Applying Machine Learning Methods to Suggest Network Involvement and Functionality of Genes in *Saccharomyces cerevisiae*

By

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Abstract

Elucidating genetic networks provides the foundation for the development of new treatments or cures for diseased pathways, and determining novel gene functionality is critical for bringing a better understanding on how an organism functions as a whole. In this dissertation, I developed a methodology that correctly locates genes that may be involved in genetic networks with a given gene based on its location over 50% of the time or based on its description over 43% of the time. I also developed a methodology that makes it easier to predict how a gene product behaves in a cellular context by suggesting the correct Gene Ontology term over 80% of the time. The designed software provides researchers with a way to focus their search for coregulated genes which will lead to better microarray chip design and limits the list of possible functions of a gene product. This ultimately saves the researcher time and money.

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1 Introduction

Several studies have challenged the notion that gene location in higher eukaryotic organisms is random. These studies [Blumenthal, 1998; Boutanaev *et al.*, 2002; Caron *et al.*, 2001; Cohen *et al.*, 2000; Lee & Sonnhammer, 2003; Lercher *et al.*, 2002; Li *et al.*, 2005; Mayor *et al.*, 2004; Roy *et al.* 2002; Spellman & Rubin, 2002] suggest that there may be patterns in gene location. After reading these studies, it became obvious that the insight that data mining has to offer was not being taken advantage of. Little work is being dedicated to determining if there are true patterns within a genome, and if we can learn from these patterns.

As we all know, in most real estate markets, the location of a house and information about the surrounding houses greatly influences its value. If a genome is analogous to a collection of neighborhoods and genomic features are analogous to houses in those neighborhoods, then this type of phenomenon has also been found in the yeast genome in my research. Knowing the location of a genomic feature and information about that feature's nearest neighbors gives us insight into what genetic network the feature belongs to and how its gene product(s) behave in a cellular context (Gene Ontology term).

In this dissertation, I developed a methodology to help locate genes that may be involved in genetic networks with a given gene based on its location or its description. This is an important concept because by making it easier to locate other genes that interact with a given gene, we are able to learn more about that given gene by seeing how it influences other genes. This is very critical in elucidating pathways because it may allow for pathway initiators (which are ideal targets for drug therapy) to be located faster. Being able to elucidate genetic networks provides the foundation on which new treatments or cures for diseased pathways to be developed. We can design drugs to target specific genes in the flawed networks.

I also developed a methodology to makes it easier to predict how a gene product behaves in a cellular context. Determining novel gene functionality is critical in bringing a better understanding on how an organism functions as a whole. Lowering the number of potential functionalities for a given gene product can make the process of identifying the true functionality faster.

My experimental results showed that my methodology is able to correctly locate areas of interest for network involvement over 50% of the time and over 80% of the time suggest the correct Gene Ontology term(s) for a given genomic feature. The major contribution of my work is in the fields of biology and bioinformatics, because it allows scientists to use what they already know to learn something new about a given genomic feature. By analyzing data from a different perspective (i.e. focusing on the location and the contribution of the nearest neighbors of each genomic feature), I was able to generate rules that can be used to focus searches for genetic networks or determine gene product functionality.

1.1 Significance of Problem

Discovering genetic networks is important. A genetic network contains information about the pathway to which a gene belongs and which genes other genes interact with. Furthermore, these networks may explain the gene's function in terms of how it influences other genes and may indicate which genes are pathway initiators and therefore reveal potential drug targets [von Someren *et al.*, 2002]. Also, understanding the position effect of genes can inform the design of gene-therapy vectors [Hurst et al., 2004]. There is a push for current research to discover more about possible patterns and rules about gene location.

One reason for this is that these rules and relationships can give us insight into finding operons. Operons are a cluster of functionally related genes regulated and transcribed as a unit. If we can discover new clusters of coregulation, we can learn more. Genes that function at different steps of the same pathway often have the same phylogenetic profile. Phylogenetic profiling is a method of assigning functional clues to proteins based on their patterns of inheritance across multiple proteomes, and is independent of their amino acid sequence similarity to proteins of known function. These profiles may have certain predictive power in that groups of genes with the same profile are more likely to be functionally connected than those with different profiles. Also, phylogenetic profile analysis facilitates the study of protein function by assigning functional clues to uncharacterized proteins. It also has the potential to assign novel functional clues to proteins of known functions [Galperin *et al.*, 2000].

An example of how this information can be used is in comparative genomic studies. Comparative genomic studies can reveal a high degree of conservation in genome structure. This concept is known as synteny. Synteny refers to loci contained within the same chromosome. Conserved synteny (colinearity) refers to some degree of conservation of gene content, order and orientation between chromosomes of different species or between nonhomologous chromosomes of a single species [Eckardt, 2001]. This has been observed in the gene content among the grasses, including the grain crops rice, wheat, maize, barley, sorghum, and millet. They appear to have high degrees of colinearity [Eckardt, 2001].

Also, the knowledge that is gained from my research can have an impact on other fields. The evidence obtained in the Lee and Sonnhammer (2003) study indicates that clustering of genes may not be limited to adjacent genes. This has an impact on gene order conservation studies.

The Lee and Sonnhammer (2003) results show that the area around a gene of interest should be expanded to include larger areas than the immediate neighborhood. Gene order conservation studies are important because establishing conserved gene order could be helpful in the prediction of both physical interactions between proteins and protein function [Dandekar *et al.*, 1998]. Dandekar *et al.* (1998) noted that:

- If products of both genes have been tentatively assigned functions, a conserved gene order can be used to predict both physical interaction and function.
- If the function of the product of one gene in a conserved gene pair is known, it can hint at the function of the product of the neighboring gene (speed up functional assignment of unknown).
- If the functions of the products of both genes are known, the fact that the genes exist as a conserved gene pair might reveal novel functional aspects.

Conserved order of genes implies an underlying selective bias and perhaps related function. If there is positive selection for the proximity of two genes, the proximity is expected to be conserved in their orthologs. Searching for conserved gene proximity across genomes is an approach for detecting functionally coupled neighbors [Yanai *et al.*, 2002].

1.2 Other Approaches

Most in research dealing with genetic networks has focused on the analysis of microarray data. There have been a multitude of modeling approaches that have been proposed for discovering genetic networks based on the analysis of the results of microarray experiments. Clustering methods are the most commonly used [Quackenbush, 2001]. These methods try to identify genes that behave in a similar manner (e.g. up regulated or down regulated) across a range of conditions or samples. Other techniques try to reconstruct and model gene-expression networks by using models. Some of these models include but are not limited to Boolean models [D'haeseleer *et al.*, 2000], models based on differential equations [Chen *et al.*, 1999], or Bayesian networks [Friedman *et al.*, 2000 and Chen, 2006]. These models are based on the notion that the expression of each gene in the network depends on the expression of some other genes, so to reconstruct such a network we have to know for each gene in the network: which genes affect it, and how they affect it.

In a typical microarray experiment, many genes in an organism are assayed under multiple conditions (i.e. different time points, different tissue samples with some common phenotype (tissue type or malignancy)). Even though microarray technology allows for studying large portions of a genome, there is only data available for a small portion of the genes, meaning a large portion of genes remain unknown. This creates a need to establish methods that facilitate the discovery of new genes and methods that help determine their functional relationships with other genes faster. Since proteins can serve different roles depending on the demands of the organism, their corresponding genes are often coexpressed with different groups of genes under different situations. This notion poses a challenge in analyzing whole genome expression data because many genes will be similarly expressed to multiple, distinct groups of genes. This means that the connections between conditionally coregulated genes are often missed because most commonly used analytical methods cannot appropriately represent these relationships. Creating a way to focus a search for coregulated genes and genetic networks that utilizes learned relationships from the genome will help with this problem. Little research has been dedicated to learning patterns the applying what is learned to focus studies.

Determining functionality of an unknown gene is commonly done using sequence information. Sequences are compared using algorithms like BLAST (Basic Local Alignment Search Tool) [Altschul *et al.*, 1990]. The premise of these searches is that if two sequences are similar, they probably share a common evolutionary ancestor (i.e. they are homologues) and possibly the same functionality. When there are no homologues for the given gene, in vivo experimentation through gene knockout and other assays can give researchers insight to how genes work in cells, but these studies can be labor intensive.

1.3 My Approach

The objective of this thesis is to develop a computational tool that uses different knowledge sources and learning algorithms to assist in focusing searches for genetic networks and help determine gene product functionality. The goal is to make the discovery of genetic networks faster and easier by limiting the search areas within the genome and to make the process of determining gene functionality faster by suggesting Gene Ontology terms for the given gene.

To build this tool, I first had to evaluate the performance of different classification learning techniques on the genomic data. The genome selected was that of *Saccharomyces cerevisiae* because of all the complete genomes, it has the most ideal characteristics for a test case [Lee and Sonnhammer 2003, Pál and Hurst, 2003, Cohen *et al.*, 2000, Kruglyak, 2000 and Hurst *et al.*, 2004].

In this research, A series of experiments was performed to determine:

1. What information is the most beneficial in classifying what networks a genomic feature belongs.
2. What information is the most beneficial in classifying genomic features to the correct Gene Ontology term.
3. If locations of interest for networks could be suggested based on a description of a feature.

Different classification learning techniques were used to analyze the genomic data. These techniques included a Bayesian classifier, a tree classifier and a lazy classifier. The Bayesian classifier used was a Naïve Bayesian classifier [Zhang, 2004]. The MultiBoostAB algorithm [Webb, 2000] using the J48 classifier [Quinlan, 1993] was the tree classifier used. The KStar classifier [Cleary and Trigg, 1995] was the lazy classifier used.

Different metrics were used to evaluate performances of these classifiers. These metrics include the percentage of correctly classified features, the Kappa statistic, precision, recall, the F-measure, and the area under the ROC curve. A description of all of these metrics can be found in Section 4.2.

Based on the performances of these classifiers, two rule-based systems were created. One suggests possible areas of interest where other genomic features that interact with a given genomic feature could be located. The other suggests the functionality of the given genomic feature.

To further analyze if locations of interest could be suggested based on a feature's description, a search engine was created. The search engine processed descriptions of features, retrieved features that it deemed similar, then based on the retrieved features, suggest possible networks that the feature may be involved in and areas in the genome to look for other features that may participate in these networks.

Results indicated that knowing the Gene Ontology terms of the nearest neighbors both upstream and downstream on both strands of a feature is important in determining the Gene Ontology term of that feature and determining network involvement of that feature.

1.4 Contributions

Through my experiments I determined, for yeast, what neighbor information was the most beneficial in classifying features to the correct network and the correct Gene Ontology term, and how many neighbors to include in this process. I found that knowing the Gene Ontology terms of a feature's two-nearest neighbors both upstream and downstream on both strands of a feature is important in determining network involvement of that feature the Gene Ontology term of that feature. Partitioning the classification process by chromosome allowed the MultiBoostAB algorithm [Webb, 2000] using the J48 classifier [Quinlan, 1993] to provide the most accurate results. The decision trees generated in the classification process became the rules in the rule-based systems I designed.

The software created acts as a filter, limiting the search area for genetic interactions for scientists and suggesting possible functionality if it is unknown. Now that I established this in yeast, this technique can be applied to other genomes to see if similar trends appear. We will then be able to determine if there are rules based on gene order or conserved synteny among the different genomes. This is beneficial to comparative genomics, and it is also helpful in understanding human disease. Animal models are commonly used in studying human disease, so discovering these relationships between animal models and humans will be easier with my software because rules can be established and then compared. Many diseases are caused by flawed networks. Being able to elucidate genetic networks provides the foundation on which new treatments or cures can be developed.

When given the location of a genomic feature, the software created can correctly suggest potential networks and thus areas of interest over 50% of the time by incorporating information about each feature's two-nearest neighbors. When only given a textual description of the feature, the software recommended the correct network and thus areas of interest about 43% of the time.

These results can help with experimental design. Little effort has been placed on analyzing the genome for network relationships before initiating the microarray experiments. My software can help design (i.e. which probe sets should be included on the microarray chip) the actual chips. The software designed here can provide researchers with a way to focus their search for coregulated genes, which will lead to better chip design, and ultimately save the researcher time and money. Scientists can then use my software to maximize the possibility that their microarray experiment represents a good coverage of potential gene interactions. This work could be pivotal for research by providing a more focused experimental approach to elucidate biological roles and relationships between genes.

When given the location of a genomic feature, the software created can correctly suggest a gene product's Gene Ontology term(s) over 80% of the time by incorporating information about each feature's two-nearest neighbors. This does not eliminate the need to confirm actual functionality in the lab, but it does help by limiting the list of possible functions of a gene product.

If we make the analogy that a genome is a collection of neighborhoods, and a genomic feature is like a house, then knowing your address and what your two-nearest neighbors on both sides of your house and across the street do tells us a lot about what you do (Gene Ontology terms) and what organizations (networks) you might be involved in. The software created in this study takes advantage of this phenomenon making it easier to come up with reliable hypotheses about the location of potential genetic regulatory networks within a genome and about possible functionality of a gene.

2 Background

2.1 Knowledge Sources

Currently, there are several biological databases that are open to the public. These databases are: Gene Ontology (GO), *Saccharomyces* Genome Database (SGD) and KEGG (Kyoto Encyclopedia of Genes and Genomes).

2.1.1 *Saccharomyces* Genome Database

SGD is a scientific database that contains information about the molecular biology and genetics of the yeast *Saccharomyces cerevisiae. Saccharomyces cerevisiae* is also known as baker's or budding yeast. This database contains the information about the known open reading frames and genes. Maps of all the sixteen chromosomes and the mitochondrial chromosome can be obtained from this database (Hong *et al*., 2006). Summaries of several genomic features can be accessed at SGD.

2.1.2 Gene Ontology

Gene Ontology is not a database of gene sequences, nor a catalog of gene products. Rather, Gene Ontology describes how gene products behave in a cellular context using three different ontologies: molecular function, biological process, and cellular component. These classifications were chosen by the Gene Ontology Consortium because they represent information about genes and gene products [Gene Ontology Consortium, 2000]. The ontology comprises a set of well-defined terms with well-defined relationships. The structure of Gene Ontology reflects the current representation of biological knowledge as well as serving as a guide for organizing new data [Gene Ontology Consortium, 2000]. The vocabulary is fluid and consistently undergoes revision. The intention of the Gene Ontology is to make possible, in a flexible and dynamic way, the annotation of homologous gene and protein sequences in multiple organisms using a common vocabulary. Sharing this common vocabulary will result in the ability to query and retrieve genes and proteins based on their shared biology [Gene Ontology Consortium, 2000].

2.1.3 KEGG

KEGG contains knowledge about known biological (regulatory, metabolic and cellular) pathways, thus it contains knowledge about genetic networks. KEGG can be indexed based on gene products. Information on the pathways in which the gene/gene product participates, the other genes/gene products in those pathways, and locations for all the genes involved can be determined.

2.2 Learning

Learning encompasses a broad range of processes. There are many definitions of learning. In general, it can be stated that learning occurs when an agent changes its structure, program, or data (based on inputs or in response to external information) in such a manner that its expected future performance improves [Nilsson, 1996]. Dietterich (1986) states that learning can be defined as an increase in knowledge. Knowledge is then defined by Dietterich as the following: An agent (program) knows a fact F if the agent has been told F or if the agent can logically infer F from its other knowledge. This form of knowledge can be called "knowledge in principle" or "deductive closure knowledge". The logical inferences are assumed to preserve correctness (i.e. they are monotonic, deductive inferences) [Dietterich, 1990]. Learning can occur under two circumstances with this definition of knowledge.

1. When an agent is told a fact F that it did not know
2. When an agent makes an "inductive leap" and chooses to believe some fact F that is not entailed by its existing knowledge [Dietterich, 1990].

The type of learning that is of interest for this research in induction. Induction uses specific examples to reach general conclusions. Inductive learning methods can be defined as those methods that systematically produce general descriptions or knowledge from the specific knowledge provided by domain examples. This type of learning will assist in determining if there are patterns in gene location and if there are rules that can be found in genetic network data. Specifically, data mining methods will be used.

Data mining is defined as the process of discovering patterns in data. Patterns allow us to make nontrivial predictions on new data. It is helpful when the patterns that are mined are represented in terms of a structure that can be examined, reasoned about, and used to inform future decisions. These are structural patterns because they capture the decision structure in an explicit way, thus, they help to explain something about the data. There are different styles of learning in data mining applications. These styles include classification learning, association learning, clustering and numeric prediction.

2.2.1 Classification learning

Classification learning is the learning style used in this research. Based on the description provided by Witten and Frank (2005), in classification learning, the learning system is presented with a set of classified examples. From these examples, the system is expected to learn a way of classifying unseen examples.

There are several data mining algorithms that perform classification learning. These can be broken down into various categories. Some of the more commonly known categories are: Bayesian classifiers, tree classifiers and functions (classifiers that can be written down as mathematical equations).

2.2.1.1 Bayesian classifiers

Bayesian classification is based on Bayes' Theorem. Bayesian classifiers are useful in predicting the probability that a sample belongs to a particular class or grouping. A common of these types of classifiers are called Naïve Bayes classifiers. A more detailed discussion follows in Section 2.2.2.1.

2.2.1.2 Tree classifiers

Decision tree classifiers are hierarchically based classifiers that compare the data with a range of properly selected features. The selection of features is determined from an assessment that depends on the algorithm being implemented. Assessment can be based on the spectral distributions or separability of the classes in the dataset. Decision trees are often referred to as a "divide-and-conquer" method. Nodes in a tree pertain to testing a particular attribute. Leaf nodes give the classification that can be applied to all instances that reach the leaf, or a set of classifications, or a probability distribution over all possible classifications. In the classification process of an unknown instance, the instance is routed down the tree according to the values of the attributes tested in successive nodes, and when a leaf is reached, the instance is classified based on the class assigned to that leaf [Witten and Frank, 2005]. Basically, a series of questions separate data into increasingly narrower categories. The goal is to ask the proper sequence of questions that will accurately model patterns in the data. The advantages of the decision tree classifier are that computing time is less than a maximum likelihood classifier and by comparison the statistical errors are avoided. However the disadvantage is that the accuracy depends fully on the design of the decision tree and the selected features/attributes.

2.2.1.3 Functions

These types of classifiers are usually based on logistic regression. Logistic regression attempts to produce accurate probability estimates by maximizing the probability of the training data. Accurate probability estimates lead to accurate classifications [Witten and Frank, 2005]. Any regression technique (linear or non-linear) can be used for classification. To do this, regression must be performed for each class, setting the output equal to one for training instances that belong to the class and zero for those that do not. The result is a linear expression for the class. To classify an unknown, calculate the value of each linear expression and choose the one that is largest. Other approaches learn a hyperplane that separates the instances pertaining to the different classes.

2.2.1.4 Lazy Classifiers

The classifiers that are mentioned above are sometimes considered "eager" because they precompute (perform statistics, build trees, etc) over the entire dataset. They construct a generalization model before receiving any new samples to classify. This makes the training of the classifier a timely activity, but prediction of the classification of a new instance is fast. Lazy classifiers do no precomputation, and they only focus on a particular set of the data. There is no training, thus the prediction of the classification of a new instance is slow because classifiers are not built until new samples need to be classified. Lazy classification uses a richer hypothesis space, which can improve classification accuracy, but the attributes are all equally weighted, which can decrease classification accuracy. A major disadvantage of lazy classification is that all training samples need to be stored, which leads to expensive storage costs and requires efficient indexing techniques. The most common of these types of classifiers use a distance function to classify instances.

2.2.2 Classification Algorithms

The types of algorithms described above for classification learning can be found in WEKA (the Waikato Environment for Knowledge Analysis). WEKA is open source software issued under the GNU General Public License. It is a collection of machine learning algorithms for data mining tasks. WEKA contains tools for data pre-processing, classification, regression, clustering, association rules, and visualization [Witten and Frank, 2005].

The specific algorithms that this research is interested in are the Bayesian classifier technique called Naïve Bayes, the tree classifier algorithm known as C4.5, and the lazy classifier known as KStar. In WEKA, C4.5 is referred to as J48. To prevent the over-fitting of data, the MultiBoostAB algorithm using the J48 classifier was used.

2.2.2.1 Naïve Bayes

A Naïve Bayes classifier is based on models that incorporate strong independence assumptions. Naïve Bayes classification does not require that you have lots of observations for each possible combination of the attributes. Rather, the attributes are assumed to be independent of one another. In other words, Naïve Bayes classifiers assume that the effect of an attribute value on a given class is independent of the values of other attributes. This assumption is called class conditional independence. It is made to simplify the computation and in this sense considered to be “Naïve”.

These assumptions make for very efficient algorithm for classification. Naïve Bayesian classifiers generate rules based on Bayes’ rule of conditional probability. It uses all the attributes and allows them to make contributions to the classification as if they were all equally important and independent of one another.

To explain how the Naïve Bayesian classifier, we need to consider a Bayesian classifier. Let us say an instance, *I*, in classification is represented by a tuple of attribute values ($x_1, x_2, \ldots, x_n$), where x_i is the value of attribute X_i. Let us assume that there are only two classes, positive or negative. Next, we let *C* represent the classification variable, and let *c* be a value of *C*. According to Bayes rule, the probability of an instance $I = (x_1, x_2, \ldots, x_n)$ being in class *c* can be calculated:

$$p(c|I) = \frac{p(I|c)p(c)}{p(I)}$$

The instance, *I*, is classified as the class positive C if and only if:

$$f_b(I) = \frac{p(C = positive|I)}{p(C = negative|I)} \geq 1$$

The function, $f_b(I)$, is considered a Bayesian classifier (Zhang, 2004).

When the assumption is made that all the attributes are independent given the value of the class variable (conditional independence), we get:

$$p(I|c) = p(x_1, x_2, \ldots, x_n|c) = \prod_{i=1}^{n} p(x_i\,|c)$$

This results in a Naïve Bayesian classifier function:

$$f_{nb}(I) = \frac{p(C = positive)}{p(C = negative)} \prod_{i=1}^{n} \frac{p(x_i|C = positive)}{p(x_i|C = negative)}$$

(Zhang, 2004).

The Naïve Bayes classifier has several properties that make it surprisingly useful in practice, despite the fact that the far-reaching independence assumptions are often violated. Like all probabilistic classifiers under the MAP decision rule (maximum *a posteriori* decision rule: a rule that picks the hypothesis that is most probable), it arrives at the correct classification as long as the correct class is more probable than any other class. The class probabilities do not have to be estimated very well because the overall classifier is robust enough to ignore serious deficiencies in its underlying naïve probability model. These types of classifiers, despite their over-simplified assumptions, often work much better in many complex "real-world" situations. Studies comparing classification algorithms have found the Naïve Bayesian classifier to be comparable in performance with classification trees and with neural network classifiers [Stewart, 2002]. They have also exhibited high accuracy and speed when applied to large databases [Zhang, 2004 and Witten and Frank, 2005].

Since attributes in these classifiers are treated as if they were independent, the addition of redundant attributes skews the learning process. Also, dependencies between attributes reduce the ability of the Naïve Bayes classifier to discern what is actually going on.

2.2.2.2 MultiBoostAB using the J48 classifier

MultiBoostAB is the WEKA version of the MultiBoosting algorithm. MultiBoosting combines AdaBoost (a boosting technique) [Freund and Schapire, 1996] with wagging (a variant of bagging) [Bauer and R. Kohavi, 1998] to form decision committees. This technique "boosts" a learning algorithm to a stronger learning algorithm by taking advantage of AdaBoost's high bias and variance reduction and wagging's strong variance reduction. It has been shown that when using the C4.5 algorithm as its base learning algorithm, MultiBoosting produces decision committees with a lower error than either AdaBoost or wagging [Webb, 2000].

This technique allows us to combine multiple models/classifiers generated by the learning algorithm. Bagging (Bootstrap aggregating) and boosting create an ensemble of classifiers from a dataset. Each of the classifiers is built using a different training set obtained from the original dataset using resampling techniques. Combining the decisions of different classifiers into one prediction is done by taking a vote in both bagging and boosting. They differ in how they derive the individual models. In bagging, an equal weight is assigned to the models. In boosting, weighting is used to give more influence to the more successful models.

Bagging works by producing replications of the training set by sampling with replacement. Each of these replications has the same size as the original set, but some instances can appear more than once and some do not appear at all. A classifier (like a decision tree) is generated for each replication, and they are used on each instance of the test set. For final classification, each of the classifiers votes for each class [Witten and Frank, 2005].

Wagging differs from bagging in that it assigns random weights to the instances in the training set. In the MultiBoosting algorithm, random instance weights are assigned using the continuous Poisson distribution. The weights are calculated using the formula:

$$Poisson(\quad) = -\log\left(\frac{Random(1\ldots999)}{1000}\right)$$

where *Random(min..max)* returns a random integer value between *min* and *max* inclusive [Webb, 2000].

Boosting differs from bagging in that the process is iterative. In bagging, the models/classifiers are built separately. In boosting, each new classifier is influenced by the performance of those built before it. This encourages new classifiers to become "experts" for instances handled incorrectly by the earlier classifiers.

The variant of boosting that MultiBoosting incorporates is AdaBoost [Freund and Schapire, 1996]. It works by first assigning an equal weight to all training instances. For each iteration, it calls the learning algorithm to form a classifier for the weighted dataset and it stores the resulting model. The error e of the model is computed. If e is equal to zero, or e is greater than or equal to 0.5, model generation is terminated. Next, each instance in the dataset gets reweighted according to the classifier's output. The weights of the correctly classified instances get decreased by using the following formula:

$$weight = weight * \left(\frac{e}{(1-e)}\right)$$

The weights of the incorrectly classified instances remain unchanged. This produces a set of "easy" instances with low weight and a set of "hard" instances with high weight.

In the subsequent iterations, a classifier is built on the reweighted dataset which focuses on classifying the "hard" instances correctly. To form a prediction, the output of the classifiers from each iteration is combined using a weighted vote. Classifiers that perform well on the weighted training data (e close to zero) receive a higher weight, and classifiers that perform poorly (e close to 0.5) receive a lower weight. The weight of the voting is determined by the formula:

$$weight = -log\left(\frac{e}{(1-e)}\right)$$

To make the prediction, the weights of all the classifiers that vote for a particular class are summed, and the class with the greatest sum is chosen [Frank and Witten, 2005].

Boosting often produces classifiers that are significantly more accurate than bagging, but due to overfitting the data, boosting can generate classifiers that are significantly less accurate than a single classifier built from the same training set [Frank and Witten, 2005]. This motivated the creation of MultiBoosting.

MultiBoosting should be used if the learning algorithm is unstable. When decision trees are built for a dataset, the process is unstable, meaning slight changes in the training data may result in different attributes being chosen at a particular node. This has an impact on the structure of the subtree beneath that node. On algorithms that are stable, like k-nearest neighbors, this technique should not be applied because it degrades the estimates of the algorithm.

J48 is the WEKA version of C4.5 [Quinlan, 1993]. C4.5 is a decision tree generating algorithm based on the ID3 algorithm [Quinlan, 1986]. C4.5 is an extension of ID3 that accounts for unavailable values, continuous attribute value ranges, pruning of decision trees and rule derivation. In building a decision tree, C4.5 can deal with training sets that have records with unknown attribute values by evaluating the gain, or the gain ratio, for an attribute by considering only the records where that attribute is defined. In using a decision tree, it can classify records that have unknown attribute values by estimating the probability of the various possible results [Witten and Frank, 2005].

In building decision trees, the algorithm needs to determine which attribute to split on given a set of examples with different classes. This attribute is selected based on information [Shannon and Weaver, 1949]. Information is measured in bits. When information is associated with a node, it represents the expected amount of information that would be needed to specify how a new instance should be classified given that instance reached that node. It is calculated using the formula:

$$I = \left(P(v_1), \dots, P(v_n)\right) = \sum_{i=1}^{n} -P(v_i) log_2 P(v_i)$$

To simplify, suppose the training set contains positive (*p*) and negative (*n*) examples, then the estimate of the information contained in the correct classification is:

$$I\left(\frac{p}{p+n},\frac{n}{p+n}\right) = -\frac{p}{p+n}log_2\frac{p}{p+n} - \frac{n}{p+n}log_2\frac{n}{p+n}$$

Calculating how much information that is still needed after the attribute test needs to be determined. Any attribute divides the training set into subsets according their values for that attribute (an attribute can have *v* distinct values). Each subset has positive (p_i) and negative (n_i) examples. So on average, after testing attribute *A*, we will need:

$$Remainder(A) = \sum_{i=1}^{v}\frac{p_i+n_i}{p+n}\, I\left(\frac{p_i}{p_i+n_i},\frac{n_i}{p_i+n_i}\right)$$

bits of information to classify the example. The information gain from the attribute test is then calculated as:

$$Gain(A) = I\left(\frac{p}{p+n},\frac{n}{p+n}\right) - Remainder(A)$$

The equations for these calculation are taken from Russell and Norvig (2003).

C4.5 builds a tree by selecting the best attribute to split the dataset on. For each attribute, it calculates the information gain from splitting the tree on that attribute. The best attribute has the highest information gain. A decision node is created that splits the dataset on that best attribute. The process is repeated on the subtrees of that node.

2.2.2.3 KStar

KStar is an instance-based classifier. An instance-based classifier classifies a test instance by finding the training instance(s) that is/are the most similar to the test instance. The KStar algorithm is a member of the *k*-nearest neighbor classifiers. *K*-nearest neighbor classifiers classifies each instance by looking at the nearest *k* data points and determining the class an instance belongs to based on the most common class amongst the nearest *k* data points. The nearest neighbors of an instance are defined in terms of a standard distance. KStar uses an entropy-based distance function. This approach is motivated by information theory [Cleary and Trigg, 1995].

The distance between two instances is defined by the complexity of transforming one instance into another. The KStar distance sums over all the possible transformations between two instances. Instances are classified into certain categories based on probability. The probability that an instance, *i*, belongs to a category C is calculated by summing over the probabilities from *i* to each instance that is a member of C:

$$PStar(C|i) = \sum_{b \in C} PStar(b|i)$$

The probabilities for each category are calculated. The category with the highest probability is selected as the classification of the new instance [Cleary and Trigg, 1995].

The KStar requires the user to specify a blend factor. It specifies how the distance function acts by setting the guideline for *k* (how many instances to consider when classifying). A lower blend factor will classify an instance based on a more specialized set of training data. A higher blend factor will classify an instance based on a more general set of training data [Cleary and Trigg, 1995].

The user also needs to specify how to handle missing values. There are four options. The missing values can be ignored when computing the distance. The missing values can be interpreted as the maximum possible distance between the instances of a particular attribute. Before the distance is computed, the missing values can be normalized over the attribute. The distance for the missing values can be determined from the average column entropy curve [Cleary and Trigg, 1995].

KStar is a simple method that is generally very accurate. It is slow because the entire set must be searched so that the k-nearest neighbors can be found. What may skew results is the fact that KStar treats all attributes as equally important [Cleary and Trigg, 1995].

2.3 Information Retrieval

In this research, similar genomic functions were determined using Information Retrieval (IR) techniques using the vector-space model (VSM). The VSM is a common approach in IR for similar-document retrieval [Salton, 1971]. In the VSM, each document is represented by a list (vector) of weighted terms. For example document *i* is equal to:

$$D_i = (w_{i1}, w_{i2}, \dots , w_{in})$$

where $w_{in}$is the weight assessed to term *n* in the document D_i.

When analyzing a term in a document, how well the term describes its document, and the term's scarcity need to be included. These two concepts are involved in determining a term's weight. This weight is associated with and describes a term's value for a document. The weighting system for each term in the document uses a *tf-idf* scheme. (*tf* = term frequency; *idf* = inverse document frequency). In this term-weighting scheme, the *tf* and *idf* are calculated in the following manner:

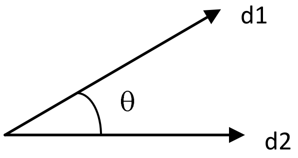
$$tf = \frac{frequency\ of\ the\ term\ in\ the\ document}{frequency\ of\ the\ most\ frequent\ word\ in\ the\ document}$$

$$idf = log_{10}\left(\frac{total\ number\ of\ documents\ in\ the\ collection}{the\ number\ of\ documents\ in\ the\ collection\ that\ contain\ the\ term}\right)$$

Thus the weight of a term is calculated by:

$$Weight = tf * idf$$

A similarity measure can be computed between pairs of weighted term vectors that reflects text similarity. Using the VSM makes it possible to compare two documents using vector algebra, as, for example, the cosine measure of similarity [Salton and McGill, 1983]. In this model, the similarity of document vector, d1, to another document vector, d2, equals the cosine of the angle between them.



$$similarity(d1, d2) = \ cosine\ \theta = \frac{d1\ \cdot d2}{|d1||d2|}$$

Cosine is the normalized dot product. The degree of similarity is determined by the cosine of the angle; the smaller the angle, the more similar the documents.

2.4 Patterns in Genomes

Several research groups have noted that genes with related function are often located close to each other on the chromosomes [Jensen *et al.*, 2003]. The existence of operons makes this grouping trend stronger in prokaryotes. Operons are a common form of gene organization in bacteria and archea. In bacterial operons, genes are coexpressed from a single promoter to make a polycistronic mRNA (an mRNA that codes for more than one protein).

An example of an operon is the *lac* operon. The *lac* operon was the first discovered example of tight integration of gene expression and function. The *lac* operon is a transcriptional unit of genes functioning in a common metabolic pathway in bacteria utilizing lactose. The genes encode a hydrolase cleaving lactose, *lac*Z, a galactoside permease, *lac*Y, and a galactoside transacetylase, *lac*A. The coexpression of these genes is achieved by their organization in a linear transcription unit that is regulated by a repressor.

Many times the genes contained within an operon are functionally related, thereby facilitating coregulation [Blumenthal, 1998]. It was believed that eukaryotic genes appeared to be transcribed without apparent organization by function or by temporospatial expression. This view is being slightly altered by the presence of examples of clustering of genes of related function (e.g. Hox genes, hemoglobin genes and immunoglobulin genes) and by the presence of tight clustering of genes whose functions are not obviously related [Blumenthal, 1998]. It has also been observed that an interesting feature of the *A. thaliana* genome is the frequent occurrence of clusters of closely related protein-coding genes adjacent on the same strand [Wambutt *et al.*, 2000]. The given examples hint that the eukaryotic organization of genes on chromosomes may not be as random as once believed.

Blumenthal (1998) stated that there are operons in eukaryotes that are clear examples of coregulation of genes whose products need to be coexpressed temporarily and spatially. It is important to note that the observed operons in eukaryotes are different from those observed in prokaryotes in terms of mechanism and gene content [Blumenthal, 1998]. Operons that have been detected in eukaryotes differ from those in prokaryotes in that eukaryotic polycistronic mRNAs are not translatable directly as in prokaryotes [Kozak, 1999].

Lee and Sonnhammer (2003) noted that there could exist some degree of selection for keeping coregulated genes in the same region of a chromosome. For instance, the gene positioning can make the genes (as a group) more efficiently available to transcription. This is supported by the fact that coregulated human genes are often linked functionally in synexpression groups [Niehrs and Pollet 1999]. Synexpression groups designate sets of genes that share a complex 'spatial' expression pattern (multiple tissues), and that function in the same process.

Képès (2003) found that in yeast, genes that are regulated by the same sequence-specific transcription factor tend to be regularly spaced along chromosomes. Co-expressed gene pairs have also been found to be regularly spaced along chromosomes in S*accharomyces cerevisiae* [Mannila et al., 2002] and in *Drosophila melanogaster* [Balázsi et al. 2003].

Positional clustering of coexpressed genes has been studied in *Caenorhabditis elegans*. After exclusion of operon and tandem duplication (the major mechanisms for observed coexpression), gene clustering is still evident [Roy *et al.*, 2002 and Lercher *et al.*, 2003].

Cho *et al.* (1998) first showed clustering of co-expressed genes in yeast on a genomic scale when they found that 25% of genes with cell-cycle dependent expression patterns were directly adjacent to genes induced in the same phase of the cell cycle. Several genes in yeast that are in co-expression clusters seem to be functionally related (i.e. they belong to the same Gene Ontology classification [Fukuoka et al., 2004] or the same MIPS (Munich Information Centre for Protein Sequences) category) [Cohen, et al., 2000].

Caron *et al.* (2001) found highly expressed genes co-localized in *Homo sapiens*. Caron *et al.* (2001) presented work on the Human Transcriptome Map. This map allows us to view the whole chromosome. When inspected, whole chromosome views reveal a high order organization of the human genome. In humans, it has been suggested that expression neighborhoods serve to regulate housekeeping functions [Lercher *et al.*, 2002]. From the Transcriptome Map, we can see most of the chromosomes show clusters of highly expressed genes, which are referred to as RIDGEs (regions of increased gene expression) (see the Figure 2.1 below from the paper by Caron *et al.* (2001)). Since there is a continuum from small to very large clusters, it is hard to quantitatively define a RIDGE. This study shows that RIDGEs most likely represent a higher order of structure in the genome.

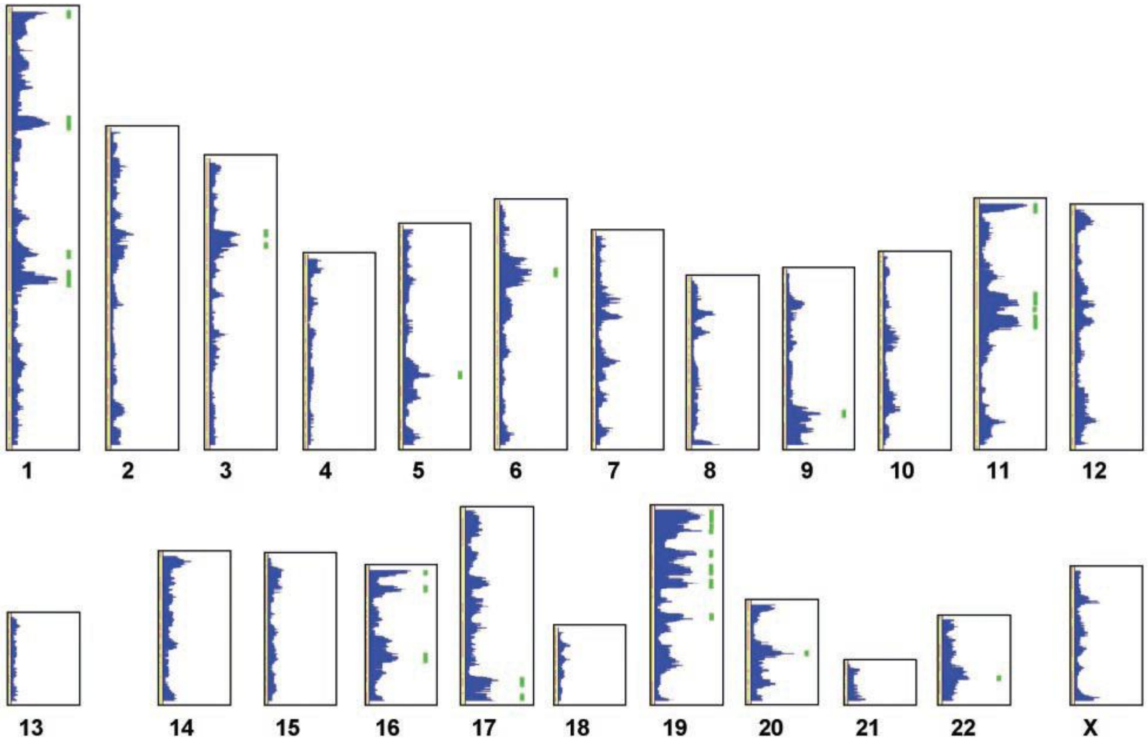


Figure 2.1. From Caron *et al.* Regional expression profiles for 23 human chromosomes show a clustering of highly expressed genes in RIDGEs. Expression levels are shown as a moving median with a window size of 39 genes. There are 74 regions with one or more consecutive moving medians that have a lower limit of four times the genomic median; 27 of them have a length of at least 10 consecutive moving medians (indicated by the bars to the right).

A study by Gabrielsson *et al.* examined genes expressed in human adipose tissue via microarray analysis. They observed clusters of adipose specific genes when they mapped these genes back to the human genome [Gabrielsson *et al.*, 2000]. This study suggests that clusters of tissue-specific genes do exist. This type of phenomenon was also demonstrated within the mouse [Li *et al.*, 2005].

Spellman and Rubin (2002) describe a transcriptional profiling study that reveals a surprising correlation between the organization of genes along *Drosophila* chromosomes and their expression levels. This study showed that more than 20% of genes clustered into co-regulated groups of 10-30 genes in the *Drosophila* genome. They noted that neighborhoods composed of an average of 15 contiguous genes show markedly similar relative expression levels. Although the average neighborhood contains 15 genes, there is a very wide range. These neighborhoods are not obviously composed of genes with related functions that might be expected to exhibit co-regulation, as is the case for the rRNA, histone, Hox, and globin gene clusters [Spellman and Rubin, 2002].

With these findings, Lee and Sonnhammer (2003) examined gene clustering of pathways in eukaryotes. The research presented in the Lee and Sonnhammer (2003) study is based on genes in metabolic pathways as defined in the Kyoto Encyclopedia for Genes and Genomes (KEGG), with missing enzymes filled in by homology. The species included in this study were: *Homo sapiens*, *Caenorhabditis elegans*, *Drosophila melanogaster*, *Arabidopsis thaliana*, and S*accharomyces cerevisiae*. This study analyzed which pathways are significantly clustered in each species, and whether the clustered pathways are the same in different species. The clustering level was measured by calculating the overall degree of gene colocalization compared to random. The 'clusters' presented in this paper are thus not necessarily compact. The clusters may correspond to rather large regions with high concentrations of pathway members, although nonmembers may also be present in such regions [Lee and Sonnhammer, 2003].

To determine whether genes in a pathway are found in closer proximity than expected by chance, Lee and Sonnhammer (2003) developed a formula for calculating a clustering score. They noted that such a formula needs to fulfill a set of criteria:

1. The score should increase monotonously with increased proximity
2. The score between genes on different chromosomes needs to be defined and to be the same as the average score between two randomly placed genes on an average chromosome.
3. The score should be normalized for genome and pathway size to allow comparative studies.

To estimate the significance of the observed average clustering score of a pathway in a genome, it was compared to the distribution of 200 iterations of placing the same number of genes on randomly picked known gene positions. Friedman and Hughes (2001) used a similar approach for determining whether observed gene patterns are expected by chance [Lee and Sonnhammer, 2003].

The results of the Lee and Sonnhammer (2003) work show between 98% and 30% of the analyzed pathways in a genome were found to exhibit significantly higher clustering levels than expected by chance. The *Saccharomyces cerevisiae* genome showed the most clustering followed by *Homo sapiens*, *Caenorhabditis elegans*, *Arabidopsis thaliana*, and *Drosophila melanogaster* in descending order. Surprisingly, Lee and Sonnhammer (2003) did not observe much agreement between genomes in terms of which pathways are most clustered. Only seven of 69 pathways found in all species were significantly clustered in all five of them [Lee and Sonnhammer, 2003].

In their study, Lee and Sonnhammer (2003) frequently found that genes in a pathway are in closer proximity than would be expected by chance. They also noted that genes that are 'clustered' are much more distant than those detected in prokaryotes; however there may still be an advantage for functionally related eukaryotic genes to be close in a genome even if separated by other genes [Lee and Sonnhammer, 2003]. From this study, it seems that the clustering of pathway members must be a selected trait. In further support of this, there is no detectable correlation between sequence similarity and clustering score in the Lee and Sonnhammer work [Lee and Sonnhammer, 2003].

The notion that genes of comparable and/or coordinated expression cluster is important in terms of understanding how genomes function and how the genomes have evolved.

2.5 Possible explanation of clusters/groups of genes in genomes

The mechanism(s) responsible for the observed similarities in expression of adjacent genes was not revealed in the Spellman and Rubin (2002) study. The authors stated that the results obtained were most consistent with regulation at the level of chromatin structure based on the following reasons:

1. The regions showing similarities in expression are quite large (average 15 genes) with each presumably having its own core promoter.
2. It is frequently the case that one or two genes in a group display a high level of differential expression. They state that "if the chromatin in a region of the chromosome that contained many genes was 'opened' so that a single target gene could be expressed, it might increase the accessibility of promoters and enhancers of other genes to the transcriptional machinery, leading to a modest parallel increase in their expression." [Spellman and Rubin, 2002]

Oliver *et al.* (2002) find the *Drosophila* data presented by Spellman and Rubin (2002) warrant closer examination to try to discover what could underlie the observed similarity of gene expression within neighborhoods.

Oliver *et al.* (2002) explored explanations for these neighborhoods. The simplest explanation is that co-regulation within an expression neighborhood may be due to incidental interactions between promoters and transcriptional enhancers (see Figure 3). In this model, transcription of one or more genes in a genomic cluster is regulated by the usual suspects (transcription factors) binding at the appropriate sites and activating nearby genes as well as the target gene. The resulting inappropriate expression of genes other than the target is tolerated because it has little biological effect. Transcription factors have a limited range of effect [Dorsett, 1999]. This means if strong activators are responsible then one might expect to see a steep fall-off in the effects of a given factor with distance from its core binding site (See the curve in Figure 2.2 below). But Oliver *et al.* (2002) state that the data presented by Spellman and Rubin (2002) suggest that in fact the pattern of gene expression within a neighborhood is essentially a 'square wave' (See the curve in the Figure 2.3 below).

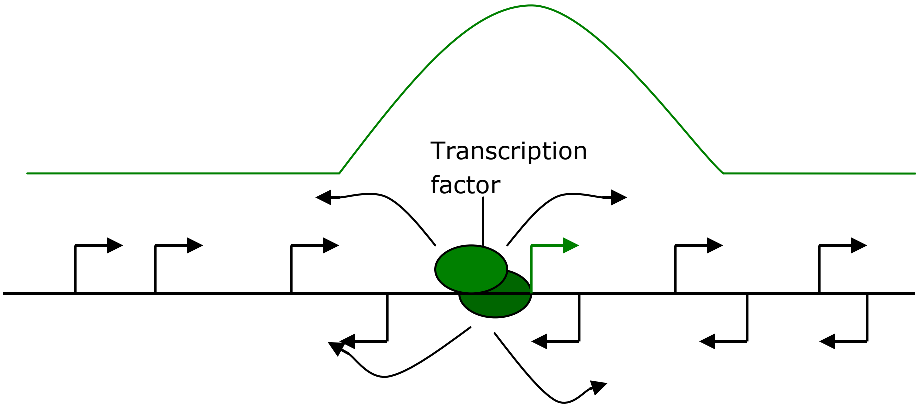


Figure 2.2. Incidental regulation. A transcription factor (green oval) binds at a target gene (green arrow) and incidentally up-regulates neighboring genes. In this model, the level of expression of neighboring genes is determined by proximity to the target gene and is expected to decrease with distance from the target gene (the green line at the top of each panel indicates the gene expression profile across the neighborhood) [Oliver et al., 2002].

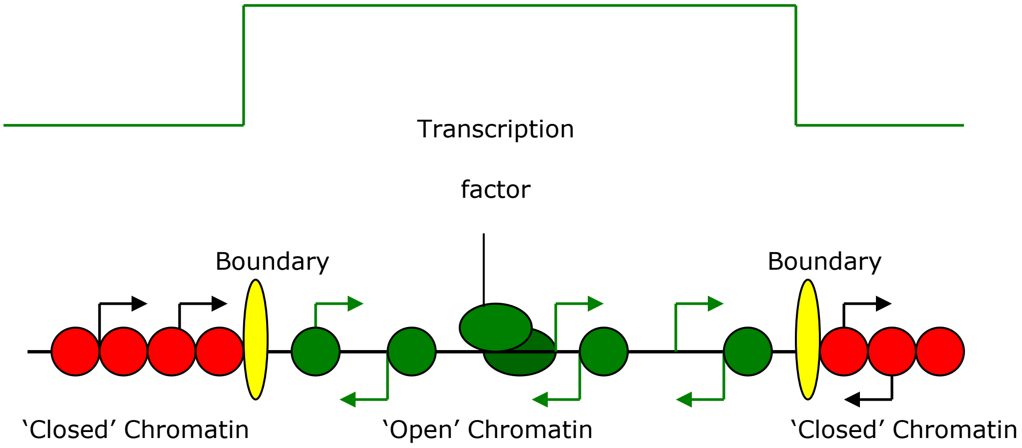


Figure 2.3. A structural domain model. A discrete 'open' chromatin domain is created as a result of activation of a target gene within the domain. Flanking boundary or insulator elements (yellow ovals) define the neighborhood and the limits of the open chromatin domain (Note the 'square wave' expression profile) [Oliver et al., 2002].

In the Spellman and Rubin (2002) paper, they favored a structural chromatin domain model (See Figure 2.3 above), involving the opening of the chromatin of an entire neighborhood as a result of activation of a target gene within the neighborhood. Spellman and Rubin (2002) stated that the creation of a domain of open chromatin structure would increase the availability of the promoters and enhancers of all the genes in the neighborhood to the transcriptional machinery. This would then lead to correlated increases in expression. Such a domain of open chromatin structure could be delimited by boundary elements or insulators, accounting for the square wave profile (See Figure 2.3 above) [Oliver *et al.*, 2002].

Oliver *et al.* (2002) find a problem with this model. They feel that the increased chromatin accessibility is just as likely to facilitate the binding of repressors as activators, the result is that some genes would be up-regulated and some down-regulated. This is not consistent with neighborhoods of co-regulation. But if increased accessibility primarily affects basal (nonactivated) expression, there could be a general increase in transcription of all the genes in the neighborhood [Oliver *et al.*, 2002].

The eukaryotic genome requires extensive compaction of DNA to fit into the nucleus. Packing is accomplished by wrapping the DNA around histones and other proteins. When genes are transcribed, a great deal of unpacking of regions of DNA is required.

The region of DNA which is unfolded contains a number of genes. It has been suggested that keeping functionally related genes near, even if not adjacent, may ease the burden of the unpacking of DNA in the cell for transcription [Lee and Sonnhammer, 2003].

2.6 Current Approach

2.6.1 Determining Networks

Thus far, a multitude of modeling approaches has been proposed for discovering genetic networks. These efforts focus on the analysis of the results of microarray experiments. Clustering methods are the most commonly used [Quackenbush, 2001]. These methods try to identify genes that behave in a similar manner (e.g. up regulated or down regulated) across a range of conditions or samples. There are various clustering techniques that have been applied to gene expression data. The most popular technique is hierarchical clustering [Eisen, 1998]. Other techniques include *k*-means clustering [Bittner *et al.*, 2000 and Datta and Datta, 2003], fuzzy *k*-means clustering [Gasch and Eisen, 2003], self-organizing maps [Tamayo *et al.*, 1999], deterministic annealing [Alon *et al.*, 1999], and graph theoretical approaches [Sharan and Shamir, 2000]. The quality of results from clustering algorithms is highly dependent on the input (i.e., on the data that is used for the analysis). It is not uncommon that more than one clustering technique is applied to a dataset. Often the results are not considered valid unless the clusters can be reproduced by various techniques. This gives confidence that the patterns observed are true biological phenomena that are independent of the analysis technique [Kaminski and Friedman, 2002].

There are several hierarchical clustering algorithms. They differ in the way they calculate distance. Michael Eisen (1998) has developed one of the most popular hierarchical clustering and visualization tools (Cluster and Treeview). This algorithm is an agglomerative process in which single member clusters are fused to bigger and bigger clusters based on a similarity metric. This algorithm begins by computing a pairwise distance matrix between all the genes, the distance matrix is then explored for the nearest genes, and these genes are defined as a cluster. After a new cluster is formed by agglomeration of two clusters, the distance matrix is updated to reflect its distance from all other clusters. The algorithm then searches for the nearest pair of clusters to agglomerate, and the process repeats. The object of this algorithm is to compute a dendrogram, in which multiple clusters are fused in nodes according to their similarity, that resulting in a single hierarchical tree [Eisen *et al.*, 1998 and Kaminski and Friedman, 2002].

k-means clustering is an iterative process. This algorithm searches for clusters that are defined in terms of their "center" points or means. The number of clusters that are going to be generated needs to be fixed in advance for this algorithm. Underestimating *k* will result in large clusters of many genes that display divergent gene-expression patterns, while overestimating *k* will over-fit the data and split groups of similarly expressed genes into multiple, small clusters. Usually another clustering algorithm, such as hierarchical clustering, is run to determine the initial cluster centers to be used in this algorithm. This method does not generate a hierarchical tree, but rather a predetermined number of clusters, so *k*-means clustering is especially useful in cases in which one knows how many distinct gene expression patterns to expect [Datta and Datta, 2003]. Once a set of cluster centers is defined, each gene is then assigned to the cluster it is closest to. The clustering algorithm then adjusts the center of each cluster of genes to minimize the sum of distances of genes in each cluster to the center. This results in a new choice of cluster centers, and so we can reassign genes to clusters and repeat the process. These iterations are applied until convergence [Kaminski and Friedman, 2002].

Fuzzy *k*-means clustering algorithms have also been used to identify clusters of genes. The essential difference between fuzzy *k*-means clustering and traditional *k*-means clustering is the partitioning of genes into clusters. Rather than the hard partitioning used in the traditional *k*-means clustering, where genes belong to only a single cluster, fuzzy *k*-means clustering considers each gene to be a member of every cluster, with a variable degree of 'membership' [Gasch and Eisen, 2003]. This provides fuzzy *k*-means clustering with the benefit of being less sensitive to over-fitting, because the genes are not forced to belong to only a single cluster. In this algorithm, each gene has a total membership of 1.0 that is apportioned to clusters on the basis of the similarity between the gene's expression pattern and that of each cluster centroid. Genes whose expression patterns are very similar to a given centroid will be assigned a high membership in that cluster, whereas genes that bear little similarity to the centroid will have a low membership [Gasch and Eisen, 2003]. Using this algorithm, genes can be assigned significant memberships to more than one cluster. This can help reveal genes whose expression is similar to multiple, distinct groups of genes.

Tamayo *et al.* (1999) introduced the use of self-organizing maps (SOMs) in the analysis of microarray data. SOMs are preferable when dealing with "messy" data that contains outliers and irrelevant parameters. Similar to the *k*-means procedure, the genes are assigned into a predetermined set of clusters. However, unlike *k*-means, what follows is an iterative process in which gene expression vectors in each cluster are "trained" to find the best distinctions between the different clusters. In other words, a partial structure is imposed on the data and then this structure is iteratively modified according to the data [Kaminski and Friedman, 2002].

In deterministic annealing, genes are input vectors that are assigned to clusters based on what Rose (1998) called the association probability in the probabilistic model he defined in his paper. This technique has some similarity to fuzzy clustering, where each gene has partial membership in clusters. However, the cluster formulation is purely probabilistic. Clusters are considered as regular (nonfuzzy) sets whose exact membership is the outcome of a random experiment. Alon *et al.* (1999) used deterministic annealing to perform hierarchical clustering. It was used to organize gene data in a binary tree.

Graph-theoretic clustering is an innovative clustering method that utilizes graph-theoretic and statistical techniques to identify tight groups of highly similar elements (kernels), which are likely to belong to the same true cluster. CLICK (Cluster Identification via Connectivity Kernels) is an example of this technique [Sharon and Shamir, 2000]. The CLICK algorithm first preprocesses the input data and forms a weighted similarity graph. Recursively it then partitions the current set of elements into two subsets. Before a partition, the algorithm tests if the subgraph induced by the current subset of elements is a kernel of a cluster. If it is a kernel, the subgraph is not partitioned further. Otherwise, a minimum weight cut is computed in the subgraph, and the current set of elements is split into the two subsets separated by that cut. The output is a list of kernels which serve as a basis for the eventual clusters [Sharon and Shamir, 2000].Graph-theoretic approaches were also used for the related problem of clustering cDNAs based on their oligonucleotide fingerprints [Hartuv *et al.*, 1999 and Lennon and Lehrach, 1991].

Recognizing that genes are not randomly distributed, Turkheimer et al. (2006) created a mathematical model (CHROMOWAVE) that is based on single value decomposition and Haar wavelets. It detects variations in expression of spatially related genes and visualizes them on chromosomes.

Many approaches try to use reverse engineering to construct genetic networks from gene expression data. Boolean networks [Kauffman, 1969] are a simple way to represent the interaction between genes. Each gene is considered a binary variable (ON or OFF) that are regulated by other genes through Boolean functions [D'haeseleer *et al.*, 2000]. These networks provide a conceptual tool for investigating network organization, but there are many criticisms on using the Boolean network approach [Akutsu *et al.*, 2000].

Other approaches have used linear differential equations to reconstruct genetic networks [Chen *et al.*, 1999]. In Chen *et al.* (1999), they used a linear transcription model for gene expression, as well as two algorithms (minimum weight solutions to linear equations and Fourier transform for stable systems) to construct the model from a set of temporal samples of mRNAs and proteins. With this model, they were able to determine most of the gene regulation in the genome level from a minor set of accurate temporal data.

Bayesian networks are also used to reverse engineer networks. These networks represent the dependence structure between expression levels of different genes. Friedman *et al.* (2000) used a technique called the Sparse Candidate algorithm [Friedman, Nachman and Pe'er 1999] to identify a small number of candidate parents for each gene. This restricts the search for networks in which only the candidate parents of a variable can be its parents, thus making the search space for finding a good network structure. In order to specify a Bayesian model, the type of local probability models that are learned need to be selected. Friedman *et al.* (2000) used two different models (multinomial and linear Gaussian), and they were able to predict sensible relations between genes of known function. Chen *et al.* (2006) developed a methodology that processes the expression data to find a suitable node ordering that can be used by the greedy search algorithm, K2 algorithm [Copper and Herskovits, 1992], to learn the structure of Bayesian networks. This method can identify networks that are close to the optimal structures [Chen *et al.*, 2006].

Little effort has been placed on analyzing the genome for these relationships before initiating the microarray experiments. My research focuses on developing software to help design (i.e. which probe sets should be included on the microarray chip) the actual chips. The software designed here can provide researchers with a way to focus their search for coregulated genes, which will lead to better chip design, and ultimately save the researcher time and money. This work could be pivotal for research by providing a more focused experimental approach to elucidate biological roles and relationships between genes.

2.6.2 Determining Functionality

Gene function can be established using sequence information. Comparing the sequence of the gene with the unknown functionality with known genes in a database (such as GenBank at the National Center for Biotechnology Information or NCBI) is a technique for establishing possible functionality of the unknown. Sequences are compared using algorithms like BLAST (Basic Local Alignment Search Tool) [Altschul *et al.*, 1990]. The premise of these searches is that if two sequences are similar, they probably share a common evolutionary ancestor (i.e. they are homologues) and possibly the same functionality. For example, if your search results contained a lot of sequences that showed a high degree of similarity with your given gene and that these similar genes belonged to the same family of genes that were known to perform "function x" then you could conclude that your given gene encoded for a gene product with a similar function. Protein motifs can also be searched for to help determine functionality. A motif is a distinctive pattern of amino acids that is conserved across many proteins, and it gives a particular function to the protein ["Determining Gene..."].

When there are no homologues for the given gene, a biological approach exists to assist in determining its function. This approach involves creating a mutation in that gene and then observing the effects of the mutation on the organism to determine the genes function. This is called a knockout study, and these studies give researchers insight to how genes work in cells. The problem with some knockout studies is that the defects resulting from such experiments can yield no apparent changes because other genes can fulfill that same function as the altered gene. Other genetic manipulations can be lethal early in development, eliminating the possibility of observing any changes at all.

The work done in my research helps start limiting the list of possible functions of a gene product by using information that is known about the gene's neighbors. It does not replace using knockouts to establish functionality. The suggestions made by the software are to be used as guides.

2.6.3 Establishing Similarity Using Text

Establishing similarity between proteins/gene products is usually done using sequence alignment and/or structural alignment. Similarity is a quantitative term that defines the degree of sequence match between two compared sequences. Other methods have expanded the definition of similarity that go beyond mere alignment. These methods investigate establishing relationships between proteins based on the functionality of the proteins. Marcotte *et al.* showed that general biochemical functions of proteins can be inferred by associating proteins on the basis of properties other than the similarity between their amino acid sequences. These properties associate proteins that are functionally related. Proteins that are functionally related participate in a common structural complex, metabolic pathway, biological process or closely related physiological function. Functional relationships can provide information that can go beyond the capabilities of traditional sequence matching [Marcotte *et al.*, 1999].

Relationships between proteins can also be established based on text. Wren *et al.* identified one of the best sources to identify relationships, commonalities, and functional groupings among a heterogeneous set of objects (e.g. genes, phenotypes, chemicals, diseases) is the use of scientific literature. The technique they described enables object sets to be scored for their cohesiveness, as judged by their co-occurrence within scientific literature (MEDLINE). This method allows other objects to be identified and evaluated for their potential cohesiveness or relevance in relation to the analyzed set (cohesiveness is the metric used – it enables researchers to infer that an experimental grouping is purposeful assuming the grouped objects are adequately represented within the literature). Prior use of term co-occurrence has been used to find tentative relationships between objects such as genes [Stapley and Benoit, 2000; Jenssen *et al.*, 2001], proteins [Blaschke *et al.*, 1999] and drugs [Rindflesch *et al.*, 2000]. Wren *et al.* noted that co-occurrence does not necessarily reflect the existence of a meaningful relationship, so Wren *et al.* used Fuzzy Set Theory to assign a weight to the relatedness of two objects based upon their frequency of co-occurrence. Ambiguous gene names are noted to be problematic in co-occurrence networks [Wren *et al.*, 2004].

Determining similar function among proteins has been explored. Altman and Raychaudhuri (2001) showed that there is an interest in using information from genes with a common function to search for additional genes that share this function. They stated that if the function of a gene is unknown, one can analyze microarray data and make an educated guess as to the function of the gene through "guilt by association". Guilt by association means that if a non-annotated gene is regulated in a similar fashion compared to a group of annotated genes, then it has a similar function to the annotated genes. The co-expression of genes may imply that they share common regulatory mechanisms. There is controversy about this notion because regulatory mechanisms can be mixed and combined in ways that could lead to both convergent regulation (similar temporal expression patterns, different control strategies) and divergent regulation (similar control regions, put together in such a way that the effect on expression is different) [Altman and Raychaudhuri, 2001].

These studies suggest that there are alternative ways to establish similarity other than sequence or structural alignment. My research utilizes a search engine to retrieve similar genomic features to suggest possible locations to look for other features that may be involved in the same network. Again, this is trying to provide a more focused experimental approach to elucidate biological roles and relationships between genes.

3. Methodology

3.1 Approach

From previous research (See Background), the location of a genomic feature and its surrounding neighborhood have an influence on the feature's network involvement and its functionality. Determining what attributes of the surrounding neighborhood had the biggest impact on classifying a feature to the correct network and functionality needed to be established. Different neighborhood attributes were tested and different sizes of neighborhoods were examined with different classifiers. Once the best neighborhood attributes, the best neighborhood size and better classifier were determined, software could be developed to suggest locations of interest for network involvement and possible functionality for a given gene.

A feature's neighborhood attributes were determined by the attributes of its nearest neighbors on both strands and both upstream and downstream to the feature. The neighbor attributes that remained constant for the experiments were: the neighbor's number (indicating how close it was to the feature, one being the closest), the neighbor's strand and the neighbor's distance (determined from the mid-point of each feature). The different attributes that were then tested separately in classifying network involvement for a feature were: the neighbor's SGDID, the neighbor's Gene Ontology information and the neighbor's network involvement. The different attributes that were then tested separately in classifying functionality for a feature were: the neighbor's SGDID and the neighbor's Gene Ontology information.

The size of the neighborhood was determined by how many nearest neighbors should be included. All experiments were repeated using different sizes of neighborhoods. These neighborhoods included information from the nearest neighbors, the two-nearest neighbors, the five-nearest neighbors and the ten-nearest neighbors of each feature on both strands and both upstream and downstream from the feature.

The *Saccharomyces cerevisiae* genome was selected for classification because of all the complete genomes, it has the most ideal characteristics for a test case. The *Saccharomyces cerevisiae* genome shows a high amount clustering of genes that are involved in the same metabolic pathway [Lee and Sonnhammer, 2003] and it shows clustering of essential genes into regions of low recombination [Pál and Hurst, 2003]. Incidences of highly coordinated expression of linked genes have also been found in yeast [Cohen *et al.*, 2000 and Kruglyak, 2000]. Clusters of co-expressed genes in yeast rarely exceed ten genes or a few kilobases, so larger clusters were not examined [Hurst *et al.*, 2004].

In this study, various classification techniques (KStar, MultiBoostAB using the J48 classifier and Naïve Bayes) were used on genomic data of *Saccharomyces cerevisiae*. All of the classifiers that were used are contained in the software package, WEKA [Frank and Witten, 2005], and this software package was used setting the Java maximum heap size set to 12 GB.

Experiments were performed to determine what classifier yielded the best results and:

1. What neighbor information is the most beneficial in classifying genomic features to the correct network, and how many neighbors should be included.
    a. Partitioning the classification process by chromosome was also investigated.
2. What neighbor information is the most beneficial in classifying genomic features to the correct Gene Ontology term, and how many neighbors should be included.
    a. Partitioning the classification process by chromosome was also investigated.

Additional experiments were performed to determine if locations of interest could be suggested based on a description of a feature. Experiments were performed to determine:

3. Whether genomic features can be classified to the correct location
    a. Classification experiments were performed to see if a feature's chromosome could be suggested based on either its network involvement or its Gene Ontology term.
    b. Classification experiments were performed to see if a feature's start position could be suggested based on its chromosome and either its network involvement or its Gene Ontology term.
4. Whether given a textual description of a feature, would finding the networks that the top ten similar features (similarity based on IR) were involved in be helpful by suggesting looking by the feature's involved in these networks as areas of possible interest.

Based on the results from the experiments mentioned in numbers 1 and 2 above, it was determined that the MultiBoosting algorithm using the J48 classifier and that partitioning the classification process by chromosome yielded the better classification of features to their networks and to their Gene Ontology terms. It was also determined that a neighborhood that included each feature's two-nearest neighbors and the neighbors' Gene Ontology information provided the best information for these classifications.

The decision trees generated from these experiments were then converted into if-then rules to be utilized by two different rule-based systems. The first rule-based system, when given the location of a genomic feature of interest, will suggest areas in the genome to look for other genomic features that may interact with the given feature (See Figure 3.1). The other system, when given the location of a genomic feature of interest, suggests how its gene product(s) behave in a cellular context (Gene Ontology term) (See Figure 3.2). A detailed discussion of how the systems work will be discussed in section 3.2.

Based on the results from the experiments mentioned in number 3, it was determined that if either a feature's network involvement or its Gene Ontology term is known, it would be hard to determine accurately which chromosome it is located on. Even if the chromosome number is determined, classifying the feature to the correct start position given either its network involvement or its Gene Ontology term is still hard to do. A Nearest-neighbor-like algorithm using non-nested generalized exemplars did obtain rules that only suggested some of the locations, not all. These rules were adapted (See Appendix G) to create a rule-based system that suggested areas of interest based on a given network.

Based on the results from the experiments mentioned in number 4, it was determined that textual descriptions are helpful. A search engine based on genomic feature descriptions was created. The search engine was developed to take as input a description of a feature. Based on the network involvement of the top ten most similar features to the given feature, locations of start positions in the genome for other features that may participate in a network with the given feature are provided. These locations are suggested using rules adapted from experiments mentioned in number 3. A diagram of the process can be seen in Figure 3.2.3, and a description of the system will be discussed in section 3.2.

3.2 Systems

Different systems were designed to utilize the knowledge gained in the experiments discussed in the previous section. The first rule-based system suggests areas in the genome to look for other genomic features that may interact with a given feature when given its location (See Figure 3.1). The user must provide the system with the chromosome number, the strand and the start position of a feature (box 1). The system then finds the two-nearest neighbors (both upstream and downstream, and on both strands) of that feature (box 2). It then looks up the Gene Ontology term (if known) for each neighbor and determines their neighbor numbers (box 3). Information from each neighbor is then ran through the rule-based system adapted from the experiments mentioned in section 3.1 number 1 (box 4). Network suggestions are then made by the rule-based system (box 5) and given to two different methods. The first method looks up all the features that are known to participate in that network (box 6a) and reports their locations, so the user can focus their search around these areas (box 7a). The second method relies on the rules adapted from the experiments mentioned in section 3.1 number 3. The rule-based system (box 6b) takes the network suggestions (box 5) and suggests areas of interest where features that may be involved with the given feature are located (box 7b).

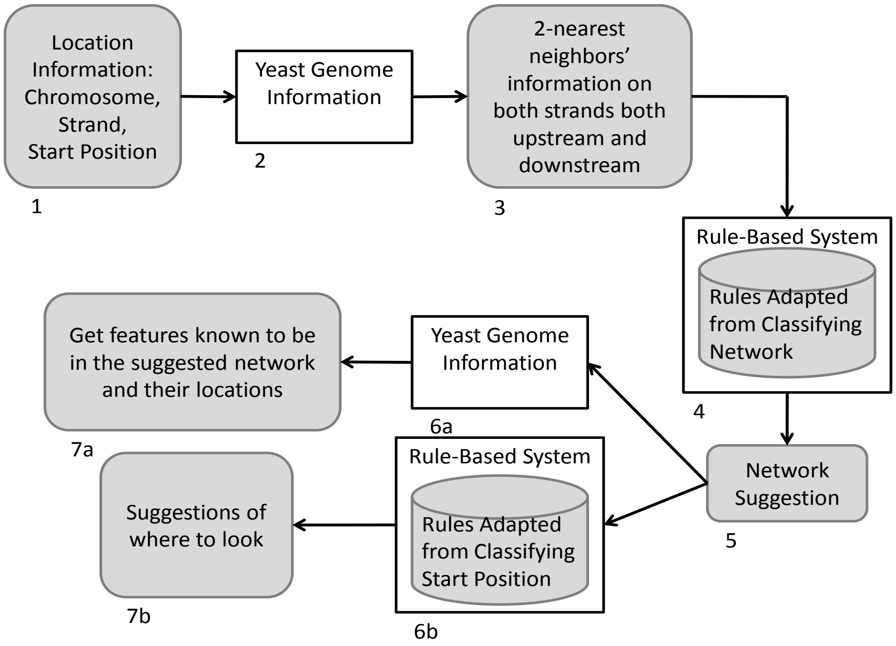


Figure 3.1. Diagram of software designed to suggest areas of interest for networks.

The other rule-based system suggests a gene product's Gene Ontology term when given its location (See Figure 3.2). The user must provide the system with the chromosome number, the strand and the start position of a feature (box 1). The system then finds the two-nearest neighbors (both upstream and downstream, and on both strands) of that feature (box 2). It then looks up the Gene Ontology term (if known) for each neighbor and determines their neighbor numbers (box 3). Information from each neighbor is then ran through the rule-based system adapted from the experiments mentioned in section 3.1 number 2 (box 4). The system then generates a list of Gene Ontology terms (box 5) to suggest to the user.

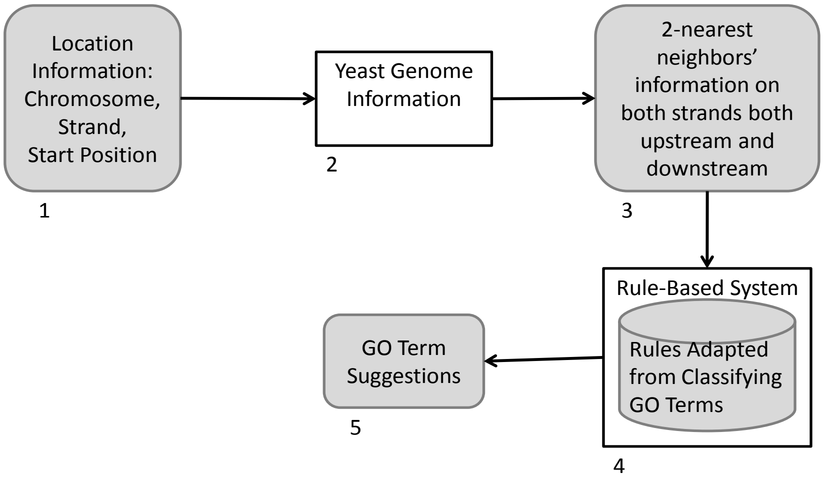


Figure 3.2. Diagram of software designed to suggest GO Terms.

The last system uses a search engine to recommend areas of interest for network involvement. A search engine was generated using the textual descriptions provided for features at the SGD website (See Figure 3.3). Each feature description was processed and the standard dictionary and posting files were created. The user provides a textual description of the feature, that description is processed in the same manner the features in the search engine were processed (box 1). The description is fed into the search engine (box 2) and the top ten most similar features are returned (box 3). For each of these features, their network involvement (if known) is looked up (box 4). The network involvement of the top ten are then fed into the rule-based system that was created based on experiments mentioned in section 3.1 number 3. The rule-based system (box 6) takes the network suggestions (box 5) and suggests areas of interest where features that may be involved with the given feature are located (box 7).

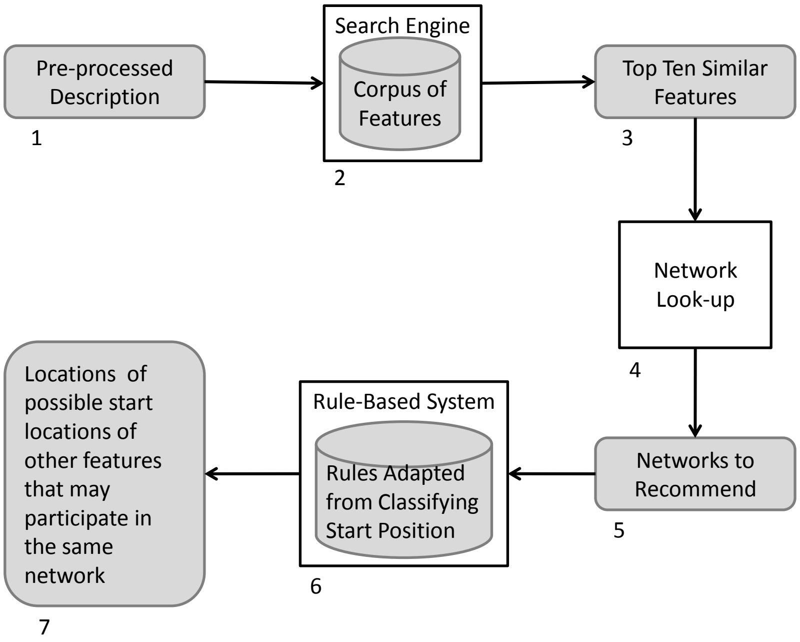


Figure 3.3. Diagram of how location suggestion is made.

These tools differ from current approaches, because they are using what is already known to help guide future work. For network involvement, little effort has been placed on developing software to help design (i.e. which probe sets should be included on the microarray chip) the actual chips. The software designed here can provide researchers with a way to focus their search for coregulated genes, which will lead to better chip design, and ultimately save the researcher time and money. This work could be pivotal for research by providing a more focused experimental approach to elucidate biological roles and relationships between genes. The user need only to provide a location or a textual description of a feature for my software to generate areas of interest in the genome.

The work done in this study helps start limiting the list of possible functions of a gene product by using information that is known about the gene's neighbors. It does not replace using knockouts to establish functionality. The suggestions made by the software are to be used as guides.

4 Experiments

4.1 Description of Experiments

4.1.1. Classifying Features to Networks

Experiments were performed to establish if classification algorithms can correctly classify network involvement (based on KEGG) of a genomic feature (a feature being: gene, ARS, etc.). The classification algorithms used include KStar, MultiBoosting the J48 classifier and Naïve Bayes. Different neighborhood attributes were used in the classification process to determine what information is the most beneficial in generating rules for classifying features to their correct network. Different neighborhood sizes were examined to determine how many nearest neighbors should be included around each feature to provide better classification rules. As a baseline, the classification process was performed using no neighbor information. Also, the classification process was performed using the entire genome, and then it was repeated on each chromosome to examine if partitioning the classification process would yield better rules. The classification process was not repeated on the mitochondrial chromosome because it only has one known network on it.

The classifiers were trained using different neighborhood attributes. A feature's neighborhood attributes were determined by the attributes of its nearest neighbors on both strands and both upstream and downstream to the feature. The feature's attributes that remained constant in the training process were: chromosome number, start position, stop position and strand. The neighbor attributes that remained constant for the training process were: the neighbor's number (indicating how close it was to the feature, one being the closest), the neighbor's strand and the neighbor's distance (determined from the mid-point of each feature). The different attributes that were then tested separately in classifying network involvement for a feature were: the neighbor's SGDID, the neighbor's Gene Ontology information and the neighbor's network involvement.

The size of the neighborhood was determined by how many nearest neighbors should be included. All experiments were repeated using different sizes of neighborhoods. These neighborhoods included information from the nearest neighbors, the two-nearest neighbors, the five-nearest neighbors and the ten-nearest neighbors of each feature on both strands and both upstream and downstream from the feature. Certain sized neighborhoods were excluded only when the heap size of the Java Virtual Machine was exceeded.

4.1.2. Classifying features to Gene Ontology terms

Experiments were performed to establish if classification algorithms can correctly classify Gene Ontology terms of a genomic feature. The classification algorithms used include KStar, MultiBoosting using the J48 classifier and Naïve Bayes. Different neighborhood attributes were used in the classification process to determine what information is the most beneficial in generating rules for classifying features to their correct network. Different neighborhood sizes were examined to determine how many nearest neighbors should be included around each feature to provide better classification rules. As a baseline, the classification process was performed using no neighbor information. Also, the classification process was performed using the entire genome, and then it was repeated on each chromosome to examine if partitioning the classification process would yield better rules.

The classifiers were trained using different neighborhood attributes. A feature's neighborhood attributes were determined by the attributes of its nearest neighbors on both strands and both upstream and downstream to the feature. The feature's attributes that remained constant in the training process were: chromosome number, start position, stop position and strand. The neighbor attributes that remained constant for the training process were: the neighbor's number (indicating how close it was to the feature, one being the closest), the neighbor's strand and the neighbor's distance (determined from the mid-point of each feature). The different attributes that were then tested separately in classifying network involvement for a feature were: the neighbor's SGDID and the neighbor's Gene Ontology information.

The size of the neighborhood was determined by how many nearest neighbors should be included. All experiments were repeated using different sizes of neighborhoods. These neighborhoods included information from the nearest neighbors, the two-nearest neighbors, the five-nearest neighbors and the ten-nearest neighbors of each feature on both strands and both upstream and downstream from the feature. The exclusion of including each feature's ten-nearest neighbors only occurred when the heap size of the Java Virtual Machine was exceeded.

4.1.3 Suggesting Locations of Interest

Experiments were performed to see if classification algorithms could correctly classify the chromosome of a genomic feature and the start position of a genomic feature. The classification algorithms used include KStar, MultiBoosting using the J48 classifier, Naïve Bayes, and a Nearest-neighbor-like algorithm using non-nested generalized exemplars. Different feature attributes were used in the classification process to determine what information would generate better rules for classifying features to their correct chromosome and their correct start position. The goal was to produce rules that would suggest areas in the genome that contained features with a certain quality (belonged to a certain network or Gene Ontology term).

When training classifiers to classify features to the correct chromosome, different feature attributes were used to determine what attributes produced better rules. Classifiers were given training data that included the feature's chromosome number and its network involvement. Classifiers were also given training data that included the feature's chromosome number and its Gene Ontology term.

When training classifiers to classify a features to the start position, different feature attributes were used to determine what attributes produced the better rules. Classifiers were given training data that included the feature's chromosome number, its discretized start position, its strand and its network involvement. Classifiers were also given training data that included the feature's chromosome number, its discretized start position, its strand and its Gene Ontology term.

Experiments were also performed to determine if textual descriptions of features could be used to suggest areas of interest in the genome for network involvement. It was examined if retrieving the network involvement of the top ten most similar features (similarity based on IR) of a given feature would be helpful in suggesting where to look for other features that may be involved with that given feature.

4.2 Datasets

For these experiments, the genome feature information was taken from the *Saccharomyces* Genome Database (http://www.yeastgenome.org/). The files were obtained from the Anonymous FTP site. Information for all genomic features that have been physically mapped was used. These features include genes, telomeric elements, autonomously replicating sequences, hypothetical proteins, putative proteins of unknown function, elements of dubious open reading frames and centromeres. The files were formatted as CSV (comma-separated values) files for processing by WEKA.

For each feature, its primary information was used. This information includes the feature's chromosome number (one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, mito), start position (in bp), stop position (in bp) and strand ("W" for Watson and "C" for Crick). Depending on what experiment was being run, additional information was included. If information was not available, it was substituted with a "?".

For experiments that pertained to classifying networks, for each network that a feature is involved in, an entry into the file that was analyzed was added. For example, for a feature that belongs to two different networks, sce00910 (nitrogen metabolism) and sce00251 (glutamate metabolism), it will have two different entries into the file. See Table 4.1 for an example.

Chromosome	**Start**	**Stop**	**Strand**	**Network**
one	31568	32941	W	sce00910
one	31568	32941	W	sce00251

Table 4.1. Shows the format of data files that included network involvement but did not include neighbor information

For experiments that analyzed how neighbors influenced the classification of networks, additional information was added. The information that was constant in all neighbor experiments included the neighbor number (1 being closest), the neighbor's strand, and the distance from the feature's midpoint to the neighbor's midpoint.

For experiments that investigated the influence of neighbor's SGDID (*Saccharomyces* Genome Database identification) on the feature's network classification, the neighbor's SGDID was included. For each of the feature's neighbors, a separate entry was created for each of the feature's different networks. See Table 4.2 for an example.

Chromosome	Start	Stop	Strand	Neighbor Number	Neighbor Strand	Distance	Neighbor SDGID	Network
one	31568	32941	W	1	W	1189	S000118317	sce00910
one	31568	32941	W	1	W	1189	S000118317	sce00251
one	31568	32941	W	2	W	9861	S000006787	sce00910
one	31568	32941	W	2	W	9861	S000006787	sce00251

Table 4.2. Shows the format of the data files that included neighbor's SGDID and feature's network involvement.

For experiments that investigated the influence of neighbor's Gene Ontology term on the feature's network classification, the neighbor's Gene Ontology term was included. For each of the neighbor's Gene Ontology terms, a separate entry was created for each of the feature's different networks. See Table 4.3 for an example.

Chromosome	Start	Stop	Strand	Neighbor Number	Neighbor Strand	Distance	Neighbor GO Term	Network
one	45023	42882	C	1	W	3123	cytoplasm	sce00010
one	45023	42882	C	1	W	3123	cytoplasm	sce00620
one	45023	42882	C	1	W	3123	cytoplasm	sce00720
one	45023	42882	C	1	W	3123	endoplasmic reticulum	sce00010
one	45023	42882	C	1	W	3123	endoplasmic reticulum	sce00620
one	45023	42882	C	1	W	3123	endoplasmic reticulum	sce00720
one	45023	42882	C	1	W	3123	transporter activity	sce00010
one	45023	42882	C	1	W	3123	transporter activity	sce00620
one	45023	42882	C	1	W	3123	transporter activity	sce00720

Table 4.3. Shows the format of the data files that included neighbor's Gene Ontology term and feature's network involvement.

For experiments that investigated the influence of neighbor's network involvement on the feature's network classification, the neighbor's network involvement was included. For each of the networks a neighbor was involved in, a separate entry was created for each of the feature's different networks. See Table 4.4 for an example.

Chromosome	**Start**	**Stop**	**Strand**	**Neighbor Number**	**Neighbor Strand**	**Distance**	**Neighbor Network**	**Network**
one	69526	68717	C	1	W	4998	?	sce00860
one	69526	68717	C	2	W	4998	sce04010	sce00860
one	69526	68717	C	1	C	2471	?	sce00860
one	69526	68717	C	2	C	2471	sce04111	sce00860
one	69526	68717	C	1	W	1253	?	sce00860
one	69526	68717	C	2	W	3417	sce00010	sce00860
one	69526	68717	C	2	W	3417	sce00230	sce00860
one	69526	68717	C	2	W	3417	sce00620	sce00860
one	69526	68717	C	2	W	3417	sce00710	sce00860

Table 4.4. Shows the format of the data files that included neighbor's network and feature's network involvement.

For experiments that pertained to classifying Gene Ontology terms, for each Gene Ontology term that a feature has, an entry into the file that was analyzed was added. For example, if a feature has three different Gene Ontology terms, cellular component, molecular function and ribosome biogenesis and assembly, it will have three different entries into the file. See Table 4.5 for an example.

Chromosome	**Start**	**Stop**	**Strand**	**GO aspect**	**GO term**
one	99306	99869	W	C	cellular component
one	99306	99869	W	F	molecular function
one	99306	99869	W	P	ribosome biogenesis and assembly

Table 4.5. Shows the format of data files that included Gene Ontology information but did not include neighbor information

For experiments that investigated the influence of neighbor's SGDID (*Saccharomyces* Genome Database identification) on the feature's Gene Ontology term classification, the neighbor's SGDID was included. For each of the feature's neighbors, a separate entry was created for each of the feature's different Gene Ontology terms. See Table 4.6 for an example.

Chromosome	**Start**	**Stop**	**Strand**	**Neighbor Number**	**Neighbor Strand**	**Neighbor SGDID**	**Distance**	**GO term**
one	99306	99869	W	1	W	S000033629	4507	cellular component
one	99306	99869	W	1	W	S000033629	4507	molecular function
one	99306	99869	W	1	W	S000033629	4507	ribosome biogenesis and assembly
one	99306	99869	W	2	W	S000000025	4507	cellular component
one	99306	99869	W	2	W	S000000025	4507	molecular function
one	99306	99869	W	2	W	S000000025	4507	ribosome biogenesis and assembly

Table 4.6. Shows the format of the data files that included neighbor's SGDID and feature's Gene Ontology information.

For experiments that investigated the influence of neighbor's Gene Ontology information on the feature's Gene Ontology term classification, the neighbor's Gene Ontology information was included. For each of the neighbor's Gene Ontology terms, a separate entry was created for each of the feature's different Gene Ontology terms. See Table 4.7 for an example.

Chromo-some	Start	Stop	Strand	Neighbor number	Neighbor strand	Distance	Neighbor GO aspect	Neighbor GO term	GO aspect	GO term
one	2169	1807	C	1	W	605	C	cellular component	C	cellular component
one	2169	1807	C	1	W	605	C	cellular component	F	molecular function
one	2169	1807	C	1	W	605	C	cellular component	P	sporulation
one	2169	1807	C	1	W	605	F	molecular function	C	cellular component
one	2169	1807	C	1	W	605	F	molecular function	F	molecular function
one	2169	1807	C	1	W	605	F	molecular function	P	sporulation
one	2169	1807	C	1	W	605	P	biological process	C	cellular component
one	2169	1807	C	1	W	605	P	biological process	F	molecular function
one	2169	1807	C	1	W	605	P	biological process	P	sporulation
one	2169	1807	C	2	W	605	?	?	C	cellular component
one	2169	1807	C	2	W	605	?	?	F	molecular function
one	2169	1807	C	2	W	605	?	?	P	sporulation

Table 4.7. Shows the format of the data files that included neighbor's Gene Ontology information and feature's Gene Ontology information.

4.3 Algorithms

All datasets were analyzed by WEKA. The algorithms used to analyze the datasets are Naïve Bayes, KStar and MultiBoostAB using the J48 classifier. An exhaustive analysis of all possible algorithms was not performed. The performance of a classifier is dataset dependent. We still do not have a single classifier that can reliably outperform all others on a given dataset [van der Walt and Barnard, 2006]. The process of selecting a classifier is a process of trial and error, so a sampling of algorithms from different families of classification was examined.

The Naïve Bayesian classifier was selected because often the simplest approach is the best, and studies that have compared various classification algorithms found the Naïve Bayesian classifier to be comparable in performance with classification trees and with neural network classifiers [Stewart, 2002]. The KStar classifier was selected because it tends to perform better than other lazy classifiers (IB1-5 [Aha *et al.*, 1991]), and in some cases it performs better than Quinlan's C4.5 [Cleary and Trigg, 1995]. J48 (Java version of C4.5) was selected because even though there are other tree classifiers, Quinlan's research has always been on the "forefront of decision tree induction" and it is an algorithm that is well studied [Witten and Frank, 2005]. MultiBoosting was used in conjunction with J48 to produce decision committees with lower error than either AdaBoost or wagging over a broad array of datasets [Webb, 2000].

For the KStar experiments, a default blend setting of 20% was used because that is the value "which seems to work well for most datasets" [Cleary and Trigg, 1995]. The missing values were replaced with the average of the entropy curve for that attribute in which the missing value belonged.

For the MultiBoostAB experiments, reweighting was used instead of resampling because past experiments produced results the suggested "reweighting is more effective than resampling" [Webb, 2000]. The other settings were set to default values.

For the experiments that required IR techniques, 8287 genomic feature descriptions were obtained from the SGD. These descriptions were pre-processed for IR retrieval. The stop-list that was used can be found in Appendix A.

4.4 Metrics

The performance of the classification process can be evaluated by several metrics. In this study, six metrics were focused on: percentage of correctly classified instances, the Kappa statistic, precision, recall, the F-measure and the area under the ROC (receiver operating characteristics) curve.

The percentage of correctly classified instances is a basic accuracy measurement that can be determined by the following:

$$Percent\ Correctly\ Classified = \frac{number\ of\ correctly\ classified\ instances}{number\ of\ instances}$$

The Kappa statistic measures the agreement between predicted and observed categorization. As a test statistic, Kappa can verify that agreement exceeds chance levels. It has possible values that range from +1 (perfect agreement) to 0 (no agreement above that expected by chance, or in other words the agreement is equal to chance) and then to -1 (perfect disagreement). When

Kappa is negative, it means that the agreement is less than what would be expected by chance. It is rare that to get perfect agreement. Kappa is calculated as:

$$\varkappa = \frac{P(A) - P(E)}{1 - P(E)}$$

where *P(A)* is the observed agreement (between the classifier and the actual truth) , and *P(E)* is the chance agreement.

There are different interpretations as to what is a good level of agreement. One possible interpretation of Kappa provided by Altman (1991) can found in Table 4.8.

Agreement	**Range of values**
Poor	Less than 0.20
Fair	0.20 to 0.40
Moderate	0.40 to 0.60
Good	0.60 to 0.80
Very Good	0.80 to 1.00

Table 4.8 Interpretation of Kappa statistic.

The precision and recall scores are similar to those used in IR. In the classification process, a precision score of 1.0 for a class *X* means that every item labeled as belonging to class *X* does indeed belong to class *X* (but says nothing about the number of items from class *X* that were not labeled correctly). In the classification process, a recall score of 1.0 means that every item from class *X* was labeled as belonging to class *X* (but says nothing about how many other items were incorrectly also labeled as belonging to class *X*). Precision and recall are calculated in the following manner:

$$Precision(X) = \frac{\text{number of correctly classified instances of class X}}{\text{number of instances classified as belonging to class X}}$$

$$Recall(X) = \frac{\text{number of correctly classified instances of class X}}{\text{number of instances in class}}$$

Often, there is an inverse relationship between precision and recall, where it is possible to increase one at the cost of reducing the other. For example, in a classification system for deciding whether or not, say, a fruit is a tomato, can achieve high precision by only classifying fruits with the exact right shape (round) and color (red) as tomatoes, but at the cost of low recall due to the number of false negatives from tomatoes that did not quite match the specification, like a green Roma tomato.

Precision and recall are rarely discussed in isolation. They can be combined into a single measure, such as the F-measure. The F-measure is a weighted harmonic mean of precision and recall. It is calculated in the following manner:

$$F = 2 * \frac{(\text{precision} \ * \ \text{recall})}{(\text{precision} \ + \ \text{recall})}$$

In statistics, the F-measure is a measure of a test's accuracy. The F-measure can be interpreted as a weighted average of the precision and recall, where an F-measure reaches its best value at 1.0 and worst score at 0.

Another way to measure accuracy is to use the area under the ROC curve. The area has a nice interpretation as the probability that the classifier ranks a randomly chosen positive instance above a randomly chosen negative one. The accuracy of the test depends on how well the classifier separates the group being tested into those that belong to a class and those that do not belong to a class.

An area of 1.0 represents a perfect test. An area of 0.5 represents a worthless test. For better understanding of the ROC curves, Thomas G. Tape provides a graph of some curves with an interpretation as follows:

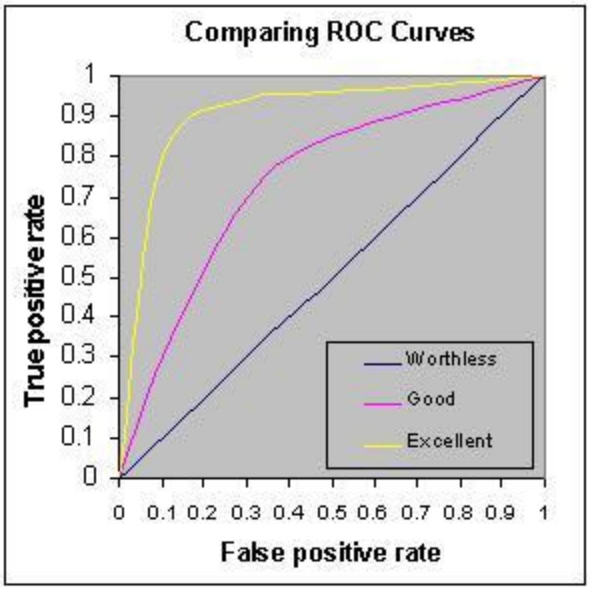


Figure 4.1. Taken from *Interpreting Diagnostic Tests* web page by Thomas G. Tape to illustrate the interpretation of the area under the ROC curve.

A rough guide for classifying the accuracy is provided by Tape (See Table 4.9).

Results	**Area ranges**
Fail	0.50 -0.60
Poor	0.60 – 0.70
Fair	0.70 – 0.80
Good	0.80 – 0.90
Excellent	0.90 – 1.0

Table 4.9. Interpretation of area under ROC curve from *Interpreting Diagnostic Tests* web page by Thomas G. Tape.

5 Results

5.1 Classifying Genomic Features to Networks

The results of experiments that determined if altering the type of neighbor information given the classifiers altered the accuracy of the classification process follow.

5.1.1 Using Neighbor's SGDID

A series of experiments was performed to determine if given the properties of chromosome number, start position, stop position, strand, neighbor number, neighbor SGDID, neighbor strand, neighbor distance (determined from the mid-point of each feature), and network involvement information from KEGG for genomic features (features being: genes, ARS, etc) could classification algorithms correctly classify network involvement. This was also performed including information from the nearest, two-, five- and ten- nearest neighbors of each feature. This was also repeated on the individual chromosomes. The mitochondrial chromosome is excluded. Having only one known network on the mitochondrial chromosome, classifiers cannot classify unary classes.

The results of the experiments are based on averages of ten different runs of each dataset being randomized and then split for training and testing. The training sets were set to contain 66% of the instances randomly selected from each dataset.

5.1.1.1 Results for Entire Genome

When using only a genomic feature's chromosome number, start position, stop position, strand, and network involvement without neighbor information, we see that the percentage of genomic features correctly classified to the correct network does not vary greatly when different classifiers are used (See Figure 5.1). When no neighbor information is included, less than 20% of the genomic features are classified to the correct network regardless of the classifier used. As more neighbor information is included, the percentage of correctly classified features increases for the KStar classifier. For the MultiBoostAB algorithm using the J48 classifier, the percentage of correctly classified features decreases with the inclusion of neighbor information. When the Naïve Bayesian classifier is used, the percentage of correctly classified genomic features decreases with the inclusion of neighbor information until information from each feature's ten-nearest neighbors is included where it then increases.

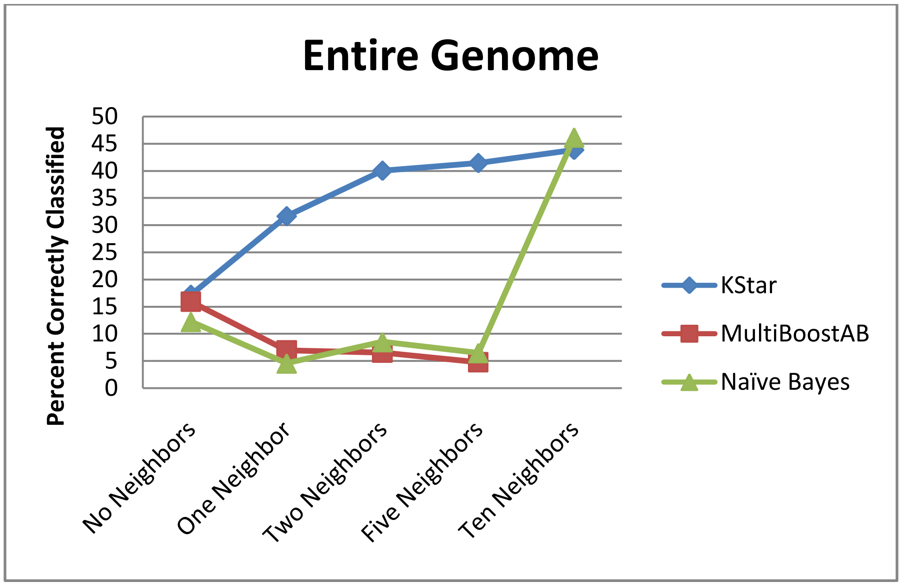


Figure 5.1. Percent of genomic features classified for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The agreement between the predicted and observed classification of the genomic features can be seen in the Kappa statistic. When no neighbor information is included, all of the classifiers have poor agreement between the predicted and observed classification (See Figure 5.2). The KStar classifier achieves moderate agreement as more neighbor information is added. A moderate agreement is achieved with the Naïve Bayesian classifier when information on the ten-nearest neighbors of a genomic feature is included. The MultiBoostAB algorithm using the J48 classifier never achieves an agreement above poor. In fact, the inclusion of neighbor information decreases the agreement between predicted and observed classification.

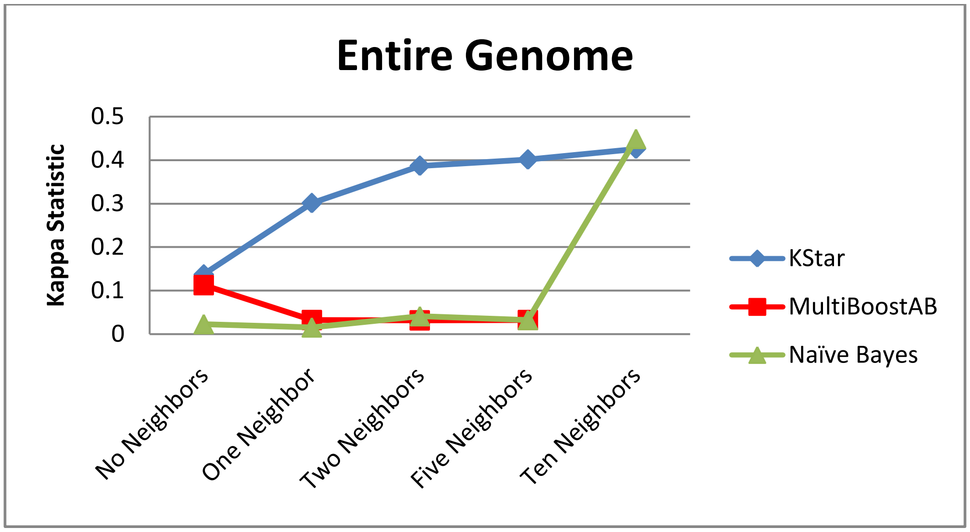


Figure 5.2. Kappa statistic for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The overall precision of the classification process is low for all classifiers (See Figure 5.3). The KStar classifier obtains a precision score above 0.2 when information from each feature's two-nearest neighbors is included. In all other instances, the precision scores are never above 0.15.

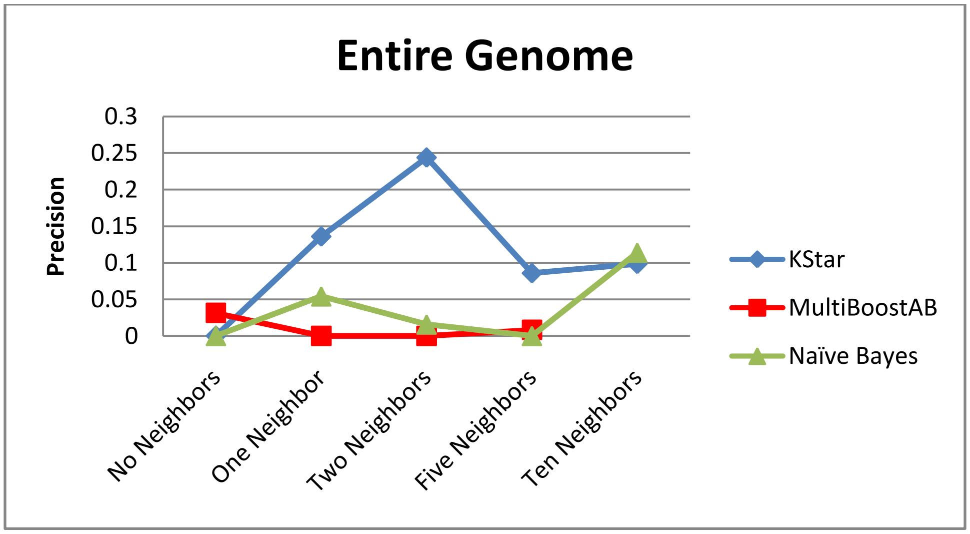


Figure 5.3. Precision for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The recall scores of the classifiers mimic the precision scores the classifiers obtained (See Figure 5.4). The highest recall score obtained by the KStar classifier is when information from each feature's two-nearest neighbors is included. The Naïve Bayesian classifier does not obtain a recall score above 0.12 even after information from each feature's ten-nearest neighbors is included. For the MultiBoostAB algorithm using the J48 classifier, the recall scores decrease with the inclusion of neighbor information.

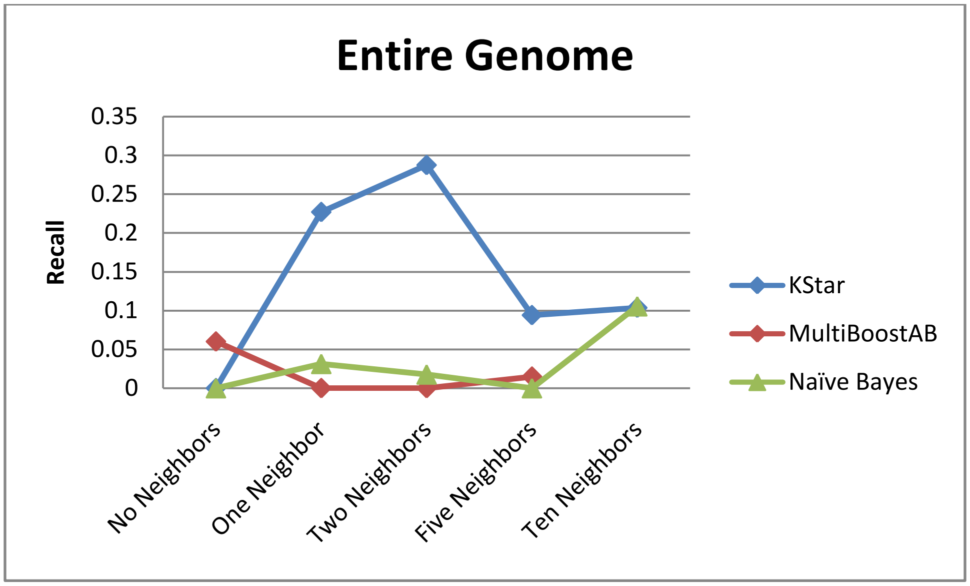


Figure 5.4. Recall for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Not surprisingly, the F-measures obtained by the different classifiers mimic their precision and recall scores (See Figure 5.5). For the KStar classifier, the highest F-measure is obtained when information from each feature's two-nearest neighbors is included. There is not a dramatic change in F-measures for the Naïve Bayesian classifier until information about the ten-nearest neighbors for each feature is included. For the MultiBoostAB algorithm using the J48 classifier, the F-measure decreases with the inclusion of neighbor information.

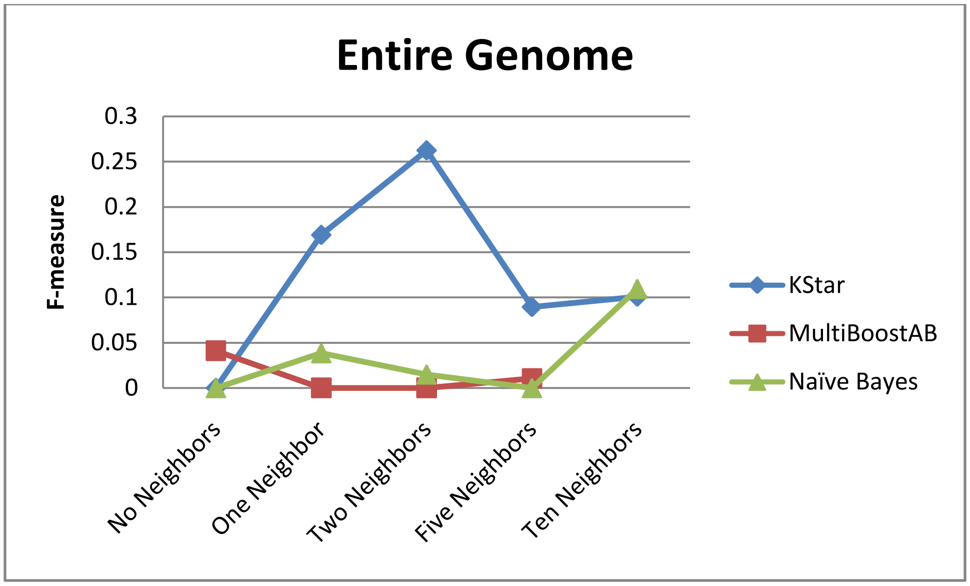


Figure 5.5. F-measure for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

When no neighbor information is included, the MultiBoostAB algorithm using the J48 classifier is the only classifier that obtains an accuracy score, according to the area under the ROC curve, that is not failing, but it is considered poor (See Figure 5.6). The accuracy does not improve when neighbor information is included. The KStar classifier improves its accuracy to excellent when information about the neighbor information is included, but the accuracy drops to failing when information from each feature's ten-nearest neighbors is included. With the Naïve Bayesian classifier, the accuracy of the classification improves to fair when information from each feature's five-nearest neighbors is included and then improves to excellent when information from the ten-nearest neighbors is included.

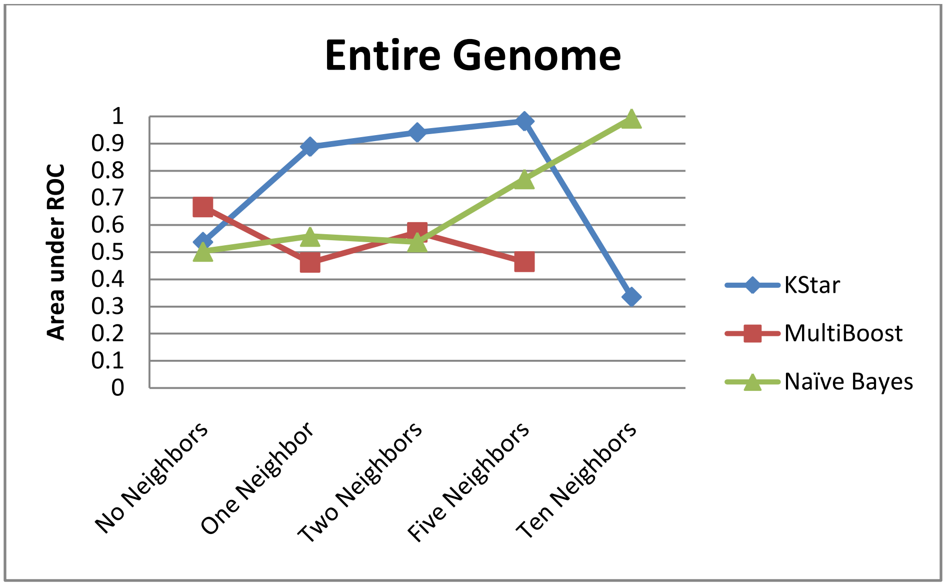


Figure 5.6. Area under ROC curve for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

To see the effect on the accuracy of the KStar classification for each network, the F-measures for each network were analyzed. The table of the F-measures can be found in Appendix B. The addition of neighbor information improves the accuracy of the classification process for most networks (See Figures 5.7-5.9).

Some networks attain F-measures that are above 0.6 with no neighbor information included implying that the location of these features alone is indicative of their network involvement. These networks are the ribosome network and the polyunsaturated fatty acid biosynthesis network. Other networks (the oxidative phosphorylation network, the SNARE interactions in vesicular transport network, the ubiquitin biosynthesis network, the proteasome network, the valine, leucine and isoleucine biosynthesis network, the glycerophospholipid metabolism network, the cell cycle network, the aminoacyl-tRNA biosynthesis network, the purine metabolism network and the starch and sucrose metabolism network) also obtain F-measures with no neighbor information included, but they are less than 0.4.

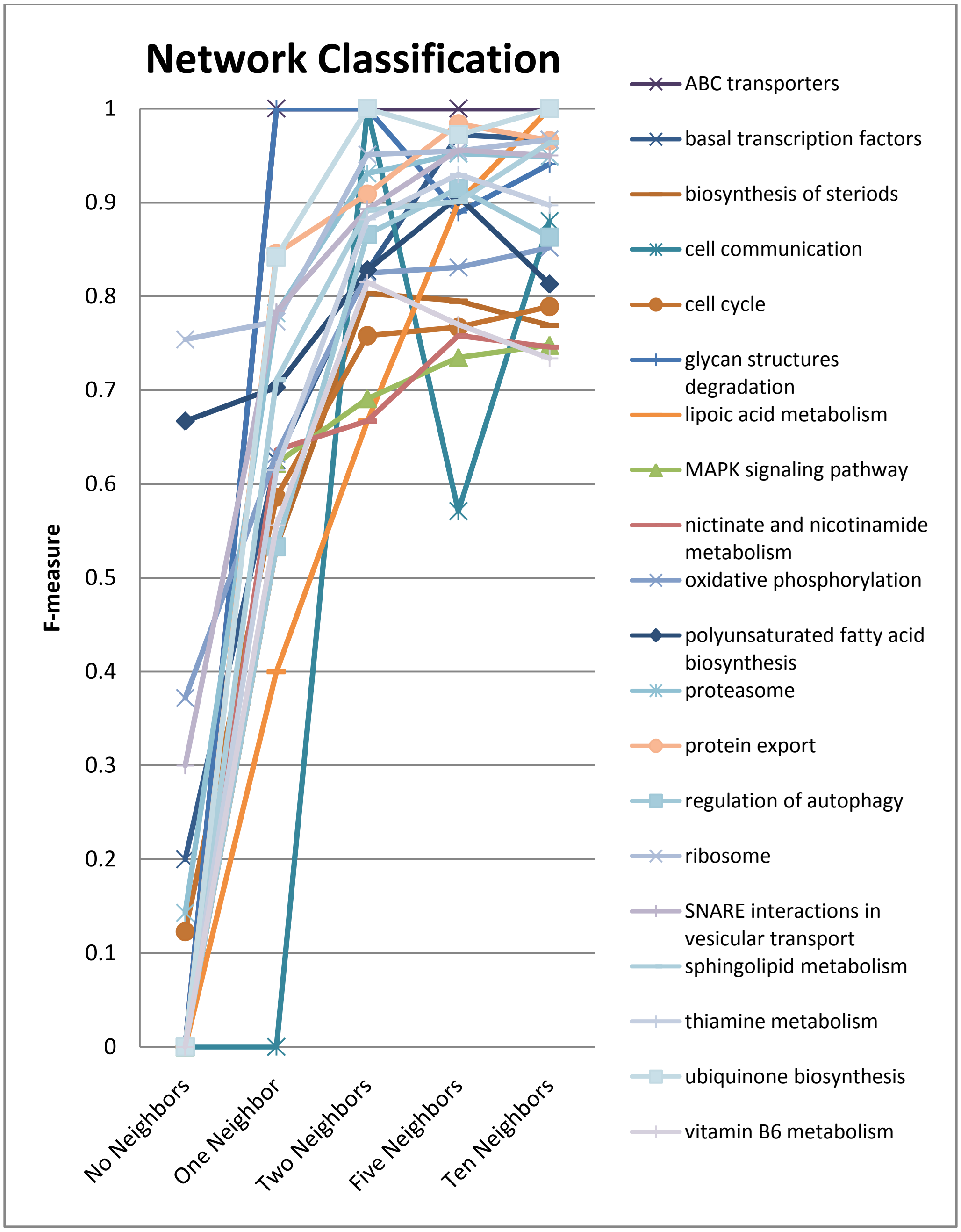


Figure 5.7. F-measures obtained using the KStar classifier for the individual networks. Only networks that obtained an F-measure above 0.7 are shown.

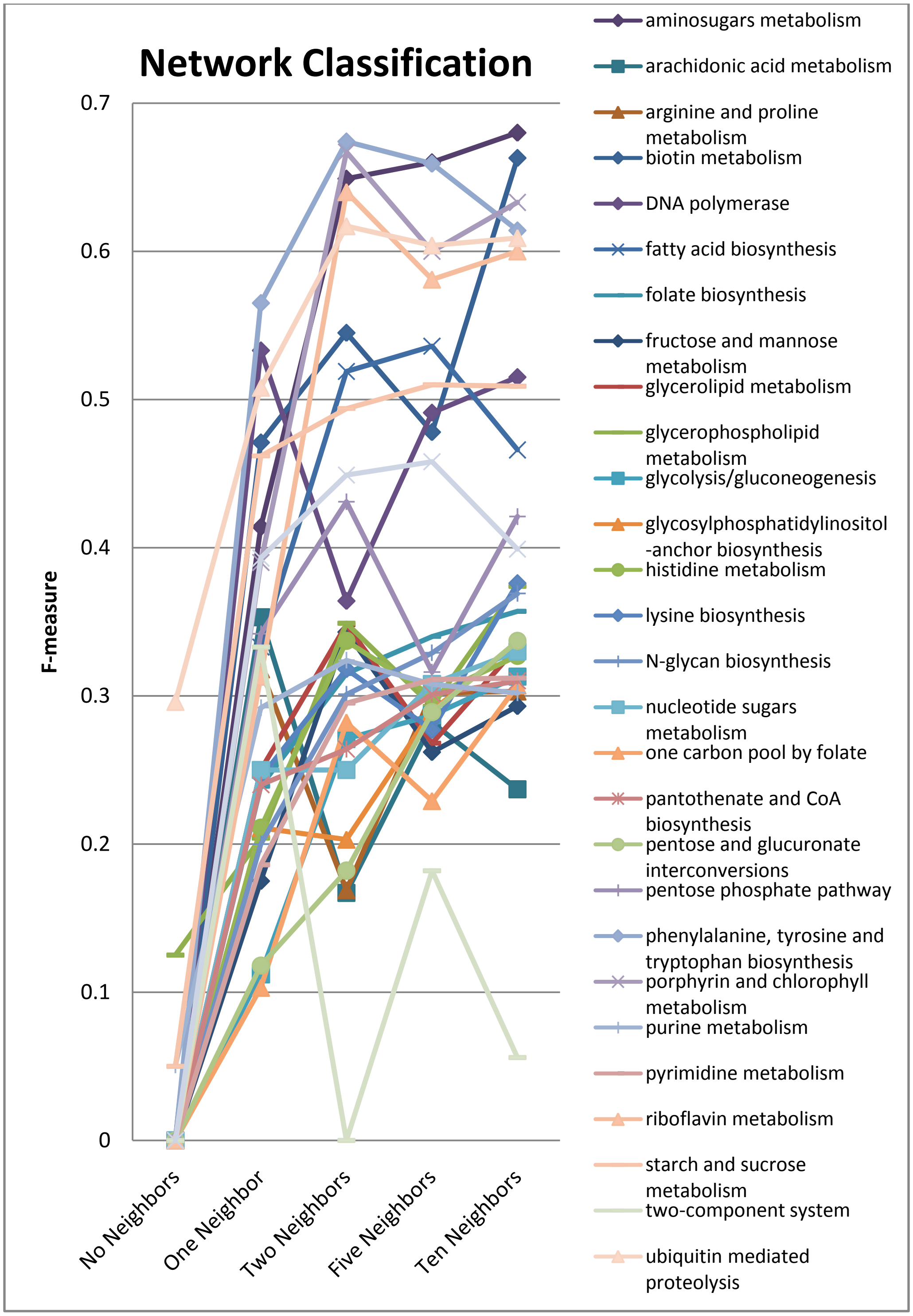


Figure 5.8. F-measures obtained using the KStar classifier for the individual networks. Only networks that obtained an F-measure above 0.3 and below 0.7 are shown.

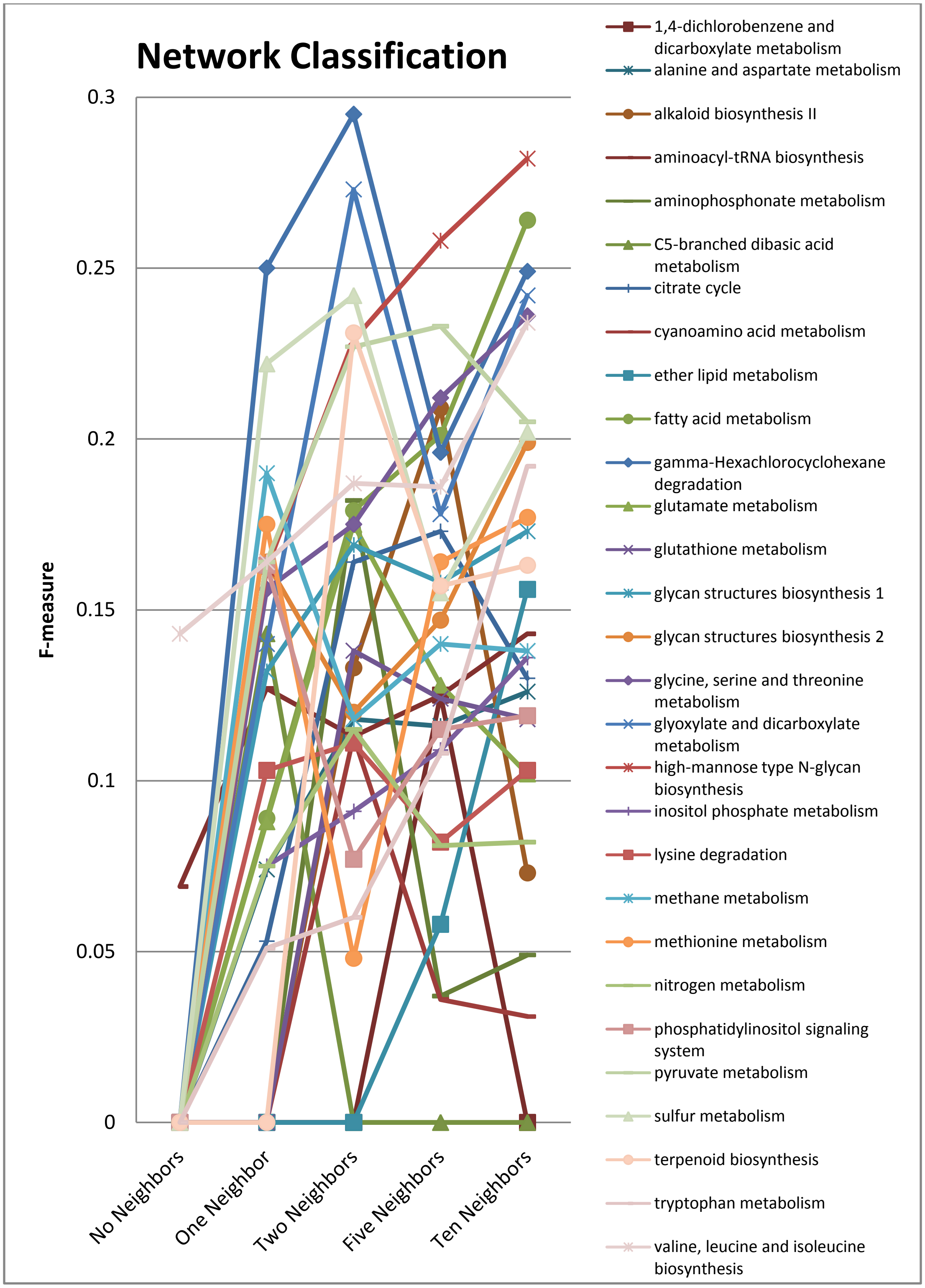


Figure 5.9. F-measures obtained using the KStar classifier for the individual networks. Only networks that obtained an F-measure above 0.1 and below 0.3 are shown.

With the networks that obtained the lower accuracies, the F-measures fluctuate depending on the amount of neighbor information that is included.

5.1.1.2 Results for Individual Chromosomes

When we look at each chromosome individually, we see that the results of classification vary from chromosome to chromosome, from the number of neighbors included, and from the classification algorithm being used.

5.1.1.2.1 Percent Correctly Classified

For all chromosomes, the percent of genomic features correctly classified to the correct network differed depending on the number of neighbors included in the dataset and the classification algorithm used.

When information about each genomic feature's neighbors is included, there is an improvement in the percent of features correctly classified for each of the classification algorithms for chromosome one (See Figure 5.10) The inclusion of information beyond each feature's two-nearest neighbors has little effect on the percentage of correctly classified features. The MultiBoostAB algorithm using the J48 classifier obtains the highest percentage of correctly classified features.

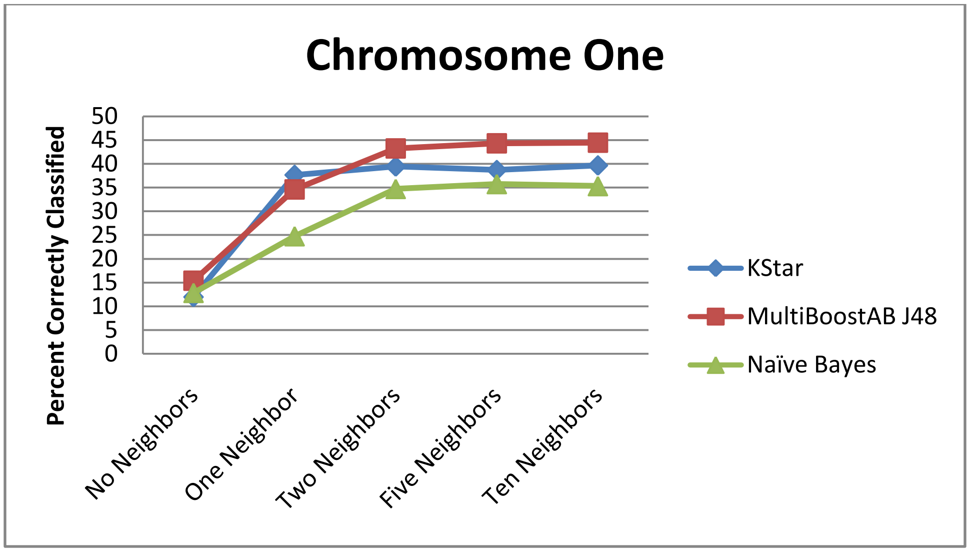
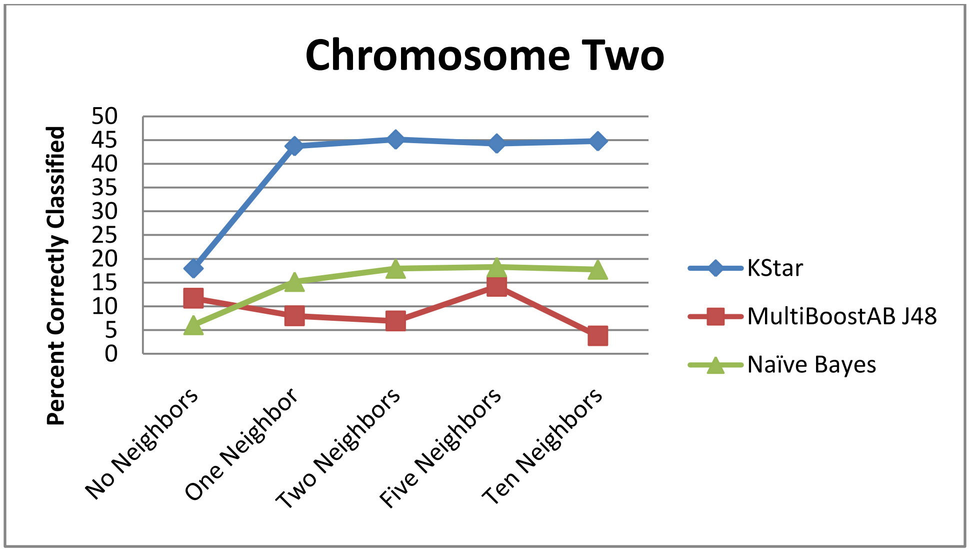


Figure 5.10. Percent of genomic features classified for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, the KStar classifier appears to be influenced the most by the inclusion of neighbor information (See Figure 5.11). The Naïve Bayesian classifier does see an increase in its percentage of correctly classified features as more neighbors are included, but it is not as drastic as that observed with the KStar classifier. The percentage fluctuates using the MultiBoostAB algorithm with the J48 classifier. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features.



5.11. Percent of genomic features classified for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, the percent of genomic features correctly classified to the correct network increases when information about each genomic feature's nearest neighbors is included (See Figure 5.12). The MultiBoostAB using the J48 classifier sees the largest improvement. Increasing the number of neighbors beyond five, does not significantly improve the classification for the any of the classifiers.

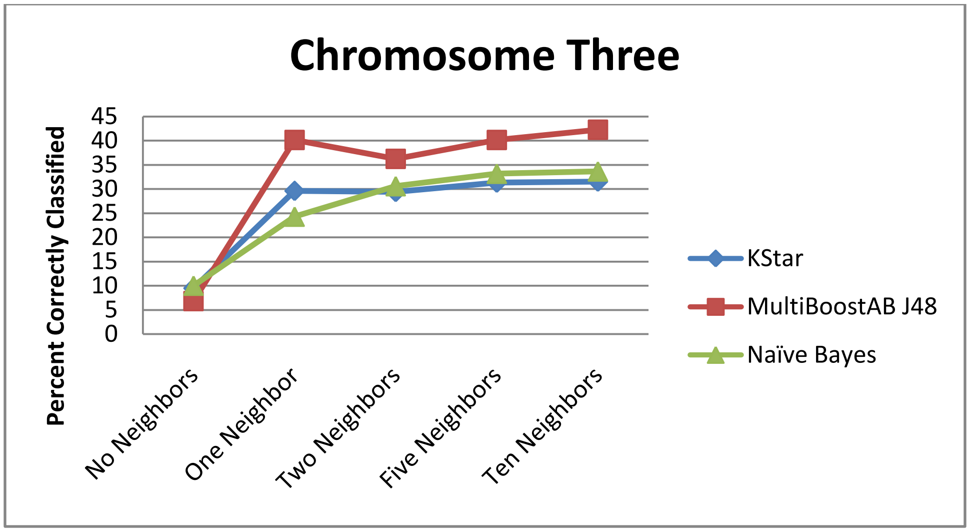


Figure 5.12. Percent of genomic features classified for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The inclusion of neighbor information for the genomic features of chromosome four increases the percentage of correctly classified genomic features for the KStar classifier and the Naïve Bayesian classifier, with the KStar classifier seeing the largest improvement (See Figure 5.13). The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on these classifiers. Including neighbor information does not improve the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier.

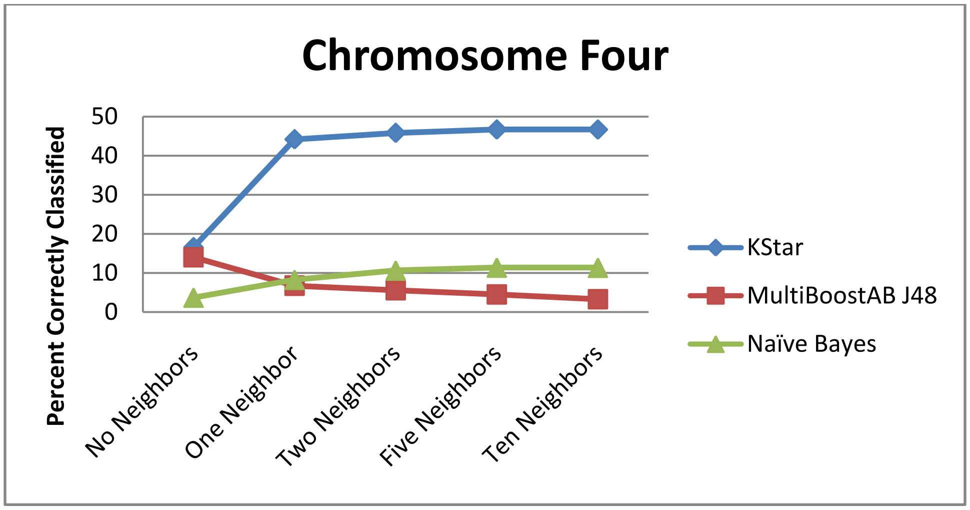


Figure 5.13. Percent of genomic features classified for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, the inclusion of neighbor information is beneficial to the KStar classifier and the Naïve Bayesian classifier. The increase in the percentage of correctly classified features plateaus for these classifiers after the inclusion of information from each feature's nearest neighbors (See Figure 5.14). The MultiBoostAB algorithm using the J48 classifier does not see an increase in percentage of correctly classified features until information from each feature's two-nearest neighbors is included, then it obtains the higher percentages of correctly classified features.

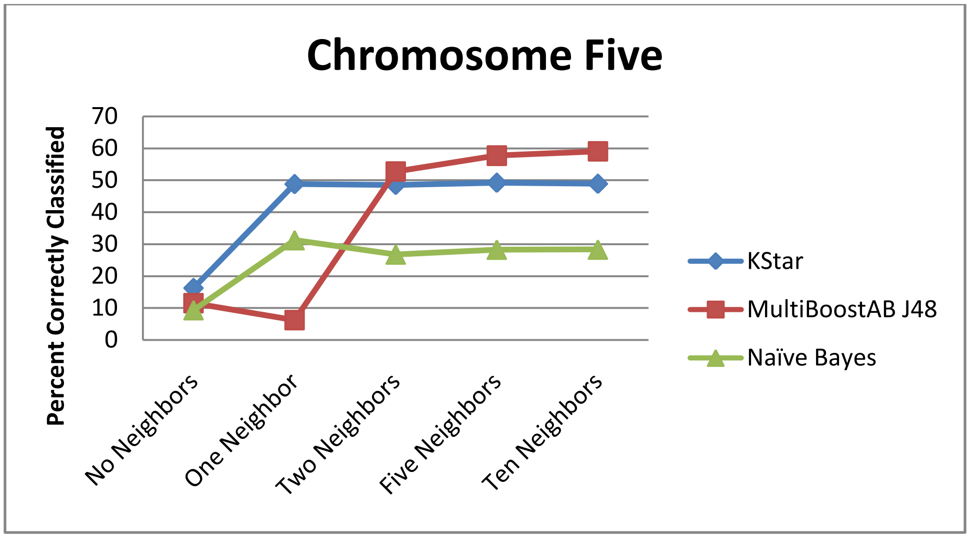


Figure 5.14. Percent of genomic features classified for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, the inclusion of neighbor information increases the percentage of correctly classified features for all classifiers (See Figure 5.15). Inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the percentages of correctly classified features.

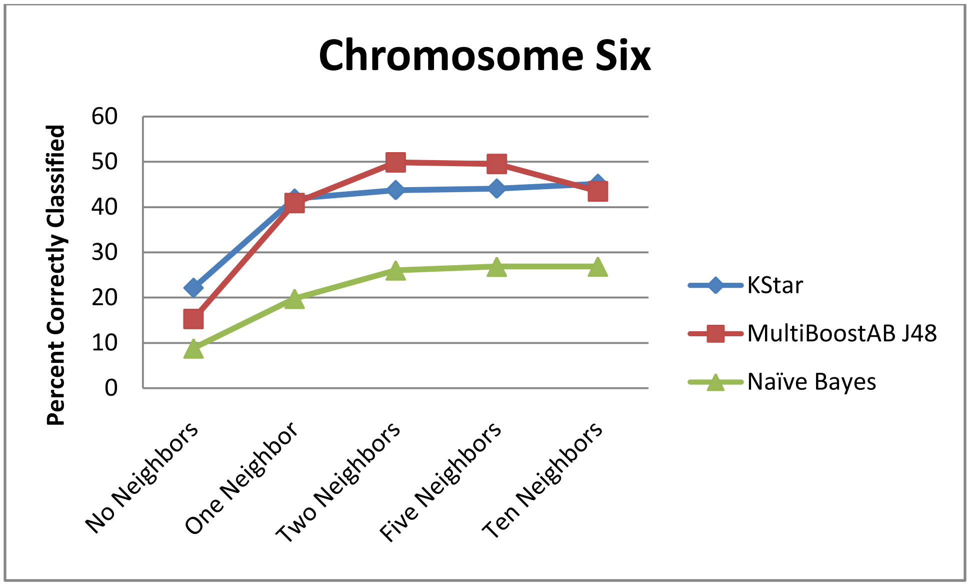


Figure 5.15. Percent of genomic features classified for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, the inclusion of neighbor information improves the percentage of correctly classified features for the KStar classifier and the Naïve Bayesian classifier. This increase is not observed for the MultiBoostAB algorithm using the J48 classifier until information from each feature's five-nearest neighbors is included (See Figure 5.16).

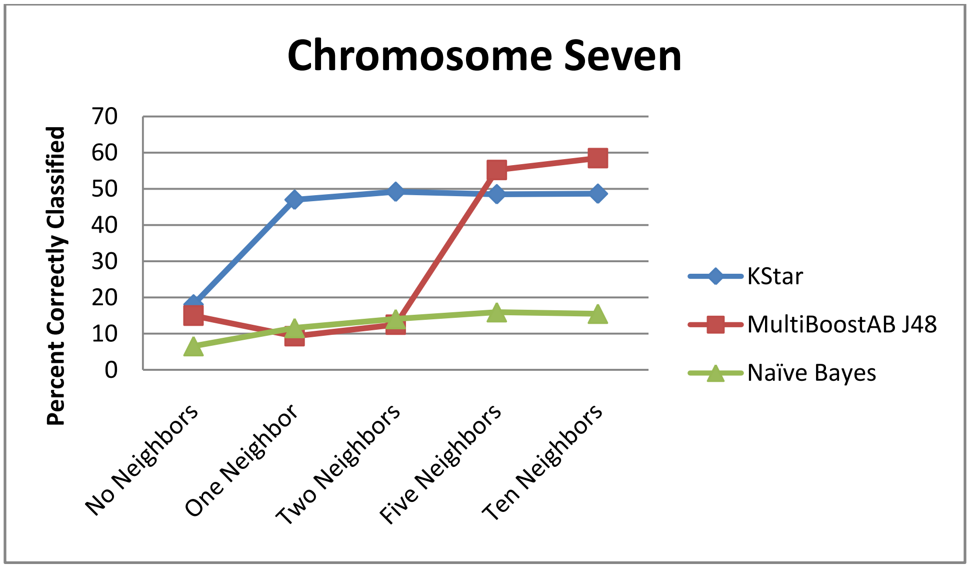


Figure 5.16. Percent of genomic features classified for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, all classifiers have an increase in the percentage of correctly classified features with the inclusion of neighbor information (See Figure 5.17). For the KStar classifier and the Naïve Bayesian classifier the inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentages of correctly classified features.

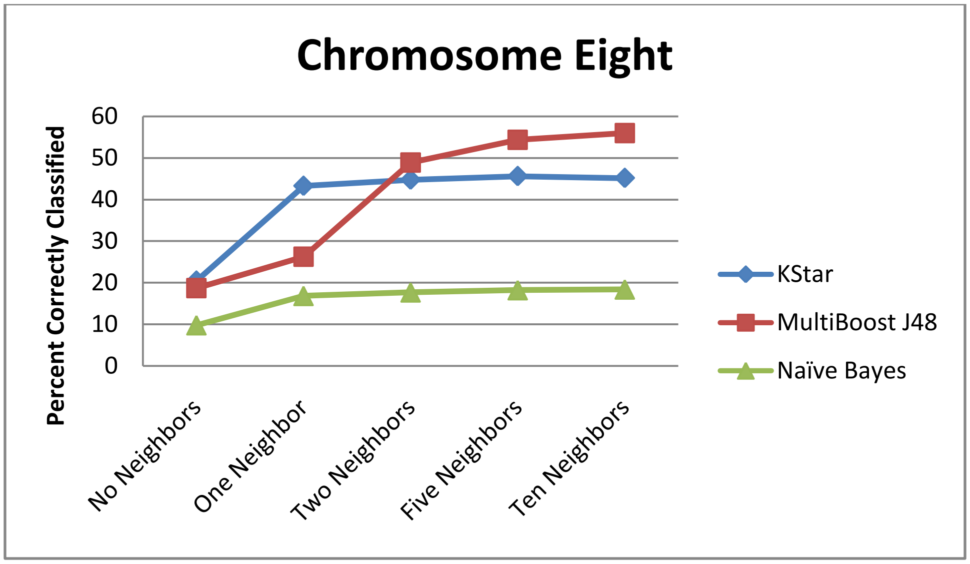


Figure 5.17. Percent of genomic features classified for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, the inclusion of neighbor information improves the percentage of features correctly classified for both the KStar classifier and the MultiBoostAB algorithm using the J48 classifier (See Figure 5.18). The inclusion of neighbor information beyond each feature's nearest neighbors does not increase the percentage of correctly classified features for the KStar classifier. The inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the MultiBoostAB algorithm using the J48 classifier. This classifier obtains the higher percentages at this point of information inclusion. There is not a drastic change in the percentage of correctly classified features using the Naïve Bayesian classifier as neighbor information is included.

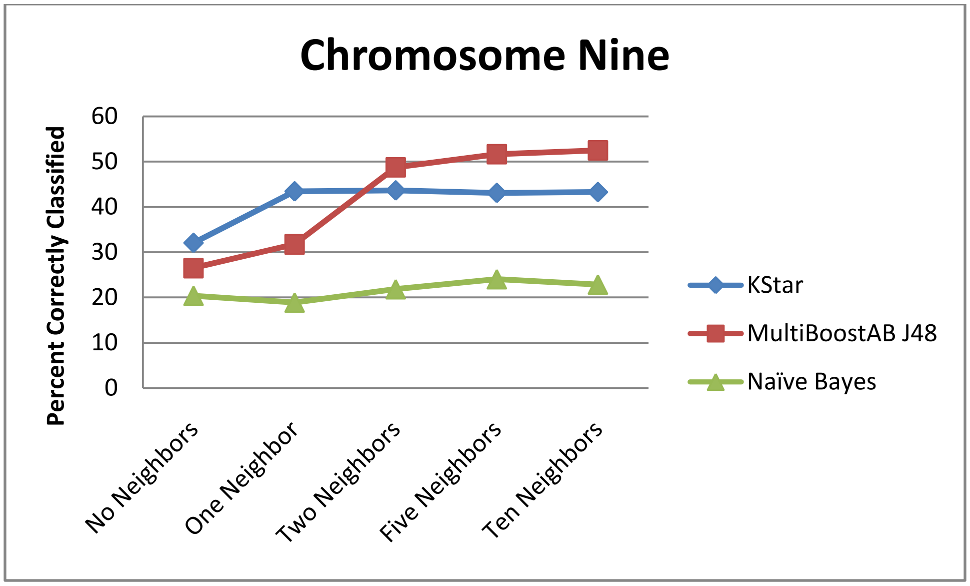


Figure 5.18. Percent of genomic features classified for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the inclusion of neighbor information is beneficial to the KStar classifier and the Naïve Bayesian classifier. The inclusion of information beyond each feature's nearest neighbors has little impact on the performance of the KStar classifier. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of neighbor information generally causes a decrease in the percentage of correctly classified features. The exception occurs with the inclusion of information from each feature's five-nearest neighbors (See Figure 5.19).

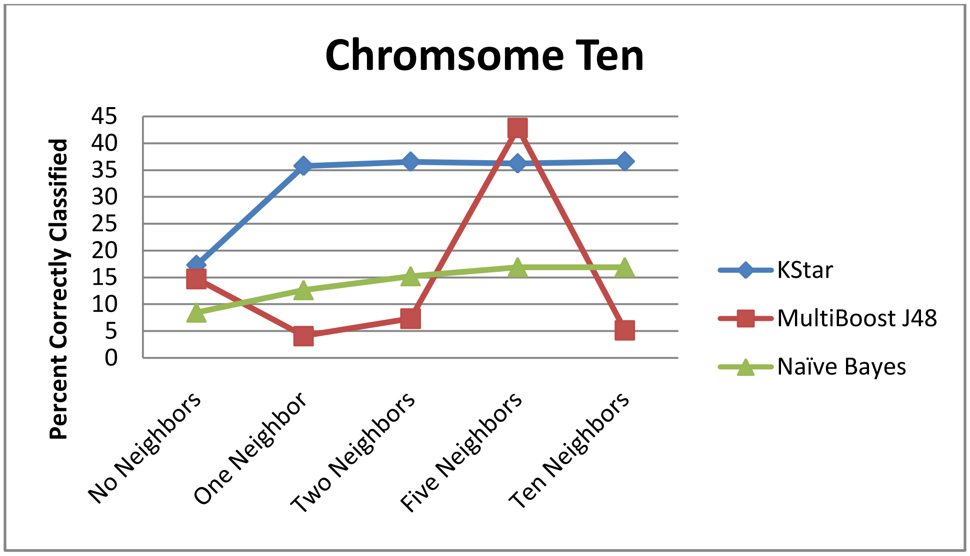


Figure 5.19. Percent of genomic features classified for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eleven, the inclusion of neighbor information improves the percentage of correctly classified features for the KStar classifier and the Naïve Bayes classifier. The inclusion of information beyond each feature's nearest neighbors for the KStar classifier has little effect on the percentage of correctly classified features. For the Naïve Bayesian classifier, the inclusion of information beyond each feature's two-nearest neighbors has little effect on the percentage of correctly classified features. The MultiBoostAB algorithm using the J48 classifier, in general, sees a decrease in the percentage of correctly classified features with a spike seen when information from each feature's five-nearest neighbors is included. (See Figure 5.20).

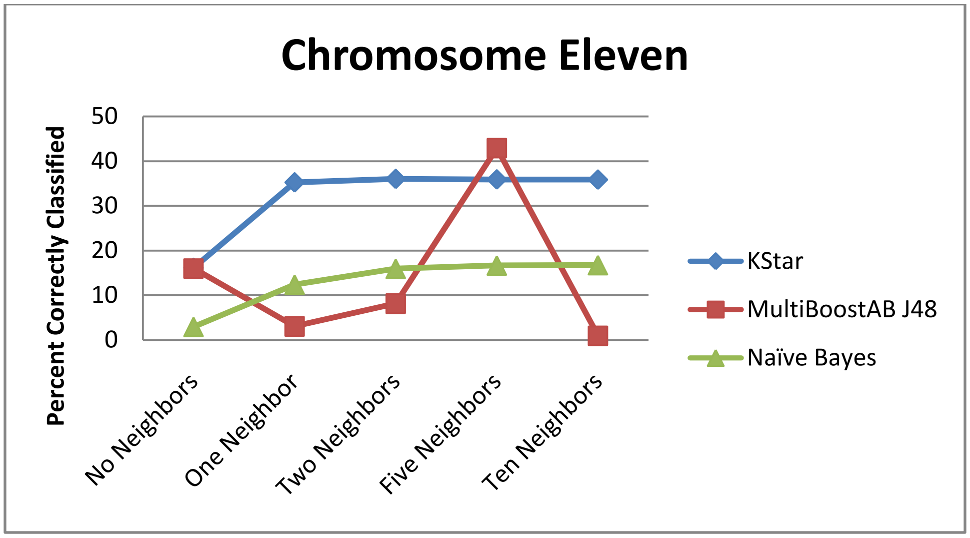


Figure 5.20. Percent of genomic features classified for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the KStar classifier and the Naïve Bayesian classifier observe an increase in the percentage of correctly classified features with the inclusion of neighbor information (See Figure 5.21). The inclusion of information beyond each feature's nearest neighbors for the KStar classifier has little effect on the percentage of correctly classified features. There is a decrease in the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier when information from the number of neighbors increases from zero to two. As more neighbor information is included, an increase in the percentage of correctly classified features is seen for the MultiBoostAB algorithm using the J48 classifier.

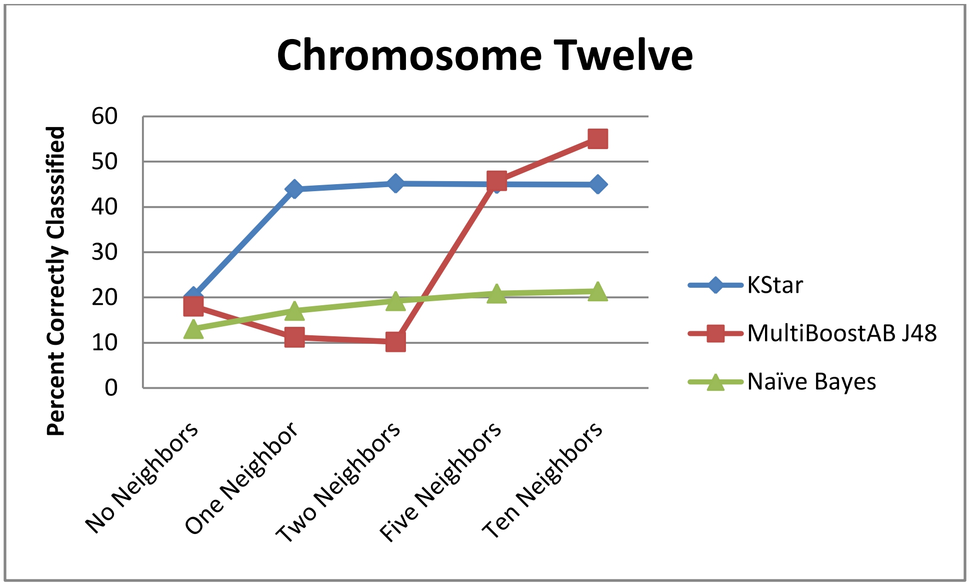


Figure 5.21. Percent of genomic features classified for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, the inclusion of more neighbor information improves the percentage of correctly classified features for the KStar and Naïve Bayesian classifiers (See Figure 5.22). The inclusion of information beyond each feature's nearest neighbors for the KStar classifier has little effect on the percentage of correctly classified features. For the MultiBoostAB algorithm using the J48 classifier, initially there is a decrease in the percentage of correctly classified features as the number of neighbors included goes from zero to two. When information from each feature's five-nearest neighbors is included, an increase in the percentage of correctly classified features is seen for the MultiBoostAB algorithm using the J48 classifier.

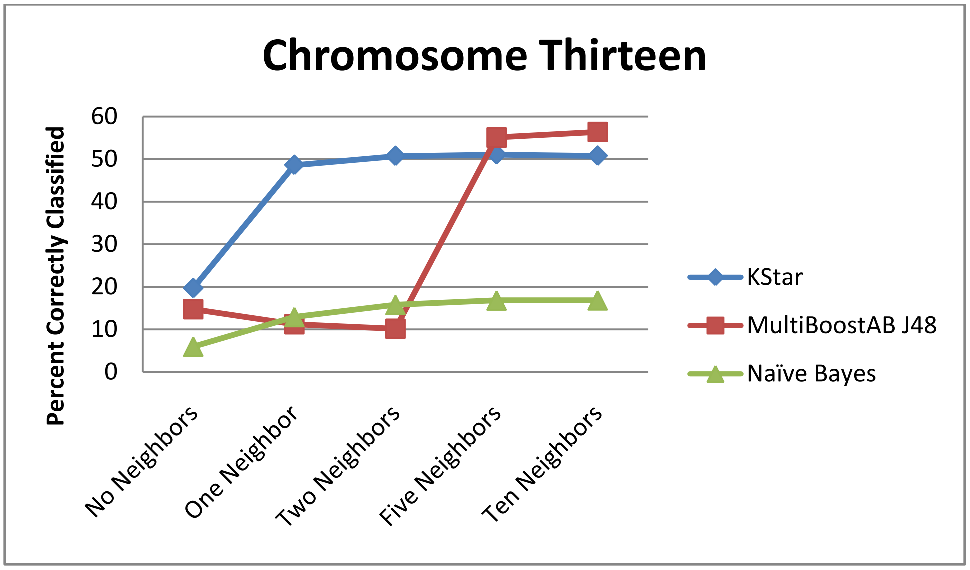


Figure 5.22. Percent of genomic features classified for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, for the KStar and Naïve Bayesian classifiers, there is an increase in the percentage of correctly classified genomic features as neighbor information is included (See Figure 5.23). The inclusion of information beyond each feature's nearest neighbors for the KStar classifier has little effect on the percentage of correctly classified features. The MultiBoostAB algorithm using the J48 classifier sees a decrease in the percentage of correctly classified features followed by a steep increase when neighbor information is expanded from each feature's two- nearest neighbors to the ten-nearest neighbors.

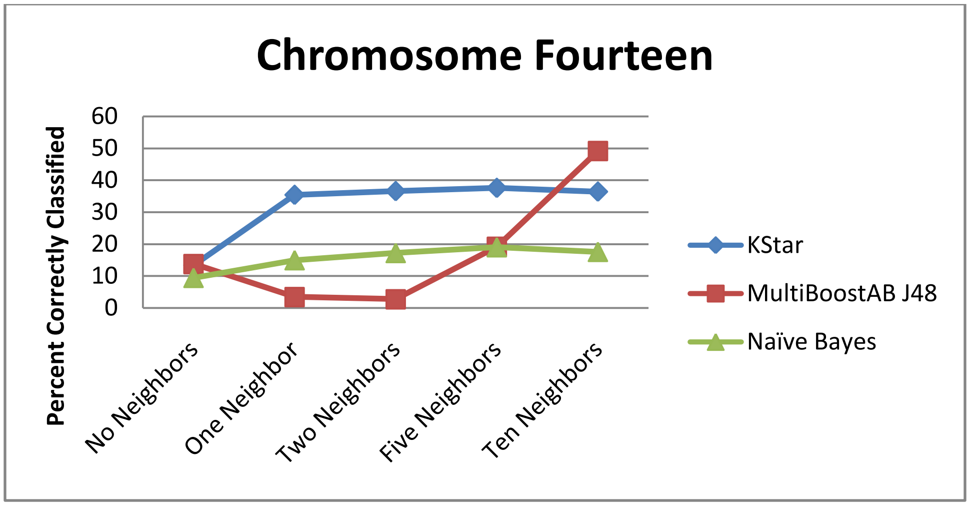


Figure 5.23. Percent of genomic features classified for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, including neighbor information increases the percent of correctly classified genomic features for the KStar and the Naïve Bayesian classifiers (See Figure 5.24). The inclusion of information beyond each feature's nearest neighbors for the KStar classifier has little effect on the percentage of correctly classified features. The MultiBoostAB algorithm using the J48 classifier experiences a decrease in the percentage of correctly classified features when neighbor information is included.

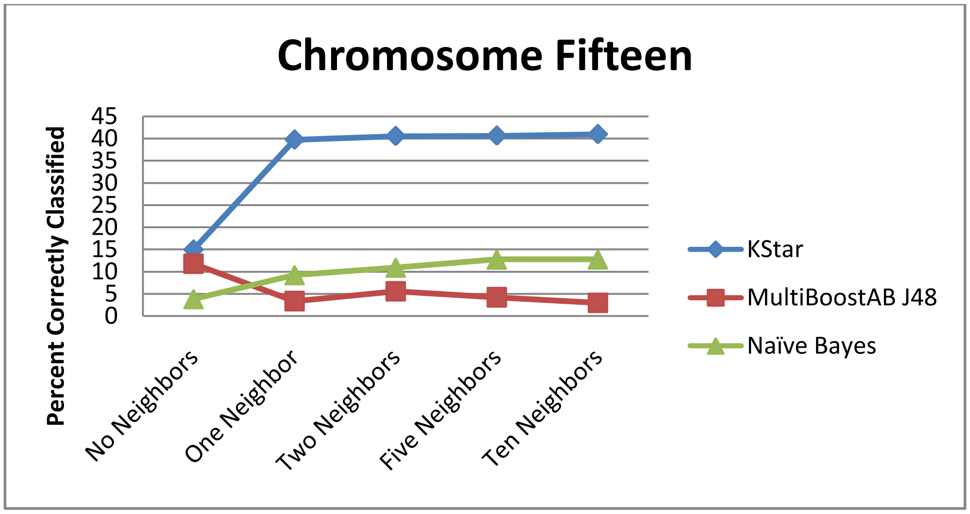


Figure 5.24. Percent of genomic features classified for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, the addition of neighbor information does increase the percentage of correctly classified genomic features for the KStar classifier and the Naïve Bayesian classifier, with the KStar classifier seeing the larger increase (See Figure 5.25). The inclusion of information beyond each feature's nearest neighbors for the KStar classifier has little effect on the percentage of correctly classified features. The MultiBoostAB algorithm using the J48 classifier, in general, sees a decrease in the percentage of correctly classified features with a spike seen when information from each feature's five-nearest neighbors is included.

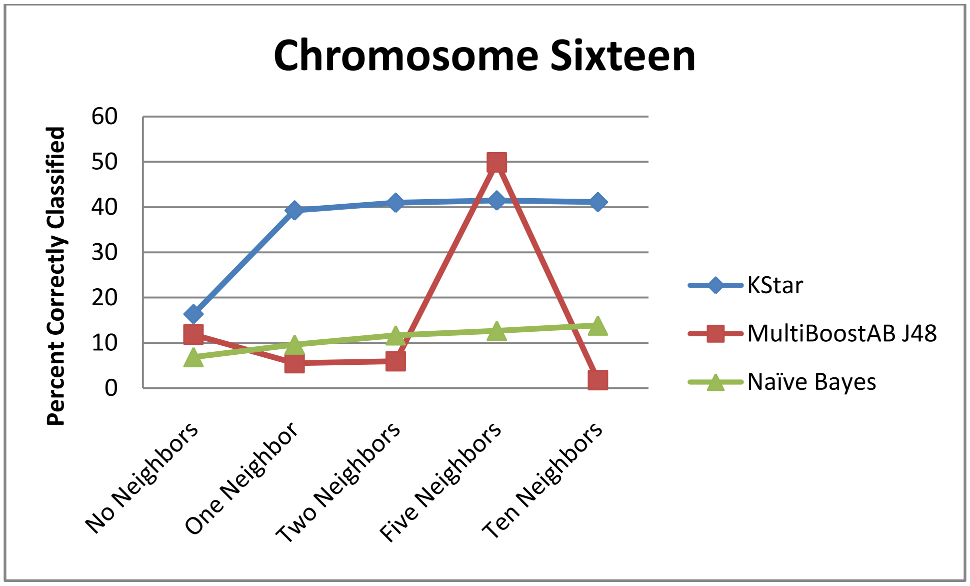


Figure 5.25. Percent of genomic features classified for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

After analyzing all the chromosomes, the KStar classifier and the Naïve Bayesian classifier show similar patterns of performance for each chromosome. The MultiBoostAB algorithm using the J48 classifier does not show a consistent pattern of performance, but it did obtain the higher percentages of correctly classified features with the inclusion of more neighbor information. The KStar classifier obtained the higher percentages of correctly classified features with the inclusion of only each feature's nearest neighbors. Partitioning the classification process by chromosome did not improve the percentage of correctly classified features. Each chromosome obtained close to a maximum of 45% using the KStar classifier, which is similar to the percentage that was obtained using the entire genome.

5.1.1.2.2. F-measures

To look at the accuracy of the classification process for each chromosome, the F-measures obtained for each chromosome can be analyzed.

For chromosome one, the F-measures are low. The higher F-measures are obtained with the MultiBoostAB algorithm using the J48 classifier, and the accuracy is affected by the number of neighbors included. The KStar classifier does not obtain F-measures above 0.11 regardless of the neighbor information included and the Naïve Bayesian classifier never achieves an F-measure above zero (See Figure 5.26).

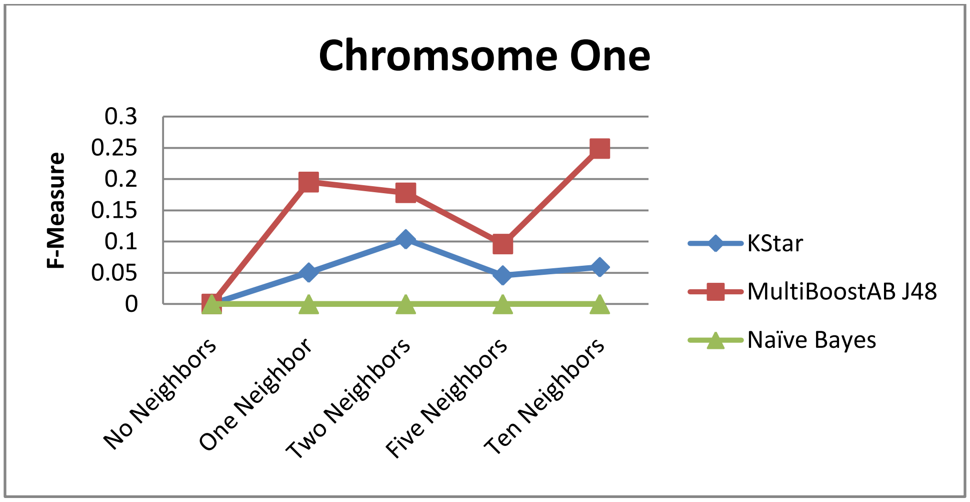


Figure 5.26. F-measure for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, the KStar classifier achieves the higher F-measures. The inclusion of neighbor information improves its accuracy. The Naïve Bayesian classifier never achieves an F-measure above zero, and the MultiBoostAB algorithm using the J48 classifier only gets an F-measure that is not zero when information from the five-nearest neighbors is included (See Figure 5.27).

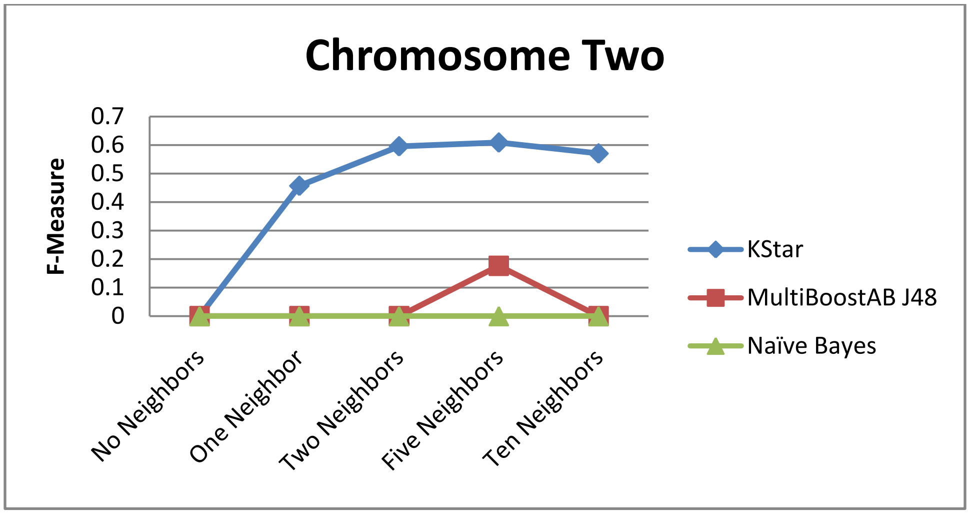


Figure 5.27. F-measure for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For the chromosome three, the F-measures are low. The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures with the inclusion of neighbor information having information from each feature's nearest neighbors obtaining the highest F-measure (See Figure 5.28). The F-measures for the KStar classifier improves when neighbor information is added, but the F-measures obtained are never above 0.1. The Naïve Bayesian classifier never achieves an F-measure above zero.

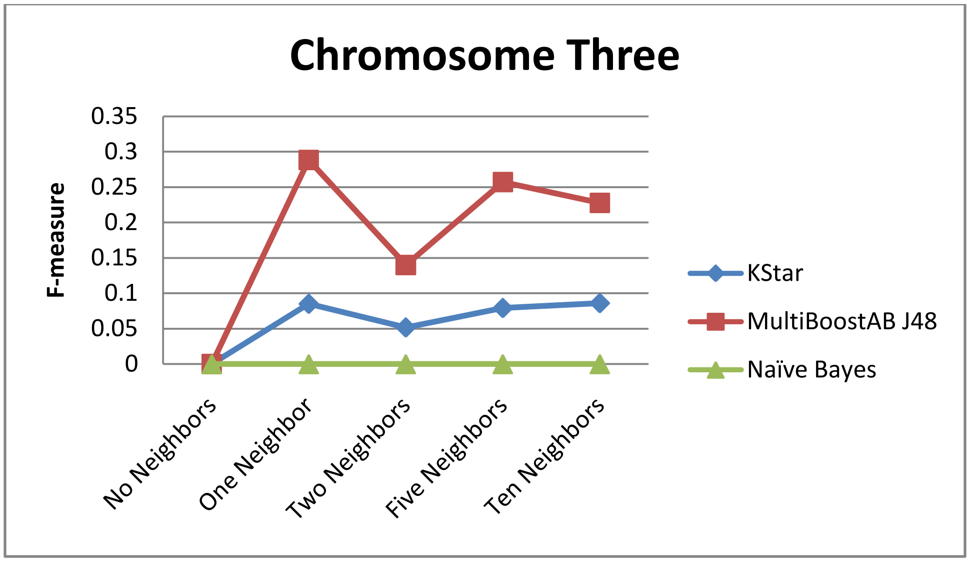


Figure 5.28. F-measure for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, the F-measures are low. The KStar classifier achieves the higher F-measures when neighbor information is included. The Naïve Bayesian classifier never obtains an F-measure above 0.15, but the inclusion of neighbor information from more than one neighbor is beneficial. The MultiBoostAB algorithm using the J48 classifier obtains its highest F-measure when no neighbor information is included (See Figure 5.29).

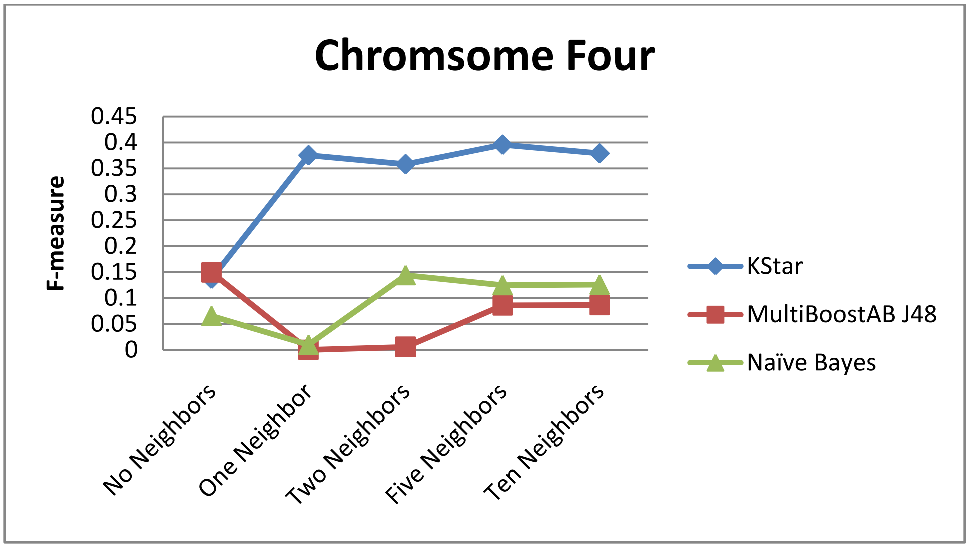


Figure 5.29. F-measure for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, the F-measures for the KStar classifier improve from zero to one when neighbor information is included. The F-measures obtained using the MultiBoostAB algorithm using the J48 classifier and the Naive Bayesian classifier improve to those levels when information from at least the two-nearest neighbors of each feature is included (See Figure 5.30).

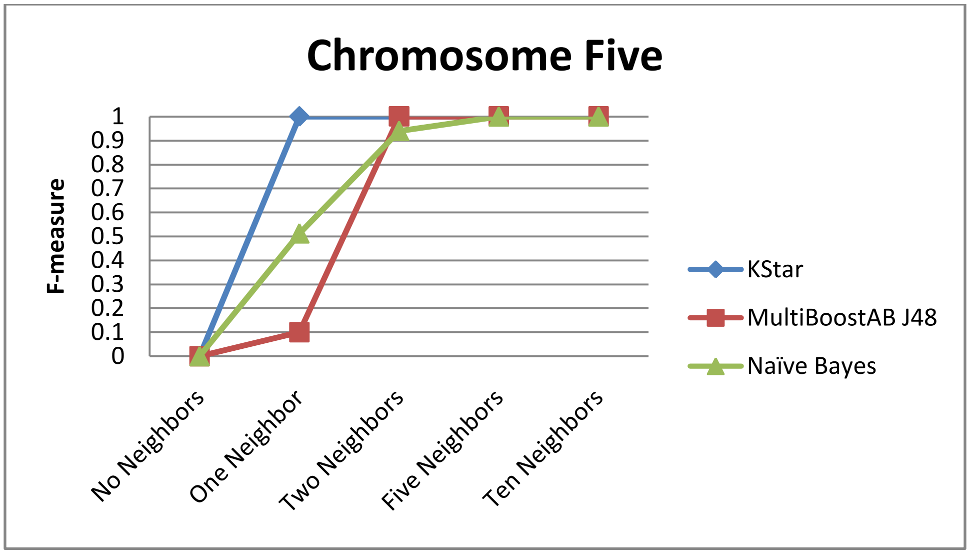


Figure 5.30. F-measure for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, all of the classifiers observe an increase in F-measures as neighbor information is included (See Figure 5.31). For the KStar classifier and the MultiBoostAB algorithm using the J48 classifier, the increase observed goes from zero, when no neighbor information is included, to one regardless of how many neighbors are included. For the Naïve Bayesian classifier, information from more than one neighbor must be included to see the increase to one.

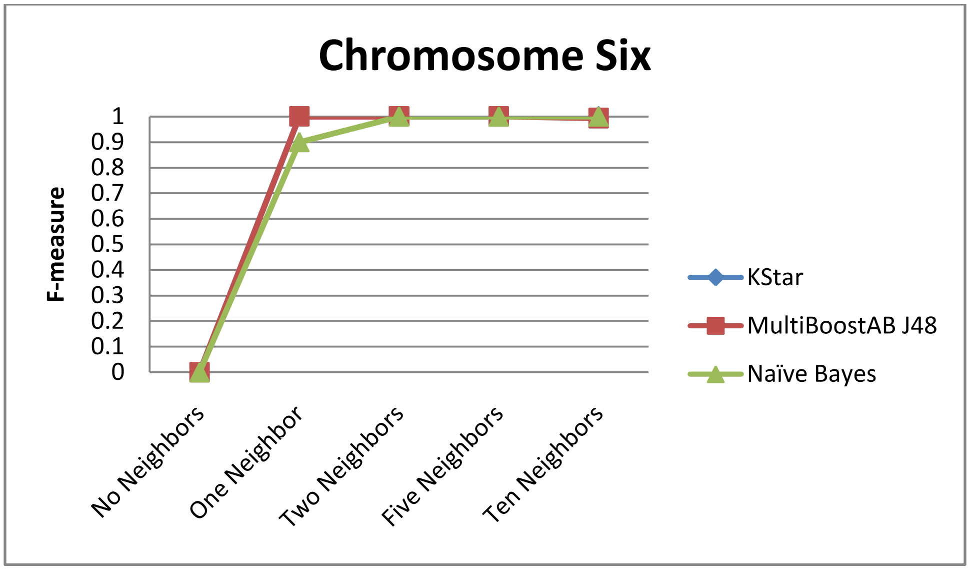


Figure 5.31. F-measure for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The F-measures obtained using the different classifiers for chromosome seven are the lowest out of all the chromosomes (See Figure 5.32). The highest F-measure is obtained using the MultiBoostAB algorithm using the J48 classifier including information from each feature's ten-nearest neighbors.

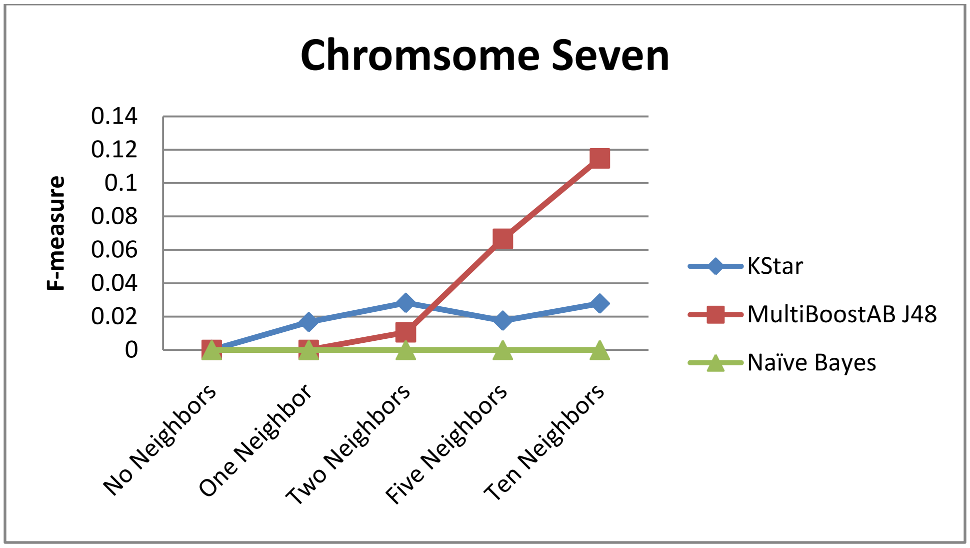


Figure 5.32. F-measure for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, the KStar classifier obtains F-measures above 0.75 independent of the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier observes an increase in the F-measure when information from the two, five or ten-nearest neighbors of each feature is included (See Figure 5.33). The Naïve Bayesian classifier never obtains an F-measure above 0.1 independent of the inclusion of neighbor information.

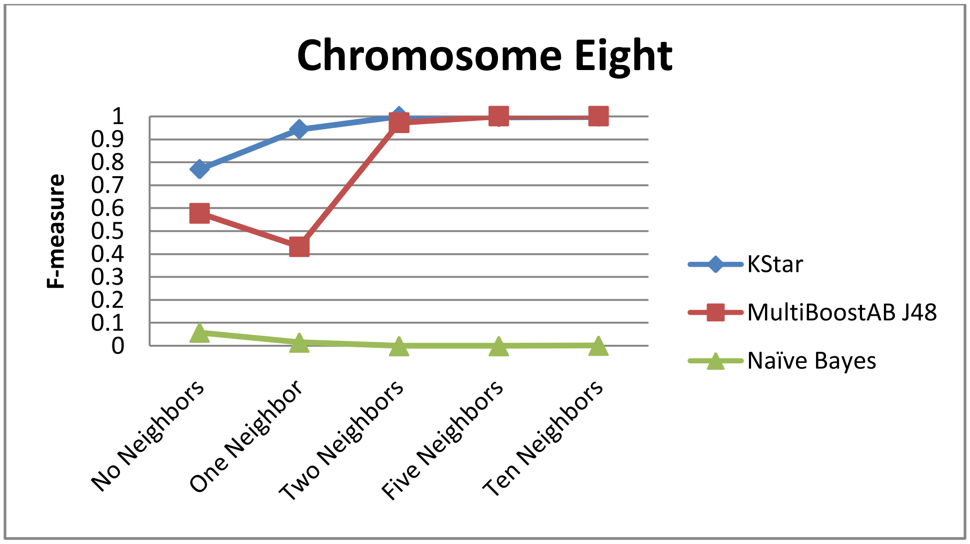


Figure 5.33. F-measure for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, all the classifiers observe an increase in F-measures as more neighbor information is included. The KStar classifier and MultiBoostAB algorithm using the J48 classifier observe a steep increase with the inclusion of just one neighbor, with the F-measure for KStar classifier going from zero to one. The MultiBoostAB algorithm using the J48 does not obtain an F-measure until the inclusion of information from each feature's two-nearest neighbors. The F-measures obtained by the Naïve Bayesian classifier never exceed 0.4 (See Figure 5.34).

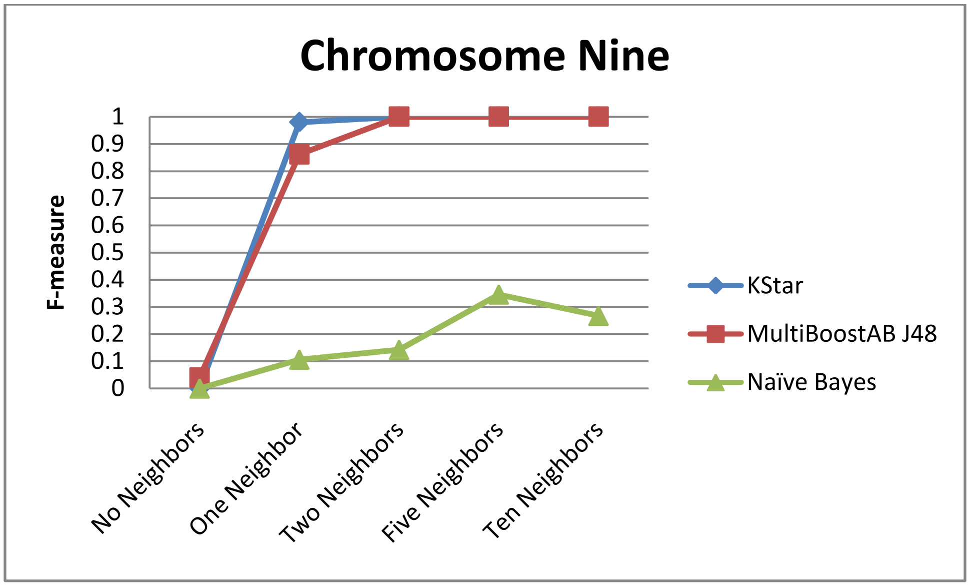


Figure 5.34. F-measure for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the KStar classifier observes an increase in F-measures when neighbor information is included. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the classifier. For the MultiBoostAB algorithm using the J48 classifier, the F-measure increases when information from the five-nearest neighbors is included. This increase is lost when information from the ten-nearest neighbors is included. The Naïve

Bayesian classifier observes little change in its F-measures as neighbor information is included (See Figure 5.35).

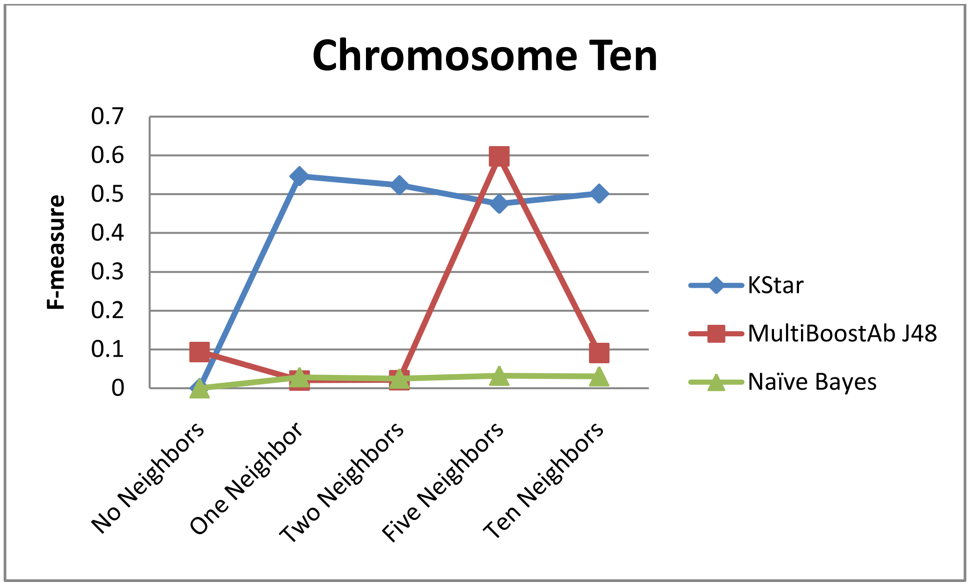


Figure 5.35. F-measure for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The F-measures for chromosome eleven have a similar pattern to those of chromosome ten (See Figure 5.36). The KStar classifier observes an increase in F-measures when neighbor information is included. For the MultiBoostAB algorithm using the J48 classifier, the F-measure increases when information from the five-nearest neighbors is included. This increase is lost when information from the ten-nearest neighbors is included. The F-measures for the Naïve Bayesian classifier remain zero independent of the inclusion of neighbor information.

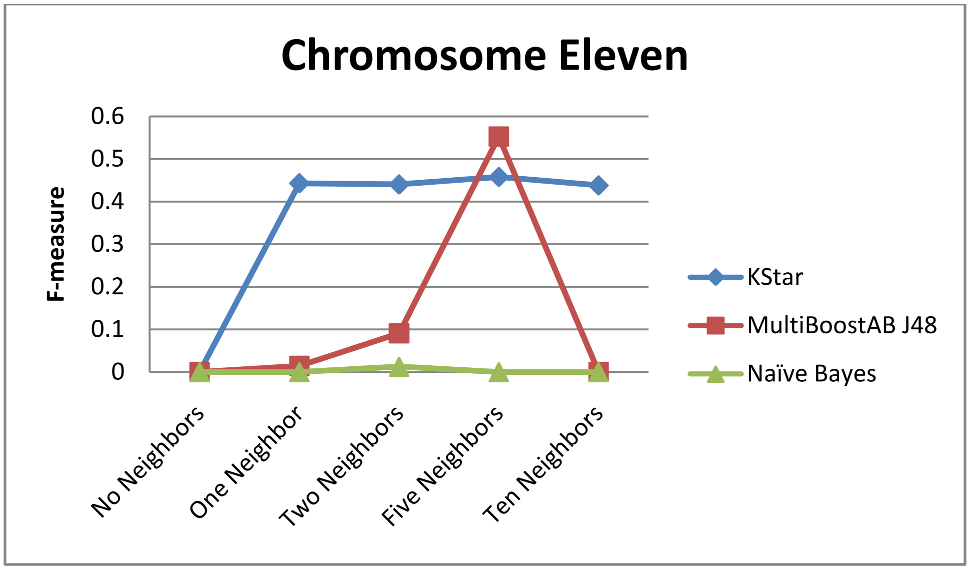


Figure 5.36. F-measure for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the F-measures obtained by the KStar classifier improve from near 0.7 to 1.0 with the inclusion of neighbor information. The inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the KStar classifier. For the Naïve Bayesian classifier, the F-measures decrease as neighbor information is included. The F-measures obtained using the MultiBoostAB algorithm using the J48 classifier increase when information from each feature's five-nearest or the ten-nearest neighbors is included, with the higher F-measure obtained when including information from the ten-nearest neighbors (See Figure 5.37).

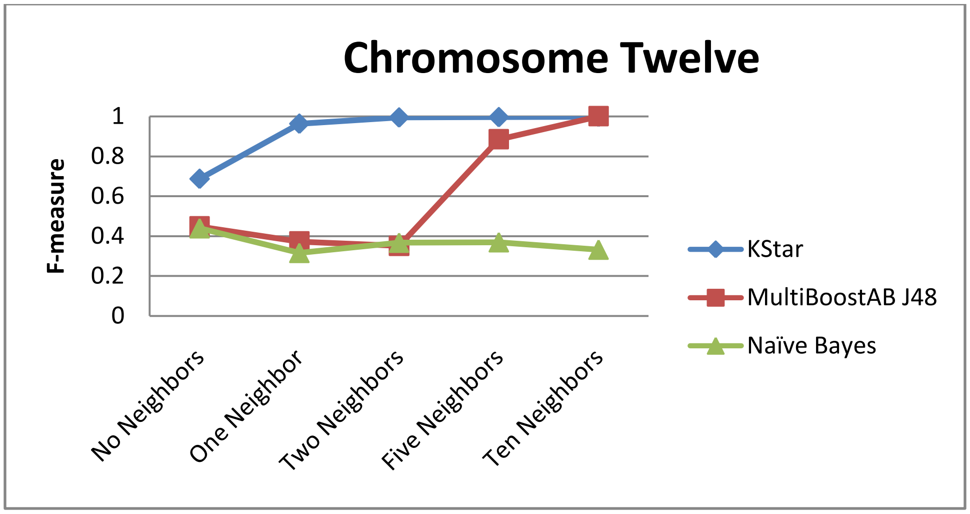


Figure 5.37. F-measure for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, the F-measures obtained are low. The KStar classifier never obtains an F-measure above 0.1 (See Figure 5.38). The F-measures obtained using the Naïve Bayesian classifier increase as more neighbor information is included, but all remain below 0.16. The F-measures obtained using the MultiBoostAB algorithm using the J48 classifier increase with the inclusion of neighbor information, with the highest F-measure obtained when information from each feature's nearest neighbors is included.

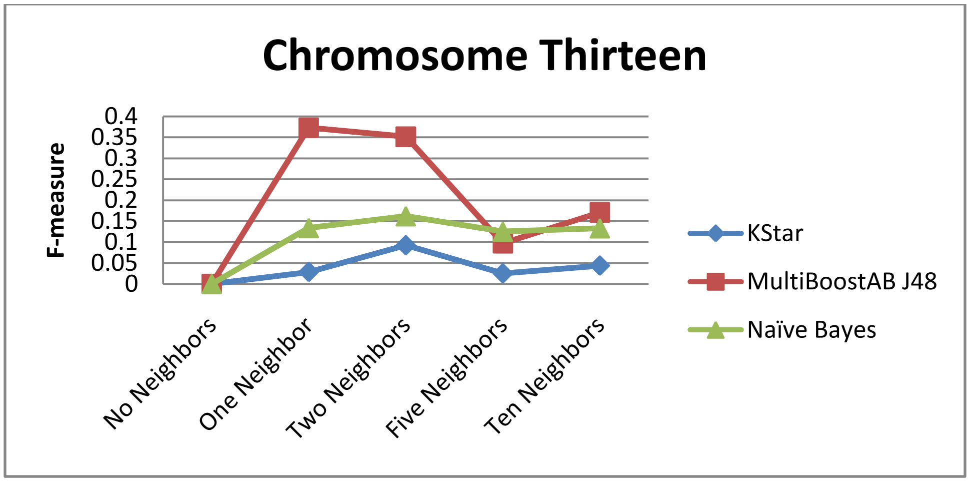


Figure 5.38. F-measure for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, the KStar classifier observes an increase in the F-measure from zero to one as more neighbor information is included (See Figure 5.39). The Naïve Bayesian classifier never achieves an F-measure above zero regardless of the amount of neighbor information included. The F-measures obtained using the MultiBoostAB algorithm using the J48 classifier increase when information from each feature's five-nearest or the ten-nearest neighbors is included, with the higher F-measure obtained by including information from the ten-nearest neighbors (equal to one).

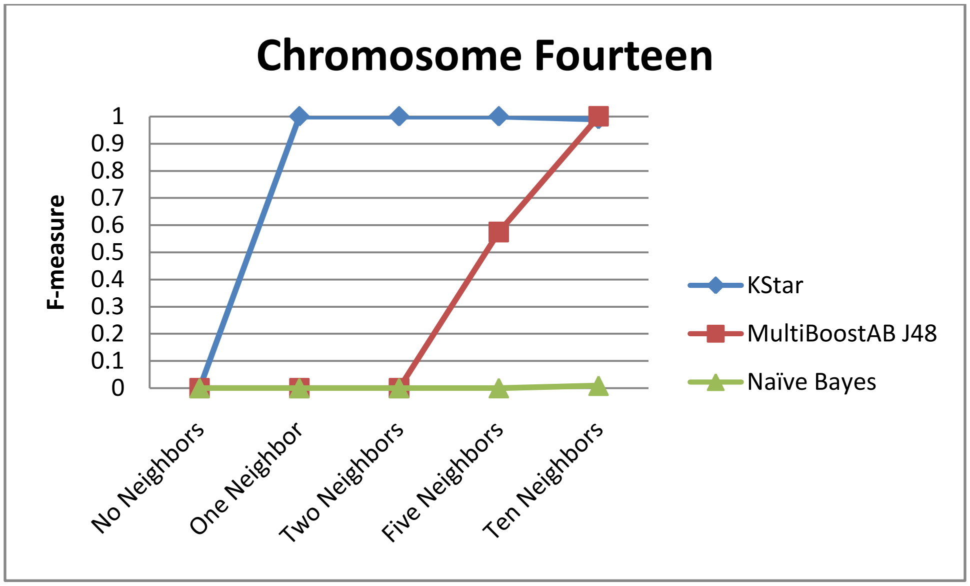


Figure 5.39. F-measure for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, the K-Star classifier observes an increase in the F-measure as neighbor information is included. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the KStar classifier. The F-measures obtained by the other classifiers do not appear to be as affected by the inclusion of neighbor information. The Naïve Bayesian classifier experiences small increases when information each feature's nearest or two-nearest neighbors is included (See Figure 5.40).

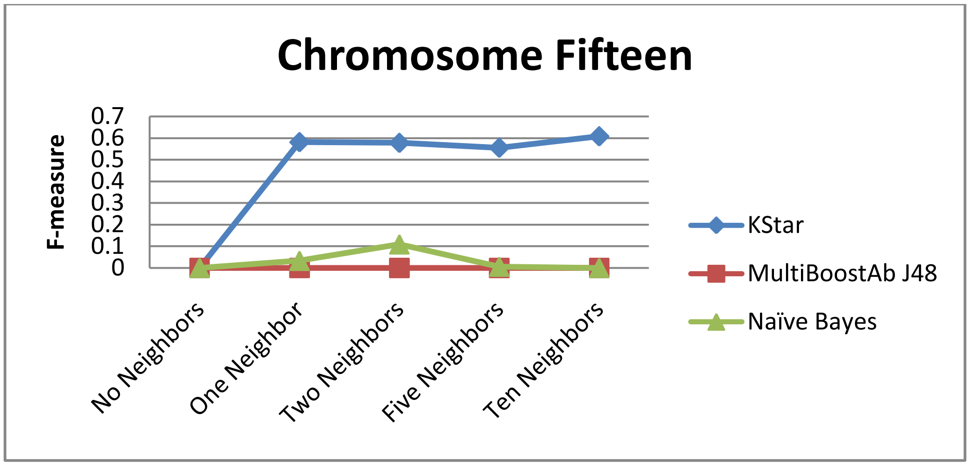


Figure 5.40. F-measure for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, the F-measures obtained for each classifier are very different (See Figure 5.41). Initially, as more neighbor information is included, the F-measure increases for the KStar classifier. The F-measure then drops when information from each feature's ten-nearest neighbors is included. For the MultiBoostAB algorithm, the F-measure increases when information from each feature's five-nearest neighbors is included then returns to zero when more neighbor information is included. The Naïve Bayesian classifier has the most consistent F-measures remaining zero or close to zero regardless of the inclusion of neighbor information.

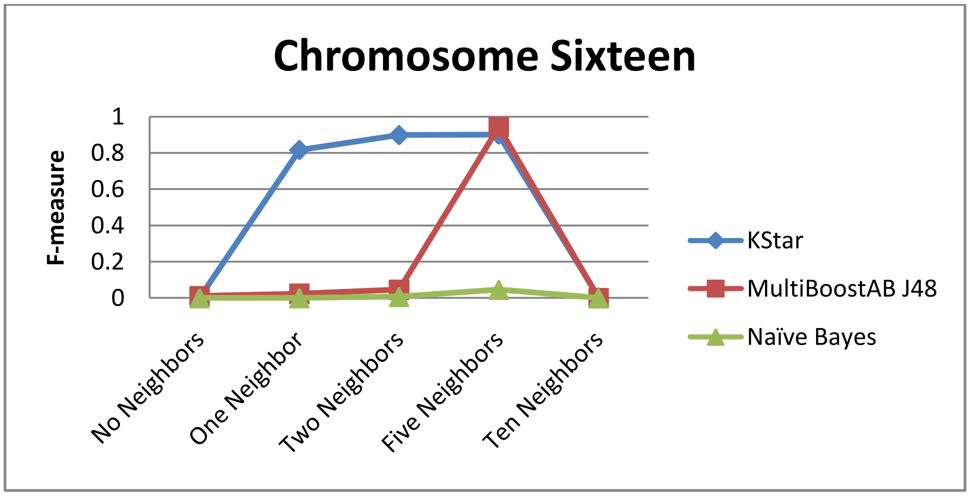


Figure 5.41. F-measure for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For a majority of the chromosome, the KStar classifier has the best accuracy, and the Naïve Bayesian classifier has the worst accuracy. Partitioning the classification process by chromosome does benefit the accuracy obtained by the classifiers.

5.1.2 Using Neighbor's Gene Ontology Term

A series of experiments was performed to determine if given the properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's Gene Ontology term, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and network involvement information from KEGG for genomic features (features being: genes, ARS, etc) for training could classification algorithms correctly classify network involvement. This was also performed including information from the nearest, two-, five- and ten-nearest neighbors of each feature. This was also repeated on the individual chromosomes. The mitochondrial chromosome is excluded. Having only one known network on the mitochondrial chromosome, classifiers cannot classify unary classes.

The results of the experiments are based on averages of ten different runs of each dataset being randomized and then split for training and testing. The training sets were set to contain 66% of the instances randomly selected from each dataset.

5.1.2.1 Results for the Entire Genome

When using only a genomic feature's chromosome number, start position, stop position, strand, and network involvement without neighbor information, we see that the percentage of genomic features correctly classified to the correct network varies depending on the classification algorithm used (See Figure 5.42). When no neighbor information is included, less than 20% of the genomic features are classified to the correct network regardless of the classifier used. As more neighbor information is added, the KStar classifier and the MultiBoostAB algorithm using the J48 classifier increase their correctly classified percentage with the MultiBoostAB algorithm using the J48 classifier achieving the higher percentages. For both classifiers, the inclusion of neighbor information beyond each feature's two-nearest neighbors does not impact the percentage of correctly classified features. When the Naïve Bayesian classifier is used, the percentage of correctly classified genomic features drops as more neighbor information is included.

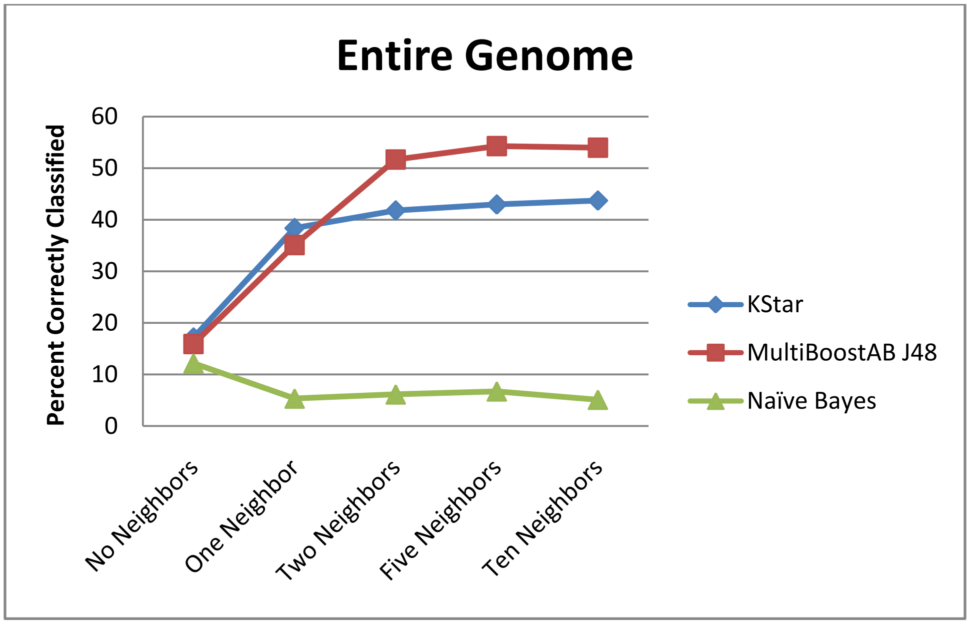


Figure 5.42. Percent of genomic features classified for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

When no neighbor information is included, all of the classifiers have poor agreement between the predicted and observed classification (See Figure 5.43). The KStar classifier and the MultiBoostAB algorithm using the J48 classifier achieve moderate agreements as more neighbor information is added with the MultiBoostAB algorithm using the J48 classifier achieving the higher Kappa statistic. The inclusion of neighbor information beyond each feature's two-nearest neighbors has little effect on the agreement between predicted and observed for the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. The Naïve Bayesian classifier never attains an agreement better than poor.

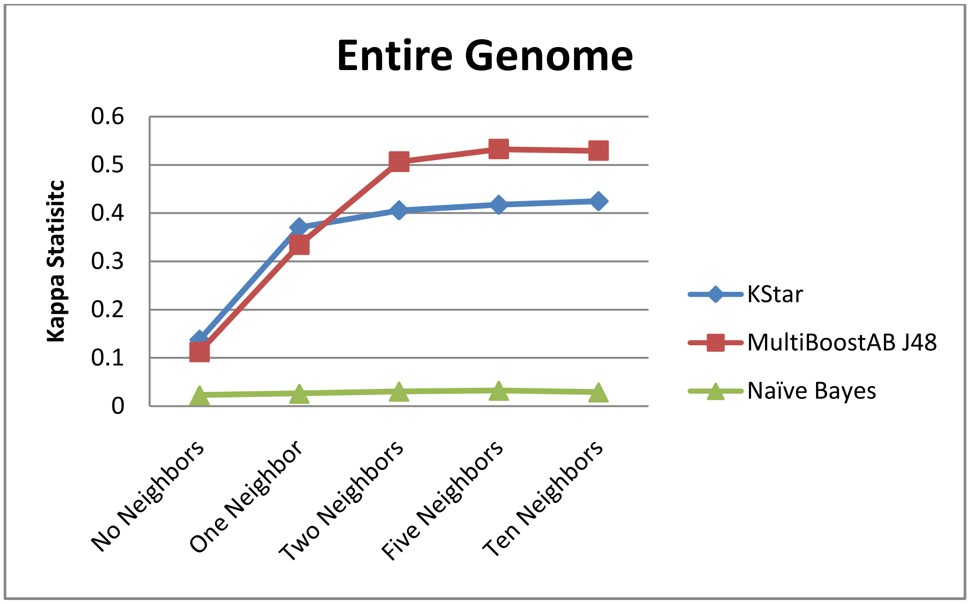


Figure 5.43. Kappa statistic for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The inclusion of neighbor information affects the precision of the classification process. For the MultiBoostAB algorithm using the J48 classifier, the precision increases with the addition of neighbor information. The inclusion of neighbor information beyond each feature's two-nearest neighbors has little effect on the precision obtained by the MultiBoostAB algorithm using the J48 classifier. For the KStar classifier, the precision increases as more neighbor information is included, but it then decreases with the inclusion of each feature's ten-nearest neighbors. The Naïve Bayesian classifier never obtains high precision scores, but it does increase and plateau upon the inclusion of information from each feature's two-nearest neighbors (See Figure 5.44).

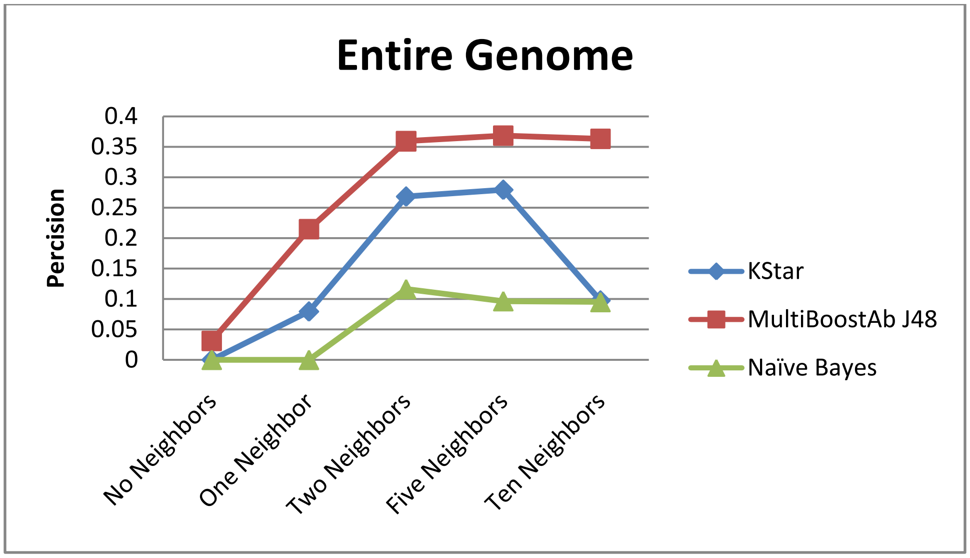


Figure 5.44. Precision for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The recall scores obtained by the MultiBoostAB algorithm using the J48 classifier improve with the inclusion of neighbor information. The inclusion of neighbor information beyond each feature's two-nearest neighbors has little effect on the recall obtained by the MultiBoostAB algorithm using the J48 classifier. The recall scores of the KStar classifier increases as more neighbor information is included then it decreases with the inclusion of each feature's ten-nearest neighbors. The recall scores obtained by the Naïve Bayes remain low regardless of the inclusion of neighbor information (See Figure 5.45).

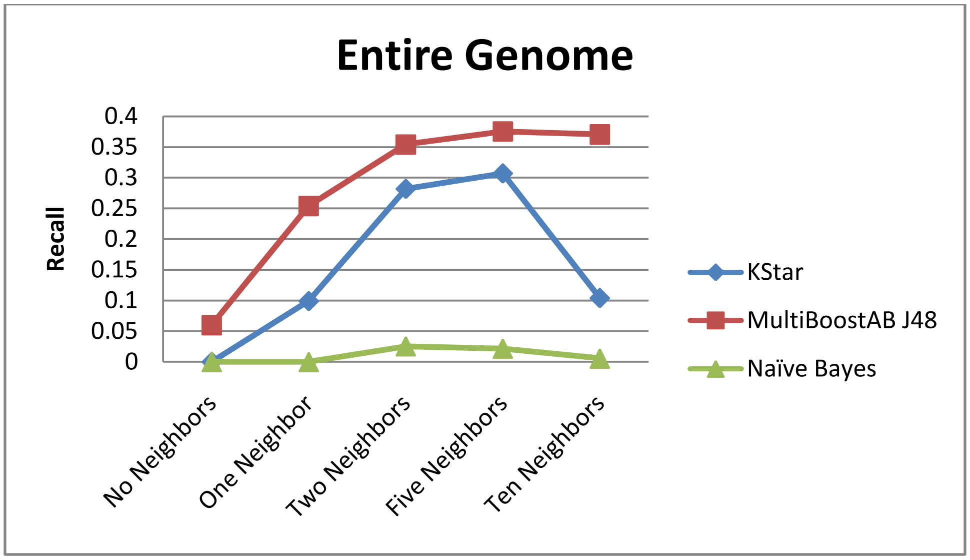


Figure 5.45. Recall for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

F-measures obtained by the different classifiers mimic their precision and recall scores (See Figure 5.46). The accuracy of the classification of a genomic feature increases as more neighbor information is included for MultiBoostAB algorithm using the J48 classifier, with the inclusion of neighbor information beyond each feature's two-nearest neighbors having little effect on the F-measures obtained. The accuracy of the KStar classifier increases as more neighbor information is included then it decreases with the inclusion of each feature's ten-nearest neighbors. The accuracy of the Naïve Bayesian classifier is not greatly affected by the inclusion of neighbor information.

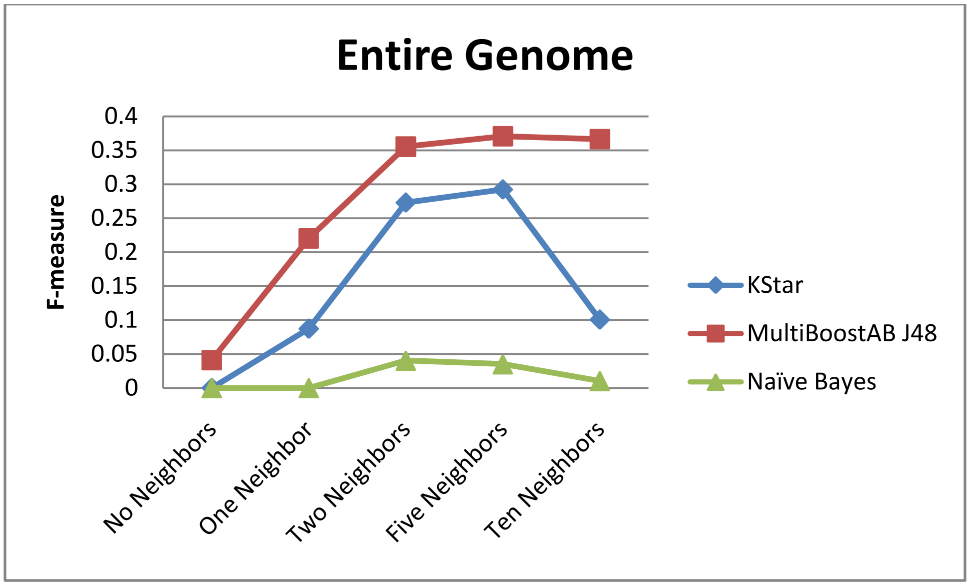


Figure 5.46. F-measure for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

When analyzing the area under the ROC curves, when no neighbor information is included, the MultiBoostAB algorithm using the J48 classifier is the only classifier that obtains an accuracy score that is not failing, but it is considered poor (See Figure 5.47). Upon the inclusion of neighbor information, the accuracy scores for both the KStar classifier and the MultiBoostAB algorithm using the J48 classifier improve to excellent. With the Naïve Bayesian classifier, the accuracy of the classification never improves above poor.

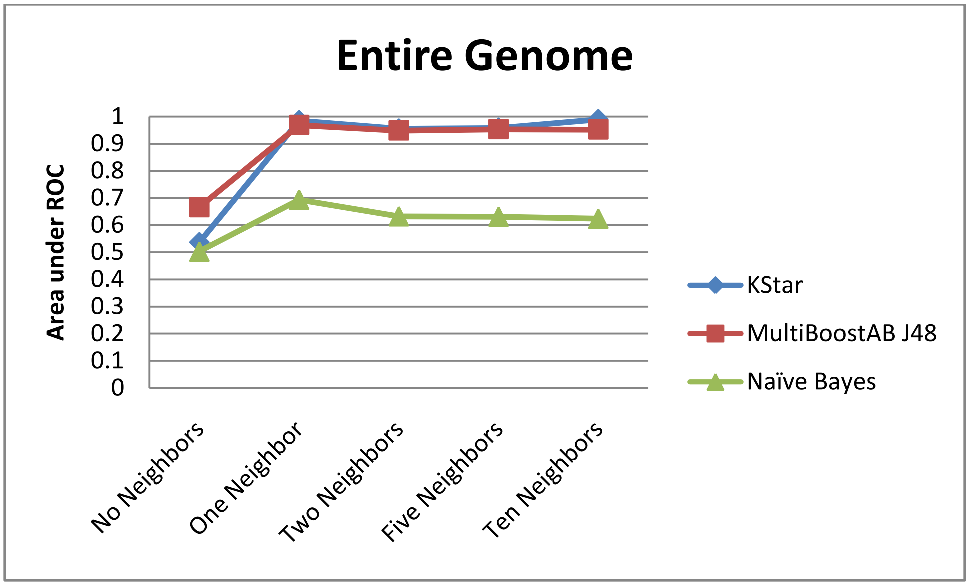


Figure 5.47. Area under ROC curve for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

In general, the MultiBoostAB algorithm using the J48 classifier performs the best, obtaining the higher values in the metrics used.

To see the effect on the accuracy of classification for each network, the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier for each network were analyzed. The table of the F-measures can be found in Appendix C. Most of the networks benefited from the addition of neighbor information (See Figures 5.48 - 5.50).

Three networks obtain F-measures when no information is included. These networks are the ribosome network, the polyunsaturated fatty acid biosynthesis network and the oxidative phosphorylation network. The F-measures are not above 0.5, so there is not a strong implication that feature location alone is an indicator for network involvement.

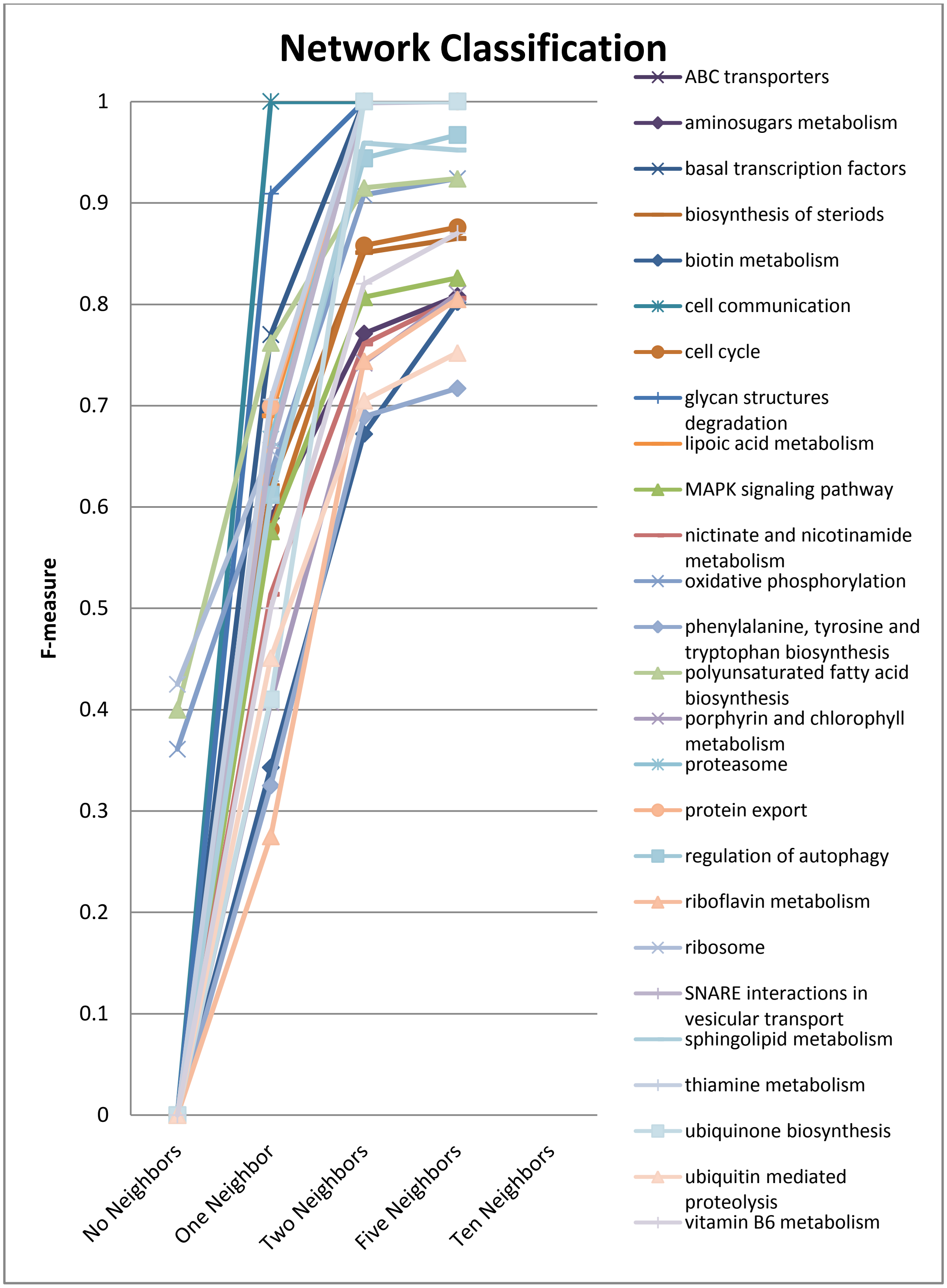


Figure 5.48. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual networks. Only networks that obtained an F-measure above 0.7 are shown.

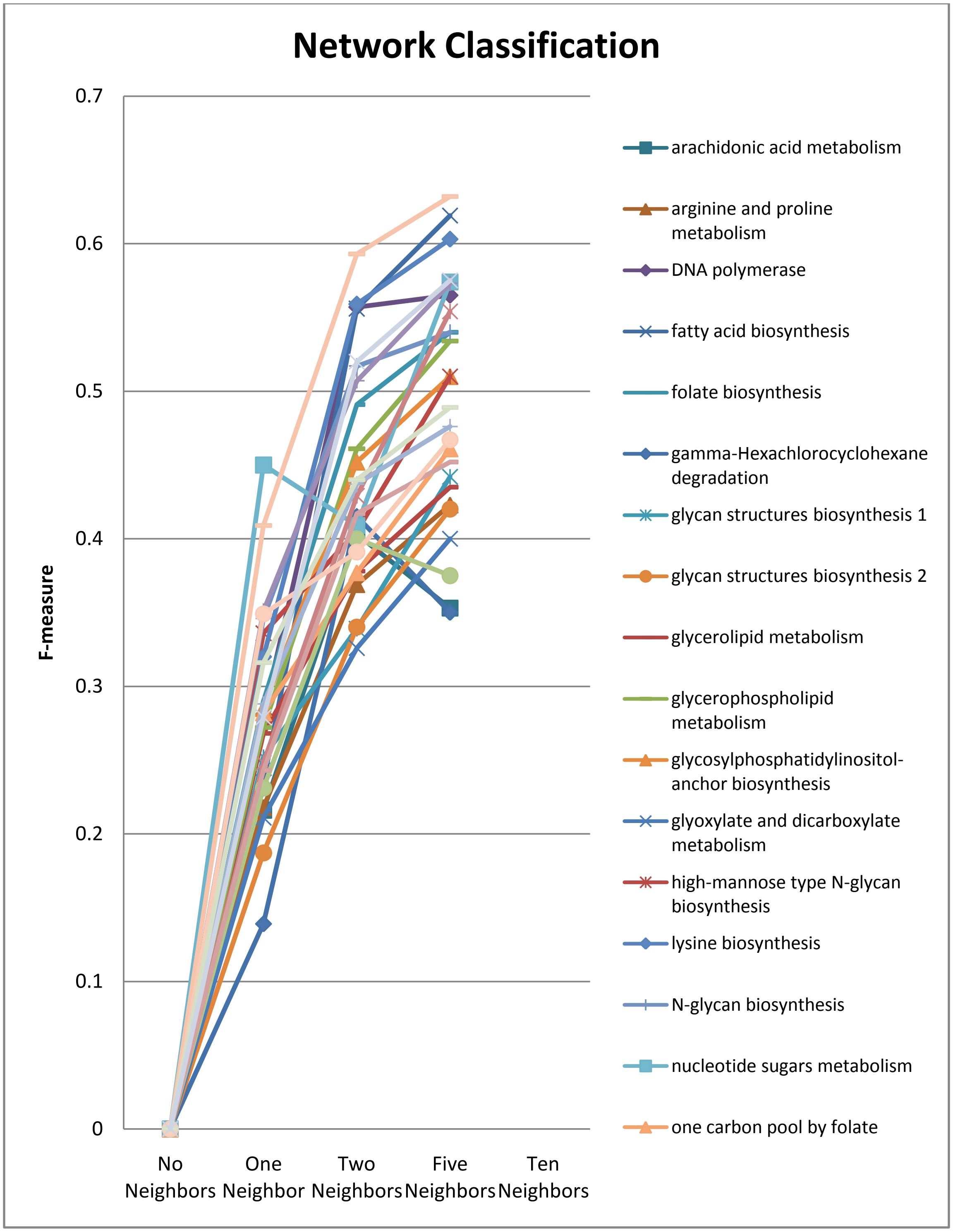


Figure 5.49. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual networks. Only networks that obtained an F-measure above 0.45 and below 0.7 are shown.

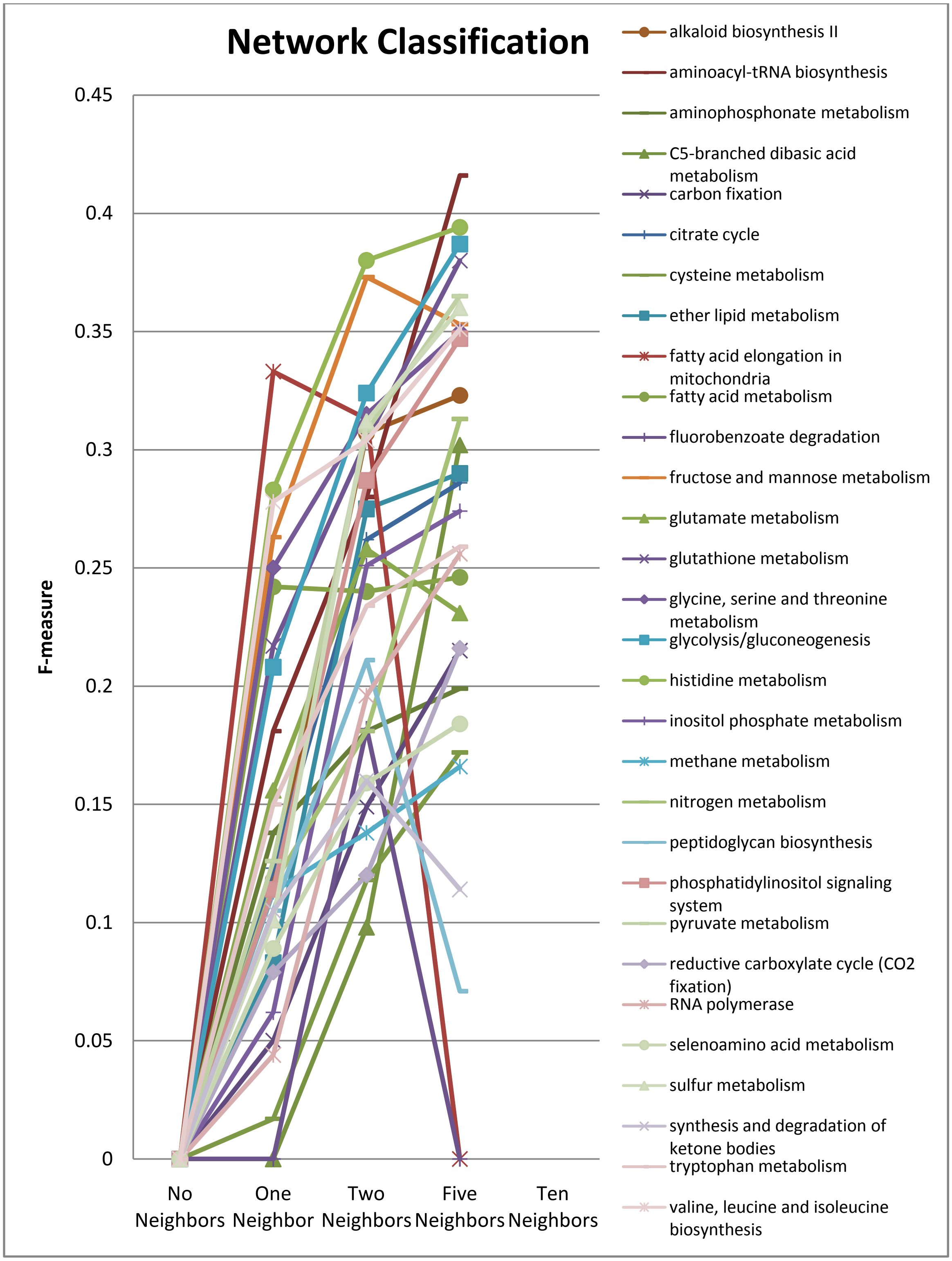


Figure 5.50. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual networks. Only networks that obtained an F-measure above 0.1 and below 0.45 are shown.

With the networks that obtained the lower accuracies, the F-measures fluctuate depending on the amount of neighbor information that is included.

5.1.2.2 Result for Individual Chromosomes

When we look at each chromosome individually, we see that the results of classification vary from chromosome to chromosome, from the number of neighbors included, and from the classification algorithm being used.

5.1.2.2.1 Percent Correctly Classified

For all chromosomes, the percent of genomic features correctly classified to the correct network differed depending on the number of neighbors included in the dataset and the classification algorithm used.

For chromosome one, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.51). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentage of correctly classified features in all instances. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features. And, for the Naïve Bayesian classifier, the inclusion of information beyond each feature's five-nearest neighbors has little effect on the percentage of classified features.

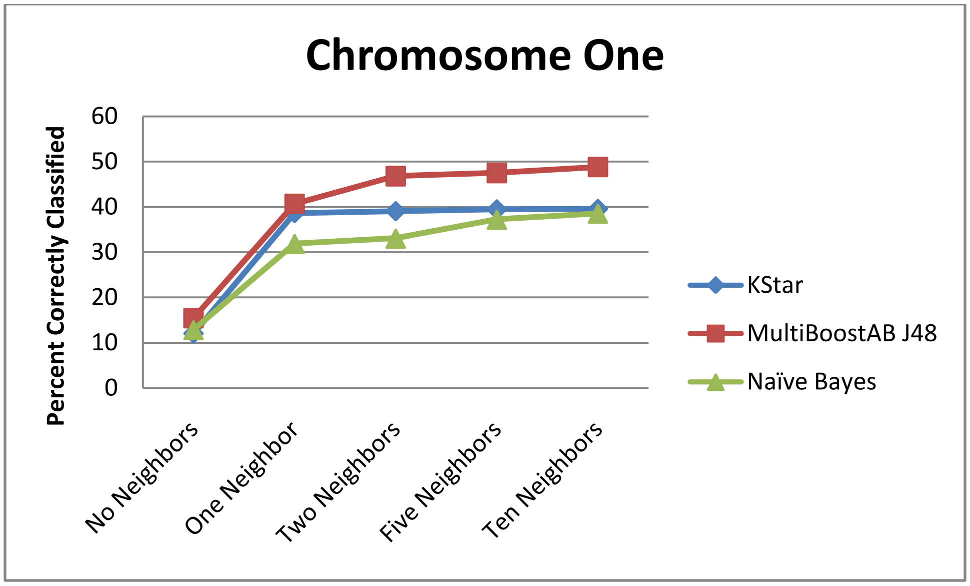


Figure 5.51. Percent of genomic features classified for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages (See Figure 5.52). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features. For the Naïve Bayesian classifier, the percentage of correctly classified features plateau after the inclusion of information from each feature's nearest neighbors; the percentage then increases upon the inclusion of information from each feature's ten-nearest neighbors.

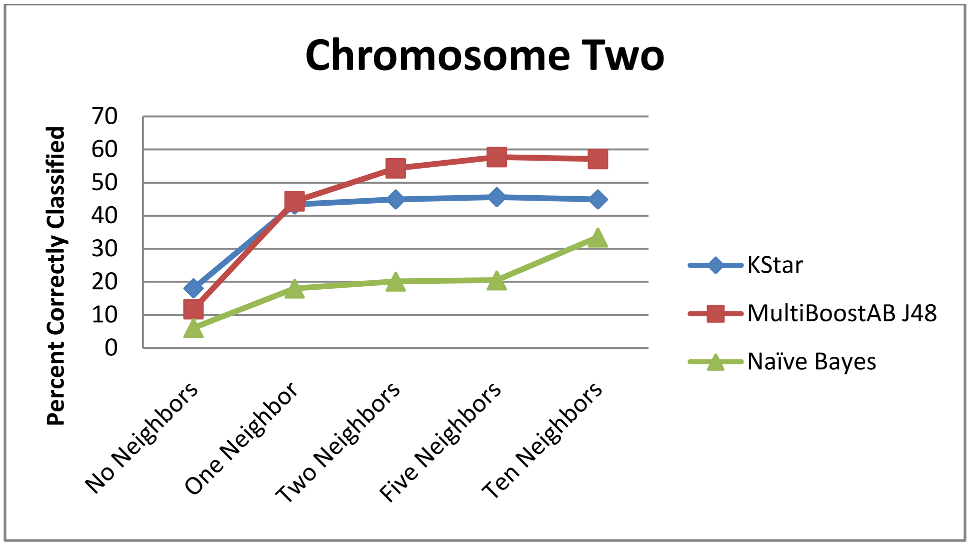


Figure 5.52. Percent of genomic features classified for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.53). The MultiBoostAB algorithm using the J48 classifier obtains the highest percentages of correctly classified features with inclusion of neighbor information followed by the Naïve Bayesian classifier and the KStar classifier respectively.

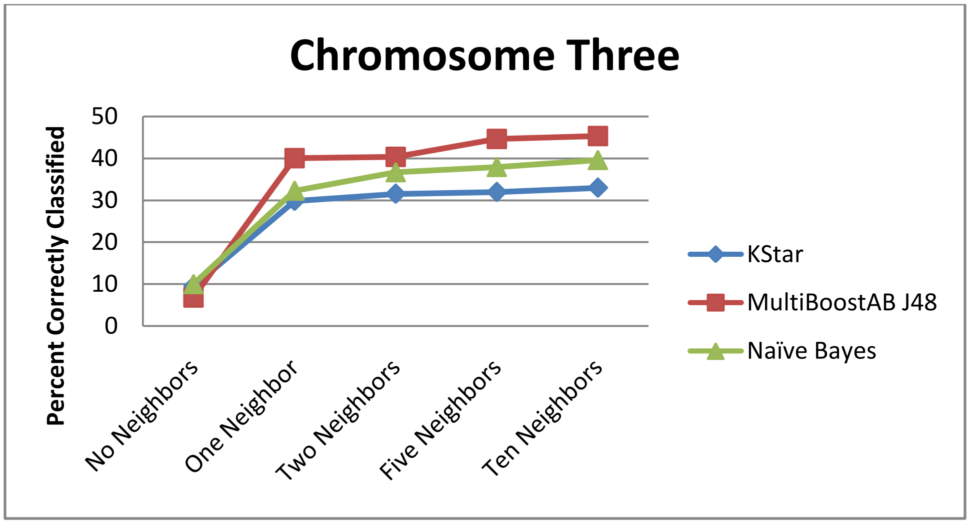


Figure 5.53. Percent of genomic features classified for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included, with the MultiBoostAB algorithm using the J48 classifier obtaining the higher percentage (See Figure 5.54). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentages obtained. For the KStar classifier and the Naïve Bayesian classifier, inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentages they obtain.

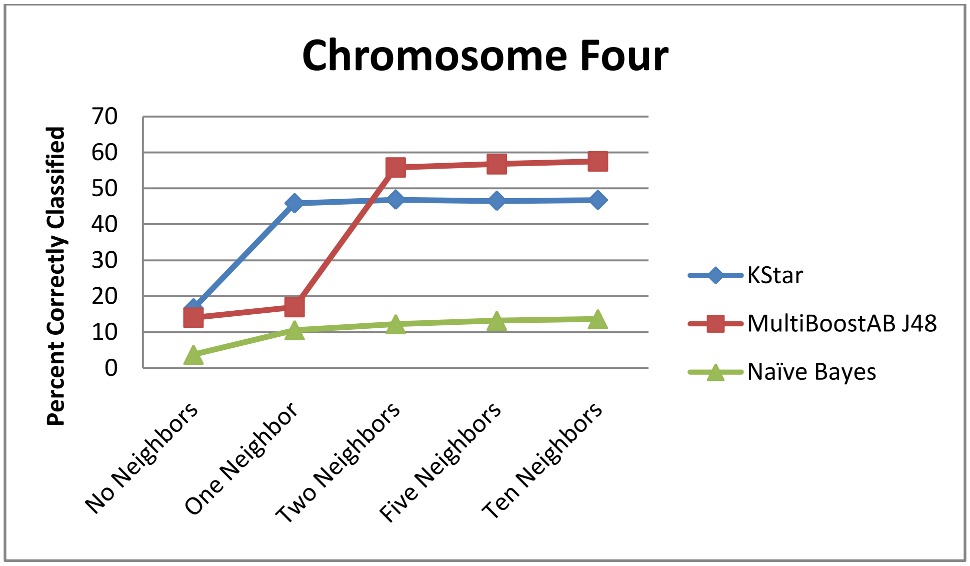


Figure 5.54. Percent of genomic features classified for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included with the MultiBoostAB algorithm using the J48 classifier obtaining the higher percentages (See Figure 5.55). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's five-nearest neighbors has little impact on the percentage of correctly classified features.

For the KStar classifier and the Naïve Bayesian classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features.

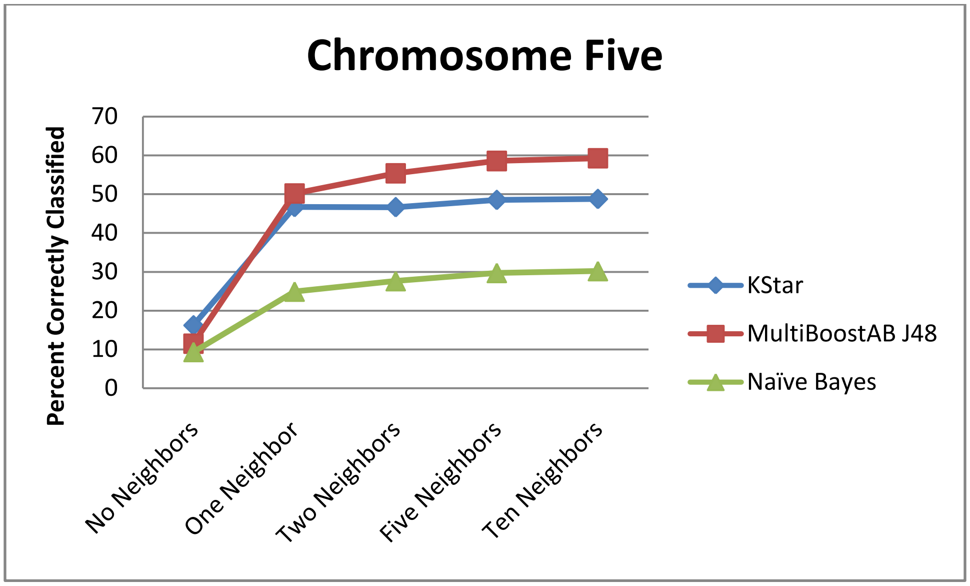


Figure 5.55. Percent of genomic features classified for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, similar to other chromosomes, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included with the MultiBoostAB algorithm using the J48 classifier obtaining the higher percentages (See Figure 5.56). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features.

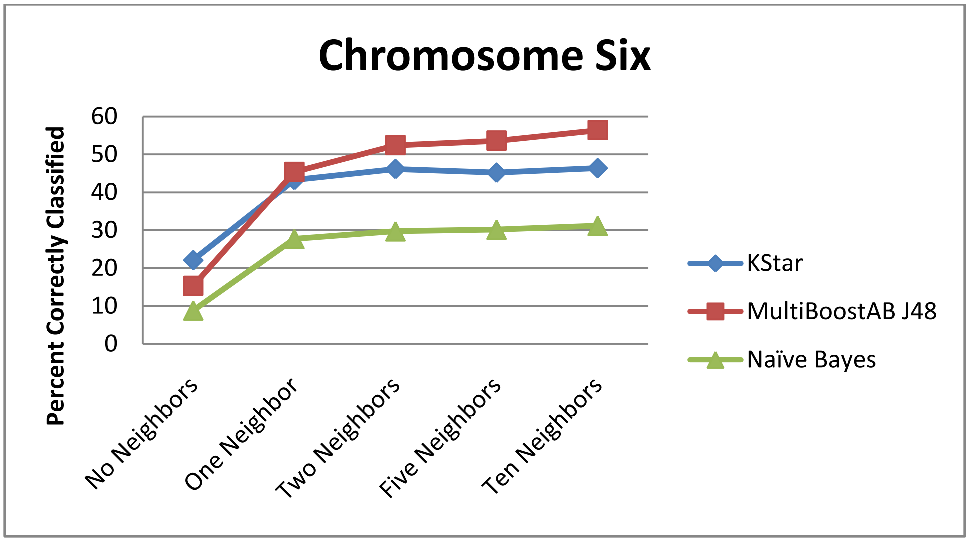


Figure 5.56. Percent of genomic features classified for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, similar to other chromosomes, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included with the MultiBoostAB algorithm using the J48 classifier obtaining the higher percentages (See Figure 5.57). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features. The Naïve Bayesian classifier does not see a drastic improvement in the percentage of correctly classified features, and obtains the lower percentages.

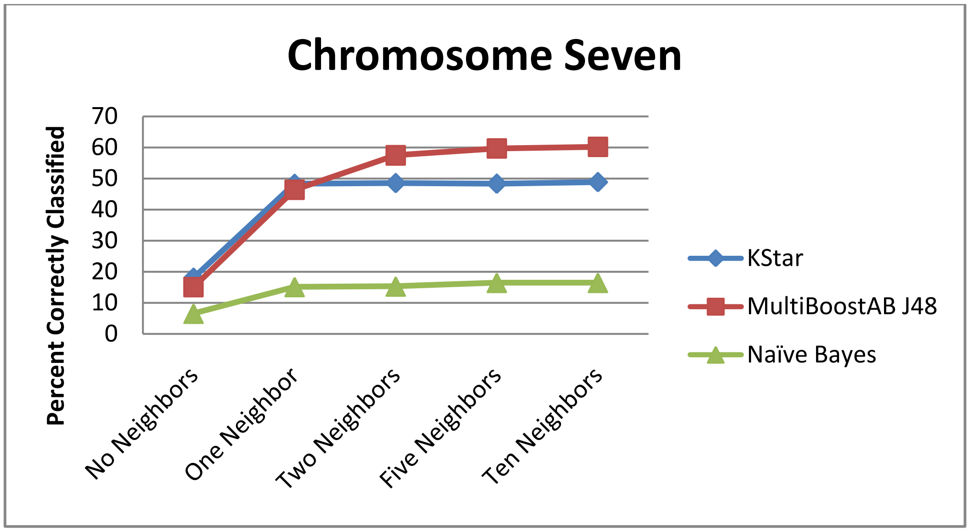


Figure 5.57. Percent of genomic features classified for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The patterns of the percentage of correctly classified features for chromosome eight are similar to those seen in chromosome seven (See Figure 5.58). All of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included, with the MultiBoostAB algorithm using the J48 classifier obtaining the higher percentages. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features. The Naïve Bayesian classifier does not see a drastic improvement in the percentage of correctly classified features, and obtains the lower percentages.

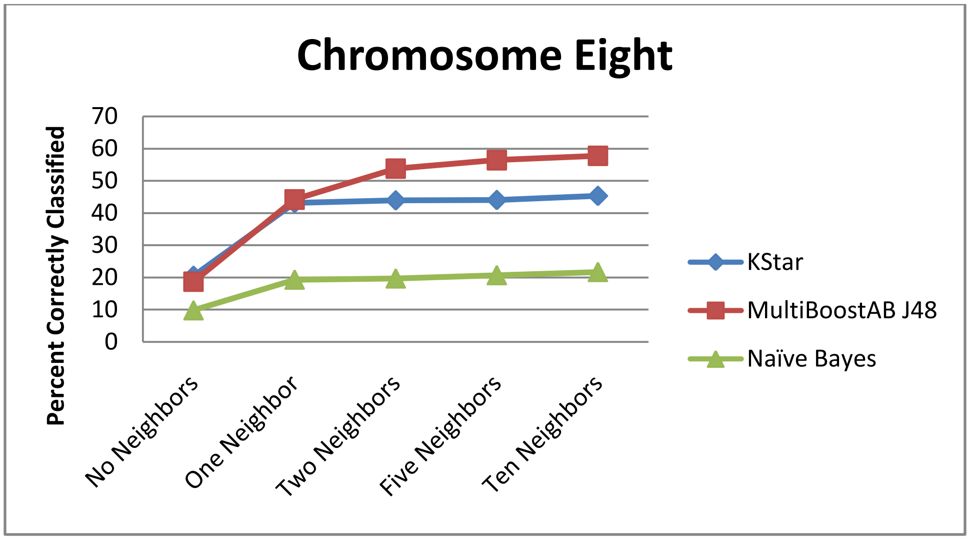


Figure 5.58. Percent of genomic features classified for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages (See Figure 5.59). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features. For the Naïve Bayesian classifier, the percentage of correctly classified features plateau after the inclusion of information from each feature's two-nearest neighbors.

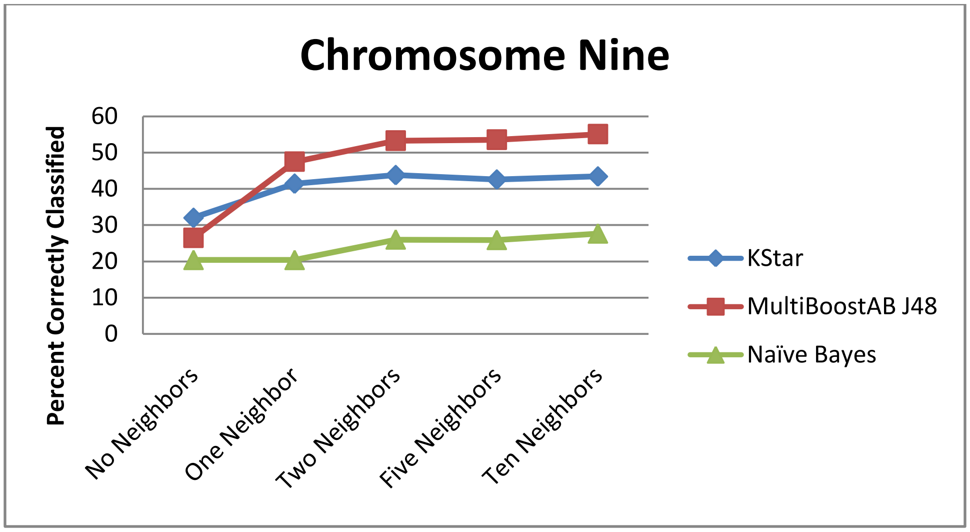


Figure 5.59. Percent of genomic features classified for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the inclusion of neighbor information increases the percentage of correctly classified features for each classifier (See Figure 5.60). As more neighbor information is added, the percentage of correctly classified features increases for the MultiBoostAB algorithm using the J48 classifier. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features. The Naïve Bayesian classifier does not see a drastic improvement in the percentage of correctly classified features, and obtains the lower percentages.

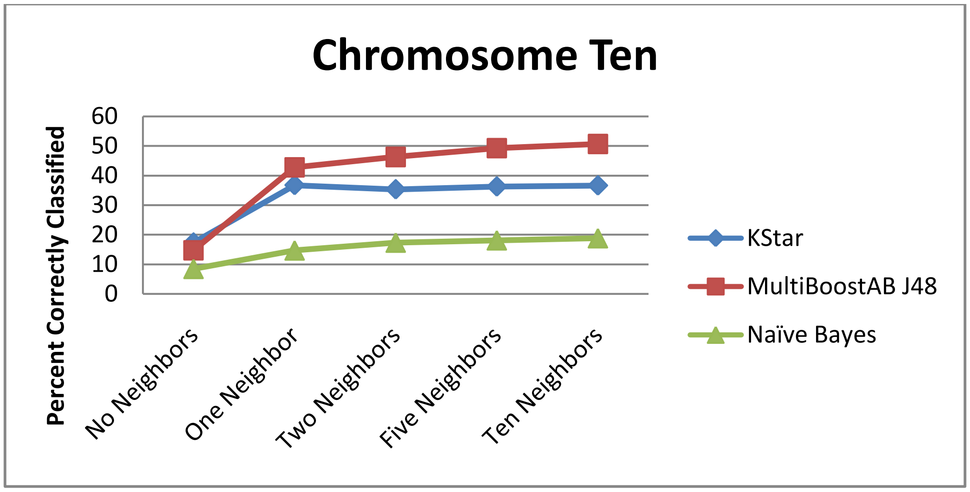


Figure 5.60. Percent of genomic features classified for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

All of the classifiers experience increases in the percentage of correctly classified features when neighbor information is included for chromosome eleven (See Figure 5.61). For all classifiers, the inclusion of information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features obtained. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentage of correctly classified features, and the Naïve Bayesian classifier obtains the lower.

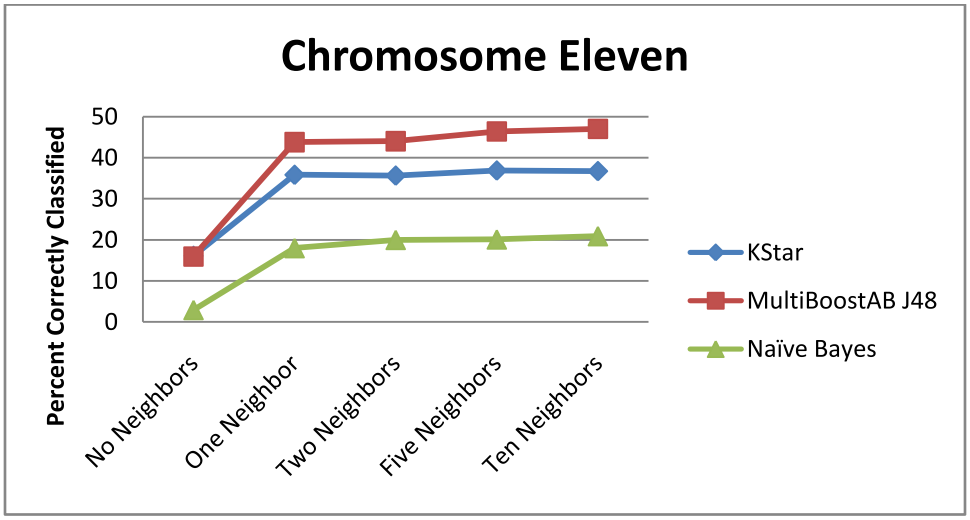


Figure 5.61. Percent of genomic features classified for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, following trends established in other chromosomes, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.62). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's five-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of correctly classified features. The Naïve Bayesian classifier does not see a drastic improvement in the percentage of correctly classified features, and obtains the lower percentages.

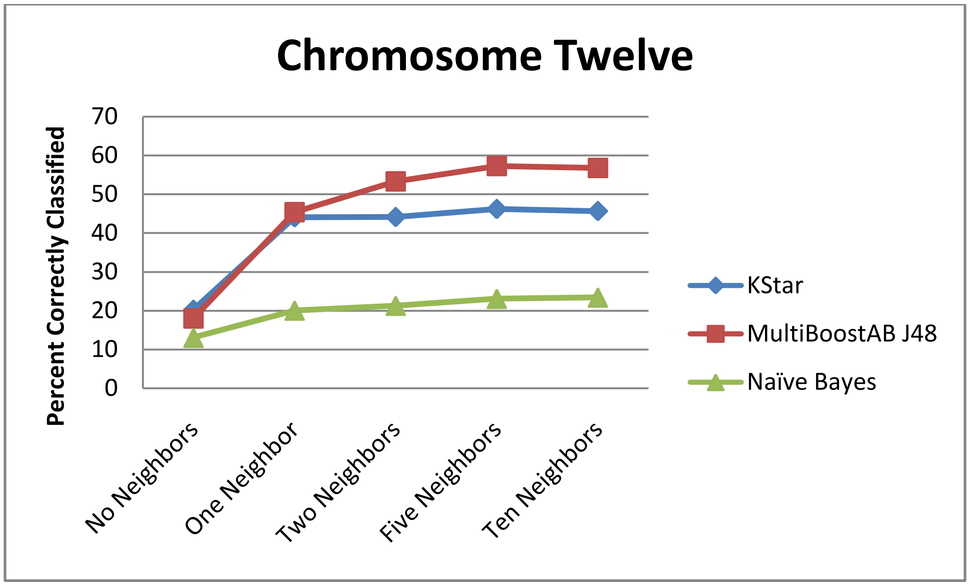


Figure 5.62. Percent of genomic features classified for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.63). For all classifiers, the inclusion of information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features obtained. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentage of correctly classified features, and the Naïve Bayesian classifier obtains the lower.

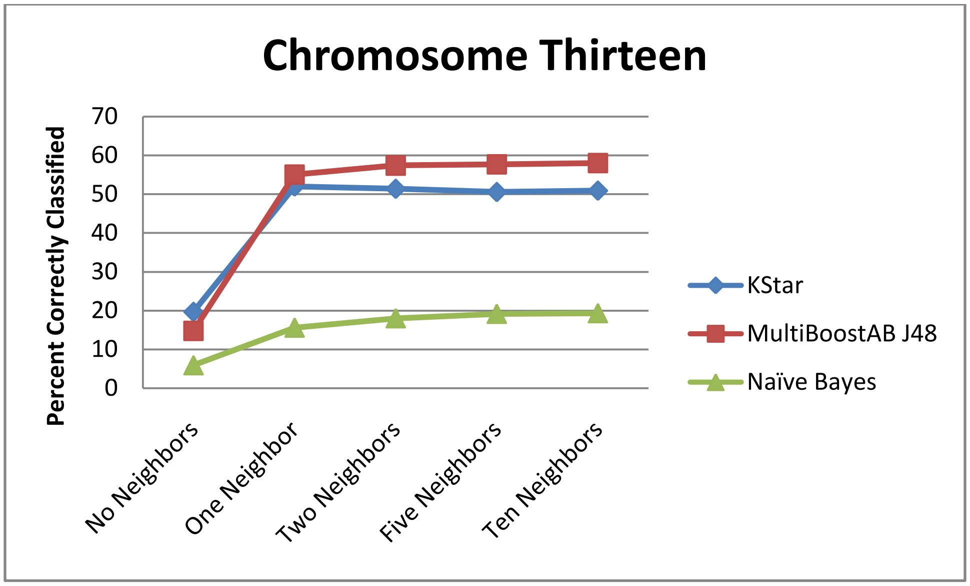


Figure 5.63. Percent of genomic features classified for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, the KStar classifier and the Naïve Bayesian classifier observe an increase in the percentage of correctly classified features upon the inclusion of information from each feature's nearest neighbor, then the percentages level off (See Figure 5.64). For the MultiBoostAB algorithm using the J48 classifier, an increase is not observed until information from each feature's two-or-more nearest neighbors is included, then it achieves the higher percentages of correctly classified features.

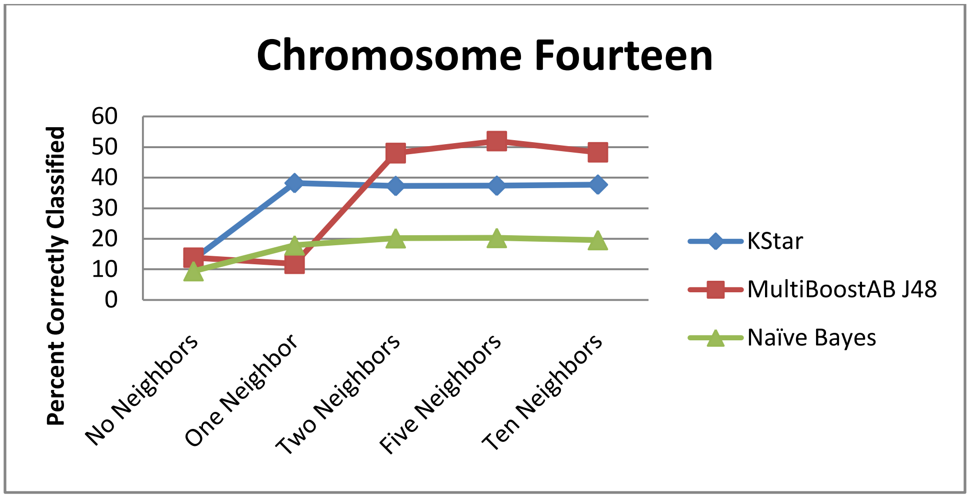


Figure 5.64. Percent of genomic features classified for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Similar to chromosome fourteen, the KStar classifier and the Naïve Bayesian classifier observe an increase in the percentage of correctly classified features upon the inclusion of information from each feature's nearest neighbor, then the percentages level off for chromosome fifteen (See Figure 5.65). For the MultiBoostAB algorithm using the J48 classifier, an increase is not observed until information from each feature's two-or-more nearest neighbors is included, then it achieves the higher percentages of correctly classified features.

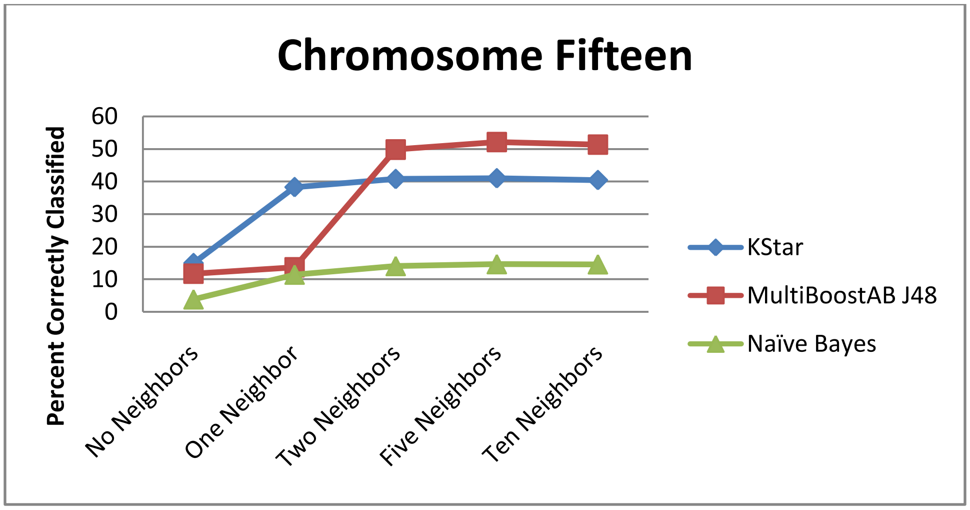


Figure 5.65. Percent of genomic features classified for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.66). Similar to other chromosomes, for the MultiBoostAB algorithm using the J48 classifier, the inclusion of information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of information beyond each feature's nearest neighbors has little effect on the percentage of classified features. The Naïve Bayesian classifier does not see a drastic improvement in the percentage of correctly classified features, and obtains the lower percentages.

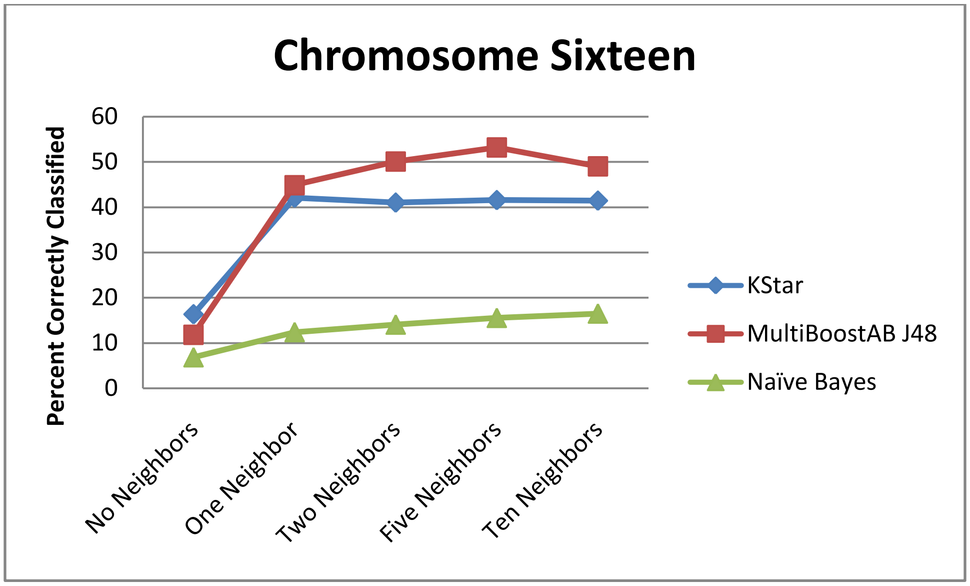


Figure 5.66. Percent of genomic features classified for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

After analyzing all the chromosomes, all the classifiers benefitted from the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier performed better than the other classifiers, with the inclusion of information beyond each feature's two-nearest neighbors having little additional benefit to the process. The partitioning of the classification process by chromosome did not affect it. Each chromosome obtained a percentage of correctly classified features that was similar to the percentage obtained using the entire genome.

5.1.2.2.2 F-measures

To look at the accuracy of the classification process for each chromosome, the F-measures obtained for each chromosome can be analyzed.

For chromosome one, the F-measures are low. The higher F-measures are obtained with the MultiBoostAB algorithm using the J48 classifier, and the accuracy increases with the addition of more neighbor information. The KStar classifier does not obtain F-measures above 0.1. The F-measures plateau for the KStar classifier after the inclusion of information from each feature's two-nearest neighbors. The Naïve Bayesian classifier never achieves an F-measure above zero (See Figure 5.67).

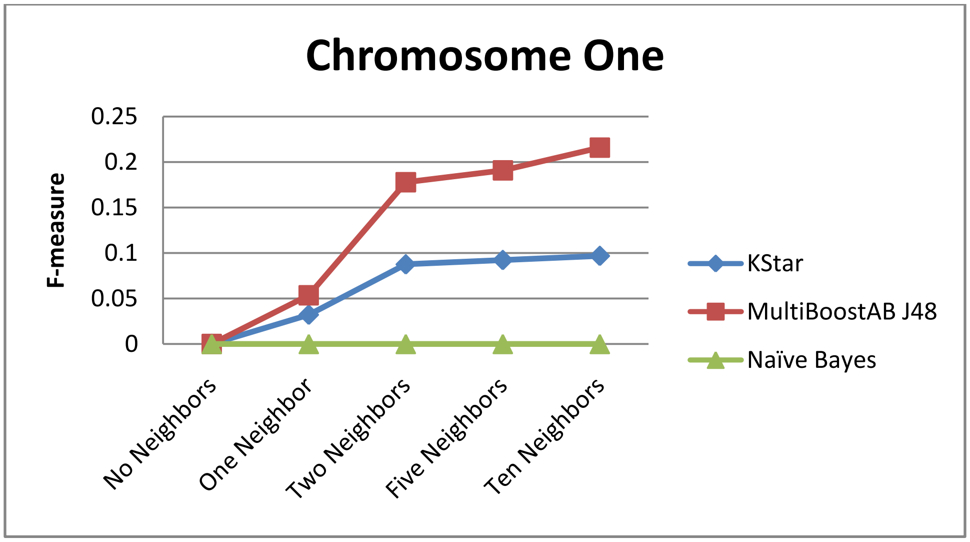


Figure 5.67. F-measure for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, the inclusion of neighbor information has an effect on all the classifiers. For the MultiBoostAB algorithm using the J48 classifier and the KStar classifier, this effect is seen upon the addition of information from each feature's nearest neighbors. At this point for the KStar classifier, the F-measures plateau. For the MultiBoostAB algorithm using the J48 classifier, the F-measures do not plateau until the addition of information from each feature's five-nearest neighbors. (See Figure 5.68). For the Naïve Bayesian classifier, an increase in the F-measure is not observed until information from each feature's ten-nearest neighbors is included.

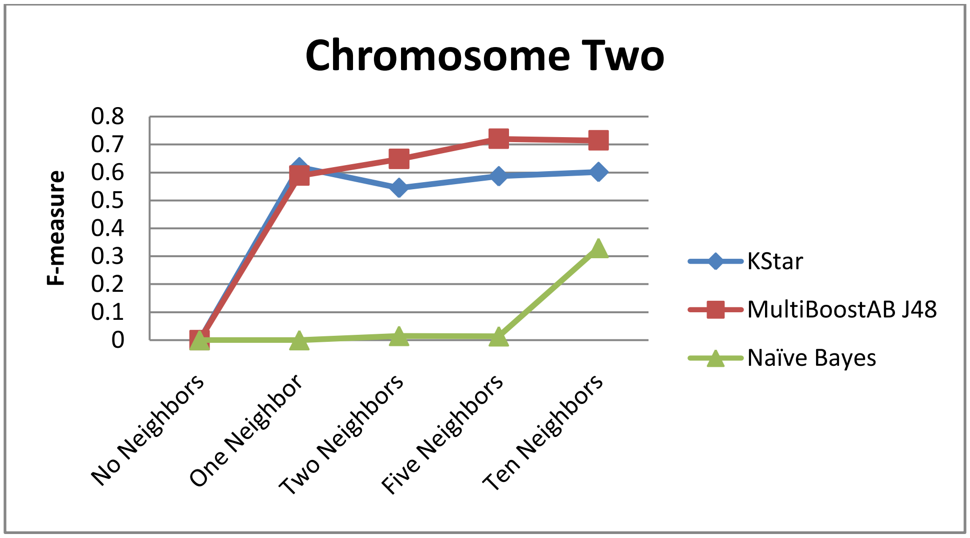


Figure 5.68. F-measure for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, like chromosome one, the F-measures are low. The higher F-measures are obtained with the MultiBoostAB algorithm using the J48 classifier, and the accuracy is affected by the amount of neighbor information included. The F-measures level off after the inclusion of information from each feature's five-nearest neighbors. The KStar classifier does not obtain F-measures above 0.1. The inclusion of information beyond each feature's nearest neighbors has little impact on the F-measures obtained by the KStar classifier. The Naïve Bayesian classifier never achieves an F-measure above zero (See Figure 5.69).

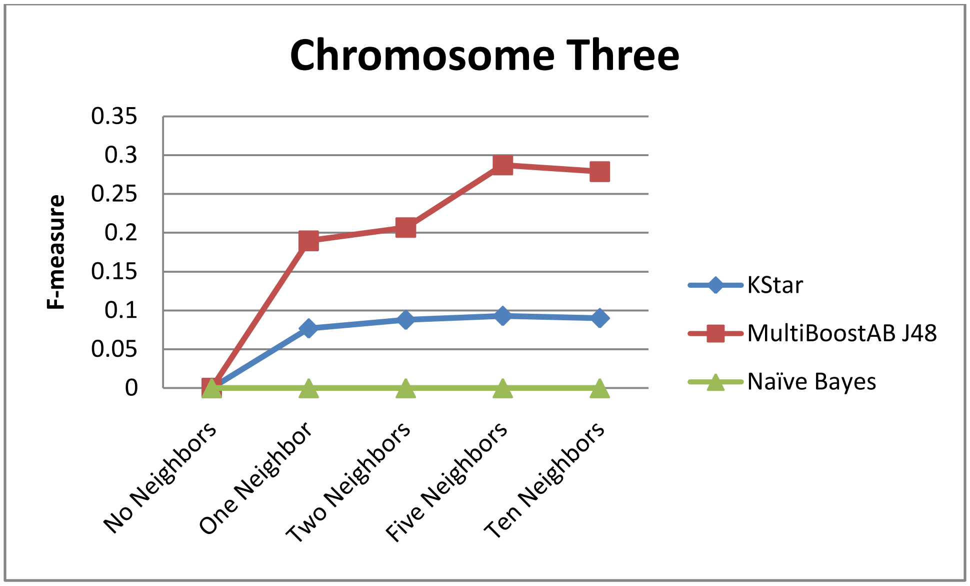


Figure 5.69. F-measure for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, after information from each feature's two-nearest neighbors is included, the MultiBoostAB algorithm using the J48 classifier obtains higher F-measures, with its highest F-measure obtained when information from each feature's two-nearest neighbors is included. The KStar classifier also obtains its highest F-measure when information from each feature's two-nearest neighbors is included. The Naïve Bayesian classifier never obtains an F-measure above 0.1 (See Figure 5.70).

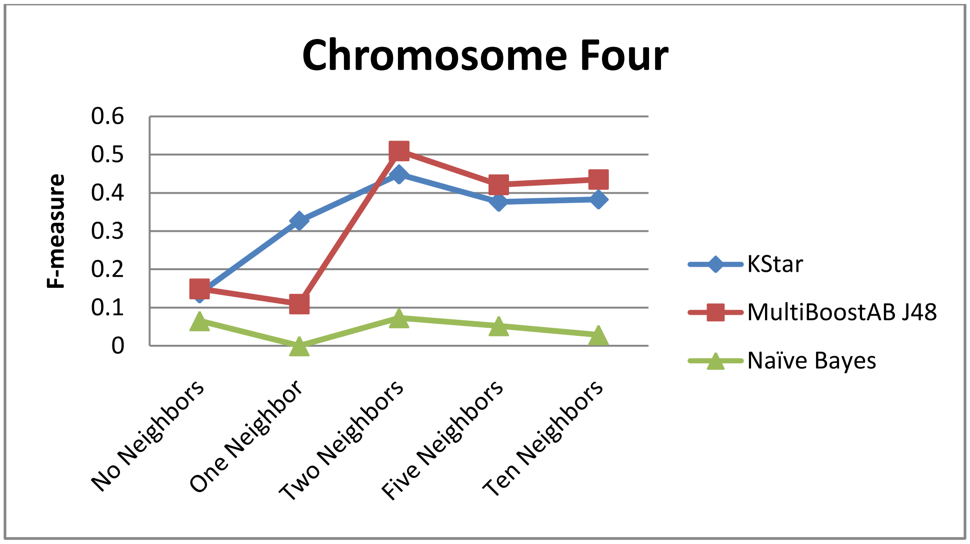


Figure 5.70. F-measure for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, all of the classifiers obtain drastic increases in their classification accuracy with the inclusion of neighbor information (Figure 5.71). The F-measures go from zero to one upon the inclusion of neighbor information for the KStar classifier and MultiBoostAB algorithm using the J48 classifier. After the inclusion of information from each feature's two-nearest neighbors, the Naïve Bayesian classifier obtains F-measures equal to one.

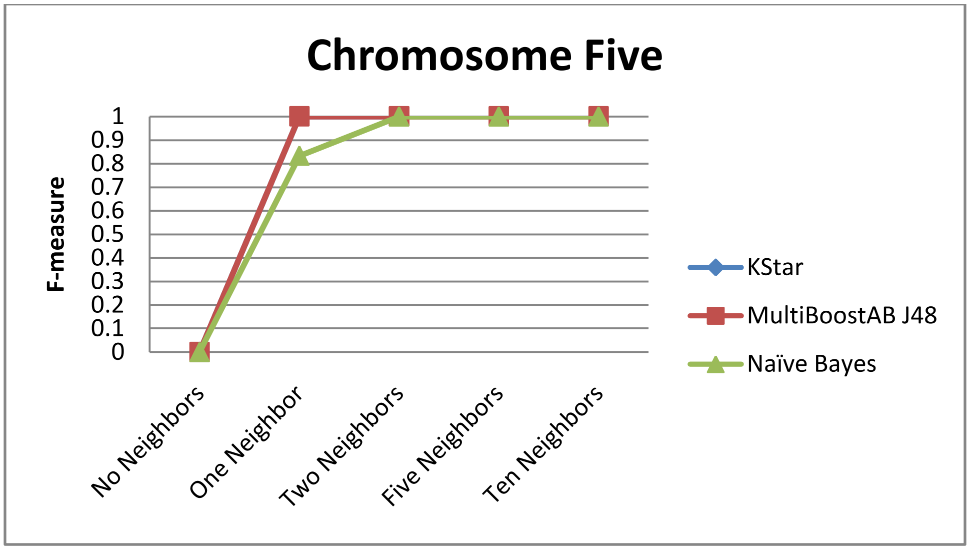


Figure 5.71. F-measure for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Upon the addition of any neighbor information, all of the classifiers improve their F-measures from zero to one for chromosome six (See Figure 5.72.)

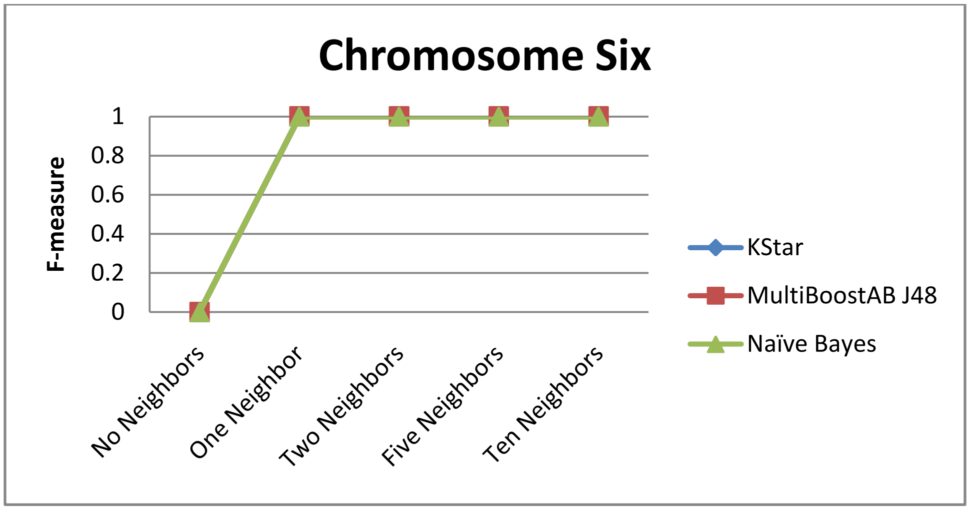


Figure 5.72. F-measure for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, all the F-measures are low. The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures, but these values do not exceed 0.16 (See Figure 5.73). The KStar classifier never obtains F-measures above 0.04, and the F-measures remain zero for the Naïve Bayesian classifier.

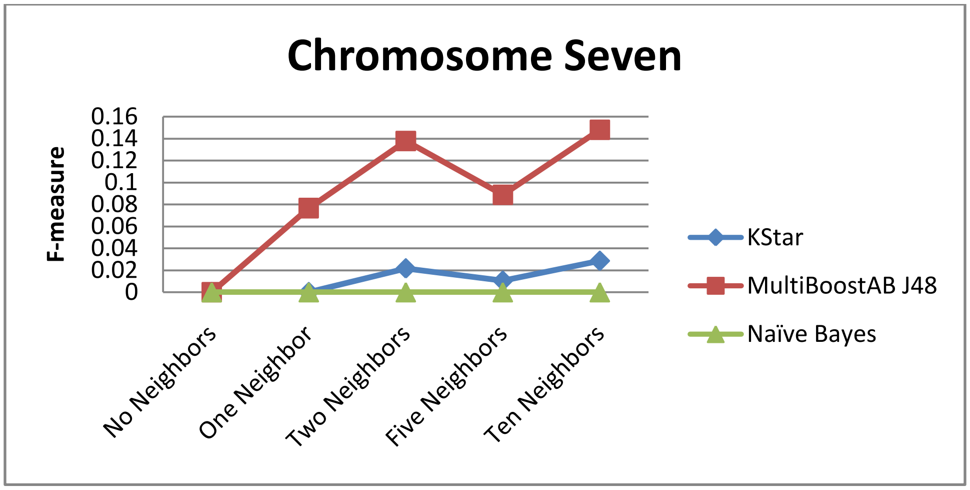


Figure 5.73. F-measure for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. The KStar classifier obtains F-measures of one after the inclusion of information from each feature's nearest neighbors. This happens for the MultiBoostAB algorithm using the J48 classifier after the inclusion of information from each feature's two-nearest neighbors. The inclusion of neighbor information decreases the accuracy of the classification process for the Naïve Bayesian classifier (See Figure 5.74).

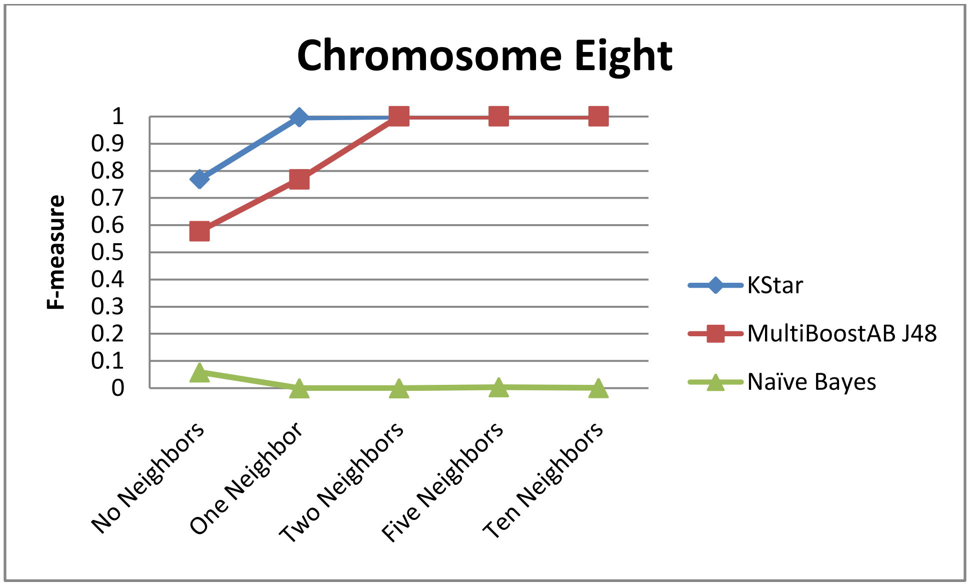


Figure 5.74. F-measure for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, the inclusion of neighbor information improves the F-measures obtained by all the classifiers. The KStar classifier obtains F-measures of one after the inclusion of information from each feature's nearest neighbors. This happens for the MultiBoostAB algorithm using the J48 classifier after the inclusion of information from each feature's two-nearest neighbors. The improvement is not as drastic for the Naïve Bayesian classifier. Its F-measures level off below 0.3 after the inclusion of information from each feature's two-nearest neighbors (See Figure 5.75).

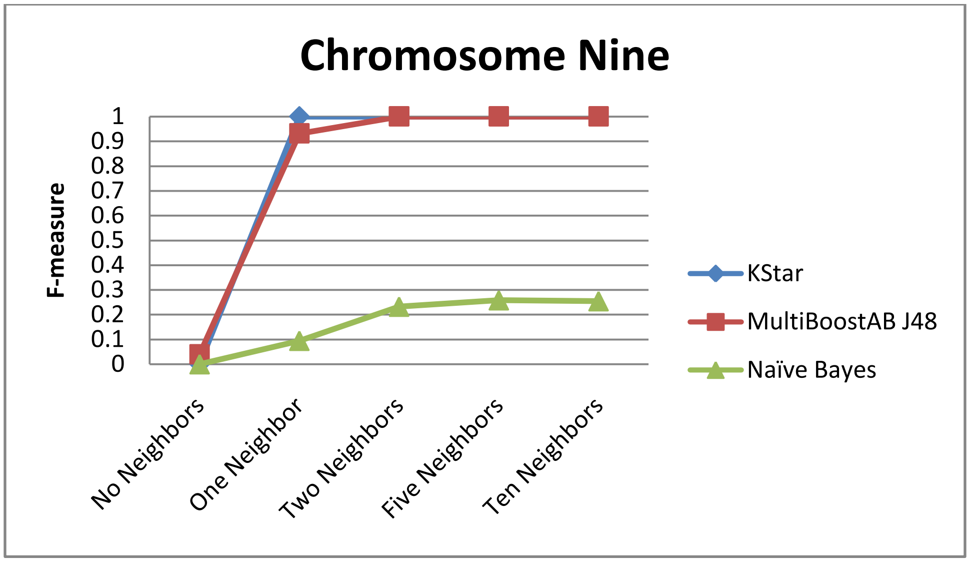


Figure 5.75. F-measure for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier, with the higher percentages obtained by the MultiBoostAB algorithm using the J48 classifier. For those classifiers, the inclusion of information from each feature's nearest neighbors has little effect on the F-measures obtained. For the Naïve Bayesian classifier, the inclusion of each feature's nearest neighbors improves its classification accuracy, but the addition of more than one neighbor lowers its accuracy (See Figure 5.76).

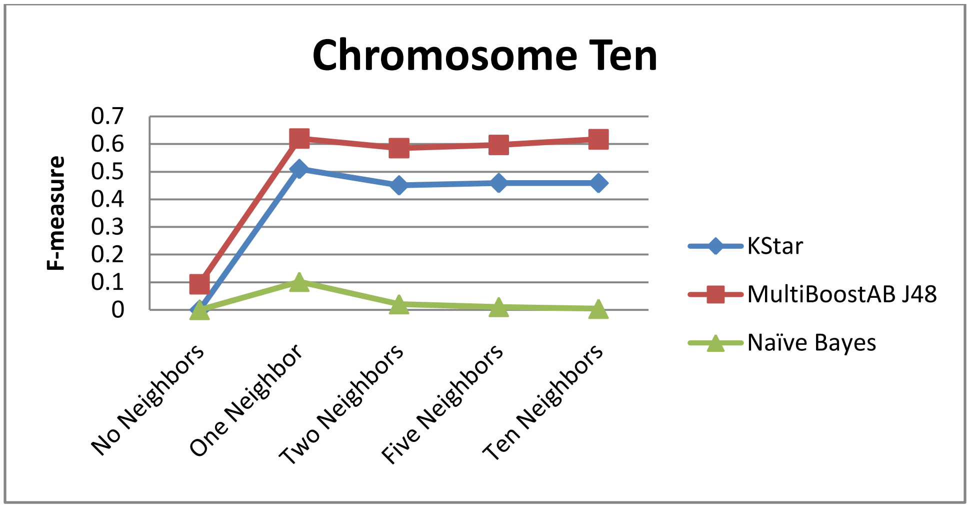


Figure 5.76. F-measure for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eleven, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier with the higher percentages obtained by the MultiBoostAB algorithm using the J48 classifier. For the Naïve Bayesian classifier, there is a slight increase in F-measure with the inclusion of neighbor information, but it returns to zero with the inclusion of information from each feature's ten-nearest neighbors (See Figure 5.77).

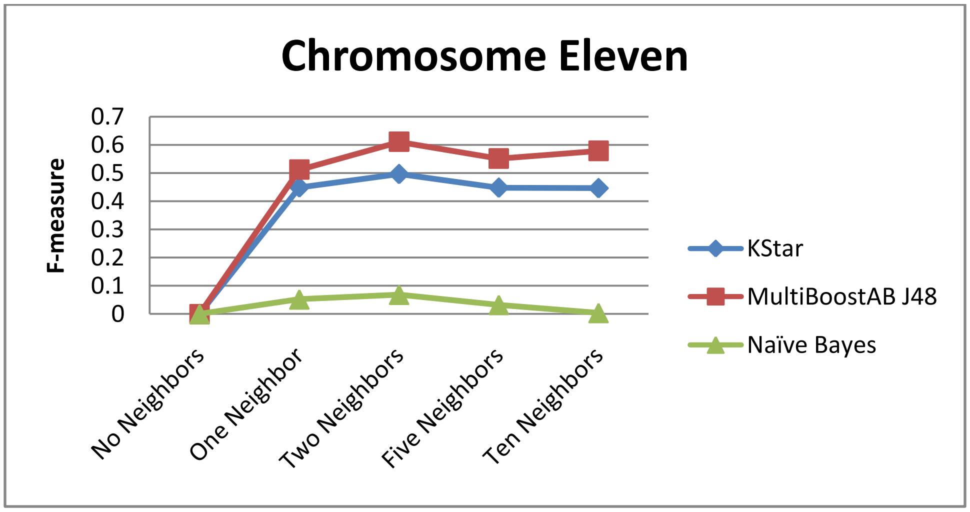


Figure 5.77. F-measure for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, similar to chromosome eight, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. The KStar classifier obtains F-measures of one after the inclusion of information from each feature's nearest neighbors. This happens for the MultiBoostAB algorithm using the J48 classifier after the inclusion of information from each feature's two-nearest neighbors. The inclusion of neighbor information decreases the accuracy of the classification process for the Naïve Bayesian classifier (See Figure 5.78).

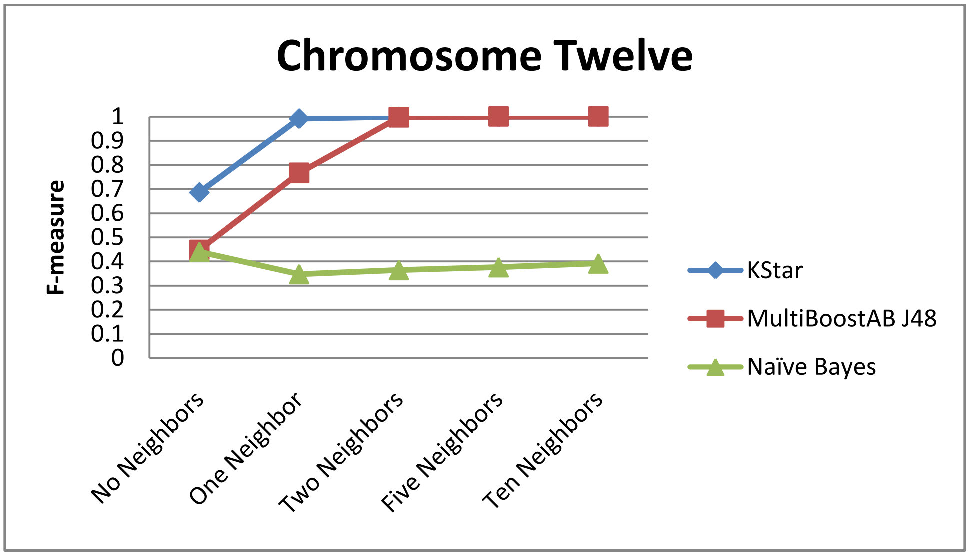


Figure 5.78. F-measure for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier experience an increase in F-measures with the inclusion of neighbor information, with the higher F-measures being obtained by the MultiBoostAB algorithm using the J48 classifier. The inclusion of information beyond each feature's nearest neighbors has little effect on the accuracy of the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier**.** The KStar classifier never obtains an F-measure above zero (See Figure 5.79).

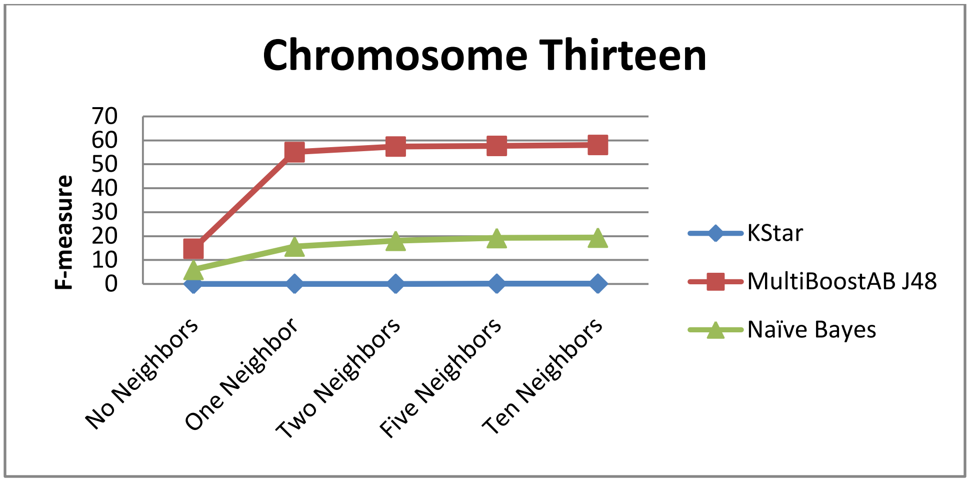


Figure 5.79. F-measure for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. The KStar classifier obtains F-measures of one after the inclusion of information from each feature's nearest neighbors. This happens for the MultiBoostAB algorithm using the J48 classifier after the inclusion of information from each feature's two-nearest neighbors. The accuracy of the Naïve Bayesian classifier does not improve above zero with the inclusion of neighbor information (See Figure 5.80).

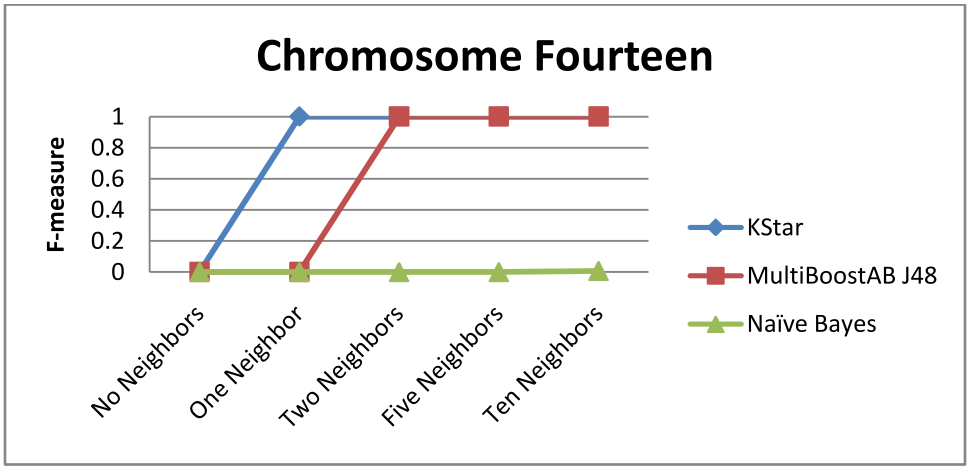


Figure 5.80. F-measure for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier, with the higher percentages obtained by the MultiBoostAB algorithm using the J48 classifier. For the KStar classifier, the inclusion of information from each feature's nearest neighbors has little effect on the F-measures obtained. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of information from each feature's two-nearest neighbors has little effect on the F-measures obtained. The accuracy of the Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See Figure 5.81).

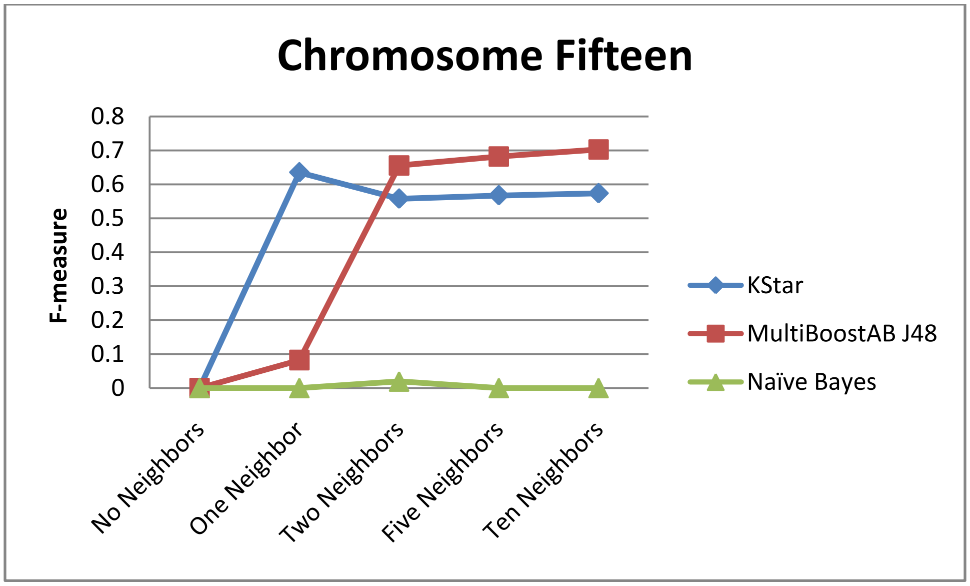


Figure 5.81. F-measure for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, the KStar classifier observes an improvement in its classification accuracy with the inclusion of neighbor information with the inclusion of information beyond each feature's nearest neighbors having little effect on the F-measures obtained. The inclusion of information from the each feature's nearest, two nearest, or five-nearest neighbors benefits the accuracy of the MultiBoostAB algorithm using the J48 classifier. Upon the inclusion of information from each feature's ten-nearest neighbors, the F-measure drops back to zero. The accuracy of the Naïve Bayesian classifier remains poor even with the inclusion of neighbor information (See Figure 5.82).

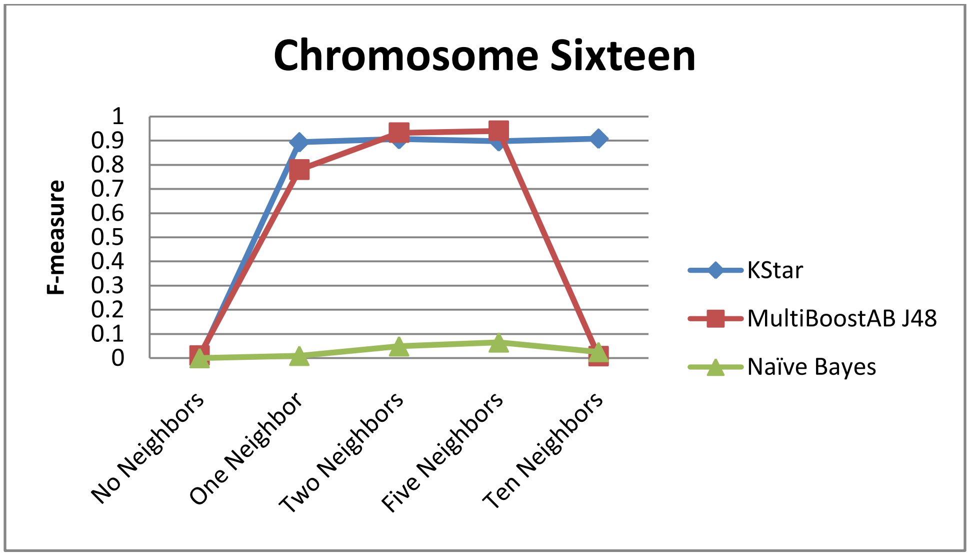


Figure 5.82. F-measure for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

In general the MultiBoostAB algorithm using the J48 classifier obtained the higher F-measures for all the chromosomes. The partitioning of the classification process by chromosome benefited the accuracy of the classification for most of the classifiers. The classifiers obtained higher F-measures on individual chromosomes than what they were able to obtain using the entire genome. The decision trees that were generated can be found in Appendix H.

5.1.2.3 Removing Location Information

A series of experiments was performed to determine if given the properties of neighbor's number, neighbor's Gene Ontology term, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and network involvement information from KEGG for genomic features (features being: genes, ARS, etc) for training could the MultiBoostAB algorithm using the J48 classifier could correctly classify network involvement. The MultiBoostAB algorithm using the J48 classifier was selected since it obtained the best performance in the prior section.

These experiments were performed to see if rules could be generated that would provided insight about a genomic feature's network involvement based only on what other features are near it regardless of that feature's location.

The rules generated did not incorporate the neighbor's Gene Ontology information. Neighbor distance was the most important attribute being selected for the root of the decision tree. Using information from each feature's two-nearest neighbors obtained the highest percentage of correctly classified features, but the percentage was low (See Figure 5.83).

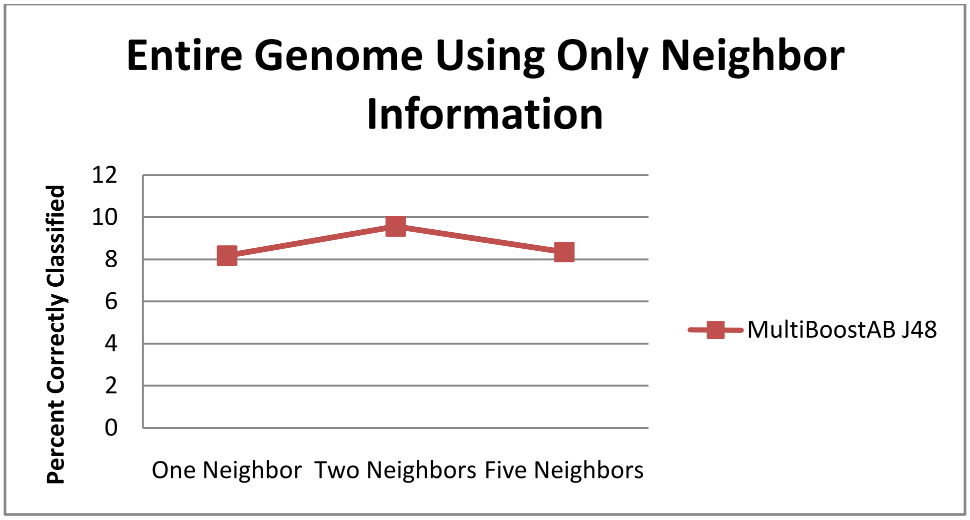


Figure 5.83. The percentage of correctly classified features using the MultiBoostAB algorithm using the J48 classifier.

The accuracy of the classification was low regardless of the number of neighbors included (See Figure 5.84).

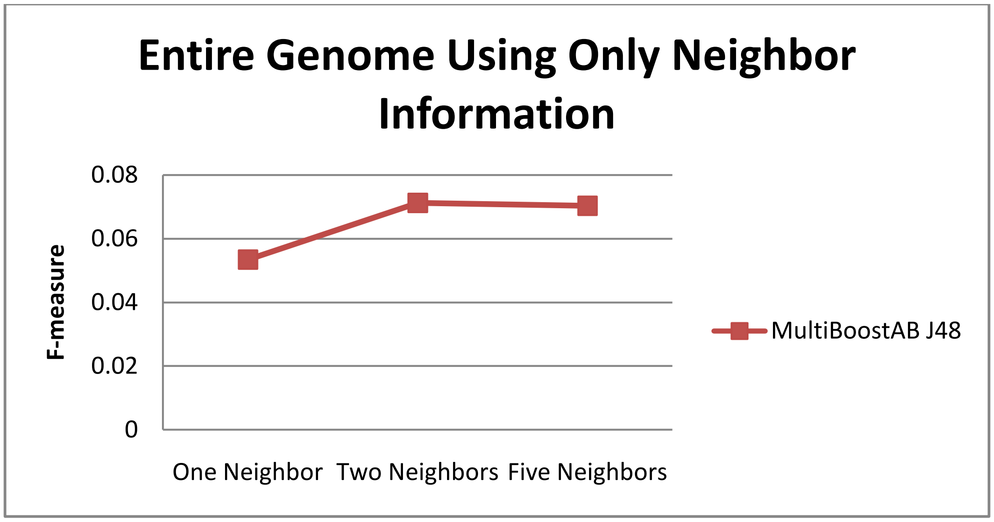


Figure 5.84. The F-measure using the MultiBoostAB algorithm using the J48 classifier.

5.1.3 Using Neighbor's Network Involvement

A series of experiments was performed to determine if given the genomic properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), neighbor's network involvement and the feature's network involvement information from KEGG for training could classification algorithms correctly classify network involvement. This was also performed including information from the nearest, two-, five- and ten- nearest neighbors of each feature. This was also repeated on the individual chromosomes. The mitochondrial chromosome is excluded. Having only one known network on the mitochondrial chromosome, classifiers cannot classify unary classes

The results of the experiments are based on averages of ten different runs of each dataset being randomized and then split for training and testing. The training sets were set to contain 66% of the instances randomly selected from each dataset.

5.1.3.1 Results for the Entire Genome

When using only a genomic feature's chromosome number, start position, stop position, strand, and network involvement without neighbor information, we see that the percentage of genomic features correctly classified to the correct net varies depending on the classification algorithm used (See Figure 5.85). When neighbor information is included, the percentage of correctly classified features increases for the KStar classifier. The percentage of correctly classified features does not change greatly with the inclusion of neighbor information for the MultiBoostAB algorithm using the J48 classifier until information from each feature's ten-nearest neighbors is included. At this point, it achieves the highest percentage of correctly classified features. For the Naïve Bayesian classifier, the percentage of correctly classified genomic features decreases when neighbor information is included.

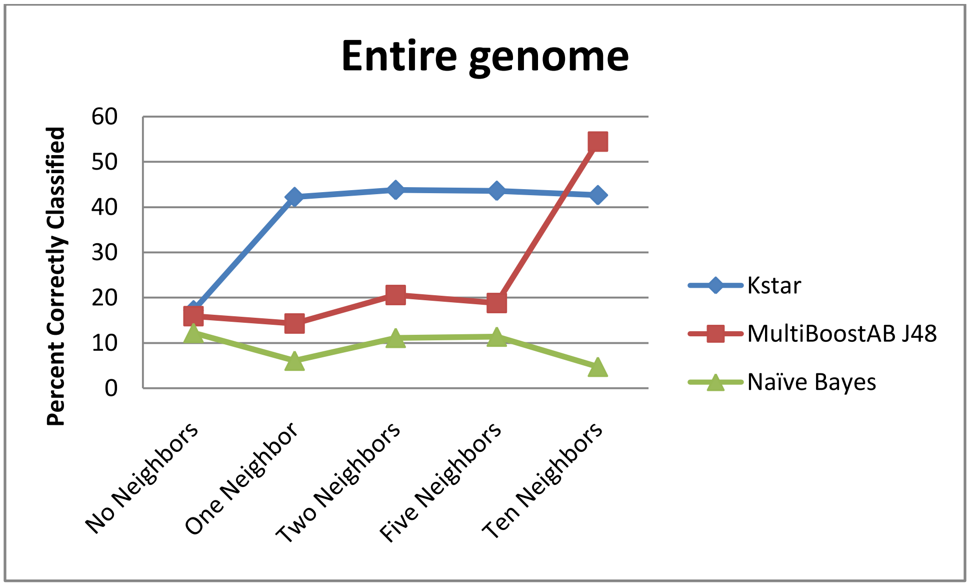


Figure 5.85. Percent of genomic features classified for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The agreement between the predicted and observed classification of the genomic features is affected by the inclusion of neighbor information. The KStar classifier achieves a moderate agreement with the inclusion of neighbor information. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the Kappa statistic for the KStar classifier. The MultiBoostAB algorithm using the J48 classifier attains an agreement that is moderate upon the addition of information from each feature's ten-nearest neighbors. The Naïve Bayesian classifier never attains an agreement above poor with the inclusion of neighbor information (See Figure 5.86).

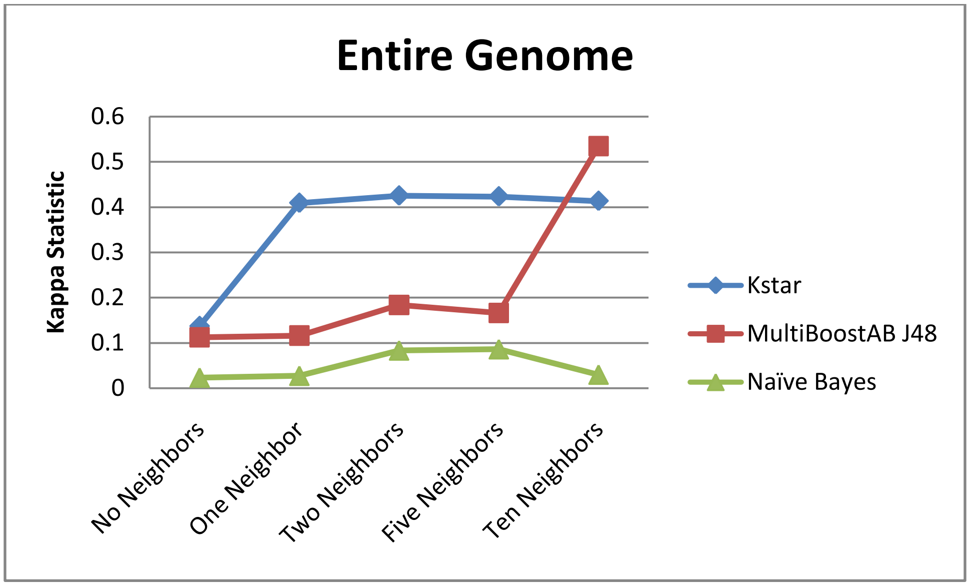


Figure 5.86. Kappa statistic for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The precision of feature classification is affected by the number of neighbors that is included (See Figure 5.87). For the KStar classifier, the inclusion of neighbor information improves the precision, with the inclusion of each feature's ten-nearest neighbors obtaining the highest precision. The MultiBoostAB algorithm using the J48 classifier obtains a precision score above 0.4 only with the inclusion of information from each feature's ten-nearest neighbors. The Naïve Bayesian classifier never obtains precision scores above 0.2.

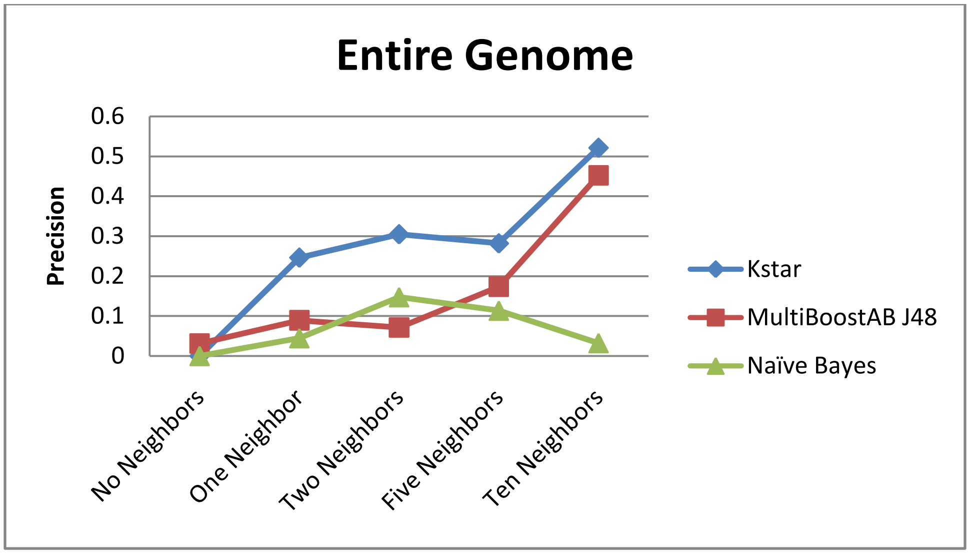


Figure 5.87. Precision for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Recall is also affected by the number of neighbors that is included (See Figure 5.88). For the KStar classifier, the inclusion of neighbor information improves the recall, with the inclusion of each feature's ten-nearest neighbors obtaining the highest recall. The recall scores remain low for the other classifiers. The MultiBoostAB algorithm using the J48 classifier obtains a recall score above 0.4 after the inclusion of information from each feature's ten-nearest neighbors. The Naïve Bayesian classifier never obtains recall scores above 0.1; its higher recall score is obtained with the inclusion of information from each feature's two-nearest neighbors.

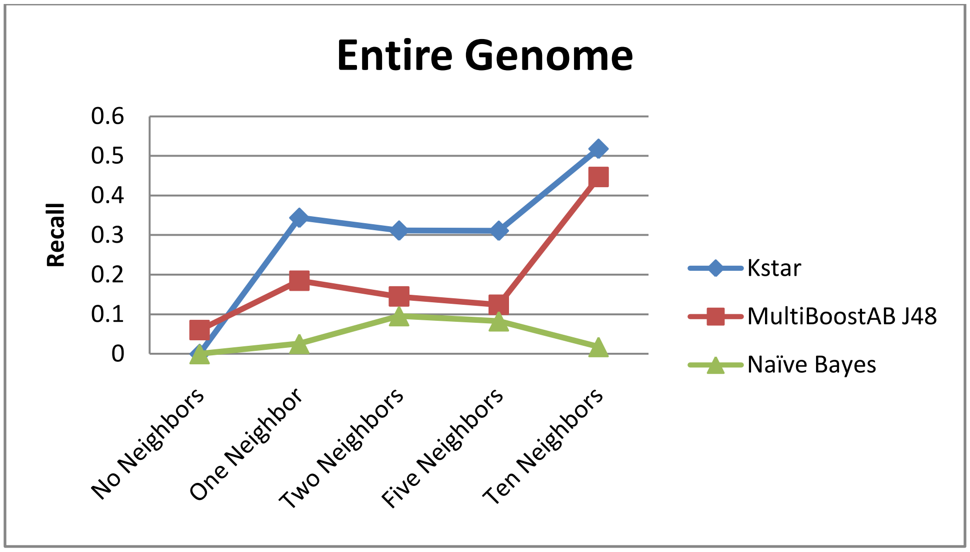


Figure 5.88. Recall for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The F-measures of the classifiers mimic the precision and recall scores obtained by the classifiers (See Figure 5.89). For the KStar classifier, the inclusion of neighbor information improves the accuracy of the classification process, with the inclusion of each feature's ten-nearest neighbors obtaining the higher F-measure. The accuracy of the MultiBoostAB algorithm using the J48 classifier and is benefitted by the inclusion of neighbor information, with the inclusion of information from each feature's ten-nearest neighbors yielding the higher F-measures. For the Naïve Bayesian classifier, the higher recall score is obtained with the inclusion of information from each feature's two-nearest neighbors.

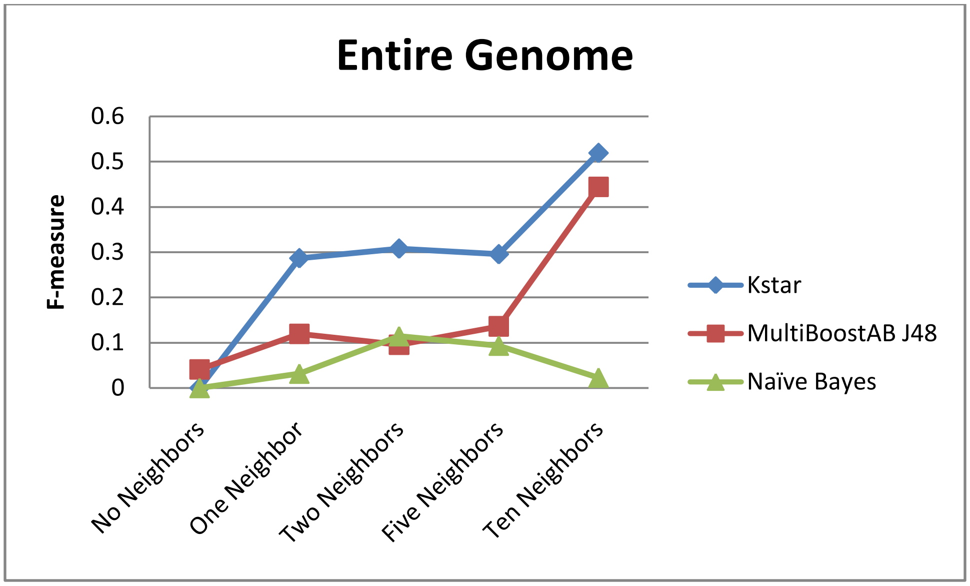


Figure 5.89. F-measure for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

When analyzing the area under the ROC curves, the accuracy improves to excellent with the inclusion of neighbor information for the KStar classifier. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the area under the ROC curve for the KStar classifier. For the MultiBoostAB algorithm using the J48 classifier, the accuracy is poor with the inclusion of no neighbors. It improves to good with the inclusion of each feature's nearest neighbors and then it decreases with the inclusion of more neighbors, then increases to excellent upon the inclusion of information from each feature's ten-nearest neighbors. With the Naïve Bayesian classifier, the accuracy of the classification never improves above poor (See Figure 5.90).

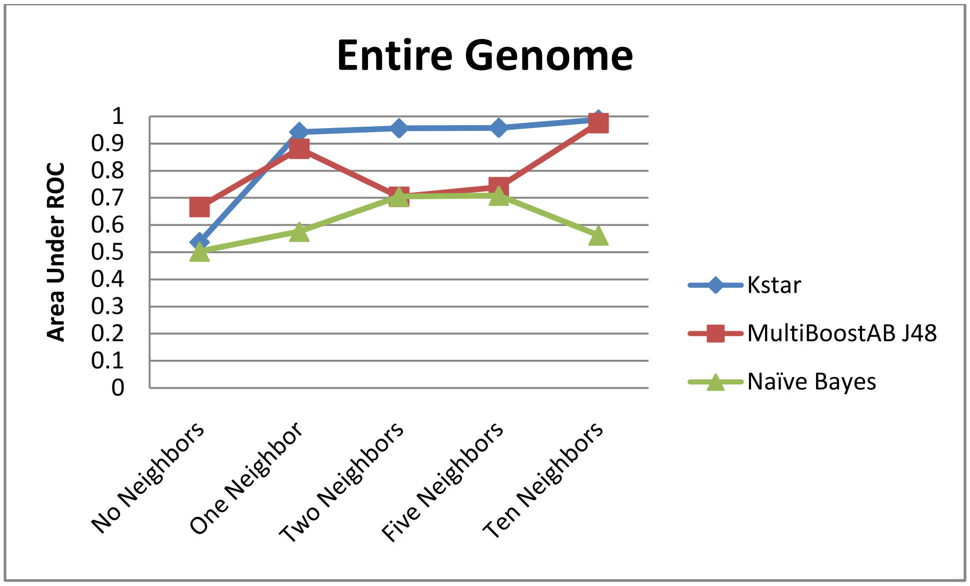


Figure 5.90. Area under ROC curve for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

In general, the KStar classifier performs the best when trained using the genomic properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), neighbor's network involvement and the feature's network involvement information from KEGG.

To see the effect on the accuracy of classification for each network, the F-measures obtained by the classifier for each network were analyzed. The table of the F-measures can be found in Appendix D. Most of the networks benefited from the addition of neighbor information (See Figures 5.91 - 5.93).

Some networks attain F-measures that are above 0.6 with no neighbor information included implying that the location of these features alone is indicative of their network involvement. These networks are the ribosome network and the polyunsaturated fatty acid biosynthesis network. The inclusion of neighbor's network involvement for feature's of the ribosome network decreases the F-measures.

Other networks (the oxidative phosphorylation network, the SNARE interactions in vesicular transport network, the ubiquitin biosynthesis network, the proteasome network, the valine, leucine and isoleucine biosynthesis network, the glycerophospholipid metabolism network, the cell cycle network, the aminoacyl-tRNA biosynthesis network, the purine metabolism network and the starch and sucrose metabolism network) also obtain F-measures with no neighbor information included, but they are less than 0.4.

For networks that obtain lower F-measures, the F-measures fluctuate depending on how many neighbor's information is included.

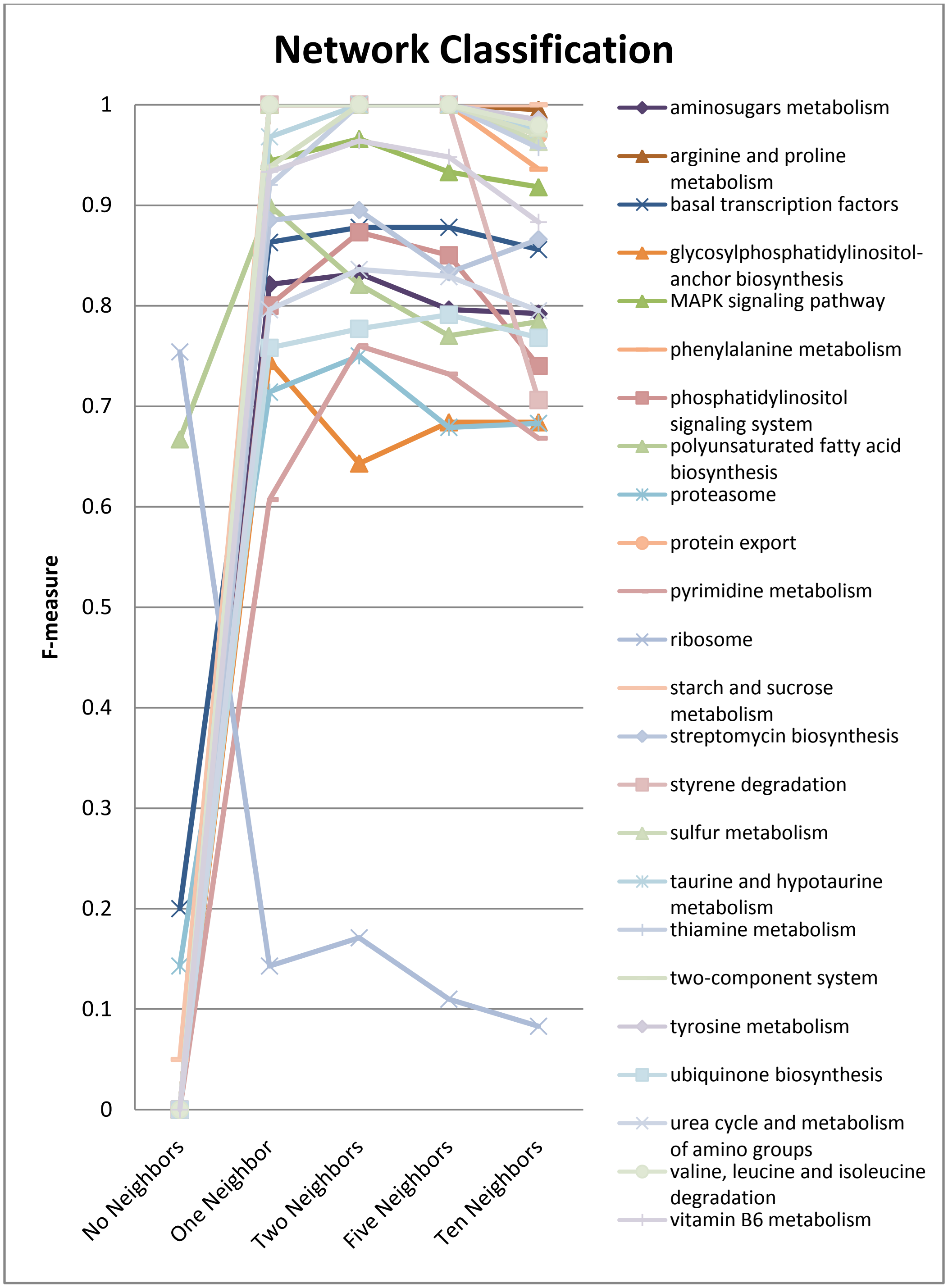


Figure 5.91. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual networks. Only networks that obtained an F-measure above 0.7 are shown.

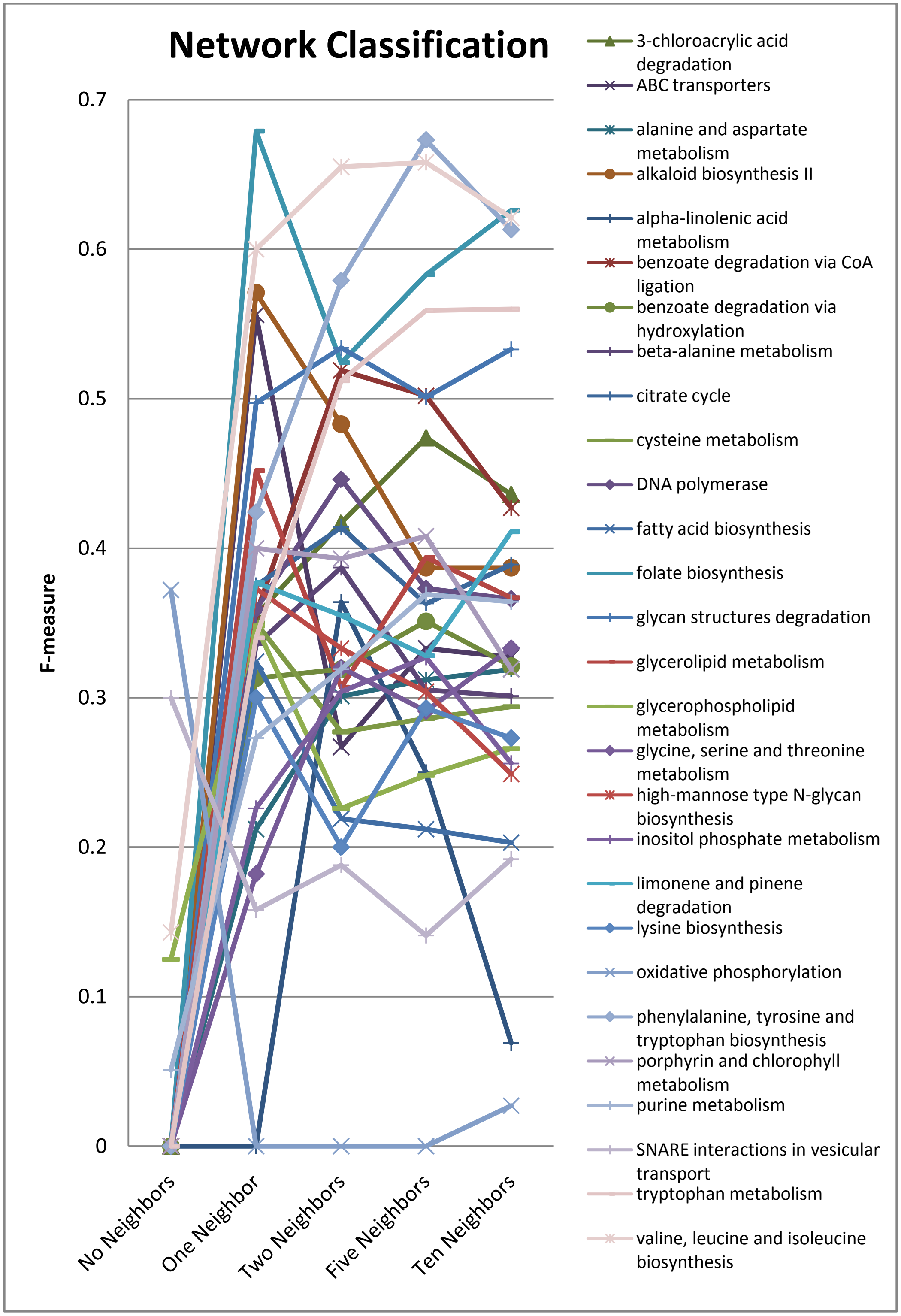


Figure 5.92. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual networks. Only networks that obtained an F-measure above 0.3 and below 0.7 are shown.

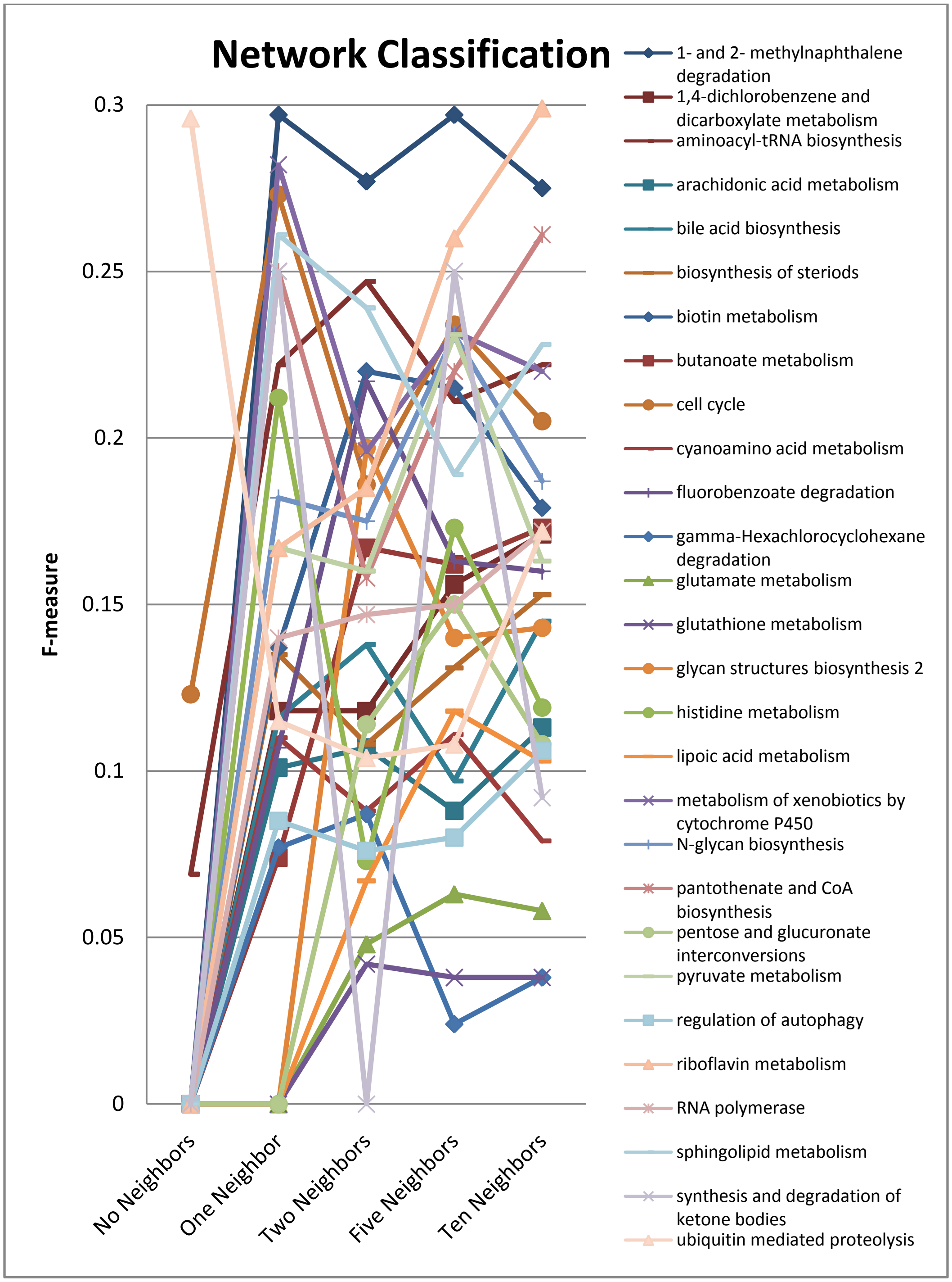


Figure 5.93. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual networks. Only networks that obtained an F-measure above 0.45 and below 0.7 are shown.

5.1.3.2 Result for Individual Chromosomes

When we look at each chromosome individually, we see that the results of classification vary from chromosome to chromosome, from the number of neighbors included, and from the classification algorithm being used.

5.1.3.2.1 Percent Correctly Classified

For all chromosomes, the percent of genomic features correctly classified to the correct network differed depending on the number of neighbors included in the dataset and the classification algorithm used.

For chromosome one, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.94). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentage of correctly classified features. The percentages obtained by the MultiBoostAB algorithm using the J48 classifier plateau after information from each features two-nearest neighbors is included. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier and the Naïve Bayesian classifier.

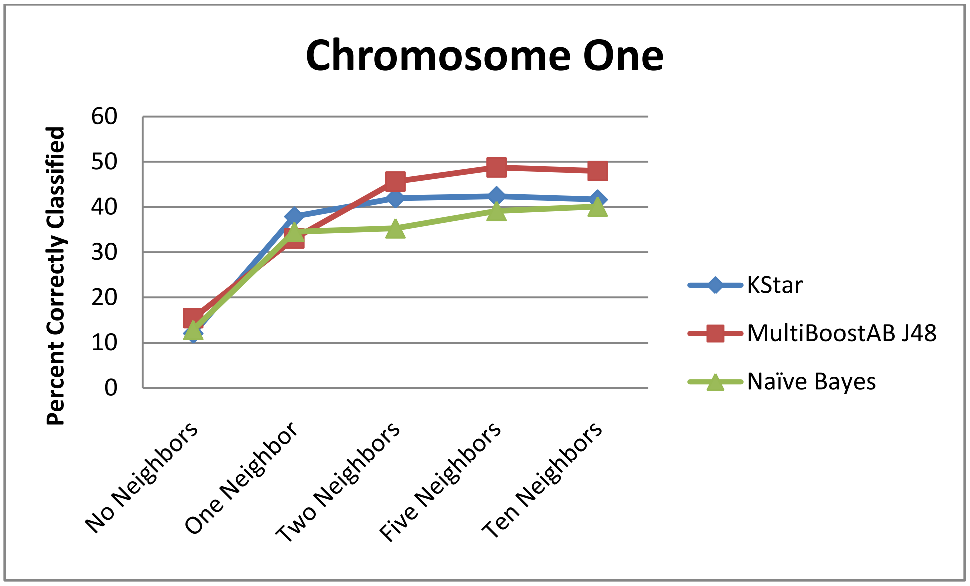


Figure 5.94. Percent of genomic features classified for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included with the MultiBoostAB algorithm using the J48 classifier obtained the larger percentages (See Figure 5.95). For the MultiBoostAB algorithm using the J48 classifier, the percentage of correctly classified features increases as more neighbor information is included. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier and the Naïve Bayesian classifier.

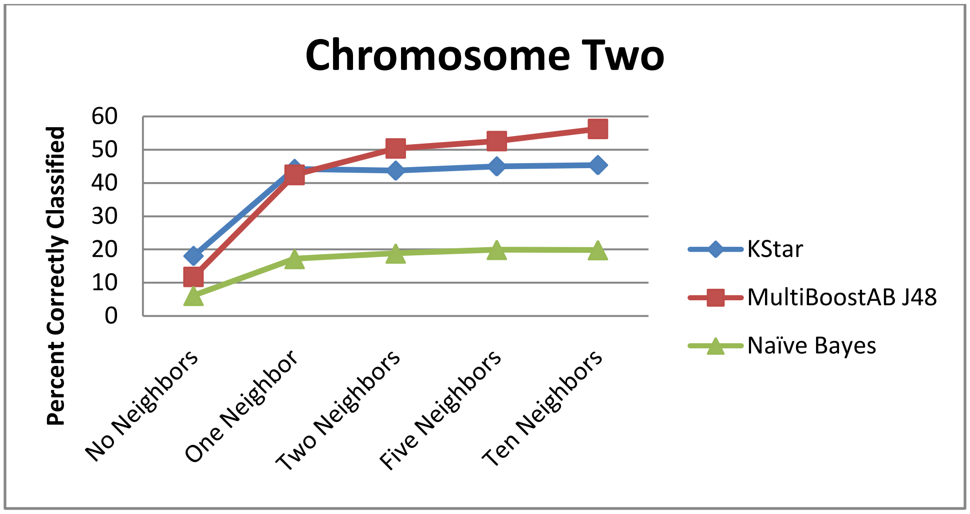


Figure 5.95. Percent of genomic features classified for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.96). For the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier, the percentage of correctly classified features increases as more neighbor information is included. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier.

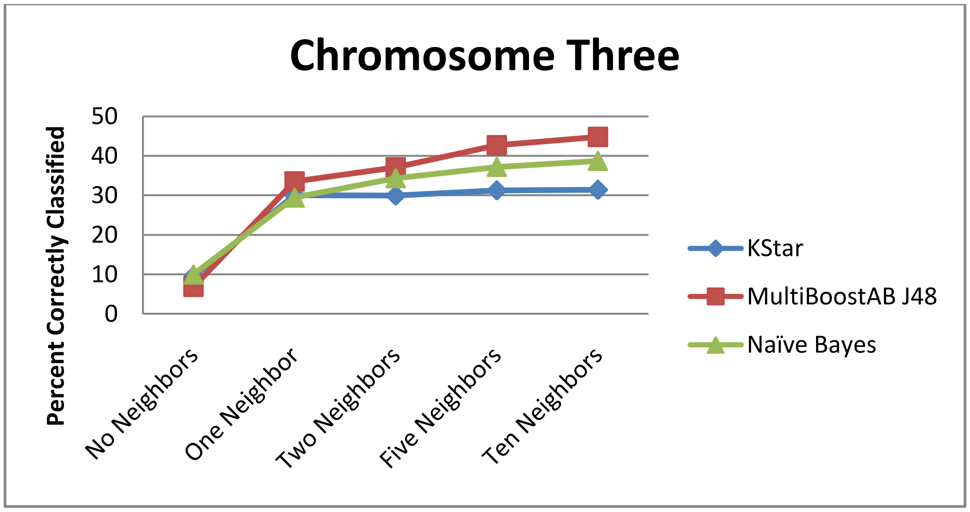


Figure 5.96. Percent of genomic features classified for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.97). For the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier, the percentage of correctly classified features increases as more neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, and the Naïve Bayesian classifier obtains the lower percentages. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier.

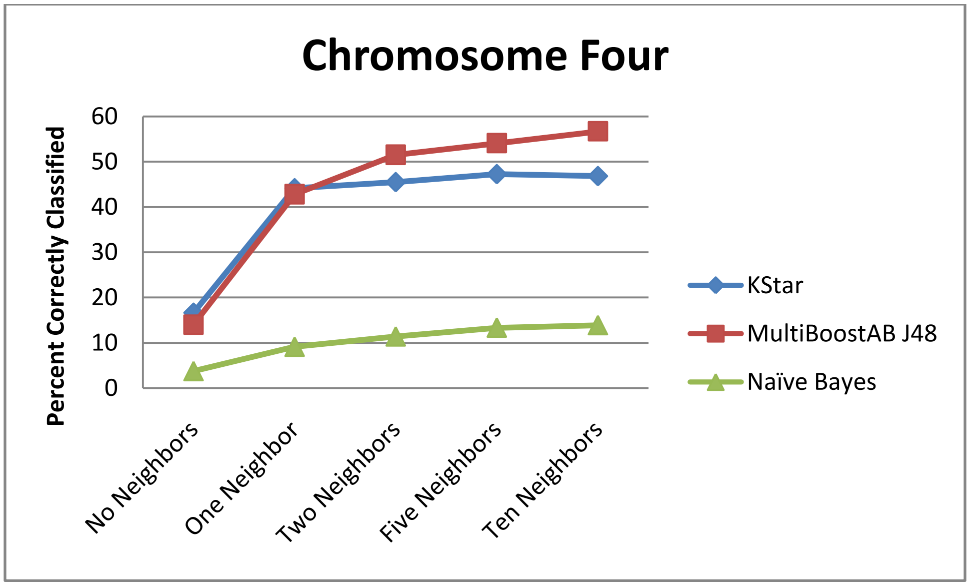


Figure 5.97. Percent of genomic features classified for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.98). For the MultiBoostAB algorithm using the J48 classifier, the percentage of correctly classified features increases as more neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the highest percentages. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier and the Naïve Bayesian classifier. The Naïve Bayesian classifier obtains the lowest percentages.

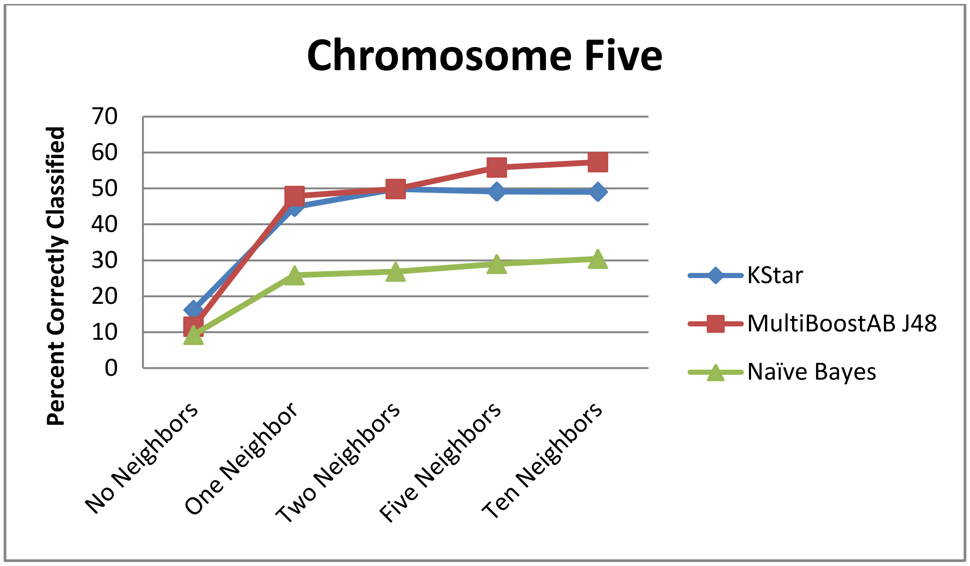


Figure 5.98. Percent of genomic features classified for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included, but the KStar classifier and the MultiBoostAB algorithm using the J48 classifier experience slight dips when information from each feature's two-nearest neighbors is included (See Figure 5.99). For the Naïve Bayesian classifier, the percentage of correctly classified features increases as more neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, and the Naïve Bayesian classifier obtains the lower percentages.

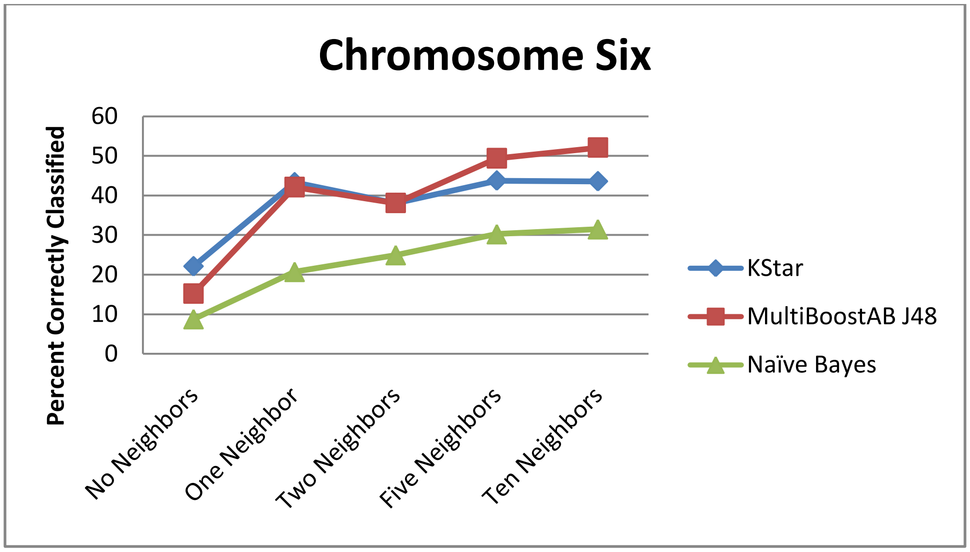


Figure 5.99. Percent of genomic features classified for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, similar to other chromosomes, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included with the MultiBoostAB algorithm using the J48 classifier obtains the higher percentages (See Figure 5.100). The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier The Naïve Bayesian classifier does not see a drastic improvement in the percentage of correctly classified features, and it obtains the lower percentages.

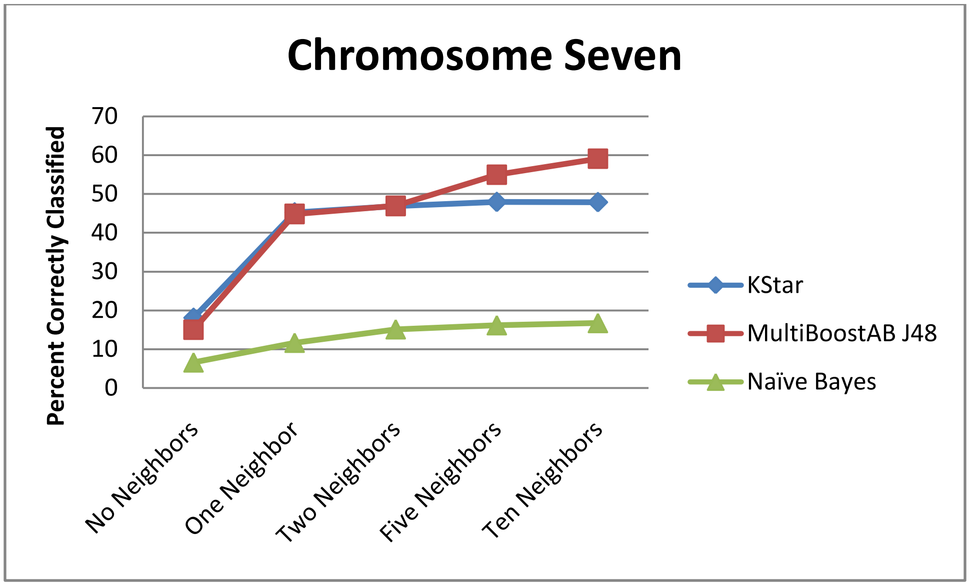


Figure 5.100. Percent of genomic features classified for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, for all classifiers, the highest percentage of correctly classified features is obtained when information from each feature's nearest neighbors is included (See Figure 5.101). When more neighbor information is included, the percentage of correctly classified features decreases, but the percentages remain higher than when no neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the highest percentages, and the Naïve Bayesian classifier obtains the lowest percentages.

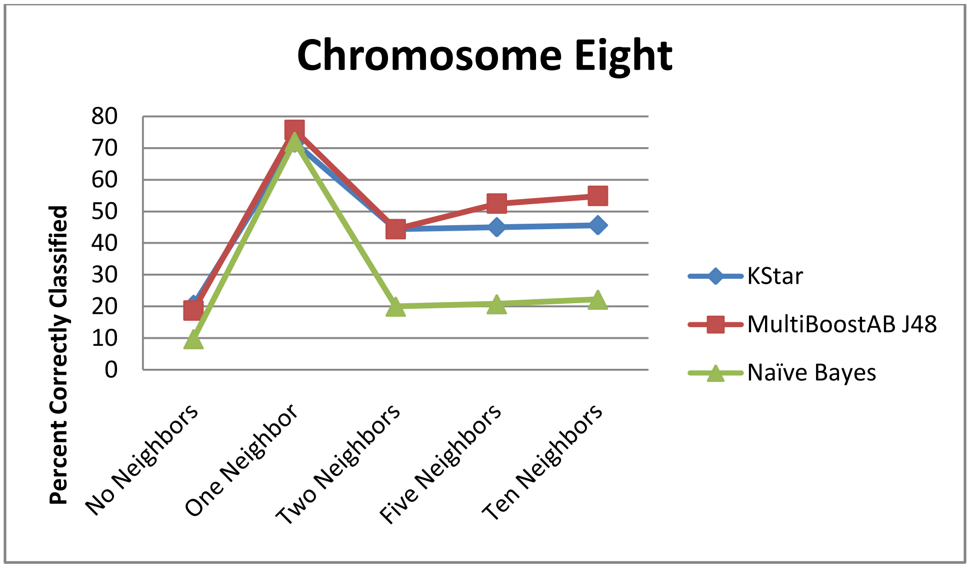


Figure 5.101. Percent of genomic features classified for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, the MultiBoostAB algorithm using the J48 classifier and the KStar classifier observe increases in the percentage of correctly classified features when neighbor information is included (See Figure 5.102). This increase is not seen in the Naïve Bayesian classifier until information from each feature's two-nearest neighbors has been included. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages after information from each feature's two-nearest neighbors is included. For the KStar classifier, the inclusion of information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features. The Naïve Bayesian classifier obtains the lower percentages.

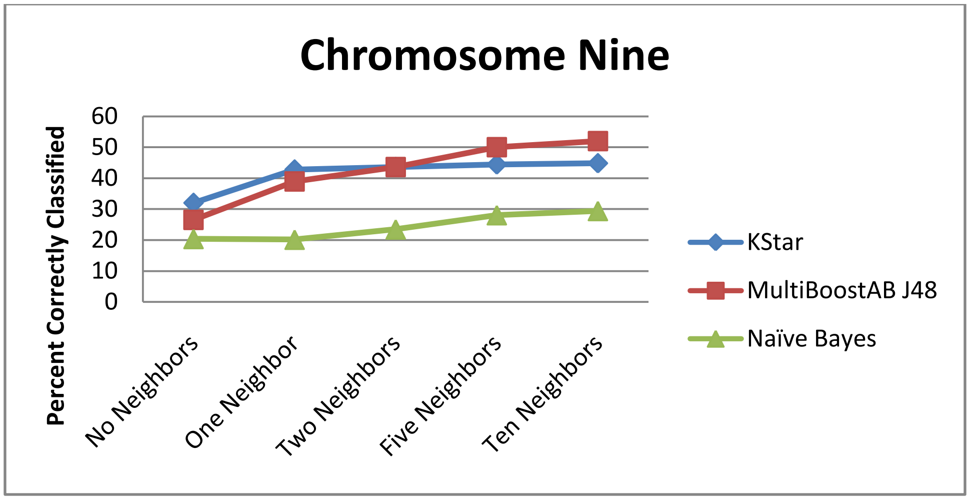


Figure 5.102. Percent of genomic features classified for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.103). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages after information from each feature's two-nearest neighbors has been included. The Naïve Bayesian classifier obtains the lower percentages. For the KStar classifier, the inclusion of information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features.

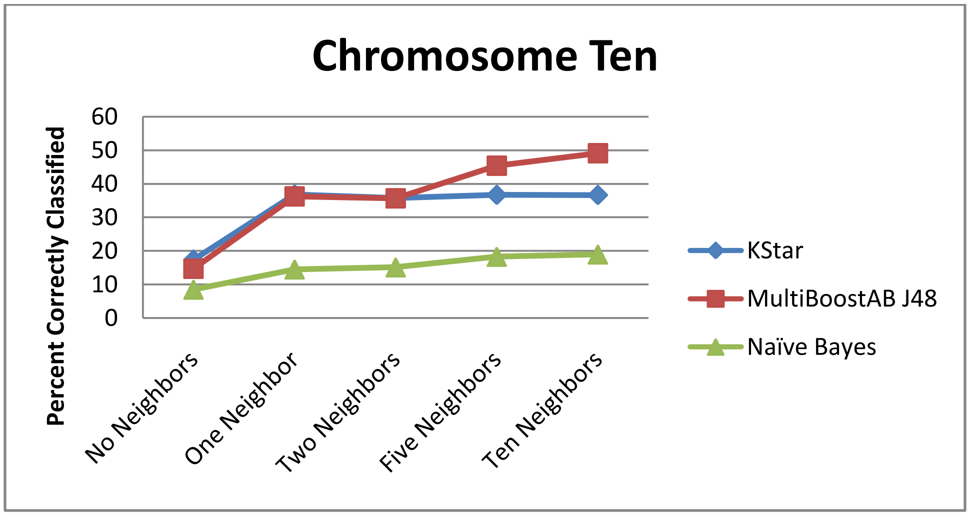


Figure 5.103. Percent of genomic features classified for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

All of the classifiers experience increases in the percentage of correctly classified features when neighbor information is included for chromosome eleven (See Figure 5.104). Similar to other chromosomes, the MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, and the Naïve Bayesian classifier obtains the lower percentages. For the KStar classifier, the higher percentage of correctly classified features is obtained when information from each feature's nearest neighbors is included.

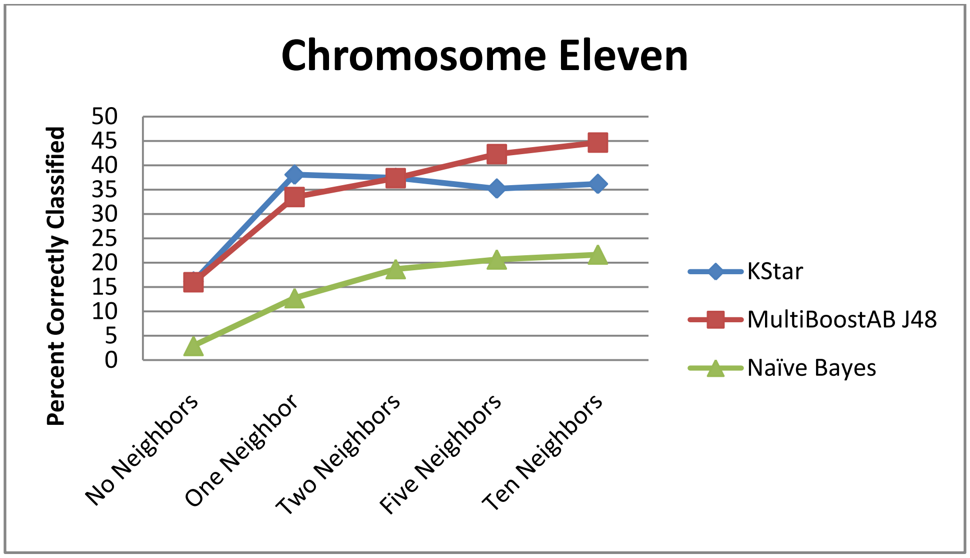


Figure 5.104. Percent of genomic features classified for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the KStar classifier and the Naïve Bayesian classifier observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.105), with the inclusion of neighbor information beyond each feature's nearest neighbor having little impact on the percentage of correctly classified features. The MultiBoostAB algorithm using the J48 classifier experiences a dip in the percentage of correctly classified features when information from each feature's nearest neighbors is included, then it increases as more neighbor information is included, achieving the higher percentages.

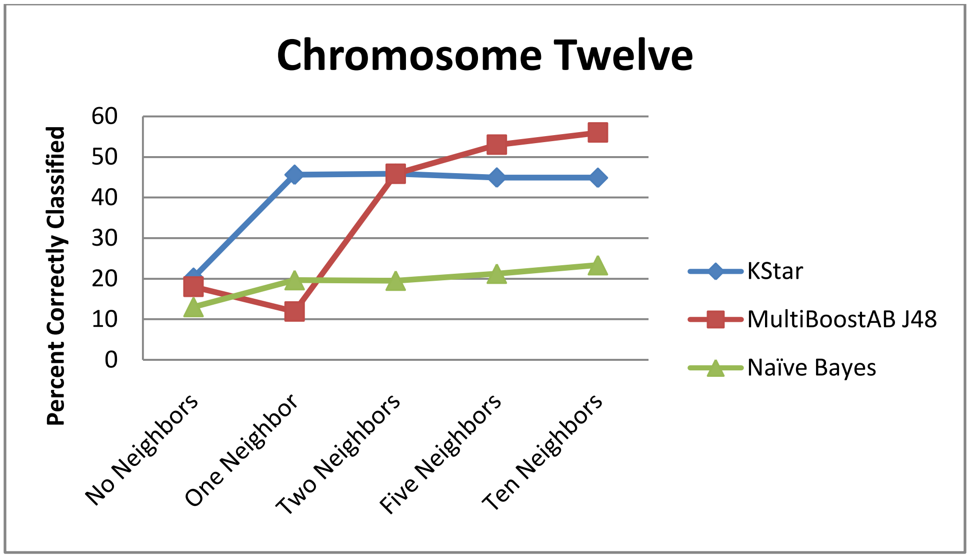


Figure 5.105. Percent of genomic features classified for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.106). Similar to other chromosomes, the MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, and the Naïve Bayesian classifier obtains the lower percentages. For the MultiBoostAB algorithm using the J48 classifier, the percentage of correctly classified features increases as more neighbor information is included. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier and the Naïve Bayesian classifier.

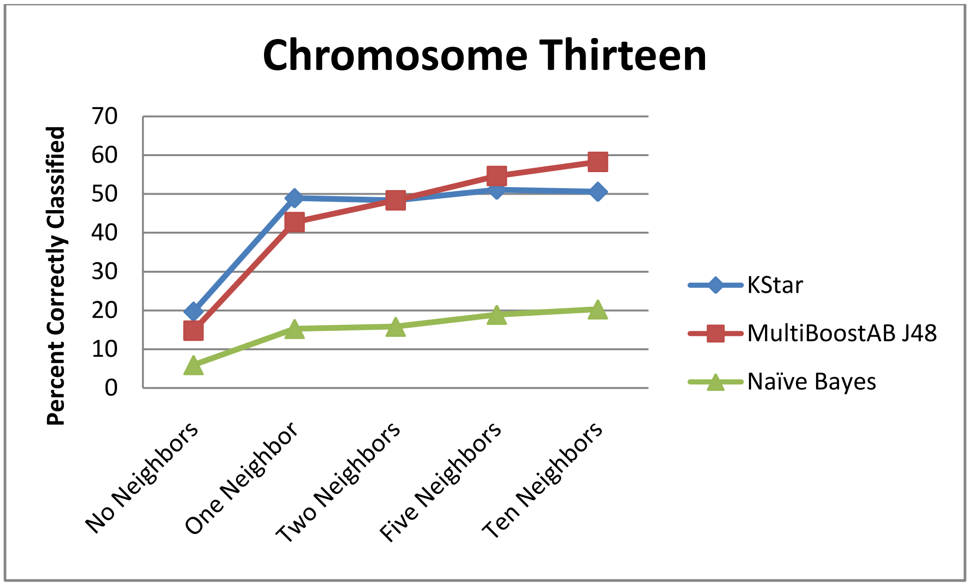


Figure 5.106. Percent of genomic features classified for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, all the classifiers obtain an increase in the percentage of correctly classified features with the inclusion of neighbor information (See Figure 5.107). For the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier, the percentage of correctly classified features increases as more neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, and the Naïve Bayesian classifier obtains the lower percentages. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier.

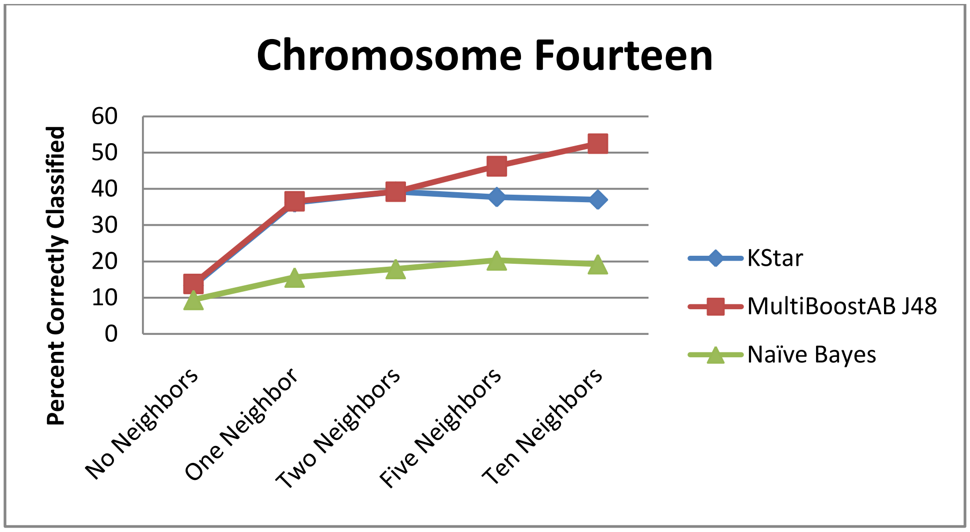


Figure 5.107. Percent of genomic features classified for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, all the classifiers obtain an increase in the percentage of correctly classified features with the inclusion of neighbor information with the MultiBoostAB algorithm using the J48 classifier obtains the higher percentage of correctly classified features (See Figure 5.108). For all classifiers, the highest percentages are obtained with the inclusion of information from each feature's ten-nearest neighbors.

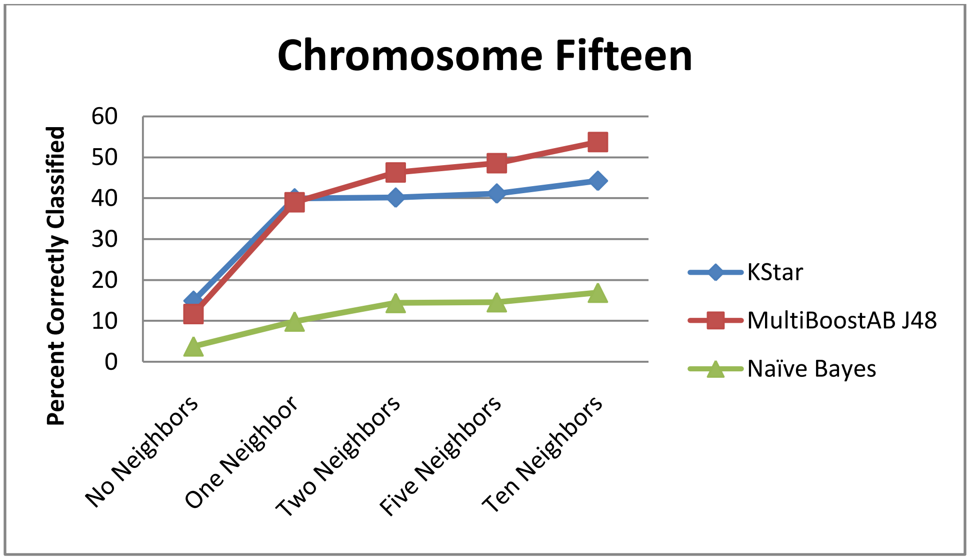


Figure 5.108. Percent of genomic features classified for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, all of the classifiers observe an increase in the percentage of correctly classified features when neighbor information is included (See Figure 5.109) For the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier, the percentage of correctly classified features increases as more neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the highest percentages, and the Naïve Bayesian classifier obtains the lowest percentages. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features of the KStar classifier.

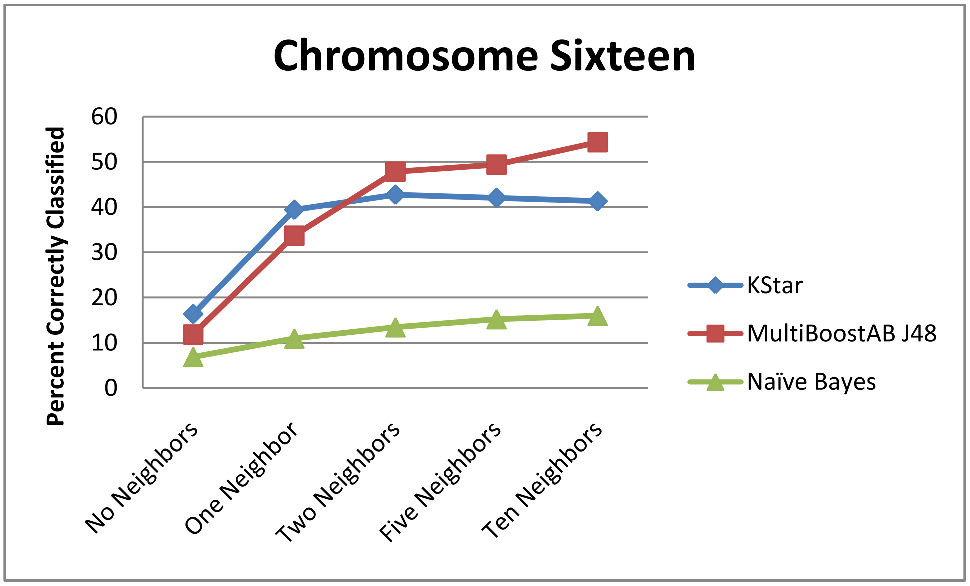


Figure 5.109. Percent of genomic features classified for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

After analyzing all the chromosomes, all the classifiers benefitted from the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier performed better than the other classifiers. This is different from what performed better using the entire genome. The partitioning of the classification process by chromosome benefitted the classification process. In general, for each chromosome, the MultiBoostAB algorithm using the J48 classifier was able to obtain a higher percentage of correctly classified features than when compared to the results using the entire genome.

5.1.3.2.2 F-measures

To look at the accuracy of the classification process for each chromosome, the F-measures obtained for each chromosome can be analyzed.

For chromosome one, the F-measures are low. The F-measures obtained by both the KStar classifier and the MultiBoostAB algorithm using the J48 classifier fluctuate depending on how many neighbors are included. For both classifiers, the higher F-measures are obtained when information from each feature's ten-nearest neighbors is included. The Naïve Bayesian classifier never achieves an F-measure above zero (See Figure 5.110).

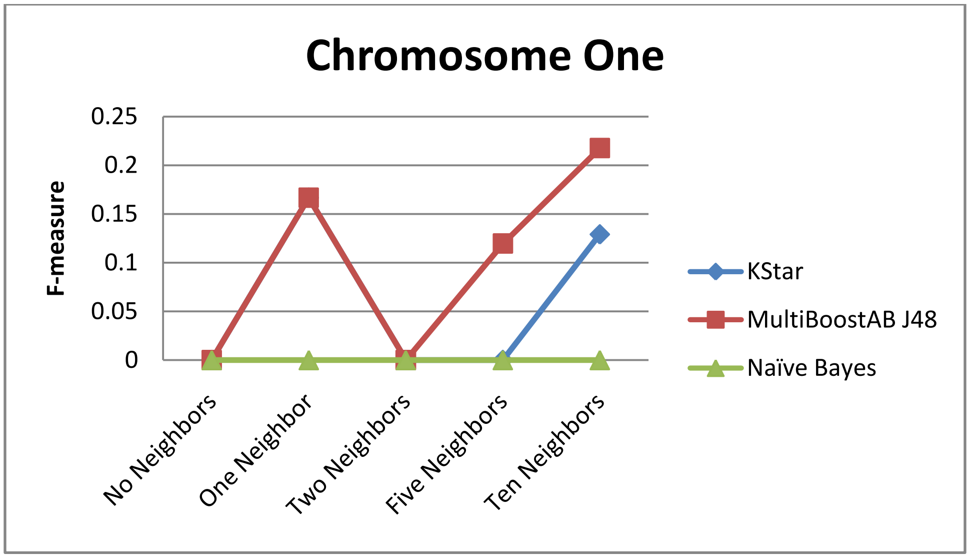


Figure 5.110. F-measure for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, F-measures above 0.5 are not obtained until information from each feature's ten-nearest neighbors is included for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier (See Figure 5.111). The accuracy of the Naïve Bayesian classifier does not benefit from the inclusion of neighbor information.

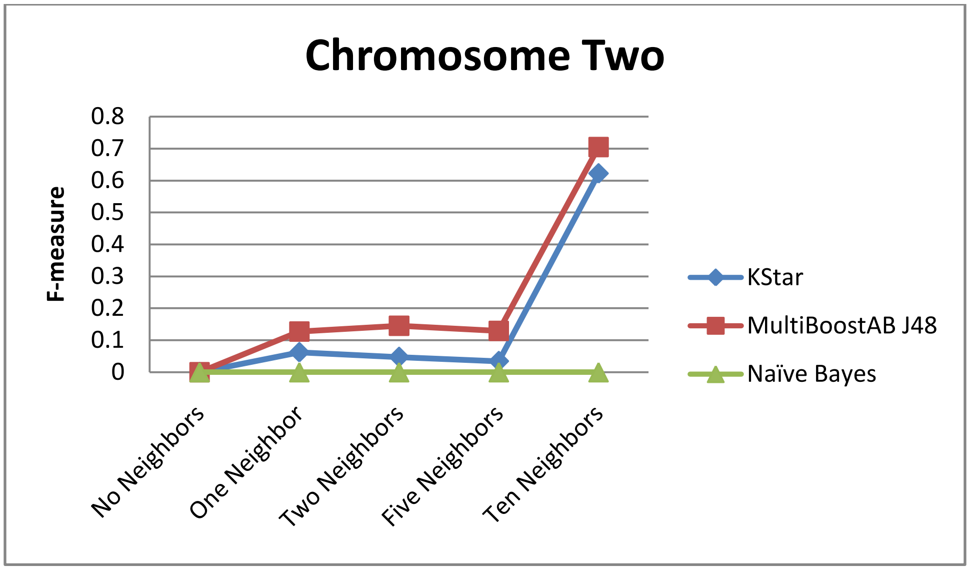


Figure 5.111. F-measure for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, like chromosome one, the F-measures are low and they fluctuate for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier. The higher F-measure for the MultiBoostAB algorithm using the J48 classifier is obtained with the inclusion of information from each feature's nearest neighbor. The higher F-measure for KStar classifier is obtained with the inclusion of information from each feature's five-nearest neighbors. The Naïve Bayesian classifier never achieves an F-measure above zero (See Figure 5.112).

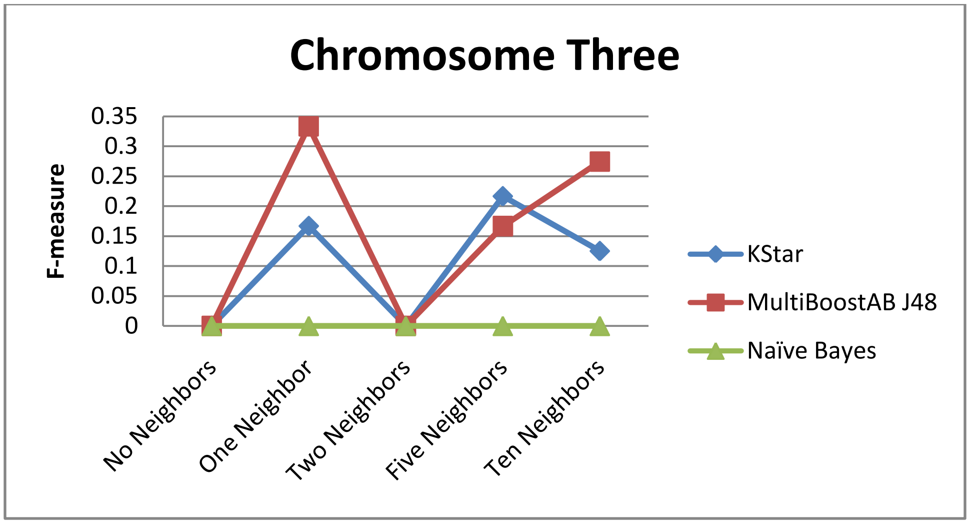


Figure 5.112. F-measure for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, the inclusion of neighbor information benefits the accuracy of the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. For both classifiers, the highest F-measures are obtained when information from each feature's five-nearest neighbors is included. The inclusion of neighbor information does not improve the accuracy of the Naïve Bayesian classifier (See Figure 5.113).

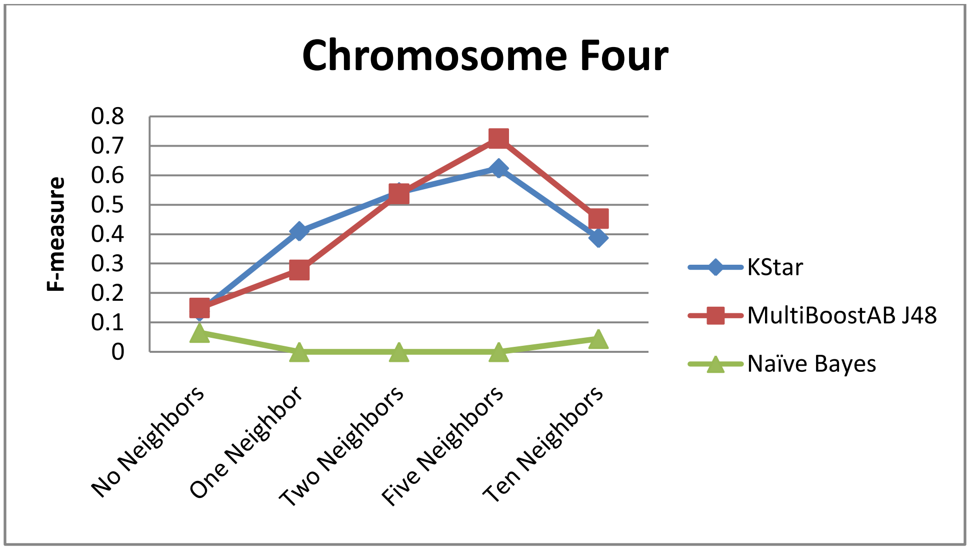


Figure 5.113. F-measure for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, the accuracy of all the classifiers improves drastically with the inclusion of information from each feature's ten-nearest neighbors (Figure 5.114). The F-measures go from zero to one.

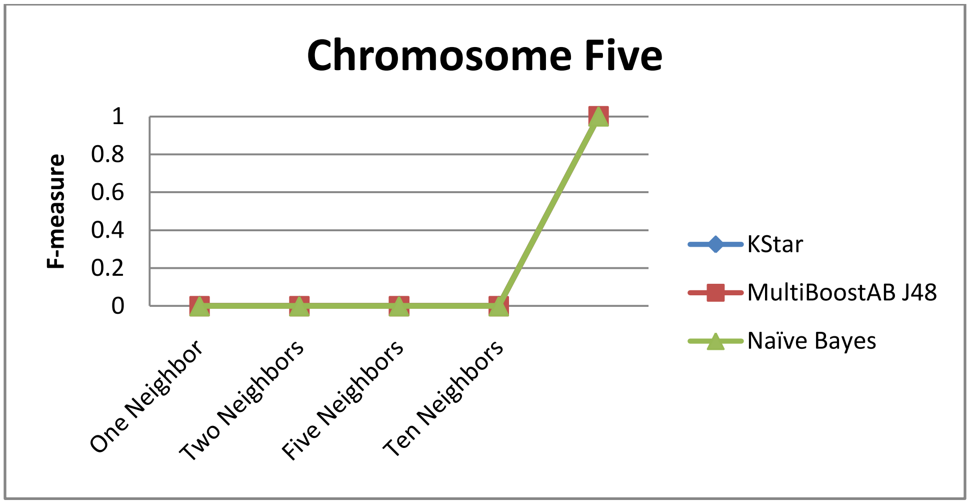


Figure 5.114. F-measure for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Similar to chromosome five, upon the addition of information from each feature's ten-nearest neighbors, all of the classifiers improve their F-measures to one for chromosome six (See Figure 5.115).

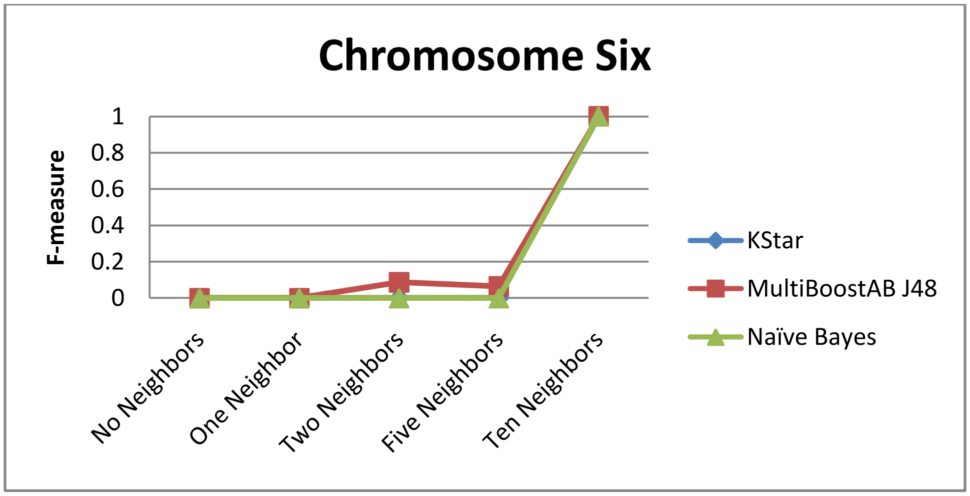


Figure 5.115. F-measure for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, the inclusion of some neighbor information is beneficial for the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. Both classifiers experience decreases in the F-measures with the inclusion of information from each feature's ten-nearest neighbors (See Figure 5.116). The Naïve Bayesian classifier never obtains an F-measure above zero.

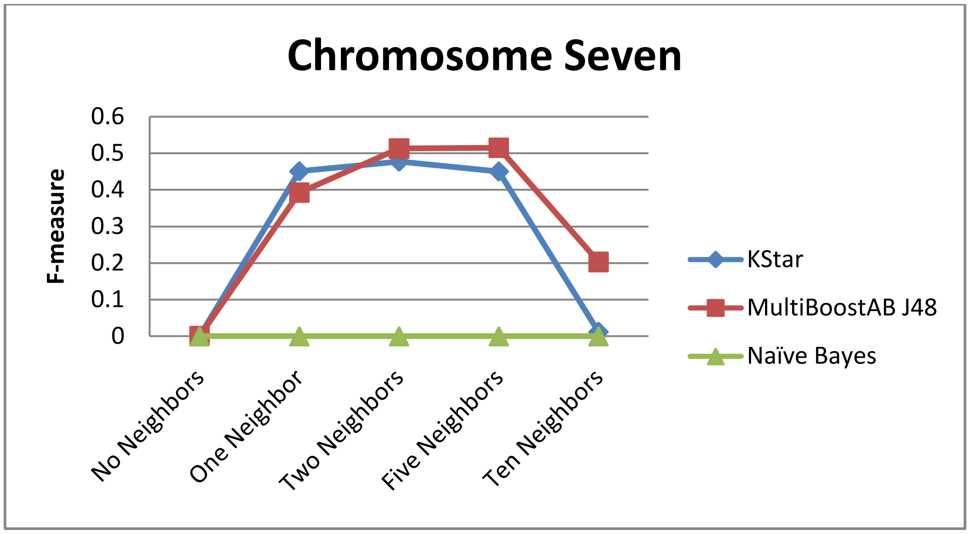


Figure 5.116. F-measure for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. For both classifiers, the inclusion of information beyond each feature's nearest neighbors has little impact on the F-measures obtained. The F-measures obtained by the Naïve Bayesian classifier fluctuate depending on the amount of neighbor information that is included with the highest F-measure being obtained with the inclusion of information from each feature's nearest neighbors (See Figure 5.117).

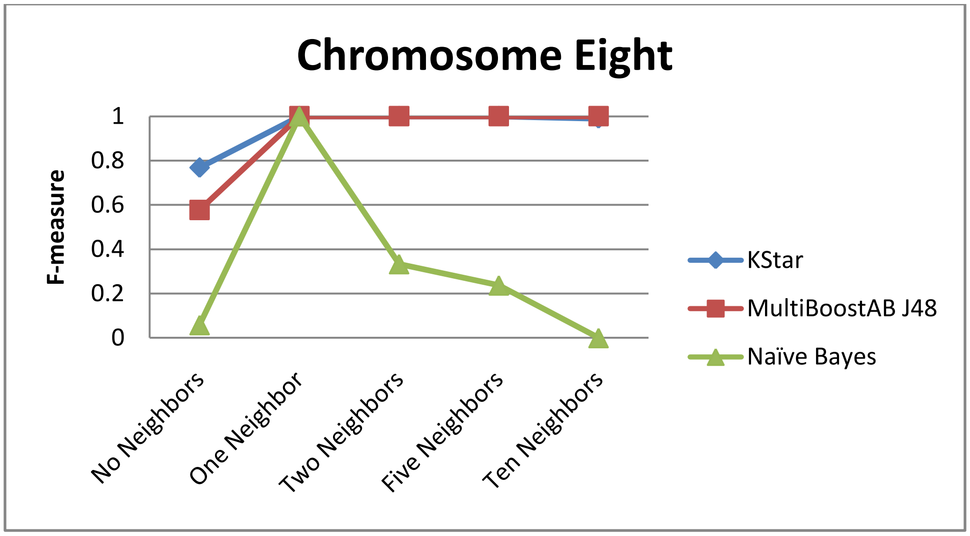


Figure 5.117. F-measure for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, upon the inclusion of information from each feature's ten-nearest neighbors, the KStar classifier and the MultiBoostAB algorithm using the J48 classifier experience a drastic increase in their F-measures. The increase obtained by the Naïve Bayesian classifier is not as great (See Figure 5.118).

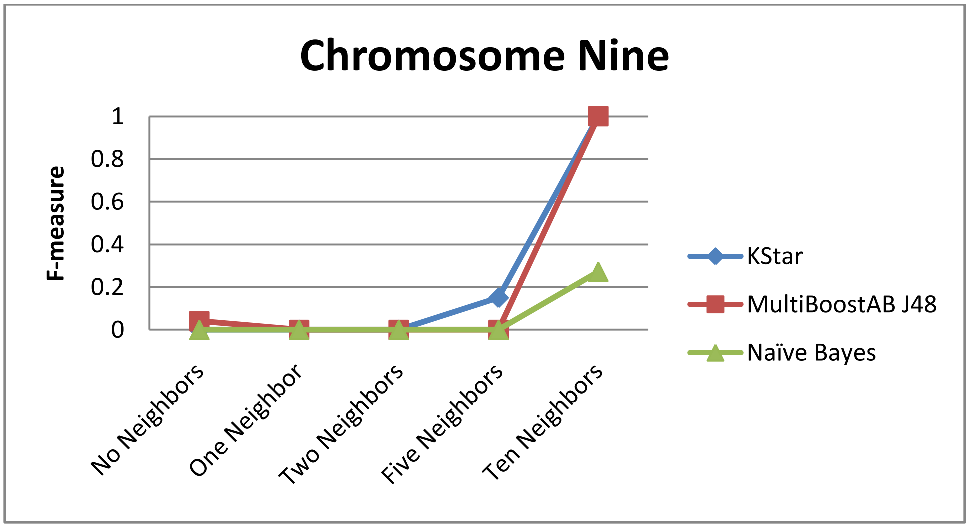


Figure 5.118. F-measure for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the inclusion of neighbor information improves the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier (both achieve F-measures of 1.0), but the F-measures with the inclusion of each feature's ten-nearest neighbors decrease. The Naïve Bayesian classifier never obtains an F-measure above zero (See Figure 5.119).

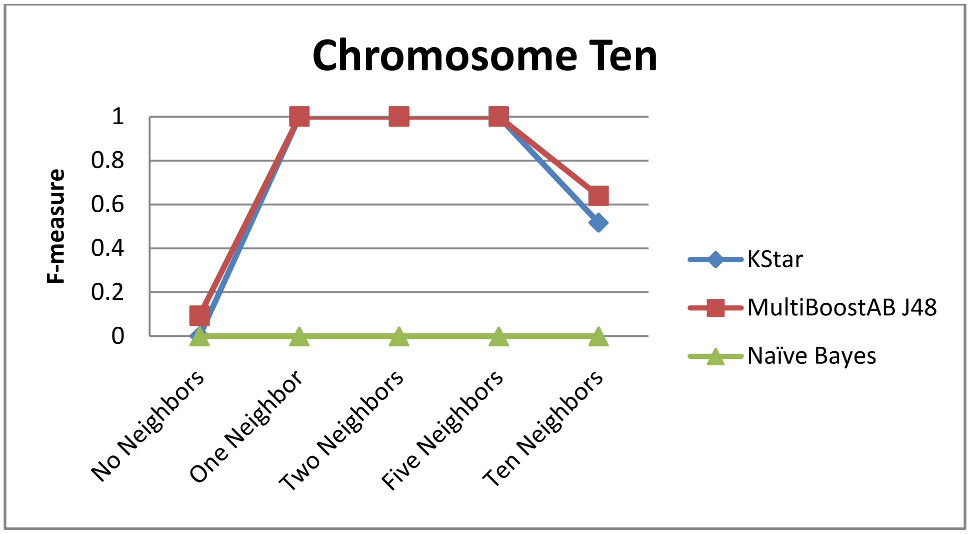


Figure 5.119. F-measure for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eleven, as more neighbor information is included, the F-measures for the MultiBoostAB algorithm using the J48 classifier increases. The F-measures obtained using the KStar classifier fluctuate depending on the number of neighbors included. The Naïve Bayesian classifier never obtains an F-measure above zero (See Figure 5.120).

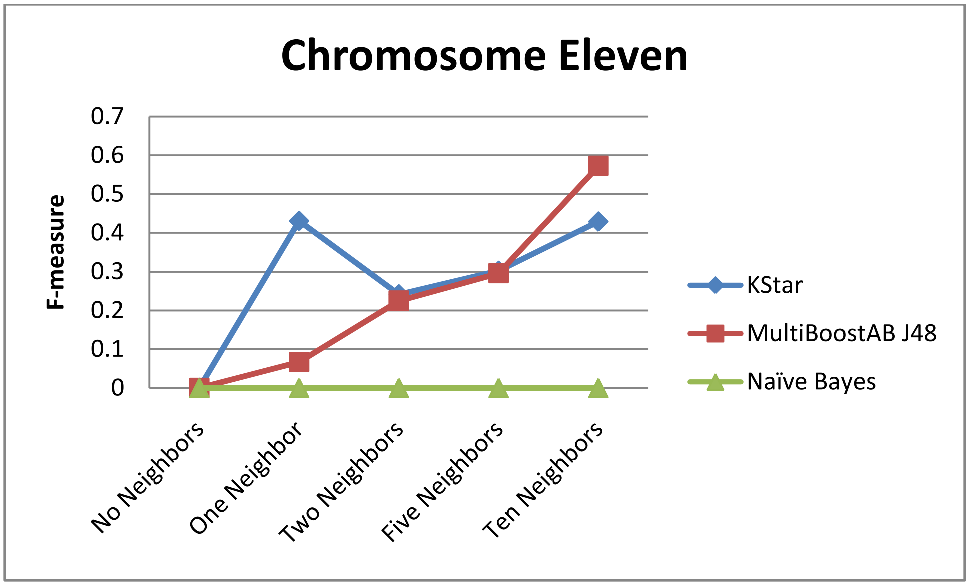


Figure 5.120. F-measure for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the inclusion of neighbor information decreases the F-measures obtained by the KStar classifier until information from each feature's ten-nearest neighbors is included. The inclusion of information from each feature's nearest neighbors or the two-nearest neighbors decreases the F-measures obtained using the MultiBoostAB algorithm using the J48 classifier. With the inclusion of more neighbor information, the F-measures then rise for the MultiBoostAB algorithm using the J48 classifier. The F-measures obtained using the Naïve Bayesian classifier with the inclusion of neighbor information are not as high as that obtained when no neighbor information is included (See Figure 5.121).

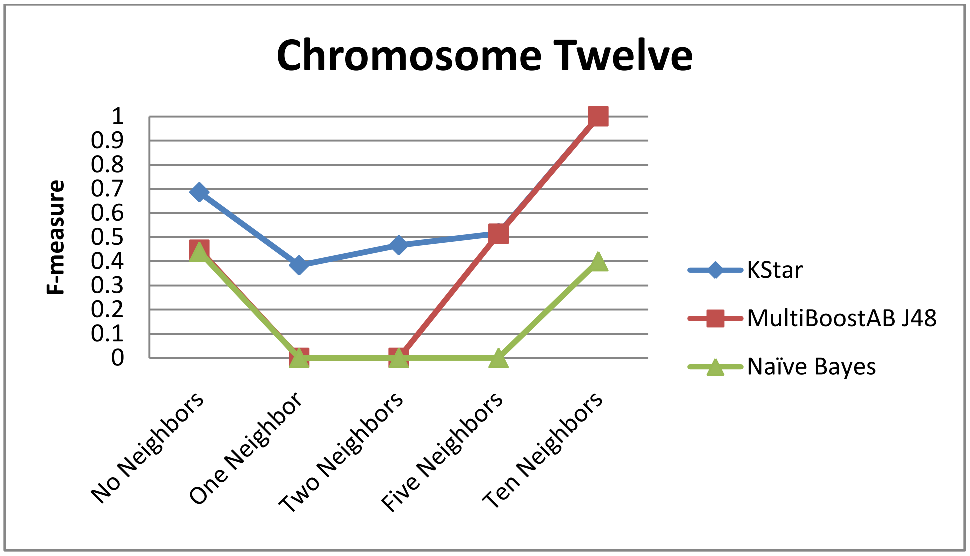


Figure 5.121. F-measure for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, the F-measures are low. For the MultiBoostAB algorithm using the J48 classifier and the KStar classifier, the higher F-measures are obtained when information from each feature's five-nearest neighbors is included. For the Naïve Bayesian classifier, the F-measures increase as information from more than two-nearest neighbors is included (See Figure 5.122).

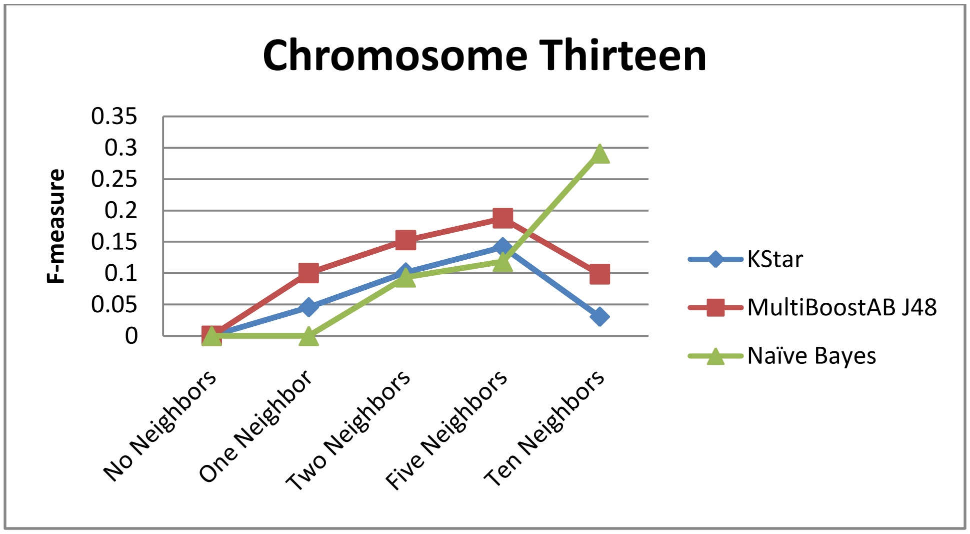


Figure 5.122. F-measure for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, upon the addition of information from each feature's ten-nearest neighbors, the KStar classifier and the MultiBoostAB algorithm using the J48 classifier drastically improve their F-measures, going from near 0.1 to 1.0. The F-measures for the Naïve Bayesian classifier fluctuate, obtaining the highest F-measure with the inclusion of information from each feature's nearest neighbors (See Figure 5.123).

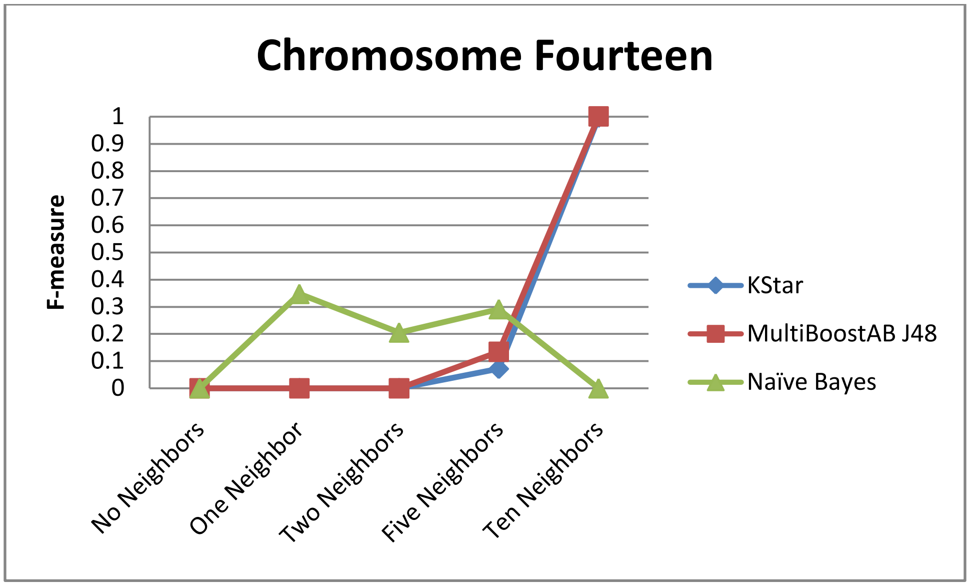


Figure 5.123. F-measure for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, the addition of neighbor information improves the accuracy of both the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The accuracy of the Naïve Bayesian classifier is improved slightly with only the inclusion of information from each feature's two-nearest neighbors (See Figure 5.124).

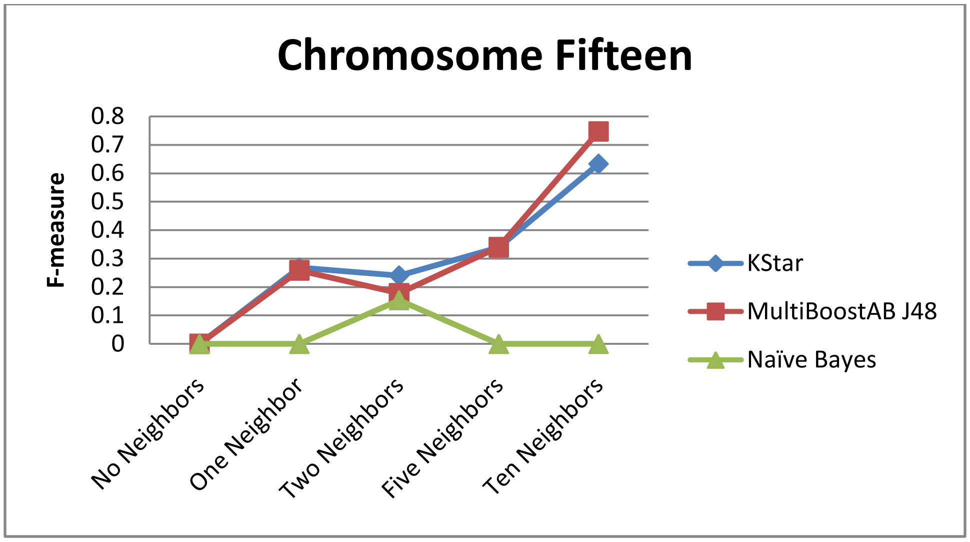


Figure 5.124. F-measure for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, the F-measures are low. The KStar classifier never obtains an F-measure above zero. With the addition of information from each feature's ten-nearest neighbors, the MultiBoostAB algorithm using the J48 classifier improves its F-measure from zero to above 0.1. The Naïve Bayesian classifier obtains its highest F-measure with the inclusion of each feature's five-nearest neighbors (See Figure 5.125).

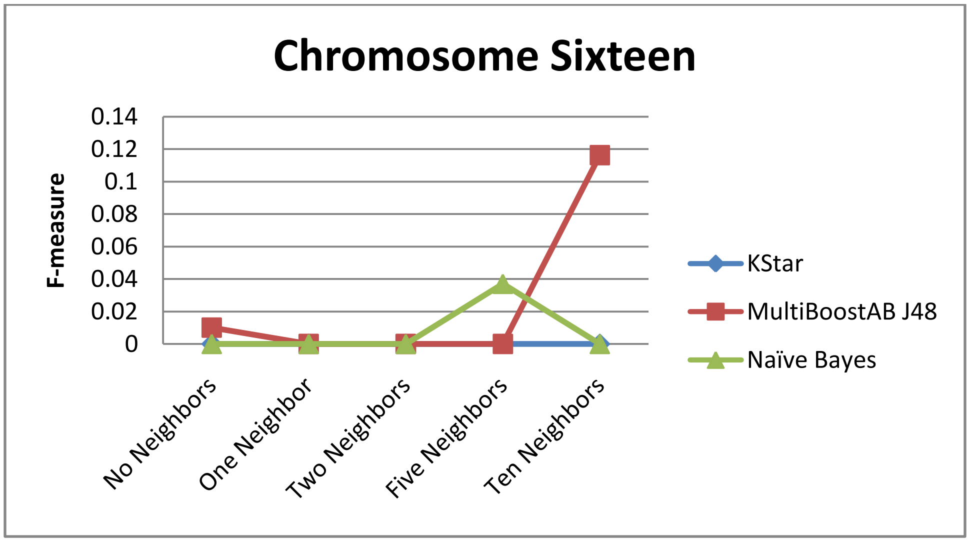


Figure 5.125. F-measure for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

From this analysis the MultiBoostAB algorithm obtains the higher accuracy in the classification process when neighbor information is included for most of the chromosomes. The partitioning of the classification process by chromosome produced in some cases higher F-measures than those that were obtained using the entire genome.

5.2 Classifying Genomic Features to Gene Ontology Terms

The results of experiments that determined if altering the type of neighbor information given the classifiers altered the accuracy of the classification process follow.

5.2.1 Using Neighbor's SGDID

A series of experiments was performed to determine if given the properties of chromosome number, start position, stop position, strand, neighbor number, neighbor's SGDID, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), Gene Ontology aspect and Gene Ontology term for genomic features (features being: genes, ARS, etc) could classification algorithms correctly classify the Gene Ontology term. This was also performed including information from the nearest, two-, five- and ten-nearest neighbors of each feature. This was also repeated on the individual chromosomes.

The results of the experiments are based on averages of ten different runs of each dataset being randomized and then split for training and testing. The training sets were set to contain 66% of the instances randomly selected from each dataset.

5.2.1.1 Results for Entire Genome

None of the classifiers obtained a percentage of correctly classified features that was above 30% (See Figure 5.126). As more neighbor information is added, the KStar classifier and the MultiBoostAB algorithm using the J48 classifier increase their correctly classified percentage, with the MultiBoostAB algorithm using the J48 classifier achieving the higher percentages. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of neighbor information beyond each feature's nearest neighbors does not impact the percentage of correctly classified features. When the Naïve Bayesian classifier is used, the percentage of correctly classified genomic features is not affected by the addition of neighbor information.

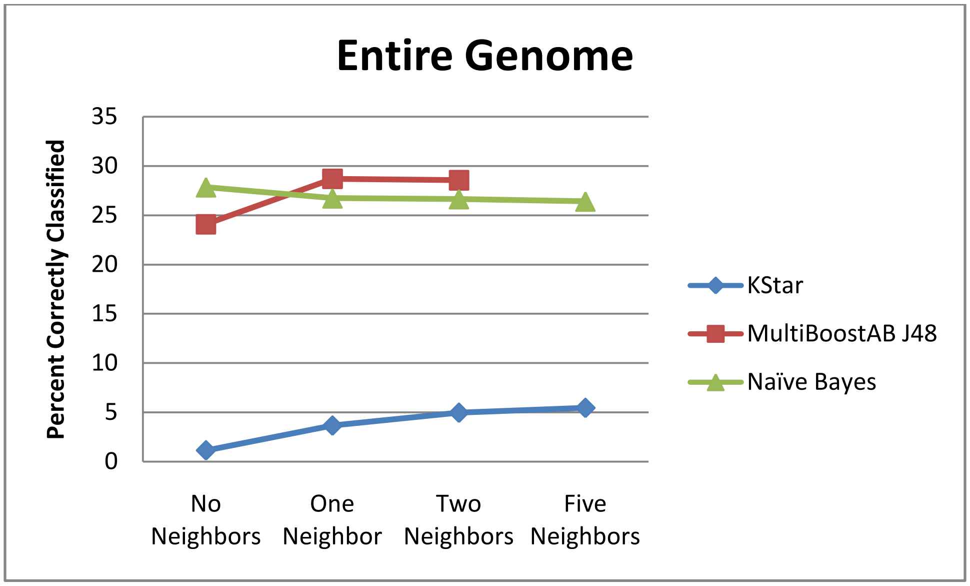


Figure 5.126. Percent of genomic features classified for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Regardless of the inclusion of neighbor information, none of the classifiers obtain a Kappa statistic above 0.25. This indicates that under all of the tested conditions, all of the classifiers obtained poor agreement between predicted and observed classification (See Figure 5.127).

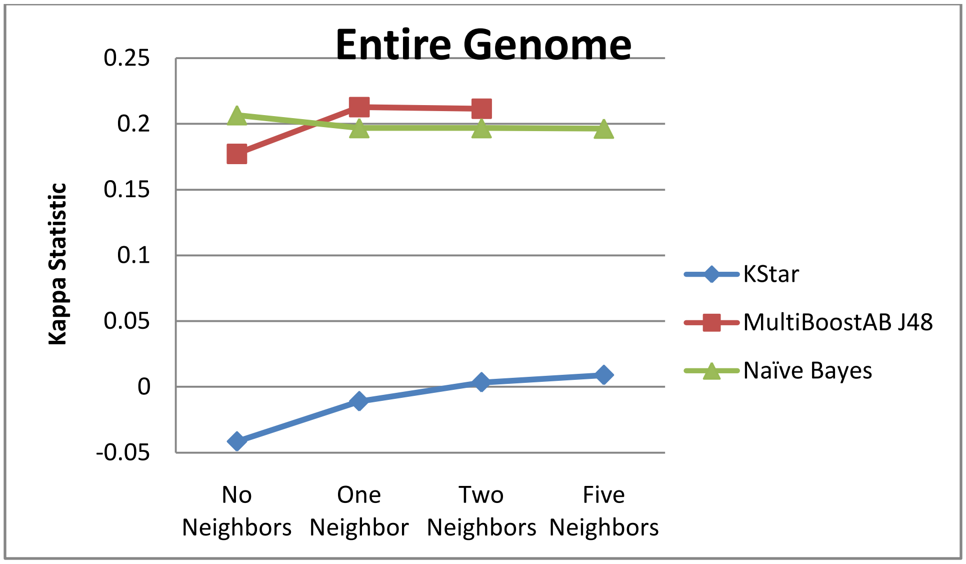


Figure 5.127. Kappa statistic for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The precision scores are low under all test conditions for all of the classifiers. For the KStar classifier, the inclusion of neighbor information improves the classification precision. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of neighbor information decreases the precision of the classification. The precision scores obtained by the Naïve Bayesian classifier are zero (See Figure 5.128).

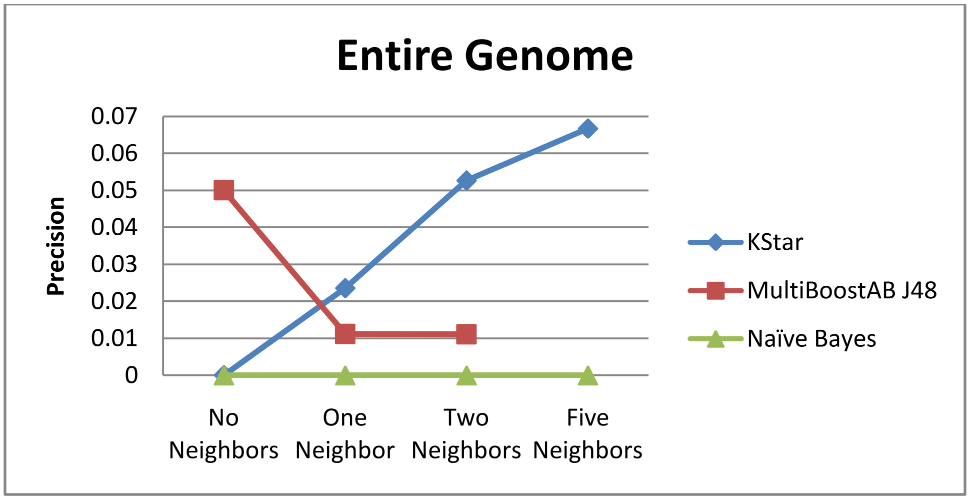


Figure 5.128. Precision for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For all classifiers, the recall scores are low regardless of the inclusion of neighbor information. The recall scores of the KStar classifier increases as more neighbor information is included but they remain low. The recall scores obtained by the MultiBoostAB algorithm using the J48 classifier increase with the inclusion neighbor information. For the Naïve Bayesian classifier, the recall scores are zero (See Figure 5.129).

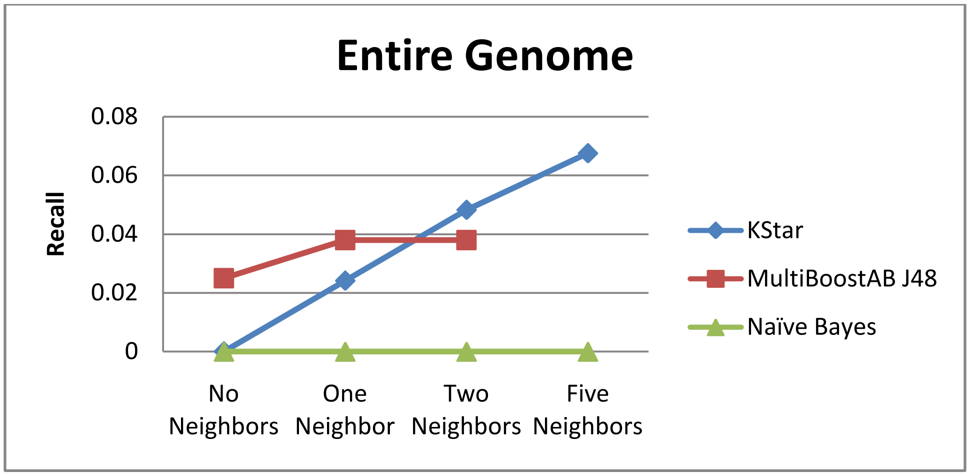


Figure 5.129. Recall scores for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

F-measures obtained by the different classifiers mimic their precision scores (See Figure 5.130). The F-measures are low under all test conditions for all of the classifiers. For the KStar classifier, the inclusion of neighbor information improves the accuracy of classification precision. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of neighbor information decreases the accuracy of the classification. The F-measures obtained by the Naïve Bayesian classifier are zero.

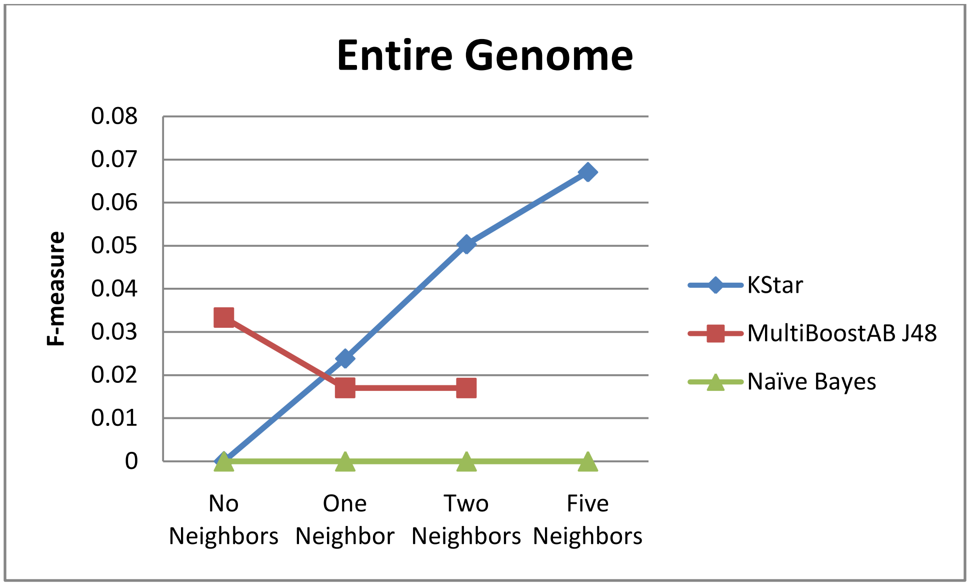


Figure 5.130. F-measure for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

When analyzing the area under the ROC curves, when no neighbor information is included, the Naïve Bayesian classifier is the only classifier that obtains an accuracy score that is deemed good. This result does not change with the inclusion of neighbor information. The KStar classifier improves from poor to excellent with the inclusion of neighbor information, and it obtains the higher accuracy scores. For the MultiBoostAB algorithm using the J48 classifier, the accuracy improves from poor to good with the inclusion of neighbor information (See Figure 5.131).

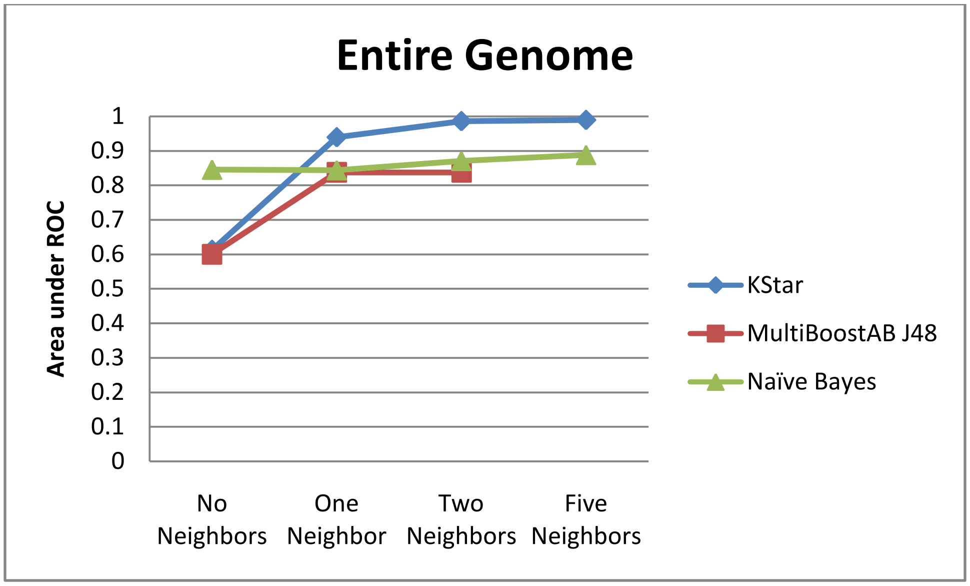


Figure 5.131. Area under ROC curve for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

None of the classifiers performed well based on the metrics used. Since the MultiBoostAB algorithm using the J48 classifier obtained the higher percentage of correctly classified features, it was used in the analysis of the classification of features to individual Gene Ontology terms.

To see the effect on the accuracy of classification for each network, the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier for each network were analyzed. The table of the F-measures can be found in Appendix D. Most of the Gene Ontology term groups did not benefit from the addition of neighbor information (See Figures 5.132 and 5.133). Only three Gene Ontology term groups (biological process, cytoplasm and molecular function) showed an increase in the classification of features to the groups with the addition of neighbor information.

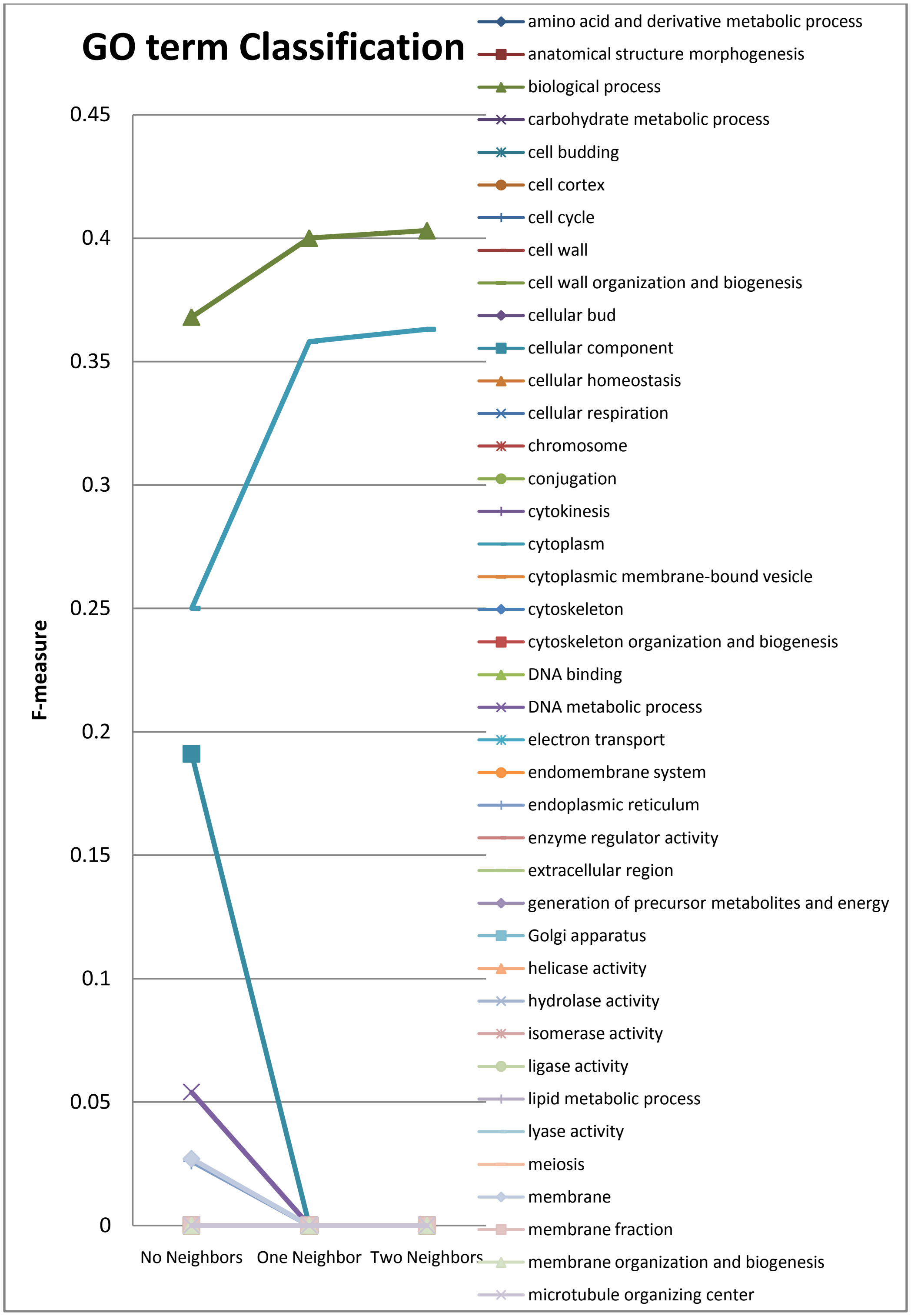


Figure 5.132. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual Gene Ontology (GO) terms.

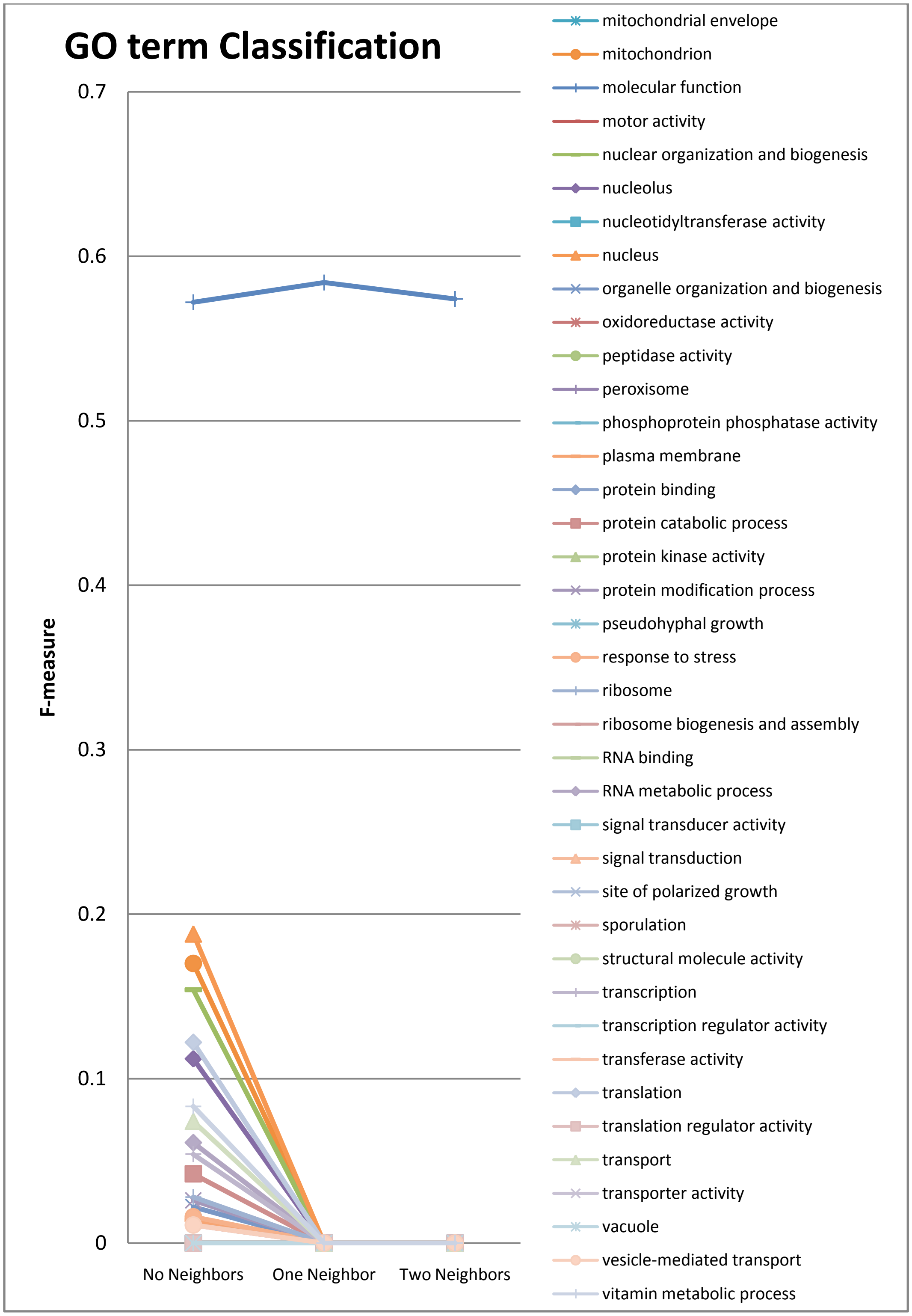


Figure 5.133. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual Gene Ontology (GO) terms.

5.2.1.2 Result for Individual Chromosomes

When we look at each chromosome individually, we see that the results of classification vary from chromosome to chromosome, from the number of neighbors included, and from the classification algorithm being used.

5.2.1.2.1 Percent Correctly Classified

For all chromosomes, the percent of genomic features correctly classified to the correct Gene Ontology term did not differ drastically as neighbor information is included, but the classifiers did perform differently.

For chromosome one, the inclusion of neighbor information increases the percentage of correctly classified features for all classifiers (See Figure 5.134). For the MultiBoostAB algorithm using the J48 classifier, the inclusion of neighbor information from each feature's ten-nearest neighbors drastically increases the percentage of correctly classified features. For the KStar classifier and the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbor has little impact on the classification process. The KStar classifier obtains the lower percentages of correctly classified features

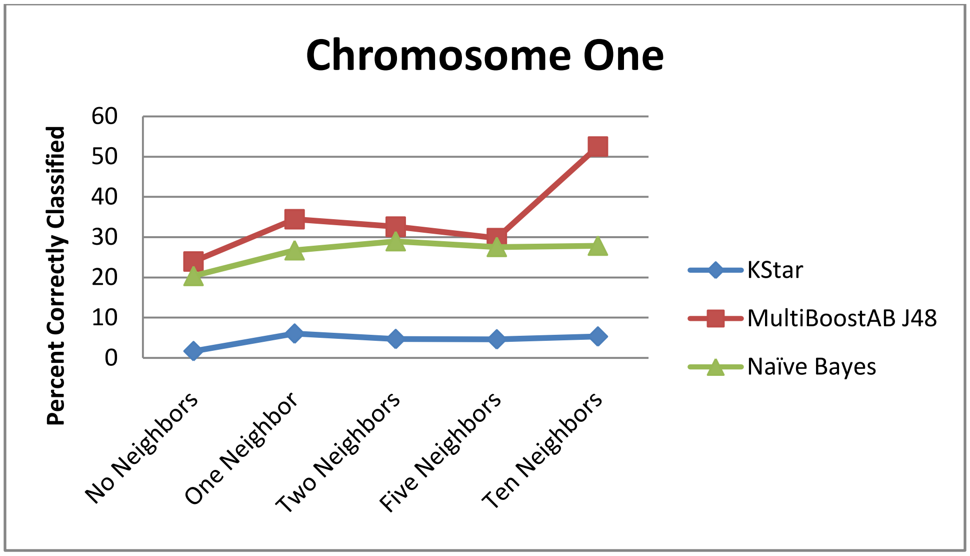
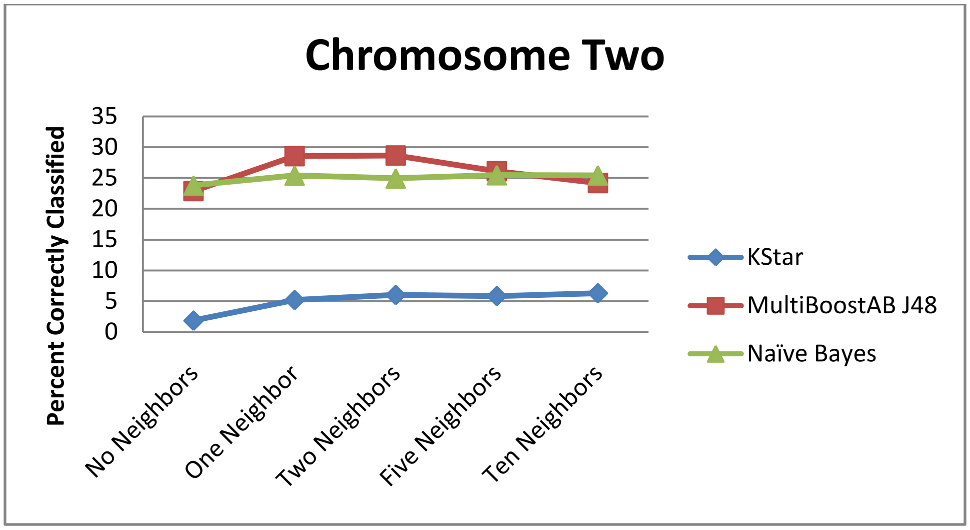


Figure 5.134. Percent of genomic features classified for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The inclusion of each feature's nearest and two-nearest neighbors produces the higher percentages of correctly classified features. The KStar classifier obtains the lowest percentages of correctly classified features, and the inclusion of information beyond each feature's nearest neighbors has little impact. For the Naïve Bayesian classifier, the percentage of correctly classified features is no affected by the inclusion of neighbor information (See Figure 5.135).



5.135. Percent of genomic features classified for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, the inclusion of neighbor information increases the percentage of correctly classified features for the KStar classifier and the Naïve Bayesian classifier. The inclusion of neighbor information beyond each feature's nearest neighbors has little effect on the percentage of correctly classified feature by the Naïve Bayesian classifier. The percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier is not as affected by the inclusion of neighbor information (See Figure 5.136), and it obtains the highest percentages. The KStar classifier obtains the lower percentages.

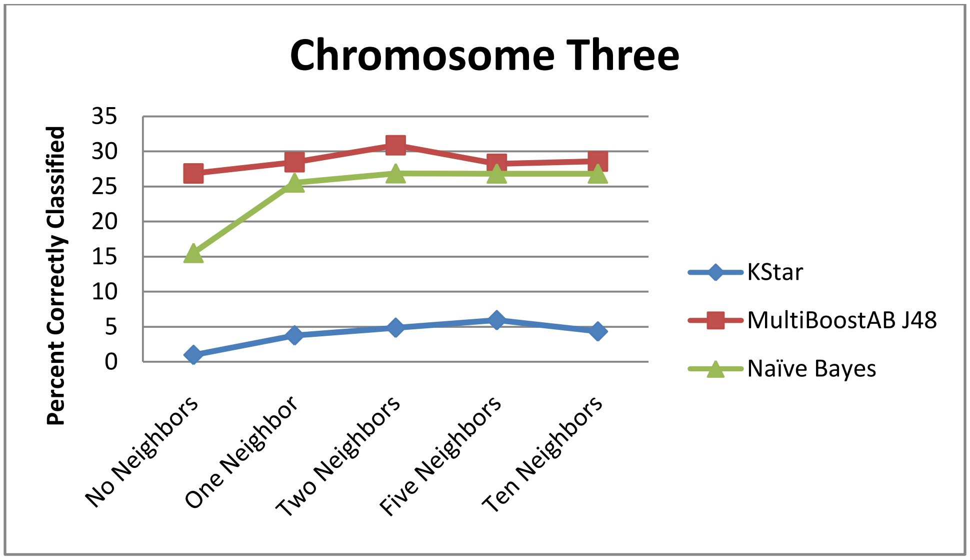


Figure 5.136. Percent of genomic features classified for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The inclusion of each feature's nearest and two-nearest neighbors produces the higher percentages of correctly classified features. The KStar classifier obtains the lower percentages of correctly classified features, and the inclusion of information beyond each feature's nearest neighbors has little impact. For the Naïve Bayesian classifier, the percentage of correctly classified features decreases slightly with the inclusion of neighbor information (See Figure 5.137).

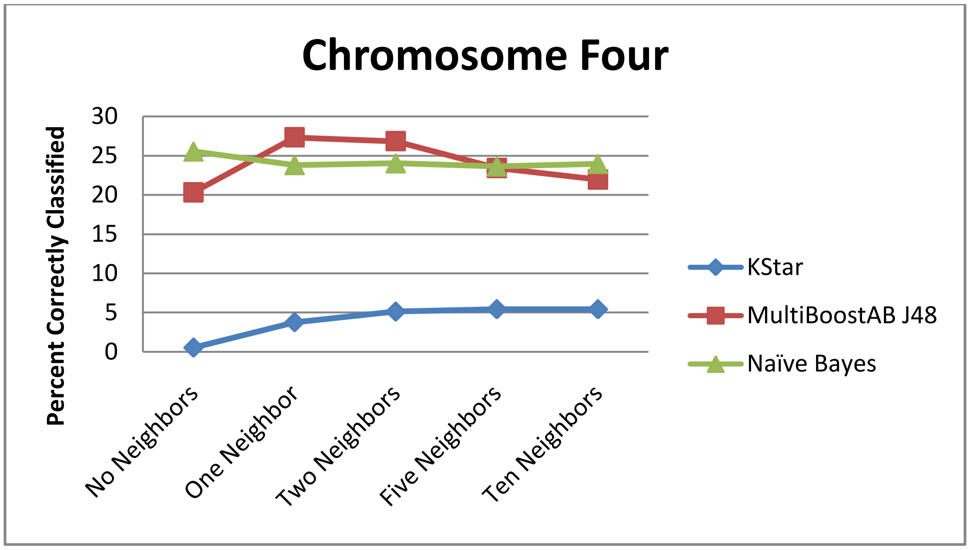


Figure 5.137. Percent of genomic features classified for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, the percentage of correctly classified features increases for all classifiers with the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, with the inclusion of each feature's nearest and two-nearest neighbors producing the higher percentages of correctly classified features. The KStar classifier obtains the lower percentages of correctly classified features. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the KStar classifier and the Naïve Bayesian classifier (See Figure 5.138).

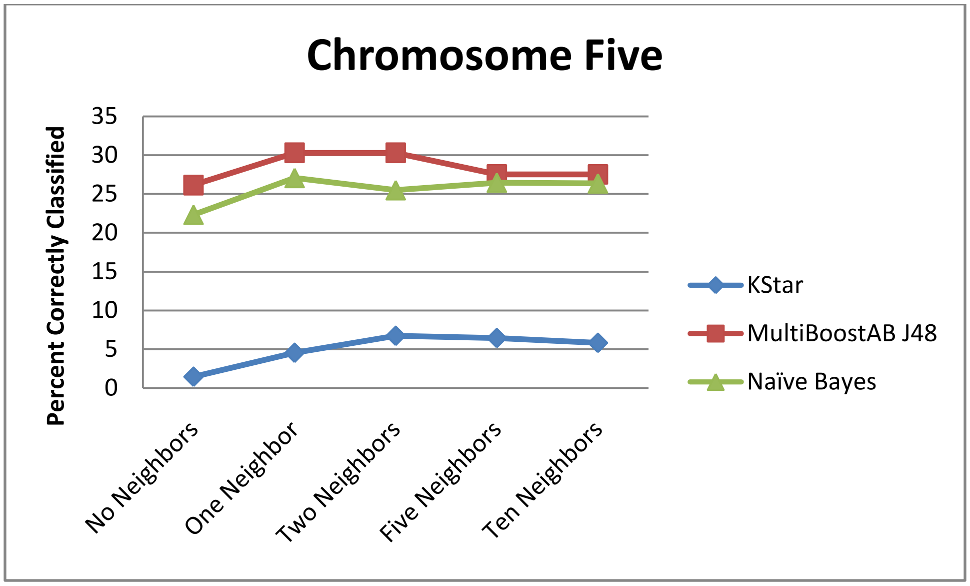


Figure 5.138. Percent of genomic features classified for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, the inclusion of neighbor information affects the Naïve Bayesian classifier the most. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentages obtained by the Naïve Bayesian classifier. The KStar classifier obtains a slight increase in the percentage of correctly classified features as more neighbor information is included. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, but the percentages are not affected by the inclusion of neighbor information until information from each feature's ten-nearest neighbors is included, then, it decreases (See Figure 5.139).

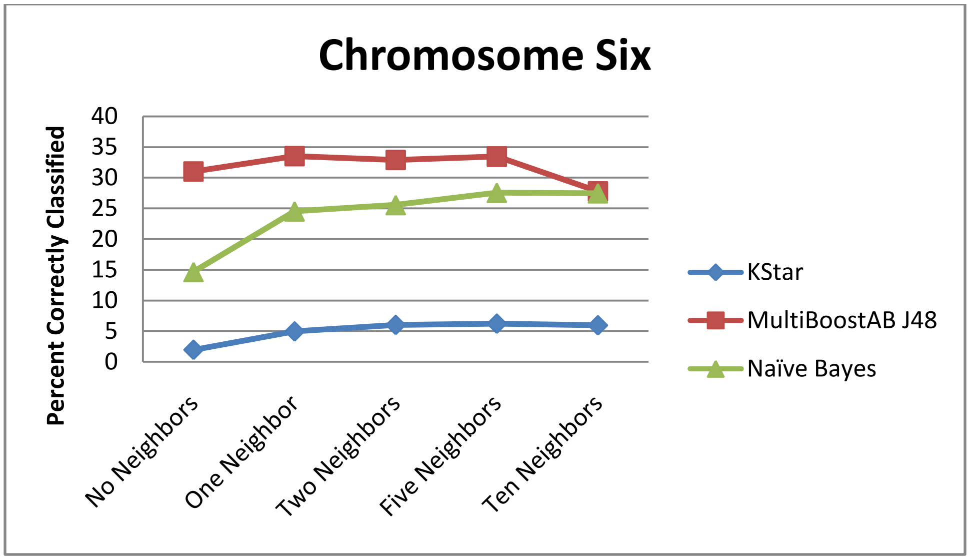


Figure 5.139. Percent of genomic features classified for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The inclusion of each feature's nearest and two-nearest neighbors produces the higher percentages of correctly classified features. The KStar classifier obtains the lower percentages of correctly classified features, and the inclusion of information beyond each feature's nearest neighbors has little impact. For the Naïve Bayesian classifier, the percentage of correctly classified features decreases slightly with the inclusion of neighbor information (See Figure 5.140).

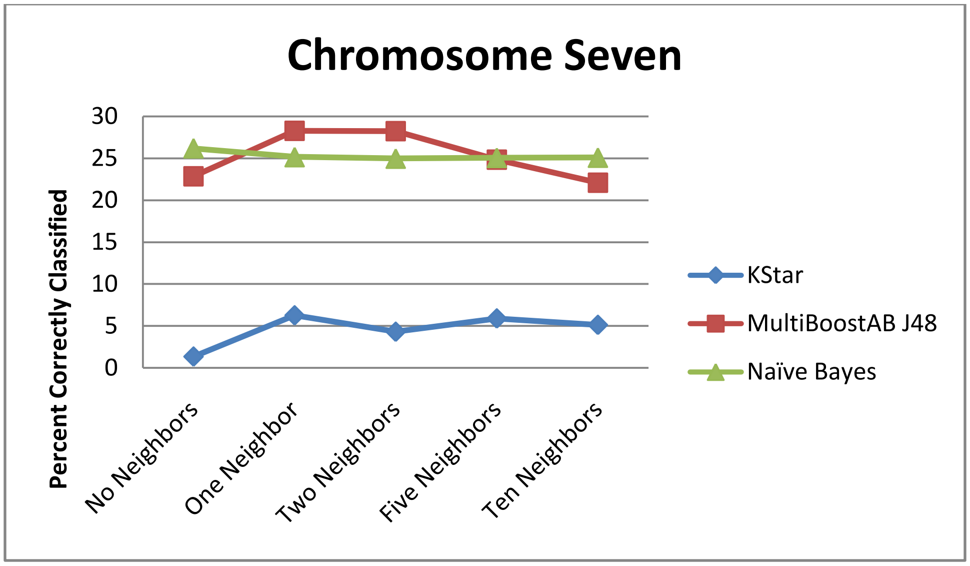


Figure 5.140. Percent of genomic features classified for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, the KStar classifier is affected most by the inclusion of neighbor information, with the inclusion of neighbor information increasing the percentage of correctly classified features. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features. The MultiBoostAB algorithm using the J48 classifier and the KStar classifier do not experience drastic changes in the percentage of correctly classified features with the inclusion information (See Figure 5.141).

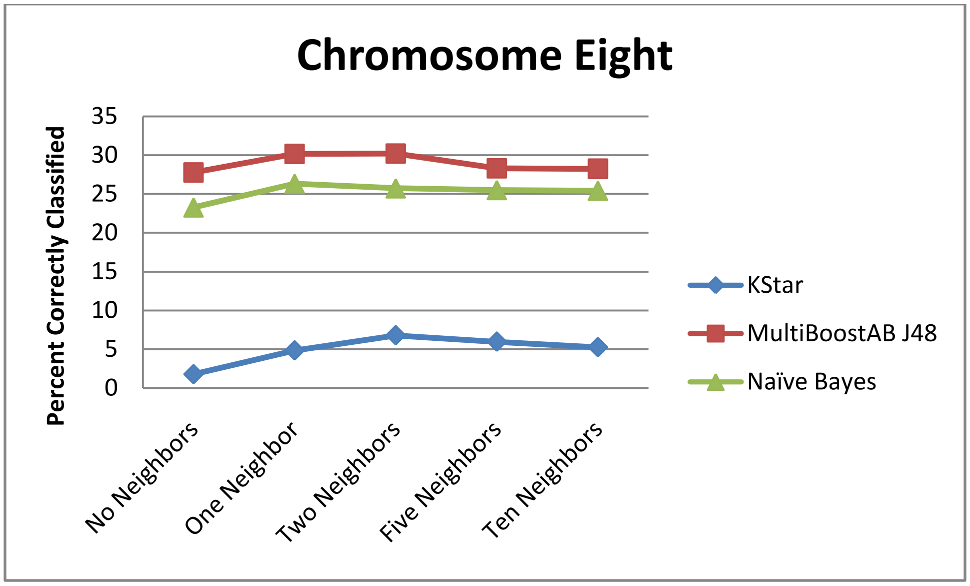


Figure 5.141. Percent of genomic features classified for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, the MultiBoostAB algorithm using the J48 classifier achieves the higher percentages of correctly classified features compared the other classifiers. The percentage of correctly classified features remains constant for the MultiBoostAB algorithm using the J48 classifier until the inclusion of neighbor information from each feature's five-nearest neighbors, then, the percentages drop. The inclusion of neighbor information slightly increase the percentage of correctly classified features for the KStar classifier and the Naïve Bayesian classifier (See Figure 5.142).

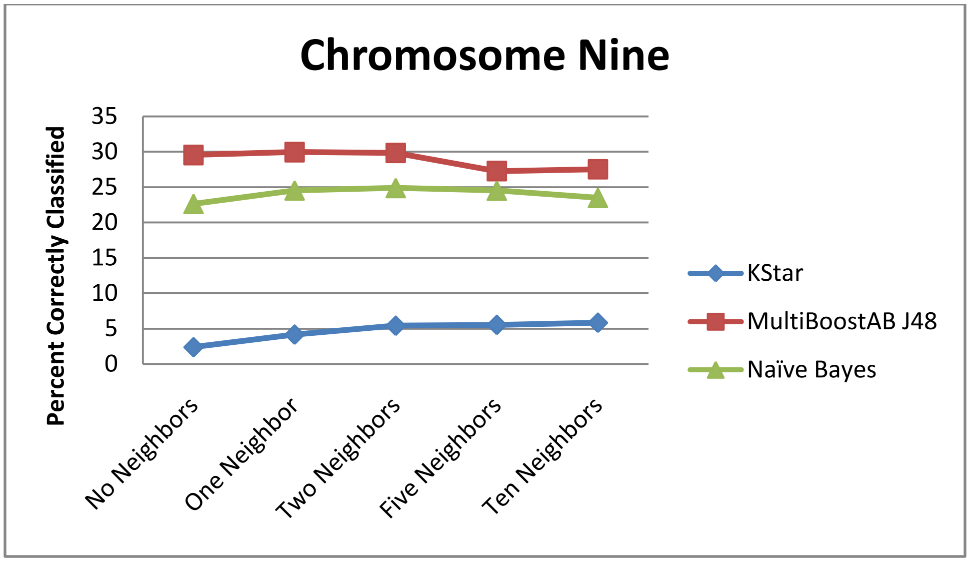


Figure 5.142. Percent of genomic features classified for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the percentage of correctly classified features increases for all classifiers with the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, with the inclusion of each feature's nearest and two-nearest neighbors producing the higher percentages of correctly classified features. The KStar classifier obtains the lower percentages of correctly classified features. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the KStar classifier and the Naïve Bayesian classifier (See Figure 5.143).

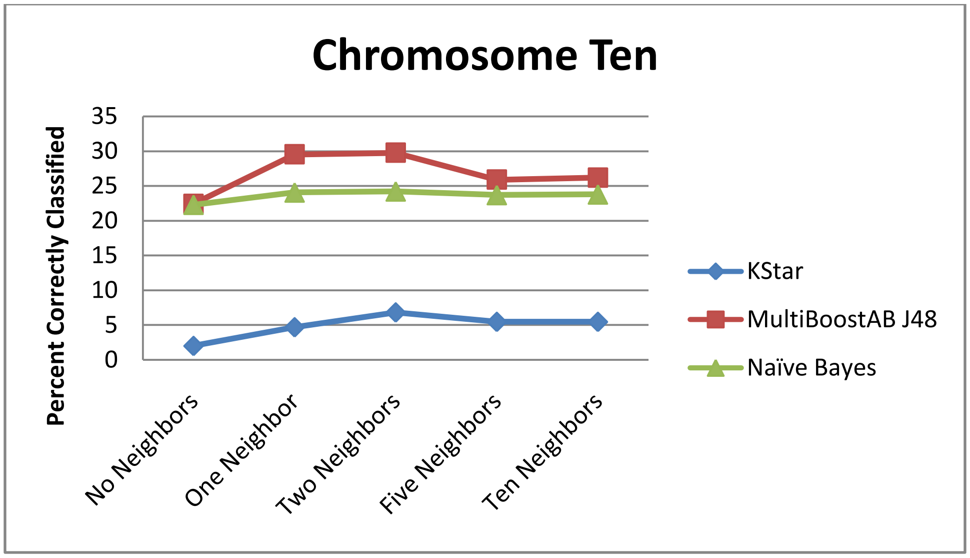


Figure 5.143. Percent of genomic features classified for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eleven, the percentage of correctly classified features increases for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier with the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, with the inclusion of each feature's nearest and two-nearest neighbors producing the higher percentages of correctly classified features, but this increase is lost as more neighbor information is included. The KStar classifier obtains the lower percentages of correctly classified features. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the KStar classifier. The percentage of correctly classified features for the Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See Figure 5.144).

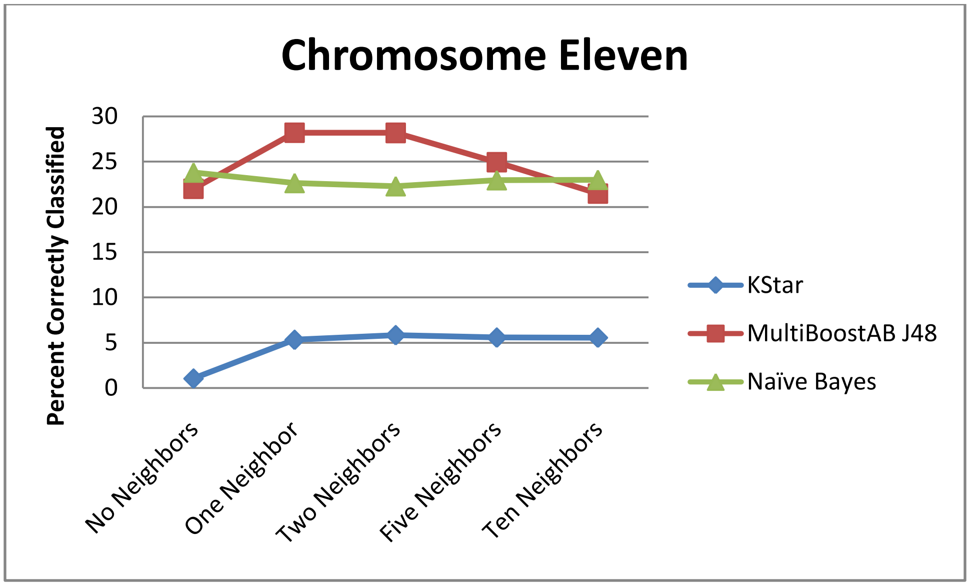


Figure 5.144. Percent of genomic features classified for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The inclusion of each feature's nearest and two-nearest neighbors produces the higher percentages of correctly classified features. The KStar classifier obtains the lower percentages of correctly classified features, and the inclusion of information beyond each feature's nearest neighbors has little impact. For the Naïve Bayesian classifier, the percentage of correctly classified features is not affected by the inclusion of neighbor information (See Figure 5.145).

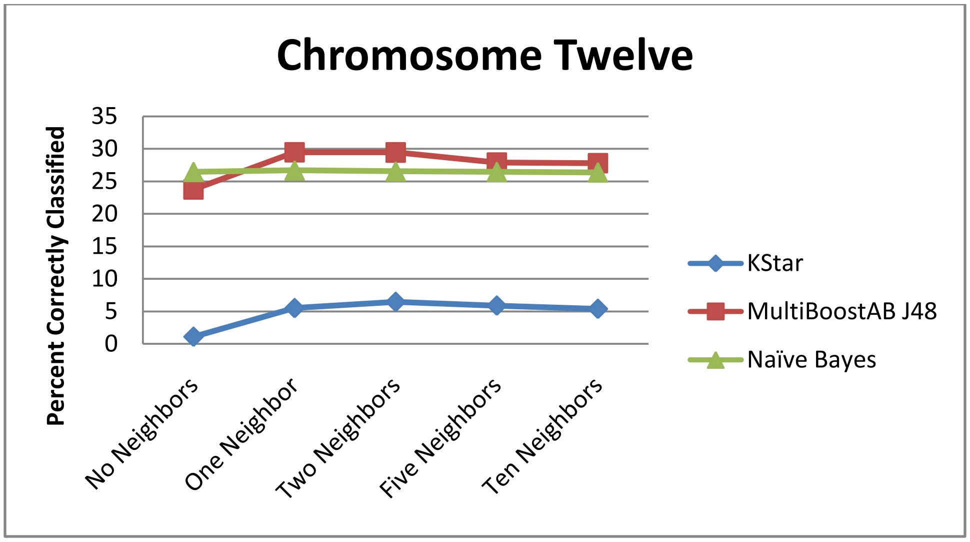


Figure 5.145. Percent of genomic features classified for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The inclusion of each feature's nearest and two-nearest neighbors produces the higher percentages of correctly classified features. The KStar classifier obtains the lower percentages of correctly classified features, and the inclusion of information beyond each feature's nearest neighbors has little impact. For the Naïve Bayesian classifier, the percentage of correctly classified features is not affected by the inclusion of neighbor information (See Figure 5.146).

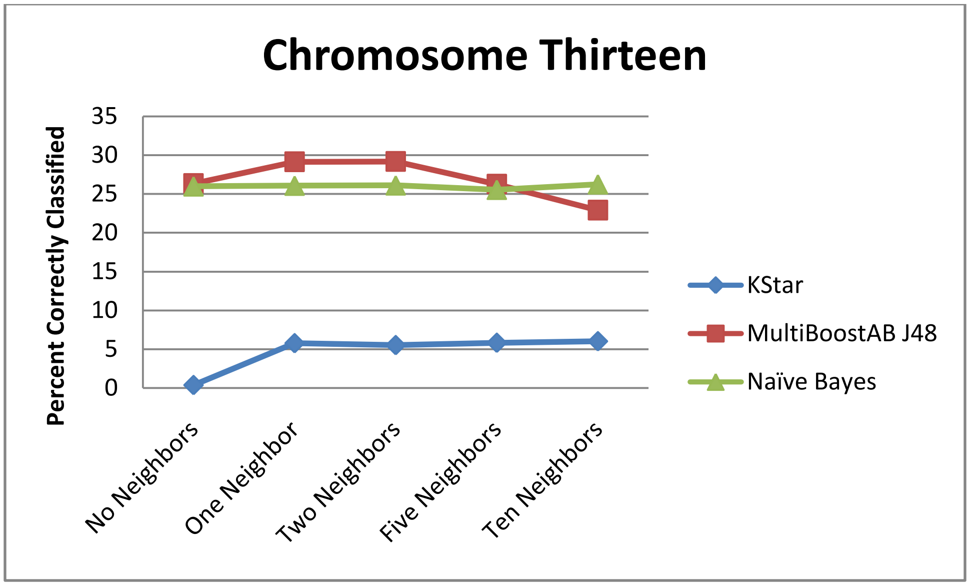


Figure 5.146. Percent of genomic features classified for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, for the KStar classifier, there is an increase in the percentage of correctly classified features with the inclusion of neighbor information, with the inclusion of neighbor information beyond each feature's nearest neighbors having little impact. The higher percentages are obtained by the MultiBoostAB algorithm using the J48 classifier. The inclusion of information from each feature's ten-nearest neighbors decreases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier (See Figure 5.147).

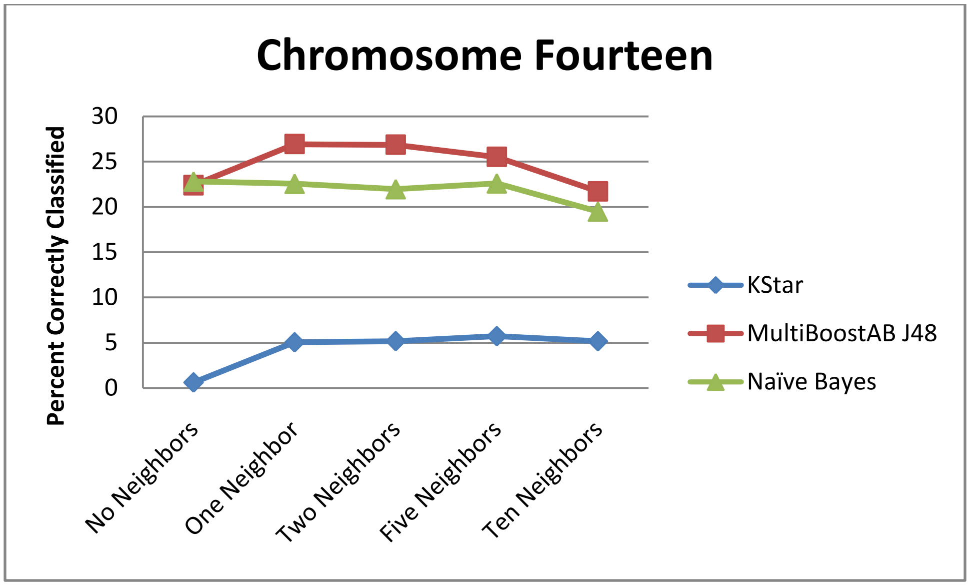


Figure 5.147. Percent of genomic features classified for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, similar to other chromosomes, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The inclusion of each feature's nearest and two-nearest neighbors produces the higher percentages of correctly classified features. The KStar classifier obtains the lower percentages of correctly classified features, and the inclusion of information beyond each feature's nearest neighbors has little impact. For the Naïve Bayesian classifier, the percentage of correctly classified features is not affected by the inclusion of neighbor information (See Figure 5.148).

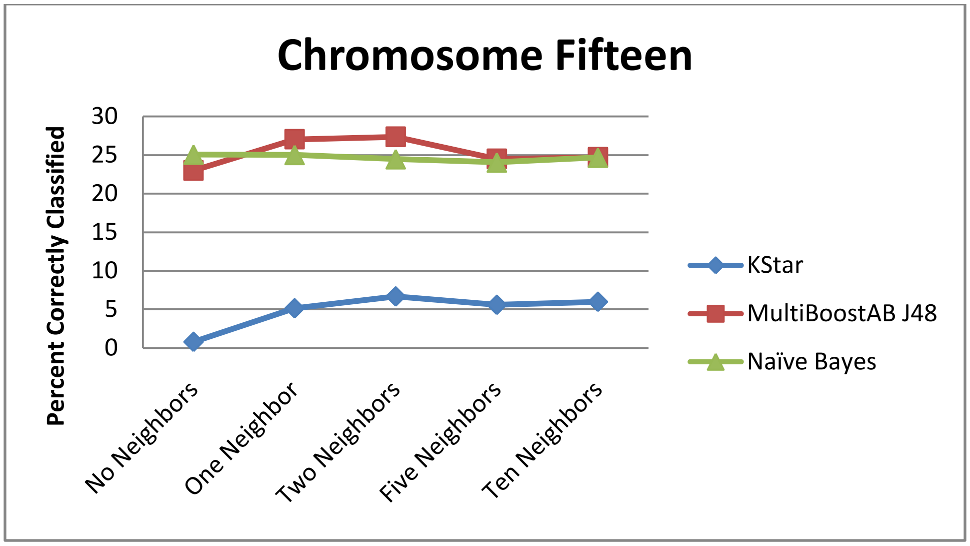


Figure 5.148. Percent of genomic features classified for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Like other chromosomes, for chromosome sixteen, the MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features. The inclusion of information from each feature's nearest and two-nearest neighbors increases the percentage of features correctly classified, but this increase is lost as more neighbor information is included. For the KStar classifier, the inclusion of neighbor information increases the percentage of correctly classified features. For the Naïve Bayesian classifier, the percentage of correctly classified features is not affected by the inclusion of neighbor information (See Figure 5.149).

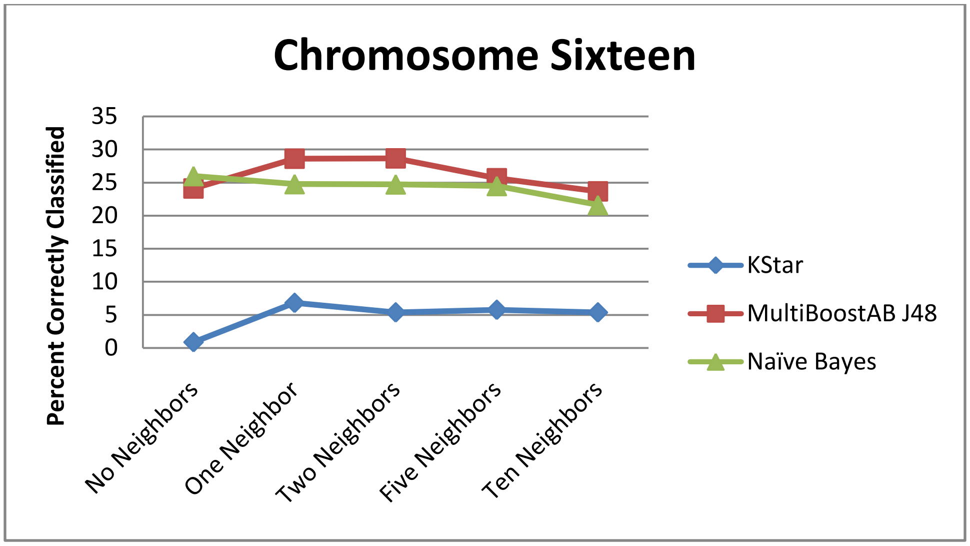


Figure 5.149. Percent of genomic features classified for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For the mitochondrial chromosome, the MultiBoostAB algorithm using the J48 classifier obtains an increase in the percentage of correctly classified features with the inclusion of information from two or more nearest neighbors of each feature. The inclusion of neighbor information does not have a drastic affect on the KStar classifier and the Naïve Bayesian classifier. The KStar classifier obtains the lower percentages of correctly classified features (See Figure 5.150).

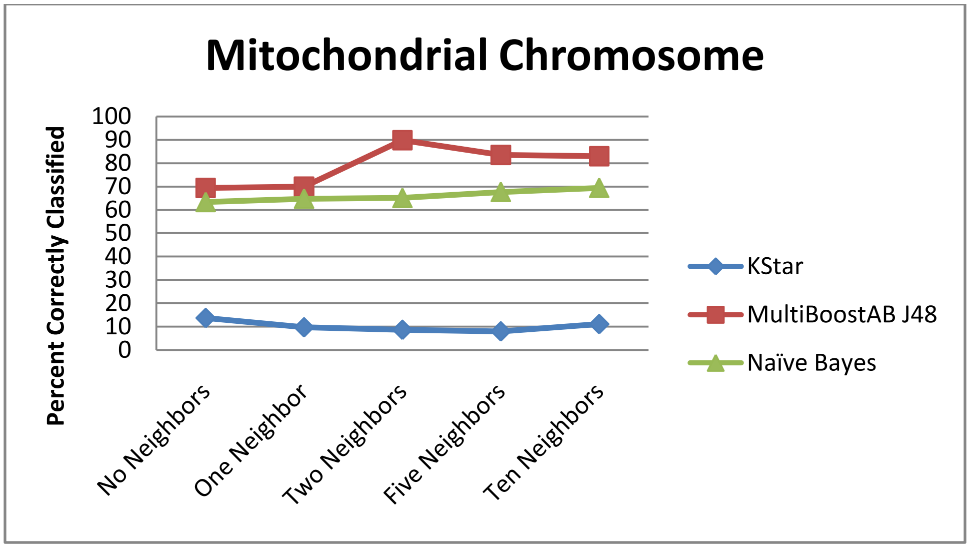


Figure 5.150. Percent of genomic features classified for the mitochondrial chromosome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For most of the chromosomes, the MultiBoostAB algorithm using the J48 classifier obtained a higher percentage of correctly classified features followed by the Naïve Bayesian classifier then the KStar classifier. The mitochondrial chromosome is the only chromosome that has classifiers that obtain percentages of correctly classified features above 60%. The partitioning of the classification process by chromosome, in general, did not improve the percentages of correctly classified features for the classifiers.

5.2.1.2.2. F-measures

To look at the accuracy of the classification process for each chromosome, the F-measures obtained for each chromosome can be analyzed. The accuracy of the classification process is affected by the inclusion of neighbor information, and the classifier is used. The F-measures for the chromosomes are low.

For chromosome one, the highest F-measure is obtained by the MultiBoostAB algorithm using the J48 classifier with the inclusion of information from each feature's nearest neighbor. The inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier. The KStar classifier obtains the lower F-measures, and it obtains slightly increased F-measures with the inclusion of neighbor information (See Figure 5.151).

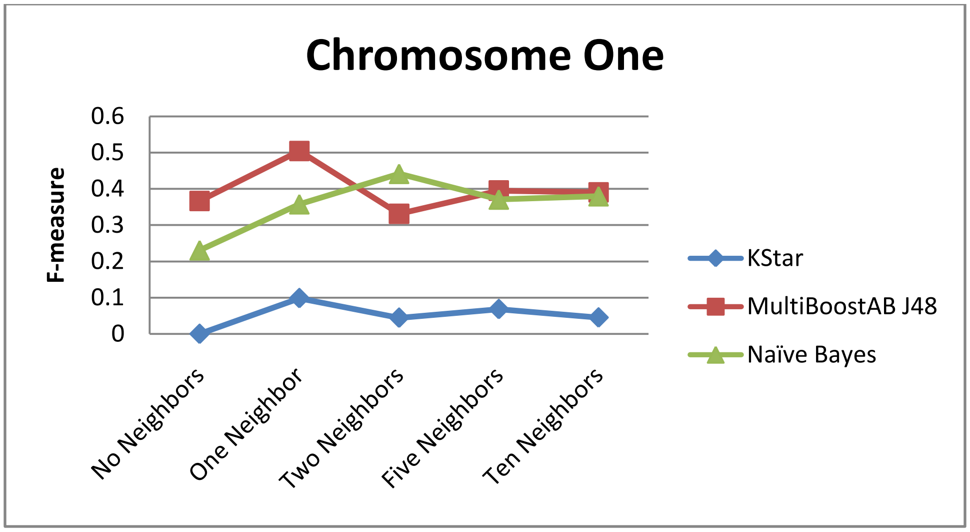


Figure 5.151. F-measure for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, the highest F-measure is obtained by the Naïve Bayesian classifier with information from each feature's five-nearest neighbors is included. The F-measures for the MultiBoostAB algorithm using the J48 classifier fluctuate depending on the amount of neighbor information that is included. The largest decrease in the F-measures is seen when information from each feature's two-nearest neighbors is included for the MultiBoostAB algorithm using the J48 classifier. The inclusion of neighbor information increases the F-measures for the KStar classifier (See Figure 5.152).

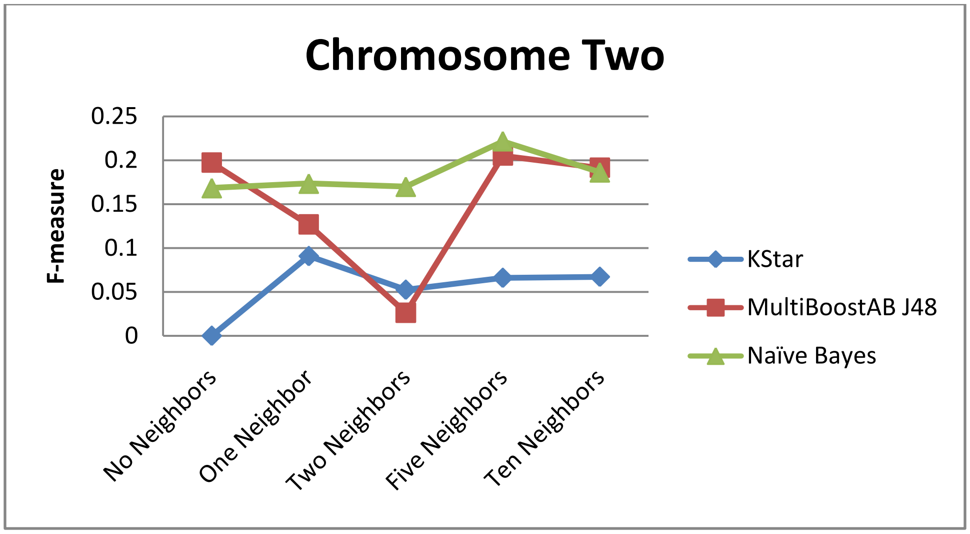


Figure 5.152. F-measure for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier. The higher F-measure is obtained with the Naïve Bayesian classifier with the inclusion of information from each feature's five-nearest neighbors. The F-measures for the MultiBoostAB algorithm using the J48 classifier fluctuate depending on the amount of neighbor information that is included. The KStar classifier has the lower F-measures. The inclusion of information from each feature's five-or-more nearest neighbors increases the F-measures obtained by the KStar classifier (See Figure 5.153).

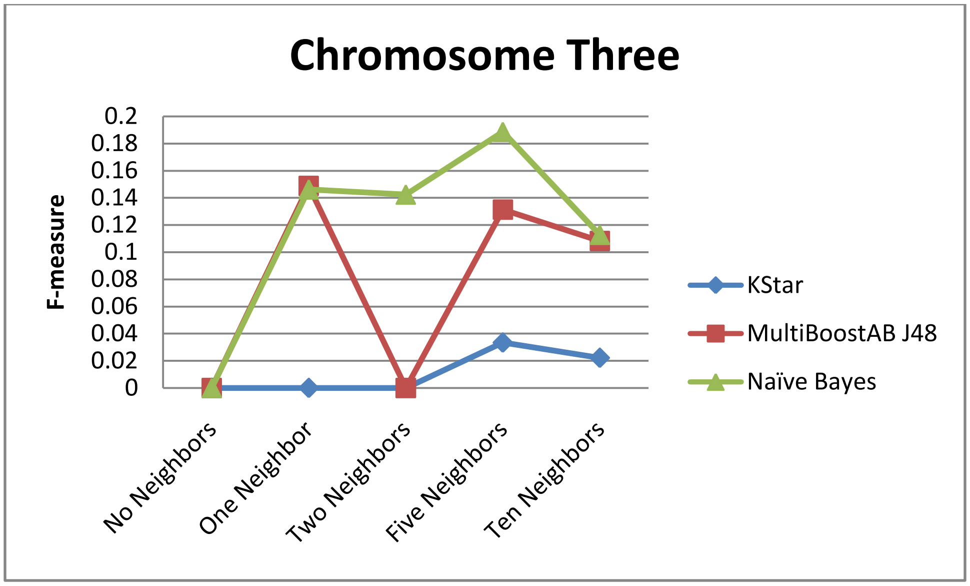


Figure 5.153. F-measure for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. This increase is not seen for the MultiBoostAB algorithm using the J48 classifier until information from each feature's five-nearest or ten-nearest neighbors is included (See Figure 5.154).

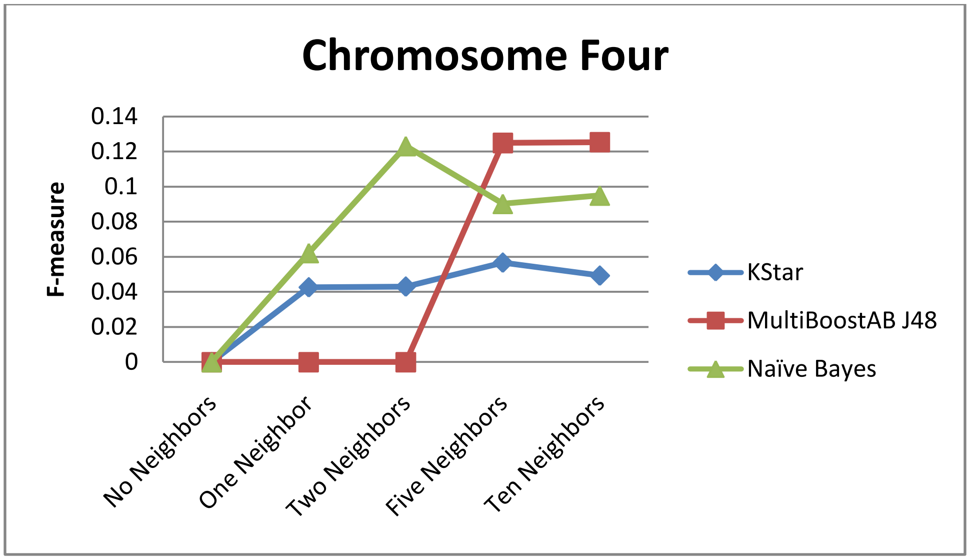


Figure 5.154. F-measure for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, the inclusion of neighbor information improves the F-measures for the Naïve Bayesian classifier and the KStar classifier, with the higher F-measures obtained by the Naïve Bayesian classifier. The inclusion of neighbor information from each feature's nearest and two-nearest neighbors decreases the F-measures for the MultiBoostAB algorithm using the J48 classifier, but the F-measures then rebound upon the inclusion of information from each feature's five-or-more-nearest neighbors (See Figure 5.155).

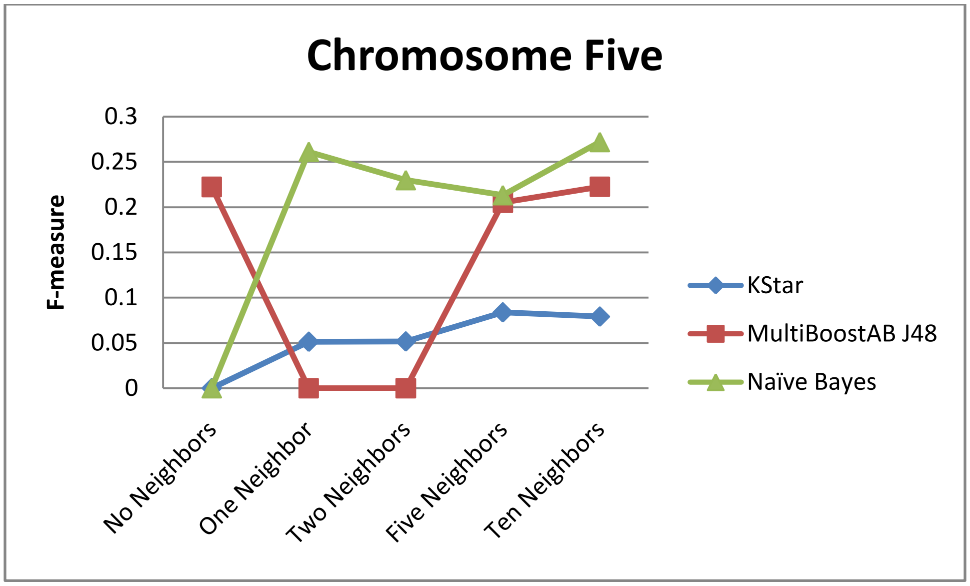


Figure 5.155. F-measure for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, the inclusion of neighbor information increased the F-measures obtained by all the classifiers. The higher F-measures are obtained by the MultiBoostAB algorithm using the J48 classifier. The inclusion of neighbor information beyond each feature's five-nearest neighbors has little impact on the accuracy of classification process for the MultiBoostAB algorithm using the J48 classifier. The inclusion of neighbor information from each feature's nearest neighbors has little impact the accuracy of the classification process for the KStar classifier and the Naïve Bayesian classifier (See Figure 5.156).

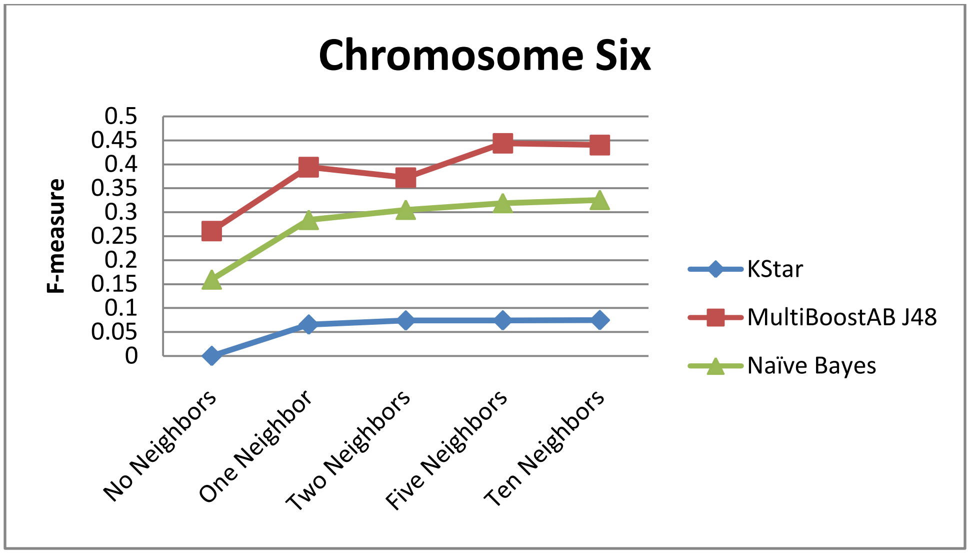


Figure 5.156. F-measure for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, like chromosome four, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. This increase is not seen for the MultiBoostAB algorithm using the J48 classifier until information from each feature's five-nearest or ten-nearest neighbors is included (See Figure 5.157).

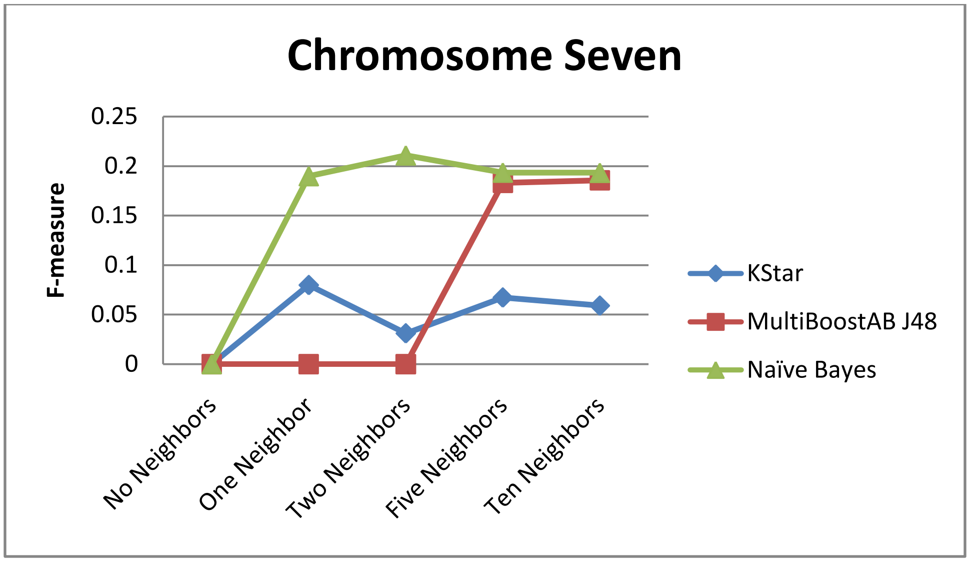


Figure 5.157. F-measure for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. The inclusion of neighbor information decreases the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier, with the largest decrease observed upon the inclusion of neighbor information from each feature's nearest neighbors (See Figure 5.158).

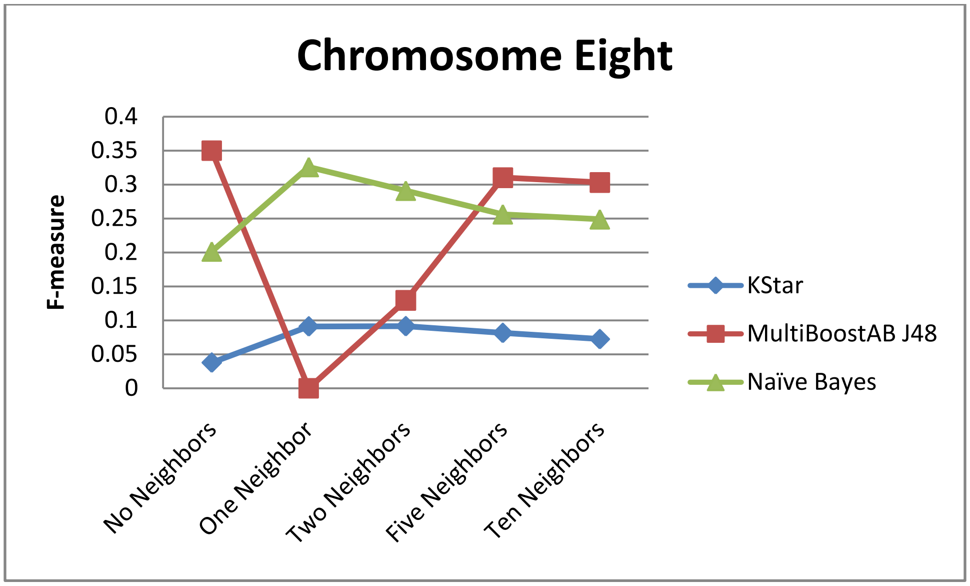


Figure 5.158. F-measure for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Similar to other chromosomes, for chromosome nine, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. This increase is not seen for the MultiBoostAB algorithm using the J48 classifier until information from each feature's five-nearest or ten-nearest neighbors is included (See Figure 5.159).

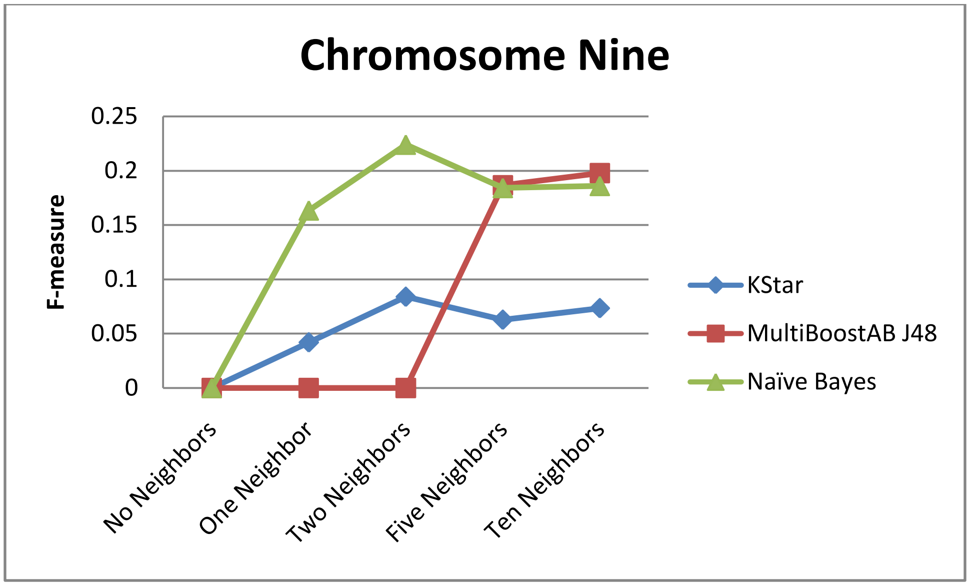


Figure 5.159. F-measure for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. The inclusion of information from each feature's nearest and two-nearest neighbors decreases the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier. With the inclusion of information from the five- or ten-nearest neighbors of each feature, the F-measures then increase for the MultiBoostAB algorithm using the J48 classifier (See Figure 5.160).

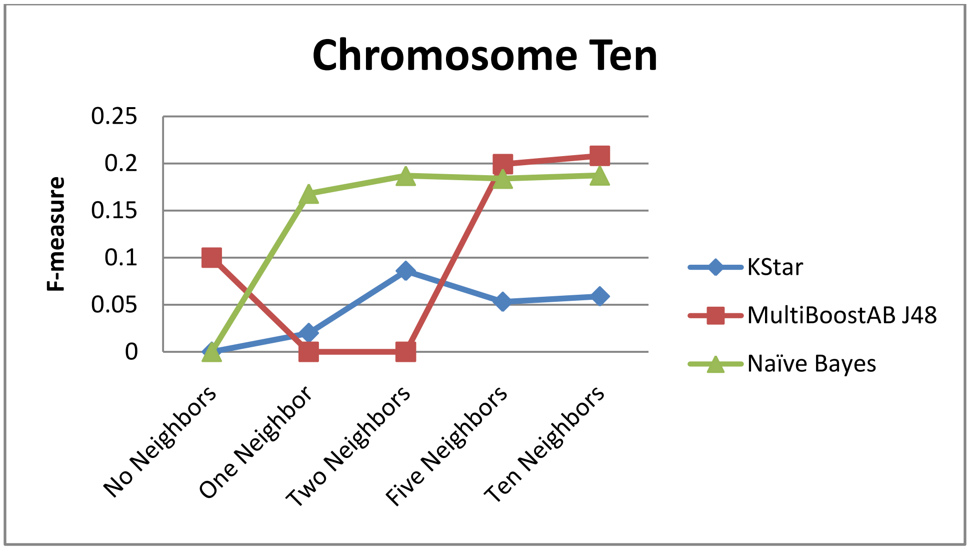


Figure 5.160. F-measure for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Like other chromosomes, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier for chromosome eleven. This increase is not seen for the MultiBoostAB algorithm using the J48 classifier until information from each feature's five-nearest or ten-nearest neighbors is included (See Figure 5.161).

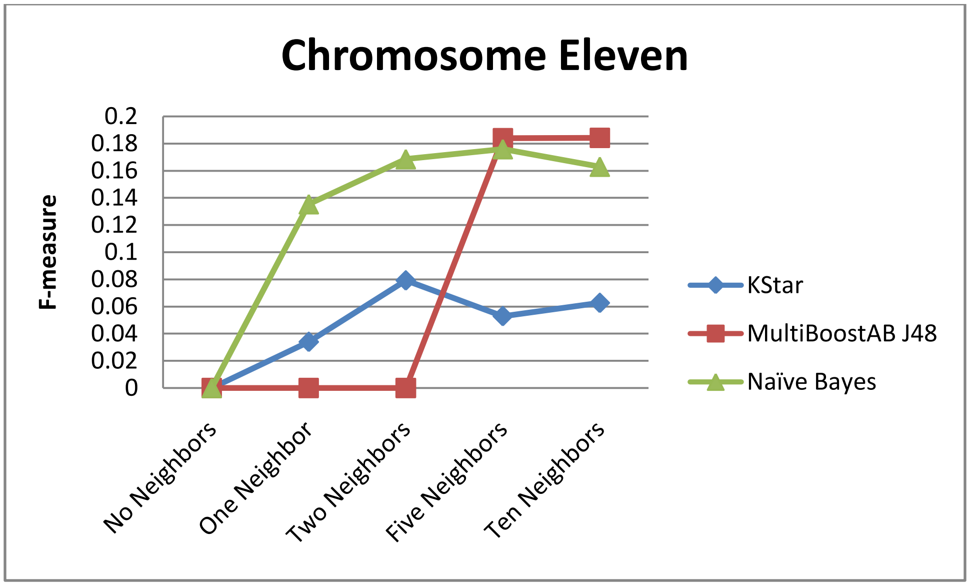


Figure 5.161. F-measure for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. The inclusion of information from each feature's nearest and two-nearest neighbors decreases the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier. With the inclusion of information from the five- or ten-nearest neighbors of each feature, the F-measures then increase for the MultiBoostAB algorithm using the J48 classifier (See Figure 5.162).

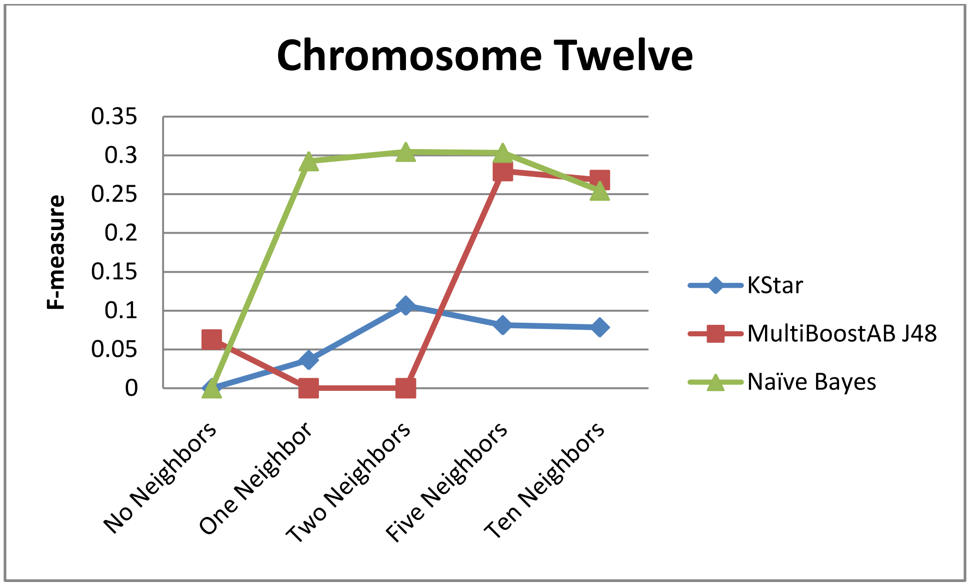


Figure 5.162. F-measure for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. The inclusion of information from each feature's nearest and two-nearest neighbors decreases the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier, with the inclusion of information from the five- or ten-nearest neighbors of each feature, the F-measures then increase and are the highest F-measures obtained by any classifier (See Figure 5.163).

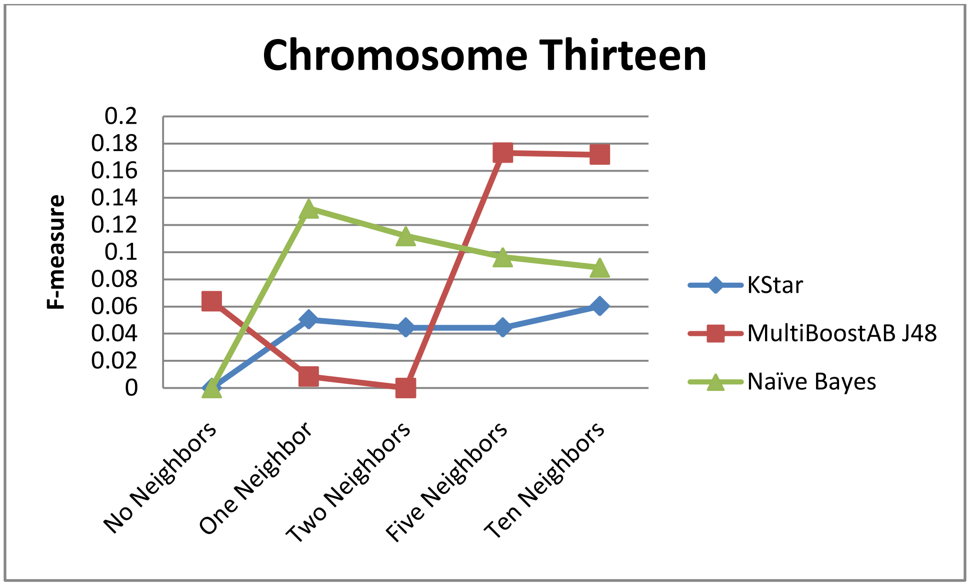


Figure 5.163. F-measure for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier (See Figure 5.164). For the Naïve Bayesian classifier, the higher F-measures are obtained with the inclusion of information from each feature's nearest, two-nearest and five-nearest neighbors, then the F-measure drops. The inclusion of neighbor information decreases the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier, with the lower F-measures obtained when information from each feature's nearest and two-nearest neighbors is included. The inclusion of information beyond each feature's nearest neighbors has little effect on the F-measures obtained by the KStar classifier. The F-measures obtained by the KStar are the lowest.

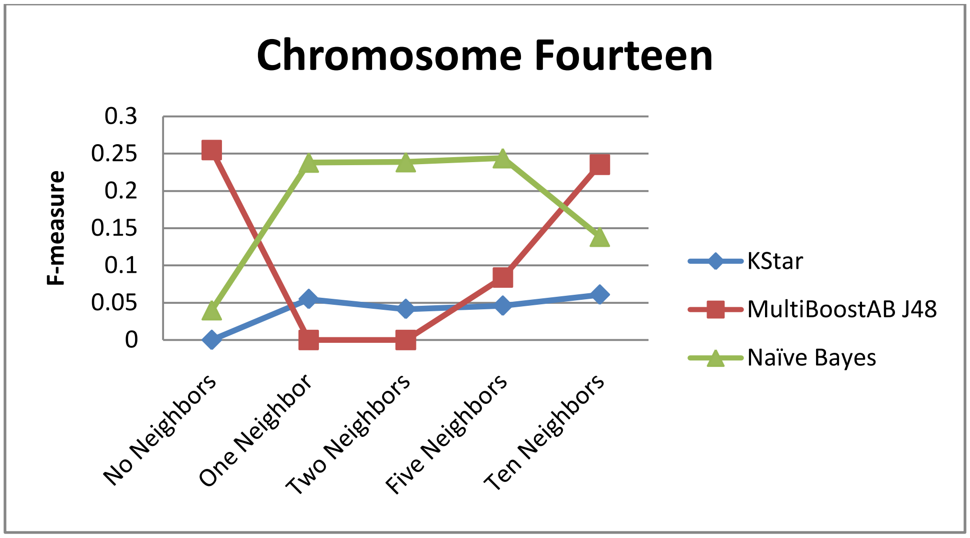


Figure 5.164. F-measure for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Like other chromosomes, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier for chromosome fifteen. This increase is not observed until the inclusion of information from each feature's five-or-more-nearest neighbors for the MultiBoostAB algorithm using the J48 classifier (See Figure 5.165).

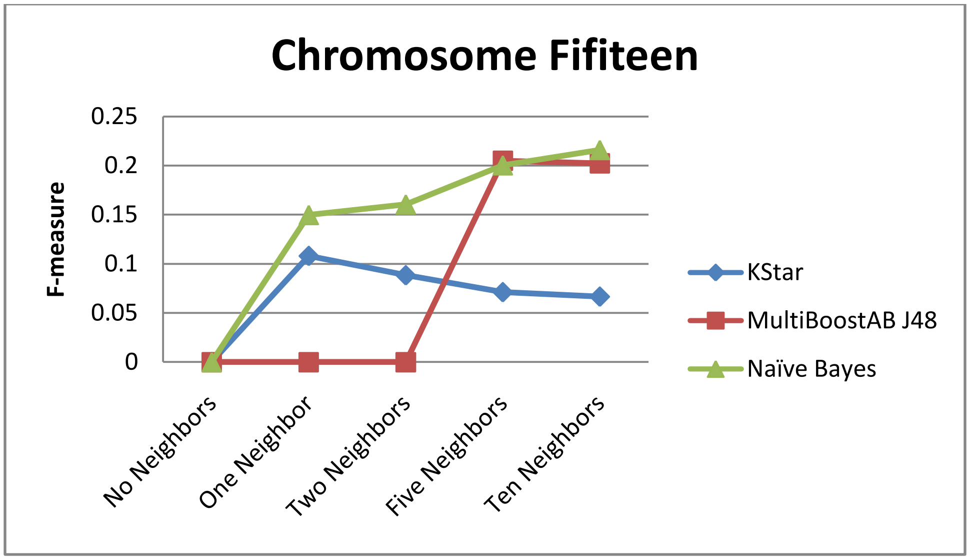


Figure 5.165. F-measure for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, the inclusion of neighbor information increases the F-measures obtained by the Naïve Bayesian classifier and the KStar classifier. The inclusion of information from each feature's nearest and two-nearest neighbors decreases the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier. With the inclusion of information from the five- or ten-nearest neighbors of each feature, the F-measures then increase for the MultiBoostAB algorithm using the J48 classifier (See Figure 5.166).

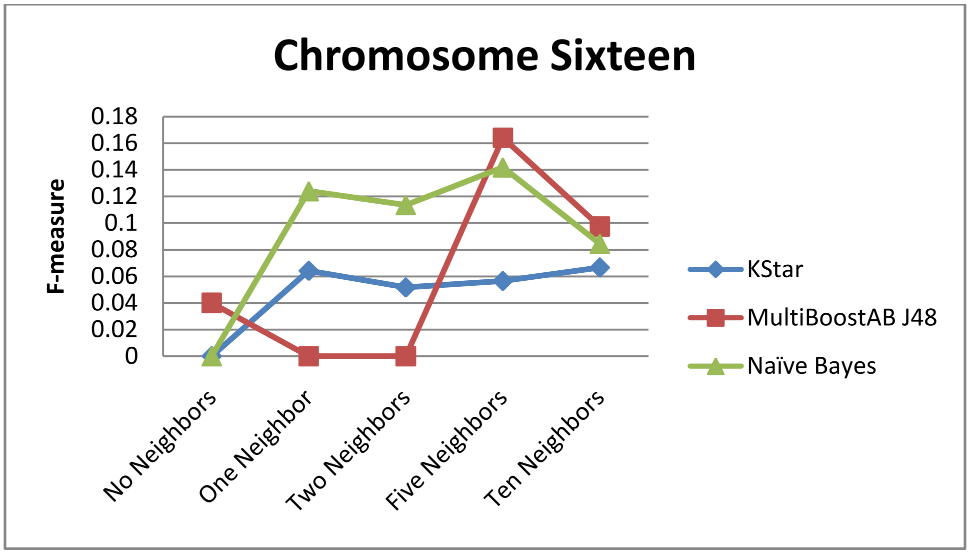


Figure 5.166. F-measure for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The F-measures obtained by the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier are excellent for all instances for the mitochondrial chromosome. The F-measures are low for the KStar classifier, and decrease with the inclusion of neighbor information (See 5.167).

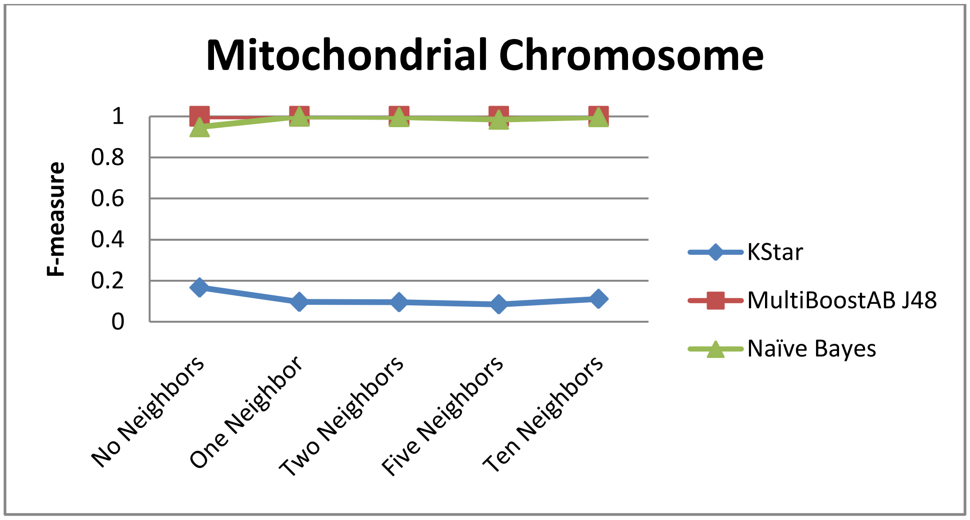


Figure 5.167. F-measure for the mitochondrial chromosome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier obtained the higher F-measures for most of the chromosomes. The partitioning of the classification process by chromosome, in general, did not improve the accuracy of the classification for the classifiers.

5.2.2. Using Neighbor Gene Ontology Information

A series of experiments was performed to determine if given the properties of chromosome number, start position, stop position, strand, neighbor number, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), neighbor's Gene Ontology aspect, neighbor's Gene Ontology term, Gene Ontology aspect and Gene Ontology term for genomic features (features being: genes, ARS, etc) could classification algorithms correctly classify Gene Ontology term. This was also performed including information from the nearest, two-, five- and ten-nearest neighbors of each feature. This was also repeated on the individual chromosomes including up to ten neighbors.

The results of the experiments are based on averages of ten different runs of each dataset being randomized and then split for training and testing. The training sets were set to contain 66% of the instances randomly selected from each dataset.

5.2.2.1 Results for Entire Genome

When using only a genomic feature's chromosome number, start position, stop position, strand, and Gene Ontology information without neighbor information, we see that the percentage of genomic features correctly classified to the correct Gene Ontology term varies depending on the classification algorithm used (See Figure 5.168). When no neighbor information is included less than 30% of the genomic features are classified to the correct network regardless of the classifier used. As more neighbor information is added, the KStar classifier and the MultiBoostAB algorithm using the J48 classifier increase their correctly classified percentage with the MultiBoostAB algorithm using the J48 classifier achieving the higher percentages. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of neighbor information beyond each feature's two-nearest neighbors does not impact the percentage of correctly classified features. When the Naïve Bayesian classifier is used, the percentage of correctly classified genomic features does not change with the addition of neighbor information.

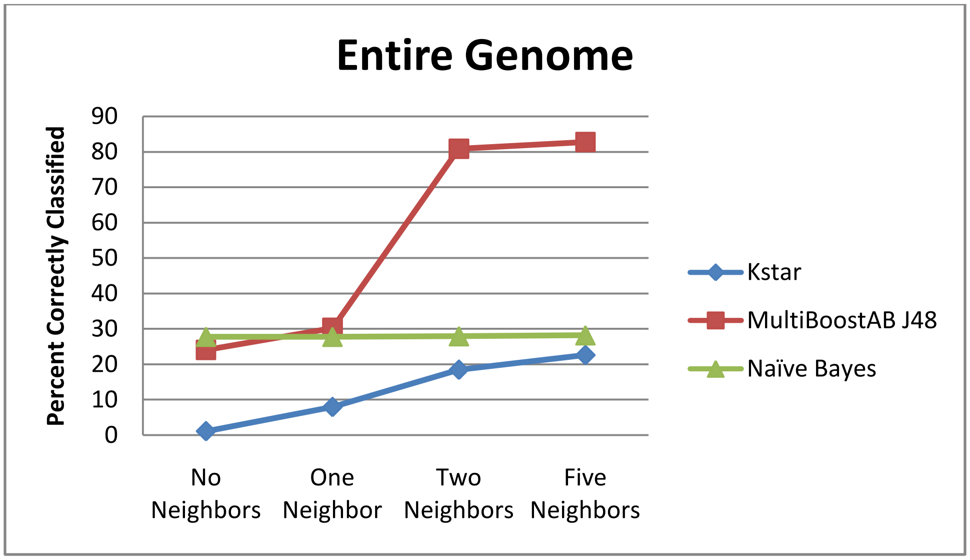


Figure 5.168. Percent of genomic features classified for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

When no neighbor information is included, all of the classifiers have poor agreement between the predicted and observed classification (See Figure 5.169). The MultiBoostAB algorithm using the J48 classifier is able to achieve a very good agreement between predicted and observed classification upon the addition of information from each feature's two-nearest neighbors. The Kappa statistic is not altered for the Naïve Bayesian classifier with the inclusion of neighbor information. The inclusion of neighbor information does improve the agreement between the predicted and observed classification for the KStar classifier, but the agreements remain poor.

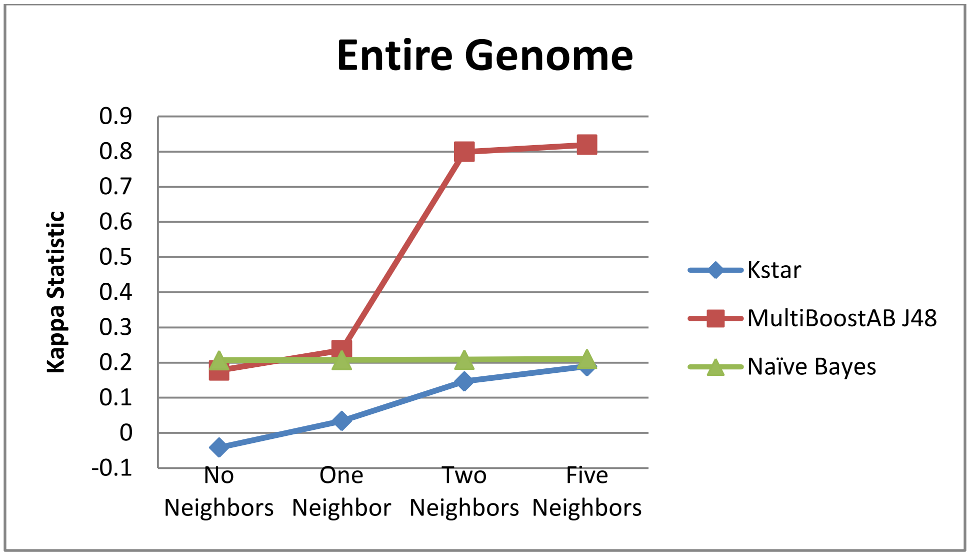


Figure 5.169. Kappa statistic for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The inclusion of neighbor information affects the precision of the classification process. For all classifiers, the inclusion of neighbor information improves the classification precision. For the MultiBoostAB algorithm using the J48 classifier, the inclusion of neighbor information beyond each feature's two-nearest neighbors has little effect on the precision. For the KStar classifier, the precision increases as more neighbor information is included, but the precision scores remain low. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors has little effect on the precision with the scores leveling out a little above 0.2 (See Figure 5.170).

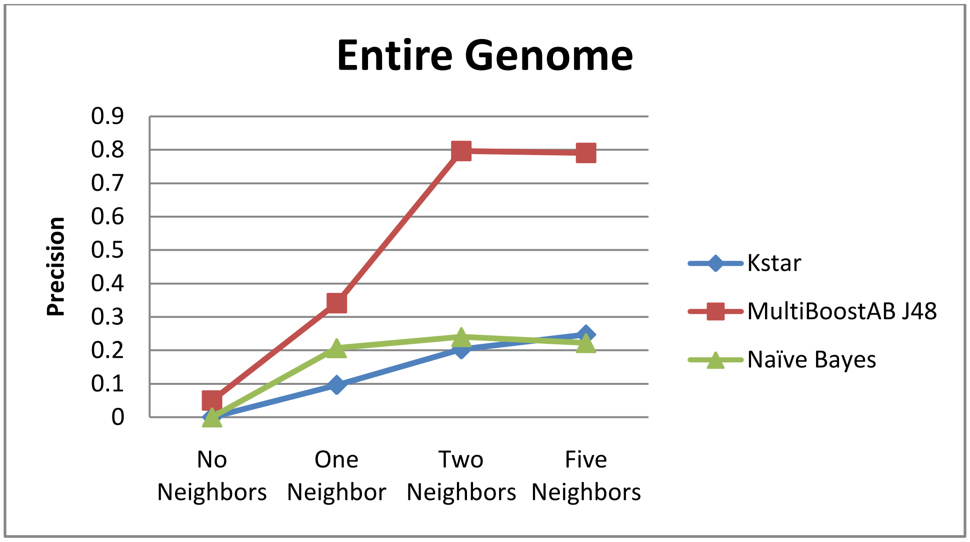


Figure 5.170. Precision for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For all classifiers, the recall scores are improved by the inclusion of neighbor information. The recall scores obtained by the MultiBoostAB algorithm using the J48 classifier are the highest, and they increase with the inclusion of more neighbor information. The recall scores of the KStar classifier increases as more neighbor information is included but they remain low. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors has little effect on the precision with the scores leveling out around 0.1 (See Figure 5.171).

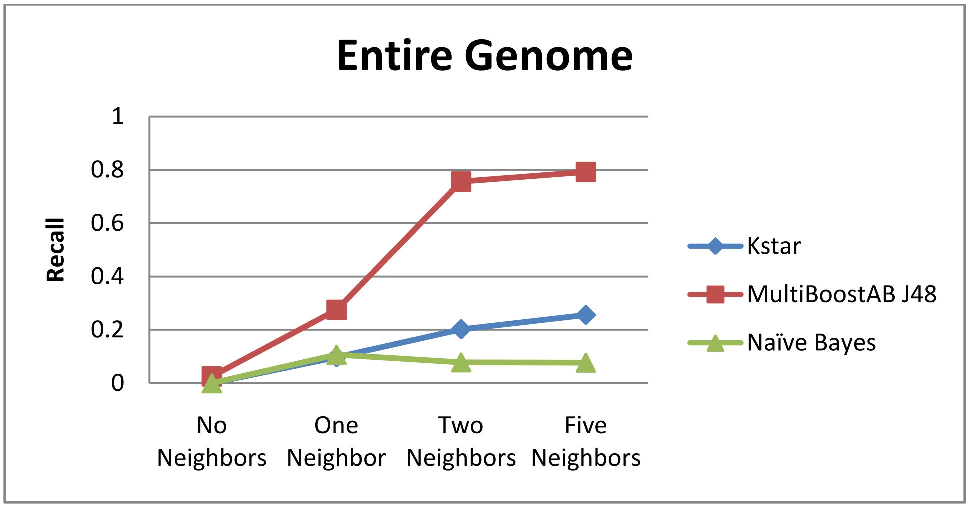


Figure 5.171. Recall scores for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

F-measures obtained by the different classifiers mimic their precision and recall scores (See Figure 5.172). The accuracy of the classification of a genomic feature increases with the inclusion of neighbor information for all classifiers. The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures, and the inclusion of neighbor information beyond each feature's two-nearest neighbors has little effect on the F-measures obtained. The accuracy of the KStar classifier increases as more neighbor information is included, but the values remain low. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors has little effect on the F-measures obtained.

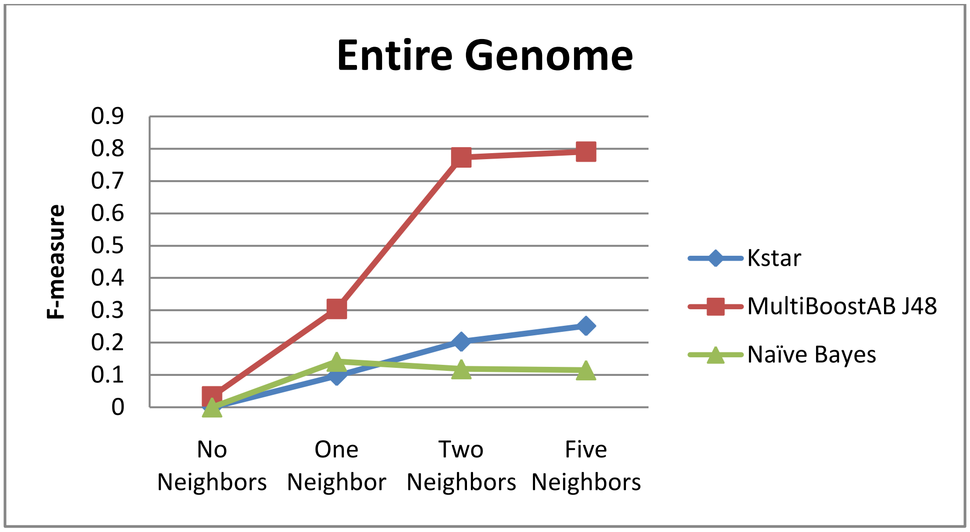


Figure 5.172. F-measure for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

When analyzing the area under the ROC curves, when no neighbor information is included, the Naïve Bayesian classifier is the only classifier that obtains an accuracy score that is deemed good. This result does not change with the inclusion of neighbor information. For the MultiBoostAB algorithm using the J48 classifier, the accuracy improves from poor to good with the inclusion of each feature's nearest neighbor. Then, it improves to excellent upon the inclusion of information from each feature's two-nearest neighbors. The KStar classifier improves in a similar manner, but its scores are not as high as those that are obtained using the MultiBoostAB algorithm using the J48 classifier (See Figure 5.173).

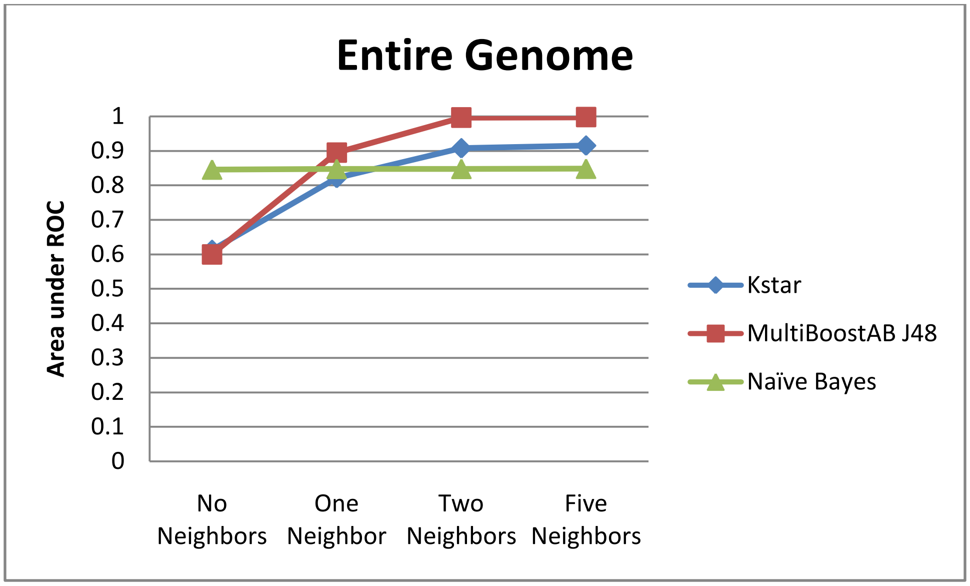


Figure 5.173. Area under ROC curve for the entire genome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Based on these results, the MultiBoostAB algorithm using the J48 classifier performs the best, achieving significantly higher scores in all of the metrics used.

To see the effect on the accuracy of classification for each Gene Ontology term, the F-measures obtained by the MultiBoostAB algorithm using the J48 classifier for each Gene Ontology term were analyzed. The table of the F-measures can be found in Appendix F. Most of the Gene Ontology term groups benefited from the addition of neighbor information (See Figures 5.174 and 5.175). Based on the results, the inclusion of neighbor information beyond each feature's two-nearest neighbors did not significantly increase the accuracy of classification of features to their correct Gene Ontology terms. When no neighbor information is included, Gene Ontology terms that represent broader functionalities (e.g. biological process, molecular function) have higher accuracy scores, meaning the classifier was able to classify features that belonged to these Gene Ontology terms better. The four Gene Ontology term groups that obtained the lowest F-measures (did not achieve an F-measure above 0.5) are: anatomical structure morphogenesis, cell cortex, cellular bud and site of polarized growth.

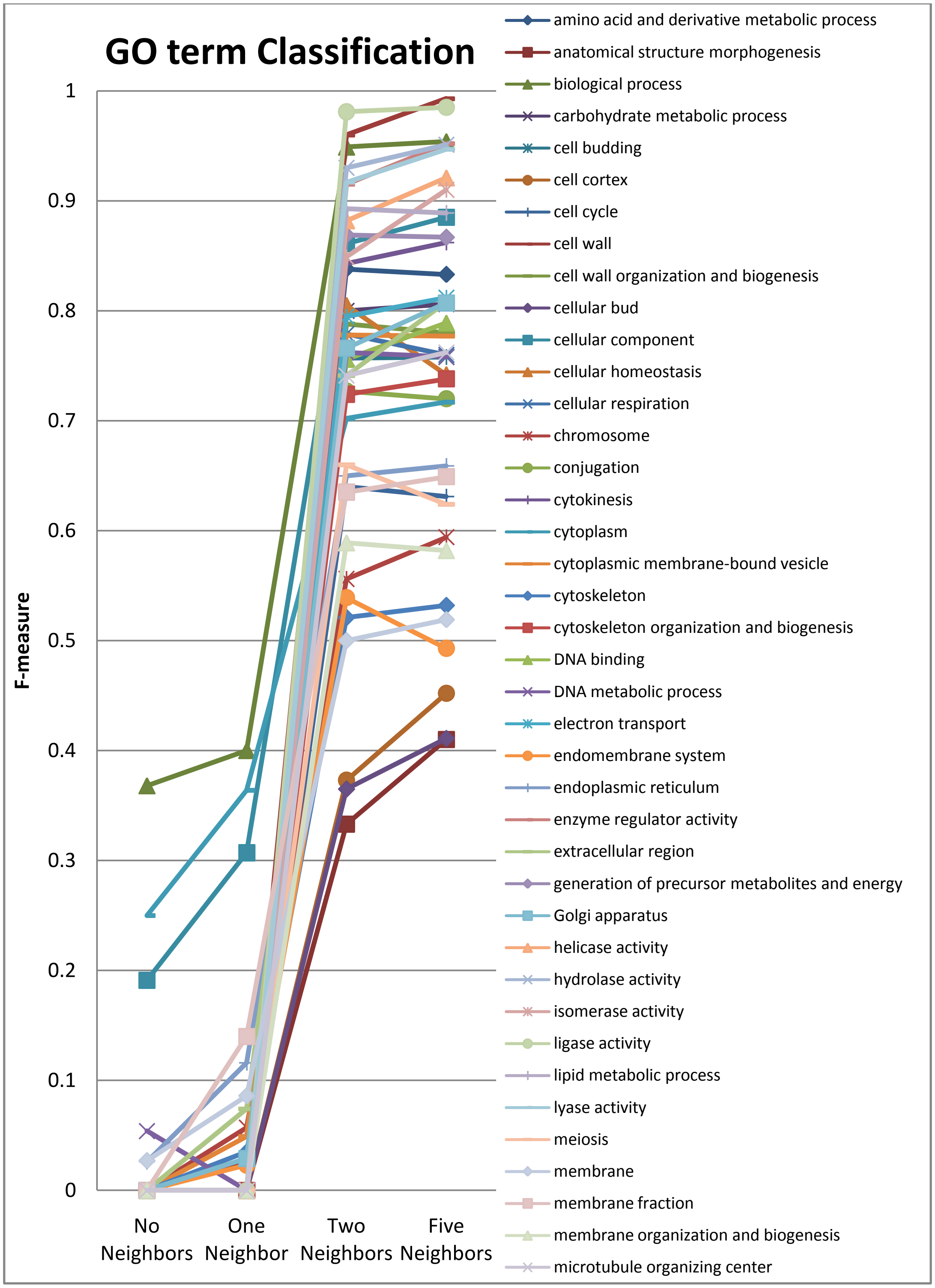


Figure 5.174. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual Gene Ontology (GO) terms.

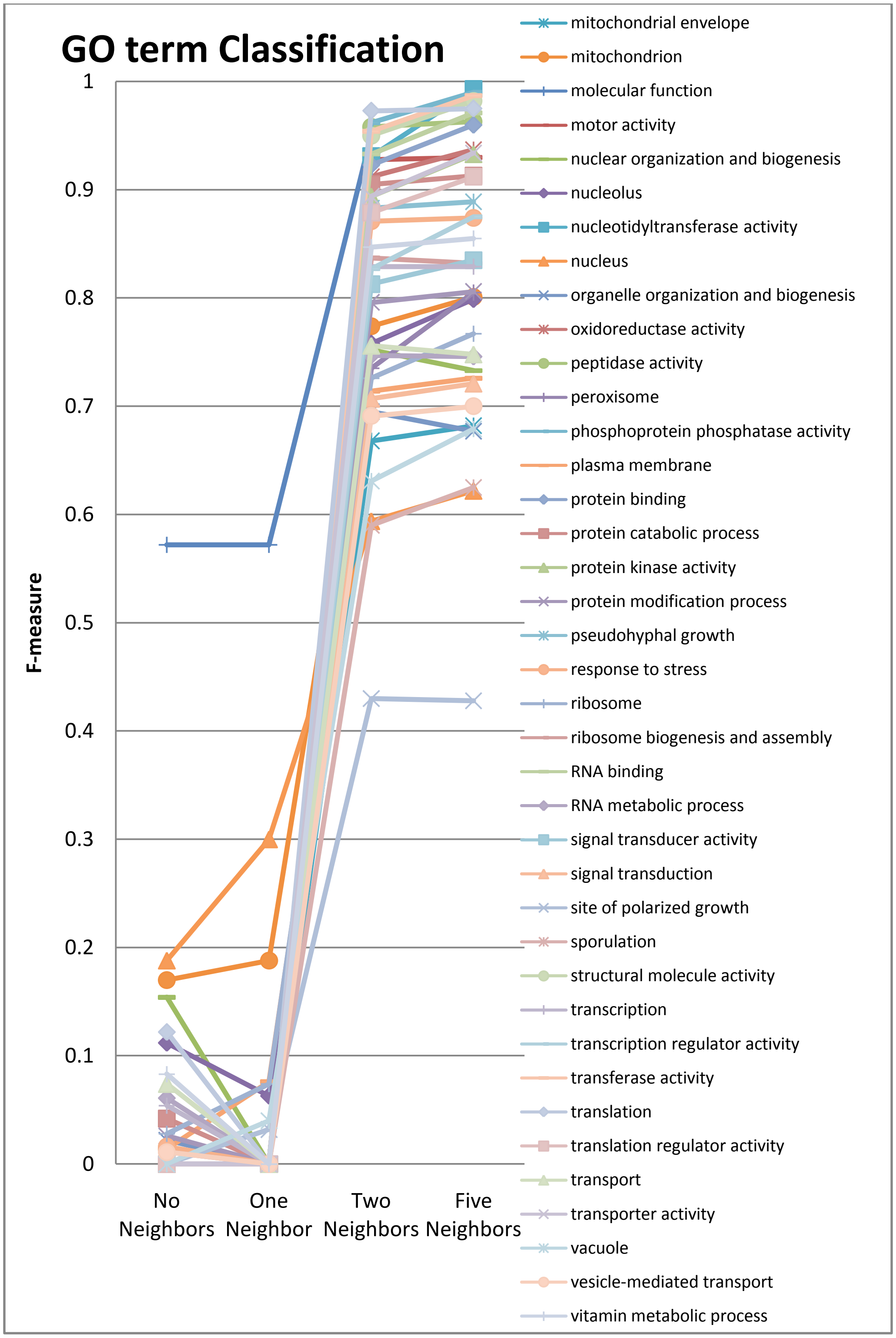


Figure 5.175. F-measures obtained using the MultiBoostAB algorithm using the J48 classifier for the individual Gene Ontology (GO) terms.

5.2.2.2 Results for Individual Chromosomes

When we look at each chromosome individually, we see that the results of classification vary from chromosome to chromosome, from the number of neighbors included, and from the classification algorithm being used.

5.2.2.2.1 Percent Correctly Classified

For all chromosomes, the percent of genomic features correctly classified to the correct Gene Ontology term differ depending on the classifier used and the amount of neighbor information included.

For chromosome one, the inclusion of neighbor information increases the percentage of correctly classified features for the classifiers (See 5.176). The larger increases are seen in the MultiBoostAB algorithm using the J48 classifier, with this classifier obtaining over 80% correctly classified features after the inclusion of information from each feature's two-nearest neighbors. The KStar classifier obtains the lowest percentages of correctly classified features.

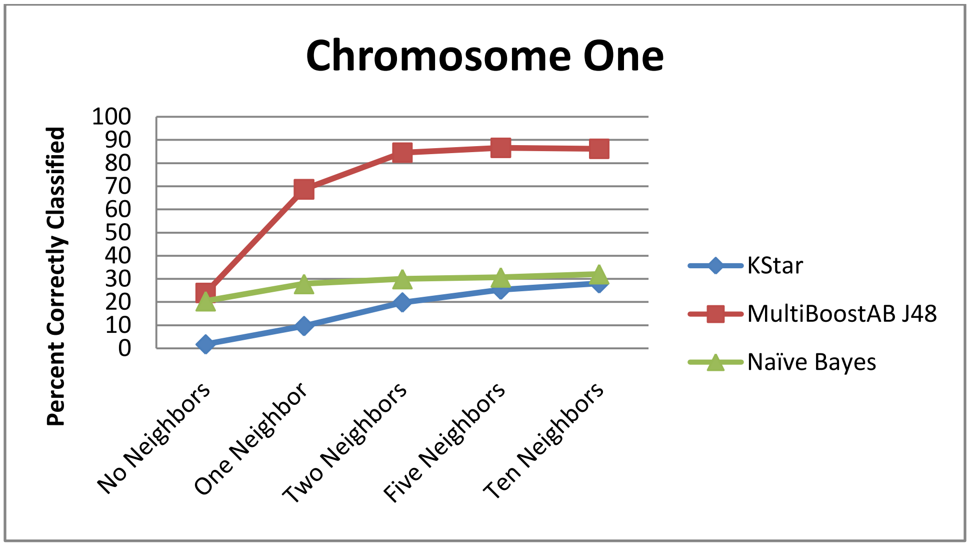
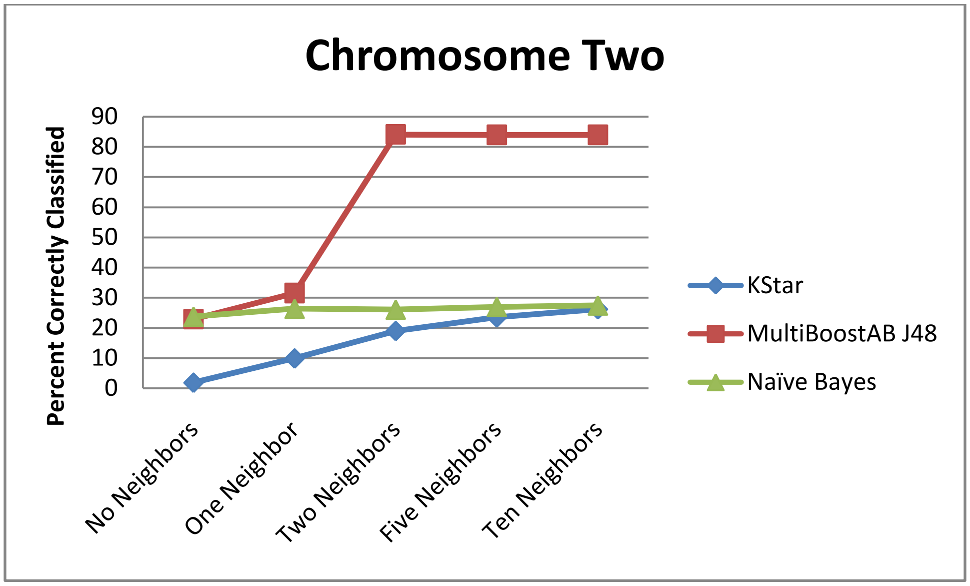


Figure 5.176. Percent of genomic features classified for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, the MultiBoostAB algorithm using the J48 classifier and the KStar classifier obtain increases in the percentage of correctly classified features with the inclusion of neighbor information with the MultiBoostAB algorithm using the J48 classifier achieving the higher percentages. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See Figure 5.177).



5.177. Percent of genomic features classified for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, the inclusion of neighbor information increases the percentage of correctly classified features for all of the classifiers. The MultiBoostAB algorithm using the J48 classifier obtains over 80% correctly classified features after the inclusion of information from the two-nearest neighbors of each feature (See Figure 5.178).

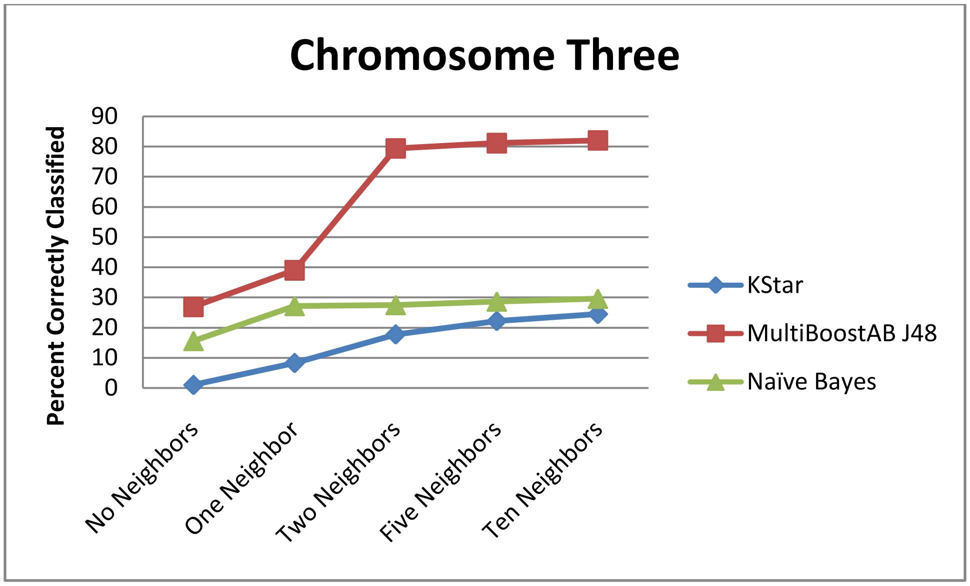


Figure 5.178. Percent of genomic features classified for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages after the inclusion of each feature's two-nearest neighbors. The KStar classifier obtains the lowest percentages of correctly classified features. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See Figure 5.179).

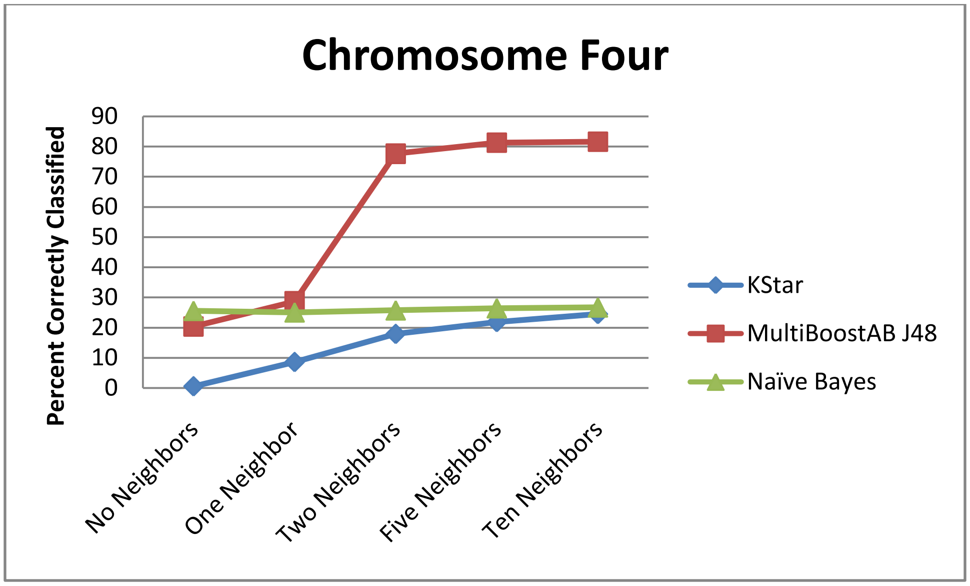


Figure 5.179. Percent of genomic features classified for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, similar to chromosomes two and four the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages, and the KStar classifier obtains the lower percentages. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information, but obtains higher percentages of correctly classified features than the KStar classifier (See Figure 5.180).

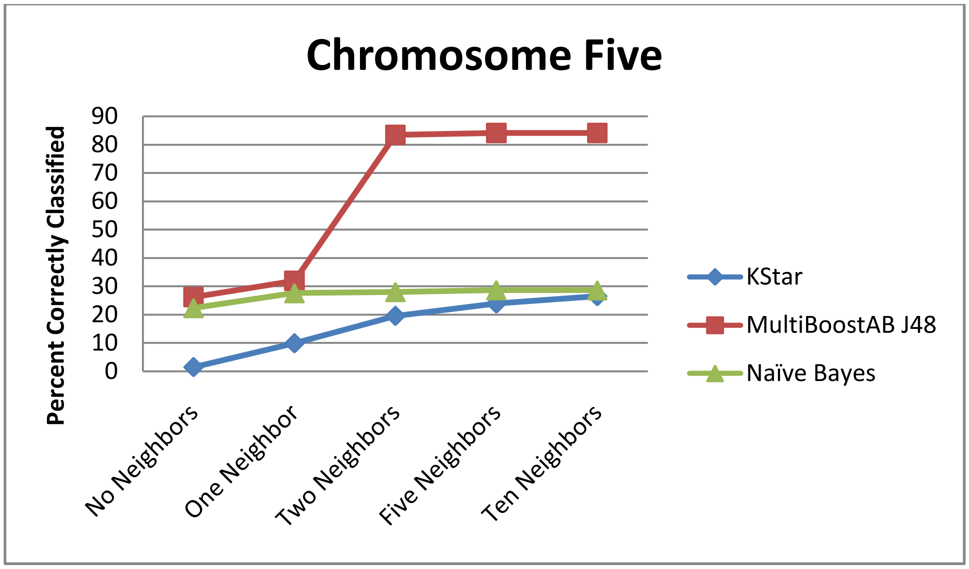


Figure 5.180. Percent of genomic features classified for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, the inclusion of neighbor information increases the percentage of correctly classified features for all of the classifiers. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentage of correctly classified features, followed by the Naïve Bayesian classifier then the KStar classifier (See Figure 5.181).

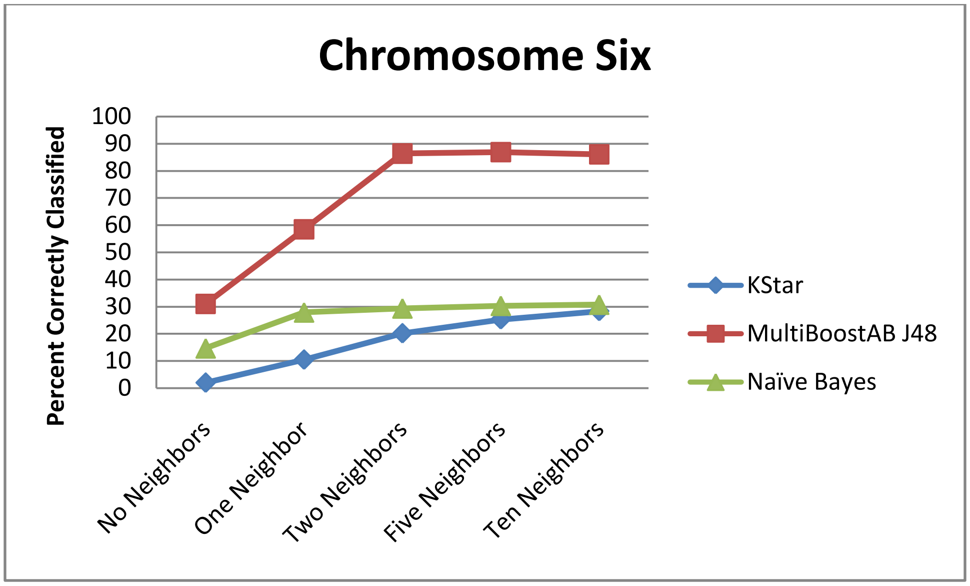


Figure 5.181. Percent of genomic features classified for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Similar to other chromosomes, for chromosome seven, the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers are the most affected by the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages after the inclusion of each feature's two-nearest neighbors. The KStar classifier obtains the lowest percentages of correctly classified features. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information, but obtains higher percentages than the KStar classifier (See Figure 5.182).

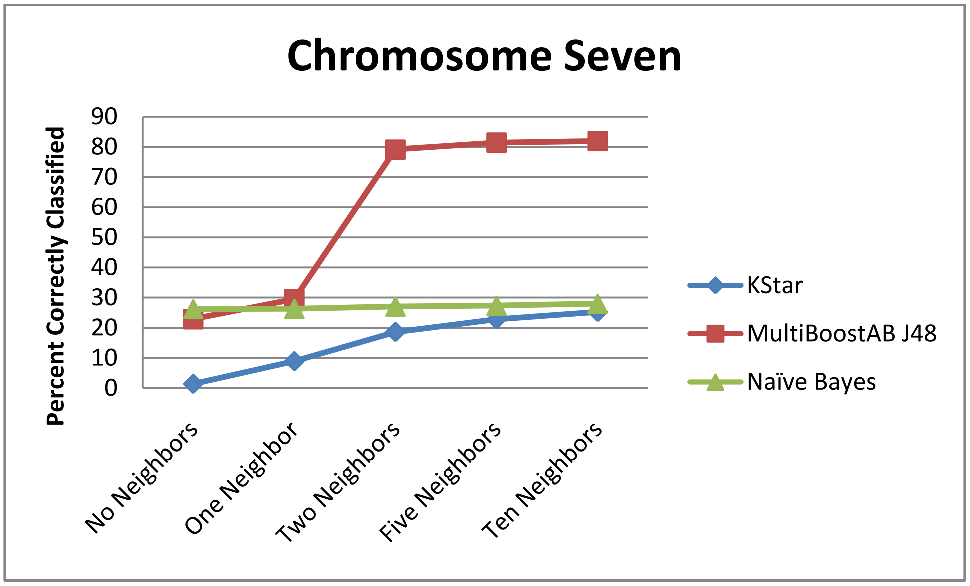


Figure 5.182. Percent of genomic features classified for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, the patterns of the percentage of correctly classified features is similar to those seen in other chromosomes with the MultiBoostAB algorithm using the J48 classifier and the KStar classifiers being the most affected by the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages after the inclusion of each feature's two-nearest neighbors. The KStar classifier obtains the lowest percentages of correctly classified features (See Figure 5.183).

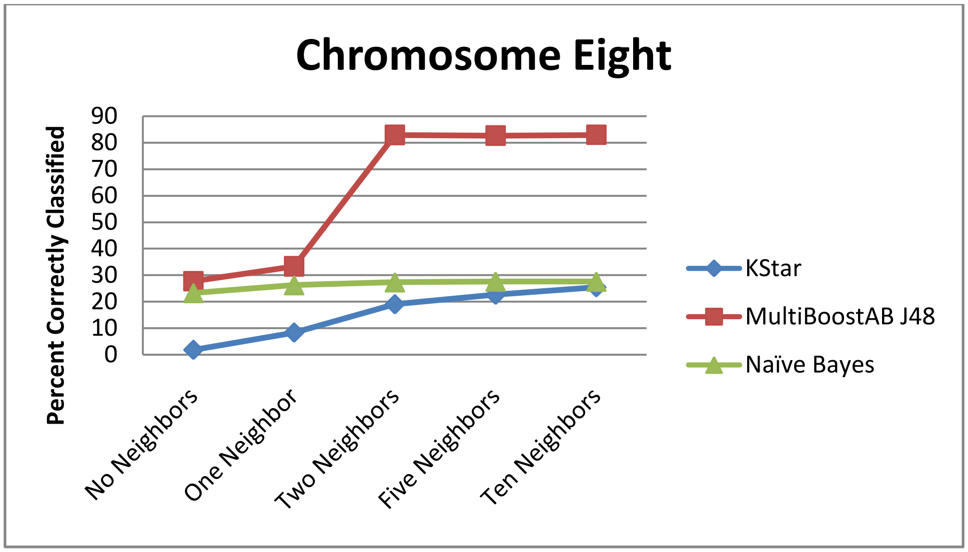


Figure 5.183. Percent of genomic features classified for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Chromosome nine repeats patterns seen in prior chromosomes. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages after the inclusion of each feature's two-nearest neighbors. The KStar classifier obtains the lower percentages of correctly classified features. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See Figure 5.184).

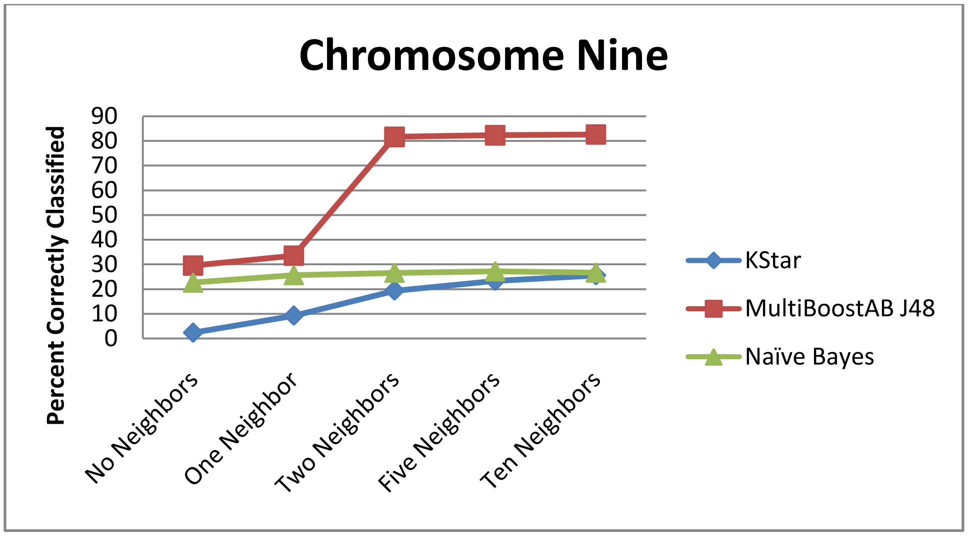


Figure 5.184. Percent of genomic features classified for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Similar to other chromosomes, for chromosome ten the MultiBoostAB algorithm using the J48 classifier obtains the higher percentages after the inclusion of each feature's two-nearest neighbors. The KStar classifier obtains the lower percentages of correctly classified features. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See Figure 5.185).

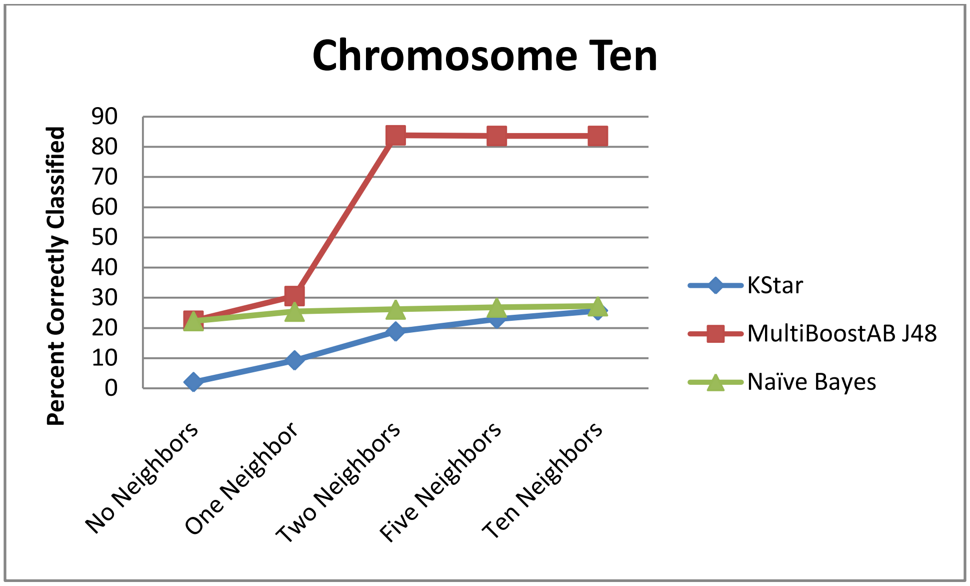


Figure 5.185. Percent of genomic features classified for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eleven, the inclusion of neighbor information increases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier (See Figure 5.186). The Naïve Bayesian classifier is not affected by the inclusion of neighbor information. The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, and the inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features.

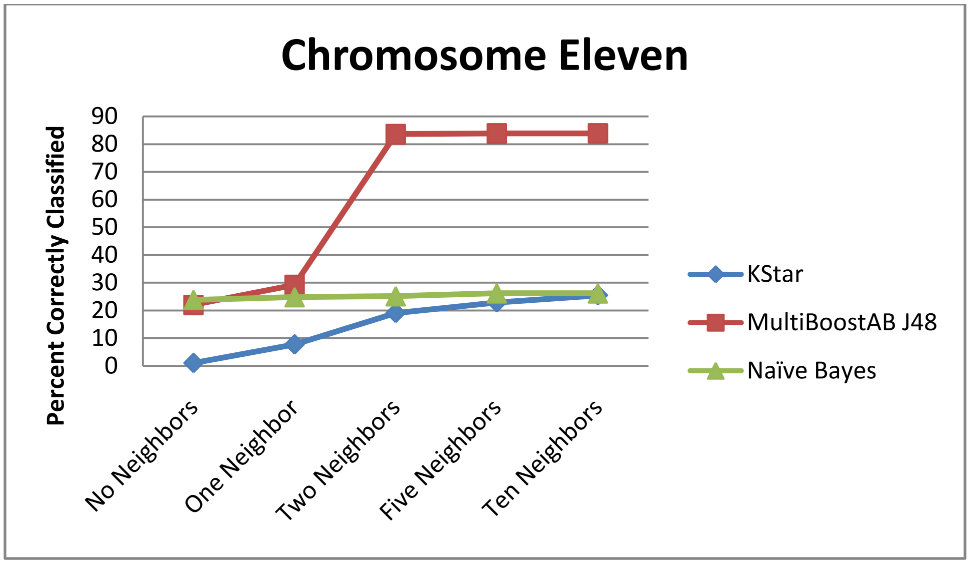


Figure 5.186. Percent of genomic features classified for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the inclusion of neighbor information increases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See Figure 5.187). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, and the inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features.

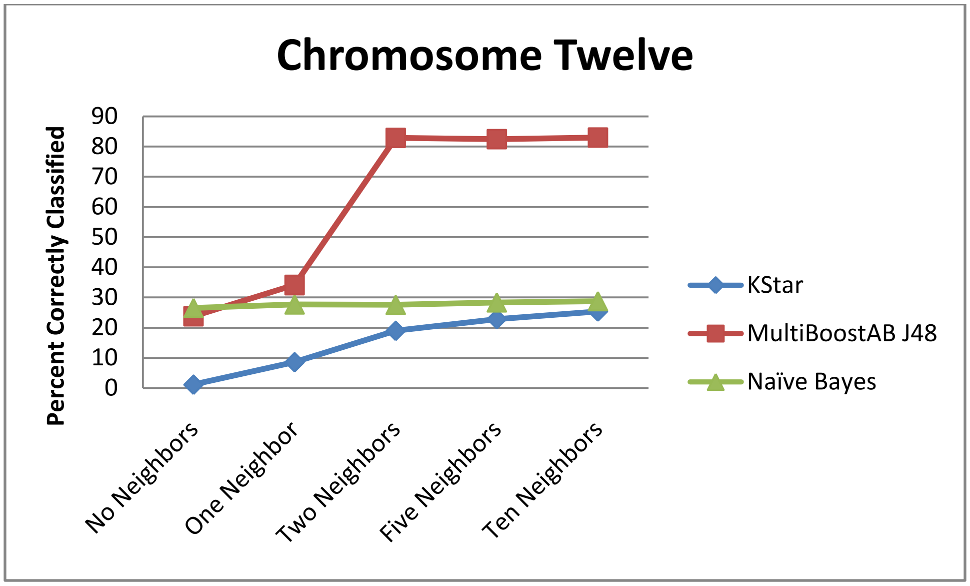


Figure 5.187. Percent of genomic features classified for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

Similar to other chromosomes, for chromosome thirteen, the inclusion of neighbor information increases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See 5.188). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, and the inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features.

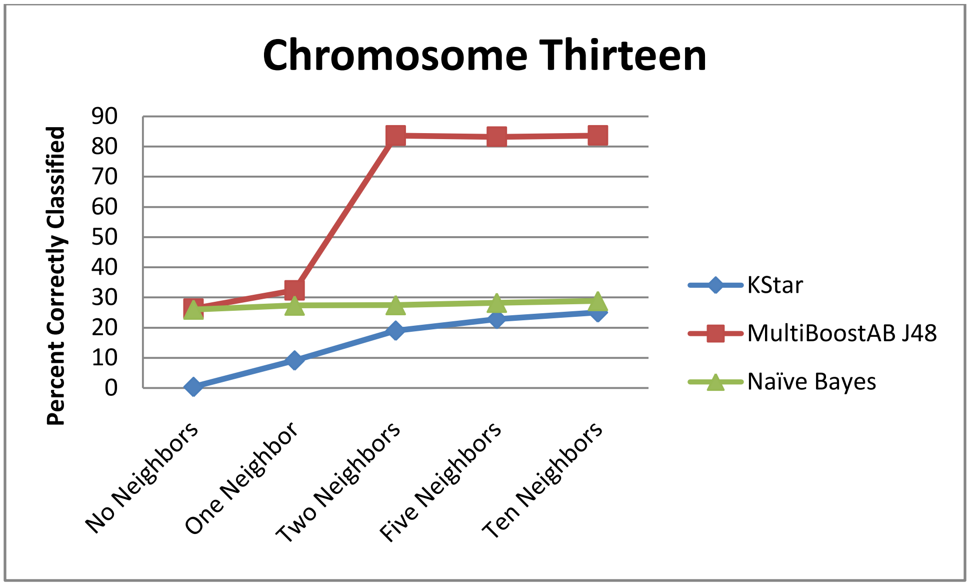


Figure 5.188. Percent of genomic features classified for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, the inclusion of neighbor information increases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier. For the Naïve Bayesian classifier, the percentage of correctly classified features decreases with the inclusion of neighbor information (See 5.189). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, and the inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features. The inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features for the KStar classifiers.

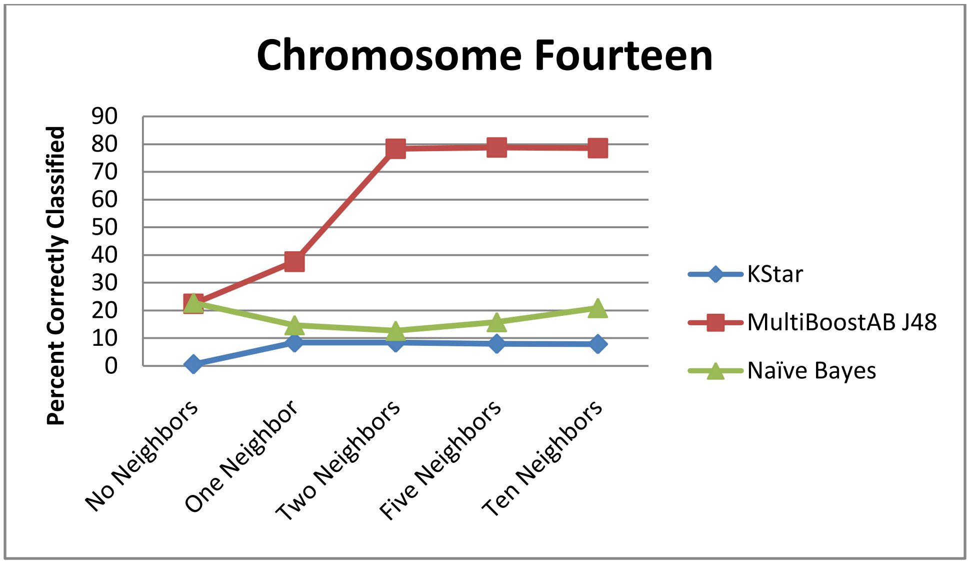


Figure 5.189. Percent of genomic features classified for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, like other chromosomes, the inclusion of neighbor information increases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See 5.190). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, and the inclusion of neighbor information beyond each feature's two-nearest neighbors has little impact on the percentage of correctly classified features.

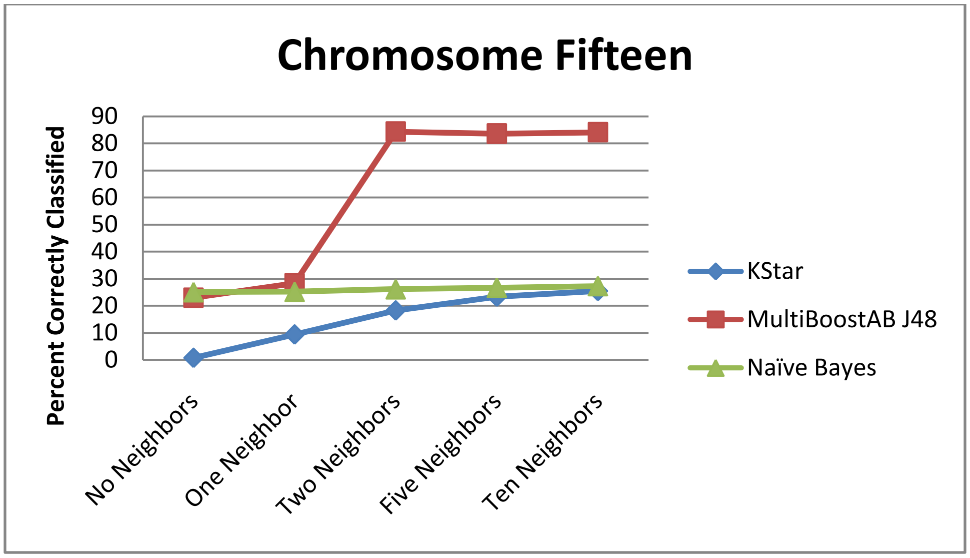


Figure 5.190. Percent of genomic features classified for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, similar to other chromosomes, the inclusion of neighbor information increases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the KStar classifier. The Naïve Bayesian classifier is not affected by the inclusion of neighbor information (See 5.191). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, and the inclusion of neighbor information beyond each feature’s two-nearest neighbors has little impact on the percentage of correctly classified features. The inclusion of neighbor information from each feature’s five-nearest neighbors obtains the highest F-measure for the KStar classifier.

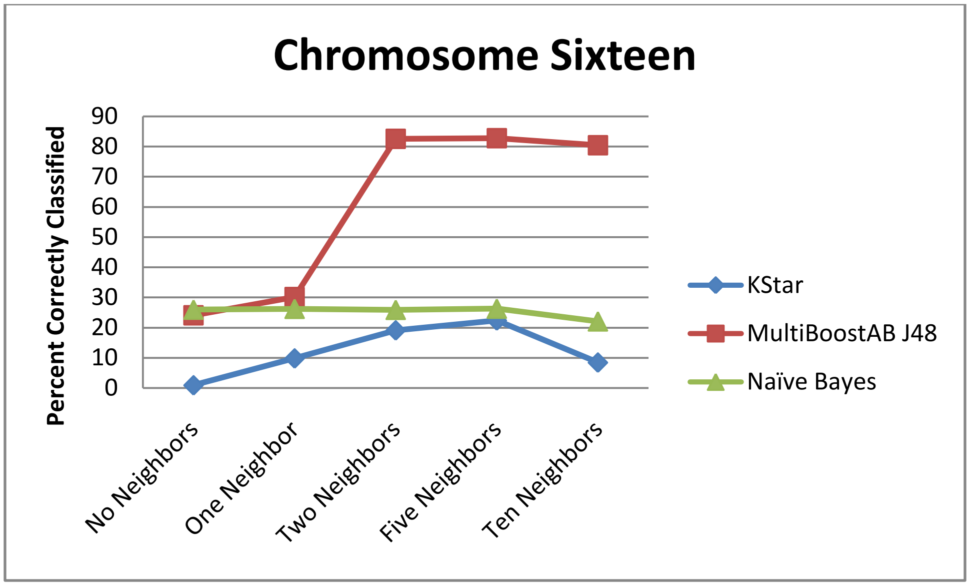


Figure 5.191. Percent of genomic features classified for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For the mitochondrial chromosome, the inclusion of neighbor information increases the percentage of correctly classified features for the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier (See 5.192). The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features, and the inclusion of neighbor information beyond each feature's nearest neighbors has little impact on the percentage of correctly classified features. The inclusion of neighbor information from each feature's five-nearest neighbors obtains the highest F-measure for the Naïve Bayesian classifier. For the KStar classifier, the inclusion of neighbor information from each feature's nearest, two-nearest, or ten-nearest neighbors does increase the percentage of correctly classified features.

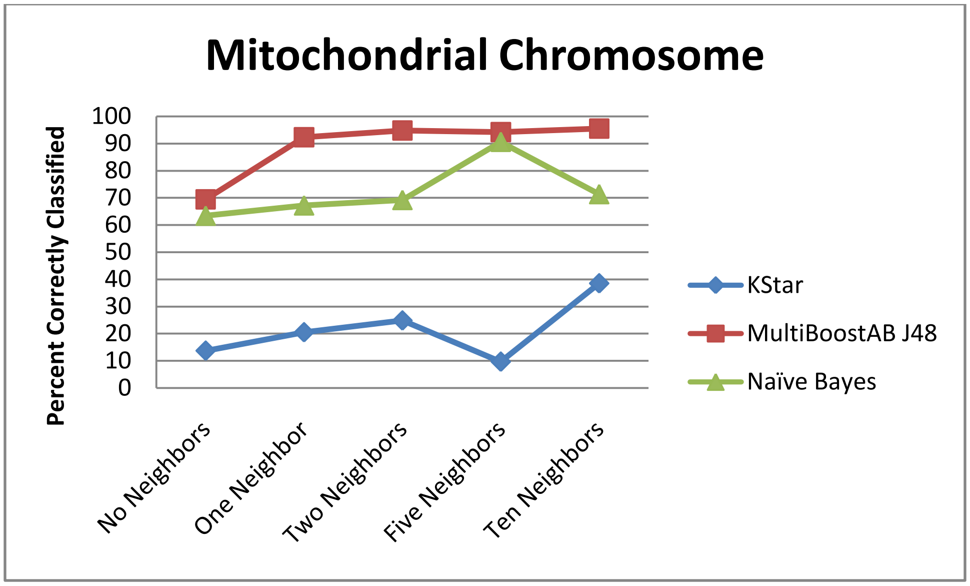


Figure 5.192. Percent of genomic features classified for the mitochondrial chromosome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The MultiBoostAB algorithm using the J48 classifier obtains the higher percentages of correctly classified features for all of the chromosomes. For most chromosomes, the inclusion of neighbor information beyond each feature's two-nearest neighbors did not have a huge effect on the percentage of correctly classified features. The partitioning of the classification process by chromosome slightly improves the percentage of correctly classified features for MultiBoostAB algorithm using the J48 classifier.

5.2.2.2.2 F-measures

To look at the accuracy of the classification process for each chromosome, the F-measures obtained for each chromosome can be analyzed.

For chromosome one, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.193). The F-measures are higher for the MultiBoostAB algorithm using the J48 classifier and lower for the KStar classifier. For the

MultiBoostAB algorithm using the J48 classifier, including neighbor information beyond the two-nearest neighbors of each feature does not add an increased benefit to the classification process.

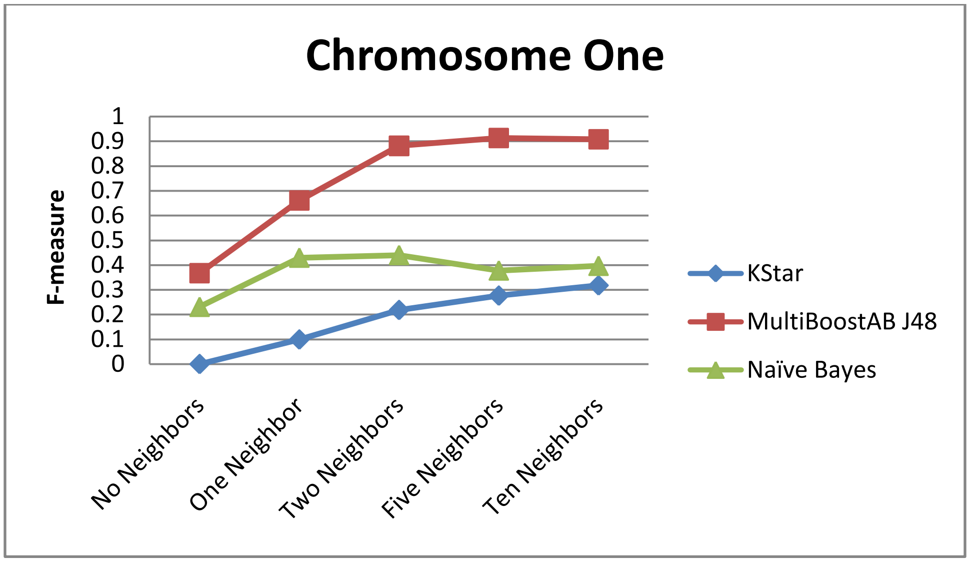


Figure 5.193. F-measure for chromosome one using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome two, the inclusion of neighbor information increases the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. Including neighbor information has little effect on the Naïve Bayesian classifier (See Figure 5.194). The higher F-measures are obtained by the MultiBoostAB algorithm using the J48 classifier. The addition of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier.

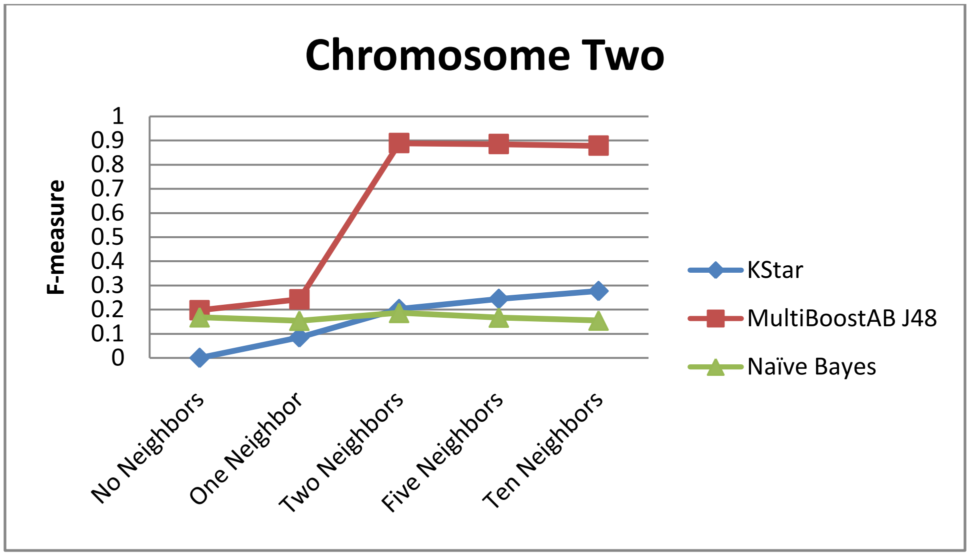


Figure 5.194. F-measure for chromosome two using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome three, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.195). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures, with the inclusion of information from each feature's five-nearest neighbors obtaining the highest F-measure.

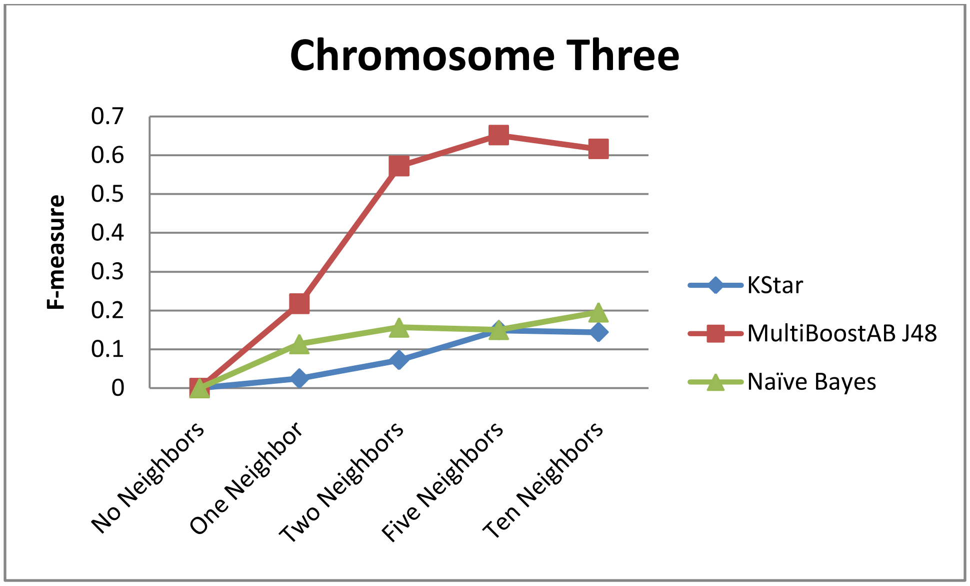


Figure 5.195. F-measure for chromosome three using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome four, the inclusion of neighbor information increases the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. Including neighbor information has little effect on the Naïve Bayesian classifier (See Figure 5.196). The higher F-measures are obtained by the MultiBoostAB algorithm using the J48 classifier. The addition of neighbor information beyond each feature's five-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier.

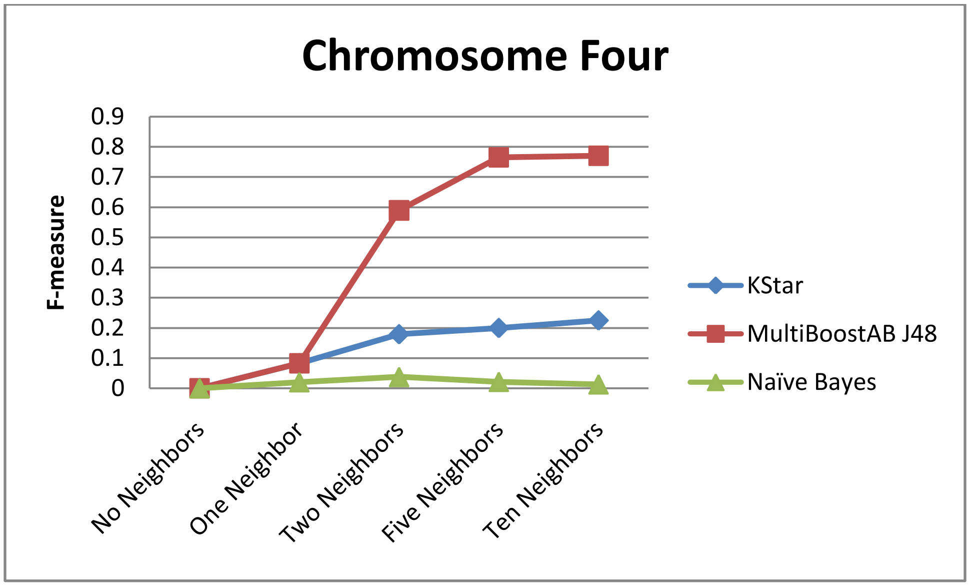


Figure 5.196. F-measure for chromosome four using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome five, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.197). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The addition of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. The Naïve Bayesian classifier obtains the lower F-measures.

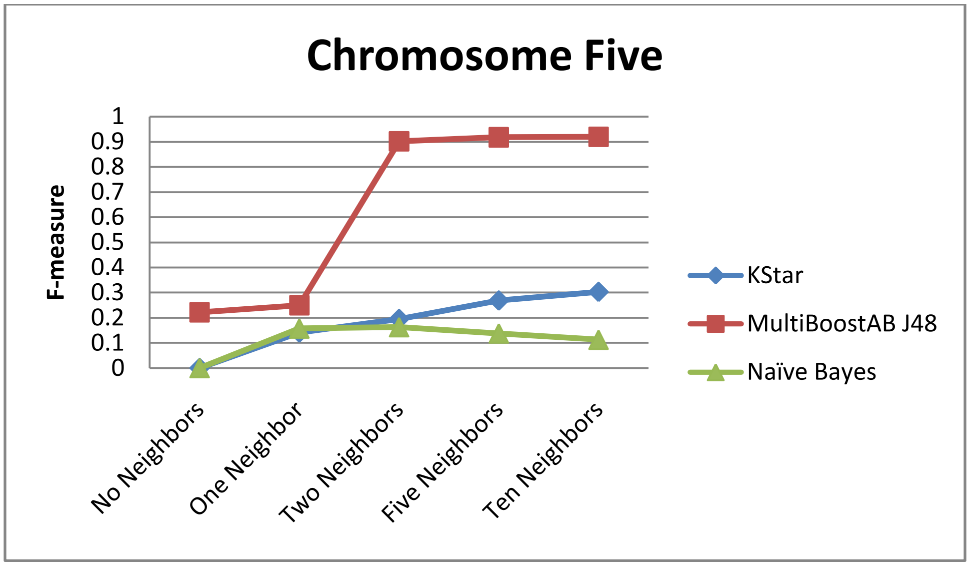


Figure 5.197. F-measure for chromosome five using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome six, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.198). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. The KStar classifier obtains the lower F-measures until the addition of information from each feature's ten-nearest neighbors when it surpasses the results obtained by the Naïve Bayesian classifier.

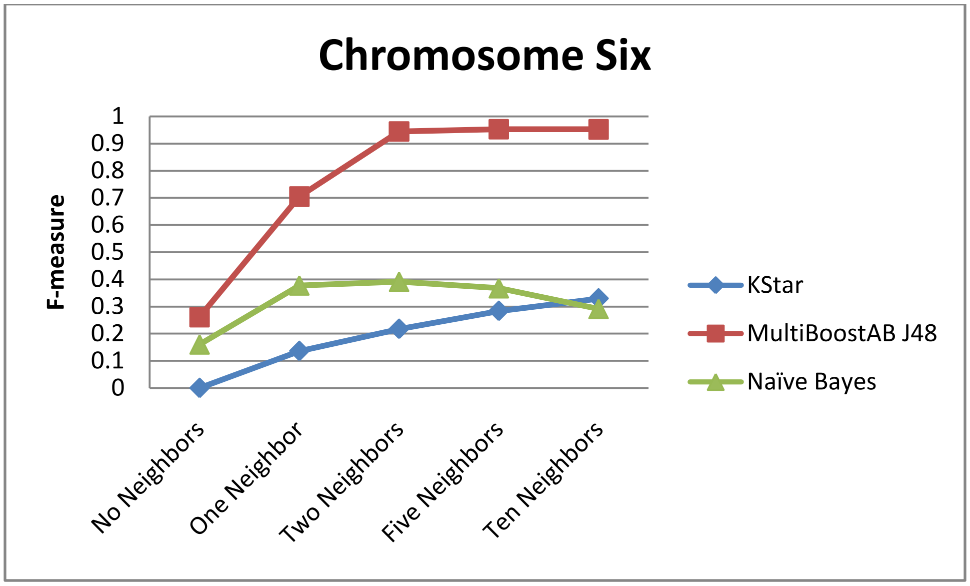


Figure 5.198. F-measure for chromosome six using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome seven, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.199). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors does not add an increased benefit to the classification process. The KStar classifier obtains the lower F-measures until the addition of information from each feature's two-nearest neighbors when it surpasses the results obtained by the Naïve Bayesian classifier.

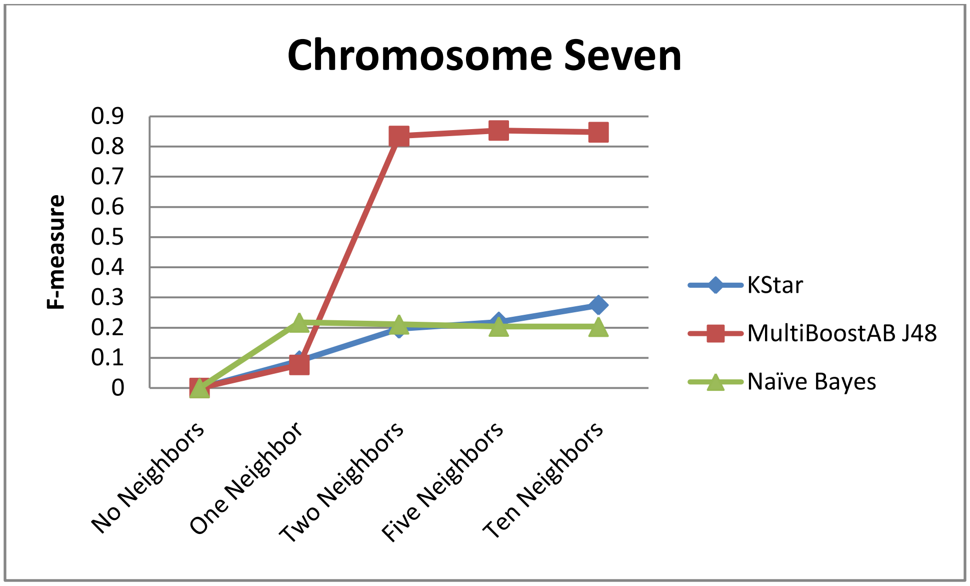


Figure 5.199. F-measure for chromosome seven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eight, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. Including neighbor information has little effect on the Naïve Bayesian classifier (See Figure 5.200). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. The KStar classifier obtains the lower F-measures until the addition of information from each feature's two-nearest neighbors when it surpasses the results obtained by the Naïve Bayesian classifier.

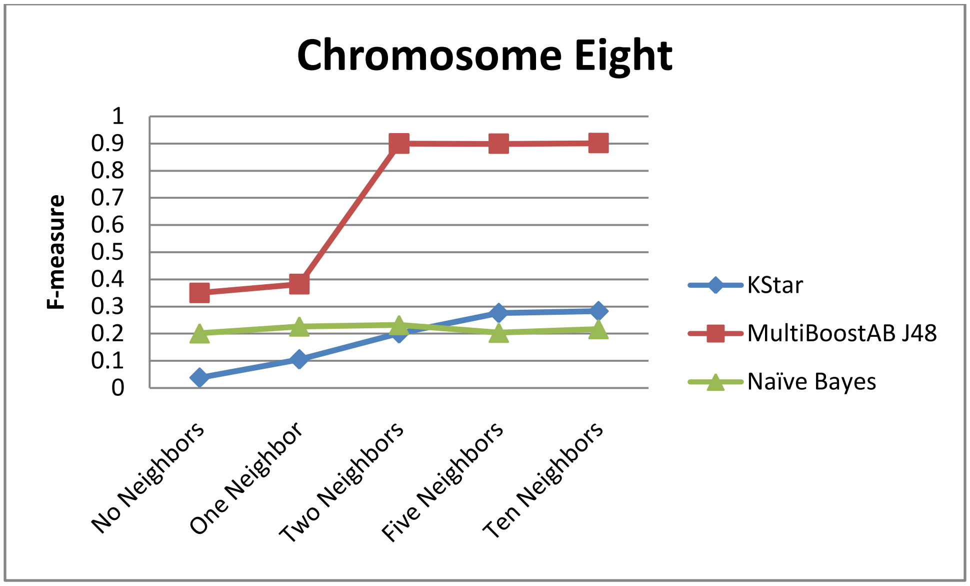


Figure 5.200. F-measure for chromosome eight using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome nine, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.201). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. The Naïve Bayesian classifier tends to obtain the lower F-measures.

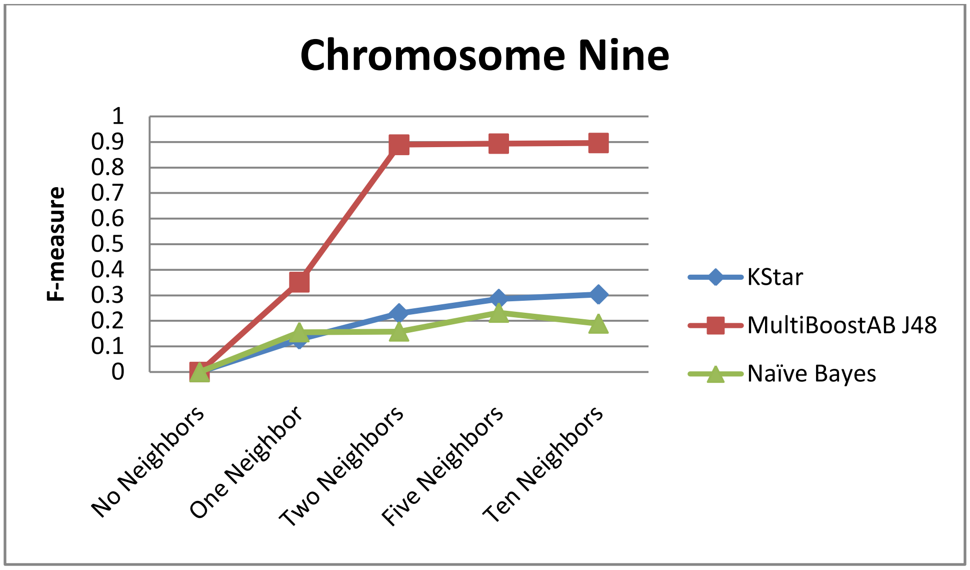


Figure 5.201. F-measure for chromosome nine using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome ten, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.202). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors does not add an increased benefit to the classification process. The KStar classifier obtains the lower F-measures until the addition of information from each feature's two-nearest neighbors when it surpasses the results obtained by the Naïve Bayesian classifier.

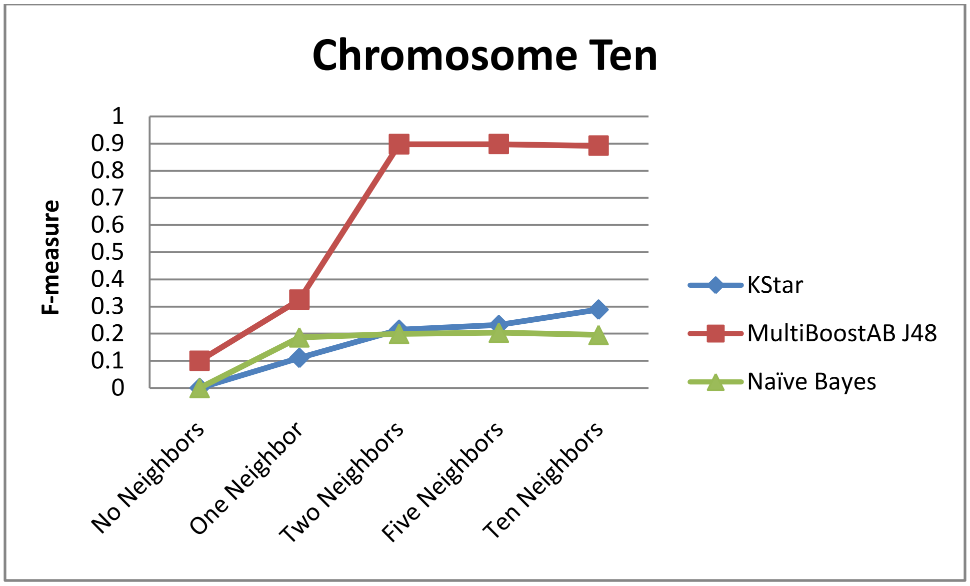


Figure 5.202. F-measure for chromosome ten using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome eleven, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers, but the increases are small for the Naïve Bayes classifier (See Figure 5.203). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. In general, the Naïve Bayesian classifier obtains the lower F-measures.

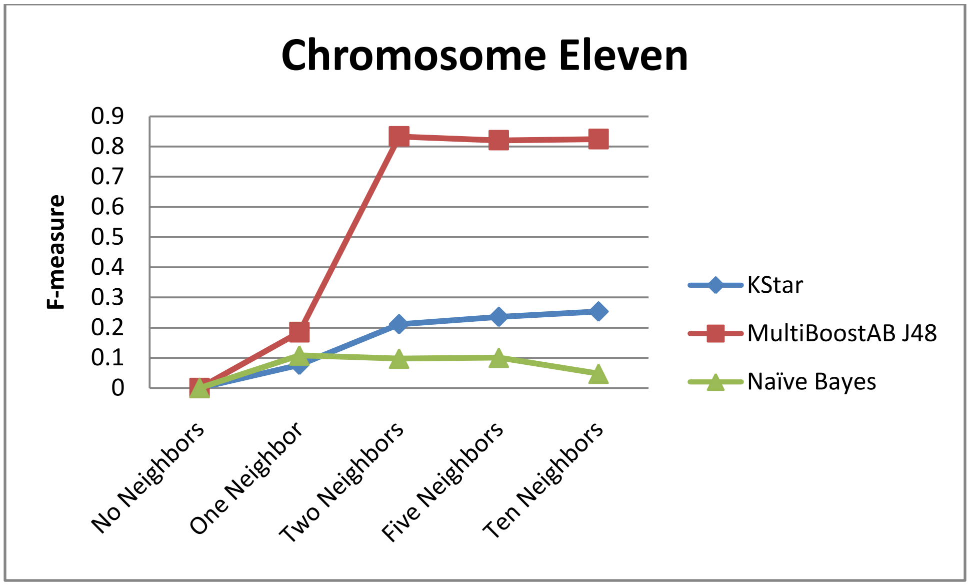


Figure 5.203. F-measure for chromosome eleven using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome twelve, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.204). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors does not add an increased benefit to the classification process. The KStar classifier obtains the lower F-measures until the addition of information from each feature's two-nearest neighbors when it surpasses the results obtained by the Naïve Bayesian classifier.

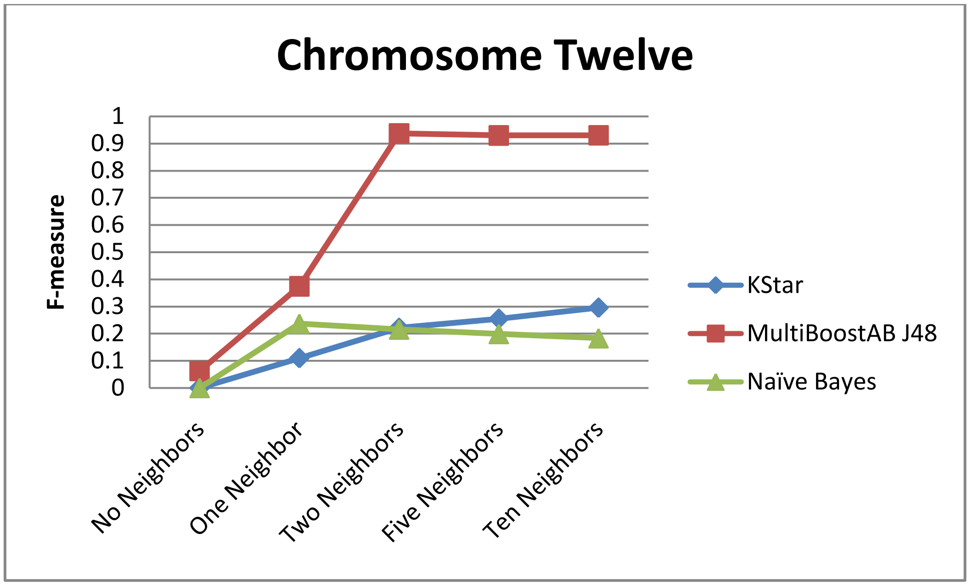


Figure 5.204. F-measure for chromosome twelve using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome thirteen, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier. Including neighbor information has little effect on the Naïve Bayesian classifier (See Figure 5.205). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. The Naïve Bayesian classifier tends to get the lower F-measures.

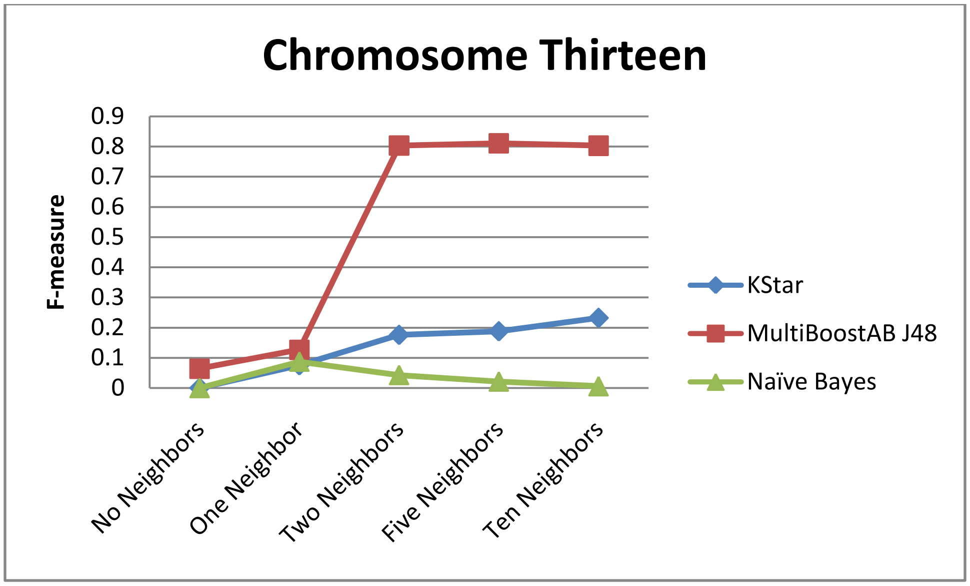


Figure 5.205. F-measure for chromosome thirteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fourteen, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by the KStar classifier and the MultiBoostAB algorithm using the J48 classifier (See Figure 5.206). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. The inclusion of neighbor information beyond each feature's nearest neighbors does not add an increased benefit to the classification process for the KStar classifier. The inclusion of information from each feature's five-nearest neighbors has the most impact on the Naïve Bayesian classifier.

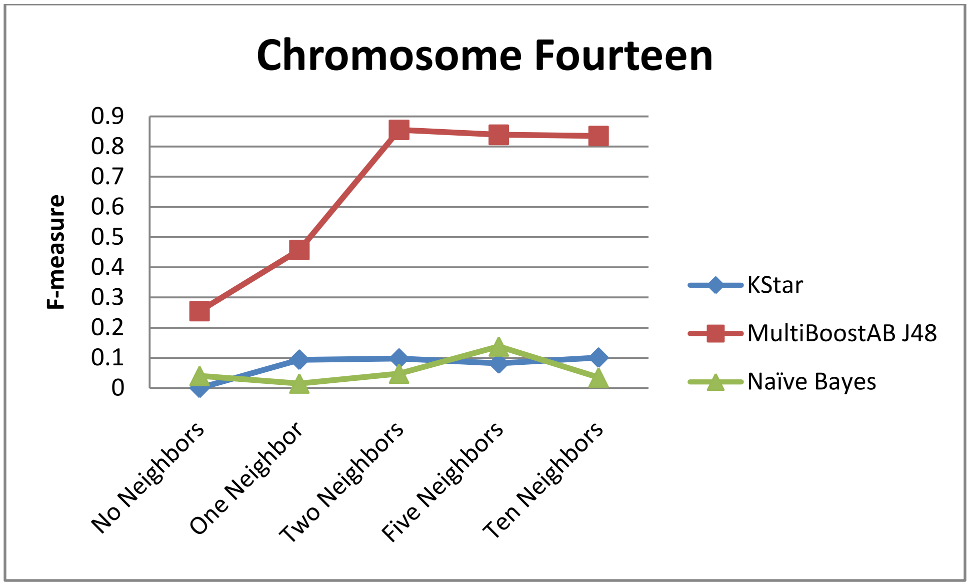


Figure 5.206. F-measure for chromosome fourteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome fifteen, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.207). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors does not add an increased benefit to the classification process, and it obtains the lower F-measures.

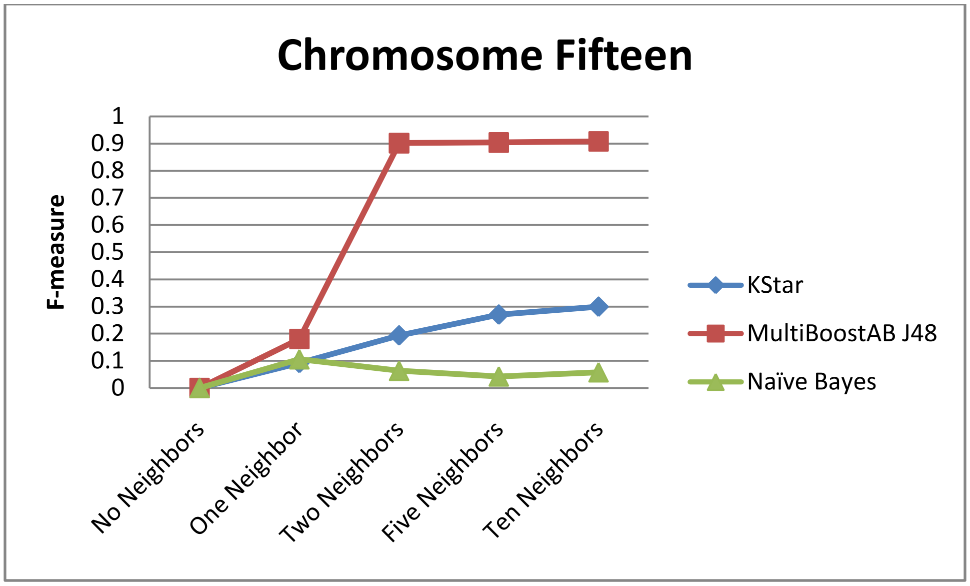


Figure 5.207. F-measure for chromosome fifteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For chromosome sixteen, the inclusion of neighbor information is beneficial, increasing the F-measures obtained by all of the classifiers (See Figure 5.208). The MultiBoostAB algorithm using the J48 classifier obtains the higher F-measures. The inclusion of neighbor information beyond each feature's two-nearest neighbors does not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. In fact, including information from each feature's ten-nearest neighbors sees a drop in F-measures. For the Naïve Bayesian classifier, the inclusion of neighbor information beyond each feature's nearest neighbors does not add an increased benefit to the classification process, and it obtains the lower F-measures. For the KStar classifier, the F-measures increase with the addition of neighbor information until the addition of information from each feature's ten-nearest neighbors.

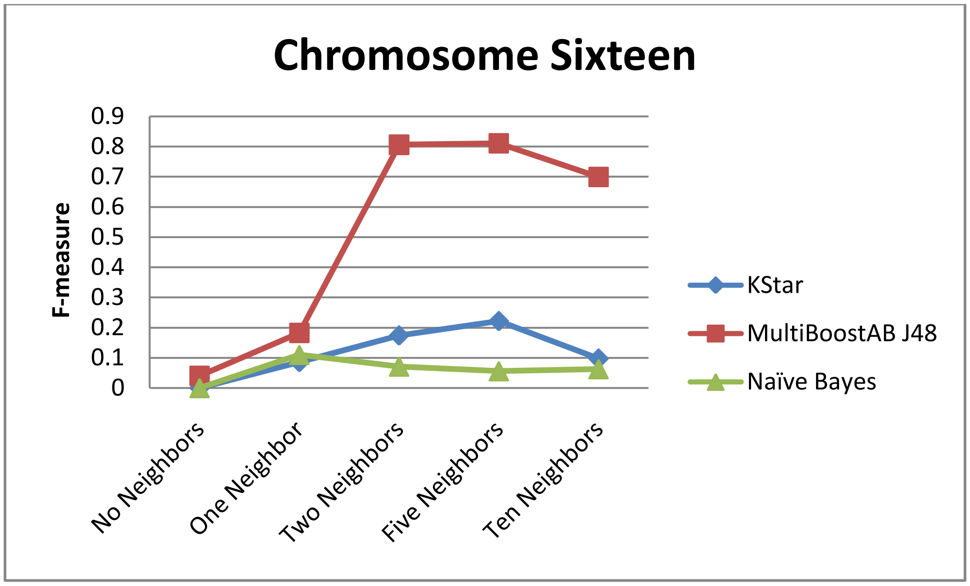


Figure 5.208. F-measure for chromosome sixteen using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

For the mitochondrial chromosome, the MultiBoostAB algorithm using the J48 classifier obtains F-measures of 1.0 independent of the inclusion of neighbor information. The Naïve Bayesian classifier performs in a similar manner to the MultiBoostAB algorithm using the J48 classifier. For the KStar classifier, the inclusion of neighbor information from each feature's nearest, two-nearest, or ten-nearest neighbors is beneficial to the classification process (See Figure 5.209).

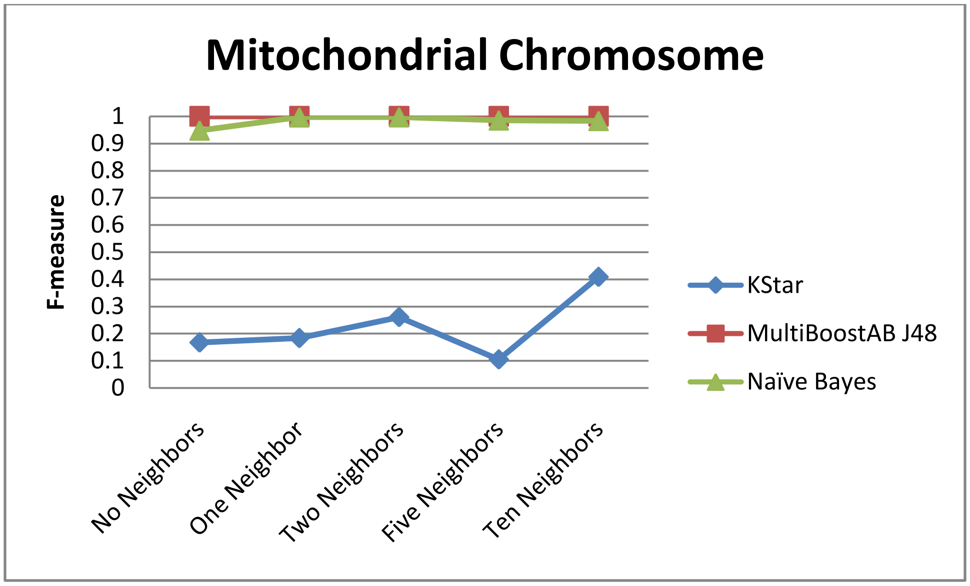


Figure 5.209. F-measure for the mitochondrial chromosome using KStar, MultiBoostAB using J48 and Naïve Bayes algorithms for classification.

The F-measures obtained by the MultiBoostAB algorithm using the J48 classifier are higher for all of the chromosomes indicating a higher accuracy of its classification process compared to the other classifiers. For most chromosomes, the inclusion of neighbor information beyond each feature's two-nearest neighbors did not add an increased benefit to the classification process for the MultiBoostAB algorithm using the J48 classifier. The partitioning of the classification process by chromosome, in general, produced a higher accuracy of classification for the MultiBoostAB algorithm using the J48 classifier. The decision trees generated can be found in Appendix I.

5.2.2.3 Removing Location Information

A series of experiments was performed to determine if given the properties of neighbor number, neighbor's Gene Ontology information, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and Gene Ontology information for genomic features (features being: genes, ARS, etc) for training could the MultiBoostAB algorithm using the J48 classifier could correctly classify Gene Ontology term. The MultiBoostAB algorithm using the J48 classifier was selected since it obtained the best performance in the prior section.

These experiments were performed to see if rules could be generated that would provided insight about a genomic feature's network involvement based only on what other features are near it regardless of that feature's location.

The rules generated did not incorporate the neighbor's Gene Ontology information. Neighbor distance was the most important attribute being selected for the root of the decision tree (See Figure 5.210). Increasing the amount of information did not alter the performance of the classification process.

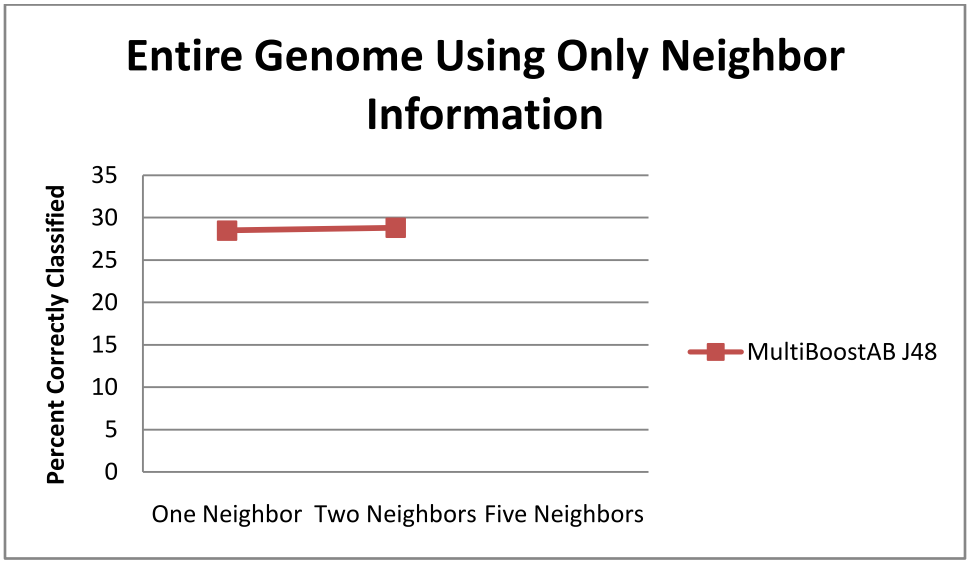


Figure 5.210. The percentage of correctly classified features using the MultiBoostAB algorithm using the J48 classifier.

The accuracy of the classification was low regardless of the number of neighbors included, but there is a slight increase in the F-measure with the inclusion of more neighbor information (See Figure 5.211).

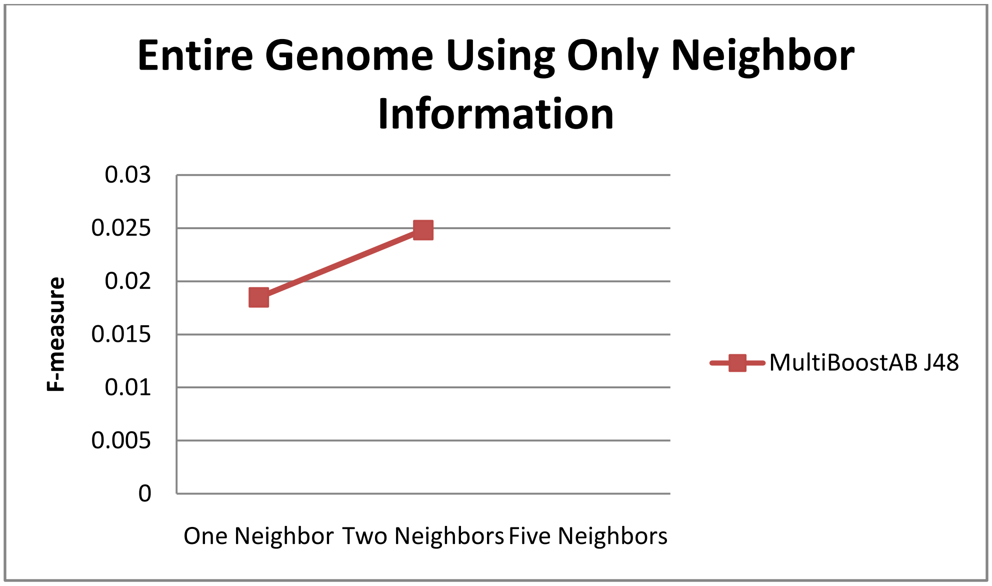


Figure 5.211. The F-measure using the MultiBoostAB algorithm using the J48 classifier.

5.3 Suggesting Locations

To see if locations of interest could be suggested given feature descriptions, different sets of experiments were performed.

5.3.1 Classifying Genomic Features to Chromosome

A series of experiments was performed to determine whether genomic features can be classified to the correct chromosome if given different properties. When given the training data of a genomic feature's chromosome number and either its network involvement from KEGG or its Gene Ontology term, the classification results are similar.

The results of the experiments are based on averages of ten different runs of each dataset being randomized and then split for training and testing. The training sets were set to contain 66% of the instances randomly selected from each dataset.

5.3.1.1 Percent of Correctly Classified

The percent of correctly classified features does not vary depending on the classifier used and the information included (See Figure 5.212). The addition of either the Gene Ontology information or network involvement does not make a significant impact on the classification process.

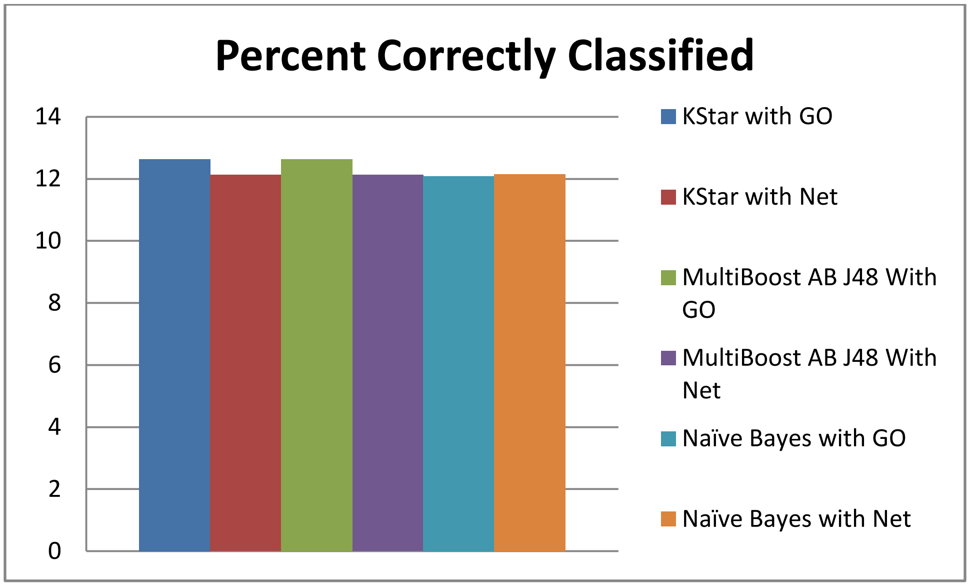


Figure 5.212. The overall correctly classified features for the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayes classifier with either KEGG network involvement included or the GO term included.

5.3.1.2 Effect on Individual Chromosomes

For a majority of chromosomes, the higher F-measures are obtained using the Naïve Bayesian classifier (See Figure 5.213). The classifiers tend to classify all features to chromosome four (the largest chromosome), and these classifications then show not very high accuracy yielding F-measures less than 0.25. The mitochondrial chromosome only has features that are involved in one network, so that explains the F-measure observed when using information from each feature's network involvement.

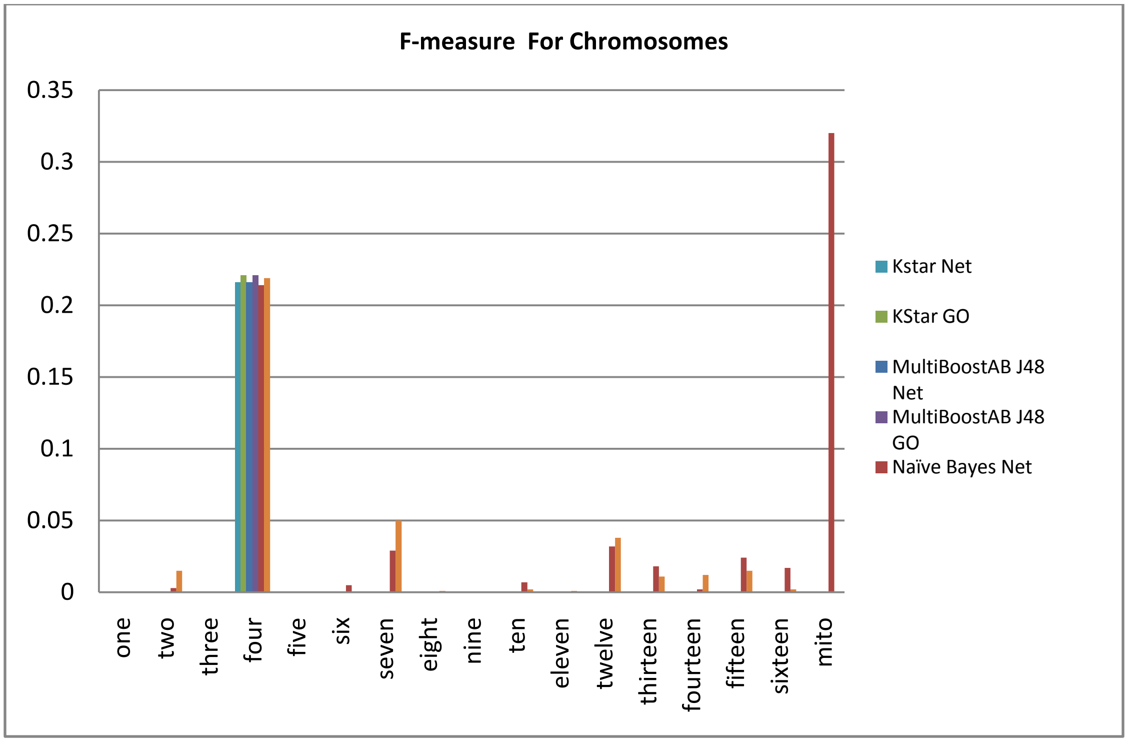


Figure 5.213. The F-measures for the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayes classifier with either KEGG network involvement included or the GO term included for each chromosome.

5.3.2 Classifying Genomic Features to Start Position Using Network Involvement

Experiments were performed to see if given the chromosome number, network involvement and discretized start position to train on that the classifiers could correctly classify the features to the correct start position.

All of the classifiers performed in a similar manner. This can be seen by examining the percentage of correctly classified features (See Table 5.1)

	KStar	**MultiBoostAB using J48**	**Naïve Bayes**
Percent Correctly Classified	22.91 %	22.61%	22.59%

Table 5.1. Percentage of correctly classified features to start position given chromosome number, network involvement and start position to train on using the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier on the entire genome.

The rules generated from these experiments tended to clump all the features to one area on the chromosome. Network involvement was not an attribute that was included in any of the rules. Table 5. 2 represents the rules generated by the MultiBoostAB algorithm using the J48 classifier. The percentage of correctly classified features to the range parallels the percentage of the chromosome the range represents.

If on Chromosome	Then start position range	Percent of correctly classified features by rules	Percent of Chromosome covered by range
One	(0-153220.1]	68.05	66.56
Two	(0-153220.1]	20.11	18.84
Three	(0-153220.1]	52.88	48.39
Four	(306406.2-459592.3]	11.34	10.00
Five	(0-153220.1]	27.42	26.56
Six	(0-153220.1]	54.77	56.72
Seven	(306406.2-459592.3]	15.99	14.04
Eight	(0-153220.1]	29.77	27.23
Nine	(153220.1-306406.2]	37.10	34.82
Ten	(0-153220.1]	22.61	20.55
Eleven	(153220.1-306406.2]	27.71	22.99
Twelve	(459592.3-612778.4]	18.50	14.21
Thirteen	(153220.1-306406.2]	18.57	16.57
Fourteen	(306406.2-459592.3]	21.92	19.53
Fifteen	(765964.5-919150.6]	15.45	14.04
Sixteen	(765964.5-919150.6]	18.17	16.16
Mitochondrial	(0-153220.1]	100.00	100.00

Table 5.2. A representation of the rules generated by the MultiBoostAB algorithm using the J48 classifier. The percent of correctly classified features for each rule was determined by dividing the number of features that were correctly classified by the rule by the total number of features that were classified by that rule then multiplying by 100.

A series of experiments was performed to determine if partitioning the classification to the individual chromosomes would impact the classification process. The classifiers were trained on each feature's network involvement and discretized start position. Each of the classifiers performed similarly (See Table 5.3).

Chromosome	KStar	MultiBoostAB using J48	Naïve Bayes
One	13.74%	13.74 %	14.70 %
Two	11.71%	11.19 %	12.15 %
Three	14.66%	13.54 %	15.40 %
Four	11.49 %	11.34 %	10.91 %
Five	14.35 %	13.18 %	13.19 %
Six	12.71 %	12.22 %	12.47 %
Seven	11.91 %	11.45 %	11.84 %
Eight	14.09 %	13.37 %	14.09 %
Nine	12.74 %	12.58 %	12.90 %
Ten	12.98 %	12.60 %	12.88 %
Eleven	11.78 %	12.36 %	11.43 %
Twelve	14.82 %	14.82 %	15.80 %
Thirteen	10.49 %	10.96 %	10.80 %
Fourteen	12.49 %	11.47 %	13.04 %
Fifteen	11.72 %	11.59 %	11.99 %
Sixteen	13.02 %	12.72 %	13.40 %
Mitochondrial	17.24 %	17.24 %	17.24 %

Table 5.3. Percentage of correctly classified features to start position given network involvement and start position to train on using the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier on the individual chromosomes.

The results from above show that if a feature's network involvement is known, it would be hard to accurately determine which chromosome it is located on. Even if the chromosome number is determined, the classifiers then only have anywhere between a 10-17% chance of locating the feature's starting position.

The classification process was performed using information from the entire genome (each feature's network involvement and start position but no chromosome number information to train on) to see if features of certain networks could be attributed to certain areas on any chromosome. The classifiers performed in a similar manner (See Table 5.4)

	KStar	MultiBoostAB using J48	Naïve Bayes
Percent Correctly Classified	21.05 %	21.05 %	21.09 %

Table 5.4. Percentage of correctly classified features to start position given network involvement and start information to train on using the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier for the entire genome.

5.3.2.1Generating Rules to Classify Start Position Using Network Involvement Information

Since network involvement was not an important attribute in generating rules for the MultiBoostAB algorithm using the J48 classifier, other rules generating classifiers were investigated. The Nearest-neighbor-like algorithm using non-nested generalized exemplars (which are hyperrectangles that can be viewed as if-then rules) obtained rules that did use network involvement to classify start position. The percentage of correctly classified features to their start position for this classifier is 22.653%. The rules that were generated were adapted and used with the IR code to make suggestions of where to look for networks (See section 5.3.4). The rule adaption is discussed in Appendix G. The suggestions of the rules tended to be correct, but they neglected to suggest all the locations that actually contained features that participated in the given network.

5.3.3 Classifying Genomic Features to Start Position Using Gene Ontology Term

Experiments were performed to see if given the chromosome number, the feature's Gene Ontology term and discretized start position to train on that the classifiers could correctly classify the features to the correct start position. Table 5.5 contains the percent of correctly classified features for the different classifiers.

	KStar	**MultiBoostAB using J48**	**Naïve Bayes**
Percent Correctly Classified	22.24 %	21.60 %	22.59 %

Table 5.5. Percentage of correctly classified features to start position given chromosome number, network involvement and start position to train on using the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier on the entire genome.

The rules generated from these experiments also tended to clump all the features to one area on the chromosome for some chromosomes.

A series of experiments was performed to determine if partitioning the classification to the individual chromosomes would impact the classification process. The classifiers were trained on each feature's Gene Ontology term and discretized start position for each chromosome separately. Each of the classifiers performed similarly (See Table 5.6). The Gene Ontology term was an attribute in the rules generated for the MultiBoostAB algorithm using the J48 classifier.

Chromosome	**KStar**	**MultiBoostAB using J48**	**Naïve Bayes**
One	13.67 %	12.17 %	12.17 %
Two	10.49 %	11.30 %	11.30 %
Three	11.81 %	12.87 %	12.55 %
Four	10.05 %	10.33 %	10.33 %
Five	11.40 %	10.76 %	11.15 %
Six	13.82 %	13.11 %	12.96 %
Seven	11.03 %	10.43 %	10.43 %
Eight	12.13 %	11.60 %	11.60 %
Nine	11.47%	10.33 %	11.03 %
Ten	11.81%	11.71 %	11.92 %
Eleven	10.85 %	11.65 %	11.28 %
Twelve	13.00 %	12.43 %	12.43 %
Thirteen	10.68 %	9.61 %	9.53 %
Fourteen	10.44 %	10.53 %	10.73 %
Fifteen	12.82 %	11.16 %	11.19 %
Sixteen	12.35 %	12.89 %	11.52 %
Mitochondrial	16.97 %	16.97 %	16.61 %

Table 5.6. Percentage of correctly classified features to start position given GO term and start position to train on using the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier on the individual chromosomes.

The results from above show that if a feature's Gene Ontology term is known, it would be hard to accurately determine which chromosome it is located on. Even if the chromosome number is determined, the classifiers then only have anywhere between a 10-16% chance of locating the feature's starting position.

The classification process was performed using information from the entire genome (each feature's Gene Ontology term and start position but no chromosome number information to train on) to see if features that have certain Gene Ontology terms could be attributed to certain areas on any chromosome. Each classifier had a similar performance (See Table 5.7).

	KStar	**MultiBoostAB using J48**	**Naïve Bayes**
Percent Correctly Classified	21.07 %	20.57 %	21.18%

Table 5.7. Percentage of correctly classified features to start position given GO term and start information to train on using the KStar classifier, the MultiBoostAB algorithm using the J48 classifier and the Naïve Bayesian classifier for the entire genome.

5.3.4 Using Genomic Feature Descriptions and Information Retrieval

A series of experiments was performed to determine whether given a description of a feature, would finding the networks that the top ten similar features (similarity based on IR) were involved in be helpful by suggesting looking by the feature's involved in these networks as areas of possible interest.

For the experiments, descriptions from 8287 genomic features obtained from the *Saccharomyces* Genome Database were used. For the other 8587 genomic features listed in the *Saccharomyces* Genome Database, descriptions could not be obtained. For each of these descriptions, the top ten most similar features from the corpus of descriptions were retrieved. To see if these top ten features could properly suggest network involvement for the given feature, the network involvement of each of the top ten features compared to the actual network involvement of the given feature. A tally was kept of how many networks were suggested and of how many of those suggestions were correct.

From the retrieval results of the 8287 features, the percentage of correct suggestions was calculated to be 42.86%. To further analyze how the retrieval process worked, each individual run was analyzed. Table 5.8 shows a summary of the runs

Number of features	Percentage of features	Description of suggestions
4669	56.34	There was no known network, and no suggestions were made
2520	30.41	There was no known network involvement, but suggestions were made
90	1.09	Network suggestion were made, but none of them matched the known network involvement
47	0.57	There was known network involvement, but no suggestions were made.
349	4.21	100% of the suggestions were accurate
28	0.34	The range of the percent of correct suggestions was $90 \le x < 100$
54	0.65	The range of the percent of correct suggestions was $80 \le x < 90$
42	0.51	The range of the percent of correct suggestions was $70 \le x < 80$
70	0.84	The range of the percent of correct suggestions was $60 \le x < 70$
123	1.48	The range of the percent of correct suggestions was $50 \le x < 60$
67	0.81	The range of the percent of correct suggestions was $40 \le x < 50$
52	0.63	The range of the percent of correct suggestions was $30 \le x < 40$
78	0.94	The range of the percent of correct suggestions was $20 \le x < 30$
75	0.91	The range of the percent of correct suggestions was $10 \le x < 20$
23	0.28	The range of the percent of correct suggestions was $0 < x < 10$

Table 5.8. Shows a summary of the retrieval results and network suggestions for the 8287 genomic features.

A search engine was developed to take as input a description of a feature. Based on the network involvement of the top ten most similar features to the given feature, locations of start positions in the genome for other features that may participate in a network with the given feature are provided. A diagram of the process can be seen in Figure 3.3. The given feature description does affect the accuracy of the results. The vaguer a description is, the less likely the user will get suggestions that would be useful.

5.4 Summary

The results of this study showed that in classifying features to their correct network, neighbor information from those features is needed. The inclusion of the Gene Ontology term for each feature's two-nearest neighbors was more beneficial to the classification process than including either the neighbor's SGDID or the neighbor's network involvement. The MultiBoostAB algorithm using the J48 classifier performed better than the KStar classifier and the Naïve Bayesian classifier. When using the Gene Ontology term for each feature's two-nearest neighbors, it was determined that partitioning of the classification process improved F-measures obtained by the MultiBoostAB algorithm using the J48 classifier, so the rules that were translated for the rule-based system were based on the rules generated using the individual chromosomes. By doing this, the average percent correctly classified became 50.63% and the average F-measure became 0.65. The rules for the rule-based system were fairly accurate and could classify features to their correct network over 50% of the time. The results did show that knowing the location of the feature is key in classifying it to the proper network. Only using neighbor information to classify a feature to a network reduces the percentage of correctly classified features by over 40 percentage points.

The results of this study also showed that in classifying features to their correct Gene Ontology term group, neighbor information from those features is also needed. The inclusion of the Gene Ontology information for each feature's two-nearest neighbors was more beneficial to the classification process than including the neighbor's SGDID. The MultiBoostAB algorithm using the J48 classifier performed better than the KStar classifier and the Naïve Bayesian classifier. When using the Gene Ontology information for each feature's two-nearest neighbors, it was determined that partitioning of the classification process improved F-measures obtained by the MultiBoostAB algorithm using the J48 classifier, so the rules that were translated for the rule-based system were based on the rules generated using the individual chromosomes. By doing this, the average percent correctly classified became 83.1% and the average F-measure became 0.85. The rules for the rule-based system were fairly accurate and could classify features to their correct Gene Ontology term over 80% of the time. The results did show that knowing the location of the feature is key in classifying it to the proper Gene Ontology term. Only using neighbor information to classify a feature to a network reduces the percentage of correctly classified features by over 50 percentage points.

When trying to suggest locations of features based on their network involvement or their Gene Ontology term, the classification process was not as successful. The locations that were recommended did not include all the known features that belonged to either the network or the Gene Ontology group. These rules only were able to suggest some locations of interest, not all. When trying to suggest areas of interest of possible network work involvement using textual feature descriptions, the search engine created in this study recommended the correct network about 43% of the time.

6 Discussion

6.1 Discussion of Results

Through my experiments, I determined what neighbor information was the most beneficial in classifying features to the correct network and the correct Gene Ontology term, and how many neighbors to include in this process for the yeast genome. I found that knowing the Gene Ontology terms of a feature's two-nearest neighbors both upstream and downstream on both strands of a feature is important in determining network involvement of that feature and the Gene Ontology term of that feature. Partitioning the classification process by chromosome allowed the MultiBoostAB algorithm [Webb, 2000] using the J48 classifier [Quinlan, 1993] to provide the most accurate results. The decision trees generated in the classification process became the rules in the rule-based systems I produced. The software created acts as a filter, limiting the search area that one needs to look for other genomic features that are involved in a network with a given feature and suggesting possible functionality for a feature if it is unknown.

It was not too surprising to find that the inclusion of information from only each feature's two-nearest neighbors had such an impact on classification since Hurst *et al.* (2004) found that clusters of co-expressed genes in yeast rarely exceed ten genes or a few kilobases. The inclusion of more neighbors, beyond the two nearest, did not significantly improve the classification process.

Lee and Sonnhammer (2003) found 98% of metabolic pathways in yeast exhibited significantly higher clustering levels than expected by chance. This suggested that the inclusion of neighbor information would be beneficial in classifying features to networks. When examining Figures 5.48–5.50, we do see that for most networks, classifying features to them accurately is benefitted from the inclusion of neighbor information supporting the notion set forth by Lee and Sonnhammer (2003). It was hoped that the rule-based system would have been able to classify features to their correct network more than it did (over 50% of the time) based on the high amount of clustering found in the yeast genome.

The rule-based system designed to suggest a feature's Gene Ontology term performed well. The rules for the rule-based system could classify features to their correct Gene Ontology term over 80% of the time. Having the inclusion of neighbor's Gene Ontology information being so beneficial in classifying features to the correct Gene Ontology term group supports finding from other studies. In a study by Fukuoka *et al.*, they investigated Gene Ontology categories of gene pairs that were considered highly correlated in chromosomal distance ranges between 0 and 20 kbp and between 980 and 1000 kbp. The results of the pairwise analysis of Gene Ontology category showed that only highly correlated pairs shared the same category and most of these pairs were not duplicates, meaning the genes did not share a common history; this was determined by BLAST analysis [Fukuoka, *et al.*, 2004].

When trying to suggest locations of features based on their network involvement or their Gene Ontology term group, the classification process was not as successful. This is in part that the rules did not cover all the locations, only some of them. When trying to suggest areas of interest of possible network work involvement using textual feature descriptions, the search engine created in this study recommended the correct network about 43% of the time. Marcotte *et al.* (1999) found that proteins that are functionally related participate in a common structural complex, metabolic pathway, biological process or closely related physiological function. Since the feature descriptions used contained information about functionality, it was thought that the results of the search engine technique would have been higher. It could be that the results are better. The search engine did make network suggestions that did not match what is currently known. It could be that the search engine made network involvement suggestions for features, and in future studies in yeast, they could be found relevant.

My experimental results showed that my methodology is able to correctly locate areas of interest for network involvement over 50% of the time and over 80% of the time suggest the correct Gene Ontology term(s) for a given genomic feature in yeast. By analyzing data from a different perspective (i.e. focusing on the location and the contribution of the nearest neighbors of each genomic feature), I was able to generate rules that can be used to focus searches for genetic networks or determine gene product functionality. Since other genomes (*Homo sapiens*, *Caenorhabditis elegans*, *Drosophila melanogaster*, *Arabidopsis thaliana*) exhibit clustering patterns, this methodology should translate to those other genomes. The optimal neighborhood size for each genome would have to be established through experimentation. The classification rules generated in the genomes where we do not know as much as we do in yeast could elucidate new relationships between genes.

If we make the analogy that a genome is a collection of neighborhoods, and a genomic feature is like a house, then knowing your address and what your two-nearest neighbors on both sides of your house and across the street do tells us a lot about what you do (Gene Ontology terms) and what organizations (networks) you might be involved in. The software created in this study takes advantage of this phenomenon making it easier to come up with reliable hypotheses about the location of potential genetic regulatory networks within a genome and about possible functionality of a gene.

6.2 Future studies

This dissertation only examined yeast. It would be beneficial to perform the same experiments on other species. This way we could determine if there are common trends in the classification process among different species. The mouse genome and the human genome are the next genomes of interest because mice are a common animal model for studying human disease.

If we compare the human genome and the mouse genome, it looks like the human chromosomes were chopped up into many pieces and then put back together to form the mouse genome (or it may have occurred the other way). These rearrangements did not occur all at one time, but they occurred over millions of years. Within each of the blocks there are many small changes at the gene level, but what is very interesting to scientists is how much of the DNA sequence is the same between mouse and humans, although the location of the genes is different. This discovery has led scientists to believe that the relative location of genes to one another may also affect the phenotype of an organism [Mouse Genome Sequencing Consortium, 2002]. Discovering patterns in gene location may offer more insight to this.

Also, understanding why genes are located where they are will be useful to scientists to help discover genes that cause disease. The software I developed utilizes patterns based on gene location and the neighborhood around it. Once these patterns have been established in different organisms, then discovering these relationships between animal models and humans will be easier. Many diseases are caused by flawed networks. When genes malfunction, they can cause diseases such as cancer, glaucoma, ADHD, diabetes, epilepsy, asthma, cystic fibrosis and muscular dystrophy. Research is critical for scientists to cultivate a greater understanding of how genes contribute to disease. This understanding and being able to elucidate genetic networks provides the foundation on which new treatments or cures can be developed.

Since results on individual networks and Gene Ontology term groups were obtained, it would be interesting to see why the classifiers could classify features to certain networks or certain Gene Ontology term groups better than others. A more detailed biological analysis would be required.

In a study by Tsai *et al.* (2007), their findings suggest that transcription factor sharing is not the sole determinant for the co-regulation of adjacent genes in yeast. These studies suggest that yeast have developed a regulatory system which integrates both transcription-factor-based and non-transcription-factor based mechanisms. They believe that the non-transcription-factor based mechanisms may play a greater role in driving co-expression of neighboring genes [Tsai *et al.,* 2007]. Based on this study, it would be interesting to incorporate transcription factor information in studies similar to the ones performed in this thesis to see if there are patterns based on the location genomic features and their neighbors and transcription factor that interact with them.

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Appendix A: Stop List Used in Information Retrieval

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Appendix B: F-measures for the networks using KStar classifier

The Table B1 shows the F-measures for the networks using the KStar classifier trained with the properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's SGDID, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and network involvement information from KEGG for genomic features (features being: genes, ARS, etc.).

F-measure	**K***				
Network	**No**	**1**	**2**	**5**	**10**
1- and 2- methylnaphthalene degradation	0	0	0	0	0
1,4-dichlorobenzene and dicarboxylate metabolism	0	0	0	0.125	0
3-chloroacrylic acid degradation	0	0	0	0	0
ABC transporters	0	1	1	1	1
alanine and aspartate metabolism	0	0.074	0.118	0.116	0.126
alkaloid biosynthesis II	0	0	0.133	0.209	0.073
alpha-linolenic acid metabolism	0	0	0	0	0
aminoacyl-tRNA biosynthesis	0.069	0.127	0.113	0.125	0.143
aminophosphonate metabolism	0	0	0.182	0.037	0.049
aminosugars metabolism	0	0.414	0.649	0.66	0.68
arachidonic acid metabolism	0	0.353	0.167	0.282	0.237
arginine and proline metabolism	0	0.318	0.169	0.302	0.303
basal transcription factors	0.2	0.625	0.827	0.972	0.967
benzoate degradation via CoA ligation	0	0.039	0.042	0.021	0.03
benzoate degradation via hydroxylation	0	0	0	0	0
beta-alanine metabolism	0	0.061	0.048	0.065	0.073
bile acid biosynthesis	0	0.054	0.045	0.08	0.092
biosynthesis of steroids	0	0.533	0.803	0.795	0.769
biotin metabolism	0	0.471	0.545	0.478	0.663
butanoate metabolism	0	0.068	0	0.022	0.019
C5-branched dibasic acid metabolism	0	0.143	0	0	0
carbon fixation	0	0.042	0.042	0.051	0.058
cell communication	0	0	1	0.571	0.88
cell cycle	0.123	0.586	0.758	0.767	0.789
citrate cycle	0	0.053	0.164	0.173	0.13

cyanoamino acid metabolism	0	0	0.113	0.036	0.031
cysteine metabolism	0	0	0.045	0.016	0.017
DNA polymerase	0	0.533	0.364	0.491	0.515
ether lipid metabolism	0	0	0	0.058	0.156
ethylbenzene degradation	0	0	0	0	0
fatty acid biosynthesis	0	0.333	0.519	0.536	0.466
fatty acid elongation in mitochondria	0	0	0	0	0.077
fatty acid metabolism	0	0.089	0.179	0.201	0.264
fluorobenzoate degradation	0	0	0	0	0
folate biosynthesis	0	0.239	0.315	0.34	0.357
fructose and mannose metabolism	0	0.175	0.343	0.262	0.293
gamma-Hexachlorocyclohexane degradation	0	0.25	0.295	0.196	0.249
geraniol degradation	0	0	0	0	0
glutamate metabolism	0	0.088	0.175	0.128	0.102
glutathione metabolism	0	0	0.138	0.124	0.118
glycan structures biosynthesis 1	0	0.132	0.169	0.158	0.173
glycan structures biosynthesis 2	0	0.164	0.12	0.147	0.199
glycan structures degradation	0	1	1	0.889	0.941
glycerolipid metabolism	0	0.25	0.348	0.268	0.333
glycerophospholipid metabolism	0.125	0.204	0.349	0.293	0.374
glycine, serine and threonine metabolism	0	0.156	0.175	0.212	0.236
glycolysis/gluconeogenesis	0	0.112	0.271	0.287	0.313
glycosylphosphatidylinositol-anchor biosynthesis	0	0.211	0.203	0.29	0.336
glyoxylate and dicarboxylate metabolism	0	0.14	0.273	0.178	0.242
high-mannose type N-glycan biosynthesis	0	0.162	0.229	0.258	0.282
histidine metabolism	0	0.211	0.337	0.3	0.327
inositol phosphate metabolism	0	0.075	0.091	0.109	0.136
limonene and pinene degradation	0	0	0	0	0.04
lipoic acid metabolism	0	0.4	0.667	0.9	1
lysine biosynthesis	0	0.245	0.318	0.277	0.376
lysine degradation	0	0.103	0.111	0.082	0.103
MAPK signaling pathway	0	0.622	0.691	0.735	0.748
metabolism of xenobiotics by cytochrome P450	0	0	0	0	0
methane metabolism	0	0.19	0.118	0.14	0.138
methionine metabolism	0	0.175	0.048	0.164	0.177
N-glycan biosynthesis	0	0.2	0.301	0.329	0.369
nictinate and nicotinamide metabolism	0	0.636	0.667	0.758	0.746
nitrogen metabolism	0	0.075	0.115	0.081	0.082
novobiocin biosynthesis	0	0	0	0	0

nucleotide sugars metabolism	0	0.25	0.25	0.308	0.33
one carbon pool by folate	0	0.103	0.282	0.229	0.307
oxidative phosphorylation	0.372	0.632	0.825	0.831	0.852
pantothenate and CoA biosynthesis	0	0.24	0.264	0.301	0.31
pentose and glucuronate interconversions	0	0.118	0.182	0.289	0.337
pentose phosphate pathway	0	0.342	0.431	0.316	0.421
peptidoglycan biosynthesis	0	0	0	0	0
phenylalanine metabolism	0	0	0	0.019	0
phenylalanine, tyrosine and tryptophan biosynthesis	0	0.565	0.674	0.659	0.614
phosphatidylinositol signaling system	0	0.163	0.077	0.115	0.119
polyunsaturated fatty acid biosynthesis	0.667	0.703	0.828	0.906	0.813
porphyrin and chlorophyll metabolism	0	0.39	0.667	0.6	0.633
proteasome	0.143	0.782	0.931	0.952	0.949
protein export	0	0.846	0.909	0.984	0.966
purine metabolism	0.051	0.292	0.324	0.308	0.302
pyrimidine metabolism	0	0.186	0.295	0.311	0.312
pyruvate metabolism	0	0.164	0.227	0.233	0.205
reductive carboxylate cycle (CO2 fixation)	0	0	0	0.033	0.012
regulation of autophagy	0	0.533	0.866	0.915	0.863
riboflavin metabolism	0	0.313	0.64	0.581	0.6
ribosome	0.754	0.773	0.951	0.955	0.967
RNA polymerase	0	0.031	0.014	0.052	0.019
selenoamino acid metabolism	0	0.031	0.04	0.023	0.063
SNARE interactions in vesicular transport	0.3	0.784	0.893	0.956	0.95
sphingolipid metabolism	0	0.711	0.892	0.901	0.964
starch and sucrose metabolism	0.05	0.462	0.494	0.51	0.509
streptomycin biosynthesis	0	0	0	0.024	0.053
styrene degradation	0	0	0	0	0
sulfur metabolism	0	0.222	0.242	0.155	0.202
synthesis and degradation of ketone bodies	0	0	0	0.057	0.043
taurine and hypotaurine metabolism	0	0	0	0	0
terpenoid biosynthesis	0	0	0.231	0.157	0.163
thiamine metabolism	0	0.615	0.882	0.93	0.897
tryptophan metabolism	0	0.051	0.06	0.108	0.192
two-component system	0	0.333	0	0.182	0.056
tyrosine metabolism	0	0	0	0	0
ubiquinone biosynthesis	0	0.842	1	0.972	1
ubiquitin mediated proteolysis	0.296	0.508	0.617	0.604	0.609
urea cycle and metabolism of amino groups	0	0.393	0.449	0.458	0.399

valine, leucine and isoleucine biosynthesis	0.143	0.164	0.187	0.186	0.234
valine, leucine and isoleucine degradation	0	0	0	0.029	0
vitamin B6 metabolism	0	0.556	0.815	0.77	0.734

Table B1

Appendix C: F-measures for the networks using the MultiBoostAB algorithm using the J48 classifier

The Table C1 below shows the F-measures for the networks using the MultiBoostAB algorithm using the J48 classifier trained with the properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's Gene Ontology term, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and network involvement information from KEGG for the genomic features (features being: genes, ARS, etc.). Measures for the ten-nearest neighbors could not be obtained.

F-measures	**Number of Neighbors**				
Network	**No**	**1**	**2**	**5**	**10**
1- and 2- methylnaphthalene degradation	0	0.017	0.02	0	
1,4-dichlorobenzene and dicarboxylate metabolism	0	0	0.148	0	
3-chloroacrylic acid degradation	0	0.022	0	0.019	
ABC transporters	0	0.7	1	1	
alanine and aspartate metabolism	0	0.14	0.228	0.276	
alkaloid biosynthesis II	0	0.118	0.307	0.323	
alpha-linolenic acid metabolism	0	0.056	0.045	0.026	
aminoacyl-tRNA biosynthesis	0	0.181	0.28	0.416	
aminophosphonate metabolism	0	0.138	0.181	0.199	
aminosugars metabolism	0	0.589	0.771	0.808	
arachidonic acid metabolism	0	0.216	0.403	0.353	
arginine and proline metabolism	0	0.218	0.369	0.423	
basal transcription factors	0	0.77	1	1	
benzoate degradation via CoA ligation	0	0.059	0.112	0.145	
benzoate degradation via hydroxylation	0	0.067	0	0	
beta-alanine metabolism	0	0.091	0.098	0.127	
bile acid biosynthesis	0	0.03	0.118	0.142	
biosynthesis of steroids	0	0.621	0.851	0.865	
biotin metabolism	0	0.343	0.672	0.802	
butanoate metabolism	0	0.088	0.072	0.146	
C5-branched dibasic acid metabolism	0	0	0.098	0.302	
carbon fixation	0	0.05	0.149	0.215	

cell communication	0	1	1	1	
cell cycle	0	0.578	0.858	0.876	
citrate cycle	0	0.123	0.262	0.286	
cyanoamino acid metabolism	0	0.061	0.092	0.124	
cysteine metabolism	0	0.017	0.118	0.172	
DNA polymerase	0	0.281	0.557	0.565	
ether lipid metabolism	0	0.083	0.275	0.29	
ethylbenzene degradation	0	0	0	0.092	
fatty acid biosynthesis	0	0.235	0.556	0.619	
fatty acid elongation in mitochondria	0	0.333	0.313	0	
fatty acid metabolism	0	0.242	0.24	0.246	
fluorobenzoate degradation	0	0	0.182	0	
folate biosynthesis	0	0.29	0.491	0.54	
fructose and mannose metabolism	0	0.263	0.373	0.353	
gamma-Hexachlorocyclohexane degradation	0	0.139	0.415	0.35	
geraniol degradation	0	0.111	0	0.091	
glutamate metabolism	0	0.156	0.258	0.231	
glutathione metabolism	0	0.217	0.304	0.38	
glycan structures biosynthesis 1	0	0.252	0.339	0.442	
glycan structures biosynthesis 2	0	0.187	0.34	0.42	
glycan structures degradation	0	0.909	1	1	
glycerolipid metabolism	0	0.268	0.378	0.435	
glycerophospholipid metabolism	0	0.272	0.461	0.534	
glycine, serine and threonine metabolism	0	0.25	0.315	0.35	
glycolysis/gluconeogenesis	0	0.208	0.324	0.387	
glycosylphosphatidylinositol-anchor biosynthesis	0	0.285	0.452	0.51	
glyoxylate and dicarboxylate metabolism	0	0.211	0.326	0.4	
high-mannose type N-glycan biosynthesis	0	0.336	0.405	0.51	
histidine metabolism	0	0.283	0.38	0.394	
inositol phosphate metabolism	0	0.062	0.251	0.274	
limonene and pinene degradation	0	0.043	0.07	0.011	
lipoic acid metabolism	0	0.69	1	1	
lysine biosynthesis	0	0.32	0.559	0.603	
lysine degradation	0	0.047	0.154	0.167	
MAPK signaling pathway	0	0.576	0.807	0.826	
metabolism of xenobiotics by cytochrome P450	0	0.022	0.016	0.008	
methane metabolism	0	0.113	0.138	0.166	
methionine metabolism	0	0.187	0.262	0.343	
N-glycan biosynthesis	0	0.346	0.517	0.54	

nictinate and nicotinamide metabolism	0	0.514	0.761	0.806	
nitrogen metabolism	0	0.116	0.181	0.313	
novobiocin biosynthesis	0	0.067	0.023	0.083	
nucleotide sugars metabolism	0	0.45	0.409	0.574	
one carbon pool by folate	0	0.282	0.377	0.461	
oxidative phosphorylation	0.361	0.633	0.908	0.924	
pantothenate and CoA biosynthesis	0	0.248	0.429	0.554	
pentose and glucuronate interconversions	0	0.231	0.4	0.375	
pentose phosphate pathway	0	0.351	0.507	0.573	
peptidoglycan biosynthesis	0	0.105	0.211	0.071	
phenylalanine metabolism	0	0.053	0.023	0.113	
phenylalanine, tyrosine and tryptophan biosynthesis	0	0.325	0.689	0.717	
phosphatidylinositol signaling system	0	0.114	0.287	0.347	
polyunsaturated fatty acid biosynthesis	0.4	0.762	0.915	0.924	
porphyrin and chlorophyll metabolism	0	0.407	0.742	0.81	
proteasome	0	0.667	1	1	
protein export	0	0.699	1	1	
purine metabolism	0	0.288	0.437	0.476	
pyrimidine metabolism	0	0.243	0.417	0.452	
pyruvate metabolism	0	0.126	0.308	0.365	
reductive carboxylate cycle (CO2 fixation)	0	0.079	0.12	0.216	
regulation of autophagy	0	0.612	0.944	0.967	
riboflavin metabolism	0	0.275	0.744	0.805	
ribosome	0.425	0.656	1	1	
RNA polymerase	0	0.044	0.196	0.256	
selenoamino acid metabolism	0	0.089	0.159	0.184	
SNARE interactions in vesicular transport	0	0.658	0.999	1	
sphingolipid metabolism	0	0.608	0.959	0.952	
starch and sucrose metabolism	0	0.409	0.593	0.632	
streptomycin biosynthesis	0	0.031	0.099	0.097	
styrene degradation	0	0	0.087	0	
sulfur metabolism	0	0.101	0.312	0.36	
synthesis and degradation of ketone bodies	0	0.105	0.16	0.114	
taurine and hypotaurine metabolism	0	0	0.059	0.089	
terpenoid biosynthesis	0	0.349	0.391	0.467	
thiamine metabolism	0	0.706	1	1	
tryptophan metabolism	0	0.15	0.234	0.259	
two-component system	0	0.316	0.44	0.489	
tyrosine metabolism	0	0.019	0.031	0.058	

ubiquinone biosynthesis	0	0.41	1	1	
ubiquitin mediated proteolysis	0	0.451	0.705	0.752	
urea cycle and metabolism of amino groups	0	0.279	0.52	0.575	
valine, leucine and isoleucine biosynthesis	0	0.278	0.304	0.351	
valine, leucine and isoleucine degradation	0	0.028	0.052	0.091	
vitamin B6 metabolism	0	0.5	0.82	0.87	

Table C1

Appendix D: F-measures for the networks using KStar classifier

The Table D1 shows the F-measures for the networks using the KStar classifier trained with the properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's network involvement information from KEGG, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and network involvement information from KEGG for genomic features (features being: genes, ARS, etc.).

F-measure	**K***				
Network	**No**	**1**	**2**	**5**	**10**
1- and 2- methylnaphthalene degradation	0	0.297	0.277	0.297	0.275
1,4-dichlorobenzene and dicarboxylate metabolism	0	0.118	0.118	0.156	0.171
3-chloroacrylic acid degradation	0	0.355	0.417	0.474	0.436
ABC transporters	0	0.556	0.267	0.333	0.327
alanine and aspartate metabolism	0	0.212	0.301	0.312	0.319
alkaloid biosynthesis II	0	0.571	0.483	0.387	0.387
alpha-linolenic acid metabolism	0	0	0.364	0.25	0.069
aminoacyl-tRNA biosynthesis	0.069	0.222	0.247	0.211	0.222
aminophosphonate metabolism	0	0	0	0	0.063
aminosugars metabolism	0	0.821	0.832	0.796	0.792
arachidonic acid metabolism	0	0.101	0.107	0.088	0.113
arginine and proline metabolism	0	1	1	1	0.995
basal transcription factors	0.2	0.863	0.878	0.878	0.856
benzoate degradation via CoA ligation	0	0.356	0.519	0.502	0.427
benzoate degradation via hydroxylation	0	0.313	0.319	0.351	0.321
beta-alanine metabolism	0	0.335	0.387	0.305	0.301
bile acid biosynthesis	0	0.116	0.138	0.097	0.145
biosynthesis of steroids	0	0.135	0.108	0.131	0.153
biotin metabolism	0	0.137	0.22	0.215	0.179
butanoate metabolism	0	0.074	0.167	0.162	0.173
C5-branched dibasic acid metabolism	0	0	0.067	0.014	0.007
carbon fixation	0	0	0.038	0	0.009
cell communication	0	0	0	0	0
cell cycle	0.123	0.273	0.186	0.234	0.205
citrate cycle	0	0.375	0.414	0.363	0.389

cyanoamino acid metabolism	0	0.11	0.088	0.111	0.079
cysteine metabolism	0	0.35	0.277	0.286	0.294
DNA polymerase	0	0.359	0.446	0.373	0.366
ether lipid metabolism	0	0	0	0	0.003
ethylbenzene degradation	0	0	0	0	0
fatty acid biosynthesis	0	0.324	0.219	0.212	0.203
fatty acid elongation in mitochondria	0	0	0	0	0
fatty acid metabolism	0	0	0	0	0
fluorobenzoate degradation	0	0.107	0.217	0.163	0.16
folate biosynthesis	0	0.679	0.524	0.583	0.626
fructose and mannose metabolism	0	0	0	0	0
gamma-Hexachlorocyclohexane degradation	0	0.077	0.087	0.024	0.038
geraniol degradation	0	0	0	0.069	0
glutamate metabolism	0	0	0.048	0.063	0.058
glutathione metabolism	0	0	0.042	0.038	0.038
glycan structures biosynthesis 1	0	0	0	0.068	0.022
glycan structures biosynthesis 2	0	0	0.197	0.14	0.143
glycan structures degradation	0	0.497	0.534	0.501	0.533
glycerolipid metabolism	0	0.452	0.307	0.394	0.367
glycerophospholipid metabolism	0.125	0.348	0.226	0.248	0.266
glycine, serine and threonine metabolism	0	0.182	0.32	0.291	0.333
glycolysis/gluconeogenesis	0	0	0	0.031	0.01
glycosylphosphatidylinositol-anchor biosynthesis	0	0.745	0.643	0.684	0.684
glyoxylate and dicarboxylate metabolism	0	0	0	0	0
high-mannose type N-glycan biosynthesis	0	0.373	0.333	0.304	0.249
histidine metabolism	0	0.212	0.073	0.173	0.119
inositol phosphate metabolism	0	0.226	0.304	0.327	0.256
limonene and pinene degradation	0	0.377	0.355	0.328	0.411
lipoic acid metabolism	0	0	0.067	0.118	0.103
lysine biosynthesis	0	0.3	0.2	0.293	0.273
lysine degradation	0	0	0	0	0
MAPK signaling pathway	0	0.944	0.966	0.933	0.918
metabolism of xenobiotics by cytochrome P450	0	0.282	0.196	0.232	0.22
methane metabolism	0	0	0	0	0
methionine metabolism	0	0	0.222	0	0
N-glycan biosynthesis	0	0.182	0.175	0.231	0.187
nictinate and nicotinamide metabolism	0	0	0.081	0.054	0.026
nitrogen metabolism	0	0	0	0	0
novobiocin biosynthesis	0	0	0	0	0

nucleotide sugars metabolism	0	0	0	0	0.08
one carbon pool by folate	0	0.027	0.015	0.029	0.028
oxidative phosphorylation	0.372	0	0	0	0.027
pantothenate and CoA biosynthesis	0	0.25	0.158	0.22	0.261
pentose and glucuronate interconversions	0	0	0.114	0.15	0.108
pentose phosphate pathway	0	0	0.053	0.009	0.064
peptidoglycan biosynthesis	0	0.067	0.034	0.034	0.054
phenylalanine metabolism	0	1	1	1	0.936
phenylalanine, tyrosine and tryptophan biosynthesis	0	0.424	0.579	0.673	0.613
phosphatidylinositol signaling system	0	0.8	0.873	0.85	0.74
polyunsaturated fatty acid biosynthesis	0.667	0.9	0.821	0.77	0.784
porphyrin and chlorophyll metabolism	0	0.4	0.393	0.408	0.319
proteasome	0.143	0.714	0.75	0.679	0.683
protein export	0	1	1	1	0.97
purine metabolism	0.051	0.273	0.319	0.369	0.364
pyrimidine metabolism	0	0.607	0.76	0.732	0.668
pyruvate metabolism	0	0.167	0.16	0.231	0.163
reductive carboxylate cycle (CO2 fixation)	0	0	0	0.027	0.02
regulation of autophagy	0	0.085	0.076	0.08	0.106
riboflavin metabolism	0	0.167	0.185	0.26	0.299
ribosome	0.754	0.143	0.171	0.11	0.083
RNA polymerase	0	0.14	0.147	0.15	0.172
selenoamino acid metabolism	0	0	0	0	0.008
SNARE interactions in vesicular transport	0.3	0.158	0.188	0.141	0.192
sphingolipid metabolism	0	0.261	0.239	0.189	0.228
starch and sucrose metabolism	0.05	1	1	1	1
streptomycin biosynthesis	0	0.885	0.895	0.833	0.866
styrene degradation	0	1	1	1	0.706
sulfur metabolism	0	1	1	1	0.963
synthesis and degradation of ketone bodies	0	0.25	0	0.25	0.092
taurine and hypotaurine metabolism	0	0.968	1	1	0.975
terpenoid biosynthesis	0	0.026	0.015	0.042	0.052
thiamine metabolism	0	0.92	1	1	0.957
tryptophan metabolism	0	0.34	0.512	0.559	0.56
two-component system	0	0.938	1	1	0.97
tyrosine metabolism	0	1	1	1	0.985
ubiquinone biosynthesis	0	0.758	0.777	0.791	0.768
ubiquitin mediated proteolysis	0.296	0.115	0.104	0.108	0.172
urea cycle and metabolism of amino groups	0	0.796	0.836	0.829	0.795

valine, leucine and isoleucine biosynthesis	0.143	0.6	0.655	0.658	0.621
valine, leucine and isoleucine degradation	0	1	1	1	0.979
vitamin B6 metabolism	0	0.933	0.964	0.948	0.883

Table D1

Appendix E: F-measures for the Gene Ontology term using the MultiBoostAB algorithm using the J48 classifier

The Table E1 below shows the F-measures for the networks using the MultiBoostAB algorithm using the J48 classifier trained with the properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's SGDID, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and Gene Ontology information for the genomic features (features being: genes, ARS, etc.).

F-measures	**Number of Neighbors**			
GO terms	**No**	**1**	**2**	**5**
amino acid and derivative metabolic process	0	0	0	
anatomical structure morphogenesis	0	0	0	
biological process	0.368	0.4	0.403	
carbohydrate metabolic process	0	0	0	
cell budding	0	0	0	
cell cortex	0	0	0	
cell cycle	0	0	0	
cell wall	0	0	0	
cell wall organization and biogenesis	0	0	0	
cellular bud	0	0	0	
cellular component	0.191	0	0	
cellular homeostasis	0	0	0	
cellular respiration	0	0	0	
chromosome	0	0	0	
conjugation	0	0	0	
cytokinesis	0	0	0	
cytoplasm	0.25	0.358	0.363	
cytoplasmic membrane-bound vesicle	0	0	0	
cytoskeleton	0	0	0	
cytoskeleton organization and biogenesis	0	0	0	
DNA binding	0	0	0	
DNA metabolic process	0.054	0	0	
electron transport	0	0	0	
endomembrane system	0	0	0	
endoplasmic reticulum	0.026	0	0	
enzyme regulator activity	0	0	0	
extracellular region	0	0	0	
generation of precursor metabolites and energy	0	0	0	
Golgi apparatus	0	0	0	
helicase activity	0	0	0	
hydrolase activity	0	0	0	
isomerase activity	0	0	0	
ligase activity	0	0	0	

lipid metabolic process	0	0	0	
lyase activity	0	0	0	
meiosis	0	0	0	
membrane	0.027	0	0	
membrane fraction	0	0	0	
membrane organization and biogenesis	0	0	0	
microtubule organizing center	0	0	0	
mitochondrial envelope	0	0	0	
mitochondrion	0.17	0	0	
molecular function	0.572	0.584	0.574	
motor activity	0	0	0	
nuclear organization and biogenesis	0.154	0	0	
nucleolus	0.112	0	0	
nucleotidyltransferase activity	0	0	0	
nucleus	0.188	0	0	
organelle organization and biogenesis	0.022	0	0	
oxidoreductase activity	0	0	0	
peptidase activity	0	0	0	
peroxisome	0	0	0	
phosphoprotein phosphatase activity	0	0	0	
plasma membrane	0.014	0	0	
protein binding	0	0	0	
protein catabolic process	0.042	0	0	
protein kinase activity	0	0	0	
protein modification process	0.026	0	0	
pseudohyphal growth	0	0	0	
response to stress	0.016	0	0	
ribosome	0.028	0	0	
ribosome biogenesis and assembly	0.011	0	0	
RNA binding	0	0	0	
RNA metabolic process	0.061	0	0	
signal transducer activity	0	0	0	
signal transduction	0	0	0	
site of polarized growth	0	0	0	
sporulation	0	0	0	
structural molecule activity	0	0	0	
transcription	0.054	0	0	
transcription regulator activity	0	0	0	
transferase activity	0	0	0	
translation	0.122	0	0	
translation regulator activity	0	0	0	
transport	0.074	0	0	
transporter activity	0	0	0	
vacuole	0	0	0	
vesicle-mediated transport	0.011	0	0	
vitamin metabolic process	0.083	0	0	

Table E1

Appendix F: F-measures for the Gene Ontology term using the MultiBoostAB algorithm using the J48 classifier

The Table F1 below shows the F-measures for the networks using the MultiBoostAB algorithm using the J48 classifier trained with the properties of chromosome number, start position, stop position, strand, neighbor's number, neighbor's Gene Ontology information, neighbor's strand, neighbor's distance (determined from the mid-point of each feature), and Gene Ontology information for the genomic features (features being: genes, ARS, etc.).

F-measures	**Number of Neighbors**			
GO terms	**No**	**1**	**2**	**5**
amino acid and derivative metabolic process	0	0	0.838	0.833
anatomical structure morphogenesis	0	0	0.333	0.41
biological process	0.368	0.4	0.949	0.954
carbohydrate metabolic process	0	0	0.8	0.806
cell budding	0	0	0.757	0.758
cell cortex	0	0	0.373	0.452
cell cycle	0	0	0.64	0.631
cell wall	0	0.025	0.96	0.993
cell wall organization and biogenesis	0	0	0.788	0.78
cellular bud	0	0	0.365	0.411
cellular component	0.191	0.307	0.861	0.885
cellular homeostasis	0	0	0.805	0.742
cellular respiration	0	0	0.779	0.76
chromosome	0	0.057	0.556	0.594
conjugation	0	0	0.727	0.72
cytokinesis	0	0	0.843	0.862
cytoplasm	0.25	0.364	0.702	0.717
cytoplasmic membrane-bound vesicle	0	0.049	0.778	0.777
cytoskeleton	0	0.035	0.521	0.532
cytoskeleton organization and biogenesis	0	0	0.724	0.738
DNA binding	0	0	0.756	0.789
DNA metabolic process	0.054	0	0.762	0.758
electron transport	0	0	0.795	0.812
endomembrane system	0	0.023	0.539	0.493
endoplasmic reticulum	0.026	0.116	0.65	0.659
enzyme regulator activity	0	0	0.915	0.952
extracellular region	0	0.074	0.741	0.808
generation of precursor metabolites and energy	0	0	0.869	0.867
Golgi apparatus	0	0.029	0.766	0.807
helicase activity	0	0	0.882	0.921
hydrolase activity	0	0	0.93	0.951
isomerase activity	0	0	0.849	0.91
ligase activity	0	0	0.981	0.985

lipid metabolic process	0	0	0.893	0.889
lyase activity	0	0	0.917	0.947
meiosis	0	0	0.66	0.624
membrane	0.027	0.086	0.5	0.519
membrane fraction	0	0.14	0.635	0.649
membrane organization and biogenesis	0	0	0.589	0.582
microtubule organizing center	0	0	0.741	0.762
mitochondrial envelope	0	0	0.668	0.682
mitochondrion	0.17	0.188	0.774	0.801
molecular function	0.572	0.572	0.951	0.987
motor activity	0	0	0.928	0.93
nuclear organization and biogenesis	0.154	0	0.752	0.733
nucleolus	0.112	0.063	0.758	0.799
nucleotidyltransferase activity	0	0	0.931	0.993
nucleus	0.188	0.3	0.594	0.622
organelle organization and biogenesis	0.022	0	0.695	0.677
oxidoreductase activity	0	0	0.912	0.937
peptidase activity	0	0	0.958	0.963
peroxisome	0	0	0.735	0.805
phosphoprotein phosphatase activity	0	0	0.962	0.99
plasma membrane	0.014	0.076	0.714	0.726
protein binding	0	0	0.923	0.96
protein catabolic process	0.042	0	0.905	0.913
protein kinase activity	0	0	0.894	0.933
protein modification process	0.026	0	0.796	0.806
pseudohyphal growth	0	0	0.883	0.889
response to stress	0.016	0	0.871	0.874
ribosome	0.028	0.074	0.726	0.767
ribosome biogenesis and assembly	0.011	0	0.837	0.832
RNA binding	0	0	0.933	0.971
RNA metabolic process	0.061	0	0.747	0.746
signal transducer activity	0	0	0.813	0.835
signal transduction	0	0	0.707	0.721
site of polarized growth	0	0.032	0.43	0.428
sporulation	0	0	0.59	0.625
structural molecule activity	0	0	0.95	0.982
transcription	0.054	0	0.829	0.829
transcription regulator activity	0	0	0.827	0.875
transferase activity	0	0	0.954	0.987
translation	0.122	0	0.973	0.975
translation regulator activity	0	0	0.879	0.912
transport	0.074	0	0.756	0.748
transporter activity	0	0	0.894	0.934
vacuole	0	0.04	0.631	0.679
vesicle-mediated transport	0.011	0	0.691	0.7
vitamin metabolic process	0.083	0	0.847	0.855

Table F1.

Appendix G: NNge Rule Adaption

The Nearest-neighbor-like algorithm uses non-nested generalized exemplars which are hyperrectangles. These hyperrectangles can be viewed as if-then rules. An example of one of these rules follows:

`class '(306406.2-459592.3]' IF : strand in {C} ^ network in {sce03022} ^ chromosome in {sixteen}`

This rule was adapted to:

If the feature is in network sce03022 then look at strand C of chromosome sixteen in the range of 306406-459592.

There were several rules that mentioned this network, so at the end of the adaption process, there were several locations that were recommended. Below is the rule generated for this network, it is written in Java:

```
if(network.equals("sce03022"))
{
      addLocation("Chromosome two, Strand C, range: 612778 -
      765964");
      addLocation("Chromosome three, Strand C, range: 153220 -
      306406");
      addLocation("Chromosome four, Strand W, range: 1072336 -
      1225522");
      addLocation("Chromosome five, Strand W or C, range: 459592 -
      612778");
      addLocation("Chromosome seven, Strand W, range: 765964 -
      919150");
      addLocation("Chromosome seven, Strand C, range: 919150 -
      1072336");
      addLocation("Chromosome eleven, Strand W, range: 459592 -
      612778");
      addLocation("Chromosome twelve, Strand W, range: 153220 -
      306406");
      addLocation("Chromosome thirteen, Strand W or C, range: 612778
      - 765964");
      addLocation("Chromosome fifteen, Strand C, range: 612778 -
      765964");
```

```
    addLocation("Chromosome sixteen, Strand C, range: 306406 -
    459592");
    addLocation("Chromosome sixteen, Strand W, range: 612778 -
    765964");
}
```

Appendix H. Decision Trees Generated for Classifying Features to Networks

In the tree structure, a colon introduces the name of the network that has been assigned to a particular leaf. The network name is followed by the number of instances that reach that leaf. The number is expressed as a decimal because of the way the classification algorithm uses fractions to handle missing values. The number of incorrectly classified instances that reach that leaf, if they exist, are reported after the "/". For example, if the numbers (2.0/1.0) are reported, it means that two instances reached the leaf, of which one is incorrectly classified.

Decision Tree Generated for Chromosome One:

```
start <= 71787
|   strand = C
|   |   start <= 45023: sce00720 (58.75/38.43)
|   |   start > 45023
|   |   |   start <= 67521: sce04111 (9.31)
|   |   |   start > 67521: sce00860 (9.85)
|   strand = W
|   |   start <= 62841
|   |   |   start <= 45023: sce00251 (21.99/9.33)
|   |   |   start > 45023: sce04010 (10.77)
|   |   start > 62841: sce00010 (63.23/42.98)
start > 71787
|   strand = C
|   |   start <= 105873: sce04111 (13.56)
|   |   start > 105873
|   |   |   start <= 130802: sce04130 (11.84)
|   |   |   start > 130802: sce04111 (8.9)
|   strand = W
|   |   start <= 130802
|   |   |   start <= 105873: sce04130 (7.54)
|   |   |   start > 105873: sce00910 (106.76/82.31)
|   |   start > 130802
|   |   |   start <= 175133: sce00230 (10.85)
|   |   |   start > 175133
|   |   |   |   start <= 190187: sce00252 (9.53)
|   |   |   |   start > 190187: sce00361 (8.11/3.17)
```

Decision Tree Generated for Chromosome Two:

```
start <= 505662
|   start <= 245669
|   |   start <= 168426
|   |   |   start <= 80728
|   |   |   |   start <= 69442
```

```
|   |   |   |   |   start <= 37050
|   |   |   |   |   |   start <= 17696
|   |   |   |   |   |   |   distance <= 7324: sce04010 (29.55/9.08)
|   |   |   |   |   |   |   distance > 7324: sce04070 (10.57/2.03)
|   |   |   |   |   |   start > 17696: sce00190 (7.96)
|   |   |   |   |   start > 37050
|   |   |   |   |   |   start <= 60735
|   |   |   |   |   |   |   start <= 40828: sce04111 (18.12)
|   |   |   |   |   |   |   start > 40828: sce03010 (27.82)
|   |   |   |   |   |   start > 60735
|   |   |   |   |   |   |   distance <= 2281: sce04120 (3.36/0.92)
|   |   |   |   |   |   |   distance > 2281: sce04111 (17.42/4.28)
|   |   |   |   start > 69442
|   |   |   |   |   start <= 71124
|   |   |   |   |   |   neigh_num <= 1: sce01030 (15.84/2.99)
|   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   distance <= 2707: sce01030 (3.72/1.04)
|   |   |   |   |   |   |   distance > 2707: sce00510 (8.63/2.5)
|   |   |   |   |   start > 71124
|   |   |   |   |   |   start <= 74692
|   |   |   |   |   |   |   neigh_strand = W: sce00252 (15.62/4.12)
|   |   |   |   |   |   |   neigh_strand = C: sce00251 (19.45/7.61)
|   |   |   |   |   |   start > 74692: sce04140 (17.04)
|   |   |   start > 80728
|   |   |   |   start <= 89123
|   |   |   |   |   start <= 84259: sce00970 (32.28/11.2)
|   |   |   |   |   start > 84259: sce03010 (25.67)
|   |   |   |   start > 89123
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 92412: sce00230 (22.14/7.31)
|   |   |   |   |   |   start > 92412
|   |   |   |   |   |   |   start <= 153613: sce03050 (13.38)
|   |   |   |   |   |   |   start > 153613: sce03010 (16.18)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 135519: sce00190 (18.27)
|   |   |   |   |   |   start > 135519
|   |   |   |   |   |   |   start <= 153613
|   |   |   |   |   |   |   |   start <= 145731: sce00240 (15.99)
|   |   |   |   |   |   |   |   start > 145731: sce03030 (48.5/31.1)
|   |   |   |   |   |   |   start > 153613: sce00740 (12.75)
|   |   start > 168426
|   |   |   start <= 194125
|   |   |   |   start <= 192454
|   |   |   |   |   start <= 182404
|   |   |   |   |   |   start <= 177529: sce04111 (21.25)
|   |   |   |   |   |   start > 177529: sce00510 (17.37)
|   |   |   |   |   start > 182404: sce04111 (31.77/14.65)
|   |   |   |   start > 192454: sce00620 (19.5)
|   |   |   start > 194125
|   |   |   |   start <= 241285
|   |   |   |   |   start <= 202059
|   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   neigh_strand = W: sce00670 (5.29/1.51)
|   |   |   |   |   |   |   neigh_strand = C
```

```
|   |   |   |   |   |   |   |   distance <= 1589: sce00670
(7.7/2.07)
|   |   |   |   |   |   |   |   distance > 1589: sce00271
(4.71/2.08)
|   |   |   |   |   |   neigh_num > 1: sce00271 (24.78/14.18)
|   |   |   |   |   start > 202059: sce00500 (13.63)
|   |   |   |   start > 241285
|   |   |   |   |   start <= 242811: sce00510 (22.76)
|   |   |   |   |   start > 242811: sce01031 (34.9/15.69)
|   start > 245669
|   |   start <= 332829
|   |   |   start <= 278352
|   |   |   |   strand = W
|   |   |   |   |   neigh_num <= 1: sce00350 (20.53/10.22)
|   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   distance <= 1842: sce00251 (8.04/2.32)
|   |   |   |   |   |   distance > 1842: sce00650 (21.69/8.39)
|   |   |   |   strand = C
|   |   |   |   |   start <= 269503
|   |   |   |   |   |   start <= 257973: sce00190 (12.21)
|   |   |   |   |   |   start > 257973
|   |   |   |   |   |   |   neigh_strand = W: sce00513 (20.78/5.07)
|   |   |   |   |   |   |   neigh_strand = C: sce01030 (19.01/4.25)
|   |   |   |   |   start > 269503: sce00520 (33.44/9.16)
|   |   |   start > 278352
|   |   |   |   start <= 297742
|   |   |   |   |   start <= 294019
|   |   |   |   |   |   start <= 287925: sce00530 (18.77)
|   |   |   |   |   |   start > 287925: sce00061 (30.5/13.94)
|   |   |   |   |   start > 294019: sce04070 (40.67/16.99)
|   |   |   |   start > 297742
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 311897
|   |   |   |   |   |   |   start <= 305976: sce03010 (17.41)
|   |   |   |   |   |   |   start > 305976: sce00530 (14.84)
|   |   |   |   |   |   start > 311897
|   |   |   |   |   |   |   start <= 315575: sce00190 (14.97)
|   |   |   |   |   |   |   start > 315575: sce03010 (9.16)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 305976
|   |   |   |   |   |   |   neigh_strand = W: sce00340 (46.92/31.61)
|   |   |   |   |   |   |   neigh_strand = C: sce00440 (48.09/35.36)
|   |   |   |   |   |   start > 305976: sce00750 (16.43)
|   |   start > 332829
|   |   |   start <= 458866
|   |   |   |   strand = W
|   |   |   |   |   start <= 436945
|   |   |   |   |   |   start <= 415255
|   |   |   |   |   |   |   start <= 409163: sce04010 (14.22)
|   |   |   |   |   |   |   start > 409163: sce00630 (24.79/11.92)
|   |   |   |   |   |   start > 415255: sce04140 (16.45)
|   |   |   |   |   start > 436945: sce01030 (47.17/18.42)
|   |   |   |   strand = C
|   |   |   |   |   start <= 411048
```

```
|   |   |   |   |   |   start <= 372732
|   |   |   |   |   |   |   start <= 362512: sce04111 (20.54)
|   |   |   |   |   |   |   start > 362512
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00650
(18.25/7.79)
|   |   |   |   |   |   |   |   neigh_num > 1: sce00960 (22.22/6.85)
|   |   |   |   |   |   start > 372732
|   |   |   |   |   |   |   start <= 379931: sce01030 (20.38/8.69)
|   |   |   |   |   |   |   start > 379931: sce04120 (17.39)
|   |   |   |   |   start > 411048
|   |   |   |   |   |   start <= 415255: sce03010 (17.65)
|   |   |   |   |   |   start > 415255
|   |   |   |   |   |   |   start <= 436945
|   |   |   |   |   |   |   |   start <= 429095
|   |   |   |   |   |   |   |   |   distance <= 1463: sce00740
(8.22/1.79)
|   |   |   |   |   |   |   |   |   distance > 1463: sce00361
(15.21/6.5)
|   |   |   |   |   |   |   |   start > 429095
|   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: sce00361
(14.32/6.57)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: sce04111
(7.36/2.46)
|   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   distance <= 4774: sce04111
(13.81/6.3)
|   |   |   |   |   |   |   |   |   |   distance > 4774: sce00740
(8.72/4.31)
|   |   |   |   |   |   |   start > 436945: sce04070 (17.46)
|   |   |   start > 458866
|   |   |   |   start <= 476431
|   |   |   |   |   start <= 465764
|   |   |   |   |   |   start <= 461867: sce00230 (20.19)
|   |   |   |   |   |   start > 461867: sce04111 (11.07)
|   |   |   |   |   start > 465764
|   |   |   |   |   |   start <= 473920: sce00310 (27.97/13.07)
|   |   |   |   |   |   start > 473920: sce00030 (30.03/13.62)
|   |   |   |   start > 476431
|   |   |   |   |   start <= 494109
|   |   |   |   |   |   start <= 490386
|   |   |   |   |   |   |   start <= 483361: sce00970 (16.19/4.7)
|   |   |   |   |   |   |   start > 483361: sce00500 (11.16)
|   |   |   |   |   |   start > 490386
|   |   |   |   |   |   |   start <= 492816: sce00190 (11.9)
|   |   |   |   |   |   |   start > 492816: sce04140 (11.02)
|   |   |   |   |   start > 494109: sce04111 (48.02)
start > 505662
|   strand = W
|   |   start <= 558679
|   |   |   start <= 533756
|   |   |   |   start <= 528311: sce00500 (32.22/15.08)
|   |   |   |   start > 528311
```

```
|   |   |   |   |   neigh_GO_term = cellular_component_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00624
(9.0/6.68)
|   |   |   |   |   neigh_GO_term = biological_process_
|   |   |   |   |   |   neigh_strand = W: sce00071 (2.9/2.03)
|   |   |   |   |   |   neigh_strand = C: sce00641 (10.73/7.43)
|   |   |   |   |   neigh_GO_term = molecular_function_: sce00010
(11.49/9.26)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00561
(19.64/15.35)
|   |   |   |   |   neigh_GO_term = translation_: sce00561
(12.32/9.41)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = nucleus_: sce00624 (3.48/2.44)
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce00980
(28.48/19.84)
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = ribosome_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00641 (13.18/9.94)
|   |   |   |   |   neigh_GO_term = transcription_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = transport_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00561 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00561
(10.72/6.34)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00561 (17.4/13.26)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = motor_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = sporulation_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00561 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = meiosis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cortex_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = conjugation_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00561
(0.0)
|   |   |   start > 533756
|   |   |   |   start <= 549003: sce00740 (17.65)
|   |   |   |   start > 549003: sce01040 (41.84)
|   |   start > 558679
|   |   |   start <= 721385
|   |   |   |   start <= 633376
|   |   |   |   |   start <= 597358
|   |   |   |   |   |   start <= 583715
|   |   |   |   |   |   |   start <= 571195: sce04111 (15.22)
|   |   |   |   |   |   |   start > 571195: sce00770 (9.97)
|   |   |   |   |   |   start > 583715: sce00600 (48.5/15.53)
|   |   |   |   |   start > 597358
|   |   |   |   |   |   start <= 606265: sce03010 (34.18)
|   |   |   |   |   |   start > 606265
|   |   |   |   |   |   |   start <= 620867: sce04010 (13.66)
|   |   |   |   |   |   |   start > 620867: sce04111 (16.97)
|   |   |   |   start > 633376
|   |   |   |   |   start <= 691964
|   |   |   |   |   |   start <= 666248
|   |   |   |   |   |   |   start <= 650363: sce00860 (14.42)
|   |   |   |   |   |   |   start > 650363: sce04140 (10.13)
|   |   |   |   |   |   start > 666248: sce00790 (34.24/15.84)
|   |   |   |   |   start > 691964
|   |   |   |   |   |   start <= 707523: sce00480 (42.08/19.97)
|   |   |   |   |   |   start > 707523: sce03010 (14.94)
|   |   |   start > 721385
|   |   |   |   start <= 736259
|   |   |   |   |   start <= 728097: sce00240 (21.36)
|   |   |   |   |   start > 728097
|   |   |   |   |   |   neigh_num <= 1: sce00670 (28.29/17.29)
|   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   distance <= 1094: sce00460 (10.83/4.92)
|   |   |   |   |   |   |   distance > 1094: sce00260 (60.23/43.08)
```

```
|   |   |   |   start > 736259
|   |   |   |   |   start <= 749589
|   |   |   |   |   |   start <= 738577: sce00600 (17.69)
|   |   |   |   |   |   start > 738577: sce04111 (14.78)
|   |   |   |   |   start > 749589
|   |   |   |   |   |   start <= 770411
|   |   |   |   |   |   |   distance <= 960: sce00240 (13.98/7.13)
|   |   |   |   |   |   |   distance > 960: sce03030 (24.88/14.58)
|   |   |   |   |   |   start > 770411: sce00500 (12.0)
|   strand = C
|   |   start <= 625767
|   |   |   start <= 571195
|   |   |   |   start <= 560072: sce00230 (76.02/45.29)
|   |   |   |   start > 560072: sce00400 (13.09)
|   |   |   start > 571195
|   |   |   |   start <= 613895
|   |   |   |   |   start <= 597358: sce03010 (14.44)
|   |   |   |   |   start > 597358
|   |   |   |   |   |   neigh_num <= 1: sce00500 (14.07/4.75)
|   |   |   |   |   |   neigh_num > 1: sce00030 (30.34/18.41)
|   |   |   |   start > 613895: sce03022 (21.69)
|   |   start > 625767
|   |   |   start <= 666248
|   |   |   |   start <= 650363
|   |   |   |   |   start <= 633376: sce00960 (28.43/11.17)
|   |   |   |   |   start > 633376: sce00220 (15.07)
|   |   |   |   start > 650363
|   |   |   |   |   start <= 662244
|   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   neigh_strand = W: sce00620 (9.09/4.73)
|   |   |   |   |   |   |   neigh_strand = C: sce00020 (6.6/2.24)
|   |   |   |   |   |   neigh_num > 1: sce00252 (32.92/16.87)
|   |   |   |   |   start > 662244
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00252 (13.21/10.03)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = biological_process_
|   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00650 (6.71/3.44)
|   |   |   |   |   |   |   |   neigh_num > 1: sce00252 (3.58/2.07)
|   |   |   |   |   |   |   neigh_strand = C: sce00010 (12.31/7.0)
|   |   |   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   |   |   neigh_strand = W: sce00010 (16.57/11.71)
|   |   |   |   |   |   |   neigh_strand = C: sce00620 (12.13/8.56)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00620
(5.99/2.95)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00650
(0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00650 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = motor_activity_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00650
(5.21/3.15)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00650
(0.0)
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00650 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00650 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00650 (0.0)
|   |   |   start > 666248
|   |   |   |   start <= 707523: sce01030 (73.99/33.78)
|   |   |   |   start > 707523
|   |   |   |   |   start <= 722606
|   |   |   |   |   |   start <= 716460: sce00340 (15.17)
|   |   |   |   |   |   start > 716460: sce00400 (19.38)
|   |   |   |   |   start > 722606
|   |   |   |   |   |   start <= 738577: sce00740 (11.0)
|   |   |   |   |   |   start > 738577: sce03060 (12.49)
```

Decision Tree Generated for Chromosome Three:

```
start <= 105548
|   start <= 68333
|   |   strand = C
|   |   |   start <= 35393
|   |   |   |   start <= 16880
|   |   |   |   |   neigh_num <= 1: sce00260 (16.25/7.72)
|   |   |   |   |   neigh_num > 1: sce00272 (12.13/5.29)
|   |   |   |   start > 16880: sce01031 (30.85/8.96)
|   |   |   start > 35393
|   |   |   |   start <= 50838: sce00920 (39.89/18.77)
|   |   |   |   start > 50838: sce00340 (17.93)
|   |   strand = W
|   |   |   start <= 38801: sce00450 (65.19/49.58)
|   |   |   start > 38801
|   |   |   |   neigh_GO_term = membrane_: sce00521 (5.95/2.38)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = transport_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00010 (12.03/3.36)
|   |   |   |   neigh_GO_term = cellular_component_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_num <= 1: sce00010 (7.92/3.25)
|   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   distance <= 994: sce00500 (4.57/1.2)
|   |   |   |   |   |   distance > 994: sce00521 (5.7/2.64)
|   |   |   |   neigh_GO_term = biological_process_: sce00010
(11.14/5.23)
|   |   |   |   neigh_GO_term = nucleus_: sce00500 (8.61/2.79)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00010 (0.0)
```

```
|   |   |   |   neigh_GO_term = transcription_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00010 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00010 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00521 (4.86/1.7)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00010 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00010 (1.81/0.59)
|   |   |   |   neigh_GO_term = translation_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00010 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00010
(0.0)
```

```
|   |   |   |   neigh_GO_term = cell_budding_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00010
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00010 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00010 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00010 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00010 (0.0)
|   start > 68333
|   |   start <= 94270
|   |   |   strand = C: sce00730 (18.85)
|   |   |   strand = W
|   |   |   |   start <= 71803: sce04010 (23.92)
|   |   |   |   start > 71803: sce00290 (17.04)
|   |   start > 94270: sce00660 (83.92/59.1)
start > 105548
|   strand = C
|   |   start <= 140931
|   |   |   start <= 122326: sce00020 (31.1/12.43)
|   |   |   start > 122326: sce03030 (14.65)
|   |   start > 140931
|   |   |   start <= 162218: sce00970 (23.12/9.75)
|   |   |   start > 162218
|   |   |   |   start <= 190588: sce03010 (21.41)
|   |   |   |   start > 190588
|   |   |   |   |   start <= 216693: sce03022 (11.55)
|   |   |   |   |   start > 216693: sce04111 (10.56)
|   strand = W
|   |   start <= 190588
|   |   |   start <= 162218
|   |   |   |   start <= 122326
|   |   |   |   |   distance <= 1334: sce00564 (15.25/5.27)
|   |   |   |   |   distance > 1334: sce00260 (20.09/5.1)
```

```
|   |   |   |   start > 122326: sce00010 (26.16/10.59)
|   |   |   start > 162218: sce01040 (47.14)
|   |   start > 190588
|   |   |   start <= 262449
|   |   |   |   start <= 211925
|   |   |   |   |   start <= 193293: sce00030 (14.3)
|   |   |   |   |   start > 193293: sce00120 (12.93)
|   |   |   |   start > 211925
|   |   |   |   |   start <= 216693: sce00260 (26.9/11.55)
|   |   |   |   |   start > 216693: sce00030 (15.71)
|   |   |   start > 262449
|   |   |   |   neigh_GO_term = membrane_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = transport_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = cellular_component_: sce00650
(30.07/22.3)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_strand = W: sce00310 (9.21/5.34)
|   |   |   |   |   neigh_strand = C: sce00650 (18.99/13.5)
|   |   |   |   neigh_GO_term = biological_process_
|   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   start <= 309067: sce00310 (8.0/5.01)
|   |   |   |   |   |   start > 309067: sce00260 (9.35/5.66)
|   |   |   |   |   neigh_num > 1: sce00051 (28.79/17.48)
|   |   |   |   neigh_GO_term = nucleus_: sce00051 (13.27/7.15)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00051 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00051 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00120 (11.88/8.32)
|   |   |   |   neigh_GO_term = meiosis_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00051
(0.0)
```

```
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00051 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = translation_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00051 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00051
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00051 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00051 (0.0)
```

```
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00051 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00051 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00051 (0.0)
```

Decision Tree Generated for Chromosome Four:

```
start <= 931125
|   start <= 159605
|   |   start <= 38488
|   |   |   strand = W
|   |   |   |   start <= 33918: sce00361 (14.28)
|   |   |   |   start > 33918: sce00510 (32.4/11.71)
|   |   |   strand = C
|   |   |   |   start <= 18566
|   |   |   |   |   start <= 9756: sce00051 (10.32)
|   |   |   |   |   start > 9756
|   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   neigh_num <= 1: sce00051 (12.49/6.41)
|   |   |   |   |   |   |   neigh_num > 1: sce00310 (17.12/9.46)
|   |   |   |   |   |   neigh_strand = C: sce00260 (30.17/22.51)
|   |   |   |   start > 18566
|   |   |   |   |   start <= 30454: sce00230 (17.06)
|   |   |   |   |   start > 30454: sce02021 (46.75/16.32)
|   |   start > 38488
|   |   |   start <= 155641
|   |   |   |   start <= 130485
|   |   |   |   |   start <= 93746
|   |   |   |   |   |   start <= 73919: sce00910 (28.04/12.22)
|   |   |   |   |   |   start > 73919: sce00860 (10.02)
|   |   |   |   |   start > 93746
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 121593: sce03010 (16.79)
|   |   |   |   |   |   |   start > 121593: sce00190 (14.47)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 121593: sce04120 (13.19)
|   |   |   |   |   |   |   start > 121593: sce03010 (14.44)
|   |   |   |   start > 130485
|   |   |   |   |   start <= 147590: sce00620 (46.64/14.87)
|   |   |   |   |   start > 147590: sce00251 (33.37/16.25)
|   |   |   start > 155641
|   |   |   |   neigh_GO_term = mitochondrion_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = biological_process_
|   |   |   |   |   neigh_strand = W: sce00071 (10.22/7.02)
|   |   |   |   |   neigh_strand = C: sce00010 (12.41/9.4)
|   |   |   |   neigh_GO_term = cellular_component_: sce00641
(6.45/4.94)
```

```
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = transport_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_num <= 1: sce00350 (11.36/9.05)
|   |   |   |   |   neigh_num > 1: sce00624 (19.86/15.3)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00120 (19.25/15.31)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = nucleus_: sce00120 (17.79/13.74)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00120
(0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = translation_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00120 (10.01/5.82)
|   |   |   |   neigh_GO_term = chromosome_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00624 (4.85/3.52)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00120 (0.0)
```

```
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00561 (10.65/7.92)
|   |   |   |   neigh_GO_term = vacuole_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00624
(10.76/8.56)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00010
(16.63/13.66)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00120 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00071 (12.85/8.37)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00680 (11.87/7.13)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00120 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00120
(0.0)
```

```
|   |   |   |   neigh_GO_term = lyase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = motor_activity_: sce00120 (0.0)
|   start > 159605
|   |   start <= 444680
|   |   |   start <= 281848
|   |   |   |   start <= 210562
|   |   |   |   |   start <= 176774
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 172482: sce04010 (15.86)
|   |   |   |   |   |   |   start > 172482: sce04111 (22.56)
|   |   |   |   |   |   strand = C: sce00790 (26.6/12.03)
|   |   |   |   |   start > 176774
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 183344: sce00240 (52.69/26.3)
|   |   |   |   |   |   |   start > 183344
|   |   |   |   |   |   |   |   start <= 190925: sce03050 (23.38)
|   |   |   |   |   |   |   |   start > 190925: sce00780 (20.14)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 203040: sce00564 (16.2)
|   |   |   |   |   |   |   start > 203040: sce00230 (58.01/33.42)
|   |   |   |   start > 210562
|   |   |   |   |   start <= 271901
|   |   |   |   |   |   start <= 229906
|   |   |   |   |   |   |   start <= 224304
|   |   |   |   |   |   |   |   start <= 221801: sce03010 (26.09)
|   |   |   |   |   |   |   |   start > 221801
|   |   |   |   |   |   |   |   |   neigh_GO_term = mitochondrion_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
biological_process_: sce04111 (6.45/2.3)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cellular_component_: sce04120 (5.01/2.36)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
plasma_membrane_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
transporter_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = transport_:
sce04120 (2.69/0.61)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
molecular_function_: sce04111 (1.46/0.12)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cytoplasm_:
sce04111 (0.0)
```

```
|   |   |   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
signal_transduction_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = membrane_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_binding_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = sporulation_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
hydrolase_activity_: sce04120 (7.79/0.86)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
transferase_activity_: sce04111 (0.45/0.15)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
response_to_stress_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = nucleus_:
sce04120 (7.9/3.81)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce04111 (1.03/0.34)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
endomembrane_system_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
endoplasmic_reticulum_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = translation_:
sce04120 (3.3/0.6)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_cortex_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce04111 (1.71/0.31)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cytokinesis_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
DNA_metabolic_process_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_cycle_:
sce04111 (5.39/0.73)
|   |   |   |   |   |   |   |   |   neigh_GO_term = RNA_binding_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = conjugation_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = chromosome_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = DNA_binding_:
sce04111 (0.0)
```

```
|   |   |   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
peptidase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = nucleolus_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = vacuole_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
RNA_metabolic_process_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = transcription_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
Golgi_apparatus_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cytoplasmic_membrane-bound_vesicle_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = ribosome_:
sce04120 (1.67/0.67)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce04111 (4.97/0.99)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
ligase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
pseudohyphal_growth_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = meiosis_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
membrane_fraction_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cellular_bud_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
mitochondrial_envelope_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce04111 (0.0)
```

```
|   |   |   |   |   |   |   |   |   neigh_GO_term = peroxisome_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
electron_transport_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
extracellular_region_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
isomerase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
helicase_activity_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_wall_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cellular_homeostasis_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cellular_respiration_: sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_budding_:
sce04111 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce04111 (0.0)
|   |   |   |   |   |   |   start > 224304
|   |   |   |   |   |   |   |   start <= 227393: sce00300
(28.83/13.65)
|   |   |   |   |   |   |   |   start > 227393: sce03010 (13.78)
|   |   |   |   |   |   start > 229906: sce04111 (47.49)
|   |   |   |   |   start > 271901
|   |   |   |   |   |   strand = W: sce03030 (57.91/30.37)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 276872: sce00530 (13.04)
|   |   |   |   |   |   |   start > 276872
|   |   |   |   |   |   |   |   neigh_GO_term = mitochondrion_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00562 (6.8/2.5)
|   |   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transporter_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transport_: sce00632
(2.49/0.88)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00562 (1.51/0.77)
|   |   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00632
(6.88/3.58)
|   |   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transduction_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = sporulation_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00632 (3.58/1.91)
|   |   |   |   |   |   |   |   neigh_GO_term =
transferase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00562 (3.68/1.67)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce00562
(5.61/1.09)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce00632 (5.05/1.68)
|   |   |   |   |   |   |   |   neigh_GO_term =
endomembrane_system_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endoplasmic_reticulum_: sce04070 (1.39/0.82)
|   |   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = translation_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cortex_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytokinesis_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
DNA_metabolic_process_: sce00632 (1.65/0.95)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cycle_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = RNA_binding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00562 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = conjugation_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = chromosome_:
sce00562 (2.11/0.7)
|   |   |   |   |   |   |   |   neigh_GO_term = DNA_binding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
RNA_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transcription_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoplasmic_membrane-bound_vesicle_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_
|   |   |   |   |   |   |   |   |   distance <= 4002: sce00632
(3.82/2.17)
|   |   |   |   |   |   |   |   |   distance > 4002: sce04070
(8.75/1.37)
|   |   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
pseudohyphal_growth_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_bud_:
sce00562 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
mitochondrial_envelope_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peroxisome_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
extracellular_region_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_homeostasis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_respiration_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_budding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce00562 (0.0)
|   |   |   start > 281848
|   |   |   |   start <= 340798
|   |   |   |   |   start <= 301413
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 292781: sce03060 (14.45)
|   |   |   |   |   |   |   start > 292781: sce00361 (46.6/27.01)
|   |   |   |   |   |   strand = C: sce03050 (20.22)
|   |   |   |   |   start > 301413
|   |   |   |   |   |   start <= 312471
|   |   |   |   |   |   |   start <= 303211: sce00190 (19.27)
|   |   |   |   |   |   |   start > 303211
|   |   |   |   |   |   |   |   start <= 310122: sce03010 (41.12)
|   |   |   |   |   |   |   |   start > 310122: sce00010 (12.69)
|   |   |   |   |   |   start > 312471
|   |   |   |   |   |   |   start <= 316388
|   |   |   |   |   |   |   |   neigh_GO_term = mitochondrion_:
sce00720 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transporter_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transport_: sce00720
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00720
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_
|   |   |   |   |   |   |   |   |   neigh_num <= 1: sce00630
(3.16/1.97)
|   |   |   |   |   |   |   |   |   neigh_num > 1: sce00720
(8.31/3.76)
|   |   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transduction_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_: sce00020
(11.0/7.42)
|   |   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = sporulation_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transferase_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce00720
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endomembrane_system_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endoplasmic_reticulum_: sce00720 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = translation_:
sce00720 (5.93/4.48)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cortex_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00620 (9.13/5.13)
|   |   |   |   |   |   |   |   neigh_GO_term = cytokinesis_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
DNA_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cycle_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = RNA_binding_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = conjugation_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = chromosome_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = DNA_binding_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00720
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce00630
(9.6/5.04)
|   |   |   |   |   |   |   |   neigh_GO_term =
RNA_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00710 (7.51/5.18)
|   |   |   |   |   |   |   |   neigh_GO_term = transcription_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoplasmic_membrane-bound_vesicle_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce00720
(6.75/4.74)
|   |   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00720 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
pseudohyphal_growth_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce00720
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_bud_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
mitochondrial_envelope_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peroxisome_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
extracellular_region_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00720
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_homeostasis_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_respiration_: sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_budding_:
sce00720 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce00720 (0.0)
|   |   |   |   |   |   |   start > 316388
|   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   start <= 334835
|   |   |   |   |   |   |   |   |   |   start <= 322226: sce03010
(14.1)
|   |   |   |   |   |   |   |   |   |   start > 322226: sce00480
(31.97/20.29)
|   |   |   |   |   |   |   |   |   start > 334835: sce04120 (17.48)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 337487: sce00190
(13.35)
|   |   |   |   |   |   |   |   |   start > 337487: sce03010 (12.96)
|   |   |   |   start > 340798
|   |   |   |   |   start <= 411822
|   |   |   |   |   |   start <= 363583
|   |   |   |   |   |   |   strand = W: sce04111 (19.68)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 356759: sce00051 (15.72)
|   |   |   |   |   |   |   |   start > 356759: sce00564
(53.02/32.56)
|   |   |   |   |   |   start > 363583
|   |   |   |   |   |   |   start <= 394214
|   |   |   |   |   |   |   |   start <= 373605: sce00740 (10.07)
|   |   |   |   |   |   |   |   start > 373605: sce00500
(45.56/11.4)
|   |   |   |   |   |   |   start > 394214
|   |   |   |   |   |   |   |   strand = W: sce00564 (5.33)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 403288: sce04111 (12.1)
|   |   |   |   |   |   |   |   |   start > 403288: sce00361
(21.47/9.38)
|   |   |   |   |   start > 411822
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 433494
|   |   |   |   |   |   |   |   start <= 416705: sce00010 (15.76)
|   |   |   |   |   |   |   |   start > 416705: sce04111
(39.14/9.84)
|   |   |   |   |   |   |   start > 433494
|   |   |   |   |   |   |   |   start <= 438044: sce03050 (21.68)
|   |   |   |   |   |   |   |   start > 438044
|   |   |   |   |   |   |   |   |   start <= 443026: sce00190
(18.67)
|   |   |   |   |   |   |   |   |   start > 443026: sce04111 (18.7)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 416705: sce03050 (15.84)
|   |   |   |   |   |   |   start > 416705: sce01040 (29.82)
|   |   start > 444680
|   |   |   start <= 679761
|   |   |   |   start <= 538464
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 521813
|   |   |   |   |   |   |   start <= 461839: sce00400 (15.3)
|   |   |   |   |   |   |   start > 461839
|   |   |   |   |   |   |   |   start <= 491512
|   |   |   |   |   |   |   |   |   start <= 489505
```

```
|   |   |   |   |   |   |   |   |   |   start <= 471850: sce03010
(12.87)
|   |   |   |   |   |   |   |   |   |   start > 471850: sce00970
(46.28/22.78)
|   |   |   |   |   |   |   |   |   start > 489505: sce03010 (14.2)
|   |   |   |   |   |   |   |   start > 491512: sce00400 (13.39)
|   |   |   |   |   |   start > 521813: sce00970 (40.15/16.16)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 491512
|   |   |   |   |   |   |   start <= 461839: sce00500 (14.41)
|   |   |   |   |   |   |   start > 461839: sce00910 (48.2/29.39)
|   |   |   |   |   |   start > 491512
|   |   |   |   |   |   |   neigh_num <= 1: sce00500 (22.9/5.26)
|   |   |   |   |   |   |   neigh_num > 1: sce00790 (52.23/18.61)
|   |   |   |   start > 538464
|   |   |   |   |   start <= 560623
|   |   |   |   |   |   strand = W: sce00860 (37.16)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 551858: sce03020 (55.67/31.57)
|   |   |   |   |   |   |   start > 551858
|   |   |   |   |   |   |   |   start <= 556470: sce00010
(29.25/15.29)
|   |   |   |   |   |   |   |   start > 556470: sce04111 (15.63)
|   |   |   |   |   start > 560623
|   |   |   |   |   |   start <= 629873
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 579456
|   |   |   |   |   |   |   |   |   start <= 574161: sce02010
(17.11)
|   |   |   |   |   |   |   |   |   start > 574161
|   |   |   |   |   |   |   |   |   |   start <= 576471: sce00600
(19.35)
|   |   |   |   |   |   |   |   |   |   start > 576471: sce03010
(13.4)
|   |   |   |   |   |   |   |   start > 579456
|   |   |   |   |   |   |   |   |   start <= 593890: sce00500
(22.83)
|   |   |   |   |   |   |   |   |   start > 593890: sce04120 (14.36)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 568701
|   |   |   |   |   |   |   |   |   start <= 562325: sce04120
(15.27)
|   |   |   |   |   |   |   |   |   start > 562325: sce00561 (15.16)
|   |   |   |   |   |   |   |   start > 568701: sce04120 (19.48)
|   |   |   |   |   |   start > 629873
|   |   |   |   |   |   |   start <= 658347: sce04010 (17.41)
|   |   |   |   |   |   |   start > 658347
|   |   |   |   |   |   |   |   distance <= 3851: sce00252
(28.38/14.76)
|   |   |   |   |   |   |   |   distance > 3851: sce00710
(14.98/6.12)
|   |   |   start > 679761
|   |   |   |   start <= 769522
|   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   start <= 694697
|   |   |   |   |   |   |   start <= 693582
|   |   |   |   |   |   |   |   start <= 685879: sce04111
(28.29/6.97)
|   |   |   |   |   |   |   |   start > 685879: sce03030
(35.96/21.95)
|   |   |   |   |   |   |   start > 693582
|   |   |   |   |   |   |   |   neigh_GO_term = mitochondrion_:
sce00562 (6.24/2.18)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce04070 (7.93/3.27)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00562 (0.95/0.46)
|   |   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transporter_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transport_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00562 (2.25/0.73)
|   |   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transduction_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = sporulation_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transferase_activity_: sce00562 (2.89/1.22)
|   |   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce00562
(3.39/1.93)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce04070 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endomembrane_system_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endoplasmic_reticulum_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = translation_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cortex_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytokinesis_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
DNA_metabolic_process_: sce00632 (5.49/2.08)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cycle_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = RNA_binding_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = conjugation_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = chromosome_:
sce04070 (3.42/1.77)
|   |   |   |   |   |   |   |   neigh_GO_term = DNA_binding_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00632 (2.46/1.2)
|   |   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
RNA_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transcription_:
sce04070 (0.73/0.42)
|   |   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoplasmic_membrane-bound_vesicle_: sce04070 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00562 (8.04/3.45)
|   |   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00632 (2.03/1.06)
|   |   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
pseudohyphal_growth_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_bud_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
mitochondrial_envelope_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce04070 (10.37/4.85)
|   |   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peroxisome_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
extracellular_region_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce04070
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_homeostasis_: sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_respiration_: sce04070 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = cell_budding_:
sce04070 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce04070 (0.0)
|   |   |   |   |   |   start > 694697
|   |   |   |   |   |   |   start <= 755063
|   |   |   |   |   |   |   |   start <= 704481: sce00400 (25.4)
|   |   |   |   |   |   |   |   start > 704481
|   |   |   |   |   |   |   |   |   start <= 746735: sce03022
(24.44)
|   |   |   |   |   |   |   |   |   start > 746735: sce00564 (13.51)
|   |   |   |   |   |   |   start > 755063
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00240
(21.89/9.32)
|   |   |   |   |   |   |   |   neigh_num > 1: sce03020
(35.43/21.23)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 751628: sce04111 (23.04)
|   |   |   |   |   |   start > 751628: sce00310 (35.56/15.5)
|   |   |   |   start > 769522
|   |   |   |   |   start <= 817947
|   |   |   |   |   |   start <= 789446
|   |   |   |   |   |   |   start <= 770354
|   |   |   |   |   |   |   |   distance <= 1459: sce00300
(10.0/2.1)
|   |   |   |   |   |   |   |   distance > 1459: sce00260
(28.66/9.38)
|   |   |   |   |   |   |   start > 770354: sce03022 (19.53)
|   |   |   |   |   |   start > 789446
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 816875: sce04120 (17.61)
|   |   |   |   |   |   |   |   start > 816875
|   |   |   |   |   |   |   |   |   neigh_num <= 1: sce00020
(19.0/8.31)
|   |   |   |   |   |   |   |   |   neigh_num > 1: sce00190
(20.15/5.93)
|   |   |   |   |   |   |   strand = C: sce00562 (17.72)
|   |   |   |   |   start > 817947
|   |   |   |   |   |   start <= 903476
|   |   |   |   |   |   |   start <= 821292: sce04111 (15.78)
|   |   |   |   |   |   |   start > 821292
|   |   |   |   |   |   |   |   start <= 868221: sce00562
(38.33/17.42)
|   |   |   |   |   |   |   |   start > 868221: sce04111 (13.79)
|   |   |   |   |   |   start > 903476
|   |   |   |   |   |   |   start <= 927448
|   |   |   |   |   |   |   |   start <= 916482: sce00230 (13.76)
|   |   |   |   |   |   |   |   start > 916482: sce00860
(31.51/14.23)
|   |   |   |   |   |   |   start > 927448: sce00300 (18.65)
start > 931125
|   start <= 1153620
|   |   start <= 1062787
|   |   |   start <= 958335
```

```
|   |   |   |   strand = W
|   |   |   |   |   start <= 946803
|   |   |   |   |   |   neigh_num <= 1: sce00643 (42.28/29.72)
|   |   |   |   |   |   neigh_num > 1: sce00220 (46.41/34.87)
|   |   |   |   |   start > 946803: sce01030 (40.15/15.22)
|   |   |   |   strand = C
|   |   |   |   |   start <= 946803: sce00740 (18.22)
|   |   |   |   |   start > 946803: sce00030 (23.9)
|   |   |   start > 958335
|   |   |   |   start <= 1009006
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 1004000: sce00380 (40.16/19.83)
|   |   |   |   |   |   start > 1004000: sce00620 (12.27)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 969676
|   |   |   |   |   |   |   neigh_num <= 1: sce00380 (8.86/2.23)
|   |   |   |   |   |   |   neigh_num > 1: sce00680 (22.45/8.27)
|   |   |   |   |   |   start > 969676: sce00500 (13.45)
|   |   |   |   start > 1009006
|   |   |   |   |   start <= 1056547
|   |   |   |   |   |   start <= 1045007: sce03060 (16.16)
|   |   |   |   |   |   start > 1045007: sce00600 (39.57)
|   |   |   |   |   start > 1056547
|   |   |   |   |   |   start <= 1058810: sce00190 (16.77)
|   |   |   |   |   |   start > 1058810: sce00220 (21.95)
|   |   start > 1062787
|   |   |   strand = W
|   |   |   |   start <= 1085062
|   |   |   |   |   start <= 1067727: sce00563 (37.18/17.19)
|   |   |   |   |   start > 1067727: sce03022 (21.43)
|   |   |   |   start > 1085062
|   |   |   |   |   start <= 1117121
|   |   |   |   |   |   start <= 1108699: sce00460 (37.87/20.33)
|   |   |   |   |   |   start > 1108699: sce04111 (13.98)
|   |   |   |   |   start > 1117121: sce01031 (38.22/17.25)
|   |   |   strand = C
|   |   |   |   start <= 1129583: sce04120 (28.21/13.83)
|   |   |   |   start > 1129583
|   |   |   |   |   distance <= 2089: sce00970 (12.43/1.62)
|   |   |   |   |   distance > 2089: sce00330 (10.7/2.7)
|   start > 1153620
|   |   start <= 1369782
|   |   |   start <= 1234210
|   |   |   |   start <= 1213896
|   |   |   |   |   start <= 1184740
|   |   |   |   |   |   start <= 1183292: sce00240 (8.76)
|   |   |   |   |   |   start > 1183292: sce00400 (12.12)
|   |   |   |   |   start > 1184740: sce00650 (69.86/53.06)
|   |   |   |   start > 1213896
|   |   |   |   |   start <= 1228603: sce00190 (19.5)
|   |   |   |   |   start > 1228603: sce00010 (13.78)
|   |   |   start > 1234210
|   |   |   |   strand = W
|   |   |   |   |   start <= 1322197
```

```
|   |   |   |   |   |   start <= 1301608
|   |   |   |   |   |   |   start <= 1277161
|   |   |   |   |   |   |   |   start <= 1239484: sce03010 (6.42)
|   |   |   |   |   |   |   |   start > 1239484: sce03050 (14.93)
|   |   |   |   |   |   |   start > 1277161: sce03010 (14.39)
|   |   |   |   |   |   start > 1301608
|   |   |   |   |   |   |   start <= 1303166: sce03030 (7.8)
|   |   |   |   |   |   |   start > 1303166: sce03050 (15.28)
|   |   |   |   |   start > 1322197
|   |   |   |   |   |   start <= 1337344
|   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   start <= 1331229: sce01031
(24.23/4.72)
|   |   |   |   |   |   |   |   start > 1331229
|   |   |   |   |   |   |   |   |   neigh_num <= 1: sce00563
(6.68/2.04)
|   |   |   |   |   |   |   |   |   neigh_num > 1: sce01031
(8.24/1.85)
|   |   |   |   |   |   |   neigh_strand = C: sce00563 (40.43/16.54)
|   |   |   |   |   |   start > 1337344
|   |   |   |   |   |   |   start <= 1345054: sce00310 (14.91)
|   |   |   |   |   |   |   start > 1345054
|   |   |   |   |   |   |   |   start <= 1359915: sce03010 (13.13)
|   |   |   |   |   |   |   |   start > 1359915: sce04120 (7.32)
|   |   |   |   strand = C
|   |   |   |   |   start <= 1273695
|   |   |   |   |   |   start <= 1261673: sce04120 (14.47)
|   |   |   |   |   |   start > 1261673
|   |   |   |   |   |   |   distance <= 1450: sce00380 (9.37/2.98)
|   |   |   |   |   |   |   distance > 1450: sce00361 (27.88/14.88)
|   |   |   |   |   start > 1273695
|   |   |   |   |   |   start <= 1277161: sce03020 (43.98/25.95)
|   |   |   |   |   |   start > 1277161
|   |   |   |   |   |   |   start <= 1345054: sce00230 (61.04/15.05)
|   |   |   |   |   |   |   start > 1345054
|   |   |   |   |   |   |   |   start <= 1359915: sce03010 (14.9)
|   |   |   |   |   |   |   |   start > 1359915: sce00230 (15.76)
|   |   start > 1369782
|   |   |   start <= 1454456
|   |   |   |   strand = W
|   |   |   |   |   start <= 1401762
|   |   |   |   |   |   start <= 1385168: sce04010 (18.17)
|   |   |   |   |   |   start > 1385168: sce03010 (29.27)
|   |   |   |   |   start > 1401762
|   |   |   |   |   |   start <= 1412365: sce00632 (33.81/21.11)
|   |   |   |   |   |   start > 1412365: sce04010 (28.43)
|   |   |   |   strand = C
|   |   |   |   |   start <= 1394566: sce00450 (57.35/38.15)
|   |   |   |   |   start > 1394566
|   |   |   |   |   |   start <= 1446986
|   |   |   |   |   |   |   start <= 1420242
|   |   |   |   |   |   |   |   start <= 1401762: sce04130 (16.04)
|   |   |   |   |   |   |   |   start > 1401762: sce00790
(29.32/12.57)
```

```
|   |   |   |   |   |   |   start > 1420242
|   |   |   |   |   |   |   |   start <= 1428972: sce00740 (14.72)
|   |   |   |   |   |   |   |   start > 1428972: sce04130 (21.41)
|   |   |   |   |   |   start > 1446986
|   |   |   |   |   |   |   start <= 1450845: sce03010 (10.2)
|   |   |   |   |   |   |   start > 1450845
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00271 (8.02/1.99)
|   |   |   |   |   |   |   |   neigh_num > 1: sce00450
(22.03/10.18)
|   |   |   start > 1454456
|   |   |   |   strand = W
|   |   |   |   |   start <= 1498224: sce00770 (19.81)
|   |   |   |   |   start > 1498224: sce00130 (15.72)
|   |   |   |   strand = C
|   |   |   |   |   start <= 1487030
|   |   |   |   |   |   start <= 1465778: sce04111 (10.56)
|   |   |   |   |   |   start > 1465778: sce00562 (49.19/31.02)
|   |   |   |   |   start > 1487030
|   |   |   |   |   |   start <= 1496540: sce00190 (18.54)
|   |   |   |   |   |   start > 1496540: sce00230 (8.67)
```

Decision Tree Generated for Chromosome Five:

```
start <= 257957
|   start <= 160549
|   |   start <= 107260
|   |   |   strand = W
|   |   |   |   start <= 43252: sce00530 (27.47)
|   |   |   |   start > 43252
|   |   |   |   |   start <= 86937
|   |   |   |   |   |   start <= 68792: sce00190 (18.42)
|   |   |   |   |   |   start > 68792: sce04111 (5.95)
|   |   |   |   |   start > 86937: sce00190 (36.02)
|   |   |   strand = C
|   |   |   |   start <= 68792
|   |   |   |   |   start <= 51539: sce03030 (14.38)
|   |   |   |   |   start > 51539
|   |   |   |   |   |   start <= 58378: sce03010 (16.57)
|   |   |   |   |   |   start > 58378: sce00260 (11.67)
|   |   |   |   start > 68792: sce00513 (38.72/17.31)
|   |   start > 107260
|   |   |   start <= 133120
|   |   |   |   start <= 128825
|   |   |   |   |   start <= 116167: sce00240 (17.71)
|   |   |   |   |   start > 116167: sce04140 (20.63)
|   |   |   |   start > 128825
|   |   |   |   |   start <= 131772: sce04120 (19.59)
|   |   |   |   |   start > 131772: sce00500 (21.87)
|   |   |   start > 133120
|   |   |   |   start <= 153519: sce01030 (45.68/15.15)
|   |   |   |   start > 153519
|   |   |   |   |   start <= 159117: sce00051 (18.61)
|   |   |   |   |   start > 159117: sce00230 (21.48/9.77)
```

```
|   start > 160549
|   |   strand = W
|   |   |   start <= 196947
|   |   |   |   start <= 182599
|   |   |   |   |   start <= 177834: sce03050 (9.91)
|   |   |   |   |   start > 177834: sce00860 (21.55)
|   |   |   |   start > 182599
|   |   |   |   |   start <= 184540: sce00071 (12.1)
|   |   |   |   |   start > 184540: sce03050 (16.43)
|   |   |   start > 196947: sce00330 (15.56)
|   |   strand = C
|   |   |   start <= 208473
|   |   |   |   neigh_num <= 1: sce00564 (8.31/1.71)
|   |   |   |   neigh_num > 1: sce00260 (30.84/14.05)
|   |   |   start > 208473
|   |   |   |   start <= 237118: sce00271 (36.04/17.55)
|   |   |   |   start > 237118: sce00260 (36.4/17.2)
start > 257957
|   start <= 318338
|   |   start <= 298948
|   |   |   strand = W
|   |   |   |   start <= 295408: sce00220 (17.08)
|   |   |   |   start > 295408: sce00230 (38.83/17.75)
|   |   |   strand = C
|   |   |   |   start <= 279624
|   |   |   |   |   start <= 270183
|   |   |   |   |   |   start <= 265784: sce00340 (13.82)
|   |   |   |   |   |   start > 265784: sce03010 (9.15)
|   |   |   |   |   start > 270183: sce00061 (20.97)
|   |   |   |   start > 279624
|   |   |   |   |   start <= 280680: sce00561 (10.68)
|   |   |   |   |   start > 280680: sce00630 (12.72)
|   |   start > 298948
|   |   |   start <= 304027
|   |   |   |   neigh_GO_term = cellular_component_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = biological_process_: sce00641
(19.26/15.13)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_strand = W: sce00310 (18.79/15.05)
|   |   |   |   |   neigh_strand = C: sce00380 (17.46/14.13)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = transport_: sce00120 (14.58/12.17)
|   |   |   |   neigh_GO_term = cytoplasm_
|   |   |   |   |   neigh_num <= 1: sce00650 (24.2/20.19)
|   |   |   |   |   neigh_num > 1: sce00340 (18.68/15.18)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = nucleus_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00340
(0.0)
```

```
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00120 (13.13/10.71)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00220
(10.91/8.25)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00340 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00220
(12.18/10.5)
|   |   |   |   neigh_GO_term = motor_activity_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00340 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00340 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00340 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00120 (20.39/16.33)
|   |   |   |   neigh_GO_term = translation_: sce00380 (36.35/29.25)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00340 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00220 (11.91/9.81)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00340 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00340 (0.0)
```

```
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00340
(0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00340 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00340 (15.75/11.36)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00340 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00340 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00340 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00340 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00340
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00340 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00340 (20.79/15.71)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00340 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00340 (0.0)
|   |   |   start > 304027
|   |   |   |   start <= 306319: sce03010 (11.86)
|   |   |   |   start > 306319: sce00310 (20.91/8.45)
|   start > 318338
|   |   start <= 525969
|   |   |   strand = W
|   |   |   |   start <= 423948
|   |   |   |   |   start <= 342163
|   |   |   |   |   |   start <= 328473
|   |   |   |   |   |   |   start <= 322682: sce00260 (10.49)
|   |   |   |   |   |   |   start > 322682
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00290 (8.89/2.05)
|   |   |   |   |   |   |   |   neigh_num > 1
```

```
|   |   |   |   |   |   |   |   |   distance <= 1789: sce00260
(12.72/4.7)
|   |   |   |   |   |   |   |   |   distance > 1789: sce00290
(12.33/4.42)
|   |   |   |   |   |   start > 328473
|   |   |   |   |   |   |   start <= 330572
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00330 (6.07/1.62)
|   |   |   |   |   |   |   |   neigh_num > 1: sce00970 (8.37/3.16)
|   |   |   |   |   |   |   start > 330572: sce00400 (9.41)
|   |   |   |   |   start > 342163
|   |   |   |   |   |   start <= 399051
|   |   |   |   |   |   |   start <= 359558: sce04120 (20.06)
|   |   |   |   |   |   |   start > 359558: sce03010 (34.24)
|   |   |   |   |   |   start > 399051
|   |   |   |   |   |   |   start <= 404809: sce04070 (46.48/26.42)
|   |   |   |   |   |   |   start > 404809
|   |   |   |   |   |   |   |   start <= 410185: sce04120 (12.12)
|   |   |   |   |   |   |   |   start > 410185: sce03010 (13.69)
|   |   |   |   start > 423948
|   |   |   |   |   start <= 465298
|   |   |   |   |   |   start <= 453454: sce00190 (24.22/9.76)
|   |   |   |   |   |   start > 453454: sce03022 (9.74)
|   |   |   |   |   start > 465298
|   |   |   |   |   |   start <= 475015: sce03060 (16.84)
|   |   |   |   |   |   start > 475015: sce00230 (20.8)
|   |   |   strand = C
|   |   |   |   start <= 363096
|   |   |   |   |   start <= 349342
|   |   |   |   |   |   start <= 342163: sce00271 (5.42)
|   |   |   |   |   |   start > 342163: sce03050 (8.04)
|   |   |   |   |   start > 349342: sce00230 (36.49/13.16)
|   |   |   |   start > 363096
|   |   |   |   |   start <= 423948: sce04010 (44.23/12.24)
|   |   |   |   |   start > 423948: sce04111 (10.82)
|   |   start > 525969
|   |   |   start <= 536295
|   |   |   |   start <= 536016: sce00790 (90.73/38.01)
|   |   |   |   start > 536016: sce04111 (12.15)
|   |   |   start > 536295
|   |   |   |   start <= 546812
|   |   |   |   |   neigh_GO_term = cellular_component_: sce00650
(9.77/5.78)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = biological_process_: sce00252
(4.79/3.1)
|   |   |   |   |   neigh_GO_term = molecular_function_: sce00650
(8.23/4.93)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = transport_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00620 (4.41/2.62)
```

```
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = nucleus_: sce00290 (10.42/7.26)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00010
(17.67/9.73)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = motor_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = sporulation_: sce00010
(3.54/2.49)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00620
(2.77/1.93)
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = transcription_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = ribosome_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = translation_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00010 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = electron_transport_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00650
(5.47/2.69)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00620
(11.43/5.72)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = meiosis_: sce00252 (3.11/2.03)
|   |   |   |   |   neigh_GO_term = conjugation_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00010 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00010 (0.0)
|   |   |   |   start > 546812: sce00670 (13.73)
```

Decision Tree Generated for Chromosome Six:

```
start <= 103121
|   start <= 54695
|   |   start <= 15431
|   |   |   start <= 10969: sce00750 (14.32)
|   |   |   start > 10969
|   |   |   |   neigh_GO_term = cellular_component_: sce00650
(10.24/7.42)
|   |   |   |   neigh_GO_term = molecular_function_: sce00650
(15.99/7.29)
|   |   |   |   neigh_GO_term = biological_process_: sce00260
(7.47/5.07)
|   |   |   |   neigh_GO_term = vacuole_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00260
(5.26/3.87)
|   |   |   |   neigh_GO_term = protein_binding_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00051
(7.2/2.68)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00260
(6.26/3.57)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00120
(15.7/7.74)
|   |   |   |   neigh_GO_term = transport_: sce00310 (6.95/4.68)
|   |   |   |   neigh_GO_term = membrane_: sce00120 (6.27/4.32)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = nucleus_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00120
(0.0)
```

```
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = translation_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00120
(0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00120 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00120 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00120 (0.0)
```

```
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00120 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00120
(0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00120 (0.0)
|   |   start > 15431
|   |   |   strand = W: sce00561 (12.99)
|   |   |   strand = C
|   |   |   |   start <= 44392: sce00051 (16.95)
|   |   |   |   start > 44392
|   |   |   |   |   start <= 45560: sce00632 (26.49/11.67)
|   |   |   |   |   start > 45560: sce01430 (9.67)
|   start > 54695
|   |   start <= 95008
|   |   |   strand = W: sce04010 (17.02)
|   |   |   strand = C
|   |   |   |   start <= 87232
|   |   |   |   |   start <= 82578
|   |   |   |   |   |   start <= 64931: sce03010 (10.69)
|   |   |   |   |   |   start > 64931: sce04111 (15.52)
|   |   |   |   |   start > 82578: sce00563 (13.36)
|   |   |   |   start > 87232
|   |   |   |   |   neigh_strand = W: sce00400 (8.48/1.17)
|   |   |   |   |   neigh_strand = C: sce00970 (18.53/6.68)
|   |   start > 95008
|   |   |   neigh_num <= 1: sce00020 (31.87/21.53)
|   |   |   neigh_num > 1: sce00260 (37.49/25.01)
start > 103121
|   start <= 226950
|   |   strand = W
|   |   |   start <= 153388
|   |   |   |   start <= 119424
|   |   |   |   |   start <= 116139
|   |   |   |   |   |   neigh_num <= 1: sce04120 (9.88/3.56)
|   |   |   |   |   |   neigh_num > 1: sce04111 (25.26/6.04)
|   |   |   |   |   start > 116139: sce04111 (17.72)
|   |   |   |   start > 119424: sce03050 (17.76)
|   |   |   start > 153388
|   |   |   |   start <= 220094
|   |   |   |   |   start <= 184490: sce04070 (19.38)
|   |   |   |   |   start > 184490
|   |   |   |   |   |   neigh_strand = W: sce00920 (7.05/1.54)
|   |   |   |   |   |   neigh_strand = C: sce00450 (11.73/3.89)
|   |   |   |   start > 220094: sce04111 (27.24/8.5)
|   |   strand = C
|   |   |   start <= 204738
|   |   |   |   start <= 119424: sce00251 (31.85/12.5)
|   |   |   |   start > 119424
|   |   |   |   |   start <= 184490: sce00500 (29.08)
|   |   |   |   |   start > 184490: sce00340 (15.06)
|   |   |   start > 204738
```

```
|   |   |   |   start <= 220094: sce04111 (38.96)
|   |   |   |   start > 220094
|   |   |   |   |   start <= 224757
|   |   |   |   |   |   start <= 223425: sce03010 (15.18)
|   |   |   |   |   |   start > 223425: sce00190 (12.83)
|   |   |   |   |   start > 224757: sce04111 (19.36)
|   start > 226950
|   |   start <= 255036
|   |   |   start <= 252492
|   |   |   |   start <= 245153: sce00760 (10.14)
|   |   |   |   start > 245153: sce03050 (28.0)
|   |   |   start > 252492
|   |   |   |   distance <= 339: sce00521 (6.95/1.41)
|   |   |   |   distance > 339
|   |   |   |   |   neigh_strand = W: sce00521 (36.85/26.99)
|   |   |   |   |   neigh_strand = C: sce00051 (15.33/7.82)
|   |   start > 255036
|   |   |   neigh_strand = W: sce00920 (29.37/19.54)
|   |   |   neigh_strand = C
|   |   |   |   neigh_num <= 1: sce00910 (7.81/4.85)
|   |   |   |   neigh_num > 1: sce00450 (9.52/3.91)
```

Decision Tree Generated for Chromosome Seven:

```
start <= 216101
|   start <= 23935
|   |   start <= 14910
|   |   |   start <= 14157
|   |   |   |   neigh_GO_term = cellular_component_: sce01031
(8.77/2.93)
|   |   |   |   neigh_GO_term = molecular_function_: sce00561
(5.7/3.39)
|   |   |   |   neigh_GO_term = biological_process_: sce00561
(3.33/1.81)
|   |   |   |   neigh_GO_term = transferase_activity_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00051 (2.29/1.27)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce01031
(6.22/3.11)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00561
(5.19/2.08)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00051 (6.5/1.36)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00561 (1.18/0.48)
|   |   |   |   neigh_GO_term = signal_transduction_: sce01031
(4.06/1.67)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce01031
(0.0)
```

```
|   |   |   |   neigh_GO_term = transport_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = nucleus_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce01031 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce01031 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = translation_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce01031 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = motor_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce01031
(0.0)
```

```
|   |   |   |   neigh_GO_term = peroxisome_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce01031
(0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce01031 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce01031 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce01031
(0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce01031 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce01031 (0.0)
|   |   |   start > 14157
|   |   |   |   neigh_GO_term = cellular_component_: sce00010
(24.49/18.07)
|   |   |   |   neigh_GO_term = molecular_function_: sce00071
(7.12/5.74)
|   |   |   |   neigh_GO_term = biological_process_: sce00980
(8.06/5.6)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00641
(11.6/8.12)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00350 (2.77/1.63)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00071
(0.0)
```

```
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00641 (11.14/6.83)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00561 (18.21/14.47)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00071
(16.79/12.68)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00350
(6.95/5.13)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00071
(12.74/7.84)
|   |   |   |   neigh_GO_term = transport_: sce00561 (11.54/8.75)
|   |   |   |   neigh_GO_term = nucleus_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = translation_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00071 (0.0)
```

```
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = motor_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00071 (0.0)
|   |   start > 14910
|   |   |   neigh_GO_term = cellular_component_: sce00530
(5.93/3.06)
```

```
|   |   |   neigh_GO_term = molecular_function_: sce00521
(6.19/2.32)
|   |   |   neigh_GO_term = biological_process_: sce00530
(7.52/4.57)
|   |   |   neigh_GO_term = transferase_activity_: sce00521
(9.1/6.23)
|   |   |   neigh_GO_term = protein_modification_process_: sce00010
(6.41/4.2)
|   |   |   neigh_GO_term = peptidase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = mitochondrion_: sce00521 (0.0)
|   |   |   neigh_GO_term = oxidoreductase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00521 (0.0)
|   |   |   neigh_GO_term = cytoplasm_: sce00010 (10.88/7.89)
|   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00500 (7.55/5.43)
|   |   |   neigh_GO_term = signal_transduction_: sce00500
(7.74/4.61)
|   |   |   neigh_GO_term = plasma_membrane_: sce00521 (0.0)
|   |   |   neigh_GO_term = transporter_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = transport_: sce00051 (5.65/2.82)
|   |   |   neigh_GO_term = nucleus_: sce00051 (8.99/6.2)
|   |   |   neigh_GO_term = DNA_binding_: sce00521 (4.73/3.16)
|   |   |   neigh_GO_term = transcription_: sce00010 (5.87/3.58)
|   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00521 (0.0)
|   |   |   neigh_GO_term = helicase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = meiosis_: sce00521 (0.0)
|   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00521
(0.0)
|   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00521 (0.0)
|   |   |   neigh_GO_term = chromosome_: sce00521 (0.0)
|   |   |   neigh_GO_term = cell_cycle_: sce00521 (0.0)
|   |   |   neigh_GO_term = hydrolase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = endomembrane_system_: sce00521 (0.0)
|   |   |   neigh_GO_term = membrane_organization_and_biogenesis_:
sce00521 (0.0)
|   |   |   neigh_GO_term = nuclear_organization_and_biogenesis_:
sce00521 (0.0)
|   |   |   neigh_GO_term = ligase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = translation_: sce00521 (0.0)
|   |   |   neigh_GO_term = DNA_metabolic_process_: sce00521 (0.0)
|   |   |   neigh_GO_term = RNA_metabolic_process_: sce00521 (0.0)
|   |   |   neigh_GO_term = protein_binding_: sce00521 (0.0)
|   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00521 (0.0)
|   |   |   neigh_GO_term = cellular_bud_: sce00521 (0.0)
|   |   |   neigh_GO_term = site_of_polarized_growth_: sce00521
(0.0)
|   |   |   neigh_GO_term = cytokinesis_: sce00521 (0.0)
|   |   |   neigh_GO_term = RNA_binding_: sce00521 (0.0)
|   |   |   neigh_GO_term = phosphoprotein_phosphatase_activity_:
sce00521 (0.0)
|   |   |   neigh_GO_term = membrane_: sce00521 (0.0)
```

```
|   |   |   neigh_GO_term = protein_catabolic_process_: sce00521
(0.0)
|   |   |   neigh_GO_term = Golgi_apparatus_: sce00521 (0.0)
|   |   |   neigh_GO_term = vesicle-mediated_transport_: sce00521
(0.0)
|   |   |   neigh_GO_term = organelle_organization_and_biogenesis_:
sce00521 (0.0)
|   |   |   neigh_GO_term = motor_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00521 (0.0)
|   |   |   neigh_GO_term = vacuole_: sce00521 (0.0)
|   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00521 (0.0)
|   |   |   neigh_GO_term = structural_molecule_activity_: sce00521
(0.0)
|   |   |   neigh_GO_term = protein_kinase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = peroxisome_: sce00521 (0.0)
|   |   |   neigh_GO_term = lipid_metabolic_process_: sce00521 (0.0)
|   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00521 (0.0)
|   |   |   neigh_GO_term = sporulation_: sce00521 (0.0)
|   |   |   neigh_GO_term = lyase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = pseudohyphal_growth_: sce00521 (0.0)
|   |   |   neigh_GO_term = cellular_respiration_: sce00521 (0.0)
|   |   |   neigh_GO_term = ribosome_: sce00521 (0.0)
|   |   |   neigh_GO_term = electron_transport_: sce00521 (0.0)
|   |   |   neigh_GO_term = cell_wall_organization_and_biogenesis_:
sce00521 (0.0)
|   |   |   neigh_GO_term = microtubule_organizing_center_: sce00521
(0.0)
|   |   |   neigh_GO_term = nucleolus_: sce00521 (0.0)
|   |   |   neigh_GO_term = isomerase_activity_: sce00521 (0.0)
|   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00521 (0.0)
|   |   |   neigh_GO_term = translation_regulator_activity_:
sce00521 (0.0)
|   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00521 (0.0)
|   |   |   neigh_GO_term = signal_transducer_activity_: sce00521
(0.0)
|   |   |   neigh_GO_term = extracellular_region_: sce00521 (0.0)
|   |   |   neigh_GO_term = conjugation_: sce00521 (0.0)
|   |   |   neigh_GO_term = response_to_stress_: sce00521 (0.0)
|   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00521
(0.0)
|   |   |   neigh_GO_term = cell_budding_: sce00521 (0.0)
|   |   |   neigh_GO_term = membrane_fraction_: sce00521 (0.0)
|   |   |   neigh_GO_term = cell_wall_: sce00521 (0.0)
|   |   |   neigh_GO_term = mitochondrial_envelope_: sce00521 (0.0)
|   |   |   neigh_GO_term = cell_cortex_: sce00521 (0.0)
|   |   |   neigh_GO_term = cytoskeleton_: sce00521 (0.0)
|   start > 23935
|   |   strand = C
|   |   |   start <= 196409
```

```
|   |   |   |   start <= 73157
|   |   |   |   |   start <= 48613: sce00790 (38.8/18.64)
|   |   |   |   |   start > 48613: sce00510 (25.98/12.86)
|   |   |   |   start > 73157
|   |   |   |   |   start <= 160071
|   |   |   |   |   |   start <= 120911: sce04111 (12.09)
|   |   |   |   |   |   start > 120911
|   |   |   |   |   |   |   start <= 148594: sce03010 (14.86)
|   |   |   |   |   |   |   start > 148594: sce00190 (9.12)
|   |   |   |   |   start > 160071: sce00790 (30.18/14.59)
|   |   |   start > 196409: sce00310 (32.11/15.56)
|   |   strand = W
|   |   |   start <= 73157
|   |   |   |   start <= 35653: sce00230 (29.86)
|   |   |   |   start > 35653
|   |   |   |   |   start <= 39023: sce00860 (47.53/29.2)
|   |   |   |   |   start > 39023
|   |   |   |   |   |   start <= 48613: sce04111 (11.13)
|   |   |   |   |   |   start > 48613: sce00230 (16.12)
|   |   |   start > 73157
|   |   |   |   start <= 108162: sce01040 (75.71/36.82)
|   |   |   |   start > 108162
|   |   |   |   |   start <= 150177
|   |   |   |   |   |   start <= 120911: sce00300 (14.44)
|   |   |   |   |   |   start > 120911: sce00190 (18.21)
|   |   |   |   |   start > 150177
|   |   |   |   |   |   start <= 160071: sce04140 (14.75)
|   |   |   |   |   |   start > 160071: sce01032 (18.24)
start > 216101
|   start <= 787784
|   |   start <= 511549
|   |   |   start <= 374830
|   |   |   |   strand = C
|   |   |   |   |   start <= 365999
|   |   |   |   |   |   start <= 254646
|   |   |   |   |   |   |   start <= 228334: sce03010 (22.46)
|   |   |   |   |   |   |   start > 228334: sce01031 (31.06/13.78)
|   |   |   |   |   |   start > 254646
|   |   |   |   |   |   |   start <= 347122
|   |   |   |   |   |   |   |   start <= 317345: sce03022 (17.13)
|   |   |   |   |   |   |   |   start > 317345: sce04010 (14.86)
|   |   |   |   |   |   |   start > 347122: sce03010 (17.41)
|   |   |   |   |   start > 365999
|   |   |   |   |   |   distance <= 2525: sce00230 (31.19/18.15)
|   |   |   |   |   |   distance > 2525: sce00240 (12.75/3.36)
|   |   |   |   strand = W
|   |   |   |   |   start <= 277623
|   |   |   |   |   |   start <= 238124: sce00400 (16.8)
|   |   |   |   |   |   start > 238124
|   |   |   |   |   |   |   start <= 254646: sce03010 (14.34)
|   |   |   |   |   |   |   start > 254646
|   |   |   |   |   |   |   |   start <= 272526
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cellular_component_: sce00670 (0.0)
```

```
|   |   |   |   |   |   |   |   |   neigh_GO_term =
molecular_function_: sce00680 (10.29/4.18)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
biological_process_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
transferase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
peptidase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = mitochondrion_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cytoplasm_:
sce00670 (1.75/0.79)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
signal_transduction_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
plasma_membrane_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
transporter_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = transport_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = nucleus_:
sce00670 (1.4/0.67)
|   |   |   |   |   |   |   |   |   neigh_GO_term = DNA_binding_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = transcription_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
helicase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = meiosis_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = chromosome_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_cycle_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
hydrolase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
endomembrane_system_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00670 (0.0)
```

```
|   |   |   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
ligase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = translation_:
sce00670 (5.48/1.24)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
DNA_metabolic_process_: sce00670 (2.22/0.47)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
RNA_metabolic_process_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_binding_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
endoplasmic_reticulum_: sce00670 (1.61/0.38)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cellular_bud_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cytokinesis_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = RNA_binding_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = membrane_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
Golgi_apparatus_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce00680 (3.61/1.46)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = vacuole_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cytoplasmic_membrane-bound_vesicle_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00680 (4.58/0.72)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = peroxisome_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce00680 (6.57/1.62)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = sporulation_:
sce00670 (0.0)
```

```
|   |   |   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
pseudohyphal_growth_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cellular_respiration_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = ribosome_:
sce00670 (6.52/0.97)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
electron_transport_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = nucleolus_:
sce00670 (0.58/0.11)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
isomerase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
extracellular_region_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = conjugation_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
response_to_stress_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_budding_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
membrane_fraction_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_wall_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term =
mitochondrial_envelope_: sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cell_cortex_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_:
sce00670 (0.0)
|   |   |   |   |   |   |   |   start > 272526: sce03010 (10.86)
|   |   |   |   |   start > 277623
|   |   |   |   |   |   start <= 299731: sce04111 (37.86/15.57)
|   |   |   |   |   |   start > 299731
|   |   |   |   |   |   |   start <= 317345
|   |   |   |   |   |   |   |   start <= 310970: sce03010 (13.54)
|   |   |   |   |   |   |   |   start > 310970: sce04130 (7.75)
|   |   |   |   |   |   |   start > 317345: sce04111 (20.04)
```

```
|   |   |   start > 374830
|   |   |   |   start <= 446148
|   |   |   |   |   start <= 398631
|   |   |   |   |   |   strand = C: sce01030 (31.52/15.29)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 385199
|   |   |   |   |   |   |   |   start <= 383657: sce00240 (12.86)
|   |   |   |   |   |   |   |   start > 383657
|   |   |   |   |   |   |   |   |   neigh_num <= 1: sce00620
(10.39/4.32)
|   |   |   |   |   |   |   |   |   neigh_num > 1: sce00020
(25.46/13.86)
|   |   |   |   |   |   |   start > 385199
|   |   |   |   |   |   |   |   start <= 393992: sce04120 (15.35)
|   |   |   |   |   |   |   |   start > 393992: sce01040 (37.01)
|   |   |   |   |   start > 398631
|   |   |   |   |   |   start <= 426810
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 411555: sce03050 (24.41)
|   |   |   |   |   |   |   |   start > 411555
|   |   |   |   |   |   |   |   |   start <= 420561: sce00860 (9.22)
|   |   |   |   |   |   |   |   |   start > 420561: sce00513 (17.32)
|   |   |   |   |   |   |   strand = W: sce00510 (18.76/5.75)
|   |   |   |   |   |   start > 426810
|   |   |   |   |   |   |   start <= 439096
|   |   |   |   |   |   |   |   start <= 427953: sce00760 (17.03)
|   |   |   |   |   |   |   |   start > 427953: sce03010 (26.78)
|   |   |   |   |   |   |   start > 439096: sce00510 (37.45/14.78)
|   |   |   |   start > 446148
|   |   |   |   |   start <= 500136
|   |   |   |   |   |   start <= 478657
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 448540: sce00400 (25.49)
|   |   |   |   |   |   |   |   start > 448540
|   |   |   |   |   |   |   |   |   start <= 475252: sce03050
(15.46)
|   |   |   |   |   |   |   |   |   start > 475252: sce00290 (10.93)
|   |   |   |   |   |   |   strand = W: sce00100 (17.73)
|   |   |   |   |   |   start > 478657
|   |   |   |   |   |   |   start <= 482671: sce00190 (13.72)
|   |   |   |   |   |   |   start > 482671
|   |   |   |   |   |   |   |   start <= 494178: sce04120
(28.09/11.71)
|   |   |   |   |   |   |   |   start > 494178
|   |   |   |   |   |   |   |   |   start <= 496506: sce00100
(15.44)
|   |   |   |   |   |   |   |   |   start > 496506: sce04120 (12.05)
|   |   |   |   |   start > 500136
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 506973: sce03022 (20.22)
|   |   |   |   |   |   |   start > 506973: sce04130 (28.7)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 506973: sce00440 (32.46/14.85)
|   |   |   |   |   |   |   start > 506973: sce00760 (20.19)
```

```
|   |   start > 511549
|   |   |   start <= 648911
|   |   |   |   start <= 527333
|   |   |   |   |   start <= 513163: sce00272 (46.47/27.15)
|   |   |   |   |   start > 513163
|   |   |   |   |   |   start <= 525233: sce00410 (63.03/39.68)
|   |   |   |   |   |   start > 525233: sce00190 (9.51)
|   |   |   |   start > 527333
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 581440
|   |   |   |   |   |   |   start <= 558872
|   |   |   |   |   |   |   |   start <= 534462: sce03010 (20.61)
|   |   |   |   |   |   |   |   start > 534462: sce00510 (23.1)
|   |   |   |   |   |   |   start > 558872: sce00030 (23.54)
|   |   |   |   |   |   start > 581440
|   |   |   |   |   |   |   start <= 615969: sce00230 (13.53)
|   |   |   |   |   |   |   start > 615969: sce03010 (32.66)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 581440
|   |   |   |   |   |   |   start <= 548268: sce04010 (21.33/9.33)
|   |   |   |   |   |   |   start > 548268
|   |   |   |   |   |   |   |   start <= 558872: sce03010 (13.7)
|   |   |   |   |   |   |   |   start > 558872: sce04010 (11.51)
|   |   |   |   |   |   start > 581440: sce00100 (18.11)
|   |   |   start > 648911
|   |   |   |   start <= 718897
|   |   |   |   |   start <= 654638
|   |   |   |   |   |   start <= 652985: sce00010 (20.61)
|   |   |   |   |   |   start > 652985: sce00380 (50.08/32.38)
|   |   |   |   |   start > 654638
|   |   |   |   |   |   start <= 672190
|   |   |   |   |   |   |   start <= 668193: sce04111 (16.73)
|   |   |   |   |   |   |   start > 668193: sce00290 (24.86/11.2)
|   |   |   |   |   |   start > 672190: sce04111 (68.06)
|   |   |   |   start > 718897
|   |   |   |   |   start <= 739949
|   |   |   |   |   |   start <= 726978: sce03010 (11.46)
|   |   |   |   |   |   start > 726978: sce00252 (29.85/11.61)
|   |   |   |   |   start > 739949
|   |   |   |   |   |   start <= 761397: sce03050 (28.64)
|   |   |   |   |   |   start > 761397: sce03010 (15.52)
|   start > 787784
|   |   start <= 958213
|   |   |   start <= 867525
|   |   |   |   start <= 842556
|   |   |   |   |   strand = C: sce00271 (50.08/29.01)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 798548: sce00271 (43.43/25.21)
|   |   |   |   |   |   start > 798548: sce00260 (51.32/22.65)
|   |   |   |   start > 842556
|   |   |   |   |   start <= 856306
|   |   |   |   |   |   start <= 848428: sce00900 (30.01/11.83)
|   |   |   |   |   |   start > 848428: sce00240 (43.75/16.53)
|   |   |   |   |   start > 856306
```

```
|   |   |   |   |   |   start <= 859481: sce00190 (13.21)
|   |   |   |   |   |   start > 859481: sce00970 (32.42/12.07)
|   |   |   start > 867525
|   |   |   |   strand = C
|   |   |   |   |   start <= 911888
|   |   |   |   |   |   start <= 883815
|   |   |   |   |   |   |   start <= 875114: sce04111 (16.5)
|   |   |   |   |   |   |   start > 875114: sce00010 (16.21)
|   |   |   |   |   |   start > 883815
|   |   |   |   |   |   |   start <= 887880: sce00040 (10.6)
|   |   |   |   |   |   |   start > 887880: sce00564 (23.97/10.7)
|   |   |   |   |   start > 911888
|   |   |   |   |   |   start <= 924467: sce00563 (31.22/11.57)
|   |   |   |   |   |   start > 924467: sce04111 (18.31)
|   |   |   |   strand = W
|   |   |   |   |   start <= 905939
|   |   |   |   |   |   start <= 883815: sce03022 (17.5)
|   |   |   |   |   |   start > 883815: sce00630 (51.15/22.0)
|   |   |   |   |   start > 905939
|   |   |   |   |   |   start <= 911888: sce00260 (23.48)
|   |   |   |   |   |   start > 911888
|   |   |   |   |   |   |   start <= 924467: sce03010 (13.86)
|   |   |   |   |   |   |   start > 924467: sce01030 (19.42/9.66)
|   |   start > 958213
|   |   |   start <= 1004630
|   |   |   |   start <= 979324
|   |   |   |   |   start <= 973739: sce00010 (40.67/23.08)
|   |   |   |   |   start > 973739: sce00720 (39.52/25.54)
|   |   |   |   start > 979324
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 1000932: sce03050 (26.48)
|   |   |   |   |   |   start > 1000932: sce00130 (17.68)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 1000932
|   |   |   |   |   |   |   start <= 985977: sce00030 (12.43)
|   |   |   |   |   |   |   start > 985977: sce00010 (10.8)
|   |   |   |   |   |   start > 1000932: sce00030 (16.24)
|   |   |   start > 1004630
|   |   |   |   start <= 1021859: sce00970 (42.06/25.01)
|   |   |   |   start > 1021859
|   |   |   |   |   start <= 1043102
|   |   |   |   |   |   start <= 1031797
|   |   |   |   |   |   |   start <= 1025741: sce00790 (13.56)
|   |   |   |   |   |   |   start > 1025741: sce00500 (21.14/8.06)
|   |   |   |   |   |   start > 1031797: sce03022 (18.33)
|   |   |   |   |   start > 1043102
|   |   |   |   |   |   start <= 1064947
|   |   |   |   |   |   |   start <= 1058731: sce00500 (19.13)
|   |   |   |   |   |   |   start > 1058731: sce00780 (36.37)
|   |   |   |   |   |   start > 1064947: sce00500 (31.18)
```

Decision Tree Generated for Chromosome Eight:

```
start <= 323412
|   start <= 126515
|   |   strand = C
|   |   |   start <= 81612
|   |   |   |   start <= 39484
|   |   |   |   |   start <= 38506
|   |   |   |   |   |   start <= 36023: sce03010 (11.24)
|   |   |   |   |   |   start > 36023: sce00561 (10.81)
|   |   |   |   |   start > 38506: sce04130 (11.56)
|   |   |   |   start > 39484: sce00230 (31.4/11.76)
|   |   |   start > 81612
|   |   |   |   start <= 114912
|   |   |   |   |   start <= 107821
|   |   |   |   |   |   start <= 97933: sce04010 (16.1)
|   |   |   |   |   |   start > 97933: sce00600 (18.01)
|   |   |   |   |   start > 107821: sce04010 (17.89)
|   |   |   |   start > 114912: sce00100 (20.18)
|   |   strand = W
|   |   |   start <= 81612
|   |   |   |   start <= 75409: sce03010 (10.64)
|   |   |   |   start > 75409
|   |   |   |   |   neigh_strand = W: sce00520 (13.2/6.44)
|   |   |   |   |   neigh_strand = C: sce00040 (25.22/11.13)
|   |   |   start > 81612
|   |   |   |   start <= 114912
|   |   |   |   |   start <= 104272: sce03010 (7.77)
|   |   |   |   |   start > 104272: sce00190 (9.22)
|   |   |   |   start > 114912: sce03010 (20.32)
|   start > 126515
|   |   start <= 286772
|   |   |   start <= 159431
|   |   |   |   start <= 143989
|   |   |   |   |   start <= 127774: sce00970 (25.29/9.23)
|   |   |   |   |   start > 127774
|   |   |   |   |   |   start <= 141395
|   |   |   |   |   |   |   neigh_num <= 1: sce00252 (16.23/8.59)
|   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   neigh_strand = W: sce00330
(5.19/1.94)
|   |   |   |   |   |   |   |   neigh_strand = C: sce00220
(6.33/2.52)
|   |   |   |   |   |   start > 141395
|   |   |   |   |   |   |   start <= 143551
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00970
(10.06/3.67)
|   |   |   |   |   |   |   |   neigh_num > 1: sce00252 (19.29/7.61)
|   |   |   |   |   |   |   start > 143551: sce00330 (33.82/15.52)
|   |   |   |   start > 143989
|   |   |   |   |   start <= 148662: sce03010 (10.35)
|   |   |   |   |   start > 148662: sce00260 (17.58)
|   |   |   start > 159431
|   |   |   |   start <= 209699
|   |   |   |   |   start <= 170337
|   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   start <= 164704: sce03050 (14.32)
|   |   |   |   |   |   |   start > 164704: sce04010 (13.6)
|   |   |   |   |   |   strand = W: sce00190 (17.01)
|   |   |   |   |   start > 170337
|   |   |   |   |   |   start <= 181970: sce00330 (29.88/14.66)
|   |   |   |   |   |   start > 181970: sce00190 (36.26)
|   |   |   |   start > 209699
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 246195
|   |   |   |   |   |   |   start <= 225171: sce00770 (14.05)
|   |   |   |   |   |   |   start > 225171: sce00790 (33.19/15.74)
|   |   |   |   |   |   start > 246195
|   |   |   |   |   |   |   neigh_strand = W: sce00970 (12.77/2.95)
|   |   |   |   |   |   |   neigh_strand = C: sce00330 (12.16/5.26)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 246195
|   |   |   |   |   |   |   start <= 239100: sce00100 (9.02)
|   |   |   |   |   |   |   start > 239100: sce00251 (23.15/8.71)
|   |   |   |   |   |   start > 246195: sce04010 (13.99)
|   |   start > 286772
|   |   |   neigh_GO_term = cellular_component_: sce00310 (0.0)
|   |   |   neigh_GO_term = helicase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = biological_process_: sce00310
(9.07/7.55)
|   |   |   neigh_GO_term = molecular_function_
|   |   |   |   distance <= 1666: sce00120 (8.13/5.03)
|   |   |   |   distance > 1666: sce00310 (16.02/11.33)
|   |   |   neigh_GO_term = endomembrane_system_: sce00310 (0.0)
|   |   |   neigh_GO_term = response_to_stress_: sce00310 (0.0)
|   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00310 (0.0)
|   |   |   neigh_GO_term = plasma_membrane_: sce00310 (0.0)
|   |   |   neigh_GO_term = transporter_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = transport_: sce00310 (0.0)
|   |   |   neigh_GO_term = cell_wall_organization_and_biogenesis_:
sce00561 (25.25/18.57)
|   |   |   neigh_GO_term = cytoplasm_
|   |   |   |   neigh_strand = W: sce00120 (22.64/15.82)
|   |   |   |   neigh_strand = C: sce00260 (15.72/11.86)
|   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00310 (0.0)
|   |   |   neigh_GO_term = mitochondrion_: sce00310 (0.0)
|   |   |   neigh_GO_term = RNA_binding_: sce00310 (0.0)
|   |   |   neigh_GO_term = RNA_metabolic_process_: sce00310 (0.0)
|   |   |   neigh_GO_term = membrane_: sce00310 (0.0)
|   |   |   neigh_GO_term = ribosome_: sce00310 (0.0)
|   |   |   neigh_GO_term = hydrolase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = nucleolus_: sce00310 (0.0)
|   |   |   neigh_GO_term = structural_molecule_activity_: sce00310
(12.86/10.34)
|   |   |   neigh_GO_term = translation_: sce00310 (0.0)
|   |   |   neigh_GO_term = transferase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = protein_binding_: sce00310 (0.0)
```

```
|   |   |   neigh_GO_term = vesicle-mediated_transport_: sce00310
(0.0)
|   |   |   neigh_GO_term = nucleus_: sce00310 (0.0)
|   |   |   neigh_GO_term = protein_catabolic_process_: sce00310
(0.0)
|   |   |   neigh_GO_term = membrane_fraction_: sce00310 (0.0)
|   |   |   neigh_GO_term = signal_transducer_activity_: sce00310
(0.0)
|   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00310 (0.0)
|   |   |   neigh_GO_term = meiosis_: sce00310 (0.0)
|   |   |   neigh_GO_term = DNA_metabolic_process_: sce00310 (0.0)
|   |   |   neigh_GO_term = sporulation_: sce00310 (0.0)
|   |   |   neigh_GO_term = chromosome_: sce00310 (0.0)
|   |   |   neigh_GO_term = cell_cycle_: sce00310 (0.0)
|   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00310 (0.0)
|   |   |   neigh_GO_term = Golgi_apparatus_: sce00310 (0.0)
|   |   |   neigh_GO_term = DNA_binding_: sce00310 (0.0)
|   |   |   neigh_GO_term = transcription_: sce00310 (0.0)
|   |   |   neigh_GO_term = vacuole_: sce00310 (0.0)
|   |   |   neigh_GO_term = site_of_polarized_growth_: sce00310
(0.0)
|   |   |   neigh_GO_term = protein_kinase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = pseudohyphal_growth_: sce00310 (0.0)
|   |   |   neigh_GO_term = oxidoreductase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = cellular_respiration_: sce00310 (0.0)
|   |   |   neigh_GO_term = electron_transport_: sce00310 (0.0)
|   |   |   neigh_GO_term = phosphoprotein_phosphatase_activity_:
sce00310 (0.0)
|   |   |   neigh_GO_term = nuclear_organization_and_biogenesis_:
sce00310 (0.0)
|   |   |   neigh_GO_term = conjugation_: sce00310 (0.0)
|   |   |   neigh_GO_term = membrane_organization_and_biogenesis_:
sce00310 (0.0)
|   |   |   neigh_GO_term = lipid_metabolic_process_: sce00310 (0.0)
|   |   |   neigh_GO_term = ligase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = cell_cortex_: sce00310 (0.0)
|   |   |   neigh_GO_term = cytoskeleton_: sce00310 (0.0)
|   |   |   neigh_GO_term = lyase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00310 (0.0)
|   |   |   neigh_GO_term = cellular_bud_: sce00310 (0.0)
|   |   |   neigh_GO_term = motor_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = cytokinesis_: sce00051 (13.02/8.56)
|   |   |   neigh_GO_term = peptidase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = protein_modification_process_: sce00310
(0.0)
|   |   |   neigh_GO_term = organelle_organization_and_biogenesis_:
sce00310 (0.0)
|   |   |   neigh_GO_term = signal_transduction_: sce00310 (0.0)
|   |   |   neigh_GO_term = translation_regulator_activity_:
sce00310 (0.0)
|   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00310 (0.0)
```

```
|   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00310 (0.0)
|   |   |   neigh_GO_term = isomerase_activity_: sce00310 (0.0)
|   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00310
(0.0)
|   |   |   neigh_GO_term = cell_budding_: sce00310 (0.0)
|   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00310
(0.0)
|   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00310 (0.0)
|   |   |   neigh_GO_term = cell_wall_: sce00310 (0.0)
|   |   |   neigh_GO_term = extracellular_region_: sce00310 (0.0)
|   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00310 (0.0)
|   |   |   neigh_GO_term = peroxisome_: sce00310 (0.0)
|   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00310 (0.0)
|   |   |   neigh_GO_term = mitochondrial_envelope_: sce00310 (0.0)
|   |   |   neigh_GO_term = microtubule_organizing_center_: sce00310
(0.0)
start > 323412
|   start <= 470960
|   |   start <= 388729
|   |   |   strand = C
|   |   |   |   start <= 374313
|   |   |   |   |   start <= 354818: sce04111 (16.52)
|   |   |   |   |   start > 354818
|   |   |   |   |   |   neigh_num <= 1: sce00632 (24.51/13.37)
|   |   |   |   |   |   neigh_num > 1: sce00562 (28.47/16.01)
|   |   |   |   start > 374313
|   |   |   |   |   start <= 382754: sce03010 (13.17)
|   |   |   |   |   start > 382754: sce00240 (18.47)
|   |   |   strand = W
|   |   |   |   start <= 354818
|   |   |   |   |   start <= 325601: sce00240 (21.83)
|   |   |   |   |   start > 325601
|   |   |   |   |   |   neigh_num <= 1: sce00440 (22.71/8.58)
|   |   |   |   |   |   neigh_num > 1: sce00564 (41.75/24.69)
|   |   |   |   start > 354818
|   |   |   |   |   start <= 374313: sce00240 (15.21)
|   |   |   |   |   start > 374313
|   |   |   |   |   |   distance <= 398: sce03020 (4.12/0.35)
|   |   |   |   |   |   distance > 398: sce00240 (29.43/18.38)
|   |   start > 388729
|   |   |   strand = C
|   |   |   |   neigh_strand = W: sce04120 (16.48/4.42)
|   |   |   |   neigh_strand = C: sce04111 (9.46/3.01)
|   |   |   strand = W
|   |   |   |   start <= 442182
|   |   |   |   |   start <= 423726: sce00030 (18.93)
|   |   |   |   |   start > 423726: sce00790 (24.93/9.44)
|   |   |   |   start > 442182
|   |   |   |   |   start <= 445713: sce04140 (20.12)
|   |   |   |   |   start > 445713
```

```
|   |   |   |   |   |   start <= 451327: sce00010 (10.75)
|   |   |   |   |   |   start > 451327: sce00030 (17.65)
|   start > 470960
|   |   start <= 499079
|   |   |   strand = C
|   |   |   |   neigh_strand = W: sce01031 (16.59/4.28)
|   |   |   |   neigh_strand = C: sce00563 (14.37/6.04)
|   |   |   strand = W
|   |   |   |   start <= 484845: sce00900 (33.72/15.5)
|   |   |   |   start > 484845: sce03050 (13.47)
|   |   start > 499079
|   |   |   strand = C
|   |   |   |   start <= 501143: sce00230 (13.16)
|   |   |   |   start > 501143: sce03010 (20.31)
|   |   |   strand = W
|   |   |   |   start <= 517532: sce00290 (80.01/41.52)
|   |   |   |   start > 517532
|   |   |   |   |   start <= 552099: sce00740 (17.35/8.32)
|   |   |   |   |   start > 552099: sce00230 (8.72)
```

Decision Tree Generated for Chromosome Nine:

```
start <= 155219
|   start <= 99416
|   |   start <= 41444
|   |   |   start <= 37385: sce00500 (28.55)
|   |   |   start > 37385
|   |   |   |   neigh_GO_term = cellular_component_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = biological_process_: sce00071
(10.27/7.69)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_strand = W: sce00592 (6.19/3.93)
|   |   |   |   |   neigh_strand = C: sce00120 (16.77/10.98)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00280 (10.68/6.92)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = transport_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00592 (8.21/6.04)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00281 (12.97/7.26)
```

```
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00362
(11.55/8.34)
|   |   |   |   neigh_GO_term = protein_binding_: sce00071
(10.48/5.83)
|   |   |   |   neigh_GO_term = cell_budding_: sce00592 (7.24/5.25)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00592
(6.96/5.19)
|   |   |   |   neigh_GO_term = translation_: sce00071 (9.78/6.9)
|   |   |   |   neigh_GO_term = vacuole_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = nucleus_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00071
(0.0)
```

```
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00071
(0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00071 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00071 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00071 (0.0)
|   |   start > 41444
|   |   |   start <= 73453
|   |   |   |   strand = C
|   |   |   |   |   start <= 53708: sce00564 (18.14)
|   |   |   |   |   start > 53708: sce02021 (19.22/9.36)
|   |   |   |   strand = W: sce03010 (14.02)
|   |   |   start > 73453
|   |   |   |   start <= 77283: sce00410 (29.09/12.8)
|   |   |   |   start > 77283
|   |   |   |   |   start <= 88716: sce03030 (9.64)
|   |   |   |   |   start > 88716: sce03010 (15.76)
|   start > 99416
|   |   start <= 126204
|   |   |   start <= 122689: sce00380 (61.01/38.04)
|   |   |   start > 122689: sce00565 (36.67/14.28)
|   |   start > 126204
|   |   |   start <= 142925
|   |   |   |   neigh_num <= 1: sce00401 (38.3/24.78)
|   |   |   |   neigh_num > 1: sce00340 (41.99/30.63)
|   |   |   start > 142925: sce00190 (18.03)
start > 155219
|   start <= 326101
|   |   start <= 222487
```

```
|   |   |   start <= 187629
|   |   |   |   strand = C
|   |   |   |   |   start <= 166412: sce00051 (23.4)
|   |   |   |   |   start > 166412: sce00300 (13.38)
|   |   |   |   strand = W
|   |   |   |   |   start <= 166412: sce04111 (20.52)
|   |   |   |   |   start > 166412: sce00500 (15.58)
|   |   |   start > 187629
|   |   |   |   strand = C
|   |   |   |   |   start <= 220697: sce03050 (25.09)
|   |   |   |   |   start > 220697: sce00260 (21.03)
|   |   |   |   strand = W: sce00260 (23.15/9.01)
|   |   start > 222487
|   |   |   start <= 312903
|   |   |   |   start <= 257061
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 232366: sce03010 (19.06)
|   |   |   |   |   |   start > 232366
|   |   |   |   |   |   |   start <= 240705: sce00240 (42.26/19.32)
|   |   |   |   |   |   |   start > 240705: sce03010 (14.63)
|   |   |   |   |   strand = W: sce00561 (8.56)
|   |   |   |   start > 257061
|   |   |   |   |   start <= 307927
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 274925: sce00530 (23.36)
|   |   |   |   |   |   |   start > 274925: sce04111 (8.65)
|   |   |   |   |   |   strand = W: sce04111 (43.74/13.51)
|   |   |   |   |   start > 307927: sce00230 (52.47/27.2)
|   |   |   start > 312903
|   |   |   |   strand = C: sce00340 (17.3)
|   |   |   |   strand = W
|   |   |   |   |   start <= 316766: sce03010 (14.93)
|   |   |   |   |   start > 316766: sce00051 (42.44/26.9)
|   start > 326101
|   |   start <= 415614
|   |   |   start <= 348502
|   |   |   |   start <= 339341: sce00071 (21.69)
|   |   |   |   start > 339341: sce04130 (19.77)
|   |   |   start > 348502
|   |   |   |   start <= 393672
|   |   |   |   |   start <= 374303: sce00240 (46.78/26.61)
|   |   |   |   |   start > 374303: sce00500 (10.43)
|   |   |   |   start > 393672
|   |   |   |   |   start <= 410804: sce00230 (27.96)
|   |   |   |   |   start > 410804
|   |   |   |   |   |   start <= 414676: sce00630 (27.31/7.26)
|   |   |   |   |   |   start > 414676: sce00230 (19.87)
|   |   start > 415614
|   |   |   start <= 420733: sce00310 (32.7/13.41)
|   |   |   start > 420733
|   |   |   |   neigh_num <= 1
|   |   |   |   |   neigh_strand = W: sce00590 (3.94/1.42)
|   |   |   |   |   neigh_strand = C: sce00480 (10.19/2.23)
|   |   |   |   neigh_num > 1: sce00590 (13.3/4.37)
```

Decision Tree Generated for Chromosome Ten:

```
start <= 424103
|   start <= 105008
|   |   start <= 26086
|   |   |   strand = C: sce00500 (31.05)
|   |   |   strand = W
|   |   |   |   neigh_GO_term = cellular_component_: sce00564
(27.35/14.49)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = biological_process_
|   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   neigh_num <= 1: sce00624 (4.32/3.03)
|   |   |   |   |   |   neigh_num > 1: sce00632 (7.77/4.31)
|   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   neigh_num <= 1: sce00564 (12.58/9.65)
|   |   |   |   |   |   neigh_num > 1: sce00903 (11.02/7.37)
|   |   |   |   neigh_GO_term = molecular_function_: sce00624
(15.94/10.93)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00632
(17.88/12.95)
|   |   |   |   neigh_GO_term = transport_: sce00624 (16.23/9.82)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00632
(7.91/5.3)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00624
(3.82/2.91)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00624 (4.37/3.41)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00624 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = nucleus_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00624
(0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00624 (0.0)
```

```
|   |   |   |   neigh_GO_term = lyase_activity_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = translation_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00624 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00624 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00624 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00624 (0.0)
```

```
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00624 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00624 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00624 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00624
(0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00624 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00624 (0.0)
|   |   start > 26086
|   |   |   start <= 79261
|   |   |   |   start <= 58813
|   |   |   |   |   start <= 36919: sce04111 (13.7)
|   |   |   |   |   start > 36919
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00020 (13.57/4.75)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00630
(1.53/0.73)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00720 (4.57/2.84)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00720
(8.91/3.59)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00720 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00020 (7.79/4.31)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00720
(7.49/3.61)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00720
(4.59/2.12)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00720 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00720 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00720 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00720
(0.0)
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00720 (0.0)
|   |   |   |   start > 58813
|   |   |   |   |   start <= 69337: sce04111 (19.33)
|   |   |   |   |   start > 69337
|   |   |   |   |   |   start <= 75932: sce03010 (35.89)
|   |   |   |   |   |   start > 75932: sce04111 (16.47)
|   |   |   start > 79261
|   |   |   |   start <= 84066
|   |   |   |   |   start <= 80153: sce00513 (15.7)
|   |   |   |   |   start > 80153: sce01030 (21.16/8.54)
|   |   |   |   start > 84066
|   |   |   |   |   start <= 90784: sce03010 (12.99)
|   |   |   |   |   start > 90784
|   |   |   |   |   |   neigh_strand = W: sce00100 (12.8/3.76)
|   |   |   |   |   |   neigh_strand = C: sce00900 (17.89/5.87)
|   start > 105008
|   |   strand = C
|   |   |   start <= 180100
|   |   |   |   start <= 150958
|   |   |   |   |   start <= 130640
|   |   |   |   |   |   start <= 126324: sce04111 (26.84/12.95)
|   |   |   |   |   |   start > 126324: sce00051 (11.8)
|   |   |   |   |   start > 130640
|   |   |   |   |   |   start <= 140434
|   |   |   |   |   |   |   neigh_num <= 1: sce00562 (8.75/2.38)
|   |   |   |   |   |   |   neigh_num > 1: sce00521 (16.5/4.38)
|   |   |   |   |   |   start > 140434: sce04070 (53.95/31.99)
|   |   |   |   start > 150958
|   |   |   |   |   start <= 172364
|   |   |   |   |   |   start <= 158185: sce03010 (14.21)
|   |   |   |   |   |   start > 158185
|   |   |   |   |   |   |   neigh_num <= 1: sce00252 (10.69/4.01)
|   |   |   |   |   |   |   neigh_num > 1: sce00251 (36.73/18.29)
|   |   |   |   |   start > 172364: sce04010 (14.99)
|   |   |   start > 180100
|   |   |   |   start <= 262547
|   |   |   |   |   start <= 191089: sce00040 (45.1/24.47)
|   |   |   |   |   start > 191089
|   |   |   |   |   |   start <= 247250: sce00480 (38.18/18.59)
|   |   |   |   |   |   start > 247250: sce00563 (14.17)
|   |   |   |   start > 262547
|   |   |   |   |   start <= 411034
|   |   |   |   |   |   start <= 268794: sce03030 (17.13)
|   |   |   |   |   |   start > 268794: sce04111 (32.2)
|   |   |   |   |   start > 411034: sce00562 (44.72/25.73)
|   |   strand = W
|   |   |   start <= 247250
|   |   |   |   start <= 150958
|   |   |   |   |   start <= 106428: sce00190 (13.28)
```

```
|   |   |   |   |   start > 106428: sce00240 (107.99/60.25)
|   |   |   |   start > 150958
|   |   |   |   |   start <= 221386
|   |   |   |   |   |   start <= 180100: sce00600 (11.09)
|   |   |   |   |   |   start > 180100: sce00632 (42.17/26.07)
|   |   |   |   |   start > 221386
|   |   |   |   |   |   start <= 245587: sce01040 (43.9)
|   |   |   |   |   |   start > 245587: sce04010 (18.09)
|   |   |   start > 247250
|   |   |   |   start <= 306127
|   |   |   |   |   start <= 262547: sce00790 (49.98/22.37)
|   |   |   |   |   start > 262547
|   |   |   |   |   |   start <= 268794: sce00220 (55.24/23.11)
|   |   |   |   |   |   start > 268794
|   |   |   |   |   |   |   start <= 295240: sce04111 (6.41)
|   |   |   |   |   |   |   start > 295240: sce00220 (15.89)
|   |   |   |   start > 306127
|   |   |   |   |   start <= 356019
|   |   |   |   |   |   start <= 352381
|   |   |   |   |   |   |   start <= 323381: sce00300 (18.24)
|   |   |   |   |   |   |   start > 323381
|   |   |   |   |   |   |   |   start <= 338266: sce00010 (12.32)
|   |   |   |   |   |   |   |   start > 338266: sce00785 (17.85)
|   |   |   |   |   |   start > 352381
|   |   |   |   |   |   |   neigh_strand = W: sce00020 (15.82/6.52)
|   |   |   |   |   |   |   neigh_strand = C: sce00190 (16.21/4.79)
|   |   |   |   |   start > 356019
|   |   |   |   |   |   start <= 383832: sce00790 (24.3/10.18)
|   |   |   |   |   |   start > 383832
|   |   |   |   |   |   |   start <= 387652: sce04111 (6.14)
|   |   |   |   |   |   |   start > 387652: sce00230 (19.66/7.87)
start > 424103
|   start <= 632935
|   |   start <= 517506
|   |   |   strand = C
|   |   |   |   start <= 460375
|   |   |   |   |   start <= 456232
|   |   |   |   |   |   start <= 435157: sce01030 (29.76/14.83)
|   |   |   |   |   |   start > 435157: sce00010 (19.91)
|   |   |   |   |   start > 456232: sce00780 (42.3/20.21)
|   |   |   |   start > 460375
|   |   |   |   |   start <= 471664
|   |   |   |   |   |   start <= 466201: sce00770 (32.46/10.29)
|   |   |   |   |   |   start > 466201: sce00380 (8.13)
|   |   |   |   |   start > 471664
|   |   |   |   |   |   neigh_strand = W: sce00230 (40.37/21.13)
|   |   |   |   |   |   neigh_strand = C: sce00240 (21.07/10.64)
|   |   |   strand = W
|   |   |   |   start <= 449195
|   |   |   |   |   start <= 435157
|   |   |   |   |   |   start <= 425151: sce00230 (16.7)
|   |   |   |   |   |   start > 425151: sce03050 (9.48)
|   |   |   |   |   start > 435157: sce00230 (62.12/36.07)
|   |   |   |   start > 449195
```

```
|   |   |   |   |   start <= 456232: sce00450 (43.83/26.23)
|   |   |   |   |   start > 456232
|   |   |   |   |   |   neigh_num <= 1: sce01031 (7.19/2.47)
|   |   |   |   |   |   neigh_num > 1: sce00563 (14.89/5.97)
|   |   start > 517506
|   |   |   start <= 594320
|   |   |   |   start <= 573974
|   |   |   |   |   start <= 555188
|   |   |   |   |   |   start <= 534020: sce04111 (9.16)
|   |   |   |   |   |   start > 534020: sce00240 (55.03/26.88)
|   |   |   |   |   start > 555188: sce01030 (47.38/21.2)
|   |   |   |   start > 573974
|   |   |   |   |   strand = C: sce04111 (32.4/11.33)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 578853: sce00380 (21.62)
|   |   |   |   |   |   start > 578853: sce04010 (13.53)
|   |   |   start > 594320
|   |   |   |   strand = C: sce00240 (33.53/16.37)
|   |   |   |   strand = W
|   |   |   |   |   start <= 620747
|   |   |   |   |   |   start <= 608301: sce03010 (15.5)
|   |   |   |   |   |   start > 608301: sce00240 (14.45)
|   |   |   |   |   start > 620747
|   |   |   |   |   |   start <= 623573: sce00230 (8.69)
|   |   |   |   |   |   start > 623573: sce00960 (26.97/12.54)
|   start > 632935
|   |   start <= 667638
|   |   |   start <= 667131
|   |   |   |   start <= 651895
|   |   |   |   |   strand = C: sce03010 (11.81)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 647601: sce00190 (18.9)
|   |   |   |   |   |   start > 647601: sce03010 (7.83)
|   |   |   |   start > 651895
|   |   |   |   |   neigh_GO_term = cellular_component_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = biological_process_: sce00450
(8.19/4.91)
|   |   |   |   |   neigh_GO_term = molecular_function_: sce00920
(7.23/1.68)
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00450
(7.72/2.33)
|   |   |   |   |   neigh_GO_term = transport_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00450
(7.17/4.51)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00920 (3.16/1.66)
```

```
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00450
(10.17/5.71)
|   |   |   |   |   neigh_GO_term = ribosome_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00272
(6.77/3.15)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = nucleus_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00271 (4.33/2.91)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00450
(3.4/1.38)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00272
(5.55/1.47)
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = translation_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00272 (5.72/3.31)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00271 (4.25/1.25)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = meiosis_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = extracellular_region_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00450 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = conjugation_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = electron_transport_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00450
(0.0)
|   |   |   |   |   neigh_GO_term = transcription_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cortex_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = sporulation_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00450 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00450
(0.0)
```

```
|   |   |   start > 667131: sce00510 (65.1/41.06)
|   |   start > 667638
|   |   |   start <= 705738
|   |   |   |   strand = C
|   |   |   |   |   start <= 690518: sce00300 (23.56/9.38)
|   |   |   |   |   start > 690518: sce03010 (5.88)
|   |   |   |   strand = W
|   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   neigh_strand = W: sce00280 (7.36/3.61)
|   |   |   |   |   |   neigh_strand = C: sce00290 (12.76/7.39)
|   |   |   |   |   neigh_num > 1: sce00770 (29.76/13.05)
|   |   |   start > 705738
|   |   |   |   start <= 722809: sce00500 (38.49/14.82)
|   |   |   |   start > 722809: sce00051 (79.29/50.29)
```

Decision Tree Generated for Chromosome Eleven:

```
start <= 327131
|   start <= 194865
|   |   start <= 100676
|   |   |   strand = C
|   |   |   |   start <= 75539
|   |   |   |   |   start <= 39164: sce00400 (22.05)
|   |   |   |   |   start > 39164: sce04130 (11.62)
|   |   |   |   start > 75539
|   |   |   |   |   start <= 78651: sce00260 (43.58/13.65)
|   |   |   |   |   start > 78651: sce00190 (18.0)
|   |   |   strand = W
|   |   |   |   start <= 39164
|   |   |   |   |   start <= 25216: sce00240 (25.77)
|   |   |   |   |   start > 25216: sce04120 (12.94)
|   |   |   |   start > 39164
|   |   |   |   |   start <= 96762: sce00220 (18.33)
|   |   |   |   |   start > 96762: sce00061 (12.1)
|   |   start > 100676
|   |   |   start <= 166549
|   |   |   |   strand = C
|   |   |   |   |   start <= 114632: sce04010 (21.35)
|   |   |   |   |   start > 114632
|   |   |   |   |   |   start <= 140696: sce01031 (26.51/13.06)
|   |   |   |   |   |   start > 140696: sce00010 (16.52)
|   |   |   |   strand = W
|   |   |   |   |   start <= 107321: sce00230 (33.4/16.15)
|   |   |   |   |   start > 107321
|   |   |   |   |   |   start <= 158619: sce03010 (36.44)
|   |   |   |   |   |   start > 158619: sce00530 (7.37)
|   |   |   start > 166549
|   |   |   |   start <= 179672
|   |   |   |   |   start <= 174218
|   |   |   |   |   |   start <= 171134: sce00020 (38.56/13.03)
|   |   |   |   |   |   start > 171134: sce03050 (6.46)
```

```
|   |   |   |   |   start > 174218
|   |   |   |   |   |   start <= 176486: sce00240 (41.94/23.97)
|   |   |   |   |   |   start > 176486: sce00020 (28.39/13.28)
|   |   |   |   start > 179672
|   |   |   |   |   start <= 180784: sce00650 (34.24/9.55)
|   |   |   |   |   start > 180784: sce00790 (12.88)
|   start > 194865
|   |   start <= 245017
|   |   |   start <= 203185
|   |   |   |   neigh_GO_term = cellular_component_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   distance <= 5681: sce00010 (7.39/4.84)
|   |   |   |   |   distance > 5681: sce00500 (7.12/3.19)
|   |   |   |   neigh_GO_term = biological_process_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = transport_: sce00500 (3.21/1.96)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00500
(9.07/5.42)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00500 (6.42/4.06)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00010 (6.13/2.77)
|   |   |   |   neigh_GO_term = nucleus_: sce00010 (5.17/3.34)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = translation_: sce00521 (8.57/5.43)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00500 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00500 (0.0)
```

```
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00030
(7.86/3.24)
|   |   |   |   neigh_GO_term = peroxisome_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00500
(0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = motor_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00500
(0.0)
```

```
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00500 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00500 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00500 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00500 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00500
(0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00500 (0.0)
|   |   |   start > 203185
|   |   |   |   start <= 237180
|   |   |   |   |   neigh_GO_term = cellular_component_
|   |   |   |   |   |   distance <= 2126
|   |   |   |   |   |   |   distance <= 1304: sce00350 (9.42/7.55)
|   |   |   |   |   |   |   distance > 1304: sce00710 (20.44/12.22)
|   |   |   |   |   |   distance > 2126: sce00272 (16.54/10.29)
|   |   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   |   neigh_num <= 1: sce00360 (18.91/14.91)
|   |   |   |   |   |   neigh_num > 1: sce00400 (20.02/15.08)
|   |   |   |   |   neigh_GO_term = biological_process_: sce00401
(25.54/21.88)
|   |   |   |   |   neigh_GO_term = ribosome_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = transport_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = nucleus_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00350 (11.65/9.18)
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00710 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00252 (11.95/8.48)
|   |   |   |   |   neigh_GO_term = translation_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00251 (9.17/6.36)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00710
(26.03/17.84)
|   |   |   |   |   neigh_GO_term = transcription_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = conjugation_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00710
(0.0)
```

```
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = electron_transport_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00401 (5.3/4.09)
|   |   |   |   |   neigh_GO_term = cell_cortex_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = motor_activity_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00710 (0.0)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00710 (0.0)
|   |   |   |   |   neigh_GO_term = extracellular_region_: sce00710
(0.0)
|   |   |   |   |   neigh_GO_term = meiosis_: sce00710 (0.0)
|   |   |   |   start > 237180: sce00530 (35.17/17.16)
|   |   start > 245017
|   |   |   start <= 278767
|   |   |   |   start <= 248564: sce04111 (9.95)
|   |   |   |   start > 248564
|   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   distance <= 2075: sce00020 (22.51/13.03)
|   |   |   |   |   |   distance > 2075: sce00620 (4.94/1.23)
|   |   |   |   |   neigh_num > 1: sce00720 (60.61/46.96)
|   |   |   start > 278767
|   |   |   |   strand = C: sce00010 (62.18/42.08)
|   |   |   |   strand = W
|   |   |   |   |   start <= 284674: sce00190 (15.35)
|   |   |   |   |   start > 284674
|   |   |   |   |   |   start <= 314456: sce00240 (21.0/8.01)
|   |   |   |   |   |   start > 314456: sce04010 (8.7)
start > 327131
```

```
|   strand = C
|   |   start <= 425518
|   |   |   start <= 389526
|   |   |   |   start <= 353137: sce04070 (46.96/28.58)
|   |   |   |   start > 353137
|   |   |   |   |   start <= 385401: sce00620 (13.88)
|   |   |   |   |   start > 385401: sce00590 (27.43/9.76)
|   |   |   start > 389526
|   |   |   |   start <= 392783: sce00240 (14.95)
|   |   |   |   start > 392783
|   |   |   |   |   start <= 396891: sce04111 (34.29/15.85)
|   |   |   |   |   start > 396891
|   |   |   |   |   |   start <= 407632: sce00190 (19.85)
|   |   |   |   |   |   start > 407632: sce04120 (13.57)
|   |   start > 425518
|   |   |   start <= 456697
|   |   |   |   start <= 439028
|   |   |   |   |   start <= 431549
|   |   |   |   |   |   start <= 428194: sce00600 (19.28)
|   |   |   |   |   |   start > 428194: sce04130 (14.24)
|   |   |   |   |   start > 431549: sce00450 (36.12/19.5)
|   |   |   |   start > 439028
|   |   |   |   |   neigh_strand = W: sce00632 (98.89/83.78)
|   |   |   |   |   neigh_strand = C: sce00624 (69.53/54.99)
|   |   |   start > 456697
|   |   |   |   start <= 506037: sce00565 (38.33/17.96)
|   |   |   |   start > 506037
|   |   |   |   |   start <= 571254: sce00600 (16.97)
|   |   |   |   |   start > 571254: sce03010 (16.37)
|   strand = W
|   |   start <= 559308
|   |   |   start <= 353137
|   |   |   |   start <= 329810: sce03022 (23.87)
|   |   |   |   start > 329810: sce03030 (48.11/28.26)
|   |   |   start > 353137
|   |   |   |   start <= 369534
|   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   distance <= 1705: sce00040 (9.47/4.05)
|   |   |   |   |   |   distance > 1705: sce00500 (17.22/6.31)
|   |   |   |   |   neigh_strand = C: sce00040 (13.39/6.88)
|   |   |   |   start > 369534
|   |   |   |   |   start <= 551299
|   |   |   |   |   |   start <= 407632: sce03022 (15.59)
|   |   |   |   |   |   start > 407632: sce03010 (34.69)
|   |   |   |   |   start > 551299: sce03022 (16.33)
|   |   start > 559308
|   |   |   start <= 619447
|   |   |   |   start <= 571254: sce00860 (19.95)
|   |   |   |   start > 571254
|   |   |   |   |   start <= 590037: sce00670 (17.59)
|   |   |   |   |   start > 590037: sce04010 (17.03)
|   |   |   start > 619447: sce00620 (61.31/37.4)
```

Decision Tree Generated for Chromosome Twelve:

```
start <= 487290
|   start <= 286560
|   |   strand = C
|   |   |   start <= 198086
|   |   |   |   start <= 166536
|   |   |   |   |   start <= 80204
|   |   |   |   |   |   start <= 52589
|   |   |   |   |   |   |   start <= 48628: sce03010 (18.25)
|   |   |   |   |   |   |   start > 48628: sce04140 (16.62)
|   |   |   |   |   |   start > 52589
|   |   |   |   |   |   |   start <= 53930: sce00020 (36.43/13.81)
|   |   |   |   |   |   |   start > 53930: sce00563 (21.82/6.09)
|   |   |   |   |   start > 80204
|   |   |   |   |   |   start <= 111574
|   |   |   |   |   |   |   neigh_strand = W: sce00252 (8.96/2.09)
|   |   |   |   |   |   |   neigh_strand = C: sce00970 (24.33/9.88)
|   |   |   |   |   |   start > 111574
|   |   |   |   |   |   |   start <= 141072: sce00190 (17.16)
|   |   |   |   |   |   |   start > 141072: sce04010 (29.47/9.66)
|   |   |   |   start > 166536
|   |   |   |   |   start <= 196473: sce04130 (22.21)
|   |   |   |   |   start > 196473
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00350
(15.89/10.98)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00350 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_
|   |   |   |   |   |   |   neigh_strand = W: sce00252 (11.19/5.81)
|   |   |   |   |   |   |   neigh_strand = C: sce00350 (8.78/7.08)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00401 (13.86/8.36)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00350
(8.06/5.86)
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00710 (11.05/7.68)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_
|   |   |   |   |   |   |   neigh_strand = W: sce00401 (11.29/8.68)
|   |   |   |   |   |   |   neigh_strand = C: sce00272 (7.33/5.78)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00350
(12.02/7.26)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00710 (8.99/5.61)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00350 (8.92/6.39)
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00350 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00272
(19.73/15.34)
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00350
(0.0)
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00350 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00350 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00350
(0.0)
|   |   |   start > 198086
|   |   |   |   start <= 242233
|   |   |   |   |   start <= 201316
|   |   |   |   |   |   neigh_strand = W: sce00230 (14.61/6.0)
|   |   |   |   |   |   neigh_strand = C: sce00670 (19.8/8.84)
|   |   |   |   |   start > 201316
|   |   |   |   |   |   start <= 204992: sce03010 (20.3)
|   |   |   |   |   |   start > 204992
|   |   |   |   |   |   |   start <= 225173: sce00190 (14.9)
|   |   |   |   |   |   |   start > 225173: sce00010 (10.14)
|   |   |   |   start > 242233
|   |   |   |   |   start <= 267170: sce00680 (92.53/68.4)
|   |   |   |   |   start > 267170
|   |   |   |   |   |   start <= 275212: sce00040 (14.15)
|   |   |   |   |   |   start > 275212: sce04130 (11.45)
|   |   strand = W
|   |   |   start <= 253862
|   |   |   |   start <= 160048
|   |   |   |   |   start <= 141072: sce04111 (15.81)
|   |   |   |   |   start > 141072: sce03022 (11.27)
|   |   |   |   start > 160048
|   |   |   |   |   start <= 242233
|   |   |   |   |   |   start <= 166536: sce03010 (17.24)
|   |   |   |   |   |   start > 166536
|   |   |   |   |   |   |   start <= 204992: sce00500 (39.18/9.94)
|   |   |   |   |   |   |   start > 204992: sce03010 (9.13)
|   |   |   |   |   start > 242233: sce00100 (20.81)
|   |   |   start > 253862
|   |   |   |   start <= 260980: sce00970 (25.94/10.66)
|   |   |   |   start > 260980
|   |   |   |   |   start <= 263195: sce03010 (16.85)
|   |   |   |   |   start > 263195
|   |   |   |   |   |   start <= 267170: sce00780 (43.9/20.94)
|   |   |   |   |   |   start > 267170: sce03010 (14.1)
|   start > 286560
|   |   start <= 408446
|   |   |   strand = C
|   |   |   |   start <= 320016: sce00251 (51.29/29.65)
|   |   |   |   start > 320016: sce04111 (86.41/38.36)
|   |   |   strand = W
|   |   |   |   start <= 320016
|   |   |   |   |   start <= 302244: sce04111 (36.94)
|   |   |   |   |   start > 302244: sce00563 (24.79)
|   |   |   |   start > 320016
|   |   |   |   |   start <= 371621
|   |   |   |   |   |   start <= 345942: sce00100 (13.19)
|   |   |   |   |   |   start > 345942: sce04010 (6.03)
|   |   |   |   |   start > 371621: sce00260 (33.24/14.85)
|   |   |   strand = N: sce04111 (0.0)
|   |   start > 408446
|   |   |   start <= 447576
|   |   |   |   start <= 433726
```

```
|   |   |   |   |   strand = C: sce00220 (28.52/10.38)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 410724: sce00010 (14.75)
|   |   |   |   |   |   start > 410724: sce00330 (18.67)
|   |   |   |   |   strand = N: sce00330 (0.0)
|   |   |   |   start > 433726
|   |   |   |   |   neigh_num <= 1: sce00010 (7.72/2.71)
|   |   |   |   |   neigh_num > 1: sce00620 (33.5/21.55)
|   |   |   start > 447576
|   |   |   |   neigh_GO_term = cellular_component_
|   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   start <= 474058: sce00460 (5.55/1.69)
|   |   |   |   |   |   start > 474058: sce00252 (11.88/5.59)
|   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   distance <= 2648: sce00252 (21.93/11.62)
|   |   |   |   |   |   distance > 2648: sce00460 (6.94/2.84)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = biological_process_
|   |   |   |   |   start <= 483638
|   |   |   |   |   |   start <= 474058: sce00910 (24.37/13.69)
|   |   |   |   |   |   start > 474058: sce00460 (12.2/5.53)
|   |   |   |   |   start > 483638: sce00910 (11.06/5.46)
|   |   |   |   neigh_GO_term = molecular_function_: sce00460
(35.19/20.22)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = transport_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00252 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = mitochondrion_: sce00910 (6.61/2.09)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00252 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00910 (11.8/7.11)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00252 (21.37/12.7)
```

```
|   |   |   |   neigh_GO_term = translation_: sce00252 (18.83/11.05)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00252 (2.3/0.91)
|   |   |   |   neigh_GO_term = electron_transport_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = nucleus_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00252
(0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00252
(0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00252 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00252 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00252
(0.0)
```

```
|   |   |   |   neigh_GO_term = ligase_activity_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00910
(3.18/1.77)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00252 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00252 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00252 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00252
(0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00252 (0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00252 (0.0)
start > 487290
|   start <= 809997
|   |   strand = C
|   |   |   start <= 626932
|   |   |   |   start <= 562010: sce00760 (69.93/43.78)
|   |   |   |   start > 562010
|   |   |   |   |   start <= 604789: sce04010 (17.99)
|   |   |   |   |   start > 604789
|   |   |   |   |   |   start <= 617535: sce00785 (27.08)
|   |   |   |   |   |   start > 617535: sce00240 (12.51)
|   |   |   start > 626932
|   |   |   |   start <= 728957
|   |   |   |   |   start <= 696832
|   |   |   |   |   |   start <= 691557: sce04111 (14.18)
|   |   |   |   |   |   start > 691557
|   |   |   |   |   |   |   neigh_num <= 1: sce00500 (7.82/2.35)
|   |   |   |   |   |   |   neigh_num > 1: sce00790 (16.29/7.35)
|   |   |   |   |   start > 696832
|   |   |   |   |   |   start <= 713160
|   |   |   |   |   |   |   start <= 710138: sce00530 (10.96)
|   |   |   |   |   |   |   start > 710138: sce03010 (9.53)
|   |   |   |   |   |   start > 713160
|   |   |   |   |   |   |   start <= 714906: sce04111 (12.81)
|   |   |   |   |   |   |   start > 714906: sce00190 (11.69)
|   |   |   |   start > 728957
|   |   |   |   |   start <= 737550: sce00020 (45.7/28.89)
|   |   |   |   |   start > 737550
|   |   |   |   |   |   start <= 747939
|   |   |   |   |   |   |   neigh_strand = W: sce04070 (14.39/4.6)
|   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   neigh_num <= 1: sce04070 (4.65/1.09)
```

```
|   |   |   |   |   |   |   |   neigh_num > 1: sce00562 (22.47/6.19)
|   |   |   |   |   |   start > 747939: sce03010 (26.73)
|   |   strand = W
|   |   |   start <= 696832
|   |   |   |   start <= 515264
|   |   |   |   |   start <= 504593
|   |   |   |   |   |   start <= 498949
|   |   |   |   |   |   |   start <= 493885: sce00190 (30.13/12.42)
|   |   |   |   |   |   |   start > 493885: sce03010 (10.72)
|   |   |   |   |   |   start > 498949: sce00480 (61.98/37.38)
|   |   |   |   |   start > 504593: sce00450 (37.83/17.98)
|   |   |   |   start > 515264
|   |   |   |   |   start <= 626932
|   |   |   |   |   |   start <= 562010
|   |   |   |   |   |   |   start <= 517942
|   |   |   |   |   |   |   |   neigh_num <= 1: sce04111
(10.69/4.25)
|   |   |   |   |   |   |   |   neigh_num > 1: sce04010 (18.41/2.66)
|   |   |   |   |   |   |   start > 517942
|   |   |   |   |   |   |   |   start <= 522665: sce03010 (14.75)
|   |   |   |   |   |   |   |   start > 522665: sce04111 (14.65)
|   |   |   |   |   |   start > 562010
|   |   |   |   |   |   |   neigh_num <= 1: sce04140 (22.7/9.87)
|   |   |   |   |   |   |   neigh_num > 1: sce04070 (27.19/14.9)
|   |   |   |   |   start > 626932
|   |   |   |   |   |   start <= 673133
|   |   |   |   |   |   |   start <= 665846
|   |   |   |   |   |   |   |   start <= 660718: sce00500 (14.45)
|   |   |   |   |   |   |   |   start > 660718: sce00600 (14.67)
|   |   |   |   |   |   |   start > 665846: sce03010 (22.59)
|   |   |   |   |   |   start > 673133
|   |   |   |   |   |   |   start <= 680202: sce04130 (13.88)
|   |   |   |   |   |   |   start > 680202: sce04111 (17.38)
|   |   |   start > 696832
|   |   |   |   start <= 737550
|   |   |   |   |   start <= 726071
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00590 (7.37/3.81)
|   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00450 (6.29/3.6)
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00460 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00460
(14.5/9.26)
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00480 (5.55/3.72)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00590
(6.15/4.37)
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00480
(6.18/3.95)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00460 (9.01/6.33)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00460 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00430 (9.9/7.41)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00450
(4.82/3.34)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00460
(0.0)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00460
(0.0)
```

```
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00460 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00460
(0.0)
|   |   |   |   |   start > 726071
|   |   |   |   |   |   start <= 728957: sce00500 (12.87)
|   |   |   |   |   |   start > 728957: sce00920 (37.1/24.36)
|   |   |   |   start > 737550
|   |   |   |   |   start <= 784913
|   |   |   |   |   |   start <= 744153: sce04120 (19.21)
|   |   |   |   |   |   start > 744153
|   |   |   |   |   |   |   start <= 747939: sce00530 (33.05)
|   |   |   |   |   |   |   start > 747939: sce00760 (16.91)
|   |   |   |   |   start > 784913
|   |   |   |   |   |   distance <= 2504: sce03010 (14.82/2.26)
|   |   |   |   |   |   distance > 2504: sce04010 (45.87/14.86)
|   start > 809997
|   |   strand = C
|   |   |   start <= 874791
|   |   |   |   start <= 856441
|   |   |   |   |   start <= 837356: sce00030 (22.9)
|   |   |   |   |   start > 837356
|   |   |   |   |   |   distance <= 4218
|   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   distance <= 2662: sce00290
(9.97/3.31)
|   |   |   |   |   |   |   |   distance > 2662: sce00770
(15.91/4.74)
|   |   |   |   |   |   |   neigh_strand = C: sce00770 (9.86/1.68)
|   |   |   |   |   |   distance > 4218: sce00290 (4.06/0.01)
|   |   |   |   start > 856441: sce00010 (91.99/61.46)
|   |   |   start > 874791
|   |   |   |   start <= 884751
|   |   |   |   |   start <= 877177: sce03060 (11.07)
|   |   |   |   |   start > 877177: sce00290 (45.19/15.78)
|   |   |   |   start > 884751
|   |   |   |   |   start <= 909965: sce00190 (16.29)
|   |   |   |   |   start > 909965
|   |   |   |   |   |   start <= 1018905
|   |   |   |   |   |   |   start <= 973167
|   |   |   |   |   |   |   |   start <= 931754: sce03010 (12.74)
|   |   |   |   |   |   |   |   start > 931754: sce04140 (21.19)
|   |   |   |   |   |   |   start > 973167: sce03010 (13.26)
|   |   |   |   |   |   start > 1018905: sce00190 (13.35)
|   |   strand = W
|   |   |   start <= 1028850
|   |   |   |   start <= 877177
```

```
|   |   |   |   |   start <= 856441
|   |   |   |   |   |   start <= 844281
|   |   |   |   |   |   |   start <= 819312: sce03010 (10.75)
|   |   |   |   |   |   |   start > 819312: sce00230 (36.56/16.07)
|   |   |   |   |   |   start > 844281
|   |   |   |   |   |   |   start <= 849865: sce04010 (18.07)
|   |   |   |   |   |   |   start > 849865: sce03010 (3.5)
|   |   |   |   |   start > 856441: sce01040 (30.97)
|   |   |   |   start > 877177
|   |   |   |   |   start <= 1012498
|   |   |   |   |   |   start <= 973167
|   |   |   |   |   |   |   start <= 909965: sce03010 (8.51)
|   |   |   |   |   |   |   start > 909965: sce00240 (17.02)
|   |   |   |   |   |   start > 973167
|   |   |   |   |   |   |   start <= 1002554: sce00230 (12.38)
|   |   |   |   |   |   |   start > 1002554: sce00330 (7.66)
|   |   |   |   |   start > 1012498: sce03010 (38.72)
|   |   |   start > 1028850
|   |   |   |   start <= 1032624: sce00100 (18.73)
|   |   |   |   start > 1032624: sce01031 (34.24/14.78)
```

Decision Tree Generated for Chromosome Thirteen:

```
start <= 396378
|   start <= 104162
|   |   strand = C
|   |   |   start <= 20536
|   |   |   |   neigh_GO_term = mitochondrion_: sce00280 (6.42/3.2)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = biological_process_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00280
(7.97/3.61)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00280 (2.87/1.27)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_num <= 1: sce00072 (2.89/1.15)
|   |   |   |   |   neigh_num > 1: sce00650 (20.12/6.03)
|   |   |   |   neigh_GO_term = cellular_component_: sce00280
(7.21/2.55)
|   |   |   |   neigh_GO_term = nucleus_
|   |   |   |   |   distance <= 2869: sce00650 (5.9/2.69)
|   |   |   |   |   distance > 2869: sce00280 (5.45/2.3)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00650
(3.18/1.01)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00650
(0.0)
```

```
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00650
(4.58/1.71)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00072 (1.2/0.49)
|   |   |   |   neigh_GO_term = meiosis_: sce00072 (1.03/0.31)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00072
(2.87/1.88)
|   |   |   |   neigh_GO_term = transcription_: sce00650 (2.08/0.94)
|   |   |   |   neigh_GO_term = transport_: sce00072 (4.29/1.84)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce00650 (0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00650 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = translation_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00650 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00650 (0.0)
```

```
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00650 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00650
(0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00650
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00650 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = motor_activity_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00650 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00650 (0.0)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00650 (0.0)
|   |   |   start > 20536
|   |   |   |   start <= 45063
|   |   |   |   |   start <= 29807: sce00190 (17.74)
|   |   |   |   |   start > 29807: sce01030 (26.78/11.72)
|   |   |   |   start > 45063
|   |   |   |   |   start <= 70624
|   |   |   |   |   |   start <= 50954: sce00130 (17.13)
|   |   |   |   |   |   start > 50954: sce03060 (18.1)
|   |   |   |   |   start > 70624
|   |   |   |   |   |   start <= 86739: sce03050 (7.73)
|   |   |   |   |   |   start > 86739: sce00190 (12.66)
|   |   strand = W
|   |   |   start <= 70624
```

```
|   |   |   |   start <= 45063
|   |   |   |   |   neigh_strand = W: sce00632 (26.96/14.8)
|   |   |   |   |   neigh_strand = C: sce04070 (17.39/7.87)
|   |   |   |   start > 45063
|   |   |   |   |   start <= 58687: sce00240 (23.35)
|   |   |   |   |   start > 58687: sce00500 (25.27)
|   |   |   start > 70624
|   |   |   |   start <= 86739: sce03022 (14.27)
|   |   |   |   start > 86739: sce00920 (66.68/46.78)
|   start > 104162
|   |   start <= 302484
|   |   |   start <= 228937
|   |   |   |   start <= 145876
|   |   |   |   |   start <= 133475
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 118898: sce00100 (14.82)
|   |   |   |   |   |   |   start > 118898: sce03010 (8.31)
|   |   |   |   |   |   strand = W: sce00561 (16.58)
|   |   |   |   |   start > 133475: sce04111 (30.16)
|   |   |   |   start > 145876
|   |   |   |   |   start <= 146482: sce03010 (17.32)
|   |   |   |   |   start > 146482
|   |   |   |   |   |   start <= 208860
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 164176: sce00230 (16.13)
|   |   |   |   |   |   |   |   start > 164176
|   |   |   |   |   |   |   |   |   start <= 167308: sce00620
(13.58)
|   |   |   |   |   |   |   |   |   start > 167308: sce00230 (9.51)
|   |   |   |   |   |   |   strand = W: sce00252 (9.32)
|   |   |   |   |   |   start > 208860
|   |   |   |   |   |   |   start <= 225889: sce03010 (20.84)
|   |   |   |   |   |   |   start > 225889: sce00230 (12.2)
|   |   |   start > 228937
|   |   |   |   start <= 243029
|   |   |   |   |   start <= 233457: sce01030 (36.15/14.16)
|   |   |   |   |   start > 233457: sce03022 (21.41)
|   |   |   |   start > 243029
|   |   |   |   |   start <= 262685
|   |   |   |   |   |   start <= 252990: sce00100 (15.67)
|   |   |   |   |   |   start > 252990: sce04010 (44.35/20.81)
|   |   |   |   |   start > 262685
|   |   |   |   |   |   start <= 296737
|   |   |   |   |   |   |   start <= 271136: sce04111 (17.38)
|   |   |   |   |   |   |   start > 271136: sce00510 (11.3)
|   |   |   |   |   |   start > 296737: sce00100 (27.61)
|   |   start > 302484
|   |   |   start <= 321874
|   |   |   |   start <= 307488: sce04130 (23.75)
|   |   |   |   start > 307488
|   |   |   |   |   start <= 318679: sce04120 (24.93)
|   |   |   |   |   start > 318679: sce03010 (12.96)
|   |   |   start > 321874
|   |   |   |   start <= 387020
```

```
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 343519: sce04111 (17.27)
|   |   |   |   |   |   start > 343519
|   |   |   |   |   |   |   start <= 353870: sce04010 (16.25)
|   |   |   |   |   |   |   start > 353870: sce04111 (15.16)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 353870: sce04010 (13.09)
|   |   |   |   |   |   start > 353870: sce00190 (14.89)
|   |   |   |   start > 387020: sce00220 (18.79)
start > 396378
|   start <= 603081
|   |   start <= 494998
|   |   |   start <= 469475
|   |   |   |   start <= 434787
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = biological_process_
|   |   |   |   |   |   distance <= 5692: sce00071 (22.98/17.13)
|   |   |   |   |   |   distance > 5692: sce00561 (13.51/9.98)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = molecular_function_: sce00561
(39.59/31.11)
|   |   |   |   |   neigh_GO_term = cellular_component_
|   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   neigh_num <= 1: sce00561 (5.53/4.41)
|   |   |   |   |   |   |   neigh_num > 1: sce00641 (10.56/5.71)
|   |   |   |   |   |   neigh_strand = C: sce00561 (8.14/5.98)
|   |   |   |   |   neigh_GO_term = nucleus_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = meiosis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00561 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = transcription_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = transport_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = electron_transport_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = ribosome_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = translation_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00561 (0.0)
```

```
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = sporulation_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = conjugation_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cortex_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = extracellular_region_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00561
(0.0)
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = motor_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00561 (0.0)
|   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00561 (0.0)
|   |   |   |   start > 434787
|   |   |   |   |   start <= 458407: sce00750 (32.6)
|   |   |   |   |   start > 458407: sce00510 (13.38)
|   |   |   start > 469475
|   |   |   |   strand = C
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = biological_process_: sce00030
(6.11/3.33)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00010
(0.0)
```

```
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00010 (5.49/1.9)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00010
(12.08/5.14)
|   |   |   |   |   neigh_GO_term = molecular_function_: sce00500
(6.87/3.36)
|   |   |   |   |   neigh_GO_term = cellular_component_: sce00030
(8.09/4.1)
|   |   |   |   |   neigh_GO_term = nucleus_: sce00010 (12.77/8.9)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00010
(2.06/1.03)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = meiosis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = transcription_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = transport_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = electron_transport_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00030
(2.8/1.33)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00030 (3.68/1.64)
|   |   |   |   |   neigh_GO_term = ribosome_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00010 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00521
(7.22/3.76)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = translation_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = sporulation_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = conjugation_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cortex_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = extracellular_region_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00010
(0.0)
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00010 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = motor_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00010 (0.0)
|   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00010 (0.0)
|   |   |   |   strand = W
|   |   |   |   |   start <= 484083: sce00290 (68.07/48.22)
|   |   |   |   |   start > 484083: sce00790 (17.14)
|   |   start > 494998
|   |   |   start <= 574927
|   |   |   |   start <= 556474
|   |   |   |   |   start <= 509279
|   |   |   |   |   |   start <= 502733: sce00190 (26.71/11.8)
|   |   |   |   |   |   start > 502733
|   |   |   |   |   |   |   neigh_strand = W: sce00230 (10.39/3.58)
|   |   |   |   |   |   |   neigh_strand = C: sce00670 (10.37/3.88)
|   |   |   |   |   start > 509279
|   |   |   |   |   |   start <= 551927: sce03010 (24.47)
|   |   |   |   |   |   start > 551927: sce00190 (13.74)
|   |   |   |   start > 556474
|   |   |   |   |   start <= 560995: sce00510 (26.6/11.97)
|   |   |   |   |   start > 560995: sce04140 (18.35)
|   |   |   start > 574927
|   |   |   |   neigh_strand = W: sce00980 (119.99/88.63)
|   |   |   |   neigh_strand = C: sce00340 (91.92/58.96)
|   start > 603081
|   |   start <= 754219
|   |   |   start <= 712315
|   |   |   |   strand = C
|   |   |   |   |   start <= 662643: sce04130 (22.64)
|   |   |   |   |   start > 662643
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00010
(6.72/3.02)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00030 (0.61/0.28)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00030 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00051 (7.47/3.04)
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00030 (3.33/1.21)
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00010 (1.44/0.46)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00010
(8.71/2.66)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00030 (2.18/0.8)
|   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00030 (11.1/5.81)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00030 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00010
(2.73/1.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00030 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = motor_activity_: sce00030
(0.0)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00030
(7.0/1.78)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00030 (0.0)
|   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00030 (0.0)
|   |   |   |   strand = W
|   |   |   |   |   start <= 662643
|   |   |   |   |   |   start <= 637499: sce00260 (14.31)
|   |   |   |   |   |   start > 637499
|   |   |   |   |   |   |   start <= 651144: sce03010 (18.05)
|   |   |   |   |   |   |   start > 651144: sce04111 (14.07)
|   |   |   |   |   start > 662643
|   |   |   |   |   |   start <= 684466: sce00100 (29.11)
|   |   |   |   |   |   start > 684466
|   |   |   |   |   |   |   start <= 701789: sce00251 (28.4/12.16)
|   |   |   |   |   |   |   start > 701789: sce00100 (15.06)
|   |   |   start > 712315
|   |   |   |   start <= 742970
|   |   |   |   |   start <= 732413
|   |   |   |   |   |   start <= 724384: sce03022 (13.55)
|   |   |   |   |   |   start > 724384: sce03010 (29.31)
|   |   |   |   |   start > 732413: sce03022 (24.35)
|   |   |   |   start > 742970: sce03010 (12.89)
|   |   start > 754219
|   |   |   start <= 867090
|   |   |   |   strand = C
|   |   |   |   |   start <= 851590
|   |   |   |   |   |   start <= 822762
|   |   |   |   |   |   |   start <= 793368
|   |   |   |   |   |   |   |   start <= 779126: sce00190 (5.58)
|   |   |   |   |   |   |   |   start > 779126: sce00500 (17.0)
|   |   |   |   |   |   |   start > 793368: sce00240 (13.16)
|   |   |   |   |   |   start > 822762
|   |   |   |   |   |   |   neigh_num <= 1: sce00500 (20.05/4.06)
|   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   distance <= 6078: sce00790
(8.83/2.68)
|   |   |   |   |   |   |   |   distance > 6078: sce00500
(4.87/1.51)
|   |   |   |   |   start > 851590
|   |   |   |   |   |   start <= 860890
|   |   |   |   |   |   |   start <= 856792: sce00251 (32.25/13.73)
|   |   |   |   |   |   |   start > 856792: sce00600 (14.64)
|   |   |   |   |   |   start > 860890: sce00230 (37.67/17.33)
|   |   |   |   strand = W
```

```
|   |   |   |   |   start <= 779126
|   |   |   |   |   |   start <= 759806: sce00071 (13.29)
|   |   |   |   |   |   start > 759806
|   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   distance <= 1695: sce00430
(11.9/6.42)
|   |   |   |   |   |   |   |   distance > 1695: sce00251
(17.82/8.92)
|   |   |   |   |   |   |   neigh_strand = C: sce00410 (30.04/21.91)
|   |   |   |   |   start > 779126
|   |   |   |   |   |   start <= 822762
|   |   |   |   |   |   |   start <= 807547: sce00190 (19.48)
|   |   |   |   |   |   |   start > 807547: sce00051 (15.29)
|   |   |   |   |   |   start > 822762
|   |   |   |   |   |   |   start <= 832338: sce01031 (26.53/9.9)
|   |   |   |   |   |   |   start > 832338: sce03010 (14.41)
|   |   |   start > 867090
|   |   |   |   strand = C
|   |   |   |   |   start <= 869626: sce02010 (16.02)
|   |   |   |   |   start > 869626
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00980
(5.37/4.16)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00641 (9.15/7.34)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00350 (15.92/12.4)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00624
(15.48/11.14)
|   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00641 (15.95/10.0)
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00980 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00980 (4.99/3.67)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00071 (15.06/12.27)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00561 (9.11/6.38)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00561 (10.34/7.97)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00980 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = motor_activity_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00980
(0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00980 (0.0)
|   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00980 (0.0)
|   |   |   |   strand = W
|   |   |   |   |   start <= 881158: sce00500 (21.88)
|   |   |   |   |   start > 881158
```

```
|   |   |   |   |   |   start <= 901708: sce03050 (21.14)
|   |   |   |   |   |   start > 901708: sce00010 (15.62)
```

Decision Tree Generated for Chromosome Fourteen:

```
start <= 529943
|   strand = W
|   |   start <= 155101
|   |   |   start <= 140879
|   |   |   |   start <= 87897
|   |   |   |   |   start <= 82806
|   |   |   |   |   |   start <= 66517: sce03030 (12.22)
|   |   |   |   |   |   start > 66517: sce00240 (25.56)
|   |   |   |   |   start > 82806: sce04111 (20.6)
|   |   |   |   start > 87897
|   |   |   |   |   start <= 117349: sce00271 (34.33/14.59)
|   |   |   |   |   start > 117349: sce04070 (25.27/11.33)
|   |   |   start > 140879
|   |   |   |   start <= 148213: sce03030 (66.72/42.21)
|   |   |   |   start > 148213: sce04111 (27.09)
|   |   start > 155101
|   |   |   start <= 331324
|   |   |   |   start <= 237664
|   |   |   |   |   start <= 197944
|   |   |   |   |   |   start <= 164624: sce00790 (16.41)
|   |   |   |   |   |   start > 164624: sce00272 (41.19/18.07)
|   |   |   |   |   start > 197944: sce00230 (50.06/21.96)
|   |   |   |   start > 237664
|   |   |   |   |   start <= 276503: sce00530 (13.12)
|   |   |   |   |   start > 276503
|   |   |   |   |   |   start <= 302682: sce03010 (13.41)
|   |   |   |   |   |   start > 302682
|   |   |   |   |   |   |   start <= 317673: sce04120 (19.93/3.44)
|   |   |   |   |   |   |   start > 317673: sce03010 (11.59)
|   |   |   start > 331324
|   |   |   |   start <= 444317
|   |   |   |   |   start <= 406360
|   |   |   |   |   |   start <= 380833
|   |   |   |   |   |   |   start <= 352416: sce04010 (9.79)
|   |   |   |   |   |   |   start > 352416: sce00230 (8.91)
|   |   |   |   |   |   start > 380833
|   |   |   |   |   |   |   neigh_num <= 1: sce00620 (18.26/6.25)
|   |   |   |   |   |   |   neigh_num > 1: sce00630 (28.96/13.06)
|   |   |   |   |   start > 406360
|   |   |   |   |   |   start <= 413641
|   |   |   |   |   |   |   start <= 412773
|   |   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce03020
(0.77/0.35)
|   |   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce00230 (3.08/1.87)
|   |   |   |   |   |   |   |   neigh_GO_term =
DNA_metabolic_process_: sce03020 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce00230
(3.46/1.15)
|   |   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce03020 (6.33/2.82)
|   |   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00240 (7.7/3.02)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_bud_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytokinesis_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peroxisome_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transduction_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
mitochondrial_envelope_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transporter_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transport_: sce03020
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transferase_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_: sce03020
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = conjugation_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce03020
(8.39/2.28)
|   |   |   |   |   |   |   |   neigh_GO_term =
endoplasmic_reticulum_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce03020 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce03020
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = mitochondrion_:
sce00240 (4.84/1.66)
|   |   |   |   |   |   |   |   neigh_GO_term = RNA_binding_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
RNA_metabolic_process_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transcription_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = chromosome_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = DNA_binding_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce03020
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cycle_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce03020
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00230 (5.88/3.01)
|   |   |   |   |   |   |   |   neigh_GO_term = translation_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce03020
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cortex_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = sporulation_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce03020 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoplasmic_membrane-bound_vesicle_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
pseudohyphal_growth_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endomembrane_system_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_budding_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
extracellular_region_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce03020 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_respiration_: sce03020 (0.0)
|   |   |   |   |   |   |   start > 412773: sce00790 (35.93/17.95)
|   |   |   |   |   |   start > 413641: sce03030 (44.66/26.95)
|   |   |   |   start > 444317
|   |   |   |   |   start <= 495002
|   |   |   |   |   |   start <= 488387: sce00970 (24.95/8.47)
|   |   |   |   |   |   start > 488387
|   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce00620
(5.54/1.91)
|   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00010 (17.01/4.51)
|   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00010 (3.3/1.36)
|   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00252 (5.65/2.63)
```

```
|   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00620 (3.45/1.51)
|   |   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00010 (3.54/1.84)
|   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = transport_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00620 (5.04/1.29)
|   |   |   |   |   |   |   neigh_GO_term = membrane_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = conjugation_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00620
(1.05/0.27)
|   |   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00010 (0.0)
```

```
|   |   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00010
(3.44/1.32)
|   |   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00620
(4.55/0.82)
|   |   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = transcription_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = chromosome_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce00620
(3.58/1.91)
|   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = translation_: sce00252
(1.38/0.82)
|   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = sporulation_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce00010 (0.0)
```

```
|   |   |   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00010
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00010 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00010 (0.0)
|   |   |   |   |   start > 495002
|   |   |   |   |   |   start <= 499682: sce03010 (18.44)
|   |   |   |   |   |   start > 499682: sce04010 (13.42)
|   strand = C
|   |   start <= 43074
|   |   |   start <= 17248
|   |   |   |   start <= 12876: sce00750 (7.13)
|   |   |   |   start > 12876: sce00051 (77.04/59.47)
|   |   |   start > 17248: sce00400 (14.09)
|   |   start > 43074
|   |   |   start <= 302682
|   |   |   |   start <= 155101
|   |   |   |   |   start <= 57573: sce00562 (59.41/28.84)
|   |   |   |   |   start > 57573
|   |   |   |   |   |   start <= 82806: sce03010 (18.43)
|   |   |   |   |   |   start > 82806
|   |   |   |   |   |   |   start <= 106695: sce04010 (18.52)
|   |   |   |   |   |   |   start > 106695
|   |   |   |   |   |   |   |   start <= 117349: sce00100 (14.36)
|   |   |   |   |   |   |   |   start > 117349: sce04010 (14.93)
|   |   |   |   start > 155101
|   |   |   |   |   start <= 197944
|   |   |   |   |   |   start <= 182876: sce00230 (43.09/24.01)
|   |   |   |   |   |   start > 182876: sce00030 (39.03/16.84)
```

```
|   |   |   |   |   start > 197944
|   |   |   |   |   |   start <= 237664: sce01030 (38.01/16.32)
|   |   |   |   |   |   start > 237664: sce04070 (37.67/19.01)
|   |   |   start > 302682
|   |   |   |   start <= 380833
|   |   |   |   |   start <= 359598
|   |   |   |   |   |   start <= 331324: sce00564 (24.65/10.45)
|   |   |   |   |   |   start > 331324: sce00230 (42.27/22.06)
|   |   |   |   |   start > 359598
|   |   |   |   |   |   distance <= 333: sce00565 (3.82/0.27)
|   |   |   |   |   |   distance > 333: sce00564 (34.96/20.54)
|   |   |   |   start > 380833
|   |   |   |   |   start <= 430089
|   |   |   |   |   |   start <= 424497: sce04070 (24.84/10.58)
|   |   |   |   |   |   start > 424497: sce00620 (26.0/10.97)
|   |   |   |   |   start > 430089
|   |   |   |   |   |   start <= 440572: sce04010 (19.46)
|   |   |   |   |   |   start > 440572: sce03010 (19.6)
start > 529943
|   start <= 678801
|   |   strand = W
|   |   |   start <= 559003
|   |   |   |   start <= 538174
|   |   |   |   |   start <= 531726: sce00190 (17.31)
|   |   |   |   |   start > 531726: sce01030 (45.77/20.2)
|   |   |   |   start > 538174
|   |   |   |   |   start <= 542964: sce00590 (21.54)
|   |   |   |   |   start > 542964: sce01031 (38.98/16.68)
|   |   |   start > 559003
|   |   |   |   start <= 640398
|   |   |   |   |   start <= 627144: sce00720 (66.28/38.98)
|   |   |   |   |   start > 627144: sce00561 (22.81)
|   |   |   |   start > 640398
|   |   |   |   |   start <= 674925
|   |   |   |   |   |   start <= 665341
|   |   |   |   |   |   |   start <= 647434: sce00240 (13.47)
|   |   |   |   |   |   |   start > 647434: sce00120 (18.38)
|   |   |   |   |   |   start > 665341: sce00750 (15.52)
|   |   |   |   |   start > 674925: sce00510 (45.79/20.29)
|   |   strand = C
|   |   |   start <= 631063
|   |   |   |   start <= 627144
|   |   |   |   |   start <= 559003: sce00020 (17.03)
|   |   |   |   |   start > 559003: sce03010 (14.26)
|   |   |   |   start > 627144: sce00020 (22.1/9.23)
|   |   |   start > 631063
|   |   |   |   start <= 635299: sce00230 (41.24/24.68)
|   |   |   |   start > 635299
|   |   |   |   |   start <= 647434: sce04140 (17.94)
|   |   |   |   |   start > 647434: sce00620 (28.14/11.15)
|   start > 678801
|   |   start <= 690323
|   |   |   strand = W
|   |   |   |   start <= 687637: sce00790 (18.83)
```

```
|   |   |   |   start > 687637: sce00030 (27.2)
|   |   |   strand = C
|   |   |   |   neigh_GO_term = nucleus_: sce00632 (9.06/4.9)
|   |   |   |   neigh_GO_term = helicase_activity_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   distance <= 4717: sce00632 (5.8/3.79)
|   |   |   |   |   distance > 4717: sce04070 (9.81/5.84)
|   |   |   |   neigh_GO_term = biological_process_: sce04070
(4.87/3.13)
|   |   |   |   neigh_GO_term = cellular_component_: sce04070
(5.06/2.75)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_
|   |   |   |   |   distance <= 3468: sce00632 (5.27/1.47)
|   |   |   |   |   distance > 3468: sce04070 (6.11/3.5)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce04010
(0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = transport_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce04010
(5.49/3.08)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce04010 (8.65/4.8)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce04010
(9.07/4.91)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce04010 (0.0)
```

```
|   |   |   |   neigh_GO_term = mitochondrion_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = lyase_activity_: sce04010 (0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = chromosome_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = translation_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce04010
(0.0)
|   |   |   |   neigh_GO_term = cytoplasmic_membrane-bound_vesicle_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00562 (3.13/1.76)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce04010 (0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce04010 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce04010 (0.0)
```

```
|   |   |   |   neigh_GO_term = extracellular_region_: sce04010
(0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce04010 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce04010
(0.0)
|   |   start > 690323
|   |   |   start <= 715390
|   |   |   |   strand = W: sce00100 (17.78)
|   |   |   |   strand = C
|   |   |   |   |   start <= 701897: sce00130 (17.88)
|   |   |   |   |   start > 701897: sce00300 (34.24/17.08)
|   |   |   start > 715390
|   |   |   |   start <= 734291: sce00780 (27.79)
|   |   |   |   start > 734291: sce00051 (29.27/19.18)
```

Decision Tree Generated for Chromosome Fifteen:

```
start <= 525279
|   start <= 263476
|   |   strand = C
|   |   |   start <= 137825
|   |   |   |   start <= 82920
|   |   |   |   |   start <= 70325
|   |   |   |   |   |   start <= 58759
|   |   |   |   |   |   |   start <= 24293: sce00500 (14.0)
|   |   |   |   |   |   |   start > 24293: sce00740 (25.15)
|   |   |   |   |   |   start > 58759: sce00051 (15.64)
|   |   |   |   |   start > 70325: sce00020 (75.42/57.15)
|   |   |   |   start > 82920
|   |   |   |   |   start <= 101475: sce03010 (40.54)
|   |   |   |   |   start > 101475
|   |   |   |   |   |   start <= 115808: sce04010 (8.09)
|   |   |   |   |   |   start > 115808: sce00970 (38.31/18.21)
|   |   |   start > 137825
|   |   |   |   start <= 160594
|   |   |   |   |   start <= 139045: sce00130 (12.76)
|   |   |   |   |   start > 139045: sce00071 (88.25/72.05)
|   |   |   |   start > 160594
|   |   |   |   |   start <= 212244
|   |   |   |   |   |   start <= 205885: sce00562 (32.39/12.48)
|   |   |   |   |   |   start > 205885: sce00920 (19.02)
|   |   |   |   |   start > 212244
|   |   |   |   |   |   start <= 226074: sce00730 (19.99)
|   |   |   |   |   |   start > 226074
|   |   |   |   |   |   |   start <= 238618: sce00220 (31.58/15.73)
|   |   |   |   |   |   |   start > 238618: sce03010 (16.64)
|   |   strand = W
|   |   |   start <= 226074
|   |   |   |   start <= 185438
|   |   |   |   |   start <= 70325
|   |   |   |   |   |   start <= 58759: sce00220 (18.44)
```

```
|   |   |   |   |   |   start > 58759: sce04111 (36.65/18.18)
|   |   |   |   |   start > 70325
|   |   |   |   |   |   start <= 139045
|   |   |   |   |   |   |   start <= 82920: sce03010 (12.08)
|   |   |   |   |   |   |   start > 82920: sce03030 (10.63)
|   |   |   |   |   |   start > 139045: sce00190 (16.2)
|   |   |   |   start > 185438
|   |   |   |   |   start <= 217126
|   |   |   |   |   |   start <= 212244: sce00230 (30.73/11.73)
|   |   |   |   |   |   start > 212244: sce00564 (20.87)
|   |   |   |   |   start > 217126: sce00220 (44.68/25.58)
|   |   |   start > 226074
|   |   |   |   start <= 254296
|   |   |   |   |   start <= 238618: sce00480 (41.84/20.76)
|   |   |   |   |   start > 238618: sce03010 (14.76)
|   |   |   |   start > 254296
|   |   |   |   |   start <= 255336: sce03050 (12.22)
|   |   |   |   |   start > 255336: sce00970 (49.43/26.71)
|   start > 263476
|   |   strand = C
|   |   |   start <= 415908
|   |   |   |   start <= 325250
|   |   |   |   |   start <= 303036
|   |   |   |   |   |   start <= 292075: sce04130 (19.35)
|   |   |   |   |   |   start > 292075: sce04120 (15.92)
|   |   |   |   |   start > 303036: sce00240 (46.53/29.3)
|   |   |   |   start > 325250
|   |   |   |   |   start <= 342415: sce04010 (7.14)
|   |   |   |   |   start > 342415
|   |   |   |   |   |   neigh_num <= 1: sce00790 (9.41/3.73)
|   |   |   |   |   |   neigh_num > 1: sce00500 (21.28/6.34)
|   |   |   start > 415908
|   |   |   |   start <= 482035
|   |   |   |   |   start <= 453464: sce00510 (37.94/16.3)
|   |   |   |   |   start > 453464: sce00240 (31.98/13.18)
|   |   |   |   start > 482035
|   |   |   |   |   start <= 505795: sce00030 (44.7/21.91)
|   |   |   |   |   start > 505795
|   |   |   |   |   |   neigh_strand = W: sce00510 (22.35/6.73)
|   |   |   |   |   |   neigh_strand = C: sce01030 (8.44/2.54)
|   |   strand = W
|   |   |   start <= 379781
|   |   |   |   start <= 342415
|   |   |   |   |   start <= 325250: sce04111 (21.5)
|   |   |   |   |   start > 325250: sce01030 (29.4/9.49)
|   |   |   |   start > 342415: sce04111 (23.7)
|   |   |   start > 379781
|   |   |   |   start <= 519122
|   |   |   |   |   start <= 415908
|   |   |   |   |   |   start <= 400348: sce04130 (11.81)
|   |   |   |   |   |   start > 400348: sce00620 (21.57)
|   |   |   |   |   start > 415908
|   |   |   |   |   |   start <= 453464
|   |   |   |   |   |   |   start <= 444688: sce03010 (20.55)
```

```
|   |   |   |   |   |   |   start > 444688: sce00190 (19.82)
|   |   |   |   |   |   start > 453464
|   |   |   |   |   |   |   start <= 482035
|   |   |   |   |   |   |   |   start <= 468214: sce04130 (20.07)
|   |   |   |   |   |   |   |   start > 468214: sce00510
(16.31/5.94)
|   |   |   |   |   |   |   start > 482035
|   |   |   |   |   |   |   |   start <= 505795: sce03010 (22.56)
|   |   |   |   |   |   |   |   start > 505795: sce04130 (20.53)
|   |   |   |   start > 519122: sce04070 (30.6/12.44)
start > 525279
|   strand = C
|   |   start <= 761266
|   |   |   start <= 690696
|   |   |   |   start <= 616672
|   |   |   |   |   start <= 602343
|   |   |   |   |   |   start <= 580251
|   |   |   |   |   |   |   start <= 551115: sce00240 (44.93/28.01)
|   |   |   |   |   |   |   start > 551115
|   |   |   |   |   |   |   |   start <= 559732: sce00130 (9.3)
|   |   |   |   |   |   |   |   start > 559732: sce00230 (15.56)
|   |   |   |   |   |   start > 580251: sce00730 (14.04)
|   |   |   |   |   start > 602343
|   |   |   |   |   |   start <= 611389: sce01031 (19.0)
|   |   |   |   |   |   start > 611389: sce00230 (54.16/30.09)
|   |   |   |   start > 616672
|   |   |   |   |   start <= 631752: sce03050 (21.44)
|   |   |   |   |   start > 631752
|   |   |   |   |   |   start <= 662402
|   |   |   |   |   |   |   start <= 649304: sce03010 (14.08)
|   |   |   |   |   |   |   start > 649304: sce00600 (9.66)
|   |   |   |   |   |   start > 662402: sce03010 (21.91)
|   |   |   start > 690696
|   |   |   |   start <= 721947
|   |   |   |   |   start <= 716838
|   |   |   |   |   |   start <= 712544: sce03022 (16.16)
|   |   |   |   |   |   start > 712544: sce00785 (15.2)
|   |   |   |   |   start > 716838
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00450 (2.27/1.67)
|   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00340 (9.86/6.51)
|   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00440 (12.17/8.25)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00380 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00380
(8.38/5.01)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00340
(3.1/1.63)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00380 (10.29/6.45)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00380 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00350
(6.48/4.11)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00340 (4.62/2.75)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00440
(5.5/2.98)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00380 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00380 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00380
(0.0)
|   |   |   |   |   |   neigh_GO_term = motor_activity_: sce00380
(0.0)
|   |   |   |   start > 721947
|   |   |   |   |   start <= 733458
|   |   |   |   |   |   neigh_strand = W: sce03020 (33.3/15.87)
|   |   |   |   |   |   neigh_strand = C: sce00230 (19.55/10.27)
|   |   |   |   |   start > 733458
|   |   |   |   |   |   start <= 742911: sce00760 (17.65)
|   |   |   |   |   |   start > 742911: sce00230 (39.56/25.99)
|   |   start > 761266
|   |   |   start <= 958829
|   |   |   |   start <= 909340
|   |   |   |   |   start <= 800732
|   |   |   |   |   |   start <= 786996: sce03010 (6.31)
|   |   |   |   |   |   start > 786996: sce04111 (30.47/15.06)
|   |   |   |   |   start > 800732
|   |   |   |   |   |   start <= 816931: sce03050 (41.1)
|   |   |   |   |   |   start > 816931
|   |   |   |   |   |   |   start <= 842816: sce00190 (16.36)
|   |   |   |   |   |   |   start > 842816: sce03010 (16.76)
|   |   |   |   start > 909340
|   |   |   |   |   start <= 943653
|   |   |   |   |   |   start <= 922902: sce00220 (13.92)
|   |   |   |   |   |   start > 922902
|   |   |   |   |   |   |   start <= 931078: sce04130 (15.66)
|   |   |   |   |   |   |   start > 931078: sce03030 (11.77)
|   |   |   |   |   start > 943653
|   |   |   |   |   |   start <= 949106
|   |   |   |   |   |   |   distance <= 3516: sce00970 (9.29/2.2)
|   |   |   |   |   |   |   distance > 3516: sce00252 (24.08/6.05)
|   |   |   |   |   |   start > 949106: sce04120 (20.55)
|   |   |   start > 958829
|   |   |   |   start <= 1014819
|   |   |   |   |   start <= 960984: sce00240 (44.51/28.16)
|   |   |   |   |   start > 960984
|   |   |   |   |   |   start <= 986459: sce00010 (61.6/42.17)
|   |   |   |   |   |   start > 986459: sce00230 (9.59)
|   |   |   |   start > 1014819
|   |   |   |   |   start <= 1028623
```

```
|   |   |   |   |   |   start <= 1018744: sce03050 (15.7)
|   |   |   |   |   |   start > 1018744: sce03010 (20.97)
|   |   |   |   |   start > 1028623
|   |   |   |   |   |   start <= 1043040
|   |   |   |   |   |   |   distance <= 3353: sce00251 (19.03/5.61)
|   |   |   |   |   |   |   distance > 3353: sce00910 (7.53/2.86)
|   |   |   |   |   |   start > 1043040: sce00680 (31.76/14.78)
|   strand = W
|   |   start <= 960984
|   |   |   start <= 690696
|   |   |   |   start <= 616672
|   |   |   |   |   start <= 559732
|   |   |   |   |   |   start <= 545030: sce03050 (13.96)
|   |   |   |   |   |   start > 545030
|   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00650 (6.87/4.48)
|   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00650 (4.59/2.39)
|   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00120 (5.36/3.43)
|   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = membrane_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = transport_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00120
(17.16/8.91)
|   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce00120
(12.4/8.7)
|   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce00310 (14.46/8.09)
|   |   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00120 (0.0)
```

```
|   |   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = chromosome_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = transcription_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00051 (14.82/7.84)
|   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = translation_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00260
(6.53/4.23)
|   |   |   |   |   |   |   neigh_GO_term = sporulation_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce00650 (4.4/2.13)
|   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = conjugation_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00120
(0.0)
```

```
|   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00260 (5.68/3.56)
|   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00120 (0.0)
```

```
|   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00120 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00120
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce00120 (0.0)
|   |   |   |   |   start > 559732: sce00020 (64.12/24.17)
|   |   |   |   start > 616672
|   |   |   |   |   start <= 653885
|   |   |   |   |   |   start <= 642742
|   |   |   |   |   |   |   neigh_num <= 1: sce00790 (10.76/2.87)
|   |   |   |   |   |   |   neigh_num > 1: sce00500 (21.89/6.95)
|   |   |   |   |   |   start > 642742
|   |   |   |   |   |   |   neigh_strand = W: sce00251 (10.34/3.42)
|   |   |   |   |   |   |   neigh_strand = C: sce00970 (7.85/2.57)
|   |   |   |   |   start > 653885
|   |   |   |   |   |   start <= 662402: sce00860 (13.68)
|   |   |   |   |   |   start > 662402
|   |   |   |   |   |   |   start <= 679358
|   |   |   |   |   |   |   |   neigh_strand = W: sce00260
(18.38/6.09)
|   |   |   |   |   |   |   |   neigh_strand = C: sce00750
(19.68/7.97)
|   |   |   |   |   |   |   start > 679358: sce00500 (11.24)
|   |   |   start > 690696
|   |   |   |   start <= 813708
|   |   |   |   |   start <= 738321
|   |   |   |   |   |   start <= 721947: sce00340 (9.96)
|   |   |   |   |   |   start > 721947: sce00240 (63.74/35.9)
|   |   |   |   |   start > 738321
|   |   |   |   |   |   start <= 772602: sce04010 (33.41)
|   |   |   |   |   |   start > 772602
|   |   |   |   |   |   |   start <= 780907
|   |   |   |   |   |   |   |   neigh_num <= 1: sce00670 (12.47/3.7)
|   |   |   |   |   |   |   |   neigh_num > 1: sce00790 (11.92/4.92)
|   |   |   |   |   |   |   start > 780907: sce00790 (10.99)
|   |   |   |   start > 813708
|   |   |   |   |   start <= 882897
|   |   |   |   |   |   start <= 867097
|   |   |   |   |   |   |   start <= 842816: sce00860 (19.0)
|   |   |   |   |   |   |   start > 842816: sce03010 (13.52)
|   |   |   |   |   |   start > 867097: sce00251 (44.91/14.91)
|   |   |   |   |   start > 882897
|   |   |   |   |   |   start <= 949106
|   |   |   |   |   |   |   start <= 922902: sce00071 (10.59)
|   |   |   |   |   |   |   start > 922902: sce00190 (11.27)
|   |   |   |   |   |   start > 949106: sce00230 (49.09/28.36)
|   |   start > 960984
|   |   |   start <= 1028623
|   |   |   |   start <= 986459: sce03030 (7.42)
|   |   |   |   start > 986459: sce04111 (18.18)
|   |   |   start > 1028623
```

```
|   |   |   |   start <= 1043040
|   |   |   |   |   neigh_GO_term = cellular_component_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = molecular_function_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = biological_process_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00650 (31.81/27.64)
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = transport_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00620
(14.39/12.56)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cytoplasmic_membrane-
bound_vesicle_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = extracellular_region_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = nucleus_
|   |   |   |   |   |   neigh_num <= 1: sce00903 (22.93/17.49)
|   |   |   |   |   |   neigh_num > 1: sce00310 (21.97/15.67)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00340 (20.57/17.1)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = transcription_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00903 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = ribosome_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = translation_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00120 (16.67/10.93)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00280
(26.97/23.02)
|   |   |   |   |   neigh_GO_term = sporulation_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = conjugation_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00071 (13.86/11.96)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00340 (19.2/16.77)
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = meiosis_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00071 (17.95/14.98)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00903 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = electron_transport_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00903
(0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cell_cortex_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00903 (0.0)
|   |   |   |   |   neigh_GO_term = motor_activity_: sce00903 (0.0)
|   |   |   |   start > 1043040: sce00010 (14.11)
```

Decision Tree Generated for Chromosome Sixteen:

```
start <= 568993
|   start <= 423889
|   |   start <= 179276
|   |   |   strand = W
|   |   |   |   start <= 103232
|   |   |   |   |   start <= 66614
|   |   |   |   |   |   start <= 35236
|   |   |   |   |   |   |   start <= 30079: sce00190 (18.68)
|   |   |   |   |   |   |   start > 30079: sce00562 (31.18/12.25)
|   |   |   |   |   |   start > 35236
|   |   |   |   |   |   |   neigh_num <= 1: sce00720 (7.31/3.3)
|   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   distance <= 1808: sce00020
(4.58/0.43)
|   |   |   |   |   |   |   |   distance > 1808: sce00720
(7.22/1.75)
|   |   |   |   |   start > 66614
|   |   |   |   |   |   start <= 88517: sce03060 (15.86)
|   |   |   |   |   |   start > 88517: sce00500 (35.77/17.09)
|   |   |   |   start > 103232
|   |   |   |   |   start <= 121167
|   |   |   |   |   |   start <= 107275: sce04130 (17.67)
|   |   |   |   |   |   start > 107275: sce01040 (55.67/17.86)
|   |   |   |   |   start > 121167
|   |   |   |   |   |   start <= 173151: sce03010 (26.69)
```

```
|   |   |   |   |   |   start > 173151: sce04111 (13.74)
|   |   |   strand = C
|   |   |   |   start <= 150190
|   |   |   |   |   start <= 88517
|   |   |   |   |   |   start <= 55153: sce00730 (16.77)
|   |   |   |   |   |   start > 55153
|   |   |   |   |   |   |   start <= 66614: sce04111 (20.55)
|   |   |   |   |   |   |   start > 66614: sce03010 (11.45)
|   |   |   |   |   start > 88517
|   |   |   |   |   |   start <= 121167
|   |   |   |   |   |   |   start <= 108652: sce00190 (14.23)
|   |   |   |   |   |   |   start > 108652: sce00510 (16.61)
|   |   |   |   |   |   start > 121167: sce00730 (23.35)
|   |   |   |   start > 150190
|   |   |   |   |   start <= 156211: sce03060 (13.13)
|   |   |   |   |   start > 156211: sce00564 (21.09)
|   |   start > 179276
|   |   |   strand = W
|   |   |   |   start <= 328729
|   |   |   |   |   start <= 246989
|   |   |   |   |   |   start <= 225740
|   |   |   |   |   |   |   start <= 193647: sce04010 (15.67)
|   |   |   |   |   |   |   start > 193647: sce01031 (29.05/12.21)
|   |   |   |   |   |   start > 225740: sce00970 (45.55/19.15)
|   |   |   |   |   start > 246989
|   |   |   |   |   |   start <= 303120
|   |   |   |   |   |   |   start <= 271309: sce04140 (14.94)
|   |   |   |   |   |   |   start > 271309
|   |   |   |   |   |   |   |   start <= 301715
|   |   |   |   |   |   |   |   |   start <= 289033: sce03010
(15.49)
|   |   |   |   |   |   |   |   |   start > 289033: sce00190 (14.47)
|   |   |   |   |   |   |   |   start > 301715: sce03010 (24.56)
|   |   |   |   |   |   start > 303120
|   |   |   |   |   |   |   start <= 305297: sce03022 (11.73)
|   |   |   |   |   |   |   start > 305297: sce04140 (19.99)
|   |   |   |   start > 328729
|   |   |   |   |   start <= 364949
|   |   |   |   |   |   start <= 339943: sce00220 (26.52/6.31)
|   |   |   |   |   |   start > 339943
|   |   |   |   |   |   |   start <= 355697: sce00252 (40.04/17.04)
|   |   |   |   |   |   |   start > 355697: sce00970 (34.88/16.93)
|   |   |   |   |   start > 364949
|   |   |   |   |   |   start <= 383452
|   |   |   |   |   |   |   start <= 378392: sce00480 (41.23/14.84)
|   |   |   |   |   |   |   start > 378392: sce00600 (9.7)
|   |   |   |   |   |   start > 383452
|   |   |   |   |   |   |   start <= 406633: sce03010 (22.79)
|   |   |   |   |   |   |   start > 406633: sce00563 (19.35/7.98)
|   |   |   strand = C
|   |   |   |   start <= 322070
|   |   |   |   |   start <= 271309
|   |   |   |   |   |   start <= 225740: sce00190 (37.07/10.29)
|   |   |   |   |   |   start > 225740
```

```
|   |   |   |   |   |   |   start <= 246989: sce03030 (14.23)
|   |   |   |   |   |   |   start > 246989: sce04111 (12.01)
|   |   |   |   |   start > 271309
|   |   |   |   |   |   start <= 303120
|   |   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00562 (5.23/3.05)
|   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = transport_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce04010
(9.61/3.88)
|   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce04070
(6.35/3.91)
|   |   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = membrane_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce04070 (0.0)
```

```
|   |   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = translation_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = conjugation_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce04070 (3.68/2.22)
|   |   |   |   |   |   |   neigh_GO_term = transcription_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_
|   |   |   |   |   |   |   |   neigh_num <= 1: sce04070 (3.76/2.06)
|   |   |   |   |   |   |   |   neigh_num > 1: sce00632 (9.87/5.61)
```

```
|   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = chromosome_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce04070
(15.25/7.68)
|   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = sporulation_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = peroxisome_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce04070 (0.0)
|   |   |   |   |   |   |   neigh_GO_term = cell_budding_: sce04070
(0.0)
|   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce04070 (0.0)
|   |   |   |   |   |   start > 303120: sce03022 (23.17)
|   |   |   |   start > 322070
```

```
|   |   |   |   |   start <= 326263: sce00790 (29.83/11.57)
|   |   |   |   |   start > 326263
|   |   |   |   |   |   start <= 383452
|   |   |   |   |   |   |   start <= 339943: sce00100 (36.1/13.31)
|   |   |   |   |   |   |   start > 339943
|   |   |   |   |   |   |   |   start <= 378392: sce03010 (15.88)
|   |   |   |   |   |   |   |   start > 378392: sce04010 (19.64)
|   |   |   |   |   |   start > 383452
|   |   |   |   |   |   |   start <= 410440: sce00190 (10.88)
|   |   |   |   |   |   |   start > 410440: sce00100 (47.2/19.27)
|   start > 423889
|   |   strand = W
|   |   |   start <= 432585
|   |   |   |   neigh_GO_term = mitochondrion_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = cellular_component_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = biological_process_: sce00120
(23.45/19.74)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_num <= 1: sce00380 (24.97/21.34)
|   |   |   |   |   neigh_num > 1: sce00220 (18.69/14.59)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00650
(14.92/12.62)
|   |   |   |   neigh_GO_term = transport_
|   |   |   |   |   neigh_strand = W: sce00620 (23.74/17.36)
|   |   |   |   |   neigh_strand = C: sce00561 (5.27/4.28)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00903 (20.22/14.15)
|   |   |   |   neigh_GO_term = nucleus_: sce00220 (20.77/18.66)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00903
(0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00903 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00903 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00903 (0.0)
```

```
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = translation_: sce00903 (24.22/20.34)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = motor_activity_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00903
(0.0)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00310 (33.9/27.11)
|   |   |   |   neigh_GO_term = chromosome_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00903
(0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00903 (0.0)
```

```
|   |   |   |   neigh_GO_term = meiosis_: sce00903 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00903
(0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00903
(0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = peroxisome_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00620
(17.01/14.95)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00903 (0.0)
|   |   |   |   neigh_GO_term = cell_budding_: sce00903 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00903 (0.0)
|   |   |   start > 432585
|   |   |   |   start <= 520231
|   |   |   |   |   start <= 482841: sce00190 (9.93)
|   |   |   |   |   start > 482841
|   |   |   |   |   |   neigh_GO_term = mitochondrion_: sce00620
(11.35/6.35)
|   |   |   |   |   |   neigh_GO_term = helicase_activity_: sce00072
(15.48/9.23)
|   |   |   |   |   |   neigh_GO_term = DNA_metabolic_process_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce00280 (10.91/8.83)
|   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_binding_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00620 (12.72/9.35)
|   |   |   |   |   |   neigh_GO_term = lyase_activity_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = transporter_activity_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = transport_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00632
(16.43/13.36)
```

```
|   |   |   |   |   |   neigh_GO_term = nucleus_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = transferase_activity_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = membrane_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_respiration_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cortex_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = pseudohyphal_growth_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transduction_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cell_cycle_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = translation_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = conjugation_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = motor_activity_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = transcription_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = ribosome_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_binding_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = DNA_binding_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_bud_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00620 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = cytokinesis_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = RNA_metabolic_process_:
sce00071 (15.15/11.1)
|   |   |   |   |   |   neigh_GO_term = vacuole_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00620 (13.99/9.31)
|   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = chromosome_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = endomembrane_system_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00310 (10.47/5.2)
|   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = cellular_homeostasis_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00650 (10.27/7.2)
|   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = meiosis_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = extracellular_region_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = ligase_activity_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = sporulation_: sce00650
(12.59/9.23)
|   |   |   |   |   |   neigh_GO_term = peroxisome_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00620 (0.0)
|   |   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00620 (0.0)
```

```
|   |   |   |   |   |   neigh_GO_term = cell_budding_: sce00620
(0.0)
|   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00620 (0.0)
|   |   |   |   start > 520231: sce00020 (24.85/9.52)
|   |   strand = C
|   |   |   start <= 482841
|   |   |   |   start <= 466940
|   |   |   |   |   start <= 461963: sce00513 (55.11/25.65)
|   |   |   |   |   start > 461963
|   |   |   |   |   |   start <= 463836: sce04010 (15.13)
|   |   |   |   |   |   start > 463836: sce04120 (17.51)
|   |   |   |   start > 466940
|   |   |   |   |   start <= 474704
|   |   |   |   |   |   neigh_strand = W: sce00632 (26.38/14.9)
|   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   neigh_num <= 1: sce04070 (4.72/1.49)
|   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   neigh_GO_term = mitochondrion_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = helicase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
DNA_metabolic_process_: sce00562 (8.08/2.58)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_component_:
sce04070 (3.87/1.01)
|   |   |   |   |   |   |   |   neigh_GO_term = peptidase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = protein_binding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = biological_process_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = molecular_function_:
sce00562 (2.94/1.52)
|   |   |   |   |   |   |   |   neigh_GO_term = lyase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_fraction_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = plasma_membrane_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transporter_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transport_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoplasm_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleus_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transferase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00562 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = membrane_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = hydrolase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_respiration_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cortex_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
pseudohyphal_growth_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transduction_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_cycle_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = nucleolus_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
carbohydrate_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = Golgi_apparatus_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = vesicle-
mediated_transport_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
vitamin_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = translation_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
enzyme_regulator_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = conjugation_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
microtubule_organizing_center_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
structural_molecule_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = motor_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = transcription_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
oxidoreductase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ribosome_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = RNA_binding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = DNA_binding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cellular_bud_:
sce00562 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term =
site_of_polarized_growth_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytokinesis_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = response_to_stress_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
translation_regulator_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
RNA_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = vacuole_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_kinase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = chromosome_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cytoskeleton_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endomembrane_system_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
endoplasmic_reticulum_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_modification_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
lipid_metabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cellular_homeostasis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = isomerase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = meiosis_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
extracellular_region_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
protein_catabolic_process_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = ligase_activity_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_wall_: sce00562
(0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = sporulation_:
sce00562 (0.0)
```

```
|   |   |   |   |   |   |   |   neigh_GO_term = peroxisome_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
mitochondrial_envelope_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term =
signal_transducer_activity_: sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = cell_budding_:
sce00562 (0.0)
|   |   |   |   |   |   |   |   neigh_GO_term = electron_transport_:
sce00562 (0.0)
|   |   |   |   |   start > 474704: sce00970 (32.65/14.4)
|   |   |   start > 482841
|   |   |   |   start <= 498094: sce04111 (16.05)
|   |   |   |   start > 498094
|   |   |   |   |   start <= 520231: sce00020 (127.35/102.55)
|   |   |   |   |   start > 520231: sce00630 (13.46)
start > 568993
|   strand = W
|   |   start <= 664957
|   |   |   start <= 657526
|   |   |   |   start <= 643833
|   |   |   |   |   start <= 615376
|   |   |   |   |   |   start <= 596747: sce04111 (19.03)
|   |   |   |   |   |   start > 596747
|   |   |   |   |   |   |   start <= 599867: sce00190 (13.25)
|   |   |   |   |   |   |   start > 599867: sce00500 (18.5)
|   |   |   |   |   start > 615376
|   |   |   |   |   |   start <= 642205: sce00550 (57.65/36.71)
|   |   |   |   |   |   start > 642205: sce00190 (20.13)
|   |   |   |   start > 643833
|   |   |   |   |   start <= 654163: sce03010 (12.06)
|   |   |   |   |   start > 654163: sce00970 (31.62/14.18)
|   |   |   start > 657526
|   |   |   |   neigh_GO_term = mitochondrion_: sce00360
(14.15/11.03)
|   |   |   |   neigh_GO_term = helicase_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00350
(10.98/8.53)
|   |   |   |   neigh_GO_term = cellular_component_: sce00960
(12.27/9.6)
|   |   |   |   neigh_GO_term = peptidase_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = protein_binding_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = biological_process_: sce00350
(7.63/5.89)
|   |   |   |   neigh_GO_term = molecular_function_
|   |   |   |   |   neigh_strand = W: sce00360 (12.67/7.29)
|   |   |   |   |   neigh_strand = C: sce00564 (19.99/15.67)
|   |   |   |   neigh_GO_term = lyase_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = membrane_fraction_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = plasma_membrane_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = transporter_activity_: sce00360
(0.0)
```

```
|   |   |   |   neigh_GO_term = transport_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = cytoplasm_: sce00642 (12.08/7.71)
|   |   |   |   neigh_GO_term = nucleus_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = transferase_activity_: sce00360
(0.0)
|   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00360 (0.0)
|   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = membrane_: sce00350 (6.82/3.76)
|   |   |   |   neigh_GO_term = hydrolase_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = cellular_respiration_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = cell_cortex_: sce00360 (0.0)
|   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = signal_transduction_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = cell_cycle_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = nucleolus_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = ribosome_biogenesis_and_assembly_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = vitamin_metabolic_process_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = translation_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = enzyme_regulator_activity_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = conjugation_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = motor_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = transcription_regulator_activity_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = transcription_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = oxidoreductase_activity_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = ribosome_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = RNA_binding_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = DNA_binding_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = cellular_bud_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = site_of_polarized_growth_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = cytokinesis_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = response_to_stress_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00360 (0.0)
```

```
|   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = vacuole_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = protein_kinase_activity_: sce00360
(9.93/7.9)
|   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00360 (12.05/9.48)
|   |   |   |   neigh_GO_term = chromosome_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = cytoskeleton_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = endomembrane_system_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = protein_modification_process_:
sce00632 (10.8/7.58)
|   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = lipid_metabolic_process_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00360
(0.0)
|   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00350 (10.06/7.73)
|   |   |   |   neigh_GO_term = isomerase_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = meiosis_: sce00360 (0.0)
|   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = extracellular_region_: sce00360
(0.0)
|   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = protein_catabolic_process_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = nucleotidyltransferase_activity_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = ligase_activity_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = cell_wall_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = sporulation_: sce00624 (9.85/7.53)
|   |   |   |   neigh_GO_term = peroxisome_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = mitochondrial_envelope_: sce00360
(0.0)
|   |   |   |   neigh_GO_term = anatomical_structure_morphogenesis_:
sce00360 (0.0)
|   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00642 (11.25/8.22)
|   |   |   |   neigh_GO_term = cell_budding_: sce00360 (0.0)
|   |   |   |   neigh_GO_term = electron_transport_: sce00360 (0.0)
|   |   start > 664957
|   |   |   start <= 822616
|   |   |   |   start <= 742452
|   |   |   |   |   start <= 713026
|   |   |   |   |   |   start <= 677162
|   |   |   |   |   |   |   start <= 671123: sce03022 (22.35)
|   |   |   |   |   |   |   start > 671123: sce00240 (15.49)
|   |   |   |   |   |   start > 677162
```

```
|   |   |   |   |   |   |   start <= 694835: sce04120 (15.13)
|   |   |   |   |   |   |   start > 694835: sce03022 (10.74)
|   |   |   |   |   start > 713026: sce03050 (26.04)
|   |   |   |   start > 742452
|   |   |   |   |   start <= 775180
|   |   |   |   |   |   start <= 752255
|   |   |   |   |   |   |   start <= 747304: sce04111 (12.69)
|   |   |   |   |   |   |   start > 747304: sce04070 (33.26/14.0)
|   |   |   |   |   |   start > 752255
|   |   |   |   |   |   |   start <= 767750: sce00271 (23.76)
|   |   |   |   |   |   |   start > 767750: sce04111 (16.82)
|   |   |   |   |   start > 775180
|   |   |   |   |   |   start <= 794961: sce03010 (8.88)
|   |   |   |   |   |   start > 794961: sce00252 (46.42/20.54)
|   |   |   start > 822616
|   |   |   |   start <= 902040
|   |   |   |   |   start <= 888970
|   |   |   |   |   |   start <= 877628
|   |   |   |   |   |   |   start <= 868300: sce00500 (6.36)
|   |   |   |   |   |   |   start > 868300: sce04010 (15.33)
|   |   |   |   |   |   start > 877628: sce00240 (54.19/31.52)
|   |   |   |   |   start > 888970
|   |   |   |   |   |   start <= 900751
|   |   |   |   |   |   |   start <= 895957: sce04120 (15.4)
|   |   |   |   |   |   |   start > 895957: sce00510 (12.02)
|   |   |   |   |   |   start > 900751: sce00500 (18.29)
|   |   |   |   start > 902040
|   |   |   |   |   start <= 907214: sce04140 (16.6)
|   |   |   |   |   start > 907214
|   |   |   |   |   |   start <= 911253: sce00230 (55.92/31.09)
|   |   |   |   |   |   start > 911253: sce00190 (11.29)
|   strand = C
|   |   start <= 703968
|   |   |   start <= 677162
|   |   |   |   start <= 599867
|   |   |   |   |   neigh_GO_term = mitochondrion_: sce03020
(2.55/1.41)
|   |   |   |   |   neigh_GO_term = helicase_activity_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = DNA_metabolic_process_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = cellular_component_: sce00230
(7.02/4.23)
|   |   |   |   |   neigh_GO_term = peptidase_activity_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = protein_binding_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = biological_process_: sce00230
(9.11/3.22)
|   |   |   |   |   neigh_GO_term = molecular_function_: sce00240
(4.8/2.43)
|   |   |   |   |   neigh_GO_term = lyase_activity_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_fraction_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = plasma_membrane_: sce00240 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = transporter_activity_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = transport_: sce00230 (5.95/2.99)
|   |   |   |   |   neigh_GO_term = cytoplasm_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = nucleus_: sce00240 (3.36/0.83)
|   |   |   |   |   neigh_GO_term = transferase_activity_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term =
amino_acid_and_derivative_metabolic_process_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
generation_of_precursor_metabolites_and_energy_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = membrane_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = hydrolase_activity_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = cellular_respiration_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = cell_cortex_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
cytoskeleton_organization_and_biogenesis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = pseudohyphal_growth_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = signal_transduction_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = cell_cycle_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = nucleolus_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
ribosome_biogenesis_and_assembly_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = carbohydrate_metabolic_process_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = Golgi_apparatus_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = vesicle-mediated_transport_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = vitamin_metabolic_process_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = translation_: sce00240
(8.43/2.51)
|   |   |   |   |   neigh_GO_term = enzyme_regulator_activity_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = conjugation_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = microtubule_organizing_center_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = structural_molecule_activity_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = motor_activity_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
transcription_regulator_activity_: sce00230 (1.56/0.94)
|   |   |   |   |   neigh_GO_term = transcription_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = oxidoreductase_activity_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = ribosome_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_binding_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = DNA_binding_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_bud_: sce00240 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = site_of_polarized_growth_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = cytokinesis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = response_to_stress_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = translation_regulator_activity_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = RNA_metabolic_process_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = vacuole_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = protein_kinase_activity_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
organelle_organization_and_biogenesis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = chromosome_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = cytoskeleton_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = endomembrane_system_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = endoplasmic_reticulum_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = protein_modification_process_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
membrane_organization_and_biogenesis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = lipid_metabolic_process_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = cellular_homeostasis_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term =
cell_wall_organization_and_biogenesis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = isomerase_activity_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term = meiosis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
nuclear_organization_and_biogenesis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = extracellular_region_: sce00240
(0.0)
|   |   |   |   |   neigh_GO_term =
phosphoprotein_phosphatase_activity_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = protein_catabolic_process_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
nucleotidyltransferase_activity_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = ligase_activity_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = cell_wall_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = sporulation_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = peroxisome_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = mitochondrial_envelope_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term =
anatomical_structure_morphogenesis_: sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = signal_transducer_activity_:
sce00240 (0.0)
|   |   |   |   |   neigh_GO_term = cell_budding_: sce00240 (0.0)
```

```
|   |   |   |   |   neigh_GO_term = electron_transport_: sce00240
(0.0)
|   |   |   |   start > 599867
|   |   |   |   |   start <= 643833: sce00340 (38.79/17.0)
|   |   |   |   |   start > 643833
|   |   |   |   |   |   start <= 664957: sce04140 (12.86)
|   |   |   |   |   |   start > 664957: sce00400 (21.29)
|   |   |   start > 677162
|   |   |   |   start <= 692415
|   |   |   |   |   start <= 685434: sce00220 (61.23/29.33)
|   |   |   |   |   start > 685434: sce00361 (23.96/11.98)
|   |   |   |   start > 692415
|   |   |   |   |   start <= 694835: sce00710 (33.25/15.16)
|   |   |   |   |   start > 694835: sce00260 (37.31/14.79)
|   |   start > 703968
|   |   |   start <= 732347
|   |   |   |   start <= 713026: sce03060 (17.23)
|   |   |   |   start > 713026: sce03010 (20.47)
|   |   |   start > 732347
|   |   |   |   start <= 868300
|   |   |   |   |   start <= 752255: sce03020 (37.99/22.07)
|   |   |   |   |   start > 752255: sce04111 (29.76)
|   |   |   |   start > 868300
|   |   |   |   |   start <= 895957: sce00920 (17.29)
|   |   |   |   |   start > 895957: sce03020 (61.15/38.61)
```

Appendix I. Decision Trees Generated for Classifying Features to Gene Ontology Terms

In the tree structure, a colon introduces the name of the Gene Ontology term that has been assigned to a particular leaf. The Gene Ontology Term is followed by the number of instances that reach that leaf. The number is expressed as a decimal because of the way the classification algorithm uses fractions to handle missing values. The number of incorrectly classified instances that reach that leaf, if they exist, are reported after the "/". For example, if the numbers (2.0/1.0) are reported, it means that two instances reached the leaf, of which one is incorrectly classified.

Decision Tree Generated for Chromosome One:

For Cellular Component

```
|   start <= 166268
|   |   start <= 27969
|   |   |   start <= 22687
|   |   |   |   start <= 9017
|   |   |   |   |   start <= 2480: cellular_component_ (24.79)
|   |   |   |   |   start > 2480: membrane_ (15.92)
|   |   |   |   start > 9017: cellular_component_ (76.01)
|   |   |   start > 22687: cell_wall_ (15.31)
|   |   start > 27969
|   |   |   start <= 108552
|   |   |   |   start <= 54790
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 52596
|   |   |   |   |   |   |   start <= 48565: mitochondrion_ (11.53)
|   |   |   |   |   |   |   start > 48565: cytoplasm_ (12.04)
|   |   |   |   |   |   start > 52596: mitochondrion_ (15.09)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 36510
|   |   |   |   |   |   |   start <= 35156
|   |   |   |   |   |   |   |   start <= 31568: mitochondrion_
(17.85/7.42)
|   |   |   |   |   |   |   |   start > 31568
|   |   |   |   |   |   |   |   |   start <= 33449: nucleus_
(35.65/16.29)
|   |   |   |   |   |   |   |   |   start > 33449: cytoplasm_
(15.28)
|   |   |   |   |   |   |   start > 35156: nucleolus_ (22.86/11.29)
|   |   |   |   |   |   start > 36510
|   |   |   |   |   |   |   start <= 39260
|   |   |   |   |   |   |   |   start <= 37465:
endoplasmic_reticulum_ (20.28)
|   |   |   |   |   |   |   |   start > 37465
```

```
|   |   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_
(16.31/10.06)
|   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
mitochondrion_ (20.05/9.52)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(3.99/1.99)
|   |   |   |   |   |   |   start > 39260
|   |   |   |   |   |   |   |   start <= 42178: peroxisome_ (17.77)
|   |   |   |   |   |   |   |   start > 42178
|   |   |   |   |   |   |   |   |   start <= 45900: cytoplasm_
(35.68/14.11)
|   |   |   |   |   |   |   |   |   start > 45900: nucleus_ (13.66)
|   |   |   |   start > 54790
|   |   |   |   |   start <= 87287
|   |   |   |   |   |   start <= 81952
|   |   |   |   |   |   |   start <= 67521
|   |   |   |   |   |   |   |   start <= 58463
|   |   |   |   |   |   |   |   |   start <= 56858: cytoskeleton_
(26.41/9.34)
|   |   |   |   |   |   |   |   |   start > 56858
|   |   |   |   |   |   |   |   |   |   start <= 57519:
cellular_component_ (31.99)
|   |   |   |   |   |   |   |   |   |   start > 57519:
mitochondrion_ (16.88)
|   |   |   |   |   |   |   |   start > 58463
|   |   |   |   |   |   |   |   |   strand = C: nucleus_
(45.29/8.92)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 61317:
cytoplasmic_membrane-bound_vesicle_ (9.14)
|   |   |   |   |   |   |   |   |   |   start > 61317: nucleus_
(12.28)
|   |   |   |   |   |   |   start > 67521
|   |   |   |   |   |   |   |   start <= 76428
|   |   |   |   |   |   |   |   |   start <= 76153
|   |   |   |   |   |   |   |   |   |   start <= 69526:
mitochondrion_ (16.83)
|   |   |   |   |   |   |   |   |   |   start > 69526
|   |   |   |   |   |   |   |   |   |   |   start <= 71787:
cytoplasm_ (18.36)
|   |   |   |   |   |   |   |   |   |   |   start > 71787
|   |   |   |   |   |   |   |   |   |   |   |   start <= 74021:
cellular_component_ (31.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 74021:
cytoplasm_ (9.88)
|   |   |   |   |   |   |   |   |   start > 76153: mitochondrion_
(19.57)
|   |   |   |   |   |   |   |   start > 76428
|   |   |   |   |   |   |   |   |   start <= 79719: cytoskeleton_
(21.34)
|   |   |   |   |   |   |   |   |   start > 79719:
cellular_component_ (12.94)
|   |   |   |   |   |   start > 81952
```

```
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 84475: nucleus_ (22.8)
|   |   |   |   |   |   |   |   start > 84475: cytoplasm_ (18.96)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 84475: nucleolus_ (14.29)
|   |   |   |   |   |   |   |   start > 84475: cytoplasmic_membrane-
bound_vesicle_ (8.3)
|   |   |   |   |   start > 87287
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 99698
|   |   |   |   |   |   |   |   start <= 94688
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
mitochondrion_ (8.72/2.22)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cellular_bud_ (3.97/1.59)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cellular_bud_ (7.02/2.59)
|   |   |   |   |   |   |   |   start > 94688: Golgi_apparatus_
(13.94)
|   |   |   |   |   |   |   start > 99698
|   |   |   |   |   |   |   |   start <= 101146: nucleolus_ (19.82)
|   |   |   |   |   |   |   |   start > 101146
|   |   |   |   |   |   |   |   |   start <= 105873: cellular_bud_
(20.04)
|   |   |   |   |   |   |   |   |   start > 105873:
endoplasmic_reticulum_ (12.25)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 94688
|   |   |   |   |   |   |   |   start <= 92901:
endoplasmic_reticulum_ (10.42)
|   |   |   |   |   |   |   |   start > 92901: nucleus_ (10.56)
|   |   |   |   |   |   |   start > 94688: cellular_component_
(16.0)
|   |   |   start > 108552
|   |   |   |   start <= 141433
|   |   |   |   |   start <= 132202
|   |   |   |   |   |   start <= 110431: membrane_ (14.39)
|   |   |   |   |   |   start > 110431
|   |   |   |   |   |   |   start <= 114616: cytoplasm_ (23.75)
|   |   |   |   |   |   |   start > 114616
|   |   |   |   |   |   |   |   start <= 119542
|   |   |   |   |   |   |   |   |   start <= 114920: mitochondrion_
(27.98/13.54)
|   |   |   |   |   |   |   |   |   start > 114920:
cellular_component_ (8.09)
|   |   |   |   |   |   |   |   start > 119542
|   |   |   |   |   |   |   |   |   start <= 130802
|   |   |   |   |   |   |   |   |   |   start <= 128103
|   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (33.74/15.07)
|   |   |   |   |   |   |   |   |   |   |   strand = W: cytoplasm_
(22.11/5.76)
|   |   |   |   |   |   |   |   |   |   start > 128103
```

```
|   |   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(18.05)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 129271:
nucleus_ (9.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 129271:
cytoplasm_ (13.97)
|   |   |   |   |   |   |   |   |   start > 130802: mitochondrion_
(26.32/11.38)
|   |   |   |   |   start > 132202
|   |   |   |   |   |   start <= 136916
|   |   |   |   |   |   |   strand = C: mitochondrial_envelope_
(27.77)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 135856:
endomembrane_system_ (16.43)
|   |   |   |   |   |   |   |   start > 135856: mitochondrion_
(21.99)
|   |   |   |   |   |   start > 136916
|   |   |   |   |   |   |   start <= 138347: cytoplasmic_membrane-
bound_vesicle_ (17.58)
|   |   |   |   |   |   |   start > 138347: cytoplasm_ (30.87/5.99)
|   |   |   |   start > 141433
|   |   |   |   |   start <= 143709
|   |   |   |   |   |   stop <= 142470: nucleolus_ (15.94)
|   |   |   |   |   |   stop > 142470
|   |   |   |   |   |   |   start <= 142369: ribosome_ (14.95)
|   |   |   |   |   |   |   start > 142369: membrane_fraction_
(13.05)
|   |   |   |   |   start > 143709
|   |   |   |   |   |   start <= 155007
|   |   |   |   |   |   |   strand = C: mitochondrion_ (41.0)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 152259: membrane_
(56.36/33.46)
|   |   |   |   |   |   |   |   start > 152259: cellular_component_
(46.02/16.93)
|   |   |   |   |   |   start > 155007
|   |   |   |   |   |   |   distance <= 3592
|   |   |   |   |   |   |   |   distance <= 1133: mitochondrion_
(4.0/1.28)
|   |   |   |   |   |   |   |   distance > 1133: cytoplasm_
(27.84/1.44)
|   |   |   |   |   |   |   distance > 3592: mitochondrion_
(7.3/1.04)
|   start > 166268
|   |   start <= 186315
|   |   |   strand = C
|   |   |   |   start <= 175133
|   |   |   |   |   start <= 171698
|   |   |   |   |   |   start <= 169370
|   |   |   |   |   |   |   neigh_num <= 1:
site_of_polarized_growth_ (19.43/6.14)
```

```
|   |   |   |   |   |   |   neigh_num > 1: cellular_bud_
(12.31/3.42)
|   |   |   |   |   |   start > 169370: cellular_component_ (18.68)
|   |   |   |   |   start > 171698: site_of_polarized_growth_
(46.9/29.37)
|   |   |   |   start > 175133
|   |   |   |   |   start <= 181135: cellular_component_ (28.47)
|   |   |   |   |   start > 181135: cytoplasm_ (9.21)
|   |   |   strand = W
|   |   |   |   start <= 181135: cytoplasm_ (36.43/8.89)
|   |   |   |   start > 181135
|   |   |   |   |   start <= 184886
|   |   |   |   |   |   start <= 183764: endomembrane_system_
(13.28)
|   |   |   |   |   |   start > 183764: cellular_component_ (7.8)
|   |   |   |   |   start > 184886: cytoplasm_ (15.95)
|   |   start > 186315
|   |   |   start <= 190187
|   |   |   |   start <= 188101: endoplasmic_reticulum_ (49.4/23.18)
|   |   |   |   start > 188101: mitochondrion_ (13.95)
|   |   |   start > 190187
|   |   |   |   start <= 203394
|   |   |   |   |   strand = C: cellular_component_ (10.78)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 192613: endoplasmic_reticulum_
(15.34)
|   |   |   |   |   |   start > 192613: cell_wall_ (14.71)
|   |   |   |   start > 203394
|   |   |   |   |   start <= 222397: cellular_component_ (29.06)
|   |   |   |   |   start > 222397: extracellular_region_ (4.32)
```

For Molecular Function

```
|   start <= 58463
|   |   start <= 27969
|   |   |   start <= 9017
|   |   |   |   start <= 2480: molecular_function_ (20.01)
|   |   |   |   start > 2480: transporter_activity_ (13.28)
|   |   |   start > 9017: molecular_function_ (87.27)
|   |   start > 27969
|   |   |   start <= 45023
|   |   |   |   strand = C: ligase_activity_ (18.19)
|   |   |   |   strand = W
|   |   |   |   |   start <= 35156: oxidoreductase_activity_ (54.55)
|   |   |   |   |   start > 35156
|   |   |   |   |   |   start <= 36510: molecular_function_ (8.67)
|   |   |   |   |   |   start > 36510
|   |   |   |   |   |   |   start <= 39260
|   |   |   |   |   |   |   |   start <= 37465: protein_binding_
(13.98)
|   |   |   |   |   |   |   |   start > 37465:
signal_transducer_activity_ (11.28)
|   |   |   |   |   |   |   start > 39260: protein_binding_ (15.38)
|   |   |   start > 45023
|   |   |   |   start <= 48565
```

```
|   |   |   |   |   start <= 45900: transporter_activity_ (23.41)
|   |   |   |   |   start > 45900: DNA_binding_ (16.09)
|   |   |   |   start > 48565
|   |   |   |   |   start <= 57519
|   |   |   |   |   |   start <= 54790
|   |   |   |   |   |   |   start <= 52596: molecular_function_
(14.74)
|   |   |   |   |   |   |   start > 52596: hydrolase_activity_
(17.7)
|   |   |   |   |   |   start > 54790
|   |   |   |   |   |   |   start <= 56858:
structural_molecule_activity_ (18.93)
|   |   |   |   |   |   |   start > 56858: molecular_function_
(22.98)
|   |   |   |   |   start > 57519: oxidoreductase_activity_ (19.79)
|   start > 58463
|   |   start <= 151168
|   |   |   start <= 119542
|   |   |   |   start <= 81952
|   |   |   |   |   start <= 71787
|   |   |   |   |   |   start <= 61317
|   |   |   |   |   |   |   start <= 61053: RNA_binding_ (11.73)
|   |   |   |   |   |   |   start > 61053: molecular_function_
(19.46)
|   |   |   |   |   |   start > 61317
|   |   |   |   |   |   |   start <= 67521:
enzyme_regulator_activity_ (25.04)
|   |   |   |   |   |   |   start > 67521
|   |   |   |   |   |   |   |   start <= 69526: lyase_activity_
(15.87)
|   |   |   |   |   |   |   |   start > 69526: transferase_activity_
(10.35)
|   |   |   |   |   start > 71787
|   |   |   |   |   |   start <= 76153: molecular_function_ (60.75)
|   |   |   |   |   |   start > 76153
|   |   |   |   |   |   |   start <= 76428:
translation_regulator_activity_ (13.56)
|   |   |   |   |   |   |   start > 76428: molecular_function_
(31.47)
|   |   |   |   start > 81952
|   |   |   |   |   start <= 92271
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 84475:
transcription_regulator_activity_ (16.57)
|   |   |   |   |   |   |   start > 84475
|   |   |   |   |   |   |   |   start <= 87287:
enzyme_regulator_activity_ (15.23)
|   |   |   |   |   |   |   |   start > 87287: motor_activity_
(13.58)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 84475: hydrolase_activity_
(15.37)
|   |   |   |   |   |   |   start > 84475: protein_binding_ (14.68)
|   |   |   |   |   start > 92271
```

```
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 113360
|   |   |   |   |   |   |   |   start <= 105873
|   |   |   |   |   |   |   |   |   start <= 101146
|   |   |   |   |   |   |   |   |   |   start <= 99698:
hydrolase_activity_ (8.99)
|   |   |   |   |   |   |   |   |   |   start > 99698:
molecular_function_ (15.02)
|   |   |   |   |   |   |   |   |   start > 101146:
enzyme_regulator_activity_ (12.99)
|   |   |   |   |   |   |   |   start > 105873
|   |   |   |   |   |   |   |   |   start <= 108552:
transferase_activity_ (15.79)
|   |   |   |   |   |   |   |   |   start > 108552
|   |   |   |   |   |   |   |   |   |   start <= 110431:
transporter_activity_ (8.95)
|   |   |   |   |   |   |   |   |   |   start > 110431:
hydrolase_activity_ (12.93)
|   |   |   |   |   |   |   start > 113360: molecular_function_
(30.56)
|   |   |   |   |   |   strand = W: molecular_function_ (45.3)
|   |   |   start > 119542
|   |   |   |   start <= 130802
|   |   |   |   |   start <= 124880
|   |   |   |   |   |   start <= 120226: protein_kinase_activity_
(18.15)
|   |   |   |   |   |   start > 120226:
phosphoprotein_phosphatase_activity_ (7.74)
|   |   |   |   |   start > 124880
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 128103: lyase_activity_ (7.48)
|   |   |   |   |   |   |   start > 128103: protein_binding_ (26.61)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 129271:
transcription_regulator_activity_ (16.47)
|   |   |   |   |   |   |   start > 129271: lyase_activity_ (24.75)
|   |   |   |   start > 130802
|   |   |   |   |   start <= 139154
|   |   |   |   |   |   start <= 135856
|   |   |   |   |   |   |   start <= 135667: molecular_function_
(32.17)
|   |   |   |   |   |   |   start > 135667:
phosphoprotein_phosphatase_activity_ (16.51)
|   |   |   |   |   |   start > 135856: molecular_function_ (41.57)
|   |   |   |   |   start > 139154
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 143709: protein_binding_
(11.36)
|   |   |   |   |   |   |   start > 143709:
transcription_regulator_activity_ (12.13)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   stop <= 142470: RNA_binding_ (19.75)
|   |   |   |   |   |   |   stop > 142470
```

```
|   |   |   |   |   |   |   |   start <= 142369:
translation_regulator_activity_ (16.64)
|   |   |   |   |   |   |   |   start > 142369: molecular_function_
(14.61)
|   |   start > 151168
|   |   |   start <= 175133
|   |   |   |   start <= 166268
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 155007: molecular_function_ (19.29)
|   |   |   |   |   |   start > 155007: DNA_binding_ (14.73)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 155007
|   |   |   |   |   |   |   start <= 152259:
structural_molecule_activity_ (10.92)
|   |   |   |   |   |   |   start > 152259: transferase_activity_
(17.08)
|   |   |   |   |   |   start > 155007
|   |   |   |   |   |   |   start <= 158967: hydrolase_activity_
(13.11)
|   |   |   |   |   |   |   start > 158967: molecular_function_
(10.26)
|   |   |   |   start > 166268
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 169370: enzyme_regulator_activity_
(14.88)
|   |   |   |   |   |   start > 169370: protein_kinase_activity_
(41.79)
|   |   |   |   |   strand = W: ligase_activity_ (15.23)
|   |   |   start > 175133
|   |   |   |   start <= 186830: molecular_function_ (130.98)
|   |   |   |   start > 186830
|   |   |   |   |   start <= 190187
|   |   |   |   |   |   start <= 188101: protein_binding_ (8.07)
|   |   |   |   |   |   start > 188101: transferase_activity_
(10.94)
|   |   |   |   |   start > 190187
|   |   |   |   |   |   start <= 222397: molecular_function_ (70.29)
|   |   |   |   |   |   start > 222397: hydrolase_activity_ (3.85)
```

For Biological Process

```
|   start <= 52596
|   |   start <= 33449
|   |   |   start <= 9017
|   |   |   |   strand = C
|   |   |   |   |   start <= 2480: sporulation_ (6.68)
|   |   |   |   |   start > 2480: transport_ (15.27)
|   |   |   |   strand = W: biological_process_ (8.64)
|   |   |   start > 9017
|   |   |   |   start <= 27969: biological_process_ (69.72)
|   |   |   |   start > 27969
|   |   |   |   |   start <= 31568:
amino_acid_and_derivative_metabolic_process_ (17.95)
|   |   |   |   |   start > 31568: biological_process_ (14.07)
|   |   start > 33449
```

```
|   |   |   strand = C
|   |   |   |   start <= 48565: protein_modification_process_
(38.69/17.49)
|   |   |   |   start > 48565: biological_process_ (14.71)
|   |   |   strand = W
|   |   |   |   start <= 37465
|   |   |   |   |   start <= 36510
|   |   |   |   |   |   start <= 35156:
generation_of_precursor_metabolites_and_energy_ (12.66)
|   |   |   |   |   |   start > 35156:
cell_wall_organization_and_biogenesis_ (22.54)
|   |   |   |   |   start > 36510: protein_catabolic_process_
(14.74)
|   |   |   |   start > 37465
|   |   |   |   |   start <= 42178
|   |   |   |   |   |   start <= 39260: signal_transduction_ (16.18)
|   |   |   |   |   |   start > 39260:
organelle_organization_and_biogenesis_ (25.72/11.7)
|   |   |   |   |   start > 42178
|   |   |   |   |   |   start <= 45900: transport_ (31.77/13.37)
|   |   |   |   |   |   start > 45900:
organelle_organization_and_biogenesis_ (23.8)
|   start > 52596
|   |   start <= 158967
|   |   |   start <= 120226
|   |   |   |   start <= 105873
|   |   |   |   |   start <= 69526
|   |   |   |   |   |   start <= 61317
|   |   |   |   |   |   |   start <= 57519
|   |   |   |   |   |   |   |   start <= 56858
|   |   |   |   |   |   |   |   |   start <= 54790: vesicle-
mediated_transport_ (15.35)
|   |   |   |   |   |   |   |   |   start > 54790: cell_cycle_
(14.17)
|   |   |   |   |   |   |   |   start > 56858: biological_process_
(32.12)
|   |   |   |   |   |   |   start > 57519
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 58463:
DNA_metabolic_process_ (12.66)
|   |   |   |   |   |   |   |   |   start > 58463:
RNA_metabolic_process_ (11.04)
|   |   |   |   |   |   |   |   strand = W: vesicle-
mediated_transport_ (32.84/13.16)
|   |   |   |   |   |   start > 61317
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 67521:
organelle_organization_and_biogenesis_ (11.78)
|   |   |   |   |   |   |   |   start > 67521:
protein_modification_process_ (14.52)
|   |   |   |   |   |   |   strand = W: pseudohyphal_growth_ (11.41)
|   |   |   |   |   start > 69526
|   |   |   |   |   |   start <= 87032
```

```
|   |   |   |   |   |   |   start <= 74021: biological_process_
(51.78/7.76)
|   |   |   |   |   |   |   start > 74021
|   |   |   |   |   |   |   |   start <= 76428
|   |   |   |   |   |   |   |   |   start <= 76153:
ribosome_biogenesis_and_assembly_ (10.23)
|   |   |   |   |   |   |   |   |   start > 76153: translation_
(9.48)
|   |   |   |   |   |   |   |   start > 76428
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   distance <= 978
|   |   |   |   |   |   |   |   |   |   |   start <= 82707:
biological_process_ (3.11)
|   |   |   |   |   |   |   |   |   |   |   start > 82707:
RNA_metabolic_process_ (8.08/0.58)
|   |   |   |   |   |   |   |   |   |   distance > 978:
biological_process_ (41.31/3.66)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 79719:
biological_process_ (11.58)
|   |   |   |   |   |   |   |   |   |   start > 79719:
ribosome_biogenesis_and_assembly_ (13.55)
|   |   |   |   |   |   start > 87032
|   |   |   |   |   |   |   stop <= 95631
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 94688:
organelle_organization_and_biogenesis_ (7.24)
|   |   |   |   |   |   |   |   |   start > 94688
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
membrane_organization_and_biogenesis_ (9.31/2.84)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (14.27/5.92)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 87287: vesicle-
mediated_transport_ (19.0)
|   |   |   |   |   |   |   |   |   start > 87287
|   |   |   |   |   |   |   |   |   |   start <= 92901:
response_to_stress_ (7.26)
|   |   |   |   |   |   |   |   |   |   start > 92901:
biological_process_ (12.44)
|   |   |   |   |   |   |   stop > 95631
|   |   |   |   |   |   |   |   start <= 101146:
ribosome_biogenesis_and_assembly_ (31.78)
|   |   |   |   |   |   |   |   start > 101146: vesicle-
mediated_transport_ (8.46)
|   |   |   |   start > 105873
|   |   |   |   |   start <= 113360
|   |   |   |   |   |   start <= 108552:
protein_modification_process_ (19.25)
|   |   |   |   |   |   start > 108552
|   |   |   |   |   |   |   start <= 110431: transport_ (16.17)
|   |   |   |   |   |   |   start > 110431: RNA_metabolic_process_
(16.25)
|   |   |   |   |   start > 113360
```

```
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 114920: cell_budding_
(31.62/11.46)
|   |   |   |   |   |   |   start > 114920: biological_process_
(17.98)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 114920:
organelle_organization_and_biogenesis_ (12.93)
|   |   |   |   |   |   |   start > 114920:
protein_modification_process_ (18.56)
|   |   |   start > 120226
|   |   |   |   start <= 136916
|   |   |   |   |   start <= 130802
|   |   |   |   |   |   start <= 129271
|   |   |   |   |   |   |   start <= 124880: translation_ (5.24)
|   |   |   |   |   |   |   start > 124880
|   |   |   |   |   |   |   |   start <= 128103:
DNA_metabolic_process_ (16.95)
|   |   |   |   |   |   |   |   start > 128103
|   |   |   |   |   |   |   |   |   start <= 129020: transport_
(14.2)
|   |   |   |   |   |   |   |   |   start > 129020:
DNA_metabolic_process_ (10.07)
|   |   |   |   |   |   start > 129271:
amino_acid_and_derivative_metabolic_process_ (14.97)
|   |   |   |   |   start > 130802
|   |   |   |   |   |   start <= 135667:
organelle_organization_and_biogenesis_ (32.79)
|   |   |   |   |   |   start > 135667
|   |   |   |   |   |   |   start <= 135856
|   |   |   |   |   |   |   |   neigh_num <= 1: meiosis_
(12.07/3.91)
|   |   |   |   |   |   |   |   neigh_num > 1:
nuclear_organization_and_biogenesis_ (18.3/7.36)
|   |   |   |   |   |   |   start > 135856: biological_process_
(17.49)
|   |   |   |   start > 136916
|   |   |   |   |   start <= 142176
|   |   |   |   |   |   start <= 138347
|   |   |   |   |   |   |   neigh_strand = W: transport_
(14.07/5.02)
|   |   |   |   |   |   |   neigh_strand = C: vesicle-
mediated_transport_ (13.85/1.83)
|   |   |   |   |   |   start > 138347
|   |   |   |   |   |   |   strand = C: response_to_stress_
(17.03/5.74)
|   |   |   |   |   |   |   strand = W: translation_ (33.76)
|   |   |   |   |   start > 142176
|   |   |   |   |   |   start <= 142369: RNA_metabolic_process_
(34.0/12.37)
|   |   |   |   |   |   start > 142369
|   |   |   |   |   |   |   start <= 158621
|   |   |   |   |   |   |   |   start <= 154726
|   |   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   |   start <= 152259:
transcription_ (11.34)
|   |   |   |   |   |   |   |   |   |   start > 152259: transport_
(31.81/13.14)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 143709: vesicle-
mediated_transport_ (15.37)
|   |   |   |   |   |   |   |   |   |   start > 143709:
DNA_metabolic_process_ (11.68)
|   |   |   |   |   |   |   |   start > 154726
|   |   |   |   |   |   |   |   |   start <= 155007
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
DNA_metabolic_process_ (9.36/1.94)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
transcription_ (24.21/7.03)
|   |   |   |   |   |   |   |   |   start > 155007:
DNA_metabolic_process_ (17.68)
|   |   |   |   |   |   |   start > 158621: RNA_metabolic_process_
(17.8)
|   |   start > 158967
|   |   |   start <= 186315
|   |   |   |   start <= 168866
|   |   |   |   |   start <= 166268: translation_ (17.88)
|   |   |   |   |   start > 166268:
cytoskeleton_organization_and_biogenesis_ (13.79)
|   |   |   |   start > 168866
|   |   |   |   |   start <= 179818
|   |   |   |   |   |   start <= 171698: biological_process_ (43.36)
|   |   |   |   |   |   start > 171698
|   |   |   |   |   |   |   start <= 175133: cytokinesis_ (15.67)
|   |   |   |   |   |   |   start > 175133: biological_process_
(23.19)
|   |   |   |   |   start > 179818
|   |   |   |   |   |   start <= 182597: translation_ (26.2)
|   |   |   |   |   |   start > 182597: biological_process_ (34.81)
|   |   |   start > 186315
|   |   |   |   start <= 190187
|   |   |   |   |   start <= 188101:
organelle_organization_and_biogenesis_ (31.3)
|   |   |   |   |   start > 188101: vitamin_metabolic_process_
(12.69)
|   |   |   |   start > 190187
|   |   |   |   |   start <= 192613
|   |   |   |   |   |   start <= 192411: biological_process_ (11.47)
|   |   |   |   |   |   start > 192411: vesicle-mediated_transport_
(16.06)
|   |   |   |   |   start > 192613: biological_process_ (38.34)
```

Decision Tree Generated for Chromosome Two:
For Cellular Component

```
|   start <= 496863
|   |   start <= 227639
```

```
|   |   |   start <= 164775
|   |   |   |   start <= 36395
|   |   |   |   |   start <= 7733: cellular_component_ (40.89)
|   |   |   |   |   start > 7733
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 13879
|   |   |   |   |   |   |   |   start <= 10551: cytoplasm_ (12.74)
|   |   |   |   |   |   |   |   start > 10551: plasma_membrane_
(27.33)
|   |   |   |   |   |   |   start > 13879
|   |   |   |   |   |   |   |   start <= 17696:
site_of_polarized_growth_ (72.82/48.35)
|   |   |   |   |   |   |   |   start > 17696: cytoplasm_
(77.09/12.75)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 24098
|   |   |   |   |   |   |   |   start <= 13879: cytoplasm_ (19.71)
|   |   |   |   |   |   |   |   start > 13879: endomembrane_system_
(12.76)
|   |   |   |   |   |   |   start > 24098
|   |   |   |   |   |   |   |   start <= 28427: cellular_component_
(17.07)
|   |   |   |   |   |   |   |   start > 28427: cytoplasm_ (12.37)
|   |   |   |   start > 36395
|   |   |   |   |   start <= 135519
|   |   |   |   |   |   start <= 101158
|   |   |   |   |   |   |   start <= 74692
|   |   |   |   |   |   |   |   start <= 60735
|   |   |   |   |   |   |   |   |   start <= 59379
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 49571
|   |   |   |   |   |   |   |   |   |   |   |   start <= 45975:
nucleus_ (10.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 45975
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 47177:
cellular_component_ (8.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 47177:
cytoplasm_ (9.5)
|   |   |   |   |   |   |   |   |   |   |   start > 49571:
mitochondrion_ (30.28/14.44)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 48822
|   |   |   |   |   |   |   |   |   |   |   |   start <= 43274
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 39142:
mitochondrion_ (22.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 39142
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
40828: nucleus_ (8.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
40828: mitochondrion_ (12.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 43274
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 47177:
ribosome_ (11.92)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 47177:
mitochondrion_ (19.07)
|   |   |   |   |   |   |   |   |   |   |   start > 48822:
cellular_component_ (13.77)
|   |   |   |   |   |   |   |   |   start > 59379: ribosome_ (16.81)
|   |   |   |   |   |   |   |   start > 60735
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 69442
|   |   |   |   |   |   |   |   |   |   |   start <= 63873:
cellular_component_ (20.04)
|   |   |   |   |   |   |   |   |   |   |   start > 63873: nucleus_
(15.7)
|   |   |   |   |   |   |   |   |   |   start > 69442
|   |   |   |   |   |   |   |   |   |   |   start <= 71863:
endoplasmic_reticulum_ (16.5)
|   |   |   |   |   |   |   |   |   |   |   start > 71863:
mitochondrion_ (15.67)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 63873
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cellular_bud_ (8.4/2.75)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
site_of_polarized_growth_ (9.96/2.41)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
site_of_polarized_growth_ (9.53/4.62)
|   |   |   |   |   |   |   |   |   |   start > 63873:
cellular_component_ (10.01)
|   |   |   |   |   |   |   start > 74692
|   |   |   |   |   |   |   |   start <= 92412
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 86446: cytoplasm_
(48.17)
|   |   |   |   |   |   |   |   |   |   start > 86446
|   |   |   |   |   |   |   |   |   |   |   start <= 88188: nucleus_
(22.25)
|   |   |   |   |   |   |   |   |   |   |   start > 88188
|   |   |   |   |   |   |   |   |   |   |   |   start <= 89123:
ribosome_ (15.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 89123:
cellular_component_ (15.23)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 80728: nucleus_
(47.77/29.46)
|   |   |   |   |   |   |   |   |   |   start > 80728
|   |   |   |   |   |   |   |   |   |   |   start <= 88188:
nucleolus_ (19.47)
|   |   |   |   |   |   |   |   |   |   |   start > 88188
|   |   |   |   |   |   |   |   |   |   |   |   start <= 89976:
nucleus_ (22.71/10.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 89976
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 90739:
membrane_ (14.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 90739:
cytoplasm_ (6.87)
```

```
|   |   |   |   |   |   |   |   start > 92412
|   |   |   |   |   |   |   |   |   start <= 100117:
cellular_component_ (18.05)
|   |   |   |   |   |   |   |   |   start > 100117: mitochondrion_
(13.85)
|   |   |   |   |   |   start > 101158
|   |   |   |   |   |   |   start <= 107408
|   |   |   |   |   |   |   |   start <= 101888:
microtubule_organizing_center_ (8.03)
|   |   |   |   |   |   |   |   start > 101888: cellular_bud_
(34.62/16.1)
|   |   |   |   |   |   |   start > 107408
|   |   |   |   |   |   |   |   start <= 124762
|   |   |   |   |   |   |   |   |   start <= 117592
|   |   |   |   |   |   |   |   |   |   start <= 113447
|   |   |   |   |   |   |   |   |   |   |   start <= 111439
|   |   |   |   |   |   |   |   |   |   |   |   start <= 110596
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 110541:
cytoplasm_ (44.16/12.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 110541:
mitochondrion_ (11.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 110596:
nucleus_ (29.8/9.97)
|   |   |   |   |   |   |   |   |   |   |   start > 111439
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2865:
cytoplasm_ (33.53/13.7)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2865:
mitochondrion_ (7.39/0.49)
|   |   |   |   |   |   |   |   |   |   start > 113447
|   |   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(19.43)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: cytoplasm_ (22.26/7.86)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: cytoplasm_ (1.47/0.34)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: nucleus_ (0.94/0.38)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: nucleus_ (1.88/0.64)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: cytoplasm_ (4.78/0.79)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: nucleus_ (11.13/1.97)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: cytoplasm_ (4.68/0.69)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: nucleus_ (0.84/0.1)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: nucleus_ (2.58/0.85)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (4.31/1.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
nucleus_ (5.17/1.02)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: cytoplasm_ (2.24/0.4)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: nucleus_ (7.37/1.57)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: nucleus_ (1.65/0.37)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: nucleus_ (2.74/0.49)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: cytoplasm_ (0.89/0.17)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   start > 117592
|   |   |   |   |   |   |   |   |   |   start <= 121877:
cellular_component_ (29.18/11.67)
|   |   |   |   |   |   |   |   |   |   start > 121877: cytoplasm_
(24.52)
|   |   |   |   |   |   |   |   start > 124762
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 132427
|   |   |   |   |   |   |   |   |   |   |   distance <= 3982:
cellular_bud_ (12.31/3.05)
|   |   |   |   |   |   |   |   |   |   |   distance > 3982:
site_of_polarized_growth_ (13.46/2.14)
|   |   |   |   |   |   |   |   |   |   start > 132427:
mitochondrion_ (12.95)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 125128:
membrane_fraction_ (22.82)
|   |   |   |   |   |   |   |   |   |   start > 125128
|   |   |   |   |   |   |   |   |   |   |   start <= 126831:
cellular_component_ (11.11)
|   |   |   |   |   |   |   |   |   |   |   start > 126831: nucleus_
(15.12)
|   |   |   |   |   start > 135519
|   |   |   |   |   |   start <= 151223
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 143396
```

```
|   |   |   |   |   |   |   |   |   start <= 141250:
plasma_membrane_ (15.16)
|   |   |   |   |   |   |   |   |   start > 141250:
endoplasmic_reticulum_ (9.59)
|   |   |   |   |   |   |   |   start > 143396
|   |   |   |   |   |   |   |   |   start <= 147212: cytoplasm_
(17.09)
|   |   |   |   |   |   |   |   |   start > 147212:
cellular_component_ (13.84)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 143396: cellular_component_
(61.73)
|   |   |   |   |   |   |   |   start > 143396
|   |   |   |   |   |   |   |   |   start <= 146190: mitochondrion_
(13.09)
|   |   |   |   |   |   |   |   |   start > 146190: plasma_membrane_
(10.45)
|   |   |   |   |   |   start > 151223
|   |   |   |   |   |   |   start <= 160187
|   |   |   |   |   |   |   |   start <= 158392
|   |   |   |   |   |   |   |   |   start <= 153613: nucleus_
(19.89)
|   |   |   |   |   |   |   |   |   start > 153613:
microtubule_organizing_center_ (20.66)
|   |   |   |   |   |   |   |   start > 158392
|   |   |   |   |   |   |   |   |   start <= 159696
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(17.9/5.09)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(16.75/5.61)
|   |   |   |   |   |   |   |   |   start > 159696: cytoplasm_
(18.54)
|   |   |   |   |   |   |   start > 160187
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 164000: mitochondrion_
(12.46)
|   |   |   |   |   |   |   |   |   start > 164000:
cellular_component_ (23.99)
|   |   |   |   |   |   |   |   strand = W: cytoskeleton_ (28.16)
|   |   |   start > 164775
|   |   |   |   start <= 203541
|   |   |   |   |   start <= 177529
|   |   |   |   |   |   start <= 171484
|   |   |   |   |   |   |   start <= 166137
|   |   |   |   |   |   |   |   neigh_strand = W: nucleus_
(15.45/3.86)
|   |   |   |   |   |   |   |   neigh_strand = C: cytoplasm_
(16.14/5.75)
|   |   |   |   |   |   |   start > 166137
|   |   |   |   |   |   |   |   start <= 168426
|   |   |   |   |   |   |   |   |   start <= 167841: nucleus_
(66.19/42.14)
|   |   |   |   |   |   |   |   |   start > 167841: ribosome_
(19.31)
```

```
|   |   |   |   |   |   |   |   start > 168426: nucleolus_ (36.87)
|   |   |   |   |   |   start > 171484
|   |   |   |   |   |   |   start <= 172537: nucleus_ (22.11)
|   |   |   |   |   |   |   start > 172537: cytoplasm_ (38.45/18.1)
|   |   |   |   |   start > 177529
|   |   |   |   |   |   start <= 184356
|   |   |   |   |   |   |   start <= 181278: mitochondrion_ (22.81)
|   |   |   |   |   |   |   start > 181278
|   |   |   |   |   |   |   |   start <= 182404
|   |   |   |   |   |   |   |   |   start <= 182097: nucleus_
(19.35)
|   |   |   |   |   |   |   |   |   start > 182097
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   distance <= 2176:
membrane_ (5.29/1.75)
|   |   |   |   |   |   |   |   |   |   |   distance > 2176:
endomembrane_system_ (13.07/6.39)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
endoplasmic_reticulum_ (35.82/14.26)
|   |   |   |   |   |   |   |   start > 182404: nucleus_ (30.86)
|   |   |   |   |   |   start > 184356
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 194125
|   |   |   |   |   |   |   |   |   start <= 186477: nucleolus_
(15.14)
|   |   |   |   |   |   |   |   |   start > 186477: Golgi_apparatus_
(12.67)
|   |   |   |   |   |   |   |   start > 194125
|   |   |   |   |   |   |   |   |   start <= 197702: cytoplasm_
(16.06)
|   |   |   |   |   |   |   |   |   start > 197702: nucleolus_
(18.82)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 202059
|   |   |   |   |   |   |   |   |   start <= 192454
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   distance <= 3975:
nucleus_ (5.94/2.43)
|   |   |   |   |   |   |   |   |   |   |   distance > 3975:
cytoplasm_ (4.84/2.22)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
mitochondrion_ (30.51/16.0)
|   |   |   |   |   |   |   |   |   start > 192454
|   |   |   |   |   |   |   |   |   |   start <= 194125:
mitochondrion_ (21.82)
|   |   |   |   |   |   |   |   |   |   start > 194125
|   |   |   |   |   |   |   |   |   |   |   start <= 197702:
cytoplasm_ (8.15)
|   |   |   |   |   |   |   |   |   |   |   start > 197702:
mitochondrion_ (7.1)
|   |   |   |   |   |   |   |   start > 202059:
endoplasmic_reticulum_ (13.76)
|   |   |   |   start > 203541
|   |   |   |   |   start <= 217132
```

```
|   |   |   |   |   |   start <= 209412
|   |   |   |   |   |   |   strand = C: cytoplasmic_membrane-
bound_vesicle_ (9.96)
|   |   |   |   |   |   |   strand = W: cellular_component_ (37.68)
|   |   |   |   |   |   start > 209412: nucleus_ (88.24/30.23)
|   |   |   |   |   start > 217132
|   |   |   |   |   |   start <= 217473: nucleus_ (23.37/9.56)
|   |   |   |   |   |   start > 217473: cytoplasm_ (45.48/11.32)
|   |   start > 227639
|   |   |   start <= 297742
|   |   |   |   start <= 236495: chromosome_ (82.21/36.9)
|   |   |   |   start > 236495
|   |   |   |   |   start <= 287925
|   |   |   |   |   |   start <= 245908
|   |   |   |   |   |   |   start <= 241285: cytoplasm_
(61.51/27.48)
|   |   |   |   |   |   |   start > 241285
|   |   |   |   |   |   |   |   start <= 245669
|   |   |   |   |   |   |   |   |   strand = C:
endoplasmic_reticulum_ (39.35/14.17)
|   |   |   |   |   |   |   |   |   strand = W: mitochondrion_
(14.13)
|   |   |   |   |   |   |   |   start > 245669:
endoplasmic_reticulum_ (15.28)
|   |   |   |   |   |   start > 245908
|   |   |   |   |   |   |   start <= 256329
|   |   |   |   |   |   |   |   start <= 251017
|   |   |   |   |   |   |   |   |   start <= 247012: cytoplasm_
(25.52)
|   |   |   |   |   |   |   |   |   start > 247012:
cellular_component_ (19.04)
|   |   |   |   |   |   |   |   start > 251017
|   |   |   |   |   |   |   |   |   start <= 254210:
plasma_membrane_ (18.74)
|   |   |   |   |   |   |   |   |   start > 254210: nucleus_
(33.23/10.66)
|   |   |   |   |   |   |   start > 256329
|   |   |   |   |   |   |   |   start <= 269503
|   |   |   |   |   |   |   |   |   start <= 266378
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 257973:
cytoplasm_ (7.81)
|   |   |   |   |   |   |   |   |   |   |   start > 257973:
cellular_component_ (17.27)
|   |   |   |   |   |   |   |   |   |   strand = W: cytoplasm_
(17.0)
|   |   |   |   |   |   |   |   |   start > 266378
|   |   |   |   |   |   |   |   |   |   start <= 267336:
membrane_fraction_ (14.46)
|   |   |   |   |   |   |   |   |   |   start > 267336:
Golgi_apparatus_ (21.59)
|   |   |   |   |   |   |   |   start > 269503
|   |   |   |   |   |   |   |   |   start <= 270247:
plasma_membrane_ (19.67)
```

```
|   |   |   |   |   |   |   |   |   start > 270247
|   |   |   |   |   |   |   |   |   |   start <= 275527: cytoplasm_
(32.13)
|   |   |   |   |   |   |   |   |   |   start > 275527
|   |   |   |   |   |   |   |   |   |   |   start <= 283738
|   |   |   |   |   |   |   |   |   |   |   |   start <= 279021
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 278352:
cellular_component_ (18.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 278352:
cytoplasm_ (15.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 279021
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 281443:
plasma_membrane_ (11.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 281443:
cellular_component_ (18.69)
|   |   |   |   |   |   |   |   |   |   |   start > 283738:
cytoplasm_ (17.65)
|   |   |   |   |   start > 287925
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 296002
|   |   |   |   |   |   |   |   start <= 294019
|   |   |   |   |   |   |   |   |   start <= 291865: cytoplasm_
(13.48)
|   |   |   |   |   |   |   |   |   start > 291865: mitochondrion_
(19.54)
|   |   |   |   |   |   |   |   start > 294019: cytoplasm_ (20.06)
|   |   |   |   |   |   |   start > 296002: endoplasmic_reticulum_
(41.0/18.92)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   neigh_num <= 1: mitochondrion_
(18.12/6.19)
|   |   |   |   |   |   |   neigh_num > 1: mitochondrial_envelope_
(23.34/5.71)
|   |   |   start > 297742
|   |   |   |   start <= 318266
|   |   |   |   |   start <= 310313
|   |   |   |   |   |   start <= 306955
|   |   |   |   |   |   |   start <= 300166
|   |   |   |   |   |   |   |   start <= 298292: nucleus_ (25.22)
|   |   |   |   |   |   |   |   start > 298292: ribosome_ (18.53)
|   |   |   |   |   |   |   start > 300166
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 305976: nucleus_
(14.62)
|   |   |   |   |   |   |   |   |   start > 305976:
cellular_component_ (15.58)
|   |   |   |   |   |   |   |   strand = W: cellular_component_
(14.86)
|   |   |   |   |   |   start > 306955
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 307587: nucleolus_ (15.3)
|   |   |   |   |   |   |   |   start > 307587:
endoplasmic_reticulum_ (13.43)
|   |   |   |   |   |   |   strand = W: nucleus_ (25.63/12.22)
```

```
|   |   |   |   |   start > 310313
|   |   |   |   |   |   start <= 316968
|   |   |   |   |   |   |   start <= 315575
|   |   |   |   |   |   |   |   start <= 311897
|   |   |   |   |   |   |   |   |   start <= 311451: mitochondrion_
(8.77)
|   |   |   |   |   |   |   |   |   start > 311451:
site_of_polarized_growth_ (40.25/16.07)
|   |   |   |   |   |   |   |   start > 311897: mitochondrion_
(18.72)
|   |   |   |   |   |   |   start > 315575
|   |   |   |   |   |   |   |   distance <= 5002: cell_wall_
(22.4/7.82)
|   |   |   |   |   |   |   |   distance > 5002:
site_of_polarized_growth_ (9.52/3.14)
|   |   |   |   |   |   start > 316968: peroxisome_ (30.51/14.49)
|   |   |   |   start > 318266
|   |   |   |   |   start <= 432030
|   |   |   |   |   |   start <= 356015
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 330090
|   |   |   |   |   |   |   |   |   start <= 326864
|   |   |   |   |   |   |   |   |   |   start <= 323945
|   |   |   |   |   |   |   |   |   |   |   start <= 321609:
cytoplasm_ (16.28)
|   |   |   |   |   |   |   |   |   |   |   start > 321609:
plasma_membrane_ (11.67)
|   |   |   |   |   |   |   |   |   |   start > 323945
|   |   |   |   |   |   |   |   |   |   |   start <= 326058:
mitochondrion_ (18.15)
|   |   |   |   |   |   |   |   |   |   |   start > 326058:
cytoplasm_ (10.15)
|   |   |   |   |   |   |   |   |   start > 326864: membrane_
(13.61)
|   |   |   |   |   |   |   |   start > 330090
|   |   |   |   |   |   |   |   |   start <= 347877
|   |   |   |   |   |   |   |   |   |   start <= 339350
|   |   |   |   |   |   |   |   |   |   |   start <= 336816
|   |   |   |   |   |   |   |   |   |   |   |   start <= 332829:
cytoplasm_ (29.83/9.63)
|   |   |   |   |   |   |   |   |   |   |   |   start > 332829:
nucleus_ (15.01)
|   |   |   |   |   |   |   |   |   |   |   start > 336816:
cytoplasm_ (29.9)
|   |   |   |   |   |   |   |   |   |   start > 339350
|   |   |   |   |   |   |   |   |   |   |   start <= 343099:
cellular_component_ (17.07)
|   |   |   |   |   |   |   |   |   |   |   start > 343099: nucleus_
(17.4)
|   |   |   |   |   |   |   |   |   start > 347877: cytoplasm_
(26.87)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 343099
|   |   |   |   |   |   |   |   |   start <= 336816
```

```
|   |   |   |   |   |   |   |   |   |   start <= 331831:
mitochondrion_ (18.76)
|   |   |   |   |   |   |   |   |   |   start > 331831: ribosome_
(14.27)
|   |   |   |   |   |   |   |   |   start > 336816: mitochondrion_
(19.88/8.31)
|   |   |   |   |   |   |   |   start > 343099: cytoplasm_ (43.68)
|   |   |   |   |   |   start > 356015
|   |   |   |   |   |   |   start <= 390369
|   |   |   |   |   |   |   |   start <= 382027
|   |   |   |   |   |   |   |   |   start <= 368182
|   |   |   |   |   |   |   |   |   |   start <= 356564:
membrane_fraction_ (16.73)
|   |   |   |   |   |   |   |   |   |   start > 356564
|   |   |   |   |   |   |   |   |   |   |   start <= 365717
|   |   |   |   |   |   |   |   |   |   |   |   start <= 362512
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 360185:
cytoplasm_ (17.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 360185
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasm_: cellular_component_ (9.26/4.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= molecular_function_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= biological_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endomembrane_system_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vesicle-mediated_transport_: nucleus_ (7.03/2.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_component_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= structural_molecule_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_: chromosome_ (9.79/5.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lipid_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrion_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleus_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_kinase_activity_: chromosome_ (7.52/2.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= response_to_stress_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_binding_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cycle_: chromosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nuclear_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= organelle_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleolus_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_binding_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_biogenesis_and_assembly_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peptidase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= microtubule_organizing_center_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= motor_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_organization_and_biogenesis_: nucleus_ (2.93/1.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_bud_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= site_of_polarized_growth_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= enzyme_regulator_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytokinesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= hydrolase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= phosphoprotein_phosphatase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_modification_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transferase_activity_: chromosome_ (4.76/2.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_fraction_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transport_: chromosome_ (2.22/0.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= oxidoreductase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_respiration_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= plasma_membrane_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transporter_activity_: chromosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_catabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endoplasmic_reticulum_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= isomerase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= amino_acid_and_derivative_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_binding_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= helicase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transducer_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= meiosis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cortex_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_regulator_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= chromosome_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrial_envelope_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_regulator_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= conjugation_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasmic_membrane-bound_vesicle_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= sporulation_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_budding_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vacuole_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transduction_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= generation_of_precursor_metabolites_and_energy_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vitamin_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleotidyltransferase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= Golgi_apparatus_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peroxisome_: chromosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ligase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= carbohydrate_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lyase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= pseudohyphal_growth_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= anatomical_structure_morphogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_homeostasis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 362512:
cytoplasm_ (17.95)
|   |   |   |   |   |   |   |   |   |   |   start > 365717:
cellular_component_ (28.03)
|   |   |   |   |   |   |   |   |   start > 368182
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 372732
|   |   |   |   |   |   |   |   |   |   |   |   start <= 370697:
nucleus_ (34.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 370697:
cell_wall_ (19.78)
|   |   |   |   |   |   |   |   |   |   |   start > 372732
|   |   |   |   |   |   |   |   |   |   |   |   start <= 378430:
plasma_membrane_ (29.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 378430:
membrane_fraction_ (9.61)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 380408:
cytoplasm_ (18.02)
|   |   |   |   |   |   |   |   |   |   |   start > 380408: nucleus_
(33.5/12.57)
|   |   |   |   |   |   |   |   start > 382027
|   |   |   |   |   |   |   |   |   start <= 383209
|   |   |   |   |   |   |   |   |   |   start <= 383016:
cellular_component_ (26.78)
|   |   |   |   |   |   |   |   |   |   start > 383016: nucleus_
(9.0)
|   |   |   |   |   |   |   |   |   start > 383209:
cellular_component_ (34.71)
|   |   |   |   |   |   |   start > 390369
|   |   |   |   |   |   |   |   start <= 415977
|   |   |   |   |   |   |   |   |   start <= 405954
|   |   |   |   |   |   |   |   |   |   start <= 393118
|   |   |   |   |   |   |   |   |   |   |   start <= 392287:
cytoplasm_ (17.5)
|   |   |   |   |   |   |   |   |   |   |   start > 392287
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
mitochondrion_ (5.15/2.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
plasma_membrane_ (6.0/1.93)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: mitochondrion_ (12.05/5.15)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: plasma_membrane_ (3.66/1.58)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: membrane_fraction_ (2.94/1.28)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: plasma_membrane_ (7.04/2.47)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: plasma_membrane_ (2.94/1.08)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: plasma_membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: plasma_membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: plasma_membrane_ (2.54/1.44)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: membrane_fraction_ (4.73/2.53)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: plasma_membrane_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: plasma_membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   start > 393118
|   |   |   |   |   |   |   |   |   |   |   start <= 398271:
ribosome_ (36.63/17.05)
|   |   |   |   |   |   |   |   |   |   |   start > 398271
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 400884:
cytoplasm_ (12.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 400884:
mitochondrion_ (21.65)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cytoplasm_ (31.44)
|   |   |   |   |   |   |   |   |   start > 405954
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 411048:
cellular_component_ (10.61)
|   |   |   |   |   |   |   |   |   |   |   start > 411048:
ribosome_ (10.69)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 409163:
nucleus_ (5.55)
|   |   |   |   |   |   |   |   |   |   |   start > 409163:
mitochondrion_ (24.76)
|   |   |   |   |   |   |   |   start > 415977
|   |   |   |   |   |   |   |   |   start <= 427052
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 423759
|   |   |   |   |   |   |   |   |   |   |   |   start <= 419158:
nucleus_ (20.06/8.95)
|   |   |   |   |   |   |   |   |   |   |   |   start > 419158
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= C: plasma_membrane_ (4.73/1.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= F: plasma_membrane_ (7.19/2.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= P: cellular_bud_ (9.68/1.72)
|   |   |   |   |   |   |   |   |   |   |   start > 423759
|   |   |   |   |   |   |   |   |   |   |   |   start <= 426483
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 425760:
nucleus_ (13.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 425760:
chromosome_ (20.58/8.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 426483:
cytoplasm_ (14.69/4.51)
|   |   |   |   |   |   |   |   |   |   strand = W: chromosome_
(16.08)
|   |   |   |   |   |   |   |   |   start > 427052
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 427478:
mitochondrion_ (16.29)
|   |   |   |   |   |   |   |   |   |   |   start > 427478
|   |   |   |   |   |   |   |   |   |   |   |   start <= 429095:
cellular_component_ (13.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 429095:
cell_wall_ (15.96)
|   |   |   |   |   |   |   |   |   |   strand = W: cytoplasm_
(15.17)
|   |   |   |   |   start > 432030
|   |   |   |   |   |   start <= 458866
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 444687
|   |   |   |   |   |   |   |   |   start <= 436945: nucleus_ (7.8)
|   |   |   |   |   |   |   |   |   start > 436945: ribosome_
(13.81)
```

```
|   |   |   |   |   |   |   |   start > 444687
|   |   |   |   |   |   |   |   |   start <= 452652
|   |   |   |   |   |   |   |   |   |   start <= 447703:
cellular_bud_ (30.87/9.4)
|   |   |   |   |   |   |   |   |   |   start > 447703:
cytoplasmic_membrane-bound_vesicle_ (21.98)
|   |   |   |   |   |   |   |   |   start > 452652
|   |   |   |   |   |   |   |   |   |   start <= 454816
|   |   |   |   |   |   |   |   |   |   |   distance <= 1649:
chromosome_ (12.82/3.7)
|   |   |   |   |   |   |   |   |   |   |   distance > 1649:
nucleus_ (17.18/6.83)
|   |   |   |   |   |   |   |   |   |   start > 454816:
cellular_bud_ (31.23/11.2)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 452652
|   |   |   |   |   |   |   |   |   start <= 447703
|   |   |   |   |   |   |   |   |   |   start <= 436945
|   |   |   |   |   |   |   |   |   |   |   start <= 436015:
endoplasmic_reticulum_ (14.1)
|   |   |   |   |   |   |   |   |   |   |   start > 436015:
mitochondrion_ (20.76)
|   |   |   |   |   |   |   |   |   |   start > 436945: nucleus_
(32.55)
|   |   |   |   |   |   |   |   |   start > 447703: mitochondrion_
(59.45/23.36)
|   |   |   |   |   |   |   |   start > 452652
|   |   |   |   |   |   |   |   |   start <= 454816:
plasma_membrane_ (21.89)
|   |   |   |   |   |   |   |   |   start > 454816:
endoplasmic_reticulum_ (19.79)
|   |   |   |   |   |   start > 458866
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 486685
|   |   |   |   |   |   |   |   |   start <= 484497
|   |   |   |   |   |   |   |   |   |   start <= 477665
|   |   |   |   |   |   |   |   |   |   |   start <= 462133:
mitochondrion_ (58.79/38.65)
|   |   |   |   |   |   |   |   |   |   |   start > 462133
|   |   |   |   |   |   |   |   |   |   |   |   start <= 467242:
nucleus_ (18.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 467242
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 473920:
cytoplasm_ (15.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 473920:
nucleus_ (35.38/15.38)
|   |   |   |   |   |   |   |   |   |   start > 477665:
mitochondrion_ (43.91/7.03)
|   |   |   |   |   |   |   |   |   start > 484497:
cellular_component_ (27.39/13.44)
|   |   |   |   |   |   |   |   start > 486685
|   |   |   |   |   |   |   |   |   start <= 492816: cytoplasm_
(48.83)
|   |   |   |   |   |   |   |   |   start > 492816
```

```
|   |   |   |   |   |   |   |   |   |   start <= 494109:
membrane_fraction_ (14.27)
|   |   |   |   |   |   |   |   |   |   start > 494109: cytoplasm_
(41.05/11.25)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 462133: membrane_
(45.65/24.55)
|   |   |   |   |   |   |   |   start > 462133
|   |   |   |   |   |   |   |   |   start <= 477665
|   |   |   |   |   |   |   |   |   |   start <= 467242: nucleus_
(8.78)
|   |   |   |   |   |   |   |   |   |   start > 467242: ribosome_
(18.2)
|   |   |   |   |   |   |   |   |   start > 477665: nucleus_ (17.62)
|   start > 496863
|   |   start <= 747798
|   |   |   start <= 607647
|   |   |   |   start <= 504281
|   |   |   |   |   start <= 501436
|   |   |   |   |   |   start <= 497157: membrane_ (17.08)
|   |   |   |   |   |   start > 497157
|   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   distance <= 2587: membrane_
(8.92/3.81)
|   |   |   |   |   |   |   |   distance > 2587:
endoplasmic_reticulum_ (9.66/4.63)
|   |   |   |   |   |   |   neigh_num > 1: endomembrane_system_
(30.8/18.56)
|   |   |   |   |   start > 501436: site_of_polarized_growth_
(30.13/13.83)
|   |   |   |   start > 504281
|   |   |   |   |   start <= 556543
|   |   |   |   |   |   start <= 546370
|   |   |   |   |   |   |   start <= 528311
|   |   |   |   |   |   |   |   start <= 515330
|   |   |   |   |   |   |   |   |   start <= 505662
|   |   |   |   |   |   |   |   |   |   start <= 504848
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: cytoplasm_ (1.67/0.41)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: nucleus_ (7.25/1.61)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: nucleus_ (1.25/0.29)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: cytoplasm_ (2.82/1.06)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 3079:
nucleus_ (2.28/0.67)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 3079:
cytoplasm_ (7.11/0.56)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: nucleus_ (4.53/1.48)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: cytoplasm_ (6.58/1.5)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: nucleus_ (3.1/0.41)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: nucleus_ (1.29/0.23)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: nucleus_ (1.46/0.28)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: nucleus_ (0.63/0.2)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   start > 504848
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
mitochondrion_ (23.3/8.86)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (17.14/7.79)
|   |   |   |   |   |   |   |   |   start > 505662: cytoplasm_
(28.25)
|   |   |   |   |   |   |   |   start > 515330
|   |   |   |   |   |   |   |   |   start <= 526622
|   |   |   |   |   |   |   |   |   |   start <= 515658: vacuole_
(15.96)
|   |   |   |   |   |   |   |   |   |   start > 515658:
mitochondrion_ (26.25/13.0)
|   |   |   |   |   |   |   |   |   start > 526622: nucleolus_
(32.14)
|   |   |   |   |   |   |   start > 528311
|   |   |   |   |   |   |   |   start <= 544487
|   |   |   |   |   |   |   |   |   start <= 533756
|   |   |   |   |   |   |   |   |   |   start <= 532176: cytoplasm_
(14.2)
```

```
|   |   |   |   |   |   |   |   |   |   start > 532176
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (14.81/4.39)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleus_ (8.16/2.81)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (6.49/1.25)
|   |   |   |   |   |   |   |   |   start > 533756
|   |   |   |   |   |   |   |   |   |   start <= 537870
|   |   |   |   |   |   |   |   |   |   |   start <= 536569:
mitochondrion_ (34.6)
|   |   |   |   |   |   |   |   |   |   |   start > 536569:
cellular_component_ (7.28)
|   |   |   |   |   |   |   |   |   |   start > 537870
|   |   |   |   |   |   |   |   |   |   |   start <= 539981:
cytoplasm_ (13.5)
|   |   |   |   |   |   |   |   |   |   |   start > 539981
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2498:
nucleus_ (19.97/11.1)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2498:
mitochondrion_ (26.54/14.38)
|   |   |   |   |   |   |   |   start > 544487
|   |   |   |   |   |   |   |   |   start <= 545022: cytoplasm_
(31.25/14.56)
|   |   |   |   |   |   |   |   |   start > 545022: nucleus_ (16.57)
|   |   |   |   |   |   start > 546370
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 549765: nucleolus_ (17.91)
|   |   |   |   |   |   |   |   start > 549765
|   |   |   |   |   |   |   |   |   start <= 553194: cytoskeleton_
(11.63)
|   |   |   |   |   |   |   |   |   start > 553194:
cellular_component_ (14.33)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 547454: cellular_component_
(19.63)
|   |   |   |   |   |   |   |   start > 547454
|   |   |   |   |   |   |   |   |   start <= 549765: cytoplasm_
(21.75)
|   |   |   |   |   |   |   |   |   start > 549765: nucleus_
(54.65/29.12)
|   |   |   |   |   start > 556543
|   |   |   |   |   |   start <= 597358
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 581367
|   |   |   |   |   |   |   |   |   start <= 568847
|   |   |   |   |   |   |   |   |   |   start <= 565718: cell_wall_
(18.18)
|   |   |   |   |   |   |   |   |   |   start > 565718:
Golgi_apparatus_ (14.69)
|   |   |   |   |   |   |   |   |   start > 568847
|   |   |   |   |   |   |   |   |   |   start <= 572366
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 571195:
cytoplasm_ (14.71)
|   |   |   |   |   |   |   |   |   |   |   start > 571195:
nucleolus_ (18.76)
|   |   |   |   |   |   |   |   |   |   start > 572366
|   |   |   |   |   |   |   |   |   |   |   distance <= 3971
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 1516:
endoplasmic_reticulum_ (3.38/0.32)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 1516
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: cytoplasm_ (35.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
578359
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
575991: cytoplasm_ (5.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
575991: endoplasmic_reticulum_ (4.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
578359: cytoplasm_ (10.62)
|   |   |   |   |   |   |   |   |   |   |   distance > 3971:
endoplasmic_reticulum_ (5.04)
|   |   |   |   |   |   |   |   start > 581367
|   |   |   |   |   |   |   |   |   start <= 594859
|   |   |   |   |   |   |   |   |   |   start <= 583715: nucleus_
(42.98/16.22)
|   |   |   |   |   |   |   |   |   |   start > 583715
|   |   |   |   |   |   |   |   |   |   |   start <= 589736:
mitochondrion_ (22.8)
|   |   |   |   |   |   |   |   |   |   |   start > 589736
|   |   |   |   |   |   |   |   |   |   |   |   start <= 592769:
cytoplasm_ (6.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 592769
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1343: nucleus_ (12.26/2.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 1343:
cytoplasm_ (20.13/8.16)
|   |   |   |   |   |   |   |   |   start > 594859:
cellular_component_ (12.87)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 565226
|   |   |   |   |   |   |   |   |   start <= 560072
|   |   |   |   |   |   |   |   |   |   start <= 558679:
endoplasmic_reticulum_ (24.73)
|   |   |   |   |   |   |   |   |   |   start > 558679: cytoplasm_
(53.3/27.54)
|   |   |   |   |   |   |   |   |   start > 560072
|   |   |   |   |   |   |   |   |   |   start <= 561629: vacuole_
(16.28)
|   |   |   |   |   |   |   |   |   |   start > 561629:
endoplasmic_reticulum_ (12.9)
|   |   |   |   |   |   |   |   start > 565226
|   |   |   |   |   |   |   |   |   start <= 572366
```

```
|   |   |   |   |   |   |   |   |   |   start <= 565718:
mitochondrion_ (19.64)
|   |   |   |   |   |   |   |   |   |   start > 565718
|   |   |   |   |   |   |   |   |   |   |   start <= 568847:
nucleus_ (10.31)
|   |   |   |   |   |   |   |   |   |   |   start > 568847:
peroxisome_ (16.6)
|   |   |   |   |   |   |   |   |   start > 572366
|   |   |   |   |   |   |   |   |   |   start <= 578359:
endoplasmic_reticulum_ (51.81/30.58)
|   |   |   |   |   |   |   |   |   |   start > 578359
|   |   |   |   |   |   |   |   |   |   |   start <= 586157
|   |   |   |   |   |   |   |   |   |   |   |   start <= 582403:
nucleus_ (38.99/19.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 582403:
mitochondrion_ (7.72)
|   |   |   |   |   |   |   |   |   |   |   start > 586157
|   |   |   |   |   |   |   |   |   |   |   |   start <= 596110
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 592769:
membrane_ (8.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 592769:
endoplasmic_reticulum_ (26.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 596110:
cellular_component_ (13.84)
|   |   |   |   |   |   start > 597358
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 600548: mitochondrion_
(12.02)
|   |   |   |   |   |   |   |   start > 600548: nucleus_ (23.26)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 606265
|   |   |   |   |   |   |   |   |   start <= 602629
|   |   |   |   |   |   |   |   |   |   start <= 600548: nucleolus_
(15.18)
|   |   |   |   |   |   |   |   |   |   start > 600548: vacuole_
(27.57)
|   |   |   |   |   |   |   |   |   start > 602629: ribosome_
(41.76/15.91)
|   |   |   |   |   |   |   |   start > 606265: mitochondrion_
(19.88)
|   |   |   start > 607647
|   |   |   |   start <= 664672
|   |   |   |   |   start <= 633376
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 613895
|   |   |   |   |   |   |   |   start <= 611877: cellular_component_
(78.0/38.9)
|   |   |   |   |   |   |   |   start > 611877: mitochondrion_
(16.48)
|   |   |   |   |   |   |   start > 613895
|   |   |   |   |   |   |   |   start <= 620867
|   |   |   |   |   |   |   |   |   start <= 614625:
cellular_component_ (31.96)
|   |   |   |   |   |   |   |   |   start > 614625
```

```
|   |   |   |   |   |   |   |   |   |   start <= 615851
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (21.67/5.0)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(23.8/8.97)
|   |   |   |   |   |   |   |   |   |   start > 615851
|   |   |   |   |   |   |   |   |   |   |   distance <= 4686:
cellular_component_ (20.03/8.17)
|   |   |   |   |   |   |   |   |   |   |   distance > 4686:
nucleus_ (15.13/1.91)
|   |   |   |   |   |   |   |   start > 620867: cellular_component_
(39.9)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 622978
|   |   |   |   |   |   |   |   start <= 618904
|   |   |   |   |   |   |   |   |   start <= 614168: cytoplasm_
(18.23)
|   |   |   |   |   |   |   |   |   start > 614168: Golgi_apparatus_
(20.14)
|   |   |   |   |   |   |   |   start > 618904
|   |   |   |   |   |   |   |   |   start <= 620867: cellular_bud_
(25.17/11.68)
|   |   |   |   |   |   |   |   |   start > 620867:
cellular_component_ (15.13)
|   |   |   |   |   |   |   start > 622978
|   |   |   |   |   |   |   |   start <= 623572:
endomembrane_system_ (51.69/29.34)
|   |   |   |   |   |   |   |   start > 623572
|   |   |   |   |   |   |   |   |   start <= 625767: nucleus_
(35.97/13.79)
|   |   |   |   |   |   |   |   |   start > 625767: mitochondrion_
(17.65)
|   |   |   |   |   start > 633376
|   |   |   |   |   |   start <= 635141
|   |   |   |   |   |   |   start <= 633617: membrane_fraction_
(12.07)
|   |   |   |   |   |   |   start > 633617: membrane_ (36.71/14.85)
|   |   |   |   |   |   start > 635141
|   |   |   |   |   |   |   start <= 647881
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 643073: cytoplasm_
(29.14)
|   |   |   |   |   |   |   |   |   start > 643073:
microtubule_organizing_center_ (17.35)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 645545
|   |   |   |   |   |   |   |   |   |   start <= 645162: cytoplasm_
(14.45)
|   |   |   |   |   |   |   |   |   |   start > 645162:
cytoplasmic_membrane-bound_vesicle_ (20.15)
|   |   |   |   |   |   |   |   |   start > 645545: cytoplasm_
(24.5)
|   |   |   |   |   |   |   start > 647881
|   |   |   |   |   |   |   |   start <= 662244
```

```
|   |   |   |   |   |   |   |   |   start <= 650363:
cellular_component_ (20.25)
|   |   |   |   |   |   |   |   |   start > 650363
|   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(28.34)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 653351
|   |   |   |   |   |   |   |   |   |   |   |   start <= 651410:
cytoplasm_ (14.52)
|   |   |   |   |   |   |   |   |   |   |   |   start > 651410:
nucleus_ (15.06)
|   |   |   |   |   |   |   |   |   |   |   start > 653351:
membrane_fraction_ (16.85)
|   |   |   |   |   |   |   |   start > 662244: cellular_component_
(29.32)
|   |   |   |   start > 664672
|   |   |   |   |   start <= 730382
|   |   |   |   |   |   start <= 707523
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 701837
|   |   |   |   |   |   |   |   |   start <= 680357
|   |   |   |   |   |   |   |   |   |   start <= 670622
|   |   |   |   |   |   |   |   |   |   |   start <= 666533:
mitochondrion_ (12.83)
|   |   |   |   |   |   |   |   |   |   |   start > 666533
|   |   |   |   |   |   |   |   |   |   |   |   start <= 668346:
cytoplasm_ (14.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 668346:
nucleus_ (10.77)
|   |   |   |   |   |   |   |   |   |   start > 670622:
mitochondrion_ (64.26/17.07)
|   |   |   |   |   |   |   |   |   start > 680357
|   |   |   |   |   |   |   |   |   |   start <= 691964
|   |   |   |   |   |   |   |   |   |   |   start <= 683423:
nucleus_ (29.94)
|   |   |   |   |   |   |   |   |   |   |   start > 683423
|   |   |   |   |   |   |   |   |   |   |   |   start <= 686896:
cytoskeleton_ (11.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 686896:
nucleus_ (18.46)
|   |   |   |   |   |   |   |   |   |   start > 691964
|   |   |   |   |   |   |   |   |   |   |   start <= 697297:
mitochondrion_ (49.3/20.93)
|   |   |   |   |   |   |   |   |   |   |   start > 697297
|   |   |   |   |   |   |   |   |   |   |   |   start <= 699938
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: cytoplasm_ (4.3/1.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: nucleus_ (6.34/2.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= F: nucleus_ (9.97/3.39)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= P: cytoplasm_ (10.34/2.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 699938:
nucleus_ (13.01)
|   |   |   |   |   |   |   |   start > 701837
|   |   |   |   |   |   |   |   |   start <= 704665: membrane_
(20.1)
|   |   |   |   |   |   |   |   |   start > 704665:
endoplasmic_reticulum_ (32.81)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 686896
|   |   |   |   |   |   |   |   |   start <= 681857
|   |   |   |   |   |   |   |   |   |   start <= 670622:
cellular_component_ (17.42)
|   |   |   |   |   |   |   |   |   |   start > 670622
|   |   |   |   |   |   |   |   |   |   |   start <= 675308:
nucleus_ (21.99)
|   |   |   |   |   |   |   |   |   |   |   start > 675308:
cellular_component_ (16.84)
|   |   |   |   |   |   |   |   |   start > 681857
|   |   |   |   |   |   |   |   |   |   start <= 684972
|   |   |   |   |   |   |   |   |   |   |   start <= 683423:
cytoplasm_ (13.62)
|   |   |   |   |   |   |   |   |   |   |   start > 683423
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
chromosome_ (10.57/2.5)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoskeleton_ (8.66/3.04)
|   |   |   |   |   |   |   |   |   |   start > 684972:
cellular_component_ (15.95)
|   |   |   |   |   |   |   |   start > 686896
|   |   |   |   |   |   |   |   |   start <= 697297: nucleus_
(16.41)
|   |   |   |   |   |   |   |   |   start > 697297: cytoplasm_
(58.96/24.43)
|   |   |   |   |   |   start > 707523
|   |   |   |   |   |   |   start <= 724451
|   |   |   |   |   |   |   |   start <= 723265
|   |   |   |   |   |   |   |   |   start <= 716460
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 714450
|   |   |   |   |   |   |   |   |   |   |   |   start <= 711586:
nucleus_ (35.88/17.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 711586
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
4976: nucleolus_ (22.23/7.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 4976:
nucleus_ (8.05/1.18)
|   |   |   |   |   |   |   |   |   |   |   start > 714450:
cellular_component_ (23.52)
|   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (23.33)
|   |   |   |   |   |   |   |   |   start > 716460
```

```
|   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(21.35/9.5)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 721385
|   |   |   |   |   |   |   |   |   |   |   |   start <= 719028:
cellular_component_ (15.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 719028:
mitochondrion_ (23.37)
|   |   |   |   |   |   |   |   |   |   |   start > 721385
|   |   |   |   |   |   |   |   |   |   |   |   start <= 722606:
cytoplasm_ (23.24/10.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 722606
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
4029: nucleus_ (21.56/8.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 4029:
cellular_component_ (6.64/0.71)
|   |   |   |   |   |   |   |   start > 723265
|   |   |   |   |   |   |   |   |   start <= 724258:
Golgi_apparatus_ (18.23)
|   |   |   |   |   |   |   |   |   start > 724258: cytoplasm_
(17.03)
|   |   |   |   |   |   |   start > 724451
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 728880:
cellular_component_ (35.63)
|   |   |   |   |   |   |   |   |   start > 728880: nucleus_ (17.37)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 728880: nucleolus_
(22.11)
|   |   |   |   |   |   |   |   |   start > 728880:
cellular_component_ (18.18)
|   |   |   |   |   start > 730382
|   |   |   |   |   |   start <= 734634: cellular_bud_ (14.18)
|   |   |   |   |   |   start > 734634
|   |   |   |   |   |   |   start <= 742571
|   |   |   |   |   |   |   |   start <= 739836
|   |   |   |   |   |   |   |   |   start <= 736259
|   |   |   |   |   |   |   |   |   |   start <= 735525: cytoplasm_
(23.11)
|   |   |   |   |   |   |   |   |   |   start > 735525:
mitochondrion_ (31.01)
|   |   |   |   |   |   |   |   |   start > 736259
|   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(20.22)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 738577:
endoplasmic_reticulum_ (32.85/14.53)
|   |   |   |   |   |   |   |   |   |   |   start > 738577:
cytoplasm_ (13.32)
|   |   |   |   |   |   |   |   start > 739836: mitochondrion_
(21.6)
|   |   |   |   |   |   |   start > 742571
|   |   |   |   |   |   |   |   start <= 744393: cellular_component_
(12.67)
```

```
|   |   |   |   |   |   |   |   start > 744393: cytoplasm_ (26.69)
|   |   start > 747798
|   |   |   start <= 787001
|   |   |   |   start <= 767602
|   |   |   |   |   start <= 749366: endoplasmic_reticulum_ (13.38)
|   |   |   |   |   start > 749366
|   |   |   |   |   |   start <= 764693
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 757101: nucleus_
(30.23/12.2)
|   |   |   |   |   |   |   |   start > 757101: cellular_component_
(33.26)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 749589: nucleus_ (19.65)
|   |   |   |   |   |   |   |   start > 749589
|   |   |   |   |   |   |   |   |   start <= 760290: chromosome_
(24.58)
|   |   |   |   |   |   |   |   |   start > 760290: nucleus_ (15.04)
|   |   |   |   |   |   start > 764693: nucleus_ (26.4/7.05)
|   |   |   |   start > 767602
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 779663
|   |   |   |   |   |   |   start <= 774696: endomembrane_system_
(15.22)
|   |   |   |   |   |   |   start > 774696: membrane_ (26.85/9.35)
|   |   |   |   |   |   start > 779663: mitochondrion_ (20.33)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 773918
|   |   |   |   |   |   |   start <= 768236: mitochondrion_ (18.07)
|   |   |   |   |   |   |   start > 768236: cellular_component_
(36.02)
|   |   |   |   |   |   start > 773918
|   |   |   |   |   |   |   start <= 784568
|   |   |   |   |   |   |   |   start <= 774696: vacuole_ (17.11)
|   |   |   |   |   |   |   |   start > 774696
|   |   |   |   |   |   |   |   |   start <= 779663
|   |   |   |   |   |   |   |   |   |   start <= 776567:
endoplasmic_reticulum_ (16.04)
|   |   |   |   |   |   |   |   |   |   start > 776567:
cellular_component_ (35.43/12.88)
|   |   |   |   |   |   |   |   |   start > 779663:
endoplasmic_reticulum_ (23.41)
|   |   |   |   |   |   |   start > 784568: membrane_ (18.48/5.54)
|   |   |   start > 787001
|   |   |   |   start <= 798516: plasma_membrane_ (48.94)
|   |   |   |   start > 798516
|   |   |   |   |   start <= 805345
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 800517: cellular_component_
(20.48)
|   |   |   |   |   |   |   start > 800517
|   |   |   |   |   |   |   |   start <= 804469: membrane_fraction_
(17.34)
```

```
|   |   |   |   |   |   |   |   start > 804469: cellular_component_
(12.11)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 800517: nucleus_ (20.91)
|   |   |   |   |   |   |   start > 800517: cellular_component_
(16.43)
|   |   |   |   |   start > 805345
|   |   |   |   |   |   start <= 809051: cell_wall_ (9.28)
|   |   |   |   |   |   start > 809051: vacuole_ (6.23)
```

For Molecular Function

```
|   start <= 147212
|   |   start <= 63873
|   |   |   start <= 44915
|   |   |   |   start <= 43274
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 2658: helicase_activity_ (7.41)
|   |   |   |   |   |   start > 2658
|   |   |   |   |   |   |   start <= 21293
|   |   |   |   |   |   |   |   start <= 13879: molecular_function_
(54.82)
|   |   |   |   |   |   |   |   start > 13879
|   |   |   |   |   |   |   |   |   start <= 17696:
protein_kinase_activity_ (15.48)
|   |   |   |   |   |   |   |   |   start > 17696:
molecular_function_ (18.86)
|   |   |   |   |   |   |   start > 21293
|   |   |   |   |   |   |   |   start <= 24098:
transcription_regulator_activity_ (13.81)
|   |   |   |   |   |   |   |   start > 24098: molecular_function_
(16.97)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 36395: molecular_function_ (56.83)
|   |   |   |   |   |   start > 36395
|   |   |   |   |   |   |   start <= 39142
|   |   |   |   |   |   |   |   start <= 37050:
transporter_activity_ (6.02)
|   |   |   |   |   |   |   |   start > 37050:
oxidoreductase_activity_ (9.28)
|   |   |   |   |   |   |   start > 39142: molecular_function_
(19.98)
|   |   |   |   start > 43274: transcription_regulator_activity_
(28.15)
|   |   |   start > 44915
|   |   |   |   start <= 60735
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 59379
|   |   |   |   |   |   |   start <= 49571
|   |   |   |   |   |   |   |   start <= 47177: molecular_function_
(7.71)
|   |   |   |   |   |   |   |   start > 47177: peptidase_activity_
(8.87)
```

```
|   |   |   |   |   |   |   start > 49571: protein_kinase_activity_
(17.49)
|   |   |   |   |   |   start > 59379: structural_molecule_activity_
(24.28)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 48822:
structural_molecule_activity_ (36.11)
|   |   |   |   |   |   start > 48822: transporter_activity_ (17.11)
|   |   |   |   start > 60735: molecular_function_ (26.52)
|   |   start > 63873
|   |   |   strand = C
|   |   |   |   start <= 100117
|   |   |   |   |   start <= 86446
|   |   |   |   |   |   start <= 71863
|   |   |   |   |   |   |   start <= 69442: protein_binding_ (15.9)
|   |   |   |   |   |   |   start > 69442: transferase_activity_
(18.2)
|   |   |   |   |   |   start > 71863
|   |   |   |   |   |   |   start <= 75256: molecular_function_
(12.28)
|   |   |   |   |   |   |   start > 75256
|   |   |   |   |   |   |   |   start <= 80728: protein_binding_
(11.69)
|   |   |   |   |   |   |   |   start > 80728
|   |   |   |   |   |   |   |   |   start <= 84259: ligase_activity_
(9.73)
|   |   |   |   |   |   |   |   |   start > 84259: protein_binding_
(7.64)
|   |   |   |   |   start > 86446
|   |   |   |   |   |   start <= 89123
|   |   |   |   |   |   |   start <= 88188: molecular_function_
(18.2)
|   |   |   |   |   |   |   start > 88188:
structural_molecule_activity_ (17.03)
|   |   |   |   |   |   start > 89123
|   |   |   |   |   |   |   start <= 95884
|   |   |   |   |   |   |   |   start <= 92412: molecular_function_
(11.35)
|   |   |   |   |   |   |   |   start > 92412: peptidase_activity_
(11.45)
|   |   |   |   |   |   |   start > 95884: molecular_function_
(25.41)
|   |   |   |   start > 100117
|   |   |   |   |   start <= 117592
|   |   |   |   |   |   start <= 111439
|   |   |   |   |   |   |   start <= 101888:
oxidoreductase_activity_ (27.47/12.2)
|   |   |   |   |   |   |   start > 101888
|   |   |   |   |   |   |   |   start <= 107934:
enzyme_regulator_activity_ (25.92)
|   |   |   |   |   |   |   |   start > 107934: molecular_function_
(17.17)
|   |   |   |   |   |   start > 111439: hydrolase_activity_ (39.45)
|   |   |   |   |   start > 117592
```

```
|   |   |   |   |   |   start <= 136691
|   |   |   |   |   |   |   start <= 126831
|   |   |   |   |   |   |   |   start <= 121877:
transferase_activity_ (13.22)
|   |   |   |   |   |   |   |   start > 121877: molecular_function_
(14.61)
|   |   |   |   |   |   |   start > 126831
|   |   |   |   |   |   |   |   start <= 132427: protein_binding_
(12.52)
|   |   |   |   |   |   |   |   start > 132427:
oxidoreductase_activity_ (12.49)
|   |   |   |   |   |   start > 136691
|   |   |   |   |   |   |   start <= 143396
|   |   |   |   |   |   |   |   start <= 141250:
transporter_activity_ (13.44)
|   |   |   |   |   |   |   |   start > 141250: molecular_function_
(14.64)
|   |   |   |   |   |   |   start > 143396: ligase_activity_ (14.59)
|   |   |   strand = W
|   |   |   |   start <= 101888
|   |   |   |   |   start <= 90739
|   |   |   |   |   |   distance <= 2498
|   |   |   |   |   |   |   start <= 88188
|   |   |   |   |   |   |   |   start <= 71863: molecular_function_
(14.04)
|   |   |   |   |   |   |   |   start > 71863: RNA_binding_
(13.47/0.76)
|   |   |   |   |   |   |   start > 88188: molecular_function_
(29.49)
|   |   |   |   |   |   distance > 2498
|   |   |   |   |   |   |   start <= 71863: molecular_function_
(12.12)
|   |   |   |   |   |   |   start > 71863:
structural_molecule_activity_ (12.14)
|   |   |   |   |   start > 90739
|   |   |   |   |   |   start <= 95884: transferase_activity_ (5.51)
|   |   |   |   |   |   start > 95884: motor_activity_ (39.66/12.3)
|   |   |   |   start > 101888
|   |   |   |   |   start <= 132427
|   |   |   |   |   |   distance <= 4114
|   |   |   |   |   |   |   start <= 113765
|   |   |   |   |   |   |   |   start <= 111439
|   |   |   |   |   |   |   |   |   start <= 107934:
enzyme_regulator_activity_ (19.25)
|   |   |   |   |   |   |   |   |   start > 107934
|   |   |   |   |   |   |   |   |   |   start <= 110596:
molecular_function_ (13.98)
|   |   |   |   |   |   |   |   |   |   start > 110596:
enzyme_regulator_activity_ (15.88)
|   |   |   |   |   |   |   |   start > 111439:
phosphoprotein_phosphatase_activity_ (27.31)
|   |   |   |   |   |   |   start > 113765
|   |   |   |   |   |   |   |   start <= 126831
|   |   |   |   |   |   |   |   |   distance <= 2019
```

```
|   |   |   |   |   |   |   |   |   |   start <= 125128
|   |   |   |   |   |   |   |   |   |   |   start <= 117592:
molecular_function_ (2.71)
|   |   |   |   |   |   |   |   |   |   |   start > 117592:
protein_binding_ (5.28)
|   |   |   |   |   |   |   |   |   |   start > 125128:
molecular_function_ (5.53)
|   |   |   |   |   |   |   |   |   distance > 2019:
molecular_function_ (29.28)
|   |   |   |   |   |   |   |   start > 126831:
enzyme_regulator_activity_ (19.82)
|   |   |   |   |   |   distance > 4114: protein_binding_
(12.02/0.46)
|   |   |   |   |   start > 132427
|   |   |   |   |   |   start <= 143396
|   |   |   |   |   |   |   start <= 136691: molecular_function_
(32.88)
|   |   |   |   |   |   |   start > 136691
|   |   |   |   |   |   |   |   start <= 141250: peptidase_activity_
(11.72)
|   |   |   |   |   |   |   |   start > 141250: molecular_function_
(23.34)
|   |   |   |   |   |   start > 143396
|   |   |   |   |   |   |   start <= 146190:
structural_molecule_activity_ (18.96)
|   |   |   |   |   |   |   start > 146190: molecular_function_
(31.35)
|   start > 147212
|   |   start <= 307345
|   |   |   start <= 170626
|   |   |   |   start <= 153613
|   |   |   |   |   start <= 151223: isomerase_activity_
(40.62/16.9)
|   |   |   |   |   start > 151223: nucleotidyltransferase_activity_
(16.56)
|   |   |   |   start > 153613
|   |   |   |   |   start <= 159696
|   |   |   |   |   |   start <= 158392:
structural_molecule_activity_ (20.53)
|   |   |   |   |   |   start > 158392: hydrolase_activity_ (19.92)
|   |   |   |   |   start > 159696
|   |   |   |   |   |   start <= 167841
|   |   |   |   |   |   |   start <= 160187: RNA_binding_ (23.18)
|   |   |   |   |   |   |   start > 160187
|   |   |   |   |   |   |   |   start <= 164000
|   |   |   |   |   |   |   |   |   start <= 161702:
molecular_function_ (18.55)
|   |   |   |   |   |   |   |   |   start > 161702:
transporter_activity_ (19.47)
|   |   |   |   |   |   |   |   start > 164000: molecular_function_
(48.12)
|   |   |   |   |   |   start > 167841
|   |   |   |   |   |   |   start <= 168426:
structural_molecule_activity_ (29.66)
```

```
|   |   |   |   |   |   |   start > 168426: RNA_binding_ (16.62)
|   |   |   start > 170626
|   |   |   |   start <= 217473
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 181278
|   |   |   |   |   |   |   start <= 177529: molecular_function_
(65.27/41.59)
|   |   |   |   |   |   |   start > 177529: peptidase_activity_
(19.17)
|   |   |   |   |   |   start > 181278
|   |   |   |   |   |   |   start <= 209656
|   |   |   |   |   |   |   |   start <= 186477
|   |   |   |   |   |   |   |   |   start <= 182404:
transcription_regulator_activity_ (24.75)
|   |   |   |   |   |   |   |   |   start > 182404:
hydrolase_activity_ (22.08)
|   |   |   |   |   |   |   |   start > 186477
|   |   |   |   |   |   |   |   |   start <= 197702:
molecular_function_ (34.0)
|   |   |   |   |   |   |   |   |   start > 197702
|   |   |   |   |   |   |   |   |   |   start <= 203541:
transcription_regulator_activity_ (11.46)
|   |   |   |   |   |   |   |   |   |   start > 203541:
molecular_function_ (13.38)
|   |   |   |   |   |   |   start > 209656
|   |   |   |   |   |   |   |   start <= 216369: protein_binding_
(24.19)
|   |   |   |   |   |   |   |   start > 216369: hydrolase_activity_
(10.21)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 186477
|   |   |   |   |   |   |   start <= 172537
|   |   |   |   |   |   |   |   start <= 171484:
transcription_regulator_activity_ (20.68)
|   |   |   |   |   |   |   |   start > 171484:
transferase_activity_ (25.44)
|   |   |   |   |   |   |   start > 172537
|   |   |   |   |   |   |   |   start <= 182404:
transporter_activity_ (17.29)
|   |   |   |   |   |   |   |   start > 182404: lyase_activity_
(26.11)
|   |   |   |   |   |   start > 186477
|   |   |   |   |   |   |   start <= 209412
|   |   |   |   |   |   |   |   start <= 194125
|   |   |   |   |   |   |   |   |   start <= 192454:
protein_kinase_activity_ (23.5/10.91)
|   |   |   |   |   |   |   |   |   start > 192454:
hydrolase_activity_ (13.14)
|   |   |   |   |   |   |   |   start > 194125
|   |   |   |   |   |   |   |   |   start <= 203541
|   |   |   |   |   |   |   |   |   |   start <= 197702:
molecular_function_ (14.61)
|   |   |   |   |   |   |   |   |   |   start > 197702:
transferase_activity_ (25.24)
```

```
|   |   |   |   |   |   |   |   |   start > 203541
|   |   |   |   |   |   |   |   |   |   start <= 207197:
protein_kinase_activity_ (15.46)
|   |   |   |   |   |   |   |   |   |   start > 207197:
molecular_function_ (16.0)
|   |   |   |   |   |   |   start > 209412:
transcription_regulator_activity_ (38.67)
|   |   |   |   start > 217473
|   |   |   |   |   start <= 273703
|   |   |   |   |   |   start <= 236495
|   |   |   |   |   |   |   start <= 227639
|   |   |   |   |   |   |   |   start <= 227078: molecular_function_
(8.87)
|   |   |   |   |   |   |   |   start > 227078: RNA_binding_ (25.14)
|   |   |   |   |   |   |   start > 227639: DNA_binding_ (33.05)
|   |   |   |   |   |   start > 236495
|   |   |   |   |   |   |   start <= 245669
|   |   |   |   |   |   |   |   start <= 241285
|   |   |   |   |   |   |   |   |   start <= 237469:
molecular_function_ (12.79)
|   |   |   |   |   |   |   |   |   start > 237469:
hydrolase_activity_ (18.37)
|   |   |   |   |   |   |   |   start > 241285:
transferase_activity_ (52.92)
|   |   |   |   |   |   |   start > 245669
|   |   |   |   |   |   |   |   start <= 256329
|   |   |   |   |   |   |   |   |   start <= 251017
|   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (15.74)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 245908:
molecular_function_ (12.97)
|   |   |   |   |   |   |   |   |   |   |   start > 245908:
oxidoreductase_activity_ (16.76)
|   |   |   |   |   |   |   |   |   start > 251017
|   |   |   |   |   |   |   |   |   |   start <= 254210:
transporter_activity_ (15.52)
|   |   |   |   |   |   |   |   |   |   start > 254210: DNA_binding_
(44.7)
|   |   |   |   |   |   |   |   start > 256329
|   |   |   |   |   |   |   |   |   start <= 257973:
hydrolase_activity_ (9.04)
|   |   |   |   |   |   |   |   |   start > 257973
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 267336:
molecular_function_ (21.68)
|   |   |   |   |   |   |   |   |   |   |   start > 267336
|   |   |   |   |   |   |   |   |   |   |   |   start <= 270247:
transferase_activity_ (11.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 270247:
molecular_function_ (16.84)
|   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (25.41)
|   |   |   |   |   start > 273703
```

```
|   |   |   |   |   |   start <= 281443
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 275527:
nucleotidyltransferase_activity_ (22.04)
|   |   |   |   |   |   |   |   start > 275527: isomerase_activity_
(16.7)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 279021:
transcription_regulator_activity_ (14.26)
|   |   |   |   |   |   |   |   start > 279021:
transporter_activity_ (20.74)
|   |   |   |   |   |   start > 281443
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 305976
|   |   |   |   |   |   |   |   |   start <= 294019
|   |   |   |   |   |   |   |   |   |   start <= 291865
|   |   |   |   |   |   |   |   |   |   |   start <= 289445:
transferase_activity_ (16.52)
|   |   |   |   |   |   |   |   |   |   |   start > 289445:
hydrolase_activity_ (9.57)
|   |   |   |   |   |   |   |   |   |   start > 291865:
oxidoreductase_activity_ (19.27)
|   |   |   |   |   |   |   |   |   start > 294019
|   |   |   |   |   |   |   |   |   |   start <= 300166
|   |   |   |   |   |   |   |   |   |   |   start <= 296002:
protein_kinase_activity_ (12.28)
|   |   |   |   |   |   |   |   |   |   |   start > 296002:
nucleotidyltransferase_activity_ (14.53)
|   |   |   |   |   |   |   |   |   |   start > 300166:
transferase_activity_ (14.46)
|   |   |   |   |   |   |   |   start > 305976
|   |   |   |   |   |   |   |   |   start <= 306955:
oxidoreductase_activity_ (26.05)
|   |   |   |   |   |   |   |   |   start > 306955: RNA_binding_
(16.6)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 283738: hydrolase_activity_
(13.47)
|   |   |   |   |   |   |   |   start > 283738
|   |   |   |   |   |   |   |   |   start <= 298292
|   |   |   |   |   |   |   |   |   |   start <= 291865
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
oxidoreductase_activity_ (13.03/4.38)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
molecular_function_ (6.14/2.52)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
molecular_function_ (7.68/1.31)
|   |   |   |   |   |   |   |   |   |   start > 291865:
molecular_function_ (14.66)
|   |   |   |   |   |   |   |   |   start > 298292
|   |   |   |   |   |   |   |   |   |   start <= 300166:
structural_molecule_activity_ (19.29)
|   |   |   |   |   |   |   |   |   |   start > 300166:
molecular_function_ (10.49)
```

```
|   |   start > 307345
|   |   |   start <= 757101
|   |   |   |   start <= 714450
|   |   |   |   |   start <= 560072
|   |   |   |   |   |   start <= 504281
|   |   |   |   |   |   |   start <= 356564
|   |   |   |   |   |   |   |   start <= 326058
|   |   |   |   |   |   |   |   |   start <= 311451
|   |   |   |   |   |   |   |   |   |   start <= 310313
|   |   |   |   |   |   |   |   |   |   |   start <= 307587:
molecular_function_ (19.55)
|   |   |   |   |   |   |   |   |   |   |   start > 307587:
enzyme_regulator_activity_ (21.87)
|   |   |   |   |   |   |   |   |   |   start > 310313
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
molecular_function_ (15.85/6.84)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
oxidoreductase_activity_ (23.78/9.88)
|   |   |   |   |   |   |   |   |   start > 311451
|   |   |   |   |   |   |   |   |   |   start <= 323945
|   |   |   |   |   |   |   |   |   |   |   start <= 316968
|   |   |   |   |   |   |   |   |   |   |   |   start <= 315575
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 311897:
transferase_activity_ (13.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 311897:
transporter_activity_ (20.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 315575:
molecular_function_ (20.1)
|   |   |   |   |   |   |   |   |   |   |   start > 316968
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 321609:
transferase_activity_ (17.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 321609:
transporter_activity_ (16.48)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
ligase_activity_ (12.92)
|   |   |   |   |   |   |   |   |   |   start > 323945:
protein_binding_ (12.84)
|   |   |   |   |   |   |   |   start > 326058
|   |   |   |   |   |   |   |   |   start <= 353291
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 338197
|   |   |   |   |   |   |   |   |   |   |   |   start <= 326864:
molecular_function_ (10.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 326864
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 332829
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
330090: enzyme_regulator_activity_ (14.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
330090: RNA_binding_ (14.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 332829
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
336816: transcription_regulator_activity_ (16.79)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
336816: enzyme_regulator_activity_ (15.96)
|   |   |   |   |   |   |   |   |   |   |   start > 338197
|   |   |   |   |   |   |   |   |   |   |   |   start <= 343099:
molecular_function_ (25.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 343099
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 347877:
RNA_binding_ (23.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 347877:
molecular_function_ (9.32)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 336816
|   |   |   |   |   |   |   |   |   |   |   |   start <= 331831:
molecular_function_ (16.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 331831:
structural_molecule_activity_ (20.24)
|   |   |   |   |   |   |   |   |   |   |   start > 336816:
molecular_function_ (53.43)
|   |   |   |   |   |   |   |   |   start > 353291
|   |   |   |   |   |   |   |   |   |   start <= 356015:
peptidase_activity_ (5.64)
|   |   |   |   |   |   |   |   |   |   start > 356015:
enzyme_regulator_activity_ (20.88)
|   |   |   |   |   |   |   start > 356564
|   |   |   |   |   |   |   |   start <= 458356
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 370697
|   |   |   |   |   |   |   |   |   |   |   start <= 369676
|   |   |   |   |   |   |   |   |   |   |   |   start <= 360185:
protein_kinase_activity_ (13.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 360185
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 365717
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
362512: molecular_function_ (23.6/8.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
362512: transferase_activity_ (12.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 365717:
molecular_function_ (36.51)
|   |   |   |   |   |   |   |   |   |   |   start > 369676:
transcription_regulator_activity_ (16.85)
|   |   |   |   |   |   |   |   |   |   start > 370697
|   |   |   |   |   |   |   |   |   |   |   start <= 380408
|   |   |   |   |   |   |   |   |   |   |   |   start <= 378430
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 372732:
structural_molecule_activity_ (10.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 372732:
transporter_activity_ (19.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 378430:
protein_binding_ (16.67)
|   |   |   |   |   |   |   |   |   |   |   start > 380408
|   |   |   |   |   |   |   |   |   |   |   |   start <= 436945
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 427052
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
400884
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
393118: molecular_function_ (36.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
393118
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 398271: translation_regulator_activity_ (18.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 398271: hydrolase_activity_ (14.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
400884
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
415977
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 411048
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 405954: structural_molecule_activity_ (11.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 405954: molecular_function_ (14.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 411048: structural_molecule_activity_ (12.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
415977
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 423759: molecular_function_ (29.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 423759
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 425760: enzyme_regulator_activity_ (13.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 425760: molecular_function_ (18.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 427052
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
427478: transporter_activity_ (11.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
427478: hydrolase_activity_ (33.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 436945
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 454816
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
447703
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
444687: molecular_function_ (17.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
444687: protein_binding_ (10.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
447703: molecular_function_ (50.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 454816:
protein_binding_ (14.25)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 407163
|   |   |   |   |   |   |   |   |   |   |   start <= 383209
|   |   |   |   |   |   |   |   |   |   |   |   start <= 382027
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 380408:
molecular_function_ (17.82)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 380408:
protein_binding_ (8.21)
|   |   |   |   |   |   |   |   |   |   |   start > 382027:
isomerase_activity_ (34.83/17.18)
|   |   |   |   |   |   |   |   |   |   start > 383209:
molecular_function_ (69.15)
|   |   |   |   |   |   |   |   |   |   start > 407163
|   |   |   |   |   |   |   |   |   |   |   start <= 427478
|   |   |   |   |   |   |   |   |   |   |   |   start <= 411048
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 409163:
transcription_regulator_activity_ (6.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 409163:
ligase_activity_ (16.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 411048
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 419158:
transporter_activity_ (8.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 419158:
DNA_binding_ (11.22)
|   |   |   |   |   |   |   |   |   |   |   start > 427478
|   |   |   |   |   |   |   |   |   |   |   |   start <= 447703
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 436945
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
436015: molecular_function_ (25.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
436015: protein_kinase_activity_ (9.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 436945:
transcription_regulator_activity_ (33.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 447703
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 449661:
transporter_activity_ (18.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 449661:
molecular_function_ (49.66)
|   |   |   |   |   |   |   |   start > 458356
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 490386
|   |   |   |   |   |   |   |   |   |   |   start <= 473920
|   |   |   |   |   |   |   |   |   |   |   |   start <= 462133:
hydrolase_activity_ (24.49)
|   |   |   |   |   |   |   |   |   |   |   |   start > 462133
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 467242:
transcription_regulator_activity_ (12.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 467242:
oxidoreductase_activity_ (7.83)
|   |   |   |   |   |   |   |   |   |   |   start > 473920
|   |   |   |   |   |   |   |   |   |   |   |   start <= 484497
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 480917
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
477665: transferase_activity_ (15.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
477665: molecular_function_ (7.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 480917
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
483361: ligase_activity_ (8.95)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
483361: structural_molecule_activity_ (11.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 484497
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 488374
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
486685: transcription_regulator_activity_ (10.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
486685: phosphoprotein_phosphatase_activity_ (8.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 488374:
transferase_activity_ (13.97)
|   |   |   |   |   |   |   |   |   |   start > 490386
|   |   |   |   |   |   |   |   |   |   |   start <= 495333
|   |   |   |   |   |   |   |   |   |   |   |   start <= 492816:
transporter_activity_ (31.46/14.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 492816:
molecular_function_ (22.45)
|   |   |   |   |   |   |   |   |   |   |   start > 495333
|   |   |   |   |   |   |   |   |   |   |   |   start <= 497157:
RNA_binding_ (16.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 497157
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 501436:
transporter_activity_ (11.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 501436:
transferase_activity_ (11.95)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 467242
|   |   |   |   |   |   |   |   |   |   |   start <= 458866:
transferase_activity_ (18.06)
|   |   |   |   |   |   |   |   |   |   |   start > 458866
|   |   |   |   |   |   |   |   |   |   |   |   start <= 462133:
molecular_function_ (13.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 462133:
DNA_binding_ (12.65)
|   |   |   |   |   |   |   |   |   |   start > 467242
|   |   |   |   |   |   |   |   |   |   |   start <= 477665:
translation_regulator_activity_ (19.81)
|   |   |   |   |   |   |   |   |   |   |   start > 477665
|   |   |   |   |   |   |   |   |   |   |   |   start <= 486685:
RNA_binding_ (17.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 486685:
enzyme_regulator_activity_ (12.44)
|   |   |   |   |   |   start > 504281
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 546370
|   |   |   |   |   |   |   |   |   start <= 528311
|   |   |   |   |   |   |   |   |   |   start <= 515658:
molecular_function_ (17.38)
|   |   |   |   |   |   |   |   |   |   start > 515658
|   |   |   |   |   |   |   |   |   |   |   start <= 526622:
enzyme_regulator_activity_ (10.18)
|   |   |   |   |   |   |   |   |   |   |   start > 526622:
molecular_function_ (16.22)
|   |   |   |   |   |   |   |   |   start > 528311
```

```
|   |   |   |   |   |   |   |   |   |   start <= 537870:
translation_regulator_activity_ (14.79)
|   |   |   |   |   |   |   |   |   |   start > 537870:
molecular_function_ (9.65)
|   |   |   |   |   |   |   |   start > 546370
|   |   |   |   |   |   |   |   |   start <= 549765:
nucleotidyltransferase_activity_ (18.26)
|   |   |   |   |   |   |   |   |   start > 549765
|   |   |   |   |   |   |   |   |   |   start <= 553194:
enzyme_regulator_activity_ (16.3)
|   |   |   |   |   |   |   |   |   |   start > 553194:
molecular_function_ (12.93)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 547454
|   |   |   |   |   |   |   |   |   start <= 505662
|   |   |   |   |   |   |   |   |   |   start <= 504848:
protein_binding_ (16.09)
|   |   |   |   |   |   |   |   |   |   start > 504848:
protein_kinase_activity_ (17.83)
|   |   |   |   |   |   |   |   |   start > 505662
|   |   |   |   |   |   |   |   |   |   start <= 528311
|   |   |   |   |   |   |   |   |   |   |   start <= 515658
|   |   |   |   |   |   |   |   |   |   |   |   start <= 513038:
molecular_function_ (15.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 513038:
hydrolase_activity_ (19.64)
|   |   |   |   |   |   |   |   |   |   |   start > 515658:
helicase_activity_ (16.57)
|   |   |   |   |   |   |   |   |   |   start > 528311
|   |   |   |   |   |   |   |   |   |   |   start <= 545022
|   |   |   |   |   |   |   |   |   |   |   |   start <= 535254
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 533756:
oxidoreductase_activity_ (14.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 533756:
structural_molecule_activity_ (9.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 535254
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 537870:
molecular_function_ (44.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 537870
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
539981: oxidoreductase_activity_ (25.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
539981: molecular_function_ (14.85)
|   |   |   |   |   |   |   |   |   |   |   start > 545022
|   |   |   |   |   |   |   |   |   |   |   |   start <= 546370:
protein_binding_ (12.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 546370:
hydrolase_activity_ (38.93/18.13)
|   |   |   |   |   |   |   |   start > 547454
|   |   |   |   |   |   |   |   |   start <= 556543:
protein_binding_ (29.76)
|   |   |   |   |   |   |   |   |   start > 556543
|   |   |   |   |   |   |   |   |   |   start <= 558679:
oxidoreductase_activity_ (21.11)
```

```
|   |   |   |   |   |   |   |   |   |   start > 558679:
protein_kinase_activity_ (14.0)
|   |   |   |   |   start > 560072
|   |   |   |   |   |   start <= 602629
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 589736
|   |   |   |   |   |   |   |   |   start <= 583715
|   |   |   |   |   |   |   |   |   |   start <= 572366
|   |   |   |   |   |   |   |   |   |   |   start <= 565718:
molecular_function_ (17.99)
|   |   |   |   |   |   |   |   |   |   |   start > 565718
|   |   |   |   |   |   |   |   |   |   |   |   start <= 568847:
hydrolase_activity_ (14.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 568847
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 571195:
oxidoreductase_activity_ (14.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 571195:
hydrolase_activity_ (12.02)
|   |   |   |   |   |   |   |   |   |   start > 572366:
molecular_function_ (65.65)
|   |   |   |   |   |   |   |   |   start > 583715:
hydrolase_activity_ (27.69)
|   |   |   |   |   |   |   |   start > 589736
|   |   |   |   |   |   |   |   |   start <= 594859
|   |   |   |   |   |   |   |   |   |   start <= 592769:
structural_molecule_activity_ (9.59)
|   |   |   |   |   |   |   |   |   |   start > 592769
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transcription_regulator_activity_ (10.34/2.13)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 780:
transcription_regulator_activity_ (4.24/0.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 780:
DNA_binding_ (2.45/0.76)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_binding_ (9.7/1.21)
|   |   |   |   |   |   |   |   |   start > 594859:
molecular_function_ (35.52)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 592769
|   |   |   |   |   |   |   |   |   start <= 572366
|   |   |   |   |   |   |   |   |   |   start <= 561629:
transferase_activity_ (14.75)
|   |   |   |   |   |   |   |   |   |   start > 561629:
molecular_function_ (58.63)
|   |   |   |   |   |   |   |   |   start > 572366
|   |   |   |   |   |   |   |   |   |   start <= 586157
|   |   |   |   |   |   |   |   |   |   |   start <= 578359:
transporter_activity_ (17.77)
|   |   |   |   |   |   |   |   |   |   |   start > 578359:
transferase_activity_ (35.94)
|   |   |   |   |   |   |   |   |   |   start > 586157:
transporter_activity_ (22.28)
```

```
|   |   |   |   |   |   |   |   start > 592769
|   |   |   |   |   |   |   |   |   start <= 596110:
hydrolase_activity_ (24.25)
|   |   |   |   |   |   |   |   |   start > 596110:
molecular_function_ (48.54)
|   |   |   |   |   |   start > 602629
|   |   |   |   |   |   |   start <= 613895
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 611877
|   |   |   |   |   |   |   |   |   |   start <= 606265:
RNA_binding_ (15.16)
|   |   |   |   |   |   |   |   |   |   start > 606265:
transcription_regulator_activity_ (27.86)
|   |   |   |   |   |   |   |   |   start > 611877:
isomerase_activity_ (16.13)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 606265:
structural_molecule_activity_ (33.52)
|   |   |   |   |   |   |   |   |   start > 606265
|   |   |   |   |   |   |   |   |   |   start <= 607647:
transporter_activity_ (12.08)
|   |   |   |   |   |   |   |   |   |   start > 607647:
molecular_function_ (17.7)
|   |   |   |   |   |   |   start > 613895
|   |   |   |   |   |   |   |   start <= 684972
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 664672
|   |   |   |   |   |   |   |   |   |   |   start <= 625767
|   |   |   |   |   |   |   |   |   |   |   |   start <= 615851:
molecular_function_ (58.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 615851
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 620867:
transcription_regulator_activity_ (15.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 620867:
molecular_function_ (28.03)
|   |   |   |   |   |   |   |   |   |   |   start > 625767
|   |   |   |   |   |   |   |   |   |   |   |   start <= 635141:
hydrolase_activity_ (16.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 635141
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 642205:
ligase_activity_ (10.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 642205
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
657827: molecular_function_ (38.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
657827
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
662244: ligase_activity_ (15.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
662244: molecular_function_ (31.83)
|   |   |   |   |   |   |   |   |   |   start > 664672
|   |   |   |   |   |   |   |   |   |   |   start <= 679216
|   |   |   |   |   |   |   |   |   |   |   |   start <= 668346
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 666533:
oxidoreductase_activity_ (14.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 666533:
molecular_function_ (13.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 668346
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 675308
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
670622: hydrolase_activity_ (10.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
670622: protein_binding_ (17.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 675308:
hydrolase_activity_ (16.98)
|   |   |   |   |   |   |   |   |   |   |   start > 679216
|   |   |   |   |   |   |   |   |   |   |   |   start <= 681857
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 680357:
molecular_function_ (13.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 680357:
RNA_binding_ (11.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 681857:
molecular_function_ (18.85)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 635141
|   |   |   |   |   |   |   |   |   |   |   start <= 629163
|   |   |   |   |   |   |   |   |   |   |   |   start <= 623572
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 618904:
transferase_activity_ (12.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 618904
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
620867: protein_binding_ (23.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
620867
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
622978: molecular_function_ (18.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
622978: protein_binding_ (17.63)
|   |   |   |   |   |   |   |   |   |   |   |   start > 623572
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 625767:
transcription_regulator_activity_ (15.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 625767:
molecular_function_ (19.09)
|   |   |   |   |   |   |   |   |   |   |   start > 629163
|   |   |   |   |   |   |   |   |   |   |   |   start <= 633617:
transferase_activity_ (17.17)
|   |   |   |   |   |   |   |   |   |   |   |   start > 633617:
transporter_activity_ (18.46)
|   |   |   |   |   |   |   |   |   |   start > 635141
|   |   |   |   |   |   |   |   |   |   |   start <= 650363
|   |   |   |   |   |   |   |   |   |   |   |   start <= 645545:
molecular_function_ (26.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 645545
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 647881
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: translation_regulator_activity_ (15.79/7.04)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: RNA_binding_ (18.93/5.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 647881:
lyase_activity_ (17.74)
|   |   |   |   |   |   |   |   |   |   |   start > 650363
|   |   |   |   |   |   |   |   |   |   |   |   start <= 683423
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 653351
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
651410: molecular_function_ (11.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
651410: transcription_regulator_activity_ (21.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 653351
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
670622: molecular_function_ (33.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
670622
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
675308: hydrolase_activity_ (16.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
675308: molecular_function_ (28.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 683423:
protein_binding_ (17.89)
|   |   |   |   |   |   |   |   start > 684972
|   |   |   |   |   |   |   |   |   start <= 691688
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 686896:
structural_molecule_activity_ (21.71)
|   |   |   |   |   |   |   |   |   |   |   start > 686896:
transferase_activity_ (16.58)
|   |   |   |   |   |   |   |   |   |   strand = W:
transporter_activity_ (15.07)
|   |   |   |   |   |   |   |   |   start > 691688
|   |   |   |   |   |   |   |   |   |   start <= 704665
|   |   |   |   |   |   |   |   |   |   |   start <= 699938
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (43.07)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
RNA_binding_ (12.15)
|   |   |   |   |   |   |   |   |   |   |   start > 699938
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 701837:
transcription_regulator_activity_ (17.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 701837:
transporter_activity_ (14.17)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (7.15)
|   |   |   |   |   |   |   |   |   |   start > 704665
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 711586
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 707523:
transferase_activity_ (17.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 707523:
hydrolase_activity_ (12.17)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 711586:
RNA_binding_ (19.07)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (52.5/17.0)
|   |   |   |   start > 714450
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 735525
|   |   |   |   |   |   |   start <= 719028: transferase_activity_
(41.02)
|   |   |   |   |   |   |   start > 719028
|   |   |   |   |   |   |   |   start <= 727069
|   |   |   |   |   |   |   |   |   start <= 724451:
enzyme_regulator_activity_ (21.33)
|   |   |   |   |   |   |   |   |   start > 724451:
molecular_function_ (7.97)
|   |   |   |   |   |   |   |   start > 727069
|   |   |   |   |   |   |   |   |   start <= 730382:
transferase_activity_ (29.23)
|   |   |   |   |   |   |   |   |   start > 730382
|   |   |   |   |   |   |   |   |   |   start <= 734634:
enzyme_regulator_activity_ (20.08)
|   |   |   |   |   |   |   |   |   |   start > 734634:
transferase_activity_ (20.66)
|   |   |   |   |   |   start > 735525
|   |   |   |   |   |   |   start <= 749589: molecular_function_
(89.99)
|   |   |   |   |   |   |   start > 749589: protein_binding_ (12.5)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 730382
|   |   |   |   |   |   |   start <= 723265
|   |   |   |   |   |   |   |   start <= 719028: molecular_function_
(23.17)
|   |   |   |   |   |   |   |   start > 719028
|   |   |   |   |   |   |   |   |   start <= 721385:
structural_molecule_activity_ (30.76)
|   |   |   |   |   |   |   |   |   start > 721385
|   |   |   |   |   |   |   |   |   |   start <= 722606:
hydrolase_activity_ (23.49)
|   |   |   |   |   |   |   |   |   |   start > 722606:
structural_molecule_activity_ (18.03)
|   |   |   |   |   |   |   start > 723265
|   |   |   |   |   |   |   |   start <= 724451: molecular_function_
(20.49)
|   |   |   |   |   |   |   |   start > 724451
|   |   |   |   |   |   |   |   |   start <= 728880:
hydrolase_activity_ (16.17)
|   |   |   |   |   |   |   |   |   start > 728880:
molecular_function_ (12.49)
|   |   |   |   |   |   start > 730382
|   |   |   |   |   |   |   start <= 744847
|   |   |   |   |   |   |   |   start <= 738577
|   |   |   |   |   |   |   |   |   start <= 736259:
transferase_activity_ (18.24)
```

```
|   |   |   |   |   |   |   |   |   start > 736259:
oxidoreductase_activity_ (11.39)
|   |   |   |   |   |   |   |   start > 738577
|   |   |   |   |   |   |   |   |   start <= 739836:
molecular_function_ (14.02)
|   |   |   |   |   |   |   |   |   start > 739836
|   |   |   |   |   |   |   |   |   |   start <= 742571:
structural_molecule_activity_ (10.71)
|   |   |   |   |   |   |   |   |   |   start > 742571:
transferase_activity_ (13.88)
|   |   |   |   |   |   |   start > 744847: protein_kinase_activity_
(13.82)
|   |   |   start > 757101
|   |   |   |   start <= 779459
|   |   |   |   |   start <= 761253
|   |   |   |   |   |   strand = C:
phosphoprotein_phosphatase_activity_ (12.36)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 760290:
nucleotidyltransferase_activity_ (13.72)
|   |   |   |   |   |   |   start > 760290:
transcription_regulator_activity_ (16.45)
|   |   |   |   |   start > 761253
|   |   |   |   |   |   start <= 770411
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 764693: molecular_function_
(14.77)
|   |   |   |   |   |   |   |   start > 764693
|   |   |   |   |   |   |   |   |   start <= 768236:
peptidase_activity_ (17.69)
|   |   |   |   |   |   |   |   |   start > 768236:
transporter_activity_ (14.54)
|   |   |   |   |   |   |   strand = W:
structural_molecule_activity_ (22.26)
|   |   |   |   |   |   start > 770411
|   |   |   |   |   |   |   start <= 774696
|   |   |   |   |   |   |   |   start <= 773918: molecular_function_
(31.62)
|   |   |   |   |   |   |   |   start > 773918: peptidase_activity_
(15.8)
|   |   |   |   |   |   |   start > 774696: molecular_function_
(38.59)
|   |   |   |   start > 779459
|   |   |   |   |   start <= 782587
|   |   |   |   |   |   start <= 779663:
transcription_regulator_activity_ (23.65)
|   |   |   |   |   |   start > 779663: protein_binding_ (17.46)
|   |   |   |   |   start > 782587
|   |   |   |   |   |   start <= 798516: transporter_activity_
(98.41/23.96)
|   |   |   |   |   |   start > 798516
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 804469
```

```
|   |   |   |   |   |   |   |   |   start <= 800517:
molecular_function_ (14.96)
|   |   |   |   |   |   |   |   |   start > 800517:
transporter_activity_ (11.74)
|   |   |   |   |   |   |   |   start > 804469: molecular_function_
(18.53)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 800517
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
transcription_regulator_activity_ (24.12/6.86)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
DNA_binding_ (18.52/3.81)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
transcription_regulator_activity_ (17.96/8.79)
|   |   |   |   |   |   |   |   start > 800517
|   |   |   |   |   |   |   |   |   start <= 805345:
hydrolase_activity_ (14.89)
|   |   |   |   |   |   |   |   |   start > 805345:
molecular_function_ (12.17)
```

For Biological Process

```
|   start <= 744847
|   |   start <= 454524
|   |   |   start <= 398271
|   |   |   |   start <= 166137
|   |   |   |   |   start <= 132427
|   |   |   |   |   |   start <= 48822
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 13879
|   |   |   |   |   |   |   |   |   start <= 10551:
biological_process_ (57.19)
|   |   |   |   |   |   |   |   |   start > 10551: vesicle-
mediated_transport_ (19.2)
|   |   |   |   |   |   |   |   start > 13879
|   |   |   |   |   |   |   |   |   start <= 36395
|   |   |   |   |   |   |   |   |   |   start <= 17696
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: signal_transduction_ (1.56/0.62)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: cell_wall_organization_and_biogenesis_
(13.12/4.48)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: signal_transduction_ (5.9/1.38)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: signal_transduction_ (1.56/0.32)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: cell_wall_organization_and_biogenesis_
(8.33/2.91)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: signal_transduction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: signal_transduction_ (3.49/0.55)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: signal_transduction_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: signal_transduction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: signal_transduction_ (0.7/0.25)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: signal_transduction_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: signal_transduction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: signal_transduction_ (0.0)
|   |   |   |   |   |   |   |   |   |   start > 17696
|   |   |   |   |   |   |   |   |   |   |   start <= 21293:
biological_process_ (28.66)
|   |   |   |   |   |   |   |   |   |   |   start > 21293
|   |   |   |   |   |   |   |   |   |   |   |   start <= 24098:
signal_transduction_ (9.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 24098:
cell_wall_organization_and_biogenesis_ (11.08)
|   |   |   |   |   |   |   |   |   start > 36395
|   |   |   |   |   |   |   |   |   |   start <= 47177
|   |   |   |   |   |   |   |   |   |   |   start <= 45975:
transcription_ (9.65)
|   |   |   |   |   |   |   |   |   |   |   start > 45975:
lipid_metabolic_process_ (11.91)
|   |   |   |   |   |   |   |   |   |   start > 47177:
biological_process_ (20.77)
|   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   start <= 24098
|   |   |   |   |   |   |   |   |   start <= 13879: translation_
(12.78)
|   |   |   |   |   |   |   |   |   start > 13879: vesicle-
mediated_transport_ (14.87)
|   |   |   |   |   |   |   |   start > 24098
|   |   |   |   |   |   |   |   |   start <= 43274
|   |   |   |   |   |   |   |   |   |   start <= 37050
|   |   |   |   |   |   |   |   |   |   |   start <= 28427:
biological_process_ (14.07)
|   |   |   |   |   |   |   |   |   |   |   start > 28427
|   |   |   |   |   |   |   |   |   |   |   |   start <= 36395:
translation_ (15.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 36395:
generation_of_precursor_metabolites_and_energy_ (8.04)
|   |   |   |   |   |   |   |   |   |   start > 37050
|   |   |   |   |   |   |   |   |   |   |   start <= 40828
|   |   |   |   |   |   |   |   |   |   |   |   start <= 39142:
vitamin_metabolic_process_ (5.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 39142:
cell_cycle_ (15.6)
|   |   |   |   |   |   |   |   |   |   |   start > 40828:
biological_process_ (10.56)
|   |   |   |   |   |   |   |   |   start > 43274: translation_
(26.09)
|   |   |   |   |   |   start > 48822
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 117592
|   |   |   |   |   |   |   |   |   start <= 84259
|   |   |   |   |   |   |   |   |   |   start <= 69442
|   |   |   |   |   |   |   |   |   |   |   start <= 60735
|   |   |   |   |   |   |   |   |   |   |   |   start <= 59379:
response_to_stress_ (20.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 59379:
translation_ (20.46)
|   |   |   |   |   |   |   |   |   |   |   start > 60735
|   |   |   |   |   |   |   |   |   |   |   |   start <= 63873:
biological_process_ (18.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 63873:
cell_cycle_ (13.96)
|   |   |   |   |   |   |   |   |   |   start > 69442
|   |   |   |   |   |   |   |   |   |   |   start <= 71863:
protein_modification_process_ (20.4)
|   |   |   |   |   |   |   |   |   |   |   start > 71863
|   |   |   |   |   |   |   |   |   |   |   |   start <= 75256:
translation_ (16.79)
|   |   |   |   |   |   |   |   |   |   |   |   start > 75256
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 80728:
organelle_organization_and_biogenesis_ (36.63/17.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 80728:
translation_ (9.69)
|   |   |   |   |   |   |   |   |   start > 84259
|   |   |   |   |   |   |   |   |   |   start <= 111439
|   |   |   |   |   |   |   |   |   |   |   start <= 101888
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 86446:
response_to_stress_ (18.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 86446
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 100117
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
89123
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
88188: biological_process_ (24.2/9.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
88188: translation_ (15.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
89123: biological_process_ (37.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 100117:
response_to_stress_ (10.37)
|   |   |   |   |   |   |   |   |   |   |   start > 101888
|   |   |   |   |   |   |   |   |   |   |   |   start <= 107934:
cytokinesis_ (22.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 107934:
biological_process_ (15.71)
|   |   |   |   |   |   |   |   |   |   start > 111439
|   |   |   |   |   |   |   |   |   |   |   start <= 113765:
translation_ (15.81)
|   |   |   |   |   |   |   |   |   |   |   start > 113765:
response_to_stress_ (17.74)
|   |   |   |   |   |   |   |   start > 117592
|   |   |   |   |   |   |   |   |   start <= 121877:
DNA_metabolic_process_ (26.56/10.79)
|   |   |   |   |   |   |   |   |   start > 121877
|   |   |   |   |   |   |   |   |   |   start <= 126831: cell_cycle_
(20.61)
|   |   |   |   |   |   |   |   |   |   start > 126831: vesicle-
mediated_transport_ (8.47)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 101888
|   |   |   |   |   |   |   |   |   start <= 80728
|   |   |   |   |   |   |   |   |   |   start <= 63873
|   |   |   |   |   |   |   |   |   |   |   start <= 49571:
transport_ (17.49)
|   |   |   |   |   |   |   |   |   |   |   start > 49571:
cytokinesis_ (24.42/11.88)
|   |   |   |   |   |   |   |   |   |   start > 63873
|   |   |   |   |   |   |   |   |   |   |   start <= 71863:
biological_process_ (24.07)
|   |   |   |   |   |   |   |   |   |   |   start > 71863:
nuclear_organization_and_biogenesis_ (15.19)
|   |   |   |   |   |   |   |   |   start > 80728
|   |   |   |   |   |   |   |   |   |   start <= 95884
|   |   |   |   |   |   |   |   |   |   |   start <= 89976:
RNA_metabolic_process_ (45.52/14.92)
|   |   |   |   |   |   |   |   |   |   |   start > 89976
|   |   |   |   |   |   |   |   |   |   |   |   start <= 90739:
transport_ (9.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 90739:
ribosome_biogenesis_and_assembly_ (12.86)
```

```
|   |   |   |   |   |   |   |   |   |   start > 95884:
cytoskeleton_organization_and_biogenesis_ (14.04)
|   |   |   |   |   |   |   |   start > 101888
|   |   |   |   |   |   |   |   |   start <= 111439
|   |   |   |   |   |   |   |   |   |   start <= 110596:
biological_process_ (21.72)
|   |   |   |   |   |   |   |   |   |   start > 110596: sporulation_
(24.74/12.3)
|   |   |   |   |   |   |   |   |   start > 111439
|   |   |   |   |   |   |   |   |   |   start <= 125128
|   |   |   |   |   |   |   |   |   |   |   start <= 117592
|   |   |   |   |   |   |   |   |   |   |   |   start <= 113765:
protein_modification_process_ (16.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 113765:
ribosome_biogenesis_and_assembly_ (9.68)
|   |   |   |   |   |   |   |   |   |   |   start > 117592
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
organelle_organization_and_biogenesis_ (21.0/12.0)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
vesicle-mediated_transport_ (25.58/16.24)
|   |   |   |   |   |   |   |   |   |   start > 125128
|   |   |   |   |   |   |   |   |   |   |   start <= 126831:
biological_process_ (18.09)
|   |   |   |   |   |   |   |   |   |   |   start > 126831:
protein_modification_process_ (13.94)
|   |   |   |   |   start > 132427
|   |   |   |   |   |   start <= 151223
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 143396
|   |   |   |   |   |   |   |   |   start <= 136691:
cellular_respiration_ (13.95)
|   |   |   |   |   |   |   |   |   start > 136691
|   |   |   |   |   |   |   |   |   |   start <= 141250: transport_
(13.39)
|   |   |   |   |   |   |   |   |   |   start > 141250: vesicle-
mediated_transport_ (29.66/11.07)
|   |   |   |   |   |   |   |   start > 143396
|   |   |   |   |   |   |   |   |   start <= 147212:
lipid_metabolic_process_ (19.45)
|   |   |   |   |   |   |   |   |   start > 147212:
amino_acid_and_derivative_metabolic_process_ (14.39)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 143396
|   |   |   |   |   |   |   |   |   start <= 136691
|   |   |   |   |   |   |   |   |   |   start <= 136001:
biological_process_ (10.75)
|   |   |   |   |   |   |   |   |   |   start > 136001:
cell_wall_organization_and_biogenesis_ (13.83)
|   |   |   |   |   |   |   |   |   start > 136691
|   |   |   |   |   |   |   |   |   |   start <= 141250:
protein_catabolic_process_ (18.6)
|   |   |   |   |   |   |   |   |   |   start > 141250:
biological_process_ (7.76)
|   |   |   |   |   |   |   |   start > 143396
```

```
|   |   |   |   |   |   |   |   |   start <= 146190: translation_
(15.21)
|   |   |   |   |   |   |   |   |   start > 146190: vesicle-
mediated_transport_ (13.96)
|   |   |   |   |   |   start > 151223
|   |   |   |   |   |   |   start <= 160187
|   |   |   |   |   |   |   |   start <= 158392
|   |   |   |   |   |   |   |   |   start <= 153613:
DNA_metabolic_process_ (19.06)
|   |   |   |   |   |   |   |   |   start > 153613:
cytoskeleton_organization_and_biogenesis_ (25.7)
|   |   |   |   |   |   |   |   start > 158392
|   |   |   |   |   |   |   |   |   start <= 159696
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
vitamin_metabolic_process_ (10.12/2.63)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
biological_process_ (5.27/1.53)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
biological_process_ (8.49/2.26)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
vitamin_metabolic_process_ (5.0/1.48)
|   |   |   |   |   |   |   |   |   start > 159696:
DNA_metabolic_process_ (15.73)
|   |   |   |   |   |   |   start > 160187
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 164000:
cellular_respiration_ (26.77)
|   |   |   |   |   |   |   |   |   start > 164000:
biological_process_ (20.46)
|   |   |   |   |   |   |   |   strand = W: biological_process_
(41.32)
|   |   |   |   start > 166137
|   |   |   |   |   start <= 273703
|   |   |   |   |   |   start <= 191586
|   |   |   |   |   |   |   start <= 172537
|   |   |   |   |   |   |   |   start <= 168426
|   |   |   |   |   |   |   |   |   start <= 167841:
ribosome_biogenesis_and_assembly_ (26.73)
|   |   |   |   |   |   |   |   |   start > 167841: translation_
(23.91)
|   |   |   |   |   |   |   |   start > 168426
|   |   |   |   |   |   |   |   |   start <= 171484
|   |   |   |   |   |   |   |   |   |   start <= 170626:
RNA_metabolic_process_ (11.2)
|   |   |   |   |   |   |   |   |   |   start > 170626:
transcription_ (22.91)
|   |   |   |   |   |   |   |   |   start > 171484:
ribosome_biogenesis_and_assembly_ (18.41)
|   |   |   |   |   |   |   start > 172537
|   |   |   |   |   |   |   |   start <= 182097
|   |   |   |   |   |   |   |   |   start <= 177529:
DNA_metabolic_process_ (23.24)
|   |   |   |   |   |   |   |   |   start > 177529
```

```
|   |   |   |   |   |   |   |   |   |   start <= 181278:
response_to_stress_ (20.99)
|   |   |   |   |   |   |   |   |   |   start > 181278:
transcription_ (19.53)
|   |   |   |   |   |   |   |   start > 182097
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 186477:
ribosome_biogenesis_and_assembly_ (25.54)
|   |   |   |   |   |   |   |   |   |   start > 186477: transport_
(12.31)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 182404: transport_
(25.45/10.57)
|   |   |   |   |   |   |   |   |   |   start > 182404:
DNA_metabolic_process_ (21.26)
|   |   |   |   |   |   start > 191586
|   |   |   |   |   |   |   start <= 227639
|   |   |   |   |   |   |   |   start <= 209412
|   |   |   |   |   |   |   |   |   start <= 202059
|   |   |   |   |   |   |   |   |   |   start <= 194125
|   |   |   |   |   |   |   |   |   |   |   start <= 192454:
protein_modification_process_ (14.17)
|   |   |   |   |   |   |   |   |   |   |   start > 192454:
biological_process_ (26.26)
|   |   |   |   |   |   |   |   |   |   start > 194125
|   |   |   |   |   |   |   |   |   |   |   start <= 197702:
translation_ (26.63)
|   |   |   |   |   |   |   |   |   |   |   start > 197702
|   |   |   |   |   |   |   |   |   |   |   |   start <= 201751:
transcription_ (10.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 201751:
translation_ (6.32)
|   |   |   |   |   |   |   |   |   start > 202059
|   |   |   |   |   |   |   |   |   |   start <= 203541:
lipid_metabolic_process_ (15.45)
|   |   |   |   |   |   |   |   |   |   start > 203541
|   |   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (21.46)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 207197:
meiosis_ (14.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 207197:
biological_process_ (15.82)
|   |   |   |   |   |   |   |   start > 209412
|   |   |   |   |   |   |   |   |   start <= 217132
|   |   |   |   |   |   |   |   |   |   start <= 216369
|   |   |   |   |   |   |   |   |   |   |   start <= 209656:
RNA_metabolic_process_ (14.63)
|   |   |   |   |   |   |   |   |   |   |   start > 209656:
cell_wall_organization_and_biogenesis_ (20.07)
|   |   |   |   |   |   |   |   |   |   start > 216369
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
RNA_metabolic_process_ (17.41/7.55)
```

```
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (16.24/5.6)
|   |   |   |   |   |   |   |   |   start > 217132
|   |   |   |   |   |   |   |   |   |   start <= 227078
|   |   |   |   |   |   |   |   |   |   |   start <= 217473:
biological_process_ (16.44)
|   |   |   |   |   |   |   |   |   |   |   start > 217473:
translation_ (14.0)
|   |   |   |   |   |   |   |   |   |   start > 227078:
ribosome_biogenesis_and_assembly_ (20.46)
|   |   |   |   |   |   |   start > 227639
|   |   |   |   |   |   |   |   start <= 256329
|   |   |   |   |   |   |   |   |   start <= 236495:
DNA_metabolic_process_ (45.77)
|   |   |   |   |   |   |   |   |   start > 236495
|   |   |   |   |   |   |   |   |   |   start <= 247012
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 241285
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 237469:
cell_wall_organization_and_biogenesis_ (22.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 237469:
response_to_stress_ (14.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 241285:
protein_modification_process_ (38.02)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 242811:
biological_process_ (19.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 242811
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 245908
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: cell_wall_organization_and_biogenesis_ (16.33/6.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: vesicle-mediated_transport_ (26.9/9.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 245908:
response_to_stress_ (10.44)
|   |   |   |   |   |   |   |   |   |   start > 247012
|   |   |   |   |   |   |   |   |   |   |   start <= 254210:
biological_process_ (29.2)
|   |   |   |   |   |   |   |   |   |   |   start > 254210:
DNA_metabolic_process_ (29.07)
|   |   |   |   |   |   |   |   start > 256329
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 267336:
biological_process_ (42.63)
|   |   |   |   |   |   |   |   |   |   start > 267336
|   |   |   |   |   |   |   |   |   |   |   start <= 270247:
protein_modification_process_ (12.89)
|   |   |   |   |   |   |   |   |   |   |   start > 270247:
cell_cycle_ (15.67)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 267336:
translation_ (14.96)
|   |   |   |   |   |   |   |   |   |   start > 267336:
response_to_stress_ (21.78)
```

```
|   |   |   |   |   start > 273703
|   |   |   |   |   |   start <= 323945
|   |   |   |   |   |   |   start <= 289445
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 281443:
carbohydrate_metabolic_process_ (27.88)
|   |   |   |   |   |   |   |   |   start > 281443: cytokinesis_
(29.63)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 281443: transport_
(32.18)
|   |   |   |   |   |   |   |   |   start > 281443
|   |   |   |   |   |   |   |   |   |   start <= 283738:
RNA_metabolic_process_ (17.69)
|   |   |   |   |   |   |   |   |   |   start > 283738: transport_
(10.89)
|   |   |   |   |   |   |   start > 289445
|   |   |   |   |   |   |   |   start <= 310313
|   |   |   |   |   |   |   |   |   start <= 301944
|   |   |   |   |   |   |   |   |   |   start <= 296002
|   |   |   |   |   |   |   |   |   |   |   start <= 291865:
biological_process_ (15.52)
|   |   |   |   |   |   |   |   |   |   |   start > 291865
|   |   |   |   |   |   |   |   |   |   |   |   start <= 294019:
cellular_respiration_ (16.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 294019:
biological_process_ (10.62)
|   |   |   |   |   |   |   |   |   |   start > 296002
|   |   |   |   |   |   |   |   |   |   |   start <= 298292:
lipid_metabolic_process_ (29.63)
|   |   |   |   |   |   |   |   |   |   |   start > 298292
|   |   |   |   |   |   |   |   |   |   |   |   start <= 300166:
translation_ (22.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 300166:
biological_process_ (17.64)
|   |   |   |   |   |   |   |   |   start > 301944
|   |   |   |   |   |   |   |   |   |   start <= 307587
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 306955
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 305976:
ribosome_biogenesis_and_assembly_ (17.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 305976
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: DNA_metabolic_process_ (31.63/12.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: lipid_metabolic_process_ (21.58/5.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 306955:
ribosome_biogenesis_and_assembly_ (28.58/12.16)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
DNA_metabolic_process_ (23.25)
|   |   |   |   |   |   |   |   |   |   start > 307587:
biological_process_ (20.51)
|   |   |   |   |   |   |   |   start > 310313
|   |   |   |   |   |   |   |   |   start <= 315575
```

```
|   |   |   |   |   |   |   |   |   |   strand = C:
response_to_stress_ (15.18)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 311897:
cytokinesis_ (19.28)
|   |   |   |   |   |   |   |   |   |   |   start > 311897:
generation_of_precursor_metabolites_and_energy_ (15.69)
|   |   |   |   |   |   |   |   |   start > 315575
|   |   |   |   |   |   |   |   |   |   start <= 316968:
conjugation_ (10.85)
|   |   |   |   |   |   |   |   |   |   start > 316968
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 321609:
lipid_metabolic_process_ (14.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 321609:
transport_ (14.49)
|   |   |   |   |   |   |   |   |   |   |   strand = W: transport_
(18.74)
|   |   |   |   |   |   start > 323945
|   |   |   |   |   |   |   start <= 350825
|   |   |   |   |   |   |   |   start <= 331509
|   |   |   |   |   |   |   |   |   start <= 326864
|   |   |   |   |   |   |   |   |   |   start <= 326058:
biological_process_ (12.35)
|   |   |   |   |   |   |   |   |   |   start > 326058: translation_
(12.8)
|   |   |   |   |   |   |   |   |   start > 326864
|   |   |   |   |   |   |   |   |   |   start <= 330090:
sporulation_ (27.51/7.38)
|   |   |   |   |   |   |   |   |   |   start > 330090:
response_to_stress_ (9.18)
|   |   |   |   |   |   |   |   start > 331509
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 338197:
transcription_ (27.38)
|   |   |   |   |   |   |   |   |   |   start > 338197
|   |   |   |   |   |   |   |   |   |   |   start <= 343099:
biological_process_ (30.6)
|   |   |   |   |   |   |   |   |   |   |   start > 343099:
RNA_metabolic_process_ (13.89)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 331831:
biological_process_ (15.86)
|   |   |   |   |   |   |   |   |   |   start > 331831
|   |   |   |   |   |   |   |   |   |   |   start <= 347877
|   |   |   |   |   |   |   |   |   |   |   |   start <= 347601
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 343099
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
336816: translation_ (7.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
336816: biological_process_ (14.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 343099:
translation_ (10.05)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 347601:
biological_process_ (13.3)
|   |   |   |   |   |   |   |   |   |   |   start > 347877:
translation_ (7.32)
|   |   |   |   |   |   |   start > 350825
|   |   |   |   |   |   |   |   start <= 386281
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 368182
|   |   |   |   |   |   |   |   |   |   |   start <= 356564
|   |   |   |   |   |   |   |   |   |   |   |   start <= 356015
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 353291:
DNA_metabolic_process_ (7.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 353291:
carbohydrate_metabolic_process_ (37.57/22.79)
|   |   |   |   |   |   |   |   |   |   |   |   start > 356015:
biological_process_ (37.77/14.36)
|   |   |   |   |   |   |   |   |   |   |   start > 356564
|   |   |   |   |   |   |   |   |   |   |   |   start <= 360185:
cytoskeleton_organization_and_biogenesis_ (35.59/18.63)
|   |   |   |   |   |   |   |   |   |   |   |   start > 360185
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 365717
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
362512: DNA_metabolic_process_ (9.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
362512: translation_ (9.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 365717:
biological_process_ (19.05)
|   |   |   |   |   |   |   |   |   |   start > 368182
|   |   |   |   |   |   |   |   |   |   |   start <= 372732
|   |   |   |   |   |   |   |   |   |   |   |   start <= 370697
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 369676:
cell_wall_organization_and_biogenesis_ (8.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 369676:
pseudohyphal_growth_ (14.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 370697:
cell_wall_organization_and_biogenesis_ (11.8)
|   |   |   |   |   |   |   |   |   |   |   start > 372732
|   |   |   |   |   |   |   |   |   |   |   |   start <= 378430:
transport_ (30.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 378430
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 380408:
protein_modification_process_ (12.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 380408:
biological_process_ (14.24)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 382027
|   |   |   |   |   |   |   |   |   |   |   start <= 380408:
biological_process_ (11.95)
|   |   |   |   |   |   |   |   |   |   |   start > 380408:
response_to_stress_ (12.7)
|   |   |   |   |   |   |   |   |   |   start > 382027
|   |   |   |   |   |   |   |   |   |   |   start <= 383209:
DNA_metabolic_process_ (10.87)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 383209:
biological_process_ (17.58)
|   |   |   |   |   |   |   |   start > 386281
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 393118:
signal_transduction_ (15.78)
|   |   |   |   |   |   |   |   |   |   start > 393118: translation_
(23.08)
|   |   |   |   |   |   |   |   |   strand = W:
cell_wall_organization_and_biogenesis_ (28.42)
|   |   |   start > 398271
|   |   |   |   start <= 444687
|   |   |   |   |   start <= 415977
|   |   |   |   |   |   start <= 405245
|   |   |   |   |   |   |   start <= 400884:
organelle_organization_and_biogenesis_ (57.12/34.48)
|   |   |   |   |   |   |   start > 400884: conjugation_ (15.14)
|   |   |   |   |   |   start > 405245
|   |   |   |   |   |   |   start <= 407163
|   |   |   |   |   |   |   |   strand = C: response_to_stress_
(12.97)
|   |   |   |   |   |   |   |   strand = W: translation_ (29.0)
|   |   |   |   |   |   |   start > 407163
|   |   |   |   |   |   |   |   strand = C: translation_ (10.63)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 409163:
pseudohyphal_growth_ (17.68)
|   |   |   |   |   |   |   |   |   start > 409163
|   |   |   |   |   |   |   |   |   |   start <= 411048:
ribosome_biogenesis_and_assembly_ (20.57)
|   |   |   |   |   |   |   |   |   |   start > 411048:
cellular_respiration_ (8.96)
|   |   |   |   |   start > 415977
|   |   |   |   |   |   start <= 436015
|   |   |   |   |   |   |   start <= 426483
|   |   |   |   |   |   |   |   start <= 423035
|   |   |   |   |   |   |   |   |   start <= 419158:
biological_process_ (18.56)
|   |   |   |   |   |   |   |   |   start > 419158:
response_to_stress_ (17.74)
|   |   |   |   |   |   |   |   start > 423035:
DNA_metabolic_process_ (37.39)
|   |   |   |   |   |   |   start > 426483
|   |   |   |   |   |   |   |   start <= 429095
|   |   |   |   |   |   |   |   |   start <= 427478
|   |   |   |   |   |   |   |   |   |   start <= 427052:
biological_process_ (8.73)
|   |   |   |   |   |   |   |   |   |   start > 427052:
membrane_organization_and_biogenesis_ (14.89)
|   |   |   |   |   |   |   |   |   start > 427478:
vitamin_metabolic_process_ (18.53)
|   |   |   |   |   |   |   |   start > 429095
|   |   |   |   |   |   |   |   |   start <= 430945:
response_to_stress_ (40.53/26.75)
```

```
|   |   |   |   |   |   |   |   |   start > 430945
|   |   |   |   |   |   |   |   |   |   strand = C: conjugation_
(10.83)
|   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (26.15)
|   |   |   |   |   |   start > 436015
|   |   |   |   |   |   |   strand = C: translation_ (7.7)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 436945
|   |   |   |   |   |   |   |   |   neigh_strand = W:
protein_modification_process_ (20.17/9.18)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (9.86/3.78)
|   |   |   |   |   |   |   |   start > 436945
|   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_metabolic_process_ (14.93/6.1)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
response_to_stress_ (9.15/2.44)
|   |   |   |   start > 444687
|   |   |   |   |   start <= 452652
|   |   |   |   |   |   strand = C: vesicle-mediated_transport_
(33.32)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 449661
|   |   |   |   |   |   |   |   start <= 447703: meiosis_ (11.68)
|   |   |   |   |   |   |   |   start > 447703
|   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (17.0/7.22)
|   |   |   |   |   |   |   |   |   neigh_strand = C: transport_
(10.13/3.27)
|   |   |   |   |   |   |   start > 449661: DNA_metabolic_process_
(22.88)
|   |   |   |   |   start > 452652
|   |   |   |   |   |   NeighGO_term = cytoplasm_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = molecular_function_
|   |   |   |   |   |   |   neigh_num <= 1: cell_cycle_ (6.53/3.56)
|   |   |   |   |   |   |   neigh_num > 1: sporulation_ (13.12/6.31)
|   |   |   |   |   |   NeighGO_term = biological_process_:
biological_process_ (8.35/4.72)
|   |   |   |   |   |   NeighGO_term = endomembrane_system_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = vesicle-mediated_transport_:
biological_process_ (3.99/2.22)
|   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = cellular_component_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = ribosome_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = translation_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = lipid_metabolic_process_:
cell_cycle_ (0.0)
```

```
|   |   |   |   |   |   NeighGO_term = mitochondrion_: cell_cycle_
(4.9/2.57)
|   |   |   |   |   |   NeighGO_term = nucleus_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = protein_kinase_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = response_to_stress_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = protein_binding_:
sporulation_ (7.64/3.31)
|   |   |   |   |   |   NeighGO_term = cell_cycle_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = membrane_: sporulation_
(6.9/3.44)
|   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = nucleolus_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = RNA_binding_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = RNA_metabolic_process_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = peptidase_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = motor_activity_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: biological_process_
(4.98/2.7)
|   |   |   |   |   |   NeighGO_term = cellular_bud_: cell_cycle_
(7.59/3.15)
|   |   |   |   |   |   NeighGO_term = site_of_polarized_growth_:
cell_cycle_ (10.26/5.99)
|   |   |   |   |   |   NeighGO_term = enzyme_regulator_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = cytokinesis_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
protein_modification_process_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = transferase_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = DNA_metabolic_process_:
cell_cycle_ (6.95/3.75)
```

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|   |   |   |   |   |   NeighGO_term = membrane_fraction_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = transport_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = oxidoreductase_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = cellular_respiration_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = plasma_membrane_: cell_cycle_
(7.62/3.78)
|   |   |   |   |   |   NeighGO_term = transporter_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = protein_catabolic_process_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = endoplasmic_reticulum_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = isomerase_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = DNA_binding_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = helicase_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = signal_transducer_activity_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = meiosis_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = cell_cortex_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = chromosome_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = mitochondrial_envelope_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = transcription_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = conjugation_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: sporulation_ (4.7/2.72)
|   |   |   |   |   |   NeighGO_term = sporulation_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = cell_budding_: sporulation_
(1.44/0.74)
|   |   |   |   |   |   NeighGO_term = vacuole_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = signal_transduction_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = vitamin_metabolic_process_:
cell_cycle_ (0.0)
```

```
|   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = cytoskeleton_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = cell_wall_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = Golgi_apparatus_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = peroxisome_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = ligase_activity_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = lyase_activity_: cell_cycle_
(0.0)
|   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: cell_cycle_ (0.0)
|   |   |   |   |   |   NeighGO_term = cellular_homeostasis_:
cell_cycle_ (0.0)
|   |   start > 454524
|   |   |   start <= 561629
|   |   |   |   strand = C
|   |   |   |   |   start <= 486685
|   |   |   |   |   |   start <= 462133
|   |   |   |   |   |   |   start <= 458866
|   |   |   |   |   |   |   |   neigh_num <= 1: cell_budding_
(9.66/2.87)
|   |   |   |   |   |   |   |   neigh_num > 1:
cytoskeleton_organization_and_biogenesis_ (25.29/8.56)
|   |   |   |   |   |   |   start > 458866: biological_process_
(16.1)
|   |   |   |   |   |   start > 462133
|   |   |   |   |   |   |   start <= 477665
|   |   |   |   |   |   |   |   start <= 473920
|   |   |   |   |   |   |   |   |   start <= 467242
|   |   |   |   |   |   |   |   |   |   distance <= 5808:
transcription_ (17.9/5.13)
|   |   |   |   |   |   |   |   |   |   distance > 5808:
DNA_metabolic_process_ (5.39/0.81)
|   |   |   |   |   |   |   |   |   start > 467242:
amino_acid_and_derivative_metabolic_process_ (27.54)
|   |   |   |   |   |   |   |   start > 473920:
carbohydrate_metabolic_process_ (30.42/14.45)
|   |   |   |   |   |   |   start > 477665
|   |   |   |   |   |   |   |   start <= 484497
|   |   |   |   |   |   |   |   |   start <= 483361
|   |   |   |   |   |   |   |   |   |   start <= 480917:
translation_ (16.82)
|   |   |   |   |   |   |   |   |   |   start > 480917:
transcription_ (20.33/7.56)
|   |   |   |   |   |   |   |   |   start > 483361: translation_
(17.44)
```

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|   |   |   |   |   |   |   |   start > 484497: transcription_
(13.67)
|   |   |   |   |   start > 486685
|   |   |   |   |   |   start <= 501436
|   |   |   |   |   |   |   start <= 494109
|   |   |   |   |   |   |   |   start <= 490386
|   |   |   |   |   |   |   |   |   start <= 488374:
biological_process_ (18.15)
|   |   |   |   |   |   |   |   |   start > 488374:
carbohydrate_metabolic_process_ (30.66/12.72)
|   |   |   |   |   |   |   |   start > 490386
|   |   |   |   |   |   |   |   |   start <= 492816:
organelle_organization_and_biogenesis_ (17.15)
|   |   |   |   |   |   |   |   |   start > 492816:
biological_process_ (16.89)
|   |   |   |   |   |   |   start > 494109
|   |   |   |   |   |   |   |   start <= 497157
|   |   |   |   |   |   |   |   |   start <= 495333: conjugation_
(16.35)
|   |   |   |   |   |   |   |   |   start > 495333:
organelle_organization_and_biogenesis_ (19.07)
|   |   |   |   |   |   |   |   start > 497157: response_to_stress_
(19.75)
|   |   |   |   |   |   start > 501436
|   |   |   |   |   |   |   start <= 528311
|   |   |   |   |   |   |   |   start <= 505662: cell_cycle_ (24.59)
|   |   |   |   |   |   |   |   start > 505662
|   |   |   |   |   |   |   |   |   start <= 515658:
biological_process_ (15.92)
|   |   |   |   |   |   |   |   |   start > 515658
|   |   |   |   |   |   |   |   |   |   start <= 526622:
signal_transduction_ (11.13)
|   |   |   |   |   |   |   |   |   |   start > 526622:
biological_process_ (13.72)
|   |   |   |   |   |   |   start > 528311
|   |   |   |   |   |   |   |   distance <= 1718: transcription_
(12.41/1.42)
|   |   |   |   |   |   |   |   distance > 1718
|   |   |   |   |   |   |   |   |   start <= 553194
|   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 547454
|   |   |   |   |   |   |   |   |   |   |   |   start <= 537870:
cytokinesis_ (12.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 537870:
biological_process_ (6.28)
|   |   |   |   |   |   |   |   |   |   |   start > 547454:
cytokinesis_ (21.13)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 549765
|   |   |   |   |   |   |   |   |   |   |   |   start <= 546370:
cytokinesis_ (3.26/1.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 546370:
transcription_ (10.63)
```

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|   |   |   |   |   |   |   |   |   |   |   start > 549765:
cytokinesis_ (6.87)
|   |   |   |   |   |   |   |   |   start > 553194:
biological_process_ (7.83)
|   |   |   |   strand = W
|   |   |   |   |   start <= 505662
|   |   |   |   |   |   start <= 458866
|   |   |   |   |   |   |   start <= 454816: biological_process_
(18.66)
|   |   |   |   |   |   |   start > 454816: lipid_metabolic_process_
(41.1/20.52)
|   |   |   |   |   |   start > 458866
|   |   |   |   |   |   |   start <= 477665
|   |   |   |   |   |   |   |   start <= 462133: transcription_
(21.39)
|   |   |   |   |   |   |   |   start > 462133
|   |   |   |   |   |   |   |   |   start <= 467242:
organelle_organization_and_biogenesis_ (16.37/8.12)
|   |   |   |   |   |   |   |   |   start > 467242: translation_
(20.53)
|   |   |   |   |   |   |   start > 477665
|   |   |   |   |   |   |   |   start <= 497157
|   |   |   |   |   |   |   |   |   start <= 486685:
RNA_metabolic_process_ (16.86)
|   |   |   |   |   |   |   |   |   start > 486685: vesicle-
mediated_transport_ (11.21)
|   |   |   |   |   |   |   |   start > 497157
|   |   |   |   |   |   |   |   |   start <= 504848: transcription_
(14.69)
|   |   |   |   |   |   |   |   |   start > 504848:
DNA_metabolic_process_ (19.44)
|   |   |   |   |   start > 505662
|   |   |   |   |   |   start <= 549765
|   |   |   |   |   |   |   start <= 535254
|   |   |   |   |   |   |   |   start <= 528311
|   |   |   |   |   |   |   |   |   start <= 515658:
biological_process_ (29.27)
|   |   |   |   |   |   |   |   |   start > 515658:
ribosome_biogenesis_and_assembly_ (17.13)
|   |   |   |   |   |   |   |   start > 528311
|   |   |   |   |   |   |   |   |   start <= 533756:
generation_of_precursor_metabolites_and_energy_ (34.83/15.14)
|   |   |   |   |   |   |   |   |   start > 533756: translation_
(20.03)
|   |   |   |   |   |   |   start > 535254
|   |   |   |   |   |   |   |   start <= 545022
|   |   |   |   |   |   |   |   |   start <= 537870:
biological_process_ (25.45)
|   |   |   |   |   |   |   |   |   start > 537870
|   |   |   |   |   |   |   |   |   |   start <= 539981:
carbohydrate_metabolic_process_ (21.61)
|   |   |   |   |   |   |   |   |   |   start > 539981:
biological_process_ (22.71)
|   |   |   |   |   |   |   |   start > 545022
```

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|   |   |   |   |   |   |   |   |   start <= 546370:
RNA_metabolic_process_ (26.69)
|   |   |   |   |   |   |   |   |   start > 546370
|   |   |   |   |   |   |   |   |   |   start <= 547454:
vitamin_metabolic_process_ (16.98)
|   |   |   |   |   |   |   |   |   |   start > 547454:
biological_process_ (14.91)
|   |   |   |   |   |   start > 549765
|   |   |   |   |   |   |   start <= 556543: cell_cycle_ (17.27)
|   |   |   |   |   |   |   start > 556543
|   |   |   |   |   |   |   |   start <= 558679:
lipid_metabolic_process_ (19.65)
|   |   |   |   |   |   |   |   start > 558679
|   |   |   |   |   |   |   |   |   start <= 560072: transcription_
(14.03)
|   |   |   |   |   |   |   |   |   start > 560072:
lipid_metabolic_process_ (15.07)
|   |   |   start > 561629
|   |   |   |   start <= 691964
|   |   |   |   |   start <= 602629
|   |   |   |   |   |   start <= 581367
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 575991
|   |   |   |   |   |   |   |   |   start <= 571195
|   |   |   |   |   |   |   |   |   |   start <= 568847
|   |   |   |   |   |   |   |   |   |   |   start <= 565718:
biological_process_ (12.59)
|   |   |   |   |   |   |   |   |   |   |   start > 565718: vesicle-
mediated_transport_ (17.74)
|   |   |   |   |   |   |   |   |   |   start > 568847:
amino_acid_and_derivative_metabolic_process_ (14.54)
|   |   |   |   |   |   |   |   |   start > 571195
|   |   |   |   |   |   |   |   |   |   start <= 572366:
ribosome_biogenesis_and_assembly_ (16.32)
|   |   |   |   |   |   |   |   |   |   start > 572366:
biological_process_ (17.67)
|   |   |   |   |   |   |   |   start > 575991
|   |   |   |   |   |   |   |   |   start <= 578359:
protein_catabolic_process_ (18.85)
|   |   |   |   |   |   |   |   |   start > 578359:
cytoskeleton_organization_and_biogenesis_ (27.57)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 568847
|   |   |   |   |   |   |   |   |   start <= 565718:
biological_process_ (29.61)
|   |   |   |   |   |   |   |   |   start > 565718:
protein_modification_process_ (21.66)
|   |   |   |   |   |   |   |   start > 568847
|   |   |   |   |   |   |   |   |   start <= 572366:
organelle_organization_and_biogenesis_ (15.52)
|   |   |   |   |   |   |   |   |   start > 572366:
biological_process_ (16.51)
|   |   |   |   |   |   start > 581367
|   |   |   |   |   |   |   start <= 597358
```

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|   |   |   |   |   |   |   |   start <= 582403
|   |   |   |   |   |   |   |   |   start <= 582167:
response_to_stress_ (15.23)
|   |   |   |   |   |   |   |   |   start > 582167:
DNA_metabolic_process_ (17.03)
|   |   |   |   |   |   |   |   start > 582403
|   |   |   |   |   |   |   |   |   start <= 592769
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 589736
|   |   |   |   |   |   |   |   |   |   |   |   start <= 586157:
lipid_metabolic_process_ (12.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 586157:
organelle_organization_and_biogenesis_ (19.41)
|   |   |   |   |   |   |   |   |   |   |   start > 589736:
translation_ (14.57)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 586157:
biological_process_ (19.26)
|   |   |   |   |   |   |   |   |   |   |   start > 586157:
transport_ (14.28)
|   |   |   |   |   |   |   |   |   start > 592769
|   |   |   |   |   |   |   |   |   |   start <= 594859:
response_to_stress_ (17.49)
|   |   |   |   |   |   |   |   |   |   start > 594859
|   |   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (22.66)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 596110:
lipid_metabolic_process_ (18.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 596110:
biological_process_ (17.21)
|   |   |   |   |   |   |   start > 597358
|   |   |   |   |   |   |   |   strand = C: cellular_respiration_
(19.2)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 600548: meiosis_
(10.07)
|   |   |   |   |   |   |   |   |   start > 600548:
ribosome_biogenesis_and_assembly_ (17.0)
|   |   |   |   |   start > 602629
|   |   |   |   |   |   start <= 651410
|   |   |   |   |   |   |   start <= 625767
|   |   |   |   |   |   |   |   start <= 609748
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 606265:
RNA_metabolic_process_ (16.78)
|   |   |   |   |   |   |   |   |   |   start > 606265:
transcription_ (16.16)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 606265:
translation_ (29.54)
|   |   |   |   |   |   |   |   |   |   start > 606265:
organelle_organization_and_biogenesis_ (22.18)
|   |   |   |   |   |   |   |   start > 609748
```

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|   |   |   |   |   |   |   |   |   start <= 615851
|   |   |   |   |   |   |   |   |   |   start <= 613895
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 611877:
DNA_metabolic_process_ (14.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 611877:
carbohydrate_metabolic_process_ (14.96)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (15.46)
|   |   |   |   |   |   |   |   |   |   start > 613895:
biological_process_ (53.83)
|   |   |   |   |   |   |   |   |   start > 615851
|   |   |   |   |   |   |   |   |   |   start <= 618904
|   |   |   |   |   |   |   |   |   |   |   start <= 618518
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
4686: DNA_metabolic_process_ (12.14/5.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 4686:
protein_modification_process_ (3.88/1.07)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cell_cycle_ (28.68/18.12)
|   |   |   |   |   |   |   |   |   |   |   start > 618518:
protein_modification_process_ (15.48)
|   |   |   |   |   |   |   |   |   |   start > 618904
|   |   |   |   |   |   |   |   |   |   |   start <= 624692
|   |   |   |   |   |   |   |   |   |   |   |   start <= 622978:
biological_process_ (52.03/15.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 622978
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 623572:
protein_catabolic_process_ (20.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 623572:
biological_process_ (13.38)
|   |   |   |   |   |   |   |   |   |   |   start > 624692:
DNA_metabolic_process_ (23.93)
|   |   |   |   |   |   |   start > 625767
|   |   |   |   |   |   |   |   start <= 633617
|   |   |   |   |   |   |   |   |   strand = C: biological_process_
(12.28)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 629163:
signal_transduction_ (15.8)
|   |   |   |   |   |   |   |   |   |   start > 629163:
cell_wall_organization_and_biogenesis_ (13.82)
|   |   |   |   |   |   |   |   start > 633617
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 643073
|   |   |   |   |   |   |   |   |   |   |   start <= 642205:
biological_process_ (12.37)
|   |   |   |   |   |   |   |   |   |   |   start > 642205:
translation_ (11.99)
|   |   |   |   |   |   |   |   |   |   start > 643073:
cytoskeleton_organization_and_biogenesis_ (13.29)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 645545
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 635141:
vesicle-mediated_transport_ (18.15)
|   |   |   |   |   |   |   |   |   |   |   start > 635141
|   |   |   |   |   |   |   |   |   |   |   |   start <= 645162:
translation_ (13.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 645162:
cell_budding_ (17.45)
|   |   |   |   |   |   |   |   |   |   start > 645545
|   |   |   |   |   |   |   |   |   |   |   start <= 647881:
organelle_organization_and_biogenesis_ (19.37)
|   |   |   |   |   |   |   |   |   |   |   start > 647881
|   |   |   |   |   |   |   |   |   |   |   |   start <= 650363:
biological_process_ (16.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 650363:
vesicle-mediated_transport_ (19.04)
|   |   |   |   |   |   start > 651410
|   |   |   |   |   |   |   start <= 680357
|   |   |   |   |   |   |   |   start <= 653351
|   |   |   |   |   |   |   |   |   neigh_strand = W:
RNA_metabolic_process_ (21.15/9.22)
|   |   |   |   |   |   |   |   |   neigh_strand = C: cell_cycle_
(22.01/9.23)
|   |   |   |   |   |   |   |   start > 653351
|   |   |   |   |   |   |   |   |   start <= 662244
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 657827:
response_to_stress_ (10.34)
|   |   |   |   |   |   |   |   |   |   |   start > 657827:
carbohydrate_metabolic_process_ (21.55)
|   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (17.28)
|   |   |   |   |   |   |   |   |   start > 662244
|   |   |   |   |   |   |   |   |   |   start <= 675129
|   |   |   |   |   |   |   |   |   |   |   start <= 668346:
biological_process_ (75.44)
|   |   |   |   |   |   |   |   |   |   |   start > 668346
|   |   |   |   |   |   |   |   |   |   |   |   start <= 670292:
DNA_metabolic_process_ (12.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 670292:
biological_process_ (32.33)
|   |   |   |   |   |   |   |   |   |   start > 675129
|   |   |   |   |   |   |   |   |   |   |   start <= 679216
|   |   |   |   |   |   |   |   |   |   |   |   start <= 675308:
response_to_stress_ (18.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 675308:
cell_wall_organization_and_biogenesis_ (15.49)
|   |   |   |   |   |   |   |   |   |   |   start > 679216:
biological_process_ (23.28)
|   |   |   |   |   |   |   start > 680357
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 683423
|   |   |   |   |   |   |   |   |   |   start <= 681857:
RNA_metabolic_process_ (19.62)
```

```
|   |   |   |   |   |   |   |   |   |   start > 681857:
DNA_metabolic_process_ (17.56)
|   |   |   |   |   |   |   |   |   start > 683423
|   |   |   |   |   |   |   |   |   |   start <= 686896:
organelle_organization_and_biogenesis_ (14.98)
|   |   |   |   |   |   |   |   |   |   start > 686896:
RNA_metabolic_process_ (15.4)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 686896
|   |   |   |   |   |   |   |   |   |   start <= 684972
|   |   |   |   |   |   |   |   |   |   |   start <= 683423:
biological_process_ (11.44)
|   |   |   |   |   |   |   |   |   |   |   start > 683423:
cell_cycle_ (13.92)
|   |   |   |   |   |   |   |   |   |   start > 684972:
biological_process_ (12.61)
|   |   |   |   |   |   |   |   |   start > 686896:
RNA_metabolic_process_ (12.35)
|   |   |   |   start > 691964
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 724451
|   |   |   |   |   |   |   start <= 714450
|   |   |   |   |   |   |   |   start <= 701837
|   |   |   |   |   |   |   |   |   start <= 699938
|   |   |   |   |   |   |   |   |   |   start <= 697297:
ribosome_biogenesis_and_assembly_ (16.94)
|   |   |   |   |   |   |   |   |   |   start > 697297:
biological_process_ (16.72)
|   |   |   |   |   |   |   |   |   start > 699938:
vitamin_metabolic_process_ (16.95)
|   |   |   |   |   |   |   |   start > 701837
|   |   |   |   |   |   |   |   |   start <= 707523
|   |   |   |   |   |   |   |   |   |   start <= 704665: transport_
(18.88)
|   |   |   |   |   |   |   |   |   |   start > 704665:
cellular_respiration_ (14.34)
|   |   |   |   |   |   |   |   |   start > 707523
|   |   |   |   |   |   |   |   |   |   start <= 711586:
RNA_metabolic_process_ (18.82)
|   |   |   |   |   |   |   |   |   |   start > 711586:
ribosome_biogenesis_and_assembly_ (15.92)
|   |   |   |   |   |   |   start > 714450
|   |   |   |   |   |   |   |   start <= 719028:
amino_acid_and_derivative_metabolic_process_ (32.98)
|   |   |   |   |   |   |   |   start > 719028: vesicle-
mediated_transport_ (42.71/17.03)
|   |   |   |   |   |   start > 724451
|   |   |   |   |   |   |   start <= 734634
|   |   |   |   |   |   |   |   start <= 730382
|   |   |   |   |   |   |   |   |   start <= 728880
|   |   |   |   |   |   |   |   |   |   start <= 727069:
biological_process_ (10.95)
|   |   |   |   |   |   |   |   |   |   start > 727069:
vitamin_metabolic_process_ (9.4)
```

```
|   |   |   |   |   |   |   |   |   start > 728880:
protein_modification_process_ (21.8)
|   |   |   |   |   |   |   |   start > 730382: response_to_stress_
(21.38/9.79)
|   |   |   |   |   |   |   start > 734634
|   |   |   |   |   |   |   |   start <= 736259: biological_process_
(39.45)
|   |   |   |   |   |   |   |   start > 736259
|   |   |   |   |   |   |   |   |   start <= 739836:
organelle_organization_and_biogenesis_ (11.47)
|   |   |   |   |   |   |   |   |   start > 739836:
biological_process_ (22.18)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 724451
|   |   |   |   |   |   |   start <= 719028
|   |   |   |   |   |   |   |   start <= 714450
|   |   |   |   |   |   |   |   |   start <= 707523
|   |   |   |   |   |   |   |   |   |   start <= 704665:
biological_process_ (13.25)
|   |   |   |   |   |   |   |   |   |   start > 704665:
response_to_stress_ (17.84)
|   |   |   |   |   |   |   |   |   start > 707523:
biological_process_ (17.53)
|   |   |   |   |   |   |   |   start > 714450: meiosis_ (23.58)
|   |   |   |   |   |   |   start > 719028
|   |   |   |   |   |   |   |   start <= 721385: translation_
(21.31)
|   |   |   |   |   |   |   |   start > 721385
|   |   |   |   |   |   |   |   |   start <= 722606:
biological_process_ (21.12)
|   |   |   |   |   |   |   |   |   start > 722606
|   |   |   |   |   |   |   |   |   |   start <= 723265:
transcription_ (21.86)
|   |   |   |   |   |   |   |   |   |   start > 723265:
biological_process_ (15.85)
|   |   |   |   |   |   start > 724451
|   |   |   |   |   |   |   start <= 738577
|   |   |   |   |   |   |   |   start <= 728880:
ribosome_biogenesis_and_assembly_ (17.08)
|   |   |   |   |   |   |   |   start > 728880
|   |   |   |   |   |   |   |   |   start <= 736259:
biological_process_ (29.07)
|   |   |   |   |   |   |   |   |   start > 736259:
lipid_metabolic_process_ (29.35/8.07)
|   |   |   |   |   |   |   start > 738577
|   |   |   |   |   |   |   |   distance <= 1329
|   |   |   |   |   |   |   |   |   start <= 739836:
ribosome_biogenesis_and_assembly_ (3.93)
|   |   |   |   |   |   |   |   |   start > 739836: translation_
(10.45/0.07)
|   |   |   |   |   |   |   |   distance > 1329:
ribosome_biogenesis_and_assembly_ (30.29)
|   start > 744847
|   |   start <= 779663
```

```
|   |   |   start <= 761253
|   |   |   |   start <= 749366
|   |   |   |   |   start <= 747798: DNA_metabolic_process_ (19.37)
|   |   |   |   |   start > 747798: sporulation_ (22.91)
|   |   |   |   start > 749366
|   |   |   |   |   start <= 749589: protein_modification_process_
(20.09)
|   |   |   |   |   start > 749589
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 757101: DNA_metabolic_process_
(16.71)
|   |   |   |   |   |   |   start > 757101:
protein_modification_process_ (10.4)
|   |   |   |   |   |   strand = W: DNA_metabolic_process_ (30.28)
|   |   |   start > 761253
|   |   |   |   start <= 776567
|   |   |   |   |   start <= 768236
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 764693:
protein_catabolic_process_ (12.3)
|   |   |   |   |   |   |   start > 764693: biological_process_
(9.78)
|   |   |   |   |   |   strand = W: translation_ (18.59)
|   |   |   |   |   start > 768236
|   |   |   |   |   |   start <= 771235: DNA_metabolic_process_
(24.84)
|   |   |   |   |   |   start > 771235
|   |   |   |   |   |   |   start <= 773918: biological_process_
(18.65)
|   |   |   |   |   |   |   start > 773918
|   |   |   |   |   |   |   |   start <= 774696:
protein_catabolic_process_ (36.59/13.85)
|   |   |   |   |   |   |   |   start > 774696: biological_process_
(15.36)
|   |   |   |   start > 776567
|   |   |   |   |   start <= 779459: vesicle-mediated_transport_
(17.87)
|   |   |   |   |   start > 779459: DNA_metabolic_process_ (21.68)
|   |   start > 779663
|   |   |   start <= 798516: transport_ (121.87/23.28)
|   |   |   start > 798516
|   |   |   |   strand = C
|   |   |   |   |   start <= 800517: biological_process_ (17.6)
|   |   |   |   |   start > 800517
|   |   |   |   |   |   start <= 804469: transport_ (18.59)
|   |   |   |   |   |   start > 804469: biological_process_ (16.95)
|   |   |   |   strand = W
|   |   |   |   |   start <= 805345: carbohydrate_metabolic_process_
(38.53)
|   |   |   |   |   start > 805345: biological_process_ (13.0)
```

Decision Tree Generated for Chromosome Three:

For Cellular Component

```
|   start <= 265065
|   |   start <= 176434
|   |   |   start <= 56527
|   |   |   |   start <= 23584
|   |   |   |   |   start <= 22106
|   |   |   |   |   |   start <= 12285
|   |   |   |   |   |   |   start <= 9706
|   |   |   |   |   |   |   |   start <= 8326: membrane_ (18.14)
|   |   |   |   |   |   |   |   start > 8326: vacuole_ (27.53/10.55)
|   |   |   |   |   |   |   start > 9706: cellular_component_
(14.59)
|   |   |   |   |   |   start > 12285
|   |   |   |   |   |   |   start <= 16880
|   |   |   |   |   |   |   |   start <= 13282: nucleus_ (33.84)
|   |   |   |   |   |   |   |   start > 13282: mitochondrion_
(12.33)
|   |   |   |   |   |   |   start > 16880
|   |   |   |   |   |   |   |   start <= 17290
|   |   |   |   |   |   |   |   |   distance <= 790: membrane_
(2.38/0.03)
|   |   |   |   |   |   |   |   |   distance > 790: vacuole_
(27.37/8.76)
|   |   |   |   |   |   |   |   start > 17290: nucleus_ (13.78)
|   |   |   |   |   start > 22106
|   |   |   |   |   |   start <= 23379: nucleolus_ (16.83)
|   |   |   |   |   |   start > 23379: cellular_component_ (23.1)
|   |   |   |   start > 23584
|   |   |   |   |   start <= 52645
|   |   |   |   |   |   start <= 27359
|   |   |   |   |   |   |   start <= 24768: mitochondrion_
(54.95/11.42)
|   |   |   |   |   |   |   start > 24768: cytoplasm_ (32.3)
|   |   |   |   |   |   start > 27359
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 38801
|   |   |   |   |   |   |   |   |   start <= 35865:
endoplasmic_reticulum_ (24.57)
|   |   |   |   |   |   |   |   |   start > 35865: nucleus_
(30.07/13.93)
|   |   |   |   |   |   |   |   start > 38801
|   |   |   |   |   |   |   |   |   start <= 44437
|   |   |   |   |   |   |   |   |   |   start <= 42165:
membrane_fraction_ (17.25)
|   |   |   |   |   |   |   |   |   |   start > 42165:
cellular_component_ (7.82)
|   |   |   |   |   |   |   |   |   start > 44437
|   |   |   |   |   |   |   |   |   |   start <= 46905:
endoplasmic_reticulum_ (17.58)
|   |   |   |   |   |   |   |   |   |   start > 46905
|   |   |   |   |   |   |   |   |   |   |   start <= 48364:
mitochondrion_ (13.47)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 48364:
endoplasmic_reticulum_ (12.93)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 41488
|   |   |   |   |   |   |   |   |   start <= 31449
|   |   |   |   |   |   |   |   |   |   start <= 27929: cytoplasm_
(23.16/10.15)
|   |   |   |   |   |   |   |   |   |   start > 27929: nucleolus_
(17.61/7.86)
|   |   |   |   |   |   |   |   |   start > 31449
|   |   |   |   |   |   |   |   |   |   start <= 35865: cell_wall_
(18.03)
|   |   |   |   |   |   |   |   |   |   start > 35865:
cellular_component_ (18.3)
|   |   |   |   |   |   |   |   start > 41488
|   |   |   |   |   |   |   |   |   start <= 44437: plasma_membrane_
(11.48)
|   |   |   |   |   |   |   |   |   start > 44437: cytoplasm_
(62.85/14.39)
|   |   |   |   |   start > 52645: membrane_ (34.88/11.27)
|   |   |   start > 56527
|   |   |   |   start <= 104350
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 83620
|   |   |   |   |   |   |   start <= 68333
|   |   |   |   |   |   |   |   start <= 63441
|   |   |   |   |   |   |   |   |   start <= 61658
|   |   |   |   |   |   |   |   |   |   start <= 59026:
cellular_component_ (22.16)
|   |   |   |   |   |   |   |   |   |   start > 59026: cytoplasm_
(25.61/8.26)
|   |   |   |   |   |   |   |   |   start > 61658:
cellular_component_ (27.77)
|   |   |   |   |   |   |   |   start > 63441
|   |   |   |   |   |   |   |   |   start <= 65568: nucleus_
(30.44/15.19)
|   |   |   |   |   |   |   |   |   start > 65568:
cellular_component_ (18.22)
|   |   |   |   |   |   |   start > 68333
|   |   |   |   |   |   |   |   start <= 71803: cell_cortex_ (13.11)
|   |   |   |   |   |   |   |   start > 71803
|   |   |   |   |   |   |   |   |   start <= 75285: cytoplasm_
(79.49/38.08)
|   |   |   |   |   |   |   |   |   start > 75285
|   |   |   |   |   |   |   |   |   |   start <= 79162:
plasma_membrane_ (8.88)
|   |   |   |   |   |   |   |   |   |   start > 79162: cytoplasm_
(18.32)
|   |   |   |   |   |   start > 83620
|   |   |   |   |   |   |   start <= 96281
|   |   |   |   |   |   |   |   start <= 94270: nucleus_
(31.32/13.16)
|   |   |   |   |   |   |   |   start > 94270: chromosome_ (19.43)
|   |   |   |   |   |   |   start > 96281
```

```
|   |   |   |   |   |   |   |   start <= 101788: cellular_component_
(15.71)
|   |   |   |   |   |   |   |   start > 101788: nucleus_
(45.55/8.69)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 75285
|   |   |   |   |   |   |   start <= 61658
|   |   |   |   |   |   |   |   start <= 59026: cellular_component_
(13.82)
|   |   |   |   |   |   |   |   start > 59026: cell_cortex_ (23.94)
|   |   |   |   |   |   |   start > 61658
|   |   |   |   |   |   |   |   start <= 70150: cytoplasm_ (34.07)
|   |   |   |   |   |   |   |   start > 70150: plasma_membrane_
(14.18)
|   |   |   |   |   |   start > 75285
|   |   |   |   |   |   |   start <= 91324
|   |   |   |   |   |   |   |   start <= 79162:
site_of_polarized_growth_ (31.18/14.66)
|   |   |   |   |   |   |   |   start > 79162
|   |   |   |   |   |   |   |   |   start <= 90859
|   |   |   |   |   |   |   |   |   |   start <= 83620:
cellular_component_ (16.35)
|   |   |   |   |   |   |   |   |   |   start > 83620: cytoplasm_
(17.63)
|   |   |   |   |   |   |   |   |   start > 90859:
cellular_component_ (20.21)
|   |   |   |   |   |   |   start > 91324: site_of_polarized_growth_
(34.43/13.82)
|   |   |   |   start > 104350
|   |   |   |   |   start <= 131540
|   |   |   |   |   |   start <= 109105
|   |   |   |   |   |   |   start <= 107023
|   |   |   |   |   |   |   |   start <= 105548: mitochondrion_
(13.96)
|   |   |   |   |   |   |   |   start > 105548
|   |   |   |   |   |   |   |   |   start <= 106853: cytoplasm_
(49.11/19.42)
|   |   |   |   |   |   |   |   |   start > 106853: vacuole_
(19.19/9.15)
|   |   |   |   |   |   |   start > 107023
|   |   |   |   |   |   |   |   strand = C: nucleolus_ (10.61)
|   |   |   |   |   |   |   |   strand = W: mitochondrion_ (31.28)
|   |   |   |   |   |   start > 109105
|   |   |   |   |   |   |   start <= 113768
|   |   |   |   |   |   |   |   start <= 111914
|   |   |   |   |   |   |   |   |   start <= 111674:
cellular_component_ (12.51)
|   |   |   |   |   |   |   |   |   start > 111674:
cytoplasmic_membrane-bound_vesicle_ (20.7)
|   |   |   |   |   |   |   |   start > 111914: cellular_component_
(28.88)
|   |   |   |   |   |   |   start > 113768
|   |   |   |   |   |   |   |   start <= 122326
```

```
|   |   |   |   |   |   |   |   |   start <= 118346: cell_cortex_
(31.5/14.35)
|   |   |   |   |   |   |   |   |   start > 118346
|   |   |   |   |   |   |   |   |   |   start <= 120316
|   |   |   |   |   |   |   |   |   |   |   start <= 118618:
mitochondrion_ (14.34)
|   |   |   |   |   |   |   |   |   |   |   start > 118618:
cytoplasm_ (30.29/12.83)
|   |   |   |   |   |   |   |   |   |   start > 120316:
mitochondrion_ (28.53/11.62)
|   |   |   |   |   |   |   |   start > 122326
|   |   |   |   |   |   |   |   |   start <= 128468
|   |   |   |   |   |   |   |   |   |   start <= 127714
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 123646:
cytoplasm_ (11.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 123646:
cellular_component_ (13.4)
|   |   |   |   |   |   |   |   |   |   |   strand = W: cytoplasm_
(21.49)
|   |   |   |   |   |   |   |   |   |   start > 127714:
cellular_component_ (17.02)
|   |   |   |   |   |   |   |   |   start > 128468
|   |   |   |   |   |   |   |   |   |   distance <= 953:
cell_cortex_ (6.95/1.44)
|   |   |   |   |   |   |   |   |   |   distance > 953:
plasma_membrane_ (26.85/15.47)
|   |   |   |   |   start > 131540
|   |   |   |   |   |   start <= 155318
|   |   |   |   |   |   |   start <= 137744
|   |   |   |   |   |   |   |   start <= 133122: plasma_membrane_
(40.02/18.44)
|   |   |   |   |   |   |   |   start > 133122: cytoplasm_
(46.26/16.96)
|   |   |   |   |   |   |   start > 137744
|   |   |   |   |   |   |   |   start <= 147632
|   |   |   |   |   |   |   |   |   start <= 143632
|   |   |   |   |   |   |   |   |   |   start <= 142168
|   |   |   |   |   |   |   |   |   |   |   start <= 140931:
nucleus_ (12.37)
|   |   |   |   |   |   |   |   |   |   |   start > 140931:
cellular_component_ (15.68)
|   |   |   |   |   |   |   |   |   |   start > 142168
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 142544:
nucleolus_ (16.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 142544:
cytoplasm_ (20.59)
|   |   |   |   |   |   |   |   |   |   |   strand = W: nucleolus_
(29.67/14.68)
|   |   |   |   |   |   |   |   |   start > 143632:
site_of_polarized_growth_ (23.97/10.19)
|   |   |   |   |   |   |   |   start > 147632
|   |   |   |   |   |   |   |   |   start <= 155094
```

```
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 149918:
cytoplasm_ (37.73/16.9)
|   |   |   |   |   |   |   |   |   |   |   start > 149918
|   |   |   |   |   |   |   |   |   |   |   |   start <= 152835:
mitochondrion_ (16.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 152835:
cytoplasm_ (23.91)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 151354:
cytoplasm_ (11.8)
|   |   |   |   |   |   |   |   |   |   |   start > 151354:
cellular_component_ (7.8)
|   |   |   |   |   |   |   |   |   start > 155094: nucleus_
(27.25/8.19)
|   |   |   |   |   |   start > 155318
|   |   |   |   |   |   |   start <= 173436
|   |   |   |   |   |   |   |   start <= 166335
|   |   |   |   |   |   |   |   |   start <= 162861
|   |   |   |   |   |   |   |   |   |   start <= 157103:
plasma_membrane_ (10.33)
|   |   |   |   |   |   |   |   |   |   start > 157103
|   |   |   |   |   |   |   |   |   |   |   start <= 162218
|   |   |   |   |   |   |   |   |   |   |   |   start <= 160369:
cellular_component_ (11.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 160369:
mitochondrion_ (23.52)
|   |   |   |   |   |   |   |   |   |   |   start > 162218:
cellular_component_ (13.98)
|   |   |   |   |   |   |   |   |   start > 162861
|   |   |   |   |   |   |   |   |   |   start <= 163063:
plasma_membrane_ (28.67/12.99)
|   |   |   |   |   |   |   |   |   |   start > 163063:
cellular_component_ (7.64)
|   |   |   |   |   |   |   |   start > 166335
|   |   |   |   |   |   |   |   |   start <= 172420
|   |   |   |   |   |   |   |   |   |   start <= 167995:
plasma_membrane_ (18.07)
|   |   |   |   |   |   |   |   |   |   start > 167995
|   |   |   |   |   |   |   |   |   |   |   start <= 168368:
cytoplasm_ (15.07)
|   |   |   |   |   |   |   |   |   |   |   start > 168368:
plasma_membrane_ (15.9)
|   |   |   |   |   |   |   |   |   start > 172420: mitochondrion_
(18.2)
|   |   |   |   |   |   |   start > 173436: cellular_bud_
(31.02/12.87)
|   |   start > 176434
|   |   |   start <= 236318
|   |   |   |   start <= 179516
|   |   |   |   |   start <= 178794: nucleolus_ (59.32/13.15)
|   |   |   |   |   start > 178794: mitochondrion_ (22.87)
|   |   |   |   start > 179516
|   |   |   |   |   start <= 214990
```

```
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 199545
|   |   |   |   |   |   |   |   start <= 193293: cytoplasm_
(31.94/11.61)
|   |   |   |   |   |   |   |   start > 193293
|   |   |   |   |   |   |   |   |   start <= 197181: membrane_
(9.43)
|   |   |   |   |   |   |   |   |   start > 197181: cellular_bud_
(27.87/13.58)
|   |   |   |   |   |   |   start > 199545
|   |   |   |   |   |   |   |   start <= 207946
|   |   |   |   |   |   |   |   |   start <= 205393
|   |   |   |   |   |   |   |   |   |   start <= 200438: nucleus_
(16.6)
|   |   |   |   |   |   |   |   |   |   start > 200438
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(6.84/0.59)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_component_ (16.16/6.44)
|   |   |   |   |   |   |   |   |   start > 205393
|   |   |   |   |   |   |   |   |   |   start <= 206640:
Golgi_apparatus_ (18.06)
|   |   |   |   |   |   |   |   |   |   start > 206640:
endoplasmic_reticulum_ (7.66)
|   |   |   |   |   |   |   |   start > 207946
|   |   |   |   |   |   |   |   |   start <= 210419
|   |   |   |   |   |   |   |   |   |   start <= 209606:
cellular_component_ (12.04)
|   |   |   |   |   |   |   |   |   |   start > 209606:
mitochondrion_ (13.79)
|   |   |   |   |   |   |   |   |   start > 210419
|   |   |   |   |   |   |   |   |   |   start <= 211925: nucleus_
(22.73/10.11)
|   |   |   |   |   |   |   |   |   |   start > 211925:
cellular_component_ (13.16)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 186485: nucleus_ (43.04/17.35)
|   |   |   |   |   |   |   start > 186485
|   |   |   |   |   |   |   |   start <= 214067
|   |   |   |   |   |   |   |   |   start <= 190588:
endoplasmic_reticulum_ (16.95)
|   |   |   |   |   |   |   |   |   start > 190588
|   |   |   |   |   |   |   |   |   |   start <= 205393: nucleus_
(39.53/14.69)
|   |   |   |   |   |   |   |   |   |   start > 205393
|   |   |   |   |   |   |   |   |   |   |   start <= 211925:
endoplasmic_reticulum_ (13.55)
|   |   |   |   |   |   |   |   |   |   |   start > 211925: nucleus_
(37.61/18.1)
|   |   |   |   |   |   |   |   start > 214067
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
cellular_component_ (9.06/2.21)
|   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(20.85/8.22)
```

```
|   |   |   |   |   start > 214990
|   |   |   |   |   |   start <= 227938
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 223224: cytoplasm_
(47.75/12.92)
|   |   |   |   |   |   |   |   start > 223224: nucleus_
(28.07/11.97)
|   |   |   |   |   |   |   strand = W: cytoplasm_ (96.5/33.95)
|   |   |   |   |   |   start > 227938
|   |   |   |   |   |   |   strand = C: endoplasmic_reticulum_
(22.13)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 229306: nucleus_ (32.98)
|   |   |   |   |   |   |   |   start > 229306: chromosome_
(27.54/11.13)
|   |   |   start > 236318
|   |   |   |   start <= 252625
|   |   |   |   |   start <= 242348
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 240539: mitochondrion_ (17.61)
|   |   |   |   |   |   |   start > 240539: nucleolus_ (40.31/19.53)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 237210: vacuole_ (19.42)
|   |   |   |   |   |   |   start > 237210: membrane_ (26.75)
|   |   |   |   |   start > 242348
|   |   |   |   |   |   start <= 250042
|   |   |   |   |   |   |   start <= 248812
|   |   |   |   |   |   |   |   start <= 246580: cellular_component_
(17.66)
|   |   |   |   |   |   |   |   start > 246580: cytoplasm_
(66.03/22.12)
|   |   |   |   |   |   |   start > 248812: cellular_component_
(36.59)
|   |   |   |   |   |   start > 250042: ribosome_ (25.85/10.76)
|   |   |   |   start > 252625
|   |   |   |   |   start <= 262449
|   |   |   |   |   |   start <= 252842: mitochondrion_ (20.32)
|   |   |   |   |   |   start > 252842
|   |   |   |   |   |   |   start <= 258880: nucleus_ (53.4/23.07)
|   |   |   |   |   |   |   start > 258880
|   |   |   |   |   |   |   |   start <= 259575: mitochondrion_
(8.69)
|   |   |   |   |   |   |   |   start > 259575: nucleus_ (9.45)
|   |   |   |   |   start > 262449
|   |   |   |   |   |   start <= 264464: nucleolus_ (26.56)
|   |   |   |   |   |   start > 264464
|   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_
(7.35/2.21)
|   |   |   |   |   |   |   |   neigh_strand = C: cell_cortex_
(14.81/6.12)
|   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   distance <= 2807: cell_cortex_
(10.21/5.4)
```

```
|   |   |   |   |   |   |   |   distance > 2807: cytoskeleton_
(9.76/4.04)
|   start > 265065
|   |   start <= 295481
|   |   |   start <= 267431: cell_wall_ (15.06)
|   |   |   start > 267431
|   |   |   |   strand = C
|   |   |   |   |   start <= 289636
|   |   |   |   |   |   start <= 280114: nucleus_ (65.71/30.27)
|   |   |   |   |   |   start > 280114: cytoplasm_ (21.1)
|   |   |   |   |   start > 289636: cellular_component_ (6.06)
|   |   |   |   strand = W
|   |   |   |   |   start <= 274401: cellular_component_ (16.45)
|   |   |   |   |   start > 274401
|   |   |   |   |   |   start <= 286759
|   |   |   |   |   |   |   start <= 280114: cytoplasm_
(28.69/13.98)
|   |   |   |   |   |   |   start > 280114: membrane_fraction_
(16.46)
|   |   |   |   |   |   start > 286759
|   |   |   |   |   |   |   start <= 289636: cellular_component_
(14.3)
|   |   |   |   |   |   |   start > 289636
|   |   |   |   |   |   |   |   start <= 293832: nucleus_ (14.18)
|   |   |   |   |   |   |   |   start > 293832: cytoplasm_ (11.24)
|   |   start > 295481
|   |   |   start <= 298602: plasma_membrane_ (9.25)
|   |   |   start > 298602
|   |   |   |   start <= 309067
|   |   |   |   |   start <= 303027
|   |   |   |   |   |   start <= 302218: cellular_component_ (29.16)
|   |   |   |   |   |   start > 302218: membrane_fraction_ (12.53)
|   |   |   |   |   start > 303027: cellular_component_ (48.24)
|   |   |   |   start > 309067
|   |   |   |   |   start <= 310955: nucleus_ (15.12)
|   |   |   |   |   start > 310955: cellular_component_ (24.1)
```

For Molecular Function

```
|   start <= 224395
|   |   start <= 133122
|   |   |   start <= 35865
|   |   |   |   start <= 27359
|   |   |   |   |   start <= 17290
|   |   |   |   |   |   start <= 12285
|   |   |   |   |   |   |   start <= 9706: transporter_activity_
(25.95)
|   |   |   |   |   |   |   start > 9706: molecular_function_
(14.95)
|   |   |   |   |   |   start > 12285
|   |   |   |   |   |   |   start <= 13282:
transcription_regulator_activity_ (26.32)
|   |   |   |   |   |   |   start > 13282
```

```
|   |   |   |   |   |   |   |   start <= 16880: lyase_activity_
(14.21)
|   |   |   |   |   |   |   |   start > 16880: protein_binding_
(7.19)
|   |   |   |   |   start > 17290
|   |   |   |   |   |   start <= 24325
|   |   |   |   |   |   |   start <= 23379
|   |   |   |   |   |   |   |   start <= 22106: molecular_function_
(19.46)
|   |   |   |   |   |   |   |   start > 22106: RNA_binding_ (15.04)
|   |   |   |   |   |   |   start > 23379: molecular_function_
(37.64)
|   |   |   |   |   |   start > 24325
|   |   |   |   |   |   |   start <= 24768: peptidase_activity_
(16.39)
|   |   |   |   |   |   |   start > 24768: molecular_function_
(16.75)
|   |   |   |   start > 27359
|   |   |   |   |   strand = C: transferase_activity_ (15.2)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 27929:
transcription_regulator_activity_ (33.98/13.61)
|   |   |   |   |   |   start > 27929
|   |   |   |   |   |   |   start <= 31449: transferase_activity_
(8.73)
|   |   |   |   |   |   |   start > 31449:
transcription_regulator_activity_ (16.23)
|   |   |   start > 35865
|   |   |   |   start <= 113768
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 75285
|   |   |   |   |   |   |   start <= 59026
|   |   |   |   |   |   |   |   start <= 56527
|   |   |   |   |   |   |   |   |   start <= 38801:
hydrolase_activity_ (9.31)
|   |   |   |   |   |   |   |   |   start > 38801
|   |   |   |   |   |   |   |   |   |   start <= 48364:
molecular_function_ (52.81)
|   |   |   |   |   |   |   |   |   |   start > 48364
|   |   |   |   |   |   |   |   |   |   |   start <= 52645:
oxidoreductase_activity_ (15.47)
|   |   |   |   |   |   |   |   |   |   |   start > 52645:
molecular_function_ (15.17)
|   |   |   |   |   |   |   |   start > 56527: RNA_binding_ (18.27)
|   |   |   |   |   |   |   start > 59026
|   |   |   |   |   |   |   |   start <= 65568
|   |   |   |   |   |   |   |   |   start <= 63441
|   |   |   |   |   |   |   |   |   |   distance <= 2492:
oxidoreductase_activity_ (43.53/9.99)
|   |   |   |   |   |   |   |   |   |   distance > 2492:
transferase_activity_ (16.22/5.79)
|   |   |   |   |   |   |   |   |   start > 63441:
molecular_function_ (20.94)
|   |   |   |   |   |   |   |   start > 65568
```

```
|   |   |   |   |   |   |   |   |   start <= 71803
|   |   |   |   |   |   |   |   |   |   start <= 68333:
oxidoreductase_activity_ (17.34)
|   |   |   |   |   |   |   |   |   |   start > 68333:
protein_binding_ (22.45)
|   |   |   |   |   |   |   |   |   start > 71803:
oxidoreductase_activity_ (32.12)
|   |   |   |   |   |   start > 75285
|   |   |   |   |   |   |   start <= 101788
|   |   |   |   |   |   |   |   start <= 79162:
transporter_activity_ (13.44)
|   |   |   |   |   |   |   |   start > 79162
|   |   |   |   |   |   |   |   |   start <= 94270
|   |   |   |   |   |   |   |   |   |   start <= 83620:
molecular_function_ (11.96)
|   |   |   |   |   |   |   |   |   |   start > 83620:
lyase_activity_ (17.28)
|   |   |   |   |   |   |   |   |   start > 94270:
molecular_function_ (47.86)
|   |   |   |   |   |   |   start > 101788
|   |   |   |   |   |   |   |   start <= 103358: RNA_binding_
(19.98)
|   |   |   |   |   |   |   |   start > 103358
|   |   |   |   |   |   |   |   |   start <= 105548
|   |   |   |   |   |   |   |   |   |   start <= 104350:
molecular_function_ (19.59)
|   |   |   |   |   |   |   |   |   |   start > 104350:
enzyme_regulator_activity_ (21.55)
|   |   |   |   |   |   |   |   |   start > 105548
|   |   |   |   |   |   |   |   |   |   start <= 107023:
protein_binding_ (16.41)
|   |   |   |   |   |   |   |   |   |   start > 107023
|   |   |   |   |   |   |   |   |   |   |   start <= 109105:
RNA_binding_ (9.88)
|   |   |   |   |   |   |   |   |   |   |   start > 109105:
molecular_function_ (15.09)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 90859
|   |   |   |   |   |   |   start <= 61658
|   |   |   |   |   |   |   |   start <= 50838
|   |   |   |   |   |   |   |   |   start <= 50584:
molecular_function_ (44.49)
|   |   |   |   |   |   |   |   |   start > 50584:
transferase_activity_ (20.07)
|   |   |   |   |   |   |   |   start > 50838: molecular_function_
(59.03)
|   |   |   |   |   |   |   start > 61658
|   |   |   |   |   |   |   |   start <= 65568:
enzyme_regulator_activity_ (33.23/13.68)
|   |   |   |   |   |   |   |   start > 65568
|   |   |   |   |   |   |   |   |   start <= 75285:
molecular_function_ (35.04)
|   |   |   |   |   |   |   |   |   start > 75285
```

```
|   |   |   |   |   |   |   |   |   |   start <= 79162:
protein_kinase_activity_ (9.4)
|   |   |   |   |   |   |   |   |   |   start > 79162:
molecular_function_ (27.09)
|   |   |   |   |   |   start > 90859
|   |   |   |   |   |   |   start <= 107023
|   |   |   |   |   |   |   |   start <= 96281
|   |   |   |   |   |   |   |   |   start <= 91324:
oxidoreductase_activity_ (11.91)
|   |   |   |   |   |   |   |   |   start > 91324:
molecular_function_ (11.84)
|   |   |   |   |   |   |   |   start > 96281
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
transporter_activity_ (10.24/2.04)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
hydrolase_activity_ (20.24/7.55)
|   |   |   |   |   |   |   start > 107023
|   |   |   |   |   |   |   |   start <= 109105
|   |   |   |   |   |   |   |   |   start <= 108021:
molecular_function_ (11.16)
|   |   |   |   |   |   |   |   |   start > 108021:
transferase_activity_ (20.83)
|   |   |   |   |   |   |   |   start > 109105: molecular_function_
(63.88)
|   |   |   |   start > 113768
|   |   |   |   |   start <= 122326
|   |   |   |   |   |   start <= 118618:
structural_molecule_activity_ (35.24)
|   |   |   |   |   |   start > 118618
|   |   |   |   |   |   |   start <= 120316:
oxidoreductase_activity_ (21.01)
|   |   |   |   |   |   |   start > 120316: transferase_activity_
(14.32)
|   |   |   |   |   start > 122326
|   |   |   |   |   |   start <= 127714: molecular_function_ (51.81)
|   |   |   |   |   |   start > 127714
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 131540: protein_binding_
(16.43)
|   |   |   |   |   |   |   |   start > 131540:
transporter_activity_ (19.05)
|   |   |   |   |   |   |   strand = W: protein_kinase_activity_
(9.92)
|   |   start > 133122
|   |   |   start <= 162861
|   |   |   |   start <= 140931
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 137744: hydrolase_activity_ (9.77)
|   |   |   |   |   |   start > 137744:
nucleotidyltransferase_activity_ (16.4)
|   |   |   |   |   strand = W: transferase_activity_ (7.92)
|   |   |   |   start > 140931
|   |   |   |   |   start <= 142544
|   |   |   |   |   |   start <= 142168: molecular_function_ (14.78)
```

```
|   |   |   |   |   |   start > 142168: RNA_binding_ (14.08)
|   |   |   |   |   start > 142544
|   |   |   |   |   |   start <= 154657: molecular_function_
(107.73)
|   |   |   |   |   |   start > 154657
|   |   |   |   |   |   |   start <= 155094: transferase_activity_
(15.45)
|   |   |   |   |   |   |   start > 155094
|   |   |   |   |   |   |   |   start <= 160369: molecular_function_
(37.86)
|   |   |   |   |   |   |   |   start > 160369
|   |   |   |   |   |   |   |   |   start <= 162218:
ligase_activity_ (7.98)
|   |   |   |   |   |   |   |   |   start > 162218:
molecular_function_ (13.2)
|   |   |   start > 162861
|   |   |   |   start <= 200174
|   |   |   |   |   start <= 179516
|   |   |   |   |   |   start <= 167995
|   |   |   |   |   |   |   start <= 163063:
enzyme_regulator_activity_ (12.82)
|   |   |   |   |   |   |   start > 163063: hydrolase_activity_
(22.69)
|   |   |   |   |   |   start > 167995
|   |   |   |   |   |   |   start <= 176434
|   |   |   |   |   |   |   |   start <= 172420
|   |   |   |   |   |   |   |   |   start <= 168368:
molecular_function_ (15.84)
|   |   |   |   |   |   |   |   |   start > 168368:
transporter_activity_ (13.39)
|   |   |   |   |   |   |   |   start > 172420
|   |   |   |   |   |   |   |   |   start <= 173436: DNA_binding_
(18.62)
|   |   |   |   |   |   |   |   |   start > 173436:
molecular_function_ (13.18)
|   |   |   |   |   |   |   start > 176434
|   |   |   |   |   |   |   |   start <= 178794: RNA_binding_
(45.63)
|   |   |   |   |   |   |   |   start > 178794: molecular_function_
(18.17)
|   |   |   |   |   start > 179516
|   |   |   |   |   |   start <= 193293
|   |   |   |   |   |   |   strand = C: hydrolase_activity_ (26.23)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 186485: hydrolase_activity_
(19.33)
|   |   |   |   |   |   |   |   start > 186485:
transferase_activity_ (40.23)
|   |   |   |   |   |   start > 193293
|   |   |   |   |   |   |   start <= 199545
|   |   |   |   |   |   |   |   start <= 197181:
transporter_activity_ (15.54)
|   |   |   |   |   |   |   |   start > 197181:
enzyme_regulator_activity_ (14.67)
```

```
|   |   |   |   |   |   |   start > 199545: DNA_binding_ (18.17)
|   |   |   |   start > 200174
|   |   |   |   |   start <= 211925
|   |   |   |   |   |   start <= 207946
|   |   |   |   |   |   |   start <= 205393:
transcription_regulator_activity_ (25.01)
|   |   |   |   |   |   |   start > 205393: molecular_function_
(21.15)
|   |   |   |   |   |   start > 207946
|   |   |   |   |   |   |   start <= 210419
|   |   |   |   |   |   |   |   start <= 209606: peptidase_activity_
(11.57)
|   |   |   |   |   |   |   |   start > 209606:
structural_molecule_activity_ (8.87)
|   |   |   |   |   |   |   start > 210419: transferase_activity_
(29.36)
|   |   |   |   |   start > 211925
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 220063: molecular_function_
(37.54)
|   |   |   |   |   |   |   start > 220063
|   |   |   |   |   |   |   |   start <= 223224: RNA_binding_
(14.73)
|   |   |   |   |   |   |   |   start > 223224: molecular_function_
(20.34)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 214990
|   |   |   |   |   |   |   |   start <= 214067: molecular_function_
(22.62)
|   |   |   |   |   |   |   |   start > 214067: hydrolase_activity_
(16.03)
|   |   |   |   |   |   |   start > 214990
|   |   |   |   |   |   |   |   start <= 220063: lyase_activity_
(15.67)
|   |   |   |   |   |   |   |   start > 220063: protein_binding_
(12.25)
|   start > 224395
|   |   strand = C
|   |   |   start <= 246960
|   |   |   |   start <= 242348
|   |   |   |   |   start <= 240539
|   |   |   |   |   |   start <= 237210: molecular_function_ (15.36)
|   |   |   |   |   |   start > 237210:
structural_molecule_activity_ (20.92)
|   |   |   |   |   start > 240539: molecular_function_ (21.04)
|   |   |   |   start > 242348: signal_transducer_activity_
(38.71/15.11)
|   |   |   start > 246960
|   |   |   |   start <= 248972: transporter_activity_ (23.04)
|   |   |   |   start > 248972
|   |   |   |   |   start <= 280114
|   |   |   |   |   |   start <= 274401
|   |   |   |   |   |   |   start <= 263389
```

```
|   |   |   |   |   |   |   |   start <= 254368: molecular_function_
(37.48)
|   |   |   |   |   |   |   |   start > 254368:
transcription_regulator_activity_ (11.54)
|   |   |   |   |   |   |   start > 263389: molecular_function_
(39.29)
|   |   |   |   |   |   start > 274401: DNA_binding_ (26.07)
|   |   |   |   |   start > 280114
|   |   |   |   |   |   start <= 298602
|   |   |   |   |   |   |   start <= 295481: molecular_function_
(25.0)
|   |   |   |   |   |   |   start > 295481: transporter_activity_
(12.76)
|   |   |   |   |   |   start > 298602: molecular_function_ (82.78)
|   |   strand = W
|   |   |   start <= 307798
|   |   |   |   start <= 252842
|   |   |   |   |   start <= 231496
|   |   |   |   |   |   start <= 228314: molecular_function_ (34.2)
|   |   |   |   |   |   start > 228314: DNA_binding_ (30.44)
|   |   |   |   |   start > 231496
|   |   |   |   |   |   start <= 242348
|   |   |   |   |   |   |   start <= 237210: hydrolase_activity_
(21.87)
|   |   |   |   |   |   |   start > 237210: isomerase_activity_
(17.0)
|   |   |   |   |   |   start > 242348
|   |   |   |   |   |   |   start <= 250042: molecular_function_
(32.19)
|   |   |   |   |   |   |   start > 250042:
phosphoprotein_phosphatase_activity_ (15.3)
|   |   |   |   start > 252842
|   |   |   |   |   start <= 267431
|   |   |   |   |   |   start <= 254368:
transcription_regulator_activity_ (19.61)
|   |   |   |   |   |   start > 254368
|   |   |   |   |   |   |   start <= 259575
|   |   |   |   |   |   |   |   start <= 258880: molecular_function_
(8.59)
|   |   |   |   |   |   |   |   start > 258880:
oxidoreductase_activity_ (9.74)
|   |   |   |   |   |   |   start > 259575
|   |   |   |   |   |   |   |   start <= 265065
|   |   |   |   |   |   |   |   |   start <= 263389:
molecular_function_ (12.61)
|   |   |   |   |   |   |   |   |   start > 263389: protein_binding_
(14.07)
|   |   |   |   |   |   |   |   start > 265065: molecular_function_
(20.88)
|   |   |   |   |   start > 267431
|   |   |   |   |   |   start <= 286759
|   |   |   |   |   |   |   start <= 274401:
protein_kinase_activity_ (17.62)
```

```
|   |   |   |   |   |   |   start > 274401: hydrolase_activity_
(31.79)
|   |   |   |   |   |   start > 286759
|   |   |   |   |   |   |   start <= 293832
|   |   |   |   |   |   |   |   start <= 289636: molecular_function_
(11.77)
|   |   |   |   |   |   |   |   start > 289636:
transcription_regulator_activity_ (8.03)
|   |   |   |   |   |   |   start > 293832: molecular_function_
(16.91)
|   |   |   start > 307798
|   |   |   |   start <= 309067: oxidoreductase_activity_ (22.4)
|   |   |   |   start > 309067
|   |   |   |   |   start <= 310955: DNA_binding_ (14.74)
|   |   |   |   |   start > 310955: oxidoreductase_activity_ (11.09)
```

For Biological Process

```
|   start <= 193293
|   |   start <= 50584
|   |   |   start <= 22106
|   |   |   |   start <= 13282
|   |   |   |   |   start <= 9706: transport_ (25.02)
|   |   |   |   |   start > 9706
|   |   |   |   |   |   start <= 12285: biological_process_ (22.61)
|   |   |   |   |   |   start > 12285: transcription_ (30.44/5.39)
|   |   |   |   start > 13282
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 17290:
amino_acid_and_derivative_metabolic_process_ (18.14)
|   |   |   |   |   |   start > 17290: DNA_metabolic_process_
(12.34)
|   |   |   |   |   strand = W:
organelle_organization_and_biogenesis_ (14.27)
|   |   |   start > 22106
|   |   |   |   start <= 31449
|   |   |   |   |   start <= 27359
|   |   |   |   |   |   start <= 23379:
ribosome_biogenesis_and_assembly_ (22.22)
|   |   |   |   |   |   start > 23379: biological_process_ (84.21)
|   |   |   |   |   start > 27359
|   |   |   |   |   |   start <= 27929: meiosis_ (14.73)
|   |   |   |   |   |   start > 27929:
ribosome_biogenesis_and_assembly_ (24.88/10.99)
|   |   |   |   start > 31449
|   |   |   |   |   start <= 35865
|   |   |   |   |   |   start <= 35393:
protein_modification_process_ (11.59)
|   |   |   |   |   |   start > 35393:
cell_wall_organization_and_biogenesis_ (19.48)
|   |   |   |   |   start > 35865
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 46905: biological_process_
(45.22)
```

```
|   |   |   |   |   |   |   start > 46905
|   |   |   |   |   |   |   |   start <= 48364:
organelle_organization_and_biogenesis_ (9.35)
|   |   |   |   |   |   |   |   start > 48364: biological_process_
(16.12)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 41488: biological_process_
(14.46)
|   |   |   |   |   |   |   start > 41488
|   |   |   |   |   |   |   |   start <= 44437:
cell_wall_organization_and_biogenesis_ (15.28)
|   |   |   |   |   |   |   |   start > 44437: biological_process_
(10.97)
|   |   start > 50584
|   |   |   start <= 105548
|   |   |   |   start <= 65568
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 59026
|   |   |   |   |   |   |   start <= 56527: biological_process_
(13.19)
|   |   |   |   |   |   |   start > 56527:
ribosome_biogenesis_and_assembly_ (45.42/21.04)
|   |   |   |   |   |   start > 59026
|   |   |   |   |   |   |   start <= 63441: response_to_stress_
(41.85)
|   |   |   |   |   |   |   start > 63441:
ribosome_biogenesis_and_assembly_ (16.88)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 59026
|   |   |   |   |   |   |   start <= 52645:
carbohydrate_metabolic_process_ (38.11)
|   |   |   |   |   |   |   start > 52645: biological_process_
(26.18)
|   |   |   |   |   |   start > 59026
|   |   |   |   |   |   |   start <= 61658: vesicle-
mediated_transport_ (25.86)
|   |   |   |   |   |   |   start > 61658: signal_transduction_
(21.41)
|   |   |   |   start > 65568
|   |   |   |   |   start <= 90859
|   |   |   |   |   |   start <= 69921
|   |   |   |   |   |   |   start <= 68333:
amino_acid_and_derivative_metabolic_process_ (16.51)
|   |   |   |   |   |   |   start > 68333
|   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   neigh_strand = W: conjugation_
(11.77/1.8)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
nuclear_organization_and_biogenesis_ (3.67/0.98)
|   |   |   |   |   |   |   |   neigh_num > 1:
nuclear_organization_and_biogenesis_ (21.88/5.6)
|   |   |   |   |   |   start > 69921
|   |   |   |   |   |   |   start <= 75285
|   |   |   |   |   |   |   |   start <= 73986
```

```
|   |   |   |   |   |   |   |   |   start <= 70150:
biological_process_ (21.79)
|   |   |   |   |   |   |   |   |   start > 70150
|   |   |   |   |   |   |   |   |   |   start <= 71803: conjugation_
(12.55)
|   |   |   |   |   |   |   |   |   |   start > 71803:
biological_process_ (18.01)
|   |   |   |   |   |   |   |   start > 73986:
lipid_metabolic_process_ (21.46/10.05)
|   |   |   |   |   |   |   start > 75285
|   |   |   |   |   |   |   |   start <= 79162
|   |   |   |   |   |   |   |   |   start <= 77919: transport_
(13.16)
|   |   |   |   |   |   |   |   |   start > 77919: cell_budding_
(7.96)
|   |   |   |   |   |   |   |   start > 79162
|   |   |   |   |   |   |   |   |   start <= 83620
|   |   |   |   |   |   |   |   |   |   start <= 82533: translation_
(5.73)
|   |   |   |   |   |   |   |   |   |   start > 82533:
biological_process_ (16.78)
|   |   |   |   |   |   |   |   |   start > 83620: translation_
(12.73)
|   |   |   |   |   start > 90859
|   |   |   |   |   |   start <= 101788
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 94270: biological_process_
(35.88/16.13)
|   |   |   |   |   |   |   |   start > 94270
|   |   |   |   |   |   |   |   |   start <= 96281:
response_to_stress_ (24.06)
|   |   |   |   |   |   |   |   |   start > 96281:
biological_process_ (19.7)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 91324:
amino_acid_and_derivative_metabolic_process_ (18.71)
|   |   |   |   |   |   |   |   start > 91324: cytokinesis_ (10.83)
|   |   |   |   |   |   start > 101788
|   |   |   |   |   |   |   start <= 103358: DNA_metabolic_process_
(19.05)
|   |   |   |   |   |   |   start > 103358
|   |   |   |   |   |   |   |   start <= 104350:
protein_modification_process_ (22.56)
|   |   |   |   |   |   |   |   start > 104350:
amino_acid_and_derivative_metabolic_process_ (15.52)
|   |   |   start > 105548
|   |   |   |   start <= 176434
|   |   |   |   |   start <= 118346
|   |   |   |   |   |   start <= 107712
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 107023:
DNA_metabolic_process_ (22.08)
|   |   |   |   |   |   |   |   start > 107023
```

```
|   |   |   |   |   |   |   |   |   neigh_strand = W:
RNA_metabolic_process_ (13.72/4.12)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
ribosome_biogenesis_and_assembly_ (9.21/1.84)
|   |   |   |   |   |   |   strand = W:
organelle_organization_and_biogenesis_ (14.1)
|   |   |   |   |   |   start > 107712
|   |   |   |   |   |   |   start <= 113768
|   |   |   |   |   |   |   |   start <= 111674
|   |   |   |   |   |   |   |   |   strand = C: biological_process_
(16.18)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 108021:
biological_process_ (10.75)
|   |   |   |   |   |   |   |   |   |   start > 108021:
lipid_metabolic_process_ (10.65)
|   |   |   |   |   |   |   |   start > 111674
|   |   |   |   |   |   |   |   |   start <= 111914: vesicle-
mediated_transport_ (43.96/20.97)
|   |   |   |   |   |   |   |   |   start > 111914:
biological_process_ (26.83)
|   |   |   |   |   |   |   start > 113768: cytokinesis_
(21.97/9.05)
|   |   |   |   |   start > 118346
|   |   |   |   |   |   start <= 137744
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 128468
|   |   |   |   |   |   |   |   |   start <= 122326
|   |   |   |   |   |   |   |   |   |   start <= 120316:
biological_process_ (23.41)
|   |   |   |   |   |   |   |   |   |   start > 120316:
carbohydrate_metabolic_process_ (14.95)
|   |   |   |   |   |   |   |   |   start > 122326
|   |   |   |   |   |   |   |   |   |   start <= 123646:
translation_ (9.97)
|   |   |   |   |   |   |   |   |   |   start > 123646:
biological_process_ (21.11)
|   |   |   |   |   |   |   |   start > 128468
|   |   |   |   |   |   |   |   |   start <= 131540
|   |   |   |   |   |   |   |   |   |   distance <= 1659:
response_to_stress_ (30.21/12.4)
|   |   |   |   |   |   |   |   |   |   distance > 1659: vesicle-
mediated_transport_ (37.46/20.92)
|   |   |   |   |   |   |   |   |   start > 131540
|   |   |   |   |   |   |   |   |   |   start <= 133122:
biological_process_ (23.74)
|   |   |   |   |   |   |   |   |   |   start > 133122: transport_
(14.67)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 127714: translation_
(30.12)
|   |   |   |   |   |   |   |   start > 127714
|   |   |   |   |   |   |   |   |   start <= 131540: cell_cycle_
(10.47)
```

```
|   |   |   |   |   |   |   |   |   start > 131540:
carbohydrate_metabolic_process_ (17.5)
|   |   |   |   |   |   start > 137744
|   |   |   |   |   |   |   start <= 151354
|   |   |   |   |   |   |   |   start <= 142544
|   |   |   |   |   |   |   |   |   start <= 142168
|   |   |   |   |   |   |   |   |   |   start <= 140931:
DNA_metabolic_process_ (12.75)
|   |   |   |   |   |   |   |   |   |   start > 140931:
biological_process_ (17.17)
|   |   |   |   |   |   |   |   |   start > 142168:
ribosome_biogenesis_and_assembly_ (36.04/14.31)
|   |   |   |   |   |   |   |   start > 142544
|   |   |   |   |   |   |   |   |   start <= 142769: translation_
(25.51)
|   |   |   |   |   |   |   |   |   start > 142769
|   |   |   |   |   |   |   |   |   |   start <= 148901
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 147632:
signal_transduction_ (28.94/12.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 147632:
ribosome_biogenesis_and_assembly_ (13.02)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
ribosome_biogenesis_and_assembly_ (12.61)
|   |   |   |   |   |   |   |   |   |   start > 148901: translation_
(22.84)
|   |   |   |   |   |   |   start > 151354
|   |   |   |   |   |   |   |   start <= 166335
|   |   |   |   |   |   |   |   |   start <= 155094
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 154657:
organelle_organization_and_biogenesis_ (19.54)
|   |   |   |   |   |   |   |   |   |   |   start > 154657:
DNA_metabolic_process_ (16.98)
|   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (13.87)
|   |   |   |   |   |   |   |   |   start > 155094
|   |   |   |   |   |   |   |   |   |   start <= 157103:
response_to_stress_ (25.98)
|   |   |   |   |   |   |   |   |   |   start > 157103
|   |   |   |   |   |   |   |   |   |   |   start <= 162861
|   |   |   |   |   |   |   |   |   |   |   |   start <= 160369:
biological_process_ (16.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 160369
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 162218:
translation_ (9.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 162218:
biological_process_ (12.91)
|   |   |   |   |   |   |   |   |   |   |   start > 162861
|   |   |   |   |   |   |   |   |   |   |   |   start <= 163063:
transport_ (19.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 163063:
response_to_stress_ (6.0)
|   |   |   |   |   |   |   |   start > 166335
```

```
|   |   |   |   |   |   |   |   |   start <= 172420
|   |   |   |   |   |   |   |   |   |   start <= 167995: vesicle-
mediated_transport_ (18.45)
|   |   |   |   |   |   |   |   |   |   start > 167995
|   |   |   |   |   |   |   |   |   |   |   start <= 168368:
translation_ (15.8)
|   |   |   |   |   |   |   |   |   |   |   start > 168368: vesicle-
mediated_transport_ (12.1)
|   |   |   |   |   |   |   |   |   start > 172420
|   |   |   |   |   |   |   |   |   |   start <= 173436:
DNA_metabolic_process_ (24.56/12.13)
|   |   |   |   |   |   |   |   |   |   start > 173436:
biological_process_ (12.16)
|   |   |   |   start > 176434
|   |   |   |   |   start <= 179516
|   |   |   |   |   |   start <= 178794
|   |   |   |   |   |   |   start <= 178216
|   |   |   |   |   |   |   |   start <= 177179:
RNA_metabolic_process_ (28.81/13.68)
|   |   |   |   |   |   |   |   start > 177179: translation_ (13.74)
|   |   |   |   |   |   |   start > 178216:
ribosome_biogenesis_and_assembly_ (37.05/18.08)
|   |   |   |   |   |   start > 178794:
cell_wall_organization_and_biogenesis_ (26.32)
|   |   |   |   |   start > 179516
|   |   |   |   |   |   strand = C: RNA_metabolic_process_
(26.45/10.25)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 186485: meiosis_ (19.46)
|   |   |   |   |   |   |   start > 186485
|   |   |   |   |   |   |   |   start <= 190588: vesicle-
mediated_transport_ (18.75)
|   |   |   |   |   |   |   |   start > 190588:
carbohydrate_metabolic_process_ (18.66)
|   start > 193293
|   |   strand = C
|   |   |   start <= 242348
|   |   |   |   start <= 220063
|   |   |   |   |   start <= 205393
|   |   |   |   |   |   start <= 199545
|   |   |   |   |   |   |   start <= 197181: DNA_metabolic_process_
(17.95)
|   |   |   |   |   |   |   start > 197181: pseudohyphal_growth_
(12.53)
|   |   |   |   |   |   start > 199545
|   |   |   |   |   |   |   start <= 200438: transcription_
(22.68/10.81)
|   |   |   |   |   |   |   start > 200438: cell_cycle_ (12.74)
|   |   |   |   |   start > 205393
|   |   |   |   |   |   start <= 210419
|   |   |   |   |   |   |   start <= 209606
|   |   |   |   |   |   |   |   start <= 206640: biological_process_
(19.42)
|   |   |   |   |   |   |   |   start > 206640
```

```
|   |   |   |   |   |   |   |   |   start <= 207946:
protein_modification_process_ (6.22)
|   |   |   |   |   |   |   |   |   start > 207946:
biological_process_ (14.77)
|   |   |   |   |   |   |   start > 209606: translation_ (17.7)
|   |   |   |   |   |   start > 210419
|   |   |   |   |   |   |   start <= 211925: cytokinesis_ (13.15)
|   |   |   |   |   |   |   start > 211925: biological_process_
(37.51)
|   |   |   |   start > 220063
|   |   |   |   |   start <= 229306
|   |   |   |   |   |   start <= 223224
|   |   |   |   |   |   |   neigh_strand = W:
ribosome_biogenesis_and_assembly_ (22.86/6.78)
|   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   neigh_num <= 1:
ribosome_biogenesis_and_assembly_ (2.63/0.59)
|   |   |   |   |   |   |   |   neigh_num > 1: cytokinesis_
(13.08/4.18)
|   |   |   |   |   |   start > 223224:
amino_acid_and_derivative_metabolic_process_ (22.98)
|   |   |   |   |   start > 229306
|   |   |   |   |   |   start <= 237210: vesicle-mediated_transport_
(34.47/16.24)
|   |   |   |   |   |   start > 237210
|   |   |   |   |   |   |   start <= 240539: translation_ (20.53)
|   |   |   |   |   |   |   start > 240539:
ribosome_biogenesis_and_assembly_ (23.15)
|   |   |   start > 242348
|   |   |   |   start <= 248972
|   |   |   |   |   start <= 246960: protein_modification_process_
(52.33/31.18)
|   |   |   |   |   start > 246960: transport_ (24.05)
|   |   |   |   start > 248972
|   |   |   |   |   start <= 263389
|   |   |   |   |   |   start <= 254368: biological_process_
(43.76/10.27)
|   |   |   |   |   |   start > 254368: transcription_ (13.34)
|   |   |   |   |   start > 263389
|   |   |   |   |   |   start <= 280114
|   |   |   |   |   |   |   start <= 274401: biological_process_
(23.27)
|   |   |   |   |   |   |   start > 274401: DNA_metabolic_process_
(13.77)
|   |   |   |   |   |   start > 280114
|   |   |   |   |   |   |   start <= 298602
|   |   |   |   |   |   |   |   start <= 295481: biological_process_
(17.34)
|   |   |   |   |   |   |   |   start > 295481: transport_ (5.71)
|   |   |   |   |   |   |   start > 298602: biological_process_
(57.51)
|   |   strand = W
|   |   |   start <= 263389
|   |   |   |   start <= 229306
```

```
|   |   |   |   |   start <= 211925
|   |   |   |   |   |   start <= 205393: transcription_ (12.83)
|   |   |   |   |   |   start > 205393: lipid_metabolic_process_
(13.57)
|   |   |   |   |   start > 211925
|   |   |   |   |   |   start <= 228314
|   |   |   |   |   |   |   start <= 220063
|   |   |   |   |   |   |   |   start <= 214990
|   |   |   |   |   |   |   |   |   start <= 214067:
biological_process_ (12.48)
|   |   |   |   |   |   |   |   |   start > 214067
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: cell_cycle_
(10.99/3.61)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cell_cycle_ (9.81/4.18)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
RNA_metabolic_process_ (15.05/4.42)
|   |   |   |   |   |   |   |   start > 214990: vesicle-
mediated_transport_ (17.68)
|   |   |   |   |   |   |   start > 220063
|   |   |   |   |   |   |   |   start <= 225559
|   |   |   |   |   |   |   |   |   start <= 224395:
biological_process_ (11.93)
|   |   |   |   |   |   |   |   |   start > 224395:
anatomical_structure_morphogenesis_ (19.09/7.17)
|   |   |   |   |   |   |   |   start > 225559
|   |   |   |   |   |   |   |   |   start <= 227938: translation_
(9.27)
|   |   |   |   |   |   |   |   |   start > 227938:
RNA_metabolic_process_ (13.65)
|   |   |   |   |   |   start > 228314
|   |   |   |   |   |   |   neigh_num <= 1:
organelle_organization_and_biogenesis_ (21.04/12.6)
|   |   |   |   |   |   |   neigh_num > 1: DNA_metabolic_process_
(19.5/10.92)
|   |   |   |   start > 229306
|   |   |   |   |   start <= 252842
|   |   |   |   |   |   start <= 237210
|   |   |   |   |   |   |   start <= 231496: DNA_metabolic_process_
(23.86)
|   |   |   |   |   |   |   start > 231496:
membrane_organization_and_biogenesis_ (23.57)
|   |   |   |   |   |   start > 237210
|   |   |   |   |   |   |   start <= 246960
|   |   |   |   |   |   |   |   start <= 242348: biological_process_
(32.21)
|   |   |   |   |   |   |   |   start > 242348:
DNA_metabolic_process_ (47.1/22.26)
|   |   |   |   |   |   |   start > 246960: biological_process_
(40.72)
|   |   |   |   |   start > 252842
|   |   |   |   |   |   start <= 258880: DNA_metabolic_process_
(32.55)
```

```
|   |   |   |   |   |   start > 258880
|   |   |   |   |   |   |   start <= 259575: response_to_stress_
(17.42)
|   |   |   |   |   |   |   start > 259575
|   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
DNA_metabolic_process_ (7.06/1.77)
|   |   |   |   |   |   |   |   Neigh_GO_aspect = F: meiosis_
(9.54/2.52)
|   |   |   |   |   |   |   |   Neigh_GO_aspect = P: meiosis_
(2.83/1.15)
|   |   |   start > 263389
|   |   |   |   start <= 280114
|   |   |   |   |   start <= 265065
|   |   |   |   |   |   Neigh_GO_aspect = C:
cytoskeleton_organization_and_biogenesis_ (13.44/5.13)
|   |   |   |   |   |   Neigh_GO_aspect = F:
cytoskeleton_organization_and_biogenesis_ (9.08/4.09)
|   |   |   |   |   |   Neigh_GO_aspect = P: biological_process_
(9.63/2.28)
|   |   |   |   |   start > 265065
|   |   |   |   |   |   start <= 274401
|   |   |   |   |   |   |   start <= 267431: conjugation_ (19.21)
|   |   |   |   |   |   |   start > 267431:
protein_modification_process_ (11.48)
|   |   |   |   |   |   start > 274401: pseudohyphal_growth_ (20.61)
|   |   |   |   start > 280114
|   |   |   |   |   start <= 286759
|   |   |   |   |   |   neigh_num <= 1:
membrane_organization_and_biogenesis_ (14.63/5.09)
|   |   |   |   |   |   neigh_num > 1: vesicle-mediated_transport_
(20.01/7.15)
|   |   |   |   |   start > 286759
|   |   |   |   |   |   start <= 301296
|   |   |   |   |   |   |   start <= 293832
|   |   |   |   |   |   |   |   start <= 289636: biological_process_
(8.32)
|   |   |   |   |   |   |   |   start > 289636: transcription_
(9.12)
|   |   |   |   |   |   |   start > 293832: translation_ (12.31)
|   |   |   |   |   |   start > 301296: biological_process_ (52.73)
```

Decision Tree Generated for Chromosome Four:
For Cellular Component

```
|   strand = W
|   |   start <= 142098
|   |   |   start <= 114673
|   |   |   |   start <= 36798
|   |   |   |   |   start <= 30657: cellular_component_
(92.25/40.89)
|   |   |   |   |   start > 30657: nucleus_ (77.56/36.45)
```

```
|   |   |   |   start > 36798
|   |   |   |   |   start <= 84271
|   |   |   |   |   |   start <= 83549
|   |   |   |   |   |   |   start <= 38488: endoplasmic_reticulum_
(60.06/32.53)
|   |   |   |   |   |   |   start > 38488
|   |   |   |   |   |   |   |   start <= 48032: mitochondrion_
(42.49/21.12)
|   |   |   |   |   |   |   |   start > 48032: cytoplasm_
(91.96/46.31)
|   |   |   |   |   |   start > 83549: vacuole_ (32.59/15.63)
|   |   |   |   |   start > 84271
|   |   |   |   |   |   start <= 90177
|   |   |   |   |   |   |   start <= 88249: mitochondrion_
(32.22/15.32)
|   |   |   |   |   |   |   start > 88249: cellular_component_
(19.73)
|   |   |   |   |   |   start > 90177
|   |   |   |   |   |   |   start <= 98476
|   |   |   |   |   |   |   |   start <= 94606:
endoplasmic_reticulum_ (27.74)
|   |   |   |   |   |   |   |   start > 94606: mitochondrion_
(19.04)
|   |   |   |   |   |   |   start > 98476
|   |   |   |   |   |   |   |   start <= 107209: Golgi_apparatus_
(28.84/10.89)
|   |   |   |   |   |   |   |   start > 107209:
endoplasmic_reticulum_ (42.02/18.06)
|   |   |   start > 114673
|   |   |   |   start <= 122217
|   |   |   |   |   start <= 116322: cytoplasmic_membrane-
bound_vesicle_ (14.85)
|   |   |   |   |   start > 116322: cytoplasm_ (35.19/16.09)
|   |   |   |   start > 122217
|   |   |   |   |   start <= 139523
|   |   |   |   |   |   start <= 126788: cellular_component_
(38.93/21.54)
|   |   |   |   |   |   start > 126788: mitochondrion_ (96.46/47.14)
|   |   |   |   |   start > 139523: cellular_component_ (13.9)
|   |   start > 142098
|   |   |   start <= 668077
|   |   |   |   start <= 482264
|   |   |   |   |   start <= 216529
|   |   |   |   |   |   start <= 183344
|   |   |   |   |   |   |   start <= 172183
|   |   |   |   |   |   |   |   start <= 164291
|   |   |   |   |   |   |   |   |   start <= 156319: nucleus_
(31.6/13.7)
|   |   |   |   |   |   |   |   |   start > 156319: cytoplasm_
(62.15/36.66)
|   |   |   |   |   |   |   |   start > 164291: cellular_component_
(35.29/22.93)
|   |   |   |   |   |   |   start > 172183
```

```
|   |   |   |   |   |   |   |   start <= 174919: cytoplasm_
(56.92/21.91)
|   |   |   |   |   |   |   |   start > 174919: nucleus_
(75.3/17.48)
|   |   |   |   |   |   start > 183344: cytoplasm_ (198.55/118.68)
|   |   |   |   |   start > 216529
|   |   |   |   |   |   start <= 326613
|   |   |   |   |   |   |   start <= 241418
|   |   |   |   |   |   |   |   start <= 229906: ribosome_
(99.61/64.45)
|   |   |   |   |   |   |   |   start > 229906
|   |   |   |   |   |   |   |   |   start <= 234927: vacuole_
(91.26/63.54)
|   |   |   |   |   |   |   |   |   start > 234927
|   |   |   |   |   |   |   |   |   |   start <= 240259: cytoplasm_
(45.26/21.99)
|   |   |   |   |   |   |   |   |   |   start > 240259: vacuole_
(31.03/13.92)
|   |   |   |   |   |   |   start > 241418
|   |   |   |   |   |   |   |   start <= 294759
|   |   |   |   |   |   |   |   |   start <= 248581
|   |   |   |   |   |   |   |   |   |   start <= 242552: cytoplasm_
(28.29/8.73)
|   |   |   |   |   |   |   |   |   |   start > 242552
|   |   |   |   |   |   |   |   |   |   |   start <= 247612:
mitochondrion_ (35.02/15.32)
|   |   |   |   |   |   |   |   |   |   |   start > 247612:
cytoplasm_ (21.77)
|   |   |   |   |   |   |   |   |   start > 248581
|   |   |   |   |   |   |   |   |   |   start <= 272389
|   |   |   |   |   |   |   |   |   |   |   distance <= 3037
|   |   |   |   |   |   |   |   |   |   |   |   start <= 251566:
membrane_ (29.96/18.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 251566
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 258915:
cellular_component_ (17.33/3.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 258915:
nucleus_ (40.48/18.28)
|   |   |   |   |   |   |   |   |   |   |   distance > 3037
|   |   |   |   |   |   |   |   |   |   |   |   start <= 258915:
cytoplasm_ (28.49/11.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 258915:
nucleus_ (26.66/13.91)
|   |   |   |   |   |   |   |   |   |   start > 272389: cytoplasm_
(116.27/81.54)
|   |   |   |   |   |   |   |   start > 294759
|   |   |   |   |   |   |   |   |   start <= 303211
|   |   |   |   |   |   |   |   |   |   start <= 296820:
cellular_component_ (15.72)
|   |   |   |   |   |   |   |   |   |   start > 296820:
mitochondrion_ (48.26/9.73)
|   |   |   |   |   |   |   |   |   start > 303211
|   |   |   |   |   |   |   |   |   |   start <= 323471: ribosome_
(52.74/22.17)
```

```
|   |   |   |   |   |   |   |   |   |   start > 323471:
cellular_component_ (11.72)
|   |   |   |   |   |   start > 326613
|   |   |   |   |   |   |   start <= 444680
|   |   |   |   |   |   |   |   start <= 345665
|   |   |   |   |   |   |   |   |   start <= 337487: nucleus_
(43.65/16.73)
|   |   |   |   |   |   |   |   |   start > 337487: nucleolus_
(47.98/29.81)
|   |   |   |   |   |   |   |   start > 345665: nucleus_
(391.5/251.75)
|   |   |   |   |   |   |   start > 444680
|   |   |   |   |   |   |   |   start <= 471850: cytoplasm_
(167.88/80.34)
|   |   |   |   |   |   |   |   start > 471850
|   |   |   |   |   |   |   |   |   start <= 474043: nucleus_
(52.19/19.43)
|   |   |   |   |   |   |   |   |   start > 474043: chromosome_
(12.47)
|   |   |   |   start > 482264
|   |   |   |   |   start <= 603061
|   |   |   |   |   |   start <= 570646
|   |   |   |   |   |   |   start <= 558058
|   |   |   |   |   |   |   |   start <= 497315
|   |   |   |   |   |   |   |   |   start <= 486801: nucleolus_
(14.64)
|   |   |   |   |   |   |   |   |   start > 486801: ribosome_
(30.44/12.21)
|   |   |   |   |   |   |   |   start > 497315
|   |   |   |   |   |   |   |   |   distance <= 3139: cytoplasm_
(179.84/99.52)
|   |   |   |   |   |   |   |   |   distance > 3139: mitochondrion_
(105.6/68.56)
|   |   |   |   |   |   |   start > 558058
|   |   |   |   |   |   |   |   start <= 565925
|   |   |   |   |   |   |   |   |   start <= 563525:
plasma_membrane_ (26.63)
|   |   |   |   |   |   |   |   |   start > 563525:
endoplasmic_reticulum_ (12.48)
|   |   |   |   |   |   |   |   start > 565925: cytoplasm_
(56.21/14.77)
|   |   |   |   |   |   start > 570646
|   |   |   |   |   |   |   start <= 576471
|   |   |   |   |   |   |   |   start <= 574161: mitochondrion_
(14.01)
|   |   |   |   |   |   |   |   start > 574161: membrane_fraction_
(15.44)
|   |   |   |   |   |   |   start > 576471
|   |   |   |   |   |   |   |   start <= 579456: ribosome_
(36.43/21.26)
|   |   |   |   |   |   |   |   start > 579456
|   |   |   |   |   |   |   |   |   start <= 598465
|   |   |   |   |   |   |   |   |   |   start <= 580685:
mitochondrion_ (11.92)
```

```
|   |   |   |   |   |   |   |   |   |   start > 580685
|   |   |   |   |   |   |   |   |   |   |   start <= 587717:
cytoplasm_ (15.4)
|   |   |   |   |   |   |   |   |   |   |   start > 587717: nucleus_
(85.67/45.24)
|   |   |   |   |   |   |   |   |   start > 598465: mitochondrion_
(51.79/12.17)
|   |   |   |   |   start > 603061
|   |   |   |   |   |   start <= 622109: membrane_ (127.55/82.55)
|   |   |   |   |   |   start > 622109
|   |   |   |   |   |   |   start <= 653604: nucleus_ (91.21/45.97)
|   |   |   |   |   |   |   start > 653604: cytoplasm_ (81.7/45.86)
|   |   |   start > 668077
|   |   |   |   start <= 1431004
|   |   |   |   |   start <= 1234210
|   |   |   |   |   |   start <= 1171819
|   |   |   |   |   |   |   start <= 776160
|   |   |   |   |   |   |   |   start <= 771874
|   |   |   |   |   |   |   |   |   start <= 728256
|   |   |   |   |   |   |   |   |   |   start <= 683578:
mitochondrion_ (46.32/28.32)
|   |   |   |   |   |   |   |   |   |   start > 683578
|   |   |   |   |   |   |   |   |   |   |   start <= 718457
|   |   |   |   |   |   |   |   |   |   |   |   start <= 700312
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 688224:
nucleus_ (38.84/23.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 688224:
cellular_component_ (89.94/54.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 700312:
cytoplasm_ (76.31/49.79)
|   |   |   |   |   |   |   |   |   |   |   start > 718457:
Golgi_apparatus_ (15.59)
|   |   |   |   |   |   |   |   |   start > 728256
|   |   |   |   |   |   |   |   |   |   start <= 770354
|   |   |   |   |   |   |   |   |   |   |   start <= 755625
|   |   |   |   |   |   |   |   |   |   |   |   start <= 751628:
nucleus_ (101.48/49.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 751628:
mitochondrion_ (25.36/8.72)
|   |   |   |   |   |   |   |   |   |   |   start > 755625:
cytoplasm_ (81.25/32.12)
|   |   |   |   |   |   |   |   |   |   start > 770354: membrane_
(74.02/42.63)
|   |   |   |   |   |   |   |   start > 771874: plasma_membrane_
(20.24)
|   |   |   |   |   |   |   start > 776160
|   |   |   |   |   |   |   |   start <= 1037191
|   |   |   |   |   |   |   |   |   start <= 912095
|   |   |   |   |   |   |   |   |   |   start <= 851225
|   |   |   |   |   |   |   |   |   |   |   start <= 812107
|   |   |   |   |   |   |   |   |   |   |   |   start <= 789446
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 779040:
cytoplasm_ (38.84/16.61)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 779040:
nucleus_ (61.33/17.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 789446:
cytoplasm_ (152.29/52.5)
|   |   |   |   |   |   |   |   |   |   |   start > 812107
|   |   |   |   |   |   |   |   |   |   |   |   start <= 819430
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 816875:
cellular_component_ (58.34/18.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 816875
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
817947: mitochondrion_ (10.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
817947: cellular_component_ (19.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 819430
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 848068
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
827579: nucleus_ (26.78/7.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
827579: cytoplasm_ (146.21/89.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 848068:
nucleus_ (54.35/25.6)
|   |   |   |   |   |   |   |   |   |   start > 851225
|   |   |   |   |   |   |   |   |   |   |   start <= 859343
|   |   |   |   |   |   |   |   |   |   |   |   start <= 858134:
microtubule_organizing_center_ (38.63/13.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 858134:
endoplasmic_reticulum_ (55.44/33.29)
|   |   |   |   |   |   |   |   |   |   |   start > 859343:
cytoplasm_ (208.55/94.12)
|   |   |   |   |   |   |   |   |   start > 912095
|   |   |   |   |   |   |   |   |   |   start <= 1004000
|   |   |   |   |   |   |   |   |   |   |   start <= 955129
|   |   |   |   |   |   |   |   |   |   |   |   start <= 946308
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 924781:
chromosome_ (157.17/113.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 924781:
mitochondrion_ (68.09/25.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 946308:
cellular_component_ (88.42/47.88)
|   |   |   |   |   |   |   |   |   |   |   start > 955129
|   |   |   |   |   |   |   |   |   |   |   |   start <= 992828:
cytoplasm_ (88.92/58.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 992828
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 998860:
peroxisome_ (40.96/19.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 998860:
mitochondrion_ (16.12)
|   |   |   |   |   |   |   |   |   |   start > 1004000
|   |   |   |   |   |   |   |   |   |   |   start <= 1005671:
cytoplasmic_membrane-bound_vesicle_ (46.44/17.85)
|   |   |   |   |   |   |   |   |   |   |   start > 1005671
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1015698:
cytoplasm_ (33.51/7.59)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 1015698:
nucleus_ (118.54/52.5)
|   |   |   |   |   |   |   |   start > 1037191
|   |   |   |   |   |   |   |   |   start <= 1145086
|   |   |   |   |   |   |   |   |   |   start <= 1095458
|   |   |   |   |   |   |   |   |   |   |   start <= 1085062:
nucleus_ (164.16/100.81)
|   |   |   |   |   |   |   |   |   |   |   start > 1085062
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1090076:
nucleolus_ (17.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1090076:
mitochondrial_envelope_ (30.24/14.68)
|   |   |   |   |   |   |   |   |   |   start > 1095458
|   |   |   |   |   |   |   |   |   |   |   start <= 1127867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1105824:
cellular_component_ (66.98/32.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1105824:
cytoplasm_ (100.15/71.8)
|   |   |   |   |   |   |   |   |   |   |   start > 1127867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1130996:
membrane_ (46.2/26.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1130996:
cellular_component_ (42.72/20.2)
|   |   |   |   |   |   |   |   |   start > 1145086: mitochondrion_
(34.45)
|   |   |   |   |   |   start > 1171819
|   |   |   |   |   |   |   start <= 1181794
|   |   |   |   |   |   |   |   start <= 1178659
|   |   |   |   |   |   |   |   |   start <= 1175823: cytoplasm_
(8.77)
|   |   |   |   |   |   |   |   |   start > 1175823:
Golgi_apparatus_ (23.64)
|   |   |   |   |   |   |   |   start > 1178659: membrane_
(49.45/24.41)
|   |   |   |   |   |   |   start > 1181794
|   |   |   |   |   |   |   |   start <= 1219405: cytoplasm_
(210.69/135.12)
|   |   |   |   |   |   |   |   start > 1219405
|   |   |   |   |   |   |   |   |   start <= 1230159
|   |   |   |   |   |   |   |   |   |   start <= 1222751: membrane_
(15.88)
|   |   |   |   |   |   |   |   |   |   start > 1222751:
mitochondrion_ (70.76/32.5)
|   |   |   |   |   |   |   |   |   start > 1230159: cytoplasm_
(15.9)
|   |   |   |   |   start > 1234210
|   |   |   |   |   |   start <= 1337344
|   |   |   |   |   |   |   start <= 1301608
|   |   |   |   |   |   |   |   start <= 1261673
|   |   |   |   |   |   |   |   |   start <= 1250178
|   |   |   |   |   |   |   |   |   |   start <= 1246076: ribosome_
(47.08/22.45)
|   |   |   |   |   |   |   |   |   |   start > 1246076:
cytoskeleton_ (34.63/16.65)
```

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|   |   |   |   |   |   |   |   |   start > 1250178:
cellular_component_ (102.57/39.87)
|   |   |   |   |   |   |   |   start > 1261673
|   |   |   |   |   |   |   |   |   start <= 1279202: nucleus_
(153.08/98.53)
|   |   |   |   |   |   |   |   |   start > 1279202
|   |   |   |   |   |   |   |   |   |   start <= 1294685
|   |   |   |   |   |   |   |   |   |   |   distance <= 3250:
cytoplasm_ (30.65/18.47)
|   |   |   |   |   |   |   |   |   |   |   distance > 3250:
cell_cortex_ (15.44/9.17)
|   |   |   |   |   |   |   |   |   |   start > 1294685: nucleus_
(19.5/5.76)
|   |   |   |   |   |   |   start > 1301608
|   |   |   |   |   |   |   |   start <= 1328775
|   |   |   |   |   |   |   |   |   start <= 1306259
|   |   |   |   |   |   |   |   |   |   start <= 1305622:
chromosome_ (20.56/9.51)
|   |   |   |   |   |   |   |   |   |   start > 1305622:
plasma_membrane_ (19.17)
|   |   |   |   |   |   |   |   |   start > 1306259: nucleus_
(54.14/32.19)
|   |   |   |   |   |   |   |   start > 1328775:
endoplasmic_reticulum_ (58.41/25.78)
|   |   |   |   |   |   start > 1337344
|   |   |   |   |   |   |   start <= 1417391
|   |   |   |   |   |   |   |   start <= 1362870
|   |   |   |   |   |   |   |   |   start <= 1359915
|   |   |   |   |   |   |   |   |   |   start <= 1338266:
mitochondrion_ (20.8)
|   |   |   |   |   |   |   |   |   |   start > 1338266: nucleus_
(113.2/57.17)
|   |   |   |   |   |   |   |   |   start > 1359915: membrane_
(31.48/14.59)
|   |   |   |   |   |   |   |   start > 1362870
|   |   |   |   |   |   |   |   |   start <= 1367477: cytoplasm_
(19.43)
|   |   |   |   |   |   |   |   |   start > 1367477: nucleus_
(266.61/152.63)
|   |   |   |   |   |   |   start > 1417391
|   |   |   |   |   |   |   |   start <= 1422755: Golgi_apparatus_
(28.51)
|   |   |   |   |   |   |   |   start > 1422755: nucleus_
(67.28/43.31)
|   |   |   |   start > 1431004
|   |   |   |   |   start <= 1471055
|   |   |   |   |   |   start <= 1434916: endoplasmic_reticulum_
(35.62/15.1)
|   |   |   |   |   |   start > 1434916: mitochondrion_
(106.15/35.33)
|   |   |   |   |   start > 1471055
|   |   |   |   |   |   start <= 1483395
|   |   |   |   |   |   |   start <= 1477231: cytoplasm_ (35.13)
```

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|   |   |   |   |   |   |   start > 1477231: endoplasmic_reticulum_
(57.17/29.19)
|   |   |   |   |   |   start > 1483395: cytoplasm_ (174.77/103.94)
|   strand = C
|   |   start <= 1005671
|   |   |   start <= 794720
|   |   |   |   start <= 525437
|   |   |   |   |   start <= 219288
|   |   |   |   |   |   start <= 172482
|   |   |   |   |   |   |   start <= 61802
|   |   |   |   |   |   |   |   start <= 60406
|   |   |   |   |   |   |   |   |   start <= 28775
|   |   |   |   |   |   |   |   |   |   start <= 22823:
cellular_component_ (36.96/14.03)
|   |   |   |   |   |   |   |   |   |   start > 22823: membrane_
(24.3)
|   |   |   |   |   |   |   |   |   start > 28775: cytoplasm_
(138.83/62.73)
|   |   |   |   |   |   |   |   start > 60406: cell_cortex_
(31.27/15.34)
|   |   |   |   |   |   |   start > 61802
|   |   |   |   |   |   |   |   start <= 122217
|   |   |   |   |   |   |   |   |   start <= 83549
|   |   |   |   |   |   |   |   |   |   start <= 76546: nucleus_
(101.25/54.86)
|   |   |   |   |   |   |   |   |   |   start > 76546: nucleolus_
(35.31/14.56)
|   |   |   |   |   |   |   |   |   start > 83549: nucleus_
(148.75/70.65)
|   |   |   |   |   |   |   |   start > 122217
|   |   |   |   |   |   |   |   |   start <= 159605
|   |   |   |   |   |   |   |   |   |   start <= 145519
|   |   |   |   |   |   |   |   |   |   |   start <= 142098:
cellular_component_ (87.99/39.63)
|   |   |   |   |   |   |   |   |   |   |   start > 142098: nucleus_
(13.78)
|   |   |   |   |   |   |   |   |   |   start > 145519:
mitochondrion_ (39.24/18.13)
|   |   |   |   |   |   |   |   |   start > 159605
|   |   |   |   |   |   |   |   |   |   start <= 167715: nucleus_
(88.67/49.87)
|   |   |   |   |   |   |   |   |   |   start > 167715
|   |   |   |   |   |   |   |   |   |   |   start <= 169609:
cellular_component_ (15.76)
|   |   |   |   |   |   |   |   |   |   |   start > 169609:
cytoplasm_ (19.79)
|   |   |   |   |   |   start > 172482
|   |   |   |   |   |   |   start <= 213352
|   |   |   |   |   |   |   |   start <= 192751: mitochondrion_
(79.72/37.23)
|   |   |   |   |   |   |   |   start > 192751
|   |   |   |   |   |   |   |   |   start <= 199997: nucleus_
(63.02/35.06)
```

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|   |   |   |   |   |   |   |   |   start > 199997: mitochondrion_
(79.26/50.51)
|   |   |   |   |   |   |   start > 213352:
site_of_polarized_growth_ (27.97/12.65)
|   |   |   |   |   start > 219288
|   |   |   |   |   |   start <= 345665
|   |   |   |   |   |   |   start <= 281848
|   |   |   |   |   |   |   |   start <= 268921
|   |   |   |   |   |   |   |   |   start <= 248581
|   |   |   |   |   |   |   |   |   |   start <= 242552: nucleus_
(73.55/37.16)
|   |   |   |   |   |   |   |   |   |   start > 242552:
mitochondrion_ (14.97/7.16)
|   |   |   |   |   |   |   |   |   start > 248581
|   |   |   |   |   |   |   |   |   |   start <= 264110: cytoplasm_
(95.54/50.67)
|   |   |   |   |   |   |   |   |   |   start > 264110:
cellular_component_ (76.89/53.86)
|   |   |   |   |   |   |   |   start > 268921
|   |   |   |   |   |   |   |   |   distance <= 1432: mitochondrion_
(9.27/2.49)
|   |   |   |   |   |   |   |   |   distance > 1432: nucleus_
(70.8/20.88)
|   |   |   |   |   |   |   start > 281848
|   |   |   |   |   |   |   |   start <= 300003
|   |   |   |   |   |   |   |   |   start <= 285165:
endoplasmic_reticulum_ (35.97/13.84)
|   |   |   |   |   |   |   |   |   start > 285165:
cellular_component_ (89.57/38.78)
|   |   |   |   |   |   |   |   start > 300003
|   |   |   |   |   |   |   |   |   start <= 326613
|   |   |   |   |   |   |   |   |   |   start <= 310122
|   |   |   |   |   |   |   |   |   |   |   distance <= 3922:
nucleus_ (48.95/23.74)
|   |   |   |   |   |   |   |   |   |   |   distance > 3922:
ribosome_ (19.04/6.17)
|   |   |   |   |   |   |   |   |   |   start > 310122
|   |   |   |   |   |   |   |   |   |   |   start <= 323471
|   |   |   |   |   |   |   |   |   |   |   |   start <= 322226:
nucleus_ (79.06/52.36)
|   |   |   |   |   |   |   |   |   |   |   |   start > 322226:
nucleolus_ (8.43)
|   |   |   |   |   |   |   |   |   |   |   start > 323471: nucleus_
(17.97)
|   |   |   |   |   |   |   |   |   start > 326613
|   |   |   |   |   |   |   |   |   |   start <= 337487:
mitochondrion_ (56.15/22.63)
|   |   |   |   |   |   |   |   |   |   start > 337487
|   |   |   |   |   |   |   |   |   |   |   start <= 340134:
cytoplasm_ (32.8/14.16)
|   |   |   |   |   |   |   |   |   |   |   start > 340134: nucleus_
(34.32/12.44)
|   |   |   |   |   |   start > 345665
|   |   |   |   |   |   |   start <= 438044
```

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|   |   |   |   |   |   |   |   start <= 388898
|   |   |   |   |   |   |   |   |   start <= 382330: cytoplasm_
(210.93/137.82)
|   |   |   |   |   |   |   |   |   start > 382330
|   |   |   |   |   |   |   |   |   |   start <= 385584:
cellular_component_ (27.88)
|   |   |   |   |   |   |   |   |   |   start > 385584: cytoplasm_
(37.67/23.19)
|   |   |   |   |   |   |   |   start > 388898
|   |   |   |   |   |   |   |   |   start <= 416705
|   |   |   |   |   |   |   |   |   |   start <= 404954:
mitochondrion_ (50.62/26.49)
|   |   |   |   |   |   |   |   |   |   start > 404954:
cellular_component_ (41.29/6.12)
|   |   |   |   |   |   |   |   |   start > 416705
|   |   |   |   |   |   |   |   |   |   start <= 432327:
plasma_membrane_ (85.6/47.29)
|   |   |   |   |   |   |   |   |   |   start > 432327:
cellular_component_ (39.37/12.16)
|   |   |   |   |   |   |   start > 438044
|   |   |   |   |   |   |   |   start <= 512106
|   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(118.03/71.29)
|   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   start <= 491512: cytoplasm_
(134.49/81.33)
|   |   |   |   |   |   |   |   |   |   start > 491512: nucleus_
(108.0/70.06)
|   |   |   |   |   |   |   |   start > 512106: mitochondrion_
(25.2/8.12)
|   |   |   |   start > 525437
|   |   |   |   |   start <= 676099
|   |   |   |   |   |   start <= 603061
|   |   |   |   |   |   |   start <= 574161
|   |   |   |   |   |   |   |   start <= 563525
|   |   |   |   |   |   |   |   |   start <= 541697:
membrane_fraction_ (158.59/103.66)
|   |   |   |   |   |   |   |   |   start > 541697
|   |   |   |   |   |   |   |   |   |   start <= 553252: nucleus_
(66.12/31.42)
|   |   |   |   |   |   |   |   |   |   start > 553252: cytoplasm_
(104.64/60.83)
|   |   |   |   |   |   |   |   start > 563525
|   |   |   |   |   |   |   |   |   start <= 565925:
endoplasmic_reticulum_ (30.88/12.4)
|   |   |   |   |   |   |   |   |   start > 565925:
cellular_component_ (22.68)
|   |   |   |   |   |   |   start > 574161
|   |   |   |   |   |   |   |   start <= 583711: cytoplasm_ (41.73)
|   |   |   |   |   |   |   |   start > 583711
|   |   |   |   |   |   |   |   |   start <= 588377: mitochondrion_
(50.25/16.18)
|   |   |   |   |   |   |   |   |   start > 588377: cytoplasm_
(44.04/24.53)
```

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|   |   |   |   |   |   start > 603061
|   |   |   |   |   |   |   start <= 668077
|   |   |   |   |   |   |   |   start <= 619642
|   |   |   |   |   |   |   |   |   start <= 616147
|   |   |   |   |   |   |   |   |   |   start <= 610438: nucleus_
(36.59)
|   |   |   |   |   |   |   |   |   |   start > 610438
|   |   |   |   |   |   |   |   |   |   |   start <= 614001:
cytoplasm_ (17.2)
|   |   |   |   |   |   |   |   |   |   |   start > 614001:
cellular_component_ (17.94)
|   |   |   |   |   |   |   |   |   start > 616147
|   |   |   |   |   |   |   |   |   |   start <= 617167: membrane_
(48.05/28.01)
|   |   |   |   |   |   |   |   |   |   start > 617167: nucleus_
(64.28/22.67)
|   |   |   |   |   |   |   |   start > 619642
|   |   |   |   |   |   |   |   |   start <= 658347
|   |   |   |   |   |   |   |   |   |   start <= 625995
|   |   |   |   |   |   |   |   |   |   |   start <= 622109:
cytoplasm_ (16.61)
|   |   |   |   |   |   |   |   |   |   |   start > 622109:
membrane_ (14.48)
|   |   |   |   |   |   |   |   |   |   start > 625995: cytoplasm_
(81.1/32.82)
|   |   |   |   |   |   |   |   |   start > 658347
|   |   |   |   |   |   |   |   |   |   start <= 667001: cell_wall_
(38.63/17.97)
|   |   |   |   |   |   |   |   |   |   start > 667001: cytoplasm_
(8.46)
|   |   |   |   |   |   |   start > 668077
|   |   |   |   |   |   |   |   start <= 671266: membrane_fraction_
(15.44)
|   |   |   |   |   |   |   |   start > 671266: cellular_component_
(17.57)
|   |   |   |   |   start > 676099
|   |   |   |   |   |   start <= 718457
|   |   |   |   |   |   |   start <= 704481
|   |   |   |   |   |   |   |   start <= 682223: nucleus_
(69.7/39.36)
|   |   |   |   |   |   |   |   start > 682223: mitochondrion_
(85.52/30.29)
|   |   |   |   |   |   |   start > 704481: cytoskeleton_
(63.14/43.27)
|   |   |   |   |   |   start > 718457
|   |   |   |   |   |   |   start <= 741597
|   |   |   |   |   |   |   |   start <= 739994: cytoplasm_
(95.42/60.52)
|   |   |   |   |   |   |   |   start > 739994: peroxisome_ (21.03)
|   |   |   |   |   |   |   start > 741597
|   |   |   |   |   |   |   |   start <= 771874: nucleus_
(141.58/63.62)
|   |   |   |   |   |   |   |   start > 771874: cytoplasm_
(116.19/87.23)
```

```
|   |   |   start > 794720
|   |   |   |   start <= 832470
|   |   |   |   |   start <= 806618: cytoplasmic_membrane-
bound_vesicle_ (46.28/21.53)
|   |   |   |   |   start > 806618
|   |   |   |   |   |   start <= 831510: nucleus_ (103.87/38.69)
|   |   |   |   |   |   start > 831510: mitochondrion_ (21.91)
|   |   |   |   start > 832470
|   |   |   |   |   start <= 977225
|   |   |   |   |   |   start <= 936611
|   |   |   |   |   |   |   start <= 931125
|   |   |   |   |   |   |   |   start <= 838389: cytoplasm_
(34.55/16.71)
|   |   |   |   |   |   |   |   start > 838389
|   |   |   |   |   |   |   |   |   start <= 924781
|   |   |   |   |   |   |   |   |   |   start <= 851225
|   |   |   |   |   |   |   |   |   |   |   start <= 844858:
nucleus_ (65.92/28.67)
|   |   |   |   |   |   |   |   |   |   |   start > 844858:
mitochondrion_ (47.89/21.2)
|   |   |   |   |   |   |   |   |   |   start > 851225
|   |   |   |   |   |   |   |   |   |   |   start <= 862051:
cytoplasm_ (60.89/17.77)
|   |   |   |   |   |   |   |   |   |   |   start > 862051: nucleus_
(163.62/108.55)
|   |   |   |   |   |   |   |   |   start > 924781: mitochondrion_
(60.82/30.58)
|   |   |   |   |   |   |   start > 931125: membrane_fraction_
(32.38/12.35)
|   |   |   |   |   |   start > 936611
|   |   |   |   |   |   |   start <= 943416: cytoplasmic_membrane-
bound_vesicle_ (55.6/32.12)
|   |   |   |   |   |   |   start > 943416
|   |   |   |   |   |   |   |   start <= 954284: nucleus_ (21.11)
|   |   |   |   |   |   |   |   start > 954284
|   |   |   |   |   |   |   |   |   start <= 967818
|   |   |   |   |   |   |   |   |   |   start <= 960610
|   |   |   |   |   |   |   |   |   |   |   start <= 958335:
cytoplasm_ (22.24)
|   |   |   |   |   |   |   |   |   |   |   start > 958335:
cellular_component_ (13.66)
|   |   |   |   |   |   |   |   |   |   start > 960610: cytoplasm_
(29.4/12.65)
|   |   |   |   |   |   |   |   |   start > 967818: nucleus_
(63.79/18.46)
|   |   |   |   |   start > 977225
|   |   |   |   |   |   start <= 998860
|   |   |   |   |   |   |   start <= 995530: mitochondrion_
(47.94/29.39)
|   |   |   |   |   |   |   start > 995530: membrane_ (13.8)
|   |   |   |   |   |   start > 998860: cytoplasm_ (75.12/45.58)
|   |   start > 1005671
|   |   |   start <= 1045007
|   |   |   |   start <= 1013639: plasma_membrane_ (17.98)
```

```
|   |   |   |   start > 1013639
|   |   |   |   |   start <= 1039724: cellular_component_
(145.88/69.21)
|   |   |   |   |   start > 1039724: membrane_ (48.24/29.03)
|   |   |   start > 1045007
|   |   |   |   start <= 1190052
|   |   |   |   |   start <= 1169172
|   |   |   |   |   |   start <= 1108098
|   |   |   |   |   |   |   start <= 1105824
|   |   |   |   |   |   |   |   start <= 1073484
|   |   |   |   |   |   |   |   |   distance <= 6469: cytoplasm_
(163.24/96.22)
|   |   |   |   |   |   |   |   |   distance > 6469: nucleus_
(23.29/12.48)
|   |   |   |   |   |   |   |   start > 1073484
|   |   |   |   |   |   |   |   |   start <= 1075167:
cellular_component_ (10.94)
|   |   |   |   |   |   |   |   |   start > 1075167: nucleus_
(228.96/165.56)
|   |   |   |   |   |   |   start > 1105824: endomembrane_system_
(42.89/25.39)
|   |   |   |   |   |   start > 1108098
|   |   |   |   |   |   |   start <= 1153620
|   |   |   |   |   |   |   |   start <= 1124920: mitochondrion_
(96.47/63.19)
|   |   |   |   |   |   |   |   start > 1124920
|   |   |   |   |   |   |   |   |   start <= 1141162
|   |   |   |   |   |   |   |   |   |   start <= 1126013: cytoplasm_
(34.41/11.94)
|   |   |   |   |   |   |   |   |   |   start > 1126013:
endoplasmic_reticulum_ (32.06/10.45)
|   |   |   |   |   |   |   |   |   start > 1141162
|   |   |   |   |   |   |   |   |   |   start <= 1150514:
cellular_component_ (30.16/11.14)
|   |   |   |   |   |   |   |   |   |   start > 1150514: cytoplasm_
(43.6/15.62)
|   |   |   |   |   |   |   start > 1153620
|   |   |   |   |   |   |   |   start <= 1164654: plasma_membrane_
(99.2/61.51)
|   |   |   |   |   |   |   |   start > 1164654: nucleus_
(28.57/13.6)
|   |   |   |   |   start > 1169172
|   |   |   |   |   |   start <= 1175823
|   |   |   |   |   |   |   start <= 1171819:
site_of_polarized_growth_ (34.02/14.67)
|   |   |   |   |   |   |   start > 1171819
|   |   |   |   |   |   |   |   distance <= 2395:
endoplasmic_reticulum_ (19.87/5.79)
|   |   |   |   |   |   |   |   distance > 2395: cytoplasm_
(12.07/2.88)
|   |   |   |   |   |   start > 1175823: cytoplasm_ (33.26/14.78)
|   |   |   |   start > 1190052
|   |   |   |   |   start <= 1422755
|   |   |   |   |   |   start <= 1289398
```

```
|   |   |   |   |   |   |   start <= 1224749
|   |   |   |   |   |   |   |   start <= 1222751
|   |   |   |   |   |   |   |   |   start <= 1199175
|   |   |   |   |   |   |   |   |   |   start <= 1196255: nucleus_
(68.22/32.82)
|   |   |   |   |   |   |   |   |   |   start > 1196255:
cellular_component_ (33.04/13.99)
|   |   |   |   |   |   |   |   |   start > 1199175
|   |   |   |   |   |   |   |   |   |   start <= 1217572: nucleus_
(71.01/28.3)
|   |   |   |   |   |   |   |   |   |   start > 1217572: cytoplasm_
(45.83/10.39)
|   |   |   |   |   |   |   |   start > 1222751: cellular_component_
(24.94)
|   |   |   |   |   |   |   start > 1224749
|   |   |   |   |   |   |   |   start <= 1252529: mitochondrion_
(93.96/47.98)
|   |   |   |   |   |   |   |   start > 1252529: nucleus_
(177.06/83.85)
|   |   |   |   |   |   start > 1289398
|   |   |   |   |   |   |   start <= 1296678: endoplasmic_reticulum_
(76.7/44.32)
|   |   |   |   |   |   |   start > 1296678
|   |   |   |   |   |   |   |   start <= 1410086
|   |   |   |   |   |   |   |   |   start <= 1362870
|   |   |   |   |   |   |   |   |   |   start <= 1350282: cytoplasm_
(184.57/128.19)
|   |   |   |   |   |   |   |   |   |   start > 1350282
|   |   |   |   |   |   |   |   |   |   |   start <= 1353717:
mitochondrion_ (12.27)
|   |   |   |   |   |   |   |   |   |   |   start > 1353717:
nucleolus_ (42.12/26.02)
|   |   |   |   |   |   |   |   |   start > 1362870
|   |   |   |   |   |   |   |   |   |   start <= 1405846
|   |   |   |   |   |   |   |   |   |   |   start <= 1388864
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1369782:
cytoplasm_ (55.48/13.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1369782:
cellular_component_ (35.89/16.62)
|   |   |   |   |   |   |   |   |   |   |   start > 1388864:
nucleus_ (85.51/37.23)
|   |   |   |   |   |   |   |   |   |   start > 1405846:
cellular_component_ (21.42)
|   |   |   |   |   |   |   |   start > 1410086
|   |   |   |   |   |   |   |   |   start <= 1417391:
endoplasmic_reticulum_ (43.72/16.11)
|   |   |   |   |   |   |   |   |   start > 1417391: nucleus_
(40.7/20.21)
|   |   |   |   |   start > 1422755
|   |   |   |   |   |   start <= 1455858
|   |   |   |   |   |   |   start <= 1443395
|   |   |   |   |   |   |   |   distance <= 1546: cytoskeleton_
(24.61/15.03)
|   |   |   |   |   |   |   |   distance > 1546
```

```
|   |   |   |   |   |   |   |   |   distance <= 4942: cytoplasm_
(105.91/49.36)
|   |   |   |   |   |   |   |   |   distance > 4942: nucleus_
(47.91/26.35)
|   |   |   |   |   |   |   start > 1443395: membrane_ (91.41/61.46)
|   |   |   |   |   |   start > 1455858
|   |   |   |   |   |   |   start <= 1473421
|   |   |   |   |   |   |   |   start <= 1465778: cytoplasm_
(100.57/66.51)
|   |   |   |   |   |   |   |   start > 1465778: mitochondrion_
(80.45/49.78)
|   |   |   |   |   |   |   start > 1473421
|   |   |   |   |   |   |   |   start <= 1488982: cytoplasm_
(102.16/39.17)
|   |   |   |   |   |   |   |   start > 1488982
|   |   |   |   |   |   |   |   |   start <= 1496540: mitochondrion_
(48.93/25.24)
|   |   |   |   |   |   |   |   |   start > 1496540: nucleus_
(109.11/83.84)
```

For Molecular Function

```
|   start <= 550574
|   |   start <= 521813
|   |   |   start <= 378442
|   |   |   |   start <= 267201
|   |   |   |   |   start <= 114673
|   |   |   |   |   |   start <= 52174
|   |   |   |   |   |   |   start <= 18566
|   |   |   |   |   |   |   |   start <= 13360
|   |   |   |   |   |   |   |   |   start <= 1802:
signal_transducer_activity_ (8.02)
|   |   |   |   |   |   |   |   |   start > 1802
|   |   |   |   |   |   |   |   |   |   start <= 9756
|   |   |   |   |   |   |   |   |   |   |   start <= 5985:
transporter_activity_ (14.88)
|   |   |   |   |   |   |   |   |   |   |   start > 5985:
oxidoreductase_activity_ (11.3)
|   |   |   |   |   |   |   |   |   |   start > 9756:
transporter_activity_ (18.42)
|   |   |   |   |   |   |   |   start > 13360
|   |   |   |   |   |   |   |   |   start <= 16204:
molecular_function_ (14.34)
|   |   |   |   |   |   |   |   |   start > 16204:
oxidoreductase_activity_ (14.72)
|   |   |   |   |   |   |   start > 18566
|   |   |   |   |   |   |   |   start <= 42245
|   |   |   |   |   |   |   |   |   start <= 36478
|   |   |   |   |   |   |   |   |   |   start <= 32296
|   |   |   |   |   |   |   |   |   |   |   start <= 28775
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 20635:
molecular_function_ (11.16)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 20635:
enzyme_regulator_activity_ (17.39)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
protein_binding_ (13.8)
|   |   |   |   |   |   |   |   |   |   |   start > 28775
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 30657:
molecular_function_ (19.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 30657:
hydrolase_activity_ (13.28)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
hydrolase_activity_ (19.06)
|   |   |   |   |   |   |   |   |   |   start > 32296
|   |   |   |   |   |   |   |   |   |   |   start <= 33918:
transferase_activity_ (11.27)
|   |   |   |   |   |   |   |   |   |   |   start > 33918:
enzyme_regulator_activity_ (14.84)
|   |   |   |   |   |   |   |   |   start > 36478
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 36798:
molecular_function_ (19.36)
|   |   |   |   |   |   |   |   |   |   |   start > 36798:
protein_binding_ (16.61)
|   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (19.3)
|   |   |   |   |   |   |   |   start > 42245
|   |   |   |   |   |   |   |   |   start <= 42701:
phosphoprotein_phosphatase_activity_ (13.03)
|   |   |   |   |   |   |   |   |   start > 42701
|   |   |   |   |   |   |   |   |   |   start <= 48032
|   |   |   |   |   |   |   |   |   |   |   start <= 44066:
protein_binding_ (11.35)
|   |   |   |   |   |   |   |   |   |   |   start > 44066:
hydrolase_activity_ (17.27)
|   |   |   |   |   |   |   |   |   |   start > 48032:
protein_binding_ (16.19)
|   |   |   |   |   |   start > 52174
|   |   |   |   |   |   |   start <= 77967
|   |   |   |   |   |   |   |   start <= 66494
|   |   |   |   |   |   |   |   |   start <= 56347
|   |   |   |   |   |   |   |   |   |   start <= 52446:
structural_molecule_activity_ (12.42)
|   |   |   |   |   |   |   |   |   |   start > 52446: RNA_binding_
(14.53)
|   |   |   |   |   |   |   |   |   start > 56347
|   |   |   |   |   |   |   |   |   |   start <= 61802:
molecular_function_ (35.36)
|   |   |   |   |   |   |   |   |   |   start > 61802
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 65243:
hydrolase_activity_ (10.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 65243:
molecular_function_ (6.77)
```

```
|   |   |   |   |   |   |   |   |   |   |   strand = C: DNA_binding_
(14.81)
|   |   |   |   |   |   |   |   start > 66494
|   |   |   |   |   |   |   |   |   start <= 73919
|   |   |   |   |   |   |   |   |   |   start <= 68607:
transporter_activity_ (19.86)
|   |   |   |   |   |   |   |   |   |   start > 68607
|   |   |   |   |   |   |   |   |   |   |   start <= 70320:
peptidase_activity_ (17.15)
|   |   |   |   |   |   |   |   |   |   |   start > 70320:
oxidoreductase_activity_ (14.35)
|   |   |   |   |   |   |   |   |   start > 73919
|   |   |   |   |   |   |   |   |   |   start <= 76546:
protein_kinase_activity_ (37.2/17.58)
|   |   |   |   |   |   |   |   |   |   start > 76546: RNA_binding_
(18.38)
|   |   |   |   |   |   |   start > 77967
|   |   |   |   |   |   |   |   start <= 97954
|   |   |   |   |   |   |   |   |   start <= 78427: protein_binding_
(18.8)
|   |   |   |   |   |   |   |   |   start > 78427
|   |   |   |   |   |   |   |   |   |   start <= 87513
|   |   |   |   |   |   |   |   |   |   |   start <= 87227
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 83549:
molecular_function_ (15.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 83549:
transporter_activity_ (10.38)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (34.51)
|   |   |   |   |   |   |   |   |   |   |   start > 87227:
RNA_binding_ (16.62)
|   |   |   |   |   |   |   |   |   |   start > 87513
|   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (54.45)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 94606:
transferase_activity_ (14.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 94606:
molecular_function_ (16.75)
|   |   |   |   |   |   |   |   start > 97954
|   |   |   |   |   |   |   |   |   start <= 99562
|   |   |   |   |   |   |   |   |   |   start <= 98476:
structural_molecule_activity_ (13.41)
|   |   |   |   |   |   |   |   |   |   start > 98476:
protein_binding_ (17.47)
|   |   |   |   |   |   |   |   |   start > 99562
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 111581
|   |   |   |   |   |   |   |   |   |   |   |   start <= 107209:
structural_molecule_activity_ (8.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 107209:
signal_transducer_activity_ (12.01)
```

```
|   |   |   |   |   |   |   |   |   |   start > 111581:
transferase_activity_ (22.22)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 101068:
transferase_activity_ (11.71)
|   |   |   |   |   |   |   |   |   |   start > 101068
|   |   |   |   |   |   |   |   |   |   |   start <= 104552:
transporter_activity_ (37.72)
|   |   |   |   |   |   |   |   |   |   |   start > 104552:
molecular_function_ (8.44)
|   |   |   |   |   start > 114673
|   |   |   |   |   |   start <= 212047
|   |   |   |   |   |   |   start <= 164043
|   |   |   |   |   |   |   |   start <= 142098
|   |   |   |   |   |   |   |   |   start <= 130485
|   |   |   |   |   |   |   |   |   |   start <= 117665
|   |   |   |   |   |   |   |   |   |   |   start <= 116322:
hydrolase_activity_ (11.59)
|   |   |   |   |   |   |   |   |   |   |   start > 116322:
structural_molecule_activity_ (14.17)
|   |   |   |   |   |   |   |   |   |   start > 117665
|   |   |   |   |   |   |   |   |   |   |   start <= 125617
|   |   |   |   |   |   |   |   |   |   |   |   start <= 122217:
molecular_function_ (34.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 122217
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 124999:
phosphoprotein_phosphatase_activity_ (11.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 124999:
molecular_function_ (14.75)
|   |   |   |   |   |   |   |   |   |   |   start > 125617
|   |   |   |   |   |   |   |   |   |   |   |   start <= 126788:
hydrolase_activity_ (13.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 126788:
structural_molecule_activity_ (9.87)
|   |   |   |   |   |   |   |   |   start > 130485
|   |   |   |   |   |   |   |   |   |   start <= 138292
|   |   |   |   |   |   |   |   |   |   |   start <= 133438
|   |   |   |   |   |   |   |   |   |   |   |   start <= 131834:
molecular_function_ (26.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 131834:
transferase_activity_ (9.97)
|   |   |   |   |   |   |   |   |   |   |   start > 133438
|   |   |   |   |   |   |   |   |   |   |   |   start <= 135897
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 135180:
enzyme_regulator_activity_ (10.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 135180:
molecular_function_ (16.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 135897:
enzyme_regulator_activity_ (19.31)
|   |   |   |   |   |   |   |   |   |   start > 138292
|   |   |   |   |   |   |   |   |   |   |   start <= 139523:
protein_binding_ (22.65)
|   |   |   |   |   |   |   |   |   |   |   start > 139523:
molecular_function_ (39.13)
```

```
|   |   |   |   |   |   |   |   start > 142098
|   |   |   |   |   |   |   |   |   start <= 163155
|   |   |   |   |   |   |   |   |   |   start <= 145519:
nucleotidyltransferase_activity_ (22.49)
|   |   |   |   |   |   |   |   |   |   start > 145519
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 148192:
molecular_function_ (35.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 148192
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 156319:
transcription_regulator_activity_ (34.07/14.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 156319:
oxidoreductase_activity_ (30.53)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 156319:
oxidoreductase_activity_ (26.66)
|   |   |   |   |   |   |   |   |   |   |   |   start > 156319:
molecular_function_ (44.23)
|   |   |   |   |   |   |   |   |   start > 163155:
hydrolase_activity_ (31.69)
|   |   |   |   |   |   |   start > 164043
|   |   |   |   |   |   |   |   start <= 199997
|   |   |   |   |   |   |   |   |   start <= 172482
|   |   |   |   |   |   |   |   |   |   start <= 172183
|   |   |   |   |   |   |   |   |   |   |   start <= 167255
|   |   |   |   |   |   |   |   |   |   |   |   start <= 164291:
molecular_function_ (14.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 164291:
ligase_activity_ (17.1)
|   |   |   |   |   |   |   |   |   |   |   start > 167255
|   |   |   |   |   |   |   |   |   |   |   |   start <= 171931
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 169609
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
167715: protein_binding_ (8.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
167715: molecular_function_ (10.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 169609:
protein_binding_ (14.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 171931:
molecular_function_ (6.28)
|   |   |   |   |   |   |   |   |   |   start > 172183:
protein_kinase_activity_ (13.01)
|   |   |   |   |   |   |   |   |   start > 172482
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 183344
|   |   |   |   |   |   |   |   |   |   |   |   start <= 178335
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 174919:
molecular_function_ (19.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 174919
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
176774: enzyme_regulator_activity_ (16.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
176774: molecular_function_ (12.72)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 178335:
nucleotidyltransferase_activity_ (9.1)
|   |   |   |   |   |   |   |   |   |   |   start > 183344
|   |   |   |   |   |   |   |   |   |   |   |   start <= 192751
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 184926:
protein_binding_ (12.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 184926:
molecular_function_ (46.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 192751:
protein_binding_ (14.07)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 192751
|   |   |   |   |   |   |   |   |   |   |   |   start <= 178335:
molecular_function_ (16.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 178335:
RNA_binding_ (19.16)
|   |   |   |   |   |   |   |   |   |   |   start > 192751:
molecular_function_ (47.14)
|   |   |   |   |   |   |   |   start > 199997
|   |   |   |   |   |   |   |   |   strand = W: ligase_activity_
(16.81)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 203040:
transferase_activity_ (20.55)
|   |   |   |   |   |   |   |   |   |   start > 203040
|   |   |   |   |   |   |   |   |   |   |   start <= 210562:
nucleotidyltransferase_activity_ (18.87)
|   |   |   |   |   |   |   |   |   |   |   start > 210562:
molecular_function_ (18.09)
|   |   |   |   |   |   start > 212047
|   |   |   |   |   |   |   start <= 221801
|   |   |   |   |   |   |   |   start <= 216529
|   |   |   |   |   |   |   |   |   start <= 213352:
signal_transducer_activity_ (17.29)
|   |   |   |   |   |   |   |   |   start > 213352:
hydrolase_activity_ (23.08)
|   |   |   |   |   |   |   |   start > 216529
|   |   |   |   |   |   |   |   |   start <= 219288
|   |   |   |   |   |   |   |   |   |   start <= 217600:
structural_molecule_activity_ (21.66)
|   |   |   |   |   |   |   |   |   |   start > 217600:
enzyme_regulator_activity_ (15.96)
|   |   |   |   |   |   |   |   |   start > 219288
|   |   |   |   |   |   |   |   |   |   start <= 220771:
phosphoprotein_phosphatase_activity_ (17.96)
|   |   |   |   |   |   |   |   |   |   start > 220771:
structural_molecule_activity_ (14.31)
|   |   |   |   |   |   |   start > 221801
|   |   |   |   |   |   |   |   start <= 227393
|   |   |   |   |   |   |   |   |   start <= 224304
|   |   |   |   |   |   |   |   |   |   start <= 222427:
molecular_function_ (17.87)
|   |   |   |   |   |   |   |   |   |   start > 222427:
protein_binding_ (18.35)
```

```
|   |   |   |   |   |   |   |   |   start > 224304:
transferase_activity_ (17.91)
|   |   |   |   |   |   |   |   start > 227393
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 245923
|   |   |   |   |   |   |   |   |   |   |   start <= 232652
|   |   |   |   |   |   |   |   |   |   |   |   start <= 231024
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 229171:
molecular_function_ (29.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 229171
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
229906: structural_molecule_activity_ (16.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
229906: molecular_function_ (14.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 231024:
transporter_activity_ (17.64)
|   |   |   |   |   |   |   |   |   |   |   start > 232652
|   |   |   |   |   |   |   |   |   |   |   |   start <= 240259
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 234927:
enzyme_regulator_activity_ (20.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 234927:
oxidoreductase_activity_ (15.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 240259
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 241418:
molecular_function_ (13.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 241418
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
242552: peptidase_activity_ (14.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
242552: enzyme_regulator_activity_ (8.28)
|   |   |   |   |   |   |   |   |   |   start > 245923
|   |   |   |   |   |   |   |   |   |   |   start <= 255604
|   |   |   |   |   |   |   |   |   |   |   |   start <= 248581:
molecular_function_ (36.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 248581
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 251566:
structural_molecule_activity_ (19.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 251566:
molecular_function_ (11.14)
|   |   |   |   |   |   |   |   |   |   |   start > 255604:
transferase_activity_ (12.85)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 242552:
hydrolase_activity_ (39.19)
|   |   |   |   |   |   |   |   |   |   start > 242552
|   |   |   |   |   |   |   |   |   |   |   start <= 258915
|   |   |   |   |   |   |   |   |   |   |   |   start <= 248581
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 245923:
molecular_function_ (18.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 245923:
transporter_activity_ (13.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 248581:
molecular_function_ (28.05)
|   |   |   |   |   |   |   |   |   |   |   start > 258915
```

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|   |   |   |   |   |   |   |   |   |   |   |   start <= 264110:
hydrolase_activity_ (30.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 264110:
molecular_function_ (52.4)
|   |   |   |   start > 267201
|   |   |   |   |   start <= 281848
|   |   |   |   |   |   start <= 271901
|   |   |   |   |   |   |   start <= 267698:
protein_kinase_activity_ (34.59/16.25)
|   |   |   |   |   |   |   start > 267698
|   |   |   |   |   |   |   |   start <= 268921:
transporter_activity_ (9.21)
|   |   |   |   |   |   |   |   start > 268921:
transcription_regulator_activity_ (25.62/11.45)
|   |   |   |   |   |   start > 271901
|   |   |   |   |   |   |   start <= 274876: molecular_function_
(30.5)
|   |   |   |   |   |   |   start > 274876
|   |   |   |   |   |   |   |   start <= 276872:
nucleotidyltransferase_activity_ (44.71)
|   |   |   |   |   |   |   |   start > 276872:
protein_kinase_activity_ (20.96)
|   |   |   |   |   start > 281848
|   |   |   |   |   |   start <= 344953
|   |   |   |   |   |   |   start <= 302670
|   |   |   |   |   |   |   |   start <= 283176: hydrolase_activity_
(20.75)
|   |   |   |   |   |   |   |   start > 283176
|   |   |   |   |   |   |   |   |   start <= 300003
|   |   |   |   |   |   |   |   |   |   start <= 285165
|   |   |   |   |   |   |   |   |   |   |   start <= 283419:
molecular_function_ (20.26)
|   |   |   |   |   |   |   |   |   |   |   start > 283419:
RNA_binding_ (16.21)
|   |   |   |   |   |   |   |   |   |   start > 285165
|   |   |   |   |   |   |   |   |   |   |   start <= 296820
|   |   |   |   |   |   |   |   |   |   |   |   start <= 289909
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
transferase_activity_ (20.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
structural_molecule_activity_ (10.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 289909
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (31.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
294759: molecular_function_ (15.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
294759: transferase_activity_ (16.47)
|   |   |   |   |   |   |   |   |   |   |   start > 296820:
structural_molecule_activity_ (16.01)
|   |   |   |   |   |   |   |   |   start > 300003
|   |   |   |   |   |   |   |   |   |   strand = W:
hydrolase_activity_ (16.26)
```

```
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 301413:
RNA_binding_ (20.78)
|   |   |   |   |   |   |   |   |   |   |   start > 301413:
molecular_function_ (9.11)
|   |   |   |   |   |   |   start > 302670
|   |   |   |   |   |   |   |   start <= 323471
|   |   |   |   |   |   |   |   |   start <= 316388
|   |   |   |   |   |   |   |   |   |   start <= 305237
|   |   |   |   |   |   |   |   |   |   |   start <= 303211:
oxidoreductase_activity_ (10.83)
|   |   |   |   |   |   |   |   |   |   |   start > 303211:
protein_binding_ (30.38/12.52)
|   |   |   |   |   |   |   |   |   |   start > 305237
|   |   |   |   |   |   |   |   |   |   |   start <= 310122:
structural_molecule_activity_ (35.77)
|   |   |   |   |   |   |   |   |   |   |   start > 310122
|   |   |   |   |   |   |   |   |   |   |   |   start <= 314748
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 312471:
transcription_regulator_activity_ (8.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 312471:
protein_kinase_activity_ (9.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 314748:
oxidoreductase_activity_ (11.44)
|   |   |   |   |   |   |   |   |   start > 316388
|   |   |   |   |   |   |   |   |   |   strand = W:
structural_molecule_activity_ (13.24)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 322226
|   |   |   |   |   |   |   |   |   |   |   |   start <= 320120:
enzyme_regulator_activity_ (14.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 320120:
hydrolase_activity_ (14.08)
|   |   |   |   |   |   |   |   |   |   |   start > 322226:
RNA_binding_ (18.44)
|   |   |   |   |   |   |   |   start > 323471
|   |   |   |   |   |   |   |   |   start <= 334835
|   |   |   |   |   |   |   |   |   |   start <= 333810
|   |   |   |   |   |   |   |   |   |   |   start <= 331025:
molecular_function_ (37.82)
|   |   |   |   |   |   |   |   |   |   |   start > 331025:
translation_regulator_activity_ (4.78)
|   |   |   |   |   |   |   |   |   |   start > 333810:
oxidoreductase_activity_ (41.47)
|   |   |   |   |   |   |   |   |   start > 334835
|   |   |   |   |   |   |   |   |   |   start <= 341619
|   |   |   |   |   |   |   |   |   |   |   start <= 337277:
protein_binding_ (15.7)
|   |   |   |   |   |   |   |   |   |   |   start > 337277
|   |   |   |   |   |   |   |   |   |   |   |   start <= 340134:
molecular_function_ (33.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 340134
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 340798:
structural_molecule_activity_ (12.17)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 340798:
molecular_function_ (8.65)
|   |   |   |   |   |   |   |   |   |   start > 341619:
protein_binding_ (16.5)
|   |   |   |   |   |   start > 344953
|   |   |   |   |   |   |   start <= 371237
|   |   |   |   |   |   |   |   start <= 361285
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 351434:
molecular_function_ (32.26)
|   |   |   |   |   |   |   |   |   |   start > 351434
|   |   |   |   |   |   |   |   |   |   |   start <= 352877:
DNA_binding_ (15.01)
|   |   |   |   |   |   |   |   |   |   |   start > 352877:
molecular_function_ (9.68)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 356759:
nucleotidyltransferase_activity_ (13.06)
|   |   |   |   |   |   |   |   |   |   start > 356759:
transporter_activity_ (13.72)
|   |   |   |   |   |   |   |   start > 361285
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 369769
|   |   |   |   |   |   |   |   |   |   |   start <= 365874:
RNA_binding_ (10.26)
|   |   |   |   |   |   |   |   |   |   |   start > 365874:
phosphoprotein_phosphatase_activity_ (25.01)
|   |   |   |   |   |   |   |   |   |   start > 369769:
molecular_function_ (21.06)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 363952
|   |   |   |   |   |   |   |   |   |   |   start <= 362256:
molecular_function_ (17.4)
|   |   |   |   |   |   |   |   |   |   |   start > 362256:
transferase_activity_ (12.0)
|   |   |   |   |   |   |   |   |   |   start > 363952:
molecular_function_ (48.28)
|   |   |   |   |   |   |   start > 371237
|   |   |   |   |   |   |   |   strand = W:
structural_molecule_activity_ (15.11)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 373605:
nucleotidyltransferase_activity_ (14.17)
|   |   |   |   |   |   |   |   |   start > 373605
|   |   |   |   |   |   |   |   |   |   start <= 376477:
RNA_binding_ (25.94)
|   |   |   |   |   |   |   |   |   |   start > 376477:
hydrolase_activity_ (13.09)
|   |   |   start > 378442
|   |   |   |   strand = W
|   |   |   |   |   start <= 465916
|   |   |   |   |   |   start <= 427361
|   |   |   |   |   |   |   start <= 403288
|   |   |   |   |   |   |   |   start <= 397534
```

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|   |   |   |   |   |   |   |   |   start <= 394214:
helicase_activity_ (13.8)
|   |   |   |   |   |   |   |   |   start > 394214: RNA_binding_
(12.97)
|   |   |   |   |   |   |   |   start > 397534:
structural_molecule_activity_ (17.37)
|   |   |   |   |   |   |   start > 403288
|   |   |   |   |   |   |   |   start <= 416705
|   |   |   |   |   |   |   |   |   start <= 411822
|   |   |   |   |   |   |   |   |   |   start <= 410376:
molecular_function_ (13.29)
|   |   |   |   |   |   |   |   |   |   start > 410376:
oxidoreductase_activity_ (5.52)
|   |   |   |   |   |   |   |   |   start > 411822:
molecular_function_ (16.37)
|   |   |   |   |   |   |   |   start > 416705
|   |   |   |   |   |   |   |   |   start <= 424206:
protein_kinase_activity_ (19.1)
|   |   |   |   |   |   |   |   |   start > 424206:
transferase_activity_ (15.35)
|   |   |   |   |   |   start > 427361
|   |   |   |   |   |   |   start <= 458100
|   |   |   |   |   |   |   |   start <= 439906
|   |   |   |   |   |   |   |   |   start <= 437769
|   |   |   |   |   |   |   |   |   |   start <= 429064:
protein_binding_ (17.15)
|   |   |   |   |   |   |   |   |   |   start > 429064
|   |   |   |   |   |   |   |   |   |   |   start <= 434333
|   |   |   |   |   |   |   |   |   |   |   |   start <= 432327:
molecular_function_ (13.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 432327:
protein_binding_ (11.63)
|   |   |   |   |   |   |   |   |   |   |   start > 434333:
molecular_function_ (15.45)
|   |   |   |   |   |   |   |   |   start > 437769
|   |   |   |   |   |   |   |   |   |   start <= 438044:
peptidase_activity_ (11.22)
|   |   |   |   |   |   |   |   |   |   start > 438044:
phosphoprotein_phosphatase_activity_ (22.39)
|   |   |   |   |   |   |   |   start > 439906
|   |   |   |   |   |   |   |   |   start <= 443026:
transporter_activity_ (16.4)
|   |   |   |   |   |   |   |   |   start > 443026
|   |   |   |   |   |   |   |   |   |   start <= 454779
|   |   |   |   |   |   |   |   |   |   |   start <= 453042
|   |   |   |   |   |   |   |   |   |   |   |   start <= 447981:
molecular_function_ (23.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 447981:
protein_binding_ (15.46)
|   |   |   |   |   |   |   |   |   |   |   start > 453042:
molecular_function_ (32.24)
|   |   |   |   |   |   |   |   |   |   start > 454779:
protein_binding_ (11.81)
|   |   |   |   |   |   |   start > 458100
```

```
|   |   |   |   |   |   |   |   start <= 463431
|   |   |   |   |   |   |   |   |   start <= 461839:
isomerase_activity_ (8.39)
|   |   |   |   |   |   |   |   |   start > 461839:
transcription_regulator_activity_ (10.02)
|   |   |   |   |   |   |   |   start > 463431:
transporter_activity_ (11.4)
|   |   |   |   |   start > 465916
|   |   |   |   |   |   start <= 497315
|   |   |   |   |   |   |   start <= 482264
|   |   |   |   |   |   |   |   start <= 471850:
structural_molecule_activity_ (23.47)
|   |   |   |   |   |   |   |   start > 471850: molecular_function_
(34.0)
|   |   |   |   |   |   |   start > 482264
|   |   |   |   |   |   |   |   start <= 486801: helicase_activity_
(14.41)
|   |   |   |   |   |   |   |   start > 486801
|   |   |   |   |   |   |   |   |   start <= 489505:
ligase_activity_ (18.22)
|   |   |   |   |   |   |   |   |   start > 489505:
structural_molecule_activity_ (14.16)
|   |   |   |   |   |   start > 497315
|   |   |   |   |   |   |   start <= 521311: molecular_function_
(79.07)
|   |   |   |   |   |   |   start > 521311: transferase_activity_
(9.97)
|   |   |   |   strand = C
|   |   |   |   |   start <= 407203
|   |   |   |   |   |   start <= 397534
|   |   |   |   |   |   |   start <= 385584
|   |   |   |   |   |   |   |   start <= 381435:
transferase_activity_ (7.76)
|   |   |   |   |   |   |   |   start > 381435: molecular_function_
(40.9)
|   |   |   |   |   |   |   start > 385584
|   |   |   |   |   |   |   |   start <= 388898: isomerase_activity_
(16.08)
|   |   |   |   |   |   |   |   start > 388898
|   |   |   |   |   |   |   |   |   start <= 392054:
signal_transducer_activity_ (11.16)
|   |   |   |   |   |   |   |   |   start > 392054:
transferase_activity_ (15.86)
|   |   |   |   |   |   start > 397534
|   |   |   |   |   |   |   start <= 404954
|   |   |   |   |   |   |   |   start <= 403288:
protein_kinase_activity_ (7.03)
|   |   |   |   |   |   |   |   start > 403288: molecular_function_
(13.58)
|   |   |   |   |   |   |   start > 404954: protein_kinase_activity_
(22.51)
|   |   |   |   |   start > 407203
|   |   |   |   |   |   start <= 416705
```

```
|   |   |   |   |   |   |   start <= 411822: hydrolase_activity_
(14.83)
|   |   |   |   |   |   |   start > 411822:
transcription_regulator_activity_ (43.39/16.7)
|   |   |   |   |   |   start > 416705
|   |   |   |   |   |   |   start <= 485362
|   |   |   |   |   |   |   |   start <= 465916
|   |   |   |   |   |   |   |   |   start <= 438044
|   |   |   |   |   |   |   |   |   |   start <= 429064
|   |   |   |   |   |   |   |   |   |   |   start <= 424206:
molecular_function_ (31.44)
|   |   |   |   |   |   |   |   |   |   |   start > 424206:
oxidoreductase_activity_ (21.93)
|   |   |   |   |   |   |   |   |   |   start > 429064:
molecular_function_ (41.29)
|   |   |   |   |   |   |   |   |   start > 438044
|   |   |   |   |   |   |   |   |   |   start <= 458100
|   |   |   |   |   |   |   |   |   |   |   start <= 447981
|   |   |   |   |   |   |   |   |   |   |   |   start <= 444680:
transcription_regulator_activity_ (11.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 444680:
molecular_function_ (15.68)
|   |   |   |   |   |   |   |   |   |   |   start > 447981
|   |   |   |   |   |   |   |   |   |   |   |   start <= 455198:
hydrolase_activity_ (13.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 455198:
transcription_regulator_activity_ (16.14)
|   |   |   |   |   |   |   |   |   |   start > 458100:
molecular_function_ (15.21)
|   |   |   |   |   |   |   |   start > 465916
|   |   |   |   |   |   |   |   |   start <= 483857
|   |   |   |   |   |   |   |   |   |   start <= 478755:
structural_molecule_activity_ (9.22)
|   |   |   |   |   |   |   |   |   |   start > 478755:
transferase_activity_ (28.73)
|   |   |   |   |   |   |   |   |   start > 483857:
oxidoreductase_activity_ (14.09)
|   |   |   |   |   |   |   start > 485362
|   |   |   |   |   |   |   |   start <= 508144
|   |   |   |   |   |   |   |   |   start <= 497315
|   |   |   |   |   |   |   |   |   |   start <= 491512:
molecular_function_ (49.2)
|   |   |   |   |   |   |   |   |   |   start > 491512
|   |   |   |   |   |   |   |   |   |   |   start <= 494265:
DNA_binding_ (10.25)
|   |   |   |   |   |   |   |   |   |   |   start > 494265:
molecular_function_ (13.22)
|   |   |   |   |   |   |   |   |   start > 497315
|   |   |   |   |   |   |   |   |   |   start <= 500876:
enzyme_regulator_activity_ (13.35)
|   |   |   |   |   |   |   |   |   |   start > 500876:
molecular_function_ (32.92)
|   |   |   |   |   |   |   |   start > 508144
```

```
|   |   |   |   |   |   |   |   |   start <= 512106:
transcription_regulator_activity_ (18.83)
|   |   |   |   |   |   |   |   |   start > 512106:
molecular_function_ (13.74)
|   |   start > 521813
|   |   |   strand = W
|   |   |   |   start <= 530694: ligase_activity_ (13.98)
|   |   |   |   start > 530694
|   |   |   |   |   start <= 541697: structural_molecule_activity_
(20.82)
|   |   |   |   |   start > 541697: oxidoreductase_activity_ (10.39)
|   |   |   strand = C
|   |   |   |   start <= 539800
|   |   |   |   |   start <= 525437: hydrolase_activity_ (19.28)
|   |   |   |   |   start > 525437
|   |   |   |   |   |   Neigh_GO_aspect = C: transporter_activity_
(42.53/17.7)
|   |   |   |   |   |   Neigh_GO_aspect = F: hydrolase_activity_
(33.63/10.57)
|   |   |   |   |   |   Neigh_GO_aspect = P
|   |   |   |   |   |   |   neigh_num <= 1: hydrolase_activity_
(17.09/6.08)
|   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   start <= 530694: hydrolase_activity_
(6.54/2.06)
|   |   |   |   |   |   |   |   start > 530694:
transporter_activity_ (8.38/2.84)
|   |   |   |   start > 539800
|   |   |   |   |   start <= 541697
|   |   |   |   |   |   start <= 541200: molecular_function_ (16.37)
|   |   |   |   |   |   start > 541200: RNA_binding_ (19.33)
|   |   |   |   |   start > 541697
|   |   |   |   |   |   start <= 548308
|   |   |   |   |   |   |   start <= 543367: DNA_binding_ (14.97)
|   |   |   |   |   |   |   start > 543367:
nucleotidyltransferase_activity_ (13.38)
|   |   |   |   |   |   start > 548308: transporter_activity_
(19.03)
|   start > 550574
|   |   start <= 927448
|   |   |   start <= 743871
|   |   |   |   strand = W
|   |   |   |   |   start <= 691011
|   |   |   |   |   |   start <= 597153
|   |   |   |   |   |   |   start <= 587717
|   |   |   |   |   |   |   |   start <= 551858: lyase_activity_
(13.98)
|   |   |   |   |   |   |   |   start > 551858
|   |   |   |   |   |   |   |   |   start <= 574161:
molecular_function_ (99.37)
|   |   |   |   |   |   |   |   |   start > 574161
|   |   |   |   |   |   |   |   |   |   start <= 576471:
transferase_activity_ (13.79)
|   |   |   |   |   |   |   |   |   |   start > 576471
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 579456
|   |   |   |   |   |   |   |   |   |   |   |   start <= 578661:
molecular_function_ (9.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 578661:
structural_molecule_activity_ (12.72)
|   |   |   |   |   |   |   |   |   |   |   start > 579456:
molecular_function_ (25.17)
|   |   |   |   |   |   |   start > 587717
|   |   |   |   |   |   |   |   start <= 593890
|   |   |   |   |   |   |   |   |   start <= 592436:
transcription_regulator_activity_ (20.09)
|   |   |   |   |   |   |   |   |   start > 592436:
hydrolase_activity_ (22.94)
|   |   |   |   |   |   |   |   start > 593890:
phosphoprotein_phosphatase_activity_ (22.74)
|   |   |   |   |   |   start > 597153
|   |   |   |   |   |   |   start <= 616147
|   |   |   |   |   |   |   |   start <= 603061
|   |   |   |   |   |   |   |   |   start <= 600790
|   |   |   |   |   |   |   |   |   |   start <= 598465:
protein_binding_ (18.94)
|   |   |   |   |   |   |   |   |   |   start > 598465:
structural_molecule_activity_ (23.03)
|   |   |   |   |   |   |   |   |   start > 600790: protein_binding_
(20.08)
|   |   |   |   |   |   |   |   start > 603061
|   |   |   |   |   |   |   |   |   start <= 610438
|   |   |   |   |   |   |   |   |   |   start <= 604005:
enzyme_regulator_activity_ (11.46)
|   |   |   |   |   |   |   |   |   |   start > 604005: DNA_binding_
(22.09)
|   |   |   |   |   |   |   |   |   start > 610438:
transferase_activity_ (18.28)
|   |   |   |   |   |   |   start > 616147
|   |   |   |   |   |   |   |   start <= 658347
|   |   |   |   |   |   |   |   |   start <= 645221
|   |   |   |   |   |   |   |   |   |   start <= 629873:
molecular_function_ (39.38)
|   |   |   |   |   |   |   |   |   |   start > 629873
|   |   |   |   |   |   |   |   |   |   |   start <= 631279:
hydrolase_activity_ (7.23)
|   |   |   |   |   |   |   |   |   |   |   start > 631279:
DNA_binding_ (7.97)
|   |   |   |   |   |   |   |   |   start > 645221
|   |   |   |   |   |   |   |   |   |   start <= 653604:
protein_binding_ (4.69)
|   |   |   |   |   |   |   |   |   |   start > 653604:
molecular_function_ (62.05/19.78)
|   |   |   |   |   |   |   |   start > 658347
|   |   |   |   |   |   |   |   |   start <= 683578
|   |   |   |   |   |   |   |   |   |   start <= 668077:
structural_molecule_activity_ (26.89)
|   |   |   |   |   |   |   |   |   |   start > 668077
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 671266:
molecular_function_ (17.1)
|   |   |   |   |   |   |   |   |   |   |   start > 671266
|   |   |   |   |   |   |   |   |   |   |   |   start <= 676099:
DNA_binding_ (14.54)
|   |   |   |   |   |   |   |   |   |   |   |   start > 676099:
structural_molecule_activity_ (11.85)
|   |   |   |   |   |   |   |   |   start > 683578
|   |   |   |   |   |   |   |   |   |   start <= 685879:
protein_binding_ (9.46)
|   |   |   |   |   |   |   |   |   |   start > 685879:
molecular_function_ (27.27)
|   |   |   |   |   start > 691011
|   |   |   |   |   |   start <= 694697
|   |   |   |   |   |   |   start <= 693582:
nucleotidyltransferase_activity_ (23.15)
|   |   |   |   |   |   |   start > 693582: protein_kinase_activity_
(15.54)
|   |   |   |   |   |   start > 694697
|   |   |   |   |   |   |   start <= 704481
|   |   |   |   |   |   |   |   start <= 700312: molecular_function_
(8.03)
|   |   |   |   |   |   |   |   start > 700312:
transferase_activity_ (35.01)
|   |   |   |   |   |   |   start > 704481
|   |   |   |   |   |   |   |   start <= 730575
|   |   |   |   |   |   |   |   |   start <= 718457:
molecular_function_ (15.25)
|   |   |   |   |   |   |   |   |   start > 718457
|   |   |   |   |   |   |   |   |   |   start <= 728256:
enzyme_regulator_activity_ (10.52)
|   |   |   |   |   |   |   |   |   |   start > 728256:
molecular_function_ (14.75)
|   |   |   |   |   |   |   |   start > 730575:
transferase_activity_ (18.43)
|   |   |   |   strand = C
|   |   |   |   |   start <= 588377
|   |   |   |   |   |   start <= 563525
|   |   |   |   |   |   |   start <= 558058
|   |   |   |   |   |   |   |   start <= 556470: isomerase_activity_
(9.55)
|   |   |   |   |   |   |   |   start > 556470: molecular_function_
(15.84)
|   |   |   |   |   |   |   start > 558058
|   |   |   |   |   |   |   |   start <= 560623: DNA_binding_ (12.9)
|   |   |   |   |   |   |   |   start > 560623: protein_binding_
(10.97)
|   |   |   |   |   |   start > 563525
|   |   |   |   |   |   |   start <= 568962
|   |   |   |   |   |   |   |   start <= 565925: molecular_function_
(14.59)
|   |   |   |   |   |   |   |   start > 565925: hydrolase_activity_
(17.39)
|   |   |   |   |   |   |   start > 568962
```

```
|   |   |   |   |   |   |   |   start <= 583711: molecular_function_
(57.92)
|   |   |   |   |   |   |   |   start > 583711
|   |   |   |   |   |   |   |   |   start <= 587717:
hydrolase_activity_ (15.85)
|   |   |   |   |   |   |   |   |   start > 587717:
molecular_function_ (15.3)
|   |   |   |   |   start > 588377
|   |   |   |   |   |   start <= 616147
|   |   |   |   |   |   |   start <= 593890: transferase_activity_
(33.91)
|   |   |   |   |   |   |   start > 593890
|   |   |   |   |   |   |   |   start <= 614001
|   |   |   |   |   |   |   |   |   start <= 610438
|   |   |   |   |   |   |   |   |   |   start <= 603061:
molecular_function_ (9.58)
|   |   |   |   |   |   |   |   |   |   start > 603061:
transcription_regulator_activity_ (39.07)
|   |   |   |   |   |   |   |   |   start > 610438:
molecular_function_ (14.26)
|   |   |   |   |   |   |   |   start > 614001:
signal_transducer_activity_ (19.63)
|   |   |   |   |   |   start > 616147
|   |   |   |   |   |   |   start <= 671266
|   |   |   |   |   |   |   |   start <= 619642
|   |   |   |   |   |   |   |   |   start <= 618303
|   |   |   |   |   |   |   |   |   |   start <= 617167:
protein_binding_ (11.62)
|   |   |   |   |   |   |   |   |   |   start > 617167:
molecular_function_ (19.61)
|   |   |   |   |   |   |   |   |   start > 618303: RNA_binding_
(15.59)
|   |   |   |   |   |   |   |   start > 619642
|   |   |   |   |   |   |   |   |   start <= 645032
|   |   |   |   |   |   |   |   |   |   start <= 631279:
molecular_function_ (64.61/12.18)
|   |   |   |   |   |   |   |   |   |   start > 631279
|   |   |   |   |   |   |   |   |   |   |   start <= 643834:
DNA_binding_ (10.1)
|   |   |   |   |   |   |   |   |   |   |   start > 643834:
oxidoreductase_activity_ (19.31)
|   |   |   |   |   |   |   |   |   start > 645032:
molecular_function_ (94.12)
|   |   |   |   |   |   |   start > 671266
|   |   |   |   |   |   |   |   start <= 700312
|   |   |   |   |   |   |   |   |   start <= 682223
|   |   |   |   |   |   |   |   |   |   start <= 679761:
transferase_activity_ (36.65)
|   |   |   |   |   |   |   |   |   |   start > 679761
|   |   |   |   |   |   |   |   |   |   |   start <= 681614:
protein_binding_ (19.79)
|   |   |   |   |   |   |   |   |   |   |   start > 681614:
molecular_function_ (13.42)
|   |   |   |   |   |   |   |   |   start > 682223
```

```
|   |   |   |   |   |   |   |   |   |   start <= 688224
|   |   |   |   |   |   |   |   |   |   |   start <= 683578:
structural_molecule_activity_ (13.4)
|   |   |   |   |   |   |   |   |   |   |   start > 683578:
RNA_binding_ (16.92)
|   |   |   |   |   |   |   |   |   |   start > 688224
|   |   |   |   |   |   |   |   |   |   |   start <= 694697:
transferase_activity_ (18.51)
|   |   |   |   |   |   |   |   |   |   |   start > 694697:
transcription_regulator_activity_ (14.33)
|   |   |   |   |   |   |   |   start > 700312
|   |   |   |   |   |   |   |   |   start <= 716619
|   |   |   |   |   |   |   |   |   |   start <= 704481:
molecular_function_ (31.21)
|   |   |   |   |   |   |   |   |   |   start > 704481
|   |   |   |   |   |   |   |   |   |   |   start <= 715376:
protein_binding_ (8.57)
|   |   |   |   |   |   |   |   |   |   |   start > 715376:
structural_molecule_activity_ (8.74)
|   |   |   |   |   |   |   |   |   start > 716619
|   |   |   |   |   |   |   |   |   |   start <= 730575
|   |   |   |   |   |   |   |   |   |   |   start <= 720300:
molecular_function_ (31.58)
|   |   |   |   |   |   |   |   |   |   |   start > 720300:
hydrolase_activity_ (12.15)
|   |   |   |   |   |   |   |   |   |   start > 730575:
molecular_function_ (86.43)
|   |   |   start > 743871
|   |   |   |   start <= 770354
|   |   |   |   |   start <= 765152
|   |   |   |   |   |   start <= 746098: peptidase_activity_ (24.81)
|   |   |   |   |   |   start > 746098
|   |   |   |   |   |   |   start <= 755063
|   |   |   |   |   |   |   |   start <= 750739:
transcription_regulator_activity_ (36.72)
|   |   |   |   |   |   |   |   start > 750739:
transferase_activity_ (31.12)
|   |   |   |   |   |   |   start > 755063
|   |   |   |   |   |   |   |   start <= 755625: protein_binding_
(6.58)
|   |   |   |   |   |   |   |   start > 755625:
transcription_regulator_activity_ (35.37/17.4)
|   |   |   |   |   start > 765152
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 769522
|   |   |   |   |   |   |   |   start <= 765703: molecular_function_
(13.66)
|   |   |   |   |   |   |   |   start > 765703:
nucleotidyltransferase_activity_ (20.26)
|   |   |   |   |   |   |   start > 769522: oxidoreductase_activity_
(15.07)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 767968: protein_binding_
(19.08)
```

```
|   |   |   |   |   |   |   start > 767968: isomerase_activity_
(19.83)
|   |   |   |   start > 770354
|   |   |   |   |   start <= 841992
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 814449
|   |   |   |   |   |   |   |   start <= 806618
|   |   |   |   |   |   |   |   |   start <= 781420
|   |   |   |   |   |   |   |   |   |   start <= 771874:
protein_binding_ (23.2)
|   |   |   |   |   |   |   |   |   |   start > 771874:
molecular_function_ (51.8)
|   |   |   |   |   |   |   |   |   start > 781420
|   |   |   |   |   |   |   |   |   |   start <= 789446
|   |   |   |   |   |   |   |   |   |   |   start <= 784868:
protein_binding_ (17.02)
|   |   |   |   |   |   |   |   |   |   |   start > 784868:
transcription_regulator_activity_ (15.64)
|   |   |   |   |   |   |   |   |   |   start > 789446:
protein_binding_ (30.65)
|   |   |   |   |   |   |   |   start > 806618
|   |   |   |   |   |   |   |   |   start <= 808321:
translation_regulator_activity_ (24.6)
|   |   |   |   |   |   |   |   |   start > 808321:
transcription_regulator_activity_ (46.25)
|   |   |   |   |   |   |   start > 814449
|   |   |   |   |   |   |   |   start <= 829148
|   |   |   |   |   |   |   |   |   start <= 817947
|   |   |   |   |   |   |   |   |   |   start <= 816875:
molecular_function_ (14.76)
|   |   |   |   |   |   |   |   |   |   start > 816875:
oxidoreductase_activity_ (21.27)
|   |   |   |   |   |   |   |   |   start > 817947:
molecular_function_ (70.68)
|   |   |   |   |   |   |   |   start > 829148: protein_binding_
(43.51)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 802219
|   |   |   |   |   |   |   |   start <= 794720
|   |   |   |   |   |   |   |   |   start <= 790325
|   |   |   |   |   |   |   |   |   |   start <= 781420:
molecular_function_ (11.98)
|   |   |   |   |   |   |   |   |   |   start > 781420:
protein_binding_ (29.71)
|   |   |   |   |   |   |   |   |   start > 790325:
molecular_function_ (22.17)
|   |   |   |   |   |   |   |   start > 794720:
enzyme_regulator_activity_ (18.77)
|   |   |   |   |   |   |   start > 802219
|   |   |   |   |   |   |   |   start <= 838389
|   |   |   |   |   |   |   |   |   start <= 829148
|   |   |   |   |   |   |   |   |   |   start <= 806618:
molecular_function_ (18.42)
|   |   |   |   |   |   |   |   |   |   start > 806618
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 814449
|   |   |   |   |   |   |   |   |   |   |   |   start <= 812107:
transferase_activity_ (17.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 812107:
structural_molecule_activity_ (22.43)
|   |   |   |   |   |   |   |   |   |   |   start > 814449
|   |   |   |   |   |   |   |   |   |   |   |   start <= 821292:
molecular_function_ (17.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 821292:
transferase_activity_ (17.03)
|   |   |   |   |   |   |   |   |   start > 829148:
molecular_function_ (55.2)
|   |   |   |   |   |   |   |   start > 838389: helicase_activity_
(23.32)
|   |   |   |   |   start > 841992
|   |   |   |   |   |   start <= 884358
|   |   |   |   |   |   |   start <= 848596
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 848068
|   |   |   |   |   |   |   |   |   |   start <= 844858:
DNA_binding_ (24.19)
|   |   |   |   |   |   |   |   |   |   start > 844858:
molecular_function_ (16.87)
|   |   |   |   |   |   |   |   |   start > 848068: DNA_binding_
(39.69/17.28)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 844858:
structural_molecule_activity_ (19.59)
|   |   |   |   |   |   |   |   |   start > 844858: RNA_binding_
(17.2)
|   |   |   |   |   |   |   start > 848596
|   |   |   |   |   |   |   |   start <= 853969
|   |   |   |   |   |   |   |   |   strand = W: molecular_function_
(8.94)
|   |   |   |   |   |   |   |   |   strand = C:
transferase_activity_ (37.54)
|   |   |   |   |   |   |   |   start > 853969
|   |   |   |   |   |   |   |   |   start <= 862051
|   |   |   |   |   |   |   |   |   |   start <= 858134
|   |   |   |   |   |   |   |   |   |   |   start <= 856314
|   |   |   |   |   |   |   |   |   |   |   |   start <= 856090:
molecular_function_ (14.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 856090:
structural_molecule_activity_ (8.3)
|   |   |   |   |   |   |   |   |   |   |   start > 856314:
molecular_function_ (41.34)
|   |   |   |   |   |   |   |   |   |   start > 858134
|   |   |   |   |   |   |   |   |   |   |   start <= 859343:
transporter_activity_ (17.35)
|   |   |   |   |   |   |   |   |   |   |   start > 859343:
molecular_function_ (26.22)
|   |   |   |   |   |   |   |   |   start > 862051
|   |   |   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 868221:
transferase_activity_ (16.13)
|   |   |   |   |   |   |   |   |   |   |   start > 868221:
molecular_function_ (27.6)
|   |   |   |   |   |   |   |   |   |   strand = C: DNA_binding_
(31.27/13.5)
|   |   |   |   |   |   start > 884358
|   |   |   |   |   |   |   start <= 915526
|   |   |   |   |   |   |   |   start <= 906848
|   |   |   |   |   |   |   |   |   start <= 884724:
translation_regulator_activity_ (19.77/4.58)
|   |   |   |   |   |   |   |   |   start > 884724
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 892872
|   |   |   |   |   |   |   |   |   |   |   |   start <= 889748
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 887229:
protein_binding_ (9.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 887229:
transcription_regulator_activity_ (12.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 889748:
protein_binding_ (13.78)
|   |   |   |   |   |   |   |   |   |   |   start > 892872:
transcription_regulator_activity_ (42.61/14.45)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 903476:
protein_binding_ (17.54)
|   |   |   |   |   |   |   |   |   |   |   start > 903476
|   |   |   |   |   |   |   |   |   |   |   |   start <= 905048:
structural_molecule_activity_ (15.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 905048:
protein_binding_ (15.87)
|   |   |   |   |   |   |   |   start > 906848
|   |   |   |   |   |   |   |   |   start <= 910050
|   |   |   |   |   |   |   |   |   |   start <= 907326:
hydrolase_activity_ (17.24)
|   |   |   |   |   |   |   |   |   |   start > 907326:
molecular_function_ (20.6)
|   |   |   |   |   |   |   |   |   start > 910050
|   |   |   |   |   |   |   |   |   |   start <= 912095:
transcription_regulator_activity_ (12.33)
|   |   |   |   |   |   |   |   |   |   start > 912095: DNA_binding_
(28.4)
|   |   |   |   |   |   |   start > 915526
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 917567
|   |   |   |   |   |   |   |   |   |   start <= 916482:
transferase_activity_ (16.22)
|   |   |   |   |   |   |   |   |   |   start > 916482:
protein_binding_ (29.22/11.2)
|   |   |   |   |   |   |   |   |   start > 917567
|   |   |   |   |   |   |   |   |   |   start <= 924781:
molecular_function_ (13.9)
|   |   |   |   |   |   |   |   |   |   start > 924781:
transferase_activity_ (16.68)
```

```
|   |   |   |   |   |   |   |   strand = C: protein_binding_ (30.84)
|   |   start > 927448
|   |   |   start <= 1054643
|   |   |   |   start <= 954284
|   |   |   |   |   start <= 950280
|   |   |   |   |   |   start <= 946308
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 933500
|   |   |   |   |   |   |   |   |   start <= 931125: lyase_activity_
(12.43)
|   |   |   |   |   |   |   |   |   start > 931125: RNA_binding_
(20.78)
|   |   |   |   |   |   |   |   start > 933500
|   |   |   |   |   |   |   |   |   start <= 940812:
structural_molecule_activity_ (16.22)
|   |   |   |   |   |   |   |   |   start > 940812:
molecular_function_ (6.99)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 943416
|   |   |   |   |   |   |   |   |   start <= 936611
|   |   |   |   |   |   |   |   |   |   start <= 931125:
molecular_function_ (19.38)
|   |   |   |   |   |   |   |   |   |   start > 931125:
transferase_activity_ (12.52)
|   |   |   |   |   |   |   |   |   start > 936611:
molecular_function_ (30.67)
|   |   |   |   |   |   |   |   start > 943416: RNA_binding_ (10.04)
|   |   |   |   |   |   start > 946308
|   |   |   |   |   |   |   start <= 946803: hydrolase_activity_
(18.43)
|   |   |   |   |   |   |   start > 946803: RNA_binding_ (14.74)
|   |   |   |   |   start > 950280
|   |   |   |   |   |   start <= 950559: protein_binding_ (15.19)
|   |   |   |   |   |   start > 950559
|   |   |   |   |   |   |   start <= 952796: transferase_activity_
(20.27)
|   |   |   |   |   |   |   start > 952796:
enzyme_regulator_activity_ (15.06)
|   |   |   |   start > 954284
|   |   |   |   |   start <= 1045007
|   |   |   |   |   |   start <= 977225
|   |   |   |   |   |   |   start <= 960610
|   |   |   |   |   |   |   |   start <= 956009
|   |   |   |   |   |   |   |   |   start <= 955129:
molecular_function_ (17.93)
|   |   |   |   |   |   |   |   |   start > 955129:
protein_kinase_activity_ (10.25)
|   |   |   |   |   |   |   |   start > 956009: molecular_function_
(53.87)
|   |   |   |   |   |   |   start > 960610
|   |   |   |   |   |   |   |   start <= 965109
|   |   |   |   |   |   |   |   |   start <= 963408:
protein_binding_ (8.32)
```

```
|   |   |   |   |   |   |   |   |   start > 963408: DNA_binding_
(28.62)
|   |   |   |   |   |   |   |   start > 965109
|   |   |   |   |   |   |   |   |   start <= 971470:
molecular_function_ (59.66/11.89)
|   |   |   |   |   |   |   |   |   start > 971470
|   |   |   |   |   |   |   |   |   |   start <= 974239:
protein_binding_ (15.81)
|   |   |   |   |   |   |   |   |   |   start > 974239
|   |   |   |   |   |   |   |   |   |   |   start <= 975778:
transcription_regulator_activity_ (11.37)
|   |   |   |   |   |   |   |   |   |   |   start > 975778:
molecular_function_ (13.7)
|   |   |   |   |   |   start > 977225
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 1004000
|   |   |   |   |   |   |   |   |   start <= 995530:
molecular_function_ (20.61)
|   |   |   |   |   |   |   |   |   start > 995530
|   |   |   |   |   |   |   |   |   |   start <= 998860:
protein_binding_ (16.98)
|   |   |   |   |   |   |   |   |   |   start > 998860:
ligase_activity_ (13.56)
|   |   |   |   |   |   |   |   start > 1004000
|   |   |   |   |   |   |   |   |   start <= 1035991
|   |   |   |   |   |   |   |   |   |   start <= 1032432
|   |   |   |   |   |   |   |   |   |   |   start <= 1024751
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1015698
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1009006: hydrolase_activity_ (30.63/9.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1009006:
molecular_function_ (16.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1015698:
hydrolase_activity_ (23.48)
|   |   |   |   |   |   |   |   |   |   |   start > 1024751:
molecular_function_ (12.75)
|   |   |   |   |   |   |   |   |   |   start > 1032432:
hydrolase_activity_ (22.2)
|   |   |   |   |   |   |   |   |   start > 1035991
|   |   |   |   |   |   |   |   |   |   start <= 1037191:
DNA_binding_ (17.08)
|   |   |   |   |   |   |   |   |   |   start > 1037191:
molecular_function_ (13.95)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 998860
|   |   |   |   |   |   |   |   |   start <= 995530
|   |   |   |   |   |   |   |   |   |   start <= 979205:
hydrolase_activity_ (16.68)
|   |   |   |   |   |   |   |   |   |   start > 979205
|   |   |   |   |   |   |   |   |   |   |   start <= 981051:
molecular_function_ (19.76)
|   |   |   |   |   |   |   |   |   |   |   start > 981051:
hydrolase_activity_ (15.42)
```

```
|   |   |   |   |   |   |   |   |   start > 995530:
transferase_activity_ (17.44)
|   |   |   |   |   |   |   |   start > 998860
|   |   |   |   |   |   |   |   |   start <= 1024751:
molecular_function_ (107.24)
|   |   |   |   |   |   |   |   |   start > 1024751
|   |   |   |   |   |   |   |   |   |   start <= 1032432
|   |   |   |   |   |   |   |   |   |   |   start <= 1030045:
protein_kinase_activity_ (12.59)
|   |   |   |   |   |   |   |   |   |   |   start > 1030045:
hydrolase_activity_ (23.39)
|   |   |   |   |   |   |   |   |   |   start > 1032432:
molecular_function_ (56.17)
|   |   |   |   |   start > 1045007
|   |   |   |   |   |   start <= 1052224
|   |   |   |   |   |   |   start <= 1049388: RNA_binding_ (18.1)
|   |   |   |   |   |   |   start > 1049388: lyase_activity_ (15.69)
|   |   |   |   |   |   start > 1052224: hydrolase_activity_ (21.79)
|   |   |   start > 1054643
|   |   |   |   start <= 1455858
|   |   |   |   |   start <= 1305622
|   |   |   |   |   |   start <= 1093760
|   |   |   |   |   |   |   start <= 1058810
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 1055208:
transcription_regulator_activity_ (15.53)
|   |   |   |   |   |   |   |   |   start > 1055208:
oxidoreductase_activity_ (19.87)
|   |   |   |   |   |   |   |   strand = C: transporter_activity_
(18.37)
|   |   |   |   |   |   |   start > 1058810
|   |   |   |   |   |   |   |   start <= 1075167
|   |   |   |   |   |   |   |   |   start <= 1067727
|   |   |   |   |   |   |   |   |   |   start <= 1059623:
molecular_function_ (16.48)
|   |   |   |   |   |   |   |   |   |   start > 1059623
|   |   |   |   |   |   |   |   |   |   |   start <= 1063348
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1062787:
transferase_activity_ (12.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1062787:
RNA_binding_ (19.15)
|   |   |   |   |   |   |   |   |   |   |   start > 1063348:
transferase_activity_ (22.54)
|   |   |   |   |   |   |   |   |   start > 1067727
|   |   |   |   |   |   |   |   |   |   start <= 1072553
|   |   |   |   |   |   |   |   |   |   |   start <= 1071382:
DNA_binding_ (15.56)
|   |   |   |   |   |   |   |   |   |   |   start > 1071382:
isomerase_activity_ (20.98)
|   |   |   |   |   |   |   |   |   |   start > 1072553
|   |   |   |   |   |   |   |   |   |   |   start <= 1073484:
hydrolase_activity_ (15.85)
|   |   |   |   |   |   |   |   |   |   |   start > 1073484:
protein_binding_ (13.23)
```

```
|   |   |   |   |   |   |   |   start > 1075167
|   |   |   |   |   |   |   |   |   start <= 1092508
|   |   |   |   |   |   |   |   |   |   start <= 1085062
|   |   |   |   |   |   |   |   |   |   |   start <= 1075861:
molecular_function_ (37.92)
|   |   |   |   |   |   |   |   |   |   |   start > 1075861
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1080195
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1078445: transcription_regulator_activity_ (12.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1078445:
enzyme_regulator_activity_ (17.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1080195:
transcription_regulator_activity_ (42.38)
|   |   |   |   |   |   |   |   |   |   start > 1085062
|   |   |   |   |   |   |   |   |   |   |   strand = W: RNA_binding_
(23.33)
|   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (29.84)
|   |   |   |   |   |   |   |   |   start > 1092508:
transferase_activity_ (33.21)
|   |   |   |   |   |   start > 1093760
|   |   |   |   |   |   |   start <= 1267463
|   |   |   |   |   |   |   |   start <= 1202120
|   |   |   |   |   |   |   |   |   start <= 1141162
|   |   |   |   |   |   |   |   |   |   start <= 1108495
|   |   |   |   |   |   |   |   |   |   |   start <= 1105824
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1102181: molecular_function_ (12.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1102181:
protein_binding_ (11.5)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (19.83)
|   |   |   |   |   |   |   |   |   |   |   start > 1105824:
protein_binding_ (31.56)
|   |   |   |   |   |   |   |   |   |   start > 1108495
|   |   |   |   |   |   |   |   |   |   |   start <= 1112290
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1108699:
hydrolase_activity_ (18.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1108699:
structural_molecule_activity_ (45.9)
|   |   |   |   |   |   |   |   |   |   |   start > 1112290
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1135426
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1127867
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1124920: molecular_function_ (69.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1124920
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   strand =
W: molecular_function_ (23.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   strand =
C: protein_binding_ (23.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1127867
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1129583: hydrolase_activity_ (15.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
1129583: molecular_function_ (30.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1135426
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1135927: structural_molecule_activity_ (9.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1135927:
protein_binding_ (11.3)
|   |   |   |   |   |   |   |   |   start > 1141162
|   |   |   |   |   |   |   |   |   |   start <= 1164654
|   |   |   |   |   |   |   |   |   |   |   start <= 1150935
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1145086: molecular_function_ (17.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1145086:
RNA_binding_ (13.96)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (51.04)
|   |   |   |   |   |   |   |   |   |   |   start > 1150935
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1153620:
ligase_activity_ (11.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1153620:
transporter_activity_ (35.25)
|   |   |   |   |   |   |   |   |   |   start > 1164654
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1186100
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1183292
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1171819: structural_molecule_activity_ (15.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1171819: molecular_function_ (70.23/10.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1183292
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1184740: transferase_activity_ (12.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1184740: structural_molecule_activity_ (9.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1186100
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1190052: protein_binding_ (10.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1190052:
molecular_function_ (62.32)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1196255
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1175823
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1171819: molecular_function_ (33.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1171819: peptidase_activity_ (12.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1175823:
molecular_function_ (77.54)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1196255:
transcription_regulator_activity_ (10.41)
|   |   |   |   |   |   |   |   start > 1202120
```

```
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 1234210
|   |   |   |   |   |   |   |   |   |   |   start <= 1226814
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1224749
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1219405
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1212840: molecular_function_ (16.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1212840
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1213896: oxidoreductase_activity_ (13.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1213896: molecular_function_ (13.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1219405
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1222751: enzyme_regulator_activity_ (24.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1222751: molecular_function_ (11.94)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1224749:
oxidoreductase_activity_ (17.26)
|   |   |   |   |   |   |   |   |   |   |   start > 1226814
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1230159
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1228603: transporter_activity_ (15.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1228603:
enzyme_regulator_activity_ (11.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1230159:
lyase_activity_ (15.45)
|   |   |   |   |   |   |   |   |   |   start > 1234210
|   |   |   |   |   |   |   |   |   |   |   start <= 1246076
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1240668
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1236550: RNA_binding_ (10.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1236550:
structural_molecule_activity_ (6.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1240668
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1243222: translation_regulator_activity_ (14.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1243222:
hydrolase_activity_ (15.48)
|   |   |   |   |   |   |   |   |   |   |   start > 1246076
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1258688
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1250178: protein_binding_ (21.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1250178
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1252529: enzyme_regulator_activity_ (17.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1252529: transcription_regulator_activity_ (14.52)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1258688
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1261673
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1259893: molecular_function_ (13.77)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1259893: peptidase_activity_ (15.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1261673
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1263316: protein_binding_ (11.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1263316: RNA_binding_ (11.6)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 1230159
|   |   |   |   |   |   |   |   |   |   |   start <= 1206375:
RNA_binding_ (38.39)
|   |   |   |   |   |   |   |   |   |   |   start > 1206375
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1224749
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1217572
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1213896: molecular_function_ (15.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1213896
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 2903: DNA_binding_ (16.69/5.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 2903: protein_binding_ (19.23/5.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1217572:
molecular_function_ (46.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1224749
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1226814: hydrolase_activity_ (16.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1226814:
RNA_binding_ (20.52)
|   |   |   |   |   |   |   |   |   |   start > 1230159
|   |   |   |   |   |   |   |   |   |   |   start <= 1261673
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1252529
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1240668: molecular_function_ (50.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1240668:
transporter_activity_ (29.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1252529:
molecular_function_ (52.81)
|   |   |   |   |   |   |   |   |   |   |   start > 1261673:
transcription_regulator_activity_ (7.89)
|   |   |   |   |   |   |   start > 1267463
|   |   |   |   |   |   |   |   start <= 1293083
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 1270060:
transferase_activity_ (20.45)
|   |   |   |   |   |   |   |   |   |   start > 1270060
|   |   |   |   |   |   |   |   |   |   |   start <= 1279202
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1274594
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1271055: hydrolase_activity_ (19.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1271055:
molecular_function_ (15.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1274594
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1277638: structural_molecule_activity_ (22.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1277638:
hydrolase_activity_ (21.39)
|   |   |   |   |   |   |   |   |   |   |   start > 1279202:
ligase_activity_ (11.21)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 1279202
|   |   |   |   |   |   |   |   |   |   |   start <= 1274594:
oxidoreductase_activity_ (16.37)
|   |   |   |   |   |   |   |   |   |   |   start > 1274594:
nucleotidyltransferase_activity_ (8.89)
|   |   |   |   |   |   |   |   |   |   start > 1279202
|   |   |   |   |   |   |   |   |   |   |   start <= 1287930:
enzyme_regulator_activity_ (16.11)
|   |   |   |   |   |   |   |   |   |   |   start > 1287930:
transferase_activity_ (24.72)
|   |   |   |   |   |   |   |   start > 1293083
|   |   |   |   |   |   |   |   |   start <= 1298424:
molecular_function_ (77.41)
|   |   |   |   |   |   |   |   |   start > 1298424
|   |   |   |   |   |   |   |   |   |   start <= 1303166
|   |   |   |   |   |   |   |   |   |   |   start <= 1301608:
structural_molecule_activity_ (7.84)
|   |   |   |   |   |   |   |   |   |   |   start > 1301608:
nucleotidyltransferase_activity_ (13.55)
|   |   |   |   |   |   |   |   |   |   start > 1303166:
molecular_function_ (10.58)
|   |   |   |   |   start > 1305622
|   |   |   |   |   |   start <= 1328462
|   |   |   |   |   |   |   start <= 1319833
|   |   |   |   |   |   |   |   start <= 1306259:
signal_transducer_activity_ (13.65)
|   |   |   |   |   |   |   |   start > 1306259
|   |   |   |   |   |   |   |   |   start <= 1319267
|   |   |   |   |   |   |   |   |   |   start <= 1317765
|   |   |   |   |   |   |   |   |   |   |   start <= 1312032:
transcription_regulator_activity_ (10.48)
|   |   |   |   |   |   |   |   |   |   |   start > 1312032:
protein_kinase_activity_ (16.27)
|   |   |   |   |   |   |   |   |   |   start > 1317765:
transcription_regulator_activity_ (16.86)
|   |   |   |   |   |   |   |   |   start > 1319267: motor_activity_
(12.44)
|   |   |   |   |   |   |   start > 1319833
|   |   |   |   |   |   |   |   start <= 1324231
|   |   |   |   |   |   |   |   |   start <= 1320056:
molecular_function_ (14.8)
|   |   |   |   |   |   |   |   |   start > 1320056
|   |   |   |   |   |   |   |   |   |   start <= 1322197:
structural_molecule_activity_ (15.41)
|   |   |   |   |   |   |   |   |   |   start > 1322197:
molecular_function_ (8.66)
|   |   |   |   |   |   |   |   start > 1324231
```

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|   |   |   |   |   |   |   |   |   start <= 1325293:
translation_regulator_activity_ (16.62)
|   |   |   |   |   |   |   |   |   start > 1325293:
peptidase_activity_ (17.89)
|   |   |   |   |   |   start > 1328462
|   |   |   |   |   |   |   start <= 1394566
|   |   |   |   |   |   |   |   start <= 1337344
|   |   |   |   |   |   |   |   |   start <= 1331229
|   |   |   |   |   |   |   |   |   |   start <= 1328775:
RNA_binding_ (6.51)
|   |   |   |   |   |   |   |   |   |   start > 1328775:
hydrolase_activity_ (15.16)
|   |   |   |   |   |   |   |   |   start > 1331229
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 1334813:
phosphoprotein_phosphatase_activity_ (12.84)
|   |   |   |   |   |   |   |   |   |   |   start > 1334813:
transferase_activity_ (12.09)
|   |   |   |   |   |   |   |   |   |   strand = C:
transferase_activity_ (14.25)
|   |   |   |   |   |   |   |   start > 1337344
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 1353717
|   |   |   |   |   |   |   |   |   |   |   start <= 1339668:
molecular_function_ (30.1)
|   |   |   |   |   |   |   |   |   |   |   start > 1339668
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1345054:
transferase_activity_ (13.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1345054:
molecular_function_ (23.12)
|   |   |   |   |   |   |   |   |   |   start > 1353717
|   |   |   |   |   |   |   |   |   |   |   start <= 1367477
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1359915
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1356057: transcription_regulator_activity_ (16.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1356057:
structural_molecule_activity_ (15.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1359915
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1362870: hydrolase_activity_ (11.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1362870:
transporter_activity_ (15.53)
|   |   |   |   |   |   |   |   |   |   |   start > 1367477
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1385168
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1383803
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1369782: molecular_function_ (10.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1369782: transcription_regulator_activity_ (22.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1383803:
protein_binding_ (16.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1385168
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1386808
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1386065: structural_molecule_activity_ (10.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
1386065: transcription_regulator_activity_ (26.23/10.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1386808:
molecular_function_ (15.23)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 1362870
|   |   |   |   |   |   |   |   |   |   |   start <= 1353717
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1345054:
molecular_function_ (10.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1345054
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1350282: transcription_regulator_activity_ (9.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1350282:
molecular_function_ (10.32)
|   |   |   |   |   |   |   |   |   |   |   start > 1353717
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1359915
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1356057: structural_molecule_activity_ (10.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1356057:
RNA_binding_ (11.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1359915:
DNA_binding_ (16.51)
|   |   |   |   |   |   |   |   |   |   start > 1362870
|   |   |   |   |   |   |   |   |   |   |   start <= 1365654:
molecular_function_ (38.02/17.08)
|   |   |   |   |   |   |   |   |   |   |   start > 1365654
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1369782:
transferase_activity_ (14.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1369782
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1382038: molecular_function_ (16.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1382038
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1383803: transferase_activity_ (14.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1383803
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1388864: molecular_function_ (12.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1388864: transferase_activity_ (7.9)
|   |   |   |   |   |   |   start > 1394566
|   |   |   |   |   |   |   |   start <= 1443395
|   |   |   |   |   |   |   |   |   start <= 1405846
|   |   |   |   |   |   |   |   |   |   start <= 1401206
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1395113:
protein_kinase_activity_ (21.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1395113:
transferase_activity_ (22.39)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1399007:
protein_binding_ (14.2)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 1399007:
transporter_activity_ (14.96)
|   |   |   |   |   |   |   |   |   |   start > 1401206
|   |   |   |   |   |   |   |   |   |   |   start <= 1401762:
structural_molecule_activity_ (13.5)
|   |   |   |   |   |   |   |   |   |   |   start > 1401762
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1402911:
RNA_binding_ (20.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1402911
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1403314: enzyme_regulator_activity_ (16.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1403314:
RNA_binding_ (17.02)
|   |   |   |   |   |   |   |   |   start > 1405846
|   |   |   |   |   |   |   |   |   |   start <= 1427199
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1414567
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1412365: protein_kinase_activity_ (19.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1412365:
RNA_binding_ (13.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1414567
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1421149
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1417391: protein_binding_ (13.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1417391: transferase_activity_ (23.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1421149:
protein_binding_ (18.23)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1422755
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1417391: molecular_function_ (54.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1417391
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1420242: hydrolase_activity_ (13.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1420242: molecular_function_ (20.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1422755:
protein_binding_ (18.38)
|   |   |   |   |   |   |   |   |   |   start > 1427199
|   |   |   |   |   |   |   |   |   |   |   start <= 1441142
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1436209
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1431004
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1428972: molecular_function_ (35.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1428972
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1430781: motor_activity_ (17.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1430781: molecular_function_ (16.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1431004
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (29.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
protein_kinase_activity_ (17.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1436209
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1436922: structural_molecule_activity_ (22.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1436922:
molecular_function_ (21.6)
|   |   |   |   |   |   |   |   |   |   |   start > 1441142:
RNA_binding_ (21.76)
|   |   |   |   |   |   |   |   start > 1443395
|   |   |   |   |   |   |   |   |   start <= 1447822
|   |   |   |   |   |   |   |   |   |   start <= 1445459:
transporter_activity_ (19.19)
|   |   |   |   |   |   |   |   |   |   start > 1445459:
protein_binding_ (31.51)
|   |   |   |   |   |   |   |   |   start > 1447822
|   |   |   |   |   |   |   |   |   |   strand = W: DNA_binding_
(24.88/10.83)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 1454456
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1451345:
structural_molecule_activity_ (11.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1451345:
transferase_activity_ (10.3)
|   |   |   |   |   |   |   |   |   |   |   start > 1454456:
hydrolase_activity_ (15.21)
|   |   |   |   start > 1455858
|   |   |   |   |   start <= 1500545
|   |   |   |   |   |   start <= 1470009
|   |   |   |   |   |   |   start <= 1461821: molecular_function_
(53.48)
|   |   |   |   |   |   |   start > 1461821
|   |   |   |   |   |   |   |   strand = W: molecular_function_
(23.79)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 1465778:
protein_kinase_activity_ (13.06)
|   |   |   |   |   |   |   |   |   start > 1465778:
transporter_activity_ (23.34)
|   |   |   |   |   |   start > 1470009
|   |   |   |   |   |   |   start <= 1496540
|   |   |   |   |   |   |   |   start <= 1471009:
transferase_activity_ (26.15/10.89)
|   |   |   |   |   |   |   |   start > 1471009
|   |   |   |   |   |   |   |   |   start <= 1494578
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 1473421:
RNA_binding_ (17.17)
|   |   |   |   |   |   |   |   |   |   |   start > 1473421
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1483395
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1478600
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1477231: molecular_function_ (15.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1477231: oxidoreductase_activity_ (17.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1478600:
isomerase_activity_ (16.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1483395:
molecular_function_ (60.49)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 1485295:
molecular_function_ (88.18)
|   |   |   |   |   |   |   |   |   |   |   start > 1485295
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1488982
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1487030: protein_kinase_activity_ (12.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1487030:
enzyme_regulator_activity_ (17.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1488982
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1491086: molecular_function_ (9.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1491086:
RNA_binding_ (12.05)
|   |   |   |   |   |   |   |   |   start > 1494578:
oxidoreductase_activity_ (17.12)
|   |   |   |   |   |   |   start > 1496540
|   |   |   |   |   |   |   |   strand = W: transferase_activity_
(22.26)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 1498224:
hydrolase_activity_ (15.74)
|   |   |   |   |   |   |   |   |   start > 1498224:
molecular_function_ (29.86)
|   |   |   |   |   start > 1500545
|   |   |   |   |   |   start <= 1502152: peptidase_activity_
(52.81/25.52)
|   |   |   |   |   |   start > 1502152
|   |   |   |   |   |   |   start <= 1510892
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 1507996:
transporter_activity_ (9.05)
|   |   |   |   |   |   |   |   |   start > 1507996: lyase_activity_
(12.62)
|   |   |   |   |   |   |   |   strand = C: molecular_function_
(15.03)
|   |   |   |   |   |   |   start > 1510892
|   |   |   |   |   |   |   |   start <= 1523234
|   |   |   |   |   |   |   |   |   strand = W: molecular_function_
(27.2)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 1517659:
molecular_function_ (10.19)
|   |   |   |   |   |   |   |   |   |   start > 1517659:
oxidoreductase_activity_ (10.32)
```

```
|   |   |   |   |   |   |   |   start > 1523234: helicase_activity_
(4.51)
```

For Biological Process

```
|   start <= 241418
|   |   start <= 130485
|   |   |   start <= 97954
|   |   |   |   start <= 78427
|   |   |   |   |   start <= 30657
|   |   |   |   |   |   start <= 16204: transport_ (68.13/44.38)
|   |   |   |   |   |   start > 16204: biological_process_
(124.9/48.54)
|   |   |   |   |   start > 30657
|   |   |   |   |   |   start <= 76546
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 42701:
protein_modification_process_ (69.89/22.8)
|   |   |   |   |   |   |   |   start > 42701: translation_
(58.8/31.43)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 52446: vesicle-
mediated_transport_ (134.81/69.44)
|   |   |   |   |   |   |   |   start > 52446
|   |   |   |   |   |   |   |   |   start <= 68607
|   |   |   |   |   |   |   |   |   |   start <= 60406:
biological_process_ (43.16/28.39)
|   |   |   |   |   |   |   |   |   |   start > 60406:
membrane_organization_and_biogenesis_ (40.57/24.23)
|   |   |   |   |   |   |   |   |   start > 68607
|   |   |   |   |   |   |   |   |   |   start <= 70320:
protein_modification_process_ (37.58/16.5)
|   |   |   |   |   |   |   |   |   |   start > 70320:
biological_process_ (39.94/17.45)
|   |   |   |   |   |   start > 76546: transport_ (56.06/34.63)
|   |   |   |   start > 78427
|   |   |   |   |   start <= 88249
|   |   |   |   |   |   strand = W: transport_ (94.03/57.52)
|   |   |   |   |   |   strand = C: RNA_metabolic_process_
(35.85/16.11)
|   |   |   |   |   start > 88249: biological_process_ (68.27)
|   |   |   start > 97954
|   |   |   |   start <= 116322
|   |   |   |   |   start <= 101068
|   |   |   |   |   |   start <= 98476: translation_ (20.95)
|   |   |   |   |   |   start > 98476: DNA_metabolic_process_
(25.57/11.04)
|   |   |   |   |   start > 101068
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 114673
|   |   |   |   |   |   |   |   start <= 107209: vesicle-
mediated_transport_ (23.7/11.25)
|   |   |   |   |   |   |   |   start > 107209: signal_transduction_
(43.14/16.42)
```

```
|   |   |   |   |   |   |   start > 114673: transport_ (49.31/29.0)
|   |   |   |   |   |   strand = C: transcription_ (47.97/30.15)
|   |   |   |   start > 116322: translation_ (110.1/66.55)
|   |   start > 130485
|   |   |   start <= 192751
|   |   |   |   strand = W
|   |   |   |   |   start <= 159605
|   |   |   |   |   |   start <= 135180:
generation_of_precursor_metabolites_and_energy_ (42.66/17.66)
|   |   |   |   |   |   start > 135180
|   |   |   |   |   |   |   start <= 138292
|   |   |   |   |   |   |   |   start <= 135897: biological_process_
(11.55)
|   |   |   |   |   |   |   |   start > 135897: cell_cycle_ (15.71)
|   |   |   |   |   |   |   start > 138292: biological_process_
(137.33/33.57)
|   |   |   |   |   start > 159605
|   |   |   |   |   |   start <= 172482
|   |   |   |   |   |   |   start <= 169609: vesicle-
mediated_transport_ (49.33/29.43)
|   |   |   |   |   |   |   start > 169609: pseudohyphal_growth_
(33.92/16.1)
|   |   |   |   |   |   start > 172482
|   |   |   |   |   |   |   start <= 178335
|   |   |   |   |   |   |   |   start <= 176774
|   |   |   |   |   |   |   |   |   distance <= 2721:
biological_process_ (23.32/7.2)
|   |   |   |   |   |   |   |   |   distance > 2721: cell_cycle_
(20.09/3.54)
|   |   |   |   |   |   |   |   start > 176774:
DNA_metabolic_process_ (35.58/20.58)
|   |   |   |   |   |   |   start > 178335
|   |   |   |   |   |   |   |   start <= 190925: transcription_
(61.13/38.82)
|   |   |   |   |   |   |   |   start > 190925: biological_process_
(16.93)
|   |   |   |   strand = C
|   |   |   |   |   start <= 178335: biological_process_
(208.39/126.36)
|   |   |   |   |   start > 178335:
ribosome_biogenesis_and_assembly_ (36.12)
|   |   |   start > 192751
|   |   |   |   start <= 216529
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 203040:
cytoskeleton_organization_and_biogenesis_ (35.89/12.93)
|   |   |   |   |   |   start > 203040: transport_ (46.23/26.46)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 198177: vesicle-mediated_transport_
(47.68/20.43)
|   |   |   |   |   |   start > 198177
|   |   |   |   |   |   |   start <= 203040:
membrane_organization_and_biogenesis_ (37.94/12.78)
```

```
|   |   |   |   |   |   |   start > 203040: transcription_
(41.65/26.13)
|   |   |   |   start > 216529
|   |   |   |   |   start <= 221801
|   |   |   |   |   |   start <= 219288: signal_transduction_
(28.85/13.59)
|   |   |   |   |   |   start > 219288: translation_ (41.44)
|   |   |   |   |   start > 221801
|   |   |   |   |   |   start <= 238664: cell_cycle_ (197.67/134.54)
|   |   |   |   |   |   start > 238664: biological_process_ (62.53)
|   start > 241418
|   |   start <= 1127867
|   |   |   start <= 388898
|   |   |   |   start <= 305237
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 301413
|   |   |   |   |   |   |   start <= 276872
|   |   |   |   |   |   |   |   start <= 268921
|   |   |   |   |   |   |   |   |   start <= 251566
|   |   |   |   |   |   |   |   |   |   start <= 245923:
protein_modification_process_ (30.65/11.17)
|   |   |   |   |   |   |   |   |   |   start > 245923
|   |   |   |   |   |   |   |   |   |   |   distance <= 2276:
DNA_metabolic_process_ (20.63/2.55)
|   |   |   |   |   |   |   |   |   |   |   distance > 2276:
cytokinesis_ (24.9/9.59)
|   |   |   |   |   |   |   |   |   start > 251566
|   |   |   |   |   |   |   |   |   |   start <= 258915:
RNA_metabolic_process_ (37.41/12.48)
|   |   |   |   |   |   |   |   |   |   start > 258915:
biological_process_ (26.67/9.58)
|   |   |   |   |   |   |   |   start > 268921:
DNA_metabolic_process_ (35.1)
|   |   |   |   |   |   |   start > 276872
|   |   |   |   |   |   |   |   start <= 294759:
protein_modification_process_ (85.04/48.74)
|   |   |   |   |   |   |   |   start > 294759: biological_process_
(45.89)
|   |   |   |   |   |   start > 301413:
generation_of_precursor_metabolites_and_energy_ (57.22/36.67)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 272389
|   |   |   |   |   |   |   start <= 264964
|   |   |   |   |   |   |   |   start <= 255604
|   |   |   |   |   |   |   |   |   start <= 248581:
biological_process_ (17.67/8.7)
|   |   |   |   |   |   |   |   |   start > 248581: meiosis_ (16.46)
|   |   |   |   |   |   |   |   start > 255604: biological_process_
(74.47/38.09)
|   |   |   |   |   |   |   start > 264964: lipid_metabolic_process_
(36.68/14.03)
|   |   |   |   |   |   start > 272389
|   |   |   |   |   |   |   start <= 276872: biological_process_
(38.4/16.19)
```

```
|   |   |   |   |   |   |   start > 276872
|   |   |   |   |   |   |   |   start <= 285165
|   |   |   |   |   |   |   |   |   start <= 281848:
protein_modification_process_ (38.76/19.02)
|   |   |   |   |   |   |   |   |   start > 281848:
response_to_stress_ (40.01/15.23)
|   |   |   |   |   |   |   |   start > 285165: biological_process_
(94.21/50.81)
|   |   |   |   start > 305237
|   |   |   |   |   start <= 352877
|   |   |   |   |   |   start <= 334835
|   |   |   |   |   |   |   start <= 326149
|   |   |   |   |   |   |   |   start <= 322226: translation_
(117.22/66.83)
|   |   |   |   |   |   |   |   start > 322226:
RNA_metabolic_process_ (37.87/23.66)
|   |   |   |   |   |   |   start > 326149
|   |   |   |   |   |   |   |   start <= 331025: biological_process_
(40.06)
|   |   |   |   |   |   |   |   start > 331025:
carbohydrate_metabolic_process_ (45.56/22.96)
|   |   |   |   |   |   start > 334835
|   |   |   |   |   |   |   start <= 341619
|   |   |   |   |   |   |   |   start <= 337277: transport_
(39.23/17.76)
|   |   |   |   |   |   |   |   start > 337277:
ribosome_biogenesis_and_assembly_ (66.92/37.01)
|   |   |   |   |   |   |   start > 341619
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 345665: vesicle-
mediated_transport_ (39.88/16.13)
|   |   |   |   |   |   |   |   |   start > 345665:
biological_process_ (38.73/17.98)
|   |   |   |   |   |   |   |   strand = C: DNA_metabolic_process_
(8.13)
|   |   |   |   |   start > 352877
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 371237
|   |   |   |   |   |   |   |   start <= 369769:
cell_wall_organization_and_biogenesis_ (49.68/28.09)
|   |   |   |   |   |   |   |   start > 369769: transport_ (24.89)
|   |   |   |   |   |   |   start > 371237: translation_ (17.1)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 365874
|   |   |   |   |   |   |   |   start <= 363952
|   |   |   |   |   |   |   |   |   start <= 356759:
protein_modification_process_ (13.48)
|   |   |   |   |   |   |   |   |   start > 356759: transport_
(44.24/25.25)
|   |   |   |   |   |   |   |   start > 363952:
carbohydrate_metabolic_process_ (44.05/21.79)
|   |   |   |   |   |   |   start > 365874
|   |   |   |   |   |   |   |   start <= 382330
```

```
|   |   |   |   |   |   |   |   |   start <= 373605:
biological_process_ (40.0/15.23)
|   |   |   |   |   |   |   |   |   start > 373605: translation_
(59.12/40.43)
|   |   |   |   |   |   |   |   start > 382330
|   |   |   |   |   |   |   |   |   start <= 385584:
biological_process_ (22.23)
|   |   |   |   |   |   |   |   |   start > 385584:
RNA_metabolic_process_ (9.9)
|   |   |   start > 388898
|   |   |   |   start <= 709546
|   |   |   |   |   start <= 569768
|   |   |   |   |   |   start <= 461244
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 432327
|   |   |   |   |   |   |   |   |   start <= 427361
|   |   |   |   |   |   |   |   |   |   start <= 411822:
RNA_metabolic_process_ (53.5/40.16)
|   |   |   |   |   |   |   |   |   |   start > 411822:
biological_process_ (56.95/31.96)
|   |   |   |   |   |   |   |   |   start > 427361:
response_to_stress_ (38.34/17.69)
|   |   |   |   |   |   |   |   start > 432327
|   |   |   |   |   |   |   |   |   start <= 438044
|   |   |   |   |   |   |   |   |   |   start <= 437769: cell_cycle_
(28.56/13.47)
|   |   |   |   |   |   |   |   |   |   start > 437769:
protein_catabolic_process_ (21.13)
|   |   |   |   |   |   |   |   |   start > 438044
|   |   |   |   |   |   |   |   |   |   start <= 443026
|   |   |   |   |   |   |   |   |   |   |   start <= 439906:
organelle_organization_and_biogenesis_ (48.34/28.36)
|   |   |   |   |   |   |   |   |   |   |   start > 439906:
generation_of_precursor_metabolites_and_energy_ (21.16)
|   |   |   |   |   |   |   |   |   |   start > 443026
|   |   |   |   |   |   |   |   |   |   |   start <= 453042:
cell_cycle_ (40.86/12.03)
|   |   |   |   |   |   |   |   |   |   |   start > 453042:
biological_process_ (41.12/24.46)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 416705
|   |   |   |   |   |   |   |   |   start <= 411822
|   |   |   |   |   |   |   |   |   |   start <= 403288: cell_cycle_
(36.25/23.09)
|   |   |   |   |   |   |   |   |   |   start > 403288:
biological_process_ (29.38/8.42)
|   |   |   |   |   |   |   |   |   start > 411822:
DNA_metabolic_process_ (55.0/38.39)
|   |   |   |   |   |   |   |   start > 416705
|   |   |   |   |   |   |   |   |   start <= 429064
|   |   |   |   |   |   |   |   |   |   start <= 421511: vesicle-
mediated_transport_ (16.87)
|   |   |   |   |   |   |   |   |   |   start > 421511:
lipid_metabolic_process_ (21.16/9.55)
```

```
|   |   |   |   |   |   |   |   |   start > 429064
|   |   |   |   |   |   |   |   |   |   start <= 438044:
biological_process_ (53.08/11.94)
|   |   |   |   |   |   |   |   |   |   start > 438044:
transcription_ (74.2/41.21)
|   |   |   |   |   |   start > 461244
|   |   |   |   |   |   |   start <= 560623
|   |   |   |   |   |   |   |   start <= 541200
|   |   |   |   |   |   |   |   |   start <= 508144
|   |   |   |   |   |   |   |   |   |   start <= 491512
|   |   |   |   |   |   |   |   |   |   |   start <= 488659:
biological_process_ (204.55/137.98)
|   |   |   |   |   |   |   |   |   |   |   start > 488659:
translation_ (50.86)
|   |   |   |   |   |   |   |   |   |   start > 491512
|   |   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (20.73)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 494265:
biological_process_ (7.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 494265
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 500876:
carbohydrate_metabolic_process_ (35.84/21.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 500876:
DNA_metabolic_process_ (33.32/13.74)
|   |   |   |   |   |   |   |   |   start > 508144
|   |   |   |   |   |   |   |   |   |   strand = W: translation_
(83.13/28.48)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 512106:
amino_acid_and_derivative_metabolic_process_ (21.82)
|   |   |   |   |   |   |   |   |   |   |   start > 512106:
biological_process_ (117.65/78.24)
|   |   |   |   |   |   |   |   start > 541200
|   |   |   |   |   |   |   |   |   strand = W: biological_process_
(46.77)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 553252:
transcription_ (86.25/66.79)
|   |   |   |   |   |   |   |   |   |   start > 553252
|   |   |   |   |   |   |   |   |   |   |   start <= 558058:
biological_process_ (20.4/8.13)
|   |   |   |   |   |   |   |   |   |   |   start > 558058:
DNA_metabolic_process_ (15.39)
|   |   |   |   |   |   |   start > 560623
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 565925
|   |   |   |   |   |   |   |   |   |   start <= 563525:
cell_wall_organization_and_biogenesis_ (19.52)
|   |   |   |   |   |   |   |   |   |   start > 563525:
protein_catabolic_process_ (12.83)
|   |   |   |   |   |   |   |   |   start > 565925: translation_
(30.57)
|   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   start <= 565925
|   |   |   |   |   |   |   |   |   |   start <= 563525: cell_cycle_
(14.3)
|   |   |   |   |   |   |   |   |   |   start > 563525:
biological_process_ (17.82)
|   |   |   |   |   |   |   |   |   start > 565925
|   |   |   |   |   |   |   |   |   |   start <= 568962:
lipid_metabolic_process_ (15.04)
|   |   |   |   |   |   |   |   |   |   start > 568962:
response_to_stress_ (14.9)
|   |   |   |   |   start > 569768
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 616147
|   |   |   |   |   |   |   |   start <= 587717
|   |   |   |   |   |   |   |   |   start <= 570646:
ribosome_biogenesis_and_assembly_ (18.94)
|   |   |   |   |   |   |   |   |   start > 570646
|   |   |   |   |   |   |   |   |   |   start <= 579456
|   |   |   |   |   |   |   |   |   |   |   start <= 574161:
biological_process_ (15.28)
|   |   |   |   |   |   |   |   |   |   |   start > 574161:
lipid_metabolic_process_ (35.7/18.68)
|   |   |   |   |   |   |   |   |   |   start > 579456
|   |   |   |   |   |   |   |   |   |   |   start <= 580685:
organelle_organization_and_biogenesis_ (20.01)
|   |   |   |   |   |   |   |   |   |   |   start > 580685:
biological_process_ (21.97)
|   |   |   |   |   |   |   |   start > 587717
|   |   |   |   |   |   |   |   |   start <= 598465
|   |   |   |   |   |   |   |   |   |   start <= 593890:
DNA_metabolic_process_ (33.22/15.85)
|   |   |   |   |   |   |   |   |   |   start > 593890
|   |   |   |   |   |   |   |   |   |   |   start <= 597153:
protein_modification_process_ (41.28/14.62)
|   |   |   |   |   |   |   |   |   |   |   start > 597153:
DNA_metabolic_process_ (19.5)
|   |   |   |   |   |   |   |   |   start > 598465
|   |   |   |   |   |   |   |   |   |   start <= 604005:
cellular_respiration_ (83.31/58.53)
|   |   |   |   |   |   |   |   |   |   start > 604005:
DNA_metabolic_process_ (44.22/17.62)
|   |   |   |   |   |   |   start > 616147
|   |   |   |   |   |   |   |   start <= 685879
|   |   |   |   |   |   |   |   |   start <= 655010
|   |   |   |   |   |   |   |   |   |   start <= 622109:
membrane_organization_and_biogenesis_ (17.3)
|   |   |   |   |   |   |   |   |   |   start > 622109
|   |   |   |   |   |   |   |   |   |   |   start <= 629873:
DNA_metabolic_process_ (17.16)
|   |   |   |   |   |   |   |   |   |   |   start > 629873: vesicle-
mediated_transport_ (72.93/45.76)
|   |   |   |   |   |   |   |   |   start > 655010
|   |   |   |   |   |   |   |   |   |   start <= 658347:
conjugation_ (55.12/32.91)
```

```
|   |   |   |   |   |   |   |   |   |   start > 658347: cell_cycle_
(78.23/43.5)
|   |   |   |   |   |   |   |   start > 685879
|   |   |   |   |   |   |   |   |   start <= 700312:
biological_process_ (101.7/38.86)
|   |   |   |   |   |   |   |   |   start > 700312
|   |   |   |   |   |   |   |   |   |   start <= 703231:
sporulation_ (71.7/47.84)
|   |   |   |   |   |   |   |   |   |   start > 703231:
amino_acid_and_derivative_metabolic_process_ (56.73/25.67)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 617167
|   |   |   |   |   |   |   |   start <= 588377: biological_process_
(69.61/18.98)
|   |   |   |   |   |   |   |   start > 588377
|   |   |   |   |   |   |   |   |   start <= 604005
|   |   |   |   |   |   |   |   |   |   start <= 589400:
DNA_metabolic_process_ (17.31)
|   |   |   |   |   |   |   |   |   |   start > 589400
|   |   |   |   |   |   |   |   |   |   |   start <= 593890:
lipid_metabolic_process_ (13.17)
|   |   |   |   |   |   |   |   |   |   |   start > 593890:
DNA_metabolic_process_ (37.35)
|   |   |   |   |   |   |   |   |   start > 604005
|   |   |   |   |   |   |   |   |   |   start <= 616147:
transcription_ (55.57/33.77)
|   |   |   |   |   |   |   |   |   |   start > 616147: transport_
(17.2)
|   |   |   |   |   |   |   start > 617167
|   |   |   |   |   |   |   |   start <= 658347
|   |   |   |   |   |   |   |   |   start <= 625995
|   |   |   |   |   |   |   |   |   |   start <= 622109
|   |   |   |   |   |   |   |   |   |   |   start <= 619642
|   |   |   |   |   |   |   |   |   |   |   |   start <= 618303:
ribosome_biogenesis_and_assembly_ (28.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 618303:
RNA_metabolic_process_ (17.51)
|   |   |   |   |   |   |   |   |   |   |   start > 619642:
translation_ (18.31)
|   |   |   |   |   |   |   |   |   |   start > 622109:
biological_process_ (23.11)
|   |   |   |   |   |   |   |   |   start > 625995:
ribosome_biogenesis_and_assembly_ (83.27/55.87)
|   |   |   |   |   |   |   |   start > 658347
|   |   |   |   |   |   |   |   |   start <= 688224
|   |   |   |   |   |   |   |   |   |   start <= 664907:
cell_wall_organization_and_biogenesis_ (42.25/16.65)
|   |   |   |   |   |   |   |   |   |   start > 664907
|   |   |   |   |   |   |   |   |   |   |   start <= 679761
|   |   |   |   |   |   |   |   |   |   |   |   start <= 668077
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 667001:
biological_process_ (16.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 667001:
translation_ (24.61)
```

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|   |   |   |   |   |   |   |   |   |   |   |   start > 668077:
biological_process_ (40.74)
|   |   |   |   |   |   |   |   |   |   |   start > 679761
|   |   |   |   |   |   |   |   |   |   |   |   start <= 681614:
DNA_metabolic_process_ (34.87/10.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 681614:
biological_process_ (42.78/10.64)
|   |   |   |   |   |   |   |   |   start > 688224
|   |   |   |   |   |   |   |   |   |   distance <= 1628:
ribosome_biogenesis_and_assembly_ (15.31/5.47)
|   |   |   |   |   |   |   |   |   |   distance > 1628:
cell_wall_organization_and_biogenesis_ (54.5/34.32)
|   |   |   |   start > 709546
|   |   |   |   |   start <= 956009
|   |   |   |   |   |   start <= 930353
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 858134
|   |   |   |   |   |   |   |   |   start <= 784868
|   |   |   |   |   |   |   |   |   |   start <= 776160
|   |   |   |   |   |   |   |   |   |   |   start <= 746735:
DNA_metabolic_process_ (113.73/79.36)
|   |   |   |   |   |   |   |   |   |   |   start > 746735
|   |   |   |   |   |   |   |   |   |   |   |   start <= 769522
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 765703
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
751628: lipid_metabolic_process_ (38.23/23.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
751628: cytoskeleton_organization_and_biogenesis_ (47.31/29.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 765703:
transcription_ (27.99/11.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 769522
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 771874:
cytoskeleton_organization_and_biogenesis_ (54.03/28.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 771874:
biological_process_ (18.3)
|   |   |   |   |   |   |   |   |   |   start > 776160
|   |   |   |   |   |   |   |   |   |   |   start <= 779040:
ribosome_biogenesis_and_assembly_ (19.6)
|   |   |   |   |   |   |   |   |   |   |   start > 779040:
RNA_metabolic_process_ (29.83/13.09)
|   |   |   |   |   |   |   |   |   start > 784868
|   |   |   |   |   |   |   |   |   |   start <= 808321
|   |   |   |   |   |   |   |   |   |   |   start <= 794720:
cell_cycle_ (113.83/74.03)
|   |   |   |   |   |   |   |   |   |   |   start > 794720:
translation_ (55.24/28.85)
|   |   |   |   |   |   |   |   |   |   start > 808321
|   |   |   |   |   |   |   |   |   |   |   start <= 819430
|   |   |   |   |   |   |   |   |   |   |   |   start <= 814449
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
biological_process_ (49.16/28.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (83.93/52.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 814449
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 816875:
vesicle-mediated_transport_ (35.33/11.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 816875:
biological_process_ (39.5/18.15)
|   |   |   |   |   |   |   |   |   |   |   start > 819430
|   |   |   |   |   |   |   |   |   |   |   |   start <= 832470
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 827579:
cell_cycle_ (30.51/12.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 827579
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
829148: biological_process_ (12.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
829148: transcription_ (10.44)
|   |   |   |   |   |   |   |   |   |   |   |   start > 832470
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 848596
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
848068: biological_process_ (108.16/82.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
848068: RNA_metabolic_process_ (32.38/13.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 848596:
biological_process_ (53.62/32.77)
|   |   |   |   |   |   |   |   start > 858134
|   |   |   |   |   |   |   |   |   start <= 887229
|   |   |   |   |   |   |   |   |   |   start <= 859343:
cellular_homeostasis_ (19.05)
|   |   |   |   |   |   |   |   |   |   start > 859343
|   |   |   |   |   |   |   |   |   |   |   start <= 862051:
translation_ (46.7/19.62)
|   |   |   |   |   |   |   |   |   |   |   start > 862051
|   |   |   |   |   |   |   |   |   |   |   |   start <= 868221:
cytoskeleton_organization_and_biogenesis_ (39.39/16.84)
|   |   |   |   |   |   |   |   |   |   |   |   start > 868221:
translation_ (60.48/36.22)
|   |   |   |   |   |   |   |   |   start > 887229
|   |   |   |   |   |   |   |   |   |   start <= 907326
|   |   |   |   |   |   |   |   |   |   |   start <= 895031:
transcription_ (47.22/29.41)
|   |   |   |   |   |   |   |   |   |   |   start > 895031:
protein_modification_process_ (31.58/14.85)
|   |   |   |   |   |   |   |   |   |   start > 907326:
transcription_ (122.96/79.93)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 802219
|   |   |   |   |   |   |   |   |   start <= 741597
|   |   |   |   |   |   |   |   |   |   start <= 734135
|   |   |   |   |   |   |   |   |   |   |   start <= 715376:
vesicle-mediated_transport_ (36.07/21.1)
|   |   |   |   |   |   |   |   |   |   |   start > 715376:
protein_modification_process_ (57.16/34.81)
|   |   |   |   |   |   |   |   |   |   start > 734135:
organelle_organization_and_biogenesis_ (65.27/25.89)
|   |   |   |   |   |   |   |   |   start > 741597
|   |   |   |   |   |   |   |   |   |   start <= 781420
|   |   |   |   |   |   |   |   |   |   |   start <= 767968
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 751628:
response_to_stress_ (55.6/31.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 751628:
carbohydrate_metabolic_process_ (60.54/42.59)
|   |   |   |   |   |   |   |   |   |   |   start > 767968:
sporulation_ (39.48/17.09)
|   |   |   |   |   |   |   |   |   |   start > 781420
|   |   |   |   |   |   |   |   |   |   |   start <= 794720
|   |   |   |   |   |   |   |   |   |   |   |   start <= 790325:
cytokinesis_ (36.07/17.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 790325:
biological_process_ (37.09)
|   |   |   |   |   |   |   |   |   |   |   start > 794720:
transport_ (39.58/16.58)
|   |   |   |   |   |   |   |   start > 802219
|   |   |   |   |   |   |   |   |   start <= 856314
|   |   |   |   |   |   |   |   |   |   start <= 831510
|   |   |   |   |   |   |   |   |   |   |   start <= 821292
|   |   |   |   |   |   |   |   |   |   |   |   start <= 814449:
translation_ (80.58/31.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 814449:
conjugation_ (33.99/12.64)
|   |   |   |   |   |   |   |   |   |   |   start > 821292
|   |   |   |   |   |   |   |   |   |   |   |   start <= 829148:
transcription_ (13.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 829148:
response_to_stress_ (29.27/9.86)
|   |   |   |   |   |   |   |   |   |   start > 831510
|   |   |   |   |   |   |   |   |   |   |   start <= 851225:
biological_process_ (106.81/50.49)
|   |   |   |   |   |   |   |   |   |   |   start > 851225:
conjugation_ (44.79/29.66)
|   |   |   |   |   |   |   |   |   start > 856314
|   |   |   |   |   |   |   |   |   |   start <= 917567
|   |   |   |   |   |   |   |   |   |   |   start <= 862051:
organelle_organization_and_biogenesis_ (16.69)
|   |   |   |   |   |   |   |   |   |   |   start > 862051:
DNA_metabolic_process_ (154.31/100.88)
|   |   |   |   |   |   |   |   |   |   start > 917567:
RNA_metabolic_process_ (65.01/46.87)
|   |   |   |   |   |   |   start > 930353
|   |   |   |   |   |   |   |   start <= 955129
|   |   |   |   |   |   |   |   |   start <= 935888
|   |   |   |   |   |   |   |   |   |   strand = W:
RNA_metabolic_process_ (45.83/21.97)
|   |   |   |   |   |   |   |   |   |   strand = C:
vitamin_metabolic_process_ (17.03)
|   |   |   |   |   |   |   |   |   start > 935888
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 946803:
translation_ (51.78/17.87)
|   |   |   |   |   |   |   |   |   |   |   start > 946803: transport_
(97.86/62.83)
|   |   |   |   |   |   |   |   |   |   strand = C
```

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|   |   |   |   |   |   |   |   |   |   start <= 943416: transport_
(41.09/25.17)
|   |   |   |   |   |   |   |   |   |   start > 943416:
RNA_metabolic_process_ (48.56/11.4)
|   |   |   |   |   |   |   start > 955129:
protein_modification_process_ (42.79/21.27)
|   |   |   |   |   start > 956009
|   |   |   |   |   |   start <= 1052224
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 1005671
|   |   |   |   |   |   |   |   |   start <= 995530:
biological_process_ (74.73/29.85)
|   |   |   |   |   |   |   |   |   start > 995530
|   |   |   |   |   |   |   |   |   |   start <= 998860:
organelle_organization_and_biogenesis_ (34.56/13.73)
|   |   |   |   |   |   |   |   |   |   start > 998860: translation_
(31.32/11.31)
|   |   |   |   |   |   |   |   start > 1005671
|   |   |   |   |   |   |   |   |   start <= 1035991
|   |   |   |   |   |   |   |   |   |   start <= 1024751
|   |   |   |   |   |   |   |   |   |   |   start <= 1010172:
meiosis_ (18.32/8.52)
|   |   |   |   |   |   |   |   |   |   |   start > 1010172
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1015698:
biological_process_ (9.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1015698:
DNA_metabolic_process_ (23.93/10.63)
|   |   |   |   |   |   |   |   |   |   start > 1024751
|   |   |   |   |   |   |   |   |   |   |   start <= 1032432:
meiosis_ (32.49/13.14)
|   |   |   |   |   |   |   |   |   |   |   start > 1032432:
carbohydrate_metabolic_process_ (17.37)
|   |   |   |   |   |   |   |   |   start > 1035991
|   |   |   |   |   |   |   |   |   |   distance <= 2345:
DNA_metabolic_process_ (18.17/2.03)
|   |   |   |   |   |   |   |   |   |   distance > 2345:
biological_process_ (14.68)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 974239
|   |   |   |   |   |   |   |   |   start <= 965109
|   |   |   |   |   |   |   |   |   |   start <= 960610:
biological_process_ (42.16)
|   |   |   |   |   |   |   |   |   |   start > 960610:
amino_acid_and_derivative_metabolic_process_ (16.16)
|   |   |   |   |   |   |   |   |   start > 965109
|   |   |   |   |   |   |   |   |   |   start <= 967818:
carbohydrate_metabolic_process_ (12.64)
|   |   |   |   |   |   |   |   |   |   start > 967818:
response_to_stress_ (51.39/15.38)
|   |   |   |   |   |   |   |   start > 974239
|   |   |   |   |   |   |   |   |   start <= 998860
|   |   |   |   |   |   |   |   |   |   start <= 981051:
cell_wall_organization_and_biogenesis_ (81.54/47.53)
|   |   |   |   |   |   |   |   |   |   start > 981051
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 995530: 
DNA_metabolic_process_ (25.05)
|   |   |   |   |   |   |   |   |   |   |   start > 995530: vesicle-
mediated_transport_ (16.94)
|   |   |   |   |   |   |   |   |   start > 998860
|   |   |   |   |   |   |   |   |   |   start <= 1037191
|   |   |   |   |   |   |   |   |   |   |   start <= 1013639
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1005671: 
biological_process_ (34.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1005671: 
transport_ (10.69)
|   |   |   |   |   |   |   |   |   |   |   start > 1013639
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1032432
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1024751
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <= 
1019364: signal_transduction_ (24.0/8.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start > 
1019364: biological_process_ (42.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1024751
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <= 
1030045: protein_modification_process_ (55.91/34.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start > 
1030045: signal_transduction_ (15.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1032432: 
biological_process_ (25.61)
|   |   |   |   |   |   |   |   |   |   start > 1037191
|   |   |   |   |   |   |   |   |   |   |   start <= 1039724: 
DNA_metabolic_process_ (27.9/10.05)
|   |   |   |   |   |   |   |   |   |   |   start > 1039724: 
cell_wall_organization_and_biogenesis_ (41.49/25.19)
|   |   |   |   |   |   start > 1052224
|   |   |   |   |   |   |   start <= 1071382
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 1059623: 
organelle_organization_and_biogenesis_ (51.82/29.19)
|   |   |   |   |   |   |   |   |   start > 1059623: 
RNA_metabolic_process_ (60.23/37.98)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 1056547: 
DNA_metabolic_process_ (45.68/22.39)
|   |   |   |   |   |   |   |   |   start > 1056547: 
ribosome_biogenesis_and_assembly_ (96.89/71.39)
|   |   |   |   |   |   |   start > 1071382
|   |   |   |   |   |   |   |   start <= 1105824
|   |   |   |   |   |   |   |   |   start <= 1075167
|   |   |   |   |   |   |   |   |   |   start <= 1073484: 
biological_process_ (35.76)
|   |   |   |   |   |   |   |   |   |   start > 1073484: 
protein_catabolic_process_ (18.48)
|   |   |   |   |   |   |   |   |   start > 1075167
|   |   |   |   |   |   |   |   |   |   start <= 1092508
|   |   |   |   |   |   |   |   |   |   |   start <= 1080195: 
cell_budding_ (62.49/43.62)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 1080195:
DNA_metabolic_process_ (106.5/54.14)
|   |   |   |   |   |   |   |   |   |   start > 1092508:
biological_process_ (77.19/35.14)
|   |   |   |   |   |   |   |   start > 1105824
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 1117121
|   |   |   |   |   |   |   |   |   |   |   start <= 1112290:
translation_ (40.53/19.71)
|   |   |   |   |   |   |   |   |   |   |   start > 1112290:
cell_cycle_ (13.53)
|   |   |   |   |   |   |   |   |   |   start > 1117121:
protein_catabolic_process_ (18.22)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 1114024:
cell_cycle_ (57.41/33.72)
|   |   |   |   |   |   |   |   |   |   start > 1114024
|   |   |   |   |   |   |   |   |   |   |   distance <= 3583:
cytokinesis_ (43.51/28.83)
|   |   |   |   |   |   |   |   |   |   |   distance > 3583:
biological_process_ (23.43/11.92)
|   |   start > 1127867
|   |   |   strand = W
|   |   |   |   distance <= 7637
|   |   |   |   |   start <= 1414567
|   |   |   |   |   |   start <= 1183292
|   |   |   |   |   |   |   start <= 1129583:
protein_modification_process_ (20.28)
|   |   |   |   |   |   |   start > 1129583
|   |   |   |   |   |   |   |   start <= 1175823
|   |   |   |   |   |   |   |   |   start <= 1145086
|   |   |   |   |   |   |   |   |   |   distance <= 3358:
biological_process_ (28.79/1.38)
|   |   |   |   |   |   |   |   |   |   distance > 3358:
DNA_metabolic_process_ (26.61/13.35)
|   |   |   |   |   |   |   |   |   start > 1145086: translation_
(27.66)
|   |   |   |   |   |   |   |   start > 1175823
|   |   |   |   |   |   |   |   |   start <= 1178659:
cell_wall_organization_and_biogenesis_ (14.37)
|   |   |   |   |   |   |   |   |   start > 1178659:
response_to_stress_ (21.1/9.55)
|   |   |   |   |   |   start > 1183292
|   |   |   |   |   |   |   start <= 1259893
|   |   |   |   |   |   |   |   start <= 1228603
|   |   |   |   |   |   |   |   |   start <= 1206375: vesicle-
mediated_transport_ (83.86/57.06)
|   |   |   |   |   |   |   |   |   start > 1206375:
biological_process_ (107.91/56.57)
|   |   |   |   |   |   |   |   start > 1228603
|   |   |   |   |   |   |   |   |   start <= 1246076
|   |   |   |   |   |   |   |   |   |   start <= 1234210:
pseudohyphal_growth_ (43.07/17.5)
|   |   |   |   |   |   |   |   |   |   start > 1234210
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 1236550:
DNA_metabolic_process_ (10.02)
|   |   |   |   |   |   |   |   |   |   |   start > 1236550:
translation_ (56.53/31.85)
|   |   |   |   |   |   |   |   |   start > 1246076
|   |   |   |   |   |   |   |   |   |   start <= 1252529
|   |   |   |   |   |   |   |   |   |   |   start <= 1250178:
vesicle-mediated_transport_ (22.09)
|   |   |   |   |   |   |   |   |   |   |   start > 1250178:
cell_cycle_ (34.38/16.51)
|   |   |   |   |   |   |   |   |   |   start > 1252529:
organelle_organization_and_biogenesis_ (44.22/19.44)
|   |   |   |   |   |   |   start > 1259893
|   |   |   |   |   |   |   |   start <= 1362870
|   |   |   |   |   |   |   |   |   start <= 1328775
|   |   |   |   |   |   |   |   |   |   start <= 1294685
|   |   |   |   |   |   |   |   |   |   |   start <= 1289398
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1271055:
protein_catabolic_process_ (80.68/49.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1271055:
biological_process_ (65.31/41.55)
|   |   |   |   |   |   |   |   |   |   |   start > 1289398:
ribosome_biogenesis_and_assembly_ (20.98)
|   |   |   |   |   |   |   |   |   |   start > 1294685
|   |   |   |   |   |   |   |   |   |   |   start <= 1306259
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1301608:
cell_cycle_ (27.8/9.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1301608
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
2320: DNA_metabolic_process_ (12.31/4.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 2320:
cell_wall_organization_and_biogenesis_ (17.57/6.3)
|   |   |   |   |   |   |   |   |   |   |   start > 1306259:
pseudohyphal_growth_ (50.92/35.47)
|   |   |   |   |   |   |   |   |   start > 1328775
|   |   |   |   |   |   |   |   |   |   start <= 1345054
|   |   |   |   |   |   |   |   |   |   |   start <= 1338266:
protein_modification_process_ (55.63/28.02)
|   |   |   |   |   |   |   |   |   |   |   start > 1338266
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1339668:
cell_cycle_ (32.59/14.96)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1339668:
meiosis_ (10.68)
|   |   |   |   |   |   |   |   |   |   start > 1345054:
biological_process_ (94.86/70.1)
|   |   |   |   |   |   |   |   start > 1362870
|   |   |   |   |   |   |   |   |   start <= 1383803: vesicle-
mediated_transport_ (43.48/25.56)
|   |   |   |   |   |   |   |   |   start > 1383803
|   |   |   |   |   |   |   |   |   |   start <= 1401762
|   |   |   |   |   |   |   |   |   |   |   start <= 1385168:
signal_transduction_ (35.5/15.51)
|   |   |   |   |   |   |   |   |   |   |   start > 1385168:
translation_ (79.45/51.98)
```

```
|   |   |   |   |   |   |   |   |   |   start > 1401762:
ribosome_biogenesis_and_assembly_ (118.95/70.45)
|   |   |   |   |   start > 1414567
|   |   |   |   |   |   start <= 1469392
|   |   |   |   |   |   |   start <= 1436209
|   |   |   |   |   |   |   |   start <= 1422755:
protein_modification_process_ (37.64/22.58)
|   |   |   |   |   |   |   |   start > 1422755:
DNA_metabolic_process_ (44.46/25.75)
|   |   |   |   |   |   |   start > 1436209
|   |   |   |   |   |   |   |   start <= 1441142: translation_
(14.05)
|   |   |   |   |   |   |   |   start > 1441142:
protein_modification_process_ (36.33/19.67)
|   |   |   |   |   |   start > 1469392
|   |   |   |   |   |   |   start <= 1477231
|   |   |   |   |   |   |   |   start <= 1470009:
biological_process_ (18.65)
|   |   |   |   |   |   |   |   start > 1470009
|   |   |   |   |   |   |   |   |   start <= 1473421: translation_
(26.23/9.75)
|   |   |   |   |   |   |   |   |   start > 1473421:
organelle_organization_and_biogenesis_ (15.33)
|   |   |   |   |   |   |   start > 1477231
|   |   |   |   |   |   |   |   start <= 1490588:
biological_process_ (71.16)
|   |   |   |   |   |   |   |   start > 1490588
|   |   |   |   |   |   |   |   |   start <= 1494578:
cell_wall_organization_and_biogenesis_ (26.9/12.84)
|   |   |   |   |   |   |   |   |   start > 1494578:
biological_process_ (70.83/13.63)
|   |   |   |   distance > 7637
|   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   start <= 1417391: signal_transduction_
(15.12/10.24)
|   |   |   |   |   |   start > 1417391: biological_process_
(30.87/18.66)
|   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   start <= 1322197
|   |   |   |   |   |   |   start <= 1141162: DNA_metabolic_process_
(8.12/3.95)
|   |   |   |   |   |   |   start > 1141162: translation_
(24.65/14.27)
|   |   |   |   |   |   start > 1322197: cellular_homeostasis_
(17.81/5.93)
|   |   |   strand = C
|   |   |   |   start <= 1427199
|   |   |   |   |   start <= 1252529
|   |   |   |   |   |   start <= 1206375
|   |   |   |   |   |   |   start <= 1190052
|   |   |   |   |   |   |   |   start <= 1153620
|   |   |   |   |   |   |   |   |   start <= 1150514
|   |   |   |   |   |   |   |   |   |   start <= 1149460:
biological_process_ (24.08)
```

```
|   |   |   |   |   |   |   |   |   |   start > 1149460:
organelle_organization_and_biogenesis_ (26.22/11.89)
|   |   |   |   |   |   |   |   |   start > 1150514: translation_
(27.75)
|   |   |   |   |   |   |   |   start > 1153620
|   |   |   |   |   |   |   |   |   start <= 1169172: transport_
(45.75/20.33)
|   |   |   |   |   |   |   |   |   start > 1169172:
biological_process_ (52.05)
|   |   |   |   |   |   |   start > 1190052
|   |   |   |   |   |   |   |   start <= 1194877:
DNA_metabolic_process_ (9.66)
|   |   |   |   |   |   |   |   start > 1194877
|   |   |   |   |   |   |   |   |   start <= 1199175:
ribosome_biogenesis_and_assembly_ (38.03/15.22)
|   |   |   |   |   |   |   |   |   start > 1199175: cell_cycle_
(38.24/14.31)
|   |   |   |   |   |   start > 1206375
|   |   |   |   |   |   |   start <= 1219405: biological_process_
(56.33/16.68)
|   |   |   |   |   |   |   start > 1219405
|   |   |   |   |   |   |   |   start <= 1222751: transport_ (13.04)
|   |   |   |   |   |   |   |   start > 1222751
|   |   |   |   |   |   |   |   |   start <= 1226814
|   |   |   |   |   |   |   |   |   |   start <= 1224749:
biological_process_ (14.88)
|   |   |   |   |   |   |   |   |   |   start > 1224749:
cellular_respiration_ (18.94/8.69)
|   |   |   |   |   |   |   |   |   start > 1226814:
biological_process_ (83.95/34.43)
|   |   |   |   |   start > 1252529
|   |   |   |   |   |   start <= 1356057
|   |   |   |   |   |   |   start <= 1345054
|   |   |   |   |   |   |   |   start <= 1296678
|   |   |   |   |   |   |   |   |   start <= 1289398
|   |   |   |   |   |   |   |   |   |   start <= 1257071
|   |   |   |   |   |   |   |   |   |   |   start <= 1256839:
protein_modification_process_ (25.96)
|   |   |   |   |   |   |   |   |   |   |   start > 1256839:
translation_ (17.49)
|   |   |   |   |   |   |   |   |   |   start > 1257071
|   |   |   |   |   |   |   |   |   |   |   start <= 1261673:
biological_process_ (24.51)
|   |   |   |   |   |   |   |   |   |   |   start > 1261673:
transcription_ (94.59/61.65)
|   |   |   |   |   |   |   |   |   start > 1289398:
protein_modification_process_ (51.36/18.28)
|   |   |   |   |   |   |   |   start > 1296678
|   |   |   |   |   |   |   |   |   start <= 1319267
|   |   |   |   |   |   |   |   |   |   start <= 1306259:
biological_process_ (21.95)
|   |   |   |   |   |   |   |   |   |   start > 1306259:
signal_transduction_ (25.25/8.0)
```

```
|   |   |   |   |   |   |   |   |   start > 1319267: 
biological_process_ (79.49/43.18)
|   |   |   |   |   |   |   start > 1345054
|   |   |   |   |   |   |   |   start <= 1350282: 
DNA_metabolic_process_ (13.01)
|   |   |   |   |   |   |   |   start > 1350282: translation_ 
(36.28)
|   |   |   |   |   |   start > 1356057
|   |   |   |   |   |   |   start <= 1365654
|   |   |   |   |   |   |   |   distance <= 3235: 
response_to_stress_ (37.17/15.8)
|   |   |   |   |   |   |   |   distance > 3235: meiosis_ 
(10.12/3.73)
|   |   |   |   |   |   |   start > 1365654
|   |   |   |   |   |   |   |   start <= 1412365
|   |   |   |   |   |   |   |   |   start <= 1388864: 
biological_process_ (70.46/18.43)
|   |   |   |   |   |   |   |   |   start > 1388864
|   |   |   |   |   |   |   |   |   |   start <= 1403314: vesicle-
mediated_transport_ (35.8/21.81)
|   |   |   |   |   |   |   |   |   |   start > 1403314: 
biological_process_ (49.25/20.18)
|   |   |   |   |   |   |   |   start > 1412365
|   |   |   |   |   |   |   |   |   start <= 1420242: 
organelle_organization_and_biogenesis_ (34.06/15.08)
|   |   |   |   |   |   |   |   |   start > 1420242: 
biological_process_ (44.26/18.32)
|   |   |   |   start > 1427199
|   |   |   |   |   start <= 1488982
|   |   |   |   |   |   start <= 1465778
|   |   |   |   |   |   |   start <= 1447822
|   |   |   |   |   |   |   |   start <= 1431004
|   |   |   |   |   |   |   |   |   start <= 1428972: 
cellular_respiration_ (47.86/30.5)
|   |   |   |   |   |   |   |   |   start > 1428972: 
cytoskeleton_organization_and_biogenesis_ (25.36)
|   |   |   |   |   |   |   |   start > 1431004
|   |   |   |   |   |   |   |   |   start <= 1436922
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: 
cell_wall_organization_and_biogenesis_ (9.05/2.65)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (21.25/9.72)
|   |   |   |   |   |   |   |   |   start > 1436922: 
DNA_metabolic_process_ (78.29/55.53)
|   |   |   |   |   |   |   start > 1447822
|   |   |   |   |   |   |   |   start <= 1455858: 
lipid_metabolic_process_ (56.55/32.8)
|   |   |   |   |   |   |   |   start > 1455858
|   |   |   |   |   |   |   |   |   start <= 1461546: 
biological_process_ (46.05)
|   |   |   |   |   |   |   |   |   start > 1461546: translation_ 
(20.31/7.54)
|   |   |   |   |   |   start > 1465778
|   |   |   |   |   |   |   start <= 1487030
```

```
|   |   |   |   |   |   |   |   start <= 1483395: sporulation_
(84.43/43.11)
|   |   |   |   |   |   |   |   start > 1483395:
cell_wall_organization_and_biogenesis_ (102.91/52.88)
|   |   |   |   |   |   |   start > 1487030: transport_
(31.85/13.41)
|   |   |   |   |   start > 1488982
|   |   |   |   |   |   start <= 1496540
|   |   |   |   |   |   |   start <= 1494578: RNA_metabolic_process_
(35.77/18.53)
|   |   |   |   |   |   |   start > 1494578: electron_transport_
(39.38/19.65)
|   |   |   |   |   |   start > 1496540: biological_process_
(87.06/43.89)
```

Decision Tree Generated for Chromosome Five:
For Cellular Component

```
|   start <= 166884
|   |   start <= 45721
|   |   |   strand = C
|   |   |   |   start <= 13720: cellular_component_ (64.73)
|   |   |   |   start > 13720
|   |   |   |   |   start <= 39537
|   |   |   |   |   |   start <= 23231: plasma_membrane_ (17.08)
|   |   |   |   |   |   start > 23231
|   |   |   |   |   |   |   start <= 31239
|   |   |   |   |   |   |   |   start <= 27657: mitochondrion_
(15.77)
|   |   |   |   |   |   |   |   start > 27657:
endoplasmic_reticulum_ (13.01)
|   |   |   |   |   |   |   start > 31239: mitochondrion_
(42.49/14.18)
|   |   |   |   |   start > 39537
|   |   |   |   |   |   start <= 43252
|   |   |   |   |   |   |   start <= 41953: vacuole_ (11.92)
|   |   |   |   |   |   |   start > 41953: mitochondrial_envelope_
(15.44)
|   |   |   |   |   |   start > 43252: cellular_component_ (24.24)
|   |   |   strand = W
|   |   |   |   start <= 19589
|   |   |   |   |   start <= 16355
|   |   |   |   |   |   start <= 13720: cellular_component_ (17.33)
|   |   |   |   |   |   start > 13720: cytoplasm_ (17.66)
|   |   |   |   |   start > 16355: cellular_component_ (30.29)
|   |   |   |   start > 19589
|   |   |   |   |   start <= 27657
|   |   |   |   |   |   start <= 26776
|   |   |   |   |   |   |   Neigh_GO_aspect = C: nucleus_
(11.11/2.12)
|   |   |   |   |   |   |   Neigh_GO_aspect = F: cytoplasm_
(7.9/2.82)
|   |   |   |   |   |   |   Neigh_GO_aspect = P: cytoplasm_
(13.2/5.45)
```

```
|   |   |   |   |   |   start > 26776: cytoplasmic_membrane-
bound_vesicle_ (19.46)
|   |   |   |   |   start > 27657
|   |   |   |   |   |   start <= 34407: cellular_component_ (10.63)
|   |   |   |   |   |   start > 34407: cytoplasm_ (28.78/13.86)
|   |   start > 45721
|   |   |   start <= 146754
|   |   |   |   start <= 85676
|   |   |   |   |   start <= 61699
|   |   |   |   |   |   start <= 56102
|   |   |   |   |   |   |   start <= 52320
|   |   |   |   |   |   |   |   strand = C: nucleolus_ (31.98)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(7.74/2.89)
|   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(12.93/3.68)
|   |   |   |   |   |   |   start > 52320
|   |   |   |   |   |   |   |   start <= 53218: ribosome_ (16.16)
|   |   |   |   |   |   |   |   start > 53218: cytoplasm_ (13.68)
|   |   |   |   |   |   start > 56102
|   |   |   |   |   |   |   start <= 60851
|   |   |   |   |   |   |   |   start <= 56571: mitochondrion_
(15.81)
|   |   |   |   |   |   |   |   start > 56571
|   |   |   |   |   |   |   |   |   start <= 58378: vacuole_
(32.09/14.31)
|   |   |   |   |   |   |   |   |   start > 58378: mitochondrion_
(12.89)
|   |   |   |   |   |   |   start > 60851: nucleolus_ (20.65)
|   |   |   |   |   start > 61699
|   |   |   |   |   |   start <= 65167
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 61960: cytoplasm_ (9.72)
|   |   |   |   |   |   |   |   start > 61960: cytoplasmic_membrane-
bound_vesicle_ (18.72)
|   |   |   |   |   |   |   strand = W: cellular_component_ (16.74)
|   |   |   |   |   |   start > 65167
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 82603
|   |   |   |   |   |   |   |   |   start <= 73771
|   |   |   |   |   |   |   |   |   |   start <= 66797
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
mitochondrion_ (6.85/1.66)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
mitochondrion_ (7.96/2.24)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
ribosome_ (9.9/3.36)
|   |   |   |   |   |   |   |   |   |   start > 66797: cytoplasm_
(12.18)
|   |   |   |   |   |   |   |   |   start > 73771: mitochondrion_
(35.54)
|   |   |   |   |   |   |   |   start > 82603
```

```
|   |   |   |   |   |   |   |   |   start <= 84552: Golgi_apparatus_
(17.71)
|   |   |   |   |   |   |   |   |   start > 84552:
cellular_component_ (13.35)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 78053
|   |   |   |   |   |   |   |   |   start <= 70478
|   |   |   |   |   |   |   |   |   |   start <= 69757: nucleus_
(17.56)
|   |   |   |   |   |   |   |   |   |   start > 69757
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
ribosome_ (9.54/4.07)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
endoplasmic_reticulum_ (16.96/4.77)
|   |   |   |   |   |   |   |   |   start > 70478
|   |   |   |   |   |   |   |   |   |   start <= 75944
|   |   |   |   |   |   |   |   |   |   |   start <= 73771:
Golgi_apparatus_ (11.83)
|   |   |   |   |   |   |   |   |   |   |   start > 73771:
cellular_component_ (9.8)
|   |   |   |   |   |   |   |   |   |   start > 75944:
membrane_fraction_ (16.04)
|   |   |   |   |   |   |   |   start > 78053
|   |   |   |   |   |   |   |   |   start <= 82603: cytoplasm_
(32.82/14.32)
|   |   |   |   |   |   |   |   |   start > 82603
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_
(19.77/9.72)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   distance <= 300:
cytoplasm_ (6.76/1.92)
|   |   |   |   |   |   |   |   |   |   |   distance > 300:
ribosome_ (12.5/5.67)
|   |   |   |   start > 85676
|   |   |   |   |   start <= 126218
|   |   |   |   |   |   start <= 121471
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 111421
|   |   |   |   |   |   |   |   |   start <= 107260
|   |   |   |   |   |   |   |   |   |   start <= 101943:
cellular_component_ (9.79)
|   |   |   |   |   |   |   |   |   |   start > 101943
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (24.46/9.96)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasm_ (14.46/5.22)
|   |   |   |   |   |   |   |   |   start > 107260:
cellular_component_ (16.67)
|   |   |   |   |   |   |   |   start > 111421
|   |   |   |   |   |   |   |   |   start <= 118035: nucleolus_
(10.4)
|   |   |   |   |   |   |   |   |   start > 118035
|   |   |   |   |   |   |   |   |   |   start <= 120299: cytoplasm_
(12.17)
```

```
|   |   |   |   |   |   |   |   |   |   start > 120299
|   |   |   |   |   |   |   |   |   |   |   distance <= 903:
cytoplasm_ (2.14/0.02)
|   |   |   |   |   |   |   |   |   |   |   distance > 903: nucleus_
(14.28/5.19)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 100769
|   |   |   |   |   |   |   |   |   start <= 100133
|   |   |   |   |   |   |   |   |   |   start <= 86937
|   |   |   |   |   |   |   |   |   |   |   start <= 86604:
cytoplasm_ (13.91)
|   |   |   |   |   |   |   |   |   |   |   start > 86604
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cytoplasm_ (14.94/6.01)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (7.7/1.9)
|   |   |   |   |   |   |   |   |   |   start > 86937
|   |   |   |   |   |   |   |   |   |   |   start <= 94644:
mitochondrion_ (13.48)
|   |   |   |   |   |   |   |   |   |   |   start > 94644:
cytoplasm_ (22.81)
|   |   |   |   |   |   |   |   |   start > 100133: membrane_
(22.65/9.99)
|   |   |   |   |   |   |   |   start > 100769
|   |   |   |   |   |   |   |   |   start <= 101943: nucleolus_
(23.08)
|   |   |   |   |   |   |   |   |   start > 101943
|   |   |   |   |   |   |   |   |   |   start <= 118035
|   |   |   |   |   |   |   |   |   |   |   start <= 111421
|   |   |   |   |   |   |   |   |   |   |   |   start <= 107260:
mitochondrion_ (26.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 107260:
cytoplasmic_membrane-bound_vesicle_ (16.16)
|   |   |   |   |   |   |   |   |   |   |   start > 111421
|   |   |   |   |   |   |   |   |   |   |   |   start <= 116167:
cytoplasm_ (11.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 116167:
mitochondrion_ (16.17)
|   |   |   |   |   |   |   |   |   |   start > 118035: nucleus_
(11.6)
|   |   |   |   |   |   start > 121471
|   |   |   |   |   |   |   start <= 122929: membrane_ (11.29)
|   |   |   |   |   |   |   start > 122929: cellular_component_
(26.22)
|   |   |   |   |   start > 126218
|   |   |   |   |   |   start <= 133120
|   |   |   |   |   |   |   start <= 128825
|   |   |   |   |   |   |   |   start <= 126629: cytoplasm_ (19.12)
|   |   |   |   |   |   |   |   start > 126629: vacuole_ (20.11)
|   |   |   |   |   |   |   start > 128825: cytoplasm_ (37.35)
|   |   |   |   |   |   start > 133120
|   |   |   |   |   |   |   start <= 135497: mitochondrion_ (11.6)
|   |   |   |   |   |   |   start > 135497
|   |   |   |   |   |   |   |   start <= 141891
```

```
|   |   |   |   |   |   |   |   |   start <= 138666: cytoplasm_
(11.83)
|   |   |   |   |   |   |   |   |   start > 138666: nucleus_
(35.89/11.46)
|   |   |   |   |   |   |   |   start > 141891
|   |   |   |   |   |   |   |   |   start <= 144326: mitochondrion_
(14.9)
|   |   |   |   |   |   |   |   |   start > 144326: cytoplasm_
(15.62)
|   |   |   start > 146754
|   |   |   |   start <= 162722
|   |   |   |   |   start <= 150977
|   |   |   |   |   |   strand = C: endoplasmic_reticulum_ (24.6)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 146950: endoplasmic_reticulum_
(20.52)
|   |   |   |   |   |   |   start > 146950: cytoplasm_ (9.39)
|   |   |   |   |   start > 150977
|   |   |   |   |   |   strand = C: cytoplasm_ (36.93/13.11)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 160549
|   |   |   |   |   |   |   |   start <= 156802
|   |   |   |   |   |   |   |   |   start <= 153519:
Golgi_apparatus_ (16.17)
|   |   |   |   |   |   |   |   |   start > 153519: nucleolus_
(30.08/12.39)
|   |   |   |   |   |   |   |   start > 156802
|   |   |   |   |   |   |   |   |   start <= 159579:
endoplasmic_reticulum_ (30.22/10.46)
|   |   |   |   |   |   |   |   |   start > 159579
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
Golgi_apparatus_ (12.43/3.67)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: membrane_
(20.37/7.63)
|   |   |   |   |   |   |   start > 160549: nucleolus_ (34.97/13.32)
|   |   |   |   start > 162722
|   |   |   |   |   start <= 164526: cellular_component_ (8.95)
|   |   |   |   |   start > 164526
|   |   |   |   |   |   neigh_num <= 1: cytoplasm_ (16.76/7.41)
|   |   |   |   |   |   neigh_num > 1: ribosome_ (14.76/5.98)
|   start > 166884
|   |   start <= 385872
|   |   |   start <= 215062
|   |   |   |   start <= 198811
|   |   |   |   |   start <= 178840
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 172114
|   |   |   |   |   |   |   |   start <= 167585: nucleus_ (16.87)
|   |   |   |   |   |   |   |   start > 167585:
site_of_polarized_growth_ (17.79)
|   |   |   |   |   |   |   start > 172114: cellular_component_
(17.4)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 175247
```

```
|   |   |   |   |   |   |   |   start <= 173337:
endomembrane_system_ (14.97)
|   |   |   |   |   |   |   |   start > 173337: cell_wall_ (16.89)
|   |   |   |   |   |   |   start > 175247
|   |   |   |   |   |   |   |   start <= 177098: cytoplasm_ (16.89)
|   |   |   |   |   |   |   |   start > 177098: nucleus_ (27.98)
|   |   |   |   |   start > 178840
|   |   |   |   |   |   start <= 192623
|   |   |   |   |   |   |   start <= 191787
|   |   |   |   |   |   |   |   stop <= 183730: cellular_component_
(13.14)
|   |   |   |   |   |   |   |   stop > 183730
|   |   |   |   |   |   |   |   |   start <= 184699: mitochondrion_
(52.19/16.6)
|   |   |   |   |   |   |   |   |   start > 184699
|   |   |   |   |   |   |   |   |   |   start <= 188276:
microtubule_organizing_center_ (20.77)
|   |   |   |   |   |   |   |   |   |   start > 188276:
mitochondrion_ (13.35)
|   |   |   |   |   |   |   start > 191787: chromosome_ (23.84)
|   |   |   |   |   |   start > 192623
|   |   |   |   |   |   |   start <= 195167
|   |   |   |   |   |   |   |   start <= 194538:
endoplasmic_reticulum_ (72.08/25.55)
|   |   |   |   |   |   |   |   start > 194538: plasma_membrane_
(29.76/11.81)
|   |   |   |   |   |   |   start > 195167: cellular_component_
(36.84/11.58)
|   |   |   |   start > 198811
|   |   |   |   |   start <= 213436
|   |   |   |   |   |   start <= 208473
|   |   |   |   |   |   |   strand = C: endoplasmic_reticulum_
(13.0)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 202191: cytoplasm_ (28.77)
|   |   |   |   |   |   |   |   start > 202191
|   |   |   |   |   |   |   |   |   start <= 205250: ribosome_
(16.3)
|   |   |   |   |   |   |   |   |   start > 205250: cytoplasm_
(7.47)
|   |   |   |   |   |   start > 208473: nucleus_ (77.74/14.77)
|   |   |   |   |   start > 213436
|   |   |   |   |   |   start <= 214746: Golgi_apparatus_ (12.36)
|   |   |   |   |   |   start > 214746
|   |   |   |   |   |   |   distance <= 4514: cellular_bud_
(31.14/12.47)
|   |   |   |   |   |   |   distance > 4514:
site_of_polarized_growth_ (11.1/2.88)
|   |   |   start > 215062
|   |   |   |   start <= 330572
|   |   |   |   |   start <= 237118
|   |   |   |   |   |   start <= 221286: mitochondrion_ (55.62/27.1)
|   |   |   |   |   |   start > 221286
```

```
|   |   |   |   |   |   |   start <= 228251: nucleus_
(250.39/133.58)
|   |   |   |   |   |   |   start > 228251
|   |   |   |   |   |   |   |   start <= 229480: cellular_component_
(32.52)
|   |   |   |   |   |   |   |   start > 229480
|   |   |   |   |   |   |   |   |   strand = C: cytoplasm_ (25.31)
|   |   |   |   |   |   |   |   |   strand = W: nucleus_
(56.48/14.4)
|   |   |   |   |   start > 237118
|   |   |   |   |   |   start <= 239773
|   |   |   |   |   |   |   start <= 238015
|   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transport_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_
|   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   distance <= 4082:
endomembrane_system_ (3.75/1.09)
|   |   |   |   |   |   |   |   |   |   distance > 4082: membrane_
(2.43/0.79)
|   |   |   |   |   |   |   |   |   neigh_strand = C: membrane_
(4.76/1.67)
|   |   |   |   |   |   |   |   NeighGO_term = nucleus_: membrane_
(1.46/0.62)
|   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = molecular_function_:
membrane_ (8.32/3.3)
|   |   |   |   |   |   |   |   NeighGO_term = biological_process_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_component_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
endoplasmic_reticulum_ (7.08/1.77)
|   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: endomembrane_system_ (6.08/2.93)
|   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleolus_: membrane_
(0.0)
```

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|   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transcription_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
membrane_ (2.55/1.05)
|   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = translation_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: endoplasmic_reticulum_ (1.95/1.01)
|   |   |   |   |   |   |   |   NeighGO_term = electron_transport_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ribosome_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
endoplasmic_reticulum_ (2.19/0.83)
|   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: membrane_ (9.29/5.11)
|   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: endomembrane_system_
(2.64/0.42)
|   |   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
membrane_ (6.07/3.55)
|   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
membrane_ (1.91/0.65)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
endoplasmic_reticulum_ (8.61/3.52)
|   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_wall_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vacuole_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
membrane_ (0.0)
|   |   |   |   |   |   |   start > 238015: chromosome_ (15.11)
|   |   |   |   |   |   start > 239773
|   |   |   |   |   |   |   start <= 302325
|   |   |   |   |   |   |   |   start <= 279624
|   |   |   |   |   |   |   |   |   start <= 271124
|   |   |   |   |   |   |   |   |   |   start <= 254386
|   |   |   |   |   |   |   |   |   |   |   start <= 250285
|   |   |   |   |   |   |   |   |   |   |   |   start <= 241500:
nucleus_ (21.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 241500
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 246502:
cytoplasm_ (28.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 246502
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
248156: nucleus_ (15.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
248156: cytoplasm_ (10.53)
|   |   |   |   |   |   |   |   |   |   |   start > 250285
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (19.26)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 250717:
mitochondrion_ (16.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 250717:
nucleus_ (9.63)
|   |   |   |   |   |   |   |   |   |   start > 254386
|   |   |   |   |   |   |   |   |   |   |   start <= 265784
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 263697
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
259638
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
257957: cytoplasm_ (10.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
257957: mitochondrion_ (12.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
259638
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
261045: endoplasmic_reticulum_ (15.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
261045: cytoplasm_ (16.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 263697:
cellular_component_ (13.13)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (17.35)
|   |   |   |   |   |   |   |   |   |   |   start > 265784
|   |   |   |   |   |   |   |   |   |   |   |   start <= 270183
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 268112:
plasma_membrane_ (9.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 268112:
ribosome_ (8.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 270183:
cytoplasm_ (21.29/9.12)
|   |   |   |   |   |   |   |   |   start > 271124
|   |   |   |   |   |   |   |   |   |   start <= 272622
|   |   |   |   |   |   |   |   |   |   |   start <= 271766:
mitochondrion_ (20.68)
|   |   |   |   |   |   |   |   |   |   |   start > 271766:
cellular_component_ (17.25)
|   |   |   |   |   |   |   |   |   |   start > 272622
|   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (24.93)
|   |   |   |   |   |   |   |   |   |   |   strand = W: membrane_
(40.56)
|   |   |   |   |   |   |   |   start > 279624
|   |   |   |   |   |   |   |   |   start <= 292064
|   |   |   |   |   |   |   |   |   |   start <= 284220
|   |   |   |   |   |   |   |   |   |   |   start <= 280680
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleus_ (14.3/3.33)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (16.85/6.65)
|   |   |   |   |   |   |   |   |   |   |   start > 280680: nucleus_
(43.08)
|   |   |   |   |   |   |   |   |   |   start > 284220
|   |   |   |   |   |   |   |   |   |   |   start <= 290240
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 286912:
cellular_component_ (8.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 286912:
cytoplasm_ (12.71)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (9.61)
|   |   |   |   |   |   |   |   |   |   |   start > 290240
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 987:
cytoplasm_ (6.07/1.22)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 987:
nucleus_ (15.24/4.84)
|   |   |   |   |   |   |   |   |   start > 292064
|   |   |   |   |   |   |   |   |   |   start <= 295408
|   |   |   |   |   |   |   |   |   |   |   start <= 293048:
cytoplasm_ (13.9)
|   |   |   |   |   |   |   |   |   |   |   start > 293048:
mitochondrion_ (15.57)
|   |   |   |   |   |   |   |   |   |   start > 295408: cytoplasm_
(30.21)
|   |   |   |   |   |   |   start > 302325
|   |   |   |   |   |   |   |   start <= 307649
|   |   |   |   |   |   |   |   |   start <= 306319
|   |   |   |   |   |   |   |   |   |   start <= 302804:
endoplasmic_reticulum_ (12.34)
```

```
|   |   |   |   |   |   |   |   |   |   start > 302804:
mitochondrion_ (32.64)
|   |   |   |   |   |   |   |   |   start > 306319
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
membrane_ (9.83/6.54)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
endomembrane_system_ (20.32/10.84)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
endoplasmic_reticulum_ (13.81/8.01)
|   |   |   |   |   |   |   |   start > 307649
|   |   |   |   |   |   |   |   |   start <= 322682
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 312091:
cytoplasm_ (20.75)
|   |   |   |   |   |   |   |   |   |   |   start > 312091:
mitochondrion_ (51.14/11.05)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 318642:
cellular_component_ (16.41)
|   |   |   |   |   |   |   |   |   |   |   start > 318642
|   |   |   |   |   |   |   |   |   |   |   |   start <= 318916
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleus_ (6.11/2.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (25.4/8.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 318916
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 319959:
mitochondrion_ (16.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 319959
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
322208: nucleus_ (16.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
322208: cytoplasm_ (9.58)
|   |   |   |   |   |   |   |   |   start > 322682
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 325932:
nucleolus_ (19.18)
|   |   |   |   |   |   |   |   |   |   |   start > 325932
|   |   |   |   |   |   |   |   |   |   |   |   start <= 327027:
endoplasmic_reticulum_ (10.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 327027:
cellular_component_ (10.11)
|   |   |   |   |   |   |   |   |   |   strand = W: mitochondrion_
(31.31)
|   |   |   |   start > 330572
|   |   |   |   |   start <= 363096
|   |   |   |   |   |   start <= 349342
|   |   |   |   |   |   |   start <= 342851
|   |   |   |   |   |   |   |   start <= 332826:
endomembrane_system_ (38.36/24.78)
|   |   |   |   |   |   |   |   start > 332826
|   |   |   |   |   |   |   |   |   start <= 342163
|   |   |   |   |   |   |   |   |   |   start <= 337336: nucleus_
(49.6/17.95)
```

```
|   |   |   |   |   |   |   |   |   |   start > 337336: cytoplasm_
(16.99)
|   |   |   |   |   |   |   |   |   start > 342163: nucleus_ (9.87)
|   |   |   |   |   |   |   start > 342851
|   |   |   |   |   |   |   |   start <= 347608: membrane_fraction_
(19.09)
|   |   |   |   |   |   |   |   start > 347608: cellular_component_
(21.45)
|   |   |   |   |   |   start > 349342
|   |   |   |   |   |   |   start <= 351694
|   |   |   |   |   |   |   |   start <= 349976: chromosome_ (22.19)
|   |   |   |   |   |   |   |   start > 349976: membrane_ (11.56)
|   |   |   |   |   |   |   start > 351694
|   |   |   |   |   |   |   |   start <= 361790
|   |   |   |   |   |   |   |   |   strand = C: cytoplasm_ (36.15)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 355462: cytoplasm_
(16.82)
|   |   |   |   |   |   |   |   |   |   start > 355462:
endomembrane_system_ (37.97/21.55)
|   |   |   |   |   |   |   |   start > 361790: ribosome_ (12.35)
|   |   |   |   |   start > 363096
|   |   |   |   |   |   start <= 374541
|   |   |   |   |   |   |   start <= 366798: nucleus_ (70.69/29.44)
|   |   |   |   |   |   |   start > 366798
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   neigh_strand = W: nucleus_
(40.73/24.52)
|   |   |   |   |   |   |   |   |   neigh_strand = C: membrane_
(69.36/41.05)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: chromosome_
(6.61/2.6)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_component_ (15.53/5.81)
|   |   |   |   |   |   |   |   |   neigh_strand = C: chromosome_
(38.93/19.74)
|   |   |   |   |   |   start > 374541: nucleus_ (79.5/25.04)
|   |   start > 385872
|   |   |   start <= 467465
|   |   |   |   strand = C
|   |   |   |   |   start <= 410185
|   |   |   |   |   |   start <= 402371
|   |   |   |   |   |   |   start <= 393708
|   |   |   |   |   |   |   |   start <= 390048: Golgi_apparatus_
(16.04)
|   |   |   |   |   |   |   |   start > 390048
|   |   |   |   |   |   |   |   |   neigh_strand = W: cellular_bud_
(15.58/5.4)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
site_of_polarized_growth_ (14.4/3.54)
|   |   |   |   |   |   |   start > 393708
```

```
|   |   |   |   |   |   |   |   start <= 396765: cellular_component_
(32.73)
|   |   |   |   |   |   |   |   start > 396765
|   |   |   |   |   |   |   |   |   start <= 399051:
plasma_membrane_ (10.03)
|   |   |   |   |   |   |   |   |   start > 399051: vacuole_ (11.6)
|   |   |   |   |   |   start > 402371
|   |   |   |   |   |   |   start <= 404809: cytoplasmic_membrane-
bound_vesicle_ (47.96/26.12)
|   |   |   |   |   |   |   start > 404809: cellular_bud_
(43.91/14.89)
|   |   |   |   |   start > 410185
|   |   |   |   |   |   start <= 456314
|   |   |   |   |   |   |   start <= 424694
|   |   |   |   |   |   |   |   start <= 417277: nucleus_ (20.71)
|   |   |   |   |   |   |   |   start > 417277: cellular_component_
(15.05)
|   |   |   |   |   |   |   start > 424694
|   |   |   |   |   |   |   |   start <= 435820
|   |   |   |   |   |   |   |   |   start <= 434608
|   |   |   |   |   |   |   |   |   |   start <= 430445: cytoplasm_
(16.11)
|   |   |   |   |   |   |   |   |   |   start > 430445
|   |   |   |   |   |   |   |   |   |   |   start <= 432491:
nucleolus_ (13.93)
|   |   |   |   |   |   |   |   |   |   |   start > 432491:
cytoplasm_ (8.33)
|   |   |   |   |   |   |   |   |   start > 434608: mitochondrion_
(6.67)
|   |   |   |   |   |   |   |   start > 435820
|   |   |   |   |   |   |   |   |   start <= 453454
|   |   |   |   |   |   |   |   |   |   start <= 441983
|   |   |   |   |   |   |   |   |   |   |   start <= 439612:
nucleus_ (16.16/4.57)
|   |   |   |   |   |   |   |   |   |   |   start > 439612:
cellular_component_ (11.11)
|   |   |   |   |   |   |   |   |   |   start > 441983: cytoplasm_
(18.64)
|   |   |   |   |   |   |   |   |   start > 453454: nucleus_ (12.07)
|   |   |   |   |   |   start > 456314
|   |   |   |   |   |   |   start <= 460218
|   |   |   |   |   |   |   |   neigh_num <= 1: cellular_bud_
(16.8/6.46)
|   |   |   |   |   |   |   |   neigh_num > 1:
site_of_polarized_growth_ (22.2/7.64)
|   |   |   |   |   |   |   start > 460218
|   |   |   |   |   |   |   |   start <= 465298
|   |   |   |   |   |   |   |   |   start <= 462580:
plasma_membrane_ (11.42)
|   |   |   |   |   |   |   |   |   start > 462580: nucleus_ (11.45)
|   |   |   |   |   |   |   |   start > 465298:
site_of_polarized_growth_ (12.59)
|   |   |   |   strand = W
|   |   |   |   |   start <= 402371
```

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|   |   |   |   |   |   start <= 396765
|   |   |   |   |   |   |   start <= 390048: nucleolus_ (17.47)
|   |   |   |   |   |   |   start > 390048: ribosome_ (7.92)
|   |   |   |   |   |   start > 396765
|   |   |   |   |   |   |   start <= 401131: endoplasmic_reticulum_
(9.95)
|   |   |   |   |   |   |   start > 401131: cellular_component_
(23.57)
|   |   |   |   |   start > 402371
|   |   |   |   |   |   start <= 410185
|   |   |   |   |   |   |   start <= 404809
|   |   |   |   |   |   |   |   neigh_strand = W: nucleus_
(15.84/4.42)
|   |   |   |   |   |   |   |   neigh_strand = C: plasma_membrane_
(29.8/12.97)
|   |   |   |   |   |   |   start > 404809: mitochondrion_
(68.58/47.88)
|   |   |   |   |   |   start > 410185
|   |   |   |   |   |   |   start <= 449470
|   |   |   |   |   |   |   |   start <= 414477: nucleus_
(37.19/12.77)
|   |   |   |   |   |   |   |   start > 414477
|   |   |   |   |   |   |   |   |   start <= 434608
|   |   |   |   |   |   |   |   |   |   start <= 417277
|   |   |   |   |   |   |   |   |   |   |   start <= 415855:
cellular_component_ (11.03)
|   |   |   |   |   |   |   |   |   |   |   start > 415855:
cytoplasm_ (15.64)
|   |   |   |   |   |   |   |   |   |   start > 417277
|   |   |   |   |   |   |   |   |   |   |   start <= 423948:
ribosome_ (20.77)
|   |   |   |   |   |   |   |   |   |   |   start > 423948:
nucleolus_ (26.36)
|   |   |   |   |   |   |   |   |   start > 434608
|   |   |   |   |   |   |   |   |   |   start <= 443271
|   |   |   |   |   |   |   |   |   |   |   start <= 439612
|   |   |   |   |   |   |   |   |   |   |   |   start <= 438696:
cytoplasm_ (12.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 438696:
membrane_fraction_ (8.12)
|   |   |   |   |   |   |   |   |   |   |   start > 439612:
cytoplasm_ (12.98)
|   |   |   |   |   |   |   |   |   |   start > 443271:
cellular_component_ (20.79)
|   |   |   |   |   |   |   start > 449470
|   |   |   |   |   |   |   |   start <= 456314
|   |   |   |   |   |   |   |   |   start <= 453454: mitochondrion_
(31.24)
|   |   |   |   |   |   |   |   |   start > 453454: plasma_membrane_
(15.67)
|   |   |   |   |   |   |   |   start > 456314
|   |   |   |   |   |   |   |   |   start <= 462580: nucleolus_
(14.65)
|   |   |   |   |   |   |   |   |   start > 462580: nucleus_ (16.86)
```

```
|   |   |   start > 467465
|   |   |   |   start <= 525969
|   |   |   |   |   start <= 472419
|   |   |   |   |   |   start <= 468365: cell_wall_ (20.22)
|   |   |   |   |   |   start > 468365: cytoplasm_ (39.57)
|   |   |   |   |   start > 472419
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 482843
|   |   |   |   |   |   |   |   start <= 473983: nucleus_
(27.05/13.08)
|   |   |   |   |   |   |   |   start > 473983: mitochondrion_
(21.84)
|   |   |   |   |   |   |   start > 482843
|   |   |   |   |   |   |   |   start <= 490573
|   |   |   |   |   |   |   |   |   start <= 487397: cytoplasm_
(42.72/12.42)
|   |   |   |   |   |   |   |   |   start > 487397:
cellular_component_ (10.2)
|   |   |   |   |   |   |   |   start > 490573
|   |   |   |   |   |   |   |   |   start <= 512739
|   |   |   |   |   |   |   |   |   |   start <= 492419
|   |   |   |   |   |   |   |   |   |   |   start <= 491953:
nucleus_ (9.36)
|   |   |   |   |   |   |   |   |   |   |   start > 491953:
cytoplasm_ (9.86)
|   |   |   |   |   |   |   |   |   |   start > 492419: nucleus_
(43.82/5.35)
|   |   |   |   |   |   |   |   |   start > 512739
|   |   |   |   |   |   |   |   |   |   distance <= 9943: cytoplasm_
(29.17/16.12)
|   |   |   |   |   |   |   |   |   |   distance > 9943: nucleus_
(6.3/2.46)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 505387
|   |   |   |   |   |   |   |   start <= 475015: mitochondrion_
(15.72)
|   |   |   |   |   |   |   |   start > 475015
|   |   |   |   |   |   |   |   |   start <= 492419:
membrane_fraction_ (12.27)
|   |   |   |   |   |   |   |   |   start > 492419: mitochondrion_
(11.61)
|   |   |   |   |   |   |   start > 505387
|   |   |   |   |   |   |   |   start <= 510368
|   |   |   |   |   |   |   |   |   neigh_strand = W: ribosome_
(32.9/18.09)
|   |   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(23.11/13.25)
|   |   |   |   |   |   |   |   start > 510368
|   |   |   |   |   |   |   |   |   start <= 512739
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
plasma_membrane_ (25.48/9.02)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
mitochondrion_ (12.88/5.3)
|   |   |   |   |   |   |   |   |   start > 512739
```

```
|   |   |   |   |   |   |   |   |   |   start <= 523364: nucleus_
(43.16/14.95)
|   |   |   |   |   |   |   |   |   |   start > 523364:
mitochondrion_ (16.6)
|   |   |   |   start > 525969
|   |   |   |   |   start <= 551353
|   |   |   |   |   |   start <= 550522
|   |   |   |   |   |   |   start <= 540358
|   |   |   |   |   |   |   |   start <= 539163
|   |   |   |   |   |   |   |   |   start <= 527077:
cellular_component_ (29.25/13.45)
|   |   |   |   |   |   |   |   |   start > 527077: nucleus_ (63.21)
|   |   |   |   |   |   |   |   start > 539163: cytoplasm_ (13.63)
|   |   |   |   |   |   |   start > 540358
|   |   |   |   |   |   |   |   start <= 541685: cellular_component_
(46.31)
|   |   |   |   |   |   |   |   start > 541685
|   |   |   |   |   |   |   |   |   strand = C: cellular_component_
(13.42)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 546812
|   |   |   |   |   |   |   |   |   |   |   start <= 545606:
nucleus_ (20.09)
|   |   |   |   |   |   |   |   |   |   |   start > 545606:
mitochondrion_ (14.15)
|   |   |   |   |   |   |   |   |   |   start > 546812: nucleus_
(21.0)
|   |   |   |   |   |   start > 550522: cytoplasm_ (30.53)
|   |   |   |   |   start > 551353
|   |   |   |   |   |   start <= 553964: mitochondrion_ (31.63)
|   |   |   |   |   |   start > 553964
|   |   |   |   |   |   |   stop <= 575675
|   |   |   |   |   |   |   |   strand = C: cellular_component_
(44.28)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 562620: membrane_
(12.18)
|   |   |   |   |   |   |   |   |   start > 562620:
cellular_component_ (17.86)
|   |   |   |   |   |   |   stop > 575675: nucleus_ (8.17)
```

For Molecular Function

```
|   start <= 173337
|   |   start <= 45721
|   |   |   start <= 34407
|   |   |   |   start <= 19589
|   |   |   |   |   start <= 4097: helicase_activity_ (13.3)
|   |   |   |   |   start > 4097
|   |   |   |   |   |   start <= 13720: molecular_function_ (57.2)
|   |   |   |   |   |   start > 13720
|   |   |   |   |   |   |   start <= 16355: oxidoreductase_activity_
(14.39)
```

```
|   |   |   |   |   |   |   start > 16355: molecular_function_
(24.5)
|   |   |   |   start > 19589
|   |   |   |   |   stop <= 31694
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 27657
|   |   |   |   |   |   |   |   start <= 23231:
transporter_activity_ (15.94)
|   |   |   |   |   |   |   |   start > 23231: molecular_function_
(12.86)
|   |   |   |   |   |   |   start > 27657: transporter_activity_
(21.9)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 26776: transferase_activity_
(12.58)
|   |   |   |   |   |   |   start > 26776: transporter_activity_
(15.35)
|   |   |   |   |   stop > 31694: molecular_function_ (18.8)
|   |   |   start > 34407
|   |   |   |   strand = C
|   |   |   |   |   start <= 41953
|   |   |   |   |   |   start <= 39537: motor_activity_ (16.43)
|   |   |   |   |   |   start > 39537: peptidase_activity_ (12.54)
|   |   |   |   |   start > 41953: molecular_function_ (25.98)
|   |   |   |   strand = W: isomerase_activity_ (20.34)
|   |   start > 45721
|   |   |   start <= 61699
|   |   |   |   start <= 51539
|   |   |   |   |   start <= 47168: protein_binding_ (20.17)
|   |   |   |   |   start > 47168: nucleotidyltransferase_activity_
(16.77)
|   |   |   |   start > 51539
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 52320: RNA_binding_ (20.97)
|   |   |   |   |   |   start > 52320
|   |   |   |   |   |   |   start <= 58378
|   |   |   |   |   |   |   |   start <= 53218:
structural_molecule_activity_ (13.76)
|   |   |   |   |   |   |   |   start > 53218: transferase_activity_
(9.72)
|   |   |   |   |   |   |   start > 58378:
structural_molecule_activity_ (15.2)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 56571: molecular_function_ (28.11)
|   |   |   |   |   |   start > 56571
|   |   |   |   |   |   |   start <= 58378
|   |   |   |   |   |   |   |   neigh_strand = W:
hydrolase_activity_ (9.26/2.71)
|   |   |   |   |   |   |   |   neigh_strand = C:
transporter_activity_ (16.76/4.9)
|   |   |   |   |   |   |   start > 58378: RNA_binding_ (22.71)
|   |   |   start > 61699
|   |   |   |   start <= 141891
|   |   |   |   |   start <= 117211
```

```
|   |   |   |   |   |   start <= 100133
|   |   |   |   |   |   |   start <= 80462
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 65167:
molecular_function_ (37.09)
|   |   |   |   |   |   |   |   |   start > 65167
|   |   |   |   |   |   |   |   |   |   start <= 66797:
oxidoreductase_activity_ (16.11)
|   |   |   |   |   |   |   |   |   |   start > 66797
|   |   |   |   |   |   |   |   |   |   |   start <= 73771:
lyase_activity_ (20.32)
|   |   |   |   |   |   |   |   |   |   |   start > 73771:
oxidoreductase_activity_ (14.34)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 73771
|   |   |   |   |   |   |   |   |   |   start <= 70478:
molecular_function_ (46.99)
|   |   |   |   |   |   |   |   |   |   start > 70478:
hydrolase_activity_ (9.3)
|   |   |   |   |   |   |   |   |   start > 73771
|   |   |   |   |   |   |   |   |   |   start <= 75944:
transferase_activity_ (14.09)
|   |   |   |   |   |   |   |   |   |   start > 75944:
molecular_function_ (37.17)
|   |   |   |   |   |   |   start > 80462
|   |   |   |   |   |   |   |   start <= 86937
|   |   |   |   |   |   |   |   |   start <= 84552
|   |   |   |   |   |   |   |   |   |   start <= 82603:
protein_binding_ (32.88/15.22)
|   |   |   |   |   |   |   |   |   |   start > 82603:
transferase_activity_ (16.13)
|   |   |   |   |   |   |   |   |   start > 84552
|   |   |   |   |   |   |   |   |   |   start <= 86604
|   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (17.04)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 85676:
protein_binding_ (12.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 85676:
molecular_function_ (7.44)
|   |   |   |   |   |   |   |   |   |   start > 86604
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_binding_ (20.53/6.4)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
molecular_function_ (9.76/3.34)
|   |   |   |   |   |   |   |   start > 86937
|   |   |   |   |   |   |   |   |   start <= 90258:
hydrolase_activity_ (24.45/7.68)
|   |   |   |   |   |   |   |   |   start > 90258:
molecular_function_ (28.84)
|   |   |   |   |   |   start > 100133
|   |   |   |   |   |   |   strand = C: molecular_function_ (24.44)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 107260
```

```
|   |   |   |   |   |   |   |   |   start <= 101943
|   |   |   |   |   |   |   |   |   |   start <= 100769:
transporter_activity_ (12.74)
|   |   |   |   |   |   |   |   |   |   start > 100769: RNA_binding_
(18.47)
|   |   |   |   |   |   |   |   |   start > 101943:
oxidoreductase_activity_ (19.21)
|   |   |   |   |   |   |   |   start > 107260
|   |   |   |   |   |   |   |   |   start <= 116167
|   |   |   |   |   |   |   |   |   |   start <= 111421:
enzyme_regulator_activity_ (10.68)
|   |   |   |   |   |   |   |   |   |   start > 111421:
lyase_activity_ (15.65)
|   |   |   |   |   |   |   |   |   start > 116167: protein_binding_
(13.16)
|   |   |   |   |   start > 117211
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 135497
|   |   |   |   |   |   |   |   start <= 126629
|   |   |   |   |   |   |   |   |   start <= 123657
|   |   |   |   |   |   |   |   |   |   start <= 118035:
hydrolase_activity_ (10.01)
|   |   |   |   |   |   |   |   |   |   start > 118035
|   |   |   |   |   |   |   |   |   |   |   start <= 120299:
molecular_function_ (22.68)
|   |   |   |   |   |   |   |   |   |   |   start > 120299
|   |   |   |   |   |   |   |   |   |   |   |   start <= 121471:
ligase_activity_ (16.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 121471:
molecular_function_ (9.39)
|   |   |   |   |   |   |   |   |   start > 123657:
hydrolase_activity_ (18.89)
|   |   |   |   |   |   |   |   start > 126629: molecular_function_
(41.06)
|   |   |   |   |   |   |   start > 135497: DNA_binding_ (14.2)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 131772
|   |   |   |   |   |   |   |   start <= 126629: molecular_function_
(53.98)
|   |   |   |   |   |   |   |   start > 126629
|   |   |   |   |   |   |   |   |   start <= 128825:
protein_binding_ (10.88)
|   |   |   |   |   |   |   |   |   start > 128825:
molecular_function_ (18.17)
|   |   |   |   |   |   |   start > 131772
|   |   |   |   |   |   |   |   start <= 135497:
transferase_activity_ (18.19)
|   |   |   |   |   |   |   |   start > 135497: molecular_function_
(16.78)
|   |   |   |   start > 141891
|   |   |   |   |   start <= 159579
|   |   |   |   |   |   start <= 148175
|   |   |   |   |   |   |   start <= 146950
|   |   |   |   |   |   |   |   strand = C: protein_binding_ (8.56)
```

```
|   |   |   |   |   |   |   |   strand = W: transporter_activity_
(18.62)
|   |   |   |   |   |   |   start > 146950: protein_binding_ (19.71)
|   |   |   |   |   |   start > 148175
|   |   |   |   |   |   |   start <= 153519
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 150013:
transferase_activity_ (12.2)
|   |   |   |   |   |   |   |   |   start > 150013:
molecular_function_ (11.81)
|   |   |   |   |   |   |   |   strand = W: transferase_activity_
(24.31)
|   |   |   |   |   |   |   start > 153519
|   |   |   |   |   |   |   |   strand = C: isomerase_activity_
(15.8)
|   |   |   |   |   |   |   |   strand = W: molecular_function_
(32.43)
|   |   |   |   |   start > 159579
|   |   |   |   |   |   start <= 162722: hydrolase_activity_ (22.3)
|   |   |   |   |   |   start > 162722
|   |   |   |   |   |   |   start <= 172114
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 167585: RNA_binding_
(28.39)
|   |   |   |   |   |   |   |   |   start > 167585: protein_binding_
(10.26)
|   |   |   |   |   |   |   |   strand = W: protein_binding_ (39.72)
|   |   |   |   |   |   |   start > 172114: molecular_function_
(12.37)
|   start > 173337
|   |   start <= 484783
|   |   |   start <= 385872
|   |   |   |   start <= 281708
|   |   |   |   |   start <= 254655
|   |   |   |   |   |   start <= 210231
|   |   |   |   |   |   |   start <= 192623
|   |   |   |   |   |   |   |   stop <= 183730
|   |   |   |   |   |   |   |   |   start <= 175247:
structural_molecule_activity_ (19.58)
|   |   |   |   |   |   |   |   |   start > 175247
|   |   |   |   |   |   |   |   |   |   start <= 177834
|   |   |   |   |   |   |   |   |   |   |   start <= 177098:
molecular_function_ (15.8)
|   |   |   |   |   |   |   |   |   |   |   start > 177098:
peptidase_activity_ (20.05)
|   |   |   |   |   |   |   |   |   |   start > 177834
|   |   |   |   |   |   |   |   |   |   |   start <= 178840:
RNA_binding_ (9.68)
|   |   |   |   |   |   |   |   |   |   |   start > 178840:
molecular_function_ (11.54)
|   |   |   |   |   |   |   |   stop > 183730
|   |   |   |   |   |   |   |   |   start <= 184699
|   |   |   |   |   |   |   |   |   |   start <= 182599:
oxidoreductase_activity_ (14.22)
```

```
|   |   |   |   |   |   |   |   |   |   start > 182599:
ligase_activity_ (17.08)
|   |   |   |   |   |   |   |   |   start > 184699
|   |   |   |   |   |   |   |   |   |   start <= 191787
|   |   |   |   |   |   |   |   |   |   |   start <= 188276:
structural_molecule_activity_ (11.85)
|   |   |   |   |   |   |   |   |   |   |   start > 188276:
peptidase_activity_ (12.66)
|   |   |   |   |   |   |   |   |   |   start > 191787:
structural_molecule_activity_ (14.5)
|   |   |   |   |   |   |   start > 192623
|   |   |   |   |   |   |   |   start <= 195167
|   |   |   |   |   |   |   |   |   strand = C:
enzyme_regulator_activity_ (15.16)
|   |   |   |   |   |   |   |   |   strand = W: hydrolase_activity_
(33.58)
|   |   |   |   |   |   |   |   start > 195167
|   |   |   |   |   |   |   |   |   start <= 201075
|   |   |   |   |   |   |   |   |   |   start <= 196947:
molecular_function_ (16.96)
|   |   |   |   |   |   |   |   |   |   start > 196947
|   |   |   |   |   |   |   |   |   |   |   start <= 198811:
transcription_regulator_activity_ (6.75)
|   |   |   |   |   |   |   |   |   |   |   start > 198811:
oxidoreductase_activity_ (14.36)
|   |   |   |   |   |   |   |   |   start > 201075
|   |   |   |   |   |   |   |   |   |   start <= 208473
|   |   |   |   |   |   |   |   |   |   |   start <= 205250
|   |   |   |   |   |   |   |   |   |   |   |   start <= 202191:
transferase_activity_ (13.66)
|   |   |   |   |   |   |   |   |   |   |   |   start > 202191:
translation_regulator_activity_ (13.97)
|   |   |   |   |   |   |   |   |   |   |   start > 205250
|   |   |   |   |   |   |   |   |   |   |   |   start <= 207356:
molecular_function_ (9.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 207356:
transferase_activity_ (20.85)
|   |   |   |   |   |   |   |   |   |   start > 208473:
protein_kinase_activity_ (12.57)
|   |   |   |   |   |   start > 210231
|   |   |   |   |   |   |   start <= 237118
|   |   |   |   |   |   |   |   start <= 229480
|   |   |   |   |   |   |   |   |   start <= 213436
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 211875:
DNA_binding_ (23.13)
|   |   |   |   |   |   |   |   |   |   |   start > 211875:
RNA_binding_ (8.76)
|   |   |   |   |   |   |   |   |   |   strand = W: protein_binding_
(17.42)
|   |   |   |   |   |   |   |   |   start > 213436
|   |   |   |   |   |   |   |   |   |   start <= 214746:
hydrolase_activity_ (17.89)
|   |   |   |   |   |   |   |   |   |   start > 214746
```

```
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 225888
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 222638:
molecular_function_ (21.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 222638:
hydrolase_activity_ (19.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 225888:
molecular_function_ (51.7)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 221845:
molecular_function_ (45.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 221845
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 222638:
RNA_binding_ (21.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 222638:
molecular_function_ (11.61)
|   |   |   |   |   |   |   |   start > 229480
|   |   |   |   |   |   |   |   |   start <= 229794: DNA_binding_
(38.34/18.1)
|   |   |   |   |   |   |   |   |   start > 229794
|   |   |   |   |   |   |   |   |   |   strand = C:
hydrolase_activity_ (20.65)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 232460:
hydrolase_activity_ (12.22)
|   |   |   |   |   |   |   |   |   |   |   start > 232460:
oxidoreductase_activity_ (11.29)
|   |   |   |   |   |   |   start > 237118
|   |   |   |   |   |   |   |   start <= 238015: protein_binding_
(32.65)
|   |   |   |   |   |   |   |   start > 238015
|   |   |   |   |   |   |   |   |   start <= 251727
|   |   |   |   |   |   |   |   |   |   start <= 241500
|   |   |   |   |   |   |   |   |   |   |   start <= 239773:
molecular_function_ (19.83)
|   |   |   |   |   |   |   |   |   |   |   start > 239773:
transcription_regulator_activity_ (14.48)
|   |   |   |   |   |   |   |   |   |   start > 241500
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 246502:
hydrolase_activity_ (11.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 246502:
molecular_function_ (14.76)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (62.35)
|   |   |   |   |   |   |   |   |   start > 251727
|   |   |   |   |   |   |   |   |   |   start <= 254386:
structural_molecule_activity_ (10.73)
|   |   |   |   |   |   |   |   |   |   start > 254386:
protein_binding_ (15.52)
|   |   |   |   |   start > 254655
|   |   |   |   |   |   start <= 279624
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 268112
```

```
|   |   |   |   |   |   |   |   |   start <= 257957:
transferase_activity_ (23.89)
|   |   |   |   |   |   |   |   |   start > 257957
|   |   |   |   |   |   |   |   |   |   start <= 263697
|   |   |   |   |   |   |   |   |   |   |   start <= 259638:
transporter_activity_ (16.77)
|   |   |   |   |   |   |   |   |   |   |   start > 259638
|   |   |   |   |   |   |   |   |   |   |   |   start <= 261045:
molecular_function_ (13.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 261045:
enzyme_regulator_activity_ (12.1)
|   |   |   |   |   |   |   |   |   |   start > 263697
|   |   |   |   |   |   |   |   |   |   |   start <= 265784:
transferase_activity_ (17.62)
|   |   |   |   |   |   |   |   |   |   |   start > 265784:
transporter_activity_ (14.62)
|   |   |   |   |   |   |   |   start > 268112
|   |   |   |   |   |   |   |   |   start <= 274565
|   |   |   |   |   |   |   |   |   |   start <= 270183:
structural_molecule_activity_ (11.15)
|   |   |   |   |   |   |   |   |   |   start > 270183:
molecular_function_ (9.39)
|   |   |   |   |   |   |   |   |   start > 274565:
transferase_activity_ (14.51)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 272622
|   |   |   |   |   |   |   |   |   start <= 271766:
molecular_function_ (10.1)
|   |   |   |   |   |   |   |   |   start > 271766:
enzyme_regulator_activity_ (20.24)
|   |   |   |   |   |   |   |   start > 272622:
transporter_activity_ (47.47)
|   |   |   |   |   |   start > 279624
|   |   |   |   |   |   |   start <= 280680: hydrolase_activity_
(14.63)
|   |   |   |   |   |   |   start > 280680: RNA_binding_ (21.94)
|   |   |   |   start > 281708
|   |   |   |   |   start <= 361790
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 328473
|   |   |   |   |   |   |   |   start <= 286912
|   |   |   |   |   |   |   |   |   start <= 284220:
molecular_function_ (15.31)
|   |   |   |   |   |   |   |   |   start > 284220: lyase_activity_
(21.66)
|   |   |   |   |   |   |   |   start > 286912
|   |   |   |   |   |   |   |   |   start <= 311195
|   |   |   |   |   |   |   |   |   |   start <= 306319:
molecular_function_ (14.74)
|   |   |   |   |   |   |   |   |   |   start > 306319:
phosphoprotein_phosphatase_activity_ (12.31)
|   |   |   |   |   |   |   |   |   start > 311195
|   |   |   |   |   |   |   |   |   |   start <= 316596:
molecular_function_ (35.68)
```

```
|   |   |   |   |   |   |   |   |   |   start > 316596
|   |   |   |   |   |   |   |   |   |   |   start <= 319959:
peptidase_activity_ (11.22)
|   |   |   |   |   |   |   |   |   |   |   start > 319959:
molecular_function_ (29.18)
|   |   |   |   |   |   |   start > 328473
|   |   |   |   |   |   |   |   start <= 347608
|   |   |   |   |   |   |   |   |   start <= 337945
|   |   |   |   |   |   |   |   |   |   start <= 335184
|   |   |   |   |   |   |   |   |   |   |   start <= 332826:
protein_binding_ (13.06)
|   |   |   |   |   |   |   |   |   |   |   start > 332826:
molecular_function_ (5.48)
|   |   |   |   |   |   |   |   |   |   start > 335184:
phosphoprotein_phosphatase_activity_ (13.71)
|   |   |   |   |   |   |   |   |   start > 337945
|   |   |   |   |   |   |   |   |   |   start <= 342851:
transferase_activity_ (16.89)
|   |   |   |   |   |   |   |   |   |   start > 342851:
protein_binding_ (12.77)
|   |   |   |   |   |   |   |   start > 347608
|   |   |   |   |   |   |   |   |   start <= 351694
|   |   |   |   |   |   |   |   |   |   start <= 348396:
molecular_function_ (13.55)
|   |   |   |   |   |   |   |   |   |   start > 348396:
peptidase_activity_ (10.76)
|   |   |   |   |   |   |   |   |   start > 351694
|   |   |   |   |   |   |   |   |   |   start <= 359558:
transferase_activity_ (14.1)
|   |   |   |   |   |   |   |   |   |   start > 359558:
molecular_function_ (15.45)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 322682
|   |   |   |   |   |   |   |   start <= 293048
|   |   |   |   |   |   |   |   |   start <= 292064:
molecular_function_ (27.44)
|   |   |   |   |   |   |   |   |   start > 292064:
transcription_regulator_activity_ (13.36)
|   |   |   |   |   |   |   |   start > 293048
|   |   |   |   |   |   |   |   |   start <= 298948
|   |   |   |   |   |   |   |   |   |   start <= 295408
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
oxidoreductase_activity_ (7.13/1.88)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
transferase_activity_ (17.89/5.28)
|   |   |   |   |   |   |   |   |   |   start > 295408:
oxidoreductase_activity_ (17.57)
|   |   |   |   |   |   |   |   |   start > 298948
|   |   |   |   |   |   |   |   |   |   start <= 322208
|   |   |   |   |   |   |   |   |   |   |   start <= 306319
|   |   |   |   |   |   |   |   |   |   |   |   start <= 302804:
molecular_function_ (13.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 302804
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 304027:
oxidoreductase_activity_ (16.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 304027:
structural_molecule_activity_ (9.59)
|   |   |   |   |   |   |   |   |   |   |   start > 306319:
molecular_function_ (63.76)
|   |   |   |   |   |   |   |   |   |   start > 322208:
oxidoreductase_activity_ (16.31)
|   |   |   |   |   |   |   start > 322682
|   |   |   |   |   |   |   |   start <= 337945
|   |   |   |   |   |   |   |   |   start <= 332826
|   |   |   |   |   |   |   |   |   |   start <= 328473:
lyase_activity_ (11.75)
|   |   |   |   |   |   |   |   |   |   start > 328473:
ligase_activity_ (10.06)
|   |   |   |   |   |   |   |   |   start > 332826: lyase_activity_
(11.88)
|   |   |   |   |   |   |   |   start > 337945
|   |   |   |   |   |   |   |   |   start <= 354930
|   |   |   |   |   |   |   |   |   |   start <= 349976:
molecular_function_ (23.71)
|   |   |   |   |   |   |   |   |   |   start > 349976
|   |   |   |   |   |   |   |   |   |   |   start <= 351694:
enzyme_regulator_activity_ (19.06)
|   |   |   |   |   |   |   |   |   |   |   start > 351694:
molecular_function_ (7.93)
|   |   |   |   |   |   |   |   |   start > 354930
|   |   |   |   |   |   |   |   |   |   start <= 355462:
peptidase_activity_ (13.5)
|   |   |   |   |   |   |   |   |   |   start > 355462:
molecular_function_ (12.57)
|   |   |   |   |   start > 361790
|   |   |   |   |   |   start <= 374541
|   |   |   |   |   |   |   strand = C:
structural_molecule_activity_ (50.32)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 364585
|   |   |   |   |   |   |   |   |   start <= 363096:
structural_molecule_activity_ (19.67)
|   |   |   |   |   |   |   |   |   start > 363096: protein_binding_
(9.14)
|   |   |   |   |   |   |   |   start > 364585: molecular_function_
(36.68)
|   |   |   |   |   |   start > 374541
|   |   |   |   |   |   |   start <= 382099
|   |   |   |   |   |   |   |   start <= 377610:
transcription_regulator_activity_ (18.9)
|   |   |   |   |   |   |   |   start > 377610: protein_binding_
(6.62)
|   |   |   |   |   |   |   start > 382099: DNA_binding_ (21.94)
|   |   |   start > 385872
|   |   |   |   start <= 451560
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 404809
```

```
|   |   |   |   |   |   |   start <= 396765: molecular_function_
(85.46)
|   |   |   |   |   |   |   start > 396765
|   |   |   |   |   |   |   |   start <= 402371
|   |   |   |   |   |   |   |   |   start <= 399051:
signal_transducer_activity_ (11.14)
|   |   |   |   |   |   |   |   |   start > 399051:
transporter_activity_ (11.38)
|   |   |   |   |   |   |   |   start > 402371:
enzyme_regulator_activity_ (14.95)
|   |   |   |   |   |   start > 404809
|   |   |   |   |   |   |   start <= 430445: molecular_function_
(71.87)
|   |   |   |   |   |   |   start > 430445
|   |   |   |   |   |   |   |   start <= 432491: RNA_binding_
(18.59)
|   |   |   |   |   |   |   |   start > 432491: molecular_function_
(63.8)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 424694
|   |   |   |   |   |   |   start <= 401131
|   |   |   |   |   |   |   |   start <= 396765
|   |   |   |   |   |   |   |   |   start <= 390048: RNA_binding_
(15.49)
|   |   |   |   |   |   |   |   |   start > 390048:
structural_molecule_activity_ (8.87)
|   |   |   |   |   |   |   |   start > 396765: protein_binding_
(20.79)
|   |   |   |   |   |   |   start > 401131
|   |   |   |   |   |   |   |   start <= 417277
|   |   |   |   |   |   |   |   |   start <= 415855
|   |   |   |   |   |   |   |   |   |   start <= 404809
|   |   |   |   |   |   |   |   |   |   |   start <= 402371:
molecular_function_ (15.71)
|   |   |   |   |   |   |   |   |   |   |   start > 402371:
protein_kinase_activity_ (20.29)
|   |   |   |   |   |   |   |   |   |   start > 404809
|   |   |   |   |   |   |   |   |   |   |   start <= 414477
|   |   |   |   |   |   |   |   |   |   |   |   start <= 410185:
molecular_function_ (18.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 410185:
RNA_binding_ (15.49)
|   |   |   |   |   |   |   |   |   |   |   start > 414477:
molecular_function_ (19.52)
|   |   |   |   |   |   |   |   |   start > 415855:
protein_kinase_activity_ (12.44)
|   |   |   |   |   |   |   |   start > 417277
|   |   |   |   |   |   |   |   |   start <= 423948:
structural_molecule_activity_ (14.29)
|   |   |   |   |   |   |   |   |   start > 423948: RNA_binding_
(21.5)
|   |   |   |   |   |   start > 424694
|   |   |   |   |   |   |   start <= 434608:
phosphoprotein_phosphatase_activity_ (15.13)
```

```
|   |   |   |   |   |   |   start > 434608
|   |   |   |   |   |   |   |   start <= 439612
|   |   |   |   |   |   |   |   |   start <= 438696:
molecular_function_ (11.78)
|   |   |   |   |   |   |   |   |   start > 438696:
enzyme_regulator_activity_ (11.99)
|   |   |   |   |   |   |   |   start > 439612: molecular_function_
(34.78)
|   |   |   |   start > 451560
|   |   |   |   |   start <= 456314
|   |   |   |   |   |   strand = C: hydrolase_activity_ (21.68)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 453454:
oxidoreductase_activity_ (16.89)
|   |   |   |   |   |   |   start > 453454: protein_binding_ (15.95)
|   |   |   |   |   start > 456314
|   |   |   |   |   |   start <= 473983
|   |   |   |   |   |   |   start <= 462580
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 460218:
peptidase_activity_ (25.1)
|   |   |   |   |   |   |   |   |   start > 460218:
transporter_activity_ (15.94)
|   |   |   |   |   |   |   |   strand = W: RNA_binding_ (18.02)
|   |   |   |   |   |   |   start > 462580
|   |   |   |   |   |   |   |   start <= 469452
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 465298:
molecular_function_ (13.76)
|   |   |   |   |   |   |   |   |   |   start > 465298:
protein_binding_ (7.44)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 465298:
DNA_binding_ (10.17)
|   |   |   |   |   |   |   |   |   |   start > 465298:
molecular_function_ (26.95)
|   |   |   |   |   |   |   |   start > 469452
|   |   |   |   |   |   |   |   |   start <= 472419:
peptidase_activity_ (18.52)
|   |   |   |   |   |   |   |   |   start > 472419:
molecular_function_ (8.18)
|   |   |   |   |   |   start > 473983
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 475015:
translation_regulator_activity_ (21.39)
|   |   |   |   |   |   |   |   start > 475015
|   |   |   |   |   |   |   |   |   start <= 482843:
enzyme_regulator_activity_ (23.02)
|   |   |   |   |   |   |   |   |   start > 482843:
molecular_function_ (12.72)
|   |   |   |   |   |   |   strand = W: transporter_activity_
(24.66)
|   |   start > 484783
|   |   |   start <= 540358
```

```
|   |   |   |   start <= 523364
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 492419
|   |   |   |   |   |   |   start <= 490573: molecular_function_
(26.11)
|   |   |   |   |   |   |   start > 490573
|   |   |   |   |   |   |   |   start <= 491953:
transcription_regulator_activity_ (15.06)
|   |   |   |   |   |   |   |   start > 491953: molecular_function_
(8.57)
|   |   |   |   |   |   start > 492419
|   |   |   |   |   |   |   start <= 502889: DNA_binding_ (20.01)
|   |   |   |   |   |   |   start > 502889
|   |   |   |   |   |   |   |   start <= 512739: molecular_function_
(16.71)
|   |   |   |   |   |   |   |   start > 512739:
nucleotidyltransferase_activity_ (9.56)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 512739
|   |   |   |   |   |   |   start <= 505387:
transcription_regulator_activity_ (12.08)
|   |   |   |   |   |   |   start > 505387
|   |   |   |   |   |   |   |   start <= 510368: RNA_binding_
(16.39)
|   |   |   |   |   |   |   |   start > 510368: hydrolase_activity_
(9.19)
|   |   |   |   |   |   start > 512739
|   |   |   |   |   |   |   start <= 518211: molecular_function_
(16.95)
|   |   |   |   |   |   |   start > 518211:
transcription_regulator_activity_ (18.59)
|   |   |   |   start > 523364
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 539163
|   |   |   |   |   |   |   start <= 536295: RNA_binding_ (19.99)
|   |   |   |   |   |   |   start > 536295: oxidoreductase_activity_
(15.61)
|   |   |   |   |   |   start > 539163: transferase_activity_
(26.27)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 525969: transferase_activity_
(21.19)
|   |   |   |   |   |   start > 525969: DNA_binding_ (23.6)
|   |   |   start > 540358
|   |   |   |   start <= 548416
|   |   |   |   |   start <= 541685
|   |   |   |   |   |   start <= 540645: molecular_function_ (19.69)
|   |   |   |   |   |   start > 540645: helicase_activity_ (20.86)
|   |   |   |   |   start > 541685
|   |   |   |   |   |   start <= 546812
|   |   |   |   |   |   |   start <= 545606: protein_binding_
(17.13)
|   |   |   |   |   |   |   start > 545606: oxidoreductase_activity_
(14.61)
```

```
|   |   |   |   |   |   start > 546812: DNA_binding_ (17.29)
|   |   |   |   start > 548416
|   |   |   |   |   stop <= 575675
|   |   |   |   |   |   start <= 551117
|   |   |   |   |   |   |   start <= 550522: molecular_function_
(20.65)
|   |   |   |   |   |   |   start > 550522:
enzyme_regulator_activity_ (13.13)
|   |   |   |   |   |   start > 551117
|   |   |   |   |   |   |   start <= 553964
|   |   |   |   |   |   |   |   start <= 552520: molecular_function_
(27.9)
|   |   |   |   |   |   |   |   start > 552520: ligase_activity_
(10.77)
|   |   |   |   |   |   |   start > 553964: molecular_function_
(87.62)
|   |   |   |   |   stop > 575675: helicase_activity_ (9.56)
```

For Biological Process

```
|   start <= 364585
|   |   start <= 167585
|   |   |   start <= 42624
|   |   |   |   start <= 19589: biological_process_ (98.93)
|   |   |   |   start > 19589
|   |   |   |   |   start <= 34407
|   |   |   |   |   |   start <= 26776
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 23231: transport_ (16.62)
|   |   |   |   |   |   |   |   start > 23231: biological_process_
(13.28)
|   |   |   |   |   |   |   strand = W:
protein_modification_process_ (12.77)
|   |   |   |   |   |   start > 26776: transport_ (58.84)
|   |   |   |   |   start > 34407
|   |   |   |   |   |   start <= 41953
|   |   |   |   |   |   |   start <= 39537: cell_cycle_ (11.19)
|   |   |   |   |   |   |   start > 39537: sporulation_ (10.63)
|   |   |   |   |   |   start > 41953: biological_process_ (19.27)
|   |   |   start > 42624
|   |   |   |   start <= 61960
|   |   |   |   |   start <= 51539
|   |   |   |   |   |   start <= 43252:
carbohydrate_metabolic_process_ (22.7/8.37)
|   |   |   |   |   |   start > 43252
|   |   |   |   |   |   |   start <= 47168: DNA_metabolic_process_
(50.49/14.44)
|   |   |   |   |   |   |   start > 47168: transcription_ (17.28)
|   |   |   |   |   start > 51539
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 52320: RNA_metabolic_process_
(44.9/21.34)
|   |   |   |   |   |   |   start > 52320
|   |   |   |   |   |   |   |   start <= 58378
```

```
|   |   |   |   |   |   |   |   |   start <= 53218: translation_
(21.53)
|   |   |   |   |   |   |   |   |   start > 53218:
DNA_metabolic_process_ (15.89)
|   |   |   |   |   |   |   |   start > 58378: translation_ (31.07)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 58378
|   |   |   |   |   |   |   |   start <= 56571: response_to_stress_
(14.99)
|   |   |   |   |   |   |   |   start > 56571:
organelle_organization_and_biogenesis_ (13.22)
|   |   |   |   |   |   |   start > 58378
|   |   |   |   |   |   |   |   Neigh_GO_aspect = C
|   |   |   |   |   |   |   |   |   neigh_strand = W:
RNA_metabolic_process_ (7.08/2.98)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
ribosome_biogenesis_and_assembly_ (6.74/1.53)
|   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
RNA_metabolic_process_ (20.04/5.28)
|   |   |   |   |   |   |   |   Neigh_GO_aspect = P
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
RNA_metabolic_process_ (11.39/4.45)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
ribosome_biogenesis_and_assembly_ (9.15/3.16)
|   |   |   |   start > 61960
|   |   |   |   |   start <= 85545
|   |   |   |   |   |   start <= 70478
|   |   |   |   |   |   |   start <= 66797: biological_process_
(50.97)
|   |   |   |   |   |   |   start > 66797
|   |   |   |   |   |   |   |   strand = C:
amino_acid_and_derivative_metabolic_process_ (16.21)
|   |   |   |   |   |   |   |   strand = W: biological_process_
(22.31)
|   |   |   |   |   |   start > 70478
|   |   |   |   |   |   |   start <= 79977
|   |   |   |   |   |   |   |   strand = C: electron_transport_
(18.19)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 75944
|   |   |   |   |   |   |   |   |   |   start <= 73771:
protein_modification_process_ (15.88)
|   |   |   |   |   |   |   |   |   |   start > 73771:
vitamin_metabolic_process_ (23.29)
|   |   |   |   |   |   |   |   |   start > 75944:
cell_wall_organization_and_biogenesis_ (19.64)
|   |   |   |   |   |   |   start > 79977
|   |   |   |   |   |   |   |   start <= 82603
|   |   |   |   |   |   |   |   |   start <= 80462:
biological_process_ (16.83)
|   |   |   |   |   |   |   |   |   start > 80462:
protein_catabolic_process_ (22.99)
|   |   |   |   |   |   |   |   start > 82603
```

```
|   |   |   |   |   |   |   |   |   start <= 84552:
protein_modification_process_ (16.59)
|   |   |   |   |   |   |   |   |   start > 84552:
biological_process_ (15.77)
|   |   |   |   |   start > 85545
|   |   |   |   |   |   start <= 138666
|   |   |   |   |   |   |   start <= 128825
|   |   |   |   |   |   |   |   start <= 101943
|   |   |   |   |   |   |   |   |   start <= 100133
|   |   |   |   |   |   |   |   |   |   start <= 86604: translation_
(36.36)
|   |   |   |   |   |   |   |   |   |   start > 86604
|   |   |   |   |   |   |   |   |   |   |   start <= 97796
|   |   |   |   |   |   |   |   |   |   |   |   start <= 90258
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 86937:
DNA_metabolic_process_ (13.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 86937:
protein_modification_process_ (9.95)
|   |   |   |   |   |   |   |   |   |   |   |   start > 90258
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 94644
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: transport_ (5.29/1.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: organelle_organization_and_biogenesis_ (12.23/3.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 94644:
DNA_metabolic_process_ (12.19)
|   |   |   |   |   |   |   |   |   |   |   start > 97796:
translation_ (10.98)
|   |   |   |   |   |   |   |   |   start > 100133
|   |   |   |   |   |   |   |   |   |   start <= 100769:
organelle_organization_and_biogenesis_ (34.4/13.78)
|   |   |   |   |   |   |   |   |   |   start > 100769:
ribosome_biogenesis_and_assembly_ (17.34)
|   |   |   |   |   |   |   |   start > 101943
|   |   |   |   |   |   |   |   |   start <= 111421
|   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (29.34)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 107260:
electron_transport_ (38.28/16.89)
|   |   |   |   |   |   |   |   |   |   |   start > 107260: vesicle-
mediated_transport_ (36.39/21.75)
|   |   |   |   |   |   |   |   |   start > 111421
|   |   |   |   |   |   |   |   |   |   start <= 126218
|   |   |   |   |   |   |   |   |   |   |   start <= 118035
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
RNA_metabolic_process_ (7.63)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 116167:
biological_process_ (12.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 116167:
membrane_organization_and_biogenesis_ (16.2)
|   |   |   |   |   |   |   |   |   |   |   start > 118035
|   |   |   |   |   |   |   |   |   |   |   |   start <= 121471
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 120299:
biological_process_ (11.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 120299:
DNA_metabolic_process_ (28.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 121471
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 122929:
transport_ (10.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 122929:
biological_process_ (36.44)
|   |   |   |   |   |   |   |   |   |   start > 126218
|   |   |   |   |   |   |   |   |   |   |   start <= 126629:
RNA_metabolic_process_ (16.9)
|   |   |   |   |   |   |   |   |   |   |   start > 126629
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
organelle_organization_and_biogenesis_ (15.72/5.42)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
2351: membrane_organization_and_biogenesis_ (5.16/1.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 2351:
organelle_organization_and_biogenesis_ (6.88/2.06)
|   |   |   |   |   |   |   start > 128825
|   |   |   |   |   |   |   |   strand = C: translation_ (31.3)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 135497
|   |   |   |   |   |   |   |   |   |   start <= 131772:
carbohydrate_metabolic_process_ (8.41)
|   |   |   |   |   |   |   |   |   |   start > 131772:
generation_of_precursor_metabolites_and_energy_ (26.49/11.14)
|   |   |   |   |   |   |   |   |   start > 135497: translation_
(10.01)
|   |   |   |   |   |   start > 138666
|   |   |   |   |   |   |   start <= 150977
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 141891:
amino_acid_and_derivative_metabolic_process_ (6.58)
|   |   |   |   |   |   |   |   |   start > 141891
|   |   |   |   |   |   |   |   |   |   start <= 150013
|   |   |   |   |   |   |   |   |   |   |   start <= 148175:
biological_process_ (12.8)
|   |   |   |   |   |   |   |   |   |   |   start > 148175:
cell_cycle_ (11.91)
|   |   |   |   |   |   |   |   |   |   start > 150013:
biological_process_ (18.84)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 141891:
biological_process_ (16.88)
|   |   |   |   |   |   |   |   |   start > 141891
|   |   |   |   |   |   |   |   |   |   start <= 146950
|   |   |   |   |   |   |   |   |   |   |   start <= 144326:
transport_ (16.23)
|   |   |   |   |   |   |   |   |   |   |   start > 144326:
cell_wall_organization_and_biogenesis_ (40.37/21.92)
|   |   |   |   |   |   |   |   |   |   start > 146950:
biological_process_ (14.42)
```

```
|   |   |   |   |   |   |   start > 150977
|   |   |   |   |   |   |   |   start <= 166884
|   |   |   |   |   |   |   |   |   start <= 159117
|   |   |   |   |   |   |   |   |   |   start <= 153519:
protein_modification_process_ (18.77)
|   |   |   |   |   |   |   |   |   |   start > 153519
|   |   |   |   |   |   |   |   |   |   |   start <= 156802:
ribosome_biogenesis_and_assembly_ (14.16)
|   |   |   |   |   |   |   |   |   |   |   start > 156802:
protein_modification_process_ (15.44)
|   |   |   |   |   |   |   |   |   start > 159117
|   |   |   |   |   |   |   |   |   |   start <= 160549
|   |   |   |   |   |   |   |   |   |   |   start <= 159579:
biological_process_ (17.42)
|   |   |   |   |   |   |   |   |   |   |   start > 159579:
protein_modification_process_ (10.28)
|   |   |   |   |   |   |   |   |   |   start > 160549
|   |   |   |   |   |   |   |   |   |   |   strand = C:
ribosome_biogenesis_and_assembly_ (13.96)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 162722:
ribosome_biogenesis_and_assembly_ (11.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 162722:
biological_process_ (13.82)
|   |   |   |   |   |   |   |   start > 166884:
RNA_metabolic_process_ (11.33)
|   |   start > 167585
|   |   |   start <= 222638
|   |   |   |   start <= 211875
|   |   |   |   |   start <= 194538
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 192796
|   |   |   |   |   |   |   |   start <= 184699
|   |   |   |   |   |   |   |   |   start <= 178840
|   |   |   |   |   |   |   |   |   |   start <= 172114:
cytokinesis_ (15.07)
|   |   |   |   |   |   |   |   |   |   start > 172114:
biological_process_ (13.44)
|   |   |   |   |   |   |   |   |   start > 178840: cytokinesis_
(18.63)
|   |   |   |   |   |   |   |   start > 184699
|   |   |   |   |   |   |   |   |   start <= 191787:
protein_modification_process_ (12.35)
|   |   |   |   |   |   |   |   |   start > 191787:
biological_process_ (11.25)
|   |   |   |   |   |   |   start > 192796: transport_ (20.09)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 177834
|   |   |   |   |   |   |   |   start <= 173337: transport_ (13.07)
|   |   |   |   |   |   |   |   start > 173337
|   |   |   |   |   |   |   |   |   start <= 177098
|   |   |   |   |   |   |   |   |   |   start <= 175247:
response_to_stress_ (14.99)
```

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|   |   |   |   |   |   |   |   |   |   start > 175247: translation_ 
(21.48)
|   |   |   |   |   |   |   |   |   start > 177098: 
response_to_stress_ (16.41)
|   |   |   |   |   |   |   start > 177834
|   |   |   |   |   |   |   |   start <= 184699
|   |   |   |   |   |   |   |   |   start <= 182599
|   |   |   |   |   |   |   |   |   |   start <= 178840: 
RNA_metabolic_process_ (14.26)
|   |   |   |   |   |   |   |   |   |   start > 178840: 
biological_process_ (12.49)
|   |   |   |   |   |   |   |   |   start > 182599: 
lipid_metabolic_process_ (17.35)
|   |   |   |   |   |   |   |   start > 184699
|   |   |   |   |   |   |   |   |   start <= 188276: cell_cycle_ 
(14.77)
|   |   |   |   |   |   |   |   |   start > 188276: 
response_to_stress_ (17.15)
|   |   |   |   |   start > 194538
|   |   |   |   |   |   start <= 202191
|   |   |   |   |   |   |   start <= 196947
|   |   |   |   |   |   |   |   start <= 195167
|   |   |   |   |   |   |   |   |   neigh_strand = W: 
pseudohyphal_growth_ (15.79/6.45)
|   |   |   |   |   |   |   |   |   neigh_strand = C: 
signal_transduction_ (13.91/5.07)
|   |   |   |   |   |   |   |   start > 195167: 
protein_catabolic_process_ (10.55)
|   |   |   |   |   |   |   start > 196947
|   |   |   |   |   |   |   |   start <= 201075
|   |   |   |   |   |   |   |   |   start <= 198811: transcription_ 
(9.43)
|   |   |   |   |   |   |   |   |   start > 198811: 
amino_acid_and_derivative_metabolic_process_ (16.84)
|   |   |   |   |   |   |   |   start > 201075: 
vitamin_metabolic_process_ (10.46)
|   |   |   |   |   |   start > 202191
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 208473: 
lipid_metabolic_process_ (20.45)
|   |   |   |   |   |   |   |   start > 208473
|   |   |   |   |   |   |   |   |   start <= 210231: 
signal_transduction_ (17.06)
|   |   |   |   |   |   |   |   |   start > 210231: 
response_to_stress_ (14.44)
|   |   |   |   |   |   |   strand = W: translation_ (31.73)
|   |   |   |   start > 211875
|   |   |   |   |   start <= 214746
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 213436: RNA_metabolic_process_ 
(8.44)
|   |   |   |   |   |   |   start > 213436: vesicle-
mediated_transport_ (16.65)
|   |   |   |   |   |   strand = W: DNA_metabolic_process_ (22.59)
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|   |   |   |   |   start > 214746
|   |   |   |   |   |   start <= 215062: RNA_metabolic_process_
(20.69)
|   |   |   |   |   |   start > 215062
|   |   |   |   |   |   |   start <= 221845: biological_process_
(30.45)
|   |   |   |   |   |   |   start > 221845: RNA_metabolic_process_
(12.46)
|   |   |   start > 222638
|   |   |   |   start <= 243179
|   |   |   |   |   start <= 234936
|   |   |   |   |   |   start <= 232460
|   |   |   |   |   |   |   start <= 228251
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 225888:
ribosome_biogenesis_and_assembly_ (7.56)
|   |   |   |   |   |   |   |   |   start > 225888:
DNA_metabolic_process_ (10.88)
|   |   |   |   |   |   |   |   strand = W: biological_process_
(21.76)
|   |   |   |   |   |   |   start > 228251: biological_process_
(84.84/15.93)
|   |   |   |   |   |   start > 232460: response_to_stress_ (20.09)
|   |   |   |   |   start > 234936
|   |   |   |   |   |   start <= 238015
|   |   |   |   |   |   |   start <= 237118:
amino_acid_and_derivative_metabolic_process_ (17.5)
|   |   |   |   |   |   |   start > 237118: lipid_metabolic_process_
(21.81)
|   |   |   |   |   |   start > 238015
|   |   |   |   |   |   |   start <= 239773: cell_cycle_
(76.72/52.89)
|   |   |   |   |   |   |   start > 239773
|   |   |   |   |   |   |   |   start <= 241500: transcription_
(15.14)
|   |   |   |   |   |   |   |   start > 241500:
cell_wall_organization_and_biogenesis_ (26.85/10.18)
|   |   |   |   start > 243179
|   |   |   |   |   start <= 322208
|   |   |   |   |   |   start <= 280680
|   |   |   |   |   |   |   start <= 270183
|   |   |   |   |   |   |   |   start <= 254386
|   |   |   |   |   |   |   |   |   start <= 250717
|   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (24.21)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 250285:
translation_ (10.58)
|   |   |   |   |   |   |   |   |   |   |   start > 250285:
biological_process_ (13.95)
|   |   |   |   |   |   |   |   |   start > 250717
|   |   |   |   |   |   |   |   |   |   start <= 251727:
ribosome_biogenesis_and_assembly_ (13.11)
```

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|   |   |   |   |   |   |   |   |   |   start > 251727: translation_
(14.92)
|   |   |   |   |   |   |   |   start > 254386
|   |   |   |   |   |   |   |   |   start <= 265784
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 261045
|   |   |   |   |   |   |   |   |   |   |   |   start <= 257957
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: biological_process_ (17.58/5.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: amino_acid_and_derivative_metabolic_process_ (13.1/5.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 257957
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 259638:
transport_ (12.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 259638:
biological_process_ (17.53)
|   |   |   |   |   |   |   |   |   |   |   start > 261045
|   |   |   |   |   |   |   |   |   |   |   |   start <= 263697:
protein_modification_process_ (12.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 263697:
amino_acid_and_derivative_metabolic_process_ (18.05)
|   |   |   |   |   |   |   |   |   |   strand = W:
protein_modification_process_ (11.1)
|   |   |   |   |   |   |   |   |   start > 265784
|   |   |   |   |   |   |   |   |   |   start <= 268112: transport_
(13.96)
|   |   |   |   |   |   |   |   |   |   start > 268112: translation_
(12.31)
|   |   |   |   |   |   |   start > 270183
|   |   |   |   |   |   |   |   start <= 276570
|   |   |   |   |   |   |   |   |   start <= 272622
|   |   |   |   |   |   |   |   |   |   start <= 271766:
biological_process_ (23.02)
|   |   |   |   |   |   |   |   |   |   start > 271766:
carbohydrate_metabolic_process_ (16.79)
|   |   |   |   |   |   |   |   |   start > 272622:
biological_process_ (31.11)
|   |   |   |   |   |   |   |   start > 276570
|   |   |   |   |   |   |   |   |   start <= 279624:
lipid_metabolic_process_ (18.21)
|   |   |   |   |   |   |   |   |   start > 279624:
carbohydrate_metabolic_process_ (14.19)
|   |   |   |   |   |   start > 280680
|   |   |   |   |   |   |   start <= 298948
|   |   |   |   |   |   |   |   start <= 295408
|   |   |   |   |   |   |   |   |   start <= 288522
|   |   |   |   |   |   |   |   |   |   start <= 284220:
transcription_ (28.09)
|   |   |   |   |   |   |   |   |   |   start > 284220
|   |   |   |   |   |   |   |   |   |   |   start <= 286912:
carbohydrate_metabolic_process_ (7.46)
|   |   |   |   |   |   |   |   |   |   |   start > 286912:
translation_ (8.69)
|   |   |   |   |   |   |   |   |   start > 288522
```

```
|   |   |   |   |   |   |   |   |   |   start <= 292064:
biological_process_ (33.5)
|   |   |   |   |   |   |   |   |   |   start > 292064
|   |   |   |   |   |   |   |   |   |   |   start <= 293048:
conjugation_ (9.43)
|   |   |   |   |   |   |   |   |   |   |   start > 293048:
transcription_ (14.11)
|   |   |   |   |   |   |   |   start > 295408:
DNA_metabolic_process_ (24.16)
|   |   |   |   |   |   |   start > 298948
|   |   |   |   |   |   |   |   start <= 312091
|   |   |   |   |   |   |   |   |   start <= 304027
|   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (9.91)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 302804:
transport_ (45.45/29.01)
|   |   |   |   |   |   |   |   |   |   |   start > 302804:
electron_transport_ (12.35)
|   |   |   |   |   |   |   |   |   start > 304027
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 311195:
protein_modification_process_ (13.46)
|   |   |   |   |   |   |   |   |   |   |   start > 311195:
translation_ (8.56)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 306319:
translation_ (22.95)
|   |   |   |   |   |   |   |   |   |   |   start > 306319:
transport_ (21.47/8.48)
|   |   |   |   |   |   |   |   start > 312091
|   |   |   |   |   |   |   |   |   start <= 319959:
biological_process_ (80.72)
|   |   |   |   |   |   |   |   |   start > 319959: transcription_
(21.23)
|   |   |   |   |   start > 322208
|   |   |   |   |   |   start <= 348396
|   |   |   |   |   |   |   start <= 327027
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 325932:
ribosome_biogenesis_and_assembly_ (13.58)
|   |   |   |   |   |   |   |   |   start > 325932:
cell_wall_organization_and_biogenesis_ (18.96)
|   |   |   |   |   |   |   |   strand = W:
amino_acid_and_derivative_metabolic_process_ (13.99)
|   |   |   |   |   |   |   start > 327027
|   |   |   |   |   |   |   |   start <= 342163
|   |   |   |   |   |   |   |   |   start <= 335184
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 332826
|   |   |   |   |   |   |   |   |   |   |   |   start <= 328473:
biological_process_ (8.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 328473:
transport_ (17.14)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 332826:
biological_process_ (14.68)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 328473:
amino_acid_and_derivative_metabolic_process_ (16.19)
|   |   |   |   |   |   |   |   |   |   |   start > 328473:
biological_process_ (7.94)
|   |   |   |   |   |   |   |   |   start > 335184
|   |   |   |   |   |   |   |   |   |   start <= 337336:
response_to_stress_ (9.37)
|   |   |   |   |   |   |   |   |   |   start > 337336:
amino_acid_and_derivative_metabolic_process_ (19.38)
|   |   |   |   |   |   |   |   start > 342163
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 347608:
cell_wall_organization_and_biogenesis_ (12.36)
|   |   |   |   |   |   |   |   |   |   start > 347608:
biological_process_ (11.3)
|   |   |   |   |   |   |   |   |   strand = W: biological_process_
(26.05)
|   |   |   |   |   |   start > 348396
|   |   |   |   |   |   |   start <= 359558
|   |   |   |   |   |   |   |   start <= 354930
|   |   |   |   |   |   |   |   |   strand = C:
protein_catabolic_process_ (8.0)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 349976:
DNA_metabolic_process_ (13.2)
|   |   |   |   |   |   |   |   |   |   start > 349976
|   |   |   |   |   |   |   |   |   |   |   start <= 351694:
sporulation_ (14.04)
|   |   |   |   |   |   |   |   |   |   |   start > 351694:
translation_ (4.69)
|   |   |   |   |   |   |   |   start > 354930
|   |   |   |   |   |   |   |   |   strand = C:
amino_acid_and_derivative_metabolic_process_ (12.69)
|   |   |   |   |   |   |   |   |   strand = W:
protein_modification_process_ (39.14/10.93)
|   |   |   |   |   |   |   start > 359558
|   |   |   |   |   |   |   |   strand = C: biological_process_
(25.61)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 363096: translation_
(16.85)
|   |   |   |   |   |   |   |   |   start > 363096:
response_to_stress_ (16.41)
|   start > 364585
|   |   start <= 414477
|   |   |   start <= 374541
|   |   |   |   strand = C
|   |   |   |   |   start <= 372322:
nuclear_organization_and_biogenesis_ (26.19)
|   |   |   |   |   start > 372322:
membrane_organization_and_biogenesis_ (40.17/18.7)
```

```
|   |   |   |   strand = W
|   |   |   |   |   start <= 366798: DNA_metabolic_process_ (20.03)
|   |   |   |   |   start > 366798: meiosis_ (21.21)
|   |   |   start > 374541
|   |   |   |   start <= 404348
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 393708
|   |   |   |   |   |   |   start <= 387228
|   |   |   |   |   |   |   |   start <= 377610:
pseudohyphal_growth_ (13.74)
|   |   |   |   |   |   |   |   start > 377610
|   |   |   |   |   |   |   |   |   start <= 382099: transport_
(17.81)
|   |   |   |   |   |   |   |   |   start > 382099: transcription_
(13.6)
|   |   |   |   |   |   |   start > 387228
|   |   |   |   |   |   |   |   start <= 390048: biological_process_
(12.22)
|   |   |   |   |   |   |   |   start > 390048: cell_budding_
(34.4/10.64)
|   |   |   |   |   |   start > 393708
|   |   |   |   |   |   |   start <= 399051
|   |   |   |   |   |   |   |   start <= 394863: sporulation_
(12.43)
|   |   |   |   |   |   |   |   start > 394863
|   |   |   |   |   |   |   |   |   start <= 396765:
response_to_stress_ (13.96)
|   |   |   |   |   |   |   |   |   start > 396765:
pseudohyphal_growth_ (8.93)
|   |   |   |   |   |   |   start > 399051
|   |   |   |   |   |   |   |   start <= 402371: transport_ (8.15)
|   |   |   |   |   |   |   |   start > 402371
|   |   |   |   |   |   |   |   |   distance <= 1521: transport_
(9.17/1.98)
|   |   |   |   |   |   |   |   |   distance > 1521
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: transport_
(5.83/2.27)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (15.39/3.96)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 396765
|   |   |   |   |   |   |   start <= 390048: RNA_metabolic_process_
(18.62)
|   |   |   |   |   |   |   start > 390048: translation_ (19.03)
|   |   |   |   |   |   start > 396765
|   |   |   |   |   |   |   start <= 401131: transport_ (11.65)
|   |   |   |   |   |   |   start > 401131: biological_process_
(17.5)
|   |   |   |   start > 404348
|   |   |   |   |   start <= 410185
|   |   |   |   |   |   strand = C: cytokinesis_ (18.11)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 404809:
protein_modification_process_ (13.61)
```

```
|   |   |   |   |   |   |   start > 404809: transcription_ (19.28)
|   |   |   |   |   start > 410185:
ribosome_biogenesis_and_assembly_ (43.75)
|   |   start > 414477
|   |   |   start <= 536016
|   |   |   |   strand = C
|   |   |   |   |   start <= 492419
|   |   |   |   |   |   start <= 432491
|   |   |   |   |   |   |   start <= 430445
|   |   |   |   |   |   |   |   start <= 424694: biological_process_
(17.64)
|   |   |   |   |   |   |   |   start > 424694: sporulation_ (12.32)
|   |   |   |   |   |   |   start > 430445: RNA_metabolic_process_
(27.29/11.09)
|   |   |   |   |   |   start > 432491
|   |   |   |   |   |   |   start <= 472419
|   |   |   |   |   |   |   |   start <= 453454
|   |   |   |   |   |   |   |   |   start <= 435820: translation_
(19.44)
|   |   |   |   |   |   |   |   |   start > 435820
|   |   |   |   |   |   |   |   |   |   start <= 441983:
biological_process_ (17.26)
|   |   |   |   |   |   |   |   |   |   start > 441983
|   |   |   |   |   |   |   |   |   |   |   start <= 443271:
translation_ (12.41)
|   |   |   |   |   |   |   |   |   |   |   start > 443271:
biological_process_ (17.25)
|   |   |   |   |   |   |   |   start > 453454
|   |   |   |   |   |   |   |   |   start <= 465298
|   |   |   |   |   |   |   |   |   |   start <= 462580
|   |   |   |   |   |   |   |   |   |   |   start <= 460218
|   |   |   |   |   |   |   |   |   |   |   |   start <= 456314:
DNA_metabolic_process_ (14.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 456314:
protein_modification_process_ (12.88)
|   |   |   |   |   |   |   |   |   |   |   start > 460218:
transport_ (14.74)
|   |   |   |   |   |   |   |   |   |   start > 462580
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
DNA_metabolic_process_ (12.58/5.46)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
biological_process_ (18.13/8.48)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
organelle_organization_and_biogenesis_ (13.16/6.8)
|   |   |   |   |   |   |   |   |   start > 465298
|   |   |   |   |   |   |   |   |   |   start <= 469452:
pseudohyphal_growth_ (14.58)
|   |   |   |   |   |   |   |   |   |   start > 469452:
protein_modification_process_ (39.12/16.74)
|   |   |   |   |   |   |   start > 472419
|   |   |   |   |   |   |   |   start <= 490573
|   |   |   |   |   |   |   |   |   distance <= 3845
```

```
|   |   |   |   |   |   |   |   |   |   start <= 473983:
biological_process_ (12.97)
|   |   |   |   |   |   |   |   |   |   start > 473983
|   |   |   |   |   |   |   |   |   |   |   start <= 487397
|   |   |   |   |   |   |   |   |   |   |   |   start <= 484783
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 475015:
translation_ (16.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 475015:
biological_process_ (14.92/0.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 484783:
translation_ (18.26)
|   |   |   |   |   |   |   |   |   |   |   start > 487397:
biological_process_ (11.91)
|   |   |   |   |   |   |   |   |   distance > 3845
|   |   |   |   |   |   |   |   |   |   start <= 482843:
cell_wall_organization_and_biogenesis_ (23.48/1.61)
|   |   |   |   |   |   |   |   |   |   start > 482843:
biological_process_ (9.91/0.38)
|   |   |   |   |   |   |   |   start > 490573
|   |   |   |   |   |   |   |   |   start <= 491953: transcription_
(11.6)
|   |   |   |   |   |   |   |   |   start > 491953: translation_
(12.3)
|   |   |   |   |   start > 492419
|   |   |   |   |   |   start <= 502889: DNA_metabolic_process_
(63.04/23.02)
|   |   |   |   |   |   start > 502889
|   |   |   |   |   |   |   start <= 512739: biological_process_
(15.66)
|   |   |   |   |   |   |   start > 512739: RNA_metabolic_process_
(33.32)
|   |   |   |   strand = W
|   |   |   |   |   start <= 453454
|   |   |   |   |   |   start <= 438696
|   |   |   |   |   |   |   start <= 424694
|   |   |   |   |   |   |   |   start <= 417277
|   |   |   |   |   |   |   |   |   start <= 415855:
biological_process_ (19.98)
|   |   |   |   |   |   |   |   |   start > 415855:
protein_modification_process_ (26.06/12.86)
|   |   |   |   |   |   |   |   start > 417277
|   |   |   |   |   |   |   |   |   start <= 423948: translation_
(9.68)
|   |   |   |   |   |   |   |   |   start > 423948:
biological_process_ (12.29)
|   |   |   |   |   |   |   start > 424694
|   |   |   |   |   |   |   |   start <= 434608: meiosis_
(25.68/8.38)
|   |   |   |   |   |   |   |   start > 434608: translation_ (7.36)
|   |   |   |   |   |   start > 438696
|   |   |   |   |   |   |   start <= 443271
|   |   |   |   |   |   |   |   start <= 439612: vesicle-
mediated_transport_ (8.3)
|   |   |   |   |   |   |   |   start > 439612: transport_ (12.97)
```

```
|   |   |   |   |   |   |   start > 443271: biological_process_
(49.72)
|   |   |   |   |   start > 453454
|   |   |   |   |   |   start <= 512739
|   |   |   |   |   |   |   start <= 468365
|   |   |   |   |   |   |   |   start <= 462580
|   |   |   |   |   |   |   |   |   start <= 456314: vesicle-
mediated_transport_ (14.37)
|   |   |   |   |   |   |   |   |   start > 456314:
RNA_metabolic_process_ (18.88)
|   |   |   |   |   |   |   |   start > 462580
|   |   |   |   |   |   |   |   |   start <= 465298: transcription_
(12.04)
|   |   |   |   |   |   |   |   |   start > 465298:
biological_process_ (16.38)
|   |   |   |   |   |   |   start > 468365
|   |   |   |   |   |   |   |   start <= 510368
|   |   |   |   |   |   |   |   |   start <= 475015
|   |   |   |   |   |   |   |   |   |   start <= 469452:
translation_ (16.93)
|   |   |   |   |   |   |   |   |   |   start > 469452:
membrane_organization_and_biogenesis_ (18.54)
|   |   |   |   |   |   |   |   |   start > 475015
|   |   |   |   |   |   |   |   |   |   start <= 492419
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transport_ (3.32/1.15)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
vesicle-mediated_transport_ (7.0/1.93)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
transport_ (14.36/4.1)
|   |   |   |   |   |   |   |   |   |   start > 492419
|   |   |   |   |   |   |   |   |   |   |   start <= 505387:
RNA_metabolic_process_ (14.13)
|   |   |   |   |   |   |   |   |   |   |   start > 505387:
translation_ (19.27)
|   |   |   |   |   |   |   |   start > 510368:
membrane_organization_and_biogenesis_ (29.59/13.61)
|   |   |   |   |   |   start > 512739
|   |   |   |   |   |   |   start <= 523364
|   |   |   |   |   |   |   |   start <= 518211: cell_cycle_ (13.26)
|   |   |   |   |   |   |   |   start > 518211:
DNA_metabolic_process_ (10.51)
|   |   |   |   |   |   |   start > 523364
|   |   |   |   |   |   |   |   start <= 525969: biological_process_
(26.05)
|   |   |   |   |   |   |   |   start > 525969: transcription_
(20.43)
|   |   |   start > 536016
|   |   |   |   start <= 539163
|   |   |   |   |   start <= 536295: meiosis_ (42.82/23.33)
|   |   |   |   |   start > 536295: response_to_stress_ (16.71)
|   |   |   |   start > 539163
|   |   |   |   |   start <= 551353
```

```
|   |   |   |   |   |   start <= 546812
|   |   |   |   |   |   |   start <= 540645: biological_process_
(34.4)
|   |   |   |   |   |   |   start > 540645
|   |   |   |   |   |   |   |   start <= 545606
|   |   |   |   |   |   |   |   |   start <= 541685: translation_
(15.49)
|   |   |   |   |   |   |   |   |   start > 541685:
pseudohyphal_growth_ (8.91)
|   |   |   |   |   |   |   |   start > 545606: biological_process_
(19.2)
|   |   |   |   |   |   start > 546812
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 551117
|   |   |   |   |   |   |   |   |   start <= 550522: sporulation_
(9.21)
|   |   |   |   |   |   |   |   |   start > 550522: transport_
(9.65)
|   |   |   |   |   |   |   |   start > 551117: translation_ (12.33)
|   |   |   |   |   |   |   strand = W: meiosis_ (17.61)
|   |   |   |   |   start > 551353
|   |   |   |   |   |   stop <= 575675: biological_process_ (103.78)
|   |   |   |   |   |   stop > 575675: DNA_metabolic_process_ (4.95)
```

Decision Tree Generated for Chromosome Six:
For Cellular Component

```
|   start <= 56335
|   |   start <= 48734
|   |   |   start <= 35848
|   |   |   |   start <= 15431
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 6426
|   |   |   |   |   |   |   start <= 3338: cellular_component_
(18.61)
|   |   |   |   |   |   |   start > 3338: vacuole_ (6.51)
|   |   |   |   |   |   start > 6426: cellular_component_ (44.83)
|   |   |   |   |   strand = C: cellular_component_ (84.1)
|   |   |   |   start > 15431
|   |   |   |   |   start <= 22787
|   |   |   |   |   |   start <= 17004: plasma_membrane_ (12.8)
|   |   |   |   |   |   start > 17004: membrane_ (15.99)
|   |   |   |   |   start > 22787
|   |   |   |   |   |   start <= 30540: cellular_component_ (39.4)
|   |   |   |   |   |   start > 30540: plasma_membrane_ (9.49)
|   |   |   start > 35848
|   |   |   |   start <= 45560
|   |   |   |   |   start <= 40180
|   |   |   |   |   |   start <= 36803: nucleus_ (12.96)
|   |   |   |   |   |   start > 36803: Golgi_apparatus_ (10.22)
|   |   |   |   |   start > 40180
|   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   start <= 40421: cytoplasm_ (18.68)
|   |   |   |   |   |   |   start > 40421: mitochondrion_ (14.63)
|   |   |   |   |   |   strand = C: cytoplasm_ (48.11/10.9)
|   |   |   |   start > 45560: cellular_component_ (49.53)
|   |   start > 48734
|   |   |   strand = W
|   |   |   |   start <= 51350: membrane_ (60.46/18.22)
|   |   |   |   start > 51350: microtubule_organizing_center_
(31.73)
|   |   |   strand = C
|   |   |   |   start <= 54695: cytoskeleton_ (64.02/43.34)
|   |   |   |   start > 54695: mitochondrion_ (22.48)
|   start > 56335
|   |   strand = W
|   |   |   start <= 153388
|   |   |   |   start <= 130329
|   |   |   |   |   start <= 107250
|   |   |   |   |   |   start <= 82578
|   |   |   |   |   |   |   start <= 79159
|   |   |   |   |   |   |   |   start <= 65475
|   |   |   |   |   |   |   |   |   start <= 58781: mitochondrion_
(16.92)
|   |   |   |   |   |   |   |   |   start > 58781: membrane_ (10.06)
|   |   |   |   |   |   |   |   start > 65475
|   |   |   |   |   |   |   |   |   start <= 75177: nucleus_ (13.63)
|   |   |   |   |   |   |   |   |   start > 75177: mitochondrion_
(8.5)
|   |   |   |   |   |   |   start > 79159: membrane_fraction_
(12.56)
|   |   |   |   |   |   start > 82578
|   |   |   |   |   |   |   start <= 90984: cytoplasm_ (17.56)
|   |   |   |   |   |   |   start > 90984
|   |   |   |   |   |   |   |   start <= 95964: nucleus_ (13.33)
|   |   |   |   |   |   |   |   start > 95964
|   |   |   |   |   |   |   |   |   start <= 101370: cytoplasm_
(11.08)
|   |   |   |   |   |   |   |   |   start > 101370: nucleus_
(36.53/14.49)
|   |   |   |   |   start > 107250
|   |   |   |   |   |   start <= 114984
|   |   |   |   |   |   |   start <= 112339
|   |   |   |   |   |   |   |   start <= 110641: cellular_component_
(15.51)
|   |   |   |   |   |   |   |   start > 110641
|   |   |   |   |   |   |   |   |   neigh_strand = W:
plasma_membrane_ (14.48/3.74)
|   |   |   |   |   |   |   |   |   neigh_strand = C: mitochondrion_
(18.22/5.82)
|   |   |   |   |   |   |   start > 112339: cellular_component_
(19.48)
|   |   |   |   |   |   start > 114984
|   |   |   |   |   |   |   start <= 123474: nucleus_ (50.43/12.03)
|   |   |   |   |   |   |   start > 123474: mitochondrion_ (24.02)
|   |   |   |   start > 130329
```

```
|   |   |   |   |   start <= 137554: endoplasmic_reticulum_ (14.78)
|   |   |   |   |   start > 137554: nucleus_ (109.7/37.26)
|   |   |   start > 153388
|   |   |   |   start <= 169216
|   |   |   |   |   start <= 167430
|   |   |   |   |   |   start <= 160529
|   |   |   |   |   |   |   start <= 156139: cytoplasm_ (7.38)
|   |   |   |   |   |   |   start > 156139: cellular_component_
(27.71)
|   |   |   |   |   |   start > 160529
|   |   |   |   |   |   |   start <= 162482
|   |   |   |   |   |   |   |   start <= 162222: cytoplasm_ (16.28)
|   |   |   |   |   |   |   |   start > 162222: ribosome_ (13.29)
|   |   |   |   |   |   |   start > 162482
|   |   |   |   |   |   |   |   start <= 165060: cellular_component_
(13.31)
|   |   |   |   |   |   |   |   start > 165060: cytoplasm_ (11.01)
|   |   |   |   |   start > 167430: cellular_component_ (25.1)
|   |   |   |   start > 169216
|   |   |   |   |   start <= 226950
|   |   |   |   |   |   start <= 203421
|   |   |   |   |   |   |   start <= 184490
|   |   |   |   |   |   |   |   start <= 176383: cellular_component_
(19.18/8.89)
|   |   |   |   |   |   |   |   start > 176383: mitochondrion_
(20.52)
|   |   |   |   |   |   |   start > 184490
|   |   |   |   |   |   |   |   start <= 194800: cytoplasm_ (15.29)
|   |   |   |   |   |   |   |   start > 194800: cellular_component_
(25.56)
|   |   |   |   |   |   start > 203421
|   |   |   |   |   |   |   start <= 207440: nucleus_ (30.59/14.0)
|   |   |   |   |   |   |   start > 207440
|   |   |   |   |   |   |   |   start <= 220094
|   |   |   |   |   |   |   |   |   start <= 210925:
plasma_membrane_ (14.86)
|   |   |   |   |   |   |   |   |   start > 210925: cytoplasm_
(14.36)
|   |   |   |   |   |   |   |   start > 220094: nucleus_ (15.2)
|   |   |   |   |   start > 226950
|   |   |   |   |   |   start <= 246133
|   |   |   |   |   |   |   start <= 239814
|   |   |   |   |   |   |   |   start <= 234229
|   |   |   |   |   |   |   |   |   start <= 229367:
cellular_component_ (6.47)
|   |   |   |   |   |   |   |   |   start > 229367: cytoplasm_
(13.92)
|   |   |   |   |   |   |   |   start > 234229: cellular_component_
(18.68)
|   |   |   |   |   |   |   start > 239814
|   |   |   |   |   |   |   |   start <= 241985:
mitochondrial_envelope_ (16.33)
|   |   |   |   |   |   |   |   start > 241985: cytoplasm_ (17.76)
|   |   |   |   |   |   start > 246133
```

```
|   |   |   |   |   |   |   start <= 249853: mitochondrion_ (22.25)
|   |   |   |   |   |   |   start > 249853: cellular_component_
(30.81)
|   |   strand = C
|   |   |   start <= 220094
|   |   |   |   start <= 99593
|   |   |   |   |   start <= 65475
|   |   |   |   |   |   start <= 63992: nucleus_ (28.21/12.29)
|   |   |   |   |   |   start > 63992: ribosome_ (14.01)
|   |   |   |   |   start > 65475
|   |   |   |   |   |   start <= 80211
|   |   |   |   |   |   |   start <= 75177
|   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_ (7.77/1.88)
|   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(7.43/2.61)
|   |   |   |   |   |   |   start > 75177: cytoplasm_ (27.21)
|   |   |   |   |   |   start > 80211
|   |   |   |   |   |   |   start <= 87232
|   |   |   |   |   |   |   |   start <= 82578: cellular_component_
(11.64)
|   |   |   |   |   |   |   |   start > 82578:
endoplasmic_reticulum_ (17.81)
|   |   |   |   |   |   |   start > 87232
|   |   |   |   |   |   |   |   start <= 90984: cellular_component_
(32.82/11.34)
|   |   |   |   |   |   |   |   start > 90984
|   |   |   |   |   |   |   |   |   start <= 95964: cytoplasm_
(12.07)
|   |   |   |   |   |   |   |   |   start > 95964:
cellular_component_ (14.22)
|   |   |   |   start > 99593
|   |   |   |   |   start <= 156139
|   |   |   |   |   |   start <= 137554
|   |   |   |   |   |   |   start <= 123474
|   |   |   |   |   |   |   |   start <= 103693: mitochondrion_
(12.86)
|   |   |   |   |   |   |   |   start > 103693
|   |   |   |   |   |   |   |   |   start <= 104456
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
nucleus_ (9.74/2.83)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cytoplasm_ (10.08/3.47)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cytoplasm_ (12.68/3.12)
|   |   |   |   |   |   |   |   |   start > 104456
|   |   |   |   |   |   |   |   |   |   start <= 107250:
mitochondrion_ (13.33)
|   |   |   |   |   |   |   |   |   |   start > 107250
|   |   |   |   |   |   |   |   |   |   |   start <= 112339:
nucleus_ (8.78)
|   |   |   |   |   |   |   |   |   |   |   start > 112339:
mitochondrion_ (37.19/15.97)
|   |   |   |   |   |   |   start > 123474
|   |   |   |   |   |   |   |   start <= 137152: chromosome_ (14.01)
```

```
|   |   |   |   |   |   |   |   start > 137152: cytoplasm_ (13.35)
|   |   |   |   |   |   start > 137554
|   |   |   |   |   |   |   start <= 150011: nucleolus_ (12.65)
|   |   |   |   |   |   |   start > 150011: nucleus_ (38.28)
|   |   |   |   |   start > 156139
|   |   |   |   |   |   start <= 182849: cytoplasm_ (173.95/55.63)
|   |   |   |   |   |   start > 182849
|   |   |   |   |   |   |   start <= 207440
|   |   |   |   |   |   |   |   start <= 184490: cellular_component_
(14.48)
|   |   |   |   |   |   |   |   start > 184490
|   |   |   |   |   |   |   |   |   start <= 203421
|   |   |   |   |   |   |   |   |   |   start <= 196821: cytoplasm_
(7.32)
|   |   |   |   |   |   |   |   |   |   start > 196821
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (9.28/3.93)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
mitochondrion_ (16.22/6.13)
|   |   |   |   |   |   |   |   |   start > 203421
|   |   |   |   |   |   |   |   |   |   start <= 204984
|   |   |   |   |   |   |   |   |   |   |   start <= 204738:
cellular_component_ (11.55)
|   |   |   |   |   |   |   |   |   |   |   start > 204738:
cytoplasm_ (16.51)
|   |   |   |   |   |   |   |   |   |   start > 204984:
cellular_component_ (14.21)
|   |   |   |   |   |   |   start > 207440
|   |   |   |   |   |   |   |   start <= 210056: nucleus_
(39.89/16.06)
|   |   |   |   |   |   |   |   start > 210056
|   |   |   |   |   |   |   |   |   start <= 213300: cytoplasm_
(17.86)
|   |   |   |   |   |   |   |   |   start > 213300: mitochondrion_
(11.75)
|   |   |   start > 220094
|   |   |   |   start <= 241985
|   |   |   |   |   start <= 239814
|   |   |   |   |   |   start <= 229367
|   |   |   |   |   |   |   start <= 223961
|   |   |   |   |   |   |   |   start <= 221406: ribosome_ (7.2)
|   |   |   |   |   |   |   |   start > 221406
|   |   |   |   |   |   |   |   |   start <= 223425
|   |   |   |   |   |   |   |   |   |   start <= 222947:
cellular_component_ (7.03)
|   |   |   |   |   |   |   |   |   |   start > 222947: cytoplasm_
(10.69)
|   |   |   |   |   |   |   |   |   start > 223425:
cellular_component_ (13.33)
|   |   |   |   |   |   |   start > 223961
|   |   |   |   |   |   |   |   start <= 225946
|   |   |   |   |   |   |   |   |   start <= 224757: mitochondrion_
(11.63)
|   |   |   |   |   |   |   |   |   start > 224757
```

```
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(5.05/0.7)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(24.08/10.6)
|   |   |   |   |   |   |   |   start > 225946
|   |   |   |   |   |   |   |   |   start <= 226453:
cellular_component_ (15.77)
|   |   |   |   |   |   |   |   |   start > 226453
|   |   |   |   |   |   |   |   |   |   start <= 226950:
mitochondrion_ (17.54)
|   |   |   |   |   |   |   |   |   |   start > 226950: nucleus_
(15.68)
|   |   |   |   |   |   start > 229367
|   |   |   |   |   |   |   start <= 234229: cellular_component_
(21.8)
|   |   |   |   |   |   |   start > 234229
|   |   |   |   |   |   |   |   start <= 238445:
endoplasmic_reticulum_ (16.98)
|   |   |   |   |   |   |   |   start > 238445: cellular_component_
(20.25)
|   |   |   |   |   start > 239814: cytoplasm_ (39.56/25.6)
|   |   |   |   start > 241985
|   |   |   |   |   start <= 246133: nucleus_ (50.94/13.94)
|   |   |   |   |   start > 246133
|   |   |   |   |   |   start <= 249853: cellular_component_ (20.55)
|   |   |   |   |   |   start > 249853
|   |   |   |   |   |   |   start <= 252492: Golgi_apparatus_
(12.58)
|   |   |   |   |   |   |   start > 252492: cytoplasm_ (10.28)
```

For Molecular Function

```
|   start <= 153119
|   |   start <= 51350
|   |   |   start <= 12929
|   |   |   |   start <= 10969: molecular_function_ (78.44)
|   |   |   |   start > 10969
|   |   |   |   |   start <= 11363: protein_binding_ (28.68)
|   |   |   |   |   start > 11363: molecular_function_ (15.77)
|   |   |   start > 12929
|   |   |   |   start <= 28232
|   |   |   |   |   start <= 22787
|   |   |   |   |   |   start <= 15431: oxidoreductase_activity_
(29.26)
|   |   |   |   |   |   start > 15431: transporter_activity_ (38.71)
|   |   |   |   |   start > 22787
|   |   |   |   |   |   start <= 23423: transferase_activity_
(25.47)
|   |   |   |   |   |   start > 23423: DNA_binding_ (18.41)
|   |   |   |   start > 28232
|   |   |   |   |   start <= 48734
|   |   |   |   |   |   start <= 40421
|   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   start <= 36803:
transcription_regulator_activity_ (16.69)
|   |   |   |   |   |   |   |   start > 36803:
enzyme_regulator_activity_ (17.34)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 36803
|   |   |   |   |   |   |   |   |   start <= 30540:
molecular_function_ (9.23)
|   |   |   |   |   |   |   |   |   start > 30540:
transporter_activity_ (12.62)
|   |   |   |   |   |   |   |   start > 36803: molecular_function_
(12.61)
|   |   |   |   |   |   start > 40421
|   |   |   |   |   |   |   strand = W: molecular_function_ (42.08)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 44392: isomerase_activity_
(17.58)
|   |   |   |   |   |   |   |   start > 44392
|   |   |   |   |   |   |   |   |   start <= 45560:
peptidase_activity_ (16.03)
|   |   |   |   |   |   |   |   |   start > 45560:
molecular_function_ (15.08)
|   |   |   |   |   start > 48734
|   |   |   |   |   |   start <= 49139: oxidoreductase_activity_
(12.73)
|   |   |   |   |   |   start > 49139: transporter_activity_ (17.75)
|   |   start > 51350
|   |   |   start <= 90343
|   |   |   |   start <= 65475
|   |   |   |   |   start <= 56335
|   |   |   |   |   |   strand = W: structural_molecule_activity_
(30.67)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 54695:
structural_molecule_activity_ (17.51)
|   |   |   |   |   |   |   start > 54695: hydrolase_activity_
(15.1)
|   |   |   |   |   start > 56335
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 58781:
nucleotidyltransferase_activity_ (20.33)
|   |   |   |   |   |   |   start > 58781: molecular_function_
(7.13)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 63992:
enzyme_regulator_activity_ (20.1)
|   |   |   |   |   |   |   start > 63992:
structural_molecule_activity_ (10.38)
|   |   |   |   start > 65475
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 75177: DNA_binding_ (27.17/7.47)
|   |   |   |   |   |   start > 75177
|   |   |   |   |   |   |   start <= 79159: transferase_activity_
(13.49)
```

```
|   |   |   |   |   |   |   start > 79159:
signal_transducer_activity_ (17.49)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 79159: protein_kinase_activity_
(22.11)
|   |   |   |   |   |   start > 79159
|   |   |   |   |   |   |   start <= 87232
|   |   |   |   |   |   |   |   start <= 82578
|   |   |   |   |   |   |   |   |   start <= 80211:
hydrolase_activity_ (19.21)
|   |   |   |   |   |   |   |   |   start > 80211:
enzyme_regulator_activity_ (13.94)
|   |   |   |   |   |   |   |   start > 82578: hydrolase_activity_
(24.34)
|   |   |   |   |   |   |   start > 87232: transferase_activity_
(18.83)
|   |   |   start > 90343
|   |   |   |   start <= 116139
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 95964
|   |   |   |   |   |   |   start <= 90984: molecular_function_
(12.4)
|   |   |   |   |   |   |   start > 90984:
transcription_regulator_activity_ (20.92)
|   |   |   |   |   |   start > 95964
|   |   |   |   |   |   |   start <= 110641
|   |   |   |   |   |   |   |   start <= 104456
|   |   |   |   |   |   |   |   |   start <= 101370:
molecular_function_ (11.97)
|   |   |   |   |   |   |   |   |   start > 101370: RNA_binding_
(6.45)
|   |   |   |   |   |   |   |   start > 104456: molecular_function_
(21.69)
|   |   |   |   |   |   |   start > 110641
|   |   |   |   |   |   |   |   start <= 112339:
transporter_activity_ (18.35)
|   |   |   |   |   |   |   |   start > 112339: molecular_function_
(27.59)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 103693
|   |   |   |   |   |   |   start <= 99593
|   |   |   |   |   |   |   |   start <= 95964: ligase_activity_
(16.0)
|   |   |   |   |   |   |   |   start > 95964: molecular_function_
(11.89)
|   |   |   |   |   |   |   start > 99593: oxidoreductase_activity_
(22.45)
|   |   |   |   |   |   start > 103693
|   |   |   |   |   |   |   start <= 107250
|   |   |   |   |   |   |   |   start <= 104456:
transferase_activity_ (11.59)
|   |   |   |   |   |   |   |   start > 104456: protein_binding_
(10.42)
```

```
|   |   |   |   |   |   |   start > 107250: molecular_function_ 
(24.8)
|   |   |   |   start > 116139
|   |   |   |   |   start <= 146929
|   |   |   |   |   |   start <= 130329
|   |   |   |   |   |   |   start <= 123474
|   |   |   |   |   |   |   |   start <= 119424: DNA_binding_ (8.79)
|   |   |   |   |   |   |   |   start > 119424: 
enzyme_regulator_activity_ (19.61)
|   |   |   |   |   |   |   start > 123474: hydrolase_activity_ 
(12.13)
|   |   |   |   |   |   start > 130329
|   |   |   |   |   |   |   start <= 137554
|   |   |   |   |   |   |   |   strand = W: molecular_function_ 
(16.67)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 137152: DNA_binding_ 
(3.28)
|   |   |   |   |   |   |   |   |   start > 137152: 
molecular_function_ (6.06)
|   |   |   |   |   |   |   start > 137554: helicase_activity_ 
(5.62)
|   |   |   |   |   start > 146929
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 147126: isomerase_activity_ 
(17.61)
|   |   |   |   |   |   |   start > 147126
|   |   |   |   |   |   |   |   start <= 149105: RNA_binding_ 
(13.34)
|   |   |   |   |   |   |   |   start > 149105: 
structural_molecule_activity_ (15.33)
|   |   |   |   |   |   strand = C: enzyme_regulator_activity_ 
(26.62)
|   start > 153119
|   |   start <= 207440
|   |   |   start <= 156139
|   |   |   |   strand = W: peptidase_activity_ (38.21)
|   |   |   |   strand = C: RNA_binding_ (16.62)
|   |   |   start > 156139
|   |   |   |   start <= 173869
|   |   |   |   |   start <= 169216
|   |   |   |   |   |   start <= 162482
|   |   |   |   |   |   |   start <= 162222: molecular_function_ 
(51.68)
|   |   |   |   |   |   |   start > 162222: hydrolase_activity_ 
(16.14)
|   |   |   |   |   |   start > 162482
|   |   |   |   |   |   |   start <= 165060: peptidase_activity_ 
(11.16)
|   |   |   |   |   |   |   start > 165060: molecular_function_ 
(50.3)
|   |   |   |   |   start > 169216
|   |   |   |   |   |   start <= 169914: protein_binding_ (16.92)
```

```
|   |   |   |   |   |   start > 169914: protein_kinase_activity_
(16.92)
|   |   |   |   start > 173869
|   |   |   |   |   start <= 176383: transferase_activity_ (18.01)
|   |   |   |   |   start > 176383
|   |   |   |   |   |   start <= 203421
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 184490
|   |   |   |   |   |   |   |   |   neigh_strand = W:
molecular_function_ (12.02/4.49)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
transferase_activity_ (20.05/5.27)
|   |   |   |   |   |   |   |   start > 184490: molecular_function_
(30.56)
|   |   |   |   |   |   |   strand = C: molecular_function_ (117.94)
|   |   |   |   |   |   start > 203421
|   |   |   |   |   |   |   start <= 204738: hydrolase_activity_
(19.96)
|   |   |   |   |   |   |   start > 204738: molecular_function_
(48.96)
|   |   start > 207440
|   |   |   start <= 239814
|   |   |   |   start <= 225946
|   |   |   |   |   start <= 210925
|   |   |   |   |   |   start <= 210056:
phosphoprotein_phosphatase_activity_ (13.43)
|   |   |   |   |   |   start > 210056: molecular_function_ (28.41)
|   |   |   |   |   start > 210925
|   |   |   |   |   |   start <= 224757
|   |   |   |   |   |   |   start <= 220094
|   |   |   |   |   |   |   |   start <= 213300:
oxidoreductase_activity_ (15.14)
|   |   |   |   |   |   |   |   start > 213300: DNA_binding_ (10.99)
|   |   |   |   |   |   |   start > 220094
|   |   |   |   |   |   |   |   start <= 223961
|   |   |   |   |   |   |   |   |   start <= 223425
|   |   |   |   |   |   |   |   |   |   start <= 222947
|   |   |   |   |   |   |   |   |   |   |   start <= 221406:
structural_molecule_activity_ (8.46)
|   |   |   |   |   |   |   |   |   |   |   start > 221406:
molecular_function_ (7.78)
|   |   |   |   |   |   |   |   |   |   start > 222947:
structural_molecule_activity_ (9.48)
|   |   |   |   |   |   |   |   |   start > 223425:
molecular_function_ (12.34)
|   |   |   |   |   |   |   |   start > 223961:
oxidoreductase_activity_ (9.77)
|   |   |   |   |   |   start > 224757
|   |   |   |   |   |   |   neigh_num <= 1: DNA_binding_
(10.41/3.34)
|   |   |   |   |   |   |   neigh_num > 1:
transcription_regulator_activity_ (16.7/6.23)
|   |   |   |   start > 225946
|   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   start <= 226950: protein_binding_ (26.71)
|   |   |   |   |   |   start > 226950
|   |   |   |   |   |   |   start <= 234229
|   |   |   |   |   |   |   |   start <= 229367: molecular_function_
(10.55)
|   |   |   |   |   |   |   |   start > 229367:
phosphoprotein_phosphatase_activity_ (14.86)
|   |   |   |   |   |   |   start > 234229: molecular_function_
(14.76)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 229367
|   |   |   |   |   |   |   start <= 226950: molecular_function_
(40.99)
|   |   |   |   |   |   |   start > 226950: hydrolase_activity_
(7.97)
|   |   |   |   |   |   start > 229367: molecular_function_ (48.02)
|   |   |   start > 239814
|   |   |   |   start <= 241985
|   |   |   |   |   start <= 241424: peptidase_activity_ (19.02)
|   |   |   |   |   start > 241424: transporter_activity_ (20.69)
|   |   |   |   start > 241985
|   |   |   |   |   start <= 248510
|   |   |   |   |   |   start <= 246133
|   |   |   |   |   |   |   start <= 244146: molecular_function_
(18.04)
|   |   |   |   |   |   |   start > 244146
|   |   |   |   |   |   |   |   start <= 245153:
transferase_activity_ (14.3)
|   |   |   |   |   |   |   |   start > 245153: molecular_function_
(13.37)
|   |   |   |   |   |   start > 246133:
structural_molecule_activity_ (17.88)
|   |   |   |   |   start > 248510
|   |   |   |   |   |   start <= 252492
|   |   |   |   |   |   |   start <= 249853: peptidase_activity_
(16.27)
|   |   |   |   |   |   |   start > 249853
|   |   |   |   |   |   |   |   start <= 251790: protein_binding_
(15.87)
|   |   |   |   |   |   |   |   start > 251790: peptidase_activity_
(12.44)
|   |   |   |   |   |   start > 252492
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 264191: lyase_activity_
(6.81)
|   |   |   |   |   |   |   |   start > 264191: molecular_function_
(5.91)
|   |   |   |   |   |   |   strand = C: transferase_activity_
(15.28)
```

For Biological Process

```
|   start <= 55985
|   |   start <= 15431
|   |   |   start <= 9545: biological_process_ (88.17)
```

```
|   |   |   start > 9545
|   |   |   |   start <= 12929: vitamin_metabolic_process_ (41.98)
|   |   |   |   start > 12929: biological_process_ (36.7)
|   |   start > 15431
|   |   |   start <= 48734
|   |   |   |   start <= 23423
|   |   |   |   |   start <= 22787: transport_ (31.55)
|   |   |   |   |   start > 22787: response_to_stress_ (13.61)
|   |   |   |   start > 23423
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 40421
|   |   |   |   |   |   |   start <= 36803
|   |   |   |   |   |   |   |   start <= 30540: biological_process_
(13.39)
|   |   |   |   |   |   |   |   start > 30540: transcription_
(19.05)
|   |   |   |   |   |   |   start > 36803: signal_transduction_
(19.43)
|   |   |   |   |   |   start > 40421: biological_process_ (33.64)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 44392
|   |   |   |   |   |   |   start <= 30540: biological_process_
(10.22)
|   |   |   |   |   |   |   start > 30540
|   |   |   |   |   |   |   |   start <= 40421
|   |   |   |   |   |   |   |   |   start <= 36803: transport_
(16.18)
|   |   |   |   |   |   |   |   |   start > 36803: vesicle-
mediated_transport_ (27.39/11.76)
|   |   |   |   |   |   |   |   start > 40421: transport_ (21.46)
|   |   |   |   |   |   start > 44392
|   |   |   |   |   |   |   start <= 45560: transcription_ (12.62)
|   |   |   |   |   |   |   start > 45560: biological_process_
(15.95)
|   |   |   start > 48734
|   |   |   |   strand = W: transport_ (36.94)
|   |   |   |   strand = C
|   |   |   |   |   start <= 54695: cytokinesis_ (32.01/14.2)
|   |   |   |   |   start > 54695: transport_ (38.92/18.85)
|   start > 55985
|   |   start <= 155868
|   |   |   start <= 137554
|   |   |   |   start <= 107250
|   |   |   |   |   start <= 63992
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 56335: cell_cycle_
(42.94/15.18)
|   |   |   |   |   |   |   start > 56335:
organelle_organization_and_biogenesis_ (34.44/12.07)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   neigh_num <= 1:
protein_modification_process_ (13.36/3.57)
|   |   |   |   |   |   |   neigh_num > 1: biological_process_
(15.71/6.28)
```

```
|   |   |   |   |   start > 63992
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 79159
|   |   |   |   |   |   |   |   start <= 65475: biological_process_
(16.66)
|   |   |   |   |   |   |   |   start > 65475
|   |   |   |   |   |   |   |   |   start <= 75177
|   |   |   |   |   |   |   |   |   |   distance <= 2260:
response_to_stress_ (21.29/10.45)
|   |   |   |   |   |   |   |   |   |   distance > 2260:
lipid_metabolic_process_ (14.28/7.87)
|   |   |   |   |   |   |   |   |   start > 75177:
amino_acid_and_derivative_metabolic_process_ (5.96)
|   |   |   |   |   |   |   start > 79159
|   |   |   |   |   |   |   |   start <= 90984
|   |   |   |   |   |   |   |   |   start <= 82578: conjugation_
(14.95)
|   |   |   |   |   |   |   |   |   start > 82578: cytokinesis_
(14.7)
|   |   |   |   |   |   |   |   start > 90984
|   |   |   |   |   |   |   |   |   start <= 101370
|   |   |   |   |   |   |   |   |   |   start <= 95964:
transcription_ (13.14)
|   |   |   |   |   |   |   |   |   |   start > 95964: translation_
(7.26)
|   |   |   |   |   |   |   |   |   start > 101370
|   |   |   |   |   |   |   |   |   |   start <= 104456:
RNA_metabolic_process_ (8.31)
|   |   |   |   |   |   |   |   |   |   start > 104456:
response_to_stress_ (11.12)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 95964
|   |   |   |   |   |   |   |   start <= 80211
|   |   |   |   |   |   |   |   |   start <= 75177
|   |   |   |   |   |   |   |   |   |   start <= 65475: translation_
(11.62)
|   |   |   |   |   |   |   |   |   |   start > 65475:
response_to_stress_ (5.47)
|   |   |   |   |   |   |   |   |   start > 75177
|   |   |   |   |   |   |   |   |   |   start <= 79159: meiosis_
(13.73)
|   |   |   |   |   |   |   |   |   |   start > 79159:
transcription_ (16.3)
|   |   |   |   |   |   |   |   start > 80211
|   |   |   |   |   |   |   |   |   start <= 87232
|   |   |   |   |   |   |   |   |   |   start <= 82578: vesicle-
mediated_transport_ (16.24)
|   |   |   |   |   |   |   |   |   |   start > 82578:
organelle_organization_and_biogenesis_ (9.0)
|   |   |   |   |   |   |   |   |   start > 87232
|   |   |   |   |   |   |   |   |   |   start <= 90984:
DNA_metabolic_process_ (15.63)
|   |   |   |   |   |   |   |   |   |   start > 90984: translation_
(13.18)
```

```
|   |   |   |   |   |   |   start > 95964
|   |   |   |   |   |   |   |   start <= 103693
|   |   |   |   |   |   |   |   |   start <= 99593:
biological_process_ (17.9)
|   |   |   |   |   |   |   |   |   start > 99593:
amino_acid_and_derivative_metabolic_process_ (11.69)
|   |   |   |   |   |   |   |   start > 103693
|   |   |   |   |   |   |   |   |   start <= 104456:
carbohydrate_metabolic_process_ (8.94)
|   |   |   |   |   |   |   |   |   start > 104456:
biological_process_ (11.05)
|   |   |   |   start > 107250
|   |   |   |   |   start <= 115737
|   |   |   |   |   |   start <= 109924: DNA_metabolic_process_
(19.33)
|   |   |   |   |   |   start > 109924
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 110641: biological_process_
(12.06)
|   |   |   |   |   |   |   |   start > 110641: transport_ (53.46)
|   |   |   |   |   |   |   strand = C: biological_process_ (13.4)
|   |   |   |   |   start > 115737
|   |   |   |   |   |   start <= 130329
|   |   |   |   |   |   |   start <= 119424
|   |   |   |   |   |   |   |   start <= 116139: meiosis_ (10.34)
|   |   |   |   |   |   |   |   start > 116139: cell_cycle_
(25.08/8.81)
|   |   |   |   |   |   |   start > 119424
|   |   |   |   |   |   |   |   start <= 123474:
protein_catabolic_process_ (15.75)
|   |   |   |   |   |   |   |   start > 123474: cytokinesis_ (19.08)
|   |   |   |   |   |   start > 130329
|   |   |   |   |   |   |   strand = W:
membrane_organization_and_biogenesis_ (35.77/21.22)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 137152
|   |   |   |   |   |   |   |   |   neigh_strand = W: cell_cycle_
(14.53/5.68)
|   |   |   |   |   |   |   |   |   neigh_strand = C: meiosis_
(11.48/5.86)
|   |   |   |   |   |   |   |   start > 137152: translation_ (13.83)
|   |   |   start > 137554
|   |   |   |   start <= 150011
|   |   |   |   |   start <= 149105
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 147126: RNA_metabolic_process_
(11.66)
|   |   |   |   |   |   |   start > 147126:
ribosome_biogenesis_and_assembly_ (13.14)
|   |   |   |   |   |   strand = C:
ribosome_biogenesis_and_assembly_ (17.68)
|   |   |   |   |   start > 149105:
nuclear_organization_and_biogenesis_ (22.31)
|   |   |   |   start > 150011
```

```
|   |   |   |   |   strand = W: protein_catabolic_process_ (15.46)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 153388:
protein_modification_process_ (21.03)
|   |   |   |   |   |   start > 153388: RNA_metabolic_process_
(13.5)
|   |   start > 155868
|   |   |   start <= 204984
|   |   |   |   start <= 184210
|   |   |   |   |   start <= 167430
|   |   |   |   |   |   start <= 160529
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 159293: biological_process_
(29.43)
|   |   |   |   |   |   |   |   start > 159293: conjugation_ (12.9)
|   |   |   |   |   |   |   strand = C: translation_ (12.58)
|   |   |   |   |   |   start > 160529
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 162482: translation_ (28.7)
|   |   |   |   |   |   |   |   start > 162482
|   |   |   |   |   |   |   |   |   start <= 165060:
protein_modification_process_ (9.19)
|   |   |   |   |   |   |   |   |   start > 165060: translation_
(12.13)
|   |   |   |   |   |   |   strand = C: biological_process_ (9.79)
|   |   |   |   |   start > 167430
|   |   |   |   |   |   start <= 176383
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 169216: biological_process_
(24.64)
|   |   |   |   |   |   |   |   start > 169216:
DNA_metabolic_process_ (6.41)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 173869:
signal_transduction_ (20.75)
|   |   |   |   |   |   |   |   start > 173869
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
carbohydrate_metabolic_process_ (25.37/7.01)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
generation_of_precursor_metabolites_and_energy_ (16.84/6.57)
|   |   |   |   |   |   start > 176383
|   |   |   |   |   |   |   start <= 181036
|   |   |   |   |   |   |   |   start <= 180735: biological_process_
(12.21)
|   |   |   |   |   |   |   |   start > 180735: translation_ (25.33)
|   |   |   |   |   |   |   start > 181036: biological_process_
(43.67)
|   |   |   |   start > 184210
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 194800:
organelle_organization_and_biogenesis_ (29.06)
|   |   |   |   |   |   start > 194800: biological_process_ (17.86)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 203421
```

```
|   |   |   |   |   |   |   start <= 196821: translation_ (7.01)
|   |   |   |   |   |   |   start > 196821:
cytoskeleton_organization_and_biogenesis_ (17.17)
|   |   |   |   |   |   start > 203421
|   |   |   |   |   |   |   start <= 204738:
amino_acid_and_derivative_metabolic_process_ (10.03)
|   |   |   |   |   |   |   start > 204738: translation_ (15.65)
|   |   |   start > 204984
|   |   |   |   start <= 241424
|   |   |   |   |   start <= 226950
|   |   |   |   |   |   start <= 207440
|   |   |   |   |   |   |   start <= 206245: biological_process_
(20.13)
|   |   |   |   |   |   |   start > 206245: DNA_metabolic_process_
(14.5)
|   |   |   |   |   |   start > 207440
|   |   |   |   |   |   |   start <= 223961
|   |   |   |   |   |   |   |   start <= 210056: cell_cycle_ (23.79)
|   |   |   |   |   |   |   |   start > 210056
|   |   |   |   |   |   |   |   |   start <= 210695: translation_
(12.95)
|   |   |   |   |   |   |   |   |   start > 210695
|   |   |   |   |   |   |   |   |   |   start <= 220094
|   |   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (26.55)
|   |   |   |   |   |   |   |   |   |   |   strand = C: cell_cycle_
(15.02)
|   |   |   |   |   |   |   |   |   |   start > 220094
|   |   |   |   |   |   |   |   |   |   |   start <= 221406:
translation_ (8.03)
|   |   |   |   |   |   |   |   |   |   |   start > 221406
|   |   |   |   |   |   |   |   |   |   |   |   start <= 223425
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 222947:
biological_process_ (7.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 222947:
translation_ (5.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 223425:
biological_process_ (12.19)
|   |   |   |   |   |   |   start > 223961
|   |   |   |   |   |   |   |   strand = W: cell_cycle_ (15.53)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 225946
|   |   |   |   |   |   |   |   |   |   start <= 224757
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
electron_transport_ (8.24/2.7)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_respiration_ (19.82/7.77)
|   |   |   |   |   |   |   |   |   |   start > 224757:
response_to_stress_ (8.33)
|   |   |   |   |   |   |   |   |   start > 225946
|   |   |   |   |   |   |   |   |   |   start <= 226453:
biological_process_ (14.85)
|   |   |   |   |   |   |   |   |   |   start > 226453: translation_
(13.4)
```

```
|   |   |   |   |   start > 226950
|   |   |   |   |   |   start <= 229173: transcription_ (14.5)
|   |   |   |   |   |   start > 229173
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 229367: biological_process_
(19.95)
|   |   |   |   |   |   |   |   start > 229367
|   |   |   |   |   |   |   |   |   start <= 234229: cell_cycle_
(18.76)
|   |   |   |   |   |   |   |   |   start > 234229:
biological_process_ (18.22)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 238445
|   |   |   |   |   |   |   |   |   start <= 234229:
biological_process_ (23.08)
|   |   |   |   |   |   |   |   |   start > 234229:
DNA_metabolic_process_ (13.23)
|   |   |   |   |   |   |   |   start > 238445: biological_process_
(34.72)
|   |   |   |   start > 241424
|   |   |   |   |   start <= 248510
|   |   |   |   |   |   start <= 246133
|   |   |   |   |   |   |   start <= 241985: transport_ (12.92)
|   |   |   |   |   |   |   start > 241985
|   |   |   |   |   |   |   |   start <= 244146: biological_process_
(21.49)
|   |   |   |   |   |   |   |   start > 244146
|   |   |   |   |   |   |   |   |   start <= 245153:
vitamin_metabolic_process_ (16.88)
|   |   |   |   |   |   |   |   |   start > 245153:
biological_process_ (14.87)
|   |   |   |   |   |   start > 246133: translation_ (18.69)
|   |   |   |   |   start > 248510
|   |   |   |   |   |   start <= 252492
|   |   |   |   |   |   |   strand = W: protein_catabolic_process_
(13.64)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 249853:
protein_catabolic_process_ (11.92)
|   |   |   |   |   |   |   |   start > 249853
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C: transport_
(9.04/2.3)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: vesicle-
mediated_transport_ (8.39/1.63)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: transport_
(2.84/0.67)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P: transport_
(7.41/2.37)
|   |   |   |   |   |   start > 252492
|   |   |   |   |   |   |   strand = W: biological_process_ (12.49)
|   |   |   |   |   |   |   strand = C:
carbohydrate_metabolic_process_ (12.14)
```

Decision Tree Generated for Chromosome Seven:
For Cellular Component

```
|   start <= 299731
|   |   start <= 62075
|   |   |   start <= 20978
|   |   |   |   start <= 14157: cellular_component_ (110.35)
|   |   |   |   start > 14157
|   |   |   |   |   start <= 14910: mitochondrion_ (22.2)
|   |   |   |   |   start > 14910: plasma_membrane_ (13.26)
|   |   |   start > 20978
|   |   |   |   start <= 55796
|   |   |   |   |   start <= 45445
|   |   |   |   |   |   start <= 33098
|   |   |   |   |   |   |   start <= 31910
|   |   |   |   |   |   |   |   start <= 23935: nucleus_
(51.08/14.51)
|   |   |   |   |   |   |   |   start > 23935
|   |   |   |   |   |   |   |   |   start <= 27484: cytoplasm_
(25.0)
|   |   |   |   |   |   |   |   |   start > 27484: nucleus_
(51.32/14.46)
|   |   |   |   |   |   |   start > 31910: chromosome_ (31.57/10.86)
|   |   |   |   |   |   start > 33098
|   |   |   |   |   |   |   start <= 36933
|   |   |   |   |   |   |   |   start <= 35653: cellular_component_
(13.23)
|   |   |   |   |   |   |   |   start > 35653: endomembrane_system_
(13.14)
|   |   |   |   |   |   |   start > 36933
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 39023: cytoplasm_
(15.45)
|   |   |   |   |   |   |   |   |   start > 39023: nucleus_
(62.74/9.28)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 41498: nucleus_ (14.89)
|   |   |   |   |   |   |   |   |   start > 41498:
cellular_component_ (12.2)
|   |   |   |   |   start > 45445
|   |   |   |   |   |   stop <= 53787
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 48613: mitochondrion_
(23.28)
|   |   |   |   |   |   |   |   start > 48613: endomembrane_system_
(11.25)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 53528: nucleus_ (10.96)
|   |   |   |   |   |   |   |   start > 53528: mitochondrion_
(12.71)
|   |   |   |   |   |   stop > 53787: cellular_component_ (17.88)
|   |   |   |   start > 55796
|   |   |   |   |   start <= 59122
|   |   |   |   |   |   start <= 56482: cytoplasm_ (20.71)
```

```
|   |   |   |   |   |   start > 56482
|   |   |   |   |   |   |   Neigh_GO_aspect = C: cellular_bud_
(11.3/3.15)
|   |   |   |   |   |   |   Neigh_GO_aspect = F:
site_of_polarized_growth_ (8.56/2.98)
|   |   |   |   |   |   |   Neigh_GO_aspect = P:
site_of_polarized_growth_ (16.48/6.96)
|   |   |   |   |   start > 59122
|   |   |   |   |   |   neigh_num <= 1: nucleus_ (12.62/2.91)
|   |   |   |   |   |   neigh_num > 1: cytoplasm_ (14.91/5.42)
|   |   start > 62075
|   |   |   start <= 124703
|   |   |   |   start <= 98973
|   |   |   |   |   start <= 84256
|   |   |   |   |   |   start <= 80364
|   |   |   |   |   |   |   start <= 73901
|   |   |   |   |   |   |   |   start <= 67598
|   |   |   |   |   |   |   |   |   start <= 63620:
endoplasmic_reticulum_ (12.27)
|   |   |   |   |   |   |   |   |   start > 63620
|   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (22.58)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 64215:
cellular_component_ (17.59)
|   |   |   |   |   |   |   |   |   |   |   start > 64215:
cytoplasm_ (30.81/14.05)
|   |   |   |   |   |   |   |   start > 67598
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 69671: cytoplasm_
(31.74/15.56)
|   |   |   |   |   |   |   |   |   |   start > 69671:
mitochondrion_ (19.43)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 73339: membrane_
(26.32/10.52)
|   |   |   |   |   |   |   |   |   |   start > 73339: cytoplasm_
(14.6)
|   |   |   |   |   |   |   start > 73901
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   neigh_strand = W:
Golgi_apparatus_ (25.2/11.32)
|   |   |   |   |   |   |   |   |   neigh_strand = C: mitochondrion_
(18.15/7.41)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 78856:
cellular_component_ (26.98)
|   |   |   |   |   |   |   |   |   start > 78856: Golgi_apparatus_
(20.87)
|   |   |   |   |   |   start > 80364: cytoplasm_ (129.37/46.2)
|   |   |   |   |   start > 84256
|   |   |   |   |   |   start <= 93797
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 91436
```

```
|   |   |   |   |   |   |   |   |   start <= 87980
|   |   |   |   |   |   |   |   |   |   start <= 84884: nucleus_
(13.91)
|   |   |   |   |   |   |   |   |   |   start > 84884:
cellular_component_ (12.3)
|   |   |   |   |   |   |   |   |   start > 87980: membrane_
(34.39/17.09)
|   |   |   |   |   |   |   |   start > 91436
|   |   |   |   |   |   |   |   |   start <= 92516: mitochondrion_
(20.46)
|   |   |   |   |   |   |   |   |   start > 92516: Golgi_apparatus_
(16.27)
|   |   |   |   |   |   |   strand = C: chromosome_ (15.79)
|   |   |   |   |   |   start > 93797
|   |   |   |   |   |   |   start <= 97342
|   |   |   |   |   |   |   |   start <= 95862: nucleus_ (28.99)
|   |   |   |   |   |   |   |   start > 95862: cytoplasm_
(45.07/22.42)
|   |   |   |   |   |   |   start > 97342: cellular_component_
(62.05/35.96)
|   |   |   |   start > 98973
|   |   |   |   |   start <= 108162
|   |   |   |   |   |   start <= 107508
|   |   |   |   |   |   |   distance <= 9983: cytoplasm_
(32.87/16.26)
|   |   |   |   |   |   |   distance > 9983
|   |   |   |   |   |   |   |   neigh_num <= 1: membrane_
(2.59/0.77)
|   |   |   |   |   |   |   |   neigh_num > 1: cytoplasmic_membrane-
bound_vesicle_ (14.93/7.14)
|   |   |   |   |   |   start > 107508: peroxisome_ (16.93)
|   |   |   |   |   start > 108162
|   |   |   |   |   |   start <= 120911
|   |   |   |   |   |   |   start <= 114668
|   |   |   |   |   |   |   |   start <= 110700: cytoplasm_ (17.37)
|   |   |   |   |   |   |   |   start > 110700: Golgi_apparatus_
(18.82)
|   |   |   |   |   |   |   start > 114668: cytoplasm_ (58.48/15.28)
|   |   |   |   |   |   start > 120911
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 123596
|   |   |   |   |   |   |   |   |   start <= 122273: mitochondrion_
(19.49)
|   |   |   |   |   |   |   |   |   start > 122273: Golgi_apparatus_
(30.39)
|   |   |   |   |   |   |   |   start > 123596: cytoplasm_
(20.43/8.07)
|   |   |   |   |   |   |   strand = C: endoplasmic_reticulum_
(16.76)
|   |   |   start > 124703
|   |   |   |   start <= 190474
|   |   |   |   |   start <= 152782
|   |   |   |   |   |   start <= 150177
|   |   |   |   |   |   |   start <= 142252
```

```
|   |   |   |   |   |   |   |   start <= 131531
|   |   |   |   |   |   |   |   |   start <= 129888:
cellular_component_ (18.65)
|   |   |   |   |   |   |   |   |   start > 129888: mitochondrion_
(13.49)
|   |   |   |   |   |   |   |   start > 131531: cellular_component_
(93.49/14.03)
|   |   |   |   |   |   |   start > 142252
|   |   |   |   |   |   |   |   start <= 148594
|   |   |   |   |   |   |   |   |   strand = W: mitochondrion_
(24.62)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 147395: nucleus_
(11.87)
|   |   |   |   |   |   |   |   |   |   start > 147395: ribosome_
(17.23)
|   |   |   |   |   |   |   |   start > 148594
|   |   |   |   |   |   |   |   |   start <= 148970:
cellular_component_ (21.94)
|   |   |   |   |   |   |   |   |   start > 148970: mitochondrion_
(15.0)
|   |   |   |   |   |   start > 150177: plasma_membrane_ (18.53)
|   |   |   |   |   start > 152782
|   |   |   |   |   |   start <= 180119
|   |   |   |   |   |   |   start <= 157291
|   |   |   |   |   |   |   |   start <= 156018
|   |   |   |   |   |   |   |   |   start <= 154312: cytoplasm_
(17.25)
|   |   |   |   |   |   |   |   |   start > 154312:
cellular_component_ (25.59)
|   |   |   |   |   |   |   |   start > 156018: chromosome_ (17.95)
|   |   |   |   |   |   |   start > 157291
|   |   |   |   |   |   |   |   start <= 167358: cytoplasm_
(62.3/7.57)
|   |   |   |   |   |   |   |   start > 167358
|   |   |   |   |   |   |   |   |   start <= 173085:
cellular_component_ (19.95)
|   |   |   |   |   |   |   |   |   start > 173085
|   |   |   |   |   |   |   |   |   |   start <= 174551: nucleus_
(45.47/12.93)
|   |   |   |   |   |   |   |   |   |   start > 174551: cytoplasm_
(15.77)
|   |   |   |   |   |   start > 180119
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 182396
|   |   |   |   |   |   |   |   |   start <= 180706:
endomembrane_system_ (19.33)
|   |   |   |   |   |   |   |   |   start > 180706: nucleolus_
(33.27)
|   |   |   |   |   |   |   |   start > 182396
|   |   |   |   |   |   |   |   |   start <= 186065: cytoplasm_
(14.71)
|   |   |   |   |   |   |   |   |   start > 186065:
cellular_component_ (16.67)
```

```
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 185400:
microtubule_organizing_center_ (20.34)
|   |   |   |   |   |   |   |   start > 185400
|   |   |   |   |   |   |   |   |   start <= 187470: mitochondrion_
(19.36)
|   |   |   |   |   |   |   |   |   start > 187470:
endomembrane_system_ (17.05)
|   |   |   |   start > 190474
|   |   |   |   |   start <= 287461
|   |   |   |   |   |   start <= 200148
|   |   |   |   |   |   |   start <= 198144: nucleus_ (85.83/11.24)
|   |   |   |   |   |   |   start > 198144: Golgi_apparatus_ (28.85)
|   |   |   |   |   |   start > 200148
|   |   |   |   |   |   |   start <= 229691
|   |   |   |   |   |   |   |   start <= 226404
|   |   |   |   |   |   |   |   |   start <= 200567: ribosome_
(30.57/11.9)
|   |   |   |   |   |   |   |   |   start > 200567
|   |   |   |   |   |   |   |   |   |   start <= 216101
|   |   |   |   |   |   |   |   |   |   |   start <= 209011
|   |   |   |   |   |   |   |   |   |   |   |   start <= 207038
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 205527
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
202727: cellular_component_ (13.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
202727: cytoplasm_ (16.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 205527:
cellular_component_ (15.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 207038:
cytoplasm_ (23.95/11.65)
|   |   |   |   |   |   |   |   |   |   |   start > 209011
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 210421:
membrane_ (36.55/17.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 210421:
cellular_component_ (19.39)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasm_ (13.57)
|   |   |   |   |   |   |   |   |   |   start > 216101
|   |   |   |   |   |   |   |   |   |   |   start <= 225578
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 216278:
peroxisome_ (5.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 216278:
nucleus_ (30.72/9.3)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cellular_component_ (32.92/10.98)
|   |   |   |   |   |   |   |   |   |   |   start > 225578:
cytoplasm_ (15.78)
|   |   |   |   |   |   |   |   start > 226404
|   |   |   |   |   |   |   |   |   start <= 228334: ribosome_
(17.9)
```

```
|   |   |   |   |   |   |   |   |   start > 228334: membrane_
(13.32)
|   |   |   |   |   |   |   start > 229691
|   |   |   |   |   |   |   |   start <= 271003
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 249874
|   |   |   |   |   |   |   |   |   |   |   start <= 245721
|   |   |   |   |   |   |   |   |   |   |   |   start <= 238358
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 230248:
endoplasmic_reticulum_ (19.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 230248:
nucleus_ (23.55/7.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 238358
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
5789: endoplasmic_reticulum_ (21.02/8.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 5789:
mitochondrion_ (13.86/5.98)
|   |   |   |   |   |   |   |   |   |   |   start > 245721:
Golgi_apparatus_ (18.95)
|   |   |   |   |   |   |   |   |   |   start > 249874
|   |   |   |   |   |   |   |   |   |   |   start <= 254646:
ribosome_ (17.21)
|   |   |   |   |   |   |   |   |   |   |   start > 254646
|   |   |   |   |   |   |   |   |   |   |   |   start <= 266150
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 255668:
cellular_component_ (18.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 255668:
nucleus_ (40.32/11.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 266150:
endoplasmic_reticulum_ (16.04)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 249874
|   |   |   |   |   |   |   |   |   |   |   start <= 238358
|   |   |   |   |   |   |   |   |   |   |   |   start <= 235963
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 234512:
cellular_component_ (10.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 234512:
mitochondrion_ (16.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 235963:
membrane_ (14.18)
|   |   |   |   |   |   |   |   |   |   |   start > 238358:
cellular_component_ (37.26)
|   |   |   |   |   |   |   |   |   |   start > 249874
|   |   |   |   |   |   |   |   |   |   |   start <= 269194
|   |   |   |   |   |   |   |   |   |   |   |   start <= 266150
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 257712:
mitochondrion_ (18.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 257712
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: cytoplasm_ (6.67/1.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: nucleus_ (12.07/5.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 266150:
mitochondrion_ (19.49)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 269194: nucleus_
(25.76)
|   |   |   |   |   |   |   |   start > 271003
|   |   |   |   |   |   |   |   |   start <= 280529
|   |   |   |   |   |   |   |   |   |   start <= 276720
|   |   |   |   |   |   |   |   |   |   |   start <= 272526
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
mitochondrion_ (15.08/4.91)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (28.91/11.82)
|   |   |   |   |   |   |   |   |   |   |   start > 272526:
cytoplasm_ (15.9)
|   |   |   |   |   |   |   |   |   |   start > 276720
|   |   |   |   |   |   |   |   |   |   |   start <= 277623
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleolus_ (6.05/1.76)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
ribosome_ (19.93/6.36)
|   |   |   |   |   |   |   |   |   |   |   start > 277623
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleus_ (11.17/2.98)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (13.76/4.58)
|   |   |   |   |   |   |   |   |   start > 280529
|   |   |   |   |   |   |   |   |   |   start <= 281163:
cellular_component_ (14.91)
|   |   |   |   |   |   |   |   |   |   start > 281163
|   |   |   |   |   |   |   |   |   |   |   start <= 284448:
mitochondrion_ (31.88)
|   |   |   |   |   |   |   |   |   |   |   start > 284448:
cytoplasm_ (11.15)
|   |   |   |   |   start > 287461
|   |   |   |   |   |   start <= 293463
|   |   |   |   |   |   |   start <= 292036
|   |   |   |   |   |   |   |   start <= 288518: cellular_component_
(22.79)
|   |   |   |   |   |   |   |   start > 288518: nucleus_
(77.74/27.42)
|   |   |   |   |   |   |   start > 292036: membrane_ (22.92)
|   |   |   |   |   |   start > 293463
|   |   |   |   |   |   |   start <= 295935
|   |   |   |   |   |   |   |   NeighGO_term = cellular_component_:
chromosome_ (6.64/2.08)
|   |   |   |   |   |   |   |   NeighGO_term = molecular_function_:
cellular_component_ (11.63/4.4)
|   |   |   |   |   |   |   |   NeighGO_term = biological_process_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: chromosome_ (1.49/0.52)
|   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
chromosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: chromosome_ (5.99/2.17)
|   |   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleus_: chromosome_
(12.48/7.26)
|   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: chromosome_ (6.09/2.57)
|   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = translation_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transport_: nucleus_
(6.47/3.76)
|   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_: nucleus_
(2.69/1.22)
|   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: cellular_component_ (4.14/1.98)
|   |   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
cellular_component_ (4.13/1.23)
|   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vacuole_: chromosome_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: chromosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: nucleus_ (1.34/0.67)
|   |   |   |   |   |   |   |   NeighGO_term = meiosis_: chromosome_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transcription_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleolus_: nucleus_
(4.4/1.5)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
chromosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
chromosome_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
chromosome_ (0.0)
|   |   |   |   |   |   |   start > 295935: cellular_component_
(35.51/17.72)
|   start > 299731
|   |   start <= 402592
|   |   |   start <= 397624
|   |   |   |   strand = W
|   |   |   |   |   start <= 347122
|   |   |   |   |   |   start <= 306563
|   |   |   |   |   |   |   start <= 299981: nucleolus_
(38.99/17.03)
|   |   |   |   |   |   |   start > 299981:
site_of_polarized_growth_ (26.03/11.52)
|   |   |   |   |   |   start > 306563
|   |   |   |   |   |   |   start <= 330610
|   |   |   |   |   |   |   |   start <= 313237
|   |   |   |   |   |   |   |   |   start <= 312196
|   |   |   |   |   |   |   |   |   |   start <= 307440: cytoplasm_
(14.03)
|   |   |   |   |   |   |   |   |   |   start > 307440
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 310970:
nucleus_ (18.19)
|   |   |   |   |   |   |   |   |   |   |   start > 310970:
cytoplasm_ (23.91/10.45)
|   |   |   |   |   |   |   |   |   start > 312196: membrane_
(40.45/21.06)
|   |   |   |   |   |   |   |   start > 313237
|   |   |   |   |   |   |   |   |   start <= 319784
|   |   |   |   |   |   |   |   |   |   start <= 316791
|   |   |   |   |   |   |   |   |   |   |   start <= 314634:
cytoplasm_ (23.85)
|   |   |   |   |   |   |   |   |   |   |   start > 314634:
nucleolus_ (10.98)
|   |   |   |   |   |   |   |   |   |   start > 316791
|   |   |   |   |   |   |   |   |   |   |   start <= 317345:
endoplasmic_reticulum_ (6.97)
|   |   |   |   |   |   |   |   |   |   |   start > 317345:
cytoplasm_ (18.66)
|   |   |   |   |   |   |   |   |   start > 319784
|   |   |   |   |   |   |   |   |   |   start <= 325334: nucleus_
(24.45)
|   |   |   |   |   |   |   |   |   |   start > 325334: cytoplasm_
(4.98)
|   |   |   |   |   |   |   start > 330610
|   |   |   |   |   |   |   |   start <= 334889: mitochondrion_
(24.84)
|   |   |   |   |   |   |   |   start > 334889
|   |   |   |   |   |   |   |   |   start <= 337909: membrane_
(44.42/27.72)
|   |   |   |   |   |   |   |   |   start > 337909
|   |   |   |   |   |   |   |   |   |   start <= 343322: nucleus_
(23.61)
|   |   |   |   |   |   |   |   |   |   start > 343322
|   |   |   |   |   |   |   |   |   |   |   start <= 345989:
nucleolus_ (18.03)
|   |   |   |   |   |   |   |   |   |   |   start > 345989: nucleus_
(16.54)
|   |   |   |   |   start > 347122
|   |   |   |   |   |   start <= 353061
|   |   |   |   |   |   |   start <= 349619: mitochondrion_ (13.25)
|   |   |   |   |   |   |   start > 349619: cytoplasmic_membrane-
bound_vesicle_ (28.52)
|   |   |   |   |   |   start > 353061
|   |   |   |   |   |   |   start <= 357380
|   |   |   |   |   |   |   |   start <= 355830
|   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(11.78/3.81)
|   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(20.38/6.78)
|   |   |   |   |   |   |   |   start > 355830: cellular_component_
(15.93)
|   |   |   |   |   |   |   start > 357380
|   |   |   |   |   |   |   |   start <= 375090
|   |   |   |   |   |   |   |   |   start <= 372015
```

```
|   |   |   |   |   |   |   |   |   |   start <= 358639:
mitochondrion_ (16.48)
|   |   |   |   |   |   |   |   |   |   start > 358639
|   |   |   |   |   |   |   |   |   |   |   start <= 363919:
cytoplasm_ (22.3)
|   |   |   |   |   |   |   |   |   |   |   start > 363919: nucleus_
(61.83/27.77)
|   |   |   |   |   |   |   |   |   start > 372015: mitochondrion_
(19.25)
|   |   |   |   |   |   |   |   start > 375090
|   |   |   |   |   |   |   |   |   start <= 376104: cytoplasm_
(39.87/19.34)
|   |   |   |   |   |   |   |   |   start > 376104
|   |   |   |   |   |   |   |   |   |   start <= 377612: nucleus_
(25.89/12.89)
|   |   |   |   |   |   |   |   |   |   start > 377612
|   |   |   |   |   |   |   |   |   |   |   start <= 392228
|   |   |   |   |   |   |   |   |   |   |   |   start <= 383657:
mitochondrion_ (11.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 383657
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 390070:
cytoplasm_ (22.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 390070:
mitochondrion_ (11.86)
|   |   |   |   |   |   |   |   |   |   |   start > 392228: nucleus_
(35.79/15.82)
|   |   |   |   strand = C
|   |   |   |   |   start <= 347122
|   |   |   |   |   |   start <= 330610
|   |   |   |   |   |   |   start <= 304074
|   |   |   |   |   |   |   |   start <= 303414: cytoplasm_ (12.99)
|   |   |   |   |   |   |   |   start > 303414: cellular_component_
(10.07)
|   |   |   |   |   |   |   start > 304074
|   |   |   |   |   |   |   |   start <= 319784: mitochondrion_
(24.78)
|   |   |   |   |   |   |   |   start > 319784: endomembrane_system_
(7.83)
|   |   |   |   |   |   start > 330610
|   |   |   |   |   |   |   start <= 343322: cytoplasm_
(58.54/22.03)
|   |   |   |   |   |   |   start > 343322
|   |   |   |   |   |   |   |   start <= 345989:
extracellular_region_ (21.41)
|   |   |   |   |   |   |   |   start > 345989: cytoplasm_
(35.38/15.88)
|   |   |   |   |   start > 347122
|   |   |   |   |   |   start <= 366472
|   |   |   |   |   |   |   start <= 355830: membrane_ (43.65/26.55)
|   |   |   |   |   |   |   start > 355830
|   |   |   |   |   |   |   |   start <= 365254
|   |   |   |   |   |   |   |   |   start <= 361862: nucleolus_
(23.43)
|   |   |   |   |   |   |   |   |   start > 361862
```

```
|   |   |   |   |   |   |   |   |   |   start <= 363919:
plasma_membrane_ (21.06)
|   |   |   |   |   |   |   |   |   |   start > 363919: nucleolus_
(21.75)
|   |   |   |   |   |   |   |   start > 365254
|   |   |   |   |   |   |   |   |   start <= 365999: ribosome_
(18.13)
|   |   |   |   |   |   |   |   |   start > 365999: nucleolus_
(10.65)
|   |   |   |   |   |   start > 366472
|   |   |   |   |   |   |   start <= 395835
|   |   |   |   |   |   |   |   start <= 377612
|   |   |   |   |   |   |   |   |   start <= 368756:
endomembrane_system_ (29.75/12.04)
|   |   |   |   |   |   |   |   |   start > 368756: nucleus_ (12.23)
|   |   |   |   |   |   |   |   start > 377612
|   |   |   |   |   |   |   |   |   start <= 381274:
endoplasmic_reticulum_ (22.51)
|   |   |   |   |   |   |   |   |   start > 381274
|   |   |   |   |   |   |   |   |   |   start <= 385199:
mitochondrion_ (18.91)
|   |   |   |   |   |   |   |   |   |   start > 385199
|   |   |   |   |   |   |   |   |   |   |   start <= 392228:
microtubule_organizing_center_ (8.67)
|   |   |   |   |   |   |   |   |   |   |   start > 392228:
mitochondrion_ (14.26)
|   |   |   |   |   |   |   start > 395835: cytoplasm_ (47.77/20.87)
|   |   |   start > 397624
|   |   |   |   start <= 401290
|   |   |   |   |   start <= 398631: endoplasmic_reticulum_
(59.9/32.69)
|   |   |   |   |   start > 398631: cytoplasmic_membrane-
bound_vesicle_ (72.11/48.93)
|   |   |   |   start > 401290
|   |   |   |   |   start <= 401601: cytoplasm_ (9.63)
|   |   |   |   |   start > 401601
|   |   |   |   |   |   neigh_num <= 1: plasma_membrane_ (5.05/0.69)
|   |   |   |   |   |   neigh_num > 1: endoplasmic_reticulum_
(17.71/7.44)
|   |   start > 402592
|   |   |   start <= 1046738
|   |   |   |   start <= 442914
|   |   |   |   |   start <= 433067
|   |   |   |   |   |   start <= 418891
|   |   |   |   |   |   |   start <= 412370
|   |   |   |   |   |   |   |   start <= 409607
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 403690:
Golgi_apparatus_ (21.59/10.13)
|   |   |   |   |   |   |   |   |   |   start > 403690
|   |   |   |   |   |   |   |   |   |   |   start <= 405473:
cytoplasm_ (18.51)
|   |   |   |   |   |   |   |   |   |   |   start > 405473:
cellular_component_ (16.97)
```

```
|   |   |   |   |   |   |   |   |   strand = C: ribosome_ (19.94)
|   |   |   |   |   |   |   |   start > 409607
|   |   |   |   |   |   |   |   |   start <= 411555
|   |   |   |   |   |   |   |   |   |   start <= 411289: nucleus_
(16.48)
|   |   |   |   |   |   |   |   |   |   start > 411289
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: cytoplasm_ (5.06/2.75)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (4.05/1.37)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasm_ (3.29/1.88)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: endoplasmic_reticulum_ (10.8/6.28)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
cytoplasm_ (5.02/2.19)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: endoplasmic_reticulum_ (6.39/3.78)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: endoplasmic_reticulum_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: endoplasmic_reticulum_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: endoplasmic_reticulum_ (2.31/1.37)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: endoplasmic_reticulum_ (0.0)
```

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|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: endoplasmic_reticulum_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: endoplasmic_reticulum_ (7.66/4.76)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: membrane_fraction_ (9.64/5.49)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: endoplasmic_reticulum_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   start > 411555: cytoplasm_
(21.82)
|   |   |   |   |   |   |   start > 412370
|   |   |   |   |   |   |   |   start <= 414106: cellular_component_
(18.55)
|   |   |   |   |   |   |   |   start > 414106
|   |   |   |   |   |   |   |   |   strand = W: nucleus_ (10.0)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 417487
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (17.31/5.84)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cellular_component_ (6.61/2.45)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_component_ (17.56/5.69)
|   |   |   |   |   |   |   |   |   |   start > 417487:
cellular_component_ (8.01)
|   |   |   |   |   |   start > 418891
|   |   |   |   |   |   |   strand = W: cytoplasm_ (40.51)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 426810
|   |   |   |   |   |   |   |   |   start <= 423098: nucleus_
(26.88/12.25)
|   |   |   |   |   |   |   |   |   start > 423098: Golgi_apparatus_
(10.4)
|   |   |   |   |   |   |   |   start > 426810
|   |   |   |   |   |   |   |   |   start <= 428606: peroxisome_
(53.4/29.57)
|   |   |   |   |   |   |   |   |   start > 428606
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(17.04/4.37)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cytoplasm_ (7.38/1.72)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (20.48/8.42)
|   |   |   |   |   start > 433067
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 436838: chromosome_ (14.15)
|   |   |   |   |   |   |   start > 436838
|   |   |   |   |   |   |   |   start <= 439096: cytoplasm_ (10.0)
|   |   |   |   |   |   |   |   start > 439096: nucleolus_ (13.48)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 440812
|   |   |   |   |   |   |   |   start <= 436838: cell_wall_ (9.1)
```

```
|   |   |   |   |   |   |   |   start > 436838
|   |   |   |   |   |   |   |   |   start <= 439096: ribosome_
(10.84)
|   |   |   |   |   |   |   |   |   start > 439096: cytoplasm_
(7.44)
|   |   |   |   |   |   |   start > 440812: cell_wall_ (22.79)
|   |   |   |   start > 442914
|   |   |   |   |   start <= 627810
|   |   |   |   |   |   start <= 506973
|   |   |   |   |   |   |   start <= 496506
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 485428
|   |   |   |   |   |   |   |   |   |   start <= 452409:
endoplasmic_reticulum_ (42.14/19.44)
|   |   |   |   |   |   |   |   |   |   start > 452409
|   |   |   |   |   |   |   |   |   |   |   start <= 458161:
cellular_component_ (47.38)
|   |   |   |   |   |   |   |   |   |   |   start > 458161
|   |   |   |   |   |   |   |   |   |   |   |   start <= 466146:
cytoplasm_ (42.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 466146
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 478657:
endoplasmic_reticulum_ (26.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 478657:
cellular_component_ (13.17)
|   |   |   |   |   |   |   |   |   start > 485428
|   |   |   |   |   |   |   |   |   |   start <= 485925
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
membrane_ (10.12/3.27)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: vacuole_
(12.82/4.04)
|   |   |   |   |   |   |   |   |   |   start > 485925:
mitochondrion_ (22.23)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 446148: membrane_
(32.28/20.7)
|   |   |   |   |   |   |   |   |   start > 446148
|   |   |   |   |   |   |   |   |   |   start <= 490551
|   |   |   |   |   |   |   |   |   |   |   start <= 449962:
nucleus_ (66.43/29.36)
|   |   |   |   |   |   |   |   |   |   |   start > 449962
|   |   |   |   |   |   |   |   |   |   |   |   start <= 461671
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 458161
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
454790: mitochondrion_ (11.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
454790: endoplasmic_reticulum_ (28.47/10.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 458161:
mitochondrion_ (16.52)
|   |   |   |   |   |   |   |   |   |   |   |   start > 461671
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 472860
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
466146: cellular_component_ (12.95)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
466146: nucleus_ (16.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 472860
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
475550: mitochondrion_ (16.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
475550
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
485925
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 482671
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 478657: cellular_component_ (12.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 478657: plasma_membrane_ (39.71/23.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 482671: cellular_component_ (15.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
485925: mitochondrion_ (10.69)
|   |   |   |   |   |   |   |   |   |   start > 490551
|   |   |   |   |   |   |   |   |   |   |   start <= 494521
|   |   |   |   |   |   |   |   |   |   |   |   start <= 491960:
cytoplasm_ (18.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 491960:
nucleus_ (46.71/17.95)
|   |   |   |   |   |   |   |   |   |   |   start > 494521:
endoplasmic_reticulum_ (20.78)
|   |   |   |   |   |   |   start > 496506
|   |   |   |   |   |   |   |   start <= 502942
|   |   |   |   |   |   |   |   |   start <= 500136
|   |   |   |   |   |   |   |   |   |   start <= 498038: cytoplasm_
(15.0)
|   |   |   |   |   |   |   |   |   |   start > 498038
|   |   |   |   |   |   |   |   |   |   |   start <= 499910:
nucleus_ (14.46)
|   |   |   |   |   |   |   |   |   |   |   start > 499910:
cytoplasm_ (33.89/15.46)
|   |   |   |   |   |   |   |   |   start > 500136: peroxisome_
(16.85)
|   |   |   |   |   |   |   |   start > 502942
|   |   |   |   |   |   |   |   |   strand = W: nucleus_
(58.23/15.32)
|   |   |   |   |   |   |   |   |   strand = C: cellular_component_
(30.36/13.67)
|   |   |   |   |   |   start > 506973
|   |   |   |   |   |   |   start <= 522080
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 514558
|   |   |   |   |   |   |   |   |   |   start <= 513163
|   |   |   |   |   |   |   |   |   |   |   start <= 511549:
nucleus_ (18.57)
|   |   |   |   |   |   |   |   |   |   |   start > 511549:
mitochondrion_ (12.25)
```

```
|   |   |   |   |   |   |   |   |   |   start > 513163: nucleus_
(20.63)
|   |   |   |   |   |   |   |   |   start > 514558:
site_of_polarized_growth_ (25.68)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 508368: membrane_
(77.51/45.45)
|   |   |   |   |   |   |   |   |   start > 508368
|   |   |   |   |   |   |   |   |   |   start <= 514558:
plasma_membrane_ (23.94/8.48)
|   |   |   |   |   |   |   |   |   |   start > 514558:
mitochondrion_ (14.05)
|   |   |   |   |   |   |   start > 522080
|   |   |   |   |   |   |   |   start <= 596697
|   |   |   |   |   |   |   |   |   start <= 554971
|   |   |   |   |   |   |   |   |   |   start <= 541854
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 525233
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 523791
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
522265: cellular_component_ (20.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
522265: cytoplasm_ (32.95/16.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 523791:
cellular_component_ (23.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 525233
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 529268
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
527636: mitochondrion_ (12.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
527636: plasma_membrane_ (14.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 529268
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
534462
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
531614: cytoplasm_ (13.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
531614: cellular_component_ (10.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
534462: cytoplasm_ (16.84)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 529268:
membrane_ (24.71/9.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 529268
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 532989
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
2430: nucleus_ (19.73/5.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
2430: cytoplasm_ (9.55/1.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 532989:
ribosome_ (11.06)
|   |   |   |   |   |   |   |   |   |   start > 541854
|   |   |   |   |   |   |   |   |   |   |   start <= 546161
|   |   |   |   |   |   |   |   |   |   |   |   start <= 544652
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
mitochondrion_ (18.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasm_ (14.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 544652:
nucleolus_ (38.74)
|   |   |   |   |   |   |   |   |   |   |   start > 546161
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 546445:
mitochondrion_ (11.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 546445:
membrane_fraction_ (17.19)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (18.24)
|   |   |   |   |   |   |   |   |   start > 554971
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 581440
|   |   |   |   |   |   |   |   |   |   |   |   start <= 561747
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 555816:
ribosome_ (14.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 555816
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
558872: cellular_component_ (7.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
558872: endoplasmic_reticulum_ (8.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 561747
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 577491
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
575402: nucleus_ (9.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
575402: cellular_bud_ (29.67/13.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 577491
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 783: cytoplasm_ (2.18/0.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 783: nucleus_ (13.04/2.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 6754: cytoplasm_ (12.75/4.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 6754: nucleus_ (2.21/0.49)
|   |   |   |   |   |   |   |   |   |   |   start > 581440
|   |   |   |   |   |   |   |   |   |   |   |   start <= 593600
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 589830
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
584899: mitochondrion_ (14.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
584899: endoplasmic_reticulum_ (14.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 589830:
mitochondrion_ (28.91)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 593600:
ribosome_ (23.02)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 558872
|   |   |   |   |   |   |   |   |   |   |   |   start <= 557569:
cellular_component_ (14.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 557569:
endoplasmic_reticulum_ (23.33)
|   |   |   |   |   |   |   |   |   |   |   start > 558872
|   |   |   |   |   |   |   |   |   |   |   |   start <= 584899
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 561747:
cytoplasm_ (51.15/15.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 561747:
nucleus_ (25.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 584899
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 591318
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
4069: cellular_component_ (26.03/5.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
4069: nucleus_ (6.11/0.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 591318:
cellular_component_ (13.03)
|   |   |   |   |   |   |   |   start > 596697
|   |   |   |   |   |   |   |   |   start <= 619862
|   |   |   |   |   |   |   |   |   |   start <= 607567
|   |   |   |   |   |   |   |   |   |   |   start <= 601665
|   |   |   |   |   |   |   |   |   |   |   |   start <= 599421:
plasma_membrane_ (14.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 599421:
nucleus_ (45.64/17.39)
|   |   |   |   |   |   |   |   |   |   |   start > 601665
|   |   |   |   |   |   |   |   |   |   |   |   start <= 606140
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 605505:
membrane_ (38.89/21.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 605505:
nucleus_ (61.57/38.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 606140:
membrane_ (23.1)
|   |   |   |   |   |   |   |   |   |   start > 607567
|   |   |   |   |   |   |   |   |   |   |   start <= 609588:
nucleolus_ (13.57)
|   |   |   |   |   |   |   |   |   |   |   start > 609588
|   |   |   |   |   |   |   |   |   |   |   |   start <= 615969
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 610568:
plasma_membrane_ (19.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 610568:
cytoplasm_ (11.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 615969
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 617282:
mitochondrial_envelope_ (13.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 617282
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
617828: nucleus_ (7.41)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
617828: plasma_membrane_ (11.2)
|   |   |   |   |   |   |   |   |   start > 619862:
cellular_component_ (52.17)
|   |   |   |   |   start > 627810
|   |   |   |   |   |   start <= 695421
|   |   |   |   |   |   |   start <= 642014
|   |   |   |   |   |   |   |   start <= 640375
|   |   |   |   |   |   |   |   |   start <= 636879: nucleus_
(80.06/17.27)
|   |   |   |   |   |   |   |   |   start > 636879
|   |   |   |   |   |   |   |   |   |   start <= 637581:
mitochondrion_ (18.59)
|   |   |   |   |   |   |   |   |   |   start > 637581
|   |   |   |   |   |   |   |   |   |   |   start <= 639517:
peroxisome_ (17.95)
|   |   |   |   |   |   |   |   |   |   |   start > 639517:
cytoplasm_ (15.77)
|   |   |   |   |   |   |   |   start > 640375
|   |   |   |   |   |   |   |   |   start <= 640724:
cellular_component_ (23.87)
|   |   |   |   |   |   |   |   |   start > 640724: cell_cortex_
(33.38/16.62)
|   |   |   |   |   |   |   start > 642014
|   |   |   |   |   |   |   |   start <= 668193
|   |   |   |   |   |   |   |   |   start <= 666345
|   |   |   |   |   |   |   |   |   |   start <= 643784: nucleus_
(41.0/19.65)
|   |   |   |   |   |   |   |   |   |   start > 643784
|   |   |   |   |   |   |   |   |   |   |   start <= 661753
|   |   |   |   |   |   |   |   |   |   |   |   start <= 650621
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
mitochondrion_ (17.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
646819: cytoplasm_ (25.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
646819
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
648911
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 648146: mitochondrion_ (13.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 648146: ribosome_ (27.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
648911: cytoplasm_ (42.39/20.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 650621
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 654638:
cytoplasm_ (28.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 654638
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
656964: membrane_fraction_ (14.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
656964: cytoplasm_ (18.73)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 661753
|   |   |   |   |   |   |   |   |   |   |   |   start <= 662362:
nucleolus_ (28.76/14.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 662362:
mitochondrion_ (17.31)
|   |   |   |   |   |   |   |   |   start > 666345: cellular_bud_
(34.93/19.71)
|   |   |   |   |   |   |   |   start > 668193
|   |   |   |   |   |   |   |   |   start <= 690249
|   |   |   |   |   |   |   |   |   |   start <= 687462
|   |   |   |   |   |   |   |   |   |   |   start <= 670392:
nucleus_ (20.64)
|   |   |   |   |   |   |   |   |   |   |   start > 670392
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 672190
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: mitochondrion_ (14.15/5.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: cytoplasm_ (20.81/9.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 672190
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
676625: mitochondrial_envelope_ (25.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
676625: cytoplasm_ (24.36)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 678699:
cytoplasm_ (36.96/17.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 678699:
nucleus_ (57.01/29.64)
|   |   |   |   |   |   |   |   |   |   start > 687462
|   |   |   |   |   |   |   |   |   |   |   start <= 687903:
chromosome_ (41.11/20.21)
|   |   |   |   |   |   |   |   |   |   |   start > 687903:
cytoplasm_ (20.7)
|   |   |   |   |   |   |   |   |   start > 690249
|   |   |   |   |   |   |   |   |   |   start <= 695139:
mitochondrion_ (45.85)
|   |   |   |   |   |   |   |   |   |   start > 695139
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleolus_ (20.63/4.03)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (21.08/6.77)
|   |   |   |   |   |   start > 695421
|   |   |   |   |   |   |   start <= 931026
|   |   |   |   |   |   |   |   start <= 797873
|   |   |   |   |   |   |   |   |   start <= 699790
|   |   |   |   |   |   |   |   |   |   start <= 698372: nucleus_
(44.01/18.23)
|   |   |   |   |   |   |   |   |   |   start > 698372
|   |   |   |   |   |   |   |   |   |   |   start <= 698603:
endoplasmic_reticulum_ (51.78/32.28)
|   |   |   |   |   |   |   |   |   |   |   start > 698603: vacuole_
(34.66/15.04)
|   |   |   |   |   |   |   |   |   start > 699790
```

```
|   |   |   |   |   |   |   |   |   |   start <= 745840
|   |   |   |   |   |   |   |   |   |   |   start <= 729676
|   |   |   |   |   |   |   |   |   |   |   |   start <= 726483
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 715832
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
703640: cytoplasm_ (60.59/9.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
703640
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
713713
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
strand = W: cellular_component_ (16.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 706505: cellular_component_ (10.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 706505: cytoplasm_ (17.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
713713
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: cytoplasm_ (13.65/4.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: nucleus_ (8.09/2.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 715832
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
718897
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 717362: mitochondrion_ (14.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 717362: cytoskeleton_ (13.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
718897
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C: mitochondrion_ (5.19/2.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F: mitochondrion_ (12.87/4.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: nucleus_ (5.93/1.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: mitochondrion_ (2.42/0.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasm_ (19.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 726483
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 726978:
ribosome_ (10.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 726978:
cellular_component_ (48.2/28.32)
|   |   |   |   |   |   |   |   |   |   |   start > 729676
|   |   |   |   |   |   |   |   |   |   |   |   start <= 733417
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
731142: cytoplasm_ (18.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
731142: cellular_component_ (12.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
731142: membrane_fraction_ (21.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
731142: plasma_membrane_ (19.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 733417
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 739949:
cytoplasm_ (85.76/11.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 739949
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
742330: vacuole_ (22.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
742330: cytoplasm_ (34.63/17.19)
|   |   |   |   |   |   |   |   |   |   start > 745840
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 770574
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 762433
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
761397
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
756901
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 754731
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 750405
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start <= 746803: cellular_component_ (10.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start > 746803: nucleus_ (12.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 750405: cellular_component_ (16.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 754731: peroxisome_ (28.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
756901
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 757775: nucleus_ (22.96/8.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 757775: cellular_component_ (17.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
761397
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: nucleus_ (15.55/6.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: cytoplasm_ (14.42/5.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 762433
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
767434
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: cytoskeleton_ (5.81/1.92)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: chromosome_ (22.18/8.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
767434: cellular_component_ (16.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 770574
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 794422
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
774354: cytoplasm_ (31.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
774354
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
780404
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 779621
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 775198: membrane_ (11.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 775198: cytoplasm_ (11.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 779621: mitochondrion_ (13.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
780404
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 784863: nucleolus_ (12.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 784863
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 789036: membrane_ (15.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 789036: cytoplasm_ (11.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 794422:
cellular_component_ (17.7)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 786925
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 750405:
nucleolus_ (15.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 750405
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
775198
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
757775
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 754731: cytoplasm_ (11.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 754731: mitochondrion_ (26.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
757775: plasma_membrane_ (12.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
775198
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
785442: cellular_component_ (26.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
785442
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: mitochondrion_ (17.31/6.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: cytoplasm_ (20.04/6.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 786925
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 793058
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
789036: ribosome_ (17.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
789036: mitochondrion_ (8.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 793058
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
796097: plasma_membrane_ (12.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
796097: peroxisome_ (17.25)
|   |   |   |   |   |   |   |   start > 797873
|   |   |   |   |   |   |   |   |   start <= 865758
|   |   |   |   |   |   |   |   |   |   start <= 830520
|   |   |   |   |   |   |   |   |   |   |   start <= 809425
|   |   |   |   |   |   |   |   |   |   |   |   start <= 798548:
mitochondrion_ (37.34/14.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 798548
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
800551: nucleus_ (29.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
800551: endoplasmic_reticulum_ (15.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
806026: cytoplasm_ (35.53/12.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
806026
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
807661
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_component_: nucleolus_ (4.24/1.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = molecular_function_: nucleus_ (5.91/3.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = biological_process_: mitochondrion_ (4.84/2.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transferase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_modification_process_: mitochondrion_
(3.97/1.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrion_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = oxidoreductase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = generation_of_precursor_metabolites_and_energy_:
mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasm_: nucleolus_ (9.29/5.25)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_regulator_activity_: mitochondrion_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transduction_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleus_: nucleus_ (8.39/3.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = enzyme_regulator_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_biogenesis_and_assembly_: nucleolus_
(5.38/2.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ligase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_binding_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transport_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endoplasmic_reticulum_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = Golgi_apparatus_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transporter_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = hydrolase_activity_: mitochondrion_ (4.77/1.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = organelle_organization_and_biogenesis_:
mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = motor_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cycle_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_organization_and_biogenesis_:
mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = chromosome_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_metabolic_process_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vacuole_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vesicle-mediated_transport_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasmic_membrane-bound_vesicle_: mitochondrion_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = structural_molecule_activity_: mitochondrion_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peroxisome_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lipid_metabolic_process_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_binding_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = helicase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_metabolic_process_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = meiosis_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = phosphoprotein_phosphatase_activity_: mitochondrion_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = pseudohyphal_growth_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_kinase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_binding_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_organization_and_biogenesis_:
mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytokinesis_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endomembrane_system_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nuclear_organization_and_biogenesis_: mitochondrion_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = microtubule_organizing_center_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = sporulation_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_respiration_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lyase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = amino_acid_and_derivative_metabolic_process_:
mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleotidyltransferase_activity_: mitochondrion_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleolus_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_bud_: mitochondrion_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = site_of_polarized_growth_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = extracellular_region_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = conjugation_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = response_to_stress_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = plasma_membrane_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = isomerase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_budding_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_regulator_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_fraction_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peptidase_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_catabolic_process_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrial_envelope_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vitamin_metabolic_process_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transducer_activity_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_organization_and_biogenesis_: mitochondrion_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = carbohydrate_metabolic_process_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = anatomical_structure_morphogenesis_: mitochondrion_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cortex_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_: mitochondrion_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
807661: cytoplasm_ (18.02/5.77)
|   |   |   |   |   |   |   |   |   |   |   start > 809425
|   |   |   |   |   |   |   |   |   |   |   |   start <= 829121
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 810232:
cellular_component_ (8.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 810232
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
824064
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
823487: cytoplasm_ (12.15)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
823487: ribosome_ (29.71/14.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
824064
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
828799: cytoplasm_ (42.43/9.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
828799: mitochondrion_ (9.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 829121:
Golgi_apparatus_ (16.11)
|   |   |   |   |   |   |   |   |   |   start > 830520
|   |   |   |   |   |   |   |   |   |   |   start <= 850441
|   |   |   |   |   |   |   |   |   |   |   |   start <= 846660
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 843596
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
836670
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   strand =
W: membrane_ (39.33/25.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   strand =
C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 834487: cellular_component_ (18.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 834487
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 835908
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   |   distance <= 2119: cytoplasm_ (4.19/0.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   |   distance > 2119: mitochondrion_ (5.16/1.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   neigh_num > 1: cytoplasm_ (9.5/2.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 835908: cellular_component_ (14.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
836670
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
842556
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 837147: endomembrane_system_ (7.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 837147: mitochondrion_ (22.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
842556
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_component_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = molecular_function_: cytoplasmic_membrane-
bound_vesicle_ (8.35/4.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = biological_process_: endomembrane_system_ (5.83/4.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transferase_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_modification_process_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrion_: cytoplasmic_membrane-bound_vesicle_
(12.26/5.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = oxidoreductase_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = generation_of_precursor_metabolites_and_energy_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasm_: membrane_ (1.35/0.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_regulator_activity_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transduction_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleus_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = enzyme_regulator_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_biogenesis_and_assembly_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ligase_activity_: membrane_ (5.12/2.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_: endoplasmic_reticulum_ (7.25/4.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_binding_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transport_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endoplasmic_reticulum_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = Golgi_apparatus_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transporter_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = hydrolase_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = organelle_organization_and_biogenesis_: membrane_
(4.26/2.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = motor_activity_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cycle_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_organization_and_biogenesis_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = chromosome_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_metabolic_process_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vacuole_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vesicle-mediated_transport_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasmic_membrane-bound_vesicle_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = structural_molecule_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peroxisome_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lipid_metabolic_process_: endomembrane_system_
(3.22/1.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_binding_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = helicase_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_metabolic_process_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = meiosis_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = phosphoprotein_phosphatase_activity_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = pseudohyphal_growth_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_kinase_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_binding_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_organization_and_biogenesis_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytokinesis_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endomembrane_system_: endomembrane_system_
(6.72/3.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nuclear_organization_and_biogenesis_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = microtubule_organizing_center_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = sporulation_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_respiration_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lyase_activity_: endomembrane_system_ (13.75/8.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = amino_acid_and_derivative_metabolic_process_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleotidyltransferase_activity_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleolus_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_bud_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = site_of_polarized_growth_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = extracellular_region_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = conjugation_: cytoplasmic_membrane-bound_vesicle_
(0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = response_to_stress_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = plasma_membrane_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = isomerase_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_budding_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_regulator_activity_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_fraction_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_: cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peptidase_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_catabolic_process_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrial_envelope_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vitamin_metabolic_process_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transducer_activity_: cytoplasmic_membrane-
bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_organization_and_biogenesis_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = carbohydrate_metabolic_process_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = anatomical_structure_morphogenesis_:
cytoplasmic_membrane-bound_vesicle_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cortex_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_: cytoplasmic_membrane-bound_vesicle_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 843596
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
845654: cytoplasm_ (29.4)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
845654: cellular_component_ (15.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (11.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 846660:
endoplasmic_reticulum_ (44.7/11.63)
|   |   |   |   |   |   |   |   |   |   |   start > 850441
|   |   |   |   |   |   |   |   |   |   |   |   start <= 857496
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 853220:
cytoplasm_ (58.12/29.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 853220
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
854900: nucleus_ (51.4/30.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
854900
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
856306: nucleus_ (24.63/9.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
856306: cytoplasm_ (8.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 857496
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 859481:
mitochondrion_ (27.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 859481:
cellular_component_ (13.45)
|   |   |   |   |   |   |   |   |   start > 865758
|   |   |   |   |   |   |   |   |   |   start <= 915246
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 897507
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 878197
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
871421: nucleus_ (34.37/16.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
871421: mitochondrion_ (7.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 878197
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
894698
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
888887
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 883815: plasma_membrane_ (8.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 883815
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: cytoplasm_ (13.94/4.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: nucleus_ (17.76/6.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
888887: plasma_membrane_ (44.81/27.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
894698: endoplasmic_reticulum_ (13.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 897507
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 909218:
nucleus_ (104.99/46.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 909218
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
910437: cytoplasm_ (34.79/13.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
910437
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: nucleus_ (36.06/11.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: cytoplasm_ (31.13/12.66)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 902275
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 892191
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
878197
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
876399
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 871421
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 867779
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   neigh_strand = W: cytoplasm_ (13.61/5.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   neigh_strand = C: nucleus_ (12.99/5.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 867779: cytoplasm_ (12.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 871421: nucleus_ (20.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
876399: cell_wall_ (14.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
878197
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
885746
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 880425: cytoplasm_ (19.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 880425: mitochondrion_ (24.22/6.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
885746: cytoplasm_ (36.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 892191
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
897507: membrane_ (24.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
897507: nucleus_ (30.66/10.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 902275
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 909218
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
903202: cellular_component_ (20.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
903202
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
905939: Golgi_apparatus_ (27.91/12.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
905939: cellular_component_ (18.89)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 909218
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
911888: mitochondrion_ (14.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
911888: cytoplasm_ (48.82/11.8)
|   |   |   |   |   |   |   |   |   |   start > 915246
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 920580
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 917045:
plasma_membrane_ (16.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 917045:
ribosome_ (14.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 920580
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 922180:
mitochondrion_ (13.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 922180:
plasma_membrane_ (13.37)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 924699:
membrane_ (24.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 924699:
cytoplasm_ (12.32)
|   |   |   |   |   |   |   start > 931026
|   |   |   |   |   |   |   |   start <= 979324
|   |   |   |   |   |   |   |   |   start <= 950902
|   |   |   |   |   |   |   |   |   |   start <= 939926
|   |   |   |   |   |   |   |   |   |   |   start <= 938995
|   |   |   |   |   |   |   |   |   |   |   |   strand = W: nucleus_
(8.52)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 936886:
mitochondrion_ (15.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 936886:
site_of_polarized_growth_ (33.83/11.3)
|   |   |   |   |   |   |   |   |   |   |   start > 938995
|   |   |   |   |   |   |   |   |   |   |   |   start <= 939675:
nucleus_ (23.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 939675:
mitochondrion_ (18.36)
|   |   |   |   |   |   |   |   |   |   start > 939926
|   |   |   |   |   |   |   |   |   |   |   start <= 942809
|   |   |   |   |   |   |   |   |   |   |   |   start <= 942218:
cytoplasm_ (9.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 942218:
plasma_membrane_ (6.14)
|   |   |   |   |   |   |   |   |   |   |   start > 942809
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 945148:
nucleus_ (9.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 945148
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: endomembrane_system_ (11.05/6.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: membrane_ (12.47/6.59)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   strand = C: nucleus_
(14.48)
|   |   |   |   |   |   |   |   |   start > 950902
|   |   |   |   |   |   |   |   |   |   start <= 965660
|   |   |   |   |   |   |   |   |   |   |   start <= 953963
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (31.01)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (19.07)
|   |   |   |   |   |   |   |   |   |   |   start > 953963
|   |   |   |   |   |   |   |   |   |   |   |   start <= 958213:
nucleus_ (27.87/12.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 958213
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 962821:
mitochondrion_ (88.96/15.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 962821:
cytoplasm_ (13.41)
|   |   |   |   |   |   |   |   |   |   start > 965660
|   |   |   |   |   |   |   |   |   |   |   start <= 970058
|   |   |   |   |   |   |   |   |   |   |   |   start <= 968692:
site_of_polarized_growth_ (31.57/14.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 968692:
peroxisome_ (17.77)
|   |   |   |   |   |   |   |   |   |   |   start > 970058
|   |   |   |   |   |   |   |   |   |   |   |   start <= 974782
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 973739:
cytoplasm_ (24.8/12.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 973739:
cellular_component_ (15.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 974782
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 976586:
cytoskeleton_ (22.49/7.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 976586:
mitochondrion_ (20.45)
|   |   |   |   |   |   |   |   start > 979324
|   |   |   |   |   |   |   |   |   start <= 999145
|   |   |   |   |   |   |   |   |   |   start <= 993526
|   |   |   |   |   |   |   |   |   |   |   start <= 984971
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cytoplasmic_membrane-bound_vesicle_ (22.03)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 982073:
nucleus_ (13.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 982073:
cellular_component_ (32.08/14.23)
|   |   |   |   |   |   |   |   |   |   |   start > 984971
|   |   |   |   |   |   |   |   |   |   |   |   strand = W: nucleus_
(48.62/13.54)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasm_ (19.16)
|   |   |   |   |   |   |   |   |   |   start > 993526
|   |   |   |   |   |   |   |   |   |   |   start <= 995644:
nucleolus_ (32.04/15.84)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 995644:
cellular_component_ (48.54/10.74)
|   |   |   |   |   |   |   |   |   start > 999145
|   |   |   |   |   |   |   |   |   |   start <= 1022662
|   |   |   |   |   |   |   |   |   |   |   start <= 1021859
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1012491
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1007311
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1000932: mitochondrion_ (29.07/11.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1000932: cytoplasm_ (34.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1007311: mitochondrion_ (19.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1007311: mitochondrion_ (30.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1007311: nucleus_ (12.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1012491
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1016756: membrane_ (30.5/14.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1016756
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1017765
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: cytoplasm_ (13.32/5.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: nucleus_ (18.96/6.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1017765
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1019247: endoplasmic_reticulum_ (13.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1019247: cytoplasm_ (18.83)
|   |   |   |   |   |   |   |   |   |   |   start > 1021859:
plasma_membrane_ (33.45/13.44)
|   |   |   |   |   |   |   |   |   |   start > 1022662
|   |   |   |   |   |   |   |   |   |   |   start <= 1038507
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1031797
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1027376
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
nucleus_ (17.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasm_ (45.5/16.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1027376:
cytoplasm_ (16.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1031797:
nucleolus_ (19.68)
|   |   |   |   |   |   |   |   |   |   |   start > 1038507
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1043102
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1039245: cellular_component_ (21.13)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1039245
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: cellular_component_ (18.11/6.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C: cellular_component_ (6.63/1.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F: nucleus_ (10.5/2.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P: nucleus_ (8.36/3.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1043102
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
nucleus_ (46.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1045487: nucleus_ (19.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1045487: cytoplasm_ (38.74/17.16)
|   |   |   start > 1046738
|   |   |   |   strand = W
|   |   |   |   |   start <= 1060047: plasma_membrane_ (33.79/15.19)
|   |   |   |   |   start > 1060047
|   |   |   |   |   |   start <= 1070300: nucleus_ (16.29)
|   |   |   |   |   |   start > 1070300
|   |   |   |   |   |   |   start <= 1080313: cellular_component_
(12.54)
|   |   |   |   |   |   |   start > 1080313: nucleus_ (7.97)
|   |   |   |   strand = C
|   |   |   |   |   start <= 1061597
|   |   |   |   |   |   start <= 1058731
|   |   |   |   |   |   |   start <= 1052831
|   |   |   |   |   |   |   |   start <= 1049965: cell_wall_ (13.0)
|   |   |   |   |   |   |   |   start > 1049965: nucleolus_ (18.07)
|   |   |   |   |   |   |   start > 1052831: cell_wall_ (17.27)
|   |   |   |   |   |   start > 1058731
|   |   |   |   |   |   |   start <= 1060047: nucleolus_
(43.18/18.88)
|   |   |   |   |   |   |   start > 1060047: cytoplasmic_membrane-
bound_vesicle_ (12.74)
|   |   |   |   |   start > 1061597
|   |   |   |   |   |   start <= 1070300
|   |   |   |   |   |   |   start <= 1063160: ribosome_ (55.5/34.99)
|   |   |   |   |   |   |   start > 1063160
|   |   |   |   |   |   |   |   start <= 1064947: mitochondrion_
(21.58)
|   |   |   |   |   |   |   |   start > 1064947: ribosome_
(39.4/18.6)
|   |   |   |   |   |   start > 1070300
|   |   |   |   |   |   |   start <= 1076606: membrane_fraction_
(9.18)
|   |   |   |   |   |   |   start > 1076606: vacuole_ (6.62)
```

For Molecular Function

```
|   start <= 1004630
|   |   start <= 392228
|   |   |   start <= 226404
|   |   |   |   start <= 93797
|   |   |   |   |   start <= 31636
|   |   |   |   |   |   start <= 11110
|   |   |   |   |   |   |   start <= 6860: molecular_function_
(54.46)
|   |   |   |   |   |   |   start > 6860
|   |   |   |   |   |   |   |   start <= 8470: peptidase_activity_
(17.39)
|   |   |   |   |   |   |   |   start > 8470: molecular_function_
(38.5)
|   |   |   |   |   |   start > 11110
|   |   |   |   |   |   |   start <= 20978
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 14910:
oxidoreductase_activity_ (9.58)
|   |   |   |   |   |   |   |   |   start > 14910:
transporter_activity_ (18.89)
|   |   |   |   |   |   |   |   strand = C: transferase_activity_
(12.13)
|   |   |   |   |   |   |   start > 20978
|   |   |   |   |   |   |   |   start <= 27484
|   |   |   |   |   |   |   |   |   start <= 22304: DNA_binding_
(37.23/18.44)
|   |   |   |   |   |   |   |   |   start > 22304
|   |   |   |   |   |   |   |   |   |   start <= 23935:
transferase_activity_ (15.65)
|   |   |   |   |   |   |   |   |   |   start > 23935:
transcription_regulator_activity_ (22.95)
|   |   |   |   |   |   |   |   start > 27484: helicase_activity_
(15.57)
|   |   |   |   |   start > 31636
|   |   |   |   |   |   start <= 59122
|   |   |   |   |   |   |   start <= 36933
|   |   |   |   |   |   |   |   start <= 33098: molecular_function_
(28.91)
|   |   |   |   |   |   |   |   start > 33098
|   |   |   |   |   |   |   |   |   start <= 35653:
hydrolase_activity_ (16.63)
|   |   |   |   |   |   |   |   |   start > 35653:
molecular_function_ (14.96)
|   |   |   |   |   |   |   start > 36933
|   |   |   |   |   |   |   |   start <= 55796
|   |   |   |   |   |   |   |   |   start <= 39023
|   |   |   |   |   |   |   |   |   |   start <= 38780:
enzyme_regulator_activity_ (14.97)
|   |   |   |   |   |   |   |   |   |   start > 38780:
ligase_activity_ (15.88)
|   |   |   |   |   |   |   |   |   start > 39023
|   |   |   |   |   |   |   |   |   |   start <= 45197
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 41498:
transcription_regulator_activity_ (13.32)
|   |   |   |   |   |   |   |   |   |   |   start > 41498:
molecular_function_ (39.88)
|   |   |   |   |   |   |   |   |   |   start > 45197
|   |   |   |   |   |   |   |   |   |   |   start <= 49552
|   |   |   |   |   |   |   |   |   |   |   |   start <= 45445:
protein_binding_ (12.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 45445
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 48613:
enzyme_regulator_activity_ (17.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 48613:
protein_binding_ (11.82)
|   |   |   |   |   |   |   |   |   |   |   start > 49552
|   |   |   |   |   |   |   |   |   |   |   |   start <= 53528:
transcription_regulator_activity_ (14.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 53528:
molecular_function_ (27.22)
|   |   |   |   |   |   |   |   start > 55796
|   |   |   |   |   |   |   |   |   start <= 56482: ligase_activity_
(20.57)
|   |   |   |   |   |   |   |   |   start > 56482: protein_binding_
(12.34)
|   |   |   |   |   |   start > 59122
|   |   |   |   |   |   |   start <= 84256
|   |   |   |   |   |   |   |   start <= 73157
|   |   |   |   |   |   |   |   |   start <= 69671
|   |   |   |   |   |   |   |   |   |   start <= 62075: RNA_binding_
(15.37)
|   |   |   |   |   |   |   |   |   |   start > 62075
|   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (34.52)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 64215:
molecular_function_ (20.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 64215:
phosphoprotein_phosphatase_activity_ (9.36)
|   |   |   |   |   |   |   |   |   start > 69671:
transferase_activity_ (24.78)
|   |   |   |   |   |   |   |   start > 73157
|   |   |   |   |   |   |   |   |   start <= 78856
|   |   |   |   |   |   |   |   |   |   start <= 73901:
molecular_function_ (33.91)
|   |   |   |   |   |   |   |   |   |   start > 73901
|   |   |   |   |   |   |   |   |   |   |   start <= 76893:
transporter_activity_ (19.4)
|   |   |   |   |   |   |   |   |   |   |   start > 76893:
hydrolase_activity_ (18.05)
|   |   |   |   |   |   |   |   |   start > 78856
|   |   |   |   |   |   |   |   |   |   start <= 81185
|   |   |   |   |   |   |   |   |   |   |   start <= 80364:
molecular_function_ (22.01)
|   |   |   |   |   |   |   |   |   |   |   start > 80364:
RNA_binding_ (17.09)
```

```
|   |   |   |   |   |   |   |   |   |   start > 81185:
molecular_function_ (56.24)
|   |   |   |   |   |   |   start > 84256
|   |   |   |   |   |   |   |   start <= 92516
|   |   |   |   |   |   |   |   |   start <= 87980
|   |   |   |   |   |   |   |   |   |   start <= 84884:
motor_activity_ (11.6)
|   |   |   |   |   |   |   |   |   |   start > 84884:
enzyme_regulator_activity_ (11.31)
|   |   |   |   |   |   |   |   |   start > 87980
|   |   |   |   |   |   |   |   |   |   start <= 91436
|   |   |   |   |   |   |   |   |   |   |   start <= 91251:
molecular_function_ (13.73)
|   |   |   |   |   |   |   |   |   |   |   start > 91251:
protein_binding_ (25.73)
|   |   |   |   |   |   |   |   |   |   start > 91436:
molecular_function_ (18.12)
|   |   |   |   |   |   |   |   start > 92516: hydrolase_activity_
(27.11)
|   |   |   |   start > 93797
|   |   |   |   |   start <= 190474
|   |   |   |   |   |   start <= 165097
|   |   |   |   |   |   |   start <= 148970
|   |   |   |   |   |   |   |   start <= 108162
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 97342
|   |   |   |   |   |   |   |   |   |   |   start <= 95862:
DNA_binding_ (15.01)
|   |   |   |   |   |   |   |   |   |   |   start > 95862:
protein_kinase_activity_ (15.4)
|   |   |   |   |   |   |   |   |   |   start > 97342
|   |   |   |   |   |   |   |   |   |   |   start <= 98973:
transcription_regulator_activity_ (21.13)
|   |   |   |   |   |   |   |   |   |   |   start > 98973:
oxidoreductase_activity_ (15.96)
|   |   |   |   |   |   |   |   |   strand = C:
structural_molecule_activity_ (24.82)
|   |   |   |   |   |   |   |   start > 108162
|   |   |   |   |   |   |   |   |   start <= 142252
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 124703
|   |   |   |   |   |   |   |   |   |   |   |   start <= 116063
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 115492:
molecular_function_ (14.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 115492:
transferase_activity_ (18.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 116063
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 122273:
molecular_function_ (18.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 122273
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
123596: protein_binding_ (14.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
123596: molecular_function_ (11.24)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 124703
|   |   |   |   |   |   |   |   |   |   |   |   start <= 129888:
lyase_activity_ (19.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 129888
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 131531:
molecular_function_ (12.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 131531:
transferase_activity_ (8.16)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 120911
|   |   |   |   |   |   |   |   |   |   |   |   start <= 116063
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 110700:
molecular_function_ (13.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 110700:
peptidase_activity_ (16.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 116063
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
DNA_binding_ (7.5/2.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
helicase_activity_ (15.93/4.63)
|   |   |   |   |   |   |   |   |   |   |   start > 120911
|   |   |   |   |   |   |   |   |   |   |   |   start <= 139967:
molecular_function_ (29.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 139967
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 141732:
hydrolase_activity_ (12.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 141732:
molecular_function_ (16.61)
|   |   |   |   |   |   |   |   |   start > 142252
|   |   |   |   |   |   |   |   |   |   strand = W:
enzyme_regulator_activity_ (21.22)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 147395:
phosphoprotein_phosphatase_activity_ (15.29)
|   |   |   |   |   |   |   |   |   |   |   start > 147395
|   |   |   |   |   |   |   |   |   |   |   |   start <= 148594:
structural_molecule_activity_ (19.84)
|   |   |   |   |   |   |   |   |   |   |   |   start > 148594:
molecular_function_ (13.27)
|   |   |   |   |   |   |   start > 148970
|   |   |   |   |   |   |   |   start <= 156018
|   |   |   |   |   |   |   |   |   start <= 154312
|   |   |   |   |   |   |   |   |   |   start <= 150177:
oxidoreductase_activity_ (14.02)
|   |   |   |   |   |   |   |   |   |   start > 150177
|   |   |   |   |   |   |   |   |   |   |   start <= 152782:
transporter_activity_ (14.62)
|   |   |   |   |   |   |   |   |   |   |   start > 152782:
oxidoreductase_activity_ (10.93)
|   |   |   |   |   |   |   |   |   start > 154312: lyase_activity_
(22.41)
|   |   |   |   |   |   |   |   start > 156018
|   |   |   |   |   |   |   |   |   start <= 157912
```

```
|   |   |   |   |   |   |   |   |   |   start <= 157291:
protein_binding_ (14.83)
|   |   |   |   |   |   |   |   |   |   start > 157291:
transcription_regulator_activity_ (12.82)
|   |   |   |   |   |   |   |   |   start > 157912:
protein_kinase_activity_ (28.77)
|   |   |   |   |   |   start > 165097
|   |   |   |   |   |   |   start <= 167358: RNA_binding_ (18.0)
|   |   |   |   |   |   |   start > 167358
|   |   |   |   |   |   |   |   start <= 180119: molecular_function_
(85.95)
|   |   |   |   |   |   |   |   start > 180119
|   |   |   |   |   |   |   |   |   start <= 185400
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 180706:
structural_molecule_activity_ (16.64)
|   |   |   |   |   |   |   |   |   |   |   start > 180706:
helicase_activity_ (14.43)
|   |   |   |   |   |   |   |   |   |   strand = C:
structural_molecule_activity_ (19.32)
|   |   |   |   |   |   |   |   |   start > 185400:
molecular_function_ (56.17)
|   |   |   |   |   start > 190474
|   |   |   |   |   |   start <= 200148
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 193306:
transcription_regulator_activity_ (14.08)
|   |   |   |   |   |   |   |   start > 193306: DNA_binding_
(37.66/18.2)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 198144
|   |   |   |   |   |   |   |   |   start <= 193306:
protein_binding_ (17.73)
|   |   |   |   |   |   |   |   |   start > 193306
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
DNA_binding_ (7.95/2.02)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
DNA_binding_ (8.04/3.99)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
isomerase_activity_ (11.45/2.83)
|   |   |   |   |   |   |   |   start > 198144: protein_binding_
(22.13)
|   |   |   |   |   |   start > 200148
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 210421
|   |   |   |   |   |   |   |   |   start <= 209011
|   |   |   |   |   |   |   |   |   |   start <= 205527
|   |   |   |   |   |   |   |   |   |   |   start <= 200567:
oxidoreductase_activity_ (10.93)
|   |   |   |   |   |   |   |   |   |   |   start > 200567:
molecular_function_ (30.25)
|   |   |   |   |   |   |   |   |   |   start > 205527
|   |   |   |   |   |   |   |   |   |   |   start <= 207038:
protein_kinase_activity_ (13.93)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 207038:
oxidoreductase_activity_ (19.26)
|   |   |   |   |   |   |   |   |   start > 209011:
hydrolase_activity_ (17.89)
|   |   |   |   |   |   |   |   start > 210421
|   |   |   |   |   |   |   |   |   start <= 217529
|   |   |   |   |   |   |   |   |   |   start <= 214086:
transferase_activity_ (16.93)
|   |   |   |   |   |   |   |   |   |   start > 214086
|   |   |   |   |   |   |   |   |   |   |   start <= 216278:
protein_binding_ (16.56)
|   |   |   |   |   |   |   |   |   |   |   start > 216278:
molecular_function_ (9.42)
|   |   |   |   |   |   |   |   |   start > 217529: lyase_activity_
(37.63/17.02)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 217529:
transferase_activity_ (12.98)
|   |   |   |   |   |   |   |   start > 217529: helicase_activity_
(17.77)
|   |   |   start > 226404
|   |   |   |   start <= 359447
|   |   |   |   |   start <= 277623
|   |   |   |   |   |   start <= 253864
|   |   |   |   |   |   |   start <= 235963
|   |   |   |   |   |   |   |   start <= 230248
|   |   |   |   |   |   |   |   |   start <= 228334:
structural_molecule_activity_ (13.58)
|   |   |   |   |   |   |   |   |   start > 228334:
molecular_function_ (34.06)
|   |   |   |   |   |   |   |   start > 230248
|   |   |   |   |   |   |   |   |   start <= 234512:
hydrolase_activity_ (13.44)
|   |   |   |   |   |   |   |   |   start > 234512:
translation_regulator_activity_ (15.93)
|   |   |   |   |   |   |   start > 235963
|   |   |   |   |   |   |   |   start <= 238124:
transferase_activity_ (11.93)
|   |   |   |   |   |   |   |   start > 238124
|   |   |   |   |   |   |   |   |   start <= 249874
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 245721
|   |   |   |   |   |   |   |   |   |   |   |   start <= 238358:
molecular_function_ (11.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 238358:
transporter_activity_ (21.62)
|   |   |   |   |   |   |   |   |   |   |   start > 245721:
molecular_function_ (15.53)
|   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (33.04)
|   |   |   |   |   |   |   |   |   start > 249874:
transferase_activity_ (9.13)
|   |   |   |   |   |   start > 253864
|   |   |   |   |   |   |   start <= 269194
```

```
|   |   |   |   |   |   |   |   start <= 257712
|   |   |   |   |   |   |   |   |   start <= 254646:
structural_molecule_activity_ (23.97)
|   |   |   |   |   |   |   |   |   start > 254646
|   |   |   |   |   |   |   |   |   |   start <= 255668:
enzyme_regulator_activity_ (11.33)
|   |   |   |   |   |   |   |   |   |   start > 255668:
molecular_function_ (10.57)
|   |   |   |   |   |   |   |   start > 257712
|   |   |   |   |   |   |   |   |   strand = W:
nucleotidyltransferase_activity_ (10.26)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 266150:
DNA_binding_ (16.03)
|   |   |   |   |   |   |   |   |   |   start > 266150:
structural_molecule_activity_ (13.77)
|   |   |   |   |   |   |   start > 269194
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 271003:
molecular_function_ (12.56)
|   |   |   |   |   |   |   |   |   start > 271003:
structural_molecule_activity_ (28.35)
|   |   |   |   |   |   |   |   strand = C: molecular_function_
(44.32)
|   |   |   |   |   start > 277623
|   |   |   |   |   |   start <= 345989
|   |   |   |   |   |   |   start <= 312196
|   |   |   |   |   |   |   |   start <= 283943
|   |   |   |   |   |   |   |   |   start <= 281163
|   |   |   |   |   |   |   |   |   |   start <= 280529:
RNA_binding_ (14.15)
|   |   |   |   |   |   |   |   |   |   start > 280529:
signal_transducer_activity_ (10.21)
|   |   |   |   |   |   |   |   |   start > 281163: RNA_binding_
(16.62)
|   |   |   |   |   |   |   |   start > 283943
|   |   |   |   |   |   |   |   |   start <= 306563
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 299981
|   |   |   |   |   |   |   |   |   |   |   |   start <= 292036
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 288518:
molecular_function_ (14.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 288518
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
289812: protein_binding_ (11.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
289812: protein_kinase_activity_ (10.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 292036
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 293463:
transporter_activity_ (20.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 293463:
molecular_function_ (36.72)
|   |   |   |   |   |   |   |   |   |   |   start > 299981:
protein_binding_ (18.07)
```

```
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 299981
|   |   |   |   |   |   |   |   |   |   |   |   start <= 293463:
molecular_function_ (9.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 293463:
transcription_regulator_activity_ (14.68)
|   |   |   |   |   |   |   |   |   |   |   start > 299981:
molecular_function_ (50.34)
|   |   |   |   |   |   |   |   |   start > 306563
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 310970
|   |   |   |   |   |   |   |   |   |   |   |   start <= 307440:
enzyme_regulator_activity_ (31.93/12.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 307440:
RNA_binding_ (9.05)
|   |   |   |   |   |   |   |   |   |   |   start > 310970:
molecular_function_ (21.01)
|   |   |   |   |   |   |   |   |   |   strand = C:
transporter_activity_ (18.88)
|   |   |   |   |   |   |   start > 312196
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 325334
|   |   |   |   |   |   |   |   |   |   start <= 317345
|   |   |   |   |   |   |   |   |   |   |   start <= 314634
|   |   |   |   |   |   |   |   |   |   |   |   start <= 313237:
structural_molecule_activity_ (18.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 313237:
hydrolase_activity_ (13.48)
|   |   |   |   |   |   |   |   |   |   |   start > 314634
|   |   |   |   |   |   |   |   |   |   |   |   start <= 316791:
RNA_binding_ (12.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 316791:
protein_binding_ (7.45)
|   |   |   |   |   |   |   |   |   |   start > 317345
|   |   |   |   |   |   |   |   |   |   |   start <= 321785
|   |   |   |   |   |   |   |   |   |   |   |   start <= 319784:
molecular_function_ (14.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 319784:
signal_transducer_activity_ (15.15)
|   |   |   |   |   |   |   |   |   |   |   start > 321785
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: DNA_binding_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: DNA_binding_ (1.87/0.44)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: DNA_binding_ (2.0/0.41)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: DNA_binding_ (1.88/0.55)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: DNA_binding_ (7.81/3.29)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: DNA_binding_ (0.0)
```

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|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
lipid_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
DNA_binding_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
helicase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
DNA_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
meiosis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
phosphoprotein_phosphatase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
pseudohyphal_growth_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
transcription_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
protein_kinase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
RNA_binding_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
cell_wall_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
cytokinesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
endomembrane_system_: DNA_binding_ (2.64/0.55)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
nuclear_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
microtubule_organizing_center_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
sporulation_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
cellular_respiration_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
ribosome_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
lyase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
amino_acid_and_derivative_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
nucleotidyltransferase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
nucleolus_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
cellular_bud_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
site_of_polarized_growth_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
extracellular_region_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
conjugation_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term = 
response_to_stress_: DNA_binding_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: transcription_regulator_activity_
(9.36/2.08)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   start > 325334
|   |   |   |   |   |   |   |   |   |   start <= 343322
|   |   |   |   |   |   |   |   |   |   |   start <= 337909
|   |   |   |   |   |   |   |   |   |   |   |   start <= 330610:
molecular_function_ (14.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 330610
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 334889:
structural_molecule_activity_ (20.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 334889:
RNA_binding_ (35.99/17.08)
|   |   |   |   |   |   |   |   |   |   |   start > 337909:
molecular_function_ (15.77)
|   |   |   |   |   |   |   |   |   |   start > 343322: RNA_binding_
(21.38)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 337909
|   |   |   |   |   |   |   |   |   |   start <= 330610:
protein_binding_ (13.41)
|   |   |   |   |   |   |   |   |   |   start > 330610:
hydrolase_activity_ (14.66)
|   |   |   |   |   |   |   |   |   start > 337909
```

```
|   |   |   |   |   |   |   |   |   |   start <= 343322:
molecular_function_ (15.59)
|   |   |   |   |   |   |   |   |   |   start > 343322:
protein_binding_ (20.9)
|   |   |   |   |   |   start > 345989
|   |   |   |   |   |   |   strand = W: molecular_function_ (142.56)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 347122: molecular_function_
(17.72)
|   |   |   |   |   |   |   |   start > 347122:
transferase_activity_ (12.63)
|   |   |   |   start > 359447
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 372015:
transcription_regulator_activity_ (73.53/32.78)
|   |   |   |   |   |   start > 372015
|   |   |   |   |   |   |   start <= 377612
|   |   |   |   |   |   |   |   start <= 376104
|   |   |   |   |   |   |   |   |   start <= 375090:
structural_molecule_activity_ (16.76)
|   |   |   |   |   |   |   |   |   start > 375090:
hydrolase_activity_ (10.07)
|   |   |   |   |   |   |   |   start > 376104:
structural_molecule_activity_ (19.31)
|   |   |   |   |   |   |   start > 377612
|   |   |   |   |   |   |   |   start <= 385199
|   |   |   |   |   |   |   |   |   start <= 383657:
isomerase_activity_ (8.48)
|   |   |   |   |   |   |   |   |   start > 383657: ligase_activity_
(9.12)
|   |   |   |   |   |   |   |   start > 385199
|   |   |   |   |   |   |   |   |   start <= 390070:
molecular_function_ (15.79)
|   |   |   |   |   |   |   |   |   start > 390070:
protein_kinase_activity_ (14.01)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 368756
|   |   |   |   |   |   |   start <= 363919
|   |   |   |   |   |   |   |   start <= 361862: helicase_activity_
(19.51)
|   |   |   |   |   |   |   |   start > 361862:
transporter_activity_ (9.2)
|   |   |   |   |   |   |   start > 363919
|   |   |   |   |   |   |   |   start <= 365254: RNA_binding_
(22.37)
|   |   |   |   |   |   |   |   start > 365254
|   |   |   |   |   |   |   |   |   start <= 365999:
structural_molecule_activity_ (23.69)
|   |   |   |   |   |   |   |   |   start > 365999
|   |   |   |   |   |   |   |   |   |   start <= 366472:
RNA_binding_ (13.95)
|   |   |   |   |   |   |   |   |   |   start > 366472:
structural_molecule_activity_ (15.15)
|   |   |   |   |   |   start > 368756
```

```
|   |   |   |   |   |   |   start <= 381274
|   |   |   |   |   |   |   |   start <= 377612:
nucleotidyltransferase_activity_ (11.06)
|   |   |   |   |   |   |   |   start > 377612:
transferase_activity_ (17.13)
|   |   |   |   |   |   |   start > 381274
|   |   |   |   |   |   |   |   start <= 385199: helicase_activity_
(15.85)
|   |   |   |   |   |   |   |   start > 385199:
structural_molecule_activity_ (11.49)
|   |   start > 392228
|   |   |   start <= 601665
|   |   |   |   start <= 414106
|   |   |   |   |   start <= 405779
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 398631
|   |   |   |   |   |   |   |   start <= 395835: molecular_function_
(14.09)
|   |   |   |   |   |   |   |   start > 395835:
oxidoreductase_activity_ (24.36)
|   |   |   |   |   |   |   start > 398631
|   |   |   |   |   |   |   |   start <= 403690
|   |   |   |   |   |   |   |   |   start <= 402592:
molecular_function_ (15.64)
|   |   |   |   |   |   |   |   |   start > 402592: protein_binding_
(10.78)
|   |   |   |   |   |   |   |   start > 403690: molecular_function_
(24.25)
|   |   |   |   |   |   strand = C: molecular_function_ (73.65)
|   |   |   |   |   start > 405779
|   |   |   |   |   |   start <= 411289
|   |   |   |   |   |   |   start <= 409607:
translation_regulator_activity_ (25.86)
|   |   |   |   |   |   |   start > 409607: peptidase_activity_
(17.3)
|   |   |   |   |   |   start > 411289
|   |   |   |   |   |   |   start <= 411555: transferase_activity_
(14.45)
|   |   |   |   |   |   |   start > 411555: molecular_function_
(43.08)
|   |   |   |   start > 414106
|   |   |   |   |   start <= 514558
|   |   |   |   |   |   start <= 502942
|   |   |   |   |   |   |   start <= 472303
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 446148
|   |   |   |   |   |   |   |   |   |   start <= 423967
|   |   |   |   |   |   |   |   |   |   |   start <= 423098
|   |   |   |   |   |   |   |   |   |   |   |   start <= 418891:
transcription_regulator_activity_ (6.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 418891:
molecular_function_ (14.53)
|   |   |   |   |   |   |   |   |   |   |   start > 423098:
oxidoreductase_activity_ (18.3)
```

```
|   |   |   |   |   |   |   |   |   |   start > 423967
|   |   |   |   |   |   |   |   |   |   |   start <= 436838
|   |   |   |   |   |   |   |   |   |   |   |   start <= 428606:
molecular_function_ (20.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 428606:
protein_binding_ (10.91)
|   |   |   |   |   |   |   |   |   |   |   start > 436838
|   |   |   |   |   |   |   |   |   |   |   |   start <= 439096:
structural_molecule_activity_ (10.49)
|   |   |   |   |   |   |   |   |   |   |   |   start > 439096:
molecular_function_ (13.67)
|   |   |   |   |   |   |   |   |   start > 446148
|   |   |   |   |   |   |   |   |   |   start <= 459859
|   |   |   |   |   |   |   |   |   |   |   start <= 454790
|   |   |   |   |   |   |   |   |   |   |   |   start <= 452409:
transferase_activity_ (22.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 452409:
protein_kinase_activity_ (23.86)
|   |   |   |   |   |   |   |   |   |   |   start > 454790
|   |   |   |   |   |   |   |   |   |   |   |   start <= 458161:
enzyme_regulator_activity_ (17.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 458161:
transferase_activity_ (15.4)
|   |   |   |   |   |   |   |   |   |   start > 459859
|   |   |   |   |   |   |   |   |   |   |   start <= 461671:
protein_binding_ (16.36)
|   |   |   |   |   |   |   |   |   |   |   start > 461671:
RNA_binding_ (23.6)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 448540
|   |   |   |   |   |   |   |   |   |   start <= 440812
|   |   |   |   |   |   |   |   |   |   |   start <= 428606
|   |   |   |   |   |   |   |   |   |   |   |   start <= 423098
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 417487:
RNA_binding_ (9.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 417487
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
418891: molecular_function_ (10.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
418891: lyase_activity_ (5.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 423098
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 426810:
transferase_activity_ (15.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 426810:
hydrolase_activity_ (19.44)
|   |   |   |   |   |   |   |   |   |   |   start > 428606
|   |   |   |   |   |   |   |   |   |   |   |   start <= 436838
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 433067:
DNA_binding_ (19.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 433067:
protein_binding_ (12.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 436838
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 439096:
RNA_binding_ (16.14)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 439096:
molecular_function_ (4.74)
|   |   |   |   |   |   |   |   |   |   start > 440812
|   |   |   |   |   |   |   |   |   |   |   start <= 446148:
hydrolase_activity_ (23.92)
|   |   |   |   |   |   |   |   |   |   |   start > 446148:
lyase_activity_ (24.39)
|   |   |   |   |   |   |   |   |   start > 448540
|   |   |   |   |   |   |   |   |   |   start <= 449962:
transcription_regulator_activity_ (16.65)
|   |   |   |   |   |   |   |   |   |   start > 449962
|   |   |   |   |   |   |   |   |   |   |   start <= 466146
|   |   |   |   |   |   |   |   |   |   |   |   start <= 458161:
molecular_function_ (41.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 458161
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 461671:
protein_binding_ (30.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 461671:
molecular_function_ (17.78)
|   |   |   |   |   |   |   |   |   |   |   start > 466146:
transcription_regulator_activity_ (11.04)
|   |   |   |   |   |   |   start > 472303
|   |   |   |   |   |   |   |   start <= 491960
|   |   |   |   |   |   |   |   |   start <= 475252
|   |   |   |   |   |   |   |   |   |   start <= 472860:
oxidoreductase_activity_ (16.22)
|   |   |   |   |   |   |   |   |   |   start > 472860:
peptidase_activity_ (13.37)
|   |   |   |   |   |   |   |   |   start > 475252
|   |   |   |   |   |   |   |   |   |   start <= 478657
|   |   |   |   |   |   |   |   |   |   |   start <= 475550:
molecular_function_ (12.35)
|   |   |   |   |   |   |   |   |   |   |   start > 475550:
lyase_activity_ (12.22)
|   |   |   |   |   |   |   |   |   |   start > 478657
|   |   |   |   |   |   |   |   |   |   |   start <= 482671:
transporter_activity_ (26.12/9.61)
|   |   |   |   |   |   |   |   |   |   |   start > 482671
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 485428:
molecular_function_ (11.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 485428
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C: transporter_activity_ (6.36/1.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F: hydrolase_activity_ (4.52/1.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P: hydrolase_activity_ (11.27/4.14)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (54.88)
|   |   |   |   |   |   |   |   start > 491960
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 496506:
molecular_function_ (22.17)
```

```
|   |   |   |   |   |   |   |   |   |   start > 496506
|   |   |   |   |   |   |   |   |   |   |   start <= 500136:
protein_binding_ (19.94)
|   |   |   |   |   |   |   |   |   |   |   start > 500136:
molecular_function_ (16.81)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 496506
|   |   |   |   |   |   |   |   |   |   |   start <= 494521:
protein_binding_ (21.86)
|   |   |   |   |   |   |   |   |   |   |   start > 494521:
oxidoreductase_activity_ (23.43)
|   |   |   |   |   |   |   |   |   |   start > 496506
|   |   |   |   |   |   |   |   |   |   |   start <= 498038:
transferase_activity_ (14.57)
|   |   |   |   |   |   |   |   |   |   |   start > 498038:
DNA_binding_ (20.77)
|   |   |   |   |   |   start > 502942
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 511549
|   |   |   |   |   |   |   |   |   start <= 506074: RNA_binding_
(24.38)
|   |   |   |   |   |   |   |   |   start > 506074:
nucleotidyltransferase_activity_ (26.69)
|   |   |   |   |   |   |   |   start > 511549
|   |   |   |   |   |   |   |   |   start <= 513163: lyase_activity_
(16.98)
|   |   |   |   |   |   |   |   |   start > 513163: RNA_binding_
(18.49)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 506973:
transcription_regulator_activity_ (20.39)
|   |   |   |   |   |   |   |   start > 506973
|   |   |   |   |   |   |   |   |   start <= 508368:
molecular_function_ (19.82)
|   |   |   |   |   |   |   |   |   start > 508368: protein_binding_
(19.08)
|   |   |   |   |   start > 514558
|   |   |   |   |   |   start <= 595841
|   |   |   |   |   |   |   start <= 561747
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 541854
|   |   |   |   |   |   |   |   |   |   start <= 516947:
signal_transducer_activity_ (13.05)
|   |   |   |   |   |   |   |   |   |   start > 516947
|   |   |   |   |   |   |   |   |   |   |   start <= 525233
|   |   |   |   |   |   |   |   |   |   |   |   start <= 523791:
molecular_function_ (25.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 523791:
transferase_activity_ (13.09)
|   |   |   |   |   |   |   |   |   |   |   start > 525233:
molecular_function_ (70.77)
|   |   |   |   |   |   |   |   |   start > 541854
|   |   |   |   |   |   |   |   |   |   start <= 543557
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 542207:
hydrolase_activity_ (11.66)
|   |   |   |   |   |   |   |   |   |   |   start > 542207:
oxidoreductase_activity_ (17.41)
|   |   |   |   |   |   |   |   |   |   start > 543557
|   |   |   |   |   |   |   |   |   |   |   distance <= 3419
|   |   |   |   |   |   |   |   |   |   |   |   start <= 555816
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 545374:
RNA_binding_ (10.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 545374
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
546445: molecular_function_ (16.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
546445: RNA_binding_ (10.92/0.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 555816:
molecular_function_ (27.16)
|   |   |   |   |   |   |   |   |   |   |   distance > 3419
|   |   |   |   |   |   |   |   |   |   |   |   start <= 548268
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 546445:
molecular_function_ (2.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 546445:
transferase_activity_ (18.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 548268:
RNA_binding_ (5.17/0.67)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 534462
|   |   |   |   |   |   |   |   |   |   start <= 529268
|   |   |   |   |   |   |   |   |   |   |   start <= 523791:
molecular_function_ (18.77)
|   |   |   |   |   |   |   |   |   |   |   start > 523791
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transporter_activity_ (18.11/3.33)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
hydrolase_activity_ (3.49/0.85)
|   |   |   |   |   |   |   |   |   |   start > 529268
|   |   |   |   |   |   |   |   |   |   |   start <= 532989:
nucleotidyltransferase_activity_ (10.01)
|   |   |   |   |   |   |   |   |   |   |   start > 532989:
structural_molecule_activity_ (11.47)
|   |   |   |   |   |   |   |   |   start > 534462
|   |   |   |   |   |   |   |   |   |   start <= 558872
|   |   |   |   |   |   |   |   |   |   |   start <= 557569
|   |   |   |   |   |   |   |   |   |   |   |   start <= 548268
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 545374:
molecular_function_ (10.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 545374:
hydrolase_activity_ (10.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 548268:
molecular_function_ (26.52)
|   |   |   |   |   |   |   |   |   |   |   start > 557569:
hydrolase_activity_ (11.8)
|   |   |   |   |   |   |   |   |   |   start > 558872
|   |   |   |   |   |   |   |   |   |   |   start <= 560686:
transporter_activity_ (35.46/16.17)
```

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|   |   |   |   |   |   |   |   |   |   |   start > 560686:
molecular_function_ (18.55)
|   |   |   |   |   |   |   start > 561747
|   |   |   |   |   |   |   |   start <= 575402: protein_binding_
(14.36)
|   |   |   |   |   |   |   |   start > 575402
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 591318
|   |   |   |   |   |   |   |   |   |   |   start <= 584899:
molecular_function_ (44.78)
|   |   |   |   |   |   |   |   |   |   |   start > 584899
|   |   |   |   |   |   |   |   |   |   |   |   start <= 589830:
protein_binding_ (17.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 589830:
molecular_function_ (14.35)
|   |   |   |   |   |   |   |   |   |   start > 591318:
transferase_activity_ (13.51)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 581440:
transferase_activity_ (17.54)
|   |   |   |   |   |   |   |   |   |   start > 581440
|   |   |   |   |   |   |   |   |   |   |   start <= 591318:
transcription_regulator_activity_ (29.27)
|   |   |   |   |   |   |   |   |   |   |   start > 591318:
molecular_function_ (14.32)
|   |   |   |   |   |   start > 595841
|   |   |   |   |   |   |   start <= 596697:
translation_regulator_activity_ (27.39)
|   |   |   |   |   |   |   start > 596697
|   |   |   |   |   |   |   |   start <= 599421:
transporter_activity_ (14.35)
|   |   |   |   |   |   |   |   start > 599421: hydrolase_activity_
(23.58)
|   |   |   start > 601665
|   |   |   |   start <= 732932
|   |   |   |   |   start <= 676625
|   |   |   |   |   |   start <= 650621
|   |   |   |   |   |   |   start <= 644048
|   |   |   |   |   |   |   |   start <= 619862
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 607567
|   |   |   |   |   |   |   |   |   |   |   start <= 606140:
molecular_function_ (18.9)
|   |   |   |   |   |   |   |   |   |   |   start > 606140:
structural_molecule_activity_ (19.74)
|   |   |   |   |   |   |   |   |   |   start > 607567
|   |   |   |   |   |   |   |   |   |   |   start <= 609588:
RNA_binding_ (19.37)
|   |   |   |   |   |   |   |   |   |   |   start > 609588:
oxidoreductase_activity_ (14.21)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 615969
|   |   |   |   |   |   |   |   |   |   |   start <= 610568:
transporter_activity_ (15.01)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 610568:
ligase_activity_ (26.03)
|   |   |   |   |   |   |   |   |   |   start > 615969
|   |   |   |   |   |   |   |   |   |   |   start <= 617282:
transporter_activity_ (15.13)
|   |   |   |   |   |   |   |   |   |   |   start > 617282
|   |   |   |   |   |   |   |   |   |   |   |   start <= 617828:
transcription_regulator_activity_ (12.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 617828:
transporter_activity_ (9.79)
|   |   |   |   |   |   |   |   start > 619862
|   |   |   |   |   |   |   |   |   start <= 634308
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 627810:
signal_transducer_activity_ (17.89)
|   |   |   |   |   |   |   |   |   |   |   start > 627810:
molecular_function_ (15.56)
|   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (54.23)
|   |   |   |   |   |   |   |   |   start > 634308
|   |   |   |   |   |   |   |   |   |   start <= 637581
|   |   |   |   |   |   |   |   |   |   |   start <= 636879:
RNA_binding_ (31.46)
|   |   |   |   |   |   |   |   |   |   |   start > 636879:
structural_molecule_activity_ (17.14)
|   |   |   |   |   |   |   |   |   |   start > 637581
|   |   |   |   |   |   |   |   |   |   |   start <= 642014
|   |   |   |   |   |   |   |   |   |   |   |   start <= 640724
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (29.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
639517: molecular_function_ (20.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
639517: protein_binding_ (21.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 640724:
protein_binding_ (17.38)
|   |   |   |   |   |   |   |   |   |   |   start > 642014
|   |   |   |   |   |   |   |   |   |   |   |   start <= 643784:
RNA_binding_ (14.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 643784:
transporter_activity_ (18.97)
|   |   |   |   |   |   |   start > 644048
|   |   |   |   |   |   |   |   start <= 648911
|   |   |   |   |   |   |   |   |   start <= 646819:
enzyme_regulator_activity_ (14.97)
|   |   |   |   |   |   |   |   |   start > 646819:
structural_molecule_activity_ (41.62)
|   |   |   |   |   |   |   |   start > 648911:
enzyme_regulator_activity_ (15.88)
|   |   |   |   |   |   start > 650621
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 670392
|   |   |   |   |   |   |   |   |   start <= 661753
```

```
|   |   |   |   |   |   |   |   |   |   start <= 654638:
oxidoreductase_activity_ (37.22/17.3)
|   |   |   |   |   |   |   |   |   |   start > 654638:
molecular_function_ (22.36)
|   |   |   |   |   |   |   |   |   start > 661753
|   |   |   |   |   |   |   |   |   |   start <= 666345:
RNA_binding_ (36.46)
|   |   |   |   |   |   |   |   |   |   start > 666345
|   |   |   |   |   |   |   |   |   |   |   start <= 668193:
protein_kinase_activity_ (11.45)
|   |   |   |   |   |   |   |   |   |   |   start > 668193:
molecular_function_ (17.66)
|   |   |   |   |   |   |   |   start > 670392
|   |   |   |   |   |   |   |   |   start <= 672190:
ligase_activity_ (9.88)
|   |   |   |   |   |   |   |   |   start > 672190:
transporter_activity_ (24.67)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 662362: lyase_activity_
(16.99)
|   |   |   |   |   |   |   |   start > 662362: hydrolase_activity_
(21.68)
|   |   |   |   |   start > 676625
|   |   |   |   |   |   start <= 693367
|   |   |   |   |   |   |   start <= 678699:
transcription_regulator_activity_ (15.42)
|   |   |   |   |   |   |   start > 678699
|   |   |   |   |   |   |   |   start <= 687903
|   |   |   |   |   |   |   |   |   start <= 687462:
peptidase_activity_ (22.63)
|   |   |   |   |   |   |   |   |   start > 687462: DNA_binding_
(21.21)
|   |   |   |   |   |   |   |   start > 687903
|   |   |   |   |   |   |   |   |   start <= 690249:
enzyme_regulator_activity_ (26.99)
|   |   |   |   |   |   |   |   |   start > 690249:
peptidase_activity_ (19.59)
|   |   |   |   |   |   start > 693367
|   |   |   |   |   |   |   start <= 715832
|   |   |   |   |   |   |   |   start <= 701052
|   |   |   |   |   |   |   |   |   start <= 698372
|   |   |   |   |   |   |   |   |   |   start <= 695421:
molecular_function_ (41.05)
|   |   |   |   |   |   |   |   |   |   start > 695421:
transcription_regulator_activity_ (24.22)
|   |   |   |   |   |   |   |   |   start > 698372:
molecular_function_ (65.24)
|   |   |   |   |   |   |   |   start > 701052
|   |   |   |   |   |   |   |   |   start <= 706505:
enzyme_regulator_activity_ (22.99)
|   |   |   |   |   |   |   |   |   start > 706505:
molecular_function_ (33.89)
|   |   |   |   |   |   |   start > 715832
|   |   |   |   |   |   |   |   start <= 731142
```

```
|   |   |   |   |   |   |   |   |   start <= 729676
|   |   |   |   |   |   |   |   |   |   start <= 717362:
protein_binding_ (17.73)
|   |   |   |   |   |   |   |   |   |   start > 717362
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 718897:
structural_molecule_activity_ (16.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 718897
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 720413:
transcription_regulator_activity_ (10.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 720413:
structural_molecule_activity_ (16.24)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 726978:
molecular_function_ (22.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 726978:
structural_molecule_activity_ (14.71)
|   |   |   |   |   |   |   |   |   start > 729676
|   |   |   |   |   |   |   |   |   |   start <= 730826:
protein_binding_ (24.65)
|   |   |   |   |   |   |   |   |   |   start > 730826:
molecular_function_ (14.47)
|   |   |   |   |   |   |   |   start > 731142:
transporter_activity_ (22.44)
|   |   |   |   start > 732932
|   |   |   |   |   start <= 982073
|   |   |   |   |   |   start <= 846660
|   |   |   |   |   |   |   start <= 774354
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 757775
|   |   |   |   |   |   |   |   |   |   start <= 746803
|   |   |   |   |   |   |   |   |   |   |   start <= 739949
|   |   |   |   |   |   |   |   |   |   |   |   start <= 739127:
molecular_function_ (45.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 739127:
ligase_activity_ (14.15)
|   |   |   |   |   |   |   |   |   |   |   start > 739949:
molecular_function_ (47.13)
|   |   |   |   |   |   |   |   |   |   start > 746803
|   |   |   |   |   |   |   |   |   |   |   start <= 750405:
RNA_binding_ (14.76)
|   |   |   |   |   |   |   |   |   |   |   start > 750405:
molecular_function_ (45.59)
|   |   |   |   |   |   |   |   |   start > 757775
|   |   |   |   |   |   |   |   |   |   start <= 761397:
peptidase_activity_ (22.1)
|   |   |   |   |   |   |   |   |   |   start > 761397
|   |   |   |   |   |   |   |   |   |   |   start <= 767434
|   |   |   |   |   |   |   |   |   |   |   |   start <= 762433:
molecular_function_ (10.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 762433:
DNA_binding_ (11.73)
|   |   |   |   |   |   |   |   |   |   |   start > 767434
|   |   |   |   |   |   |   |   |   |   |   |   start <= 772459
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 770574:
molecular_function_ (19.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 770574:
protein_binding_ (11.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 772459:
molecular_function_ (26.17)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 750405
|   |   |   |   |   |   |   |   |   |   start <= 742330:
phosphoprotein_phosphatase_activity_ (16.2)
|   |   |   |   |   |   |   |   |   |   start > 742330: RNA_binding_
(14.79)
|   |   |   |   |   |   |   |   |   start > 750405
|   |   |   |   |   |   |   |   |   |   start <= 757775:
molecular_function_ (19.57)
|   |   |   |   |   |   |   |   |   |   start > 757775:
transporter_activity_ (8.58)
|   |   |   |   |   |   |   start > 774354
|   |   |   |   |   |   |   |   start <= 807661
|   |   |   |   |   |   |   |   |   start <= 796097
|   |   |   |   |   |   |   |   |   |   start <= 775198:
hydrolase_activity_ (11.15)
|   |   |   |   |   |   |   |   |   |   start > 775198
|   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (74.36)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 793058
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 786925
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
785442: molecular_function_ (22.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
785442: transferase_activity_ (18.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 786925
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
789036: RNA_binding_ (13.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
789036: molecular_function_ (15.96)
|   |   |   |   |   |   |   |   |   |   |   |   start > 793058:
signal_transducer_activity_ (14.19)
|   |   |   |   |   |   |   |   |   start > 796097
|   |   |   |   |   |   |   |   |   |   start <= 798548
|   |   |   |   |   |   |   |   |   |   |   start <= 797873:
transferase_activity_ (25.03)
|   |   |   |   |   |   |   |   |   |   |   start > 797873:
lyase_activity_ (12.58)
|   |   |   |   |   |   |   |   |   |   start > 798548
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 800551:
RNA_binding_ (17.52)
|   |   |   |   |   |   |   |   |   |   |   |   start > 800551:
transferase_activity_ (12.58)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 806026:
hydrolase_activity_ (13.96)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 806026:
RNA_binding_ (31.19)
|   |   |   |   |   |   |   |   start > 807661
|   |   |   |   |   |   |   |   |   start <= 832461
|   |   |   |   |   |   |   |   |   |   start <= 828799
|   |   |   |   |   |   |   |   |   |   |   start <= 823487:
molecular_function_ (38.27)
|   |   |   |   |   |   |   |   |   |   |   start > 823487
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 824064:
translation_regulator_activity_ (10.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 824064:
hydrolase_activity_ (9.19)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (9.78)
|   |   |   |   |   |   |   |   |   |   start > 828799
|   |   |   |   |   |   |   |   |   |   |   start <= 829121:
structural_molecule_activity_ (12.4)
|   |   |   |   |   |   |   |   |   |   |   start > 829121
|   |   |   |   |   |   |   |   |   |   |   |   start <= 830520:
molecular_function_ (17.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 830520:
structural_molecule_activity_ (10.02)
|   |   |   |   |   |   |   |   |   start > 832461
|   |   |   |   |   |   |   |   |   |   start <= 842556
|   |   |   |   |   |   |   |   |   |   |   start <= 837147
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
lyase_activity_ (10.95)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 834487:
molecular_function_ (15.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 834487
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
835908: lyase_activity_ (9.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
835908: molecular_function_ (12.4)
|   |   |   |   |   |   |   |   |   |   |   start > 837147:
ligase_activity_ (18.97)
|   |   |   |   |   |   |   |   |   |   start > 842556:
molecular_function_ (96.8)
|   |   |   |   |   |   start > 846660
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 913232
|   |   |   |   |   |   |   |   |   start <= 883815
|   |   |   |   |   |   |   |   |   |   start <= 871421
|   |   |   |   |   |   |   |   |   |   |   start <= 859481:
transporter_activity_ (14.02)
|   |   |   |   |   |   |   |   |   |   |   start > 859481:
transcription_regulator_activity_ (13.71)
|   |   |   |   |   |   |   |   |   |   start > 871421
|   |   |   |   |   |   |   |   |   |   |   start <= 878197:
molecular_function_ (13.94)
|   |   |   |   |   |   |   |   |   |   |   start > 878197:
transporter_activity_ (5.72)
```

```
|   |   |   |   |   |   |   |   |   start > 883815
|   |   |   |   |   |   |   |   |   |   start <= 905242
|   |   |   |   |   |   |   |   |   |   |   start <= 894698
|   |   |   |   |   |   |   |   |   |   |   |   start <= 888887:
hydrolase_activity_ (11.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 888887:
molecular_function_ (16.98)
|   |   |   |   |   |   |   |   |   |   |   start > 894698
|   |   |   |   |   |   |   |   |   |   |   |   start <= 897507:
transferase_activity_ (18.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 897507:
phosphoprotein_phosphatase_activity_ (18.01)
|   |   |   |   |   |   |   |   |   |   start > 905242
|   |   |   |   |   |   |   |   |   |   |   start <= 905939:
ligase_activity_ (21.15)
|   |   |   |   |   |   |   |   |   |   |   start > 905939
|   |   |   |   |   |   |   |   |   |   |   |   start <= 910437:
molecular_function_ (42.42)
|   |   |   |   |   |   |   |   |   |   |   |   start > 910437:
hydrolase_activity_ (11.57)
|   |   |   |   |   |   |   |   start > 913232
|   |   |   |   |   |   |   |   |   start <= 947423
|   |   |   |   |   |   |   |   |   |   start <= 922180
|   |   |   |   |   |   |   |   |   |   |   start <= 917045
|   |   |   |   |   |   |   |   |   |   |   |   start <= 915246:
protein_binding_ (18.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 915246:
transferase_activity_ (11.26)
|   |   |   |   |   |   |   |   |   |   |   start > 917045:
structural_molecule_activity_ (27.81)
|   |   |   |   |   |   |   |   |   |   start > 922180
|   |   |   |   |   |   |   |   |   |   |   start <= 942809
|   |   |   |   |   |   |   |   |   |   |   |   start <= 932544
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 924699:
transporter_activity_ (24.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 924699:
protein_binding_ (7.96)
|   |   |   |   |   |   |   |   |   |   |   |   start > 932544
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 939926:
RNA_binding_ (20.84/7.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 939926:
transporter_activity_ (17.52)
|   |   |   |   |   |   |   |   |   |   |   start > 942809
|   |   |   |   |   |   |   |   |   |   |   |   start <= 945148:
enzyme_regulator_activity_ (13.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 945148:
transferase_activity_ (8.41)
|   |   |   |   |   |   |   |   |   start > 947423
|   |   |   |   |   |   |   |   |   |   start <= 953963:
molecular_function_ (29.39)
|   |   |   |   |   |   |   |   |   |   start > 953963
|   |   |   |   |   |   |   |   |   |   |   start <= 965660:
oxidoreductase_activity_ (19.34)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 965660:
molecular_function_ (16.51)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 888887
|   |   |   |   |   |   |   |   |   start <= 883815
|   |   |   |   |   |   |   |   |   |   start <= 850441
|   |   |   |   |   |   |   |   |   |   |   start <= 848428:
molecular_function_ (26.44/11.84)
|   |   |   |   |   |   |   |   |   |   |   start > 848428:
transferase_activity_ (21.8)
|   |   |   |   |   |   |   |   |   |   start > 850441
|   |   |   |   |   |   |   |   |   |   |   start <= 859481
|   |   |   |   |   |   |   |   |   |   |   |   start <= 854900
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 853220:
molecular_function_ (19.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 853220:
protein_binding_ (19.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 854900
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 856306:
oxidoreductase_activity_ (21.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 856306
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
858292: molecular_function_ (19.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
858292: oxidoreductase_activity_ (11.01)
|   |   |   |   |   |   |   |   |   |   |   start > 859481
|   |   |   |   |   |   |   |   |   |   |   |   start <= 871421
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 867779
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
865758: molecular_function_ (9.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
865758: ligase_activity_ (16.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 867779:
molecular_function_ (19.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 871421
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 876399
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_component_: protein_binding_ (0.92/0.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= molecular_function_: protein_kinase_activity_ (8.5/1.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= biological_process_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transferase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_modification_process_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrion_: protein_kinase_activity_ (1.88/0.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= oxidoreductase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= generation_of_precursor_metabolites_and_energy_: protein_binding_
(0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasm_: protein_kinase_activity_ (1.21/0.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_regulator_activity_: protein_binding_ (1.86/0.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transduction_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleus_: protein_kinase_activity_ (1.55/0.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= enzyme_regulator_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_biogenesis_and_assembly_: protein_binding_ (2.21/0.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ligase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_: protein_kinase_activity_ (0.47/0.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_binding_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transport_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endoplasmic_reticulum_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= Golgi_apparatus_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transporter_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= hydrolase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= organelle_organization_and_biogenesis_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= motor_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cycle_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_organization_and_biogenesis_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= chromosome_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_metabolic_process_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vacuole_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vesicle-mediated_transport_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasmic_membrane-bound_vesicle_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= structural_molecule_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peroxisome_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lipid_metabolic_process_: protein_binding_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_binding_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= helicase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_metabolic_process_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= meiosis_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= phosphoprotein_phosphatase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= pseudohyphal_growth_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_: protein_kinase_activity_ (3.33/1.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_kinase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_binding_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_organization_and_biogenesis_: protein_binding_
(2.55/0.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytokinesis_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endomembrane_system_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nuclear_organization_and_biogenesis_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= microtubule_organizing_center_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= sporulation_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_respiration_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lyase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= amino_acid_and_derivative_metabolic_process_: protein_binding_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleotidyltransferase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleolus_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_bud_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= site_of_polarized_growth_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= extracellular_region_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= conjugation_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= response_to_stress_: protein_binding_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= plasma_membrane_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= isomerase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_budding_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_regulator_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_fraction_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_: protein_binding_ (5.32/0.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peptidase_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_catabolic_process_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrial_envelope_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vitamin_metabolic_process_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transducer_activity_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_organization_and_biogenesis_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= carbohydrate_metabolic_process_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= anatomical_structure_morphogenesis_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cortex_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_: protein_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 876399
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
880425: molecular_function_ (24.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
880425: oxidoreductase_activity_ (9.25)
|   |   |   |   |   |   |   |   |   start > 883815
|   |   |   |   |   |   |   |   |   |   start <= 885746:
protein_binding_ (13.01)
|   |   |   |   |   |   |   |   |   |   start > 885746:
transferase_activity_ (14.76)
|   |   |   |   |   |   |   |   start > 888887
|   |   |   |   |   |   |   |   |   start <= 920580
|   |   |   |   |   |   |   |   |   |   start <= 911888
|   |   |   |   |   |   |   |   |   |   |   start <= 903202:
molecular_function_ (77.38)
|   |   |   |   |   |   |   |   |   |   |   start > 903202
|   |   |   |   |   |   |   |   |   |   |   |   start <= 905939:
nucleotidyltransferase_activity_ (20.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 905939:
molecular_function_ (33.88)
|   |   |   |   |   |   |   |   |   |   start > 911888
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 913232:
oxidoreductase_activity_ (11.74)
|   |   |   |   |   |   |   |   |   |   |   start > 913232:
molecular_function_ (28.43)
|   |   |   |   |   |   |   |   |   start > 920580
|   |   |   |   |   |   |   |   |   |   start <= 939926
|   |   |   |   |   |   |   |   |   |   |   start <= 938995
|   |   |   |   |   |   |   |   |   |   |   |   start <= 924699:
transferase_activity_ (18.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 924699
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 936886
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
932544: molecular_function_ (8.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
932544: structural_molecule_activity_ (12.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 936886:
molecular_function_ (16.59)
|   |   |   |   |   |   |   |   |   |   |   start > 938995:
RNA_binding_ (27.68)
|   |   |   |   |   |   |   |   |   |   start > 939926
|   |   |   |   |   |   |   |   |   |   |   start <= 968692
|   |   |   |   |   |   |   |   |   |   |   |   start <= 959908
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 953963:
molecular_function_ (59.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 953963:
enzyme_regulator_activity_ (15.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 959908:
molecular_function_ (63.72)
|   |   |   |   |   |   |   |   |   |   |   start > 968692
|   |   |   |   |   |   |   |   |   |   |   |   start <= 973739
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 970058:
protein_binding_ (12.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 970058:
transferase_activity_ (14.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 973739
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 2203
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
974782: molecular_function_ (3.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
974782
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
977341: protein_binding_ (10.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
977341: ligase_activity_ (2.76/0.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 2203
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
979324
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
976586: molecular_function_ (8.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
976586: ligase_activity_ (4.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
979324: molecular_function_ (17.17)
|   |   |   |   |   start > 982073
```

```
|   |   |   |   |   |   start <= 993526
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 985977: hydrolase_activity_
(43.29)
|   |   |   |   |   |   |   |   start > 985977: DNA_binding_ (24.3)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 988054:
transcription_regulator_activity_ (15.76)
|   |   |   |   |   |   |   |   start > 988054: RNA_binding_ (16.24)
|   |   |   |   |   |   start > 993526
|   |   |   |   |   |   |   start <= 1000932
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 995644:
molecular_function_ (19.48)
|   |   |   |   |   |   |   |   |   start > 995644
|   |   |   |   |   |   |   |   |   |   start <= 996874:
transcription_regulator_activity_ (19.3)
|   |   |   |   |   |   |   |   |   |   start > 996874:
lyase_activity_ (13.33)
|   |   |   |   |   |   |   |   strand = C: peptidase_activity_
(19.35)
|   |   |   |   |   |   |   start > 1000932
|   |   |   |   |   |   |   |   start <= 1004222:
molecular_function_ (51.96)
|   |   |   |   |   |   |   |   start > 1004222:
oxidoreductase_activity_ (17.65)
|   start > 1004630
|   |   strand = W
|   |   |   start <= 1060047
|   |   |   |   start <= 1046738
|   |   |   |   |   start <= 1016756: transporter_activity_ (15.01)
|   |   |   |   |   start > 1016756
|   |   |   |   |   |   start <= 1031797
|   |   |   |   |   |   |   start <= 1027376
|   |   |   |   |   |   |   |   start <= 1022662:
molecular_function_ (10.91)
|   |   |   |   |   |   |   |   start > 1022662: hydrolase_activity_
(14.56)
|   |   |   |   |   |   |   start > 1027376: helicase_activity_
(16.04)
|   |   |   |   |   |   start > 1031797: molecular_function_ (32.97)
|   |   |   |   start > 1046738: transporter_activity_ (20.8)
|   |   |   start > 1060047
|   |   |   |   start <= 1070300: DNA_binding_ (41.17/17.37)
|   |   |   |   start > 1070300
|   |   |   |   |   start <= 1076606: hydrolase_activity_ (14.76)
|   |   |   |   |   start > 1076606
|   |   |   |   |   |   start <= 1080313: molecular_function_ (8.66)
|   |   |   |   |   |   start > 1080313: helicase_activity_ (14.44)
|   |   strand = C
|   |   |   start <= 1049965
|   |   |   |   start <= 1043283
|   |   |   |   |   start <= 1012491
```

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|   |   |   |   |   |   start <= 1007311: transporter_activity_
(17.85)
|   |   |   |   |   |   start > 1007311: hydrolase_activity_ (13.83)
|   |   |   |   |   start > 1012491
|   |   |   |   |   |   start <= 1039245
|   |   |   |   |   |   |   start <= 1022662
|   |   |   |   |   |   |   |   start <= 1019247
|   |   |   |   |   |   |   |   |   start <= 1017765
|   |   |   |   |   |   |   |   |   |   start <= 1016756:
molecular_function_ (13.15)
|   |   |   |   |   |   |   |   |   |   start > 1016756:
protein_kinase_activity_ (15.05)
|   |   |   |   |   |   |   |   |   start > 1017765:
molecular_function_ (18.44)
|   |   |   |   |   |   |   |   start > 1019247: ligase_activity_
(16.56)
|   |   |   |   |   |   |   start > 1022662
|   |   |   |   |   |   |   |   start <= 1025741:
hydrolase_activity_ (13.55)
|   |   |   |   |   |   |   |   start > 1025741: molecular_function_
(42.65)
|   |   |   |   |   |   start > 1039245: protein_kinase_activity_
(19.67)
|   |   |   |   start > 1043283
|   |   |   |   |   start <= 1045487: hydrolase_activity_ (24.29)
|   |   |   |   |   start > 1045487
|   |   |   |   |   |   start <= 1046738:
nucleotidyltransferase_activity_ (15.01)
|   |   |   |   |   |   start > 1046738: hydrolase_activity_ (15.74)
|   |   |   start > 1049965
|   |   |   |   start <= 1064947
|   |   |   |   |   start <= 1061597
|   |   |   |   |   |   start <= 1058731
|   |   |   |   |   |   |   start <= 1052831: molecular_function_
(16.55)
|   |   |   |   |   |   |   start > 1052831: transferase_activity_
(15.62)
|   |   |   |   |   |   start > 1058731: molecular_function_ (36.61)
|   |   |   |   |   start > 1061597
|   |   |   |   |   |   start <= 1063160: protein_binding_ (12.38)
|   |   |   |   |   |   start > 1063160: transferase_activity_
(28.06)
|   |   |   |   start > 1064947
|   |   |   |   |   start <= 1070300: hydrolase_activity_ (17.0)
|   |   |   |   |   start > 1070300
|   |   |   |   |   |   start <= 1076606: transporter_activity_
(9.29)
|   |   |   |   |   |   start > 1076606: molecular_function_ (13.78)
```

For Biological Process

```
|   start <= 343322
|   |   start <= 107508
|   |   |   start <= 38780
```

```
|   |   |   |   start <= 23935
|   |   |   |   |   start <= 14157
|   |   |   |   |   |   start <= 11110: biological_process_ (89.81)
|   |   |   |   |   |   start > 11110: protein_modification_process_
(15.06)
|   |   |   |   |   start > 14157
|   |   |   |   |   |   start <= 22304
|   |   |   |   |   |   |   start <= 14910:
generation_of_precursor_metabolites_and_energy_ (15.89)
|   |   |   |   |   |   |   start > 14910: transport_ (66.84/22.56)
|   |   |   |   |   |   start > 22304
|   |   |   |   |   |   |   neigh_strand = W:
anatomical_structure_morphogenesis_ (19.9/7.63)
|   |   |   |   |   |   |   neigh_strand = C: biological_process_
(13.83/3.89)
|   |   |   |   start > 23935
|   |   |   |   |   start <= 35653
|   |   |   |   |   |   start <= 31910
|   |   |   |   |   |   |   strand = W: biological_process_ (18.96)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 27484: signal_transduction_
(16.51)
|   |   |   |   |   |   |   |   start > 27484: meiosis_ (21.71)
|   |   |   |   |   |   start > 31910
|   |   |   |   |   |   |   start <= 33098: cell_cycle_
(38.26/18.14)
|   |   |   |   |   |   |   start > 33098: signal_transduction_
(11.1)
|   |   |   |   |   start > 35653
|   |   |   |   |   |   start <= 36933:
nuclear_organization_and_biogenesis_ (29.88/9.51)
|   |   |   |   |   |   start > 36933:
ribosome_biogenesis_and_assembly_ (15.32)
|   |   |   start > 38780
|   |   |   |   start <= 82373
|   |   |   |   |   stop <= 53787
|   |   |   |   |   |   start <= 45197
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 39023: translation_ (13.49)
|   |   |   |   |   |   |   |   start > 39023:
RNA_metabolic_process_ (64.17/26.24)
|   |   |   |   |   |   |   strand = C: biological_process_ (14.57)
|   |   |   |   |   |   start > 45197
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 48613
|   |   |   |   |   |   |   |   |   start <= 45445: transport_
(15.81)
|   |   |   |   |   |   |   |   |   start > 45445: cell_cycle_
(27.26)
|   |   |   |   |   |   |   |   start > 48613: transport_ (16.49)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 53528: transcription_
(15.29)
|   |   |   |   |   |   |   |   start > 53528: translation_ (10.0)
```

```
|   |   |   |   |   stop > 53787
|   |   |   |   |   |   start <= 69671
|   |   |   |   |   |   |   start <= 64215
|   |   |   |   |   |   |   |   start <= 59122
|   |   |   |   |   |   |   |   |   start <= 56482:
biological_process_ (37.75)
|   |   |   |   |   |   |   |   |   start > 56482: cytokinesis_
(17.59)
|   |   |   |   |   |   |   |   start > 59122
|   |   |   |   |   |   |   |   |   strand = W:
RNA_metabolic_process_ (13.84)
|   |   |   |   |   |   |   |   |   strand = C: biological_process_
(25.02)
|   |   |   |   |   |   |   start > 64215
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 67598:
biological_process_ (12.48)
|   |   |   |   |   |   |   |   |   start > 67598:
protein_catabolic_process_ (12.76)
|   |   |   |   |   |   |   |   strand = C: cell_cycle_ (14.08)
|   |   |   |   |   |   start > 69671
|   |   |   |   |   |   |   start <= 76893
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 73901:
biological_process_ (10.92)
|   |   |   |   |   |   |   |   |   start > 73901
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: transport_ (2.61/0.6)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: protein_modification_process_ (5.56/2.06)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: transport_ (17.15/6.15)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: protein_modification_process_ (5.98/2.57)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
protein_modification_process_ (9.14/2.24)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
protein_modification_process_ (0.94/0.18)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: protein_modification_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
transport_ (2.25/0.57)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: protein_modification_process_ (2.56/0.95)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: protein_modification_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: protein_modification_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: protein_modification_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: protein_modification_process_ (0.0)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 73339:
protein_modification_process_ (19.88)
|   |   |   |   |   |   |   |   |   start > 73339: translation_
(18.15)
|   |   |   |   |   |   |   start > 76893
|   |   |   |   |   |   |   |   start <= 80364
|   |   |   |   |   |   |   |   |   start <= 78856:
biological_process_ (15.33)
|   |   |   |   |   |   |   |   |   start > 78856: transport_
(35.82/15.34)
|   |   |   |   |   |   |   |   start > 80364
|   |   |   |   |   |   |   |   |   start <= 81185:
RNA_metabolic_process_ (19.13)
|   |   |   |   |   |   |   |   |   start > 81185:
biological_process_ (38.11)
|   |   |   |   start > 82373
|   |   |   |   |   start <= 91251
|   |   |   |   |   |   start <= 84256:
organelle_organization_and_biogenesis_ (19.62)
|   |   |   |   |   |   start > 84256
```

```
|   |   |   |   |   |   |   start <= 84884:
cytoskeleton_organization_and_biogenesis_ (33.8/13.47)
|   |   |   |   |   |   |   start > 84884
|   |   |   |   |   |   |   |   start <= 87980: cell_cycle_ (8.3)
|   |   |   |   |   |   |   |   start > 87980
|   |   |   |   |   |   |   |   |   neigh_strand = W: translation_
(20.48/10.73)
|   |   |   |   |   |   |   |   |   neigh_strand = C: cell_cycle_
(22.88/9.6)
|   |   |   |   |   start > 91251
|   |   |   |   |   |   start <= 93797
|   |   |   |   |   |   |   start <= 91436: vesicle-
mediated_transport_ (18.26)
|   |   |   |   |   |   |   start > 91436
|   |   |   |   |   |   |   |   start <= 92516
|   |   |   |   |   |   |   |   |   neigh_strand = W:
biological_process_ (12.08/4.93)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
protein_modification_process_ (20.01/5.66)
|   |   |   |   |   |   |   |   start > 92516: vesicle-
mediated_transport_ (17.16)
|   |   |   |   |   |   start > 93797
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 95862: transcription_
(17.95)
|   |   |   |   |   |   |   |   start > 95862
|   |   |   |   |   |   |   |   |   start <= 97342:
signal_transduction_ (22.36)
|   |   |   |   |   |   |   |   |   start > 97342:
RNA_metabolic_process_ (17.53)
|   |   |   |   |   |   |   strand = C: vesicle-mediated_transport_
(17.72)
|   |   start > 107508
|   |   |   start <= 249874
|   |   |   |   start <= 186065
|   |   |   |   |   start <= 173085
|   |   |   |   |   |   start <= 124703
|   |   |   |   |   |   |   start <= 122273
|   |   |   |   |   |   |   |   start <= 115492
|   |   |   |   |   |   |   |   |   start <= 108162:
lipid_metabolic_process_ (12.97)
|   |   |   |   |   |   |   |   |   start > 108162
|   |   |   |   |   |   |   |   |   |   strand = W: translation_
(18.31)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 110700:
translation_ (16.58)
|   |   |   |   |   |   |   |   |   |   |   start > 110700:
protein_modification_process_ (14.49)
|   |   |   |   |   |   |   |   start > 115492
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 116063:
amino_acid_and_derivative_metabolic_process_ (18.65)
```

```
|   |   |   |   |   |   |   |   |   |   start > 116063: translation_
(13.68)
|   |   |   |   |   |   |   |   |   strand = C:
DNA_metabolic_process_ (7.39)
|   |   |   |   |   |   |   start > 122273
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 123596: vesicle-
mediated_transport_ (12.83)
|   |   |   |   |   |   |   |   |   start > 123596: sporulation_
(7.21)
|   |   |   |   |   |   |   |   strand = C:
organelle_organization_and_biogenesis_ (18.26)
|   |   |   |   |   |   start > 124703
|   |   |   |   |   |   |   start <= 154312
|   |   |   |   |   |   |   |   start <= 142252
|   |   |   |   |   |   |   |   |   start <= 139967
|   |   |   |   |   |   |   |   |   |   start <= 129888:
biological_process_ (14.36)
|   |   |   |   |   |   |   |   |   |   start > 129888
|   |   |   |   |   |   |   |   |   |   |   start <= 131531:
translation_ (12.46)
|   |   |   |   |   |   |   |   |   |   |   start > 131531:
biological_process_ (11.73)
|   |   |   |   |   |   |   |   |   start > 139967
|   |   |   |   |   |   |   |   |   |   start <= 141732
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: meiosis_ (13.15/7.24)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
meiosis_ (2.32/1.19)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (5.98/3.18)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 1112:
DNA_metabolic_process_ (3.71/1.75)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 1112:
transcription_ (6.9/1.94)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: DNA_metabolic_process_ (3.8/1.22)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: meiosis_ (3.39/1.45)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: transcription_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: transcription_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: meiosis_ (2.2/0.93)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: transcription_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
transcription_ (3.61/1.59)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: transcription_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: transcription_ (0.0)
|   |   |   |   |   |   |   |   |   |   start > 141732
|   |   |   |   |   |   |   |   |   |   |   start <= 142233:
biological_process_ (23.63)
|   |   |   |   |   |   |   |   |   |   |   start > 142233: meiosis_
(15.7)
|   |   |   |   |   |   |   |   start > 142252
|   |   |   |   |   |   |   |   |   start <= 148594
|   |   |   |   |   |   |   |   |   |   strand = W:
cellular_respiration_ (11.04)
|   |   |   |   |   |   |   |   |   |   strand = C: translation_
(56.92/12.19)
|   |   |   |   |   |   |   |   |   start > 148594
|   |   |   |   |   |   |   |   |   |   start <= 150177
|   |   |   |   |   |   |   |   |   |   |   start <= 148970:
biological_process_ (9.63)
|   |   |   |   |   |   |   |   |   |   |   start > 148970:
electron_transport_ (28.44/11.39)
|   |   |   |   |   |   |   |   |   |   start > 150177
|   |   |   |   |   |   |   |   |   |   |   start <= 152782:
transport_ (15.88)
|   |   |   |   |   |   |   |   |   |   |   start > 152782:
biological_process_ (17.45)
|   |   |   |   |   |   |   start > 154312
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 157912
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
transcription_ (14.77/5.43)
```

```
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (12.16/4.9)
|   |   |   |   |   |   |   |   |   start > 157912
|   |   |   |   |   |   |   |   |   |   start <= 160071:
organelle_organization_and_biogenesis_ (14.42)
|   |   |   |   |   |   |   |   |   |   start > 160071:
cell_wall_organization_and_biogenesis_ (8.31)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 160071
|   |   |   |   |   |   |   |   |   |   start <= 156018:
amino_acid_and_derivative_metabolic_process_ (20.93)
|   |   |   |   |   |   |   |   |   |   start > 156018: meiosis_
(47.45/30.29)
|   |   |   |   |   |   |   |   |   start > 160071
|   |   |   |   |   |   |   |   |   |   start <= 167358:
protein_modification_process_ (13.49)
|   |   |   |   |   |   |   |   |   |   start > 167358:
biological_process_ (12.71)
|   |   |   |   |   start > 173085
|   |   |   |   |   |   start <= 182396
|   |   |   |   |   |   |   start <= 174551
|   |   |   |   |   |   |   |   start <= 174328: cell_cycle_ (16.21)
|   |   |   |   |   |   |   |   start > 174328:
RNA_metabolic_process_ (29.3/12.83)
|   |   |   |   |   |   |   start > 174551
|   |   |   |   |   |   |   |   start <= 180706
|   |   |   |   |   |   |   |   |   start <= 180119:
ribosome_biogenesis_and_assembly_ (9.68)
|   |   |   |   |   |   |   |   |   start > 180119:
nuclear_organization_and_biogenesis_ (12.5)
|   |   |   |   |   |   |   |   start > 180706:
ribosome_biogenesis_and_assembly_ (16.38)
|   |   |   |   |   |   start > 182396
|   |   |   |   |   |   |   strand = W: cellular_respiration_
(17.07)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 185400: sporulation_
(17.21)
|   |   |   |   |   |   |   |   start > 185400: translation_ (17.77)
|   |   |   |   start > 186065
|   |   |   |   |   start <= 225578
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 209011
|   |   |   |   |   |   |   |   start <= 198144
|   |   |   |   |   |   |   |   |   start <= 187470:
DNA_metabolic_process_ (20.11)
|   |   |   |   |   |   |   |   |   start > 187470: transcription_
(29.74)
|   |   |   |   |   |   |   |   start > 198144
|   |   |   |   |   |   |   |   |   start <= 202727:
biological_process_ (46.28)
|   |   |   |   |   |   |   |   |   start > 202727
|   |   |   |   |   |   |   |   |   |   start <= 207038
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 205527:
translation_ (5.35)
|   |   |   |   |   |   |   |   |   |   |   start > 205527: meiosis_
(28.05)
|   |   |   |   |   |   |   |   |   |   start > 207038:
biological_process_ (14.74)
|   |   |   |   |   |   |   start > 209011
|   |   |   |   |   |   |   |   start <= 214086
|   |   |   |   |   |   |   |   |   start <= 210421:
carbohydrate_metabolic_process_ (19.39)
|   |   |   |   |   |   |   |   |   start > 210421:
signal_transduction_ (22.17)
|   |   |   |   |   |   |   |   start > 214086
|   |   |   |   |   |   |   |   |   start <= 216278:
organelle_organization_and_biogenesis_ (40.99/17.81)
|   |   |   |   |   |   |   |   |   start > 216278: transcription_
(8.76)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 193306
|   |   |   |   |   |   |   |   start <= 191135: transport_
(36.86/16.55)
|   |   |   |   |   |   |   |   start > 191135: biological_process_
(13.7)
|   |   |   |   |   |   |   start > 193306
|   |   |   |   |   |   |   |   start <= 207038
|   |   |   |   |   |   |   |   |   start <= 198144:
DNA_metabolic_process_ (27.36)
|   |   |   |   |   |   |   |   |   start > 198144: vesicle-
mediated_transport_ (21.18)
|   |   |   |   |   |   |   |   start > 207038
|   |   |   |   |   |   |   |   |   start <= 217529:
protein_modification_process_ (16.0)
|   |   |   |   |   |   |   |   |   start > 217529:
DNA_metabolic_process_ (18.85)
|   |   |   |   |   start > 225578
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 226404:
amino_acid_and_derivative_metabolic_process_ (15.93)
|   |   |   |   |   |   |   start > 226404
|   |   |   |   |   |   |   |   start <= 238358
|   |   |   |   |   |   |   |   |   start <= 230248: vesicle-
mediated_transport_ (33.39/11.08)
|   |   |   |   |   |   |   |   |   start > 230248:
protein_modification_process_ (13.89)
|   |   |   |   |   |   |   |   start > 238358
|   |   |   |   |   |   |   |   |   start <= 245721: transport_
(16.22)
|   |   |   |   |   |   |   |   |   start > 245721
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: transport_
(7.67/2.55)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (17.94/5.24)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 235963
```

```
|   |   |   |   |   |   |   |   start <= 230248
|   |   |   |   |   |   |   |   |   start <= 228334: translation_
(20.15)
|   |   |   |   |   |   |   |   |   start > 228334:
biological_process_ (18.49)
|   |   |   |   |   |   |   |   start > 230248
|   |   |   |   |   |   |   |   |   start <= 234512:
lipid_metabolic_process_ (10.92)
|   |   |   |   |   |   |   |   |   start > 234512: translation_
(11.59)
|   |   |   |   |   |   |   start > 235963
|   |   |   |   |   |   |   |   start <= 238358:
protein_modification_process_ (18.0)
|   |   |   |   |   |   |   |   start > 238358: biological_process_
(32.39)
|   |   |   start > 249874
|   |   |   |   start <= 281163
|   |   |   |   |   start <= 270781
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 255668
|   |   |   |   |   |   |   |   start <= 254646: translation_
(13.49)
|   |   |   |   |   |   |   |   start > 254646:
carbohydrate_metabolic_process_ (12.89)
|   |   |   |   |   |   |   start > 255668
|   |   |   |   |   |   |   |   start <= 257712:
DNA_metabolic_process_ (10.43)
|   |   |   |   |   |   |   |   start > 257712:
RNA_metabolic_process_ (16.06)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 257712: DNA_metabolic_process_
(22.67)
|   |   |   |   |   |   |   start > 257712
|   |   |   |   |   |   |   |   start <= 270150
|   |   |   |   |   |   |   |   |   start <= 266150:
biological_process_ (17.97)
|   |   |   |   |   |   |   |   |   start > 266150
|   |   |   |   |   |   |   |   |   |   start <= 269194:
translation_ (13.78)
|   |   |   |   |   |   |   |   |   |   start > 269194:
biological_process_ (11.34)
|   |   |   |   |   |   |   |   start > 270150:
DNA_metabolic_process_ (20.08)
|   |   |   |   |   start > 270781
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 271003:
lipid_metabolic_process_ (12.96)
|   |   |   |   |   |   |   start > 271003: translation_ (47.43)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 280529
|   |   |   |   |   |   |   |   start <= 277623: vesicle-
mediated_transport_ (8.39)
|   |   |   |   |   |   |   |   start > 277623:
RNA_metabolic_process_ (15.61)
```

```
|   |   |   |   |   |   |   start > 280529: signal_transduction_
(11.59)
|   |   |   |   start > 281163
|   |   |   |   |   start <= 328586
|   |   |   |   |   |   start <= 299731
|   |   |   |   |   |   |   start <= 292036
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 288518
|   |   |   |   |   |   |   |   |   |   start <= 284448:
cellular_respiration_ (14.2)
|   |   |   |   |   |   |   |   |   |   start > 284448:
biological_process_ (14.41)
|   |   |   |   |   |   |   |   |   start > 288518
|   |   |   |   |   |   |   |   |   |   start <= 289812:
protein_catabolic_process_ (24.09)
|   |   |   |   |   |   |   |   |   |   start > 289812:
organelle_organization_and_biogenesis_ (12.51)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 284448:
ribosome_biogenesis_and_assembly_ (10.67)
|   |   |   |   |   |   |   |   |   start > 284448: translation_
(13.49)
|   |   |   |   |   |   |   start > 292036
|   |   |   |   |   |   |   |   start <= 293463: transport_ (19.3)
|   |   |   |   |   |   |   |   start > 293463
|   |   |   |   |   |   |   |   |   start <= 295935:
DNA_metabolic_process_ (32.13)
|   |   |   |   |   |   |   |   |   start > 295935:
protein_modification_process_ (45.92/22.65)
|   |   |   |   |   |   start > 299731
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 313237
|   |   |   |   |   |   |   |   |   start <= 306563
|   |   |   |   |   |   |   |   |   |   start <= 299981:
ribosome_biogenesis_and_assembly_ (23.13)
|   |   |   |   |   |   |   |   |   |   start > 299981: cytokinesis_
(16.0)
|   |   |   |   |   |   |   |   |   start > 306563
|   |   |   |   |   |   |   |   |   |   start <= 310970:
translation_ (35.22)
|   |   |   |   |   |   |   |   |   |   start > 310970
|   |   |   |   |   |   |   |   |   |   |   start <= 312196:
biological_process_ (9.5)
|   |   |   |   |   |   |   |   |   |   |   start > 312196:
nuclear_organization_and_biogenesis_ (15.43)
|   |   |   |   |   |   |   |   start > 313237
|   |   |   |   |   |   |   |   |   start <= 316791
|   |   |   |   |   |   |   |   |   |   start <= 314634:
ribosome_biogenesis_and_assembly_ (17.66)
|   |   |   |   |   |   |   |   |   |   start > 314634:
RNA_metabolic_process_ (20.08/7.55)
|   |   |   |   |   |   |   |   |   start > 316791
|   |   |   |   |   |   |   |   |   |   start <= 317345: transport_
(23.25/7.99)
```

```
|   |   |   |   |   |   |   |   |   |   start > 317345
|   |   |   |   |   |   |   |   |   |   |   start <= 319784:
translation_ (13.02)
|   |   |   |   |   |   |   |   |   |   |   start > 319784
|   |   |   |   |   |   |   |   |   |   |   |   start <= 321785:
ribosome_biogenesis_and_assembly_ (11.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 321785
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 325334:
cell_cycle_ (6.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 325334:
translation_ (6.42)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 304074: biological_process_
(28.98)
|   |   |   |   |   |   |   |   start > 304074
|   |   |   |   |   |   |   |   |   start <= 307440
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: translation_
(17.33/3.77)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_respiration_ (12.82/3.98)
|   |   |   |   |   |   |   |   |   start > 307440: transport_
(10.07)
|   |   |   |   |   start > 328586
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 337909
|   |   |   |   |   |   |   |   start <= 334889:
cytoskeleton_organization_and_biogenesis_ (27.73)
|   |   |   |   |   |   |   |   start > 334889:
nuclear_organization_and_biogenesis_ (16.15)
|   |   |   |   |   |   |   start > 337909: DNA_metabolic_process_
(27.85)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 330610:
organelle_organization_and_biogenesis_ (21.39)
|   |   |   |   |   |   |   start > 330610
|   |   |   |   |   |   |   |   start <= 337909:
DNA_metabolic_process_ (35.05/15.86)
|   |   |   |   |   |   |   |   start > 337909: biological_process_
(19.91)
|   start > 343322
|   |   start <= 720413
|   |   |   start <= 440812
|   |   |   |   start <= 363919
|   |   |   |   |   start <= 346907
|   |   |   |   |   |   strand = W:
ribosome_biogenesis_and_assembly_ (14.77)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 345989: conjugation_
(32.94/15.36)
|   |   |   |   |   |   |   start > 345989: response_to_stress_
(11.12)
|   |   |   |   |   start > 346907
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 347122: transport_ (19.15)
```

```
|   |   |   |   |   |   |   start > 347122: biological_process_
(125.62)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 355830: DNA_metabolic_process_
(25.55/10.13)
|   |   |   |   |   |   |   start > 355830
|   |   |   |   |   |   |   |   start <= 361862:
ribosome_biogenesis_and_assembly_ (16.48)
|   |   |   |   |   |   |   |   start > 361862: transport_ (20.13)
|   |   |   |   start > 363919
|   |   |   |   |   start <= 389714
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 376104
|   |   |   |   |   |   |   |   start <= 372015
|   |   |   |   |   |   |   |   |   start <= 368756:
response_to_stress_ (16.12)
|   |   |   |   |   |   |   |   |   start > 368756: transcription_
(15.55)
|   |   |   |   |   |   |   |   start > 372015
|   |   |   |   |   |   |   |   |   start <= 375090: translation_
(22.72)
|   |   |   |   |   |   |   |   |   start > 375090:
vitamin_metabolic_process_ (9.93)
|   |   |   |   |   |   |   start > 376104
|   |   |   |   |   |   |   |   start <= 377612:
DNA_metabolic_process_ (32.66/15.19)
|   |   |   |   |   |   |   |   start > 377612
|   |   |   |   |   |   |   |   |   start <= 383657:
RNA_metabolic_process_ (14.92)
|   |   |   |   |   |   |   |   |   start > 383657:
carbohydrate_metabolic_process_ (12.95)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 366472
|   |   |   |   |   |   |   |   stop <= 364338: translation_ (15.24)
|   |   |   |   |   |   |   |   stop > 364338:
RNA_metabolic_process_ (74.27/36.82)
|   |   |   |   |   |   |   start > 366472
|   |   |   |   |   |   |   |   start <= 377612
|   |   |   |   |   |   |   |   |   start <= 368756: cell_cycle_
(18.71)
|   |   |   |   |   |   |   |   |   start > 368756:
response_to_stress_ (17.75)
|   |   |   |   |   |   |   |   start > 377612
|   |   |   |   |   |   |   |   |   start <= 381274:
lipid_metabolic_process_ (15.1)
|   |   |   |   |   |   |   |   |   start > 381274
|   |   |   |   |   |   |   |   |   |   start <= 385199:
ribosome_biogenesis_and_assembly_ (21.64)
|   |   |   |   |   |   |   |   |   |   start > 385199: cell_cycle_
(7.16)
|   |   |   |   |   start > 389714
|   |   |   |   |   |   start <= 403690
|   |   |   |   |   |   |   start <= 397624
|   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   start <= 392228:
biological_process_ (22.59)
|   |   |   |   |   |   |   |   |   start > 392228:
DNA_metabolic_process_ (13.91)
|   |   |   |   |   |   |   |   strand = C: biological_process_
(46.48)
|   |   |   |   |   |   |   start > 397624
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 398631:
organelle_organization_and_biogenesis_ (26.25)
|   |   |   |   |   |   |   |   |   start > 398631
|   |   |   |   |   |   |   |   |   |   start <= 402592:
conjugation_ (13.1)
|   |   |   |   |   |   |   |   |   |   start > 402592:
organelle_organization_and_biogenesis_ (12.41)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 401290: cell_budding_
(17.11)
|   |   |   |   |   |   |   |   |   start > 401290: translation_
(19.78)
|   |   |   |   |   |   start > 403690
|   |   |   |   |   |   |   start <= 417487
|   |   |   |   |   |   |   |   start <= 412370
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 405779
|   |   |   |   |   |   |   |   |   |   |   start <= 405473:
translation_ (14.52)
|   |   |   |   |   |   |   |   |   |   |   start > 405473:
RNA_metabolic_process_ (20.8)
|   |   |   |   |   |   |   |   |   |   start > 405779:
protein_modification_process_ (20.73)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 411555
|   |   |   |   |   |   |   |   |   |   |   start <= 409607:
translation_ (9.75)
|   |   |   |   |   |   |   |   |   |   |   start > 409607:
protein_catabolic_process_ (29.15)
|   |   |   |   |   |   |   |   |   |   start > 411555: translation_
(24.22)
|   |   |   |   |   |   |   |   start > 412370
|   |   |   |   |   |   |   |   |   start <= 414106: meiosis_
(24.37)
|   |   |   |   |   |   |   |   |   start > 414106:
RNA_metabolic_process_ (65.66/34.49)
|   |   |   |   |   |   |   start > 417487
|   |   |   |   |   |   |   |   start <= 428606
|   |   |   |   |   |   |   |   |   start <= 426810
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 423098:
translation_ (11.22)
|   |   |   |   |   |   |   |   |   |   |   start > 423098:
DNA_metabolic_process_ (11.79)
|   |   |   |   |   |   |   |   |   |   strand = C
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 423098:
biological_process_ (18.19)
|   |   |   |   |   |   |   |   |   |   |   start > 423098:
protein_modification_process_ (16.45)
|   |   |   |   |   |   |   |   |   start > 426810
|   |   |   |   |   |   |   |   |   |   start <= 427953:
vitamin_metabolic_process_ (27.2/12.68)
|   |   |   |   |   |   |   |   |   |   start > 427953:
biological_process_ (31.43)
|   |   |   |   |   |   |   |   start > 428606
|   |   |   |   |   |   |   |   |   start <= 436838
|   |   |   |   |   |   |   |   |   |   strand = W:
DNA_metabolic_process_ (28.24/16.79)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 433067:
transcription_ (16.65)
|   |   |   |   |   |   |   |   |   |   |   start > 433067:
conjugation_ (14.1)
|   |   |   |   |   |   |   |   |   start > 436838
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 439096:
translation_ (4.82)
|   |   |   |   |   |   |   |   |   |   |   start > 439096:
ribosome_biogenesis_and_assembly_ (15.57)
|   |   |   |   |   |   |   |   |   |   strand = C: translation_
(31.96)
|   |   |   start > 440812
|   |   |   |   start <= 527333
|   |   |   |   |   start <= 459859
|   |   |   |   |   |   start <= 452109
|   |   |   |   |   |   |   start <= 448540
|   |   |   |   |   |   |   |   start <= 446148
|   |   |   |   |   |   |   |   |   start <= 442914: cytokinesis_
(9.28)
|   |   |   |   |   |   |   |   |   start > 442914:
cell_wall_organization_and_biogenesis_ (14.73)
|   |   |   |   |   |   |   |   start > 446148:
amino_acid_and_derivative_metabolic_process_ (23.68)
|   |   |   |   |   |   |   start > 448540
|   |   |   |   |   |   |   |   start <= 449962: transcription_
(35.43/17.28)
|   |   |   |   |   |   |   |   start > 449962: vesicle-
mediated_transport_ (27.1)
|   |   |   |   |   |   start > 452109
|   |   |   |   |   |   |   start <= 458161
|   |   |   |   |   |   |   |   start <= 454790:
protein_modification_process_ (40.36)
|   |   |   |   |   |   |   |   start > 454790
|   |   |   |   |   |   |   |   |   start <= 457875:
organelle_organization_and_biogenesis_ (52.49/26.67)
|   |   |   |   |   |   |   |   |   start > 457875:
response_to_stress_ (15.63)
|   |   |   |   |   |   |   start > 458161
```

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|   |   |   |   |   |   |   |   start <= 459669:
cellular_respiration_ (21.67)
|   |   |   |   |   |   |   |   start > 459669:
protein_modification_process_ (17.05)
|   |   |   |   |   start > 459859
|   |   |   |   |   |   start <= 500136
|   |   |   |   |   |   |   start <= 490551
|   |   |   |   |   |   |   |   start <= 475550
|   |   |   |   |   |   |   |   |   start <= 472303
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 461671:
biological_process_ (34.76/21.31)
|   |   |   |   |   |   |   |   |   |   |   start > 461671:
RNA_metabolic_process_ (19.09)
|   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (33.31)
|   |   |   |   |   |   |   |   |   start > 472303
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 472860:
lipid_metabolic_process_ (13.91)
|   |   |   |   |   |   |   |   |   |   |   start > 472860:
biological_process_ (14.09)
|   |   |   |   |   |   |   |   |   |   strand = C:
protein_catabolic_process_ (18.69)
|   |   |   |   |   |   |   |   start > 475550
|   |   |   |   |   |   |   |   |   start <= 478657:
amino_acid_and_derivative_metabolic_process_ (12.18)
|   |   |   |   |   |   |   |   |   start > 478657
|   |   |   |   |   |   |   |   |   |   start <= 485428
|   |   |   |   |   |   |   |   |   |   |   start <= 482671:
transport_ (21.2)
|   |   |   |   |   |   |   |   |   |   |   start > 482671:
biological_process_ (23.04)
|   |   |   |   |   |   |   |   |   |   start > 485428
|   |   |   |   |   |   |   |   |   |   |   start <= 485925:
transport_ (18.51)
|   |   |   |   |   |   |   |   |   |   |   start > 485925
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
vesicle-mediated_transport_ (9.77/2.48)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
transport_ (17.82/7.16)
|   |   |   |   |   |   |   start > 490551
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 496506: transport_
(19.1)
|   |   |   |   |   |   |   |   |   start > 496506:
protein_catabolic_process_ (36.59/16.4)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 491960:
protein_catabolic_process_ (25.22)
|   |   |   |   |   |   |   |   |   start > 491960
|   |   |   |   |   |   |   |   |   |   start <= 494521: cell_cycle_
(42.88/16.44)
|   |   |   |   |   |   |   |   |   |   start > 494521
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 496506:
lipid_metabolic_process_ (18.71)
|   |   |   |   |   |   |   |   |   |   |   start > 496506
|   |   |   |   |   |   |   |   |   |   |   |   start <= 498038:
biological_process_ (15.44)
|   |   |   |   |   |   |   |   |   |   |   |   start > 498038:
DNA_metabolic_process_ (9.57)
|   |   |   |   |   |   start > 500136
|   |   |   |   |   |   |   start <= 506074
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 502942:
organelle_organization_and_biogenesis_ (21.62)
|   |   |   |   |   |   |   |   |   start > 502942:
RNA_metabolic_process_ (17.68)
|   |   |   |   |   |   |   |   strand = C: transcription_ (19.01)
|   |   |   |   |   |   |   start > 506074
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   distance <= 2663
|   |   |   |   |   |   |   |   |   |   start <= 511549
|   |   |   |   |   |   |   |   |   |   |   start <= 508368
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: biological_process_ (9.1/3.9)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: amino_acid_and_derivative_metabolic_process_
(4.05/1.86)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: amino_acid_and_derivative_metabolic_process_
(3.01/1.09)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: lipid_metabolic_process_
(8.74/2.29)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: biological_process_ (9.2/3.89)
```

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|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: lipid_metabolic_process_ (6.35/2.38)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: amino_acid_and_derivative_metabolic_process_
(3.43/1.73)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: lipid_metabolic_process_ (3.76/1.93)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: biological_process_ (4.97/1.8)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
amino_acid_and_derivative_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: amino_acid_and_derivative_metabolic_process_
(4.77/0.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: amino_acid_and_derivative_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_:
amino_acid_and_derivative_metabolic_process_ (4.1/1.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_:
amino_acid_and_derivative_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_:
amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: amino_acid_and_derivative_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   start > 508368:
vitamin_metabolic_process_ (4.46)
|   |   |   |   |   |   |   |   |   |   start > 511549
|   |   |   |   |   |   |   |   |   |   |   start <= 523791
|   |   |   |   |   |   |   |   |   |   |   |   start <= 516947
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 513163:
biological_process_ (9.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 513163
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
867: response_to_stress_ (2.46/1.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
867: RNA_metabolic_process_ (5.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 516947:
biological_process_ (22.5)
|   |   |   |   |   |   |   |   |   |   |   start > 523791:
amino_acid_and_derivative_metabolic_process_ (27.78/11.01)
|   |   |   |   |   |   |   |   |   distance > 2663
|   |   |   |   |   |   |   |   |   |   start <= 514558
|   |   |   |   |   |   |   |   |   |   |   start <= 513163
|   |   |   |   |   |   |   |   |   |   |   |   start <= 511549:
vitamin_metabolic_process_ (3.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 511549:
biological_process_ (9.62)
|   |   |   |   |   |   |   |   |   |   |   start > 513163:
RNA_metabolic_process_ (20.88)
|   |   |   |   |   |   |   |   |   |   start > 514558
|   |   |   |   |   |   |   |   |   |   |   start <= 516947:
signal_transduction_ (28.0/12.3)
|   |   |   |   |   |   |   |   |   |   |   start > 516947:
biological_process_ (5.1)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 514558
|   |   |   |   |   |   |   |   |   |   start <= 508368:
response_to_stress_ (17.16)
|   |   |   |   |   |   |   |   |   |   start > 508368: vesicle-
mediated_transport_ (12.91)
|   |   |   |   |   |   |   |   |   start > 514558
|   |   |   |   |   |   |   |   |   |   start <= 523791:
biological_process_ (19.69)
|   |   |   |   |   |   |   |   |   |   start > 523791:
organelle_organization_and_biogenesis_ (16.74)
|   |   |   |   start > 527333
|   |   |   |   |   start <= 676625
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 601665
|   |   |   |   |   |   |   |   start <= 561747
|   |   |   |   |   |   |   |   |   start <= 542207
```

```
|   |   |   |   |   |   |   |   |   |   start <= 541854
|   |   |   |   |   |   |   |   |   |   |   start <= 529268
|   |   |   |   |   |   |   |   |   |   |   |   start <= 527636:
biological_process_ (22.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 527636:
cell_wall_organization_and_biogenesis_ (13.81)
|   |   |   |   |   |   |   |   |   |   |   start > 529268
|   |   |   |   |   |   |   |   |   |   |   |   start <= 531614:
translation_ (9.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 531614
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 534462:
biological_process_ (15.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 534462:
translation_ (7.82)
|   |   |   |   |   |   |   |   |   |   start > 541854: transport_
(19.21/9.14)
|   |   |   |   |   |   |   |   |   start > 542207
|   |   |   |   |   |   |   |   |   |   start <= 545374
|   |   |   |   |   |   |   |   |   |   |   start <= 543557:
response_to_stress_ (12.82)
|   |   |   |   |   |   |   |   |   |   |   start > 543557:
ribosome_biogenesis_and_assembly_ (34.38/11.61)
|   |   |   |   |   |   |   |   |   |   start > 545374
|   |   |   |   |   |   |   |   |   |   |   start <= 558872
|   |   |   |   |   |   |   |   |   |   |   |   start <= 548268
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 546445:
biological_process_ (16.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 546445:
cell_wall_organization_and_biogenesis_ (30.53/11.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 548268
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 555816:
translation_ (11.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 555816:
biological_process_ (13.94)
|   |   |   |   |   |   |   |   |   |   |   start > 558872:
response_to_stress_ (14.59)
|   |   |   |   |   |   |   |   start > 561747
|   |   |   |   |   |   |   |   |   start <= 581440
|   |   |   |   |   |   |   |   |   |   start <= 577491
|   |   |   |   |   |   |   |   |   |   |   start <= 575402:
signal_transduction_ (15.27)
|   |   |   |   |   |   |   |   |   |   |   start > 575402:
cytokinesis_ (15.64)
|   |   |   |   |   |   |   |   |   |   start > 577491:
DNA_metabolic_process_ (15.72)
|   |   |   |   |   |   |   |   |   start > 581440
|   |   |   |   |   |   |   |   |   |   start <= 591318
|   |   |   |   |   |   |   |   |   |   |   start <= 589830:
transport_ (49.44/15.12)
|   |   |   |   |   |   |   |   |   |   |   start > 589830:
cell_cycle_ (10.25)
|   |   |   |   |   |   |   |   |   |   start > 591318
|   |   |   |   |   |   |   |   |   |   |   start <= 596697
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 593600:
biological_process_ (11.44)
|   |   |   |   |   |   |   |   |   |   |   start > 593600:
translation_ (17.28)
|   |   |   |   |   |   |   |   |   |   start > 596697
|   |   |   |   |   |   |   |   |   |   |   start <= 599421:
transport_ (17.74)
|   |   |   |   |   |   |   |   |   |   |   start > 599421:
sporulation_ (16.48)
|   |   |   |   |   |   |   start > 601665
|   |   |   |   |   |   |   |   start <= 637581
|   |   |   |   |   |   |   |   |   start <= 606140: cell_budding_
(22.58)
|   |   |   |   |   |   |   |   |   start > 606140
|   |   |   |   |   |   |   |   |   |   start <= 627810
|   |   |   |   |   |   |   |   |   |   |   start <= 609588
|   |   |   |   |   |   |   |   |   |   |   |   start <= 607567:
cell_wall_organization_and_biogenesis_ (23.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 607567
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
4383: RNA_metabolic_process_ (25.44/8.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 4383:
ribosome_biogenesis_and_assembly_ (11.85/4.66)
|   |   |   |   |   |   |   |   |   |   |   start > 609588
|   |   |   |   |   |   |   |   |   |   |   |   start <= 617828:
lipid_metabolic_process_ (17.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 617828:
cell_wall_organization_and_biogenesis_ (21.85)
|   |   |   |   |   |   |   |   |   |   start > 627810:
RNA_metabolic_process_ (35.47/9.13)
|   |   |   |   |   |   |   |   start > 637581
|   |   |   |   |   |   |   |   |   start <= 656964
|   |   |   |   |   |   |   |   |   |   start <= 642014
|   |   |   |   |   |   |   |   |   |   |   start <= 640724:
biological_process_ (31.49)
|   |   |   |   |   |   |   |   |   |   |   start > 640724:
cell_budding_ (18.83)
|   |   |   |   |   |   |   |   |   |   start > 642014
|   |   |   |   |   |   |   |   |   |   |   start <= 648911:
transport_ (35.2/17.13)
|   |   |   |   |   |   |   |   |   |   |   start > 648911
|   |   |   |   |   |   |   |   |   |   |   |   start <= 654638:
response_to_stress_ (18.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 654638:
biological_process_ (20.69)
|   |   |   |   |   |   |   |   |   start > 656964
|   |   |   |   |   |   |   |   |   |   start <= 666345
|   |   |   |   |   |   |   |   |   |   |   start <= 662362
|   |   |   |   |   |   |   |   |   |   |   |   start <= 661753:
translation_ (10.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 661753:
ribosome_biogenesis_and_assembly_ (13.67)
|   |   |   |   |   |   |   |   |   |   |   start > 662362:
RNA_metabolic_process_ (34.18)
```

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|   |   |   |   |   |   |   |   |   |   start > 666345
|   |   |   |   |   |   |   |   |   |   |   start <= 670392
|   |   |   |   |   |   |   |   |   |   |   |   start <= 668193:
protein_modification_process_ (34.73/16.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 668193:
biological_process_ (21.1)
|   |   |   |   |   |   |   |   |   |   |   start > 670392
|   |   |   |   |   |   |   |   |   |   |   |   start <= 672190:
translation_ (9.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 672190:
transport_ (25.63)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 636879
|   |   |   |   |   |   |   |   start <= 561747
|   |   |   |   |   |   |   |   |   start <= 557569
|   |   |   |   |   |   |   |   |   |   start <= 548268
|   |   |   |   |   |   |   |   |   |   |   start <= 545374
|   |   |   |   |   |   |   |   |   |   |   |   start <= 532989:
RNA_metabolic_process_ (11.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 532989:
translation_ (30.36)
|   |   |   |   |   |   |   |   |   |   |   start > 545374:
ribosome_biogenesis_and_assembly_ (18.21)
|   |   |   |   |   |   |   |   |   |   start > 548268
|   |   |   |   |   |   |   |   |   |   |   start <= 555816
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transport_ (13.19/3.49)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
organelle_organization_and_biogenesis_ (8.78/3.04)
|   |   |   |   |   |   |   |   |   |   |   start > 555816:
biological_process_ (21.3)
|   |   |   |   |   |   |   |   |   start > 557569
|   |   |   |   |   |   |   |   |   |   start <= 560686:
lipid_metabolic_process_ (78.23/36.66)
|   |   |   |   |   |   |   |   |   |   start > 560686: translation_
(17.96)
|   |   |   |   |   |   |   |   start > 561747
|   |   |   |   |   |   |   |   |   start <= 617282
|   |   |   |   |   |   |   |   |   |   start <= 591318
|   |   |   |   |   |   |   |   |   |   |   start <= 584899
|   |   |   |   |   |   |   |   |   |   |   |   start <= 581440:
biological_process_ (12.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 581440:
meiosis_ (12.56)
|   |   |   |   |   |   |   |   |   |   |   start > 584899:
transcription_ (13.88)
|   |   |   |   |   |   |   |   |   |   start > 591318
|   |   |   |   |   |   |   |   |   |   |   start <= 610568
|   |   |   |   |   |   |   |   |   |   |   |   start <= 599421:
biological_process_ (18.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 599421:
vesicle-mediated_transport_ (18.25)
|   |   |   |   |   |   |   |   |   |   |   start > 610568:
biological_process_ (36.92)
```

```
|   |   |   |   |   |   |   |   |   start > 617282
|   |   |   |   |   |   |   |   |   |   start <= 619862
|   |   |   |   |   |   |   |   |   |   |   start <= 617828
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 62:
DNA_metabolic_process_ (5.32/1.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 62:
biological_process_ (8.32/4.17)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
RNA_metabolic_process_ (32.48/21.27)
|   |   |   |   |   |   |   |   |   |   |   start > 617828:
transport_ (22.52)
|   |   |   |   |   |   |   |   |   |   start > 619862
|   |   |   |   |   |   |   |   |   |   |   start <= 634308:
biological_process_ (44.11)
|   |   |   |   |   |   |   |   |   |   |   start > 634308:
RNA_metabolic_process_ (12.61)
|   |   |   |   |   |   |   start > 636879
|   |   |   |   |   |   |   |   start <= 648911
|   |   |   |   |   |   |   |   |   start <= 642014
|   |   |   |   |   |   |   |   |   |   start <= 637581:
translation_ (22.26)
|   |   |   |   |   |   |   |   |   |   start > 637581
|   |   |   |   |   |   |   |   |   |   |   start <= 639517:
organelle_organization_and_biogenesis_ (14.05)
|   |   |   |   |   |   |   |   |   |   |   start > 639517:
biological_process_ (19.62)
|   |   |   |   |   |   |   |   |   start > 642014
|   |   |   |   |   |   |   |   |   |   start <= 644048:
ribosome_biogenesis_and_assembly_ (15.88)
|   |   |   |   |   |   |   |   |   |   start > 644048: translation_
(52.93)
|   |   |   |   |   |   |   |   start > 648911
|   |   |   |   |   |   |   |   |   start <= 650621: vesicle-
mediated_transport_ (26.75/13.01)
|   |   |   |   |   |   |   |   |   start > 650621
|   |   |   |   |   |   |   |   |   |   start <= 662362:
biological_process_ (16.76)
|   |   |   |   |   |   |   |   |   |   start > 662362:
ribosome_biogenesis_and_assembly_ (20.58)
|   |   |   |   |   start > 676625
|   |   |   |   |   |   start <= 699790
|   |   |   |   |   |   |   start <= 693367
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 687903
|   |   |   |   |   |   |   |   |   |   start <= 678699:
transcription_ (20.49)
|   |   |   |   |   |   |   |   |   |   start > 678699:
DNA_metabolic_process_ (12.15)
|   |   |   |   |   |   |   |   |   start > 687903
|   |   |   |   |   |   |   |   |   |   start <= 690249: transport_
(21.62)
|   |   |   |   |   |   |   |   |   |   start > 690249:
organelle_organization_and_biogenesis_ (24.46)
```

```
|   |   |   |   |   |   |   |   strand = C: cell_cycle_ (12.32)
|   |   |   |   |   |   |   start > 693367
|   |   |   |   |   |   |   |   start <= 695421
|   |   |   |   |   |   |   |   |   start <= 695139:
biological_process_ (25.66)
|   |   |   |   |   |   |   |   |   start > 695139:
ribosome_biogenesis_and_assembly_ (37.09/15.03)
|   |   |   |   |   |   |   |   start > 695421
|   |   |   |   |   |   |   |   |   start <= 698372: transcription_
(25.69/10.18)
|   |   |   |   |   |   |   |   |   start > 698372:
biological_process_ (56.63)
|   |   |   |   |   |   start > 699790
|   |   |   |   |   |   |   start <= 707183
|   |   |   |   |   |   |   |   start <= 701052: translation_
(29.82)
|   |   |   |   |   |   |   |   start > 701052
|   |   |   |   |   |   |   |   |   start <= 706505
|   |   |   |   |   |   |   |   |   |   start <= 703640
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cell_cycle_ (15.39/4.02)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: meiosis_
(5.69/1.9)
|   |   |   |   |   |   |   |   |   |   start > 703640:
DNA_metabolic_process_ (26.82/9.64)
|   |   |   |   |   |   |   |   |   start > 706505: translation_
(12.22)
|   |   |   |   |   |   |   start > 707183
|   |   |   |   |   |   |   |   start <= 717362
|   |   |   |   |   |   |   |   |   start <= 715832
|   |   |   |   |   |   |   |   |   |   start <= 713713:
biological_process_ (11.66)
|   |   |   |   |   |   |   |   |   |   start > 713713:
anatomical_structure_morphogenesis_ (30.74/9.72)
|   |   |   |   |   |   |   |   |   start > 715832:
cellular_respiration_ (9.74)
|   |   |   |   |   |   |   |   start > 717362
|   |   |   |   |   |   |   |   |   start <= 718897: cell_cycle_
(22.39)
|   |   |   |   |   |   |   |   |   start > 718897
|   |   |   |   |   |   |   |   |   |   distance <= 3943:
transcription_ (33.18/18.78)
|   |   |   |   |   |   |   |   |   |   distance > 3943:
RNA_metabolic_process_ (13.88/7.6)
|   |   start > 720413
|   |   |   start <= 911888
|   |   |   |   start <= 798548
|   |   |   |   |   start <= 772459
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 739949
|   |   |   |   |   |   |   |   start <= 739127
|   |   |   |   |   |   |   |   |   start <= 733417
|   |   |   |   |   |   |   |   |   |   start <= 731142:
translation_ (28.86)
```

```
|   |   |   |   |   |   |   |   |   |   start > 731142:
biological_process_ (8.37)
|   |   |   |   |   |   |   |   |   start > 733417
|   |   |   |   |   |   |   |   |   |   start <= 733940:
transcription_ (12.13)
|   |   |   |   |   |   |   |   |   |   start > 733940: translation_
(23.76)
|   |   |   |   |   |   |   |   start > 739127:
amino_acid_and_derivative_metabolic_process_ (19.13)
|   |   |   |   |   |   |   start > 739949
|   |   |   |   |   |   |   |   start <= 767434
|   |   |   |   |   |   |   |   |   start <= 754731
|   |   |   |   |   |   |   |   |   |   start <= 746803:
biological_process_ (51.27)
|   |   |   |   |   |   |   |   |   |   start > 746803
|   |   |   |   |   |   |   |   |   |   |   start <= 750405:
cell_cycle_ (15.17)
|   |   |   |   |   |   |   |   |   |   |   start > 750405:
biological_process_ (11.21)
|   |   |   |   |   |   |   |   |   start > 754731
|   |   |   |   |   |   |   |   |   |   start <= 757775
|   |   |   |   |   |   |   |   |   |   |   start <= 756901:
organelle_organization_and_biogenesis_ (15.57)
|   |   |   |   |   |   |   |   |   |   |   start > 756901:
transcription_ (23.65)
|   |   |   |   |   |   |   |   |   |   start > 757775:
biological_process_ (39.01)
|   |   |   |   |   |   |   |   start > 767434: transport_
(34.76/8.68)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 731142
|   |   |   |   |   |   |   |   start <= 729676
|   |   |   |   |   |   |   |   |   start <= 726978:
biological_process_ (17.78)
|   |   |   |   |   |   |   |   |   start > 726978:
nuclear_organization_and_biogenesis_ (19.36)
|   |   |   |   |   |   |   |   start > 729676: transport_
(32.99/8.72)
|   |   |   |   |   |   |   start > 731142
|   |   |   |   |   |   |   |   start <= 750405
|   |   |   |   |   |   |   |   |   start <= 733940:
biological_process_ (10.46)
|   |   |   |   |   |   |   |   |   start > 733940:
ribosome_biogenesis_and_assembly_ (26.49)
|   |   |   |   |   |   |   |   start > 750405
|   |   |   |   |   |   |   |   |   start <= 757775:
biological_process_ (38.68)
|   |   |   |   |   |   |   |   |   start > 757775: transport_
(10.05)
|   |   |   |   |   start > 772459
|   |   |   |   |   |   start <= 781772
|   |   |   |   |   |   |   start <= 779621
|   |   |   |   |   |   |   |   start <= 775198
```

```
|   |   |   |   |   |   |   |   |   start <= 774354: translation_
(12.44)
|   |   |   |   |   |   |   |   |   start > 774354:
cell_wall_organization_and_biogenesis_ (13.2)
|   |   |   |   |   |   |   |   start > 775198: translation_ (12.68)
|   |   |   |   |   |   |   start > 779621
|   |   |   |   |   |   |   |   start <= 780404:
organelle_organization_and_biogenesis_ (10.59)
|   |   |   |   |   |   |   |   start > 780404:
ribosome_biogenesis_and_assembly_ (9.07)
|   |   |   |   |   |   start > 781772
|   |   |   |   |   |   |   start <= 794422
|   |   |   |   |   |   |   |   start <= 786925
|   |   |   |   |   |   |   |   |   start <= 785442:
biological_process_ (25.72)
|   |   |   |   |   |   |   |   |   start > 785442:
protein_modification_process_ (13.6)
|   |   |   |   |   |   |   |   start > 786925
|   |   |   |   |   |   |   |   |   start <= 787784: translation_
(19.37)
|   |   |   |   |   |   |   |   |   start > 787784
|   |   |   |   |   |   |   |   |   |   start <= 793058:
biological_process_ (19.44)
|   |   |   |   |   |   |   |   |   |   start > 793058: translation_
(11.57)
|   |   |   |   |   |   |   start > 794422
|   |   |   |   |   |   |   |   start <= 795497: cell_budding_
(18.13)
|   |   |   |   |   |   |   |   start > 795497: biological_process_
(52.07)
|   |   |   |   start > 798548
|   |   |   |   |   start <= 878820
|   |   |   |   |   |   start <= 856306
|   |   |   |   |   |   |   start <= 827557
|   |   |   |   |   |   |   |   start <= 802445
|   |   |   |   |   |   |   |   |   start <= 800551:
RNA_metabolic_process_ (13.43)
|   |   |   |   |   |   |   |   |   start > 800551:
DNA_metabolic_process_ (18.8)
|   |   |   |   |   |   |   |   start > 802445
|   |   |   |   |   |   |   |   |   start <= 824064
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 823487
|   |   |   |   |   |   |   |   |   |   |   |   start <= 810232:
biological_process_ (8.17)
|   |   |   |   |   |   |   |   |   |   |   |   start > 810232:
translation_ (14.28)
|   |   |   |   |   |   |   |   |   |   |   start > 823487:
ribosome_biogenesis_and_assembly_ (16.21)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 807661:
ribosome_biogenesis_and_assembly_ (26.53)
|   |   |   |   |   |   |   |   |   |   |   start > 807661:
protein_modification_process_ (17.1)
```

```
|   |   |   |   |   |   |   |   |   start > 824064
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_metabolic_process_ (8.52/2.21)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
membrane_organization_and_biogenesis_ (12.67/5.09)
|   |   |   |   |   |   |   start > 827557
|   |   |   |   |   |   |   |   start <= 832461
|   |   |   |   |   |   |   |   |   start <= 829121: translation_
(21.94)
|   |   |   |   |   |   |   |   |   start > 829121: vesicle-
mediated_transport_ (57.97/18.21)
|   |   |   |   |   |   |   |   start > 832461
|   |   |   |   |   |   |   |   |   start <= 854900
|   |   |   |   |   |   |   |   |   |   start <= 836670
|   |   |   |   |   |   |   |   |   |   |   start <= 834487:
biological_process_ (18.58)
|   |   |   |   |   |   |   |   |   |   |   start > 834487
|   |   |   |   |   |   |   |   |   |   |   |   start <= 835908:
RNA_metabolic_process_ (18.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 835908:
biological_process_ (18.33)
|   |   |   |   |   |   |   |   |   |   start > 836670
|   |   |   |   |   |   |   |   |   |   |   start <= 843596
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
lipid_metabolic_process_ (10.96)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 842556:
translation_ (16.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 842556:
vesicle-mediated_transport_ (12.0)
|   |   |   |   |   |   |   |   |   |   |   start > 843596
|   |   |   |   |   |   |   |   |   |   |   |   start <= 846660
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
843859: biological_process_ (19.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
843859
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
845654: translation_ (20.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
845654: biological_process_ (14.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
organelle_organization_and_biogenesis_ (17.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 846660
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 850441:
lipid_metabolic_process_ (30.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 850441
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
853220: translation_ (21.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
853220: biological_process_ (17.38)
|   |   |   |   |   |   |   |   |   start > 854900:
DNA_metabolic_process_ (22.79)
|   |   |   |   |   |   start > 856306
```

```
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 871421
|   |   |   |   |   |   |   |   |   start <= 859481:
membrane_organization_and_biogenesis_ (8.66)
|   |   |   |   |   |   |   |   |   start > 859481: transcription_
(17.79)
|   |   |   |   |   |   |   |   start > 871421: translation_ (9.53)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 859481
|   |   |   |   |   |   |   |   |   start <= 858292: translation_
(9.3)
|   |   |   |   |   |   |   |   |   start > 858292:
cellular_respiration_ (20.53/10.2)
|   |   |   |   |   |   |   |   start > 859481
|   |   |   |   |   |   |   |   |   start <= 876399
|   |   |   |   |   |   |   |   |   |   start <= 867779
|   |   |   |   |   |   |   |   |   |   |   start <= 865758:
protein_modification_process_ (17.56)
|   |   |   |   |   |   |   |   |   |   |   start > 865758:
translation_ (19.31)
|   |   |   |   |   |   |   |   |   |   start > 867779
|   |   |   |   |   |   |   |   |   |   |   start <= 871421:
ribosome_biogenesis_and_assembly_ (22.04)
|   |   |   |   |   |   |   |   |   |   |   start > 871421:
protein_modification_process_ (14.54)
|   |   |   |   |   |   |   |   |   start > 876399
|   |   |   |   |   |   |   |   |   |   start <= 878197:
cell_wall_organization_and_biogenesis_ (13.92)
|   |   |   |   |   |   |   |   |   |   start > 878197: translation_
(15.61)
|   |   |   |   |   start > 878820
|   |   |   |   |   |   start <= 911633
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 897507
|   |   |   |   |   |   |   |   |   start <= 888887
|   |   |   |   |   |   |   |   |   |   start <= 883815: transport_
(12.21)
|   |   |   |   |   |   |   |   |   |   start > 883815:
ribosome_biogenesis_and_assembly_ (20.5)
|   |   |   |   |   |   |   |   |   start > 888887
|   |   |   |   |   |   |   |   |   |   start <= 894698: vesicle-
mediated_transport_ (20.56)
|   |   |   |   |   |   |   |   |   |   start > 894698:
protein_modification_process_ (13.76)
|   |   |   |   |   |   |   |   start > 897507
|   |   |   |   |   |   |   |   |   start <= 909218:
biological_process_ (61.18)
|   |   |   |   |   |   |   |   |   start > 909218: transport_
(10.68)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 897507
|   |   |   |   |   |   |   |   |   start <= 888887
|   |   |   |   |   |   |   |   |   |   start <= 885746:
biological_process_ (30.93)
```

```
|   |   |   |   |   |   |   |   |   |   start > 885746:
carbohydrate_metabolic_process_ (11.2)
|   |   |   |   |   |   |   |   |   start > 888887:
biological_process_ (40.34)
|   |   |   |   |   |   |   |   start > 897507
|   |   |   |   |   |   |   |   |   start <= 902275:
RNA_metabolic_process_ (13.23)
|   |   |   |   |   |   |   |   |   start > 902275
|   |   |   |   |   |   |   |   |   |   start <= 905939
|   |   |   |   |   |   |   |   |   |   |   start <= 903202:
biological_process_ (20.38)
|   |   |   |   |   |   |   |   |   |   |   start > 903202:
lipid_metabolic_process_ (12.8)
|   |   |   |   |   |   |   |   |   |   start > 905939:
biological_process_ (35.27)
|   |   |   |   |   |   start > 911633:
amino_acid_and_derivative_metabolic_process_ (26.97)
|   |   |   start > 911888
|   |   |   |   start <= 965660
|   |   |   |   |   start <= 947423
|   |   |   |   |   |   start <= 919470
|   |   |   |   |   |   |   start <= 915246
|   |   |   |   |   |   |   |   start <= 913232: response_to_stress_
(18.71)
|   |   |   |   |   |   |   |   start > 913232
|   |   |   |   |   |   |   |   |   start <= 914743:
biological_process_ (15.04)
|   |   |   |   |   |   |   |   |   start > 914743:
response_to_stress_ (16.53)
|   |   |   |   |   |   |   start > 915246: biological_process_
(24.62)
|   |   |   |   |   |   start > 919470
|   |   |   |   |   |   |   start <= 939926
|   |   |   |   |   |   |   |   start <= 936886
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 922180:
translation_ (26.77)
|   |   |   |   |   |   |   |   |   |   start > 922180
|   |   |   |   |   |   |   |   |   |   |   start <= 924699:
transport_ (12.63)
|   |   |   |   |   |   |   |   |   |   |   start > 924699:
ribosome_biogenesis_and_assembly_ (3.94)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 924699:
protein_modification_process_ (16.5)
|   |   |   |   |   |   |   |   |   |   start > 924699: translation_
(23.47)
|   |   |   |   |   |   |   |   start > 936886
|   |   |   |   |   |   |   |   |   strand = W: translation_ (7.21)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 938995:
cell_budding_ (12.64)
|   |   |   |   |   |   |   |   |   |   start > 938995:
RNA_metabolic_process_ (29.5)
```

```
|   |   |   |   |   |   |   start > 939926
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 942809: transport_
(14.0)
|   |   |   |   |   |   |   |   |   start > 942809
|   |   |   |   |   |   |   |   |   |   start <= 945148:
protein_catabolic_process_ (8.19)
|   |   |   |   |   |   |   |   |   |   start > 945148:
protein_modification_process_ (9.0)
|   |   |   |   |   |   |   |   strand = C: biological_process_
(15.92)
|   |   |   |   |   start > 947423
|   |   |   |   |   |   start <= 951897
|   |   |   |   |   |   |   start <= 950902:
cell_wall_organization_and_biogenesis_ (10.16)
|   |   |   |   |   |   |   start > 950902: meiosis_ (18.09)
|   |   |   |   |   |   start > 951897
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 953963: biological_process_
(10.33)
|   |   |   |   |   |   |   |   start > 953963: response_to_stress_
(14.71)
|   |   |   |   |   |   |   strand = C: biological_process_ (67.67)
|   |   |   |   start > 965660
|   |   |   |   |   start <= 1043102
|   |   |   |   |   |   start <= 1016756
|   |   |   |   |   |   |   start <= 995644
|   |   |   |   |   |   |   |   start <= 970058
|   |   |   |   |   |   |   |   |   start <= 968692: conjugation_
(11.75)
|   |   |   |   |   |   |   |   |   start > 968692
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: transport_ (6.58/2.06)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: transport_ (4.54/1.36)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: organelle_organization_and_biogenesis_ (7.15/2.56)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: organelle_organization_and_biogenesis_
(2.48/1.08)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
organelle_organization_and_biogenesis_ (10.59/2.91)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_:
organelle_organization_and_biogenesis_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
organelle_organization_and_biogenesis_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: transport_ (2.82/0.69)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: organelle_organization_and_biogenesis_
(2.31/1.03)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
transport_ (4.27/0.77)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: organelle_organization_and_biogenesis_
(4.69/1.22)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: transport_ (1.58/0.32)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
organelle_organization_and_biogenesis_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   start > 970058
|   |   |   |   |   |   |   |   |   start <= 979324
|   |   |   |   |   |   |   |   |   |   start <= 977341
|   |   |   |   |   |   |   |   |   |   |   start <= 973739:
carbohydrate_metabolic_process_ (14.47)
|   |   |   |   |   |   |   |   |   |   |   start > 973739
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (26.85)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 974782:
biological_process_ (11.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 974782:
vesicle-mediated_transport_ (10.68)
|   |   |   |   |   |   |   |   |   |   start > 977341:
cellular_respiration_ (34.46/16.13)
|   |   |   |   |   |   |   |   |   start > 979324
|   |   |   |   |   |   |   |   |   |   start <= 984277
|   |   |   |   |   |   |   |   |   |   |   start <= 982073:
ribosome_biogenesis_and_assembly_ (16.45)
|   |   |   |   |   |   |   |   |   |   |   start > 982073:
transcription_ (16.01)
|   |   |   |   |   |   |   |   |   |   start > 984277
|   |   |   |   |   |   |   |   |   |   |   start <= 993526
|   |   |   |   |   |   |   |   |   |   |   |   start <= 985977
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 984971:
biological_process_ (16.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 984971:
carbohydrate_metabolic_process_ (19.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 985977:
biological_process_ (30.86)
|   |   |   |   |   |   |   |   |   |   |   start > 993526:
ribosome_biogenesis_and_assembly_ (18.89)
|   |   |   |   |   |   |   start > 995644
|   |   |   |   |   |   |   |   start <= 1003967
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 996874:
protein_modification_process_ (36.48/15.42)
|   |   |   |   |   |   |   |   |   |   start > 996874
|   |   |   |   |   |   |   |   |   |   |   distance <= 3438:
organelle_organization_and_biogenesis_ (17.86/7.91)
|   |   |   |   |   |   |   |   |   |   |   distance > 3438:
membrane_organization_and_biogenesis_ (6.18/0.46)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 1000932:
response_to_stress_ (21.19)
|   |   |   |   |   |   |   |   |   |   start > 1000932:
biological_process_ (18.03)
|   |   |   |   |   |   |   |   start > 1003967
|   |   |   |   |   |   |   |   |   start <= 1004630
|   |   |   |   |   |   |   |   |   |   start <= 1004222:
translation_ (18.11)
```

```
|   |   |   |   |   |   |   |   |   |   start > 1004222:
carbohydrate_metabolic_process_ (17.81)
|   |   |   |   |   |   |   |   |   start > 1004630
|   |   |   |   |   |   |   |   |   |   start <= 1012491
|   |   |   |   |   |   |   |   |   |   |   start <= 1007311:
transport_ (20.83)
|   |   |   |   |   |   |   |   |   |   |   start > 1007311
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1010772:
transcription_ (14.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1010772:
transport_ (10.29)
|   |   |   |   |   |   |   |   |   |   start > 1012491: vesicle-
mediated_transport_ (18.95)
|   |   |   |   |   |   start > 1016756
|   |   |   |   |   |   |   start <= 1039245
|   |   |   |   |   |   |   |   start <= 1017765
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
protein_modification_process_ (9.47/2.62)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (18.06/7.09)
|   |   |   |   |   |   |   |   start > 1017765
|   |   |   |   |   |   |   |   |   start <= 1031797
|   |   |   |   |   |   |   |   |   |   start <= 1025741
|   |   |   |   |   |   |   |   |   |   |   start <= 1021859
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1019247:
biological_process_ (14.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1019247:
translation_ (17.79)
|   |   |   |   |   |   |   |   |   |   |   start > 1021859:
biological_process_ (31.24)
|   |   |   |   |   |   |   |   |   |   start > 1025741
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1027376:
protein_catabolic_process_ (9.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1027376:
translation_ (16.58)
|   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoskeleton_organization_and_biogenesis_ (12.0)
|   |   |   |   |   |   |   |   |   start > 1031797:
biological_process_ (46.24)
|   |   |   |   |   |   |   start > 1039245:
protein_modification_process_ (40.42/13.39)
|   |   |   |   |   start > 1043102
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 1046738: RNA_metabolic_process_
(50.9/12.69)
|   |   |   |   |   |   |   start > 1046738
|   |   |   |   |   |   |   |   start <= 1076606
|   |   |   |   |   |   |   |   |   start <= 1060047: transport_
(15.63)
|   |   |   |   |   |   |   |   |   start > 1060047:
carbohydrate_metabolic_process_ (29.54)
|   |   |   |   |   |   |   |   start > 1076606
```

```
|   |   |   |   |   |   |   |   |   start <= 1080313:
biological_process_ (7.18)
|   |   |   |   |   |   |   |   |   start > 1080313:
DNA_metabolic_process_ (12.0)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 1060047
|   |   |   |   |   |   |   |   start <= 1049965
|   |   |   |   |   |   |   |   |   start <= 1046738
|   |   |   |   |   |   |   |   |   |   start <= 1045487:
ribosome_biogenesis_and_assembly_ (15.83)
|   |   |   |   |   |   |   |   |   |   start > 1045487:
biological_process_ (23.43)
|   |   |   |   |   |   |   |   |   start > 1046738: conjugation_
(20.37)
|   |   |   |   |   |   |   |   start > 1049965
|   |   |   |   |   |   |   |   |   start <= 1052831:
ribosome_biogenesis_and_assembly_ (21.1)
|   |   |   |   |   |   |   |   |   start > 1052831
|   |   |   |   |   |   |   |   |   |   start <= 1058731:
cell_wall_organization_and_biogenesis_ (22.21)
|   |   |   |   |   |   |   |   |   |   start > 1058731:
ribosome_biogenesis_and_assembly_ (17.13)
|   |   |   |   |   |   |   start > 1060047
|   |   |   |   |   |   |   |   start <= 1063160
|   |   |   |   |   |   |   |   |   start <= 1061597: transport_
(39.38/18.28)
|   |   |   |   |   |   |   |   |   start > 1061597: translation_
(29.18)
|   |   |   |   |   |   |   |   start > 1063160
|   |   |   |   |   |   |   |   |   start <= 1064947:
vitamin_metabolic_process_ (19.21)
|   |   |   |   |   |   |   |   |   start > 1064947
|   |   |   |   |   |   |   |   |   |   start <= 1070300:
biological_process_ (21.22)
|   |   |   |   |   |   |   |   |   |   start > 1070300
|   |   |   |   |   |   |   |   |   |   |   start <= 1076606:
transport_ (14.08)
|   |   |   |   |   |   |   |   |   |   |   start > 1076606:
biological_process_ (6.7)
```

Decision Tree Generated for Chromosome Eight:
For Cellular Component

```
|   start <= 517532
|   |   start <= 222480
|   |   |   start <= 148662
|   |   |   |   start <= 74696
|   |   |   |   |   start <= 20968
|   |   |   |   |   |   start <= 6400
|   |   |   |   |   |   |   strand = C: cellular_component_ (24.42)
|   |   |   |   |   |   |   strand = W: endomembrane_system_ (16.35)
|   |   |   |   |   |   start > 6400
|   |   |   |   |   |   |   start <= 15665
|   |   |   |   |   |   |   |   start <= 10211
```

```
|   |   |   |   |   |   |   |   |   neigh_strand = W:
cytoplasmic_membrane-bound_vesicle_ (7.47/1.91)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
plasma_membrane_ (14.5/4.55)
|   |   |   |   |   |   |   |   start > 10211
|   |   |   |   |   |   |   |   |   start <= 13563
|   |   |   |   |   |   |   |   |   |   start <= 12283:
cellular_component_ (14.44)
|   |   |   |   |   |   |   |   |   |   start > 12283:
plasma_membrane_ (10.72)
|   |   |   |   |   |   |   |   |   start > 13563:
cellular_component_ (24.74)
|   |   |   |   |   |   |   start > 15665: cytoplasmic_membrane-
bound_vesicle_ (11.95)
|   |   |   |   |   start > 20968
|   |   |   |   |   |   start <= 48761
|   |   |   |   |   |   |   start <= 39484
|   |   |   |   |   |   |   |   start <= 21780: cytoplasm_ (24.64)
|   |   |   |   |   |   |   |   start > 21780
|   |   |   |   |   |   |   |   |   start <= 36023
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 32754
|   |   |   |   |   |   |   |   |   |   |   |   start <= 26239:
mitochondrion_ (8.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 26239
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
2207: ribosome_ (2.96/0.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
2207: mitochondrion_ (7.08/2.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
ribosome_ (11.71/3.66)
|   |   |   |   |   |   |   |   |   |   |   start > 32754
|   |   |   |   |   |   |   |   |   |   |   |   start <= 34075:
nucleolus_ (14.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 34075:
ribosome_ (14.44)
|   |   |   |   |   |   |   |   |   |   strand = W: membrane_
(11.91)
|   |   |   |   |   |   |   |   |   start > 36023
|   |   |   |   |   |   |   |   |   |   start <= 38506: cytoplasm_
(6.2)
|   |   |   |   |   |   |   |   |   |   start > 38506: membrane_
(13.51)
|   |   |   |   |   |   |   start > 39484
|   |   |   |   |   |   |   |   start <= 47966: cytoplasm_
(53.21/12.94)
|   |   |   |   |   |   |   |   start > 47966: membrane_fraction_
(12.01)
|   |   |   |   |   |   start > 48761
|   |   |   |   |   |   |   start <= 64155
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 62753:
cellular_component_ (37.74)
```

```
|   |   |   |   |   |   |   |   |   start > 62753: chromosome_
(15.16)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 54849
|   |   |   |   |   |   |   |   |   |   start <= 51109: nucleus_
(20.93)
|   |   |   |   |   |   |   |   |   |   start > 51109:
cellular_component_ (25.84/12.37)
|   |   |   |   |   |   |   |   |   start > 54849: cytoplasm_
(25.52)
|   |   |   |   |   |   |   start > 64155
|   |   |   |   |   |   |   |   start <= 69705
|   |   |   |   |   |   |   |   |   start <= 67453
|   |   |   |   |   |   |   |   |   |   start <= 65856:
mitochondrion_ (18.79)
|   |   |   |   |   |   |   |   |   |   start > 65856
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
endoplasmic_reticulum_ (6.94/1.53)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (18.07/6.91)
|   |   |   |   |   |   |   |   |   start > 67453
|   |   |   |   |   |   |   |   |   |   start <= 69545:
Golgi_apparatus_ (14.67)
|   |   |   |   |   |   |   |   |   |   start > 69545:
mitochondrion_ (9.42)
|   |   |   |   |   |   |   |   start > 69705
|   |   |   |   |   |   |   |   |   strand = C: plasma_membrane_
(13.75)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 70273:
cytoplasmic_membrane-bound_vesicle_ (23.49)
|   |   |   |   |   |   |   |   |   |   start > 70273:
cellular_component_ (17.95)
|   |   |   |   start > 74696
|   |   |   |   |   start <= 127774
|   |   |   |   |   |   start <= 98791
|   |   |   |   |   |   |   start <= 78350
|   |   |   |   |   |   |   |   start <= 77311
|   |   |   |   |   |   |   |   |   start <= 75409: ribosome_
(13.46)
|   |   |   |   |   |   |   |   |   start > 75409: mitochondrion_
(20.53)
|   |   |   |   |   |   |   |   start > 77311
|   |   |   |   |   |   |   |   |   neigh_num <= 1: ribosome_
(17.42/5.21)
|   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(23.56/9.58)
|   |   |   |   |   |   |   start > 78350
|   |   |   |   |   |   |   |   start <= 85367
|   |   |   |   |   |   |   |   |   start <= 83717
|   |   |   |   |   |   |   |   |   |   start <= 81612
|   |   |   |   |   |   |   |   |   |   |   start <= 78932:
cellular_component_ (13.56)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 78932:
cytoplasm_ (17.07)
|   |   |   |   |   |   |   |   |   |   start > 81612:
cellular_component_ (14.98)
|   |   |   |   |   |   |   |   |   start > 83717
|   |   |   |   |   |   |   |   |   |   start <= 85056: nucleus_
(10.03)
|   |   |   |   |   |   |   |   |   |   start > 85056: cytoplasm_
(16.04)
|   |   |   |   |   |   |   |   start > 85367
|   |   |   |   |   |   |   |   |   start <= 97933
|   |   |   |   |   |   |   |   |   |   start <= 94506: vacuole_
(9.68)
|   |   |   |   |   |   |   |   |   |   start > 94506:
site_of_polarized_growth_ (15.03)
|   |   |   |   |   |   |   |   |   start > 97933: nucleus_ (13.94)
|   |   |   |   |   |   start > 98791
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 115896
|   |   |   |   |   |   |   |   |   start <= 106050:
endoplasmic_reticulum_ (8.23)
|   |   |   |   |   |   |   |   |   start > 106050
|   |   |   |   |   |   |   |   |   |   start <= 113089:
mitochondrion_ (40.64)
|   |   |   |   |   |   |   |   |   |   start > 113089
|   |   |   |   |   |   |   |   |   |   |   start <= 114912:
plasma_membrane_ (22.04)
|   |   |   |   |   |   |   |   |   |   |   start > 114912:
mitochondrion_ (15.21)
|   |   |   |   |   |   |   |   start > 115896
|   |   |   |   |   |   |   |   |   start <= 122760
|   |   |   |   |   |   |   |   |   |   start <= 121678
|   |   |   |   |   |   |   |   |   |   |   start <= 117809:
cytoplasm_ (11.21)
|   |   |   |   |   |   |   |   |   |   |   start > 117809:
endoplasmic_reticulum_ (8.33)
|   |   |   |   |   |   |   |   |   |   start > 121678:
cellular_component_ (15.57)
|   |   |   |   |   |   |   |   |   start > 122760
|   |   |   |   |   |   |   |   |   |   start <= 123585:
mitochondrion_ (16.32)
|   |   |   |   |   |   |   |   |   |   start > 123585: cytoplasm_
(19.19)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 99215: mitochondrion_
(17.38)
|   |   |   |   |   |   |   |   start > 99215
|   |   |   |   |   |   |   |   |   start <= 106050
|   |   |   |   |   |   |   |   |   |   start <= 104272
|   |   |   |   |   |   |   |   |   |   |   start <= 102607:
cytoplasm_ (13.99)
|   |   |   |   |   |   |   |   |   |   |   start > 102607:
ribosome_ (8.82)
```

```
|   |   |   |   |   |   |   |   |   |   start > 104272: cytoplasm_
(15.33)
|   |   |   |   |   |   |   |   |   start > 106050
|   |   |   |   |   |   |   |   |   |   start <= 113089:
mitochondrion_ (34.75)
|   |   |   |   |   |   |   |   |   |   start > 113089
|   |   |   |   |   |   |   |   |   |   |   start <= 126515
|   |   |   |   |   |   |   |   |   |   |   |   start <= 121678:
nucleus_ (11.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 121678:
ribosome_ (13.09)
|   |   |   |   |   |   |   |   |   |   |   start > 126515:
cytoplasm_ (23.1/10.92)
|   |   |   |   |   start > 127774
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 132040: ribosome_ (16.07)
|   |   |   |   |   |   |   start > 132040
|   |   |   |   |   |   |   |   start <= 138687
|   |   |   |   |   |   |   |   |   start <= 134547: cytoplasm_
(19.94)
|   |   |   |   |   |   |   |   |   start > 134547
|   |   |   |   |   |   |   |   |   |   distance <= 1861:
cell_cortex_ (13.36/1.64)
|   |   |   |   |   |   |   |   |   |   distance > 1861:
cytoskeleton_ (26.33/7.4)
|   |   |   |   |   |   |   |   start > 138687
|   |   |   |   |   |   |   |   |   start <= 146307: cytoplasm_
(36.2)
|   |   |   |   |   |   |   |   |   start > 146307: ribosome_ (4.62)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 134547
|   |   |   |   |   |   |   |   start <= 129475:
endomembrane_system_ (15.39)
|   |   |   |   |   |   |   |   start > 129475
|   |   |   |   |   |   |   |   |   start <= 134314
|   |   |   |   |   |   |   |   |   |   start <= 133100: nucleus_
(8.82)
|   |   |   |   |   |   |   |   |   |   start > 133100: cytoplasm_
(9.99)
|   |   |   |   |   |   |   |   |   start > 134314
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
membrane_ (8.98/3.02)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(13.21/7.76)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
membrane_ (2.75/1.34)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: membrane_ (2.09/0.79)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: membrane_ (2.45/0.93)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
nucleus_ (1.23/0.6)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: cellular_component_ (8.06/2.49)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
nucleus_ (4.83/2.41)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: nucleus_ (2.3/0.76)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: membrane_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: membrane_ (0.0)
|   |   |   |   |   |   |   start > 134547
|   |   |   |   |   |   |   |   start <= 138687: mitochondrion_
(18.35)
|   |   |   |   |   |   |   |   start > 138687: ribosome_ (13.13)
|   |   |   start > 148662
|   |   |   |   start <= 159431
|   |   |   |   |   start <= 151299: cellular_component_ (56.4)
|   |   |   |   |   start > 151299
|   |   |   |   |   |   strand = C: mitochondrion_ (17.82)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 151659
|   |   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = molecular_function_:
site_of_polarized_growth_ (9.57/2.14)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transport_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
cellular_bud_ (1.41/0.53)
|   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = biological_process_:
cellular_bud_ (1.19/0.49)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_component_:
cellular_bud_ (8.29/3.1)
|   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = translation_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: cellular_bud_ (3.03/1.01)
|   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: site_of_polarized_growth_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transcription_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: cellular_bud_
(6.94/1.79)
|   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: site_of_polarized_growth_
(5.26/1.06)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
cellular_bud_ (1.1/0.21)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: site_of_polarized_growth_ (3.4/0.8)
|   |   |   |   |   |   |   |   NeighGO_term = electron_transport_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
site_of_polarized_growth_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: site_of_polarized_growth_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: site_of_polarized_growth_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: site_of_polarized_growth_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: site_of_polarized_growth_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: site_of_polarized_growth_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: site_of_polarized_growth_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: site_of_polarized_growth_ (0.0)
```

```
|   |   |   |   |   |   |   start > 151659: cellular_component_
(33.08)
|   |   |   |   start > 159431
|   |   |   |   |   start <= 220110
|   |   |   |   |   |   start <= 206455
|   |   |   |   |   |   |   start <= 167427
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 164704:
endoplasmic_reticulum_ (51.5/29.5)
|   |   |   |   |   |   |   |   |   start > 164704: vacuole_
(30.9/14.15)
|   |   |   |   |   |   |   |   strand = W: vacuole_ (37.0/17.87)
|   |   |   |   |   |   |   start > 167427
|   |   |   |   |   |   |   |   start <= 178212
|   |   |   |   |   |   |   |   |   start <= 168554:
cellular_component_ (22.01)
|   |   |   |   |   |   |   |   |   start > 168554
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 170337:
cytoplasm_ (32.9/14.29)
|   |   |   |   |   |   |   |   |   |   |   start > 170337
|   |   |   |   |   |   |   |   |   |   |   |   start <= 173337:
chromosome_ (10.44)
|   |   |   |   |   |   |   |   |   |   |   |   start > 173337:
cytoplasm_ (32.29/13.1)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 175541
|   |   |   |   |   |   |   |   |   |   |   |   start <= 173337:
cellular_component_ (17.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 173337:
cytoplasm_ (12.43)
|   |   |   |   |   |   |   |   |   |   |   start > 175541:
cellular_component_ (21.79)
|   |   |   |   |   |   |   |   start > 178212
|   |   |   |   |   |   |   |   |   start <= 187672
|   |   |   |   |   |   |   |   |   |   start <= 186802
|   |   |   |   |   |   |   |   |   |   |   strand = C:
endoplasmic_reticulum_ (26.37)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 180338:
endoplasmic_reticulum_ (18.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 180338:
mitochondrion_ (28.52)
|   |   |   |   |   |   |   |   |   |   start > 186802: vacuole_
(16.51)
|   |   |   |   |   |   |   |   |   start > 187672
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 195544
|   |   |   |   |   |   |   |   |   |   |   |   start <= 193538
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 190536:
nucleus_ (26.93/9.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 190536
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C: nucleus_ (8.56/2.49)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F: cytoplasm_ (8.09/2.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P: cytoplasm_ (7.3/2.94)
|   |   |   |   |   |   |   |   |   |   |   |   start > 193538:
cellular_component_ (11.97)
|   |   |   |   |   |   |   |   |   |   |   start > 195544:
cytoplasm_ (60.73/26.64)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 190536
|   |   |   |   |   |   |   |   |   |   |   |   start <= 187917:
cytoplasm_ (40.24/15.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 187917:
mitochondrion_ (12.32)
|   |   |   |   |   |   |   |   |   |   |   start > 190536
|   |   |   |   |   |   |   |   |   |   |   |   start <= 204600
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 198278:
endoplasmic_reticulum_ (26.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 198278:
membrane_ (20.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 204600
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1544: cytoplasm_ (8.31/1.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 1544:
nucleus_ (22.96/8.57)
|   |   |   |   |   |   start > 206455
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 214720
|   |   |   |   |   |   |   |   |   start <= 212722: cytoplasm_
(12.42)
|   |   |   |   |   |   |   |   |   start > 212722
|   |   |   |   |   |   |   |   |   |   start <= 214409:
cellular_component_ (21.05)
|   |   |   |   |   |   |   |   |   |   start > 214409: cytoplasm_
(11.57)
|   |   |   |   |   |   |   |   start > 214720: cellular_component_
(77.93/25.74)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 207648:
cytoplasmic_membrane-bound_vesicle_ (31.31/13.68)
|   |   |   |   |   |   |   |   start > 207648
|   |   |   |   |   |   |   |   |   start <= 214720
|   |   |   |   |   |   |   |   |   |   start <= 209699
|   |   |   |   |   |   |   |   |   |   |   start <= 209469:
cellular_component_ (9.14)
|   |   |   |   |   |   |   |   |   |   |   start > 209469:
mitochondrion_ (23.36)
|   |   |   |   |   |   |   |   |   |   start > 209699
|   |   |   |   |   |   |   |   |   |   |   start <= 210842:
nucleolus_ (6.52)
|   |   |   |   |   |   |   |   |   |   |   start > 210842:
cellular_component_ (28.32)
|   |   |   |   |   |   |   |   |   start > 214720: mitochondrion_
(23.31)
```

```
|   |   |   |   |   start > 220110
|   |   |   |   |   |   start <= 220727
|   |   |   |   |   |   |   neigh_strand = W: membrane_ (17.12/7.92)
|   |   |   |   |   |   |   neigh_strand = C: endoplasmic_reticulum_
(32.66/20.31)
|   |   |   |   |   |   start > 220727: site_of_polarized_growth_
(29.47/14.69)
|   |   start > 222480
|   |   |   strand = C
|   |   |   |   start <= 298612
|   |   |   |   |   start <= 286772
|   |   |   |   |   |   start <= 256362
|   |   |   |   |   |   |   start <= 230972
|   |   |   |   |   |   |   |   start <= 223760: nucleolus_ (20.27)
|   |   |   |   |   |   |   |   start > 223760
|   |   |   |   |   |   |   |   |   start <= 227143: cytoplasm_
(32.77)
|   |   |   |   |   |   |   |   |   start > 227143: nucleolus_
(11.38)
|   |   |   |   |   |   |   start > 230972
|   |   |   |   |   |   |   |   start <= 242584
|   |   |   |   |   |   |   |   |   start <= 234883: nucleus_
(41.71/17.38)
|   |   |   |   |   |   |   |   |   start > 234883: cytoplasm_
(16.57)
|   |   |   |   |   |   |   |   start > 242584
|   |   |   |   |   |   |   |   |   start <= 251103:
cellular_component_ (23.78)
|   |   |   |   |   |   |   |   |   start > 251103: cytoplasm_
(16.05)
|   |   |   |   |   |   start > 256362
|   |   |   |   |   |   |   start <= 262555
|   |   |   |   |   |   |   |   start <= 261593: nucleus_ (20.01)
|   |   |   |   |   |   |   |   start > 261593: chromosome_ (16.58)
|   |   |   |   |   |   |   start > 262555
|   |   |   |   |   |   |   |   start <= 267540
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C: ribosome_
(14.97/5.34)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
mitochondrion_ (6.38/1.75)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
mitochondrion_ (10.3/2.12)
|   |   |   |   |   |   |   |   start > 267540
|   |   |   |   |   |   |   |   |   start <= 284627
|   |   |   |   |   |   |   |   |   |   start <= 276766: nucleus_
(14.82)
|   |   |   |   |   |   |   |   |   |   start > 276766
|   |   |   |   |   |   |   |   |   |   |   start <= 283300:
nucleolus_ (10.59)
|   |   |   |   |   |   |   |   |   |   |   start > 283300: nucleus_
(8.02)
|   |   |   |   |   |   |   |   |   start > 284627: mitochondrion_
(13.97)
|   |   |   |   |   start > 286772
```

```
|   |   |   |   |   |   start <= 296450: membrane_fraction_
(95.84/45.53)
|   |   |   |   |   |   start > 296450: cytoplasm_ (25.84/12.24)
|   |   |   |   start > 298612
|   |   |   |   |   start <= 475778
|   |   |   |   |   |   start <= 393537
|   |   |   |   |   |   |   start <= 377702
|   |   |   |   |   |   |   |   start <= 342352
|   |   |   |   |   |   |   |   |   start <= 320417
|   |   |   |   |   |   |   |   |   |   start <= 314676
|   |   |   |   |   |   |   |   |   |   |   start <= 302764:
endoplasmic_reticulum_ (9.85)
|   |   |   |   |   |   |   |   |   |   |   start > 302764:
mitochondrion_ (13.4)
|   |   |   |   |   |   |   |   |   |   start > 314676:
endoplasmic_reticulum_ (19.01)
|   |   |   |   |   |   |   |   |   start > 320417: cytoplasm_
(54.04)
|   |   |   |   |   |   |   |   start > 342352
|   |   |   |   |   |   |   |   |   start <= 349577:
cellular_component_ (62.0/32.11)
|   |   |   |   |   |   |   |   |   start > 349577
|   |   |   |   |   |   |   |   |   |   start <= 370057
|   |   |   |   |   |   |   |   |   |   |   start <= 367895
|   |   |   |   |   |   |   |   |   |   |   |   start <= 362118
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 358572:
cytoplasm_ (18.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 358572:
cellular_component_ (13.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 362118
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 364156:
cytoskeleton_ (13.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 364156:
cytoplasm_ (10.49)
|   |   |   |   |   |   |   |   |   |   |   start > 367895: vacuole_
(13.77)
|   |   |   |   |   |   |   |   |   |   start > 370057
|   |   |   |   |   |   |   |   |   |   |   start <= 374313
|   |   |   |   |   |   |   |   |   |   |   |   start <= 371752:
endoplasmic_reticulum_ (17.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 371752:
mitochondrion_ (47.59/28.28)
|   |   |   |   |   |   |   |   |   |   |   start > 374313
|   |   |   |   |   |   |   |   |   |   |   |   start <= 375712:
cytoplasm_ (21.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 375712:
cellular_component_ (18.97)
|   |   |   |   |   |   |   start > 377702
|   |   |   |   |   |   |   |   start <= 385513
|   |   |   |   |   |   |   |   |   start <= 380575: cell_wall_
(11.63)
|   |   |   |   |   |   |   |   |   start > 380575: ribosome_
(14.46)
|   |   |   |   |   |   |   |   start > 385513
```

```
|   |   |   |   |   |   |   |   |   start <= 390303: cytoplasm_
(36.71)
|   |   |   |   |   |   |   |   |   start > 390303: mitochondrion_
(13.07)
|   |   |   |   |   |   start > 393537
|   |   |   |   |   |   |   start <= 407106
|   |   |   |   |   |   |   |   start <= 397254: cell_cortex_
(20.14)
|   |   |   |   |   |   |   |   start > 397254: cellular_component_
(35.82)
|   |   |   |   |   |   |   start > 407106
|   |   |   |   |   |   |   |   start <= 456591
|   |   |   |   |   |   |   |   |   start <= 420075
|   |   |   |   |   |   |   |   |   |   start <= 412910: nucleus_
(23.72)
|   |   |   |   |   |   |   |   |   |   start > 412910
|   |   |   |   |   |   |   |   |   |   |   start <= 417552:
cytoplasm_ (20.92)
|   |   |   |   |   |   |   |   |   |   |   start > 417552:
peroxisome_ (23.34)
|   |   |   |   |   |   |   |   |   start > 420075
|   |   |   |   |   |   |   |   |   |   start <= 423726:
cytoskeleton_ (31.06/11.11)
|   |   |   |   |   |   |   |   |   |   start > 423726: nucleus_
(55.42)
|   |   |   |   |   |   |   |   start > 456591
|   |   |   |   |   |   |   |   |   start <= 475340:
cellular_component_ (16.41)
|   |   |   |   |   |   |   |   |   start > 475340: cytoplasm_
(18.74)
|   |   |   |   |   start > 475778
|   |   |   |   |   |   start <= 486826
|   |   |   |   |   |   |   start <= 480990
|   |   |   |   |   |   |   |   neigh_strand = W: mitochondrion_
(29.42/16.82)
|   |   |   |   |   |   |   |   neigh_strand = C: plasma_membrane_
(31.41/20.34)
|   |   |   |   |   |   |   start > 480990
|   |   |   |   |   |   |   |   start <= 484845: membrane_
(45.4/20.92)
|   |   |   |   |   |   |   |   start > 484845: chromosome_ (14.53)
|   |   |   |   |   |   start > 486826
|   |   |   |   |   |   |   start <= 499079
|   |   |   |   |   |   |   |   start <= 498422
|   |   |   |   |   |   |   |   |   start <= 491931: cytoplasm_
(14.8)
|   |   |   |   |   |   |   |   |   start > 491931: mitochondrion_
(38.88)
|   |   |   |   |   |   |   |   start > 498422: cellular_component_
(19.87)
|   |   |   |   |   |   |   start > 499079
|   |   |   |   |   |   |   |   start <= 509363
|   |   |   |   |   |   |   |   |   start <= 502388
```

```
|   |   |   |   |   |   |   |   |   |   distance <= 3124:
plasma_membrane_ (19.41/6.39)
|   |   |   |   |   |   |   |   |   |   distance > 3124: cytoplasm_
(5.86/2.0)
|   |   |   |   |   |   |   |   |   start > 502388: ribosome_
(12.27)
|   |   |   |   |   |   |   |   start > 509363: cytoplasm_
(27.15/8.83)
|   |   |   strand = W
|   |   |   |   start <= 377702
|   |   |   |   |   start <= 302764
|   |   |   |   |   |   start <= 251103
|   |   |   |   |   |   |   start <= 230972
|   |   |   |   |   |   |   |   start <= 229337: nucleolus_ (17.37)
|   |   |   |   |   |   |   |   start > 229337: mitochondrion_
(14.63)
|   |   |   |   |   |   |   start > 230972
|   |   |   |   |   |   |   |   start <= 237941
|   |   |   |   |   |   |   |   |   start <= 234883
|   |   |   |   |   |   |   |   |   |   start <= 232135: cytoplasm_
(21.74)
|   |   |   |   |   |   |   |   |   |   start > 232135
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (9.54/1.76)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(33.48/14.55)
|   |   |   |   |   |   |   |   |   start > 234883:
cellular_component_ (17.39)
|   |   |   |   |   |   |   |   start > 237941
|   |   |   |   |   |   |   |   |   start <= 241666
|   |   |   |   |   |   |   |   |   |   start <= 239100:
endoplasmic_reticulum_ (24.76/11.41)
|   |   |   |   |   |   |   |   |   |   start > 239100: nucleolus_
(14.1)
|   |   |   |   |   |   |   |   |   start > 241666
|   |   |   |   |   |   |   |   |   |   start <= 246195
|   |   |   |   |   |   |   |   |   |   |   start <= 242584:
cytoplasm_ (7.73)
|   |   |   |   |   |   |   |   |   |   |   start > 242584
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
4348: nucleus_ (7.59/1.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 4348:
cytoplasm_ (2.91/0.86)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasm_ (11.11/4.47)
|   |   |   |   |   |   |   |   |   |   start > 246195:
mitochondrion_ (17.42)
|   |   |   |   |   |   start > 251103
|   |   |   |   |   |   |   start <= 278155
|   |   |   |   |   |   |   |   start <= 261593: cellular_component_
(10.14)
|   |   |   |   |   |   |   |   start > 261593
|   |   |   |   |   |   |   |   |   start <= 272629
```

```
|   |   |   |   |   |   |   |   |   |   start <= 267540: nucleus_
(20.06)
|   |   |   |   |   |   |   |   |   |   start > 267540:
mitochondrion_ (11.5)
|   |   |   |   |   |   |   |   |   start > 272629: nucleus_ (53.28)
|   |   |   |   |   |   |   start > 278155
|   |   |   |   |   |   |   |   start <= 280822
|   |   |   |   |   |   |   |   |   start <= 280233:
cellular_component_ (15.47)
|   |   |   |   |   |   |   |   |   start > 280233: cytoplasm_
(29.83/12.84)
|   |   |   |   |   |   |   |   start > 280822
|   |   |   |   |   |   |   |   |   start <= 288814: nucleolus_
(11.56)
|   |   |   |   |   |   |   |   |   start > 288814
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(13.06/5.14)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_component_ (18.56/5.53)
|   |   |   |   |   start > 302764
|   |   |   |   |   |   start <= 342352
|   |   |   |   |   |   |   start <= 333075
|   |   |   |   |   |   |   |   start <= 324769: cytoplasm_
(75.6/18.3)
|   |   |   |   |   |   |   |   start > 324769
|   |   |   |   |   |   |   |   |   start <= 328306
|   |   |   |   |   |   |   |   |   |   start <= 325601:
mitochondrion_ (7.04)
|   |   |   |   |   |   |   |   |   |   start > 325601:
Golgi_apparatus_ (14.89)
|   |   |   |   |   |   |   |   |   start > 328306
|   |   |   |   |   |   |   |   |   |   start <= 330313: cytoplasm_
(18.01)
|   |   |   |   |   |   |   |   |   |   start > 330313
|   |   |   |   |   |   |   |   |   |   |   start <= 332285:
membrane_ (13.69)
|   |   |   |   |   |   |   |   |   |   |   start > 332285:
cytoplasm_ (16.68)
|   |   |   |   |   |   |   start > 333075
|   |   |   |   |   |   |   |   start <= 338086
|   |   |   |   |   |   |   |   |   start <= 336340: ribosome_
(33.81/13.5)
|   |   |   |   |   |   |   |   |   start > 336340: cytoplasm_
(15.67)
|   |   |   |   |   |   |   |   start > 338086: mitochondrion_
(51.38/17.41)
|   |   |   |   |   |   start > 342352
|   |   |   |   |   |   |   start <= 349577
|   |   |   |   |   |   |   |   start <= 346046: cellular_component_
(29.55/14.19)
|   |   |   |   |   |   |   |   start > 346046: mitochondrion_
(17.4)
|   |   |   |   |   |   |   start > 349577
|   |   |   |   |   |   |   |   start <= 353628
```

```
|   |   |   |   |   |   |   |   |   start <= 352759
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
ribosome_ (6.51/2.79)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(4.23/1.06)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
ribosome_ (7.64/2.41)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: ribosome_ (4.27/1.91)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
ribosome_ (6.35/2.61)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: nucleus_ (3.4/0.71)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: ribosome_ (6.2/3.77)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
nucleus_ (2.45/1.03)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
cytoplasm_ (1.44/0.42)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: cytoplasm_ (4.03/0.56)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
ribosome_ (3.49/1.69)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (20.85/9.79)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: ribosome_ (1.27/0.2)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   start > 352759: cytoplasm_
(35.99/15.42)
|   |   |   |   |   |   |   |   start > 353628
|   |   |   |   |   |   |   |   |   start <= 358572
|   |   |   |   |   |   |   |   |   |   start <= 354818:
endoplasmic_reticulum_ (16.08)
|   |   |   |   |   |   |   |   |   |   start > 354818: chromosome_
(9.85)
|   |   |   |   |   |   |   |   |   start > 358572
|   |   |   |   |   |   |   |   |   |   start <= 360916: nucleus_
(12.37)
|   |   |   |   |   |   |   |   |   |   start > 360916
|   |   |   |   |   |   |   |   |   |   |   start <= 371752
|   |   |   |   |   |   |   |   |   |   |   |   start <= 370057
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 364156:
cellular_component_ (12.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 364156:
cytoplasm_ (29.92/10.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 370057:
cellular_component_ (18.67)
|   |   |   |   |   |   |   |   |   |   |   start > 371752
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (16.0/4.06)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasm_ (7.53/2.51)
|   |   |   |   start > 377702
|   |   |   |   |   start <= 412910
|   |   |   |   |   |   start <= 385513
|   |   |   |   |   |   |   start <= 381543
|   |   |   |   |   |   |   |   start <= 380575: membrane_ (17.88)
|   |   |   |   |   |   |   |   start > 380575: nucleolus_ (20.19)
|   |   |   |   |   |   |   start > 381543
|   |   |   |   |   |   |   |   start <= 383541:
endoplasmic_reticulum_ (42.87/25.92)
|   |   |   |   |   |   |   |   start > 383541:
extracellular_region_ (11.9)
|   |   |   |   |   |   start > 385513
|   |   |   |   |   |   |   start <= 402969
|   |   |   |   |   |   |   |   start <= 397254
|   |   |   |   |   |   |   |   |   start <= 393537
|   |   |   |   |   |   |   |   |   |   start <= 388729: nucleolus_
(12.94)
|   |   |   |   |   |   |   |   |   |   start > 388729
|   |   |   |   |   |   |   |   |   |   |   start <= 390303:
nucleus_ (11.74)
|   |   |   |   |   |   |   |   |   |   |   start > 390303:
nucleolus_ (7.27)
|   |   |   |   |   |   |   |   |   start > 393537: peroxisome_
(14.8)
```

```
|   |   |   |   |   |   |   |   start > 397254: nucleus_
(52.05/18.65)
|   |   |   |   |   |   |   start > 402969
|   |   |   |   |   |   |   |   start <= 411231
|   |   |   |   |   |   |   |   |   start <= 407106: mitochondrion_
(12.68)
|   |   |   |   |   |   |   |   |   start > 407106: nucleolus_
(15.65)
|   |   |   |   |   |   |   |   start > 411231: chromosome_ (18.49)
|   |   |   |   |   start > 412910
|   |   |   |   |   |   start <= 451327
|   |   |   |   |   |   |   start <= 445713
|   |   |   |   |   |   |   |   start <= 439344
|   |   |   |   |   |   |   |   |   start <= 423075
|   |   |   |   |   |   |   |   |   |   start <= 420075: cytoplasm_
(20.96)
|   |   |   |   |   |   |   |   |   |   start > 420075:
mitochondrion_ (16.38)
|   |   |   |   |   |   |   |   |   start > 423075
|   |   |   |   |   |   |   |   |   |   start <= 429180: cytoplasm_
(36.51/11.83)
|   |   |   |   |   |   |   |   |   |   start > 429180: nucleus_
(12.78)
|   |   |   |   |   |   |   |   start > 439344
|   |   |   |   |   |   |   |   |   start <= 442182
|   |   |   |   |   |   |   |   |   |   start <= 440379: membrane_
(24.24/9.82)
|   |   |   |   |   |   |   |   |   |   start > 440379: nucleolus_
(14.68)
|   |   |   |   |   |   |   |   |   start > 442182
|   |   |   |   |   |   |   |   |   |   start <= 443829: cytoplasm_
(29.22/12.37)
|   |   |   |   |   |   |   |   |   |   start > 443829:
mitochondrion_ (28.84/16.88)
|   |   |   |   |   |   |   start > 445713
|   |   |   |   |   |   |   |   start <= 448335: cytoskeleton_
(32.72/11.28)
|   |   |   |   |   |   |   |   start > 448335: mitochondrion_
(17.01)
|   |   |   |   |   |   start > 451327
|   |   |   |   |   |   |   start <= 456591
|   |   |   |   |   |   |   |   start <= 452872: vacuole_
(27.63/8.19)
|   |   |   |   |   |   |   |   start > 452872
|   |   |   |   |   |   |   |   |   start <= 454229
|   |   |   |   |   |   |   |   |   |   start <= 453558:
cellular_component_ (13.21)
|   |   |   |   |   |   |   |   |   |   start > 453558
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 1819:
endoplasmic_reticulum_ (4.92/1.46)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 1819:
membrane_ (4.57/2.5)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F
```

```
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 1819:
endomembrane_system_ (4.88/1.44)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 1819:
membrane_ (5.48/2.74)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
endoplasmic_reticulum_ (11.35/5.71)
|   |   |   |   |   |   |   |   |   start > 454229:
cellular_component_ (17.48)
|   |   |   |   |   |   |   start > 456591
|   |   |   |   |   |   |   |   start <= 486826
|   |   |   |   |   |   |   |   |   start <= 484028
|   |   |   |   |   |   |   |   |   |   start <= 468219
|   |   |   |   |   |   |   |   |   |   |   start <= 462502
|   |   |   |   |   |   |   |   |   |   |   |   start <= 459299:
nucleus_ (11.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 459299
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1809: mitochondrion_ (5.46/2.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
1809: nucleus_ (5.9/2.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (19.2/9.06)
|   |   |   |   |   |   |   |   |   |   |   start > 462502
|   |   |   |   |   |   |   |   |   |   |   |   start <= 467228
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 466990:
cytoplasm_ (6.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 466990:
endoplasmic_reticulum_ (11.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 467228:
cytoplasm_ (12.38)
|   |   |   |   |   |   |   |   |   |   start > 468219
|   |   |   |   |   |   |   |   |   |   |   start <= 475778
|   |   |   |   |   |   |   |   |   |   |   |   start <= 470960:
mitochondrion_ (30.55/11.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 470960:
membrane_ (19.3)
|   |   |   |   |   |   |   |   |   |   |   start > 475778
|   |   |   |   |   |   |   |   |   |   |   |   start <= 480990:
cytoplasm_ (39.0/19.36)
|   |   |   |   |   |   |   |   |   |   |   |   start > 480990:
mitochondrion_ (15.11)
|   |   |   |   |   |   |   |   |   start > 484028
|   |   |   |   |   |   |   |   |   |   start <= 484845:
endoplasmic_reticulum_ (19.29)
|   |   |   |   |   |   |   |   |   |   start > 484845: cytoplasm_
(21.41)
|   |   |   |   |   |   |   |   start > 486826
|   |   |   |   |   |   |   |   |   start <= 499079
|   |   |   |   |   |   |   |   |   |   start <= 493896
|   |   |   |   |   |   |   |   |   |   |   start <= 490747
|   |   |   |   |   |   |   |   |   |   |   |   start <= 488657:
nucleus_ (19.51)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 488657:
endomembrane_system_ (15.05)
|   |   |   |   |   |   |   |   |   |   |   start > 490747
|   |   |   |   |   |   |   |   |   |   |   |   start <= 491931:
nucleolus_ (21.8/8.17)
|   |   |   |   |   |   |   |   |   |   |   |   start > 491931:
nucleus_ (17.63)
|   |   |   |   |   |   |   |   |   |   start > 493896:
cellular_component_ (12.34)
|   |   |   |   |   |   |   |   |   start > 499079
|   |   |   |   |   |   |   |   |   |   start <= 506319
|   |   |   |   |   |   |   |   |   |   |   start <= 502388:
vacuole_ (16.85)
|   |   |   |   |   |   |   |   |   |   |   start > 502388:
endoplasmic_reticulum_ (13.57)
|   |   |   |   |   |   |   |   |   |   start > 506319
|   |   |   |   |   |   |   |   |   |   |   start <= 512732:
nucleus_ (47.59/9.86)
|   |   |   |   |   |   |   |   |   |   |   start > 512732:
mitochondrion_ (19.57)
|   start > 517532
|   |   start <= 551499
|   |   |   start <= 525392
|   |   |   |   start <= 521737: cellular_component_ (45.05)
|   |   |   |   start > 521737: cell_wall_ (14.22)
|   |   |   start > 525392: cellular_component_ (98.67)
|   |   start > 551499
|   |   |   start <= 554396
|   |   |   |   start <= 552099: vacuole_ (9.41)
|   |   |   |   start > 552099: cytoplasm_ (9.9)
|   |   |   start > 554396: cellular_component_ (18.2)
```

For Molecular Function

```
|   start <= 209699
|   |   start <= 151299
|   |   |   start <= 117809
|   |   |   |   start <= 85367
|   |   |   |   |   start <= 34075
|   |   |   |   |   |   start <= 21780
|   |   |   |   |   |   |   start <= 3310: helicase_activity_ (5.29)
|   |   |   |   |   |   |   start > 3310
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 15665
|   |   |   |   |   |   |   |   |   |   start <= 6400:
molecular_function_ (17.28)
|   |   |   |   |   |   |   |   |   |   start > 6400
|   |   |   |   |   |   |   |   |   |   |   start <= 10211:
transporter_activity_ (6.44)
|   |   |   |   |   |   |   |   |   |   |   start > 10211:
molecular_function_ (11.25)
|   |   |   |   |   |   |   |   |   start > 15665:
transporter_activity_ (12.29)
```

```
|   |   |   |   |   |   |   |   strand = W: molecular_function_
(60.12)
|   |   |   |   |   |   start > 21780
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 26239: RNA_binding_ (13.89)
|   |   |   |   |   |   |   |   start > 26239
|   |   |   |   |   |   |   |   |   start <= 32754:
hydrolase_activity_ (5.53)
|   |   |   |   |   |   |   |   |   start > 32754: RNA_binding_
(10.47)
|   |   |   |   |   |   |   strand = W: transporter_activity_
(12.69)
|   |   |   |   |   start > 34075
|   |   |   |   |   |   start <= 40082
|   |   |   |   |   |   |   start <= 38506
|   |   |   |   |   |   |   |   start <= 36023:
structural_molecule_activity_ (13.19)
|   |   |   |   |   |   |   |   start > 36023: transferase_activity_
(13.64)
|   |   |   |   |   |   |   start > 38506: protein_binding_ (25.43)
|   |   |   |   |   |   start > 40082
|   |   |   |   |   |   |   start <= 69545
|   |   |   |   |   |   |   |   start <= 67453
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 65856
|   |   |   |   |   |   |   |   |   |   |   start <= 62753:
molecular_function_ (63.35)
|   |   |   |   |   |   |   |   |   |   |   start > 62753
|   |   |   |   |   |   |   |   |   |   |   |   start <= 64155:
hydrolase_activity_ (10.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 64155:
molecular_function_ (9.42)
|   |   |   |   |   |   |   |   |   |   start > 65856:
transcription_regulator_activity_ (10.52)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 54849
|   |   |   |   |   |   |   |   |   |   |   start <= 48761:
signal_transducer_activity_ (14.45)
|   |   |   |   |   |   |   |   |   |   |   start > 48761:
transcription_regulator_activity_ (45.23)
|   |   |   |   |   |   |   |   |   |   start > 54849
|   |   |   |   |   |   |   |   |   |   |   start <= 56647:
RNA_binding_ (8.14)
|   |   |   |   |   |   |   |   |   |   |   start > 56647:
molecular_function_ (11.13)
|   |   |   |   |   |   |   |   start > 67453: protein_binding_
(19.05)
|   |   |   |   |   |   |   start > 69545
|   |   |   |   |   |   |   |   start <= 78932
|   |   |   |   |   |   |   |   |   start <= 74241
|   |   |   |   |   |   |   |   |   |   strand = C:
transporter_activity_ (11.22)
|   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (28.66)
```

```
|   |   |   |   |   |   |   |   |   start > 74241
|   |   |   |   |   |   |   |   |   |   start <= 75409
|   |   |   |   |   |   |   |   |   |   |   start <= 74696:
molecular_function_ (16.41)
|   |   |   |   |   |   |   |   |   |   |   start > 74696:
structural_molecule_activity_ (13.15)
|   |   |   |   |   |   |   |   |   |   start > 75409:
molecular_function_ (61.48)
|   |   |   |   |   |   |   |   start > 78932
|   |   |   |   |   |   |   |   |   start <= 81612:
transferase_activity_ (10.72)
|   |   |   |   |   |   |   |   |   start > 81612
|   |   |   |   |   |   |   |   |   |   start <= 85056
|   |   |   |   |   |   |   |   |   |   |   start <= 83717:
molecular_function_ (6.31)
|   |   |   |   |   |   |   |   |   |   |   start > 83717:
transcription_regulator_activity_ (25.7/11.67)
|   |   |   |   |   |   |   |   |   |   start > 85056:
molecular_function_ (11.01)
|   |   |   |   start > 85367
|   |   |   |   |   start <= 104272
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 97933
|   |   |   |   |   |   |   |   start <= 94506:
transporter_activity_ (4.42)
|   |   |   |   |   |   |   |   start > 94506:
protein_kinase_activity_ (16.58)
|   |   |   |   |   |   |   start > 97933
|   |   |   |   |   |   |   |   start <= 99215: molecular_function_
(9.32)
|   |   |   |   |   |   |   |   start > 99215: transferase_activity_
(18.37)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 99215
|   |   |   |   |   |   |   |   neigh_strand = W:
structural_molecule_activity_ (8.01/3.01)
|   |   |   |   |   |   |   |   neigh_strand = C: RNA_binding_
(18.83/6.48)
|   |   |   |   |   |   |   start > 99215
|   |   |   |   |   |   |   |   start <= 102607: protein_binding_
(13.81)
|   |   |   |   |   |   |   |   start > 102607: RNA_binding_ (9.1)
|   |   |   |   |   start > 104272
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 114912
|   |   |   |   |   |   |   |   start <= 113089
|   |   |   |   |   |   |   |   |   start <= 111312:
molecular_function_ (6.21)
|   |   |   |   |   |   |   |   |   start > 111312:
phosphoprotein_phosphatase_activity_ (16.03)
|   |   |   |   |   |   |   |   start > 113089: hydrolase_activity_
(13.11)
|   |   |   |   |   |   |   start > 114912
```

```
|   |   |   |   |   |   |   |   start <= 115896: protein_binding_
(14.09)
|   |   |   |   |   |   |   |   start > 115896: molecular_function_
(13.27)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 107821
|   |   |   |   |   |   |   |   start <= 106050: molecular_function_
(13.79)
|   |   |   |   |   |   |   |   start > 106050:
oxidoreductase_activity_ (9.67)
|   |   |   |   |   |   |   start > 107821
|   |   |   |   |   |   |   |   start <= 113089:
transporter_activity_ (14.68)
|   |   |   |   |   |   |   |   start > 113089:
transcription_regulator_activity_ (9.53)
|   |   |   start > 117809
|   |   |   |   strand = C
|   |   |   |   |   start <= 138687
|   |   |   |   |   |   start <= 123585
|   |   |   |   |   |   |   start <= 122760: molecular_function_
(52.24/11.35)
|   |   |   |   |   |   |   start > 122760: oxidoreductase_activity_
(10.56)
|   |   |   |   |   |   start > 123585
|   |   |   |   |   |   |   start <= 132040
|   |   |   |   |   |   |   |   start <= 127774: molecular_function_
(12.47)
|   |   |   |   |   |   |   |   start > 127774:
transferase_activity_ (8.24)
|   |   |   |   |   |   |   start > 132040: molecular_function_
(26.28)
|   |   |   |   |   start > 138687
|   |   |   |   |   |   start <= 143989
|   |   |   |   |   |   |   start <= 141395: lyase_activity_ (11.02)
|   |   |   |   |   |   |   start > 141395: ligase_activity_ (13.42)
|   |   |   |   |   |   start > 143989
|   |   |   |   |   |   |   start <= 149218
|   |   |   |   |   |   |   |   start <= 146307: molecular_function_
(12.1)
|   |   |   |   |   |   |   |   start > 146307:
structural_molecule_activity_ (9.65)
|   |   |   |   |   |   |   start > 149218: molecular_function_
(25.67)
|   |   |   |   strand = W
|   |   |   |   |   start <= 133100
|   |   |   |   |   |   start <= 127774
|   |   |   |   |   |   |   start <= 126515:
structural_molecule_activity_ (16.13)
|   |   |   |   |   |   |   start > 126515: ligase_activity_ (14.45)
|   |   |   |   |   |   start > 127774
|   |   |   |   |   |   |   start <= 129475: transporter_activity_
(13.92)
|   |   |   |   |   |   |   start > 129475: protein_binding_ (21.31)
|   |   |   |   |   start > 133100
```

```
|   |   |   |   |   |   start <= 138687
|   |   |   |   |   |   |   start <= 134314: molecular_function_
(19.42)
|   |   |   |   |   |   |   start > 134314
|   |   |   |   |   |   |   |   start <= 134547: RNA_binding_
(12.66)
|   |   |   |   |   |   |   |   start > 134547: molecular_function_
(15.32)
|   |   |   |   |   |   start > 138687
|   |   |   |   |   |   |   start <= 146307: ligase_activity_
(15.86)
|   |   |   |   |   |   |   start > 146307: molecular_function_
(11.62)
|   |   start > 151299
|   |   |   start <= 172963
|   |   |   |   strand = C
|   |   |   |   |   start <= 167427: peptidase_activity_
(71.76/16.76)
|   |   |   |   |   start > 167427
|   |   |   |   |   |   start <= 170337
|   |   |   |   |   |   |   start <= 168554: molecular_function_
(10.81)
|   |   |   |   |   |   |   start > 168554: protein_kinase_activity_
(30.87/11.75)
|   |   |   |   |   |   start > 170337: helicase_activity_ (15.27)
|   |   |   |   strand = W
|   |   |   |   |   start <= 159431
|   |   |   |   |   |   start <= 151659: motor_activity_ (18.37)
|   |   |   |   |   |   start > 151659: transferase_activity_
(23.64)
|   |   |   |   |   start > 159431: hydrolase_activity_
(46.34/20.09)
|   |   |   start > 172963
|   |   |   |   start <= 186802
|   |   |   |   |   start <= 180338: molecular_function_ (70.85)
|   |   |   |   |   start > 180338
|   |   |   |   |   |   strand = C: molecular_function_ (17.43)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 181970:
oxidoreductase_activity_ (17.02)
|   |   |   |   |   |   |   start > 181970:
translation_regulator_activity_ (16.19)
|   |   |   |   start > 186802
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 198278
|   |   |   |   |   |   |   start <= 190536
|   |   |   |   |   |   |   |   start <= 187917: hydrolase_activity_
(38.33/17.14)
|   |   |   |   |   |   |   |   start > 187917:
transcription_regulator_activity_ (12.96)
|   |   |   |   |   |   |   start > 190536: hydrolase_activity_
(52.56)
|   |   |   |   |   |   start > 198278: peptidase_activity_ (13.05)
|   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   start <= 198278
|   |   |   |   |   |   |   start <= 190536
|   |   |   |   |   |   |   |   start <= 187917: molecular_function_
(15.07)
|   |   |   |   |   |   |   |   start > 187917:
oxidoreductase_activity_ (25.59)
|   |   |   |   |   |   |   start > 190536: molecular_function_
(22.98)
|   |   |   |   |   |   start > 198278
|   |   |   |   |   |   |   start <= 207648
|   |   |   |   |   |   |   |   start <= 204600:
transporter_activity_ (19.73)
|   |   |   |   |   |   |   |   start > 204600
|   |   |   |   |   |   |   |   |   start <= 206455:
hydrolase_activity_ (22.09)
|   |   |   |   |   |   |   |   |   start > 206455:
transporter_activity_ (17.09)
|   |   |   |   |   |   |   start > 207648
|   |   |   |   |   |   |   |   start <= 209469: molecular_function_
(12.26)
|   |   |   |   |   |   |   |   start > 209469:
oxidoreductase_activity_ (16.18)
|   start > 209699
|   |   strand = C
|   |   |   start <= 296450
|   |   |   |   start <= 276766
|   |   |   |   |   start <= 222480
|   |   |   |   |   |   start <= 214720: molecular_function_ (43.61)
|   |   |   |   |   |   start > 214720
|   |   |   |   |   |   |   start <= 218845
|   |   |   |   |   |   |   |   start <= 217836: DNA_binding_
(17.07)
|   |   |   |   |   |   |   |   start > 217836: isomerase_activity_
(15.41)
|   |   |   |   |   |   |   start > 218845
|   |   |   |   |   |   |   |   start <= 220727:
transcription_regulator_activity_ (11.26)
|   |   |   |   |   |   |   |   start > 220727:
enzyme_regulator_activity_ (13.11)
|   |   |   |   |   start > 222480
|   |   |   |   |   |   start <= 256362
|   |   |   |   |   |   |   start <= 225171
|   |   |   |   |   |   |   |   start <= 223760: hydrolase_activity_
(16.95)
|   |   |   |   |   |   |   |   start > 223760:
oxidoreductase_activity_ (17.55)
|   |   |   |   |   |   |   start > 225171
|   |   |   |   |   |   |   |   start <= 234883
|   |   |   |   |   |   |   |   |   start <= 227143:
protein_binding_ (12.51)
|   |   |   |   |   |   |   |   |   start > 227143
|   |   |   |   |   |   |   |   |   |   start <= 230972:
helicase_activity_ (11.61)
```

```
|   |   |   |   |   |   |   |   |   |   start > 230972: RNA_binding_
(8.6)
|   |   |   |   |   |   |   |   start > 234883
|   |   |   |   |   |   |   |   |   start <= 242584:
molecular_function_ (14.43)
|   |   |   |   |   |   |   |   |   start > 242584
|   |   |   |   |   |   |   |   |   |   start <= 251103:
hydrolase_activity_ (13.53)
|   |   |   |   |   |   |   |   |   |   start > 251103:
protein_binding_ (8.36)
|   |   |   |   |   |   start > 256362
|   |   |   |   |   |   |   start <= 267540
|   |   |   |   |   |   |   |   start <= 261593:
protein_kinase_activity_ (12.2)
|   |   |   |   |   |   |   |   start > 261593: molecular_function_
(30.05)
|   |   |   |   |   |   |   start > 267540: protein_kinase_activity_
(20.41)
|   |   |   |   start > 276766
|   |   |   |   |   start <= 286772
|   |   |   |   |   |   start <= 283300: RNA_binding_ (20.12)
|   |   |   |   |   |   start > 283300
|   |   |   |   |   |   |   start <= 284627: protein_binding_
(12.84)
|   |   |   |   |   |   |   start > 284627: ligase_activity_ (9.15)
|   |   |   |   |   start > 286772: transporter_activity_ (42.22)
|   |   |   start > 296450
|   |   |   |   start <= 385513
|   |   |   |   |   start <= 367895
|   |   |   |   |   |   start <= 320417: molecular_function_ (66.42)
|   |   |   |   |   |   start > 320417
|   |   |   |   |   |   |   start <= 338086
|   |   |   |   |   |   |   |   start <= 330313:
structural_molecule_activity_ (15.02)
|   |   |   |   |   |   |   |   start > 330313: lyase_activity_
(24.08)
|   |   |   |   |   |   |   start > 338086
|   |   |   |   |   |   |   |   start <= 349577
|   |   |   |   |   |   |   |   |   start <= 342352:
molecular_function_ (16.11)
|   |   |   |   |   |   |   |   |   start > 342352: DNA_binding_
(12.03)
|   |   |   |   |   |   |   |   start > 349577
|   |   |   |   |   |   |   |   |   start <= 362118:
molecular_function_ (21.46)
|   |   |   |   |   |   |   |   |   start > 362118
|   |   |   |   |   |   |   |   |   |   start <= 364156:
structural_molecule_activity_ (12.03)
|   |   |   |   |   |   |   |   |   |   start > 364156:
molecular_function_ (18.93)
|   |   |   |   |   start > 367895
|   |   |   |   |   |   start <= 374313
|   |   |   |   |   |   |   start <= 371752
```

```
|   |   |   |   |   |   |   |   start <= 370057: peptidase_activity_
(12.57)
|   |   |   |   |   |   |   |   start > 370057: protein_binding_
(23.09)
|   |   |   |   |   |   |   start > 371752: protein_kinase_activity_
(17.73)
|   |   |   |   |   |   start > 374313
|   |   |   |   |   |   |   start <= 377702:
enzyme_regulator_activity_ (26.53)
|   |   |   |   |   |   |   start > 377702
|   |   |   |   |   |   |   |   start <= 380575: molecular_function_
(18.97)
|   |   |   |   |   |   |   |   start > 380575:
structural_molecule_activity_ (16.8)
|   |   |   |   start > 385513
|   |   |   |   |   start <= 456591
|   |   |   |   |   |   start <= 417552
|   |   |   |   |   |   |   start <= 388729: hydrolase_activity_
(29.59/12.75)
|   |   |   |   |   |   |   start > 388729
|   |   |   |   |   |   |   |   start <= 407106
|   |   |   |   |   |   |   |   |   start <= 393537
|   |   |   |   |   |   |   |   |   |   start <= 390303:
molecular_function_ (16.02)
|   |   |   |   |   |   |   |   |   |   start > 390303:
structural_molecule_activity_ (6.61)
|   |   |   |   |   |   |   |   |   start > 393537:
molecular_function_ (43.15)
|   |   |   |   |   |   |   |   start > 407106
|   |   |   |   |   |   |   |   |   start <= 412910:
protein_binding_ (14.22)
|   |   |   |   |   |   |   |   |   start > 412910:
molecular_function_ (19.51)
|   |   |   |   |   |   start > 417552
|   |   |   |   |   |   |   start <= 423726: protein_binding_
(34.83)
|   |   |   |   |   |   |   start > 423726
|   |   |   |   |   |   |   |   start <= 429180: helicase_activity_
(21.75)
|   |   |   |   |   |   |   |   start > 429180
|   |   |   |   |   |   |   |   |   start <= 436950: RNA_binding_
(15.17)
|   |   |   |   |   |   |   |   |   start > 436950: protein_binding_
(18.66)
|   |   |   |   |   start > 456591
|   |   |   |   |   |   start <= 502388
|   |   |   |   |   |   |   start <= 499079
|   |   |   |   |   |   |   |   start <= 484845
|   |   |   |   |   |   |   |   |   start <= 480990:
molecular_function_ (49.24)
|   |   |   |   |   |   |   |   |   start > 480990:
hydrolase_activity_ (16.51)
|   |   |   |   |   |   |   |   start > 484845
|   |   |   |   |   |   |   |   |   start <= 491931
```

```
|   |   |   |   |   |   |   |   |   |   start <= 486826:
molecular_function_ (14.84)
|   |   |   |   |   |   |   |   |   |   start > 486826:
protein_binding_ (11.48)
|   |   |   |   |   |   |   |   |   start > 491931:
molecular_function_ (49.38)
|   |   |   |   |   |   |   start > 499079: hydrolase_activity_
(11.88)
|   |   |   |   |   |   start > 502388
|   |   |   |   |   |   |   start <= 509363:
structural_molecule_activity_ (15.91)
|   |   |   |   |   |   |   start > 509363: molecular_function_
(55.6)
|   |   strand = W
|   |   |   start <= 272629
|   |   |   |   start <= 234883
|   |   |   |   |   start <= 223760
|   |   |   |   |   |   start <= 210842: protein_binding_ (18.2)
|   |   |   |   |   |   start > 210842
|   |   |   |   |   |   |   start <= 220110: molecular_function_
(49.01)
|   |   |   |   |   |   |   start > 220110: protein_binding_ (18.1)
|   |   |   |   |   start > 223760
|   |   |   |   |   |   start <= 230972
|   |   |   |   |   |   |   start <= 229337: RNA_binding_ (11.03)
|   |   |   |   |   |   |   start > 229337: lyase_activity_ (20.27)
|   |   |   |   |   |   start > 230972: transferase_activity_
(33.74)
|   |   |   |   start > 234883
|   |   |   |   |   start <= 241666
|   |   |   |   |   |   start <= 237941: enzyme_regulator_activity_
(18.85)
|   |   |   |   |   |   start > 237941
|   |   |   |   |   |   |   start <= 239100: isomerase_activity_
(11.06)
|   |   |   |   |   |   |   start > 239100: RNA_binding_ (15.93)
|   |   |   |   |   start > 241666
|   |   |   |   |   |   start <= 267540
|   |   |   |   |   |   |   start <= 251103
|   |   |   |   |   |   |   |   start <= 246195
|   |   |   |   |   |   |   |   |   start <= 242584:
molecular_function_ (11.41)
|   |   |   |   |   |   |   |   |   start > 242584:
hydrolase_activity_ (8.28)
|   |   |   |   |   |   |   |   start > 246195:
phosphoprotein_phosphatase_activity_ (17.05)
|   |   |   |   |   |   |   start > 251103: molecular_function_
(32.08)
|   |   |   |   |   |   start > 267540: protein_binding_ (13.5)
|   |   |   start > 272629
|   |   |   |   start <= 491931
|   |   |   |   |   start <= 380575
|   |   |   |   |   |   start <= 274176:
transcription_regulator_activity_ (32.18/11.31)
```

```
|   |   |   |   |   |   start > 274176
|   |   |   |   |   |   |   start <= 341668
|   |   |   |   |   |   |   |   start <= 330313
|   |   |   |   |   |   |   |   |   start <= 288814
|   |   |   |   |   |   |   |   |   |   start <= 280822
|   |   |   |   |   |   |   |   |   |   |   start <= 278155
|   |   |   |   |   |   |   |   |   |   |   |   start <= 276766:
molecular_function_ (18.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 276766:
RNA_binding_ (12.38)
|   |   |   |   |   |   |   |   |   |   |   start > 278155:
molecular_function_ (37.34)
|   |   |   |   |   |   |   |   |   |   start > 280822: RNA_binding_
(13.99)
|   |   |   |   |   |   |   |   |   start > 288814
|   |   |   |   |   |   |   |   |   |   start <= 316575:
transferase_activity_ (32.33)
|   |   |   |   |   |   |   |   |   |   start > 316575
|   |   |   |   |   |   |   |   |   |   |   start <= 325601
|   |   |   |   |   |   |   |   |   |   |   |   start <= 320417:
molecular_function_ (17.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 320417
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 323412:
oxidoreductase_activity_ (20.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 323412:
molecular_function_ (40.96/12.23)
|   |   |   |   |   |   |   |   |   |   |   start > 325601
|   |   |   |   |   |   |   |   |   |   |   |   start <= 328306:
protein_binding_ (16.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 328306:
transferase_activity_ (14.23)
|   |   |   |   |   |   |   |   start > 330313
|   |   |   |   |   |   |   |   |   start <= 336340
|   |   |   |   |   |   |   |   |   |   start <= 333075:
molecular_function_ (34.21)
|   |   |   |   |   |   |   |   |   |   start > 333075:
peptidase_activity_ (19.5)
|   |   |   |   |   |   |   |   |   start > 336340:
molecular_function_ (41.59)
|   |   |   |   |   |   |   start > 341668
|   |   |   |   |   |   |   |   start <= 352759
|   |   |   |   |   |   |   |   |   start <= 346046
|   |   |   |   |   |   |   |   |   |   start <= 342352:
transporter_activity_ (19.71)
|   |   |   |   |   |   |   |   |   |   start > 342352:
transferase_activity_ (11.44)
|   |   |   |   |   |   |   |   |   start > 346046
|   |   |   |   |   |   |   |   |   |   start <= 349577:
DNA_binding_ (17.77)
|   |   |   |   |   |   |   |   |   |   start > 349577: RNA_binding_
(13.05)
|   |   |   |   |   |   |   |   start > 352759
|   |   |   |   |   |   |   |   |   start <= 353628:
molecular_function_ (24.53)
```

```
|   |   |   |   |   |   |   |   |   start > 353628
|   |   |   |   |   |   |   |   |   |   start <= 358572
|   |   |   |   |   |   |   |   |   |   |   start <= 354818:
transferase_activity_ (18.41)
|   |   |   |   |   |   |   |   |   |   |   start > 354818
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transcription_regulator_activity_ (4.01/0.53)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_binding_ (16.02/6.33)
|   |   |   |   |   |   |   |   |   |   start > 358572
|   |   |   |   |   |   |   |   |   |   |   start <= 360916:
molecular_function_ (19.41)
|   |   |   |   |   |   |   |   |   |   |   start > 360916
|   |   |   |   |   |   |   |   |   |   |   |   start <= 364156:
transferase_activity_ (9.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 364156
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 371752:
molecular_function_ (27.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 371752
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
377702: transferase_activity_ (15.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
377702: molecular_function_ (11.81)
|   |   |   |   |   start > 380575
|   |   |   |   |   |   start <= 442182
|   |   |   |   |   |   |   start <= 393537
|   |   |   |   |   |   |   |   start <= 385513
|   |   |   |   |   |   |   |   |   start <= 383541
|   |   |   |   |   |   |   |   |   |   start <= 381543:
RNA_binding_ (10.74)
|   |   |   |   |   |   |   |   |   |   start > 381543:
molecular_function_ (13.17)
|   |   |   |   |   |   |   |   |   start > 383541:
hydrolase_activity_ (20.52)
|   |   |   |   |   |   |   |   start > 385513
|   |   |   |   |   |   |   |   |   start <= 390303
|   |   |   |   |   |   |   |   |   |   start <= 388729:
nucleotidyltransferase_activity_ (13.34)
|   |   |   |   |   |   |   |   |   |   start > 388729: DNA_binding_
(13.94)
|   |   |   |   |   |   |   |   |   start > 390303: RNA_binding_
(19.91)
|   |   |   |   |   |   |   start > 393537
|   |   |   |   |   |   |   |   start <= 440379
|   |   |   |   |   |   |   |   |   start <= 411231
|   |   |   |   |   |   |   |   |   |   start <= 407106:
molecular_function_ (59.12)
|   |   |   |   |   |   |   |   |   |   start > 407106: RNA_binding_
(25.95)
|   |   |   |   |   |   |   |   |   start > 411231
|   |   |   |   |   |   |   |   |   |   start <= 423075:
molecular_function_ (53.05)
|   |   |   |   |   |   |   |   |   |   start > 423075
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 429180:
hydrolase_activity_ (13.25)
|   |   |   |   |   |   |   |   |   |   |   start > 429180:
molecular_function_ (32.46)
|   |   |   |   |   |   |   |   start > 440379: helicase_activity_
(14.99)
|   |   |   |   |   |   start > 442182
|   |   |   |   |   |   |   start <= 470960
|   |   |   |   |   |   |   |   start <= 452872
|   |   |   |   |   |   |   |   |   start <= 445713
|   |   |   |   |   |   |   |   |   |   start <= 443829:
protein_binding_ (33.06/11.76)
|   |   |   |   |   |   |   |   |   |   start > 443829:
molecular_function_ (19.21)
|   |   |   |   |   |   |   |   |   start > 445713
|   |   |   |   |   |   |   |   |   |   start <= 448335:
structural_molecule_activity_ (12.41)
|   |   |   |   |   |   |   |   |   |   start > 448335
|   |   |   |   |   |   |   |   |   |   |   start <= 451327:
lyase_activity_ (13.63)
|   |   |   |   |   |   |   |   |   |   |   start > 451327:
transporter_activity_ (11.16)
|   |   |   |   |   |   |   |   start > 452872
|   |   |   |   |   |   |   |   |   start <= 459299
|   |   |   |   |   |   |   |   |   |   start <= 456591
|   |   |   |   |   |   |   |   |   |   |   start <= 454229
|   |   |   |   |   |   |   |   |   |   |   |   start <= 453558:
molecular_function_ (10.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 453558:
oxidoreductase_activity_ (9.19)
|   |   |   |   |   |   |   |   |   |   |   start > 454229:
molecular_function_ (13.46)
|   |   |   |   |   |   |   |   |   |   start > 456591: DNA_binding_
(25.82/11.32)
|   |   |   |   |   |   |   |   |   start > 459299
|   |   |   |   |   |   |   |   |   |   start <= 462502:
oxidoreductase_activity_ (14.29)
|   |   |   |   |   |   |   |   |   |   start > 462502
|   |   |   |   |   |   |   |   |   |   |   start <= 468219
|   |   |   |   |   |   |   |   |   |   |   |   start <= 467228
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 466990:
molecular_function_ (6.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 466990:
protein_binding_ (21.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 467228:
molecular_function_ (12.24)
|   |   |   |   |   |   |   |   |   |   |   start > 468219:
oxidoreductase_activity_ (9.13)
|   |   |   |   |   |   |   start > 470960
|   |   |   |   |   |   |   |   start <= 488657
|   |   |   |   |   |   |   |   |   start <= 484028
|   |   |   |   |   |   |   |   |   |   start <= 480990:
molecular_function_ (34.07)
```

```
|   |   |   |   |   |   |   |   |   |   start > 480990:
hydrolase_activity_ (12.22)
|   |   |   |   |   |   |   |   |   start > 484028
|   |   |   |   |   |   |   |   |   |   start <= 484845:
transferase_activity_ (21.12)
|   |   |   |   |   |   |   |   |   |   start > 484845:
molecular_function_ (32.44)
|   |   |   |   |   |   |   |   start > 488657
|   |   |   |   |   |   |   |   |   start <= 490747:
protein_binding_ (17.68)
|   |   |   |   |   |   |   |   |   start > 490747: RNA_binding_
(19.31)
|   |   |   |   start > 491931
|   |   |   |   |   start <= 512732
|   |   |   |   |   |   start <= 506319
|   |   |   |   |   |   |   start <= 499079
|   |   |   |   |   |   |   |   start <= 493896: molecular_function_
(17.91)
|   |   |   |   |   |   |   |   start > 493896: peptidase_activity_
(14.64)
|   |   |   |   |   |   |   start > 499079: molecular_function_
(37.22)
|   |   |   |   |   |   start > 506319
|   |   |   |   |   |   |   start <= 509363:
protein_kinase_activity_ (22.34)
|   |   |   |   |   |   |   start > 509363: DNA_binding_
(48.3/30.44)
|   |   |   |   |   start > 512732
|   |   |   |   |   |   start <= 521737: transferase_activity_
(38.99)
|   |   |   |   |   |   start > 521737
|   |   |   |   |   |   |   start <= 541651: molecular_function_
(78.06)
|   |   |   |   |   |   |   start > 541651
|   |   |   |   |   |   |   |   start <= 554396
|   |   |   |   |   |   |   |   |   start <= 552099:
hydrolase_activity_ (10.53)
|   |   |   |   |   |   |   |   |   start > 552099:
oxidoreductase_activity_ (6.69)
|   |   |   |   |   |   |   |   start > 554396: molecular_function_
(19.14)
```

For Biological Process

```
|   start <= 452872
|   |   start <= 219886
|   |   |   stop <= 149568
|   |   |   |   start <= 48761
|   |   |   |   |   start <= 34075
|   |   |   |   |   |   start <= 15665
|   |   |   |   |   |   |   start <= 10211
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 6400:
biological_process_ (22.31)
```

```
|   |   |   |   |   |   |   |   |   start > 6400: transport_ (5.9)
|   |   |   |   |   |   |   |   strand = W: response_to_stress_
(20.85)
|   |   |   |   |   |   |   start > 10211
|   |   |   |   |   |   |   |   start <= 13563: biological_process_
(22.02)
|   |   |   |   |   |   |   |   start > 13563
|   |   |   |   |   |   |   |   |   start <= 14899:
cell_wall_organization_and_biogenesis_ (16.02)
|   |   |   |   |   |   |   |   |   start > 14899:
biological_process_ (12.38)
|   |   |   |   |   |   start > 15665
|   |   |   |   |   |   |   start <= 25506
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 21780: transport_
(8.23)
|   |   |   |   |   |   |   |   |   start > 21780:
RNA_metabolic_process_ (12.24)
|   |   |   |   |   |   |   |   strand = W:
ribosome_biogenesis_and_assembly_ (17.89)
|   |   |   |   |   |   |   start > 25506
|   |   |   |   |   |   |   |   start <= 32754: transport_ (36.31)
|   |   |   |   |   |   |   |   start > 32754:
ribosome_biogenesis_and_assembly_ (9.94)
|   |   |   |   |   start > 34075
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 36023: translation_ (11.58)
|   |   |   |   |   |   |   start > 36023
|   |   |   |   |   |   |   |   start <= 38506: biological_process_
(16.44)
|   |   |   |   |   |   |   |   start > 38506
|   |   |   |   |   |   |   |   |   start <= 40082: vesicle-
mediated_transport_ (12.57)
|   |   |   |   |   |   |   |   |   start > 40082:
biological_process_ (15.83)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 40082:
protein_catabolic_process_ (20.52)
|   |   |   |   |   |   |   start > 40082: response_to_stress_
(25.53)
|   |   |   |   start > 48761
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 85056
|   |   |   |   |   |   |   start <= 78932
|   |   |   |   |   |   |   |   start <= 65856
|   |   |   |   |   |   |   |   |   start <= 62753:
biological_process_ (28.41)
|   |   |   |   |   |   |   |   |   start > 62753
|   |   |   |   |   |   |   |   |   |   start <= 64155: cell_cycle_
(11.11)
|   |   |   |   |   |   |   |   |   |   start > 64155:
biological_process_ (15.95)
|   |   |   |   |   |   |   |   start > 65856
|   |   |   |   |   |   |   |   |   start <= 75409
```

```
|   |   |   |   |   |   |   |   |   |   start <= 70273
|   |   |   |   |   |   |   |   |   |   |   start <= 67453:
DNA_metabolic_process_ (9.89)
|   |   |   |   |   |   |   |   |   |   |   start > 67453: vesicle-
mediated_transport_ (11.87)
|   |   |   |   |   |   |   |   |   |   start > 70273: transport_
(12.59)
|   |   |   |   |   |   |   |   |   start > 75409:
biological_process_ (28.16)
|   |   |   |   |   |   |   start > 78932
|   |   |   |   |   |   |   |   start <= 81612:
ribosome_biogenesis_and_assembly_ (15.79)
|   |   |   |   |   |   |   |   start > 81612
|   |   |   |   |   |   |   |   |   start <= 83717:
biological_process_ (14.64)
|   |   |   |   |   |   |   |   |   start > 83717: transcription_
(10.6)
|   |   |   |   |   |   start > 85056
|   |   |   |   |   |   |   start <= 115896
|   |   |   |   |   |   |   |   start <= 111312
|   |   |   |   |   |   |   |   |   start <= 97933
|   |   |   |   |   |   |   |   |   |   start <= 94506
|   |   |   |   |   |   |   |   |   |   |   start <= 85367:
translation_ (13.58)
|   |   |   |   |   |   |   |   |   |   |   start > 85367:
biological_process_ (7.16)
|   |   |   |   |   |   |   |   |   |   start > 94506:
pseudohyphal_growth_ (15.02)
|   |   |   |   |   |   |   |   |   start > 97933
|   |   |   |   |   |   |   |   |   |   start <= 99215:
DNA_metabolic_process_ (17.62)
|   |   |   |   |   |   |   |   |   |   start > 99215:
biological_process_ (25.24)
|   |   |   |   |   |   |   |   start > 111312
|   |   |   |   |   |   |   |   |   start <= 114912
|   |   |   |   |   |   |   |   |   |   start <= 113089:
nuclear_organization_and_biogenesis_ (12.46)
|   |   |   |   |   |   |   |   |   |   start > 113089: conjugation_
(17.76)
|   |   |   |   |   |   |   |   |   start > 114912:
membrane_organization_and_biogenesis_ (13.29)
|   |   |   |   |   |   |   start > 115896
|   |   |   |   |   |   |   |   start <= 132040
|   |   |   |   |   |   |   |   |   start <= 121678
|   |   |   |   |   |   |   |   |   |   start <= 117809:
translation_ (8.51)
|   |   |   |   |   |   |   |   |   |   start > 117809:
lipid_metabolic_process_ (12.98)
|   |   |   |   |   |   |   |   |   start > 121678
|   |   |   |   |   |   |   |   |   |   start <= 127774
|   |   |   |   |   |   |   |   |   |   |   start <= 122760:
biological_process_ (17.43)
|   |   |   |   |   |   |   |   |   |   |   start > 122760
|   |   |   |   |   |   |   |   |   |   |   |   start <= 123585
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
biological_process_ (18.12/6.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
response_to_stress_ (13.22/2.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 123585:
biological_process_ (16.92)
|   |   |   |   |   |   |   |   |   |   start > 127774:
DNA_metabolic_process_ (15.0)
|   |   |   |   |   |   |   |   start > 132040
|   |   |   |   |   |   |   |   |   start <= 138687
|   |   |   |   |   |   |   |   |   |   start <= 134547:
translation_ (11.54)
|   |   |   |   |   |   |   |   |   |   start > 134547: vesicle-
mediated_transport_ (11.91)
|   |   |   |   |   |   |   |   |   start > 138687
|   |   |   |   |   |   |   |   |   |   start <= 141395
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
biological_process_ (13.51/3.39)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
amino_acid_and_derivative_metabolic_process_ (13.65/5.75)
|   |   |   |   |   |   |   |   |   |   start > 141395
|   |   |   |   |   |   |   |   |   |   |   start <= 149218:
translation_ (30.66)
|   |   |   |   |   |   |   |   |   |   |   start > 149218:
biological_process_ (19.18)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 56647
|   |   |   |   |   |   |   start <= 54849
|   |   |   |   |   |   |   |   start <= 51109: meiosis_ (18.25)
|   |   |   |   |   |   |   |   start > 51109:
DNA_metabolic_process_ (11.57)
|   |   |   |   |   |   |   start > 54849
|   |   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = molecular_function_:
meiosis_ (9.58/2.78)
|   |   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transport_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
sporulation_ (1.9/0.5)
|   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: sporulation_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = membrane_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleus_: meiosis_
(3.04/0.7)
|   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = biological_process_:
sporulation_ (4.47/1.74)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_component_:
sporulation_ (7.41/1.42)
|   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: sporulation_ (1.58/0.54)
|   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: sporulation_ (1.28/0.64)
|   |   |   |   |   |   |   |   NeighGO_term = translation_:
meiosis_ (2.68/0.71)
|   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transcription_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
sporulation_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = electron_transport_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: sporulation_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: sporulation_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: sporulation_ (0.0)
|   |   |   |   |   |   start > 56647
|   |   |   |   |   |   |   start <= 107821
|   |   |   |   |   |   |   |   start <= 99215
|   |   |   |   |   |   |   |   |   start <= 74696
|   |   |   |   |   |   |   |   |   |   start <= 65856: translation_
(15.7)
|   |   |   |   |   |   |   |   |   |   start > 65856:
biological_process_ (46.25)
|   |   |   |   |   |   |   |   |   start > 74696
|   |   |   |   |   |   |   |   |   |   start <= 75409: translation_
(17.55)
|   |   |   |   |   |   |   |   |   |   start > 75409
|   |   |   |   |   |   |   |   |   |   |   start <= 85367:
DNA_metabolic_process_ (11.25)
|   |   |   |   |   |   |   |   |   |   |   start > 85367:
translation_ (7.96)
|   |   |   |   |   |   |   |   start > 99215
|   |   |   |   |   |   |   |   |   start <= 106050
|   |   |   |   |   |   |   |   |   |   start <= 102607: vesicle-
mediated_transport_ (24.5)
|   |   |   |   |   |   |   |   |   |   start > 102607
|   |   |   |   |   |   |   |   |   |   |   start <= 104272:
translation_ (7.81)
|   |   |   |   |   |   |   |   |   |   |   start > 104272: vesicle-
mediated_transport_ (18.53)
|   |   |   |   |   |   |   |   |   start > 106050:
cellular_respiration_ (22.22/10.91)
|   |   |   |   |   |   |   start > 107821
```

```
|   |   |   |   |   |   |   |   start <= 133100
|   |   |   |   |   |   |   |   |   start <= 127774
|   |   |   |   |   |   |   |   |   |   start <= 121678
|   |   |   |   |   |   |   |   |   |   |   start <= 113089:
transport_ (10.58)
|   |   |   |   |   |   |   |   |   |   |   start > 113089:
transcription_ (18.63)
|   |   |   |   |   |   |   |   |   |   start > 121678
|   |   |   |   |   |   |   |   |   |   |   start <= 126515:
translation_ (10.74)
|   |   |   |   |   |   |   |   |   |   |   start > 126515:
pseudohyphal_growth_ (17.13)
|   |   |   |   |   |   |   |   |   start > 127774
|   |   |   |   |   |   |   |   |   |   start <= 129475: vesicle-
mediated_transport_ (13.56)
|   |   |   |   |   |   |   |   |   |   start > 129475: meiosis_
(26.51/11.2)
|   |   |   |   |   |   |   |   start > 133100
|   |   |   |   |   |   |   |   |   start <= 134314: translation_
(27.62)
|   |   |   |   |   |   |   |   |   start > 134314
|   |   |   |   |   |   |   |   |   |   start <= 138687
|   |   |   |   |   |   |   |   |   |   |   start <= 134547
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2172:
transport_ (17.5/6.74)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2172:
biological_process_ (6.21/0.57)
|   |   |   |   |   |   |   |   |   |   |   start > 134547:
biological_process_ (16.98)
|   |   |   |   |   |   |   |   |   |   start > 138687: translation_
(8.67)
|   |   |   stop > 149568
|   |   |   |   start <= 187672
|   |   |   |   |   start <= 178212
|   |   |   |   |   |   start <= 167427
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 151659: biological_process_
(19.68)
|   |   |   |   |   |   |   |   start > 151659
|   |   |   |   |   |   |   |   |   start <= 160837:
protein_modification_process_ (18.04)
|   |   |   |   |   |   |   |   |   start > 160837
|   |   |   |   |   |   |   |   |   |   start <= 164704:
protein_catabolic_process_ (15.63)
|   |   |   |   |   |   |   |   |   |   start > 164704:
protein_modification_process_ (14.29)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 151659
|   |   |   |   |   |   |   |   |   start <= 150338:
cell_wall_organization_and_biogenesis_ (18.94)
|   |   |   |   |   |   |   |   |   start > 150338: cytokinesis_
(22.9)
|   |   |   |   |   |   |   |   start > 151659
```

```
|   |   |   |   |   |   |   |   |   start <= 159431:
amino_acid_and_derivative_metabolic_process_ (34.68)
|   |   |   |   |   |   |   |   |   start > 159431:
organelle_organization_and_biogenesis_ (18.4)
|   |   |   |   |   |   start > 167427
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 170337
|   |   |   |   |   |   |   |   |   start <= 168554:
biological_process_ (17.32)
|   |   |   |   |   |   |   |   |   start > 168554:
cell_wall_organization_and_biogenesis_ (22.12/9.39)
|   |   |   |   |   |   |   |   start > 170337
|   |   |   |   |   |   |   |   |   start <= 173337:
DNA_metabolic_process_ (18.8)
|   |   |   |   |   |   |   |   |   start > 173337:
ribosome_biogenesis_and_assembly_ (19.63)
|   |   |   |   |   |   |   strand = W: biological_process_ (51.53)
|   |   |   |   |   start > 178212
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 186802: DNA_metabolic_process_
(49.99/29.93)
|   |   |   |   |   |   |   start > 186802:
organelle_organization_and_biogenesis_ (17.45)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 180338
|   |   |   |   |   |   |   |   neigh_num <= 1:
nuclear_organization_and_biogenesis_ (11.71/3.14)
|   |   |   |   |   |   |   |   neigh_num > 1:
membrane_organization_and_biogenesis_ (17.35/4.82)
|   |   |   |   |   |   |   start > 180338
|   |   |   |   |   |   |   |   start <= 181970:
amino_acid_and_derivative_metabolic_process_ (23.08)
|   |   |   |   |   |   |   |   start > 181970: translation_ (15.96)
|   |   |   |   start > 187672
|   |   |   |   |   start <= 194801
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 190536: DNA_metabolic_process_
(20.24/9.2)
|   |   |   |   |   |   |   start > 190536
|   |   |   |   |   |   |   |   start <= 193538: response_to_stress_
(14.36)
|   |   |   |   |   |   |   |   start > 193538:
carbohydrate_metabolic_process_ (14.59)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 187917: RNA_metabolic_process_
(13.46)
|   |   |   |   |   |   |   start > 187917: electron_transport_
(17.37)
|   |   |   |   |   start > 194801
|   |   |   |   |   |   start <= 210842
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 198278:
carbohydrate_metabolic_process_ (7.29)
```

```
|   |   |   |   |   |   |   |   start > 198278:
generation_of_precursor_metabolites_and_energy_ (10.36)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 209469
|   |   |   |   |   |   |   |   |   start <= 198278:
biological_process_ (20.94)
|   |   |   |   |   |   |   |   |   start > 198278
|   |   |   |   |   |   |   |   |   |   start <= 207648
|   |   |   |   |   |   |   |   |   |   |   start <= 206455
|   |   |   |   |   |   |   |   |   |   |   |   start <= 204600:
transport_ (13.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 204600:
biological_process_ (14.72)
|   |   |   |   |   |   |   |   |   |   |   start > 206455:
transport_ (18.73)
|   |   |   |   |   |   |   |   |   |   start > 207648:
biological_process_ (12.89)
|   |   |   |   |   |   |   |   start > 209469
|   |   |   |   |   |   |   |   |   start <= 209699:
electron_transport_ (14.9)
|   |   |   |   |   |   |   |   |   start > 209699:
protein_catabolic_process_ (26.14/12.58)
|   |   |   |   |   |   start > 210842
|   |   |   |   |   |   |   start <= 214720: biological_process_
(65.67)
|   |   |   |   |   |   |   start > 214720
|   |   |   |   |   |   |   |   start <= 217836: transcription_
(18.08/6.9)
|   |   |   |   |   |   |   |   start > 217836
|   |   |   |   |   |   |   |   |   start <= 218845:
biological_process_ (18.28)
|   |   |   |   |   |   |   |   |   start > 218845: transcription_
(16.83)
|   |   start > 219886
|   |   |   start <= 333075
|   |   |   |   start <= 286772
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 242584
|   |   |   |   |   |   |   start <= 222480: cell_budding_ (23.63)
|   |   |   |   |   |   |   start > 222480
|   |   |   |   |   |   |   |   start <= 225171
|   |   |   |   |   |   |   |   |   start <= 223760:
ribosome_biogenesis_and_assembly_ (10.6)
|   |   |   |   |   |   |   |   |   start > 223760:
biological_process_ (19.15)
|   |   |   |   |   |   |   |   start > 225171
|   |   |   |   |   |   |   |   |   start <= 227143: translation_
(18.79)
|   |   |   |   |   |   |   |   |   start > 227143
|   |   |   |   |   |   |   |   |   |   start <= 234883:
ribosome_biogenesis_and_assembly_ (31.65)
|   |   |   |   |   |   |   |   |   |   start > 234883: translation_
(17.63)
|   |   |   |   |   |   start > 242584
```

```
|   |   |   |   |   |   |   start <= 276766
|   |   |   |   |   |   |   |   start <= 261593
|   |   |   |   |   |   |   |   |   start <= 256362
|   |   |   |   |   |   |   |   |   |   start <= 251103:
protein_modification_process_ (14.08)
|   |   |   |   |   |   |   |   |   |   start > 251103:
RNA_metabolic_process_ (24.02/10.43)
|   |   |   |   |   |   |   |   |   start > 256362:
protein_modification_process_ (25.76/10.54)
|   |   |   |   |   |   |   |   start > 261593
|   |   |   |   |   |   |   |   |   start <= 262555
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: cell_cycle_ (17.41/9.68)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: meiosis_ (2.33/1.16)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
DNA_metabolic_process_ (12.93/6.56)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: DNA_metabolic_process_ (4.4/2.52)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: DNA_metabolic_process_ (2.97/1.09)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: cell_cycle_ (2.8/0.95)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: DNA_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: meiosis_ (7.55/2.71)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: DNA_metabolic_process_ (1.72/0.58)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: DNA_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
DNA_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: DNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   start > 262555
|   |   |   |   |   |   |   |   |   |   start <= 267540:
biological_process_ (10.94)
|   |   |   |   |   |   |   |   |   |   start > 267540:
protein_modification_process_ (18.63)
|   |   |   |   |   |   |   start > 276766
|   |   |   |   |   |   |   |   start <= 284627
|   |   |   |   |   |   |   |   |   start <= 283300:
ribosome_biogenesis_and_assembly_ (16.24)
|   |   |   |   |   |   |   |   |   start > 283300:
DNA_metabolic_process_ (12.07)
|   |   |   |   |   |   |   |   start > 284627: translation_ (23.44)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 241666
|   |   |   |   |   |   |   start <= 229337
|   |   |   |   |   |   |   |   start <= 220110:
DNA_metabolic_process_ (13.87)
|   |   |   |   |   |   |   |   start > 220110
|   |   |   |   |   |   |   |   |   start <= 223760:
organelle_organization_and_biogenesis_ (13.09)
|   |   |   |   |   |   |   |   |   start > 223760: conjugation_
(12.98)
|   |   |   |   |   |   |   start > 229337
|   |   |   |   |   |   |   |   start <= 232135
|   |   |   |   |   |   |   |   |   start <= 230972:
lipid_metabolic_process_ (16.29)
|   |   |   |   |   |   |   |   |   start > 230972:
protein_modification_process_ (16.8)
|   |   |   |   |   |   |   |   start > 232135
|   |   |   |   |   |   |   |   |   start <= 234883:
ribosome_biogenesis_and_assembly_ (19.94)
|   |   |   |   |   |   |   |   |   start > 234883
|   |   |   |   |   |   |   |   |   |   start <= 237941: cell_cycle_
(15.39)
|   |   |   |   |   |   |   |   |   |   start > 237941
|   |   |   |   |   |   |   |   |   |   |   start <= 239100:
lipid_metabolic_process_ (6.3)
|   |   |   |   |   |   |   |   |   |   |   start > 239100:
ribosome_biogenesis_and_assembly_ (9.05)
|   |   |   |   |   |   start > 241666
|   |   |   |   |   |   |   start <= 274176
|   |   |   |   |   |   |   |   start <= 261593
|   |   |   |   |   |   |   |   |   start <= 246195
```

```
|   |   |   |   |   |   |   |   |   |   start <= 242584:
pseudohyphal_growth_ (12.37)
|   |   |   |   |   |   |   |   |   |   start > 242584:
vitamin_metabolic_process_ (7.92)
|   |   |   |   |   |   |   |   |   start > 246195:
biological_process_ (29.2)
|   |   |   |   |   |   |   |   start > 261593
|   |   |   |   |   |   |   |   |   start <= 267540:
DNA_metabolic_process_ (18.12)
|   |   |   |   |   |   |   |   |   start > 267540
|   |   |   |   |   |   |   |   |   |   start <= 272629:
membrane_organization_and_biogenesis_ (22.07)
|   |   |   |   |   |   |   |   |   |   start > 272629:
pseudohyphal_growth_ (17.79)
|   |   |   |   |   |   |   start > 274176
|   |   |   |   |   |   |   |   start <= 280233
|   |   |   |   |   |   |   |   |   start <= 276766:
ribosome_biogenesis_and_assembly_ (15.92)
|   |   |   |   |   |   |   |   |   start > 276766:
biological_process_ (35.38)
|   |   |   |   |   |   |   |   start > 280233
|   |   |   |   |   |   |   |   |   start <= 280822:
RNA_metabolic_process_ (15.31)
|   |   |   |   |   |   |   |   |   start > 280822:
ribosome_biogenesis_and_assembly_ (19.47)
|   |   |   |   start > 286772
|   |   |   |   |   start <= 328306
|   |   |   |   |   |   start <= 314676
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 296450: transport_ (44.29)
|   |   |   |   |   |   |   |   start > 296450
|   |   |   |   |   |   |   |   |   start <= 302764
|   |   |   |   |   |   |   |   |   |   start <= 298612:
biological_process_ (12.77)
|   |   |   |   |   |   |   |   |   |   start > 298612
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
transport_ (13.1/5.5)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (8.6/3.34)
|   |   |   |   |   |   |   |   |   start > 302764:
biological_process_ (14.23)
|   |   |   |   |   |   |   strand = W: DNA_metabolic_process_
(25.45)
|   |   |   |   |   |   start > 314676
|   |   |   |   |   |   |   start <= 328039
|   |   |   |   |   |   |   |   start <= 320417:
cell_wall_organization_and_biogenesis_ (39.33)
|   |   |   |   |   |   |   |   start > 320417
|   |   |   |   |   |   |   |   |   strand = C:
cell_wall_organization_and_biogenesis_ (30.96/11.22)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 323412:
response_to_stress_ (22.58)
|   |   |   |   |   |   |   |   |   |   start > 323412
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 324769:
biological_process_ (13.12)
|   |   |   |   |   |   |   |   |   |   |   start > 324769:
response_to_stress_ (15.89)
|   |   |   |   |   |   |   start > 328039: vesicle-
mediated_transport_ (18.83)
|   |   |   |   |   start > 328306
|   |   |   |   |   |   start <= 332285
|   |   |   |   |   |   |   start <= 330313:
protein_modification_process_ (23.03)
|   |   |   |   |   |   |   start > 330313: transport_ (27.67)
|   |   |   |   |   |   start > 332285:
protein_modification_process_ (61.36/39.84)
|   |   |   start > 333075
|   |   |   |   start <= 380575
|   |   |   |   |   start <= 352759
|   |   |   |   |   |   start <= 342352
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 338086: biological_process_
(21.88)
|   |   |   |   |   |   |   |   start > 338086: cell_cycle_
(33.13/14.36)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 338086
|   |   |   |   |   |   |   |   |   start <= 336340:
biological_process_ (13.66)
|   |   |   |   |   |   |   |   |   start > 336340: vesicle-
mediated_transport_ (19.26)
|   |   |   |   |   |   |   |   start > 338086
|   |   |   |   |   |   |   |   |   start <= 341668:
cellular_respiration_ (19.75)
|   |   |   |   |   |   |   |   |   start > 341668:
biological_process_ (25.04)
|   |   |   |   |   |   start > 342352
|   |   |   |   |   |   |   start <= 349577
|   |   |   |   |   |   |   |   start <= 346046
|   |   |   |   |   |   |   |   |   start <= 345631:
DNA_metabolic_process_ (17.33)
|   |   |   |   |   |   |   |   |   start > 345631: sporulation_
(47.86/17.19)
|   |   |   |   |   |   |   |   start > 346046:
DNA_metabolic_process_ (58.18/23.59)
|   |   |   |   |   |   |   start > 349577: RNA_metabolic_process_
(19.61)
|   |   |   |   |   start > 352759
|   |   |   |   |   |   start <= 375712
|   |   |   |   |   |   |   start <= 371600
|   |   |   |   |   |   |   |   start <= 358572
|   |   |   |   |   |   |   |   |   strand = C: translation_ (15.87)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 354818
|   |   |   |   |   |   |   |   |   |   |   start <= 353628:
transcription_ (14.85)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 353628:
lipid_metabolic_process_ (50.96/31.33)
|   |   |   |   |   |   |   |   |   |   start > 354818:
transcription_ (20.43/7.78)
|   |   |   |   |   |   |   |   start > 358572
|   |   |   |   |   |   |   |   |   start <= 370057
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 367895
|   |   |   |   |   |   |   |   |   |   |   |   start <= 362118:
biological_process_ (13.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 362118
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 364156:
cell_cycle_ (8.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 364156:
biological_process_ (11.41)
|   |   |   |   |   |   |   |   |   |   |   start > 367895:
cell_wall_organization_and_biogenesis_ (8.39)
|   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (46.89)
|   |   |   |   |   |   |   |   |   start > 370057:
lipid_metabolic_process_ (20.23)
|   |   |   |   |   |   |   start > 371600
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 374313: cytokinesis_
(32.0)
|   |   |   |   |   |   |   |   |   start > 374313:
biological_process_ (18.65)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 371752:
response_to_stress_ (23.83)
|   |   |   |   |   |   |   |   |   start > 371752:
amino_acid_and_derivative_metabolic_process_ (15.37)
|   |   |   |   |   |   start > 375712
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 377702:
membrane_organization_and_biogenesis_ (24.32/7.2)
|   |   |   |   |   |   |   |   start > 377702
|   |   |   |   |   |   |   |   |   neigh_strand = W: sporulation_
(31.4/17.86)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
cell_wall_organization_and_biogenesis_ (35.53/12.51)
|   |   |   |   |   |   |   strand = W: biological_process_ (20.55)
|   |   |   |   start > 380575
|   |   |   |   |   start <= 396662
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 393537
|   |   |   |   |   |   |   |   start <= 388729
|   |   |   |   |   |   |   |   |   start <= 385513: translation_
(17.3)
|   |   |   |   |   |   |   |   |   start > 385513:
biological_process_ (17.03)
|   |   |   |   |   |   |   |   start > 388729: translation_ (30.42)
|   |   |   |   |   |   |   start > 393537: biological_process_
(16.97)
```

```
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 383541
|   |   |   |   |   |   |   |   start <= 381543:
ribosome_biogenesis_and_assembly_ (35.15/16.19)
|   |   |   |   |   |   |   |   start > 381543: transport_
(39.44/19.39)
|   |   |   |   |   |   |   start > 383541
|   |   |   |   |   |   |   |   start <= 388729
|   |   |   |   |   |   |   |   |   start <= 385513:
pseudohyphal_growth_ (17.16)
|   |   |   |   |   |   |   |   |   start > 385513: transcription_
(19.03)
|   |   |   |   |   |   |   |   start > 388729
|   |   |   |   |   |   |   |   |   start <= 390303:
biological_process_ (11.75)
|   |   |   |   |   |   |   |   |   start > 390303:
ribosome_biogenesis_and_assembly_ (20.23)
|   |   |   |   |   start > 396662
|   |   |   |   |   |   start <= 439344
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 417552
|   |   |   |   |   |   |   |   |   start <= 412910
|   |   |   |   |   |   |   |   |   |   start <= 407106
|   |   |   |   |   |   |   |   |   |   |   start <= 401437:
biological_process_ (13.19)
|   |   |   |   |   |   |   |   |   |   |   start > 401437:
sporulation_ (17.25)
|   |   |   |   |   |   |   |   |   |   start > 407106:
biological_process_ (14.86)
|   |   |   |   |   |   |   |   |   start > 412910
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
conjugation_ (32.59/18.76)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
anatomical_structure_morphogenesis_ (30.66/15.88)
|   |   |   |   |   |   |   |   start > 417552
|   |   |   |   |   |   |   |   |   start <= 423726
|   |   |   |   |   |   |   |   |   |   start <= 420075:
organelle_organization_and_biogenesis_ (38.26/16.79)
|   |   |   |   |   |   |   |   |   |   start > 420075: vesicle-
mediated_transport_ (18.93)
|   |   |   |   |   |   |   |   |   start > 423726
|   |   |   |   |   |   |   |   |   |   start <= 436950
|   |   |   |   |   |   |   |   |   |   |   start <= 429180:
DNA_metabolic_process_ (16.23)
|   |   |   |   |   |   |   |   |   |   |   start > 429180:
RNA_metabolic_process_ (32.93/15.74)
|   |   |   |   |   |   |   |   |   |   start > 436950: cell_cycle_
(18.64)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 412910
|   |   |   |   |   |   |   |   |   start <= 401437
|   |   |   |   |   |   |   |   |   |   start <= 397254:
organelle_organization_and_biogenesis_ (12.12)
```

```
|   |   |   |   |   |   |   |   |   |   start > 397254: cell_cycle_
(27.13/11.22)
|   |   |   |   |   |   |   |   |   start > 401437
|   |   |   |   |   |   |   |   |   |   start <= 411231
|   |   |   |   |   |   |   |   |   |   |   start <= 407106
|   |   |   |   |   |   |   |   |   |   |   |   start <= 402969:
DNA_metabolic_process_ (13.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 402969:
biological_process_ (13.77)
|   |   |   |   |   |   |   |   |   |   |   start > 407106:
RNA_metabolic_process_ (33.57/15.06)
|   |   |   |   |   |   |   |   |   |   start > 411231: meiosis_
(63.15/39.51)
|   |   |   |   |   |   |   |   start > 412910
|   |   |   |   |   |   |   |   |   start <= 423075:
biological_process_ (35.1)
|   |   |   |   |   |   |   |   |   start > 423075
|   |   |   |   |   |   |   |   |   |   start <= 429180:
carbohydrate_metabolic_process_ (10.35)
|   |   |   |   |   |   |   |   |   |   start > 429180:
DNA_metabolic_process_ (15.87)
|   |   |   |   |   |   start > 439344
|   |   |   |   |   |   |   start <= 443829
|   |   |   |   |   |   |   |   start <= 440379: translation_
(16.47)
|   |   |   |   |   |   |   |   start > 440379:
ribosome_biogenesis_and_assembly_ (48.7)
|   |   |   |   |   |   |   start > 443829
|   |   |   |   |   |   |   |   start <= 448335
|   |   |   |   |   |   |   |   |   start <= 445713:
protein_modification_process_ (8.11)
|   |   |   |   |   |   |   |   |   start > 445713:
cytoskeleton_organization_and_biogenesis_ (13.88)
|   |   |   |   |   |   |   |   start > 448335
|   |   |   |   |   |   |   |   |   start <= 451327
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (19.82/5.74)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
membrane_organization_and_biogenesis_ (8.89/2.53)
|   |   |   |   |   |   |   |   |   start > 451327: transport_
(14.98)
|   start > 452872
|   |   start <= 486631
|   |   |   start <= 475340
|   |   |   |   start <= 466990
|   |   |   |   |   start <= 456591: biological_process_ (42.05)
|   |   |   |   |   start > 456591
|   |   |   |   |   |   start <= 459299: transcription_ (10.83)
|   |   |   |   |   |   start > 459299
|   |   |   |   |   |   |   start <= 462502: biological_process_
(8.15)
|   |   |   |   |   |   |   start > 462502: translation_ (5.76)
|   |   |   |   start > 466990
|   |   |   |   |   start <= 470960
```

```
|   |   |   |   |   |   start <= 467228:
cell_wall_organization_and_biogenesis_ (12.59)
|   |   |   |   |   |   start > 467228
|   |   |   |   |   |   |   start <= 468219: biological_process_
(6.41)
|   |   |   |   |   |   |   start > 468219: response_to_stress_
(5.46)
|   |   |   |   |   start > 470960: sporulation_ (67.69/27.85)
|   |   |   start > 475340
|   |   |   |   start <= 484028
|   |   |   |   |   start <= 480672
|   |   |   |   |   |   start <= 475778: translation_ (25.79)
|   |   |   |   |   |   start > 475778: signal_transduction_
(28.04/10.36)
|   |   |   |   |   start > 480672
|   |   |   |   |   |   strand = C: protein_modification_process_
(19.03)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 480990: RNA_metabolic_process_
(12.45)
|   |   |   |   |   |   |   start > 480990: translation_ (17.72)
|   |   |   |   start > 484028
|   |   |   |   |   start <= 484845: lipid_metabolic_process_
(13.84)
|   |   |   |   |   start > 484845: response_to_stress_ (12.5)
|   |   start > 486631
|   |   |   start <= 506319
|   |   |   |   start <= 502388
|   |   |   |   |   strand = C: biological_process_ (83.58)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 490747
|   |   |   |   |   |   |   start <= 486826: biological_process_
(26.51)
|   |   |   |   |   |   |   start > 486826
|   |   |   |   |   |   |   |   start <= 488657:
organelle_organization_and_biogenesis_ (13.51)
|   |   |   |   |   |   |   |   start > 488657:
membrane_organization_and_biogenesis_ (17.17)
|   |   |   |   |   |   start > 490747
|   |   |   |   |   |   |   start <= 493896:
ribosome_biogenesis_and_assembly_ (28.79)
|   |   |   |   |   |   |   start > 493896
|   |   |   |   |   |   |   |   start <= 499079:
protein_catabolic_process_ (10.96)
|   |   |   |   |   |   |   |   start > 499079: biological_process_
(14.59)
|   |   |   |   start > 502388
|   |   |   |   |   start <= 505530: translation_ (24.8)
|   |   |   |   |   start > 505530: protein_catabolic_process_
(14.6)
|   |   |   start > 506319
|   |   |   |   start <= 512732
|   |   |   |   |   start <= 509363: protein_modification_process_
(24.72/9.7)
```

```
|   |   |   |   |   start > 509363: transcription_ (24.4)
|   |   |   |   start > 512732
|   |   |   |   |   start <= 517532
|   |   |   |   |   |   start <= 516485: biological_process_ (10.8)
|   |   |   |   |   |   start > 516485:
amino_acid_and_derivative_metabolic_process_ (18.87)
|   |   |   |   |   start > 517532: biological_process_ (158.49)
```

Decision Tree Generated for Chromosome Nine:
For Cellular Component

```
|   start <= 276524
|   |   start <= 48091
|   |   |   strand = C
|   |   |   |   start <= 37385
|   |   |   |   |   start <= 26106
|   |   |   |   |   |   start <= 11492: cellular_component_ (17.54)
|   |   |   |   |   |   start > 11492
|   |   |   |   |   |   |   start <= 18553: cytoplasm_ (8.59)
|   |   |   |   |   |   |   start > 18553: cellular_component_
(10.0)
|   |   |   |   |   start > 26106
|   |   |   |   |   |   start <= 32566: membrane_ (11.72)
|   |   |   |   |   |   start > 32566: cellular_component_ (22.02)
|   |   |   |   start > 37385
|   |   |   |   |   start <= 41825: peroxisome_ (12.24)
|   |   |   |   |   start > 41825: mitochondrion_ (7.19)
|   |   |   strand = W
|   |   |   |   start <= 39433
|   |   |   |   |   start <= 37385
|   |   |   |   |   |   start <= 18553: cytoplasm_ (10.97)
|   |   |   |   |   |   start > 18553
|   |   |   |   |   |   |   neigh_strand = W: cytoplasm_ (19.57/9.4)
|   |   |   |   |   |   |   neigh_strand = C: extracellular_region_
(20.23/8.56)
|   |   |   |   |   start > 37385: cytoplasm_ (22.4)
|   |   |   |   start > 39433
|   |   |   |   |   start <= 41825: cellular_bud_ (41.97/16.09)
|   |   |   |   |   start > 41825
|   |   |   |   |   |   start <= 47690
|   |   |   |   |   |   |   start <= 46201: vacuole_ (14.57)
|   |   |   |   |   |   |   start > 46201: cellular_component_
(12.46)
|   |   |   |   |   |   start > 47690: cytoplasm_ (15.13)
|   |   start > 48091
|   |   |   strand = C
|   |   |   |   start <= 222487
|   |   |   |   |   start <= 113806
|   |   |   |   |   |   start <= 88716
|   |   |   |   |   |   |   start <= 56545
|   |   |   |   |   |   |   |   start <= 53708: mitochondrion_
(18.9)
|   |   |   |   |   |   |   |   start > 53708: cytoplasm_ (19.79)
|   |   |   |   |   |   |   start > 56545
```

```
|   |   |   |   |   |   |   |   start <= 75773
|   |   |   |   |   |   |   |   |   start <= 68708
|   |   |   |   |   |   |   |   |   |   start <= 62728
|   |   |   |   |   |   |   |   |   |   |   start <= 60694:
cellular_component_ (21.41)
|   |   |   |   |   |   |   |   |   |   |   start > 60694: nucleus_
(9.7)
|   |   |   |   |   |   |   |   |   |   start > 62728:
mitochondrion_ (23.06)
|   |   |   |   |   |   |   |   |   start > 68708
|   |   |   |   |   |   |   |   |   |   start <= 73453:
plasma_membrane_ (10.22)
|   |   |   |   |   |   |   |   |   |   start > 73453:
cellular_component_ (28.32)
|   |   |   |   |   |   |   |   start > 75773
|   |   |   |   |   |   |   |   |   start <= 85366: nucleus_
(82.02/36.1)
|   |   |   |   |   |   |   |   |   start > 85366: mitochondrion_
(20.66)
|   |   |   |   |   |   start > 88716
|   |   |   |   |   |   |   start <= 99416
|   |   |   |   |   |   |   |   start <= 89715:
site_of_polarized_growth_ (35.91/13.41)
|   |   |   |   |   |   |   |   start > 89715
|   |   |   |   |   |   |   |   |   start <= 96375: cytoplasm_
(50.11/9.54)
|   |   |   |   |   |   |   |   |   start > 96375
|   |   |   |   |   |   |   |   |   |   start <= 97395:
cellular_component_ (15.12)
|   |   |   |   |   |   |   |   |   |   start > 97395: ribosome_
(15.9)
|   |   |   |   |   |   |   start > 99416
|   |   |   |   |   |   |   |   start <= 102782
|   |   |   |   |   |   |   |   |   start <= 100501
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(10.93/3.33)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(12.26/3.74)
|   |   |   |   |   |   |   |   |   start > 100501: nucleus_ (20.59)
|   |   |   |   |   |   |   |   start > 102782: cellular_bud_
(36.66/17.2)
|   |   |   |   |   start > 113806
|   |   |   |   |   |   start <= 148706
|   |   |   |   |   |   |   start <= 126204: nucleolus_ (19.82)
|   |   |   |   |   |   |   start > 126204
|   |   |   |   |   |   |   |   start <= 137874: nucleus_ (14.71)
|   |   |   |   |   |   |   |   start > 137874
|   |   |   |   |   |   |   |   |   start <= 142925: membrane_
(21.81)
|   |   |   |   |   |   |   |   |   start > 142925:
cellular_component_ (46.97/30.17)
|   |   |   |   |   |   start > 148706
|   |   |   |   |   |   |   start <= 169638
|   |   |   |   |   |   |   |   start <= 160884
```

```
|   |   |   |   |   |   |   |   |   start <= 151592: mitochondrion_
(20.67)
|   |   |   |   |   |   |   |   |   start > 151592: Golgi_apparatus_
(17.53)
|   |   |   |   |   |   |   |   start > 160884
|   |   |   |   |   |   |   |   |   start <= 166412: cytoplasm_
(16.42)
|   |   |   |   |   |   |   |   |   start > 166412
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(19.08/8.7)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
mitochondrion_ (15.78/7.69)
|   |   |   |   |   |   |   start > 169638
|   |   |   |   |   |   |   |   start <= 178001
|   |   |   |   |   |   |   |   |   start <= 171748: nucleus_
(16.41)
|   |   |   |   |   |   |   |   |   start > 171748
|   |   |   |   |   |   |   |   |   |   start <= 175028:
cellular_component_ (30.92)
|   |   |   |   |   |   |   |   |   |   start > 175028: nucleus_
(8.03)
|   |   |   |   |   |   |   |   start > 178001
|   |   |   |   |   |   |   |   |   start <= 220697
|   |   |   |   |   |   |   |   |   |   start <= 200116
|   |   |   |   |   |   |   |   |   |   |   start <= 195596
|   |   |   |   |   |   |   |   |   |   |   |   start <= 180424:
mitochondrion_ (16.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 180424
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 183934
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
183124: nucleus_ (38.86/9.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
183124: cytoplasm_ (16.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 183934
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
189063: mitochondrion_ (20.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
189063: nucleus_ (26.98/10.4)
|   |   |   |   |   |   |   |   |   |   |   start > 195596
|   |   |   |   |   |   |   |   |   |   |   |   start <= 199400:
plasma_membrane_ (7.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 199400:
mitochondrion_ (20.57)
|   |   |   |   |   |   |   |   |   |   start > 200116
|   |   |   |   |   |   |   |   |   |   |   start <= 204650
|   |   |   |   |   |   |   |   |   |   |   |   start <= 202040:
Golgi_apparatus_ (9.44)
|   |   |   |   |   |   |   |   |   |   |   |   start > 202040:
nucleus_ (60.8/25.05)
|   |   |   |   |   |   |   |   |   |   |   start > 204650
|   |   |   |   |   |   |   |   |   |   |   |   start <= 212496:
nucleolus_ (40.19/18.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 212496
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 216655:
mitochondrion_ (24.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 216655:
nucleus_ (18.57)
|   |   |   |   |   |   |   |   |   start > 220697: cytoplasm_
(24.95)
|   |   |   |   start > 222487
|   |   |   |   |   start <= 249989
|   |   |   |   |   |   start <= 237757
|   |   |   |   |   |   |   start <= 232366
|   |   |   |   |   |   |   |   start <= 229991
|   |   |   |   |   |   |   |   |   start <= 226599: chromosome_
(18.66)
|   |   |   |   |   |   |   |   |   start > 226599: nucleus_ (9.34)
|   |   |   |   |   |   |   |   start > 229991
|   |   |   |   |   |   |   |   |   start <= 231069: mitochondrion_
(9.46)
|   |   |   |   |   |   |   |   |   start > 231069: ribosome_
(12.52)
|   |   |   |   |   |   |   start > 232366
|   |   |   |   |   |   |   |   start <= 235471: cellular_bud_
(25.87/11.95)
|   |   |   |   |   |   |   |   start > 235471: vacuole_ (18.43)
|   |   |   |   |   |   start > 237757
|   |   |   |   |   |   |   start <= 241940
|   |   |   |   |   |   |   |   start <= 240705: cytoplasm_
(27.36/11.43)
|   |   |   |   |   |   |   |   start > 240705: mitochondrion_
(17.17)
|   |   |   |   |   |   |   start > 241940
|   |   |   |   |   |   |   |   start <= 246389
|   |   |   |   |   |   |   |   |   start <= 244459
|   |   |   |   |   |   |   |   |   |   start <= 243741: nucleus_
(14.04)
|   |   |   |   |   |   |   |   |   |   start > 243741:
mitochondrial_envelope_ (16.39)
|   |   |   |   |   |   |   |   |   start > 244459: nucleus_ (15.43)
|   |   |   |   |   |   |   |   start > 246389: cytoplasm_ (9.22)
|   |   |   |   |   start > 249989
|   |   |   |   |   |   start <= 257061
|   |   |   |   |   |   |   start <= 255113: cellular_component_
(24.48)
|   |   |   |   |   |   |   start > 255113: ribosome_ (20.18)
|   |   |   |   |   |   start > 257061
|   |   |   |   |   |   |   start <= 268650
|   |   |   |   |   |   |   |   start <= 261436: mitochondrion_
(9.71)
|   |   |   |   |   |   |   |   start > 261436: plasma_membrane_
(30.81/13.0)
|   |   |   |   |   |   |   start > 268650
|   |   |   |   |   |   |   |   start <= 273845:
cytoplasmic_membrane-bound_vesicle_ (13.67)
|   |   |   |   |   |   |   |   start > 273845: mitochondrion_
(39.02)
```

```
|   |   |   strand = W
|   |   |   |   start <= 166412
|   |   |   |   |   start <= 160884
|   |   |   |   |   |   start <= 88716
|   |   |   |   |   |   |   start <= 68708
|   |   |   |   |   |   |   |   start <= 55198
|   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(11.97/3.15)
|   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(15.46/5.93)
|   |   |   |   |   |   |   |   start > 55198
|   |   |   |   |   |   |   |   |   start <= 60694:
cellular_component_ (18.99)
|   |   |   |   |   |   |   |   |   start > 60694: ribosome_ (13.99)
|   |   |   |   |   |   |   start > 68708
|   |   |   |   |   |   |   |   start <= 83302
|   |   |   |   |   |   |   |   |   start <= 78074: chromosome_
(18.26)
|   |   |   |   |   |   |   |   |   start > 78074: cytoplasm_
(21.6/8.77)
|   |   |   |   |   |   |   |   start > 83302
|   |   |   |   |   |   |   |   |   distance <= 672: cellular_bud_
(7.46/0.13)
|   |   |   |   |   |   |   |   |   distance > 672:
site_of_polarized_growth_ (20.14/8.19)
|   |   |   |   |   |   start > 88716
|   |   |   |   |   |   |   start <= 99416
|   |   |   |   |   |   |   |   start <= 93619: mitochondrion_
(24.42)
|   |   |   |   |   |   |   |   start > 93619
|   |   |   |   |   |   |   |   |   start <= 97111: nucleolus_
(16.55)
|   |   |   |   |   |   |   |   |   start > 97111: mitochondrion_
(16.09)
|   |   |   |   |   |   |   start > 99416
|   |   |   |   |   |   |   |   start <= 130607
|   |   |   |   |   |   |   |   |   start <= 117992: nucleus_
(58.99/15.7)
|   |   |   |   |   |   |   |   |   start > 117992
|   |   |   |   |   |   |   |   |   |   start <= 126204:
mitochondrion_ (74.86/33.81)
|   |   |   |   |   |   |   |   |   |   start > 126204
|   |   |   |   |   |   |   |   |   |   |   start <= 128151:
cell_wall_ (15.92)
|   |   |   |   |   |   |   |   |   |   |   start > 128151: nucleus_
(14.29)
|   |   |   |   |   |   |   |   start > 130607
|   |   |   |   |   |   |   |   |   start <= 142925
|   |   |   |   |   |   |   |   |   |   start <= 134414:
plasma_membrane_ (26.58)
|   |   |   |   |   |   |   |   |   |   start > 134414:
cellular_component_ (27.28)
|   |   |   |   |   |   |   |   |   start > 142925
|   |   |   |   |   |   |   |   |   |   start <= 151592
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 150556:
nucleus_ (33.22/11.47)
|   |   |   |   |   |   |   |   |   |   |   start > 150556:
cellular_component_ (34.38/14.5)
|   |   |   |   |   |   |   |   |   |   start > 151592
|   |   |   |   |   |   |   |   |   |   |   start <= 155219:
mitochondrion_ (16.84)
|   |   |   |   |   |   |   |   |   |   |   start > 155219:
cytoplasm_ (50.19/11.81)
|   |   |   |   |   start > 160884
|   |   |   |   |   |   distance <= 3677: cellular_bud_ (36.37/22.9)
|   |   |   |   |   |   distance > 3677: site_of_polarized_growth_
(13.78/7.69)
|   |   |   |   start > 166412
|   |   |   |   |   start <= 193592
|   |   |   |   |   |   start <= 180424
|   |   |   |   |   |   |   start <= 178001
|   |   |   |   |   |   |   |   start <= 175028: cytoplasm_ (27.84)
|   |   |   |   |   |   |   |   start > 175028: vacuole_ (13.59)
|   |   |   |   |   |   |   start > 178001: nucleus_ (39.46/16.15)
|   |   |   |   |   |   start > 180424
|   |   |   |   |   |   |   start <= 183934: cytoskeleton_
(50.38/19.04)
|   |   |   |   |   |   |   start > 183934
|   |   |   |   |   |   |   |   start <= 189063: nucleus_
(29.42/13.02)
|   |   |   |   |   |   |   |   start > 189063:
endoplasmic_reticulum_ (13.07)
|   |   |   |   |   start > 193592
|   |   |   |   |   |   start <= 248847
|   |   |   |   |   |   |   start <= 195596: cellular_component_
(17.24)
|   |   |   |   |   |   |   start > 195596
|   |   |   |   |   |   |   |   start <= 220697: cytoplasm_
(80.17/25.7)
|   |   |   |   |   |   |   |   start > 220697
|   |   |   |   |   |   |   |   |   start <= 232366: chromosome_
(13.43)
|   |   |   |   |   |   |   |   |   start > 232366
|   |   |   |   |   |   |   |   |   |   start <= 246389
|   |   |   |   |   |   |   |   |   |   |   start <= 243741:
cytoplasm_ (7.57)
|   |   |   |   |   |   |   |   |   |   |   start > 243741:
cellular_component_ (6.82)
|   |   |   |   |   |   |   |   |   |   start > 246389: cytoplasm_
(22.52)
|   |   |   |   |   |   start > 248847
|   |   |   |   |   |   |   start <= 268650
|   |   |   |   |   |   |   |   start <= 258912
|   |   |   |   |   |   |   |   |   start <= 255113
|   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(10.29/2.97)
```

```
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (18.37/6.88)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(34.65/9.0)
|   |   |   |   |   |   |   |   |   start > 255113: nucleus_ (15.56)
|   |   |   |   |   |   |   |   start > 258912
|   |   |   |   |   |   |   |   |   start <= 268308
|   |   |   |   |   |   |   |   |   |   start <= 260157:
cellular_component_ (19.63)
|   |   |   |   |   |   |   |   |   |   start > 260157
|   |   |   |   |   |   |   |   |   |   |   start <= 261436:
Golgi_apparatus_ (12.49)
|   |   |   |   |   |   |   |   |   |   |   start > 261436:
cellular_component_ (15.61)
|   |   |   |   |   |   |   |   |   start > 268308: nucleus_ (13.2)
|   |   |   |   |   |   |   start > 268650: cytoplasm_ (36.78)
|   start > 276524
|   |   start <= 403656
|   |   |   start <= 370701
|   |   |   |   start <= 314818
|   |   |   |   |   start <= 284998
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 282651: cytoplasm_ (9.64)
|   |   |   |   |   |   |   start > 282651: membrane_ (23.55)
|   |   |   |   |   |   strand = W: endoplasmic_reticulum_ (46.48)
|   |   |   |   |   start > 284998
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 300008
|   |   |   |   |   |   |   |   start <= 290088
|   |   |   |   |   |   |   |   |   start <= 288907:
cellular_component_ (22.71)
|   |   |   |   |   |   |   |   |   start > 288907: cytoskeleton_
(37.23/16.89)
|   |   |   |   |   |   |   |   start > 290088
|   |   |   |   |   |   |   |   |   start <= 292632:
plasma_membrane_ (42.8/21.69)
|   |   |   |   |   |   |   |   |   start > 292632:
endomembrane_system_ (10.33)
|   |   |   |   |   |   |   start > 300008
|   |   |   |   |   |   |   |   start <= 300298: mitochondrion_
(9.75)
|   |   |   |   |   |   |   |   start > 300298
|   |   |   |   |   |   |   |   |   start <= 307927
|   |   |   |   |   |   |   |   |   |   start <= 304102
|   |   |   |   |   |   |   |   |   |   |   start <= 301255:
cellular_component_ (15.19)
|   |   |   |   |   |   |   |   |   |   |   start > 301255:
endoplasmic_reticulum_ (13.2)
|   |   |   |   |   |   |   |   |   |   start > 304102: nucleus_
(23.41)
|   |   |   |   |   |   |   |   |   start > 307927
|   |   |   |   |   |   |   |   |   |   start <= 311163
|   |   |   |   |   |   |   |   |   |   |   start <= 309169:
cellular_component_ (9.52)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 309169:
endoplasmic_reticulum_ (21.57)
|   |   |   |   |   |   |   |   |   |   start > 311163:
cellular_component_ (13.94)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 301255: nucleus_ (29.15)
|   |   |   |   |   |   |   start > 301255
|   |   |   |   |   |   |   |   start <= 311163: mitochondrion_
(25.05)
|   |   |   |   |   |   |   |   start > 311163: nucleus_ (16.34)
|   |   |   |   start > 314818
|   |   |   |   |   start <= 344059
|   |   |   |   |   |   start <= 320963
|   |   |   |   |   |   |   start <= 315091
|   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_
(21.8/11.53)
|   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(35.18/19.1)
|   |   |   |   |   |   |   start > 315091
|   |   |   |   |   |   |   |   start <= 316766: ribosome_ (10.29)
|   |   |   |   |   |   |   |   start > 316766: cytoplasm_
(40.44/18.35)
|   |   |   |   |   |   start > 320963
|   |   |   |   |   |   |   start <= 332440
|   |   |   |   |   |   |   |   start <= 321452: mitochondrion_
(29.51/12.08)
|   |   |   |   |   |   |   |   start > 321452
|   |   |   |   |   |   |   |   |   start <= 326101
|   |   |   |   |   |   |   |   |   |   start <= 322340:
cellular_component_ (20.55)
|   |   |   |   |   |   |   |   |   |   start > 322340
|   |   |   |   |   |   |   |   |   |   |   start <= 324372:
cytoplasm_ (18.78)
|   |   |   |   |   |   |   |   |   |   |   start > 324372
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cellular_component_ (15.95)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 325746:
cytoplasm_ (8.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 325746:
cellular_component_ (15.56)
|   |   |   |   |   |   |   |   |   start > 326101: membrane_ (8.36)
|   |   |   |   |   |   |   start > 332440
|   |   |   |   |   |   |   |   start <= 336209
|   |   |   |   |   |   |   |   |   start <= 333724: cell_wall_
(17.23)
|   |   |   |   |   |   |   |   |   start > 333724: nucleus_ (27.97)
|   |   |   |   |   |   |   |   start > 336209
|   |   |   |   |   |   |   |   |   start <= 343653
|   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(35.08)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 339341:
cellular_component_ (15.66)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 339341:
cytoplasm_ (14.81/6.93)
|   |   |   |   |   |   |   |   |   start > 343653: mitochondrion_
(17.61)
|   |   |   |   |   start > 344059
|   |   |   |   |   |   start <= 348502
|   |   |   |   |   |   |   start <= 345689: endoplasmic_reticulum_
(48.05/28.74)
|   |   |   |   |   |   |   start > 345689
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
endomembrane_system_ (5.16/2.57)
|   |   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = biological_process_
|   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: membrane_
(4.74/2.13)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasmic_membrane-bound_vesicle_ (7.15/3.56)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
endomembrane_system_ (2.47/1.22)
|   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
endomembrane_system_ (3.84/1.42)
|   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = molecular_function_
|   |   |   |   |   |   |   |   |   neigh_strand = W: membrane_
(6.97/2.81)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
endomembrane_system_ (8.67/4.2)
|   |   |   |   |   |   |   |   NeighGO_term = translation_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_component_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = nucleus_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ribosome_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transcription_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleolus_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = meiosis_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_:
endoplasmic_reticulum_ (4.15/2.46)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transport_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_
|   |   |   |   |   |   |   |   |   distance <= 1407:
endomembrane_system_ (2.24/1.14)
|   |   |   |   |   |   |   |   |   distance > 1407:
endoplasmic_reticulum_ (9.6/5.01)
|   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: membrane_ (11.02/4.53)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
membrane_ (4.23/2.31)
|   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vacuole_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: membrane_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = cell_wall_: membrane_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = electron_transport_:
membrane_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: membrane_ (0.0)
|   |   |   |   |   |   start > 348502
|   |   |   |   |   |   |   start <= 353428
|   |   |   |   |   |   |   |   strand = C: membrane_fraction_
(11.7)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 349119: cytoplasm_
(14.04)
|   |   |   |   |   |   |   |   |   start > 349119:
cellular_component_ (14.01)
|   |   |   |   |   |   |   start > 353428
|   |   |   |   |   |   |   |   start <= 364886
|   |   |   |   |   |   |   |   |   start <= 356892: cytoplasm_
(29.45)
|   |   |   |   |   |   |   |   |   start > 356892
|   |   |   |   |   |   |   |   |   |   start <= 360882
|   |   |   |   |   |   |   |   |   |   |   start <= 360393:
nucleus_ (14.45)
|   |   |   |   |   |   |   |   |   |   |   start > 360393:
ribosome_ (10.14)
|   |   |   |   |   |   |   |   |   |   start > 360882
|   |   |   |   |   |   |   |   |   |   |   start <= 363218:
cytoplasm_ (18.03)
|   |   |   |   |   |   |   |   |   |   |   start > 363218: nucleus_
(12.51)
|   |   |   |   |   |   |   |   start > 364886
|   |   |   |   |   |   |   |   |   strand = C: plasma_membrane_
(15.19)
|   |   |   |   |   |   |   |   |   strand = W: cytoplasm_ (37.26)
|   |   |   start > 370701
|   |   |   |   start <= 381083
|   |   |   |   |   start <= 378243
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 375428
|   |   |   |   |   |   |   |   neigh_strand = W:
cellular_component_ (17.89/9.78)
|   |   |   |   |   |   |   |   neigh_strand = C: chromosome_
(27.67/15.12)
|   |   |   |   |   |   |   start > 375428: nucleus_ (24.33)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 374522: nucleus_ (17.28)
|   |   |   |   |   |   |   start > 374522: cytoskeleton_
(40.91/16.72)
|   |   |   |   |   start > 378243
|   |   |   |   |   |   strand = C: nucleus_ (11.1)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 378483: cytoplasm_ (17.87)
|   |   |   |   |   |   |   start > 378483: vacuole_ (23.44)
|   |   |   |   start > 381083
```

```
|   |   |   |   |   start <= 382625
|   |   |   |   |   |   start <= 381945: nucleolus_ (18.63)
|   |   |   |   |   |   start > 381945: cellular_component_ (17.04)
|   |   |   |   |   start > 382625
|   |   |   |   |   |   start <= 398511
|   |   |   |   |   |   |   start <= 384606: nucleus_ (30.65)
|   |   |   |   |   |   |   start > 384606
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 385698: 
cellular_component_ (12.83)
|   |   |   |   |   |   |   |   |   start > 385698: plasma_membrane_ 
(10.25)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 397291: mitochondrion_ 
(10.19)
|   |   |   |   |   |   |   |   |   start > 397291: 
cellular_component_ (12.1)
|   |   |   |   |   |   start > 398511
|   |   |   |   |   |   |   strand = C: mitochondrion_ (16.18)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 398730: 
endoplasmic_reticulum_ (14.76)
|   |   |   |   |   |   |   |   start > 398730: nucleus_ (33.73)
|   |   start > 403656
|   |   |   start <= 422862
|   |   |   |   start <= 416121
|   |   |   |   |   start <= 414676
|   |   |   |   |   |   start <= 405964: cytoplasm_ (21.29)
|   |   |   |   |   |   start > 405964
|   |   |   |   |   |   |   start <= 408465
|   |   |   |   |   |   |   |   start <= 407639: cellular_component_ 
(13.28)
|   |   |   |   |   |   |   |   start > 407639: membrane_ (16.3)
|   |   |   |   |   |   |   start > 408465: cellular_component_ 
(44.43)
|   |   |   |   |   start > 414676
|   |   |   |   |   |   start <= 415614: membrane_ (9.78)
|   |   |   |   |   |   start > 415614
|   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   distance <= 2348: 
endoplasmic_reticulum_ (2.39/0.68)
|   |   |   |   |   |   |   |   distance > 2348: 
endomembrane_system_ (9.61/2.65)
|   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   Neigh_GO_aspect = C: 
endoplasmic_reticulum_ (8.32/3.49)
|   |   |   |   |   |   |   |   Neigh_GO_aspect = F: 
endoplasmic_reticulum_ (4.92/3.18)
|   |   |   |   |   |   |   |   Neigh_GO_aspect = P: membrane_ 
(5.88/2.03)
|   |   |   |   start > 416121: cytoplasm_ (53.67)
|   |   |   start > 422862
|   |   |   |   strand = C
```

```
|   |   |   |   |   start <= 424510: endoplasmic_reticulum_
(36.74/12.34)
|   |   |   |   |   start > 424510
|   |   |   |   |   |   start <= 433925: cell_wall_ (15.28)
|   |   |   |   |   |   start > 433925: cellular_component_ (7.58)
|   |   |   |   strand = W: cellular_component_ (38.44)
```

For Molecular Function

```
|   start <= 374303
|   |   start <= 344059
|   |   |   start <= 307927
|   |   |   |   start <= 257061
|   |   |   |   |   start <= 203256
|   |   |   |   |   |   start <= 117992
|   |   |   |   |   |   |   start <= 53708
|   |   |   |   |   |   |   |   start <= 39433
|   |   |   |   |   |   |   |   |   start <= 6147:
helicase_activity_ (8.04)
|   |   |   |   |   |   |   |   |   start > 6147
|   |   |   |   |   |   |   |   |   |   start <= 34077
|   |   |   |   |   |   |   |   |   |   |   start <= 26106
|   |   |   |   |   |   |   |   |   |   |   |   start <= 18553
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 11492:
molecular_function_ (14.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 11492:
hydrolase_activity_ (9.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 18553:
molecular_function_ (16.82)
|   |   |   |   |   |   |   |   |   |   |   start > 26106
|   |   |   |   |   |   |   |   |   |   |   |   start <= 32566:
transporter_activity_ (18.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 32566:
molecular_function_ (14.64)
|   |   |   |   |   |   |   |   |   |   start > 34077
|   |   |   |   |   |   |   |   |   |   |   start <= 37385:
hydrolase_activity_ (31.95)
|   |   |   |   |   |   |   |   |   |   |   start > 37385:
molecular_function_ (25.25)
|   |   |   |   |   |   |   |   start > 39433
|   |   |   |   |   |   |   |   |   start <= 41825
|   |   |   |   |   |   |   |   |   |   start <= 41444:
transferase_activity_ (18.2)
|   |   |   |   |   |   |   |   |   |   start > 41444:
protein_binding_ (14.95)
|   |   |   |   |   |   |   |   |   start > 41825
|   |   |   |   |   |   |   |   |   |   start <= 47690:
molecular_function_ (39.04)
|   |   |   |   |   |   |   |   |   |   start > 47690
|   |   |   |   |   |   |   |   |   |   |   start <= 48091:
peptidase_activity_ (18.35)
|   |   |   |   |   |   |   |   |   |   |   start > 48091:
oxidoreductase_activity_ (10.37)
|   |   |   |   |   |   |   start > 53708
```

```
|   |   |   |   |   |   |   |   start <= 89715
|   |   |   |   |   |   |   |   |   start <= 78074
|   |   |   |   |   |   |   |   |   |   start <= 55198
|   |   |   |   |   |   |   |   |   |   |   start <= 55021:
transcription_regulator_activity_ (16.76)
|   |   |   |   |   |   |   |   |   |   |   start > 55021:
isomerase_activity_ (14.19)
|   |   |   |   |   |   |   |   |   |   start > 55198
|   |   |   |   |   |   |   |   |   |   |   start <= 75773
|   |   |   |   |   |   |   |   |   |   |   |   start <= 68708
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 60694:
molecular_function_ (27.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 60694
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
62728: protein_binding_ (14.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
62728: molecular_function_ (52.25/11.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 68708
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 73453:
signal_transducer_activity_ (22.15/10.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 73453:
molecular_function_ (22.03)
|   |   |   |   |   |   |   |   |   |   |   start > 75773
|   |   |   |   |   |   |   |   |   |   |   |   start <= 77283:
ligase_activity_ (18.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 77283:
structural_molecule_activity_ (17.9)
|   |   |   |   |   |   |   |   |   start > 78074
|   |   |   |   |   |   |   |   |   |   start <= 83041:
helicase_activity_ (33.81/16.8)
|   |   |   |   |   |   |   |   |   |   start > 83041
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 88716:
nucleotidyltransferase_activity_ (20.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 88716:
protein_binding_ (18.23)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 83302:
protein_binding_ (16.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 83302:
molecular_function_ (13.8)
|   |   |   |   |   |   |   |   start > 89715
|   |   |   |   |   |   |   |   |   start <= 100501
|   |   |   |   |   |   |   |   |   |   start <= 96725:
molecular_function_ (78.37)
|   |   |   |   |   |   |   |   |   |   start > 96725
|   |   |   |   |   |   |   |   |   |   |   start <= 99416
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
RNA_binding_ (15.54)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 97111:
RNA_binding_ (11.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 97111:
transporter_activity_ (14.96)
```

```
|   |   |   |   |   |   |   |   |   |   start > 99416:
molecular_function_ (11.37)
|   |   |   |   |   |   |   |   |   start > 100501
|   |   |   |   |   |   |   |   |   |   start <= 102235:
DNA_binding_ (16.04)
|   |   |   |   |   |   |   |   |   |   start > 102235
|   |   |   |   |   |   |   |   |   |   |   start <= 117644
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (42.07)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 102782:
molecular_function_ (16.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 102782:
transcription_regulator_activity_ (18.28)
|   |   |   |   |   |   |   |   |   |   |   start > 117644:
helicase_activity_ (15.07)
|   |   |   |   |   |   start > 117992
|   |   |   |   |   |   |   start <= 166412
|   |   |   |   |   |   |   |   start <= 139749
|   |   |   |   |   |   |   |   |   strand = C:
enzyme_regulator_activity_ (18.46)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 128151
|   |   |   |   |   |   |   |   |   |   |   start <= 126204:
oxidoreductase_activity_ (33.93)
|   |   |   |   |   |   |   |   |   |   |   start > 126204:
molecular_function_ (8.57)
|   |   |   |   |   |   |   |   |   |   start > 128151
|   |   |   |   |   |   |   |   |   |   |   start <= 134414
|   |   |   |   |   |   |   |   |   |   |   |   start <= 130607:
transcription_regulator_activity_ (12.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 130607:
transporter_activity_ (28.53)
|   |   |   |   |   |   |   |   |   |   |   start > 134414:
signal_transducer_activity_ (12.51)
|   |   |   |   |   |   |   |   start > 139749
|   |   |   |   |   |   |   |   |   start <= 151592
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 142925:
molecular_function_ (21.17)
|   |   |   |   |   |   |   |   |   |   |   start > 142925
|   |   |   |   |   |   |   |   |   |   |   |   start <= 148706:
structural_molecule_activity_ (20.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 148706:
transporter_activity_ (19.66)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 142925:
transferase_activity_ (22.25)
|   |   |   |   |   |   |   |   |   |   |   start > 142925
|   |   |   |   |   |   |   |   |   |   |   |   start <= 150556:
phosphoprotein_phosphatase_activity_ (14.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 150556:
hydrolase_activity_ (18.92)
|   |   |   |   |   |   |   |   |   start > 151592
```

```
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 160884:
protein_binding_ (20.5)
|   |   |   |   |   |   |   |   |   |   |   start > 160884:
transferase_activity_ (27.37)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 156042
|   |   |   |   |   |   |   |   |   |   |   |   start <= 155219:
oxidoreductase_activity_ (11.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 155219:
transferase_activity_ (16.94)
|   |   |   |   |   |   |   |   |   |   |   start > 156042
|   |   |   |   |   |   |   |   |   |   |   |   start <= 160884:
molecular_function_ (25.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 160884:
enzyme_regulator_activity_ (11.29)
|   |   |   |   |   |   |   start > 166412
|   |   |   |   |   |   |   |   start <= 183510
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   distance <= 1549
|   |   |   |   |   |   |   |   |   |   |   start <= 178001
|   |   |   |   |   |   |   |   |   |   |   |   start <= 175028:
molecular_function_ (20.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 175028:
transcription_regulator_activity_ (16.72/6.28)
|   |   |   |   |   |   |   |   |   |   |   start > 178001:
molecular_function_ (25.83)
|   |   |   |   |   |   |   |   |   |   distance > 1549:
molecular_function_ (65.43)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 175028:
molecular_function_ (28.35)
|   |   |   |   |   |   |   |   |   |   start > 175028
|   |   |   |   |   |   |   |   |   |   |   start <= 178001:
hydrolase_activity_ (18.43)
|   |   |   |   |   |   |   |   |   |   |   start > 178001:
molecular_function_ (19.79)
|   |   |   |   |   |   |   |   start > 183510
|   |   |   |   |   |   |   |   |   start <= 188781
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 187629:
oxidoreductase_activity_ (17.26)
|   |   |   |   |   |   |   |   |   |   |   start > 187629:
structural_molecule_activity_ (15.74)
|   |   |   |   |   |   |   |   |   |   strand = W:
protein_kinase_activity_ (22.66)
|   |   |   |   |   |   |   |   |   start > 188781
|   |   |   |   |   |   |   |   |   |   start <= 200116
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 195596:
helicase_activity_ (14.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 195596
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 199400:
transporter_activity_ (12.24)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 199400:
molecular_function_ (13.2)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
molecular_function_ (59.98)
|   |   |   |   |   |   |   |   |   |   start > 200116
|   |   |   |   |   |   |   |   |   |   |   start <= 202040:
transferase_activity_ (23.73)
|   |   |   |   |   |   |   |   |   |   |   start > 202040:
hydrolase_activity_ (10.5)
|   |   |   |   |   start > 203256
|   |   |   |   |   |   start <= 220697
|   |   |   |   |   |   |   start <= 216655
|   |   |   |   |   |   |   |   start <= 212496
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 204650:
ligase_activity_ (12.28)
|   |   |   |   |   |   |   |   |   |   start > 204650:
nucleotidyltransferase_activity_ (16.97)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 210662:
molecular_function_ (20.17)
|   |   |   |   |   |   |   |   |   |   start > 210662:
ligase_activity_ (11.15)
|   |   |   |   |   |   |   |   start > 212496: molecular_function_
(32.56)
|   |   |   |   |   |   |   start > 216655: protein_binding_
(38.57/14.81)
|   |   |   |   |   |   start > 220697
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 222487:
oxidoreductase_activity_ (25.58)
|   |   |   |   |   |   |   |   start > 222487
|   |   |   |   |   |   |   |   |   start <= 243741
|   |   |   |   |   |   |   |   |   |   start <= 237757
|   |   |   |   |   |   |   |   |   |   |   start <= 231069:
molecular_function_ (36.73)
|   |   |   |   |   |   |   |   |   |   |   start > 231069
|   |   |   |   |   |   |   |   |   |   |   |   start <= 235471
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 232366:
structural_molecule_activity_ (8.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 232366:
protein_binding_ (8.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 235471:
molecular_function_ (12.23)
|   |   |   |   |   |   |   |   |   |   start > 237757
|   |   |   |   |   |   |   |   |   |   |   start <= 240705:
oxidoreductase_activity_ (17.84)
|   |   |   |   |   |   |   |   |   |   |   start > 240705:
molecular_function_ (22.67)
|   |   |   |   |   |   |   |   |   start > 243741
|   |   |   |   |   |   |   |   |   |   start <= 246389
|   |   |   |   |   |   |   |   |   |   |   start <= 244459:
structural_molecule_activity_ (11.8)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 244459:
RNA_binding_ (5.04)
|   |   |   |   |   |   |   |   |   |   start > 246389
|   |   |   |   |   |   |   |   |   |   |   start <= 255113:
molecular_function_ (32.17)
|   |   |   |   |   |   |   |   |   |   |   start > 255113:
structural_molecule_activity_ (14.03)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 243741
|   |   |   |   |   |   |   |   |   start <= 232366: DNA_binding_
(15.43)
|   |   |   |   |   |   |   |   |   start > 232366:
transferase_activity_ (17.18)
|   |   |   |   |   |   |   |   start > 243741
|   |   |   |   |   |   |   |   |   start <= 248847:
molecular_function_ (24.99)
|   |   |   |   |   |   |   |   |   start > 248847
|   |   |   |   |   |   |   |   |   |   start <= 249989:
DNA_binding_ (15.87)
|   |   |   |   |   |   |   |   |   |   start > 249989:
hydrolase_activity_ (10.57)
|   |   |   |   start > 257061
|   |   |   |   |   start <= 274925
|   |   |   |   |   |   start <= 268308
|   |   |   |   |   |   |   start <= 258912
|   |   |   |   |   |   |   |   start <= 258279: molecular_function_
(5.41)
|   |   |   |   |   |   |   |   start > 258279:
enzyme_regulator_activity_ (17.06)
|   |   |   |   |   |   |   start > 258912
|   |   |   |   |   |   |   |   start <= 261436
|   |   |   |   |   |   |   |   |   start <= 260157:
molecular_function_ (16.89)
|   |   |   |   |   |   |   |   |   start > 260157:
hydrolase_activity_ (17.21)
|   |   |   |   |   |   |   |   start > 261436: molecular_function_
(36.54)
|   |   |   |   |   |   start > 268308
|   |   |   |   |   |   |   start <= 273845
|   |   |   |   |   |   |   |   start <= 268650: protein_binding_
(13.91)
|   |   |   |   |   |   |   |   start > 268650:
enzyme_regulator_activity_ (40.25)
|   |   |   |   |   |   |   start > 273845: oxidoreductase_activity_
(14.66)
|   |   |   |   |   start > 274925
|   |   |   |   |   |   start <= 288907
|   |   |   |   |   |   |   start <= 284998
|   |   |   |   |   |   |   |   start <= 276291:
protein_kinase_activity_ (15.71)
|   |   |   |   |   |   |   |   start > 276291: molecular_function_
(107.0)
|   |   |   |   |   |   |   start > 284998
```

```
|   |   |   |   |   |   |   |   start <= 285665:
transcription_regulator_activity_ (16.65)
|   |   |   |   |   |   |   |   start > 285665:
protein_kinase_activity_ (12.11)
|   |   |   |   |   |   start > 288907
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 292632
|   |   |   |   |   |   |   |   |   start <= 290088:
protein_binding_ (23.7)
|   |   |   |   |   |   |   |   |   start > 290088:
enzyme_regulator_activity_ (14.32)
|   |   |   |   |   |   |   |   start > 292632
|   |   |   |   |   |   |   |   |   start <= 304102:
molecular_function_ (42.5)
|   |   |   |   |   |   |   |   |   start > 304102: protein_binding_
(15.09)
|   |   |   |   |   |   |   strand = W: peptidase_activity_ (11.92)
|   |   |   start > 307927
|   |   |   |   strand = C
|   |   |   |   |   start <= 316766
|   |   |   |   |   |   start <= 309169: molecular_function_ (23.5)
|   |   |   |   |   |   start > 309169
|   |   |   |   |   |   |   start <= 311163: transporter_activity_
(13.06)
|   |   |   |   |   |   |   start > 311163: isomerase_activity_
(18.2)
|   |   |   |   |   start > 316766
|   |   |   |   |   |   start <= 333724
|   |   |   |   |   |   |   start <= 326101: molecular_function_
(48.99)
|   |   |   |   |   |   |   start > 326101: hydrolase_activity_
(11.29)
|   |   |   |   |   |   start > 333724
|   |   |   |   |   |   |   start <= 336209:
nucleotidyltransferase_activity_ (13.77)
|   |   |   |   |   |   |   start > 336209: molecular_function_
(39.66)
|   |   |   |   strand = W
|   |   |   |   |   start <= 325746
|   |   |   |   |   |   start <= 312903
|   |   |   |   |   |   |   start <= 311163: transporter_activity_
(7.21)
|   |   |   |   |   |   |   start > 311163:
nucleotidyltransferase_activity_ (18.13)
|   |   |   |   |   |   start > 312903
|   |   |   |   |   |   |   start <= 321452
|   |   |   |   |   |   |   |   start <= 316766
|   |   |   |   |   |   |   |   |   start <= 315091:
molecular_function_ (14.47)
|   |   |   |   |   |   |   |   |   start > 315091:
structural_molecule_activity_ (16.58)
|   |   |   |   |   |   |   |   start > 316766: molecular_function_
(15.55)
|   |   |   |   |   |   |   start > 321452
```

```
|   |   |   |   |   |   |   |   start <= 322340: peptidase_activity_ 
(22.54)
|   |   |   |   |   |   |   |   start > 322340: molecular_function_ 
(21.47)
|   |   |   |   |   start > 325746
|   |   |   |   |   |   start <= 342533
|   |   |   |   |   |   |   start <= 326101: transferase_activity_ 
(20.71)
|   |   |   |   |   |   |   start > 326101
|   |   |   |   |   |   |   |   start <= 336417
|   |   |   |   |   |   |   |   |   start <= 333724: 
molecular_function_ (10.34)
|   |   |   |   |   |   |   |   |   start > 333724: 
oxidoreductase_activity_ (31.0/13.05)
|   |   |   |   |   |   |   |   start > 336417
|   |   |   |   |   |   |   |   |   start <= 339341: 
ligase_activity_ (8.7)
|   |   |   |   |   |   |   |   |   start > 339341: 
molecular_function_ (12.34)
|   |   |   |   |   |   start > 342533: transporter_activity_ 
(26.82)
|   |   start > 344059
|   |   |   start <= 370701
|   |   |   |   strand = C
|   |   |   |   |   start <= 353937
|   |   |   |   |   |   start <= 350298: protein_binding_ (10.82)
|   |   |   |   |   |   start > 350298: hydrolase_activity_ (21.23)
|   |   |   |   |   start > 353937
|   |   |   |   |   |   start <= 356892: RNA_binding_ (14.12)
|   |   |   |   |   |   start > 356892
|   |   |   |   |   |   |   start <= 364886: helicase_activity_ 
(13.65)
|   |   |   |   |   |   |   start > 364886: protein_binding_ (13.86)
|   |   |   |   strand = W
|   |   |   |   |   start <= 345689: protein_binding_ (23.97)
|   |   |   |   |   start > 345689
|   |   |   |   |   |   start <= 360882: molecular_function_ (46.98)
|   |   |   |   |   |   start > 360882
|   |   |   |   |   |   |   start <= 364886
|   |   |   |   |   |   |   |   start <= 363218: protein_binding_ 
(15.86)
|   |   |   |   |   |   |   |   start > 363218: RNA_binding_ (14.99)
|   |   |   |   |   |   |   start > 364886: molecular_function_ 
(26.79)
|   |   |   start > 370701: nucleotidyltransferase_activity_ (19.34)
|   start > 374303
|   |   start <= 403656
|   |   |   start <= 374522: RNA_binding_ (19.7)
|   |   |   start > 374522
|   |   |   |   strand = C
|   |   |   |   |   start <= 384606
|   |   |   |   |   |   start <= 378483: molecular_function_ (14.6)
|   |   |   |   |   |   start > 378483
```

```
|   |   |   |   |   |   |   start <= 381945:
transcription_regulator_activity_ (43.72/19.66)
|   |   |   |   |   |   |   start > 381945: DNA_binding_ (14.67)
|   |   |   |   |   start > 384606: molecular_function_ (55.71)
|   |   |   |   strand = W
|   |   |   |   |   start <= 382625
|   |   |   |   |   |   start <= 381083: molecular_function_ (59.37)
|   |   |   |   |   |   start > 381083
|   |   |   |   |   |   |   start <= 381945: hydrolase_activity_
(18.76)
|   |   |   |   |   |   |   start > 381945: molecular_function_
(13.73)
|   |   |   |   |   start > 382625
|   |   |   |   |   |   start <= 397291
|   |   |   |   |   |   |   start <= 385698:
transcription_regulator_activity_ (8.66)
|   |   |   |   |   |   |   start > 385698: RNA_binding_ (7.24)
|   |   |   |   |   |   start > 397291
|   |   |   |   |   |   |   start <= 399774
|   |   |   |   |   |   |   |   start <= 398511: molecular_function_
(16.94)
|   |   |   |   |   |   |   |   start > 398511
|   |   |   |   |   |   |   |   |   start <= 398730:
peptidase_activity_ (7.94)
|   |   |   |   |   |   |   |   |   start > 398730:
transcription_regulator_activity_ (14.24)
|   |   |   |   |   |   |   start > 399774: molecular_function_
(27.37)
|   |   start > 403656
|   |   |   start <= 415614
|   |   |   |   start <= 405964:
phosphoprotein_phosphatase_activity_ (16.28)
|   |   |   |   start > 405964
|   |   |   |   |   strand = C
|   |   |   |   |   |   distance <= 1458
|   |   |   |   |   |   |   start <= 412767: molecular_function_
(5.56/0.2)
|   |   |   |   |   |   |   start > 412767: transferase_activity_
(5.69/1.27)
|   |   |   |   |   |   distance > 1458
|   |   |   |   |   |   |   distance <= 3322: hydrolase_activity_
(47.39/1.76)
|   |   |   |   |   |   |   distance > 3322
|   |   |   |   |   |   |   |   neigh_strand = W:
transferase_activity_ (5.73)
|   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   start <= 408465:
hydrolase_activity_ (7.37)
|   |   |   |   |   |   |   |   |   start > 408465
|   |   |   |   |   |   |   |   |   |   start <= 412767:
molecular_function_ (2.29)
|   |   |   |   |   |   |   |   |   |   start > 412767:
hydrolase_activity_ (4.84)
|   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   start <= 408465: transporter_activity_
(18.3)
|   |   |   |   |   |   start > 408465: hydrolase_activity_ (12.43)
|   |   |   start > 415614
|   |   |   |   start <= 420733
|   |   |   |   |   start <= 416121:
transcription_regulator_activity_ (15.98)
|   |   |   |   |   start > 416121: oxidoreductase_activity_ (13.13)
|   |   |   |   start > 420733
|   |   |   |   |   start <= 423125: molecular_function_
(50.37/9.38)
|   |   |   |   |   start > 423125
|   |   |   |   |   |   start <= 432107
|   |   |   |   |   |   |   start <= 424510: transferase_activity_
(11.15)
|   |   |   |   |   |   |   start > 424510: peptidase_activity_
(19.61)
|   |   |   |   |   |   start > 432107: molecular_function_ (21.78)
```

For Biological Process

```
|   start <= 128151
|   |   start <= 99416
|   |   |   start <= 60694
|   |   |   |   start <= 34686
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 26106: biological_process_ (50.79)
|   |   |   |   |   |   start > 26106
|   |   |   |   |   |   |   start <= 32566: transport_ (13.77)
|   |   |   |   |   |   |   start > 32566: biological_process_
(35.87)
|   |   |   |   |   strand = W
|   |   |   |   |   |   Neigh_GO_aspect = C: vesicle-
mediated_transport_ (7.53/2.17)
|   |   |   |   |   |   Neigh_GO_aspect = F: transport_ (9.37/3.0)
|   |   |   |   |   |   Neigh_GO_aspect = P
|   |   |   |   |   |   |   neigh_num <= 1: vesicle-
mediated_transport_ (3.6/0.86)
|   |   |   |   |   |   |   neigh_num > 1: transport_ (4.61/1.28)
|   |   |   |   start > 34686
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 48091
|   |   |   |   |   |   |   start <= 41825: lipid_metabolic_process_
(16.13)
|   |   |   |   |   |   |   start > 41825: translation_ (21.63)
|   |   |   |   |   |   start > 48091
|   |   |   |   |   |   |   start <= 56545:
carbohydrate_metabolic_process_ (46.31)
|   |   |   |   |   |   |   start > 56545: biological_process_
(20.56)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 47690
|   |   |   |   |   |   |   start <= 37385:
carbohydrate_metabolic_process_ (11.98)
```

```
|   |   |   |   |   |   |   start > 37385
|   |   |   |   |   |   |   |   start <= 41825
|   |   |   |   |   |   |   |   |   start <= 39433:
biological_process_ (19.21)
|   |   |   |   |   |   |   |   |   start > 39433: cell_budding_
(31.74/12.67)
|   |   |   |   |   |   |   |   start > 41825: biological_process_
(31.06)
|   |   |   |   |   |   start > 47690
|   |   |   |   |   |   |   start <= 48091:
protein_modification_process_ (19.06)
|   |   |   |   |   |   |   start > 48091
|   |   |   |   |   |   |   |   start <= 55198
|   |   |   |   |   |   |   |   |   distance <= 555:
DNA_metabolic_process_ (3.37/0.13)
|   |   |   |   |   |   |   |   |   distance > 555
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
response_to_stress_ (5.24/1.4)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
response_to_stress_ (5.81/1.74)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (8.52/2.28)
|   |   |   |   |   |   |   |   start > 55198: biological_process_
(17.83)
|   |   |   start > 60694
|   |   |   |   strand = C
|   |   |   |   |   start <= 88716
|   |   |   |   |   |   start <= 73453
|   |   |   |   |   |   |   start <= 68708
|   |   |   |   |   |   |   |   start <= 62728:
DNA_metabolic_process_ (18.54)
|   |   |   |   |   |   |   |   start > 62728: transcription_
(15.29)
|   |   |   |   |   |   |   start > 68708: signal_transduction_
(32.17/16.07)
|   |   |   |   |   |   start > 73453
|   |   |   |   |   |   |   start <= 78074
|   |   |   |   |   |   |   |   start <= 75773:
cell_wall_organization_and_biogenesis_ (30.2)
|   |   |   |   |   |   |   |   start > 75773: biological_process_
(11.25)
|   |   |   |   |   |   |   start > 78074
|   |   |   |   |   |   |   |   start <= 85366: transcription_
(33.82/15.89)
|   |   |   |   |   |   |   |   start > 85366:
DNA_metabolic_process_ (19.16)
|   |   |   |   |   start > 88716
|   |   |   |   |   |   start <= 89715: vesicle-mediated_transport_
(15.82)
|   |   |   |   |   |   start > 89715
|   |   |   |   |   |   |   start <= 97395
|   |   |   |   |   |   |   |   start <= 96375
```

```
|   |   |   |   |   |   |   |   |   start <= 93619:
biological_process_ (13.08)
|   |   |   |   |   |   |   |   |   start > 93619: cell_cycle_
(17.22)
|   |   |   |   |   |   |   |   start > 96375: biological_process_
(22.55)
|   |   |   |   |   |   |   start > 97395: translation_ (10.65)
|   |   |   |   strand = W
|   |   |   |   |   start <= 93619
|   |   |   |   |   |   start <= 68708: translation_ (33.37/15.01)
|   |   |   |   |   |   start > 68708
|   |   |   |   |   |   |   start <= 83302
|   |   |   |   |   |   |   |   start <= 78074: biological_process_
(26.9)
|   |   |   |   |   |   |   |   start > 78074:
cytoskeleton_organization_and_biogenesis_ (21.73)
|   |   |   |   |   |   |   start > 83302
|   |   |   |   |   |   |   |   start <= 88716: cell_budding_ (8.14)
|   |   |   |   |   |   |   |   start > 88716: biological_process_
(25.25)
|   |   |   |   |   start > 93619
|   |   |   |   |   |   start <= 97111:
ribosome_biogenesis_and_assembly_ (27.15/13.55)
|   |   |   |   |   |   start > 97111: transport_ (19.9)
|   |   start > 99416
|   |   |   strand = C
|   |   |   |   start <= 102782
|   |   |   |   |   start <= 100501: meiosis_ (24.34)
|   |   |   |   |   start > 100501: pseudohyphal_growth_ (19.72)
|   |   |   |   start > 102782
|   |   |   |   |   start <= 113806: cell_budding_ (14.59)
|   |   |   |   |   start > 113806:
ribosome_biogenesis_and_assembly_ (15.37)
|   |   |   strand = W
|   |   |   |   start <= 117992
|   |   |   |   |   start <= 113806
|   |   |   |   |   |   start <= 102782: biological_process_ (11.08)
|   |   |   |   |   |   start > 102782: transcription_ (28.91/14.04)
|   |   |   |   |   start > 113806: meiosis_ (38.18/18.2)
|   |   |   |   start > 117992
|   |   |   |   |   start <= 122689: carbohydrate_metabolic_process_
(41.51/19.23)
|   |   |   |   |   start > 122689
|   |   |   |   |   |   start <= 126204: biological_process_
(43.31/19.35)
|   |   |   |   |   |   start > 126204:
cytoskeleton_organization_and_biogenesis_ (23.33)
|   start > 128151
|   |   start <= 370414
|   |   |   start <= 155219
|   |   |   |   strand = C
|   |   |   |   |   start <= 142925
|   |   |   |   |   |   start <= 137874: vitamin_metabolic_process_
(30.16/12.44)
```

```
|   |   |   |   |   |   start > 137874: conjugation_ (14.81)
|   |   |   |   |   start > 142925
|   |   |   |   |   |   start <= 148706:
ribosome_biogenesis_and_assembly_ (30.28/13.81)
|   |   |   |   |   |   start > 148706: transport_ (17.53)
|   |   |   |   strand = W
|   |   |   |   |   start <= 139749
|   |   |   |   |   |   start <= 134414
|   |   |   |   |   |   |   start <= 130607: cell_cycle_ (14.36)
|   |   |   |   |   |   |   start > 130607: transport_ (32.61)
|   |   |   |   |   |   start > 134414: vesicle-mediated_transport_
(15.9)
|   |   |   |   |   start > 139749
|   |   |   |   |   |   start <= 150556
|   |   |   |   |   |   |   start <= 142925:
amino_acid_and_derivative_metabolic_process_ (9.99)
|   |   |   |   |   |   |   start > 142925:
cell_wall_organization_and_biogenesis_ (20.75)
|   |   |   |   |   |   start > 150556
|   |   |   |   |   |   |   start <= 151592: meiosis_ (10.98)
|   |   |   |   |   |   |   start > 151592: electron_transport_
(13.42)
|   |   |   start > 155219
|   |   |   |   strand = C
|   |   |   |   |   start <= 261436
|   |   |   |   |   |   start <= 178001
|   |   |   |   |   |   |   start <= 169638
|   |   |   |   |   |   |   |   start <= 166412
|   |   |   |   |   |   |   |   |   start <= 160884
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
biological_process_ (20.75/9.66)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: transport_
(22.48/11.11)
|   |   |   |   |   |   |   |   |   start > 160884:
biological_process_ (22.71)
|   |   |   |   |   |   |   |   start > 166412
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
signal_transduction_ (6.76/2.65)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoskeleton_organization_and_biogenesis_ (6.39/1.97)
|   |   |   |   |   |   |   start > 169638
|   |   |   |   |   |   |   |   start <= 171748:
RNA_metabolic_process_ (23.28)
|   |   |   |   |   |   |   |   start > 171748
|   |   |   |   |   |   |   |   |   start <= 175028:
biological_process_ (33.82)
|   |   |   |   |   |   |   |   |   start > 175028:
response_to_stress_ (12.27)
|   |   |   |   |   |   start > 178001
|   |   |   |   |   |   |   start <= 229991
|   |   |   |   |   |   |   |   start <= 189063
|   |   |   |   |   |   |   |   |   start <= 183124
|   |   |   |   |   |   |   |   |   |   start <= 180424:
organelle_organization_and_biogenesis_ (15.41)
```

```
|   |   |   |   |   |   |   |   |   |   start > 180424:
ribosome_biogenesis_and_assembly_ (16.06)
|   |   |   |   |   |   |   |   |   start > 183124
|   |   |   |   |   |   |   |   |   |   start <= 187629
|   |   |   |   |   |   |   |   |   |   |   start <= 183934:
translation_ (18.51)
|   |   |   |   |   |   |   |   |   |   |   start > 183934:
amino_acid_and_derivative_metabolic_process_ (19.35)
|   |   |   |   |   |   |   |   |   |   start > 187629: translation_
(22.95)
|   |   |   |   |   |   |   |   start > 189063
|   |   |   |   |   |   |   |   |   start <= 216655
|   |   |   |   |   |   |   |   |   |   start <= 203256
|   |   |   |   |   |   |   |   |   |   |   start <= 200116
|   |   |   |   |   |   |   |   |   |   |   |   start <= 195596:
biological_process_ (15.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 195596
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 199400:
transport_ (10.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 199400:
biological_process_ (12.97)
|   |   |   |   |   |   |   |   |   |   |   start > 200116
|   |   |   |   |   |   |   |   |   |   |   |   start <= 202040:
cell_wall_organization_and_biogenesis_ (11.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 202040:
protein_modification_process_ (10.74)
|   |   |   |   |   |   |   |   |   |   start > 203256
|   |   |   |   |   |   |   |   |   |   |   start <= 204650:
biological_process_ (16.31)
|   |   |   |   |   |   |   |   |   |   |   start > 204650
|   |   |   |   |   |   |   |   |   |   |   |   start <= 212496:
RNA_metabolic_process_ (19.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 212496:
biological_process_ (16.23)
|   |   |   |   |   |   |   |   |   start > 216655
|   |   |   |   |   |   |   |   |   |   start <= 222487
|   |   |   |   |   |   |   |   |   |   |   start <= 220697:
protein_catabolic_process_ (19.02)
|   |   |   |   |   |   |   |   |   |   |   start > 220697:
amino_acid_and_derivative_metabolic_process_ (33.3)
|   |   |   |   |   |   |   |   |   |   start > 222487
|   |   |   |   |   |   |   |   |   |   |   start <= 226599:
meiosis_ (21.91)
|   |   |   |   |   |   |   |   |   |   |   start > 226599:
protein_modification_process_ (5.11)
|   |   |   |   |   |   |   start > 229991
|   |   |   |   |   |   |   |   start <= 235471
|   |   |   |   |   |   |   |   |   start <= 232366
|   |   |   |   |   |   |   |   |   |   start <= 231069:
cellular_respiration_ (9.82)
|   |   |   |   |   |   |   |   |   |   start > 231069: translation_
(10.47)
|   |   |   |   |   |   |   |   |   start > 232366: cytokinesis_
(13.14)
```

```
|   |   |   |   |   |   |   |   start > 235471
|   |   |   |   |   |   |   |   |   start <= 255113
|   |   |   |   |   |   |   |   |   |   start <= 244459
|   |   |   |   |   |   |   |   |   |   |   start <= 240705
|   |   |   |   |   |   |   |   |   |   |   |   start <= 237757:
biological_process_ (13.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 237757:
DNA_metabolic_process_ (10.21)
|   |   |   |   |   |   |   |   |   |   |   start > 240705
|   |   |   |   |   |   |   |   |   |   |   |   start <= 241940:
organelle_organization_and_biogenesis_ (15.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 241940
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 243741:
ribosome_biogenesis_and_assembly_ (11.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 243741:
organelle_organization_and_biogenesis_ (13.78)
|   |   |   |   |   |   |   |   |   |   start > 244459
|   |   |   |   |   |   |   |   |   |   |   start <= 246389:
RNA_metabolic_process_ (11.46)
|   |   |   |   |   |   |   |   |   |   |   start > 246389:
biological_process_ (37.3)
|   |   |   |   |   |   |   |   |   start > 255113
|   |   |   |   |   |   |   |   |   |   start <= 257061:
translation_ (20.72)
|   |   |   |   |   |   |   |   |   |   start > 257061:
organelle_organization_and_biogenesis_ (9.11)
|   |   |   |   |   start > 261436
|   |   |   |   |   |   start <= 292632
|   |   |   |   |   |   |   start <= 282651
|   |   |   |   |   |   |   |   start <= 274925
|   |   |   |   |   |   |   |   |   start <= 273845
|   |   |   |   |   |   |   |   |   |   start <= 268650:
signal_transduction_ (12.72)
|   |   |   |   |   |   |   |   |   |   start > 268650: vesicle-
mediated_transport_ (32.81/10.51)
|   |   |   |   |   |   |   |   |   start > 273845:
electron_transport_ (14.03)
|   |   |   |   |   |   |   |   start > 274925:
protein_modification_process_ (66.45/32.01)
|   |   |   |   |   |   |   start > 282651
|   |   |   |   |   |   |   |   start <= 288907
|   |   |   |   |   |   |   |   |   start <= 285665: conjugation_
(10.65)
|   |   |   |   |   |   |   |   |   start > 285665:
response_to_stress_ (13.89)
|   |   |   |   |   |   |   |   start > 288907
|   |   |   |   |   |   |   |   |   start <= 290088:
biological_process_ (20.88)
|   |   |   |   |   |   |   |   |   start > 290088:
signal_transduction_ (18.28)
|   |   |   |   |   |   start > 292632
|   |   |   |   |   |   |   start <= 345689
|   |   |   |   |   |   |   |   start <= 309169
|   |   |   |   |   |   |   |   |   start <= 300298
```

```
|   |   |   |   |   |   |   |   |   |   start <= 300008:
protein_catabolic_process_ (8.75)
|   |   |   |   |   |   |   |   |   |   start > 300008: translation_
(17.62)
|   |   |   |   |   |   |   |   |   start > 300298
|   |   |   |   |   |   |   |   |   |   start <= 304102:
biological_process_ (33.58)
|   |   |   |   |   |   |   |   |   |   start > 304102
|   |   |   |   |   |   |   |   |   |   |   start <= 307927:
cell_wall_organization_and_biogenesis_ (13.97)
|   |   |   |   |   |   |   |   |   |   |   start > 307927:
biological_process_ (13.53)
|   |   |   |   |   |   |   |   start > 309169
|   |   |   |   |   |   |   |   |   start <= 322340
|   |   |   |   |   |   |   |   |   |   start <= 316766
|   |   |   |   |   |   |   |   |   |   |   start <= 311163:
transport_ (14.75)
|   |   |   |   |   |   |   |   |   |   |   start > 311163:
amino_acid_and_derivative_metabolic_process_ (20.73)
|   |   |   |   |   |   |   |   |   |   start > 316766: sporulation_
(38.64/17.18)
|   |   |   |   |   |   |   |   |   start > 322340
|   |   |   |   |   |   |   |   |   |   start <= 339341
|   |   |   |   |   |   |   |   |   |   |   start <= 326101
|   |   |   |   |   |   |   |   |   |   |   |   start <= 324372:
translation_ (15.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 324372:
biological_process_ (21.61)
|   |   |   |   |   |   |   |   |   |   |   start > 326101
|   |   |   |   |   |   |   |   |   |   |   |   start <= 333724:
transport_ (12.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 333724
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 336209:
DNA_metabolic_process_ (11.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 336209:
translation_ (5.98)
|   |   |   |   |   |   |   |   |   |   start > 339341:
protein_catabolic_process_ (21.49)
|   |   |   |   |   |   |   start > 345689
|   |   |   |   |   |   |   |   start <= 353937
|   |   |   |   |   |   |   |   |   start <= 350298
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: vesicle-
mediated_transport_ (17.05/7.53)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: transport_
(15.93/5.23)
|   |   |   |   |   |   |   |   |   start > 350298:
cell_wall_organization_and_biogenesis_ (26.91)
|   |   |   |   |   |   |   |   start > 353937
|   |   |   |   |   |   |   |   |   start <= 356892:
RNA_metabolic_process_ (14.99)
|   |   |   |   |   |   |   |   |   start > 356892
|   |   |   |   |   |   |   |   |   |   start <= 364886:
DNA_metabolic_process_ (11.42)
```

```
|   |   |   |   |   |   |   |   |   |   start > 364886: cytokinesis_
(12.03)
|   |   |   |   strand = W
|   |   |   |   |   start <= 288907
|   |   |   |   |   |   start <= 212496
|   |   |   |   |   |   |   start <= 195596
|   |   |   |   |   |   |   |   start <= 178001
|   |   |   |   |   |   |   |   |   start <= 171748
|   |   |   |   |   |   |   |   |   |   start <= 160884:
biological_process_ (35.11)
|   |   |   |   |   |   |   |   |   |   start > 160884
|   |   |   |   |   |   |   |   |   |   |   start <= 166412:
protein_modification_process_ (15.84)
|   |   |   |   |   |   |   |   |   |   |   start > 166412:
biological_process_ (12.13)
|   |   |   |   |   |   |   |   |   start > 171748
|   |   |   |   |   |   |   |   |   |   start <= 175028:
translation_ (15.02)
|   |   |   |   |   |   |   |   |   |   start > 175028: sporulation_
(12.39)
|   |   |   |   |   |   |   |   start > 178001
|   |   |   |   |   |   |   |   |   start <= 183934
|   |   |   |   |   |   |   |   |   |   start <= 180424:
carbohydrate_metabolic_process_ (14.83)
|   |   |   |   |   |   |   |   |   |   start > 180424: cytokinesis_
(19.19)
|   |   |   |   |   |   |   |   |   start > 183934
|   |   |   |   |   |   |   |   |   |   start <= 189063:
biological_process_ (13.89)
|   |   |   |   |   |   |   |   |   |   start > 189063
|   |   |   |   |   |   |   |   |   |   |   start <= 193592:
organelle_organization_and_biogenesis_ (16.59)
|   |   |   |   |   |   |   |   |   |   |   start > 193592:
biological_process_ (13.86)
|   |   |   |   |   |   |   start > 195596: translation_ (49.69)
|   |   |   |   |   |   start > 212496
|   |   |   |   |   |   |   start <= 255113
|   |   |   |   |   |   |   |   start <= 232366
|   |   |   |   |   |   |   |   |   start <= 220697
|   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 1140:
transport_ (5.81/2.91)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 1140:
vesicle-mediated_transport_ (4.73/0.8)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
transport_ (21.59/10.11)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
membrane_organization_and_biogenesis_ (40.64/23.54)
|   |   |   |   |   |   |   |   |   start > 220697
|   |   |   |   |   |   |   |   |   |   distance <= 1606:
cell_cycle_ (10.09/2.75)
|   |   |   |   |   |   |   |   |   |   distance > 1606: meiosis_
(27.63/10.58)
```

```
|   |   |   |   |   |   |   |   start > 232366
|   |   |   |   |   |   |   |   |   start <= 248847
|   |   |   |   |   |   |   |   |   |   start <= 246389
|   |   |   |   |   |   |   |   |   |   |   start <= 243741:
ribosome_biogenesis_and_assembly_ (12.61)
|   |   |   |   |   |   |   |   |   |   |   start > 243741:
biological_process_ (15.31)
|   |   |   |   |   |   |   |   |   |   start > 246389: translation_
(16.44)
|   |   |   |   |   |   |   |   |   start > 248847
|   |   |   |   |   |   |   |   |   |   start <= 249989:
transcription_ (23.83/10.83)
|   |   |   |   |   |   |   |   |   |   start > 249989:
response_to_stress_ (22.97)
|   |   |   |   |   |   |   start > 255113
|   |   |   |   |   |   |   |   start <= 271160
|   |   |   |   |   |   |   |   |   start <= 261436
|   |   |   |   |   |   |   |   |   |   start <= 260157
|   |   |   |   |   |   |   |   |   |   |   start <= 258912:
carbohydrate_metabolic_process_ (18.16)
|   |   |   |   |   |   |   |   |   |   |   start > 258912:
pseudohyphal_growth_ (13.1)
|   |   |   |   |   |   |   |   |   |   start > 260157: vesicle-
mediated_transport_ (21.97/10.8)
|   |   |   |   |   |   |   |   |   start > 261436
|   |   |   |   |   |   |   |   |   |   start <= 268650
|   |   |   |   |   |   |   |   |   |   |   start <= 268308:
biological_process_ (18.08)
|   |   |   |   |   |   |   |   |   |   |   start > 268308:
cell_cycle_ (30.91/13.82)
|   |   |   |   |   |   |   |   |   |   start > 268650:
carbohydrate_metabolic_process_ (20.69)
|   |   |   |   |   |   |   |   start > 271160
|   |   |   |   |   |   |   |   |   start <= 278425
|   |   |   |   |   |   |   |   |   |   start <= 276524:
biological_process_ (22.09)
|   |   |   |   |   |   |   |   |   |   start > 276524: transport_
(67.88/30.36)
|   |   |   |   |   |   |   |   |   start > 278425:
DNA_metabolic_process_ (25.62)
|   |   |   |   |   start > 288907
|   |   |   |   |   |   start <= 326101
|   |   |   |   |   |   |   start <= 315091
|   |   |   |   |   |   |   |   start <= 311163
|   |   |   |   |   |   |   |   |   start <= 301255
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (18.38/11.11)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
protein_modification_process_ (16.46/7.2)
|   |   |   |   |   |   |   |   |   start > 301255: transport_
(21.22/7.45)
|   |   |   |   |   |   |   |   start > 311163
|   |   |   |   |   |   |   |   |   start <= 312903: transcription_
(10.77)
```

```
|   |   |   |   |   |   |   |   |   start > 312903:
ribosome_biogenesis_and_assembly_ (23.85)
|   |   |   |   |   |   |   start > 315091
|   |   |   |   |   |   |   |   start <= 325746
|   |   |   |   |   |   |   |   |   start <= 321452
|   |   |   |   |   |   |   |   |   |   start <= 316766:
translation_ (20.48)
|   |   |   |   |   |   |   |   |   |   start > 316766:
nuclear_organization_and_biogenesis_ (12.8)
|   |   |   |   |   |   |   |   |   start > 321452
|   |   |   |   |   |   |   |   |   |   start <= 322340:
conjugation_ (14.09)
|   |   |   |   |   |   |   |   |   |   start > 322340: translation_
(11.97)
|   |   |   |   |   |   |   |   start > 325746:
protein_modification_process_ (15.2)
|   |   |   |   |   |   start > 326101
|   |   |   |   |   |   |   start <= 360882
|   |   |   |   |   |   |   |   start <= 344059
|   |   |   |   |   |   |   |   |   start <= 339341
|   |   |   |   |   |   |   |   |   |   start <= 333724:
biological_process_ (12.55)
|   |   |   |   |   |   |   |   |   |   start > 333724
|   |   |   |   |   |   |   |   |   |   |   start <= 336417:
response_to_stress_ (21.24)
|   |   |   |   |   |   |   |   |   |   |   start > 336417:
lipid_metabolic_process_ (8.85)
|   |   |   |   |   |   |   |   |   start > 339341
|   |   |   |   |   |   |   |   |   |   start <= 342533:
cell_budding_ (13.76)
|   |   |   |   |   |   |   |   |   |   start > 342533: transport_
(26.3)
|   |   |   |   |   |   |   |   start > 344059: biological_process_
(71.55)
|   |   |   |   |   |   |   start > 360882
|   |   |   |   |   |   |   |   start <= 363218:
organelle_organization_and_biogenesis_ (27.97/8.0)
|   |   |   |   |   |   |   |   start > 363218
|   |   |   |   |   |   |   |   |   start <= 364886:
RNA_metabolic_process_ (14.77)
|   |   |   |   |   |   |   |   |   start > 364886: translation_
(21.85)
|   |   start > 370414
|   |   |   start <= 405964
|   |   |   |   start <= 403488
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 375428: DNA_metabolic_process_
(20.46)
|   |   |   |   |   |   start > 375428
|   |   |   |   |   |   |   start <= 384606
|   |   |   |   |   |   |   |   start <= 378483: biological_process_
(14.54)
|   |   |   |   |   |   |   |   start > 378483: transcription_
(49.22/21.3)
```

```
|   |   |   |   |   |   |   start > 384606
|   |   |   |   |   |   |   |   distance <= 2516:
biological_process_ (31.12/0.75)
|   |   |   |   |   |   |   |   distance > 2516
|   |   |   |   |   |   |   |   |   start <= 385698:
biological_process_ (5.66)
|   |   |   |   |   |   |   |   |   start > 385698:
pseudohyphal_growth_ (12.03)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 398511
|   |   |   |   |   |   |   start <= 382625
|   |   |   |   |   |   |   |   start <= 374522
|   |   |   |   |   |   |   |   |   start <= 370701:
biological_process_ (24.57)
|   |   |   |   |   |   |   |   |   start > 370701:
RNA_metabolic_process_ (28.5)
|   |   |   |   |   |   |   |   start > 374522
|   |   |   |   |   |   |   |   |   start <= 378483
|   |   |   |   |   |   |   |   |   |   start <= 375428:
biological_process_ (14.05)
|   |   |   |   |   |   |   |   |   |   start > 375428:
ribosome_biogenesis_and_assembly_ (16.92)
|   |   |   |   |   |   |   |   |   start > 378483
|   |   |   |   |   |   |   |   |   |   start <= 381083:
biological_process_ (14.88)
|   |   |   |   |   |   |   |   |   |   start > 381083
|   |   |   |   |   |   |   |   |   |   |   start <= 381945:
RNA_metabolic_process_ (9.95)
|   |   |   |   |   |   |   |   |   |   |   start > 381945:
biological_process_ (13.38)
|   |   |   |   |   |   |   start > 382625
|   |   |   |   |   |   |   |   start <= 385698: cell_cycle_ (13.4)
|   |   |   |   |   |   |   |   start > 385698
|   |   |   |   |   |   |   |   |   start <= 397291:
RNA_metabolic_process_ (7.85)
|   |   |   |   |   |   |   |   |   start > 397291:
biological_process_ (11.06)
|   |   |   |   |   |   start > 398511
|   |   |   |   |   |   |   start <= 398730: transport_ (17.73)
|   |   |   |   |   |   |   start > 398730: transcription_
(29.92/11.5)
|   |   |   |   start > 403488
|   |   |   |   |   start <= 403656: cell_cycle_ (63.7/38.47)
|   |   |   |   |   start > 403656:
ribosome_biogenesis_and_assembly_ (36.78/16.24)
|   |   |   start > 405964
|   |   |   |   start <= 408465
|   |   |   |   |   start <= 407639: biological_process_ (14.35)
|   |   |   |   |   start > 407639: transport_ (18.62)
|   |   |   |   start > 408465
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 420733
|   |   |   |   |   |   |   start <= 416121: biological_process_
(48.12)
```

```
|   |   |   |   |   |   |   start > 416121:
amino_acid_and_derivative_metabolic_process_ (11.5)
|   |   |   |   |   |   start > 420733: biological_process_ (66.57)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 424510
|   |   |   |   |   |   |   start <= 412767: biological_process_
(15.38)
|   |   |   |   |   |   |   start > 412767: response_to_stress_
(23.11)
|   |   |   |   |   |   start > 424510: biological_process_ (15.78)
```

Decision Tree Generated for Chromosome Ten:
For Cellular Component

```
|   start <= 96527
|   |   start <= 36919
|   |   |   start <= 26887
|   |   |   |   start <= 18536: cellular_component_ (64.94)
|   |   |   |   start > 18536
|   |   |   |   |   start <= 19497: plasma_membrane_ (18.12)
|   |   |   |   |   start > 19497
|   |   |   |   |   |   start <= 26086
|   |   |   |   |   |   |   start <= 21973: cellular_component_
(15.08)
|   |   |   |   |   |   |   start > 21973
|   |   |   |   |   |   |   |   start <= 23133: cytoplasm_ (14.49)
|   |   |   |   |   |   |   |   start > 23133: cellular_component_
(9.67)
|   |   |   |   |   |   start > 26086: plasma_membrane_ (14.01)
|   |   |   start > 26887
|   |   |   |   strand = C: endoplasmic_reticulum_ (15.0)
|   |   |   |   strand = W
|   |   |   |   |   start <= 32163: ribosome_ (5.94)
|   |   |   |   |   start > 32163: peroxisome_ (12.75)
|   |   start > 36919
|   |   |   start <= 94528
|   |   |   |   start <= 68781
|   |   |   |   |   start <= 53341
|   |   |   |   |   |   start <= 47433
|   |   |   |   |   |   |   start <= 41183
|   |   |   |   |   |   |   |   start <= 38005: mitochondrion_
(11.76)
|   |   |   |   |   |   |   |   start > 38005
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
mitochondrion_ (2.43/0.21)
|   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
nucleus_ (6.04/1.66)
|   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
nucleus_ (5.99/0.46)
|   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: mitochondrion_ (3.04/0.56)
|   |   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: nucleus_ (1.4/0.18)
|   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: nucleus_ (5.76/1.34)
|   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
mitochondrion_ (3.2/0.33)
|   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = transcription_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: nucleus_ (0.59/0.08)
|   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   start > 41183: ribosome_ (15.5)
|   |   |   |   |   |   start > 47433
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 50443: cellular_component_
(27.9)
|   |   |   |   |   |   |   |   start > 50443
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
site_of_polarized_growth_ (15.68/5.07)
|   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   distance <= 7339:
site_of_polarized_growth_ (2.39/0.18)
|   |   |   |   |   |   |   |   |   |   |   distance > 7339:
Golgi_apparatus_ (3.46/1.11)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
Golgi_apparatus_ (5.34/1.18)
|   |   |   |   |   |   |   strand = W: nucleus_ (8.68)
|   |   |   |   |   start > 53341
```

```
|   |   |   |   |   |   start <= 59172
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 58813: mitochondrion_
(23.71)
|   |   |   |   |   |   |   |   start > 58813: cytoplasm_ (9.36)
|   |   |   |   |   |   |   strand = W: cytoplasm_ (12.22)
|   |   |   |   |   |   start > 59172
|   |   |   |   |   |   |   strand = C: membrane_ (16.25)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 60843: membrane_ (10.24)
|   |   |   |   |   |   |   |   start > 60843
|   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(4.62/1.16)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(6.56/1.55)
|   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(3.85/0.68)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(9.19/2.98)
|   |   |   |   start > 68781
|   |   |   |   |   start <= 79261
|   |   |   |   |   |   start <= 73413
|   |   |   |   |   |   |   strand = C: endoplasmic_reticulum_
(10.43)
|   |   |   |   |   |   |   strand = W: cellular_component_
(41.23/10.85)
|   |   |   |   |   |   start > 73413
|   |   |   |   |   |   |   start <= 75932: ribosome_ (57.46/15.53)
|   |   |   |   |   |   |   start > 75932: nucleus_ (8.08)
|   |   |   |   |   start > 79261
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 90784
|   |   |   |   |   |   |   |   start <= 85658: cellular_component_
(22.07)
|   |   |   |   |   |   |   |   start > 85658
|   |   |   |   |   |   |   |   |   start <= 88785: mitochondrion_
(16.0)
|   |   |   |   |   |   |   |   |   start > 88785
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: mitochondrion_ (5.31/2.72)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: Golgi_apparatus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: Golgi_apparatus_ (6.94/3.33)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: Golgi_apparatus_ (4.8/1.97)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: mitochondrion_ (1.97/0.45)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
mitochondrion_ (3.28/1.34)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: mitochondrion_ (2.57/1.23)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
membrane_ (5.18/2.33)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
Golgi_apparatus_ (2.22/0.46)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: mitochondrion_ (5.01/2.5)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
membrane_ (3.84/1.15)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: membrane_ (1.26/0.77)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: Golgi_apparatus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: Golgi_apparatus_ (5.3/1.6)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: Golgi_apparatus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: Golgi_apparatus_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: Golgi_apparatus_ (0.0)
|   |   |   |   |   |   |   start > 90784: cellular_component_
(36.02/12.5)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 84066
|   |   |   |   |   |   |   |   start <= 80153: Golgi_apparatus_
(20.45)
|   |   |   |   |   |   |   |   start > 80153
|   |   |   |   |   |   |   |   |   start <= 83446
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   distance <= 542:
cellular_component_ (6.88/1.45)
|   |   |   |   |   |   |   |   |   |   |   distance > 542:
chromosome_ (7.56/2.18)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_component_ (31.04/18.24)
|   |   |   |   |   |   |   |   |   start > 83446: Golgi_apparatus_
(13.97)
|   |   |   |   |   |   |   start > 84066
|   |   |   |   |   |   |   |   start <= 88785: cellular_component_
(50.55/14.65)
|   |   |   |   |   |   |   |   start > 88785: ribosome_ (20.75)
```

```
|   |   |   start > 94528
|   |   |   |   start <= 95090: extracellular_region_ (16.44)
|   |   |   |   start > 95090: chromosome_ (13.38)
|   start > 96527
|   |   start <= 707154
|   |   |   start <= 559409
|   |   |   |   start <= 554842
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 290769
|   |   |   |   |   |   |   start <= 262547
|   |   |   |   |   |   |   |   start <= 211573
|   |   |   |   |   |   |   |   |   start <= 140434
|   |   |   |   |   |   |   |   |   |   start <= 120445
|   |   |   |   |   |   |   |   |   |   |   start <= 101773
|   |   |   |   |   |   |   |   |   |   |   |   start <= 100888:
mitochondrion_ (15.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 100888:
plasma_membrane_ (9.53)
|   |   |   |   |   |   |   |   |   |   |   start > 101773
|   |   |   |   |   |   |   |   |   |   |   |   start <= 117241
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 113329
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
106428: nucleus_ (16.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
106428
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
109455: cellular_component_ (15.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
109455
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 111153: nucleus_ (25.98/10.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 111153: cellular_component_ (7.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 113329:
cytoplasm_ (34.81/8.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 117241:
cellular_component_ (23.66)
|   |   |   |   |   |   |   |   |   |   start > 120445
|   |   |   |   |   |   |   |   |   |   |   start <= 122944
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: endoplasmic_reticulum_ (5.3/1.46)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: plasma_membrane_ (0.52/0.23)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: extracellular_region_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: plasma_membrane_ (3.34/1.33)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: extracellular_region_ (5.76/1.61)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: plasma_membrane_ (2.33/0.85)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: endoplasmic_reticulum_ (2.52/1.54)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: extracellular_region_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: endoplasmic_reticulum_ (8.13/4.83)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: extracellular_region_ (3.52/1.09)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: extracellular_region_
(3.83/1.15)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: endoplasmic_reticulum_ (8.11/4.59)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: plasma_membrane_ (1.65/0.91)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: extracellular_region_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: plasma_membrane_ (4.07/1.39)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: extracellular_region_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: extracellular_region_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   start > 122944
|   |   |   |   |   |   |   |   |   |   |   |   start <= 137376
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 128949
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
126324: membrane_ (36.23/20.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
126324: plasma_membrane_ (12.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 128949
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
135930
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
130640: cytoplasm_ (15.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
130640
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 133932: endomembrane_system_ (12.47)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   
start > 133932: cytoplasm_ (14.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start > 
135930: membrane_ (11.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 137376: 
nucleolus_ (33.21)
|   |   |   |   |   |   |   |   |   start > 140434
|   |   |   |   |   |   |   |   |   |   start <= 177303
|   |   |   |   |   |   |   |   |   |   |   start <= 152996
|   |   |   |   |   |   |   |   |   |   |   |   start <= 150958
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 146356: 
mitochondrion_ (10.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 146356: 
nucleus_ (24.46/6.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 150958: 
Golgi_apparatus_ (24.46)
|   |   |   |   |   |   |   |   |   |   |   start > 152996
|   |   |   |   |   |   |   |   |   |   |   |   start <= 158185
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 156166: 
cytoplasm_ (59.23/22.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 156166: 
ribosome_ (10.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 158185
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 172364
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <= 
165345: mitochondrion_ (29.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start > 
165345
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   
neigh_strand = W: mitochondrion_ (14.95/6.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   
neigh_strand = C: cytoplasm_ (12.3/2.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 172364: 
plasma_membrane_ (13.63)
|   |   |   |   |   |   |   |   |   |   start > 177303
|   |   |   |   |   |   |   |   |   |   |   start <= 186677
|   |   |   |   |   |   |   |   |   |   |   |   start <= 181707
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 180100: 
cytoplasm_ (12.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 180100: 
cellular_component_ (16.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 181707: 
nucleus_ (36.5)
|   |   |   |   |   |   |   |   |   |   |   start > 186677
|   |   |   |   |   |   |   |   |   |   |   |   start <= 192530
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 187643: 
cytoplasm_ (23.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 187643
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <= 
189715: Golgi_apparatus_ (60.16/32.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start > 
189715: cytoplasm_ (17.63)
|   |   |   |   |   |   |   |   |   |   |   |   start > 192530
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 194872:
cellular_component_ (15.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 194872
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
197383: cytoplasm_ (15.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
197383: nucleus_ (14.88)
|   |   |   |   |   |   |   |   start > 211573
|   |   |   |   |   |   |   |   |   start <= 242078
|   |   |   |   |   |   |   |   |   |   start <= 218852
|   |   |   |   |   |   |   |   |   |   |   start <= 217305:
nucleolus_ (48.55/22.69)
|   |   |   |   |   |   |   |   |   |   |   start > 217305:
membrane_ (15.85)
|   |   |   |   |   |   |   |   |   |   start > 218852
|   |   |   |   |   |   |   |   |   |   |   start <= 228475
|   |   |   |   |   |   |   |   |   |   |   |   start <= 221386:
cellular_component_ (16.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 221386:
nucleolus_ (27.78)
|   |   |   |   |   |   |   |   |   |   |   start > 228475:
cellular_component_ (29.68)
|   |   |   |   |   |   |   |   |   start > 242078
|   |   |   |   |   |   |   |   |   |   start <= 254437:
Golgi_apparatus_ (35.76/15.78)
|   |   |   |   |   |   |   |   |   |   start > 254437
|   |   |   |   |   |   |   |   |   |   |   start <= 257418:
plasma_membrane_ (15.43)
|   |   |   |   |   |   |   |   |   |   |   start > 257418:
membrane_ (15.78)
|   |   |   |   |   |   |   start > 262547
|   |   |   |   |   |   |   |   start <= 285266
|   |   |   |   |   |   |   |   |   start <= 265921: chromosome_
(24.99)
|   |   |   |   |   |   |   |   |   start > 265921
|   |   |   |   |   |   |   |   |   |   start <= 281180
|   |   |   |   |   |   |   |   |   |   |   start <= 272822:
nucleus_ (11.7)
|   |   |   |   |   |   |   |   |   |   |   start > 272822:
cytoplasm_ (16.2)
|   |   |   |   |   |   |   |   |   |   start > 281180: nucleus_
(11.84)
|   |   |   |   |   |   |   |   start > 285266
|   |   |   |   |   |   |   |   |   start <= 289221:
endomembrane_system_ (19.05)
|   |   |   |   |   |   |   |   |   start > 289221:
endoplasmic_reticulum_ (40.42/18.73)
|   |   |   |   |   |   start > 290769
|   |   |   |   |   |   |   start <= 467026
|   |   |   |   |   |   |   |   start <= 425151
|   |   |   |   |   |   |   |   |   start <= 398393
|   |   |   |   |   |   |   |   |   |   start <= 349228
|   |   |   |   |   |   |   |   |   |   |   start <= 327868
|   |   |   |   |   |   |   |   |   |   |   |   start <= 306127
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 295240
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
294042: cell_wall_ (16.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
294042: cellular_component_ (6.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 295240:
nucleus_ (34.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 306127
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 1254
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
314867
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
313910
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 310632: mitochondrion_ (3.78/0.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 310632: cytoplasm_ (4.86/1.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
313910
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: membrane_fraction_ (6.67/2.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: mitochondrion_ (14.7/4.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
314867
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
315552: nucleus_ (14.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
315552: mitochondrion_ (10.99/0.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 1254
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
320011
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
310632: mitochondrion_ (30.35/13.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
310632
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 312701: nucleolus_ (19.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 312701
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 313910: cytoplasm_ (6.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 313910: mitochondrion_ (6.32/1.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
320011: cytoplasm_ (21.85)
|   |   |   |   |   |   |   |   |   |   |   start > 327868
|   |   |   |   |   |   |   |   |   |   |   |   start <= 349173
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 348632
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
342517
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
334260
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 330116: cellular_component_ (18.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 330116: nucleus_ (14.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
334260: cellular_component_ (21.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
342517: nucleus_ (17.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 348632:
cellular_component_ (21.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 349173:
nucleolus_ (20.32)
|   |   |   |   |   |   |   |   |   |   start > 349228
|   |   |   |   |   |   |   |   |   |   |   start <= 383832
|   |   |   |   |   |   |   |   |   |   |   |   start <= 365779:
cytoplasm_ (57.2/29.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 365779
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 373794
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: membrane_ (16.69/7.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: cellular_component_ (23.81/13.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 373794
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
378355
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
374572: cytoplasm_ (17.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
374572: cellular_component_ (8.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
378355: cytoplasm_ (30.25/14.8)
|   |   |   |   |   |   |   |   |   |   |   start > 383832
|   |   |   |   |   |   |   |   |   |   |   |   start <= 393962
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 391306
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
387652: cellular_component_ (9.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
387652
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
390848: Golgi_apparatus_ (27.18/12.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
390848: cytoplasm_ (21.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 391306:
cellular_component_ (13.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 393962
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 396791
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
396587
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 2536: membrane_ (13.01/1.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 2536: cytoplasm_ (4.8/0.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
396587: cytoplasm_ (7.89)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 396791:
mitochondrion_ (14.58)
|   |   |   |   |   |   |   |   |   start > 398393
|   |   |   |   |   |   |   |   |   |   start <= 405583
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cell_cortex_ (10.14/3.34)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoskeleton_ (20.11/7.27)
|   |   |   |   |   |   |   |   |   |   start > 405583
|   |   |   |   |   |   |   |   |   |   |   start <= 414960
|   |   |   |   |   |   |   |   |   |   |   |   start <= 413393
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 411034:
nucleus_ (14.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 411034:
endoplasmic_reticulum_ (8.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 413393:
nucleus_ (22.81)
|   |   |   |   |   |   |   |   |   |   |   start > 414960
|   |   |   |   |   |   |   |   |   |   |   |   start <= 419556
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 416030:
cytoplasm_ (5.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 416030
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: nucleus_ (3.66/1.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: nucleolus_ (17.13/6.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 419556
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 421657:
cytoplasm_ (23.89/8.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 421657
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
424103: nucleus_ (16.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
424103: cytoplasm_ (18.74)
|   |   |   |   |   |   |   |   start > 425151
|   |   |   |   |   |   |   |   |   start <= 445916
|   |   |   |   |   |   |   |   |   |   start <= 436796
|   |   |   |   |   |   |   |   |   |   |   start <= 432638:
Golgi_apparatus_ (26.73)
|   |   |   |   |   |   |   |   |   |   |   start > 432638
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
endoplasmic_reticulum_ (11.01/4.55)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
membrane_ (8.85/1.76)
|   |   |   |   |   |   |   |   |   |   start > 436796
|   |   |   |   |   |   |   |   |   |   |   start <= 442546:
mitochondrion_ (9.54)
|   |   |   |   |   |   |   |   |   |   |   start > 442546:
cell_wall_ (19.58)
|   |   |   |   |   |   |   |   |   start > 445916
|   |   |   |   |   |   |   |   |   |   start <= 462714
|   |   |   |   |   |   |   |   |   |   |   start <= 456232
|   |   |   |   |   |   |   |   |   |   |   |   start <= 451013:
cellular_component_ (20.93)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 451013
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
mitochondrion_ (14.63/6.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (16.67/3.7)
|   |   |   |   |   |   |   |   |   |   |   start > 456232
|   |   |   |   |   |   |   |   |   |   |   |   start <= 458354:
endoplasmic_reticulum_ (43.17/19.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 458354:
cellular_component_ (35.38)
|   |   |   |   |   |   |   |   |   |   start > 462714
|   |   |   |   |   |   |   |   |   |   |   start <= 466201:
mitochondrion_ (16.26)
|   |   |   |   |   |   |   |   |   |   |   start > 466201: nucleus_
(16.07)
|   |   |   |   |   |   |   start > 467026
|   |   |   |   |   |   |   |   start <= 469777
|   |   |   |   |   |   |   |   |   start <= 468274
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
mitochondrion_ (16.42/4.48)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
peroxisome_ (24.44/10.64)
|   |   |   |   |   |   |   |   |   start > 468274: chromosome_
(21.05)
|   |   |   |   |   |   |   |   start > 469777
|   |   |   |   |   |   |   |   |   start <= 514048
|   |   |   |   |   |   |   |   |   |   start <= 497348
|   |   |   |   |   |   |   |   |   |   |   start <= 486189
|   |   |   |   |   |   |   |   |   |   |   |   start <= 471664:
cytoplasm_ (26.54)
|   |   |   |   |   |   |   |   |   |   |   |   start > 471664:
cellular_component_ (11.3)
|   |   |   |   |   |   |   |   |   |   |   start > 486189
|   |   |   |   |   |   |   |   |   |   |   |   start <= 491074:
cytoplasmic_membrane-bound_vesicle_ (16.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 491074:
cytoplasm_ (36.98)
|   |   |   |   |   |   |   |   |   |   start > 497348
|   |   |   |   |   |   |   |   |   |   |   start <= 507739:
cellular_component_ (11.49)
|   |   |   |   |   |   |   |   |   |   |   start > 507739:
nucleolus_ (16.51)
|   |   |   |   |   |   |   |   |   start > 514048
|   |   |   |   |   |   |   |   |   |   start <= 544055
|   |   |   |   |   |   |   |   |   |   |   start <= 517506:
nucleus_ (17.32)
|   |   |   |   |   |   |   |   |   |   |   start > 517506
|   |   |   |   |   |   |   |   |   |   |   |   start <= 526328
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 524086
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
519178: cytoplasm_ (34.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
519178
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
522041: mitochondrion_ (10.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
522041: cytoplasm_ (18.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 524086:
ribosome_ (26.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 526328:
cytoplasm_ (72.79/26.05)
|   |   |   |   |   |   |   |   |   |   start > 544055
|   |   |   |   |   |   |   |   |   |   |   start <= 548752:
plasma_membrane_ (17.73)
|   |   |   |   |   |   |   |   |   |   |   start > 548752:
mitochondrion_ (14.95)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 317279
|   |   |   |   |   |   |   start <= 294042
|   |   |   |   |   |   |   |   start <= 246486
|   |   |   |   |   |   |   |   |   start <= 225051
|   |   |   |   |   |   |   |   |   |   start <= 126324
|   |   |   |   |   |   |   |   |   |   |   start <= 105008
|   |   |   |   |   |   |   |   |   |   |   |   start <= 100888:
vacuole_ (10.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 100888:
cytoplasm_ (7.44)
|   |   |   |   |   |   |   |   |   |   |   start > 105008
|   |   |   |   |   |   |   |   |   |   |   |   start <= 118821:
mitochondrion_ (25.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 118821:
cell_wall_ (15.78)
|   |   |   |   |   |   |   |   |   |   start > 126324
|   |   |   |   |   |   |   |   |   |   |   start <= 172364
|   |   |   |   |   |   |   |   |   |   |   |   start <= 156166
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 140434
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
137376: cellular_component_ (16.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
137376: nucleolus_ (24.31/11.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 140434
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
152996
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
146356
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 143289: nucleus_ (41.8/19.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 143289: cytoplasm_ (42.43/14.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
146356
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 147098: mitochondrion_ (15.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 147098: nucleus_ (38.89/18.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
152996: cellular_component_ (9.75)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 156166
|   |   |   |   |   |   |   |   |   |   |   |   start <= 160616
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
158185: endoplasmic_reticulum_ (12.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
158185: mitochondrion_ (12.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 160616:
membrane_fraction_ (23.47)
|   |   |   |   |   |   |   |   |   |   start > 172364
|   |   |   |   |   |   |   |   |   |   |   start <= 192530
|   |   |   |   |   |   |   |   |   |   |   |   start <= 191638
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
186677: cellular_component_ (13.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
186677
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
189715: nucleus_ (43.55/25.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
189715: ribosome_ (16.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 191638:
endoplasmic_reticulum_ (19.77)
|   |   |   |   |   |   |   |   |   |   |   start > 192530
|   |   |   |   |   |   |   |   |   |   |   |   start <= 211573
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
197383: cellular_component_ (15.83/6.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
197383
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
205301
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 204731: cytoplasm_ (13.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 204731: mitochondrion_ (19.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
205301
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance <= 12412: cytoplasm_ (23.35/8.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance > 12412: cytoskeleton_ (4.83/0.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 211573
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
221386: nucleus_ (20.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
221386: cellular_component_ (18.18)
|   |   |   |   |   |   |   |   |   start > 225051
|   |   |   |   |   |   |   |   |   |   start <= 237259
|   |   |   |   |   |   |   |   |   |   |   start <= 231297:
mitochondrion_ (35.07)
|   |   |   |   |   |   |   |   |   |   |   start > 231297:
cytoplasm_ (74.04/27.95)
|   |   |   |   |   |   |   |   |   |   start > 237259
|   |   |   |   |   |   |   |   |   |   |   start <= 239410:
cytoplasmic_membrane-bound_vesicle_ (22.77)
|   |   |   |   |   |   |   |   |   |   |   start > 239410
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 242078:
mitochondrion_ (31.49/15.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 242078
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 245587:
endoplasmic_reticulum_ (14.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 245587:
mitochondrion_ (25.56)
|   |   |   |   |   |   |   |   start > 246486
|   |   |   |   |   |   |   |   |   start <= 265921
|   |   |   |   |   |   |   |   |   |   start <= 247250:
cellular_component_ (22.7)
|   |   |   |   |   |   |   |   |   |   start > 247250: nucleus_
(54.19)
|   |   |   |   |   |   |   |   |   start > 265921
|   |   |   |   |   |   |   |   |   |   start <= 272822
|   |   |   |   |   |   |   |   |   |   |   start <= 268794:
cytoplasm_ (14.77)
|   |   |   |   |   |   |   |   |   |   |   start > 268794:
cell_cortex_ (8.78)
|   |   |   |   |   |   |   |   |   |   start > 272822
|   |   |   |   |   |   |   |   |   |   |   start <= 285266
|   |   |   |   |   |   |   |   |   |   |   |   start <= 278836:
cellular_component_ (17.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 278836:
nucleus_ (54.59/30.09)
|   |   |   |   |   |   |   |   |   |   |   start > 285266:
cellular_component_ (23.7)
|   |   |   |   |   |   |   start > 294042
|   |   |   |   |   |   |   |   start <= 316718
|   |   |   |   |   |   |   |   |   start <= 303176
|   |   |   |   |   |   |   |   |   |   start <= 295240: nucleolus_
(10.35)
|   |   |   |   |   |   |   |   |   |   start > 295240:
endoplasmic_reticulum_ (22.62)
|   |   |   |   |   |   |   |   |   start > 303176: mitochondrion_
(24.97)
|   |   |   |   |   |   |   |   start > 316718: plasma_membrane_
(38.6/16.23)
|   |   |   |   |   |   start > 317279
|   |   |   |   |   |   |   start <= 466201
|   |   |   |   |   |   |   |   start <= 445916
|   |   |   |   |   |   |   |   |   start <= 378820
|   |   |   |   |   |   |   |   |   |   start <= 360125
|   |   |   |   |   |   |   |   |   |   |   start <= 320011:
nucleus_ (64.18/40.8)
|   |   |   |   |   |   |   |   |   |   |   start > 320011
|   |   |   |   |   |   |   |   |   |   |   |   start <= 342517
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 338266
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
333352
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
323381: mitochondrion_ (34.16/14.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
323381
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 327868: vacuole_ (14.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 327868
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C: nucleus_ (8.69/3.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   neigh_strand = W: nucleus_ (4.32/1.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   neigh_strand = C: cytoplasm_ (4.81/1.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P: cytoplasm_ (6.64/1.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
333352
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
335893
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 334260: mitochondrion_ (18.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 334260: endomembrane_system_ (12.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
335893: mitochondrion_ (42.22/14.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 338266
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
339782: cellular_bud_ (17.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
339782
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_component_: nucleus_ (3.89/1.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = hydrolase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = biological_process_: nucleolus_ (7.1/1.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = plasma_membrane_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transporter_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transport_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endoplasmic_reticulum_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peroxisome_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_binding_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = organelle_organization_and_biogenesis_: nucleolus_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrion_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleus_: nucleolus_ (4.15/1.23)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_biogenesis_and_assembly_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_binding_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_metabolic_process_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lyase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_metabolic_process_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cycle_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = molecular_function_: nucleus_ (6.19/2.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vesicle-mediated_transport_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleolus_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = structural_molecule_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = Golgi_apparatus_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transferase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_modification_process_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = chromosome_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_binding_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = response_to_stress_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasm_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_organization_and_biogenesis_: nucleolus_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = enzyme_regulator_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_regulator_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = extracellular_region_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_organization_and_biogenesis_: nucleolus_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vacuole_: nucleolus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peptidase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lipid_metabolic_process_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_kinase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_homeostasis_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleotidyltransferase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = meiosis_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = isomerase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = carbohydrate_metabolic_process_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vitamin_metabolic_process_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_regulator_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ligase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_fraction_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = helicase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cortex_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytokinesis_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nuclear_organization_and_biogenesis_: nucleolus_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = conjugation_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = oxidoreductase_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = sporulation_: nucleus_ (0.6/0.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasmic_membrane-bound_vesicle_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = microtubule_organizing_center_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transduction_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_respiration_: nucleolus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = amino_acid_and_derivative_metabolic_process_:
nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endomembrane_system_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_organization_and_biogenesis_: nucleolus_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = electron_transport_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_catabolic_process_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transducer_activity_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_bud_: nucleus_ (4.67/0.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = site_of_polarized_growth_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_budding_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = generation_of_precursor_metabolites_and_energy_:
nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = phosphoprotein_phosphatase_activity_: nucleolus_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrial_envelope_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = pseudohyphal_growth_: nucleolus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 342517
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 352381:
cellular_component_ (23.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 352381
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
355451: cytoplasm_ (37.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
355451: mitochondrion_ (70.78/28.52)
|   |   |   |   |   |   |   |   |   |   start > 360125
|   |   |   |   |   |   |   |   |   |   |   start <= 376657
|   |   |   |   |   |   |   |   |   |   |   |   start <= 361244:
cytoskeleton_ (21.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 361244
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 365779:
nucleus_ (54.78/35.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 365779:
cellular_component_ (14.8)
|   |   |   |   |   |   |   |   |   |   |   start > 376657:
cytoplasm_ (26.79)
|   |   |   |   |   |   |   |   |   start > 378820
|   |   |   |   |   |   |   |   |   |   start <= 411034
|   |   |   |   |   |   |   |   |   |   |   start <= 398393
|   |   |   |   |   |   |   |   |   |   |   |   start <= 381322:
endoplasmic_reticulum_ (15.76)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 381322
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 383832:
nucleolus_ (26.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 383832
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
392399
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
391306
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 387652: nucleus_ (6.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 387652: ribosome_ (9.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
391306
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance <= 566: cytoplasm_ (6.71/1.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance > 566: nucleus_ (15.25/4.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
392399: nucleolus_ (12.46)
|   |   |   |   |   |   |   |   |   |   |   start > 398393
|   |   |   |   |   |   |   |   |   |   |   |   start <= 402892:
cytoskeleton_ (26.85/10.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 402892:
cytoplasm_ (42.72/8.71)
|   |   |   |   |   |   |   |   |   |   start > 411034
|   |   |   |   |   |   |   |   |   |   |   start <= 432638
|   |   |   |   |   |   |   |   |   |   |   |   start <= 422931
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 416030:
mitochondrion_ (14.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 416030:
cytoplasm_ (15.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 422931
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 425151
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: plasma_membrane_ (11.96/2.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: mitochondrion_ (19.45/6.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 425151:
mitochondrion_ (16.61)
|   |   |   |   |   |   |   |   |   |   |   start > 432638
|   |   |   |   |   |   |   |   |   |   |   |   start <= 436796
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 435157:
cellular_component_ (13.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 435157:
vacuole_ (10.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 436796
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 438858
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: nucleolus_ (6.11/2.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 3408: nucleus_ (9.75/2.45)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 3408: nucleolus_ (2.1/0.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 438858:
plasma_membrane_ (13.54)
|   |   |   |   |   |   |   |   start > 445916
|   |   |   |   |   |   |   |   |   start <= 449195
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
chromosome_ (21.41/7.4)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
nucleus_ (8.7/3.16)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
nucleus_ (15.3/5.12)
|   |   |   |   |   |   |   |   |   start > 449195
|   |   |   |   |   |   |   |   |   |   start <= 456232
|   |   |   |   |   |   |   |   |   |   |   start <= 451013:
ribosome_ (45.15/21.48)
|   |   |   |   |   |   |   |   |   |   |   start > 451013
|   |   |   |   |   |   |   |   |   |   |   |   start <= 452423:
cytoplasm_ (25.64/8.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 452423:
mitochondrion_ (29.98/12.09)
|   |   |   |   |   |   |   |   |   |   start > 456232
|   |   |   |   |   |   |   |   |   |   |   start <= 460411:
endomembrane_system_ (58.88/32.53)
|   |   |   |   |   |   |   |   |   |   |   start > 460411
|   |   |   |   |   |   |   |   |   |   |   |   start <= 461822:
ribosome_ (42.15/15.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 461822:
cytoplasm_ (29.83/13.34)
|   |   |   |   |   |   |   start > 466201
|   |   |   |   |   |   |   |   start <= 545780
|   |   |   |   |   |   |   |   |   start <= 529854
|   |   |   |   |   |   |   |   |   |   start <= 507739
|   |   |   |   |   |   |   |   |   |   |   start <= 503929
|   |   |   |   |   |   |   |   |   |   |   |   start <= 491074
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 471664:
nucleus_ (6.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 471664:
cytoplasm_ (25.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 491074
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 496676:
mitochondrion_ (20.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 496676
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
497348: nucleus_ (28.52/12.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
497348: mitochondrion_ (11.66)
|   |   |   |   |   |   |   |   |   |   |   start > 503929:
Golgi_apparatus_ (14.97)
|   |   |   |   |   |   |   |   |   |   start > 507739
|   |   |   |   |   |   |   |   |   |   |   start <= 524086
|   |   |   |   |   |   |   |   |   |   |   |   start <= 517877:
nucleus_ (48.16/26.64)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 517877:
cytoplasm_ (26.66/11.41)
|   |   |   |   |   |   |   |   |   |   |   start > 524086
|   |   |   |   |   |   |   |   |   |   |   |   start <= 528690
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 526328:
mitochondrion_ (14.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 526328:
nucleus_ (9.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 528690:
mitochondrion_ (15.18)
|   |   |   |   |   |   |   |   |   start > 529854
|   |   |   |   |   |   |   |   |   |   start <= 536049
|   |   |   |   |   |   |   |   |   |   |   start <= 532055
|   |   |   |   |   |   |   |   |   |   |   |   start <= 531821:
cytoplasm_ (15.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 531821:
nucleus_ (15.94)
|   |   |   |   |   |   |   |   |   |   |   start > 532055
|   |   |   |   |   |   |   |   |   |   |   |   start <= 534020:
microtubule_organizing_center_ (12.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 534020:
vacuole_ (15.5)
|   |   |   |   |   |   |   |   |   |   start > 536049
|   |   |   |   |   |   |   |   |   |   |   start <= 544055
|   |   |   |   |   |   |   |   |   |   |   |   start <= 538548:
cytoplasm_ (9.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 538548
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: nucleus_ (36.65/11.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: cytoplasm_ (24.26/8.08)
|   |   |   |   |   |   |   |   |   |   |   start > 544055
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: plasma_membrane_ (4.39/1.23)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: plasma_membrane_ (2.27/0.88)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: nucleus_ (7.99/2.15)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: cytoplasm_ (4.99/2.38)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: nucleus_ (5.66/2.73)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: cytoplasm_ (1.67/0.66)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: cytoplasm_ (5.78/1.61)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: plasma_membrane_ (5.86/2.45)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: plasma_membrane_ (3.1/1.84)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: cytoplasm_ (5.61/1.3)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: cytoplasm_ (1.9/1.05)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: cytoplasm_ (5.61/2.79)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: cytoplasm_ (3.57/1.97)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: nucleus_ (2.82/0.79)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   start > 545780
|   |   |   |   |   |   |   |   |   start <= 548752: mitochondrion_
(54.87/19.46)
|   |   |   |   |   |   |   |   |   start > 548752:
cellular_component_ (21.13)
|   |   |   |   start > 554842
|   |   |   |   |   start <= 559151
|   |   |   |   |   |   start <= 555188: nucleolus_ (20.61)
|   |   |   |   |   |   start > 555188: cytoskeleton_ (69.61/21.97)
|   |   |   |   |   start > 559151: membrane_fraction_ (44.85/16.66)
|   |   |   start > 559409
|   |   |   |   start <= 654232
|   |   |   |   |   start <= 623573
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 572117: cytoplasm_
(108.26/38.78)
|   |   |   |   |   |   |   start > 572117
|   |   |   |   |   |   |   |   start <= 581609
|   |   |   |   |   |   |   |   |   start <= 576594
|   |   |   |   |   |   |   |   |   |   start <= 573974:
mitochondrion_ (29.78/13.35)
|   |   |   |   |   |   |   |   |   |   start > 573974: membrane_
(21.17)
|   |   |   |   |   |   |   |   |   start > 576594: mitochondrion_
(36.97/11.78)
|   |   |   |   |   |   |   |   start > 581609
|   |   |   |   |   |   |   |   |   start <= 609769
|   |   |   |   |   |   |   |   |   |   start <= 587711
|   |   |   |   |   |   |   |   |   |   |   start <= 583726
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 582248:
nucleus_ (13.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 582248:
cellular_component_ (21.08)
|   |   |   |   |   |   |   |   |   |   |   start > 583726
|   |   |   |   |   |   |   |   |   |   |   |   start <= 586061:
mitochondrion_ (13.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 586061:
endoplasmic_reticulum_ (10.07)
|   |   |   |   |   |   |   |   |   |   start > 587711
|   |   |   |   |   |   |   |   |   |   |   start <= 594320
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (11.56/2.26)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasm_ (17.08/6.89)
|   |   |   |   |   |   |   |   |   |   |   start > 594320
|   |   |   |   |   |   |   |   |   |   |   |   start <= 604199
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 598728:
cellular_component_ (22.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 598728
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: nucleus_ (14.54/5.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: cellular_component_ (22.66/7.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 604199:
nucleus_ (17.26)
|   |   |   |   |   |   |   |   |   start > 609769
|   |   |   |   |   |   |   |   |   |   start <= 618227:
mitochondrion_ (45.49/11.91)
|   |   |   |   |   |   |   |   |   |   start > 618227
|   |   |   |   |   |   |   |   |   |   |   start <= 620747:
membrane_ (25.33)
|   |   |   |   |   |   |   |   |   |   |   start > 620747:
mitochondrion_ (18.07)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 586061
|   |   |   |   |   |   |   |   start <= 573974
|   |   |   |   |   |   |   |   |   start <= 573088
|   |   |   |   |   |   |   |   |   |   start <= 569392: chromosome_
(17.25)
|   |   |   |   |   |   |   |   |   |   start > 569392: nucleus_
(16.19)
|   |   |   |   |   |   |   |   |   start > 573088: Golgi_apparatus_
(17.26)
|   |   |   |   |   |   |   |   start > 573974
|   |   |   |   |   |   |   |   |   start <= 583726
|   |   |   |   |   |   |   |   |   |   start <= 581609
|   |   |   |   |   |   |   |   |   |   |   start <= 578853:
cytoplasm_ (15.57)
|   |   |   |   |   |   |   |   |   |   |   start > 578853:
cellular_component_ (11.26)
|   |   |   |   |   |   |   |   |   |   start > 581609: nucleus_
(17.36)
|   |   |   |   |   |   |   |   |   start > 583726
```

```
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
plasma_membrane_ (12.24/3.73)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cytoplasm_ (8.49/1.97)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P
|   |   |   |   |   |   |   |   |   |   |   distance <= 827:
cytoplasm_ (2.83/0.62)
|   |   |   |   |   |   |   |   |   |   |   distance > 827:
plasma_membrane_ (3.36/0.73)
|   |   |   |   |   |   |   start > 586061
|   |   |   |   |   |   |   |   start <= 609769
|   |   |   |   |   |   |   |   |   start <= 598728
|   |   |   |   |   |   |   |   |   |   start <= 587711:
mitochondrion_ (13.8)
|   |   |   |   |   |   |   |   |   |   start > 587711:
cellular_bud_ (39.83/17.96)
|   |   |   |   |   |   |   |   |   start > 598728
|   |   |   |   |   |   |   |   |   |   start <= 608301: ribosome_
(14.32)
|   |   |   |   |   |   |   |   |   |   start > 608301:
mitochondrion_ (9.21)
|   |   |   |   |   |   |   |   start > 609769
|   |   |   |   |   |   |   |   |   start <= 612409: nucleus_
(65.73/26.77)
|   |   |   |   |   |   |   |   |   start > 612409
|   |   |   |   |   |   |   |   |   |   start <= 620747
|   |   |   |   |   |   |   |   |   |   |   start <= 617912:
cytoplasm_ (36.33)
|   |   |   |   |   |   |   |   |   |   |   start > 617912
|   |   |   |   |   |   |   |   |   |   |   |   start <= 618227:
mitochondrion_ (12.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 618227:
cytoplasm_ (16.95)
|   |   |   |   |   |   |   |   |   |   start > 620747
|   |   |   |   |   |   |   |   |   |   |   distance <= 4234:
nucleus_ (21.82/6.3)
|   |   |   |   |   |   |   |   |   |   |   distance > 4234:
cytoplasm_ (9.65/2.09)
|   |   |   |   |   start > 623573
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 640819
|   |   |   |   |   |   |   |   start <= 633609: cytoplasm_ (11.67)
|   |   |   |   |   |   |   |   start > 633609: mitochondrion_
(45.24)
|   |   |   |   |   |   |   start > 640819
|   |   |   |   |   |   |   |   start <= 649770
|   |   |   |   |   |   |   |   |   start <= 644095:
endoplasmic_reticulum_ (9.46)
|   |   |   |   |   |   |   |   |   start > 644095
|   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(9.72/0.56)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1
```

```
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2303:
cytoplasm_ (5.73/1.52)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2303:
nucleus_ (6.96/2.5)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: cytoplasm_
(12.18/2.32)
|   |   |   |   |   |   |   |   start > 649770: cellular_component_
(15.17)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 647120
|   |   |   |   |   |   |   |   start <= 640819
|   |   |   |   |   |   |   |   |   start <= 633609
|   |   |   |   |   |   |   |   |   |   start <= 628706:
cellular_component_ (51.46)
|   |   |   |   |   |   |   |   |   |   start > 628706: cytoplasm_
(10.31)
|   |   |   |   |   |   |   |   |   start > 633609
|   |   |   |   |   |   |   |   |   |   start <= 637024: chromosome_
(27.48/10.4)
|   |   |   |   |   |   |   |   |   |   start > 637024:
cellular_component_ (53.18)
|   |   |   |   |   |   |   |   start > 640819
|   |   |   |   |   |   |   |   |   start <= 644095:
mitochondrial_envelope_ (27.75)
|   |   |   |   |   |   |   |   |   start > 644095:
cellular_component_ (13.85)
|   |   |   |   |   |   |   start > 647120
|   |   |   |   |   |   |   |   start <= 649770: mitochondrion_
(33.8)
|   |   |   |   |   |   |   |   start > 649770: ribosome_ (18.81)
|   |   |   |   start > 654232
|   |   |   |   |   start <= 663743
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 655957: cell_cortex_
(32.31/13.07)
|   |   |   |   |   |   |   start > 655957
|   |   |   |   |   |   |   |   start <= 658683: cellular_component_
(11.78)
|   |   |   |   |   |   |   |   start > 658683: nucleus_ (18.8)
|   |   |   |   |   |   strand = W: nucleolus_ (19.49)
|   |   |   |   |   start > 663743
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 697135
|   |   |   |   |   |   |   |   start <= 676965
|   |   |   |   |   |   |   |   |   start <= 669516
|   |   |   |   |   |   |   |   |   |   start <= 665013: cytoplasm_
(18.47)
|   |   |   |   |   |   |   |   |   |   start > 665013: nucleus_
(32.06/12.74)
|   |   |   |   |   |   |   |   |   start > 669516
|   |   |   |   |   |   |   |   |   |   start <= 675846:
Golgi_apparatus_ (14.4)
|   |   |   |   |   |   |   |   |   |   start > 675846: nucleus_
(24.71/7.81)
```

```
|   |   |   |   |   |   |   |   start > 676965
|   |   |   |   |   |   |   |   |   start <= 684561: cytoplasm_
(47.77)
|   |   |   |   |   |   |   |   |   start > 684561
|   |   |   |   |   |   |   |   |   |   start <= 690518: cytoplasm_
(34.28/12.28)
|   |   |   |   |   |   |   |   |   |   start > 690518: nucleus_
(10.07)
|   |   |   |   |   |   |   start > 697135
|   |   |   |   |   |   |   |   start <= 700876:
endoplasmic_reticulum_ (17.18)
|   |   |   |   |   |   |   |   start > 700876: cytoplasm_ (12.94)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 667638: endoplasmic_reticulum_
(24.22)
|   |   |   |   |   |   |   start > 667638
|   |   |   |   |   |   |   |   start <= 700876
|   |   |   |   |   |   |   |   |   start <= 672985
|   |   |   |   |   |   |   |   |   |   start <= 669516: nucleus_
(19.78/8.73)
|   |   |   |   |   |   |   |   |   |   start > 669516: cytoplasm_
(19.8)
|   |   |   |   |   |   |   |   |   start > 672985
|   |   |   |   |   |   |   |   |   |   start <= 684561
|   |   |   |   |   |   |   |   |   |   |   start <= 678700:
mitochondrion_ (13.29)
|   |   |   |   |   |   |   |   |   |   |   start > 678700:
membrane_ (21.8/9.57)
|   |   |   |   |   |   |   |   |   |   start > 684561
|   |   |   |   |   |   |   |   |   |   |   start <= 697135:
cellular_component_ (28.76)
|   |   |   |   |   |   |   |   |   |   |   start > 697135:
mitochondrion_ (19.59)
|   |   |   |   |   |   |   |   start > 700876
|   |   |   |   |   |   |   |   |   start <= 705738
|   |   |   |   |   |   |   |   |   |   start <= 704190: nucleus_
(21.36/6.78)
|   |   |   |   |   |   |   |   |   |   start > 704190
|   |   |   |   |   |   |   |   |   |   |   distance <= 3091:
cytoplasm_ (22.83/8.3)
|   |   |   |   |   |   |   |   |   |   |   distance > 3091:
nucleus_ (7.34/1.97)
|   |   |   |   |   |   |   |   |   start > 705738: cytoplasm_
(11.71)
|   |   start > 707154
|   |   |   start <= 715734: cell_wall_ (22.41)
|   |   |   start > 715734
|   |   |   |   start <= 725778
|   |   |   |   |   start <= 719660
|   |   |   |   |   |   start <= 717574: cellular_component_ (16.53)
|   |   |   |   |   |   start > 717574: plasma_membrane_ (19.26)
|   |   |   |   |   start > 719660
|   |   |   |   |   |   start <= 722809: extracellular_region_
(20.91)
```

```
|   |   |   |   |   |   start > 722809: cytoplasm_ (11.81)
|   |   |   |   start > 725778
|   |   |   |   |   start <= 736038
|   |   |   |   |   |   start <= 729590: cellular_component_ (35.89)
|   |   |   |   |   |   start > 729590
|   |   |   |   |   |   |   start <= 732434: plasma_membrane_
(12.93)
|   |   |   |   |   |   |   start > 732434: cellular_component_
(19.73)
|   |   |   |   |   start > 736038
|   |   |   |   |   |   start <= 739810: plasma_membrane_ (12.38)
|   |   |   |   |   |   start > 739810: vacuole_ (8.11)
```

For Molecular Function

```
|   start <= 567636
|   |   start <= 335893
|   |   |   strand = C
|   |   |   |   start <= 133932
|   |   |   |   |   start <= 41183
|   |   |   |   |   |   start <= 11475
|   |   |   |   |   |   |   start <= 6130: helicase_activity_ (8.08)
|   |   |   |   |   |   |   start > 6130: molecular_function_ (7.68)
|   |   |   |   |   |   start > 11475
|   |   |   |   |   |   |   start <= 26887: hydrolase_activity_
(27.31)
|   |   |   |   |   |   |   start > 26887
|   |   |   |   |   |   |   |   start <= 38005:
transporter_activity_ (18.19)
|   |   |   |   |   |   |   |   start > 38005: hydrolase_activity_
(8.49)
|   |   |   |   |   start > 41183
|   |   |   |   |   |   start <= 122944
|   |   |   |   |   |   |   start <= 88785
|   |   |   |   |   |   |   |   start <= 73786
|   |   |   |   |   |   |   |   |   start <= 63804
|   |   |   |   |   |   |   |   |   |   start <= 50443:
molecular_function_ (44.31)
|   |   |   |   |   |   |   |   |   |   start > 50443
|   |   |   |   |   |   |   |   |   |   |   start <= 58813
|   |   |   |   |   |   |   |   |   |   |   |   start <= 54379:
protein_binding_ (8.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 54379:
lyase_activity_ (10.8)
|   |   |   |   |   |   |   |   |   |   |   start > 58813:
molecular_function_ (15.34)
|   |   |   |   |   |   |   |   |   start > 63804
|   |   |   |   |   |   |   |   |   |   start <= 69337:
transferase_activity_ (14.73)
|   |   |   |   |   |   |   |   |   |   start > 69337:
molecular_function_ (9.95)
|   |   |   |   |   |   |   |   start > 73786
|   |   |   |   |   |   |   |   |   start <= 80153
```

```
|   |   |   |   |   |   |   |   |   |   start <= 75932:
structural_molecule_activity_ (14.45)
|   |   |   |   |   |   |   |   |   |   start > 75932:
protein_kinase_activity_ (15.41)
|   |   |   |   |   |   |   |   |   start > 80153
|   |   |   |   |   |   |   |   |   |   start <= 85658:
molecular_function_ (11.35)
|   |   |   |   |   |   |   |   |   |   start > 85658:
protein_binding_ (19.99)
|   |   |   |   |   |   |   start > 88785
|   |   |   |   |   |   |   |   start <= 97731
|   |   |   |   |   |   |   |   |   start <= 95090
|   |   |   |   |   |   |   |   |   |   start <= 90784:
enzyme_regulator_activity_ (14.8)
|   |   |   |   |   |   |   |   |   |   start > 90784:
transcription_regulator_activity_ (13.71)
|   |   |   |   |   |   |   |   |   start > 95090: DNA_binding_
(22.55)
|   |   |   |   |   |   |   |   start > 97731
|   |   |   |   |   |   |   |   |   start <= 111153
|   |   |   |   |   |   |   |   |   |   start <= 106428
|   |   |   |   |   |   |   |   |   |   |   start <= 101773:
molecular_function_ (23.98)
|   |   |   |   |   |   |   |   |   |   |   start > 101773:
transferase_activity_ (12.23)
|   |   |   |   |   |   |   |   |   |   start > 106428:
protein_kinase_activity_ (24.71)
|   |   |   |   |   |   |   |   |   start > 111153
|   |   |   |   |   |   |   |   |   |   start <= 120445:
molecular_function_ (56.73)
|   |   |   |   |   |   |   |   |   |   start > 120445:
structural_molecule_activity_ (9.23)
|   |   |   |   |   |   start > 122944
|   |   |   |   |   |   |   start <= 128949
|   |   |   |   |   |   |   |   start <= 126324:
enzyme_regulator_activity_ (14.96)
|   |   |   |   |   |   |   |   start > 126324: peptidase_activity_
(20.85)
|   |   |   |   |   |   |   start > 128949
|   |   |   |   |   |   |   |   start <= 130640: hydrolase_activity_
(18.42)
|   |   |   |   |   |   |   |   start > 130640: protein_binding_
(9.44)
|   |   |   |   start > 133932
|   |   |   |   |   start <= 289221
|   |   |   |   |   |   start <= 231297
|   |   |   |   |   |   |   start <= 186677
|   |   |   |   |   |   |   |   start <= 150958
|   |   |   |   |   |   |   |   |   start <= 146356
|   |   |   |   |   |   |   |   |   |   start <= 135930:
isomerase_activity_ (10.97)
|   |   |   |   |   |   |   |   |   |   start > 135930
|   |   |   |   |   |   |   |   |   |   |   start <= 140434
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 137376:
molecular_function_ (10.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 137376:
RNA_binding_ (30.47)
|   |   |   |   |   |   |   |   |   |   |   start > 140434:
molecular_function_ (13.38)
|   |   |   |   |   |   |   |   |   start > 146356:
protein_kinase_activity_ (23.81)
|   |   |   |   |   |   |   |   start > 150958
|   |   |   |   |   |   |   |   |   start <= 158185
|   |   |   |   |   |   |   |   |   |   start <= 156166
|   |   |   |   |   |   |   |   |   |   |   start <= 152996:
transferase_activity_ (24.1)
|   |   |   |   |   |   |   |   |   |   |   start > 152996
|   |   |   |   |   |   |   |   |   |   |   |   start <= 154688:
helicase_activity_ (16.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 154688:
transferase_activity_ (17.51)
|   |   |   |   |   |   |   |   |   |   start > 156166:
structural_molecule_activity_ (14.58)
|   |   |   |   |   |   |   |   |   start > 158185
|   |   |   |   |   |   |   |   |   |   start <= 181707
|   |   |   |   |   |   |   |   |   |   |   start <= 172364
|   |   |   |   |   |   |   |   |   |   |   |   start <= 165345:
molecular_function_ (27.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 165345
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
8604: transferase_activity_ (21.15/6.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 8604:
ligase_activity_ (3.89/0.85)
|   |   |   |   |   |   |   |   |   |   |   start > 172364
|   |   |   |   |   |   |   |   |   |   |   |   start <= 180100
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 177303:
transporter_activity_ (6.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 177303:
protein_kinase_activity_ (8.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 180100:
molecular_function_ (18.37)
|   |   |   |   |   |   |   |   |   |   start > 181707
|   |   |   |   |   |   |   |   |   |   |   start <= 184499:
DNA_binding_ (13.19)
|   |   |   |   |   |   |   |   |   |   |   start > 184499:
transferase_activity_ (25.25)
|   |   |   |   |   |   |   start > 186677
|   |   |   |   |   |   |   |   start <= 197383
|   |   |   |   |   |   |   |   |   start <= 187643: RNA_binding_
(17.35)
|   |   |   |   |   |   |   |   |   start > 187643
|   |   |   |   |   |   |   |   |   |   start <= 192530
|   |   |   |   |   |   |   |   |   |   |   start <= 189715:
molecular_function_ (17.61)
|   |   |   |   |   |   |   |   |   |   |   start > 189715:
isomerase_activity_ (21.25)
```

```
|   |   |   |   |   |   |   |   |   |   start > 192530:
molecular_function_ (26.85)
|   |   |   |   |   |   |   |   start > 197383
|   |   |   |   |   |   |   |   |   start <= 211573: DNA_binding_
(36.11/10.37)
|   |   |   |   |   |   |   |   |   start > 211573
|   |   |   |   |   |   |   |   |   |   start <= 221386
|   |   |   |   |   |   |   |   |   |   |   start <= 217305:
RNA_binding_ (17.03)
|   |   |   |   |   |   |   |   |   |   |   start > 217305:
molecular_function_ (44.38)
|   |   |   |   |   |   |   |   |   |   start > 221386
|   |   |   |   |   |   |   |   |   |   |   start <= 228475:
RNA_binding_ (20.23)
|   |   |   |   |   |   |   |   |   |   |   start > 228475:
DNA_binding_ (10.52)
|   |   |   |   |   |   start > 231297
|   |   |   |   |   |   |   start <= 262547
|   |   |   |   |   |   |   |   start <= 242078: ligase_activity_
(26.71)
|   |   |   |   |   |   |   |   start > 242078
|   |   |   |   |   |   |   |   |   start <= 257418:
transporter_activity_ (35.44)
|   |   |   |   |   |   |   |   |   start > 257418:
transferase_activity_ (14.39)
|   |   |   |   |   |   |   start > 262547
|   |   |   |   |   |   |   |   start <= 281180
|   |   |   |   |   |   |   |   |   start <= 265921:
protein_binding_ (17.88)
|   |   |   |   |   |   |   |   |   start > 265921
|   |   |   |   |   |   |   |   |   |   start <= 272822:
ligase_activity_ (10.96)
|   |   |   |   |   |   |   |   |   |   start > 272822:
protein_binding_ (17.49)
|   |   |   |   |   |   |   |   start > 281180
|   |   |   |   |   |   |   |   |   start <= 285266:
molecular_function_ (16.91)
|   |   |   |   |   |   |   |   |   start > 285266: RNA_binding_
(19.19)
|   |   |   |   |   start > 289221
|   |   |   |   |   |   start <= 330116
|   |   |   |   |   |   |   start <= 315552
|   |   |   |   |   |   |   |   start <= 295240: molecular_function_
(50.68)
|   |   |   |   |   |   |   |   start > 295240
|   |   |   |   |   |   |   |   |   start <= 303176:
hydrolase_activity_ (11.33)
|   |   |   |   |   |   |   |   |   start > 303176
|   |   |   |   |   |   |   |   |   |   start <= 312701:
molecular_function_ (38.06)
|   |   |   |   |   |   |   |   |   |   start > 312701
|   |   |   |   |   |   |   |   |   |   |   start <= 313910:
hydrolase_activity_ (16.96)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 313910:
molecular_function_ (27.97)
|   |   |   |   |   |   |   start > 315552
|   |   |   |   |   |   |   |   start <= 320011:
structural_molecule_activity_ (14.36)
|   |   |   |   |   |   |   |   start > 320011: molecular_function_
(25.06)
|   |   |   |   |   |   start > 330116: DNA_binding_ (23.31)
|   |   |   strand = W
|   |   |   |   start <= 126324
|   |   |   |   |   start <= 73786
|   |   |   |   |   |   start <= 32163
|   |   |   |   |   |   |   start <= 21973
|   |   |   |   |   |   |   |   start <= 19497
|   |   |   |   |   |   |   |   |   start <= 11475:
molecular_function_ (14.87)
|   |   |   |   |   |   |   |   |   start > 11475:
transporter_activity_ (13.29)
|   |   |   |   |   |   |   |   start > 19497: transferase_activity_
(16.89)
|   |   |   |   |   |   |   start > 21973
|   |   |   |   |   |   |   |   start <= 26887
|   |   |   |   |   |   |   |   |   start <= 23133:
molecular_function_ (11.67)
|   |   |   |   |   |   |   |   |   start > 23133:
transporter_activity_ (10.66)
|   |   |   |   |   |   |   |   start > 26887: molecular_function_
(16.23)
|   |   |   |   |   |   start > 32163
|   |   |   |   |   |   |   start <= 53341
|   |   |   |   |   |   |   |   start <= 36919: protein_binding_
(18.1)
|   |   |   |   |   |   |   |   start > 36919: RNA_binding_ (34.67)
|   |   |   |   |   |   |   start > 53341
|   |   |   |   |   |   |   |   start <= 71365
|   |   |   |   |   |   |   |   |   start <= 63804
|   |   |   |   |   |   |   |   |   |   start <= 54379:
molecular_function_ (9.68)
|   |   |   |   |   |   |   |   |   |   start > 54379
|   |   |   |   |   |   |   |   |   |   |   start <= 60843:
transporter_activity_ (8.09)
|   |   |   |   |   |   |   |   |   |   |   start > 60843:
peptidase_activity_ (9.08)
|   |   |   |   |   |   |   |   |   start > 63804
|   |   |   |   |   |   |   |   |   |   start <= 69337:
protein_binding_ (12.36)
|   |   |   |   |   |   |   |   |   |   start > 69337:
molecular_function_ (22.32)
|   |   |   |   |   |   |   |   start > 71365: RNA_binding_ (17.1)
|   |   |   |   |   start > 73786
|   |   |   |   |   |   start <= 84066
|   |   |   |   |   |   |   start <= 75932:
structural_molecule_activity_ (10.35)
|   |   |   |   |   |   |   start > 75932
```

```
|   |   |   |   |   |   |   |   start <= 80153:
transferase_activity_ (26.81)
|   |   |   |   |   |   |   |   start > 80153
|   |   |   |   |   |   |   |   |   start <= 83446: DNA_binding_
(13.22)
|   |   |   |   |   |   |   |   |   start > 83446:
transferase_activity_ (15.37)
|   |   |   |   |   |   start > 84066
|   |   |   |   |   |   |   start <= 88785
|   |   |   |   |   |   |   |   start <= 85658: molecular_function_
(11.15)
|   |   |   |   |   |   |   |   start > 85658: protein_binding_
(19.93)
|   |   |   |   |   |   |   start > 88785
|   |   |   |   |   |   |   |   start <= 90784:
structural_molecule_activity_ (24.73)
|   |   |   |   |   |   |   |   start > 90784
|   |   |   |   |   |   |   |   |   start <= 105008
|   |   |   |   |   |   |   |   |   |   start <= 95090:
molecular_function_ (18.54)
|   |   |   |   |   |   |   |   |   |   start > 95090
|   |   |   |   |   |   |   |   |   |   |   start <= 100888:
peptidase_activity_ (10.57)
|   |   |   |   |   |   |   |   |   |   |   start > 100888:
transferase_activity_ (15.02)
|   |   |   |   |   |   |   |   |   start > 105008
|   |   |   |   |   |   |   |   |   |   start <= 111153:
oxidoreductase_activity_ (13.07)
|   |   |   |   |   |   |   |   |   |   start > 111153
|   |   |   |   |   |   |   |   |   |   |   start <= 118821:
molecular_function_ (13.26)
|   |   |   |   |   |   |   |   |   |   |   start > 118821:
structural_molecule_activity_ (12.66)
|   |   |   |   start > 126324
|   |   |   |   |   start <= 192530
|   |   |   |   |   |   start <= 152996
|   |   |   |   |   |   |   start <= 147098
|   |   |   |   |   |   |   |   start <= 143289
|   |   |   |   |   |   |   |   |   start <= 137376:
molecular_function_ (18.52)
|   |   |   |   |   |   |   |   |   start > 137376
|   |   |   |   |   |   |   |   |   |   start <= 140434:
nucleotidyltransferase_activity_ (15.83)
|   |   |   |   |   |   |   |   |   |   start > 140434:
molecular_function_ (9.34)
|   |   |   |   |   |   |   |   start > 143289
|   |   |   |   |   |   |   |   |   start <= 145157:
transporter_activity_ (15.67)
|   |   |   |   |   |   |   |   |   start > 145157
|   |   |   |   |   |   |   |   |   |   start <= 146356:
molecular_function_ (17.37)
|   |   |   |   |   |   |   |   |   |   start > 146356:
transporter_activity_ (12.99)
```

```
|   |   |   |   |   |   |   start > 147098:
nucleotidyltransferase_activity_ (20.46)
|   |   |   |   |   |   start > 152996
|   |   |   |   |   |   |   start <= 186677
|   |   |   |   |   |   |   |   start <= 156166: molecular_function_
(23.42)
|   |   |   |   |   |   |   |   start > 156166
|   |   |   |   |   |   |   |   |   start <= 160616
|   |   |   |   |   |   |   |   |   |   start <= 158185:
hydrolase_activity_ (15.2)
|   |   |   |   |   |   |   |   |   |   start > 158185:
transporter_activity_ (17.64)
|   |   |   |   |   |   |   |   |   start > 160616
|   |   |   |   |   |   |   |   |   |   start <= 172364:
molecular_function_ (16.97)
|   |   |   |   |   |   |   |   |   |   start > 172364:
hydrolase_activity_ (19.66)
|   |   |   |   |   |   |   start > 186677: molecular_function_
(62.45)
|   |   |   |   |   start > 192530
|   |   |   |   |   |   start <= 317279
|   |   |   |   |   |   |   start <= 247250
|   |   |   |   |   |   |   |   start <= 245587
|   |   |   |   |   |   |   |   |   start <= 228475
|   |   |   |   |   |   |   |   |   |   start <= 211573
|   |   |   |   |   |   |   |   |   |   |   start <= 205301
|   |   |   |   |   |   |   |   |   |   |   |   start <= 197383:
protein_binding_ (11.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 197383:
molecular_function_ (33.18)
|   |   |   |   |   |   |   |   |   |   |   start > 205301:
protein_binding_ (14.89)
|   |   |   |   |   |   |   |   |   |   start > 211573
|   |   |   |   |   |   |   |   |   |   |   start <= 221386:
protein_kinase_activity_ (13.88)
|   |   |   |   |   |   |   |   |   |   |   start > 221386
|   |   |   |   |   |   |   |   |   |   |   |   start <= 225051:
molecular_function_ (21.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 225051:
protein_binding_ (9.84)
|   |   |   |   |   |   |   |   |   start > 228475
|   |   |   |   |   |   |   |   |   |   start <= 237259
|   |   |   |   |   |   |   |   |   |   |   start <= 233935
|   |   |   |   |   |   |   |   |   |   |   |   start <= 231297:
translation_regulator_activity_ (7.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 231297:
molecular_function_ (11.56)
|   |   |   |   |   |   |   |   |   |   |   start > 233935:
transferase_activity_ (15.99)
|   |   |   |   |   |   |   |   |   |   start > 237259
|   |   |   |   |   |   |   |   |   |   |   start <= 239410:
molecular_function_ (19.49)
|   |   |   |   |   |   |   |   |   |   |   start > 239410
```

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|   |   |   |   |   |   |   |   |   |   |   |   start <= 242078:
phosphoprotein_phosphatase_activity_ (17.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 242078:
molecular_function_ (13.34)
|   |   |   |   |   |   |   |   start > 245587
|   |   |   |   |   |   |   |   |   start <= 246486:
structural_molecule_activity_ (15.88)
|   |   |   |   |   |   |   |   |   start > 246486:
signal_transducer_activity_ (37.73/16.8)
|   |   |   |   |   |   |   start > 247250
|   |   |   |   |   |   |   |   start <= 265921
|   |   |   |   |   |   |   |   |   start <= 257418:
helicase_activity_ (25.36)
|   |   |   |   |   |   |   |   |   start > 257418:
transcription_regulator_activity_ (18.66)
|   |   |   |   |   |   |   |   start > 265921
|   |   |   |   |   |   |   |   |   start <= 272822
|   |   |   |   |   |   |   |   |   |   start <= 268794:
transferase_activity_ (16.77)
|   |   |   |   |   |   |   |   |   |   start > 268794:
protein_binding_ (12.96)
|   |   |   |   |   |   |   |   |   start > 272822
|   |   |   |   |   |   |   |   |   |   start <= 295240
|   |   |   |   |   |   |   |   |   |   |   start <= 294042:
molecular_function_ (44.59)
|   |   |   |   |   |   |   |   |   |   |   start > 294042:
DNA_binding_ (11.39)
|   |   |   |   |   |   |   |   |   |   start > 295240
|   |   |   |   |   |   |   |   |   |   |   start <= 303176:
protein_binding_ (14.2)
|   |   |   |   |   |   |   |   |   |   |   start > 303176
|   |   |   |   |   |   |   |   |   |   |   |   start <= 316718
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 310632:
transferase_activity_ (9.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 310632:
molecular_function_ (9.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 316718:
transferase_activity_ (12.56)
|   |   |   |   |   |   start > 317279
|   |   |   |   |   |   |   start <= 333352
|   |   |   |   |   |   |   |   start <= 323381
|   |   |   |   |   |   |   |   |   start <= 320011:
structural_molecule_activity_ (16.35)
|   |   |   |   |   |   |   |   |   start > 320011:
hydrolase_activity_ (14.83)
|   |   |   |   |   |   |   |   start > 323381: molecular_function_
(26.04)
|   |   |   |   |   |   |   start > 333352: transporter_activity_
(40.31)
|   |   start > 335893
|   |   |   start <= 545168
|   |   |   |   start <= 413393
|   |   |   |   |   start <= 373794
|   |   |   |   |   |   start <= 360125
```

```
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 349173: molecular_function_
(55.94)
|   |   |   |   |   |   |   |   start > 349173
|   |   |   |   |   |   |   |   |   start <= 349228: RNA_binding_
(26.32)
|   |   |   |   |   |   |   |   |   start > 349228
|   |   |   |   |   |   |   |   |   |   start <= 355451:
protein_binding_ (7.95)
|   |   |   |   |   |   |   |   |   |   start > 355451:
enzyme_regulator_activity_ (17.38)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 338266:
oxidoreductase_activity_ (15.46)
|   |   |   |   |   |   |   |   start > 338266
|   |   |   |   |   |   |   |   |   start <= 355451
|   |   |   |   |   |   |   |   |   |   start <= 342517
|   |   |   |   |   |   |   |   |   |   |   start <= 339782:
molecular_function_ (22.64)
|   |   |   |   |   |   |   |   |   |   |   start > 339782:
helicase_activity_ (12.26)
|   |   |   |   |   |   |   |   |   |   start > 342517:
molecular_function_ (76.42)
|   |   |   |   |   |   |   |   |   start > 355451
|   |   |   |   |   |   |   |   |   |   start <= 356019:
oxidoreductase_activity_ (15.89)
|   |   |   |   |   |   |   |   |   |   start > 356019:
molecular_function_ (22.82)
|   |   |   |   |   |   start > 360125:
structural_molecule_activity_ (55.92)
|   |   |   |   |   start > 373794
|   |   |   |   |   |   start <= 380996: molecular_function_ (97.16)
|   |   |   |   |   |   start > 380996
|   |   |   |   |   |   |   start <= 387433
|   |   |   |   |   |   |   |   strand = C: transferase_activity_
(7.46)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 381322:
protein_binding_ (19.22)
|   |   |   |   |   |   |   |   |   start > 381322:
helicase_activity_ (9.65)
|   |   |   |   |   |   |   start > 387433
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 390848:
protein_binding_ (13.21)
|   |   |   |   |   |   |   |   |   start > 390848
|   |   |   |   |   |   |   |   |   |   distance <= 2740:
molecular_function_ (97.58/2.14)
|   |   |   |   |   |   |   |   |   |   distance > 2740
|   |   |   |   |   |   |   |   |   |   |   start <= 405583
|   |   |   |   |   |   |   |   |   |   |   |   start <= 398393:
molecular_function_ (12.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 398393:
protein_binding_ (15.07)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 405583: 
molecular_function_ (14.56)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 405583
|   |   |   |   |   |   |   |   |   |   start <= 392399
|   |   |   |   |   |   |   |   |   |   |   start <= 391306: 
molecular_function_ (34.38)
|   |   |   |   |   |   |   |   |   |   |   start > 391306: 
oxidoreductase_activity_ (9.63)
|   |   |   |   |   |   |   |   |   |   start > 392399
|   |   |   |   |   |   |   |   |   |   |   start <= 398393: 
transcription_regulator_activity_ (8.42)
|   |   |   |   |   |   |   |   |   |   |   start > 398393: 
molecular_function_ (28.1)
|   |   |   |   |   |   |   |   |   start > 405583: protein_binding_ 
(14.97)
|   |   |   |   start > 413393
|   |   |   |   |   start <= 449195
|   |   |   |   |   |   start <= 414764: 
nucleotidyltransferase_activity_ (18.97)
|   |   |   |   |   |   start > 414764
|   |   |   |   |   |   |   start <= 448751
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 424103
|   |   |   |   |   |   |   |   |   |   start <= 421657
|   |   |   |   |   |   |   |   |   |   |   start <= 419556: 
molecular_function_ (13.31)
|   |   |   |   |   |   |   |   |   |   |   start > 419556: 
protein_binding_ (6.27)
|   |   |   |   |   |   |   |   |   |   start > 421657: 
protein_kinase_activity_ (13.82)
|   |   |   |   |   |   |   |   |   start > 424103
|   |   |   |   |   |   |   |   |   |   start <= 442546
|   |   |   |   |   |   |   |   |   |   |   start <= 432638: 
molecular_function_ (29.79)
|   |   |   |   |   |   |   |   |   |   |   start > 432638
|   |   |   |   |   |   |   |   |   |   |   |   start <= 436796: 
transferase_activity_ (11.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 436796: 
molecular_function_ (22.84)
|   |   |   |   |   |   |   |   |   |   start > 442546
|   |   |   |   |   |   |   |   |   |   |   start <= 445916: 
protein_binding_ (12.24)
|   |   |   |   |   |   |   |   |   |   |   start > 445916: 
molecular_function_ (18.57)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 432638
|   |   |   |   |   |   |   |   |   |   start <= 422931: 
molecular_function_ (27.78)
|   |   |   |   |   |   |   |   |   |   start > 422931
|   |   |   |   |   |   |   |   |   |   |   start <= 425151: 
lyase_activity_ (7.48)
|   |   |   |   |   |   |   |   |   |   |   start > 425151: 
molecular_function_ (12.36)
```

```
|   |   |   |   |   |   |   |   |   start > 432638
|   |   |   |   |   |   |   |   |   |   start <= 436796
|   |   |   |   |   |   |   |   |   |   |   start <= 435157:
peptidase_activity_ (14.91)
|   |   |   |   |   |   |   |   |   |   |   start > 435157:
transporter_activity_ (9.22)
|   |   |   |   |   |   |   |   |   |   start > 436796:
molecular_function_ (30.93)
|   |   |   |   |   |   |   start > 448751:
nucleotidyltransferase_activity_ (18.22)
|   |   |   |   |   start > 449195
|   |   |   |   |   |   start <= 529854
|   |   |   |   |   |   |   start <= 524086
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 471664
|   |   |   |   |   |   |   |   |   |   start <= 456232:
oxidoreductase_activity_ (20.39)
|   |   |   |   |   |   |   |   |   |   start > 456232
|   |   |   |   |   |   |   |   |   |   |   start <= 470957
|   |   |   |   |   |   |   |   |   |   |   |   start <= 466201
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 462714:
molecular_function_ (52.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 462714:
lyase_activity_ (20.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 466201
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 468274
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
467026: transcription_regulator_activity_ (9.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
467026: hydrolase_activity_ (18.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 468274:
molecular_function_ (33.17)
|   |   |   |   |   |   |   |   |   |   |   start > 470957:
oxidoreductase_activity_ (17.67)
|   |   |   |   |   |   |   |   |   start > 471664
|   |   |   |   |   |   |   |   |   |   start <= 514048
|   |   |   |   |   |   |   |   |   |   |   start <= 491074
|   |   |   |   |   |   |   |   |   |   |   |   start <= 486189:
molecular_function_ (23.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 486189:
enzyme_regulator_activity_ (12.64)
|   |   |   |   |   |   |   |   |   |   |   start > 491074:
molecular_function_ (45.37)
|   |   |   |   |   |   |   |   |   |   start > 514048
|   |   |   |   |   |   |   |   |   |   |   start <= 517506:
nucleotidyltransferase_activity_ (13.87)
|   |   |   |   |   |   |   |   |   |   |   start > 517506
|   |   |   |   |   |   |   |   |   |   |   |   start <= 519178:
molecular_function_ (36.95)
|   |   |   |   |   |   |   |   |   |   |   |   start > 519178
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 522041:
enzyme_regulator_activity_ (12.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 522041:
molecular_function_ (21.66)
```

```
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 503929
|   |   |   |   |   |   |   |   |   |   start <= 460411
|   |   |   |   |   |   |   |   |   |   |   start <= 452423
|   |   |   |   |   |   |   |   |   |   |   |   start <= 451013:
translation_regulator_activity_ (16.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 451013:
molecular_function_ (20.37)
|   |   |   |   |   |   |   |   |   |   |   start > 452423
|   |   |   |   |   |   |   |   |   |   |   |   start <= 456232:
nucleotidyltransferase_activity_ (14.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 456232:
transferase_activity_ (22.24)
|   |   |   |   |   |   |   |   |   |   start > 460411
|   |   |   |   |   |   |   |   |   |   |   start <= 471664
|   |   |   |   |   |   |   |   |   |   |   |   start <= 461822:
RNA_binding_ (25.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 461822
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 466201:
molecular_function_ (16.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 466201:
RNA_binding_ (7.58)
|   |   |   |   |   |   |   |   |   |   |   start > 471664
|   |   |   |   |   |   |   |   |   |   |   |   start <= 491074:
protein_binding_ (11.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 491074
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 496676:
molecular_function_ (20.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 496676
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
497348: hydrolase_activity_ (9.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
497348: molecular_function_ (8.51)
|   |   |   |   |   |   |   |   |   start > 503929
|   |   |   |   |   |   |   |   |   |   start <= 507739:
transporter_activity_ (24.96)
|   |   |   |   |   |   |   |   |   |   start > 507739:
structural_molecule_activity_ (15.25)
|   |   |   |   |   |   |   start > 524086
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 526328:
translation_regulator_activity_ (22.22)
|   |   |   |   |   |   |   |   |   start > 526328:
transferase_activity_ (12.95)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 526328:
oxidoreductase_activity_ (22.96)
|   |   |   |   |   |   |   |   |   start > 526328
|   |   |   |   |   |   |   |   |   |   start <= 528690:
RNA_binding_ (10.46)
|   |   |   |   |   |   |   |   |   |   start > 528690:
oxidoreductase_activity_ (12.66)
|   |   |   |   |   |   start > 529854
|   |   |   |   |   |   |   start <= 534020
```

```
|   |   |   |   |   |   |   |   start <= 532055
|   |   |   |   |   |   |   |   |   start <= 531821:
molecular_function_ (10.86)
|   |   |   |   |   |   |   |   |   start > 531821: DNA_binding_
(16.28)
|   |   |   |   |   |   |   |   start > 532055:
enzyme_regulator_activity_ (17.88)
|   |   |   |   |   |   |   start > 534020
|   |   |   |   |   |   |   |   start <= 543037: molecular_function_
(92.12)
|   |   |   |   |   |   |   |   start > 543037
|   |   |   |   |   |   |   |   |   start <= 544055:
transferase_activity_ (22.98)
|   |   |   |   |   |   |   |   |   start > 544055:
molecular_function_ (18.39)
|   |   |   start > 545168
|   |   |   |   strand = C
|   |   |   |   |   start <= 559409
|   |   |   |   |   |   start <= 555907: hydrolase_activity_ (18.79)
|   |   |   |   |   |   start > 555907:
structural_molecule_activity_ (29.12)
|   |   |   |   |   start > 559409: molecular_function_ (25.31)
|   |   |   |   strand = W
|   |   |   |   |   start <= 555188
|   |   |   |   |   |   start <= 548752
|   |   |   |   |   |   |   start <= 545780:
protein_kinase_activity_ (21.09)
|   |   |   |   |   |   |   start > 545780: DNA_binding_ (27.64)
|   |   |   |   |   |   start > 548752
|   |   |   |   |   |   |   start <= 550504: molecular_function_
(19.9)
|   |   |   |   |   |   |   start > 550504:
nucleotidyltransferase_activity_ (22.31)
|   |   |   |   |   start > 555188
|   |   |   |   |   |   start <= 559409: protein_binding_
(50.95/13.32)
|   |   |   |   |   |   start > 559409: DNA_binding_ (27.66)
|   start > 567636
|   |   start <= 576594
|   |   |   start <= 572117
|   |   |   |   start <= 569392: hydrolase_activity_ (23.17)
|   |   |   |   start > 569392
|   |   |   |   |   start <= 570591: protein_binding_ (20.15)
|   |   |   |   |   start > 570591: hydrolase_activity_ (21.47)
|   |   |   start > 572117
|   |   |   |   start <= 573974
|   |   |   |   |   start <= 573088
|   |   |   |   |   |   start <= 572928: transferase_activity_
(16.71)
|   |   |   |   |   |   start > 572928: protein_binding_ (25.86)
|   |   |   |   |   start > 573088: transferase_activity_ (22.08)
|   |   |   |   start > 573974: structural_molecule_activity_
(20.78)
|   |   start > 576594
```

```
|   |   |   strand = C
|   |   |   |   start <= 620747
|   |   |   |   |   start <= 587711
|   |   |   |   |   |   start <= 578853: transporter_activity_
(14.5)
|   |   |   |   |   |   start > 578853
|   |   |   |   |   |   |   start <= 582248
|   |   |   |   |   |   |   |   start <= 581609: molecular_function_
(12.73)
|   |   |   |   |   |   |   |   start > 581609:
transferase_activity_ (15.73)
|   |   |   |   |   |   |   start > 582248: molecular_function_
(48.35)
|   |   |   |   |   start > 587711
|   |   |   |   |   |   start <= 609769
|   |   |   |   |   |   |   start <= 604199
|   |   |   |   |   |   |   |   start <= 594320: protein_binding_
(12.49)
|   |   |   |   |   |   |   |   start > 594320
|   |   |   |   |   |   |   |   |   start <= 598728: RNA_binding_
(14.43)
|   |   |   |   |   |   |   |   |   start > 598728: protein_binding_
(23.67/11.06)
|   |   |   |   |   |   |   start > 604199:
transcription_regulator_activity_ (12.74)
|   |   |   |   |   |   start > 609769
|   |   |   |   |   |   |   start <= 618227: molecular_function_
(41.68)
|   |   |   |   |   |   |   start > 618227: protein_binding_ (20.74)
|   |   |   |   start > 620747
|   |   |   |   |   start <= 654232
|   |   |   |   |   |   start <= 633609
|   |   |   |   |   |   |   start <= 627333:
oxidoreductase_activity_ (16.14)
|   |   |   |   |   |   |   start > 627333: ligase_activity_ (14.01)
|   |   |   |   |   |   start > 633609
|   |   |   |   |   |   |   start <= 644095
|   |   |   |   |   |   |   |   start <= 637784: molecular_function_
(17.94)
|   |   |   |   |   |   |   |   start > 637784
|   |   |   |   |   |   |   |   |   start <= 640819:
structural_molecule_activity_ (9.71)
|   |   |   |   |   |   |   |   |   start > 640819:
molecular_function_ (15.49)
|   |   |   |   |   |   |   start > 644095
|   |   |   |   |   |   |   |   start <= 649770:
oxidoreductase_activity_ (15.41)
|   |   |   |   |   |   |   |   start > 649770: molecular_function_
(16.19)
|   |   |   |   |   start > 654232
|   |   |   |   |   |   start <= 700876
|   |   |   |   |   |   |   start <= 678700
|   |   |   |   |   |   |   |   start <= 663743
|   |   |   |   |   |   |   |   |   start <= 658683
```

```
|   |   |   |   |   |   |   |   |   |   start <= 655957:
protein_binding_ (11.27)
|   |   |   |   |   |   |   |   |   |   start > 655957:
molecular_function_ (20.05)
|   |   |   |   |   |   |   |   |   start > 658683
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_binding_ (19.06/6.18)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
transcription_regulator_activity_ (13.31/3.42)
|   |   |   |   |   |   |   |   start > 663743
|   |   |   |   |   |   |   |   |   start <= 669516:
transferase_activity_ (33.52)
|   |   |   |   |   |   |   |   |   start > 669516
|   |   |   |   |   |   |   |   |   |   start <= 676965
|   |   |   |   |   |   |   |   |   |   |   start <= 675846:
molecular_function_ (12.53)
|   |   |   |   |   |   |   |   |   |   |   start > 675846:
protein_binding_ (16.18)
|   |   |   |   |   |   |   |   |   |   start > 676965:
molecular_function_ (15.26)
|   |   |   |   |   |   |   start > 678700
|   |   |   |   |   |   |   |   start <= 690518:
oxidoreductase_activity_ (40.84)
|   |   |   |   |   |   |   |   start > 690518
|   |   |   |   |   |   |   |   |   start <= 697135:
transcription_regulator_activity_ (9.38)
|   |   |   |   |   |   |   |   |   start > 697135:
transferase_activity_ (14.52)
|   |   |   |   |   |   start > 700876
|   |   |   |   |   |   |   start <= 719660
|   |   |   |   |   |   |   |   start <= 705738:
structural_molecule_activity_ (9.86)
|   |   |   |   |   |   |   |   start > 705738: molecular_function_
(22.04)
|   |   |   |   |   |   |   start > 719660
|   |   |   |   |   |   |   |   start <= 732434: protein_binding_
(20.53)
|   |   |   |   |   |   |   |   start > 732434
|   |   |   |   |   |   |   |   |   start <= 739810:
transporter_activity_ (12.57)
|   |   |   |   |   |   |   |   |   start > 739810:
molecular_function_ (8.77)
|   |   |   strand = W
|   |   |   |   start <= 655957
|   |   |   |   |   start <= 611191
|   |   |   |   |   |   start <= 598728
|   |   |   |   |   |   |   start <= 578853:
oxidoreductase_activity_ (20.84)
|   |   |   |   |   |   |   start > 578853
|   |   |   |   |   |   |   |   start <= 583726: molecular_function_
(34.93)
|   |   |   |   |   |   |   |   start > 583726
|   |   |   |   |   |   |   |   |   start <= 586061:
signal_transducer_activity_ (9.37)
```

```
|   |   |   |   |   |   |   |   |   start > 586061:
molecular_function_ (27.89)
|   |   |   |   |   |   start > 598728
|   |   |   |   |   |   |   start <= 609769
|   |   |   |   |   |   |   |   start <= 608301:
structural_molecule_activity_ (14.95)
|   |   |   |   |   |   |   |   start > 608301:
transporter_activity_ (17.61)
|   |   |   |   |   |   |   start > 609769: oxidoreductase_activity_
(22.59)
|   |   |   |   |   start > 611191
|   |   |   |   |   |   start <= 647120
|   |   |   |   |   |   |   start <= 623573
|   |   |   |   |   |   |   |   start <= 617912
|   |   |   |   |   |   |   |   |   start <= 612409:
molecular_function_ (13.81)
|   |   |   |   |   |   |   |   |   start > 612409
|   |   |   |   |   |   |   |   |   |   start <= 615569:
peptidase_activity_ (12.82)
|   |   |   |   |   |   |   |   |   |   start > 615569:
molecular_function_ (13.4)
|   |   |   |   |   |   |   |   start > 617912
|   |   |   |   |   |   |   |   |   start <= 620747
|   |   |   |   |   |   |   |   |   |   start <= 618227:
structural_molecule_activity_ (12.87)
|   |   |   |   |   |   |   |   |   |   start > 618227:
ligase_activity_ (15.75)
|   |   |   |   |   |   |   |   |   start > 620747:
transferase_activity_ (15.92)
|   |   |   |   |   |   |   start > 623573
|   |   |   |   |   |   |   |   start <= 633609
|   |   |   |   |   |   |   |   |   start <= 624830:
molecular_function_ (21.5)
|   |   |   |   |   |   |   |   |   start > 624830
|   |   |   |   |   |   |   |   |   |   start <= 628706
|   |   |   |   |   |   |   |   |   |   |   start <= 627333:
hydrolase_activity_ (14.71)
|   |   |   |   |   |   |   |   |   |   |   start > 627333:
molecular_function_ (17.15)
|   |   |   |   |   |   |   |   |   |   start > 628706:
hydrolase_activity_ (15.91)
|   |   |   |   |   |   |   |   start > 633609
|   |   |   |   |   |   |   |   |   start <= 640819:
molecular_function_ (61.3)
|   |   |   |   |   |   |   |   |   start > 640819
|   |   |   |   |   |   |   |   |   |   start <= 644095:
peptidase_activity_ (10.64)
|   |   |   |   |   |   |   |   |   |   start > 644095:
molecular_function_ (14.41)
|   |   |   |   |   |   start > 647120
|   |   |   |   |   |   |   start <= 647601: transporter_activity_
(29.68)
|   |   |   |   |   |   |   start > 647601
```

```
|   |   |   |   |   |   |   |   start <= 649770: molecular_function_
(15.61)
|   |   |   |   |   |   |   |   start > 649770:
structural_molecule_activity_ (14.02)
|   |   |   |   start > 655957
|   |   |   |   |   start <= 669516
|   |   |   |   |   |   start <= 667638
|   |   |   |   |   |   |   start <= 665013: RNA_binding_ (18.38)
|   |   |   |   |   |   |   start > 665013: hydrolase_activity_
(16.14)
|   |   |   |   |   |   start > 667638: protein_binding_ (19.71)
|   |   |   |   |   start > 669516
|   |   |   |   |   |   start <= 717574
|   |   |   |   |   |   |   start <= 678700
|   |   |   |   |   |   |   |   start <= 672985:
transferase_activity_ (17.21)
|   |   |   |   |   |   |   |   start > 672985:
transporter_activity_ (10.93)
|   |   |   |   |   |   |   start > 678700
|   |   |   |   |   |   |   |   start <= 704190
|   |   |   |   |   |   |   |   |   start <= 697135:
molecular_function_ (36.35)
|   |   |   |   |   |   |   |   |   start > 697135
|   |   |   |   |   |   |   |   |   |   start <= 700876:
DNA_binding_ (16.94)
|   |   |   |   |   |   |   |   |   |   start > 700876:
molecular_function_ (8.89)
|   |   |   |   |   |   |   |   start > 704190
|   |   |   |   |   |   |   |   |   start <= 705738:
transferase_activity_ (23.14)
|   |   |   |   |   |   |   |   |   start > 705738:
molecular_function_ (18.47)
|   |   |   |   |   |   start > 717574
|   |   |   |   |   |   |   start <= 725778
|   |   |   |   |   |   |   |   start <= 719660:
transporter_activity_ (16.27)
|   |   |   |   |   |   |   |   start > 719660
|   |   |   |   |   |   |   |   |   start <= 722809:
hydrolase_activity_ (22.88)
|   |   |   |   |   |   |   |   |   start > 722809:
molecular_function_ (14.59)
|   |   |   |   |   |   |   start > 725778
|   |   |   |   |   |   |   |   start <= 732434
|   |   |   |   |   |   |   |   |   start <= 729590:
oxidoreductase_activity_ (14.09)
|   |   |   |   |   |   |   |   |   start > 729590:
transporter_activity_ (9.84)
|   |   |   |   |   |   |   |   start > 732434:
oxidoreductase_activity_ (17.17)
```

For Biological Process

```
|   start <= 570591
|   |   start <= 295056
```

```
|   |   |   strand = C
|   |   |   |   start <= 90784
|   |   |   |   |   start <= 58813
|   |   |   |   |   |   start <= 41183
|   |   |   |   |   |   |   start <= 26887: biological_process_
(51.91)
|   |   |   |   |   |   |   start > 26887
|   |   |   |   |   |   |   |   start <= 38005: transport_ (14.65)
|   |   |   |   |   |   |   |   start > 38005:
ribosome_biogenesis_and_assembly_ (8.91)
|   |   |   |   |   |   start > 41183
|   |   |   |   |   |   |   start <= 47433: vesicle-
mediated_transport_ (16.21)
|   |   |   |   |   |   |   start > 47433
|   |   |   |   |   |   |   |   start <= 50443: biological_process_
(31.86)
|   |   |   |   |   |   |   |   start > 50443
|   |   |   |   |   |   |   |   |   start <= 54379: vesicle-
mediated_transport_ (14.69)
|   |   |   |   |   |   |   |   |   start > 54379:
biological_process_ (16.86)
|   |   |   |   |   start > 58813
|   |   |   |   |   |   start <= 75932
|   |   |   |   |   |   |   start <= 69337
|   |   |   |   |   |   |   |   start <= 63804: translation_ (19.3)
|   |   |   |   |   |   |   |   start > 63804:
lipid_metabolic_process_ (8.86)
|   |   |   |   |   |   |   start > 69337
|   |   |   |   |   |   |   |   start <= 73786: vesicle-
mediated_transport_ (30.53/13.61)
|   |   |   |   |   |   |   |   start > 73786: translation_ (14.38)
|   |   |   |   |   |   start > 75932
|   |   |   |   |   |   |   start <= 85658
|   |   |   |   |   |   |   |   start <= 80153: meiosis_ (7.87)
|   |   |   |   |   |   |   |   start > 80153: biological_process_
(12.46)
|   |   |   |   |   |   |   start > 85658:
organelle_organization_and_biogenesis_ (27.85)
|   |   |   |   start > 90784
|   |   |   |   |   start <= 231297
|   |   |   |   |   |   start <= 184499
|   |   |   |   |   |   |   start <= 126324
|   |   |   |   |   |   |   |   start <= 111153
|   |   |   |   |   |   |   |   |   start <= 101773
|   |   |   |   |   |   |   |   |   |   start <= 97731:
DNA_metabolic_process_ (29.29)
|   |   |   |   |   |   |   |   |   |   start > 97731
|   |   |   |   |   |   |   |   |   |   |   start <= 100888:
biological_process_ (16.78)
|   |   |   |   |   |   |   |   |   |   |   start > 100888:
conjugation_ (17.29)
|   |   |   |   |   |   |   |   |   start > 101773
|   |   |   |   |   |   |   |   |   |   start <= 109455
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 106428:
RNA_metabolic_process_ (20.9)
|   |   |   |   |   |   |   |   |   |   |   start > 106428:
cellular_homeostasis_ (13.34)
|   |   |   |   |   |   |   |   |   |   start > 109455:
protein_modification_process_ (23.57)
|   |   |   |   |   |   |   |   start > 111153
|   |   |   |   |   |   |   |   |   start <= 120445
|   |   |   |   |   |   |   |   |   |   start <= 115625:
biological_process_ (39.67)
|   |   |   |   |   |   |   |   |   |   start > 115625
|   |   |   |   |   |   |   |   |   |   |   start <= 117241:
translation_ (16.67)
|   |   |   |   |   |   |   |   |   |   |   start > 117241:
biological_process_ (10.63)
|   |   |   |   |   |   |   |   |   start > 120445
|   |   |   |   |   |   |   |   |   |   start <= 122944:
cell_wall_organization_and_biogenesis_ (17.3)
|   |   |   |   |   |   |   |   |   |   start > 122944: conjugation_
(37.54/15.85)
|   |   |   |   |   |   |   start > 126324
|   |   |   |   |   |   |   |   start <= 158185
|   |   |   |   |   |   |   |   |   start <= 152996
|   |   |   |   |   |   |   |   |   |   start <= 135930
|   |   |   |   |   |   |   |   |   |   |   start <= 128949:
protein_modification_process_ (14.29)
|   |   |   |   |   |   |   |   |   |   |   start > 128949
|   |   |   |   |   |   |   |   |   |   |   |   start <= 130640:
carbohydrate_metabolic_process_ (10.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 130640
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 133932:
vesicle-mediated_transport_ (14.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 133932:
carbohydrate_metabolic_process_ (6.85)
|   |   |   |   |   |   |   |   |   |   start > 135930
|   |   |   |   |   |   |   |   |   |   |   start <= 146356
|   |   |   |   |   |   |   |   |   |   |   |   start <= 139688
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 137376:
biological_process_ (9.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 137376:
ribosome_biogenesis_and_assembly_ (13.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 139688:
biological_process_ (22.61)
|   |   |   |   |   |   |   |   |   |   |   start > 146356:
protein_modification_process_ (40.56)
|   |   |   |   |   |   |   |   |   start > 152996
|   |   |   |   |   |   |   |   |   |   start <= 154688:
translation_ (25.36)
|   |   |   |   |   |   |   |   |   |   start > 154688
|   |   |   |   |   |   |   |   |   |   |   start <= 156166:
generation_of_precursor_metabolites_and_energy_ (37.6/14.58)
|   |   |   |   |   |   |   |   |   |   |   start > 156166:
translation_ (14.55)
|   |   |   |   |   |   |   |   start > 158185
```

```
|   |   |   |   |   |   |   |   |   start <= 172364
|   |   |   |   |   |   |   |   |   |   start <= 165345:
biological_process_ (31.46)
|   |   |   |   |   |   |   |   |   |   start > 165345:
amino_acid_and_derivative_metabolic_process_ (12.37)
|   |   |   |   |   |   |   |   |   start > 172364
|   |   |   |   |   |   |   |   |   |   start <= 180100
|   |   |   |   |   |   |   |   |   |   |   start <= 177303:
DNA_metabolic_process_ (19.09)
|   |   |   |   |   |   |   |   |   |   |   start > 177303:
response_to_stress_ (35.21/20.99)
|   |   |   |   |   |   |   |   |   |   start > 180100
|   |   |   |   |   |   |   |   |   |   |   start <= 181707:
biological_process_ (14.42)
|   |   |   |   |   |   |   |   |   |   |   start > 181707:
DNA_metabolic_process_ (20.61)
|   |   |   |   |   |   start > 184499
|   |   |   |   |   |   |   start <= 197383
|   |   |   |   |   |   |   |   start <= 189715
|   |   |   |   |   |   |   |   |   start <= 187643
|   |   |   |   |   |   |   |   |   |   start <= 186677:
ribosome_biogenesis_and_assembly_ (14.93)
|   |   |   |   |   |   |   |   |   |   start > 186677:
RNA_metabolic_process_ (25.98)
|   |   |   |   |   |   |   |   |   start > 187643:
biological_process_ (20.04)
|   |   |   |   |   |   |   |   start > 189715
|   |   |   |   |   |   |   |   |   start <= 192530:
carbohydrate_metabolic_process_ (28.68/13.45)
|   |   |   |   |   |   |   |   |   start > 192530
|   |   |   |   |   |   |   |   |   |   start <= 194872:
organelle_organization_and_biogenesis_ (17.71)
|   |   |   |   |   |   |   |   |   |   start > 194872: translation_
(15.05)
|   |   |   |   |   |   |   start > 197383
|   |   |   |   |   |   |   |   start <= 221386
|   |   |   |   |   |   |   |   |   start <= 211573
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
biological_process_ (24.59/9.46)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
transcription_ (12.22/3.78)
|   |   |   |   |   |   |   |   |   start > 211573
|   |   |   |   |   |   |   |   |   |   start <= 217305:
ribosome_biogenesis_and_assembly_ (25.03)
|   |   |   |   |   |   |   |   |   |   start > 217305
|   |   |   |   |   |   |   |   |   |   |   start <= 218852:
conjugation_ (12.38)
|   |   |   |   |   |   |   |   |   |   |   start > 218852:
biological_process_ (19.9)
|   |   |   |   |   |   |   |   start > 221386
|   |   |   |   |   |   |   |   |   start <= 228475:
RNA_metabolic_process_ (25.35/12.57)
|   |   |   |   |   |   |   |   |   start > 228475:
generation_of_precursor_metabolites_and_energy_ (18.02)
```

```
|   |   |   |   |   start > 231297
|   |   |   |   |   |   start <= 272822
|   |   |   |   |   |   |   start <= 257418
|   |   |   |   |   |   |   |   start <= 254437
|   |   |   |   |   |   |   |   |   start <= 242078:
response_to_stress_ (11.89)
|   |   |   |   |   |   |   |   |   start > 242078: transport_
(16.18)
|   |   |   |   |   |   |   |   start > 254437:
cellular_homeostasis_ (25.47)
|   |   |   |   |   |   |   start > 257418
|   |   |   |   |   |   |   |   start <= 265921
|   |   |   |   |   |   |   |   |   start <= 262547:
protein_modification_process_ (18.13)
|   |   |   |   |   |   |   |   |   start > 262547:
DNA_metabolic_process_ (14.62)
|   |   |   |   |   |   |   |   start > 265921: response_to_stress_
(34.05/12.9)
|   |   |   |   |   |   start > 272822
|   |   |   |   |   |   |   start <= 289221
|   |   |   |   |   |   |   |   start <= 285266
|   |   |   |   |   |   |   |   |   start <= 281180:
biological_process_ (13.71)
|   |   |   |   |   |   |   |   |   start > 281180:
DNA_metabolic_process_ (18.89)
|   |   |   |   |   |   |   |   start > 285266: meiosis_ (15.07)
|   |   |   |   |   |   |   start > 289221: biological_process_
(48.21)
|   |   |   strand = W
|   |   |   |   start <= 246486
|   |   |   |   |   start <= 197383
|   |   |   |   |   |   start <= 137376
|   |   |   |   |   |   |   start <= 71365
|   |   |   |   |   |   |   |   start <= 36919
|   |   |   |   |   |   |   |   |   start <= 32163
|   |   |   |   |   |   |   |   |   |   start <= 19497
|   |   |   |   |   |   |   |   |   |   |   start <= 11475
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transport_ (6.35/2.44)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
vesicle-mediated_transport_ (14.1/3.93)
|   |   |   |   |   |   |   |   |   |   |   start > 11475:
transport_ (11.24)
|   |   |   |   |   |   |   |   |   |   start > 19497
|   |   |   |   |   |   |   |   |   |   |   start <= 23133:
biological_process_ (31.94)
|   |   |   |   |   |   |   |   |   |   |   start > 23133
|   |   |   |   |   |   |   |   |   |   |   |   start <= 26887:
transport_ (7.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 26887:
biological_process_ (14.73)
|   |   |   |   |   |   |   |   |   start > 32163
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: transport_
(10.52/2.19)
```

```
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
organelle_organization_and_biogenesis_ (25.87/10.07)
|   |   |   |   |   |   |   |   start > 36919
|   |   |   |   |   |   |   |   |   start <= 60843
|   |   |   |   |   |   |   |   |   |   start <= 53341
|   |   |   |   |   |   |   |   |   |   |   start <= 41183:
cellular_respiration_ (16.09)
|   |   |   |   |   |   |   |   |   |   |   start > 41183:
RNA_metabolic_process_ (10.23)
|   |   |   |   |   |   |   |   |   |   start > 53341
|   |   |   |   |   |   |   |   |   |   |   start <= 54379:
cell_wall_organization_and_biogenesis_ (12.48)
|   |   |   |   |   |   |   |   |   |   |   start > 54379:
transport_ (13.42)
|   |   |   |   |   |   |   |   |   start > 60843
|   |   |   |   |   |   |   |   |   |   start <= 69337
|   |   |   |   |   |   |   |   |   |   |   start <= 63804:
biological_process_ (14.24)
|   |   |   |   |   |   |   |   |   |   |   start > 63804
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
DNA_metabolic_process_ (6.0/2.38)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
DNA_metabolic_process_ (5.13/2.01)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cell_cycle_ (13.05/4.43)
|   |   |   |   |   |   |   |   |   |   start > 69337:
biological_process_ (17.06)
|   |   |   |   |   |   |   start > 71365
|   |   |   |   |   |   |   |   start <= 90784
|   |   |   |   |   |   |   |   |   start <= 84066
|   |   |   |   |   |   |   |   |   |   start <= 75932: translation_
(18.29)
|   |   |   |   |   |   |   |   |   |   start > 75932
|   |   |   |   |   |   |   |   |   |   |   start <= 80153:
protein_modification_process_ (15.15)
|   |   |   |   |   |   |   |   |   |   |   start > 80153
|   |   |   |   |   |   |   |   |   |   |   |   start <= 83446:
response_to_stress_ (19.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 83446:
protein_modification_process_ (7.62)
|   |   |   |   |   |   |   |   |   start > 84066
|   |   |   |   |   |   |   |   |   |   start <= 88785
|   |   |   |   |   |   |   |   |   |   |   start <= 85658:
biological_process_ (12.5)
|   |   |   |   |   |   |   |   |   |   |   start > 85658:
cytoskeleton_organization_and_biogenesis_ (19.37)
|   |   |   |   |   |   |   |   |   |   start > 88785: translation_
(15.08)
|   |   |   |   |   |   |   |   start > 90784
|   |   |   |   |   |   |   |   |   start <= 111153
|   |   |   |   |   |   |   |   |   |   start <= 105008
|   |   |   |   |   |   |   |   |   |   |   start <= 100888
|   |   |   |   |   |   |   |   |   |   |   |   start <= 95090:
cell_wall_organization_and_biogenesis_ (13.56)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 95090:
biological_process_ (8.74)
|   |   |   |   |   |   |   |   |   |   |   start > 100888:
lipid_metabolic_process_ (15.34)
|   |   |   |   |   |   |   |   |   |   start > 105008:
electron_transport_ (26.22/13.05)
|   |   |   |   |   |   |   |   |   start > 111153
|   |   |   |   |   |   |   |   |   |   start <= 126324
|   |   |   |   |   |   |   |   |   |   |   start <= 118821:
biological_process_ (14.36)
|   |   |   |   |   |   |   |   |   |   |   start > 118821:
cell_wall_organization_and_biogenesis_ (18.28)
|   |   |   |   |   |   |   |   |   |   start > 126324:
biological_process_ (17.49)
|   |   |   |   |   |   start > 137376
|   |   |   |   |   |   |   start <= 147098
|   |   |   |   |   |   |   |   start <= 143289
|   |   |   |   |   |   |   |   |   start <= 140434:
ribosome_biogenesis_and_assembly_ (20.02)
|   |   |   |   |   |   |   |   |   start > 140434: meiosis_ (12.3)
|   |   |   |   |   |   |   |   start > 143289
|   |   |   |   |   |   |   |   |   start <= 146356
|   |   |   |   |   |   |   |   |   |   start <= 145157: transport_
(18.11)
|   |   |   |   |   |   |   |   |   |   start > 145157:
response_to_stress_ (20.96)
|   |   |   |   |   |   |   |   |   start > 146356
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 411:
transport_ (6.2/0.8)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 411:
organelle_organization_and_biogenesis_ (3.09/0.34)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
transport_ (3.78/0.39)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
organelle_organization_and_biogenesis_ (21.89/7.99)
|   |   |   |   |   |   |   start > 147098
|   |   |   |   |   |   |   |   start <= 160616
|   |   |   |   |   |   |   |   |   start <= 156166
|   |   |   |   |   |   |   |   |   |   start <= 152996:
transcription_ (26.95/12.01)
|   |   |   |   |   |   |   |   |   |   start > 152996:
biological_process_ (15.88)
|   |   |   |   |   |   |   |   |   start > 156166
|   |   |   |   |   |   |   |   |   |   start <= 158185:
signal_transduction_ (12.41)
|   |   |   |   |   |   |   |   |   |   start > 158185
|   |   |   |   |   |   |   |   |   |   |   distance <= 676:
RNA_metabolic_process_ (4.26/0.3)
|   |   |   |   |   |   |   |   |   |   |   distance > 676
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: organelle_organization_and_biogenesis_ (2.03/0.73)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: RNA_metabolic_process_ (10.49/4.85)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
organelle_organization_and_biogenesis_ (23.04/10.85)
|   |   |   |   |   |   |   |   start > 160616
|   |   |   |   |   |   |   |   |   start <= 191638
|   |   |   |   |   |   |   |   |   |   start <= 186677:
biological_process_ (46.21)
|   |   |   |   |   |   |   |   |   |   start > 186677
|   |   |   |   |   |   |   |   |   |   |   start <= 189715:
ribosome_biogenesis_and_assembly_ (19.94)
|   |   |   |   |   |   |   |   |   |   |   start > 189715:
biological_process_ (17.9)
|   |   |   |   |   |   |   |   |   start > 191638
|   |   |   |   |   |   |   |   |   |   start <= 192530: transport_
(14.6)
|   |   |   |   |   |   |   |   |   |   start > 192530
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1842: DNA_metabolic_process_ (3.37/0.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 1842:
protein_modification_process_ (3.12/0.54)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (9.3/2.29)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
protein_modification_process_ (9.28/3.64)
|   |   |   |   |   start > 197383
|   |   |   |   |   |   start <= 237259
|   |   |   |   |   |   |   start <= 228475
|   |   |   |   |   |   |   |   start <= 221386
|   |   |   |   |   |   |   |   |   start <= 205301
|   |   |   |   |   |   |   |   |   |   start <= 204731:
translation_ (7.57)
|   |   |   |   |   |   |   |   |   |   start > 204731:
organelle_organization_and_biogenesis_ (15.4)
|   |   |   |   |   |   |   |   |   start > 205301
|   |   |   |   |   |   |   |   |   |   start <= 211573:
cytoskeleton_organization_and_biogenesis_ (10.59)
|   |   |   |   |   |   |   |   |   |   start > 211573: meiosis_
(16.05)
|   |   |   |   |   |   |   |   start > 221386
|   |   |   |   |   |   |   |   |   start <= 225051:
biological_process_ (12.17)
|   |   |   |   |   |   |   |   |   start > 225051:
organelle_organization_and_biogenesis_ (34.15/12.99)
|   |   |   |   |   |   |   start > 228475
|   |   |   |   |   |   |   |   start <= 233935: translation_
(19.88)
|   |   |   |   |   |   |   |   start > 233935:
cytoskeleton_organization_and_biogenesis_ (20.72)
|   |   |   |   |   |   start > 237259
|   |   |   |   |   |   |   start <= 245587
```

```
|   |   |   |   |   |   |   |   start <= 239410: vesicle-
mediated_transport_ (50.35/19.05)
|   |   |   |   |   |   |   |   start > 239410
|   |   |   |   |   |   |   |   |   start <= 242078: cell_cycle_
(18.03)
|   |   |   |   |   |   |   |   |   start > 242078: transport_
(18.19)
|   |   |   |   |   |   |   start > 245587: translation_ (21.05)
|   |   |   |   start > 246486
|   |   |   |   |   start <= 257418
|   |   |   |   |   |   start <= 247250:
protein_modification_process_ (63.18/41.07)
|   |   |   |   |   |   start > 247250: DNA_metabolic_process_
(19.23)
|   |   |   |   |   start > 257418
|   |   |   |   |   |   start <= 265921
|   |   |   |   |   |   |   distance <= 6028: biological_process_
(41.15/25.22)
|   |   |   |   |   |   |   distance > 6028: transcription_
(9.02/4.58)
|   |   |   |   |   |   start > 265921
|   |   |   |   |   |   |   start <= 272822
|   |   |   |   |   |   |   |   start <= 268794:
amino_acid_and_derivative_metabolic_process_ (42.32/19.88)
|   |   |   |   |   |   |   |   start > 268794: cytokinesis_ (11.6)
|   |   |   |   |   |   |   start > 272822
|   |   |   |   |   |   |   |   start <= 278836:
cell_wall_organization_and_biogenesis_ (15.42)
|   |   |   |   |   |   |   |   start > 278836: biological_process_
(32.91)
|   |   start > 295056
|   |   |   start <= 378355
|   |   |   |   start <= 352381
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 349173
|   |   |   |   |   |   |   start <= 306127
|   |   |   |   |   |   |   |   start <= 303176
|   |   |   |   |   |   |   |   |   neigh_num <= 1: cell_cycle_
(14.8/6.71)
|   |   |   |   |   |   |   |   |   neigh_num > 1: sporulation_
(12.64/4.52)
|   |   |   |   |   |   |   |   start > 303176:
DNA_metabolic_process_ (15.22)
|   |   |   |   |   |   |   start > 306127
|   |   |   |   |   |   |   |   start <= 334260
|   |   |   |   |   |   |   |   |   start <= 314867
|   |   |   |   |   |   |   |   |   |   start <= 312701
|   |   |   |   |   |   |   |   |   |   |   start <= 310632:
biological_process_ (8.64)
|   |   |   |   |   |   |   |   |   |   |   start > 310632:
ribosome_biogenesis_and_assembly_ (14.9)
|   |   |   |   |   |   |   |   |   |   start > 312701:
biological_process_ (24.27)
|   |   |   |   |   |   |   |   |   start > 314867
```

```
|   |   |   |   |   |   |   |   |   |   start <= 320011
|   |   |   |   |   |   |   |   |   |   |   start <= 315552:
transcription_ (19.26)
|   |   |   |   |   |   |   |   |   |   |   start > 315552:
translation_ (12.54)
|   |   |   |   |   |   |   |   |   |   start > 320011
|   |   |   |   |   |   |   |   |   |   |   start <= 327868:
cell_wall_organization_and_biogenesis_ (20.89)
|   |   |   |   |   |   |   |   |   |   |   start > 327868
|   |   |   |   |   |   |   |   |   |   |   |   start <= 330116:
biological_process_ (13.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 330116:
transcription_ (11.08)
|   |   |   |   |   |   |   |   start > 334260
|   |   |   |   |   |   |   |   |   start <= 348632
|   |   |   |   |   |   |   |   |   |   start <= 342517:
biological_process_ (15.33)
|   |   |   |   |   |   |   |   |   |   start > 342517: sporulation_
(25.97)
|   |   |   |   |   |   |   |   |   start > 348632:
biological_process_ (18.28)
|   |   |   |   |   |   start > 349173
|   |   |   |   |   |   |   start <= 349228
|   |   |   |   |   |   |   |   distance <= 3171:
ribosome_biogenesis_and_assembly_ (19.87/6.21)
|   |   |   |   |   |   |   |   distance > 3171:
RNA_metabolic_process_ (8.78/1.13)
|   |   |   |   |   |   |   start > 349228
|   |   |   |   |   |   |   |   neigh_strand = W: cell_cycle_
(24.43/11.54)
|   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   distance <= 829: cell_cycle_
(4.72/1.47)
|   |   |   |   |   |   |   |   |   |   distance > 829:
protein_catabolic_process_ (5.93/0.25)
|   |   |   |   |   |   |   |   |   neigh_num > 1: cell_cycle_
(12.39/4.28)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 327868
|   |   |   |   |   |   |   start <= 320011
|   |   |   |   |   |   |   |   start <= 303176
|   |   |   |   |   |   |   |   |   start <= 295240:
nuclear_organization_and_biogenesis_ (8.91)
|   |   |   |   |   |   |   |   |   start > 295240: conjugation_
(37.67/15.53)
|   |   |   |   |   |   |   |   start > 303176
|   |   |   |   |   |   |   |   |   start <= 316718
|   |   |   |   |   |   |   |   |   |   start <= 310632:
DNA_metabolic_process_ (10.45)
|   |   |   |   |   |   |   |   |   |   start > 310632:
biological_process_ (16.03)
|   |   |   |   |   |   |   |   |   start > 316718
```

```
|   |   |   |   |   |   |   |   |   |   start <= 317279:
protein_modification_process_ (13.21)
|   |   |   |   |   |   |   |   |   |   start > 317279:
nuclear_organization_and_biogenesis_ (9.6)
|   |   |   |   |   |   |   start > 320011
|   |   |   |   |   |   |   |   start <= 323381:
vitamin_metabolic_process_ (12.66)
|   |   |   |   |   |   |   |   start > 323381: transport_ (17.51)
|   |   |   |   |   |   start > 327868
|   |   |   |   |   |   |   start <= 338266
|   |   |   |   |   |   |   |   start <= 334260
|   |   |   |   |   |   |   |   |   start <= 333352:
biological_process_ (19.58)
|   |   |   |   |   |   |   |   |   start > 333352:
membrane_organization_and_biogenesis_ (23.29)
|   |   |   |   |   |   |   |   start > 334260
|   |   |   |   |   |   |   |   |   start <= 335893: vesicle-
mediated_transport_ (9.51)
|   |   |   |   |   |   |   |   |   start > 335893:
carbohydrate_metabolic_process_ (17.01)
|   |   |   |   |   |   |   start > 338266
|   |   |   |   |   |   |   |   start <= 342517
|   |   |   |   |   |   |   |   |   start <= 339782:
biological_process_ (18.93)
|   |   |   |   |   |   |   |   |   start > 339782:
ribosome_biogenesis_and_assembly_ (18.91)
|   |   |   |   |   |   |   |   start > 342517: biological_process_
(30.77)
|   |   |   |   start > 352381
|   |   |   |   |   start <= 359671
|   |   |   |   |   |   strand = C: transport_ (12.5)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 355451: translation_ (46.37)
|   |   |   |   |   |   |   start > 355451: cellular_respiration_
(12.56)
|   |   |   |   |   start > 359671
|   |   |   |   |   |   start <= 373794
|   |   |   |   |   |   |   start <= 361244
|   |   |   |   |   |   |   |   start <= 360125: biological_process_
(16.62)
|   |   |   |   |   |   |   |   start > 360125:
cell_wall_organization_and_biogenesis_ (20.96)
|   |   |   |   |   |   |   start > 361244:
nuclear_organization_and_biogenesis_ (36.57)
|   |   |   |   |   |   start > 373794
|   |   |   |   |   |   |   start <= 374572: translation_ (20.76)
|   |   |   |   |   |   |   start > 374572
|   |   |   |   |   |   |   |   start <= 376657: biological_process_
(25.82)
|   |   |   |   |   |   |   |   start > 376657: translation_ (16.94)
|   |   |   start > 378355
|   |   |   |   start <= 550504
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 467026
```

```
|   |   |   |   |   |   |   start <= 442546
|   |   |   |   |   |   |   |   start <= 398393
|   |   |   |   |   |   |   |   |   start <= 387652
|   |   |   |   |   |   |   |   |   |   start <= 383832:
RNA_metabolic_process_ (14.72)
|   |   |   |   |   |   |   |   |   |   start > 383832:
protein_modification_process_ (10.19)
|   |   |   |   |   |   |   |   |   start > 387652
|   |   |   |   |   |   |   |   |   |   start <= 391306
|   |   |   |   |   |   |   |   |   |   |   start <= 390848:
vesicle-mediated_transport_ (15.63)
|   |   |   |   |   |   |   |   |   |   |   start > 390848:
translation_ (22.79)
|   |   |   |   |   |   |   |   |   |   start > 391306
|   |   |   |   |   |   |   |   |   |   |   distance <= 1316
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 350:
vesicle-mediated_transport_ (2.7/1.25)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 350:
biological_process_ (29.3/0.89)
|   |   |   |   |   |   |   |   |   |   |   distance > 1316
|   |   |   |   |   |   |   |   |   |   |   |   start <= 396587:
vesicle-mediated_transport_ (12.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 396587
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 396791:
translation_ (2.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 396791:
biological_process_ (3.3)
|   |   |   |   |   |   |   |   start > 398393
|   |   |   |   |   |   |   |   |   start <= 414960
|   |   |   |   |   |   |   |   |   |   start <= 411034
|   |   |   |   |   |   |   |   |   |   |   start <= 405583:
cytoskeleton_organization_and_biogenesis_ (15.12)
|   |   |   |   |   |   |   |   |   |   |   start > 405583:
cell_cycle_ (17.3)
|   |   |   |   |   |   |   |   |   |   start > 411034
|   |   |   |   |   |   |   |   |   |   |   start <= 413393:
organelle_organization_and_biogenesis_ (52.36/32.27)
|   |   |   |   |   |   |   |   |   |   |   start > 413393:
transcription_ (24.64)
|   |   |   |   |   |   |   |   |   start > 414960
|   |   |   |   |   |   |   |   |   |   start <= 425151
|   |   |   |   |   |   |   |   |   |   |   start <= 421657
|   |   |   |   |   |   |   |   |   |   |   |   start <= 416030:
translation_ (14.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 416030
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 419556:
ribosome_biogenesis_and_assembly_ (12.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 419556:
cytoskeleton_organization_and_biogenesis_ (10.49)
|   |   |   |   |   |   |   |   |   |   |   start > 421657
|   |   |   |   |   |   |   |   |   |   |   |   start <= 424103:
protein_modification_process_ (14.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 424103:
translation_ (22.08)
```

```
|   |   |   |   |   |   |   |   |   |   start > 425151
|   |   |   |   |   |   |   |   |   |   |   start <= 432638:
organelle_organization_and_biogenesis_ (17.42)
|   |   |   |   |   |   |   |   |   |   |   start > 432638
|   |   |   |   |   |   |   |   |   |   |   |   start <= 436796:
protein_modification_process_ (10.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 436796:
ribosome_biogenesis_and_assembly_ (10.6)
|   |   |   |   |   |   |   start > 442546
|   |   |   |   |   |   |   |   start <= 462714
|   |   |   |   |   |   |   |   |   start <= 445916: conjugation_
(14.96)
|   |   |   |   |   |   |   |   |   start > 445916
|   |   |   |   |   |   |   |   |   |   start <= 456232:
biological_process_ (25.51)
|   |   |   |   |   |   |   |   |   |   start > 456232
|   |   |   |   |   |   |   |   |   |   |   start <= 458354:
transport_ (23.57)
|   |   |   |   |   |   |   |   |   |   |   start > 458354
|   |   |   |   |   |   |   |   |   |   |   |   start <= 459419:
biological_process_ (17.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 459419:
transport_ (16.78)
|   |   |   |   |   |   |   |   start > 462714
|   |   |   |   |   |   |   |   |   start <= 466201:
amino_acid_and_derivative_metabolic_process_ (12.77)
|   |   |   |   |   |   |   |   |   start > 466201:
RNA_metabolic_process_ (14.52)
|   |   |   |   |   |   start > 467026
|   |   |   |   |   |   |   start <= 486189
|   |   |   |   |   |   |   |   start <= 469777
|   |   |   |   |   |   |   |   |   start <= 468274:
lipid_metabolic_process_ (15.58)
|   |   |   |   |   |   |   |   |   start > 468274
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cell_cycle_ (17.63/7.56)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (21.58/12.17)
|   |   |   |   |   |   |   |   start > 469777
|   |   |   |   |   |   |   |   |   start <= 470957:
biological_process_ (13.12)
|   |   |   |   |   |   |   |   |   start > 470957
|   |   |   |   |   |   |   |   |   |   start <= 471664:
vitamin_metabolic_process_ (10.38)
|   |   |   |   |   |   |   |   |   |   start > 471664:
biological_process_ (12.53)
|   |   |   |   |   |   |   start > 486189
|   |   |   |   |   |   |   |   start <= 517506
|   |   |   |   |   |   |   |   |   start <= 497348
|   |   |   |   |   |   |   |   |   |   start <= 491074: vesicle-
mediated_transport_ (42.17/27.57)
|   |   |   |   |   |   |   |   |   |   start > 491074
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
organelle_organization_and_biogenesis_ (18.2/4.56)
```

```
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
organelle_organization_and_biogenesis_ (7.85/2.95)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
vesicle-mediated_transport_ (12.83/3.66)
|   |   |   |   |   |   |   |   |   start > 497348
|   |   |   |   |   |   |   |   |   |   start <= 514048
|   |   |   |   |   |   |   |   |   |   |   start <= 507739:
protein_modification_process_ (15.0)
|   |   |   |   |   |   |   |   |   |   |   start > 507739:
ribosome_biogenesis_and_assembly_ (13.85)
|   |   |   |   |   |   |   |   |   |   start > 514048:
DNA_metabolic_process_ (15.85)
|   |   |   |   |   |   |   |   start > 517506
|   |   |   |   |   |   |   |   |   start <= 526328
|   |   |   |   |   |   |   |   |   |   start <= 522041
|   |   |   |   |   |   |   |   |   |   |   start <= 519178
|   |   |   |   |   |   |   |   |   |   |   |   start <= 517877:
translation_ (13.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 517877:
vesicle-mediated_transport_ (15.74)
|   |   |   |   |   |   |   |   |   |   |   start > 519178:
organelle_organization_and_biogenesis_ (20.36/6.96)
|   |   |   |   |   |   |   |   |   |   start > 522041: translation_
(30.71)
|   |   |   |   |   |   |   |   |   start > 526328
|   |   |   |   |   |   |   |   |   |   start <= 542495
|   |   |   |   |   |   |   |   |   |   |   start <= 534020:
vitamin_metabolic_process_ (15.75)
|   |   |   |   |   |   |   |   |   |   |   start > 534020:
biological_process_ (12.74)
|   |   |   |   |   |   |   |   |   |   start > 542495
|   |   |   |   |   |   |   |   |   |   |   start <= 544055:
translation_ (14.63)
|   |   |   |   |   |   |   |   |   |   |   start > 544055: vesicle-
mediated_transport_ (19.75)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 445916
|   |   |   |   |   |   |   start <= 405583
|   |   |   |   |   |   |   |   start <= 387652
|   |   |   |   |   |   |   |   |   start <= 381322
|   |   |   |   |   |   |   |   |   |   start <= 378820: transport_
(10.47)
|   |   |   |   |   |   |   |   |   |   start > 378820:
response_to_stress_ (18.08)
|   |   |   |   |   |   |   |   |   start > 381322
|   |   |   |   |   |   |   |   |   |   start <= 383832:
ribosome_biogenesis_and_assembly_ (15.62)
|   |   |   |   |   |   |   |   |   |   start > 383832:
organelle_organization_and_biogenesis_ (14.92)
|   |   |   |   |   |   |   |   start > 387652
|   |   |   |   |   |   |   |   |   start <= 392399
|   |   |   |   |   |   |   |   |   |   start <= 391306:
biological_process_ (22.21)
```

```
|   |   |   |   |   |   |   |   |   |   start > 391306:
DNA_metabolic_process_ (14.34)
|   |   |   |   |   |   |   |   |   start > 392399
|   |   |   |   |   |   |   |   |   |   start <= 398393:
transcription_ (17.37)
|   |   |   |   |   |   |   |   |   |   start > 398393
|   |   |   |   |   |   |   |   |   |   |   start <= 402892:
cell_cycle_ (15.98)
|   |   |   |   |   |   |   |   |   |   |   start > 402892:
biological_process_ (13.59)
|   |   |   |   |   |   |   start > 405583
|   |   |   |   |   |   |   |   start <= 432638
|   |   |   |   |   |   |   |   |   start <= 422931
|   |   |   |   |   |   |   |   |   |   start <= 411034:
cytoskeleton_organization_and_biogenesis_ (13.69)
|   |   |   |   |   |   |   |   |   |   start > 411034: translation_
(23.77)
|   |   |   |   |   |   |   |   |   start > 422931
|   |   |   |   |   |   |   |   |   |   start <= 425151:
signal_transduction_ (15.82)
|   |   |   |   |   |   |   |   |   |   start > 425151:
cellular_respiration_ (18.24)
|   |   |   |   |   |   |   |   start > 432638
|   |   |   |   |   |   |   |   |   start <= 436796
|   |   |   |   |   |   |   |   |   |   start <= 435157:
response_to_stress_ (13.5)
|   |   |   |   |   |   |   |   |   |   start > 435157: transport_
(10.79)
|   |   |   |   |   |   |   |   |   start > 436796
|   |   |   |   |   |   |   |   |   |   start <= 438858:
ribosome_biogenesis_and_assembly_ (13.71)
|   |   |   |   |   |   |   |   |   |   start > 438858: vesicle-
mediated_transport_ (16.21)
|   |   |   |   |   |   start > 445916
|   |   |   |   |   |   |   start <= 529854
|   |   |   |   |   |   |   |   start <= 503929
|   |   |   |   |   |   |   |   |   start <= 451013
|   |   |   |   |   |   |   |   |   |   start <= 449195:
DNA_metabolic_process_ (18.14)
|   |   |   |   |   |   |   |   |   |   start > 449195: translation_
(17.14)
|   |   |   |   |   |   |   |   |   start > 451013
|   |   |   |   |   |   |   |   |   |   start <= 460411
|   |   |   |   |   |   |   |   |   |   |   start <= 456232
|   |   |   |   |   |   |   |   |   |   |   |   start <= 452423:
biological_process_ (17.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 452423:
amino_acid_and_derivative_metabolic_process_ (5.0)
|   |   |   |   |   |   |   |   |   |   |   start > 456232:
cell_wall_organization_and_biogenesis_ (18.09)
|   |   |   |   |   |   |   |   |   |   start > 460411
|   |   |   |   |   |   |   |   |   |   |   start <= 471664
|   |   |   |   |   |   |   |   |   |   |   |   start <= 466201:
biological_process_ (44.87)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 466201:
RNA_metabolic_process_ (8.37)
|   |   |   |   |   |   |   |   |   |   |   start > 471664
|   |   |   |   |   |   |   |   |   |   |   |   start <= 491074:
response_to_stress_ (13.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 491074
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 496676:
biological_process_ (25.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 496676
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
497348: DNA_metabolic_process_ (8.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
497348: biological_process_ (8.2)
|   |   |   |   |   |   |   |   start > 503929
|   |   |   |   |   |   |   |   |   start <= 517877
|   |   |   |   |   |   |   |   |   |   start <= 507739:
cellular_homeostasis_ (18.65)
|   |   |   |   |   |   |   |   |   |   start > 507739:
membrane_organization_and_biogenesis_ (28.93/9.66)
|   |   |   |   |   |   |   |   |   start > 517877
|   |   |   |   |   |   |   |   |   |   start <= 526328
|   |   |   |   |   |   |   |   |   |   |   start <= 524086:
DNA_metabolic_process_ (11.38)
|   |   |   |   |   |   |   |   |   |   |   start > 524086:
electron_transport_ (23.74)
|   |   |   |   |   |   |   |   |   |   start > 526328
|   |   |   |   |   |   |   |   |   |   |   start <= 528690:
RNA_metabolic_process_ (11.87)
|   |   |   |   |   |   |   |   |   |   |   start > 528690:
biological_process_ (11.85)
|   |   |   |   |   |   |   start > 529854
|   |   |   |   |   |   |   |   start <= 544055
|   |   |   |   |   |   |   |   |   start <= 536049
|   |   |   |   |   |   |   |   |   |   start <= 532055
|   |   |   |   |   |   |   |   |   |   |   start <= 531821:
translation_ (9.58)
|   |   |   |   |   |   |   |   |   |   |   start > 531821:
organelle_organization_and_biogenesis_ (20.19/6.7)
|   |   |   |   |   |   |   |   |   |   start > 532055
|   |   |   |   |   |   |   |   |   |   |   start <= 534020:
cell_cycle_ (10.34)
|   |   |   |   |   |   |   |   |   |   |   start > 534020:
biological_process_ (17.09)
|   |   |   |   |   |   |   |   |   start > 536049
|   |   |   |   |   |   |   |   |   |   start <= 542495
|   |   |   |   |   |   |   |   |   |   |   start <= 538765
|   |   |   |   |   |   |   |   |   |   |   |   start <= 538548:
translation_ (9.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 538548:
DNA_metabolic_process_ (6.84)
|   |   |   |   |   |   |   |   |   |   |   start > 538765:
translation_ (16.0)
|   |   |   |   |   |   |   |   |   |   start > 542495:
DNA_metabolic_process_ (14.57)
```

```
|   |   |   |   |   |   |   |   start > 544055
|   |   |   |   |   |   |   |   |   start <= 545780: cell_cycle_
(48.77/28.86)
|   |   |   |   |   |   |   |   |   start > 545780
|   |   |   |   |   |   |   |   |   |   start <= 548752:
transcription_ (45.62/17.73)
|   |   |   |   |   |   |   |   |   |   start > 548752:
biological_process_ (11.68)
|   |   |   |   start > 550504
|   |   |   |   |   start <= 559151
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 555907:
protein_modification_process_ (31.94/15.62)
|   |   |   |   |   |   |   start > 555907:
organelle_organization_and_biogenesis_ (24.66)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 555188:
ribosome_biogenesis_and_assembly_ (13.0)
|   |   |   |   |   |   |   start > 555188:
cytoskeleton_organization_and_biogenesis_ (19.05)
|   |   |   |   |   start > 559151
|   |   |   |   |   |   start <= 559409:
ribosome_biogenesis_and_assembly_ (67.14/40.26)
|   |   |   |   |   |   start > 559409
|   |   |   |   |   |   |   start <= 567437: biological_process_
(22.07)
|   |   |   |   |   |   |   start > 567437
|   |   |   |   |   |   |   |   start <= 569392:
DNA_metabolic_process_ (35.93)
|   |   |   |   |   |   |   |   start > 569392:
ribosome_biogenesis_and_assembly_ (15.53)
|   start > 570591
|   |   start <= 628706
|   |   |   start <= 578853
|   |   |   |   start <= 572928
|   |   |   |   |   start <= 572117: biological_process_ (10.2)
|   |   |   |   |   start > 572117: lipid_metabolic_process_ (16.32)
|   |   |   |   start > 572928
|   |   |   |   |   start <= 578183
|   |   |   |   |   |   start <= 573088: transport_ (19.02)
|   |   |   |   |   |   start > 573088
|   |   |   |   |   |   |   start <= 576594:
cell_wall_organization_and_biogenesis_ (65.06/17.16)
|   |   |   |   |   |   |   start > 576594: transport_ (15.87)
|   |   |   |   |   start > 578183: vitamin_metabolic_process_
(19.2)
|   |   |   start > 578853
|   |   |   |   strand = C
|   |   |   |   |   start <= 587711
|   |   |   |   |   |   start <= 582248
|   |   |   |   |   |   |   start <= 581609: biological_process_
(17.74)
|   |   |   |   |   |   |   start > 581609: DNA_metabolic_process_
(15.65)
```

```
|   |   |   |   |   |   start > 582248
|   |   |   |   |   |   |   start <= 583726:
cytoskeleton_organization_and_biogenesis_ (9.01)
|   |   |   |   |   |   |   start > 583726: biological_process_
(32.24)
|   |   |   |   |   start > 587711
|   |   |   |   |   |   start <= 609769
|   |   |   |   |   |   |   start <= 604199
|   |   |   |   |   |   |   |   start <= 594320: response_to_stress_
(12.03)
|   |   |   |   |   |   |   |   start > 594320:
RNA_metabolic_process_ (42.24)
|   |   |   |   |   |   |   start > 604199: meiosis_ (21.85)
|   |   |   |   |   |   start > 609769
|   |   |   |   |   |   |   start <= 618227: biological_process_
(33.06)
|   |   |   |   |   |   |   start > 618227
|   |   |   |   |   |   |   |   start <= 620747:
DNA_metabolic_process_ (14.82)
|   |   |   |   |   |   |   |   start > 620747: response_to_stress_
(18.12)
|   |   |   |   strand = W
|   |   |   |   |   start <= 598728
|   |   |   |   |   |   start <= 587711
|   |   |   |   |   |   |   start <= 581609: biological_process_
(17.67)
|   |   |   |   |   |   |   start > 581609
|   |   |   |   |   |   |   |   start <= 586061
|   |   |   |   |   |   |   |   |   start <= 583726: conjugation_
(14.22)
|   |   |   |   |   |   |   |   |   start > 583726:
signal_transduction_ (34.38/10.36)
|   |   |   |   |   |   |   |   start > 586061: biological_process_
(17.54)
|   |   |   |   |   |   start > 587711: cell_budding_ (22.26)
|   |   |   |   |   start > 598728
|   |   |   |   |   |   start <= 618227
|   |   |   |   |   |   |   start <= 611191
|   |   |   |   |   |   |   |   start <= 609769
|   |   |   |   |   |   |   |   |   start <= 608301: translation_
(12.84)
|   |   |   |   |   |   |   |   |   start > 608301: transport_
(19.79)
|   |   |   |   |   |   |   |   start > 609769:
carbohydrate_metabolic_process_ (14.21)
|   |   |   |   |   |   |   start > 611191
|   |   |   |   |   |   |   |   start <= 615569
|   |   |   |   |   |   |   |   |   start <= 612409:
biological_process_ (17.3)
|   |   |   |   |   |   |   |   |   start > 612409:
protein_modification_process_ (18.6)
|   |   |   |   |   |   |   |   start > 615569: translation_ (22.05)
|   |   |   |   |   |   start > 618227
|   |   |   |   |   |   |   start <= 624830
```

```
|   |   |   |   |   |   |   |   start <= 620747:
lipid_metabolic_process_ (17.08)
|   |   |   |   |   |   |   |   start > 620747
|   |   |   |   |   |   |   |   |   start <= 623573:
DNA_metabolic_process_ (20.97)
|   |   |   |   |   |   |   |   |   start > 623573:
cell_wall_organization_and_biogenesis_ (12.13)
|   |   |   |   |   |   |   start > 624830
|   |   |   |   |   |   |   |   start <= 627333: biological_process_
(18.57)
|   |   |   |   |   |   |   |   start > 627333:
cytoskeleton_organization_and_biogenesis_ (20.71)
|   |   start > 628706
|   |   |   start <= 703062
|   |   |   |   start <= 676772
|   |   |   |   |   start <= 655957
|   |   |   |   |   |   start <= 640819
|   |   |   |   |   |   |   start <= 633609
|   |   |   |   |   |   |   |   start <= 632935:
amino_acid_and_derivative_metabolic_process_ (32.82/15.19)
|   |   |   |   |   |   |   |   start > 632935: vesicle-
mediated_transport_ (15.99)
|   |   |   |   |   |   |   start > 633609
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 637784:
biological_process_ (22.46)
|   |   |   |   |   |   |   |   |   start > 637784: translation_
(11.42)
|   |   |   |   |   |   |   |   strand = W: biological_process_
(50.29)
|   |   |   |   |   |   start > 640819
|   |   |   |   |   |   |   start <= 647601
|   |   |   |   |   |   |   |   start <= 646484
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 644095:
organelle_organization_and_biogenesis_ (15.01)
|   |   |   |   |   |   |   |   |   |   start > 644095:
protein_modification_process_ (11.17)
|   |   |   |   |   |   |   |   |   strand = W:
protein_modification_process_ (14.8)
|   |   |   |   |   |   |   |   start > 646484
|   |   |   |   |   |   |   |   |   start <= 647120:
cellular_respiration_ (12.58)
|   |   |   |   |   |   |   |   |   start > 647120:
generation_of_precursor_metabolites_and_energy_ (17.99)
|   |   |   |   |   |   |   start > 647601
|   |   |   |   |   |   |   |   start <= 654232
|   |   |   |   |   |   |   |   |   strand = C: biological_process_
(14.58)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 649770:
biological_process_ (15.34)
|   |   |   |   |   |   |   |   |   |   start > 649770: translation_
(10.17)
```

```
|   |   |   |   |   |   |   |   start > 654232: vesicle-
mediated_transport_ (14.14)
|   |   |   |   |   start > 655957
|   |   |   |   |   |   start <= 663743
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 658683: transport_ (11.55)
|   |   |   |   |   |   |   |   start > 658683: transcription_
(11.91)
|   |   |   |   |   |   |   strand = W:
ribosome_biogenesis_and_assembly_ (28.12/13.14)
|   |   |   |   |   |   start > 663743
|   |   |   |   |   |   |   strand = C: biological_process_ (68.04)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 667638:
protein_modification_process_ (19.87)
|   |   |   |   |   |   |   |   start > 667638
|   |   |   |   |   |   |   |   |   start <= 669516: transport_
(14.3)
|   |   |   |   |   |   |   |   |   start > 669516:
biological_process_ (18.56)
|   |   |   |   start > 676772
|   |   |   |   |   start <= 683279
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 678700: translation_ (13.98)
|   |   |   |   |   |   |   start > 678700:
cell_wall_organization_and_biogenesis_ (16.41)
|   |   |   |   |   |   strand = W:
membrane_organization_and_biogenesis_ (15.27)
|   |   |   |   |   start > 683279
|   |   |   |   |   |   start <= 697135
|   |   |   |   |   |   |   start <= 690518
|   |   |   |   |   |   |   |   start <= 684561: biological_process_
(7.06)
|   |   |   |   |   |   |   |   start > 684561:
amino_acid_and_derivative_metabolic_process_ (27.35/12.18)
|   |   |   |   |   |   |   start > 690518
|   |   |   |   |   |   |   |   start <= 695900:
RNA_metabolic_process_ (39.53/14.15)
|   |   |   |   |   |   |   |   start > 695900: biological_process_
(11.33)
|   |   |   |   |   |   start > 697135
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 700876:
protein_modification_process_ (15.15)
|   |   |   |   |   |   |   |   start > 700876: translation_ (9.91)
|   |   |   |   |   |   |   strand = W: DNA_metabolic_process_
(12.85)
|   |   |   start > 703062
|   |   |   |   start <= 705738
|   |   |   |   |   start <= 704190: pseudohyphal_growth_ (12.32)
|   |   |   |   |   start > 704190:
amino_acid_and_derivative_metabolic_process_ (18.01)
|   |   |   |   start > 705738
|   |   |   |   |   start <= 727399
```

```
|   |   |   |   |   |   start <= 719660
|   |   |   |   |   |   |   start <= 717574
|   |   |   |   |   |   |   |   start <= 709701
|   |   |   |   |   |   |   |   |   start <= 707154:
biological_process_ (9.3)
|   |   |   |   |   |   |   |   |   start > 707154: transport_
(13.41)
|   |   |   |   |   |   |   |   start > 709701: biological_process_
(27.58)
|   |   |   |   |   |   |   start > 717574: transport_ (13.84)
|   |   |   |   |   |   start > 719660
|   |   |   |   |   |   |   start <= 722809: pseudohyphal_growth_
(14.87)
|   |   |   |   |   |   |   start > 722809: biological_process_
(28.91)
|   |   |   |   |   start > 727399
|   |   |   |   |   |   start <= 729590: vitamin_metabolic_process_
(13.27)
|   |   |   |   |   |   start > 729590
|   |   |   |   |   |   |   start <= 739810
|   |   |   |   |   |   |   |   start <= 732434: transport_ (11.02)
|   |   |   |   |   |   |   |   start > 732434
|   |   |   |   |   |   |   |   |   start <= 736038:
carbohydrate_metabolic_process_ (18.01)
|   |   |   |   |   |   |   |   |   start > 736038: transport_
(7.89)
|   |   |   |   |   |   |   start > 739810: biological_process_
(6.87)
```

Decision Tree Generated for Chromosome Eleven:
For Cellular Component

```
|   start <= 117991
|   |   start <= 22234
|   |   |   start <= 6108
|   |   |   |   strand = C
|   |   |   |   |   start <= 2182: cellular_component_ (8.98)
|   |   |   |   |   start > 2182: ribosome_ (15.21)
|   |   |   |   strand = W: membrane_ (15.29)
|   |   |   start > 6108
|   |   |   |   start <= 18339
|   |   |   |   |   start <= 11227: plasma_membrane_ (15.66)
|   |   |   |   |   start > 11227: cellular_component_ (30.19)
|   |   |   |   start > 18339
|   |   |   |   |   neigh_strand = W: mitochondrion_ (16.26/4.61)
|   |   |   |   |   neigh_strand = C: plasma_membrane_ (20.04/6.04)
|   |   start > 22234
|   |   |   start <= 46807
|   |   |   |   start <= 39164
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 30688: cytoplasm_ (14.9)
|   |   |   |   |   |   start > 30688
|   |   |   |   |   |   |   start <= 31694: nucleus_ (21.75)
|   |   |   |   |   |   |   start > 31694: cytoplasm_ (55.31/11.87)
```

```
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 34544
|   |   |   |   |   |   |   start <= 25216: cytoplasm_ (18.52)
|   |   |   |   |   |   |   start > 25216: mitochondrion_ (16.68)
|   |   |   |   |   |   start > 34544
|   |   |   |   |   |   |   start <= 38812: nucleolus_ (16.7)
|   |   |   |   |   |   |   start > 38812: cytoplasm_ (24.03/11.27)
|   |   |   |   start > 39164
|   |   |   |   |   start <= 46296: site_of_polarized_growth_
(17.98)
|   |   |   |   |   start > 46296: cytoplasm_ (17.19)
|   |   |   start > 46807
|   |   |   |   strand = C
|   |   |   |   |   start <= 91541
|   |   |   |   |   |   start <= 74629
|   |   |   |   |   |   |   start <= 63360
|   |   |   |   |   |   |   |   start <= 53705: cytoplasm_ (21.04)
|   |   |   |   |   |   |   |   start > 53705: mitochondrion_
(55.21/34.12)
|   |   |   |   |   |   |   start > 63360
|   |   |   |   |   |   |   |   start <= 70223
|   |   |   |   |   |   |   |   |   start <= 67467: membrane_
(16.97)
|   |   |   |   |   |   |   |   |   start > 67467:
cellular_component_ (17.78)
|   |   |   |   |   |   |   |   start > 70223
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
membrane_fraction_ (4.88/0.98)
|   |   |   |   |   |   |   |   |   neigh_num > 1: peroxisome_
(23.8/8.03)
|   |   |   |   |   |   start > 74629
|   |   |   |   |   |   |   start <= 78651: mitochondrion_
(57.02/14.48)
|   |   |   |   |   |   |   start > 78651
|   |   |   |   |   |   |   |   start <= 79887
|   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(16.43/4.92)
|   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(18.96/8.19)
|   |   |   |   |   |   |   |   start > 79887
|   |   |   |   |   |   |   |   |   start <= 88791
|   |   |   |   |   |   |   |   |   |   start <= 84213:
mitochondrion_ (14.82)
|   |   |   |   |   |   |   |   |   |   start > 84213: peroxisome_
(13.51)
|   |   |   |   |   |   |   |   |   start > 88791: mitochondrion_
(26.97)
|   |   |   |   |   start > 91541
|   |   |   |   |   |   start <= 100676
|   |   |   |   |   |   |   start <= 94504
|   |   |   |   |   |   |   |   NeighGO_term = membrane_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = transport_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_component_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = molecular_function_:
nucleus_ (6.04/3.43)
|   |   |   |   |   |   |   |   NeighGO_term = biological_process_:
membrane_ (6.61/3.38)
|   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
membrane_ (3.79/1.06)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleolus_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = translation_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peroxisome_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
nucleus_ (9.36/2.83)
|   |   |   |   |   |   |   |   NeighGO_term = nucleus_: nucleus_
(2.49/0.81)
```

```
|   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: membrane_ (1.57/0.9)
|   |   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
membrane_ (2.99/1.45)
|   |   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vacuole_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_wall_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = electron_transport_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transcription_:
cellular_component_ (7.49/4.34)
|   |   |   |   |   |   |   |   NeighGO_term = chromosome_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ribosome_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = meiosis_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: nucleus_ (0.0)
|   |   |   |   |   |   |   start > 94504: cellular_component_
(13.02)
|   |   |   |   |   |   start > 100676
|   |   |   |   |   |   |   start <= 114632
|   |   |   |   |   |   |   |   start <= 112508:
endomembrane_system_ (14.07)
|   |   |   |   |   |   |   |   start > 112508: plasma_membrane_
(17.56)
|   |   |   |   |   |   |   start > 114632
|   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_
(18.73/10.8)
|   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasmic_membrane-bound_vesicle_ (15.85/7.7)
|   |   |   |   strand = W
```

```
|   |   |   |   |   start <= 82952
|   |   |   |   |   |   start <= 50052
|   |   |   |   |   |   |   start <= 48195
|   |   |   |   |   |   |   |   start <= 47158: mitochondrion_
(10.61)
|   |   |   |   |   |   |   |   start > 47158: cellular_component_
(11.98)
|   |   |   |   |   |   |   start > 48195: mitochondrion_ (26.45)
|   |   |   |   |   |   start > 50052
|   |   |   |   |   |   |   start <= 81040
|   |   |   |   |   |   |   |   start <= 63360: cellular_component_
(14.93)
|   |   |   |   |   |   |   |   start > 63360
|   |   |   |   |   |   |   |   |   start <= 74629: cytoplasm_
(15.32)
|   |   |   |   |   |   |   |   |   start > 74629
|   |   |   |   |   |   |   |   |   |   start <= 75826:
mitochondrion_ (15.78)
|   |   |   |   |   |   |   |   |   |   start > 75826: cytoplasm_
(11.72)
|   |   |   |   |   |   |   start > 81040: cellular_component_
(18.76)
|   |   |   |   |   start > 82952
|   |   |   |   |   |   start <= 94504
|   |   |   |   |   |   |   start <= 84213: cytoplasm_ (13.23)
|   |   |   |   |   |   |   start > 84213: cellular_bud_
(40.52/12.15)
|   |   |   |   |   |   start > 94504: cytoplasm_ (103.34/21.78)
|   start > 117991
|   |   strand = C
|   |   |   start <= 406884
|   |   |   |   start <= 340956
|   |   |   |   |   start <= 200163
|   |   |   |   |   |   start <= 179672
|   |   |   |   |   |   |   start <= 144406
|   |   |   |   |   |   |   |   start <= 135710
|   |   |   |   |   |   |   |   |   start <= 127480:
Golgi_apparatus_ (18.21)
|   |   |   |   |   |   |   |   |   start > 127480
|   |   |   |   |   |   |   |   |   |   start <= 134139
|   |   |   |   |   |   |   |   |   |   |   start <= 133467:
cytoplasm_ (15.88)
|   |   |   |   |   |   |   |   |   |   |   start > 133467:
mitochondrion_ (16.75)
|   |   |   |   |   |   |   |   |   |   start > 134139: cytoplasm_
(28.35/10.95)
|   |   |   |   |   |   |   |   start > 135710
|   |   |   |   |   |   |   |   |   start <= 141094
|   |   |   |   |   |   |   |   |   |   start <= 140696:
endoplasmic_reticulum_ (15.14)
|   |   |   |   |   |   |   |   |   |   start > 140696: cytoplasm_
(10.99)
|   |   |   |   |   |   |   |   |   start > 141094: cell_wall_
(19.79)
```

```
|   |   |   |   |   |   |   start > 144406
|   |   |   |   |   |   |   |   start <= 154996
|   |   |   |   |   |   |   |   |   start <= 148843: mitochondrion_
(11.1)
|   |   |   |   |   |   |   |   |   start > 148843:
cellular_component_ (35.94)
|   |   |   |   |   |   |   |   start > 154996
|   |   |   |   |   |   |   |   |   start <= 166549
|   |   |   |   |   |   |   |   |   |   start <= 164390
|   |   |   |   |   |   |   |   |   |   |   start <= 162563
|   |   |   |   |   |   |   |   |   |   |   |   start <= 161606:
mitochondrion_ (12.42)
|   |   |   |   |   |   |   |   |   |   |   |   start > 161606:
cytoplasm_ (10.0)
|   |   |   |   |   |   |   |   |   |   |   start > 162563:
mitochondrion_ (18.44)
|   |   |   |   |   |   |   |   |   |   start > 164390: cytoplasm_
(11.26)
|   |   |   |   |   |   |   |   |   start > 166549
|   |   |   |   |   |   |   |   |   |   start <= 168834: nucleus_
(17.2)
|   |   |   |   |   |   |   |   |   |   start > 168834
|   |   |   |   |   |   |   |   |   |   |   start <= 171788:
mitochondrion_ (13.41)
|   |   |   |   |   |   |   |   |   |   |   start > 171788: nucleus_
(16.36)
|   |   |   |   |   |   start > 179672
|   |   |   |   |   |   |   start <= 194865
|   |   |   |   |   |   |   |   start <= 185017: cytoskeleton_
(35.72/17.37)
|   |   |   |   |   |   |   |   start > 185017
|   |   |   |   |   |   |   |   |   start <= 188645
|   |   |   |   |   |   |   |   |   |   start <= 185962:
mitochondrion_ (15.7)
|   |   |   |   |   |   |   |   |   |   start > 185962:
Golgi_apparatus_ (13.52)
|   |   |   |   |   |   |   |   |   start > 188645
|   |   |   |   |   |   |   |   |   |   start <= 193069
|   |   |   |   |   |   |   |   |   |   |   start <= 191441:
mitochondrion_ (8.02)
|   |   |   |   |   |   |   |   |   |   |   start > 191441:
cellular_component_ (12.0)
|   |   |   |   |   |   |   |   |   |   start > 193069:
mitochondrion_ (18.26)
|   |   |   |   |   |   |   start > 194865
|   |   |   |   |   |   |   |   start <= 196027: cytoplasm_ (21.71)
|   |   |   |   |   |   |   |   start > 196027: cell_cortex_
(27.26/10.79)
|   |   |   |   |   start > 200163
|   |   |   |   |   |   start <= 286247
|   |   |   |   |   |   |   start <= 231871
|   |   |   |   |   |   |   |   start <= 219968
|   |   |   |   |   |   |   |   |   start <= 213786: nucleus_
(34.71/9.44)
```

```
|   |   |   |   |   |   |   |   |   start > 213786
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
endoplasmic_reticulum_ (17.53/8.47)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
endomembrane_system_ (23.16/10.01)
|   |   |   |   |   |   |   |   start > 219968
|   |   |   |   |   |   |   |   |   start <= 222544: cytoplasm_
(16.24)
|   |   |   |   |   |   |   |   |   start > 222544
|   |   |   |   |   |   |   |   |   |   start <= 224099
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (24.97/7.62)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
mitochondrion_ (17.23/6.07)
|   |   |   |   |   |   |   |   |   |   start > 224099: nucleus_
(46.61/13.25)
|   |   |   |   |   |   |   start > 231871
|   |   |   |   |   |   |   |   start <= 269103
|   |   |   |   |   |   |   |   |   start <= 245017:
cellular_component_ (68.84)
|   |   |   |   |   |   |   |   |   start > 245017
|   |   |   |   |   |   |   |   |   |   start <= 248564: vacuole_
(15.65)
|   |   |   |   |   |   |   |   |   |   start > 248564
|   |   |   |   |   |   |   |   |   |   |   start <= 256414
|   |   |   |   |   |   |   |   |   |   |   |   start <= 255104:
cellular_component_ (20.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 255104:
nucleolus_ (10.75)
|   |   |   |   |   |   |   |   |   |   |   start > 256414:
cellular_component_ (32.14)
|   |   |   |   |   |   |   |   start > 269103
|   |   |   |   |   |   |   |   |   start <= 273038: nucleus_
(19.08)
|   |   |   |   |   |   |   |   |   start > 273038
|   |   |   |   |   |   |   |   |   |   start <= 278767:
mitochondrion_ (17.32)
|   |   |   |   |   |   |   |   |   |   start > 278767: nucleolus_
(12.96)
|   |   |   |   |   |   start > 286247
|   |   |   |   |   |   |   start <= 322872
|   |   |   |   |   |   |   |   start <= 314456
|   |   |   |   |   |   |   |   |   start <= 299226
|   |   |   |   |   |   |   |   |   |   start <= 293952: cytoplasm_
(9.32)
|   |   |   |   |   |   |   |   |   |   start > 293952: nucleus_
(11.37)
|   |   |   |   |   |   |   |   |   start > 299226: cytoplasm_
(32.41)
|   |   |   |   |   |   |   |   start > 314456
|   |   |   |   |   |   |   |   |   start <= 317408:
endoplasmic_reticulum_ (27.7/9.39)
|   |   |   |   |   |   |   |   |   start > 317408: Golgi_apparatus_
(24.64)
```

```
|   |   |   |   |   |   |   start > 322872
|   |   |   |   |   |   |   |   start <= 335801
|   |   |   |   |   |   |   |   |   start <= 333613
|   |   |   |   |   |   |   |   |   |   start <= 327131: cytoplasm_
(50.75/21.25)
|   |   |   |   |   |   |   |   |   |   start > 327131: nucleus_
(77.46/40.87)
|   |   |   |   |   |   |   |   |   start > 333613
|   |   |   |   |   |   |   |   |   |   distance <= 526: cytoplasm_
(10.11/1.96)
|   |   |   |   |   |   |   |   |   |   distance > 526:
mitochondrion_ (56.79/19.07)
|   |   |   |   |   |   |   |   start > 335801
|   |   |   |   |   |   |   |   |   start <= 339086: nucleus_
(45.4/10.35)
|   |   |   |   |   |   |   |   |   start > 339086: cytoskeleton_
(11.04)
|   |   |   |   start > 340956
|   |   |   |   |   start <= 385401
|   |   |   |   |   |   start <= 349107
|   |   |   |   |   |   |   start <= 346408
|   |   |   |   |   |   |   |   start <= 345264: cellular_component_
(18.07)
|   |   |   |   |   |   |   |   start > 345264: chromosome_ (12.81)
|   |   |   |   |   |   |   start > 346408:
site_of_polarized_growth_ (36.83/18.1)
|   |   |   |   |   |   start > 349107
|   |   |   |   |   |   |   start <= 356392: membrane_fraction_
(18.23)
|   |   |   |   |   |   |   start > 356392
|   |   |   |   |   |   |   |   start <= 371472: mitochondrion_
(15.48)
|   |   |   |   |   |   |   |   start > 371472
|   |   |   |   |   |   |   |   |   start <= 381501: chromosome_
(7.51)
|   |   |   |   |   |   |   |   |   start > 381501: mitochondrion_
(9.18)
|   |   |   |   |   start > 385401
|   |   |   |   |   |   start <= 403745
|   |   |   |   |   |   |   start <= 393364
|   |   |   |   |   |   |   |   start <= 392783
|   |   |   |   |   |   |   |   |   start <= 389526:
cellular_component_ (9.29)
|   |   |   |   |   |   |   |   |   start > 389526: cytoplasm_
(48.72/16.3)
|   |   |   |   |   |   |   |   start > 392783: cellular_component_
(21.26)
|   |   |   |   |   |   |   start > 393364
|   |   |   |   |   |   |   |   start <= 402211
|   |   |   |   |   |   |   |   |   start <= 396891: nucleus_
(24.02)
|   |   |   |   |   |   |   |   |   start > 396891
|   |   |   |   |   |   |   |   |   |   start <= 398393:
membrane_fraction_ (16.33)
```

```
|   |   |   |   |   |   |   |   |   |   start > 398393: nucleus_ 
(19.68)
|   |   |   |   |   |   |   |   start > 402211: cytoplasm_ (22.32)
|   |   |   |   |   |   start > 403745
|   |   |   |   |   |   |   neigh_num <= 1: chromosome_ 
(23.45/14.06)
|   |   |   |   |   |   |   neigh_num > 1: cellular_component_ 
(41.56/24.43)
|   |   |   start > 406884
|   |   |   |   start <= 472992
|   |   |   |   |   start <= 431549
|   |   |   |   |   |   start <= 425885
|   |   |   |   |   |   |   start <= 420859
|   |   |   |   |   |   |   |   start <= 416556
|   |   |   |   |   |   |   |   |   start <= 408187: mitochondrion_ 
(14.6)
|   |   |   |   |   |   |   |   |   start > 408187: nucleolus_ 
(15.0)
|   |   |   |   |   |   |   |   start > 416556
|   |   |   |   |   |   |   |   |   start <= 417953: cytoskeleton_ 
(13.84)
|   |   |   |   |   |   |   |   |   start > 417953: 
mitochondrial_envelope_ (18.01)
|   |   |   |   |   |   |   start > 420859
|   |   |   |   |   |   |   |   neigh_strand = W: mitochondrion_ 
(25.15/10.76)
|   |   |   |   |   |   |   |   neigh_strand = C: cytoplasm_ 
(19.04/4.67)
|   |   |   |   |   |   start > 425885
|   |   |   |   |   |   |   start <= 430275
|   |   |   |   |   |   |   |   start <= 428945: 
endoplasmic_reticulum_ (12.89)
|   |   |   |   |   |   |   |   start > 428945: endomembrane_system_ 
(12.67)
|   |   |   |   |   |   |   start > 430275: nucleolus_ (24.49)
|   |   |   |   |   start > 431549
|   |   |   |   |   |   start <= 442875
|   |   |   |   |   |   |   start <= 437421
|   |   |   |   |   |   |   |   start <= 435223: nucleus_ (10.9)
|   |   |   |   |   |   |   |   start > 435223: mitochondrion_ 
(19.12)
|   |   |   |   |   |   |   start > 437421
|   |   |   |   |   |   |   |   start <= 439028: cytoplasm_ (12.08)
|   |   |   |   |   |   |   |   start > 439028
|   |   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_ 
(19.36/8.27)
|   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   distance <= 1491: cytoplasm_ 
(3.46/1.4)
|   |   |   |   |   |   |   |   |   |   distance > 1491: 
membrane_fraction_ (8.39/2.49)
|   |   |   |   |   |   start > 442875
|   |   |   |   |   |   |   start <= 460882
```

```
|   |   |   |   |   |   |   |   start <= 449810: cellular_component_
(33.35)
|   |   |   |   |   |   |   |   start > 449810
|   |   |   |   |   |   |   |   |   start <= 451844: mitochondrion_
(12.45)
|   |   |   |   |   |   |   |   |   start > 451844
|   |   |   |   |   |   |   |   |   |   start <= 458200: peroxisome_
(15.12)
|   |   |   |   |   |   |   |   |   |   start > 458200:
mitochondrion_ (10.32)
|   |   |   |   |   |   |   start > 460882
|   |   |   |   |   |   |   |   start <= 465714
|   |   |   |   |   |   |   |   |   start <= 463602: nucleus_ (9.37)
|   |   |   |   |   |   |   |   |   start > 463602: cytoplasm_
(14.73)
|   |   |   |   |   |   |   |   start > 465714: cellular_component_
(31.39)
|   |   |   |   start > 472992
|   |   |   |   |   start <= 534923
|   |   |   |   |   |   start <= 526282
|   |   |   |   |   |   |   start <= 510275
|   |   |   |   |   |   |   |   start <= 493900
|   |   |   |   |   |   |   |   |   start <= 478877
|   |   |   |   |   |   |   |   |   |   start <= 475543: nucleus_
(41.04/15.84)
|   |   |   |   |   |   |   |   |   |   start > 475543:
mitochondrion_ (25.48)
|   |   |   |   |   |   |   |   |   start > 478877
|   |   |   |   |   |   |   |   |   |   start <= 483062:
endoplasmic_reticulum_ (57.74/30.61)
|   |   |   |   |   |   |   |   |   |   start > 483062
|   |   |   |   |   |   |   |   |   |   |   start <= 487413:
nucleolus_ (15.4)
|   |   |   |   |   |   |   |   |   |   |   start > 487413:
cytoplasm_ (12.45)
|   |   |   |   |   |   |   |   start > 493900
|   |   |   |   |   |   |   |   |   start <= 499924
|   |   |   |   |   |   |   |   |   |   distance <= 2389: nucleus_
(14.15/3.96)
|   |   |   |   |   |   |   |   |   |   distance > 2389:
cellular_component_ (14.67/4.78)
|   |   |   |   |   |   |   |   |   start > 499924
|   |   |   |   |   |   |   |   |   |   start <= 507581: membrane_
(17.91)
|   |   |   |   |   |   |   |   |   |   start > 507581:
mitochondrion_ (12.23)
|   |   |   |   |   |   |   start > 510275
|   |   |   |   |   |   |   |   start <= 511439:
microtubule_organizing_center_ (25.28)
|   |   |   |   |   |   |   |   start > 511439: cytoplasm_
(113.49/36.42)
|   |   |   |   |   |   start > 526282
|   |   |   |   |   |   |   start <= 533106: mitochondrion_ (22.57)
```

```
|   |   |   |   |   |   |   start > 533106: endoplasmic_reticulum_
(24.03)
|   |   |   |   |   start > 534923
|   |   |   |   |   |   start <= 626435
|   |   |   |   |   |   |   start <= 571254
|   |   |   |   |   |   |   |   start <= 559308
|   |   |   |   |   |   |   |   |   start <= 552412: cytoskeleton_
(24.02)
|   |   |   |   |   |   |   |   |   start > 552412: nucleolus_
(17.19)
|   |   |   |   |   |   |   |   start > 559308
|   |   |   |   |   |   |   |   |   start <= 567560: mitochondrion_
(92.61/18.71)
|   |   |   |   |   |   |   |   |   start > 567560: Golgi_apparatus_
(18.04)
|   |   |   |   |   |   |   start > 571254
|   |   |   |   |   |   |   |   start <= 590037
|   |   |   |   |   |   |   |   |   start <= 575622: cytoplasm_
(21.59)
|   |   |   |   |   |   |   |   |   start > 575622
|   |   |   |   |   |   |   |   |   |   start <= 584594
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cytoplasm_ (23.81/8.68)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (24.17/9.21)
|   |   |   |   |   |   |   |   |   |   start > 584594
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (17.04/7.61)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(33.28/18.92)
|   |   |   |   |   |   |   |   start > 590037
|   |   |   |   |   |   |   |   |   start <= 596464
|   |   |   |   |   |   |   |   |   |   start <= 592467: nucleolus_
(21.45)
|   |   |   |   |   |   |   |   |   |   start > 592467:
cytoskeleton_ (15.12)
|   |   |   |   |   |   |   |   |   start > 596464
|   |   |   |   |   |   |   |   |   |   start <= 608588
|   |   |   |   |   |   |   |   |   |   |   start <= 603874
|   |   |   |   |   |   |   |   |   |   |   |   start <= 598532:
cytoplasm_ (20.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 598532:
mitochondrion_ (32.25)
|   |   |   |   |   |   |   |   |   |   |   start > 603874:
cytoplasm_ (35.06)
|   |   |   |   |   |   |   |   |   |   start > 608588
|   |   |   |   |   |   |   |   |   |   |   start <= 615372:
nucleolus_ (9.15)
|   |   |   |   |   |   |   |   |   |   |   start > 615372:
mitochondrion_ (14.43)
|   |   |   |   |   |   start > 626435
|   |   |   |   |   |   |   start <= 635489: cellular_component_
(15.74)
|   |   |   |   |   |   |   start > 635489
```

```
|   |   |   |   |   |   |   |   start <= 645994: cellular_bud_
(13.99)
|   |   |   |   |   |   |   |   start > 645994: cellular_component_
(12.06)
|   |   strand = W
|   |   |   start <= 317408
|   |   |   |   start <= 307861
|   |   |   |   |   start <= 277925
|   |   |   |   |   |   start <= 210237
|   |   |   |   |   |   |   start <= 203185
|   |   |   |   |   |   |   |   start <= 171788
|   |   |   |   |   |   |   |   |   start <= 158619
|   |   |   |   |   |   |   |   |   |   start <= 125764: vacuole_
(67.49/47.73)
|   |   |   |   |   |   |   |   |   |   start > 125764: cytoplasm_
(114.37/76.58)
|   |   |   |   |   |   |   |   |   start > 158619: membrane_
(55.21/32.41)
|   |   |   |   |   |   |   |   start > 171788
|   |   |   |   |   |   |   |   |   start <= 202643: mitochondrion_
(143.12/102.37)
|   |   |   |   |   |   |   |   |   start > 202643: cytoplasm_
(11.38)
|   |   |   |   |   |   |   start > 203185: plasma_membrane_
(37.5/21.85)
|   |   |   |   |   |   start > 210237
|   |   |   |   |   |   |   start <= 256414
|   |   |   |   |   |   |   |   start <= 235785
|   |   |   |   |   |   |   |   |   start <= 231871
|   |   |   |   |   |   |   |   |   |   start <= 216988:
cellular_component_ (21.12/10.37)
|   |   |   |   |   |   |   |   |   |   start > 216988
|   |   |   |   |   |   |   |   |   |   |   start <= 222544:
cytoplasm_ (51.66/18.45)
|   |   |   |   |   |   |   |   |   |   |   start > 222544
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cellular_component_ (11.75/4.28)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
nucleus_ (28.57/7.47)
|   |   |   |   |   |   |   |   |   start > 231871
|   |   |   |   |   |   |   |   |   |   start <= 234070: chromosome_
(13.61)
|   |   |   |   |   |   |   |   |   |   start > 234070:
cellular_component_ (17.86)
|   |   |   |   |   |   |   |   start > 235785
|   |   |   |   |   |   |   |   |   start <= 242227: mitochondrion_
(19.57)
|   |   |   |   |   |   |   |   |   start > 242227:
cellular_component_ (37.11/22.7)
|   |   |   |   |   |   |   start > 256414
|   |   |   |   |   |   |   |   start <= 260776: cell_wall_ (32.62)
|   |   |   |   |   |   |   |   start > 260776
|   |   |   |   |   |   |   |   |   start <= 271522
|   |   |   |   |   |   |   |   |   |   start <= 262993
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 261921:
nucleus_ (17.16)
|   |   |   |   |   |   |   |   |   |   |   start > 261921:
cytoplasm_ (20.3)
|   |   |   |   |   |   |   |   |   |   start > 262993:
cellular_component_ (24.11)
|   |   |   |   |   |   |   |   |   start > 271522: cytoplasm_
(67.76/31.39)
|   |   |   |   |   start > 277925
|   |   |   |   |   |   start <= 291097
|   |   |   |   |   |   |   start <= 282535: mitochondrion_
(48.76/17.86)
|   |   |   |   |   |   |   start > 282535
|   |   |   |   |   |   |   |   start <= 284674: membrane_
(43.59/24.1)
|   |   |   |   |   |   |   |   start > 284674
|   |   |   |   |   |   |   |   |   start <= 286247:
site_of_polarized_growth_ (27.72/12.96)
|   |   |   |   |   |   |   |   |   start > 286247: nucleolus_
(33.3/13.62)
|   |   |   |   |   |   start > 291097
|   |   |   |   |   |   |   start <= 299226: cellular_component_
(37.62/16.77)
|   |   |   |   |   |   |   start > 299226
|   |   |   |   |   |   |   |   start <= 304758: cytoplasm_ (22.6)
|   |   |   |   |   |   |   |   start > 304758
|   |   |   |   |   |   |   |   |   start <= 305855: mitochondrion_
(12.56)
|   |   |   |   |   |   |   |   |   start > 305855: cytoplasm_
(19.95/8.53)
|   |   |   |   start > 307861
|   |   |   |   |   start <= 308850: cellular_component_ (23.64)
|   |   |   |   |   start > 308850
|   |   |   |   |   |   start <= 309843
|   |   |   |   |   |   |   neigh_num <= 1: nucleus_ (18.21/9.22)
|   |   |   |   |   |   |   neigh_num > 1: membrane_ (30.15/16.85)
|   |   |   |   |   |   start > 309843
|   |   |   |   |   |   |   start <= 315598: cellular_component_
(20.19/8.13)
|   |   |   |   |   |   |   start > 315598: membrane_ (13.4)
|   |   |   start > 317408
|   |   |   |   start <= 491007
|   |   |   |   |   start <= 428945
|   |   |   |   |   |   start <= 403745
|   |   |   |   |   |   |   start <= 365248
|   |   |   |   |   |   |   |   start <= 356392
|   |   |   |   |   |   |   |   |   start <= 349107
|   |   |   |   |   |   |   |   |   |   start <= 334559
|   |   |   |   |   |   |   |   |   |   |   start <= 327131
|   |   |   |   |   |   |   |   |   |   |   |   start <= 322872:
nucleus_ (37.54/14.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 322872:
cytoplasm_ (24.17)
|   |   |   |   |   |   |   |   |   |   |   start > 327131
```

```
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: nucleus_ (3.81/0.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: cellular_component_ (8.96/2.74)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
nucleus_ (14.02/2.87)
|   |   |   |   |   |   |   |   |   |   start > 334559
|   |   |   |   |   |   |   |   |   |   |   start <= 340956:
plasma_membrane_ (6.57)
|   |   |   |   |   |   |   |   |   |   |   start > 340956:
cytoplasm_ (11.5)
|   |   |   |   |   |   |   |   |   start > 349107: nucleus_ (37.65)
|   |   |   |   |   |   |   |   start > 356392
|   |   |   |   |   |   |   |   |   start <= 359786
|   |   |   |   |   |   |   |   |   |   start <= 358119:
microtubule_organizing_center_ (40.77/17.51)
|   |   |   |   |   |   |   |   |   |   start > 358119: cytoplasm_
(12.91)
|   |   |   |   |   |   |   |   |   start > 359786
|   |   |   |   |   |   |   |   |   |   start <= 364419
|   |   |   |   |   |   |   |   |   |   |   start <= 362265:
cellular_component_ (13.55)
|   |   |   |   |   |   |   |   |   |   |   start > 362265:
nucleolus_ (9.3)
|   |   |   |   |   |   |   |   |   |   start > 364419: nucleus_
(21.38)
|   |   |   |   |   |   |   start > 365248
|   |   |   |   |   |   |   |   start <= 396891
|   |   |   |   |   |   |   |   |   start <= 374148
|   |   |   |   |   |   |   |   |   |   start <= 369534
|   |   |   |   |   |   |   |   |   |   |   start <= 369008:
cellular_component_ (9.53)
|   |   |   |   |   |   |   |   |   |   |   start > 369008:
cytoplasm_ (11.88)
|   |   |   |   |   |   |   |   |   |   start > 369534
|   |   |   |   |   |   |   |   |   |   |   start <= 371472:
Golgi_apparatus_ (19.8)
|   |   |   |   |   |   |   |   |   |   |   start > 371472:
cellular_component_ (9.93)
|   |   |   |   |   |   |   |   |   start > 374148
|   |   |   |   |   |   |   |   |   |   start <= 389526
|   |   |   |   |   |   |   |   |   |   |   start <= 381501:
cytoplasm_ (54.12/19.81)
|   |   |   |   |   |   |   |   |   |   |   start > 381501:
mitochondrion_ (29.28)
|   |   |   |   |   |   |   |   |   |   start > 389526: cytoplasm_
(18.13)
|   |   |   |   |   |   |   |   start > 396891
|   |   |   |   |   |   |   |   |   start <= 402211:
cellular_component_ (17.59)
|   |   |   |   |   |   |   |   |   start > 402211
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
nucleus_ (12.77/4.5)
```

```
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cellular_component_ (8.07/3.77)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cellular_component_ (18.08/6.86)
|   |   |   |   |   |   start > 403745
|   |   |   |   |   |   |   start <= 425885: nucleus_ (84.79/20.22)
|   |   |   |   |   |   |   start > 425885: cytoskeleton_
(41.68/18.5)
|   |   |   |   |   start > 428945
|   |   |   |   |   |   start <= 451844
|   |   |   |   |   |   |   start <= 447679
|   |   |   |   |   |   |   |   start <= 435223
|   |   |   |   |   |   |   |   |   start <= 431549: ribosome_
(12.31)
|   |   |   |   |   |   |   |   |   start > 431549: Golgi_apparatus_
(19.72)
|   |   |   |   |   |   |   |   start > 435223
|   |   |   |   |   |   |   |   |   start <= 442875
|   |   |   |   |   |   |   |   |   |   start <= 439028: cytoplasm_
(18.82)
|   |   |   |   |   |   |   |   |   |   start > 439028: nucleus_
(14.49)
|   |   |   |   |   |   |   |   |   start > 442875: cytoplasm_
(19.75)
|   |   |   |   |   |   |   start > 447679
|   |   |   |   |   |   |   |   start <= 451077: vacuole_
(40.86/19.61)
|   |   |   |   |   |   |   |   start > 451077: nucleus_
(43.98/20.43)
|   |   |   |   |   |   start > 451844
|   |   |   |   |   |   |   start <= 477981
|   |   |   |   |   |   |   |   start <= 465714
|   |   |   |   |   |   |   |   |   start <= 460882: cytoplasm_
(11.79)
|   |   |   |   |   |   |   |   |   start > 460882:
extracellular_region_ (18.29)
|   |   |   |   |   |   |   |   start > 465714
|   |   |   |   |   |   |   |   |   start <= 472992: mitochondrion_
(27.06)
|   |   |   |   |   |   |   |   |   start > 472992: Golgi_apparatus_
(26.5)
|   |   |   |   |   |   |   start > 477981
|   |   |   |   |   |   |   |   start <= 490611
|   |   |   |   |   |   |   |   |   start <= 483062
|   |   |   |   |   |   |   |   |   |   start <= 478877: cytoplasm_
(17.76)
|   |   |   |   |   |   |   |   |   |   start > 478877:
mitochondrion_ (23.7/9.74)
|   |   |   |   |   |   |   |   |   start > 483062
|   |   |   |   |   |   |   |   |   |   start <= 487413: nucleus_
(17.25)
|   |   |   |   |   |   |   |   |   |   start > 487413: cytoplasm_
(15.58)
```

```
|   |   |   |   |   |   |   |   start > 490611: mitochondrion_
(13.96)
|   |   |   |   start > 491007
|   |   |   |   |   start <= 559308
|   |   |   |   |   |   start <= 527457
|   |   |   |   |   |   |   start <= 517840
|   |   |   |   |   |   |   |   start <= 499924
|   |   |   |   |   |   |   |   |   start <= 493900: cytoplasm_
(26.71)
|   |   |   |   |   |   |   |   |   start > 493900:
endomembrane_system_ (30.26/14.01)
|   |   |   |   |   |   |   |   start > 499924
|   |   |   |   |   |   |   |   |   start <= 506540: nucleus_ (6.55)
|   |   |   |   |   |   |   |   |   start > 506540
|   |   |   |   |   |   |   |   |   |   start <= 517630
|   |   |   |   |   |   |   |   |   |   |   start <= 510275:
cytoplasm_ (14.96)
|   |   |   |   |   |   |   |   |   |   |   start > 510275
|   |   |   |   |   |   |   |   |   |   |   |   start <= 514705:
plasma_membrane_ (8.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 514705:
cytoplasm_ (14.75)
|   |   |   |   |   |   |   |   |   |   start > 517630
|   |   |   |   |   |   |   |   |   |   |   distance <= 1226:
nucleus_ (14.31/3.13)
|   |   |   |   |   |   |   |   |   |   |   distance > 1226:
cytoplasm_ (7.59/1.44)
|   |   |   |   |   |   |   start > 517840
|   |   |   |   |   |   |   |   start <= 523611
|   |   |   |   |   |   |   |   |   start <= 519169: cell_wall_
(17.36)
|   |   |   |   |   |   |   |   |   start > 519169:
endomembrane_system_ (14.2)
|   |   |   |   |   |   |   |   start > 523611: plasma_membrane_
(18.77)
|   |   |   |   |   |   start > 527457
|   |   |   |   |   |   |   start <= 554629
|   |   |   |   |   |   |   |   start <= 549090: cellular_component_
(59.62)
|   |   |   |   |   |   |   |   start > 549090
|   |   |   |   |   |   |   |   |   start <= 552412
|   |   |   |   |   |   |   |   |   |   start <= 551299: ribosome_
(21.52)
|   |   |   |   |   |   |   |   |   |   start > 551299:
cellular_component_ (9.78)
|   |   |   |   |   |   |   |   |   start > 552412: ribosome_
(25.93)
|   |   |   |   |   |   |   start > 554629
|   |   |   |   |   |   |   |   start <= 557319
|   |   |   |   |   |   |   |   |   start <= 556160: nucleus_
(33.74/14.3)
|   |   |   |   |   |   |   |   |   start > 556160: Golgi_apparatus_
(18.29)
```

```
|   |   |   |   |   |   |   |   start > 557319: nucleus_
(40.38/18.42)
|   |   |   |   |   start > 559308
|   |   |   |   |   |   start <= 590037
|   |   |   |   |   |   |   start <= 575622
|   |   |   |   |   |   |   |   start <= 567560
|   |   |   |   |   |   |   |   |   start <= 562189: cytoplasm_
(57.14/33.65)
|   |   |   |   |   |   |   |   |   start > 562189
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
endoplasmic_reticulum_ (21.77/5.35)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: cytoplasm_
(19.73/7.98)
|   |   |   |   |   |   |   |   start > 567560
|   |   |   |   |   |   |   |   |   start <= 571254:
cellular_component_ (16.12)
|   |   |   |   |   |   |   |   |   start > 571254: mitochondrion_
(14.85)
|   |   |   |   |   |   |   start > 575622
|   |   |   |   |   |   |   |   start <= 581925: cytoplasm_ (53.56)
|   |   |   |   |   |   |   |   start > 581925
|   |   |   |   |   |   |   |   |   start <= 583295: nucleus_
(40.44/17.76)
|   |   |   |   |   |   |   |   |   start > 583295: cytoplasm_
(42.72)
|   |   |   |   |   |   start > 590037
|   |   |   |   |   |   |   start <= 640106
|   |   |   |   |   |   |   |   start <= 615372
|   |   |   |   |   |   |   |   |   start <= 603874: nucleus_
(71.19/31.62)
|   |   |   |   |   |   |   |   |   start > 603874
|   |   |   |   |   |   |   |   |   |   start <= 611167: cytoplasm_
(51.87/14.13)
|   |   |   |   |   |   |   |   |   |   start > 611167:
membrane_fraction_ (26.15/12.74)
|   |   |   |   |   |   |   |   start > 615372
|   |   |   |   |   |   |   |   |   start <= 619447:
endomembrane_system_ (16.34)
|   |   |   |   |   |   |   |   |   start > 619447
|   |   |   |   |   |   |   |   |   |   start <= 630790
|   |   |   |   |   |   |   |   |   |   |   start <= 625506
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
chromosome_ (16.78/9.15)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cellular_component_ (18.42/9.71)
|   |   |   |   |   |   |   |   |   |   |   start > 625506:
cytoplasm_ (50.53/22.18)
|   |   |   |   |   |   |   |   |   |   start > 630790
|   |   |   |   |   |   |   |   |   |   |   start <= 635489:
nucleus_ (14.22)
|   |   |   |   |   |   |   |   |   |   |   start > 635489:
cellular_component_ (41.99/20.12)
|   |   |   |   |   |   |   start > 640106
|   |   |   |   |   |   |   |   start <= 645994: cell_wall_ (15.65)
```

```
|   |   |   |   |   |   |   |   start > 645994: membrane_ (33.77)
```

For Molecular Function

```
|   start <= 224099
|   |   start <= 100676
|   |   |   start <= 25216
|   |   |   |   strand = C
|   |   |   |   |   start <= 6108: molecular_function_ (18.98)
|   |   |   |   |   start > 6108
|   |   |   |   |   |   start <= 14485: oxidoreductase_activity_
(17.83)
|   |   |   |   |   |   start > 14485: lyase_activity_ (18.68)
|   |   |   |   strand = W
|   |   |   |   |   start <= 22234
|   |   |   |   |   |   start <= 18339
|   |   |   |   |   |   |   start <= 6108: transporter_activity_
(16.02)
|   |   |   |   |   |   |   start > 6108: molecular_function_
(18.48)
|   |   |   |   |   |   start > 18339: transporter_activity_ (18.97)
|   |   |   |   |   start > 22234: oxidoreductase_activity_ (14.48)
|   |   |   start > 25216
|   |   |   |   start <= 75826
|   |   |   |   |   start <= 50052
|   |   |   |   |   |   start <= 38812
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 31694
|   |   |   |   |   |   |   |   |   start <= 30688:
molecular_function_ (12.62)
|   |   |   |   |   |   |   |   |   start > 30688: RNA_binding_
(17.73)
|   |   |   |   |   |   |   |   start > 31694
|   |   |   |   |   |   |   |   |   start <= 34544: protein_binding_
(18.93)
|   |   |   |   |   |   |   |   |   start > 34544: lyase_activity_
(19.23)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 34544: hydrolase_activity_
(20.19)
|   |   |   |   |   |   |   |   start > 34544: RNA_binding_ (23.45)
|   |   |   |   |   |   start > 38812
|   |   |   |   |   |   |   start <= 49810
|   |   |   |   |   |   |   |   start <= 46296
|   |   |   |   |   |   |   |   |   start <= 39164:
molecular_function_ (13.81)
|   |   |   |   |   |   |   |   |   start > 39164:
hydrolase_activity_ (10.48)
|   |   |   |   |   |   |   |   start > 46296: molecular_function_
(78.69)
|   |   |   |   |   |   |   start > 49810: RNA_binding_ (20.88)
|   |   |   |   |   start > 50052
|   |   |   |   |   |   start <= 63360: protein_binding_ (27.82)
|   |   |   |   |   |   start > 63360
```

```
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 70223
|   |   |   |   |   |   |   |   |   start <= 67467:
molecular_function_ (15.89)
|   |   |   |   |   |   |   |   |   start > 67467:
protein_kinase_activity_ (12.87)
|   |   |   |   |   |   |   |   start > 70223: protein_binding_
(30.09)
|   |   |   |   |   |   |   strand = W: molecular_function_ (43.15)
|   |   |   |   start > 75826
|   |   |   |   |   start <= 80542
|   |   |   |   |   |   start <= 78651: ligase_activity_ (26.38)
|   |   |   |   |   |   start > 78651
|   |   |   |   |   |   |   start <= 79887:
enzyme_regulator_activity_ (10.39)
|   |   |   |   |   |   |   start > 79887: transporter_activity_
(16.18)
|   |   |   |   |   start > 80542
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 88791: hydrolase_activity_
(22.38)
|   |   |   |   |   |   |   start > 88791
|   |   |   |   |   |   |   |   start <= 91541: molecular_function_
(20.53)
|   |   |   |   |   |   |   |   start > 91541
|   |   |   |   |   |   |   |   |   start <= 94504: protein_binding_
(22.71)
|   |   |   |   |   |   |   |   |   start > 94504:
molecular_function_ (13.45)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 94504
|   |   |   |   |   |   |   |   start <= 88791
|   |   |   |   |   |   |   |   |   start <= 82952
|   |   |   |   |   |   |   |   |   |   start <= 81040:
molecular_function_ (20.12)
|   |   |   |   |   |   |   |   |   |   start > 81040:
phosphoprotein_phosphatase_activity_ (14.98)
|   |   |   |   |   |   |   |   |   start > 82952:
molecular_function_ (22.55)
|   |   |   |   |   |   |   |   start > 88791:
transcription_regulator_activity_ (7.78)
|   |   |   |   |   |   |   start > 94504
|   |   |   |   |   |   |   |   start <= 98726
|   |   |   |   |   |   |   |   |   start <= 96762: lyase_activity_
(12.75)
|   |   |   |   |   |   |   |   |   start > 96762:
molecular_function_ (21.82)
|   |   |   |   |   |   |   |   start > 98726: lyase_activity_
(23.62/9.36)
|   |   start > 100676
|   |   |   start <= 161347
|   |   |   |   start <= 122522
|   |   |   |   |   start <= 114632
|   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   start <= 112508: molecular_function_
(6.71)
|   |   |   |   |   |   |   start > 112508:
signal_transducer_activity_ (20.1)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 107321: transferase_activity_
(13.16)
|   |   |   |   |   |   |   start > 107321:
structural_molecule_activity_ (14.55)
|   |   |   |   |   start > 114632
|   |   |   |   |   |   start <= 122241: transporter_activity_
(46.7)
|   |   |   |   |   |   start > 122241: RNA_binding_ (19.11)
|   |   |   |   start > 122522
|   |   |   |   |   start <= 150692
|   |   |   |   |   |   start <= 125764: molecular_function_ (15.18)
|   |   |   |   |   |   start > 125764
|   |   |   |   |   |   |   start <= 135710
|   |   |   |   |   |   |   |   start <= 134139
|   |   |   |   |   |   |   |   |   start <= 127480:
protein_kinase_activity_ (15.1)
|   |   |   |   |   |   |   |   |   start > 127480
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 133467:
protein_kinase_activity_ (18.14)
|   |   |   |   |   |   |   |   |   |   |   start > 133467:
structural_molecule_activity_ (12.79)
|   |   |   |   |   |   |   |   |   |   strand = W:
structural_molecule_activity_ (17.35)
|   |   |   |   |   |   |   |   start > 134139:
protein_kinase_activity_ (17.53)
|   |   |   |   |   |   |   start > 135710
|   |   |   |   |   |   |   |   start <= 148843
|   |   |   |   |   |   |   |   |   start <= 140696:
transferase_activity_ (13.02)
|   |   |   |   |   |   |   |   |   start > 140696
|   |   |   |   |   |   |   |   |   |   start <= 144406
|   |   |   |   |   |   |   |   |   |   |   start <= 141094:
molecular_function_ (14.43)
|   |   |   |   |   |   |   |   |   |   |   start > 141094:
structural_molecule_activity_ (29.57)
|   |   |   |   |   |   |   |   |   |   start > 144406:
molecular_function_ (18.35)
|   |   |   |   |   |   |   |   start > 148843:
protein_kinase_activity_ (16.2)
|   |   |   |   |   start > 150692
|   |   |   |   |   |   start <= 154456
|   |   |   |   |   |   |   start <= 153274:
transcription_regulator_activity_ (20.8)
|   |   |   |   |   |   |   start > 153274:
enzyme_regulator_activity_ (26.2)
|   |   |   |   |   |   start > 154456
|   |   |   |   |   |   |   start <= 154996: peptidase_activity_
(20.81)
```

```
|   |   |   |   |   |   |   start > 154996:
structural_molecule_activity_ (23.13)
|   |   |   start > 161347
|   |   |   |   start <= 180784
|   |   |   |   |   start <= 165935
|   |   |   |   |   |   start <= 162563: molecular_function_ (24.1)
|   |   |   |   |   |   start > 162563
|   |   |   |   |   |   |   start <= 164390: isomerase_activity_
(13.13)
|   |   |   |   |   |   |   start > 164390: molecular_function_
(15.86)
|   |   |   |   |   start > 165935
|   |   |   |   |   |   start <= 176486
|   |   |   |   |   |   |   start <= 171134
|   |   |   |   |   |   |   |   start <= 168834
|   |   |   |   |   |   |   |   |   start <= 166549:
oxidoreductase_activity_ (9.32)
|   |   |   |   |   |   |   |   |   start > 166549:
hydrolase_activity_ (17.22)
|   |   |   |   |   |   |   |   start > 168834:
oxidoreductase_activity_ (15.68)
|   |   |   |   |   |   |   start > 171134
|   |   |   |   |   |   |   |   strand = C:
nucleotidyltransferase_activity_ (12.13)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 171788:
transporter_activity_ (10.1)
|   |   |   |   |   |   |   |   |   start > 171788:
peptidase_activity_ (16.62)
|   |   |   |   |   |   start > 176486
|   |   |   |   |   |   |   start <= 178520
|   |   |   |   |   |   |   |   start <= 176786: molecular_function_
(15.3)
|   |   |   |   |   |   |   |   start > 176786:
structural_molecule_activity_ (18.81)
|   |   |   |   |   |   |   start > 178520
|   |   |   |   |   |   |   |   start <= 179672:
oxidoreductase_activity_ (22.97)
|   |   |   |   |   |   |   |   start > 179672: hydrolase_activity_
(21.69)
|   |   |   |   start > 180784
|   |   |   |   |   start <= 200163
|   |   |   |   |   |   start <= 193069
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 188645
|   |   |   |   |   |   |   |   |   start <= 185017:
protein_binding_ (17.97)
|   |   |   |   |   |   |   |   |   start > 185017
|   |   |   |   |   |   |   |   |   |   start <= 185962:
structural_molecule_activity_ (18.96)
|   |   |   |   |   |   |   |   |   |   start > 185962:
protein_binding_ (9.83)
|   |   |   |   |   |   |   |   start > 188645
```

```
|   |   |   |   |   |   |   |   |   start <= 191441:
peptidase_activity_ (5.7)
|   |   |   |   |   |   |   |   |   start > 191441:
molecular_function_ (10.12)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 182963:
protein_kinase_activity_ (14.24)
|   |   |   |   |   |   |   |   start > 182963: molecular_function_
(17.06)
|   |   |   |   |   |   start > 193069
|   |   |   |   |   |   |   start <= 194865: ligase_activity_
(16.67)
|   |   |   |   |   |   |   start > 194865
|   |   |   |   |   |   |   |   start <= 196027: RNA_binding_
(10.82)
|   |   |   |   |   |   |   |   start > 196027: motor_activity_
(12.76)
|   |   |   |   |   start > 200163
|   |   |   |   |   |   start <= 219539
|   |   |   |   |   |   |   start <= 207891
|   |   |   |   |   |   |   |   start <= 202643: molecular_function_
(24.05)
|   |   |   |   |   |   |   |   start > 202643
|   |   |   |   |   |   |   |   |   start <= 205351
|   |   |   |   |   |   |   |   |   |   start <= 203185:
isomerase_activity_ (11.53)
|   |   |   |   |   |   |   |   |   |   start > 203185:
protein_kinase_activity_ (12.1)
|   |   |   |   |   |   |   |   |   start > 205351:
transcription_regulator_activity_ (11.87)
|   |   |   |   |   |   |   start > 207891
|   |   |   |   |   |   |   |   start <= 213786: molecular_function_
(39.64)
|   |   |   |   |   |   |   |   start > 213786
|   |   |   |   |   |   |   |   |   start <= 216988:
transporter_activity_ (17.42)
|   |   |   |   |   |   |   |   |   start > 216988:
molecular_function_ (23.84)
|   |   |   |   |   |   start > 219539
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 222544
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
signal_transducer_activity_ (7.1/2.24)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
protein_kinase_activity_ (5.12/1.01)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
protein_kinase_activity_ (9.47/2.89)
|   |   |   |   |   |   |   |   start > 222544: lyase_activity_
(17.21)
|   |   |   |   |   |   |   strand = W: protein_binding_ (14.61)
|   start > 224099
|   |   strand = C
|   |   |   start <= 329810
|   |   |   |   start <= 248564
```

```
|   |   |   |   |   start <= 242227
|   |   |   |   |   |   start <= 226214: hydrolase_activity_ (16.43)
|   |   |   |   |   |   start > 226214: molecular_function_ (52.33)
|   |   |   |   |   start > 242227
|   |   |   |   |   |   start <= 245017: transferase_activity_
(21.15)
|   |   |   |   |   |   start > 245017: peptidase_activity_ (16.69)
|   |   |   |   start > 248564
|   |   |   |   |   start <= 322872
|   |   |   |   |   |   start <= 299226
|   |   |   |   |   |   |   start <= 293952
|   |   |   |   |   |   |   |   start <= 269103
|   |   |   |   |   |   |   |   |   start <= 262993
|   |   |   |   |   |   |   |   |   |   start <= 256414
|   |   |   |   |   |   |   |   |   |   |   start <= 255104:
molecular_function_ (16.1)
|   |   |   |   |   |   |   |   |   |   |   start > 255104:
RNA_binding_ (11.2)
|   |   |   |   |   |   |   |   |   |   start > 256414:
molecular_function_ (17.89)
|   |   |   |   |   |   |   |   |   start > 262993:
enzyme_regulator_activity_ (16.14)
|   |   |   |   |   |   |   |   start > 269103
|   |   |   |   |   |   |   |   |   start <= 278767
|   |   |   |   |   |   |   |   |   |   start <= 273038:
molecular_function_ (20.77)
|   |   |   |   |   |   |   |   |   |   start > 273038:
lyase_activity_ (16.8)
|   |   |   |   |   |   |   |   |   start > 278767:
molecular_function_ (23.67)
|   |   |   |   |   |   |   start > 293952: RNA_binding_ (23.14)
|   |   |   |   |   |   start > 299226: molecular_function_ (64.34)
|   |   |   |   |   start > 322872
|   |   |   |   |   |   start <= 327131: lyase_activity_ (13.56)
|   |   |   |   |   |   start > 327131: RNA_binding_ (15.81)
|   |   |   start > 329810
|   |   |   |   start <= 534923
|   |   |   |   |   start <= 391922
|   |   |   |   |   |   start <= 345264
|   |   |   |   |   |   |   start <= 333613:
structural_molecule_activity_ (20.34)
|   |   |   |   |   |   |   start > 333613
|   |   |   |   |   |   |   |   start <= 335801
|   |   |   |   |   |   |   |   |   start <= 334559:
molecular_function_ (15.48)
|   |   |   |   |   |   |   |   |   start > 334559:
oxidoreductase_activity_ (20.13)
|   |   |   |   |   |   |   |   start > 335801
|   |   |   |   |   |   |   |   |   start <= 339086:
molecular_function_ (33.69)
|   |   |   |   |   |   |   |   |   start > 339086
|   |   |   |   |   |   |   |   |   |   start <= 340956:
structural_molecule_activity_ (13.09)
```

```
|   |   |   |   |   |   |   |   |   |   start > 340956:
molecular_function_ (16.53)
|   |   |   |   |   |   start > 345264
|   |   |   |   |   |   |   start <= 349107
|   |   |   |   |   |   |   |   start <= 346408: DNA_binding_
(14.96)
|   |   |   |   |   |   |   |   start > 346408:
protein_kinase_activity_ (20.77)
|   |   |   |   |   |   |   start > 349107
|   |   |   |   |   |   |   |   start <= 381501
|   |   |   |   |   |   |   |   |   start <= 356392:
hydrolase_activity_ (21.4)
|   |   |   |   |   |   |   |   |   start > 356392
|   |   |   |   |   |   |   |   |   |   start <= 371472:
molecular_function_ (11.3)
|   |   |   |   |   |   |   |   |   |   start > 371472: DNA_binding_
(13.35)
|   |   |   |   |   |   |   |   start > 381501
|   |   |   |   |   |   |   |   |   start <= 389526:
oxidoreductase_activity_ (43.83/13.43)
|   |   |   |   |   |   |   |   |   start > 389526:
hydrolase_activity_ (13.76)
|   |   |   |   |   start > 391922
|   |   |   |   |   |   start <= 451844
|   |   |   |   |   |   |   start <= 416556
|   |   |   |   |   |   |   |   start <= 403745
|   |   |   |   |   |   |   |   |   start <= 396891
|   |   |   |   |   |   |   |   |   |   start <= 393364
|   |   |   |   |   |   |   |   |   |   |   start <= 392783:
transferase_activity_ (7.11)
|   |   |   |   |   |   |   |   |   |   |   start > 392783:
molecular_function_ (20.4)
|   |   |   |   |   |   |   |   |   |   start > 393364:
protein_binding_ (16.45)
|   |   |   |   |   |   |   |   |   start > 396891
|   |   |   |   |   |   |   |   |   |   start <= 398393:
molecular_function_ (19.15)
|   |   |   |   |   |   |   |   |   |   start > 398393
|   |   |   |   |   |   |   |   |   |   |   start <= 402211:
DNA_binding_ (13.91)
|   |   |   |   |   |   |   |   |   |   |   start > 402211:
molecular_function_ (14.45)
|   |   |   |   |   |   |   |   start > 403745
|   |   |   |   |   |   |   |   |   start <= 406884:
helicase_activity_ (18.04)
|   |   |   |   |   |   |   |   |   start > 406884
|   |   |   |   |   |   |   |   |   |   start <= 408187:
transporter_activity_ (18.52)
|   |   |   |   |   |   |   |   |   |   start > 408187:
molecular_function_ (15.18)
|   |   |   |   |   |   |   start > 416556
|   |   |   |   |   |   |   |   start <= 442875
|   |   |   |   |   |   |   |   |   start <= 425885
```

```
|   |   |   |   |   |   |   |   |   |   start <= 417953:
structural_molecule_activity_ (19.05)
|   |   |   |   |   |   |   |   |   |   start > 417953
|   |   |   |   |   |   |   |   |   |   |   start <= 420859:
hydrolase_activity_ (12.09)
|   |   |   |   |   |   |   |   |   |   |   start > 420859:
molecular_function_ (13.5)
|   |   |   |   |   |   |   |   |   start > 425885
|   |   |   |   |   |   |   |   |   |   start <= 431549
|   |   |   |   |   |   |   |   |   |   |   start <= 428945:
transferase_activity_ (21.8)
|   |   |   |   |   |   |   |   |   |   |   start > 428945
|   |   |   |   |   |   |   |   |   |   |   |   start <= 430275:
protein_binding_ (8.42)
|   |   |   |   |   |   |   |   |   |   |   |   start > 430275:
RNA_binding_ (12.19)
|   |   |   |   |   |   |   |   |   |   start > 431549
|   |   |   |   |   |   |   |   |   |   |   start <= 435223:
transcription_regulator_activity_ (19.4)
|   |   |   |   |   |   |   |   |   |   |   start > 435223
|   |   |   |   |   |   |   |   |   |   |   |   start <= 437421:
structural_molecule_activity_ (24.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 437421
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 439028:
transferase_activity_ (8.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 439028:
hydrolase_activity_ (9.33)
|   |   |   |   |   |   |   |   start > 442875
|   |   |   |   |   |   |   |   |   start <= 449810:
molecular_function_ (31.16)
|   |   |   |   |   |   |   |   |   start > 449810:
structural_molecule_activity_ (17.02)
|   |   |   |   |   |   start > 451844
|   |   |   |   |   |   |   start <= 493900
|   |   |   |   |   |   |   |   start <= 483062
|   |   |   |   |   |   |   |   |   start <= 458200
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
lyase_activity_ (21.15/7.83)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
oxidoreductase_activity_ (9.85/3.38)
|   |   |   |   |   |   |   |   |   start > 458200
|   |   |   |   |   |   |   |   |   |   start <= 465714
|   |   |   |   |   |   |   |   |   |   |   start <= 463602:
molecular_function_ (28.23)
|   |   |   |   |   |   |   |   |   |   |   start > 463602:
hydrolase_activity_ (12.32)
|   |   |   |   |   |   |   |   |   |   start > 465714:
molecular_function_ (86.62)
|   |   |   |   |   |   |   |   start > 483062
|   |   |   |   |   |   |   |   |   start <= 487413:
helicase_activity_ (22.9)
|   |   |   |   |   |   |   |   |   start > 487413:
enzyme_regulator_activity_ (13.57)
|   |   |   |   |   |   |   start > 493900
```

```
|   |   |   |   |   |   |   |   start <= 526282
|   |   |   |   |   |   |   |   |   start <= 511439
|   |   |   |   |   |   |   |   |   |   start <= 510275
|   |   |   |   |   |   |   |   |   |   |   distance <= 2799:
protein_binding_ (33.01/0.35)
|   |   |   |   |   |   |   |   |   |   |   distance > 2799
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 4151:
hydrolase_activity_ (11.31)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 4151:
protein_binding_ (22.12/4.68)
|   |   |   |   |   |   |   |   |   |   start > 510275:
structural_molecule_activity_ (11.13)
|   |   |   |   |   |   |   |   |   start > 511439
|   |   |   |   |   |   |   |   |   |   start <= 512801:
DNA_binding_ (17.18)
|   |   |   |   |   |   |   |   |   |   start > 512801
|   |   |   |   |   |   |   |   |   |   |   start <= 524716:
molecular_function_ (60.36)
|   |   |   |   |   |   |   |   |   |   |   start > 524716:
protein_binding_ (16.51)
|   |   |   |   |   |   |   |   start > 526282
|   |   |   |   |   |   |   |   |   start <= 533106
|   |   |   |   |   |   |   |   |   |   start <= 527457:
oxidoreductase_activity_ (18.42)
|   |   |   |   |   |   |   |   |   |   start > 527457:
transporter_activity_ (20.86)
|   |   |   |   |   |   |   |   |   start > 533106:
hydrolase_activity_ (20.53)
|   |   |   |   start > 534923
|   |   |   |   |   start <= 592467
|   |   |   |   |   |   start <= 559308
|   |   |   |   |   |   |   start <= 552412: motor_activity_ (16.85)
|   |   |   |   |   |   |   start > 552412: RNA_binding_ (15.82)
|   |   |   |   |   |   start > 559308
|   |   |   |   |   |   |   start <= 590037
|   |   |   |   |   |   |   |   start <= 567560
|   |   |   |   |   |   |   |   |   start <= 565534:
molecular_function_ (38.63)
|   |   |   |   |   |   |   |   |   start > 565534:
oxidoreductase_activity_ (47.54/20.3)
|   |   |   |   |   |   |   |   start > 567560
|   |   |   |   |   |   |   |   |   start <= 578851
|   |   |   |   |   |   |   |   |   |   start <= 575622
|   |   |   |   |   |   |   |   |   |   |   start <= 571254:
enzyme_regulator_activity_ (13.38)
|   |   |   |   |   |   |   |   |   |   |   start > 571254:
molecular_function_ (20.22)
|   |   |   |   |   |   |   |   |   |   start > 575622:
enzyme_regulator_activity_ (28.66/9.76)
|   |   |   |   |   |   |   |   |   start > 578851:
molecular_function_ (31.26)
|   |   |   |   |   |   |   start > 590037: RNA_binding_ (17.8)
|   |   |   |   |   start > 592467
|   |   |   |   |   |   start <= 599499
```

```
|   |   |   |   |   |   |   start <= 596464:
structural_molecule_activity_ (15.53)
|   |   |   |   |   |   |   start > 596464
|   |   |   |   |   |   |   |   start <= 598532: molecular_function_
(18.63)
|   |   |   |   |   |   |   |   start > 598532:
structural_molecule_activity_ (14.53)
|   |   |   |   |   |   start > 599499
|   |   |   |   |   |   |   start <= 608588
|   |   |   |   |   |   |   |   start <= 605060
|   |   |   |   |   |   |   |   |   start <= 603874:
peptidase_activity_ (14.04)
|   |   |   |   |   |   |   |   |   start > 603874:
molecular_function_ (12.89)
|   |   |   |   |   |   |   |   start > 605060: hydrolase_activity_
(15.88)
|   |   |   |   |   |   |   start > 608588
|   |   |   |   |   |   |   |   start <= 626435
|   |   |   |   |   |   |   |   |   start <= 615372:
molecular_function_ (18.43)
|   |   |   |   |   |   |   |   |   start > 615372
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
structural_molecule_activity_ (17.15/7.25)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
molecular_function_ (9.49/2.63)
|   |   |   |   |   |   |   |   start > 626435
|   |   |   |   |   |   |   |   |   start <= 635489:
peptidase_activity_ (15.95)
|   |   |   |   |   |   |   |   |   start > 635489:
molecular_function_ (35.53)
|   |   strand = W
|   |   |   start <= 611167
|   |   |   |   start <= 278767
|   |   |   |   |   start <= 264433
|   |   |   |   |   |   start <= 231871
|   |   |   |   |   |   |   start <= 226214: DNA_binding_ (21.82)
|   |   |   |   |   |   |   start > 226214:
transcription_regulator_activity_ (15.91)
|   |   |   |   |   |   start > 231871
|   |   |   |   |   |   |   start <= 256414
|   |   |   |   |   |   |   |   start <= 235785: molecular_function_
(29.37)
|   |   |   |   |   |   |   |   start > 235785
|   |   |   |   |   |   |   |   |   start <= 242227:
transferase_activity_ (17.78)
|   |   |   |   |   |   |   |   |   start > 242227
|   |   |   |   |   |   |   |   |   |   start <= 248564:
protein_kinase_activity_ (9.1)
|   |   |   |   |   |   |   |   |   |   start > 248564:
molecular_function_ (10.7)
|   |   |   |   |   |   |   start > 256414
|   |   |   |   |   |   |   |   start <= 260776:
structural_molecule_activity_ (39.37)
|   |   |   |   |   |   |   |   start > 260776
```

```
|   |   |   |   |   |   |   |   |   start <= 261921:
molecular_function_ (16.59)
|   |   |   |   |   |   |   |   |   start > 261921
|   |   |   |   |   |   |   |   |   |   start <= 262993:
hydrolase_activity_ (8.56)
|   |   |   |   |   |   |   |   |   |   start > 262993:
molecular_function_ (14.54)
|   |   |   |   |   start > 264433
|   |   |   |   |   |   start <= 274927
|   |   |   |   |   |   |   start <= 271522: protein_binding_
(31.25)
|   |   |   |   |   |   |   start > 271522
|   |   |   |   |   |   |   |   start <= 273038: DNA_binding_ (15.7)
|   |   |   |   |   |   |   |   start > 273038: molecular_function_
(29.8/11.89)
|   |   |   |   |   |   start > 274927: oxidoreductase_activity_
(47.88)
|   |   |   |   start > 278767
|   |   |   |   |   start <= 534923
|   |   |   |   |   |   start <= 288489
|   |   |   |   |   |   |   start <= 282829
|   |   |   |   |   |   |   |   start <= 280153: molecular_function_
(13.18)
|   |   |   |   |   |   |   |   start > 280153
|   |   |   |   |   |   |   |   |   start <= 282535:
translation_regulator_activity_ (10.37)
|   |   |   |   |   |   |   |   |   start > 282535: RNA_binding_
(11.41)
|   |   |   |   |   |   |   start > 282829
|   |   |   |   |   |   |   |   start <= 284674: hydrolase_activity_
(31.74/13.66)
|   |   |   |   |   |   |   |   start > 284674
|   |   |   |   |   |   |   |   |   start <= 286247: motor_activity_
(11.93)
|   |   |   |   |   |   |   |   |   start > 286247:
helicase_activity_ (11.96)
|   |   |   |   |   |   start > 288489
|   |   |   |   |   |   |   start <= 439028
|   |   |   |   |   |   |   |   start <= 396891
|   |   |   |   |   |   |   |   |   start <= 317408
|   |   |   |   |   |   |   |   |   |   start <= 308850
|   |   |   |   |   |   |   |   |   |   |   start <= 296074
|   |   |   |   |   |   |   |   |   |   |   |   start <= 291097:
molecular_function_ (15.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 291097:
protein_binding_ (17.25)
|   |   |   |   |   |   |   |   |   |   |   start > 296074:
molecular_function_ (84.57)
|   |   |   |   |   |   |   |   |   |   start > 308850
|   |   |   |   |   |   |   |   |   |   |   start <= 314456
|   |   |   |   |   |   |   |   |   |   |   |   start <= 309843:
structural_molecule_activity_ (15.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 309843:
transferase_activity_ (10.19)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 314456
|   |   |   |   |   |   |   |   |   |   |   |   start <= 315598:
molecular_function_ (15.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 315598:
transporter_activity_ (19.39)
|   |   |   |   |   |   |   |   |   start > 317408
|   |   |   |   |   |   |   |   |   |   start <= 365248
|   |   |   |   |   |   |   |   |   |   |   start <= 356392
|   |   |   |   |   |   |   |   |   |   |   |   start <= 349107
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 322872:
transcription_regulator_activity_ (26.06/11.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 322872
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
334559
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
327131: molecular_function_ (20.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
327131: transcription_regulator_activity_ (14.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
334559: molecular_function_ (30.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 349107
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 353137:
nucleotidyltransferase_activity_ (16.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 353137:
DNA_binding_ (24.25/10.68)
|   |   |   |   |   |   |   |   |   |   |   start > 356392
|   |   |   |   |   |   |   |   |   |   |   |   start <= 359786
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 358119:
structural_molecule_activity_ (16.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 358119:
protein_binding_ (19.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 359786
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 364419
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
362265: molecular_function_ (13.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
362265: RNA_binding_ (10.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 364419:
DNA_binding_ (14.37)
|   |   |   |   |   |   |   |   |   |   start > 365248
|   |   |   |   |   |   |   |   |   |   |   start <= 369534
|   |   |   |   |   |   |   |   |   |   |   |   start <= 369008:
molecular_function_ (19.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 369008:
nucleotidyltransferase_activity_ (12.45)
|   |   |   |   |   |   |   |   |   |   |   start > 369534
|   |   |   |   |   |   |   |   |   |   |   |   start <= 381501:
molecular_function_ (48.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 381501
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 385401:
transcription_regulator_activity_ (15.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 385401:
molecular_function_ (33.0)
|   |   |   |   |   |   |   |   start > 396891
```

```
|   |   |   |   |   |   |   |   |   start <= 408187
|   |   |   |   |   |   |   |   |   |   start <= 403745:
transferase_activity_ (39.0)
|   |   |   |   |   |   |   |   |   |   start > 403745:
transcription_regulator_activity_ (18.95)
|   |   |   |   |   |   |   |   |   start > 408187
|   |   |   |   |   |   |   |   |   |   start <= 425885
|   |   |   |   |   |   |   |   |   |   |   start <= 420859:
RNA_binding_ (18.42)
|   |   |   |   |   |   |   |   |   |   |   start > 420859:
molecular_function_ (23.91)
|   |   |   |   |   |   |   |   |   |   start > 425885
|   |   |   |   |   |   |   |   |   |   |   start <= 431549
|   |   |   |   |   |   |   |   |   |   |   |   start <= 428945:
protein_binding_ (15.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 428945:
RNA_binding_ (14.24)
|   |   |   |   |   |   |   |   |   |   |   start > 431549
|   |   |   |   |   |   |   |   |   |   |   |   start <= 435223:
transferase_activity_ (12.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 435223:
protein_binding_ (13.78)
|   |   |   |   |   |   |   start > 439028
|   |   |   |   |   |   |   |   start <= 499924
|   |   |   |   |   |   |   |   |   start <= 442875:
nucleotidyltransferase_activity_ (21.58)
|   |   |   |   |   |   |   |   |   start > 442875
|   |   |   |   |   |   |   |   |   |   start <= 477981
|   |   |   |   |   |   |   |   |   |   |   start <= 472992
|   |   |   |   |   |   |   |   |   |   |   |   start <= 451844
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 451077:
molecular_function_ (35.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 451077:
hydrolase_activity_ (15.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 451844:
molecular_function_ (44.02)
|   |   |   |   |   |   |   |   |   |   |   start > 472992:
protein_binding_ (19.11)
|   |   |   |   |   |   |   |   |   |   start > 477981
|   |   |   |   |   |   |   |   |   |   |   start <= 487413
|   |   |   |   |   |   |   |   |   |   |   |   start <= 483062:
molecular_function_ (50.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 483062:
nucleotidyltransferase_activity_ (18.02)
|   |   |   |   |   |   |   |   |   |   |   start > 487413:
molecular_function_ (62.29)
|   |   |   |   |   |   |   |   start > 499924
|   |   |   |   |   |   |   |   |   start <= 506540
|   |   |   |   |   |   |   |   |   |   distance <= 778:
transcription_regulator_activity_ (10.66/4.76)
|   |   |   |   |   |   |   |   |   |   distance > 778: DNA_binding_
(11.11/1.68)
|   |   |   |   |   |   |   |   |   start > 506540
|   |   |   |   |   |   |   |   |   |   start <= 527457
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 523611
|   |   |   |   |   |   |   |   |   |   |   |   start <= 514705
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 510275:
molecular_function_ (10.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 510275:
transporter_activity_ (17.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 514705:
molecular_function_ (48.71)
|   |   |   |   |   |   |   |   |   |   |   start > 523611:
transporter_activity_ (19.82)
|   |   |   |   |   |   |   |   |   |   start > 527457:
molecular_function_ (11.68)
|   |   |   |   |   start > 534923
|   |   |   |   |   |   start <= 554629
|   |   |   |   |   |   |   start <= 551299
|   |   |   |   |   |   |   |   start <= 547858:
signal_transducer_activity_ (15.03)
|   |   |   |   |   |   |   |   start > 547858
|   |   |   |   |   |   |   |   |   start <= 549090:
hydrolase_activity_ (19.83)
|   |   |   |   |   |   |   |   |   start > 549090:
structural_molecule_activity_ (9.26)
|   |   |   |   |   |   |   start > 551299
|   |   |   |   |   |   |   |   start <= 552412:
transferase_activity_ (9.87)
|   |   |   |   |   |   |   |   start > 552412: helicase_activity_
(41.47/19.7)
|   |   |   |   |   |   start > 554629
|   |   |   |   |   |   |   start <= 583295
|   |   |   |   |   |   |   |   start <= 559308
|   |   |   |   |   |   |   |   |   start <= 557319
|   |   |   |   |   |   |   |   |   |   start <= 556160:
molecular_function_ (15.75)
|   |   |   |   |   |   |   |   |   |   start > 556160:
transferase_activity_ (17.4)
|   |   |   |   |   |   |   |   |   start > 557319:
transcription_regulator_activity_ (23.08)
|   |   |   |   |   |   |   |   start > 559308
|   |   |   |   |   |   |   |   |   start <= 562189:
molecular_function_ (25.72)
|   |   |   |   |   |   |   |   |   start > 562189
|   |   |   |   |   |   |   |   |   |   start <= 571254:
transferase_activity_ (34.74)
|   |   |   |   |   |   |   |   |   |   start > 571254
|   |   |   |   |   |   |   |   |   |   |   start <= 578851:
molecular_function_ (44.05)
|   |   |   |   |   |   |   |   |   |   |   start > 578851
|   |   |   |   |   |   |   |   |   |   |   |   start <= 581925:
transferase_activity_ (15.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 581925:
molecular_function_ (13.47)
|   |   |   |   |   |   |   start > 583295
|   |   |   |   |   |   |   |   start <= 592467
```

```
|   |   |   |   |   |   |   |   |   start <= 584594:
transporter_activity_ (15.72)
|   |   |   |   |   |   |   |   |   start > 584594
|   |   |   |   |   |   |   |   |   |   start <= 590037:
oxidoreductase_activity_ (15.53)
|   |   |   |   |   |   |   |   |   |   start > 590037:
structural_molecule_activity_ (13.84)
|   |   |   |   |   |   |   |   start > 592467
|   |   |   |   |   |   |   |   |   start <= 603874: RNA_binding_
(25.04)
|   |   |   |   |   |   |   |   |   start > 603874
|   |   |   |   |   |   |   |   |   |   start <= 608588:
protein_binding_ (18.86)
|   |   |   |   |   |   |   |   |   |   start > 608588:
molecular_function_ (20.13)
|   |   |   start > 611167
|   |   |   |   start <= 645994
|   |   |   |   |   start <= 615372: transporter_activity_ (15.25)
|   |   |   |   |   start > 615372
|   |   |   |   |   |   start <= 630790
|   |   |   |   |   |   |   start <= 626435
|   |   |   |   |   |   |   |   start <= 625506
|   |   |   |   |   |   |   |   |   start <= 619447:
molecular_function_ (9.69)
|   |   |   |   |   |   |   |   |   start > 619447: DNA_binding_
(13.36)
|   |   |   |   |   |   |   |   start > 625506: molecular_function_
(13.36)
|   |   |   |   |   |   |   start > 626435: lyase_activity_ (18.09)
|   |   |   |   |   |   start > 630790
|   |   |   |   |   |   |   start <= 640106: DNA_binding_ (39.18)
|   |   |   |   |   |   |   start > 640106: molecular_function_
(14.38)
|   |   |   |   start > 645994
|   |   |   |   |   start <= 656474: hydrolase_activity_ (33.86)
|   |   |   |   |   start > 656474: transporter_activity_ (10.79)
```

For Biological Process

```
|   start <= 179672
|   |   start <= 154996
|   |   |   start <= 46296
|   |   |   |   start <= 31694
|   |   |   |   |   start <= 18339
|   |   |   |   |   |   start <= 14485
|   |   |   |   |   |   |   start <= 5621: biological_process_
(20.61)
|   |   |   |   |   |   |   start > 5621
|   |   |   |   |   |   |   |   start <= 11227: transport_ (28.32)
|   |   |   |   |   |   |   |   start > 11227: biological_process_
(15.49)
|   |   |   |   |   |   start > 14485:
amino_acid_and_derivative_metabolic_process_ (27.2)
|   |   |   |   |   start > 18339
```

```
|   |   |   |   |   |   start <= 22234: transport_ (16.65)
|   |   |   |   |   |   start > 22234
|   |   |   |   |   |   |   start <= 30688: biological_process_
(32.23)
|   |   |   |   |   |   |   start > 30688
|   |   |   |   |   |   |   |   neigh_strand = W:
biological_process_ (29.18/12.69)
|   |   |   |   |   |   |   |   neigh_strand = C: transport_
(26.57/7.18)
|   |   |   |   start > 31694
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 39164
|   |   |   |   |   |   |   start <= 34544:
protein_modification_process_ (17.71)
|   |   |   |   |   |   |   start > 34544:
amino_acid_and_derivative_metabolic_process_ (17.99)
|   |   |   |   |   |   start > 39164: transport_ (18.32)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 34544: vesicle-mediated_transport_
(17.99)
|   |   |   |   |   |   start > 34544
|   |   |   |   |   |   |   start <= 38812
|   |   |   |   |   |   |   |   neigh_strand = W:
RNA_metabolic_process_ (11.42/4.22)
|   |   |   |   |   |   |   |   neigh_strand = C:
ribosome_biogenesis_and_assembly_ (14.13/5.26)
|   |   |   |   |   |   |   start > 38812:
protein_modification_process_ (14.67)
|   |   |   start > 46296
|   |   |   |   strand = C
|   |   |   |   |   start <= 74629
|   |   |   |   |   |   start <= 53705
|   |   |   |   |   |   |   start <= 48195: translation_ (12.04)
|   |   |   |   |   |   |   start > 48195:
protein_catabolic_process_ (18.68)
|   |   |   |   |   |   start > 53705
|   |   |   |   |   |   |   start <= 63360:
ribosome_biogenesis_and_assembly_ (49.19/25.13)
|   |   |   |   |   |   |   start > 63360
|   |   |   |   |   |   |   |   start <= 67467: response_to_stress_
(14.53)
|   |   |   |   |   |   |   |   start > 67467
|   |   |   |   |   |   |   |   |   start <= 70223: transport_
(13.2)
|   |   |   |   |   |   |   |   |   start > 70223:
signal_transduction_ (13.22)
|   |   |   |   |   start > 74629
|   |   |   |   |   |   start <= 133467
|   |   |   |   |   |   |   start <= 78651
|   |   |   |   |   |   |   |   start <= 75826: vesicle-
mediated_transport_ (16.2)
|   |   |   |   |   |   |   |   start > 75826: translation_ (21.46)
|   |   |   |   |   |   |   start > 78651
|   |   |   |   |   |   |   |   start <= 100676
```

```
|   |   |   |   |   |   |   |   |   start <= 91541
|   |   |   |   |   |   |   |   |   |   start <= 84213:
biological_process_ (31.06)
|   |   |   |   |   |   |   |   |   |   start > 84213
|   |   |   |   |   |   |   |   |   |   |   start <= 88791:
transport_ (17.65)
|   |   |   |   |   |   |   |   |   |   |   start > 88791:
biological_process_ (21.69)
|   |   |   |   |   |   |   |   |   start > 91541
|   |   |   |   |   |   |   |   |   |   start <= 94504:
ribosome_biogenesis_and_assembly_ (17.05)
|   |   |   |   |   |   |   |   |   |   start > 94504:
biological_process_ (17.95)
|   |   |   |   |   |   |   |   start > 100676
|   |   |   |   |   |   |   |   |   start <= 118798
|   |   |   |   |   |   |   |   |   |   start <= 114632
|   |   |   |   |   |   |   |   |   |   |   start <= 112508:
vesicle-mediated_transport_ (12.01)
|   |   |   |   |   |   |   |   |   |   |   start > 112508:
conjugation_ (16.33)
|   |   |   |   |   |   |   |   |   |   start > 114632: vesicle-
mediated_transport_ (12.91)
|   |   |   |   |   |   |   |   |   start > 118798
|   |   |   |   |   |   |   |   |   |   start <= 127480: transport_
(10.75)
|   |   |   |   |   |   |   |   |   |   start > 127480:
biological_process_ (13.46)
|   |   |   |   |   |   start > 133467
|   |   |   |   |   |   |   start <= 141094
|   |   |   |   |   |   |   |   start <= 134139: translation_
(16.88)
|   |   |   |   |   |   |   |   start > 134139
|   |   |   |   |   |   |   |   |   start <= 140696:
protein_modification_process_ (18.47)
|   |   |   |   |   |   |   |   |   start > 140696: translation_
(14.95)
|   |   |   |   |   |   |   start > 141094
|   |   |   |   |   |   |   |   start <= 144406:
cell_wall_organization_and_biogenesis_ (19.35)
|   |   |   |   |   |   |   |   start > 144406
|   |   |   |   |   |   |   |   |   start <= 150692:
biological_process_ (34.63)
|   |   |   |   |   |   |   |   |   start > 150692:
signal_transduction_ (12.49)
|   |   |   |   strand = W
|   |   |   |   |   start <= 94504
|   |   |   |   |   |   start <= 50052
|   |   |   |   |   |   |   start <= 48195
|   |   |   |   |   |   |   |   start <= 47158:
RNA_metabolic_process_ (8.27)
|   |   |   |   |   |   |   |   start > 47158: biological_process_
(21.1)
|   |   |   |   |   |   |   start > 48195: RNA_metabolic_process_
(18.57)
```

```
|   |   |   |   |   |   start > 50052
|   |   |   |   |   |   |   start <= 84213
|   |   |   |   |   |   |   |   start <= 74629: translation_
(48.73/16.45)
|   |   |   |   |   |   |   |   start > 74629
|   |   |   |   |   |   |   |   |   start <= 81040
|   |   |   |   |   |   |   |   |   |   start <= 75826: transport_
(19.19)
|   |   |   |   |   |   |   |   |   |   start > 75826:
ribosome_biogenesis_and_assembly_ (9.88)
|   |   |   |   |   |   |   |   |   start > 81040
|   |   |   |   |   |   |   |   |   |   start <= 82952:
cell_wall_organization_and_biogenesis_ (17.84)
|   |   |   |   |   |   |   |   |   |   start > 82952: translation_
(13.01)
|   |   |   |   |   |   |   start > 84213
|   |   |   |   |   |   |   |   start <= 88791: transcription_
(9.57)
|   |   |   |   |   |   |   |   start > 88791: pseudohyphal_growth_
(17.05)
|   |   |   |   |   start > 94504
|   |   |   |   |   |   start <= 107321
|   |   |   |   |   |   |   start <= 98726
|   |   |   |   |   |   |   |   start <= 96762:
amino_acid_and_derivative_metabolic_process_ (21.74)
|   |   |   |   |   |   |   |   start > 96762: biological_process_
(23.74)
|   |   |   |   |   |   |   start > 98726
|   |   |   |   |   |   |   |   start <= 100676:
lipid_metabolic_process_ (15.33)
|   |   |   |   |   |   |   |   start > 100676:
amino_acid_and_derivative_metabolic_process_ (23.38)
|   |   |   |   |   |   start > 107321
|   |   |   |   |   |   |   start <= 118798
|   |   |   |   |   |   |   |   start <= 112508: translation_
(10.04)
|   |   |   |   |   |   |   |   start > 112508:
cellular_homeostasis_ (25.39/9.75)
|   |   |   |   |   |   |   start > 118798
|   |   |   |   |   |   |   |   start <= 144406
|   |   |   |   |   |   |   |   |   start <= 127480
|   |   |   |   |   |   |   |   |   |   start <= 122522:
RNA_metabolic_process_ (17.13)
|   |   |   |   |   |   |   |   |   |   start > 122522
|   |   |   |   |   |   |   |   |   |   |   start <= 125764:
ribosome_biogenesis_and_assembly_ (8.9)
|   |   |   |   |   |   |   |   |   |   |   start > 125764:
biological_process_ (7.17)
|   |   |   |   |   |   |   |   |   start > 127480
|   |   |   |   |   |   |   |   |   |   start <= 135710:
translation_ (12.18)
|   |   |   |   |   |   |   |   |   |   start > 135710:
cell_wall_organization_and_biogenesis_ (17.37)
|   |   |   |   |   |   |   |   start > 144406
```

```
|   |   |   |   |   |   |   |   |   start <= 153274:
RNA_metabolic_process_ (36.92/16.9)
|   |   |   |   |   |   |   |   |   start > 153274:
biological_process_ (11.94)
|   |   start > 154996
|   |   |   start <= 165935
|   |   |   |   start <= 162563
|   |   |   |   |   strand = C: translation_ (32.11)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 158619: translation_ (13.33)
|   |   |   |   |   |   start > 158619: transport_ (11.56)
|   |   |   |   start > 162563
|   |   |   |   |   start <= 164390: carbohydrate_metabolic_process_
(13.59)
|   |   |   |   |   start > 164390: biological_process_ (6.92)
|   |   |   start > 165935
|   |   |   |   strand = C
|   |   |   |   |   start <= 171788
|   |   |   |   |   |   start <= 168834: pseudohyphal_growth_
(13.87)
|   |   |   |   |   |   start > 168834: electron_transport_ (15.0)
|   |   |   |   |   start > 171788: transcription_ (15.12)
|   |   |   |   strand = W
|   |   |   |   |   start <= 176786
|   |   |   |   |   |   start <= 174218
|   |   |   |   |   |   |   start <= 171788
|   |   |   |   |   |   |   |   start <= 168834: electron_transport_
(9.95)
|   |   |   |   |   |   |   |   start > 168834: transport_ (5.81)
|   |   |   |   |   |   |   start > 171788:
protein_catabolic_process_ (14.83)
|   |   |   |   |   |   start > 174218:
ribosome_biogenesis_and_assembly_ (18.42)
|   |   |   |   |   start > 176786
|   |   |   |   |   |   start <= 178520: translation_ (14.42)
|   |   |   |   |   |   start > 178520: electron_transport_ (28.15)
|   start > 179672
|   |   start <= 428945
|   |   |   start <= 260776
|   |   |   |   start <= 234070
|   |   |   |   |   start <= 219539
|   |   |   |   |   |   start <= 202643
|   |   |   |   |   |   |   start <= 185017
|   |   |   |   |   |   |   |   strand = C: cell_cycle_ (19.16)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 180784:
lipid_metabolic_process_ (19.11)
|   |   |   |   |   |   |   |   |   start > 180784
|   |   |   |   |   |   |   |   |   |   distance <= 1068:
protein_modification_process_ (3.02/0.29)
|   |   |   |   |   |   |   |   |   |   distance > 1068:
DNA_metabolic_process_ (24.81/10.79)
|   |   |   |   |   |   |   start > 185017
|   |   |   |   |   |   |   |   start <= 194865
```

```
|   |   |   |   |   |   |   |   |   start <= 185686: translation_
(21.69)
|   |   |   |   |   |   |   |   |   start > 185686
|   |   |   |   |   |   |   |   |   |   start <= 188645
|   |   |   |   |   |   |   |   |   |   |   start <= 185962:
biological_process_ (16.2)
|   |   |   |   |   |   |   |   |   |   |   start > 185962: vesicle-
mediated_transport_ (10.19)
|   |   |   |   |   |   |   |   |   |   start > 188645
|   |   |   |   |   |   |   |   |   |   |   start <= 191441:
protein_modification_process_ (10.3)
|   |   |   |   |   |   |   |   |   |   |   start > 191441:
biological_process_ (23.34)
|   |   |   |   |   |   |   |   start > 194865
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 196027:
DNA_metabolic_process_ (12.26)
|   |   |   |   |   |   |   |   |   |   start > 196027
|   |   |   |   |   |   |   |   |   |   |   start <= 200163:
cell_wall_organization_and_biogenesis_ (16.5)
|   |   |   |   |   |   |   |   |   |   |   start > 200163:
biological_process_ (9.15)
|   |   |   |   |   |   |   |   |   strand = W: translation_ (9.91)
|   |   |   |   |   |   start > 202643
|   |   |   |   |   |   |   start <= 210237
|   |   |   |   |   |   |   |   start <= 203185:
carbohydrate_metabolic_process_ (13.94)
|   |   |   |   |   |   |   |   start > 203185
|   |   |   |   |   |   |   |   |   start <= 205351: vesicle-
mediated_transport_ (12.19)
|   |   |   |   |   |   |   |   |   start > 205351
|   |   |   |   |   |   |   |   |   |   start <= 207891:
transcription_ (17.91)
|   |   |   |   |   |   |   |   |   |   start > 207891: vesicle-
mediated_transport_ (8.73)
|   |   |   |   |   |   |   start > 210237
|   |   |   |   |   |   |   |   start <= 216988
|   |   |   |   |   |   |   |   |   strand = C: transport_ (14.52)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 213786:
biological_process_ (12.05)
|   |   |   |   |   |   |   |   |   |   start > 213786: transport_
(15.66)
|   |   |   |   |   |   |   |   start > 216988
|   |   |   |   |   |   |   |   |   start <= 218861:
organelle_organization_and_biogenesis_ (10.86)
|   |   |   |   |   |   |   |   |   start > 218861: translation_
(12.39)
|   |   |   |   |   start > 219539
|   |   |   |   |   |   start <= 226214
|   |   |   |   |   |   |   start <= 222544
|   |   |   |   |   |   |   |   start <= 219968
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
biological_process_ (13.53/3.82)
```

```
|   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (23.77/8.59)
|   |   |   |   |   |   |   |   start > 219968: conjugation_ (18.74)
|   |   |   |   |   |   |   start > 222544: DNA_metabolic_process_
(49.7)
|   |   |   |   |   |   start > 226214
|   |   |   |   |   |   |   strand = C: biological_process_
(49.55/21.35)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 231871: transcription_
(16.34)
|   |   |   |   |   |   |   |   start > 231871:
DNA_metabolic_process_ (20.07)
|   |   |   |   start > 234070
|   |   |   |   |   start <= 242227
|   |   |   |   |   |   strand = C: biological_process_ (39.53)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 235785: biological_process_
(15.13)
|   |   |   |   |   |   |   start > 235785
|   |   |   |   |   |   |   |   neigh_num <= 1:
amino_acid_and_derivative_metabolic_process_ (12.52/4.39)
|   |   |   |   |   |   |   |   neigh_num > 1:
carbohydrate_metabolic_process_ (27.75/12.4)
|   |   |   |   |   start > 242227
|   |   |   |   |   |   start <= 248564
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 245017:
cell_wall_organization_and_biogenesis_ (43.14/16.29)
|   |   |   |   |   |   |   |   start > 245017:
protein_catabolic_process_ (15.48)
|   |   |   |   |   |   |   strand = W: cell_cycle_ (23.98/7.49)
|   |   |   |   |   |   start > 248564
|   |   |   |   |   |   |   start <= 258866
|   |   |   |   |   |   |   |   start <= 256116
|   |   |   |   |   |   |   |   |   start <= 255104:
biological_process_ (12.33)
|   |   |   |   |   |   |   |   |   start > 255104:
ribosome_biogenesis_and_assembly_ (8.75)
|   |   |   |   |   |   |   |   start > 256116: biological_process_
(22.24)
|   |   |   |   |   |   |   start > 258866:
cell_wall_organization_and_biogenesis_ (43.38)
|   |   |   start > 260776
|   |   |   |   start <= 339086
|   |   |   |   |   start <= 278767
|   |   |   |   |   |   start <= 273038
|   |   |   |   |   |   |   start <= 269103
|   |   |   |   |   |   |   |   strand = C: cell_budding_ (20.99)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 262993
|   |   |   |   |   |   |   |   |   |   start <= 261921:
RNA_metabolic_process_ (14.58)
```

```
|   |   |   |   |   |   |   |   |   |   start > 261921:
biological_process_ (10.51)
|   |   |   |   |   |   |   |   |   start > 262993:
cellular_respiration_ (22.75)
|   |   |   |   |   |   |   start > 269103: biological_process_
(51.74)
|   |   |   |   |   |   start > 273038
|   |   |   |   |   |   |   strand = C:
protein_modification_process_ (15.03)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 277925: response_to_stress_
(37.98)
|   |   |   |   |   |   |   |   start > 277925:
carbohydrate_metabolic_process_ (32.45/13.11)
|   |   |   |   |   start > 278767
|   |   |   |   |   |   start <= 325415
|   |   |   |   |   |   |   start <= 288489
|   |   |   |   |   |   |   |   start <= 280153
|   |   |   |   |   |   |   |   |   distance <= 2100
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (10.29/4.13)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: transport_
(8.92/2.51)
|   |   |   |   |   |   |   |   |   distance > 2100:
organelle_organization_and_biogenesis_ (15.01/2.71)
|   |   |   |   |   |   |   |   start > 280153
|   |   |   |   |   |   |   |   |   stop <= 282923
|   |   |   |   |   |   |   |   |   |   start <= 281973:
ribosome_biogenesis_and_assembly_ (16.52)
|   |   |   |   |   |   |   |   |   |   start > 281973:
RNA_metabolic_process_ (27.7/11.41)
|   |   |   |   |   |   |   |   |   stop > 282923
|   |   |   |   |   |   |   |   |   |   start <= 284674
|   |   |   |   |   |   |   |   |   |   |   start <= 282829:
translation_ (12.66)
|   |   |   |   |   |   |   |   |   |   |   start > 282829:
organelle_organization_and_biogenesis_ (15.35)
|   |   |   |   |   |   |   |   |   |   start > 284674
|   |   |   |   |   |   |   |   |   |   |   start <= 286247:
vesicle-mediated_transport_ (12.13)
|   |   |   |   |   |   |   |   |   |   |   start > 286247:
ribosome_biogenesis_and_assembly_ (14.21)
|   |   |   |   |   |   |   start > 288489
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 314456
|   |   |   |   |   |   |   |   |   |   start <= 299226
|   |   |   |   |   |   |   |   |   |   |   start <= 293952:
biological_process_ (16.28)
|   |   |   |   |   |   |   |   |   |   |   start > 293952:
RNA_metabolic_process_ (12.64)
|   |   |   |   |   |   |   |   |   |   start > 299226: translation_
(33.25)
|   |   |   |   |   |   |   |   |   start > 314456:
biological_process_ (35.76)
```

```
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 308850
|   |   |   |   |   |   |   |   |   |   start <= 296074
|   |   |   |   |   |   |   |   |   |   |   start <= 291097:
biological_process_ (8.69)
|   |   |   |   |   |   |   |   |   |   |   start > 291097
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 3849:
response_to_stress_ (15.76/6.28)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 3849:
transport_ (22.49/8.97)
|   |   |   |   |   |   |   |   |   |   start > 296074
|   |   |   |   |   |   |   |   |   |   |   start <= 302562
|   |   |   |   |   |   |   |   |   |   |   |   start <= 299226:
biological_process_ (11.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 299226:
translation_ (8.97)
|   |   |   |   |   |   |   |   |   |   |   start > 302562:
biological_process_ (48.71)
|   |   |   |   |   |   |   |   |   start > 308850
|   |   |   |   |   |   |   |   |   |   start <= 314456
|   |   |   |   |   |   |   |   |   |   |   start <= 309843:
nuclear_organization_and_biogenesis_ (8.25)
|   |   |   |   |   |   |   |   |   |   |   start > 309843:
DNA_metabolic_process_ (18.81/7.31)
|   |   |   |   |   |   |   |   |   |   start > 314456
|   |   |   |   |   |   |   |   |   |   |   start <= 317408
|   |   |   |   |   |   |   |   |   |   |   |   start <= 315598:
biological_process_ (11.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 315598:
transport_ (21.5)
|   |   |   |   |   |   |   |   |   |   |   start > 317408
|   |   |   |   |   |   |   |   |   |   |   |   start <= 322872:
response_to_stress_ (18.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 322872:
biological_process_ (14.41)
|   |   |   |   |   |   start > 325415
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 333613
|   |   |   |   |   |   |   |   |   start <= 327131:
carbohydrate_metabolic_process_ (25.65)
|   |   |   |   |   |   |   |   |   start > 327131
|   |   |   |   |   |   |   |   |   |   start <= 329810:
RNA_metabolic_process_ (15.46)
|   |   |   |   |   |   |   |   |   |   start > 329810:
DNA_metabolic_process_ (22.88)
|   |   |   |   |   |   |   |   start > 333613
|   |   |   |   |   |   |   |   |   start <= 335801
|   |   |   |   |   |   |   |   |   |   start <= 334559:
translation_ (14.22)
|   |   |   |   |   |   |   |   |   |   start > 334559:
cellular_respiration_ (28.01)
|   |   |   |   |   |   |   |   |   start > 335801
|   |   |   |   |   |   |   |   |   |   start <= 338397:
response_to_stress_ (12.48)
```

```
|   |   |   |   |   |   |   |   |   |   start > 338397:
organelle_organization_and_biogenesis_ (17.94)
|   |   |   |   |   |   |   strand = W: transcription_ (19.65)
|   |   |   |   start > 339086
|   |   |   |   |   start <= 361471
|   |   |   |   |   |   start <= 349107
|   |   |   |   |   |   |   start <= 346408
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 340956: cell_cycle_
(21.38)
|   |   |   |   |   |   |   |   |   start > 340956
|   |   |   |   |   |   |   |   |   |   start <= 345264:
biological_process_ (24.42)
|   |   |   |   |   |   |   |   |   |   start > 345264: cell_cycle_
(18.06)
|   |   |   |   |   |   |   |   strand = W:
organelle_organization_and_biogenesis_ (15.24)
|   |   |   |   |   |   |   start > 346408
|   |   |   |   |   |   |   |   start <= 348780:
pseudohyphal_growth_ (29.94/14.7)
|   |   |   |   |   |   |   |   start > 348780: biological_process_
(32.56)
|   |   |   |   |   |   start > 349107
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 356392: cell_budding_
(17.73)
|   |   |   |   |   |   |   |   start > 356392:
cellular_homeostasis_ (12.83)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 356392
|   |   |   |   |   |   |   |   |   start <= 353137:
DNA_metabolic_process_ (12.99)
|   |   |   |   |   |   |   |   |   start > 353137:
pseudohyphal_growth_ (13.72)
|   |   |   |   |   |   |   |   start > 356392
|   |   |   |   |   |   |   |   |   start <= 358119: cell_cycle_
(25.1/9.47)
|   |   |   |   |   |   |   |   |   start > 358119: vesicle-
mediated_transport_ (18.33)
|   |   |   |   |   start > 361471
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 406884
|   |   |   |   |   |   |   |   start <= 391922
|   |   |   |   |   |   |   |   |   start <= 385401
|   |   |   |   |   |   |   |   |   |   start <= 381501:
DNA_metabolic_process_ (14.94)
|   |   |   |   |   |   |   |   |   |   start > 381501:
amino_acid_and_derivative_metabolic_process_ (18.86)
|   |   |   |   |   |   |   |   |   start > 385401
|   |   |   |   |   |   |   |   |   |   start <= 389526:
response_to_stress_ (16.22)
|   |   |   |   |   |   |   |   |   |   start > 389526:
DNA_metabolic_process_ (18.52)
|   |   |   |   |   |   |   |   start > 391922
```

```
|   |   |   |   |   |   |   |   |   start <= 403745
|   |   |   |   |   |   |   |   |   |   start <= 396891
|   |   |   |   |   |   |   |   |   |   |   start <= 393364:
biological_process_ (29.38)
|   |   |   |   |   |   |   |   |   |   |   start > 393364:
cell_cycle_ (12.35)
|   |   |   |   |   |   |   |   |   |   start > 396891
|   |   |   |   |   |   |   |   |   |   |   start <= 398393:
ribosome_biogenesis_and_assembly_ (19.14)
|   |   |   |   |   |   |   |   |   |   |   start > 398393
|   |   |   |   |   |   |   |   |   |   |   |   start <= 402211:
response_to_stress_ (13.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 402211:
biological_process_ (13.29)
|   |   |   |   |   |   |   |   |   start > 403745:
DNA_metabolic_process_ (19.95)
|   |   |   |   |   |   |   start > 406884
|   |   |   |   |   |   |   |   start <= 417953
|   |   |   |   |   |   |   |   |   start <= 408187:
generation_of_precursor_metabolites_and_energy_ (24.43)
|   |   |   |   |   |   |   |   |   start > 408187
|   |   |   |   |   |   |   |   |   |   start <= 416556:
ribosome_biogenesis_and_assembly_ (17.83)
|   |   |   |   |   |   |   |   |   |   start > 416556:
organelle_organization_and_biogenesis_ (15.11)
|   |   |   |   |   |   |   |   start > 417953
|   |   |   |   |   |   |   |   |   start <= 425885
|   |   |   |   |   |   |   |   |   |   start <= 420859:
DNA_metabolic_process_ (16.51)
|   |   |   |   |   |   |   |   |   |   start > 420859:
protein_modification_process_ (20.41)
|   |   |   |   |   |   |   |   |   start > 425885:
biological_process_ (20.45)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 402211
|   |   |   |   |   |   |   |   start <= 365248
|   |   |   |   |   |   |   |   |   start <= 364419
|   |   |   |   |   |   |   |   |   |   start <= 362265:
biological_process_ (13.54)
|   |   |   |   |   |   |   |   |   |   start > 362265:
RNA_metabolic_process_ (32.5/12.04)
|   |   |   |   |   |   |   |   |   start > 364419: transport_
(33.47/16.28)
|   |   |   |   |   |   |   |   start > 365248
|   |   |   |   |   |   |   |   |   start <= 371472
|   |   |   |   |   |   |   |   |   |   start <= 369008:
biological_process_ (18.92)
|   |   |   |   |   |   |   |   |   |   start > 369008:
protein_modification_process_ (30.69)
|   |   |   |   |   |   |   |   |   start > 371472
|   |   |   |   |   |   |   |   |   |   start <= 396891
|   |   |   |   |   |   |   |   |   |   |   start <= 381501
|   |   |   |   |   |   |   |   |   |   |   |   start <= 375099:
biological_process_ (25.59)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 375099:
translation_ (14.58)
|   |   |   |   |   |   |   |   |   |   |   start > 381501
|   |   |   |   |   |   |   |   |   |   |   |   start <= 385401:
transcription_ (13.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 385401:
biological_process_ (29.62)
|   |   |   |   |   |   |   |   |   |   start > 396891:
protein_modification_process_ (11.93)
|   |   |   |   |   |   |   start > 402211
|   |   |   |   |   |   |   |   start <= 408187
|   |   |   |   |   |   |   |   |   start <= 403745:
DNA_metabolic_process_ (19.77)
|   |   |   |   |   |   |   |   |   start > 403745:
amino_acid_and_derivative_metabolic_process_ (24.8/10.0)
|   |   |   |   |   |   |   |   start > 408187
|   |   |   |   |   |   |   |   |   start <= 425885
|   |   |   |   |   |   |   |   |   |   start <= 420859:
RNA_metabolic_process_ (19.44)
|   |   |   |   |   |   |   |   |   |   start > 420859:
ribosome_biogenesis_and_assembly_ (19.73)
|   |   |   |   |   |   |   |   |   start > 425885:
biological_process_ (24.36)
|   |   start > 428945
|   |   |   start <= 618392
|   |   |   |   start <= 547858
|   |   |   |   |   start <= 490611
|   |   |   |   |   |   start <= 458200
|   |   |   |   |   |   |   start <= 450860
|   |   |   |   |   |   |   |   start <= 437135
|   |   |   |   |   |   |   |   |   start <= 430781
|   |   |   |   |   |   |   |   |   |   start <= 430275: vesicle-
mediated_transport_ (26.06/10.14)
|   |   |   |   |   |   |   |   |   |   start > 430275:
ribosome_biogenesis_and_assembly_ (26.7/11.62)
|   |   |   |   |   |   |   |   |   start > 430781
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 435223:
transcription_ (13.68)
|   |   |   |   |   |   |   |   |   |   |   start > 435223:
translation_ (20.49)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 431549:
translation_ (17.77)
|   |   |   |   |   |   |   |   |   |   |   start > 431549:
lipid_metabolic_process_ (14.98)
|   |   |   |   |   |   |   |   start > 437135
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 449810
|   |   |   |   |   |   |   |   |   |   |   start <= 442875
|   |   |   |   |   |   |   |   |   |   |   |   start <= 439028:
biological_process_ (22.09/10.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 439028:
organelle_organization_and_biogenesis_ (7.99)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 442875
|   |   |   |   |   |   |   |   |   |   |   |   start <= 447679:
cell_wall_organization_and_biogenesis_ (22.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 447679:
biological_process_ (7.23)
|   |   |   |   |   |   |   |   |   |   start > 449810: translation_
(17.4)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 442875
|   |   |   |   |   |   |   |   |   |   |   start <= 439028:
vesicle-mediated_transport_ (9.85)
|   |   |   |   |   |   |   |   |   |   |   start > 439028:
RNA_metabolic_process_ (11.12)
|   |   |   |   |   |   |   |   |   |   start > 442875: vesicle-
mediated_transport_ (18.0)
|   |   |   |   |   |   |   start > 450860
|   |   |   |   |   |   |   |   strand = C: lipid_metabolic_process_
(10.9)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 451077:
membrane_organization_and_biogenesis_ (46.97/22.35)
|   |   |   |   |   |   |   |   |   start > 451077
|   |   |   |   |   |   |   |   |   |   start <= 451844: cell_cycle_
(46.84/21.5)
|   |   |   |   |   |   |   |   |   |   start > 451844: translation_
(12.14)
|   |   |   |   |   |   start > 458200
|   |   |   |   |   |   |   start <= 483062
|   |   |   |   |   |   |   |   start <= 475543
|   |   |   |   |   |   |   |   |   start <= 460882:
DNA_metabolic_process_ (11.63)
|   |   |   |   |   |   |   |   |   start > 460882
|   |   |   |   |   |   |   |   |   |   start <= 465714
|   |   |   |   |   |   |   |   |   |   |   start <= 463602:
biological_process_ (18.59)
|   |   |   |   |   |   |   |   |   |   |   start > 463602: vesicle-
mediated_transport_ (18.71)
|   |   |   |   |   |   |   |   |   |   start > 465714:
biological_process_ (71.76)
|   |   |   |   |   |   |   |   start > 475543
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 478877:
cell_wall_organization_and_biogenesis_ (12.71)
|   |   |   |   |   |   |   |   |   |   start > 478877:
RNA_metabolic_process_ (18.83)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 477981:
organelle_organization_and_biogenesis_ (22.63)
|   |   |   |   |   |   |   |   |   |   start > 477981:
biological_process_ (39.1)
|   |   |   |   |   |   |   start > 483062
|   |   |   |   |   |   |   |   start <= 487413
|   |   |   |   |   |   |   |   |   start <= 487015:
ribosome_biogenesis_and_assembly_ (15.18)
```

```
|   |   |   |   |   |   |   |   |   start > 487015: transcription_
(22.08)
|   |   |   |   |   |   |   |   start > 487413: translation_ (37.23)
|   |   |   |   |   start > 490611
|   |   |   |   |   |   start <= 517630
|   |   |   |   |   |   |   start <= 507581
|   |   |   |   |   |   |   |   start <= 499924
|   |   |   |   |   |   |   |   |   strand = C: meiosis_ (14.35)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 491007: vesicle-
mediated_transport_ (23.25/10.73)
|   |   |   |   |   |   |   |   |   |   start > 491007
|   |   |   |   |   |   |   |   |   |   |   start <= 493900:
cell_cycle_ (41.34/14.86)
|   |   |   |   |   |   |   |   |   |   |   start > 493900:
transport_ (17.35)
|   |   |   |   |   |   |   |   start > 499924
|   |   |   |   |   |   |   |   |   start <= 506540
|   |   |   |   |   |   |   |   |   |   start <= 506037: vesicle-
mediated_transport_ (11.67)
|   |   |   |   |   |   |   |   |   |   start > 506037:
transcription_ (13.98)
|   |   |   |   |   |   |   |   |   start > 506540: vesicle-
mediated_transport_ (20.4)
|   |   |   |   |   |   |   start > 507581
|   |   |   |   |   |   |   |   start <= 511439
|   |   |   |   |   |   |   |   |   start <= 510275:
organelle_organization_and_biogenesis_ (29.81/13.48)
|   |   |   |   |   |   |   |   |   start > 510275: cell_cycle_
(29.65/11.99)
|   |   |   |   |   |   |   |   start > 511439
|   |   |   |   |   |   |   |   |   start <= 512801:
DNA_metabolic_process_ (11.4)
|   |   |   |   |   |   |   |   |   start > 512801
|   |   |   |   |   |   |   |   |   |   strand = C: translation_
(9.84)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 514705:
transport_ (6.63)
|   |   |   |   |   |   |   |   |   |   |   start > 514705:
translation_ (8.15)
|   |   |   |   |   |   start > 517630
|   |   |   |   |   |   |   start <= 530588
|   |   |   |   |   |   |   |   start <= 523611
|   |   |   |   |   |   |   |   |   start <= 519169
|   |   |   |   |   |   |   |   |   |   start <= 517840:
biological_process_ (10.06)
|   |   |   |   |   |   |   |   |   |   start > 517840:
organelle_organization_and_biogenesis_ (14.0)
|   |   |   |   |   |   |   |   |   start > 519169:
biological_process_ (52.54)
|   |   |   |   |   |   |   |   start > 523611
|   |   |   |   |   |   |   |   |   start <= 526282
```

```
|   |   |   |   |   |   |   |   |   |   start <= 524716:
cellular_respiration_ (11.53)
|   |   |   |   |   |   |   |   |   |   start > 524716:
cell_budding_ (23.18)
|   |   |   |   |   |   |   |   |   start > 526282
|   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (17.82)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 527457:
cellular_homeostasis_ (15.74)
|   |   |   |   |   |   |   |   |   |   |   start > 527457:
biological_process_ (12.09)
|   |   |   |   |   |   |   start > 530588
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 533106
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: organelle_organization_and_biogenesis_
(1.98/0.69)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: transport_ (6.91/2.95)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: RNA_metabolic_process_ (3.45/1.47)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
RNA_metabolic_process_ (3.03/1.49)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
transport_ (6.26/2.27)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: RNA_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: RNA_metabolic_process_ (2.05/0.77)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: organelle_organization_and_biogenesis_
(5.22/1.76)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
RNA_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: RNA_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: transport_ (4.06/1.89)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: RNA_metabolic_process_ (4.15/2.18)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: RNA_metabolic_process_ (1.11/0.22)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: transport_ (0.46/0.15)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: RNA_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
RNA_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   start > 533106
|   |   |   |   |   |   |   |   |   |   start <= 534923:
lipid_metabolic_process_ (19.5)
|   |   |   |   |   |   |   |   |   |   start > 534923: cell_cycle_
(22.94)
|   |   |   |   |   |   |   |   strand = W: signal_transduction_
(13.34)
|   |   |   |   start > 547858
|   |   |   |   |   start <= 561939
|   |   |   |   |   |   start <= 554629
|   |   |   |   |   |   |   start <= 549090:
ribosome_biogenesis_and_assembly_ (17.95)
|   |   |   |   |   |   |   start > 549090
|   |   |   |   |   |   |   |   start <= 552412
|   |   |   |   |   |   |   |   |   start <= 551299: translation_
(16.37)
|   |   |   |   |   |   |   |   |   start > 551299:
carbohydrate_metabolic_process_ (31.38/15.25)
|   |   |   |   |   |   |   |   start > 552412: translation_ (25.15)
|   |   |   |   |   |   start > 554629
|   |   |   |   |   |   |   start <= 559008
|   |   |   |   |   |   |   |   strand = C:
ribosome_biogenesis_and_assembly_ (37.34/15.4)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 556160:
ribosome_biogenesis_and_assembly_ (19.28)
|   |   |   |   |   |   |   |   |   start > 556160:
protein_modification_process_ (22.32)
|   |   |   |   |   |   |   start > 559008
|   |   |   |   |   |   |   |   start <= 559308: transcription_
(16.31)
|   |   |   |   |   |   |   |   start > 559308: cell_budding_
(14.44)
|   |   |   |   |   start > 561939
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 590037
|   |   |   |   |   |   |   |   start <= 571254
|   |   |   |   |   |   |   |   |   start <= 565534
```

```
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (22.18/10.18)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: transport_
(15.0/5.9)
|   |   |   |   |   |   |   |   |   start > 565534
|   |   |   |   |   |   |   |   |   |   start <= 567560:
response_to_stress_ (21.59)
|   |   |   |   |   |   |   |   |   |   start > 567560
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
vesicle-mediated_transport_ (15.44/5.86)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
transport_ (12.36/3.62)
|   |   |   |   |   |   |   |   start > 571254
|   |   |   |   |   |   |   |   |   start <= 584594
|   |   |   |   |   |   |   |   |   |   start <= 575622:
biological_process_ (18.83)
|   |   |   |   |   |   |   |   |   |   start > 575622
|   |   |   |   |   |   |   |   |   |   |   start <= 578851:
response_to_stress_ (27.84/8.89)
|   |   |   |   |   |   |   |   |   |   |   start > 578851:
biological_process_ (10.14)
|   |   |   |   |   |   |   |   |   start > 584594:
RNA_metabolic_process_ (13.83)
|   |   |   |   |   |   |   start > 590037
|   |   |   |   |   |   |   |   start <= 596464
|   |   |   |   |   |   |   |   |   start <= 592467:
ribosome_biogenesis_and_assembly_ (18.99)
|   |   |   |   |   |   |   |   |   start > 592467: cell_cycle_
(12.0)
|   |   |   |   |   |   |   |   start > 596464
|   |   |   |   |   |   |   |   |   start <= 603874
|   |   |   |   |   |   |   |   |   |   start <= 599499:
translation_ (45.2)
|   |   |   |   |   |   |   |   |   |   start > 599499:
protein_catabolic_process_ (24.5)
|   |   |   |   |   |   |   |   |   start > 603874
|   |   |   |   |   |   |   |   |   |   start <= 608588
|   |   |   |   |   |   |   |   |   |   |   start <= 605060:
vesicle-mediated_transport_ (18.05)
|   |   |   |   |   |   |   |   |   |   |   start > 605060:
lipid_metabolic_process_ (11.88)
|   |   |   |   |   |   |   |   |   |   start > 608588
|   |   |   |   |   |   |   |   |   |   |   start <= 615372:
ribosome_biogenesis_and_assembly_ (19.03)
|   |   |   |   |   |   |   |   |   |   |   start > 615372
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
ribosome_biogenesis_and_assembly_ (19.02/8.16)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
translation_ (14.67/4.53)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 581925
|   |   |   |   |   |   |   |   start <= 575622
|   |   |   |   |   |   |   |   |   start <= 567560
```

```
|   |   |   |   |   |   |   |   |   |   start <= 562189:
biological_process_ (16.0)
|   |   |   |   |   |   |   |   |   |   start > 562189:
lipid_metabolic_process_ (24.04)
|   |   |   |   |   |   |   |   |   start > 567560
|   |   |   |   |   |   |   |   |   |   start <= 571254:
amino_acid_and_derivative_metabolic_process_ (10.58)
|   |   |   |   |   |   |   |   |   |   start > 571254:
biological_process_ (16.03)
|   |   |   |   |   |   |   |   start > 575622
|   |   |   |   |   |   |   |   |   start <= 578851
|   |   |   |   |   |   |   |   |   |   start <= 578607:
translation_ (13.23)
|   |   |   |   |   |   |   |   |   |   start > 578607:
biological_process_ (9.15)
|   |   |   |   |   |   |   |   |   start > 578851:
cell_wall_organization_and_biogenesis_ (15.1)
|   |   |   |   |   |   |   start > 581925
|   |   |   |   |   |   |   |   start <= 611167
|   |   |   |   |   |   |   |   |   start <= 584594
|   |   |   |   |   |   |   |   |   |   start <= 583295:
biological_process_ (12.25)
|   |   |   |   |   |   |   |   |   |   start > 583295: transport_
(17.83)
|   |   |   |   |   |   |   |   |   start > 584594
|   |   |   |   |   |   |   |   |   |   start <= 592467
|   |   |   |   |   |   |   |   |   |   |   start <= 590037:
biological_process_ (27.71)
|   |   |   |   |   |   |   |   |   |   |   start > 590037:
DNA_metabolic_process_ (13.58)
|   |   |   |   |   |   |   |   |   |   start > 592467
|   |   |   |   |   |   |   |   |   |   |   start <= 603874:
RNA_metabolic_process_ (24.68)
|   |   |   |   |   |   |   |   |   |   |   start > 603874:
biological_process_ (37.54)
|   |   |   |   |   |   |   |   start > 611167: transport_ (27.39)
|   |   |   start > 618392
|   |   |   |   start <= 640106
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 635489: biological_process_ (15.38)
|   |   |   |   |   |   start > 635489:
cell_wall_organization_and_biogenesis_ (19.42)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 630790
|   |   |   |   |   |   |   start <= 625506: transcription_
(39.63/8.72)
|   |   |   |   |   |   |   start > 625506
|   |   |   |   |   |   |   |   start <= 626435: biological_process_
(16.46)
|   |   |   |   |   |   |   |   start > 626435:
carbohydrate_metabolic_process_ (23.02)
|   |   |   |   |   |   start > 630790
|   |   |   |   |   |   |   start <= 635489: DNA_metabolic_process_
(82.0/54.55)
```

```
|   |   |   |   |   |   |   start > 635489: transcription_ (12.99)
|   |   |   |   start > 640106
|   |   |   |   |   start <= 645994: biological_process_ (21.52)
|   |   |   |   |   start > 645994
|   |   |   |   |   |   strand = C: biological_process_ (10.81)
|   |   |   |   |   |   strand = W: transport_ (41.78)
```

Decision Tree Generated for Chromosome Twelve:
For Cellular Component

```
|   start <= 66517
|   |   start <= 36360
|   |   |   start <= 28305
|   |   |   |   strand = C
|   |   |   |   |   start <= 17956
|   |   |   |   |   |   start <= 16072: cellular_component_ (37.2)
|   |   |   |   |   |   start > 16072: cytoplasm_ (12.54)
|   |   |   |   |   start > 17956
|   |   |   |   |   |   start <= 23569: mitochondrion_ (13.08)
|   |   |   |   |   |   start > 23569: cellular_component_ (48.21)
|   |   |   |   strand = W
|   |   |   |   |   start <= 17956
|   |   |   |   |   |   start <= 9836: cellular_component_ (4.09)
|   |   |   |   |   |   start > 9836: plasma_membrane_ (8.44)
|   |   |   |   |   start > 17956: cellular_component_ (10.21)
|   |   |   start > 28305
|   |   |   |   strand = C
|   |   |   |   |   start <= 35203: plasma_membrane_ (19.36)
|   |   |   |   |   start > 35203
|   |   |   |   |   |   start <= 35960: cellular_component_ (17.62)
|   |   |   |   |   |   start > 35960: plasma_membrane_ (18.85)
|   |   |   |   strand = W: endoplasmic_reticulum_ (11.26)
|   |   start > 36360
|   |   |   strand = C
|   |   |   |   start <= 46264
|   |   |   |   |   start <= 39470: membrane_ (39.16/19.19)
|   |   |   |   |   start > 39470
|   |   |   |   |   |   start <= 40665
|   |   |   |   |   |   |   neigh_num <= 1: cytoskeleton_
(14.07/3.3)
|   |   |   |   |   |   |   neigh_num > 1: cell_cortex_ (19.1/8.44)
|   |   |   |   |   |   start > 40665: vacuole_ (8.77)
|   |   |   |   start > 46264
|   |   |   |   |   start <= 65206
|   |   |   |   |   |   start <= 52589
|   |   |   |   |   |   |   start <= 47462: cytoplasm_ (14.94)
|   |   |   |   |   |   |   start > 47462
|   |   |   |   |   |   |   |   start <= 49937: ribosome_ (8.52)
|   |   |   |   |   |   |   |   start > 49937: cytoplasm_ (9.62)
|   |   |   |   |   |   start > 52589
|   |   |   |   |   |   |   start <= 63644: mitochondrion_ (39.93)
|   |   |   |   |   |   |   start > 63644: cytoplasm_ (24.4)
|   |   |   |   |   start > 65206: cytoskeleton_ (39.03/12.66)
|   |   |   strand = W
```

```
|   |   |   |   start <= 40665: cellular_component_ (14.41)
|   |   |   |   start > 40665
|   |   |   |   |   distance <= 1943: plasma_membrane_ (7.85/2.98)
|   |   |   |   |   distance > 1943: cytoplasm_ (12.42/2.93)
|   start > 66517
|   |   start <= 490407
|   |   |   start <= 454697
|   |   |   |   start <= 167801
|   |   |   |   |   start <= 140545
|   |   |   |   |   |   start <= 100946
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 73408: nucleus_
(85.29/45.62)
|   |   |   |   |   |   |   |   start > 73408
|   |   |   |   |   |   |   |   |   start <= 98835
|   |   |   |   |   |   |   |   |   |   start <= 97484
|   |   |   |   |   |   |   |   |   |   |   start <= 76746:
cytoplasm_ (36.6/16.12)
|   |   |   |   |   |   |   |   |   |   |   start > 76746
|   |   |   |   |   |   |   |   |   |   |   |   start <= 88622:
endoplasmic_reticulum_ (9.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 88622:
cytoplasm_ (23.66/11.15)
|   |   |   |   |   |   |   |   |   |   start > 97484:
endoplasmic_reticulum_ (36.11/16.18)
|   |   |   |   |   |   |   |   |   start > 98835: nucleus_ (13.81)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 76746: cellular_component_
(41.66)
|   |   |   |   |   |   |   |   start > 76746
|   |   |   |   |   |   |   |   |   start <= 92547
|   |   |   |   |   |   |   |   |   |   start <= 84803
|   |   |   |   |   |   |   |   |   |   |   start <= 81460:
cytoplasm_ (17.9)
|   |   |   |   |   |   |   |   |   |   |   start > 81460:
cellular_bud_ (42.82/19.51)
|   |   |   |   |   |   |   |   |   |   start > 84803
|   |   |   |   |   |   |   |   |   |   |   start <= 87402:
mitochondrion_ (16.91)
|   |   |   |   |   |   |   |   |   |   |   start > 87402
|   |   |   |   |   |   |   |   |   |   |   |   start <= 88622
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: cytoplasm_ (10.84/3.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: nucleus_ (12.54/4.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 88622:
cytoplasm_ (16.8)
|   |   |   |   |   |   |   |   |   start > 92547
|   |   |   |   |   |   |   |   |   |   start <= 97484:
cellular_component_ (12.81)
|   |   |   |   |   |   |   |   |   |   start > 97484:
site_of_polarized_growth_ (19.83/6.56)
|   |   |   |   |   |   start > 100946
|   |   |   |   |   |   |   start <= 125533
```

```
|   |   |   |   |   |   |   |   start <= 108971
|   |   |   |   |   |   |   |   |   start <= 107898:
cellular_component_ (14.72)
|   |   |   |   |   |   |   |   |   start > 107898:
mitochondrial_envelope_ (11.72)
|   |   |   |   |   |   |   |   start > 108971
|   |   |   |   |   |   |   |   |   start <= 116431
|   |   |   |   |   |   |   |   |   |   start <= 111574: cytoplasm_
(13.07)
|   |   |   |   |   |   |   |   |   |   start > 111574: vacuole_
(22.22/10.38)
|   |   |   |   |   |   |   |   |   start > 116431
|   |   |   |   |   |   |   |   |   |   start <= 121321:
endoplasmic_reticulum_ (18.94)
|   |   |   |   |   |   |   |   |   |   start > 121321: cytoplasm_
(22.04)
|   |   |   |   |   |   |   start > 125533
|   |   |   |   |   |   |   |   start <= 131728
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 130612:
plasma_membrane_ (15.12)
|   |   |   |   |   |   |   |   |   |   start > 130612:
mitochondrion_ (12.49)
|   |   |   |   |   |   |   |   |   strand = W: nucleolus_ (28.12)
|   |   |   |   |   |   |   |   start > 131728
|   |   |   |   |   |   |   |   |   start <= 136298: cytoplasm_
(19.17)
|   |   |   |   |   |   |   |   |   start > 136298
|   |   |   |   |   |   |   |   |   |   strand = C:
cellular_component_ (14.86)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 136344:
cellular_component_ (13.3)
|   |   |   |   |   |   |   |   |   |   |   start > 136344:
mitochondrion_ (20.46)
|   |   |   |   |   start > 140545
|   |   |   |   |   |   start <= 143200
|   |   |   |   |   |   |   start <= 141072
|   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   neigh_num <= 1: chromosome_
(8.17/2.9)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_component_ (24.0/14.02)
|   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(27.35/15.91)
|   |   |   |   |   |   |   start > 141072
|   |   |   |   |   |   |   |   neigh_num <= 1: cytoskeleton_
(5.85/2.26)
|   |   |   |   |   |   |   |   neigh_num > 1:
microtubule_organizing_center_ (22.66/8.95)
|   |   |   |   |   |   start > 143200
|   |   |   |   |   |   |   start <= 166536
|   |   |   |   |   |   |   |   start <= 153976
```

```
|   |   |   |   |   |   |   |   |   start <= 146290: nucleus_
(12.03)
|   |   |   |   |   |   |   |   |   start > 146290: mitochondrion_
(28.97)
|   |   |   |   |   |   |   |   start > 153976
|   |   |   |   |   |   |   |   |   start <= 164391
|   |   |   |   |   |   |   |   |   |   start <= 159504
|   |   |   |   |   |   |   |   |   |   |   start <= 157729
|   |   |   |   |   |   |   |   |   |   |   |   start <= 156333
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
5852: nucleolus_ (7.56/2.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
5852: nucleus_ (2.55/0.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
969: nucleus_ (2.84/0.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
969: nucleolus_ (14.55/2.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 156333:
nucleus_ (12.29)
|   |   |   |   |   |   |   |   |   |   |   start > 157729:
endoplasmic_reticulum_ (20.95)
|   |   |   |   |   |   |   |   |   |   start > 159504
|   |   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(21.68)
|   |   |   |   |   |   |   |   |   |   |   strand = W: nucleus_
(30.28)
|   |   |   |   |   |   |   |   |   start > 164391
|   |   |   |   |   |   |   |   |   |   start <= 166082:
mitochondrion_ (12.55)
|   |   |   |   |   |   |   |   |   |   start > 166082: nucleolus_
(17.54)
|   |   |   |   |   |   |   start > 166536: nucleus_ (41.29/16.82)
|   |   |   |   start > 167801
|   |   |   |   |   start <= 267170
|   |   |   |   |   |   start <= 184925
|   |   |   |   |   |   |   start <= 179605
|   |   |   |   |   |   |   |   start <= 177607
|   |   |   |   |   |   |   |   |   start <= 175226
|   |   |   |   |   |   |   |   |   |   start <= 169102
|   |   |   |   |   |   |   |   |   |   |   start <= 168024:
cytoplasm_ (11.24)
|   |   |   |   |   |   |   |   |   |   |   start > 168024: nucleus_
(29.67/13.85)
|   |   |   |   |   |   |   |   |   |   start > 169102
|   |   |   |   |   |   |   |   |   |   |   start <= 170280:
cellular_component_ (17.27)
|   |   |   |   |   |   |   |   |   |   |   start > 170280
|   |   |   |   |   |   |   |   |   |   |   |   start <= 174981:
nucleus_ (35.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 174981:
cellular_component_ (29.92/14.03)
```

```
|   |   |   |   |   |   |   |   |   start > 175226: cytoplasm_
(52.41/13.39)
|   |   |   |   |   |   |   |   start > 177607
|   |   |   |   |   |   |   |   |   neigh_num <= 1: membrane_
(20.0/10.48)
|   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(23.95/13.73)
|   |   |   |   |   |   |   start > 179605
|   |   |   |   |   |   |   |   start <= 183404: plasma_membrane_
(45.96)
|   |   |   |   |   |   |   |   start > 183404
|   |   |   |   |   |   |   |   |   start <= 183622:
cellular_component_ (15.82)
|   |   |   |   |   |   |   |   |   start > 183622: nucleus_
(39.25/18.11)
|   |   |   |   |   |   start > 184925
|   |   |   |   |   |   |   start <= 201316
|   |   |   |   |   |   |   |   start <= 187128
|   |   |   |   |   |   |   |   |   neigh_num <= 1: membrane_
(7.95/1.75)
|   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   distance <= 3272:
endoplasmic_reticulum_ (17.41/6.0)
|   |   |   |   |   |   |   |   |   |   distance > 3272: membrane_
(11.13/3.33)
|   |   |   |   |   |   |   |   start > 187128
|   |   |   |   |   |   |   |   |   start <= 198086
|   |   |   |   |   |   |   |   |   |   start <= 194453: cytoplasm_
(39.1)
|   |   |   |   |   |   |   |   |   |   start > 194453
|   |   |   |   |   |   |   |   |   |   |   start <= 196473:
Golgi_apparatus_ (20.41)
|   |   |   |   |   |   |   |   |   |   |   start > 196473:
cytoplasm_ (26.08/9.59)
|   |   |   |   |   |   |   |   |   start > 198086
|   |   |   |   |   |   |   |   |   |   start <= 198785: nucleolus_
(19.71)
|   |   |   |   |   |   |   |   |   |   start > 198785: cytoplasm_
(15.84)
|   |   |   |   |   |   |   start > 201316
|   |   |   |   |   |   |   |   start <= 237704
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 211934
|   |   |   |   |   |   |   |   |   |   |   start <= 204992:
ribosome_ (12.71)
|   |   |   |   |   |   |   |   |   |   |   start > 204992:
membrane_ (33.31/15.91)
|   |   |   |   |   |   |   |   |   |   start > 211934
|   |   |   |   |   |   |   |   |   |   |   start <= 230452
|   |   |   |   |   |   |   |   |   |   |   |   start <= 222133
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 214457:
nucleus_ (16.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 214457
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
214956: cytoplasm_ (14.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
214956: cellular_component_ (13.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 222133
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 228597
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
223060: cell_wall_ (10.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
223060
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
225173: mitochondrion_ (9.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
225173: nucleus_ (10.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 228597:
cell_wall_ (26.93)
|   |   |   |   |   |   |   |   |   |   |   start > 230452
|   |   |   |   |   |   |   |   |   |   |   |   start <= 234082:
cytoplasm_ (68.28/22.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 234082:
cell_cortex_ (16.53)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 204226:
cellular_component_ (40.57)
|   |   |   |   |   |   |   |   |   |   start > 204226
|   |   |   |   |   |   |   |   |   |   |   start <= 204992:
chromosome_ (37.8/16.91)
|   |   |   |   |   |   |   |   |   |   |   start > 204992: nucleus_
(35.88/10.12)
|   |   |   |   |   |   |   |   start > 237704
|   |   |   |   |   |   |   |   |   start <= 242233
|   |   |   |   |   |   |   |   |   |   strand = C: membrane_
(48.79)
|   |   |   |   |   |   |   |   |   |   strand = W: ribosome_ (9.46)
|   |   |   |   |   |   |   |   |   start > 242233
|   |   |   |   |   |   |   |   |   |   start <= 255307
|   |   |   |   |   |   |   |   |   |   |   start <= 247202
|   |   |   |   |   |   |   |   |   |   |   |   start <= 246073
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 245173:
cellular_component_ (17.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 245173:
endoplasmic_reticulum_ (14.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 246073:
nucleus_ (55.62/11.07)
|   |   |   |   |   |   |   |   |   |   |   start > 247202
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 248427:
cellular_component_ (12.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 248427
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
250979: cytoplasm_ (20.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
250979: nucleus_ (12.57)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 253862:
endoplasmic_reticulum_ (15.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 253862:
cellular_component_ (23.36)
|   |   |   |   |   |   |   |   |   |   start > 255307
|   |   |   |   |   |   |   |   |   |   |   start <= 264158
|   |   |   |   |   |   |   |   |   |   |   |   start <= 260980
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 259402:
cytoplasm_ (23.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 259402
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
260548: mitochondrion_ (14.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
260548: cytoplasm_ (13.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 260980
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 263195:
ribosome_ (11.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 263195:
cytoplasm_ (11.24)
|   |   |   |   |   |   |   |   |   |   |   start > 264158
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cellular_component_ (12.59)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
endoplasmic_reticulum_ (53.48/20.54)
|   |   |   |   |   start > 267170
|   |   |   |   |   |   start <= 322298
|   |   |   |   |   |   |   start <= 278627
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 273916: mitochondrion_
(29.58)
|   |   |   |   |   |   |   |   |   start > 273916:
cellular_component_ (47.12/13.13)
|   |   |   |   |   |   |   |   strand = W: nucleolus_ (42.42/20.72)
|   |   |   |   |   |   |   start > 278627
|   |   |   |   |   |   |   |   start <= 301990
|   |   |   |   |   |   |   |   |   start <= 293573
|   |   |   |   |   |   |   |   |   |   start <= 283873
|   |   |   |   |   |   |   |   |   |   |   start <= 281622:
cytoplasm_ (33.46)
|   |   |   |   |   |   |   |   |   |   |   start > 281622
|   |   |   |   |   |   |   |   |   |   |   |   strand = C: nucleus_
(12.63)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 282928:
ribosome_ (10.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 282928:
mitochondrion_ (14.41)
|   |   |   |   |   |   |   |   |   |   start > 283873
|   |   |   |   |   |   |   |   |   |   |   start <= 286560:
endomembrane_system_ (25.2/13.05)
|   |   |   |   |   |   |   |   |   |   |   start > 286560
|   |   |   |   |   |   |   |   |   |   |   |   start <= 287917
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 286821:
cytoplasm_ (27.08/8.9)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 286821:
endomembrane_system_ (16.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 287917
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 290213:
plasma_membrane_ (16.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 290213:
nucleus_ (24.38/10.94)
|   |   |   |   |   |   |   |   |   start > 293573
|   |   |   |   |   |   |   |   |   |   start <= 300252
|   |   |   |   |   |   |   |   |   |   |   start <= 296095:
cytoplasm_ (23.79)
|   |   |   |   |   |   |   |   |   |   |   start > 296095:
membrane_ (33.09/13.46)
|   |   |   |   |   |   |   |   |   |   start > 300252: cytoplasm_
(25.21)
|   |   |   |   |   |   |   |   start > 301990
|   |   |   |   |   |   |   |   |   start <= 302244: nucleus_
(41.41/17.24)
|   |   |   |   |   |   |   |   |   start > 302244
|   |   |   |   |   |   |   |   |   |   start <= 316108
|   |   |   |   |   |   |   |   |   |   |   start <= 315732:
mitochondrion_ (23.27)
|   |   |   |   |   |   |   |   |   |   |   start > 315732:
membrane_ (28.71/13.95)
|   |   |   |   |   |   |   |   |   |   start > 316108:
mitochondrion_ (81.51/10.01)
|   |   |   |   |   |   start > 322298
|   |   |   |   |   |   |   start <= 346586
|   |   |   |   |   |   |   |   start <= 327416
|   |   |   |   |   |   |   |   |   start <= 323545:
plasma_membrane_ (22.02)
|   |   |   |   |   |   |   |   |   start > 323545: vacuole_
(29.43/12.12)
|   |   |   |   |   |   |   |   start > 327416
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 329239
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cytoplasm_ (9.96/3.77)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (4.77/0.69)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (17.47/5.86)
|   |   |   |   |   |   |   |   |   |   start > 329239
|   |   |   |   |   |   |   |   |   |   |   start <= 341811
|   |   |   |   |   |   |   |   |   |   |   |   start <= 339474
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 337266:
cellular_component_ (39.35/8.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 337266:
nucleus_ (16.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 339474:
cellular_component_ (15.71)
|   |   |   |   |   |   |   |   |   |   |   start > 341811: nucleus_
(35.1)
```

```
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 332591:
plasma_membrane_ (14.17)
|   |   |   |   |   |   |   |   |   |   start > 332591
|   |   |   |   |   |   |   |   |   |   |   start <= 341326:
cellular_component_ (21.85)
|   |   |   |   |   |   |   |   |   |   |   start > 341326
|   |   |   |   |   |   |   |   |   |   |   |   start <= 343768:
endoplasmic_reticulum_ (15.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 343768:
cellular_component_ (17.8)
|   |   |   |   |   |   |   start > 346586
|   |   |   |   |   |   |   |   start <= 388221
|   |   |   |   |   |   |   |   |   start <= 363739
|   |   |   |   |   |   |   |   |   |   start <= 348511
|   |   |   |   |   |   |   |   |   |   |   start <= 348181:
mitochondrion_ (17.11)
|   |   |   |   |   |   |   |   |   |   |   start > 348181:
nucleolus_ (13.87)
|   |   |   |   |   |   |   |   |   |   start > 348511
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
mitochondrion_ (17.64/6.4)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nucleus_ (13.86/4.13)
|   |   |   |   |   |   |   |   |   start > 363739
|   |   |   |   |   |   |   |   |   |   start <= 385409
|   |   |   |   |   |   |   |   |   |   |   start <= 377239
|   |   |   |   |   |   |   |   |   |   |   |   start <= 368125:
nucleus_ (70.2/16.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 368125
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 370099
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
368782: cytoplasm_ (19.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
368782: cell_wall_ (22.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 370099:
cytoplasm_ (64.71/11.05)
|   |   |   |   |   |   |   |   |   |   |   start > 377239
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 384535:
chromosome_ (15.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 384535
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: cytoplasm_ (22.44/6.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: nucleus_ (14.64/2.24)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W: nucleus_
(56.51/17.03)
|   |   |   |   |   |   |   |   |   |   start > 385409
|   |   |   |   |   |   |   |   |   |   |   start <= 385535
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cytoplasm_ (10.15/3.87)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
membrane_ (25.45/8.65)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 385535:
cell_wall_ (13.12)
|   |   |   |   |   |   |   |   start > 388221
|   |   |   |   |   |   |   |   |   start <= 433726
|   |   |   |   |   |   |   |   |   |   start <= 404063
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 395521
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 390271:
plasma_membrane_ (19.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 390271:
cytoplasm_ (12.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 395521
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 399658:
nucleus_ (12.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 399658:
plasma_membrane_ (21.37)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 398531:
cellular_component_ (22.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 398531:
nucleolus_ (15.27)
|   |   |   |   |   |   |   |   |   |   start > 404063
|   |   |   |   |   |   |   |   |   |   |   start <= 416659
|   |   |   |   |   |   |   |   |   |   |   |   start <= 408156:
nucleus_ (63.03/30.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 408156
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 408446:
cytoplasm_ (16.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 408446
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasm_ (34.74/15.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
nucleus_ (61.29/25.11)
|   |   |   |   |   |   |   |   |   |   |   start > 416659
|   |   |   |   |   |   |   |   |   |   |   |   start <= 425187
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 418438
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
417007: cellular_component_ (12.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
417007: plasma_membrane_ (14.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 418438
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (18.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
423684: nucleolus_ (14.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
423684: mitochondrion_ (17.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 425187
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
432169: cellular_component_ (14.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
432169: cytoplasm_ (13.7)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
427330: cytoplasm_ (34.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
427330
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 1553
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C: nucleus_ (8.14/3.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F: nucleolus_ (13.96/5.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P: nucleus_ (5.12/1.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 1553: cytoplasm_ (32.83/14.76)
|   |   |   |   |   |   |   |   |   start > 433726
|   |   |   |   |   |   |   |   |   |   start <= 439824
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 434642:
nucleus_ (19.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 434642:
cellular_component_ (20.13)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 433871:
cellular_component_ (21.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 433871
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: membrane_ (16.11/4.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: vacuole_ (17.18/3.69)
|   |   |   |   |   |   |   |   |   |   start > 439824
|   |   |   |   |   |   |   |   |   |   |   start <= 444689
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 442738:
peroxisome_ (6.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 442738:
cellular_component_ (15.41)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cytoplasm_ (19.12)
|   |   |   |   |   |   |   |   |   |   |   start > 444689
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 448315
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
447576: nucleus_ (9.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
447576
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: cytoplasm_ (22.16/7.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: nucleus_ (16.8/5.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 448315:
cytoplasm_ (14.69)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
mitochondrion_ (9.62)
```

```
|   |   |   start > 454697
|   |   |   |   start <= 470406
|   |   |   |   |   start <= 468959
|   |   |   |   |   |   start <= 468814
|   |   |   |   |   |   |   stop <= 460924: ribosome_ (47.06)
|   |   |   |   |   |   |   stop > 460924
|   |   |   |   |   |   |   |   start <= 462672: cellular_component_
(14.32)
|   |   |   |   |   |   |   |   start > 462672: ribosome_ (26.13)
|   |   |   |   |   |   start > 468814: cellular_component_ (18.9)
|   |   |   |   |   start > 468959: endoplasmic_reticulum_ (24.49)
|   |   |   |   start > 470406
|   |   |   |   |   strand = C: cellular_component_ (102.5)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 472114: cellular_component_ (24.32)
|   |   |   |   |   |   start > 472114
|   |   |   |   |   |   |   start <= 474058: ribosome_ (18.47)
|   |   |   |   |   |   |   start > 474058
|   |   |   |   |   |   |   |   start <= 481874: cellular_component_
(24.56)
|   |   |   |   |   |   |   |   start > 481874
|   |   |   |   |   |   |   |   |   start <= 483638: ribosome_
(20.22)
|   |   |   |   |   |   |   |   |   start > 483638
|   |   |   |   |   |   |   |   |   |   start <= 489350
|   |   |   |   |   |   |   |   |   |   |   start <= 485346:
cellular_component_ (17.25)
|   |   |   |   |   |   |   |   |   |   |   start > 485346
|   |   |   |   |   |   |   |   |   |   |   |   start <= 488998
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 487290:
ribosome_ (14.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 487290:
cellular_component_ (14.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 488998:
ribosome_ (15.48)
|   |   |   |   |   |   |   |   |   |   start > 489350:
cellular_component_ (18.12)
|   |   start > 490407
|   |   |   start <= 756995
|   |   |   |   start <= 552272
|   |   |   |   |   start <= 502423
|   |   |   |   |   |   start <= 498046
|   |   |   |   |   |   |   start <= 495260: mitochondrion_ (60.44)
|   |   |   |   |   |   |   start > 495260: cell_cortex_ (18.92)
|   |   |   |   |   |   start > 498046
|   |   |   |   |   |   |   start <= 502164
|   |   |   |   |   |   |   |   start <= 500272
|   |   |   |   |   |   |   |   |   start <= 498949: cytoplasm_
(13.64)
|   |   |   |   |   |   |   |   |   start > 498949: mitochondrion_
(9.89)
|   |   |   |   |   |   |   |   start > 500272
|   |   |   |   |   |   |   |   |   start <= 501051:
Golgi_apparatus_ (17.34)
```

```
|   |   |   |   |   |   |   |   |   start > 501051: cytoplasm_
(19.18)
|   |   |   |   |   |   |   start > 502164: cellular_component_
(14.14)
|   |   |   |   |   start > 502423
|   |   |   |   |   |   start <= 523634
|   |   |   |   |   |   |   start <= 522014
|   |   |   |   |   |   |   |   start <= 506136
|   |   |   |   |   |   |   |   |   start <= 504593: cytoplasm_
(17.9)
|   |   |   |   |   |   |   |   |   start > 504593: nucleolus_
(17.16)
|   |   |   |   |   |   |   |   start > 506136
|   |   |   |   |   |   |   |   |   start <= 515264: cytoplasm_
(106.65/25.87)
|   |   |   |   |   |   |   |   |   start > 515264
|   |   |   |   |   |   |   |   |   |   start <= 517672:
membrane_fraction_ (19.48)
|   |   |   |   |   |   |   |   |   |   start > 517672: cytoplasm_
(72.85/32.18)
|   |   |   |   |   |   |   start > 522014
|   |   |   |   |   |   |   |   start <= 522665: ribosome_ (18.98)
|   |   |   |   |   |   |   |   start > 522665: cytoplasm_
(40.76/24.53)
|   |   |   |   |   |   start > 523634
|   |   |   |   |   |   |   start <= 537274
|   |   |   |   |   |   |   |   start <= 535216
|   |   |   |   |   |   |   |   |   strand = C: cytoplasm_ (16.9)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 524867:
cellular_bud_ (42.02/19.47)
|   |   |   |   |   |   |   |   |   |   start > 524867
|   |   |   |   |   |   |   |   |   |   |   start <= 528302:
mitochondrion_ (24.99)
|   |   |   |   |   |   |   |   |   |   |   start > 528302:
cellular_bud_ (33.07/12.33)
|   |   |   |   |   |   |   |   start > 535216: peroxisome_ (11.52)
|   |   |   |   |   |   |   start > 537274
|   |   |   |   |   |   |   |   start <= 549014
|   |   |   |   |   |   |   |   |   start <= 541575
|   |   |   |   |   |   |   |   |   |   start <= 539591: cytoplasm_
(19.95)
|   |   |   |   |   |   |   |   |   |   start > 539591
|   |   |   |   |   |   |   |   |   |   |   start <= 540538:
mitochondrion_ (17.65)
|   |   |   |   |   |   |   |   |   |   |   start > 540538:
cell_wall_ (13.82)
|   |   |   |   |   |   |   |   |   start > 541575
|   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(29.77)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 546099
|   |   |   |   |   |   |   |   |   |   |   |   start <= 543970
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: cytoplasm_ (35.15/17.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: nucleolus_ (19.18/11.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 543970:
nucleus_ (26.95/13.2)
|   |   |   |   |   |   |   |   |   |   |   start > 546099:
cytoplasm_ (14.38)
|   |   |   |   |   |   |   |   start > 549014: mitochondrion_
(46.99)
|   |   |   |   start > 552272
|   |   |   |   |   start <= 556790
|   |   |   |   |   |   start <= 554580
|   |   |   |   |   |   |   start <= 553679: membrane_ (41.86/16.29)
|   |   |   |   |   |   |   start > 553679
|   |   |   |   |   |   |   |   distance <= 2419: cell_cortex_
(18.67/4.85)
|   |   |   |   |   |   |   |   distance > 2419: cytoskeleton_
(20.15/8.93)
|   |   |   |   |   |   start > 554580: endoplasmic_reticulum_
(87.36/49.68)
|   |   |   |   |   start > 556790
|   |   |   |   |   |   start <= 612369
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 568569
|   |   |   |   |   |   |   |   |   start <= 564533
|   |   |   |   |   |   |   |   |   |   start <= 562010:
cellular_component_ (18.04)
|   |   |   |   |   |   |   |   |   |   start > 562010: cytoplasm_
(14.17)
|   |   |   |   |   |   |   |   |   start > 564533
|   |   |   |   |   |   |   |   |   |   start <= 566283:
microtubule_organizing_center_ (28.36/9.19)
|   |   |   |   |   |   |   |   |   |   start > 566283: cell_wall_
(18.18)
|   |   |   |   |   |   |   |   start > 568569
|   |   |   |   |   |   |   |   |   start <= 589356
|   |   |   |   |   |   |   |   |   |   start <= 574153: cytoplasm_
(57.54/11.86)
|   |   |   |   |   |   |   |   |   |   start > 574153
|   |   |   |   |   |   |   |   |   |   |   start <= 586466:
nucleolus_ (75.42/14.36)
|   |   |   |   |   |   |   |   |   |   |   start > 586466:
cytoplasm_ (21.76)
|   |   |   |   |   |   |   |   |   start > 589356
|   |   |   |   |   |   |   |   |   |   start <= 592045:
microtubule_organizing_center_ (17.6)
|   |   |   |   |   |   |   |   |   |   start > 592045
|   |   |   |   |   |   |   |   |   |   |   start <= 604789
|   |   |   |   |   |   |   |   |   |   |   |   start <= 602465
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 592621:
cytoplasm_ (12.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 592621:
nucleus_ (6.53)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 602465:
plasma_membrane_ (15.76)
|   |   |   |   |   |   |   |   |   |   |   start > 604789
|   |   |   |   |   |   |   |   |   |   |   |   start <= 605434:
cytoplasm_ (7.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 605434:
nucleus_ (60.55/28.48)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 564533
|   |   |   |   |   |   |   |   |   start <= 559553: cytoplasm_
(26.75)
|   |   |   |   |   |   |   |   |   start > 559553
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(17.41/6.98)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(15.81/5.39)
|   |   |   |   |   |   |   |   start > 564533
|   |   |   |   |   |   |   |   |   start <= 586466
|   |   |   |   |   |   |   |   |   |   start <= 568569:
membrane_fraction_ (38.29/12.52)
|   |   |   |   |   |   |   |   |   |   start > 568569
|   |   |   |   |   |   |   |   |   |   |   start <= 579026
|   |   |   |   |   |   |   |   |   |   |   |   start <= 574153:
cellular_component_ (16.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 574153:
membrane_fraction_ (39.62/15.06)
|   |   |   |   |   |   |   |   |   |   |   start > 579026:
cellular_component_ (18.45)
|   |   |   |   |   |   |   |   |   start > 586466
|   |   |   |   |   |   |   |   |   |   start <= 609785: nucleus_
(30.07)
|   |   |   |   |   |   |   |   |   |   start > 609785:
plasma_membrane_ (21.01)
|   |   |   |   |   |   start > 612369
|   |   |   |   |   |   |   start <= 714906
|   |   |   |   |   |   |   |   start <= 624205
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 620475:
mitochondrion_ (20.62)
|   |   |   |   |   |   |   |   |   |   start > 620475:
endoplasmic_reticulum_ (49.39/20.81)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 617535
|   |   |   |   |   |   |   |   |   |   |   start <= 614757:
endoplasmic_reticulum_ (21.25)
|   |   |   |   |   |   |   |   |   |   |   start > 614757:
membrane_fraction_ (12.83)
|   |   |   |   |   |   |   |   |   |   start > 617535:
cellular_component_ (33.79)
|   |   |   |   |   |   |   |   start > 624205
|   |   |   |   |   |   |   |   |   start <= 673133
|   |   |   |   |   |   |   |   |   |   start <= 665004
|   |   |   |   |   |   |   |   |   |   |   start <= 627120
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 626333:
ribosome_ (16.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 626333:
nucleus_ (35.52/13.94)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1914: membrane_ (11.09/4.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 1914:
endoplasmic_reticulum_ (18.64/5.99)
|   |   |   |   |   |   |   |   |   |   |   start > 627120
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 636782:
mitochondrion_ (38.33/16.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 636782
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
660718
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
646417
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: nucleus_ (16.3/6.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: cytoplasm_ (11.75/2.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
646417: cytoplasm_ (7.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
660718: mitochondrion_ (8.97)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 640319
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
634254: cytoplasm_ (32.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
634254
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
636782: ribosome_ (15.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
636782: cytoplasm_ (13.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 640319
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
642629: mitochondrion_ (27.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
642629
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
646417: nucleus_ (13.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
646417: cytoplasm_ (25.33)
|   |   |   |   |   |   |   |   |   |   start > 665004
|   |   |   |   |   |   |   |   |   |   |   start <= 668893
|   |   |   |   |   |   |   |   |   |   |   |   start <= 665846:
membrane_fraction_ (10.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 665846:
Golgi_apparatus_ (12.65)
|   |   |   |   |   |   |   |   |   |   |   start > 668893
|   |   |   |   |   |   |   |   |   |   |   |   start <= 670342
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 669664:
cytoplasm_ (20.5/8.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 669664:
nucleus_ (28.01/9.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 670342:
ribosome_ (21.4)
|   |   |   |   |   |   |   |   |   start > 673133
|   |   |   |   |   |   |   |   |   |   start <= 680202
|   |   |   |   |   |   |   |   |   |   |   start <= 678214
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 673946:
cellular_component_ (11.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 673946:
nucleus_ (26.78)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (17.08)
|   |   |   |   |   |   |   |   |   |   |   start > 678214
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
endoplasmic_reticulum_ (11.67/2.13)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
Golgi_apparatus_ (32.6/14.58)
|   |   |   |   |   |   |   |   |   |   start > 680202
|   |   |   |   |   |   |   |   |   |   |   start <= 696832
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 691557
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
687204: nucleolus_ (17.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
687204: cytoplasm_ (36.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 691557:
nucleolus_ (17.82)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 681188:
nucleus_ (52.87/32.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 681188
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
691557: cytoplasm_ (58.39/23.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
691557: nucleus_ (9.92)
|   |   |   |   |   |   |   |   |   |   |   start > 696832
|   |   |   |   |   |   |   |   |   |   |   |   start <= 708340
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
704026
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
699497: cellular_component_ (26.18/12.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
699497: nucleus_ (10.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
704026
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
707362
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 705188: mitochondrion_ (6.55)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 705188: peroxisome_ (15.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
707362: cellular_component_ (13.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
705188: mitochondrion_ (9.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
705188: cytoplasm_ (9.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 708340
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 710138:
extracellular_region_ (28.7/13.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 710138
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
712060: cytoplasm_ (17.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
712060
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
713160: ribosome_ (12.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
713160: nucleus_ (15.6)
|   |   |   |   |   |   |   start > 714906
|   |   |   |   |   |   |   |   start <= 730827
|   |   |   |   |   |   |   |   |   start <= 722375
|   |   |   |   |   |   |   |   |   |   start <= 720372
|   |   |   |   |   |   |   |   |   |   |   start <= 719464:
mitochondrion_ (41.23)
|   |   |   |   |   |   |   |   |   |   |   start > 719464:
endomembrane_system_ (53.3/30.56)
|   |   |   |   |   |   |   |   |   |   start > 720372
|   |   |   |   |   |   |   |   |   |   |   start <= 721432
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleus_ (5.15/1.69)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (18.64/6.41)
|   |   |   |   |   |   |   |   |   |   |   start > 721432:
mitochondrion_ (17.8)
|   |   |   |   |   |   |   |   |   start > 722375
|   |   |   |   |   |   |   |   |   |   strand = C: nucleus_ (21.69)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 728957
|   |   |   |   |   |   |   |   |   |   |   |   start <= 724046:
vacuole_ (18.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 724046
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 726071:
cellular_component_ (13.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 726071:
cell_wall_ (8.03)
|   |   |   |   |   |   |   |   |   |   |   start > 728957
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2397:
endomembrane_system_ (32.39/18.14)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2397:
endoplasmic_reticulum_ (7.88/2.75)
|   |   |   |   |   |   |   |   start > 730827
```

```
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 744153
|   |   |   |   |   |   |   |   |   |   |   start <= 737550:
mitochondrion_ (13.12)
|   |   |   |   |   |   |   |   |   |   |   start > 737550:
plasma_membrane_ (39.05/15.96)
|   |   |   |   |   |   |   |   |   |   start > 744153
|   |   |   |   |   |   |   |   |   |   |   start <= 751771
|   |   |   |   |   |   |   |   |   |   |   |   start <= 747939:
cellular_component_ (10.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 747939:
Golgi_apparatus_ (14.36)
|   |   |   |   |   |   |   |   |   |   |   start > 751771:
plasma_membrane_ (29.55/12.5)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 737550: cytoplasm_
(53.24)
|   |   |   |   |   |   |   |   |   |   start > 737550
|   |   |   |   |   |   |   |   |   |   |   start <= 744153:
cellular_component_ (16.61)
|   |   |   |   |   |   |   |   |   |   |   start > 744153:
cell_wall_ (44.4)
|   |   |   start > 756995
|   |   |   |   start <= 862713
|   |   |   |   |   start <= 805887
|   |   |   |   |   |   start <= 779215
|   |   |   |   |   |   |   start <= 764137
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 759482:
cellular_component_ (16.23)
|   |   |   |   |   |   |   |   |   start > 759482
|   |   |   |   |   |   |   |   |   |   start <= 762342
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cellular_bud_ (13.17/4.15)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2554:
site_of_polarized_growth_ (10.13/1.76)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2554:
cellular_bud_ (6.28/2.56)
|   |   |   |   |   |   |   |   |   |   start > 762342: membrane_
(15.52)
|   |   |   |   |   |   |   |   strand = W: mitochondrion_ (23.92)
|   |   |   |   |   |   |   start > 764137
|   |   |   |   |   |   |   |   start <= 771684
|   |   |   |   |   |   |   |   |   start <= 766542
|   |   |   |   |   |   |   |   |   |   start <= 764808:
microtubule_organizing_center_ (25.96)
|   |   |   |   |   |   |   |   |   |   start > 764808
|   |   |   |   |   |   |   |   |   |   |   start <= 766358:
cytoplasm_ (19.44/9.0)
|   |   |   |   |   |   |   |   |   |   |   start > 766358:
nucleolus_ (26.86/13.15)
|   |   |   |   |   |   |   |   |   start > 766542:
microtubule_organizing_center_ (38.09/17.46)
```

```
|   |   |   |   |   |   |   |   start > 771684
|   |   |   |   |   |   |   |   |   start <= 778952
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 777864:
cellular_component_ (31.32/14.05)
|   |   |   |   |   |   |   |   |   |   |   start > 777864: nucleus_
(10.31)
|   |   |   |   |   |   |   |   |   |   strand = W: nucleus_ (19.3)
|   |   |   |   |   |   |   |   |   start > 778952: peroxisome_
(25.57)
|   |   |   |   |   |   start > 779215
|   |   |   |   |   |   |   start <= 793918
|   |   |   |   |   |   |   |   start <= 782174
|   |   |   |   |   |   |   |   |   start <= 781379: ribosome_
(19.53)
|   |   |   |   |   |   |   |   |   start > 781379:
cellular_component_ (15.12)
|   |   |   |   |   |   |   |   start > 782174
|   |   |   |   |   |   |   |   |   start <= 786442
|   |   |   |   |   |   |   |   |   |   start <= 784913: cytoplasm_
(81.36/33.97)
|   |   |   |   |   |   |   |   |   |   start > 784913: nucleus_
(21.05)
|   |   |   |   |   |   |   |   |   start > 786442
|   |   |   |   |   |   |   |   |   |   start <= 787664: cytoplasm_
(15.9)
|   |   |   |   |   |   |   |   |   |   start > 787664
|   |   |   |   |   |   |   |   |   |   |   start <= 790676:
plasma_membrane_ (14.82)
|   |   |   |   |   |   |   |   |   |   |   start > 790676:
cytoplasm_ (11.04)
|   |   |   |   |   |   |   start > 793918
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 802396
|   |   |   |   |   |   |   |   |   |   start <= 795024: nucleolus_
(60.21)
|   |   |   |   |   |   |   |   |   |   start > 795024
|   |   |   |   |   |   |   |   |   |   |   start <= 797430:
ribosome_ (12.65)
|   |   |   |   |   |   |   |   |   |   |   start > 797430
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 3272:
nucleolus_ (18.91/8.4)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 3272:
nucleus_ (5.9/1.46)
|   |   |   |   |   |   |   |   |   start > 802396
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cellular_bud_ (8.33/2.3)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
site_of_polarized_growth_ (5.04/1.56)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
site_of_polarized_growth_ (3.86/1.07)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 797430
```

```
|   |   |   |   |   |   |   |   |   |   start <= 797178: cytoplasm_
(9.86)
|   |   |   |   |   |   |   |   |   |   start > 797178:
mitochondrion_ (13.24)
|   |   |   |   |   |   |   |   |   start > 797430: ribosome_
(15.79)
|   |   |   |   |   start > 805887
|   |   |   |   |   |   start <= 854061
|   |   |   |   |   |   |   start <= 840320
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 837356
|   |   |   |   |   |   |   |   |   |   start <= 828729
|   |   |   |   |   |   |   |   |   |   |   start <= 826412
|   |   |   |   |   |   |   |   |   |   |   |   start <= 822592:
mitochondrion_ (13.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 822592:
cytoplasm_ (18.31)
|   |   |   |   |   |   |   |   |   |   |   start > 826412:
mitochondrion_ (31.49/15.08)
|   |   |   |   |   |   |   |   |   |   start > 828729: cytoplasm_
(55.05/18.58)
|   |   |   |   |   |   |   |   |   start > 837356: mitochondrion_
(20.58)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 831115
|   |   |   |   |   |   |   |   |   |   start <= 815810
|   |   |   |   |   |   |   |   |   |   |   start <= 807385:
cellular_component_ (15.15)
|   |   |   |   |   |   |   |   |   |   |   start > 807385
|   |   |   |   |   |   |   |   |   |   |   |   start <= 809997:
mitochondrion_ (27.74/8.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 809997:
cellular_component_ (11.91)
|   |   |   |   |   |   |   |   |   |   start > 815810
|   |   |   |   |   |   |   |   |   |   |   start <= 822592
|   |   |   |   |   |   |   |   |   |   |   |   start <= 818609:
cytoplasm_ (26.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 818609
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 819312:
ribosome_ (11.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 819312:
cytoplasm_ (5.88)
|   |   |   |   |   |   |   |   |   |   |   start > 822592
|   |   |   |   |   |   |   |   |   |   |   |   start <= 828729:
endoplasmic_reticulum_ (13.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 828729:
cellular_component_ (14.72)
|   |   |   |   |   |   |   |   |   start > 831115
|   |   |   |   |   |   |   |   |   |   start <= 834351:
site_of_polarized_growth_ (34.97/17.29)
|   |   |   |   |   |   |   |   |   |   start > 834351:
mitochondrion_ (19.72)
|   |   |   |   |   |   |   start > 840320
```

```
|   |   |   |   |   |   |   |   start <= 849678: cellular_component_
(90.29/9.96)
|   |   |   |   |   |   |   |   start > 849678
|   |   |   |   |   |   |   |   |   start <= 853150: cytoplasm_
(27.96)
|   |   |   |   |   |   |   |   |   start > 853150
|   |   |   |   |   |   |   |   |   |   start <= 853460: nucleus_
(7.7)
|   |   |   |   |   |   |   |   |   |   start > 853460: cytoplasm_
(10.47)
|   |   |   |   |   |   start > 854061
|   |   |   |   |   |   |   strand = C: cytoskeleton_ (17.0)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 859551
|   |   |   |   |   |   |   |   |   start <= 856709
|   |   |   |   |   |   |   |   |   |   start <= 856441: ribosome_
(10.49)
|   |   |   |   |   |   |   |   |   |   start > 856441: nucleolus_
(13.05)
|   |   |   |   |   |   |   |   |   start > 856709: mitochondrion_
(29.09)
|   |   |   |   |   |   |   |   start > 859551:
site_of_polarized_growth_ (32.25/14.8)
|   |   |   |   start > 862713
|   |   |   |   |   start <= 912310
|   |   |   |   |   |   start <= 893390
|   |   |   |   |   |   |   start <= 877177
|   |   |   |   |   |   |   |   start <= 871366
|   |   |   |   |   |   |   |   |   start <= 867353:
endoplasmic_reticulum_ (21.58)
|   |   |   |   |   |   |   |   |   start > 867353: plasma_membrane_
(19.13)
|   |   |   |   |   |   |   |   start > 871366
|   |   |   |   |   |   |   |   |   start <= 875375
|   |   |   |   |   |   |   |   |   |   start <= 871696: nucleus_
(17.69)
|   |   |   |   |   |   |   |   |   |   start > 871696: cytoplasm_
(63.45/11.2)
|   |   |   |   |   |   |   |   |   start > 875375: membrane_
(24.12/11.11)
|   |   |   |   |   |   |   start > 877177
|   |   |   |   |   |   |   |   start <= 885288
|   |   |   |   |   |   |   |   |   start <= 878282: mitochondrion_
(31.07/14.73)
|   |   |   |   |   |   |   |   |   start > 878282
|   |   |   |   |   |   |   |   |   |   start <= 879723
|   |   |   |   |   |   |   |   |   |   |   distance <= 2257:
nucleus_ (15.63/4.15)
|   |   |   |   |   |   |   |   |   |   |   distance > 2257:
chromosome_ (30.02/13.27)
|   |   |   |   |   |   |   |   |   |   start > 879723
|   |   |   |   |   |   |   |   |   |   |   start <= 884751:
mitochondrion_ (16.88)
|   |   |   |   |   |   |   |   |   |   |   start > 884751
```

```
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (28.08/11.18)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
mitochondrion_ (15.48/3.83)
|   |   |   |   |   |   |   |   start > 885288: nucleus_
(48.04/16.72)
|   |   |   |   |   |   start > 893390
|   |   |   |   |   |   |   start <= 899180
|   |   |   |   |   |   |   |   strand = C: cytoplasm_ (14.03)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 893628: vacuole_
(16.82)
|   |   |   |   |   |   |   |   |   start > 893628
|   |   |   |   |   |   |   |   |   |   start <= 898651: ribosome_
(8.48)
|   |   |   |   |   |   |   |   |   |   start > 898651: nucleolus_
(15.36)
|   |   |   |   |   |   |   start > 899180
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 909965
|   |   |   |   |   |   |   |   |   |   start <= 907950
|   |   |   |   |   |   |   |   |   |   |   start <= 903724:
membrane_ (19.18)
|   |   |   |   |   |   |   |   |   |   |   start > 903724:
cytoplasm_ (17.04)
|   |   |   |   |   |   |   |   |   |   start > 907950:
mitochondrion_ (27.43)
|   |   |   |   |   |   |   |   |   start > 909965: cytoplasm_
(48.1/29.88)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 907079: mitochondrion_
(67.85/10.24)
|   |   |   |   |   |   |   |   |   start > 907079: chromosome_
(17.99)
|   |   |   |   |   start > 912310
|   |   |   |   |   |   start <= 1014175
|   |   |   |   |   |   |   start <= 955007
|   |   |   |   |   |   |   |   start <= 937231
|   |   |   |   |   |   |   |   |   start <= 919019
|   |   |   |   |   |   |   |   |   |   start <= 914892:
cellular_component_ (21.14)
|   |   |   |   |   |   |   |   |   |   start > 914892: nucleolus_
(22.22)
|   |   |   |   |   |   |   |   |   start > 919019
|   |   |   |   |   |   |   |   |   |   start <= 928742
|   |   |   |   |   |   |   |   |   |   |   start <= 925567:
nucleus_ (62.76/21.59)
|   |   |   |   |   |   |   |   |   |   |   start > 925567:
membrane_ (20.33)
|   |   |   |   |   |   |   |   |   |   start > 928742
|   |   |   |   |   |   |   |   |   |   |   start <= 932966
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 931754:
ribosome_ (16.98)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 931754:
cellular_component_ (13.34)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (37.71)
|   |   |   |   |   |   |   |   |   |   |   start > 932966
|   |   |   |   |   |   |   |   |   |   |   |   start <= 934251:
cytoplasm_ (15.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 934251:
nucleolus_ (33.62/16.47)
|   |   |   |   |   |   |   |   start > 937231
|   |   |   |   |   |   |   |   |   start <= 948366
|   |   |   |   |   |   |   |   |   |   start <= 947251
|   |   |   |   |   |   |   |   |   |   |   start <= 937539:
cytoplasm_ (10.31)
|   |   |   |   |   |   |   |   |   |   |   start > 937539:
plasma_membrane_ (16.65)
|   |   |   |   |   |   |   |   |   |   start > 947251: cytoplasm_
(15.54)
|   |   |   |   |   |   |   |   |   start > 948366
|   |   |   |   |   |   |   |   |   |   start <= 954594
|   |   |   |   |   |   |   |   |   |   |   start <= 951153:
cellular_component_ (29.39)
|   |   |   |   |   |   |   |   |   |   |   start > 951153
|   |   |   |   |   |   |   |   |   |   |   |   start <= 954141:
cytoplasm_ (31.06/9.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 954141:
cellular_component_ (11.66)
|   |   |   |   |   |   |   |   |   |   start > 954594: membrane_
(12.87)
|   |   |   |   |   |   |   start > 955007
|   |   |   |   |   |   |   |   start <= 988425
|   |   |   |   |   |   |   |   |   start <= 976053
|   |   |   |   |   |   |   |   |   |   start <= 958092: nucleus_
(15.22)
|   |   |   |   |   |   |   |   |   |   start > 958092
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 965894
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 963782:
cytoplasm_ (12.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 963782:
cellular_component_ (13.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 965894:
cytoplasm_ (33.01)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 958425
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (15.82/4.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
mitochondrion_ (19.64/8.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 958425
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 965894:
cytoplasm_ (40.58/11.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 965894
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_component_: cytoplasm_ (6.45/1.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= molecular_function_: nucleus_ (6.6/4.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= biological_process_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 3787: cytoplasm_ (2.83/1.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 3787: nucleus_ (6.18/1.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= plasma_membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transporter_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrion_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= oxidoreductase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endoplasmic_reticulum_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vacuole_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= hydrolase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasm_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 1736: nucleus_ (3.65/1.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 1736: mitochondrion_ (2.18/0.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_modification_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_biogenesis_and_assembly_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleolus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= sporulation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= response_to_stress_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_bud_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= site_of_polarized_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= pseudohyphal_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_respiration_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= organelle_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lipid_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= phosphoprotein_phosphatase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= helicase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_organization_and_biogenesis_: cytoplasm_ (9.09/4.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= chromosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_metabolic_process_: nucleus_ (6.3/1.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= enzyme_regulator_activity_: mitochondrion_ (6.69/2.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transduction_: nucleus_ (5.22/2.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= amino_acid_and_derivative_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vesicle-mediated_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= Golgi_apparatus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= structural_molecule_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_: nucleus_ (2.5/0.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ligase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peptidase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endomembrane_system_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cycle_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= generation_of_precursor_metabolites_and_energy_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_kinase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_homeostasis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peroxisome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lyase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_fraction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= meiosis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cortex_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= microtubule_organizing_center_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= isomerase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vitamin_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytokinesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrial_envelope_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= electron_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= conjugation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= extracellular_region_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_budding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   start > 976053
```

```
|   |   |   |   |   |   |   |   |   |   start <= 982891:
cellular_component_ (19.9)
|   |   |   |   |   |   |   |   |   |   start > 982891
|   |   |   |   |   |   |   |   |   |   |   start <= 987059:
mitochondrion_ (19.0)
|   |   |   |   |   |   |   |   |   |   |   start > 987059:
cytoplasm_ (6.12)
|   |   |   |   |   |   |   |   start > 988425
|   |   |   |   |   |   |   |   |   start <= 1001700
|   |   |   |   |   |   |   |   |   |   strand = C: membrane_
(15.66)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 990774:
cytoskeleton_ (30.05/5.77)
|   |   |   |   |   |   |   |   |   |   |   start > 990774: nucleus_
(15.41)
|   |   |   |   |   |   |   |   |   start > 1001700
|   |   |   |   |   |   |   |   |   |   start <= 1012498: cytoplasm_
(102.29/22.89)
|   |   |   |   |   |   |   |   |   |   start > 1012498: nucleolus_
(10.71)
|   |   |   |   |   |   start > 1014175
|   |   |   |   |   |   |   start <= 1028850
|   |   |   |   |   |   |   |   start <= 1022248
|   |   |   |   |   |   |   |   |   start <= 1017694
|   |   |   |   |   |   |   |   |   |   start <= 1014488:
mitochondrion_ (22.89)
|   |   |   |   |   |   |   |   |   |   start > 1014488:
endoplasmic_reticulum_ (14.12)
|   |   |   |   |   |   |   |   |   start > 1017694
|   |   |   |   |   |   |   |   |   |   start <= 1018905: ribosome_
(15.07)
|   |   |   |   |   |   |   |   |   |   start > 1018905
|   |   |   |   |   |   |   |   |   |   |   distance <= 4417
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
mitochondrion_ (8.52/3.03)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
2387: nucleolus_ (5.27/1.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 2387:
mitochondrion_ (2.22/0.5)
|   |   |   |   |   |   |   |   |   |   |   distance > 4417:
nucleolus_ (7.78/0.69)
|   |   |   |   |   |   |   |   start > 1022248
|   |   |   |   |   |   |   |   |   start <= 1027890
|   |   |   |   |   |   |   |   |   |   strand = C: membrane_
(32.62/10.73)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 1022622:
membrane_ (16.59)
|   |   |   |   |   |   |   |   |   |   |   start > 1022622:
cellular_component_ (28.17)
|   |   |   |   |   |   |   |   |   start > 1027890: ribosome_
(19.66)
```

```
|   |   |   |   |   |   |   start > 1028850
|   |   |   |   |   |   |   |   start <= 1053627
|   |   |   |   |   |   |   |   |   start <= 1042984
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 1041364:
plasma_membrane_ (25.98)
|   |   |   |   |   |   |   |   |   |   |   start > 1041364:
nucleus_ (33.77/13.26)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 1032624
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1030830:
nucleus_ (10.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1030830:
endomembrane_system_ (20.24)
|   |   |   |   |   |   |   |   |   |   |   start > 1032624:
nucleus_ (23.37)
|   |   |   |   |   |   |   |   |   start > 1042984
|   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(16.89)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 1043996:
mitochondrion_ (16.19)
|   |   |   |   |   |   |   |   |   |   |   start > 1043996:
nucleus_ (7.66)
|   |   |   |   |   |   |   |   start > 1053627
|   |   |   |   |   |   |   |   |   start <= 1057332
|   |   |   |   |   |   |   |   |   |   strand = C: nucleus_ (7.88)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 1055068:
cellular_component_ (7.97)
|   |   |   |   |   |   |   |   |   |   |   start > 1055068:
membrane_ (24.48/6.98)
|   |   |   |   |   |   |   |   |   start > 1057332
|   |   |   |   |   |   |   |   |   |   start <= 1066570:
cellular_component_ (47.29)
|   |   |   |   |   |   |   |   |   |   start > 1066570
|   |   |   |   |   |   |   |   |   |   |   strand = C:
cellular_component_ (12.48)
|   |   |   |   |   |   |   |   |   |   |   strand = W: nucleus_
(16.16)
```

For Molecular Function

```
|   start <= 225173
|   |   start <= 39470
|   |   |   start <= 23569
|   |   |   |   start <= 13445
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 9836: helicase_activity_ (18.89)
|   |   |   |   |   |   start > 9836: molecular_function_ (8.87)
|   |   |   |   |   strand = W: molecular_function_ (7.88)
|   |   |   |   start > 13445
|   |   |   |   |   strand = C: transferase_activity_ (48.46)
|   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   start <= 17956: transporter_activity_
(12.58)
|   |   |   |   |   |   start > 17956: transferase_activity_ (13.88)
|   |   |   start > 23569
|   |   |   |   start <= 36360
|   |   |   |   |   start <= 28305
|   |   |   |   |   |   start <= 26994: oxidoreductase_activity_
(12.22)
|   |   |   |   |   |   start > 26994: molecular_function_ (12.19)
|   |   |   |   |   start > 28305
|   |   |   |   |   |   start <= 35203
|   |   |   |   |   |   |   start <= 30109: transporter_activity_
(19.54)
|   |   |   |   |   |   |   start > 30109:
transcription_regulator_activity_ (13.49)
|   |   |   |   |   |   start > 35203
|   |   |   |   |   |   |   start <= 35960: molecular_function_
(10.03)
|   |   |   |   |   |   |   start > 35960: transporter_activity_
(16.41)
|   |   |   |   start > 36360: oxidoreductase_activity_ (13.97)
|   |   start > 39470
|   |   |   start <= 140545
|   |   |   |   start <= 100946
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 49937
|   |   |   |   |   |   |   start <= 46264
|   |   |   |   |   |   |   |   start <= 40665: protein_binding_
(11.08)
|   |   |   |   |   |   |   |   start > 40665: hydrolase_activity_
(8.84)
|   |   |   |   |   |   |   start > 46264
|   |   |   |   |   |   |   |   start <= 47462: RNA_binding_ (13.94)
|   |   |   |   |   |   |   |   start > 47462:
structural_molecule_activity_ (14.17)
|   |   |   |   |   |   start > 49937
|   |   |   |   |   |   |   start <= 63644
|   |   |   |   |   |   |   |   start <= 53930
|   |   |   |   |   |   |   |   |   start <= 52589:
molecular_function_ (15.76)
|   |   |   |   |   |   |   |   |   start > 52589:
oxidoreductase_activity_ (14.22)
|   |   |   |   |   |   |   |   start > 53930: molecular_function_
(25.27)
|   |   |   |   |   |   |   start > 63644
|   |   |   |   |   |   |   |   start <= 73408
|   |   |   |   |   |   |   |   |   start <= 66517
|   |   |   |   |   |   |   |   |   |   start <= 65206
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
molecular_function_ (4.52/1.02)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
protein_binding_ (22.98/9.76)
|   |   |   |   |   |   |   |   |   |   start > 65206:
protein_binding_ (17.88)
```

```
|   |   |   |   |   |   |   |   |   start > 66517
|   |   |   |   |   |   |   |   |   |   start <= 68579: RNA_binding_
(14.14)
|   |   |   |   |   |   |   |   |   |   start > 68579:
hydrolase_activity_ (15.0)
|   |   |   |   |   |   |   |   start > 73408
|   |   |   |   |   |   |   |   |   start <= 88622
|   |   |   |   |   |   |   |   |   |   start <= 76746:
molecular_function_ (18.15)
|   |   |   |   |   |   |   |   |   |   start > 76746:
transferase_activity_ (16.67)
|   |   |   |   |   |   |   |   |   start > 88622
|   |   |   |   |   |   |   |   |   |   start <= 97484:
protein_binding_ (19.94)
|   |   |   |   |   |   |   |   |   |   start > 97484
|   |   |   |   |   |   |   |   |   |   |   start <= 98835:
molecular_function_ (20.02)
|   |   |   |   |   |   |   |   |   |   |   start > 98835:
protein_binding_ (19.28)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 97484
|   |   |   |   |   |   |   start <= 84803
|   |   |   |   |   |   |   |   start <= 81460
|   |   |   |   |   |   |   |   |   start <= 53930
|   |   |   |   |   |   |   |   |   |   start <= 40665:
molecular_function_ (23.0)
|   |   |   |   |   |   |   |   |   |   start > 40665:
transporter_activity_ (7.45)
|   |   |   |   |   |   |   |   |   start > 53930:
molecular_function_ (51.37)
|   |   |   |   |   |   |   |   start > 81460: transporter_activity_
(13.64)
|   |   |   |   |   |   |   start > 84803
|   |   |   |   |   |   |   |   start <= 88622
|   |   |   |   |   |   |   |   |   start <= 87402:
molecular_function_ (16.82)
|   |   |   |   |   |   |   |   |   start > 87402: protein_binding_
(7.2)
|   |   |   |   |   |   |   |   start > 88622: molecular_function_
(30.85)
|   |   |   |   |   |   start > 97484: protein_binding_ (13.78)
|   |   |   |   start > 100946
|   |   |   |   |   start <= 125533
|   |   |   |   |   |   start <= 124713
|   |   |   |   |   |   |   start <= 107898:
protein_kinase_activity_ (15.34)
|   |   |   |   |   |   |   start > 107898
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 108971:
transporter_activity_ (5.99)
|   |   |   |   |   |   |   |   |   start > 108971: RNA_binding_
(24.93)
|   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   start <= 116431:
transporter_activity_ (6.99)
|   |   |   |   |   |   |   |   |   start > 116431:
molecular_function_ (18.62)
|   |   |   |   |   |   start > 124713: hydrolase_activity_ (20.06)
|   |   |   |   |   start > 125533
|   |   |   |   |   |   start <= 131728
|   |   |   |   |   |   |   start <= 131413
|   |   |   |   |   |   |   |   start <= 130612
|   |   |   |   |   |   |   |   |   start <= 127522:
molecular_function_ (17.6)
|   |   |   |   |   |   |   |   |   start > 127522:
phosphoprotein_phosphatase_activity_ (14.86)
|   |   |   |   |   |   |   |   start > 130612
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
transporter_activity_ (9.85/3.06)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
transporter_activity_ (9.53/3.08)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
molecular_function_ (10.74/2.48)
|   |   |   |   |   |   |   start > 131413: helicase_activity_
(19.5)
|   |   |   |   |   |   start > 131728: molecular_function_ (65.34)
|   |   |   start > 140545
|   |   |   |   start <= 175226
|   |   |   |   |   start <= 170280
|   |   |   |   |   |   start <= 146290
|   |   |   |   |   |   |   start <= 143200
|   |   |   |   |   |   |   |   start <= 141072
|   |   |   |   |   |   |   |   |   neigh_num <= 1: DNA_binding_
(8.51/2.35)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
molecular_function_ (27.86/11.26)
|   |   |   |   |   |   |   |   start > 141072: molecular_function_
(21.11)
|   |   |   |   |   |   |   start > 143200: transferase_activity_
(20.05)
|   |   |   |   |   |   start > 146290
|   |   |   |   |   |   |   start <= 166082
|   |   |   |   |   |   |   |   start <= 159504
|   |   |   |   |   |   |   |   |   start <= 157729
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 156333
|   |   |   |   |   |   |   |   |   |   |   |   start <= 153976:
molecular_function_ (13.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 153976:
protein_binding_ (13.17)
|   |   |   |   |   |   |   |   |   |   |   start > 156333:
molecular_function_ (14.26)
|   |   |   |   |   |   |   |   |   |   strand = W: protein_binding_
(11.3)
|   |   |   |   |   |   |   |   |   start > 157729:
transporter_activity_ (12.98)
|   |   |   |   |   |   |   |   start > 159504
```

```
|   |   |   |   |   |   |   |   |   start <= 163892
|   |   |   |   |   |   |   |   |   |   start <= 160048:
transcription_regulator_activity_ (13.6)
|   |   |   |   |   |   |   |   |   |   start > 160048:
enzyme_regulator_activity_ (41.81/26.34)
|   |   |   |   |   |   |   |   |   start > 163892
|   |   |   |   |   |   |   |   |   |   start <= 164391:
molecular_function_ (14.86)
|   |   |   |   |   |   |   |   |   |   start > 164391:
protein_binding_ (20.09)
|   |   |   |   |   |   |   start > 166082
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 167801: DNA_binding_
(8.24)
|   |   |   |   |   |   |   |   |   start > 167801:
molecular_function_ (37.08)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 167801:
molecular_function_ (22.75)
|   |   |   |   |   |   |   |   |   start > 167801:
oxidoreductase_activity_ (12.55)
|   |   |   |   |   start > 170280
|   |   |   |   |   |   start <= 174981
|   |   |   |   |   |   |   NeighGO_term = cellular_component_:
transcription_regulator_activity_ (6.31/2.38)
|   |   |   |   |   |   |   NeighGO_term = molecular_function_:
DNA_binding_ (12.39/5.0)
|   |   |   |   |   |   |   NeighGO_term = biological_process_:
DNA_binding_ (1.81/0.67)
|   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transporter_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transport_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transferase_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = oxidoreductase_activity_:
transcription_regulator_activity_ (0.53/0.08)
|   |   |   |   |   |   |   NeighGO_term = endoplasmic_reticulum_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_
|   |   |   |   |   |   |   |   start <= 171338: DNA_binding_
(6.76/2.23)
|   |   |   |   |   |   |   |   start > 171338:
transcription_regulator_activity_ (8.57/1.1)
|   |   |   |   |   |   |   NeighGO_term = vacuole_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
transcription_regulator_activity_ (0.0)
```

```
|   |   |   |   |   |   |   NeighGO_term = cytoplasm_: DNA_binding_
(3.92/1.54)
|   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: transcription_regulator_activity_
(0.0)
|   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: transcription_regulator_activity_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = nucleolus_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = nucleus_: DNA_binding_
(15.45/5.99)
|   |   |   |   |   |   |   NeighGO_term = sporulation_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = ribosome_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = protein_binding_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
transcription_regulator_activity_ (2.82/0.23)
|   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cellular_respiration_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = lipid_metabolic_process_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = chromosome_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
DNA_binding_ (3.18/1.29)
|   |   |   |   |   |   |   NeighGO_term = DNA_metabolic_process_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: transcription_regulator_activity_ (0.0)
```

```
|   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transcription_
|   |   |   |   |   |   |   |   neigh_num <= 1: DNA_binding_
(3.66/1.0)
|   |   |   |   |   |   |   |   neigh_num > 1:
transcription_regulator_activity_ (6.29/0.62)
|   |   |   |   |   |   |   NeighGO_term = RNA_metabolic_process_:
DNA_binding_ (3.99/0.84)
|   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = membrane_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: transcription_regulator_activity_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = translation_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: transcription_regulator_activity_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = protein_kinase_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_wall_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cellular_homeostasis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = peroxisome_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
transcription_regulator_activity_ (0.0)
```

```
|   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = meiosis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: transcription_regulator_activity_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: transcription_regulator_activity_
(0.0)
|   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: transcription_regulator_activity_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = mitochondrial_envelope_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = electron_transport_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = conjugation_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = extracellular_region_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_budding_:
transcription_regulator_activity_ (0.0)
|   |   |   |   |   |   start > 174981:
transcription_regulator_activity_ (24.49)
|   |   |   |   start > 175226
|   |   |   |   |   start <= 202591
|   |   |   |   |   |   start <= 193282
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 183622
|   |   |   |   |   |   |   |   |   start <= 180287:
molecular_function_ (30.72)
|   |   |   |   |   |   |   |   |   start > 180287:
hydrolase_activity_ (21.84)
|   |   |   |   |   |   |   |   start > 183622: molecular_function_
(45.04)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 180287
```

```
|   |   |   |   |   |   |   |   |   start <= 177607:
transferase_activity_ (15.68)
|   |   |   |   |   |   |   |   |   start > 177607:
phosphoprotein_phosphatase_activity_ (16.95)
|   |   |   |   |   |   |   |   start > 180287: molecular_function_
(20.06)
|   |   |   |   |   |   start > 193282
|   |   |   |   |   |   |   start <= 198086
|   |   |   |   |   |   |   |   start <= 196473: protein_binding_
(32.24)
|   |   |   |   |   |   |   |   start > 196473:
transferase_activity_ (14.07)
|   |   |   |   |   |   |   start > 198086
|   |   |   |   |   |   |   |   start <= 201316
|   |   |   |   |   |   |   |   |   start <= 198785: RNA_binding_
(12.43)
|   |   |   |   |   |   |   |   |   start > 198785:
hydrolase_activity_ (14.95)
|   |   |   |   |   |   |   |   start > 201316: RNA_binding_ (16.42)
|   |   |   |   |   start > 202591
|   |   |   |   |   |   start <= 223060
|   |   |   |   |   |   |   start <= 204992
|   |   |   |   |   |   |   |   start <= 204226: molecular_function_
(29.02)
|   |   |   |   |   |   |   |   start > 204226: DNA_binding_ (14.82)
|   |   |   |   |   |   |   start > 204992
|   |   |   |   |   |   |   |   start <= 211934
|   |   |   |   |   |   |   |   |   start <= 208762:
molecular_function_ (20.5)
|   |   |   |   |   |   |   |   |   start > 208762:
transporter_activity_ (16.85)
|   |   |   |   |   |   |   |   start > 211934: molecular_function_
(47.16)
|   |   |   |   |   |   start > 223060: oxidoreductase_activity_
(15.16)
|   start > 225173
|   |   start <= 287917
|   |   |   start <= 283873
|   |   |   |   strand = C
|   |   |   |   |   start <= 250979
|   |   |   |   |   |   start <= 228597: enzyme_regulator_activity_
(21.35)
|   |   |   |   |   |   start > 228597
|   |   |   |   |   |   |   start <= 242233
|   |   |   |   |   |   |   |   start <= 230452: molecular_function_
(29.52)
|   |   |   |   |   |   |   |   start > 230452
|   |   |   |   |   |   |   |   |   start <= 237704
|   |   |   |   |   |   |   |   |   |   start <= 234082
|   |   |   |   |   |   |   |   |   |   |   start <= 232014:
oxidoreductase_activity_ (11.81)
|   |   |   |   |   |   |   |   |   |   |   start > 232014:
lyase_activity_ (14.16)
```

```
|   |   |   |   |   |   |   |   |   |   start > 234082:
structural_molecule_activity_ (17.81)
|   |   |   |   |   |   |   |   |   start > 237704
|   |   |   |   |   |   |   |   |   |   start <= 238814:
molecular_function_ (16.3)
|   |   |   |   |   |   |   |   |   |   start > 238814:
oxidoreductase_activity_ (15.75)
|   |   |   |   |   |   |   start > 242233: molecular_function_
(67.84)
|   |   |   |   |   start > 250979
|   |   |   |   |   |   start <= 263195
|   |   |   |   |   |   |   start <= 255307: protein_binding_
(33.66/13.13)
|   |   |   |   |   |   |   start > 255307
|   |   |   |   |   |   |   |   start <= 259402:
transferase_activity_ (15.68)
|   |   |   |   |   |   |   |   start > 259402: hydrolase_activity_
(9.8)
|   |   |   |   |   |   start > 263195
|   |   |   |   |   |   |   start <= 275212
|   |   |   |   |   |   |   |   start <= 267170: molecular_function_
(15.19)
|   |   |   |   |   |   |   |   start > 267170
|   |   |   |   |   |   |   |   |   start <= 273916:
translation_regulator_activity_ (31.57)
|   |   |   |   |   |   |   |   |   start > 273916:
oxidoreductase_activity_ (14.84)
|   |   |   |   |   |   |   start > 275212
|   |   |   |   |   |   |   |   start <= 278863:
transcription_regulator_activity_ (11.47)
|   |   |   |   |   |   |   |   start > 278863: molecular_function_
(35.54)
|   |   |   |   strand = W
|   |   |   |   |   start <= 260980
|   |   |   |   |   |   start <= 255307
|   |   |   |   |   |   |   start <= 242233:
structural_molecule_activity_ (4.83)
|   |   |   |   |   |   |   start > 242233
|   |   |   |   |   |   |   |   start <= 248427: molecular_function_
(14.76)
|   |   |   |   |   |   |   |   start > 248427
|   |   |   |   |   |   |   |   |   start <= 253862:
oxidoreductase_activity_ (14.18)
|   |   |   |   |   |   |   |   |   start > 253862:
molecular_function_ (14.36)
|   |   |   |   |   |   start > 255307: ligase_activity_ (14.99)
|   |   |   |   |   start > 260980
|   |   |   |   |   |   start <= 267170
|   |   |   |   |   |   |   start <= 265457
|   |   |   |   |   |   |   |   start <= 263195:
structural_molecule_activity_ (13.56)
|   |   |   |   |   |   |   |   start > 263195: molecular_function_
(24.16)
```

```
|   |   |   |   |   |   |   start > 265457: peptidase_activity_
(28.87)
|   |   |   |   |   |   start > 267170
|   |   |   |   |   |   |   start <= 278863: molecular_function_
(34.53)
|   |   |   |   |   |   |   start > 278863
|   |   |   |   |   |   |   |   start <= 282928:
structural_molecule_activity_ (18.29)
|   |   |   |   |   |   |   |   start > 282928: molecular_function_
(26.69)
|   |   |   start > 283873
|   |   |   |   start <= 286821
|   |   |   |   |   start <= 286560: protein_binding_ (16.61)
|   |   |   |   |   start > 286560: enzyme_regulator_activity_
(29.05)
|   |   |   |   start > 286821: protein_binding_ (18.79)
|   |   start > 287917
|   |   |   strand = C
|   |   |   |   start <= 837356
|   |   |   |   |   start <= 687934
|   |   |   |   |   |   start <= 501051
|   |   |   |   |   |   |   start <= 346586
|   |   |   |   |   |   |   |   start <= 323545
|   |   |   |   |   |   |   |   |   start <= 316108:
molecular_function_ (102.66)
|   |   |   |   |   |   |   |   |   start > 316108:
transferase_activity_ (15.36)
|   |   |   |   |   |   |   |   start > 323545
|   |   |   |   |   |   |   |   |   start <= 332591
|   |   |   |   |   |   |   |   |   |   start <= 329239
|   |   |   |   |   |   |   |   |   |   |   start <= 327416:
protein_binding_ (14.35)
|   |   |   |   |   |   |   |   |   |   |   start > 327416:
molecular_function_ (10.55)
|   |   |   |   |   |   |   |   |   |   start > 329239:
protein_binding_ (20.24)
|   |   |   |   |   |   |   |   |   start > 332591
|   |   |   |   |   |   |   |   |   |   start <= 341811
|   |   |   |   |   |   |   |   |   |   |   start <= 337266:
molecular_function_ (21.96)
|   |   |   |   |   |   |   |   |   |   |   start > 337266
|   |   |   |   |   |   |   |   |   |   |   |   start <= 339474
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: DNA_binding_ (15.26/6.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: transcription_regulator_activity_ (13.55/4.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 339474:
molecular_function_ (15.0)
|   |   |   |   |   |   |   |   |   |   start > 341811
|   |   |   |   |   |   |   |   |   |   |   start <= 343768:
protein_binding_ (15.64)
|   |   |   |   |   |   |   |   |   |   |   start > 343768:
DNA_binding_ (32.09/15.8)
|   |   |   |   |   |   |   start > 346586
```

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|   |   |   |   |   |   |   |   start <= 489574
|   |   |   |   |   |   |   |   |   start <= 434642
|   |   |   |   |   |   |   |   |   |   start <= 399658
|   |   |   |   |   |   |   |   |   |   |   start <= 364117
|   |   |   |   |   |   |   |   |   |   |   |   start <= 348181:
hydrolase_activity_ (18.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 348181
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 348511:
RNA_binding_ (15.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 348511:
hydrolase_activity_ (15.67)
|   |   |   |   |   |   |   |   |   |   |   start > 364117
|   |   |   |   |   |   |   |   |   |   |   |   start <= 380823:
molecular_function_ (45.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 380823
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 388221
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
384535: protein_binding_ (24.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
384535
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
385535: hydrolase_activity_ (15.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
385535: peptidase_activity_ (13.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 388221
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
395521
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
390271: structural_molecule_activity_ (10.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
390271: molecular_function_ (16.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
395521: protein_binding_ (12.5)
|   |   |   |   |   |   |   |   |   |   start > 399658
|   |   |   |   |   |   |   |   |   |   |   start <= 406823
|   |   |   |   |   |   |   |   |   |   |   |   start <= 404063:
transporter_activity_ (16.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 404063:
transcription_regulator_activity_ (17.32)
|   |   |   |   |   |   |   |   |   |   |   start > 406823
|   |   |   |   |   |   |   |   |   |   |   |   start <= 427330
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 410724:
molecular_function_ (17.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 410724
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
418438: RNA_binding_ (14.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
418438: molecular_function_ (12.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 427330
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 433871
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
432169: hydrolase_activity_ (12.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
432169: transferase_activity_ (11.31)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 433871:
RNA_binding_ (17.88)
|   |   |   |   |   |   |   |   |   start > 434642
|   |   |   |   |   |   |   |   |   |   start <= 466870
|   |   |   |   |   |   |   |   |   |   |   start <= 448722
|   |   |   |   |   |   |   |   |   |   |   |   start <= 444689
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 1979
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
442738: hydrolase_activity_ (13.04/0.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
442738: molecular_function_ (7.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 1979:
molecular_function_ (30.2/1.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 444689
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 447576:
ligase_activity_ (11.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 447576
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
448315: hydrolase_activity_ (19.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
448315: molecular_function_ (9.15)
|   |   |   |   |   |   |   |   |   |   |   start > 448722
|   |   |   |   |   |   |   |   |   |   |   |   start <= 462672
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 459677:
structural_molecule_activity_ (18.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 459677:
molecular_function_ (11.96)
|   |   |   |   |   |   |   |   |   |   |   |   start > 462672:
structural_molecule_activity_ (37.54)
|   |   |   |   |   |   |   |   |   |   start > 466870
|   |   |   |   |   |   |   |   |   |   |   distance <= 835:
molecular_function_ (35.85/2.45)
|   |   |   |   |   |   |   |   |   |   |   distance > 835
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2930
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: hydrolase_activity_ (27.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_component_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
470406: hydrolase_activity_ (5.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
470406
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 483638
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 482191: molecular_function_ (4.42/1.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 482191: hydrolase_activity_ (5.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 483638: molecular_function_ (3.11/0.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= molecular_function_: hydrolase_activity_ (16.09/0.3)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= biological_process_: hydrolase_activity_ (5.09/0.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= plasma_membrane_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transporter_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transport_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrion_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transferase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= oxidoreductase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endoplasmic_reticulum_: molecular_function_ (1.2/0.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_regulator_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vacuole_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= hydrolase_activity_: molecular_function_ (3.53/0.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasm_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_modification_process_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_biogenesis_and_assembly_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleolus_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleus_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= sporulation_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_binding_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= response_to_stress_: molecular_function_ (5.17/0.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_bud_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= site_of_polarized_growth_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= pseudohyphal_growth_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_binding_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_respiration_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= organelle_organization_and_biogenesis_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lipid_metabolic_process_: hydrolase_activity_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= phosphoprotein_phosphatase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= helicase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_organization_and_biogenesis_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= chromosome_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_binding_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_metabolic_process_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= enzyme_regulator_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transducer_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transduction_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_metabolic_process_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= amino_acid_and_derivative_metabolic_process_: hydrolase_activity_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vesicle-mediated_transport_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= Golgi_apparatus_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= structural_molecule_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ligase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peptidase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_regulator_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endomembrane_system_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cycle_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= generation_of_precursor_metabolites_and_energy_:
hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_kinase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_homeostasis_: hydrolase_activity_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_organization_and_biogenesis_: hydrolase_activity_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_organization_and_biogenesis_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peroxisome_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lyase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_fraction_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= meiosis_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cortex_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_catabolic_process_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= microtubule_organizing_center_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= isomerase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vitamin_metabolic_process_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= carbohydrate_metabolic_process_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleotidyltransferase_activity_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytokinesis_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrial_envelope_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= electron_transport_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nuclear_organization_and_biogenesis_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= conjugation_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= extracellular_region_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_budding_: hydrolase_activity_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 2930:
molecular_function_ (20.67/0.67)
|   |   |   |   |   |   |   |   |   start > 489574
|   |   |   |   |   |   |   |   |   |   start <= 495260
|   |   |   |   |   |   |   |   |   |   |   start <= 493885:
peptidase_activity_ (17.66)
|   |   |   |   |   |   |   |   |   |   |   start > 493885:
lyase_activity_ (20.18)
|   |   |   |   |   |   |   |   |   |   start > 495260
|   |   |   |   |   |   |   |   |   |   |   start <= 500272
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 498949:
protein_binding_ (14.38)
|   |   |   |   |   |   |   |   |   |   |   start > 498949:
molecular_function_ (14.38)
|   |   |   |   |   |   |   |   |   |   start > 500272:
protein_binding_ (16.39)
|   |   |   |   |   |   start > 501051
|   |   |   |   |   |   |   start <= 566283
|   |   |   |   |   |   |   |   start <= 524867
|   |   |   |   |   |   |   |   |   start <= 511056
|   |   |   |   |   |   |   |   |   |   start <= 506136:
transferase_activity_ (15.22)
|   |   |   |   |   |   |   |   |   |   start > 506136:
transcription_regulator_activity_ (21.3)
|   |   |   |   |   |   |   |   |   start > 511056
|   |   |   |   |   |   |   |   |   |   start <= 517942
|   |   |   |   |   |   |   |   |   |   |   start <= 515264:
molecular_function_ (53.15/17.91)
|   |   |   |   |   |   |   |   |   |   |   start > 515264:
enzyme_regulator_activity_ (22.93)
|   |   |   |   |   |   |   |   |   |   start > 517942:
transcription_regulator_activity_ (22.39/11.03)
|   |   |   |   |   |   |   |   start > 524867
|   |   |   |   |   |   |   |   |   start <= 539591
|   |   |   |   |   |   |   |   |   |   start <= 535216:
transferase_activity_ (13.68)
|   |   |   |   |   |   |   |   |   |   start > 535216: RNA_binding_
(23.35)
|   |   |   |   |   |   |   |   |   start > 539591
|   |   |   |   |   |   |   |   |   |   start <= 564533
|   |   |   |   |   |   |   |   |   |   |   start <= 541575
|   |   |   |   |   |   |   |   |   |   |   |   start <= 540538:
molecular_function_ (18.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 540538:
structural_molecule_activity_ (12.33)
|   |   |   |   |   |   |   |   |   |   |   start > 541575
|   |   |   |   |   |   |   |   |   |   |   |   start <= 543970:
transferase_activity_ (24.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 543970
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 556790
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
552272: molecular_function_ (48.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
552272: oxidoreductase_activity_ (31.37/15.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 556790
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
562010: transferase_activity_ (20.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
562010: molecular_function_ (13.8)
|   |   |   |   |   |   |   |   |   |   start > 564533:
structural_molecule_activity_ (20.89)
|   |   |   |   |   |   |   start > 566283
|   |   |   |   |   |   |   |   start <= 620475
|   |   |   |   |   |   |   |   |   start <= 605434
```

```
|   |   |   |   |   |   |   |   |   |   start <= 581773
|   |   |   |   |   |   |   |   |   |   |   start <= 568569:
hydrolase_activity_ (19.54)
|   |   |   |   |   |   |   |   |   |   |   start > 568569
|   |   |   |   |   |   |   |   |   |   |   |   start <= 579026
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 573213
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
571860: molecular_function_ (22.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
571860: protein_binding_ (14.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 573213:
molecular_function_ (22.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 579026:
RNA_binding_ (15.43)
|   |   |   |   |   |   |   |   |   |   start > 581773
|   |   |   |   |   |   |   |   |   |   |   start <= 586466:
DNA_binding_ (31.04/13.93)
|   |   |   |   |   |   |   |   |   |   |   start > 586466
|   |   |   |   |   |   |   |   |   |   |   |   start <= 592621
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 589356:
molecular_function_ (18.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 589356
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
592045: structural_molecule_activity_ (17.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
592045: molecular_function_ (16.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 592621
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 602465:
transcription_regulator_activity_ (10.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 602465
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
604789: signal_transducer_activity_ (13.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
604789: molecular_function_ (8.97)
|   |   |   |   |   |   |   |   |   start > 605434
|   |   |   |   |   |   |   |   |   |   start <= 612369
|   |   |   |   |   |   |   |   |   |   |   start <= 607121:
hydrolase_activity_ (15.33)
|   |   |   |   |   |   |   |   |   |   |   start > 607121:
RNA_binding_ (15.45)
|   |   |   |   |   |   |   |   |   |   start > 612369:
ligase_activity_ (17.2)
|   |   |   |   |   |   |   |   start > 620475
|   |   |   |   |   |   |   |   |   start <= 626333
|   |   |   |   |   |   |   |   |   |   start <= 624205:
molecular_function_ (20.71)
|   |   |   |   |   |   |   |   |   |   start > 624205:
peptidase_activity_ (24.8)
|   |   |   |   |   |   |   |   |   start > 626333
|   |   |   |   |   |   |   |   |   |   start <= 668893
|   |   |   |   |   |   |   |   |   |   |   start <= 660718
|   |   |   |   |   |   |   |   |   |   |   |   start <= 636782:
molecular_function_ (60.08/17.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 636782
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 646417:
protein_binding_ (7.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 646417:
molecular_function_ (7.59)
|   |   |   |   |   |   |   |   |   |   |   start > 660718
|   |   |   |   |   |   |   |   |   |   |   |   start <= 665846:
DNA_binding_ (16.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 665846:
hydrolase_activity_ (10.46)
|   |   |   |   |   |   |   |   |   |   start > 668893
|   |   |   |   |   |   |   |   |   |   |   start <= 675457:
molecular_function_ (67.69)
|   |   |   |   |   |   |   |   |   |   |   start > 675457
|   |   |   |   |   |   |   |   |   |   |   |   start <= 681188:
DNA_binding_ (14.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 681188:
molecular_function_ (37.48)
|   |   |   |   |   start > 687934
|   |   |   |   |   |   start <= 759482
|   |   |   |   |   |   |   start <= 699497
|   |   |   |   |   |   |   |   start <= 691557:
enzyme_regulator_activity_ (14.86)
|   |   |   |   |   |   |   |   start > 691557
|   |   |   |   |   |   |   |   |   start <= 696832:
helicase_activity_ (18.53)
|   |   |   |   |   |   |   |   |   start > 696832: RNA_binding_
(7.92)
|   |   |   |   |   |   |   start > 699497
|   |   |   |   |   |   |   |   start <= 713160
|   |   |   |   |   |   |   |   |   start <= 708340
|   |   |   |   |   |   |   |   |   |   start <= 705188:
molecular_function_ (21.06)
|   |   |   |   |   |   |   |   |   |   start > 705188
|   |   |   |   |   |   |   |   |   |   |   start <= 707362:
isomerase_activity_ (11.48)
|   |   |   |   |   |   |   |   |   |   |   start > 707362:
molecular_function_ (17.95)
|   |   |   |   |   |   |   |   |   start > 708340
|   |   |   |   |   |   |   |   |   |   start <= 710138:
hydrolase_activity_ (15.82)
|   |   |   |   |   |   |   |   |   |   start > 710138
|   |   |   |   |   |   |   |   |   |   |   start <= 712060:
molecular_function_ (16.33)
|   |   |   |   |   |   |   |   |   |   |   start > 712060:
structural_molecule_activity_ (4.31)
|   |   |   |   |   |   |   |   start > 713160
|   |   |   |   |   |   |   |   |   start <= 737550
|   |   |   |   |   |   |   |   |   |   start <= 719464
|   |   |   |   |   |   |   |   |   |   |   start <= 715091:
DNA_binding_ (21.35)
|   |   |   |   |   |   |   |   |   |   |   start > 715091
|   |   |   |   |   |   |   |   |   |   |   |   start <= 717980:
molecular_function_ (14.26)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 717980:
enzyme_regulator_activity_ (13.27)
|   |   |   |   |   |   |   |   |   |   start > 719464
|   |   |   |   |   |   |   |   |   |   |   start <= 722375
|   |   |   |   |   |   |   |   |   |   |   |   start <= 721432
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 720372:
transporter_activity_ (10.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 720372:
hydrolase_activity_ (16.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 721432:
transporter_activity_ (14.15)
|   |   |   |   |   |   |   |   |   |   |   start > 722375
|   |   |   |   |   |   |   |   |   |   |   |   start <= 730827:
RNA_binding_ (15.36)
|   |   |   |   |   |   |   |   |   |   |   |   start > 730827:
DNA_binding_ (14.86)
|   |   |   |   |   |   |   |   |   start > 737550
|   |   |   |   |   |   |   |   |   |   start <= 744153:
transferase_activity_ (17.29)
|   |   |   |   |   |   |   |   |   |   start > 744153
|   |   |   |   |   |   |   |   |   |   |   start <= 751771:
molecular_function_ (41.46)
|   |   |   |   |   |   |   |   |   |   |   start > 751771
|   |   |   |   |   |   |   |   |   |   |   |   start <= 756995:
enzyme_regulator_activity_ (9.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 756995:
molecular_function_ (8.51)
|   |   |   |   |   |   start > 759482
|   |   |   |   |   |   |   start <= 826412
|   |   |   |   |   |   |   |   start <= 787664
|   |   |   |   |   |   |   |   |   start <= 771940
|   |   |   |   |   |   |   |   |   |   start <= 764808
|   |   |   |   |   |   |   |   |   |   |   start <= 762342:
protein_binding_ (26.71)
|   |   |   |   |   |   |   |   |   |   |   start > 762342:
structural_molecule_activity_ (21.39)
|   |   |   |   |   |   |   |   |   |   start > 764808
|   |   |   |   |   |   |   |   |   |   |   start <= 766542:
molecular_function_ (16.39)
|   |   |   |   |   |   |   |   |   |   |   start > 766542:
protein_binding_ (16.7)
|   |   |   |   |   |   |   |   |   start > 771940
|   |   |   |   |   |   |   |   |   |   start <= 777864:
hydrolase_activity_ (15.64)
|   |   |   |   |   |   |   |   |   |   start > 777864
|   |   |   |   |   |   |   |   |   |   |   start <= 779215:
molecular_function_ (13.82)
|   |   |   |   |   |   |   |   |   |   |   start > 779215
|   |   |   |   |   |   |   |   |   |   |   |   start <= 782174:
structural_molecule_activity_ (22.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 782174:
molecular_function_ (10.77)
|   |   |   |   |   |   |   |   start > 787664
|   |   |   |   |   |   |   |   |   start <= 797430
```

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|   |   |   |   |   |   |   |   |   |   start <= 795024:
RNA_binding_ (46.58)
|   |   |   |   |   |   |   |   |   |   start > 795024:
structural_molecule_activity_ (10.58)
|   |   |   |   |   |   |   |   |   start > 797430
|   |   |   |   |   |   |   |   |   |   start <= 802396:
molecular_function_ (7.22)
|   |   |   |   |   |   |   |   |   |   start > 802396
|   |   |   |   |   |   |   |   |   |   |   start <= 809997:
protein_binding_ (18.16)
|   |   |   |   |   |   |   |   |   |   |   start > 809997
|   |   |   |   |   |   |   |   |   |   |   |   start <= 822592:
molecular_function_ (8.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 822592:
protein_binding_ (13.12)
|   |   |   |   |   |   |   start > 826412
|   |   |   |   |   |   |   |   start <= 831115
|   |   |   |   |   |   |   |   |   start <= 828729:
transporter_activity_ (14.87)
|   |   |   |   |   |   |   |   |   start > 828729:
hydrolase_activity_ (20.08)
|   |   |   |   |   |   |   |   start > 831115:
transferase_activity_ (21.71)
|   |   |   |   start > 837356
|   |   |   |   |   start <= 965894
|   |   |   |   |   |   start <= 914892
|   |   |   |   |   |   |   start <= 873553
|   |   |   |   |   |   |   |   start <= 849123
|   |   |   |   |   |   |   |   |   start <= 841330:
oxidoreductase_activity_ (16.58)
|   |   |   |   |   |   |   |   |   start > 841330:
phosphoprotein_phosphatase_activity_ (9.87)
|   |   |   |   |   |   |   |   start > 849123
|   |   |   |   |   |   |   |   |   start <= 857539:
molecular_function_ (36.28)
|   |   |   |   |   |   |   |   |   start > 857539
|   |   |   |   |   |   |   |   |   |   start <= 862713:
structural_molecule_activity_ (14.91)
|   |   |   |   |   |   |   |   |   |   start > 862713:
molecular_function_ (29.33)
|   |   |   |   |   |   |   start > 873553
|   |   |   |   |   |   |   |   start <= 885288
|   |   |   |   |   |   |   |   |   start <= 875375:
hydrolase_activity_ (16.58)
|   |   |   |   |   |   |   |   |   start > 875375
|   |   |   |   |   |   |   |   |   |   start <= 879723:
transporter_activity_ (24.03/7.42)
|   |   |   |   |   |   |   |   |   |   start > 879723: RNA_binding_
(15.78)
|   |   |   |   |   |   |   |   start > 885288
|   |   |   |   |   |   |   |   |   start <= 907950
|   |   |   |   |   |   |   |   |   |   start <= 899180:
molecular_function_ (56.33)
|   |   |   |   |   |   |   |   |   |   start > 899180
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 903724:
peptidase_activity_ (20.47)
|   |   |   |   |   |   |   |   |   |   |   start > 903724:
molecular_function_ (20.06)
|   |   |   |   |   |   |   |   |   start > 907950
|   |   |   |   |   |   |   |   |   |   start <= 912310
|   |   |   |   |   |   |   |   |   |   |   start <= 909965:
oxidoreductase_activity_ (21.2)
|   |   |   |   |   |   |   |   |   |   |   start > 909965:
molecular_function_ (11.68)
|   |   |   |   |   |   |   |   |   |   start > 912310:
hydrolase_activity_ (22.65)
|   |   |   |   |   |   start > 914892
|   |   |   |   |   |   |   start <= 921596
|   |   |   |   |   |   |   |   start <= 919019: helicase_activity_
(34.54/17.07)
|   |   |   |   |   |   |   |   start > 919019:
transcription_regulator_activity_ (17.63)
|   |   |   |   |   |   |   start > 921596
|   |   |   |   |   |   |   |   start <= 955007
|   |   |   |   |   |   |   |   |   start <= 931754
|   |   |   |   |   |   |   |   |   |   start <= 925567:
molecular_function_ (17.52)
|   |   |   |   |   |   |   |   |   |   start > 925567:
structural_molecule_activity_ (17.75)
|   |   |   |   |   |   |   |   |   start > 931754
|   |   |   |   |   |   |   |   |   |   start <= 937539
|   |   |   |   |   |   |   |   |   |   |   start <= 934251:
molecular_function_ (25.59)
|   |   |   |   |   |   |   |   |   |   |   start > 934251:
RNA_binding_ (14.81)
|   |   |   |   |   |   |   |   |   |   start > 937539:
molecular_function_ (49.89)
|   |   |   |   |   |   |   |   start > 955007
|   |   |   |   |   |   |   |   |   start <= 958425:
transcription_regulator_activity_ (18.84)
|   |   |   |   |   |   |   |   |   start > 958425
|   |   |   |   |   |   |   |   |   |   start <= 963782:
molecular_function_ (16.26)
|   |   |   |   |   |   |   |   |   |   start > 963782:
peptidase_activity_ (18.15)
|   |   |   |   |   start > 965894
|   |   |   |   |   |   start <= 1024186
|   |   |   |   |   |   |   start <= 1017694
|   |   |   |   |   |   |   |   start <= 973392:
enzyme_regulator_activity_ (14.66)
|   |   |   |   |   |   |   |   start > 973392
|   |   |   |   |   |   |   |   |   start <= 1012498
|   |   |   |   |   |   |   |   |   |   start <= 1002554:
molecular_function_ (37.94)
|   |   |   |   |   |   |   |   |   |   start > 1002554
|   |   |   |   |   |   |   |   |   |   |   start <= 1006375:
phosphoprotein_phosphatase_activity_ (16.53)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 1006375:
molecular_function_ (26.19)
|   |   |   |   |   |   |   |   |   start > 1012498
|   |   |   |   |   |   |   |   |   |   start <= 1014488:
RNA_binding_ (13.01)
|   |   |   |   |   |   |   |   |   |   start > 1014488:
molecular_function_ (11.19)
|   |   |   |   |   |   |   start > 1017694
|   |   |   |   |   |   |   |   start <= 1018905:
structural_molecule_activity_ (18.01)
|   |   |   |   |   |   |   |   start > 1018905: protein_binding_
(30.62/13.01)
|   |   |   |   |   |   start > 1024186
|   |   |   |   |   |   |   start <= 1041364
|   |   |   |   |   |   |   |   start <= 1032624:
hydrolase_activity_ (31.35/10.96)
|   |   |   |   |   |   |   |   start > 1032624:
enzyme_regulator_activity_ (29.96)
|   |   |   |   |   |   |   start > 1041364
|   |   |   |   |   |   |   |   start <= 1043996: DNA_binding_
(18.72)
|   |   |   |   |   |   |   |   start > 1043996: molecular_function_
(48.91)
|   |   |   strand = W
|   |   |   |   start <= 432169
|   |   |   |   |   start <= 399658
|   |   |   |   |   |   start <= 364117
|   |   |   |   |   |   |   start <= 296095: transporter_activity_
(29.79)
|   |   |   |   |   |   |   start > 296095
|   |   |   |   |   |   |   |   start <= 322298
|   |   |   |   |   |   |   |   |   start <= 316108
|   |   |   |   |   |   |   |   |   |   start <= 302244:
molecular_function_ (22.78)
|   |   |   |   |   |   |   |   |   |   start > 302244:
hydrolase_activity_ (21.87)
|   |   |   |   |   |   |   |   |   start > 316108:
molecular_function_ (32.57)
|   |   |   |   |   |   |   |   start > 322298
|   |   |   |   |   |   |   |   |   start <= 332591
|   |   |   |   |   |   |   |   |   |   start <= 327416:
transporter_activity_ (11.68)
|   |   |   |   |   |   |   |   |   |   start > 327416:
protein_kinase_activity_ (14.22)
|   |   |   |   |   |   |   |   |   start > 332591
|   |   |   |   |   |   |   |   |   |   start <= 348511
|   |   |   |   |   |   |   |   |   |   |   start <= 341326:
molecular_function_ (14.62)
|   |   |   |   |   |   |   |   |   |   |   start > 341326
|   |   |   |   |   |   |   |   |   |   |   |   start <= 343768:
oxidoreductase_activity_ (9.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 343768:
molecular_function_ (13.34)
```

```
|   |   |   |   |   |   |   |   |   |   start > 348511:
hydrolase_activity_ (14.8)
|   |   |   |   |   |   start > 364117
|   |   |   |   |   |   |   start <= 374356
|   |   |   |   |   |   |   |   start <= 366236: RNA_binding_
(16.13)
|   |   |   |   |   |   |   |   start > 366236
|   |   |   |   |   |   |   |   |   start <= 370099:
molecular_function_ (23.0/11.25)
|   |   |   |   |   |   |   |   |   start > 370099
|   |   |   |   |   |   |   |   |   |   start <= 371621
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
signal_transducer_activity_ (11.36/4.37)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
protein_kinase_activity_ (9.21/2.59)
|   |   |   |   |   |   |   |   |   |   start > 371621:
molecular_function_ (13.46)
|   |   |   |   |   |   |   start > 374356
|   |   |   |   |   |   |   |   start <= 388221
|   |   |   |   |   |   |   |   |   start <= 380823: RNA_binding_
(34.84)
|   |   |   |   |   |   |   |   |   start > 380823: protein_binding_
(11.08)
|   |   |   |   |   |   |   |   start > 388221
|   |   |   |   |   |   |   |   |   start <= 398531
|   |   |   |   |   |   |   |   |   |   start <= 395521:
molecular_function_ (16.57)
|   |   |   |   |   |   |   |   |   |   start > 395521:
enzyme_regulator_activity_ (9.52)
|   |   |   |   |   |   |   |   |   start > 398531: RNA_binding_
(16.66)
|   |   |   |   |   start > 399658
|   |   |   |   |   |   start <= 413282
|   |   |   |   |   |   |   start <= 410724
|   |   |   |   |   |   |   |   start <= 408446:
transferase_activity_ (15.81)
|   |   |   |   |   |   |   |   start > 408446: lyase_activity_
(12.16)
|   |   |   |   |   |   |   start > 410724: hydrolase_activity_
(24.48)
|   |   |   |   |   |   start > 413282
|   |   |   |   |   |   |   start <= 427330
|   |   |   |   |   |   |   |   start <= 423684
|   |   |   |   |   |   |   |   |   start <= 418438
|   |   |   |   |   |   |   |   |   |   start <= 417007:
molecular_function_ (15.15)
|   |   |   |   |   |   |   |   |   |   start > 417007:
transporter_activity_ (15.59)
|   |   |   |   |   |   |   |   |   start > 418438:
transcription_regulator_activity_ (22.31)
|   |   |   |   |   |   |   |   start > 423684
|   |   |   |   |   |   |   |   |   start <= 425187:
oxidoreductase_activity_ (10.91)
```

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|   |   |   |   |   |   |   |   |   start > 425187:
molecular_function_ (44.62)
|   |   |   |   |   |   |   start > 427330: hydrolase_activity_
(19.81)
|   |   |   |   start > 432169
|   |   |   |   |   start <= 636782
|   |   |   |   |   |   start <= 559553
|   |   |   |   |   |   |   start <= 511056
|   |   |   |   |   |   |   |   start <= 447576
|   |   |   |   |   |   |   |   |   start <= 434642
|   |   |   |   |   |   |   |   |   |   start <= 433871:
molecular_function_ (22.03)
|   |   |   |   |   |   |   |   |   |   start > 433871:
protein_binding_ (15.07)
|   |   |   |   |   |   |   |   |   start > 434642: DNA_binding_
(31.73)
|   |   |   |   |   |   |   |   start > 447576
|   |   |   |   |   |   |   |   |   start <= 502423
|   |   |   |   |   |   |   |   |   |   start <= 489350
|   |   |   |   |   |   |   |   |   |   |   start <= 488998
|   |   |   |   |   |   |   |   |   |   |   |   start <= 487290
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 485346
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
455572: molecular_function_ (14.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
455572
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
470406: structural_molecule_activity_ (21.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
470406
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance <= 183
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start <= 481874: molecular_function_ (4.01/0.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start > 481874: structural_molecule_activity_ (10.99/1.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: structural_molecule_activity_ (10.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance > 183: molecular_function_ (51.33/9.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 485346:
structural_molecule_activity_ (16.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 487290:
molecular_function_ (21.41)
|   |   |   |   |   |   |   |   |   |   |   start > 488998:
structural_molecule_activity_ (26.68)
|   |   |   |   |   |   |   |   |   |   start > 489350:
molecular_function_ (96.68/12.65)
|   |   |   |   |   |   |   |   |   start > 502423
|   |   |   |   |   |   |   |   |   |   start <= 506136
|   |   |   |   |   |   |   |   |   |   |   start <= 504593:
oxidoreductase_activity_ (16.56)
```

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|   |   |   |   |   |   |   |   |   |   |   start > 504593:
isomerase_activity_ (19.91)
|   |   |   |   |   |   |   |   |   |   start > 506136:
molecular_function_ (20.38)
|   |   |   |   |   |   |   start > 511056
|   |   |   |   |   |   |   |   start <= 523634
|   |   |   |   |   |   |   |   |   start <= 517942
|   |   |   |   |   |   |   |   |   |   start <= 515264:
transferase_activity_ (13.62)
|   |   |   |   |   |   |   |   |   |   start > 515264:
protein_binding_ (9.81)
|   |   |   |   |   |   |   |   |   start > 517942
|   |   |   |   |   |   |   |   |   |   start <= 522665:
structural_molecule_activity_ (21.57)
|   |   |   |   |   |   |   |   |   |   start > 522665: RNA_binding_
(17.77)
|   |   |   |   |   |   |   |   start > 523634
|   |   |   |   |   |   |   |   |   start <= 556790
|   |   |   |   |   |   |   |   |   |   start <= 528302
|   |   |   |   |   |   |   |   |   |   |   start <= 524867:
molecular_function_ (25.49)
|   |   |   |   |   |   |   |   |   |   |   start > 524867:
transporter_activity_ (35.75/13.11)
|   |   |   |   |   |   |   |   |   |   start > 528302
|   |   |   |   |   |   |   |   |   |   |   start <= 554580
|   |   |   |   |   |   |   |   |   |   |   |   start <= 552272
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 550295
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
546099
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
540538
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 535216: molecular_function_ (17.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 535216: protein_binding_ (19.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
540538: molecular_function_ (35.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
546099: protein_binding_ (16.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 550295:
molecular_function_ (22.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 552272:
protein_binding_ (16.87)
|   |   |   |   |   |   |   |   |   |   |   start > 554580:
molecular_function_ (18.63)
|   |   |   |   |   |   |   |   |   start > 556790:
structural_molecule_activity_ (22.91)
|   |   |   |   |   |   start > 559553
|   |   |   |   |   |   |   start <= 612369
|   |   |   |   |   |   |   |   start <= 592621
|   |   |   |   |   |   |   |   |   start <= 574153
|   |   |   |   |   |   |   |   |   |   start <= 564533:
enzyme_regulator_activity_ (22.65)
|   |   |   |   |   |   |   |   |   |   start > 564533
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 568569:
oxidoreductase_activity_ (16.74)
|   |   |   |   |   |   |   |   |   |   |   start > 568569:
molecular_function_ (17.42)
|   |   |   |   |   |   |   |   |   start > 574153
|   |   |   |   |   |   |   |   |   |   start <= 579026:
transporter_activity_ (14.7)
|   |   |   |   |   |   |   |   |   |   start > 579026
|   |   |   |   |   |   |   |   |   |   |   start <= 586466:
protein_binding_ (18.99)
|   |   |   |   |   |   |   |   |   |   |   start > 586466:
enzyme_regulator_activity_ (12.44)
|   |   |   |   |   |   |   |   start > 592621
|   |   |   |   |   |   |   |   |   start <= 609785: DNA_binding_
(40.74/17.53)
|   |   |   |   |   |   |   |   |   start > 609785:
transporter_activity_ (17.47)
|   |   |   |   |   |   |   start > 612369
|   |   |   |   |   |   |   |   start <= 628385
|   |   |   |   |   |   |   |   |   start <= 624205
|   |   |   |   |   |   |   |   |   |   start <= 617535
|   |   |   |   |   |   |   |   |   |   |   start <= 614757:
molecular_function_ (10.61)
|   |   |   |   |   |   |   |   |   |   |   start > 614757:
protein_kinase_activity_ (17.41)
|   |   |   |   |   |   |   |   |   |   start > 617535:
molecular_function_ (36.49)
|   |   |   |   |   |   |   |   |   start > 624205
|   |   |   |   |   |   |   |   |   |   start <= 627120:
transferase_activity_ (23.88)
|   |   |   |   |   |   |   |   |   |   start > 627120:
molecular_function_ (14.97)
|   |   |   |   |   |   |   |   start > 628385
|   |   |   |   |   |   |   |   |   start <= 634254:
protein_kinase_activity_ (16.7)
|   |   |   |   |   |   |   |   |   start > 634254:
translation_regulator_activity_ (18.7)
|   |   |   |   |   start > 636782
|   |   |   |   |   |   start <= 856441
|   |   |   |   |   |   |   start <= 658828
|   |   |   |   |   |   |   |   start <= 642629: molecular_function_
(51.47)
|   |   |   |   |   |   |   |   start > 642629
|   |   |   |   |   |   |   |   |   start <= 646417:
transcription_regulator_activity_ (13.67)
|   |   |   |   |   |   |   |   |   start > 646417:
molecular_function_ (23.43)
|   |   |   |   |   |   |   start > 658828
|   |   |   |   |   |   |   |   start <= 675457
|   |   |   |   |   |   |   |   |   start <= 665846:
transferase_activity_ (28.66)
|   |   |   |   |   |   |   |   |   start > 665846
|   |   |   |   |   |   |   |   |   |   start <= 670342
```

```
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
structural_molecule_activity_ (14.53/3.95)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
structural_molecule_activity_ (3.88/1.25)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
protein_binding_ (8.04/1.64)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
structural_molecule_activity_ (10.16/1.51)
|   |   |   |   |   |   |   |   |   |   start > 670342:
structural_molecule_activity_ (19.6)
|   |   |   |   |   |   |   |   start > 675457
|   |   |   |   |   |   |   |   |   start <= 751771
|   |   |   |   |   |   |   |   |   |   start <= 705188
|   |   |   |   |   |   |   |   |   |   |   start <= 681188
|   |   |   |   |   |   |   |   |   |   |   |   start <= 680202
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 678214:
molecular_function_ (13.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 678214:
protein_binding_ (14.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 680202:
hydrolase_activity_ (21.62)
|   |   |   |   |   |   |   |   |   |   |   start > 681188
|   |   |   |   |   |   |   |   |   |   |   |   start <= 691557:
molecular_function_ (51.51/13.66)
|   |   |   |   |   |   |   |   |   |   |   |   start > 691557
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 699497:
RNA_binding_ (18.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 699497:
molecular_function_ (8.58)
|   |   |   |   |   |   |   |   |   |   start > 705188
|   |   |   |   |   |   |   |   |   |   |   start <= 744153
|   |   |   |   |   |   |   |   |   |   |   |   start <= 728957
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 724046
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
719464
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
710138: transferase_activity_ (13.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
710138: hydrolase_activity_ (14.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
719464: molecular_function_ (17.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 724046
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
726071: transferase_activity_ (22.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
726071: hydrolase_activity_ (7.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 728957
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 732544
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
732092: molecular_function_ (19.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
732092
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: lyase_activity_ (10.06/3.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: transferase_activity_ (14.41/4.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 732544:
molecular_function_ (32.14)
|   |   |   |   |   |   |   |   |   |   |   start > 744153:
hydrolase_activity_ (39.42)
|   |   |   |   |   |   |   |   |   start > 751771
|   |   |   |   |   |   |   |   |   |   start <= 805887
|   |   |   |   |   |   |   |   |   |   |   start <= 797178
|   |   |   |   |   |   |   |   |   |   |   |   start <= 759482:
structural_molecule_activity_ (22.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 759482
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 784913
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
766542
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
764808: molecular_function_ (17.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
764808: DNA_binding_ (26.5/7.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
766542
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
784354: molecular_function_ (81.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
784354: nucleotidyltransferase_activity_ (10.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 784913
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
786442: protein_binding_ (15.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
786442
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
790676
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 787664: molecular_function_ (8.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 787664: signal_transducer_activity_ (16.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
790676: molecular_function_ (18.5)
|   |   |   |   |   |   |   |   |   |   |   start > 797178:
structural_molecule_activity_ (42.62)
|   |   |   |   |   |   |   |   |   |   start > 805887
|   |   |   |   |   |   |   |   |   |   |   start <= 822592
|   |   |   |   |   |   |   |   |   |   |   |   start <= 818609
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 807385:
molecular_function_ (19.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 807385
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
809997: transferase_activity_ (22.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
809997
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
815810: molecular_function_ (17.09)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
815810
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 816094: transferase_activity_ (12.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 816094: molecular_function_ (12.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 818609
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 819312:
RNA_binding_ (9.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 819312:
transferase_activity_ (13.23)
|   |   |   |   |   |   |   |   |   |   |   start > 822592
|   |   |   |   |   |   |   |   |   |   |   |   start <= 854061
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 841330
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
840320: molecular_function_ (73.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
840320: hydrolase_activity_ (14.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 841330
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
844281: lyase_activity_ (15.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
844281
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
849865
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 846102: molecular_function_ (17.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 846102: protein_binding_ (18.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
849865: molecular_function_ (37.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 854061:
structural_molecule_activity_ (13.12)
|   |   |   |   |   |   start > 856441
|   |   |   |   |   |   |   start <= 947251
|   |   |   |   |   |   |   |   start <= 907079
|   |   |   |   |   |   |   |   |   start <= 893628
|   |   |   |   |   |   |   |   |   |   start <= 875375
|   |   |   |   |   |   |   |   |   |   |   start <= 862713
|   |   |   |   |   |   |   |   |   |   |   |   start <= 857539
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 856709:
RNA_binding_ (6.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 856709:
molecular_function_ (17.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 857539
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 859551:
protein_binding_ (13.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 859551:
enzyme_regulator_activity_ (19.41)
|   |   |   |   |   |   |   |   |   |   |   start > 862713
|   |   |   |   |   |   |   |   |   |   |   |   start <= 867353:
transferase_activity_ (14.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 867353:
molecular_function_ (35.81)
```

```
|   |   |   |   |   |   |   |   |   |   start > 875375
|   |   |   |   |   |   |   |   |   |   |   start <= 879723
|   |   |   |   |   |   |   |   |   |   |   |   start <= 878282:
transporter_activity_ (17.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 878282:
protein_binding_ (18.45)
|   |   |   |   |   |   |   |   |   |   |   start > 879723
|   |   |   |   |   |   |   |   |   |   |   |   start <= 885288:
molecular_function_ (12.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 885288:
enzyme_regulator_activity_ (12.31)
|   |   |   |   |   |   |   |   |   start > 893628
|   |   |   |   |   |   |   |   |   |   start <= 903724
|   |   |   |   |   |   |   |   |   |   |   start <= 899180
|   |   |   |   |   |   |   |   |   |   |   |   start <= 898651:
structural_molecule_activity_ (15.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 898651:
RNA_binding_ (16.17)
|   |   |   |   |   |   |   |   |   |   |   start > 899180
|   |   |   |   |   |   |   |   |   |   |   |   start <= 903066:
molecular_function_ (9.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 903066:
structural_molecule_activity_ (11.58)
|   |   |   |   |   |   |   |   |   |   start > 903724:
protein_binding_ (19.37)
|   |   |   |   |   |   |   |   start > 907079
|   |   |   |   |   |   |   |   |   start <= 925567
|   |   |   |   |   |   |   |   |   |   start <= 914892:
ligase_activity_ (16.41)
|   |   |   |   |   |   |   |   |   |   start > 914892:
transcription_regulator_activity_ (22.37/9.03)
|   |   |   |   |   |   |   |   |   start > 925567
|   |   |   |   |   |   |   |   |   |   start <= 934251:
molecular_function_ (49.51)
|   |   |   |   |   |   |   |   |   |   start > 934251
|   |   |   |   |   |   |   |   |   |   |   start <= 937539:
transferase_activity_ (18.34)
|   |   |   |   |   |   |   |   |   |   |   start > 937539:
transporter_activity_ (17.19)
|   |   |   |   |   |   |   start > 947251
|   |   |   |   |   |   |   |   start <= 988425
|   |   |   |   |   |   |   |   |   start <= 965894
|   |   |   |   |   |   |   |   |   |   start <= 958425
|   |   |   |   |   |   |   |   |   |   |   start <= 951153:
molecular_function_ (29.77)
|   |   |   |   |   |   |   |   |   |   |   start > 951153
|   |   |   |   |   |   |   |   |   |   |   |   start <= 955007:
signal_transducer_activity_ (13.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 955007:
molecular_function_ (21.62)
|   |   |   |   |   |   |   |   |   |   start > 958425
|   |   |   |   |   |   |   |   |   |   |   start <= 963782:
hydrolase_activity_ (18.36)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 963782:
molecular_function_ (15.83)
|   |   |   |   |   |   |   |   |   start > 965894
|   |   |   |   |   |   |   |   |   |   start <= 982891
|   |   |   |   |   |   |   |   |   |   |   start <= 976053:
RNA_binding_ (16.4)
|   |   |   |   |   |   |   |   |   |   |   start > 976053:
enzyme_regulator_activity_ (14.19)
|   |   |   |   |   |   |   |   |   |   start > 982891:
molecular_function_ (18.31)
|   |   |   |   |   |   |   |   start > 988425
|   |   |   |   |   |   |   |   |   start <= 1036090
|   |   |   |   |   |   |   |   |   |   start <= 1025211
|   |   |   |   |   |   |   |   |   |   |   start <= 1002554
|   |   |   |   |   |   |   |   |   |   |   |   start <= 993431
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 990774:
protein_binding_ (10.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 990774:
transcription_regulator_activity_ (13.36)
|   |   |   |   |   |   |   |   |   |   |   |   start > 993431:
oxidoreductase_activity_ (16.74)
|   |   |   |   |   |   |   |   |   |   |   start > 1002554
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1017694
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 1012498
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1006375: molecular_function_ (7.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1006375: transferase_activity_ (11.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 1012498:
structural_molecule_activity_ (15.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1017694:
molecular_function_ (41.08)
|   |   |   |   |   |   |   |   |   |   start > 1025211
|   |   |   |   |   |   |   |   |   |   |   start <= 1030830
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1028850:
RNA_binding_ (17.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1028850:
protein_binding_ (11.01)
|   |   |   |   |   |   |   |   |   |   |   start > 1030830
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1032624:
oxidoreductase_activity_ (21.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1032624:
transcription_regulator_activity_ (17.27)
|   |   |   |   |   |   |   |   |   start > 1036090
|   |   |   |   |   |   |   |   |   |   start <= 1066570
|   |   |   |   |   |   |   |   |   |   |   start <= 1055068:
molecular_function_ (37.47)
|   |   |   |   |   |   |   |   |   |   |   start > 1055068
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1057332:
hydrolase_activity_ (12.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1057332:
molecular_function_ (27.34)
|   |   |   |   |   |   |   |   |   |   start > 1066570:
helicase_activity_ (11.02)
```

For Biological Process

```
|   start <= 602465
|   |   start <= 552272
|   |   |   start <= 167801
|   |   |   |   start <= 121321
|   |   |   |   |   start <= 46264
|   |   |   |   |   |   start <= 28305
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 17956
|   |   |   |   |   |   |   |   |   start <= 16072:
biological_process_ (44.52)
|   |   |   |   |   |   |   |   |   start > 16072:
amino_acid_and_derivative_metabolic_process_ (4.81)
|   |   |   |   |   |   |   |   start > 17956: biological_process_
(60.37)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 17956
|   |   |   |   |   |   |   |   |   start <= 9836:
biological_process_ (8.84)
|   |   |   |   |   |   |   |   |   start > 9836: transport_ (12.97)
|   |   |   |   |   |   |   |   start > 17956: biological_process_
(15.13)
|   |   |   |   |   |   start > 28305
|   |   |   |   |   |   |   start <= 36360
|   |   |   |   |   |   |   |   start <= 35960
|   |   |   |   |   |   |   |   |   strand = C: biological_process_
(25.7)
|   |   |   |   |   |   |   |   |   strand = W: transport_ (16.99)
|   |   |   |   |   |   |   |   start > 35960: transport_ (30.35)
|   |   |   |   |   |   |   start > 36360
|   |   |   |   |   |   |   |   start <= 40665
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 39470:
biological_process_ (8.75)
|   |   |   |   |   |   |   |   |   |   start > 39470:
cytoskeleton_organization_and_biogenesis_ (13.38)
|   |   |   |   |   |   |   |   |   strand = W: biological_process_
(13.88)
|   |   |   |   |   |   |   |   start > 40665: transport_ (12.78)
|   |   |   |   |   start > 46264
|   |   |   |   |   |   start <= 73408
|   |   |   |   |   |   |   start <= 53930
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 49937
|   |   |   |   |   |   |   |   |   |   start <= 47462:
ribosome_biogenesis_and_assembly_ (14.3)
|   |   |   |   |   |   |   |   |   |   start > 47462: translation_
(11.79)
|   |   |   |   |   |   |   |   |   start > 49937
|   |   |   |   |   |   |   |   |   |   start <= 52589:
protein_modification_process_ (13.38)
```

```
|   |   |   |   |   |   |   |   |   |   start > 52589:
electron_transport_ (18.36)
|   |   |   |   |   |   |   |   strand = W: transport_ (7.45)
|   |   |   |   |   |   |   start > 53930
|   |   |   |   |   |   |   |   start <= 66517
|   |   |   |   |   |   |   |   |   start <= 63644:
protein_catabolic_process_ (46.77/24.46)
|   |   |   |   |   |   |   |   |   start > 63644
|   |   |   |   |   |   |   |   |   |   start <= 65206:
response_to_stress_ (15.5)
|   |   |   |   |   |   |   |   |   |   start > 65206: vesicle-
mediated_transport_ (22.76)
|   |   |   |   |   |   |   |   start > 66517
|   |   |   |   |   |   |   |   |   start <= 73145
|   |   |   |   |   |   |   |   |   |   start <= 68255:
RNA_metabolic_process_ (11.75)
|   |   |   |   |   |   |   |   |   |   start > 68255:
ribosome_biogenesis_and_assembly_ (35.27)
|   |   |   |   |   |   |   |   |   start > 73145: sporulation_
(16.0)
|   |   |   |   |   |   start > 73408
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 107898
|   |   |   |   |   |   |   |   |   start <= 98835
|   |   |   |   |   |   |   |   |   |   start <= 88622
|   |   |   |   |   |   |   |   |   |   |   start <= 76746:
biological_process_ (17.96)
|   |   |   |   |   |   |   |   |   |   |   start > 76746:
protein_modification_process_ (17.39)
|   |   |   |   |   |   |   |   |   |   start > 88622
|   |   |   |   |   |   |   |   |   |   |   start <= 97484:
response_to_stress_ (13.29)
|   |   |   |   |   |   |   |   |   |   |   start > 97484:
biological_process_ (17.69)
|   |   |   |   |   |   |   |   |   start > 98835:
protein_modification_process_ (28.78)
|   |   |   |   |   |   |   |   start > 107898
|   |   |   |   |   |   |   |   |   start <= 108971: transport_
(7.71)
|   |   |   |   |   |   |   |   |   start > 108971: translation_
(11.61)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 92547
|   |   |   |   |   |   |   |   |   start <= 84803
|   |   |   |   |   |   |   |   |   |   start <= 81460:
biological_process_ (20.09)
|   |   |   |   |   |   |   |   |   |   start > 81460: transport_
(22.29)
|   |   |   |   |   |   |   |   |   start > 84803
|   |   |   |   |   |   |   |   |   |   start <= 87402:
DNA_metabolic_process_ (17.6)
|   |   |   |   |   |   |   |   |   |   start > 87402
|   |   |   |   |   |   |   |   |   |   |   start <= 88622:
response_to_stress_ (7.5)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 88622:
translation_ (13.86)
|   |   |   |   |   |   |   |   start > 92547
|   |   |   |   |   |   |   |   |   start <= 107898
|   |   |   |   |   |   |   |   |   |   start <= 97484:
biological_process_ (19.12)
|   |   |   |   |   |   |   |   |   |   start > 97484:
pseudohyphal_growth_ (21.53)
|   |   |   |   |   |   |   |   |   start > 107898
|   |   |   |   |   |   |   |   |   |   start <= 116431: transport_
(14.52)
|   |   |   |   |   |   |   |   |   |   start > 116431:
biological_process_ (24.41)
|   |   |   |   start > 121321
|   |   |   |   |   start <= 153976
|   |   |   |   |   |   start <= 131728
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 127522:
cellular_respiration_ (25.97/8.71)
|   |   |   |   |   |   |   |   start > 127522
|   |   |   |   |   |   |   |   |   start <= 130612:
response_to_stress_ (12.4)
|   |   |   |   |   |   |   |   |   start > 130612: transport_
(11.44)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 125533:
lipid_metabolic_process_ (15.59)
|   |   |   |   |   |   |   |   start > 125533:
ribosome_biogenesis_and_assembly_ (36.02)
|   |   |   |   |   |   start > 131728
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 146290
|   |   |   |   |   |   |   |   |   start <= 136585:
biological_process_ (13.73)
|   |   |   |   |   |   |   |   |   start > 136585
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cell_wall_organization_and_biogenesis_ (20.39/6.43)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: sporulation_
(13.81/5.75)
|   |   |   |   |   |   |   |   start > 146290: biological_process_
(14.26)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 141072
|   |   |   |   |   |   |   |   |   start <= 136344:
biological_process_ (19.14)
|   |   |   |   |   |   |   |   |   start > 136344
|   |   |   |   |   |   |   |   |   |   start <= 136585:
organelle_organization_and_biogenesis_ (23.88)
|   |   |   |   |   |   |   |   |   |   start > 136585:
DNA_metabolic_process_ (15.05)
|   |   |   |   |   |   |   |   start > 141072
|   |   |   |   |   |   |   |   |   start <= 143200: cell_cycle_
(25.96)
|   |   |   |   |   |   |   |   |   start > 143200
```

```
|   |   |   |   |   |   |   |   |   |   start <= 146290:
response_to_stress_ (20.32)
|   |   |   |   |   |   |   |   |   |   start > 146290:
organelle_organization_and_biogenesis_ (12.55)
|   |   |   |   |   start > 153976
|   |   |   |   |   |   start <= 157729:
ribosome_biogenesis_and_assembly_ (32.75)
|   |   |   |   |   |   start > 157729
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 166536
|   |   |   |   |   |   |   |   |   start <= 164391
|   |   |   |   |   |   |   |   |   |   start <= 160048: transport_
(16.93)
|   |   |   |   |   |   |   |   |   |   start > 160048:
signal_transduction_ (17.37)
|   |   |   |   |   |   |   |   |   start > 164391:
organelle_organization_and_biogenesis_ (33.06/14.83)
|   |   |   |   |   |   |   |   start > 166536:
DNA_metabolic_process_ (12.54)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 164391:
DNA_metabolic_process_ (33.82)
|   |   |   |   |   |   |   |   start > 164391:
ribosome_biogenesis_and_assembly_ (18.25)
|   |   |   start > 167801
|   |   |   |   start <= 416659
|   |   |   |   |   start <= 187128
|   |   |   |   |   |   start <= 175226
|   |   |   |   |   |   |   start <= 170280
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 169102: translation_
(12.28)
|   |   |   |   |   |   |   |   |   start > 169102:
biological_process_ (14.56)
|   |   |   |   |   |   |   |   strand = W: response_to_stress_
(17.58)
|   |   |   |   |   |   |   start > 170280: transcription_ (59.43)
|   |   |   |   |   |   start > 175226
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 180287
|   |   |   |   |   |   |   |   |   start <= 177607:
RNA_metabolic_process_ (21.74)
|   |   |   |   |   |   |   |   |   start > 177607: transport_
(13.35)
|   |   |   |   |   |   |   |   start > 180287
|   |   |   |   |   |   |   |   |   start <= 183622:
lipid_metabolic_process_ (31.4/14.61)
|   |   |   |   |   |   |   |   |   start > 183622
|   |   |   |   |   |   |   |   |   |   start <= 184925:
RNA_metabolic_process_ (12.89)
|   |   |   |   |   |   |   |   |   |   start > 184925:
lipid_metabolic_process_ (14.9)
|   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   start <= 177607:
amino_acid_and_derivative_metabolic_process_ (18.59)
|   |   |   |   |   |   |   |   start > 177607
|   |   |   |   |   |   |   |   |   start <= 180287:
response_to_stress_ (20.05)
|   |   |   |   |   |   |   |   |   start > 180287:
biological_process_ (12.95)
|   |   |   |   |   start > 187128
|   |   |   |   |   |   start <= 341326
|   |   |   |   |   |   |   start <= 283873
|   |   |   |   |   |   |   |   start <= 247202
|   |   |   |   |   |   |   |   |   start <= 201316
|   |   |   |   |   |   |   |   |   |   start <= 196473
|   |   |   |   |   |   |   |   |   |   |   start <= 193282:
protein_modification_process_ (26.48)
|   |   |   |   |   |   |   |   |   |   |   start > 193282: vesicle-
mediated_transport_ (33.08/10.23)
|   |   |   |   |   |   |   |   |   |   start > 196473
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 198785:
biological_process_ (21.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 198785:
cellular_respiration_ (17.07)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
ribosome_biogenesis_and_assembly_ (9.03)
|   |   |   |   |   |   |   |   |   start > 201316
|   |   |   |   |   |   |   |   |   |   start <= 230452
|   |   |   |   |   |   |   |   |   |   |   start <= 214956
|   |   |   |   |   |   |   |   |   |   |   |   start <= 211934
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 202591:
translation_ (13.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 202591
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
204992
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
204226: biological_process_ (31.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
204226: DNA_metabolic_process_ (12.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
204992
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
208762: cell_cycle_ (25.59/12.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
208762: biological_process_ (22.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 211934
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 214457:
meiosis_ (43.41/26.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 214457:
translation_ (23.82)
|   |   |   |   |   |   |   |   |   |   |   start > 214956
|   |   |   |   |   |   |   |   |   |   |   |   start <= 228597
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 225173:
biological_process_ (34.5)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 225173:
transport_ (22.73/8.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 228597:
biological_process_ (35.76)
|   |   |   |   |   |   |   |   |   |   start > 230452
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 237704
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 234082
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
232014: response_to_stress_ (11.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
232014: generation_of_precursor_metabolites_and_energy_ (33.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 234082:
cytoskeleton_organization_and_biogenesis_ (29.66/10.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 237704
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 246073
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
242233
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
238814: biological_process_ (22.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
238814: cellular_homeostasis_ (9.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
242233: biological_process_ (33.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 246073:
ribosome_biogenesis_and_assembly_ (9.12)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 242233:
translation_ (13.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 242233:
DNA_metabolic_process_ (19.8)
|   |   |   |   |   |   |   |   start > 247202
|   |   |   |   |   |   |   |   |   start <= 253862
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 248427:
biological_process_ (19.68)
|   |   |   |   |   |   |   |   |   |   |   start > 248427
|   |   |   |   |   |   |   |   |   |   |   |   start <= 250979:
sporulation_ (36.71/15.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 250979:
transcription_ (15.06)
|   |   |   |   |   |   |   |   |   |   strand = W: vesicle-
mediated_transport_ (19.44)
|   |   |   |   |   |   |   |   |   start > 253862
|   |   |   |   |   |   |   |   |   |   start <= 273916
|   |   |   |   |   |   |   |   |   |   |   start <= 266919
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 259402:
biological_process_ (25.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 259402
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
263195: ribosome_biogenesis_and_assembly_ (19.21/9.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
263195: biological_process_ (14.54)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 263195
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
255307: biological_process_ (18.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
255307: translation_ (33.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 263195:
biological_process_ (34.07)
|   |   |   |   |   |   |   |   |   |   |   start > 266919
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
translation_ (56.92/17.68)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 267170:
transport_ (11.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 267170:
ribosome_biogenesis_and_assembly_ (18.47)
|   |   |   |   |   |   |   |   |   |   start > 273916
|   |   |   |   |   |   |   |   |   |   |   start <= 278627
|   |   |   |   |   |   |   |   |   |   |   |   start <= 275212:
carbohydrate_metabolic_process_ (17.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 275212:
transcription_ (14.11)
|   |   |   |   |   |   |   |   |   |   |   start > 278627
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 281622:
biological_process_ (20.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 281622:
ribosome_biogenesis_and_assembly_ (12.78)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 282928
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
278863: biological_process_ (19.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
278863: translation_ (11.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 282928:
biological_process_ (22.63)
|   |   |   |   |   |   |   start > 283873
|   |   |   |   |   |   |   |   start <= 315732
|   |   |   |   |   |   |   |   |   start <= 290213
|   |   |   |   |   |   |   |   |   |   start <= 287917
|   |   |   |   |   |   |   |   |   |   |   start <= 286821
|   |   |   |   |   |   |   |   |   |   |   |   start <= 286560:
transport_ (21.99/9.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 286560:
cell_cycle_ (16.33)
|   |   |   |   |   |   |   |   |   |   |   start > 286821
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transport_ (22.74/8.06)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
vesicle-mediated_transport_ (17.34/4.9)
|   |   |   |   |   |   |   |   |   |   start > 287917: transport_
(37.82/16.54)
|   |   |   |   |   |   |   |   |   start > 290213
|   |   |   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 296095:
biological_process_ (28.53)
|   |   |   |   |   |   |   |   |   |   |   start > 296095
|   |   |   |   |   |   |   |   |   |   |   |   start <= 300252:
cytokinesis_ (16.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 300252
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 302244:
transport_ (17.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 302244:
generation_of_precursor_metabolites_and_energy_ (10.16)
|   |   |   |   |   |   |   |   |   |   strand = W: cell_cycle_
(15.11)
|   |   |   |   |   |   |   |   start > 315732
|   |   |   |   |   |   |   |   |   start <= 337266
|   |   |   |   |   |   |   |   |   |   start <= 322298
|   |   |   |   |   |   |   |   |   |   |   start <= 316108:
protein_modification_process_ (22.61)
|   |   |   |   |   |   |   |   |   |   |   start > 316108
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (21.01)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 320702:
DNA_metabolic_process_ (18.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 320702:
biological_process_ (22.12)
|   |   |   |   |   |   |   |   |   |   start > 322298
|   |   |   |   |   |   |   |   |   |   |   start <= 329239
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 327416:
vesicle-mediated_transport_ (13.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 327416:
signal_transduction_ (17.38)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
transport_ (12.95)
|   |   |   |   |   |   |   |   |   |   |   start > 329239
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 332591:
DNA_metabolic_process_ (12.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 332591:
protein_modification_process_ (12.81)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W: vesicle-
mediated_transport_ (13.77)
|   |   |   |   |   |   |   |   |   start > 337266
|   |   |   |   |   |   |   |   |   |   start <= 339474:
amino_acid_and_derivative_metabolic_process_ (30.29/13.38)
|   |   |   |   |   |   |   |   |   |   start > 339474:
biological_process_ (32.75)
|   |   |   |   |   |   start > 341326
|   |   |   |   |   |   |   start <= 406823
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 364117
|   |   |   |   |   |   |   |   |   |   start <= 346586
|   |   |   |   |   |   |   |   |   |   |   start <= 343768:
cell_cycle_ (21.38)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 343768:
DNA_metabolic_process_ (14.3)
|   |   |   |   |   |   |   |   |   |   start > 346586
|   |   |   |   |   |   |   |   |   |   |   start <= 348181:
RNA_metabolic_process_ (21.52)
|   |   |   |   |   |   |   |   |   |   |   start > 348181:
ribosome_biogenesis_and_assembly_ (47.11/15.05)
|   |   |   |   |   |   |   |   |   start > 364117
|   |   |   |   |   |   |   |   |   |   start <= 390271
|   |   |   |   |   |   |   |   |   |   |   start <= 380823
|   |   |   |   |   |   |   |   |   |   |   |   start <= 371621
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 368782:
biological_process_ (12.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 368782:
cell_wall_organization_and_biogenesis_ (13.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 371621:
vesicle-mediated_transport_ (31.34/14.99)
|   |   |   |   |   |   |   |   |   |   |   start > 380823
|   |   |   |   |   |   |   |   |   |   |   |   start <= 385535
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 384535:
cell_cycle_ (21.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 384535:
biological_process_ (22.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 385535
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 388221:
protein_modification_process_ (10.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 388221:
cell_wall_organization_and_biogenesis_ (13.08)
|   |   |   |   |   |   |   |   |   |   start > 390271
|   |   |   |   |   |   |   |   |   |   |   start <= 395521:
cellular_homeostasis_ (16.78)
|   |   |   |   |   |   |   |   |   |   |   start > 395521
|   |   |   |   |   |   |   |   |   |   |   |   start <= 404063
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 399658:
cell_cycle_ (8.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 399658:
transport_ (14.36)
|   |   |   |   |   |   |   |   |   |   |   |   start > 404063:
cell_cycle_ (12.96)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 380823
|   |   |   |   |   |   |   |   |   |   start <= 348511
|   |   |   |   |   |   |   |   |   |   |   start <= 343768:
lipid_metabolic_process_ (11.79)
|   |   |   |   |   |   |   |   |   |   |   start > 343768:
biological_process_ (18.99)
|   |   |   |   |   |   |   |   |   |   start > 348511
|   |   |   |   |   |   |   |   |   |   |   start <= 371621
|   |   |   |   |   |   |   |   |   |   |   |   start <= 366236:
RNA_metabolic_process_ (28.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 366236
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 370099:
response_to_stress_ (9.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 370099
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1137: response_to_stress_ (5.2/1.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
1137: signal_transduction_ (26.31/12.79)
|   |   |   |   |   |   |   |   |   |   |   start > 371621
|   |   |   |   |   |   |   |   |   |   |   |   start <= 374356:
translation_ (20.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 374356:
RNA_metabolic_process_ (37.27)
|   |   |   |   |   |   |   |   |   start > 380823
|   |   |   |   |   |   |   |   |   |   start <= 395521
|   |   |   |   |   |   |   |   |   |   |   start <= 388221:
transport_ (13.0)
|   |   |   |   |   |   |   |   |   |   |   start > 388221:
biological_process_ (7.31)
|   |   |   |   |   |   |   |   |   |   start > 395521
|   |   |   |   |   |   |   |   |   |   |   start <= 398531:
protein_modification_process_ (16.25)
|   |   |   |   |   |   |   |   |   |   |   start > 398531:
ribosome_biogenesis_and_assembly_ (10.1)
|   |   |   |   |   |   |   start > 406823
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 410724:
cellular_respiration_ (11.54)
|   |   |   |   |   |   |   |   |   start > 410724:
RNA_metabolic_process_ (17.25)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 410724
|   |   |   |   |   |   |   |   |   |   start <= 408446:
lipid_metabolic_process_ (29.5)
|   |   |   |   |   |   |   |   |   |   start > 408446:
generation_of_precursor_metabolites_and_energy_ (24.54)
|   |   |   |   |   |   |   |   |   start > 410724:
DNA_metabolic_process_ (33.7/16.85)
|   |   |   |   start > 416659
|   |   |   |   |   start <= 517672
|   |   |   |   |   |   start <= 448315
|   |   |   |   |   |   |   start <= 433871
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 432169
|   |   |   |   |   |   |   |   |   |   start <= 427330:
translation_ (13.67)
|   |   |   |   |   |   |   |   |   |   start > 427330:
cytoskeleton_organization_and_biogenesis_ (20.58)
|   |   |   |   |   |   |   |   |   start > 432169:
amino_acid_and_derivative_metabolic_process_ (21.63)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 425187
|   |   |   |   |   |   |   |   |   |   start <= 418438
|   |   |   |   |   |   |   |   |   |   |   start <= 417007:
biological_process_ (22.16)
|   |   |   |   |   |   |   |   |   |   |   start > 417007:
response_to_stress_ (13.66)
|   |   |   |   |   |   |   |   |   |   start > 418438
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 423684:
transcription_ (17.39)
|   |   |   |   |   |   |   |   |   |   |   start > 423684:
amino_acid_and_derivative_metabolic_process_ (20.19)
|   |   |   |   |   |   |   |   |   start > 425187
|   |   |   |   |   |   |   |   |   |   start <= 427133:
translation_ (23.18)
|   |   |   |   |   |   |   |   |   |   start > 427133
|   |   |   |   |   |   |   |   |   |   |   start <= 432169
|   |   |   |   |   |   |   |   |   |   |   |   start <= 427330:
biological_process_ (18.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 427330:
ribosome_biogenesis_and_assembly_ (15.34)
|   |   |   |   |   |   |   |   |   |   |   start > 432169:
biological_process_ (23.81)
|   |   |   |   |   |   |   start > 433871
|   |   |   |   |   |   |   |   start <= 434642
|   |   |   |   |   |   |   |   |   start <= 434464:
RNA_metabolic_process_ (22.66)
|   |   |   |   |   |   |   |   |   start > 434464
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
organelle_organization_and_biogenesis_ (27.21/16.96)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (35.58/19.66)
|   |   |   |   |   |   |   |   start > 434642
|   |   |   |   |   |   |   |   |   start <= 444689
|   |   |   |   |   |   |   |   |   |   strand = C:
biological_process_ (31.11)
|   |   |   |   |   |   |   |   |   |   strand = W:
DNA_metabolic_process_ (10.52)
|   |   |   |   |   |   |   |   |   start > 444689
|   |   |   |   |   |   |   |   |   |   start <= 447576:
protein_modification_process_ (15.66)
|   |   |   |   |   |   |   |   |   |   start > 447576:
DNA_metabolic_process_ (19.44)
|   |   |   |   |   |   start > 448315
|   |   |   |   |   |   |   start <= 490407
|   |   |   |   |   |   |   |   start <= 468814
|   |   |   |   |   |   |   |   |   start <= 462672
|   |   |   |   |   |   |   |   |   |   start <= 459677
|   |   |   |   |   |   |   |   |   |   |   strand = C: translation_
(46.6)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 455572:
biological_process_ (12.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 455572:
translation_ (5.62)
|   |   |   |   |   |   |   |   |   |   start > 459677:
biological_process_ (12.51)
|   |   |   |   |   |   |   |   |   start > 462672: translation_
(56.79)
|   |   |   |   |   |   |   |   start > 468814
|   |   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   |   distance <= 835:
biological_process_ (28.46/1.95)
|   |   |   |   |   |   |   |   |   |   distance > 835
|   |   |   |   |   |   |   |   |   |   |   distance <= 2655
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
response_to_stress_ (25.57)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: response_to_stress_ (6.57/2.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: response_to_stress_ (6.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: response_to_stress_ (5.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: biological_process_ (0.33/0.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: biological_process_ (8.48/1.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: biological_process_ (5.1/0.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: response_to_stress_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: response_to_stress_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: response_to_stress_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: response_to_stress_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: response_to_stress_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: response_to_stress_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   distance > 2655:
biological_process_ (27.24/5.46)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 489350
|   |   |   |   |   |   |   |   |   |   |   start <= 488998
|   |   |   |   |   |   |   |   |   |   |   |   start <= 487290
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 485346
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
472114: biological_process_ (16.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
472114
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
474058: translation_ (14.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
474058
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 481874: biological_process_ (30.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 481874
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 483638: translation_ (17.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 483638: biological_process_ (14.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 485346:
translation_ (10.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 487290:
biological_process_ (23.0)
|   |   |   |   |   |   |   |   |   |   |   start > 488998:
translation_ (23.76)
|   |   |   |   |   |   |   |   |   |   start > 489350:
biological_process_ (29.7)
|   |   |   |   |   |   |   start > 490407
|   |   |   |   |   |   |   |   start <= 498949
|   |   |   |   |   |   |   |   |   start <= 493885
|   |   |   |   |   |   |   |   |   |   start <= 493256:
protein_modification_process_ (23.13)
|   |   |   |   |   |   |   |   |   |   start > 493256:
biological_process_ (12.72)
|   |   |   |   |   |   |   |   |   start > 493885
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 495260:
RNA_metabolic_process_ (35.11/15.17)
|   |   |   |   |   |   |   |   |   |   |   start > 495260:
cytokinesis_ (17.8)
|   |   |   |   |   |   |   |   |   |   strand = W:
ribosome_biogenesis_and_assembly_ (32.19/15.36)
|   |   |   |   |   |   |   |   start > 498949
|   |   |   |   |   |   |   |   |   start <= 514715
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 506136
|   |   |   |   |   |   |   |   |   |   |   |   start <= 500272:
biological_process_ (14.52)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 500272
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 501051: 
vesicle-mediated_transport_ (7.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 501051: 
biological_process_ (11.28)
|   |   |   |   |   |   |   |   |   |   |   start > 506136
|   |   |   |   |   |   |   |   |   |   |   |   start <= 511056: 
response_to_stress_ (15.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 511056: 
biological_process_ (29.42)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 504593
|   |   |   |   |   |   |   |   |   |   |   |   start <= 502423: 
biological_process_ (15.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 502423: 
carbohydrate_metabolic_process_ (14.06)
|   |   |   |   |   |   |   |   |   |   |   start > 504593
|   |   |   |   |   |   |   |   |   |   |   |   start <= 506136: 
ribosome_biogenesis_and_assembly_ (10.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 506136: 
biological_process_ (11.35)
|   |   |   |   |   |   |   |   |   start > 514715
|   |   |   |   |   |   |   |   |   |   start <= 515264: 
amino_acid_and_derivative_metabolic_process_ (25.11)
|   |   |   |   |   |   |   |   |   |   start > 515264: vesicle-
mediated_transport_ (24.59)
|   |   |   |   |   start > 517672
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 535216
|   |   |   |   |   |   |   |   start <= 524867: cell_cycle_ (16.2)
|   |   |   |   |   |   |   |   start > 524867: 
lipid_metabolic_process_ (19.96)
|   |   |   |   |   |   |   start > 535216
|   |   |   |   |   |   |   |   start <= 543970
|   |   |   |   |   |   |   |   |   start <= 539591: translation_ 
(12.46)
|   |   |   |   |   |   |   |   |   start > 539591
|   |   |   |   |   |   |   |   |   |   start <= 541575
|   |   |   |   |   |   |   |   |   |   |   start <= 540538: 
protein_modification_process_ (12.39)
|   |   |   |   |   |   |   |   |   |   |   start > 540538: 
cell_wall_organization_and_biogenesis_ (16.67)
|   |   |   |   |   |   |   |   |   |   start > 541575: 
protein_modification_process_ (19.54)
|   |   |   |   |   |   |   |   start > 543970
|   |   |   |   |   |   |   |   |   start <= 550295
|   |   |   |   |   |   |   |   |   |   start <= 549014: 
biological_process_ (8.79)
|   |   |   |   |   |   |   |   |   |   start > 549014: 
cellular_respiration_ (10.17)
|   |   |   |   |   |   |   |   |   start > 550295: translation_ 
(15.9)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 522665
```

```
|   |   |   |   |   |   |   |   start <= 517942: transcription_
(26.94/9.96)
|   |   |   |   |   |   |   |   start > 517942: translation_ (18.29)
|   |   |   |   |   |   |   start > 522665
|   |   |   |   |   |   |   |   start <= 540538
|   |   |   |   |   |   |   |   |   start <= 524867
|   |   |   |   |   |   |   |   |   |   start <= 523634:
ribosome_biogenesis_and_assembly_ (14.14)
|   |   |   |   |   |   |   |   |   |   start > 523634:
biological_process_ (21.64)
|   |   |   |   |   |   |   |   |   start > 524867
|   |   |   |   |   |   |   |   |   |   start <= 528302: transport_
(18.96)
|   |   |   |   |   |   |   |   |   |   start > 528302:
organelle_organization_and_biogenesis_ (52.77/18.22)
|   |   |   |   |   |   |   |   start > 540538
|   |   |   |   |   |   |   |   |   start <= 546099:
ribosome_biogenesis_and_assembly_ (29.39)
|   |   |   |   |   |   |   |   |   start > 546099
|   |   |   |   |   |   |   |   |   |   start <= 550295:
biological_process_ (9.89)
|   |   |   |   |   |   |   |   |   |   start > 550295:
RNA_metabolic_process_ (19.04)
|   |   start > 552272
|   |   |   strand = C
|   |   |   |   start <= 574153
|   |   |   |   |   start <= 564533: biological_process_
(56.24/13.61)
|   |   |   |   |   start > 564533
|   |   |   |   |   |   start <= 571860
|   |   |   |   |   |   |   start <= 566283: cell_cycle_
(49.59/23.17)
|   |   |   |   |   |   |   start > 566283
|   |   |   |   |   |   |   |   start <= 568569:
cell_wall_organization_and_biogenesis_ (33.08/14.85)
|   |   |   |   |   |   |   |   start > 568569: cell_cycle_ (18.91)
|   |   |   |   |   |   start > 571860: biological_process_ (52.38)
|   |   |   |   start > 574153
|   |   |   |   |   start <= 586466
|   |   |   |   |   |   start <= 581773:
ribosome_biogenesis_and_assembly_ (27.58)
|   |   |   |   |   |   start > 581773: transcription_ (17.88)
|   |   |   |   |   start > 586466
|   |   |   |   |   |   start <= 589356: biological_process_ (19.13)
|   |   |   |   |   |   start > 589356
|   |   |   |   |   |   |   start <= 592045: sporulation_ (13.5)
|   |   |   |   |   |   |   start > 592045
|   |   |   |   |   |   |   |   start <= 592621: translation_ (6.4)
|   |   |   |   |   |   |   |   start > 592621:
lipid_metabolic_process_ (11.49)
|   |   |   strand = W
|   |   |   |   start <= 559553
|   |   |   |   |   start <= 556790
```

```
|   |   |   |   |   |   start <= 554580: vesicle-mediated_transport_
(22.83)
|   |   |   |   |   |   start > 554580: protein_catabolic_process_
(23.45)
|   |   |   |   |   start > 556790
|   |   |   |   |   |   neigh_strand = W:
nuclear_organization_and_biogenesis_ (23.05/12.56)
|   |   |   |   |   |   neigh_strand = C: vesicle-
mediated_transport_ (41.42/21.59)
|   |   |   |   start > 559553
|   |   |   |   |   start <= 574153
|   |   |   |   |   |   start <= 568569
|   |   |   |   |   |   |   start <= 564533: cell_cycle_ (21.0)
|   |   |   |   |   |   |   start > 564533: transport_ (15.44)
|   |   |   |   |   |   start > 568569: meiosis_ (51.08/30.04)
|   |   |   |   |   start > 574153
|   |   |   |   |   |   start <= 579026: transport_ (34.44/11.82)
|   |   |   |   |   |   start > 579026
|   |   |   |   |   |   |   start <= 586466:
protein_catabolic_process_ (15.59)
|   |   |   |   |   |   |   start > 586466: transcription_ (15.72)
|   start > 602465
|   |   start <= 877177
|   |   |   start <= 644975
|   |   |   |   start <= 623885
|   |   |   |   |   start <= 609785
|   |   |   |   |   |   start <= 607121
|   |   |   |   |   |   |   start <= 605434
|   |   |   |   |   |   |   |   start <= 604789:
pseudohyphal_growth_ (14.72)
|   |   |   |   |   |   |   |   start > 604789: translation_ (15.02)
|   |   |   |   |   |   |   start > 605434:
vitamin_metabolic_process_ (21.72)
|   |   |   |   |   |   start > 607121
|   |   |   |   |   |   |   start <= 609526: DNA_metabolic_process_
(18.09)
|   |   |   |   |   |   |   start > 609526
|   |   |   |   |   |   |   |   neigh_strand = W: meiosis_
(17.51/9.29)
|   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   neigh_num <= 1: cell_cycle_
(4.32/2.3)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (18.75/9.28)
|   |   |   |   |   start > 609785
|   |   |   |   |   |   start <= 617535
|   |   |   |   |   |   |   start <= 614757
|   |   |   |   |   |   |   |   start <= 612369: transport_ (16.84)
|   |   |   |   |   |   |   |   start > 612369: conjugation_ (15.26)
|   |   |   |   |   |   |   start > 614757:
protein_modification_process_ (99.53/48.92)
|   |   |   |   |   |   start > 617535
|   |   |   |   |   |   |   start <= 620475: biological_process_
(19.76)
```

```
|   |   |   |   |   |   |   start > 620475
|   |   |   |   |   |   |   |   distance <= 606: transport_
(3.71/0.0)
|   |   |   |   |   |   |   |   distance > 606:
DNA_metabolic_process_ (26.71/9.71)
|   |   |   |   start > 623885
|   |   |   |   |   start <= 642629
|   |   |   |   |   |   start <= 628385
|   |   |   |   |   |   |   start <= 626932: biological_process_
(53.52)
|   |   |   |   |   |   |   start > 626932
|   |   |   |   |   |   |   |   start <= 627120:
protein_modification_process_ (16.96)
|   |   |   |   |   |   |   |   start > 627120: translation_ (13.9)
|   |   |   |   |   |   start > 628385
|   |   |   |   |   |   |   start <= 636782
|   |   |   |   |   |   |   |   strand = C: biological_process_
(16.29)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 634254: meiosis_
(12.37)
|   |   |   |   |   |   |   |   |   start > 634254:
ribosome_biogenesis_and_assembly_ (16.71)
|   |   |   |   |   |   |   start > 636782: biological_process_
(50.85)
|   |   |   |   |   start > 642629:
cytoskeleton_organization_and_biogenesis_ (19.53)
|   |   |   start > 644975
|   |   |   |   strand = C
|   |   |   |   |   start <= 802396
|   |   |   |   |   |   start <= 751771
|   |   |   |   |   |   |   start <= 720372
|   |   |   |   |   |   |   |   start <= 687934
|   |   |   |   |   |   |   |   |   start <= 673946
|   |   |   |   |   |   |   |   |   |   start <= 670342
|   |   |   |   |   |   |   |   |   |   |   start <= 665846
|   |   |   |   |   |   |   |   |   |   |   |   start <= 660718:
translation_ (14.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 660718:
organelle_organization_and_biogenesis_ (32.49/10.87)
|   |   |   |   |   |   |   |   |   |   |   start > 665846
|   |   |   |   |   |   |   |   |   |   |   |   start <= 668893:
transport_ (24.12/10.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 668893:
translation_ (17.54)
|   |   |   |   |   |   |   |   |   |   start > 670342:
biological_process_ (15.02)
|   |   |   |   |   |   |   |   |   start > 673946
|   |   |   |   |   |   |   |   |   |   start <= 687204
|   |   |   |   |   |   |   |   |   |   |   start <= 681188
|   |   |   |   |   |   |   |   |   |   |   |   start <= 675457:
DNA_metabolic_process_ (19.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 675457:
response_to_stress_ (19.02)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 681188
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
DNA_metabolic_process_ (6.15/1.45)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cell_cycle_ (22.31/10.43)
|   |   |   |   |   |   |   |   |   |   start > 687204: translation_
(25.04)
|   |   |   |   |   |   |   |   start > 687934
|   |   |   |   |   |   |   |   |   start <= 699497
|   |   |   |   |   |   |   |   |   |   start <= 696832
|   |   |   |   |   |   |   |   |   |   |   start <= 691557:
carbohydrate_metabolic_process_ (12.72)
|   |   |   |   |   |   |   |   |   |   |   start > 691557:
ribosome_biogenesis_and_assembly_ (12.56)
|   |   |   |   |   |   |   |   |   |   start > 696832:
RNA_metabolic_process_ (15.78)
|   |   |   |   |   |   |   |   |   start > 699497
|   |   |   |   |   |   |   |   |   |   start <= 712060
|   |   |   |   |   |   |   |   |   |   |   start <= 708340
|   |   |   |   |   |   |   |   |   |   |   |   start <= 705188:
biological_process_ (20.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 705188
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 707362:
lipid_metabolic_process_ (16.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 707362:
biological_process_ (13.02)
|   |   |   |   |   |   |   |   |   |   |   start > 708340
|   |   |   |   |   |   |   |   |   |   |   |   start <= 710138:
cytokinesis_ (14.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 710138:
biological_process_ (15.18)
|   |   |   |   |   |   |   |   |   |   start > 712060
|   |   |   |   |   |   |   |   |   |   |   start <= 719464
|   |   |   |   |   |   |   |   |   |   |   |   start <= 717980
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 715091
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
713160: translation_ (7.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
713160: DNA_metabolic_process_ (7.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 715091:
biological_process_ (12.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 717980:
translation_ (15.49)
|   |   |   |   |   |   |   |   |   |   |   start > 719464:
transport_ (12.47)
|   |   |   |   |   |   |   start > 720372
|   |   |   |   |   |   |   |   start <= 744153
|   |   |   |   |   |   |   |   |   start <= 730827
|   |   |   |   |   |   |   |   |   |   start <= 722375
|   |   |   |   |   |   |   |   |   |   |   start <= 721432:
nuclear_organization_and_biogenesis_ (9.55)
|   |   |   |   |   |   |   |   |   |   |   start > 721432:
generation_of_precursor_metabolites_and_energy_ (16.44)
```

```
|   |   |   |   |   |   |   |   |   |   start > 722375:
RNA_metabolic_process_ (9.96)
|   |   |   |   |   |   |   |   |   start > 730827
|   |   |   |   |   |   |   |   |   |   start <= 737550
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: organelle_organization_and_biogenesis_
(1.75/0.56)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: carbohydrate_metabolic_process_ (13.87/3.21)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: cellular_respiration_ (7.43/4.47)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: organelle_organization_and_biogenesis_ (5.27/1.96)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: carbohydrate_metabolic_process_ (8.19/3.97)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: carbohydrate_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: organelle_organization_and_biogenesis_ (3.43/0.82)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: cellular_respiration_ (6.29/3.26)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: carbohydrate_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: carbohydrate_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: cellular_respiration_
(2.25/1.23)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: organelle_organization_and_biogenesis_ (8.89/4.93)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: carbohydrate_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: carbohydrate_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: carbohydrate_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: carbohydrate_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: carbohydrate_metabolic_process_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: carbohydrate_metabolic_process_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_:
carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: carbohydrate_metabolic_process_ (0.0)
|   |   |   |   |   |   |   |   |   |   start > 737550:
organelle_organization_and_biogenesis_ (24.73)
|   |   |   |   |   |   |   |   start > 744153
|   |   |   |   |   |   |   |   |   start <= 747939:
biological_process_ (16.33)
|   |   |   |   |   |   |   |   |   start > 747939: vesicle-
mediated_transport_ (21.19)
|   |   |   |   |   |   start > 751771
|   |   |   |   |   |   |   start <= 779215
|   |   |   |   |   |   |   |   start <= 762342
|   |   |   |   |   |   |   |   |   start <= 759482
|   |   |   |   |   |   |   |   |   |   start <= 756995
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
signal_transduction_ (6.15/1.96)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cell_cycle_ (11.88/5.32)
|   |   |   |   |   |   |   |   |   |   start > 756995:
biological_process_ (22.21)
|   |   |   |   |   |   |   |   |   start > 759482:
pseudohyphal_growth_ (21.71)
|   |   |   |   |   |   |   |   start > 762342
|   |   |   |   |   |   |   |   |   start <= 771940
|   |   |   |   |   |   |   |   |   |   start <= 764808:
cytokinesis_ (33.05/16.45)
|   |   |   |   |   |   |   |   |   |   start > 764808
|   |   |   |   |   |   |   |   |   |   |   start <= 766542:
RNA_metabolic_process_ (12.37)
|   |   |   |   |   |   |   |   |   |   |   start > 766542:
cytokinesis_ (20.39)
|   |   |   |   |   |   |   |   |   start > 771940:
biological_process_ (76.99/39.93)
|   |   |   |   |   |   |   start > 779215
|   |   |   |   |   |   |   |   start <= 787664
|   |   |   |   |   |   |   |   |   start <= 782174: translation_
(20.04)
|   |   |   |   |   |   |   |   |   start > 782174:
biological_process_ (25.65)
|   |   |   |   |   |   |   |   start > 787664
|   |   |   |   |   |   |   |   |   start <= 795024
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: RNA_metabolic_process_ (8.56/2.05)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
biological_process_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
plasma_membrane_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
transporter_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_: 
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
mitochondrion_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
transferase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
oxidoreductase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
endoplasmic_reticulum_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
transcription_regulator_activity_: ribosome_biogenesis_and_assembly_ 
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_: 
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
hydrolase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_: 
RNA_metabolic_process_ (9.53/4.61)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
protein_modification_process_: ribosome_biogenesis_and_assembly_ 
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
ribosome_biogenesis_and_assembly_: RNA_metabolic_process_ 
(11.58/5.18)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_: 
ribosome_biogenesis_and_assembly_ (17.88/5.64)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_: 
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_: 
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_: 
RNA_metabolic_process_ (6.27/1.6)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
protein_binding_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
response_to_stress_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
cellular_bud_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
site_of_polarized_growth_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = 
pseudohyphal_growth_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_
|   |   |   |   |   |   |   |   |   |   |   start <= 794794: 
RNA_metabolic_process_ (11.58/4.6)
|   |   |   |   |   |   |   |   |   |   |   start > 794794: 
ribosome_biogenesis_and_assembly_ (6.93/1.03)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_
|   |   |   |   |   |   |   |   |   |   |   start <= 794794:
RNA_metabolic_process_ (11.94/3.09)
|   |   |   |   |   |   |   |   |   |   |   start > 794794:
ribosome_biogenesis_and_assembly_ (3.15/0.85)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: RNA_metabolic_process_ (2.01/0.84)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
ribosome_biogenesis_and_assembly_ (10.52/2.66)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: ribosome_biogenesis_and_assembly_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: ribosome_biogenesis_and_assembly_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: ribosome_biogenesis_and_assembly_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: ribosome_biogenesis_and_assembly_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: ribosome_biogenesis_and_assembly_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: ribosome_biogenesis_and_assembly_ (0.0)
|   |   |   |   |   |   |   |   |   start > 795024
|   |   |   |   |   |   |   |   |   |   start <= 797430:
translation_ (14.63)
|   |   |   |   |   |   |   |   |   |   start > 797430:
biological_process_ (10.05)
|   |   |   |   |   start > 802396
|   |   |   |   |   |   start <= 831115
|   |   |   |   |   |   |   start <= 809997: vesicle-
mediated_transport_ (30.75/11.52)
|   |   |   |   |   |   |   start > 809997
|   |   |   |   |   |   |   |   start <= 826412
|   |   |   |   |   |   |   |   |   start <= 822592:
biological_process_ (7.91)
|   |   |   |   |   |   |   |   |   start > 822592:
nuclear_organization_and_biogenesis_ (9.8)
|   |   |   |   |   |   |   |   start > 826412
|   |   |   |   |   |   |   |   |   start <= 828729: transport_
(23.92)
|   |   |   |   |   |   |   |   |   start > 828729:
biological_process_ (13.58)
|   |   |   |   |   |   start > 831115
|   |   |   |   |   |   |   start <= 862713
|   |   |   |   |   |   |   |   start <= 837356:
vitamin_metabolic_process_ (42.29/19.44)
|   |   |   |   |   |   |   |   start > 837356
|   |   |   |   |   |   |   |   |   start <= 849123
|   |   |   |   |   |   |   |   |   |   start <= 841330:
organelle_organization_and_biogenesis_ (10.57)
|   |   |   |   |   |   |   |   |   |   start > 841330:
response_to_stress_ (22.59/10.35)
|   |   |   |   |   |   |   |   |   start > 849123
|   |   |   |   |   |   |   |   |   |   start <= 857539
|   |   |   |   |   |   |   |   |   |   |   start <= 849865:
biological_process_ (9.35)
|   |   |   |   |   |   |   |   |   |   |   start > 849865:
RNA_metabolic_process_ (9.84)
|   |   |   |   |   |   |   |   |   |   start > 857539:
organelle_organization_and_biogenesis_ (16.56)
|   |   |   |   |   |   |   start > 862713
|   |   |   |   |   |   |   |   start <= 873553
|   |   |   |   |   |   |   |   |   start <= 871696:
protein_catabolic_process_ (12.68)
```

```
|   |   |   |   |   |   |   |   |   start > 871696:
DNA_metabolic_process_ (11.61)
|   |   |   |   |   |   |   |   start > 873553
|   |   |   |   |   |   |   |   |   start <= 875375:
carbohydrate_metabolic_process_ (26.0)
|   |   |   |   |   |   |   |   |   start > 875375: transport_
(11.44)
|   |   |   |   strand = W
|   |   |   |   |   start <= 726071
|   |   |   |   |   |   start <= 675457
|   |   |   |   |   |   |   start <= 660718
|   |   |   |   |   |   |   |   start <= 658828
|   |   |   |   |   |   |   |   |   start <= 646417:
cellular_respiration_ (9.48)
|   |   |   |   |   |   |   |   |   start > 646417:
biological_process_ (15.2)
|   |   |   |   |   |   |   |   start > 658828:
carbohydrate_metabolic_process_ (30.79/13.15)
|   |   |   |   |   |   |   start > 660718
|   |   |   |   |   |   |   |   start <= 670342
|   |   |   |   |   |   |   |   |   start <= 665846:
response_to_stress_ (13.79)
|   |   |   |   |   |   |   |   |   start > 665846: cell_cycle_
(14.4)
|   |   |   |   |   |   |   |   start > 670342: translation_ (17.8)
|   |   |   |   |   |   start > 675457
|   |   |   |   |   |   |   start <= 699497
|   |   |   |   |   |   |   |   start <= 680202
|   |   |   |   |   |   |   |   |   start <= 678214:
biological_process_ (13.35)
|   |   |   |   |   |   |   |   |   start > 678214: vesicle-
mediated_transport_ (21.2)
|   |   |   |   |   |   |   |   start > 680202
|   |   |   |   |   |   |   |   |   start <= 682739
|   |   |   |   |   |   |   |   |   |   start <= 681188:
RNA_metabolic_process_ (14.09)
|   |   |   |   |   |   |   |   |   |   start > 681188:
biological_process_ (14.99)
|   |   |   |   |   |   |   |   |   start > 682739
|   |   |   |   |   |   |   |   |   |   start <= 691557:
DNA_metabolic_process_ (13.35)
|   |   |   |   |   |   |   |   |   |   start > 691557:
RNA_metabolic_process_ (24.61)
|   |   |   |   |   |   |   start > 699497
|   |   |   |   |   |   |   |   start <= 710138
|   |   |   |   |   |   |   |   |   start <= 705188:
biological_process_ (11.93)
|   |   |   |   |   |   |   |   |   start > 705188:
vitamin_metabolic_process_ (12.02)
|   |   |   |   |   |   |   |   start > 710138: biological_process_
(36.64)
|   |   |   |   |   start > 726071
|   |   |   |   |   |   start <= 819312
|   |   |   |   |   |   |   start <= 751771
```

```
|   |   |   |   |   |   |   |   start <= 737550
|   |   |   |   |   |   |   |   |   start <= 730827
|   |   |   |   |   |   |   |   |   |   start <= 728957:
cell_wall_organization_and_biogenesis_ (14.23)
|   |   |   |   |   |   |   |   |   |   start > 728957: transport_
(8.91)
|   |   |   |   |   |   |   |   |   start > 730827
|   |   |   |   |   |   |   |   |   |   start <= 732544
|   |   |   |   |   |   |   |   |   |   |   start <= 732092:
translation_ (8.71)
|   |   |   |   |   |   |   |   |   |   |   start > 732092:
biological_process_ (21.7/8.02)
|   |   |   |   |   |   |   |   |   |   start > 732544: translation_
(20.22)
|   |   |   |   |   |   |   |   start > 737550
|   |   |   |   |   |   |   |   |   start <= 744153:
protein_modification_process_ (17.21)
|   |   |   |   |   |   |   |   |   start > 744153: sporulation_
(68.21/30.71)
|   |   |   |   |   |   |   start > 751771
|   |   |   |   |   |   |   |   start <= 787664
|   |   |   |   |   |   |   |   |   start <= 784354
|   |   |   |   |   |   |   |   |   |   start <= 759482:
translation_ (27.98)
|   |   |   |   |   |   |   |   |   |   start > 759482
|   |   |   |   |   |   |   |   |   |   |   start <= 771940
|   |   |   |   |   |   |   |   |   |   |   |   start <= 764808:
biological_process_ (12.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 764808:
DNA_metabolic_process_ (33.68)
|   |   |   |   |   |   |   |   |   |   |   start > 771940
|   |   |   |   |   |   |   |   |   |   |   |   start <= 782174
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 779215:
organelle_organization_and_biogenesis_ (15.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 779215:
biological_process_ (16.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 782174:
translation_ (15.79)
|   |   |   |   |   |   |   |   |   start > 784354
|   |   |   |   |   |   |   |   |   |   start <= 784913:
vitamin_metabolic_process_ (14.79)
|   |   |   |   |   |   |   |   |   |   start > 784913
|   |   |   |   |   |   |   |   |   |   |   start <= 786442
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: DNA_metabolic_process_ (2.33/1.06)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: DNA_metabolic_process_ (9.56/3.5)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: meiosis_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: meiosis_ (14.32/7.04)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: meiosis_ (5.95/3.54)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: DNA_metabolic_process_ (1.99/0.83)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: meiosis_ (0.0)
```

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|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: meiosis_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
meiosis_ (2.4/1.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cell_cycle_ (8.19/3.64)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: DNA_metabolic_process_ (2.07/0.7)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: meiosis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   start > 786442:
conjugation_ (8.4)
|   |   |   |   |   |   |   |   start > 787664
|   |   |   |   |   |   |   |   |   start <= 805887
|   |   |   |   |   |   |   |   |   |   start <= 790676:
cell_wall_organization_and_biogenesis_ (15.36)
|   |   |   |   |   |   |   |   |   |   start > 790676
|   |   |   |   |   |   |   |   |   |   |   start <= 797178:
translation_ (24.05)
|   |   |   |   |   |   |   |   |   |   |   start > 797178
|   |   |   |   |   |   |   |   |   |   |   |   start <= 797430:
nuclear_organization_and_biogenesis_ (13.52)
|   |   |   |   |   |   |   |   |   |   |   |   start > 797430:
translation_ (13.07)
|   |   |   |   |   |   |   |   |   start > 805887
|   |   |   |   |   |   |   |   |   |   start <= 816094
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 809997
|   |   |   |   |   |   |   |   |   |   |   |   start <= 807385
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= C: sporulation_ (9.08/2.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= F: cell_wall_organization_and_biogenesis_ (17.3/5.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= P: cell_wall_organization_and_biogenesis_ (3.51/1.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 807385:
vesicle-mediated_transport_ (17.66)
|   |   |   |   |   |   |   |   |   |   |   start > 809997
|   |   |   |   |   |   |   |   |   |   |   |   start <= 815810:
biological_process_ (22.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 815810:
cell_wall_organization_and_biogenesis_ (27.91/10.18)
|   |   |   |   |   |   |   |   |   |   start > 816094: translation_
(30.4)
|   |   |   |   |   |   start > 819312
|   |   |   |   |   |   |   stop <= 856919
|   |   |   |   |   |   |   |   start <= 831115
|   |   |   |   |   |   |   |   |   start <= 828729
|   |   |   |   |   |   |   |   |   |   start <= 822592:
biological_process_ (10.6)
|   |   |   |   |   |   |   |   |   |   start > 822592:
response_to_stress_ (13.33)
|   |   |   |   |   |   |   |   |   start > 828729:
biological_process_ (12.91)
|   |   |   |   |   |   |   |   start > 831115
|   |   |   |   |   |   |   |   |   start <= 854061
|   |   |   |   |   |   |   |   |   |   start <= 844281
|   |   |   |   |   |   |   |   |   |   |   start <= 834351:
pseudohyphal_growth_ (17.16)
|   |   |   |   |   |   |   |   |   |   |   start > 834351:
biological_process_ (56.74/23.91)
|   |   |   |   |   |   |   |   |   |   start > 844281
|   |   |   |   |   |   |   |   |   |   |   start <= 849865
|   |   |   |   |   |   |   |   |   |   |   |   start <= 846102:
vesicle-mediated_transport_ (18.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 846102:
pseudohyphal_growth_ (23.62)
|   |   |   |   |   |   |   |   |   |   |   start > 849865:
biological_process_ (21.46)
|   |   |   |   |   |   |   |   |   start > 854061:
RNA_metabolic_process_ (15.52/4.56)
|   |   |   |   |   |   |   stop > 856919
|   |   |   |   |   |   |   |   start <= 867353
|   |   |   |   |   |   |   |   |   start <= 857539
|   |   |   |   |   |   |   |   |   |   start <= 856709:
translation_ (13.0)
|   |   |   |   |   |   |   |   |   |   start > 856709:
organelle_organization_and_biogenesis_ (7.22)
|   |   |   |   |   |   |   |   |   start > 857539
|   |   |   |   |   |   |   |   |   |   start <= 862713
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 859551:
DNA_metabolic_process_ (23.91)
|   |   |   |   |   |   |   |   |   |   |   start > 859551
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cell_wall_organization_and_biogenesis_ (8.27/3.25)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
response_to_stress_ (8.36/1.85)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cell_wall_organization_and_biogenesis_ (8.96/3.02)
|   |   |   |   |   |   |   |   |   |   start > 862713:
DNA_metabolic_process_ (56.83/30.15)
|   |   |   |   |   |   |   |   start > 867353
|   |   |   |   |   |   |   |   |   start <= 871696:
biological_process_ (20.8)
|   |   |   |   |   |   |   |   |   start > 871696: translation_
(23.01)
|   |   start > 877177
|   |   |   start <= 929788
|   |   |   |   start <= 903724
|   |   |   |   |   start <= 898651
|   |   |   |   |   |   start <= 884751
|   |   |   |   |   |   |   strand = C: translation_ (22.06)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 878282:
cell_wall_organization_and_biogenesis_ (11.74)
|   |   |   |   |   |   |   |   start > 878282: biological_process_
(15.62)
|   |   |   |   |   |   start > 884751
|   |   |   |   |   |   |   start <= 893390
|   |   |   |   |   |   |   |   start <= 892900
|   |   |   |   |   |   |   |   |   start <= 885288:
DNA_metabolic_process_ (15.76)
|   |   |   |   |   |   |   |   |   start > 885288:
RNA_metabolic_process_ (16.85)
|   |   |   |   |   |   |   |   start > 892900:
DNA_metabolic_process_ (22.33)
|   |   |   |   |   |   |   start > 893390
|   |   |   |   |   |   |   |   strand = C: biological_process_
(18.8)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 893628:
organelle_organization_and_biogenesis_ (11.46)
|   |   |   |   |   |   |   |   |   start > 893628: translation_
(11.52)
|   |   |   |   |   start > 898651
|   |   |   |   |   |   strand = C: protein_modification_process_
(11.37)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 899180:
ribosome_biogenesis_and_assembly_ (19.47/7.48)
|   |   |   |   |   |   |   start > 899180:
cell_wall_organization_and_biogenesis_ (42.72)
|   |   |   |   start > 903724
|   |   |   |   |   start <= 914892
```

```
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 909965
|   |   |   |   |   |   |   |   start <= 907950: biological_process_
(17.78)
|   |   |   |   |   |   |   |   start > 907950: electron_transport_
(21.99)
|   |   |   |   |   |   |   start > 909965
|   |   |   |   |   |   |   |   start <= 912310: vesicle-
mediated_transport_ (45.5/25.4)
|   |   |   |   |   |   |   |   start > 912310: biological_process_
(28.02)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 907079: biological_process_
(21.33)
|   |   |   |   |   |   |   start > 907079
|   |   |   |   |   |   |   |   neigh_num <= 1: cell_cycle_
(13.77/6.08)
|   |   |   |   |   |   |   |   neigh_num > 1: meiosis_ (14.6/4.99)
|   |   |   |   |   start > 914892
|   |   |   |   |   |   start <= 925567
|   |   |   |   |   |   |   start <= 921596
|   |   |   |   |   |   |   |   start <= 919019: translation_
(15.03)
|   |   |   |   |   |   |   |   start > 919019: meiosis_ (15.43)
|   |   |   |   |   |   |   start > 921596:
ribosome_biogenesis_and_assembly_ (24.71)
|   |   |   |   |   |   start > 925567
|   |   |   |   |   |   |   start <= 928742: biological_process_
(12.72)
|   |   |   |   |   |   |   start > 928742: RNA_metabolic_process_
(21.6)
|   |   |   start > 929788
|   |   |   |   start <= 1030830
|   |   |   |   |   start <= 973167
|   |   |   |   |   |   start <= 947251
|   |   |   |   |   |   |   start <= 934251
|   |   |   |   |   |   |   |   start <= 931754: translation_
(19.16)
|   |   |   |   |   |   |   |   start > 931754: biological_process_
(31.08)
|   |   |   |   |   |   |   start > 934251
|   |   |   |   |   |   |   |   strand = C:
ribosome_biogenesis_and_assembly_ (16.83)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 937539:
cytoskeleton_organization_and_biogenesis_ (12.62)
|   |   |   |   |   |   |   |   |   start > 937539: transport_
(14.14)
|   |   |   |   |   |   start > 947251
|   |   |   |   |   |   |   start <= 954594: biological_process_
(93.84)
|   |   |   |   |   |   |   start > 954594
|   |   |   |   |   |   |   |   start <= 958092:
DNA_metabolic_process_ (38.31)
```

```
|   |   |   |   |   |   |   |   start > 958092
|   |   |   |   |   |   |   |   |   start <= 963052
|   |   |   |   |   |   |   |   |   |   start <= 958425:
biological_process_ (15.74)
|   |   |   |   |   |   |   |   |   |   start > 958425: translation_
(26.83)
|   |   |   |   |   |   |   |   |   start > 963052
|   |   |   |   |   |   |   |   |   |   start <= 965894:
biological_process_ (54.9)
|   |   |   |   |   |   |   |   |   |   start > 965894
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_metabolic_process_ (22.01/8.62)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
biological_process_ (13.26/4.36)
|   |   |   |   |   start > 973167
|   |   |   |   |   |   start <= 982891
|   |   |   |   |   |   |   strand = C: translation_ (23.9)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 976053:
RNA_metabolic_process_ (19.48)
|   |   |   |   |   |   |   |   start > 976053:
cell_wall_organization_and_biogenesis_ (27.02/12.73)
|   |   |   |   |   |   start > 982891
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 1014488
|   |   |   |   |   |   |   |   |   start <= 1011242
|   |   |   |   |   |   |   |   |   |   start <= 1002554:
biological_process_ (10.66)
|   |   |   |   |   |   |   |   |   |   start > 1002554:
cell_wall_organization_and_biogenesis_ (28.19)
|   |   |   |   |   |   |   |   |   start > 1011242
|   |   |   |   |   |   |   |   |   |   start <= 1012498:
biological_process_ (12.12)
|   |   |   |   |   |   |   |   |   |   start > 1012498:
RNA_metabolic_process_ (4.95)
|   |   |   |   |   |   |   |   start > 1014488
|   |   |   |   |   |   |   |   |   start <= 1018905
|   |   |   |   |   |   |   |   |   |   start <= 1017694: transport_
(14.47)
|   |   |   |   |   |   |   |   |   |   start > 1017694:
translation_ (14.04)
|   |   |   |   |   |   |   |   |   start > 1018905
|   |   |   |   |   |   |   |   |   |   start <= 1024186:
DNA_metabolic_process_ (11.03)
|   |   |   |   |   |   |   |   |   |   start > 1024186:
organelle_organization_and_biogenesis_ (24.99/11.25)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 1012498
|   |   |   |   |   |   |   |   |   start <= 990774
|   |   |   |   |   |   |   |   |   |   start <= 987059:
biological_process_ (15.01)
|   |   |   |   |   |   |   |   |   |   start > 987059
|   |   |   |   |   |   |   |   |   |   |   start <= 988425:
DNA_metabolic_process_ (14.63)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 988425:
cytoskeleton_organization_and_biogenesis_ (10.44)
|   |   |   |   |   |   |   |   |   start > 990774
|   |   |   |   |   |   |   |   |   |   start <= 1006375
|   |   |   |   |   |   |   |   |   |   |   start <= 993431:
ribosome_biogenesis_and_assembly_ (17.68)
|   |   |   |   |   |   |   |   |   |   |   start > 993431
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1002554:
biological_process_ (17.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1002554:
ribosome_biogenesis_and_assembly_ (9.92)
|   |   |   |   |   |   |   |   |   |   start > 1006375
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 941:
biological_process_ (7.52/3.03)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 941:
amino_acid_and_derivative_metabolic_process_ (4.33/0.79)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
biological_process_ (10.2/4.17)
|   |   |   |   |   |   |   |   start > 1012498
|   |   |   |   |   |   |   |   |   start <= 1028850
|   |   |   |   |   |   |   |   |   |   start <= 1022622
|   |   |   |   |   |   |   |   |   |   |   start <= 1017694:
translation_ (14.82)
|   |   |   |   |   |   |   |   |   |   |   start > 1017694:
cell_wall_organization_and_biogenesis_ (20.52)
|   |   |   |   |   |   |   |   |   |   start > 1022622
|   |   |   |   |   |   |   |   |   |   |   start <= 1025211:
biological_process_ (29.73)
|   |   |   |   |   |   |   |   |   |   |   start > 1025211:
translation_ (22.31)
|   |   |   |   |   |   |   |   |   start > 1028850:
ribosome_biogenesis_and_assembly_ (17.49)
|   |   |   |   start > 1030830
|   |   |   |   |   start <= 1041364
|   |   |   |   |   |   strand = C: signal_transduction_ (21.86)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 1032624:
lipid_metabolic_process_ (17.42)
|   |   |   |   |   |   |   start > 1032624: transcription_ (11.97)
|   |   |   |   |   start > 1041364
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 1053627
|   |   |   |   |   |   |   |   start <= 1043996:
DNA_metabolic_process_ (15.7)
|   |   |   |   |   |   |   |   start > 1043996: translation_
(17.64)
|   |   |   |   |   |   |   start > 1053627
|   |   |   |   |   |   |   |   start <= 1057332: cell_cycle_ (8.81)
|   |   |   |   |   |   |   |   start > 1057332: biological_process_
(14.39)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 1066570
```

```
|   |   |   |   |   |   |   |   start <= 1055068:
biological_process_ (41.57)
|   |   |   |   |   |   |   |   start > 1055068
|   |   |   |   |   |   |   |   |   start <= 1057332:
protein_modification_process_ (11.9)
|   |   |   |   |   |   |   |   |   start > 1057332:
biological_process_ (40.57)
|   |   |   |   |   |   |   start > 1066570: DNA_metabolic_process_
(18.99)
```

Decision Tree Generated for Chromosome Thirteen:
For Cellular Component

```
|   start <= 413981
|   |   start <= 25801
|   |   |   strand = C
|   |   |   |   start <= 21700
|   |   |   |   |   start <= 14754
|   |   |   |   |   |   start <= 13175
|   |   |   |   |   |   |   start <= 7244: mitochondrion_ (5.62)
|   |   |   |   |   |   |   start > 7244: endoplasmic_reticulum_
(24.39)
|   |   |   |   |   |   start > 13175
|   |   |   |   |   |   |   distance <= 1786: mitochondrion_
(12.61/5.13)
|   |   |   |   |   |   |   distance > 1786: mitochondrial_envelope_
(31.74/9.87)
|   |   |   |   |   start > 14754: endoplasmic_reticulum_
(75.53/13.42)
|   |   |   |   start > 21700
|   |   |   |   |   start <= 23684: microtubule_organizing_center_
(13.88)
|   |   |   |   |   start > 23684: plasma_membrane_ (16.51)
|   |   |   strand = W
|   |   |   |   start <= 13175
|   |   |   |   |   start <= 7244: membrane_fraction_ (11.48)
|   |   |   |   |   start > 7244: cytoplasm_ (7.55)
|   |   |   |   start > 13175: nucleus_ (36.89/16.36)
|   |   start > 25801
|   |   |   start <= 318679
|   |   |   |   start <= 291133
|   |   |   |   |   start <= 164176
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 115347
|   |   |   |   |   |   |   |   start <= 79909
|   |   |   |   |   |   |   |   |   start <= 56773
|   |   |   |   |   |   |   |   |   |   start <= 51640
|   |   |   |   |   |   |   |   |   |   |   start <= 41794
|   |   |   |   |   |   |   |   |   |   |   |   start <= 34243:
mitochondrion_ (10.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 34243:
Golgi_apparatus_ (14.87)
|   |   |   |   |   |   |   |   |   |   |   start > 41794
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 46942:
nucleus_ (19.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 46942:
mitochondrion_ (22.7)
|   |   |   |   |   |   |   |   |   |   start > 51640: ribosome_
(22.57)
|   |   |   |   |   |   |   |   |   start > 56773
|   |   |   |   |   |   |   |   |   |   start <= 62322: cytoplasm_
(47.43)
|   |   |   |   |   |   |   |   |   |   start > 62322
|   |   |   |   |   |   |   |   |   |   |   start <= 68294
|   |   |   |   |   |   |   |   |   |   |   |   start <= 67549:
cellular_component_ (57.3/30.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 67549:
nucleolus_ (17.8)
|   |   |   |   |   |   |   |   |   |   |   start > 68294
|   |   |   |   |   |   |   |   |   |   |   |   start <= 70624:
cytoplasm_ (26.93/13.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 70624
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 77267:
nucleus_ (14.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 77267:
cytoplasm_ (19.61)
|   |   |   |   |   |   |   |   start > 79909
|   |   |   |   |   |   |   |   |   start <= 101862
|   |   |   |   |   |   |   |   |   |   start <= 97371
|   |   |   |   |   |   |   |   |   |   |   start <= 83090: nucleus_
(14.87)
|   |   |   |   |   |   |   |   |   |   |   start > 83090
|   |   |   |   |   |   |   |   |   |   |   |   start <= 86739:
cellular_component_ (12.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 86739
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 92235:
mitochondrion_ (31.24/10.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 92235
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
95369: cellular_component_ (11.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
95369: mitochondrion_ (13.87)
|   |   |   |   |   |   |   |   |   |   start > 97371
|   |   |   |   |   |   |   |   |   |   |   start <= 99400:
microtubule_organizing_center_ (10.29)
|   |   |   |   |   |   |   |   |   |   |   start > 99400:
cellular_component_ (14.56)
|   |   |   |   |   |   |   |   |   start > 101862
|   |   |   |   |   |   |   |   |   |   start <= 108806:
mitochondrion_ (25.54)
|   |   |   |   |   |   |   |   |   |   start > 108806: nucleus_
(32.0/12.1)
|   |   |   |   |   |   |   start > 115347
|   |   |   |   |   |   |   |   start <= 131572
|   |   |   |   |   |   |   |   |   start <= 124172
|   |   |   |   |   |   |   |   |   |   start <= 118898:
endomembrane_system_ (15.68)
```

```
|   |   |   |   |   |   |   |   |   |   start > 118898
|   |   |   |   |   |   |   |   |   |   |   start <= 121324:
nucleolus_ (18.01)
|   |   |   |   |   |   |   |   |   |   |   start > 121324:
ribosome_ (10.79)
|   |   |   |   |   |   |   |   |   start > 124172
|   |   |   |   |   |   |   |   |   |   start <= 129367:
mitochondrion_ (35.88/10.62)
|   |   |   |   |   |   |   |   |   |   start > 129367:
Golgi_apparatus_ (19.16)
|   |   |   |   |   |   |   |   start > 131572
|   |   |   |   |   |   |   |   |   start <= 146482
|   |   |   |   |   |   |   |   |   |   start <= 142210
|   |   |   |   |   |   |   |   |   |   |   start <= 135500:
cytoplasm_ (15.13)
|   |   |   |   |   |   |   |   |   |   |   start > 135500
|   |   |   |   |   |   |   |   |   |   |   |   start <= 140214:
cytoplasmic_membrane-bound_vesicle_ (8.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 140214:
cytoplasm_ (14.94)
|   |   |   |   |   |   |   |   |   |   start > 142210:
microtubule_organizing_center_ (18.22)
|   |   |   |   |   |   |   |   |   start > 146482
|   |   |   |   |   |   |   |   |   |   start <= 151871: nucleus_
(51.51/17.08)
|   |   |   |   |   |   |   |   |   |   start > 151871
|   |   |   |   |   |   |   |   |   |   |   start <= 163620
|   |   |   |   |   |   |   |   |   |   |   |   start <= 160180:
endoplasmic_reticulum_ (10.96)
|   |   |   |   |   |   |   |   |   |   |   |   start > 160180:
nucleolus_ (17.08)
|   |   |   |   |   |   |   |   |   |   |   start > 163620:
cytoplasm_ (18.68)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 110247
|   |   |   |   |   |   |   |   start <= 38196
|   |   |   |   |   |   |   |   |   start <= 26930: cytoplasm_
(32.12/14.46)
|   |   |   |   |   |   |   |   |   start > 26930
|   |   |   |   |   |   |   |   |   |   start <= 32334:
cellular_component_ (31.56)
|   |   |   |   |   |   |   |   |   |   start > 32334
|   |   |   |   |   |   |   |   |   |   |   start <= 34243:
cytoplasm_ (15.18)
|   |   |   |   |   |   |   |   |   |   |   start > 34243:
plasma_membrane_ (12.55)
|   |   |   |   |   |   |   |   start > 38196
|   |   |   |   |   |   |   |   |   start <= 70138
|   |   |   |   |   |   |   |   |   |   start <= 62322
|   |   |   |   |   |   |   |   |   |   |   start <= 45063: nucleus_
(31.21)
|   |   |   |   |   |   |   |   |   |   |   start > 45063
|   |   |   |   |   |   |   |   |   |   |   |   start <= 46942:
cytoplasm_ (10.56)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 46942
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 51640:
nucleus_ (17.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 51640
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: nucleus_ (24.69/10.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance <= 2022: cytoplasm_ (7.47/1.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance > 2022: nucleus_ (8.9/3.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F: cytoplasm_ (20.02/3.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance <= 1252: cytoplasm_ (2.93/0.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance > 1252: nucleus_ (14.59/5.21)
|   |   |   |   |   |   |   |   |   |   start > 62322
|   |   |   |   |   |   |   |   |   |   |   start <= 68294:
chromosome_ (19.36)
|   |   |   |   |   |   |   |   |   |   |   start > 68294:
cellular_component_ (18.33)
|   |   |   |   |   |   |   |   |   start > 70138
|   |   |   |   |   |   |   |   |   |   start <= 86739
|   |   |   |   |   |   |   |   |   |   |   start <= 82275
|   |   |   |   |   |   |   |   |   |   |   |   start <= 77267
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 70624:
cytoplasm_ (11.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 70624:
nucleus_ (15.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 77267:
cytoplasm_ (32.45)
|   |   |   |   |   |   |   |   |   |   |   start > 82275:
nucleolus_ (7.48)
|   |   |   |   |   |   |   |   |   |   start > 86739: nucleus_
(118.77/35.87)
|   |   |   |   |   |   |   start > 110247
|   |   |   |   |   |   |   |   start <= 121324
|   |   |   |   |   |   |   |   |   start <= 111002: mitochondrion_
(17.48)
|   |   |   |   |   |   |   |   |   start > 111002: Golgi_apparatus_
(20.72)
|   |   |   |   |   |   |   |   start > 121324
|   |   |   |   |   |   |   |   |   start <= 148683
|   |   |   |   |   |   |   |   |   |   start <= 133475: cytoplasm_
(28.1)
|   |   |   |   |   |   |   |   |   |   start > 133475
|   |   |   |   |   |   |   |   |   |   |   start <= 142210
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 1919
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 137550:
cellular_component_ (9.89/0.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 137550:
nucleus_ (2.33)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 1919:
nucleus_ (34.95/1.69)
|   |   |   |   |   |   |   |   |   |   |   start > 142210:
ribosome_ (13.19)
|   |   |   |   |   |   |   |   |   start > 148683
|   |   |   |   |   |   |   |   |   |   start <= 151871:
mitochondrion_ (14.24)
|   |   |   |   |   |   |   |   |   |   start > 151871
|   |   |   |   |   |   |   |   |   |   |   start <= 158760:
cytoplasm_ (21.86)
|   |   |   |   |   |   |   |   |   |   |   start > 158760
|   |   |   |   |   |   |   |   |   |   |   |   start <= 159383
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (13.45/4.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
nucleus_ (24.44/9.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 159383:
cytoplasm_ (19.3)
|   |   |   |   |   start > 164176
|   |   |   |   |   |   start <= 253272
|   |   |   |   |   |   |   start <= 196170
|   |   |   |   |   |   |   |   start <= 167781
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 167308:
mitochondrion_ (16.31)
|   |   |   |   |   |   |   |   |   |   start > 167308:
cellular_component_ (13.65)
|   |   |   |   |   |   |   |   |   strand = W:
endoplasmic_reticulum_ (30.56/11.88)
|   |   |   |   |   |   |   |   start > 167781
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 181474
|   |   |   |   |   |   |   |   |   |   |   start <= 178426:
nucleus_ (49.11/12.81)
|   |   |   |   |   |   |   |   |   |   |   start > 178426:
membrane_ (12.52)
|   |   |   |   |   |   |   |   |   |   start > 181474
|   |   |   |   |   |   |   |   |   |   |   start <= 192788
|   |   |   |   |   |   |   |   |   |   |   |   start <= 183968:
cytoplasm_ (17.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 183968:
nucleolus_ (13.76)
|   |   |   |   |   |   |   |   |   |   |   start > 192788
|   |   |   |   |   |   |   |   |   |   |   |   start <= 195755:
nucleus_ (15.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 195755:
cytoplasm_ (12.03)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 170402
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 168795:
cytoplasm_ (9.79)
|   |   |   |   |   |   |   |   |   |   |   start > 168795
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
mitochondrion_ (27.72/18.12)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: cell_cortex_ (21.99/12.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: plasma_membrane_ (24.47/14.29)
|   |   |   |   |   |   |   |   |   |   start > 170402
|   |   |   |   |   |   |   |   |   |   |   start <= 183968
|   |   |   |   |   |   |   |   |   |   |   |   start <= 171594:
cytoplasm_ (45.02/21.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 171594
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 178426
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
173139: cellular_component_ (14.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
173139: cytoplasm_ (11.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 178426:
nucleus_ (7.85)
|   |   |   |   |   |   |   |   |   |   |   start > 183968
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 3326:
mitochondrion_ (11.65/3.61)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 3326:
peroxisome_ (2.7/0.62)
|   |   |   |   |   |   |   start > 196170
|   |   |   |   |   |   |   |   start <= 243225
|   |   |   |   |   |   |   |   |   start <= 230813
|   |   |   |   |   |   |   |   |   |   start <= 220138
|   |   |   |   |   |   |   |   |   |   |   start <= 205642
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasmic_membrane-bound_vesicle_ (22.86)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (13.12)
|   |   |   |   |   |   |   |   |   |   |   start > 205642
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 209525:
cytoplasm_ (16.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 209525:
nucleus_ (8.68)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 216435
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
214189
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
209525: endomembrane_system_ (10.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
209525: microtubule_organizing_center_ (15.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
214189: mitochondrion_ (16.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 216435
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
217362
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance <= 1876: membrane_ (16.45/7.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance > 1876: endomembrane_system_ (13.33/5.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: endoplasmic_reticulum_ (10.35/4.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: membrane_ (9.57/2.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
217362: cytoplasm_ (12.54)
|   |   |   |   |   |   |   |   |   |   start > 220138
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 225889:
mitochondrion_ (22.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 225889
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 228937:
nucleus_ (12.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 228937:
mitochondrion_ (35.3/13.21)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 225889
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 221406:
nucleus_ (11.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 221406:
ribosome_ (22.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 225889:
nucleus_ (20.38/8.21)
|   |   |   |   |   |   |   |   |   start > 230813
|   |   |   |   |   |   |   |   |   |   start <= 235952
|   |   |   |   |   |   |   |   |   |   |   start <= 231149:
cellular_component_ (19.13)
|   |   |   |   |   |   |   |   |   |   |   start > 231149
|   |   |   |   |   |   |   |   |   |   |   |   start <= 233457:
endoplasmic_reticulum_ (30.97/11.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 233457:
vacuole_ (40.04/18.02)
|   |   |   |   |   |   |   |   |   |   start > 235952
|   |   |   |   |   |   |   |   |   |   |   start <= 241536:
cytoplasm_ (54.1/10.38)
|   |   |   |   |   |   |   |   |   |   |   start > 241536
|   |   |   |   |   |   |   |   |   |   |   |   start <= 243029:
cellular_component_ (28.92/9.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 243029:
nucleus_ (28.18/13.78)
|   |   |   |   |   |   |   |   start > 243225
|   |   |   |   |   |   |   |   |   start <= 246116
|   |   |   |   |   |   |   |   |   |   start <= 244149:
endoplasmic_reticulum_ (19.77)
```

```
|   |   |   |   |   |   |   |   |   |   start > 244149:
cytoplasmic_membrane-bound_vesicle_ (16.39)
|   |   |   |   |   |   |   |   |   start > 246116
|   |   |   |   |   |   |   |   |   |   start <= 247677
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2474:
nucleus_ (16.7/1.77)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2474:
mitochondrion_ (7.26/1.44)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(22.23/4.02)
|   |   |   |   |   |   |   |   |   |   start > 247677
|   |   |   |   |   |   |   |   |   |   |   start <= 252990
|   |   |   |   |   |   |   |   |   |   |   |   start <= 251516:
mitochondrion_ (14.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 251516:
endoplasmic_reticulum_ (40.62/18.78)
|   |   |   |   |   |   |   |   |   |   |   start > 252990:
mitochondrion_ (21.41)
|   |   |   |   |   |   start > 253272
|   |   |   |   |   |   |   start <= 276045
|   |   |   |   |   |   |   |   start <= 262685
|   |   |   |   |   |   |   |   |   start <= 260221
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 258416:
plasma_membrane_ (17.2)
|   |   |   |   |   |   |   |   |   |   |   start > 258416:
cytoplasm_ (22.89)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 253848
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cytoplasm_ (15.42/2.19)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (3.94/0.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
nucleus_ (6.88/1.14)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cytoplasm_ (8.09/3.11)
|   |   |   |   |   |   |   |   |   |   |   start > 253848:
cytoplasm_ (20.06)
|   |   |   |   |   |   |   |   |   start > 260221: nucleus_
(37.13/13.18)
|   |   |   |   |   |   |   |   start > 262685
|   |   |   |   |   |   |   |   |   start <= 267174
|   |   |   |   |   |   |   |   |   |   start <= 264541:
cellular_component_ (40.67)
|   |   |   |   |   |   |   |   |   |   start > 264541: vacuole_
(27.84/13.06)
|   |   |   |   |   |   |   |   |   start > 267174
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 271136:
nucleus_ (28.8)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 271136:
cellular_component_ (15.82)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 274017
|   |   |   |   |   |   |   |   |   |   |   |   start <= 272193:
nucleus_ (26.44/11.79)
|   |   |   |   |   |   |   |   |   |   |   |   start > 272193
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 273118:
mitochondrion_ (21.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 273118:
cytoplasm_ (9.27)
|   |   |   |   |   |   |   |   |   |   |   start > 274017: nucleus_
(20.95/6.59)
|   |   |   |   |   |   |   start > 276045
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 279681:
extracellular_region_ (12.64)
|   |   |   |   |   |   |   |   |   start > 279681: cell_wall_
(6.99)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 284101
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(12.02/4.3)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(9.55/2.75)
|   |   |   |   |   |   |   |   |   start > 284101
|   |   |   |   |   |   |   |   |   |   start <= 288078
|   |   |   |   |   |   |   |   |   |   |   start <= 285099:
cytoplasm_ (15.24)
|   |   |   |   |   |   |   |   |   |   |   start > 285099:
membrane_fraction_ (20.7/6.69)
|   |   |   |   |   |   |   |   |   |   start > 288078: cytoplasm_
(33.11)
|   |   |   |   start > 291133
|   |   |   |   |   start <= 298553
|   |   |   |   |   |   strand = C: endoplasmic_reticulum_
(50.97/28.93)
|   |   |   |   |   |   strand = W: nucleolus_ (116.82)
|   |   |   |   |   start > 298553
|   |   |   |   |   |   start <= 318417
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 302484:
endoplasmic_reticulum_ (19.27)
|   |   |   |   |   |   |   |   start > 302484: nucleus_ (41.21)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 312155
|   |   |   |   |   |   |   |   |   start <= 307488
|   |   |   |   |   |   |   |   |   |   start <= 302484: nucleus_
(20.19)
|   |   |   |   |   |   |   |   |   |   start > 302484: membrane_
(10.23)
|   |   |   |   |   |   |   |   |   start > 307488
|   |   |   |   |   |   |   |   |   |   start <= 310207:
cellular_component_ (16.67)
```

```
|   |   |   |   |   |   |   |   |   |   start > 310207: nucleus_
(19.89)
|   |   |   |   |   |   |   |   start > 312155: cytoplasm_ (15.07)
|   |   |   |   |   |   start > 318417: endoplasmic_reticulum_
(18.93)
|   |   |   start > 318679
|   |   |   |   start <= 366980
|   |   |   |   |   start <= 335297
|   |   |   |   |   |   start <= 334742
|   |   |   |   |   |   |   start <= 325876
|   |   |   |   |   |   |   |   start <= 321874
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 321016:
mitochondrion_ (11.6)
|   |   |   |   |   |   |   |   |   |   start > 321016: cytoplasm_
(13.35)
|   |   |   |   |   |   |   |   |   strand = W: mitochondrion_
(17.68)
|   |   |   |   |   |   |   |   start > 321874
|   |   |   |   |   |   |   |   |   strand = C: peroxisome_ (12.23)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 323299: nucleus_
(24.73)
|   |   |   |   |   |   |   |   |   |   start > 323299: cytoplasm_
(41.76/18.33)
|   |   |   |   |   |   |   start > 325876
|   |   |   |   |   |   |   |   start <= 330230: cellular_component_
(34.05)
|   |   |   |   |   |   |   |   start > 330230: mitochondrion_
(53.32/19.12)
|   |   |   |   |   |   start > 334742: cellular_bud_ (29.33/9.94)
|   |   |   |   |   start > 335297
|   |   |   |   |   |   start <= 341141
|   |   |   |   |   |   |   start <= 340721
|   |   |   |   |   |   |   |   strand = C: cellular_component_
(17.61)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 337312:
cellular_component_ (17.2)
|   |   |   |   |   |   |   |   |   start > 337312: nucleus_ (12.23)
|   |   |   |   |   |   |   start > 340721
|   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_component_:
mitochondrial_envelope_ (4.48/1.81)
|   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
mitochondrial_envelope_ (10.64/6.84)
|   |   |   |   |   |   |   |   NeighGO_term = molecular_function_:
membrane_ (11.02/6.74)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
mitochondrion_ (11.18/5.67)
|   |   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = transcription_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = electron_transport_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = biological_process_:
mitochondrial_envelope_ (12.9/6.81)
|   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
cellular_component_ (8.68/2.77)
|   |   |   |   |   |   |   |   NeighGO_term = transport_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
mitochondrial_envelope_ (5.09/2.84)
|   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: membrane_ (4.2/2.23)
|   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_:
mitochondrial_envelope_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = translation_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: mitochondrial_envelope_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: cellular_component_
(6.55/3.75)
|   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
mitochondrial_envelope_ (0.0)
```

```
|   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: mitochondrial_envelope_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: mitochondrial_envelope_
(0.0)
|   |   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: mitochondrial_envelope_ (0.0)
|   |   |   |   |   |   start > 341141
|   |   |   |   |   |   |   start <= 350380
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 346516
|   |   |   |   |   |   |   |   |   |   start <= 343519
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (22.28/10.27)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasm_ (15.99/4.51)
```

```
|   |   |   |   |   |   |   |   |   |   start > 343519: nucleus_
(23.74)
|   |   |   |   |   |   |   |   |   start > 346516
|   |   |   |   |   |   |   |   |   |   start <= 348259:
mitochondrial_envelope_ (41.63/18.42)
|   |   |   |   |   |   |   |   |   |   start > 348259: nucleus_
(19.14)
|   |   |   |   |   |   |   |   strand = W: ribosome_ (17.55)
|   |   |   |   |   |   |   start > 350380
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 355383:
cellular_component_ (15.76)
|   |   |   |   |   |   |   |   |   start > 355383: membrane_
(56.41/31.73)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 352279: cytoplasm_
(14.73)
|   |   |   |   |   |   |   |   |   start > 352279
|   |   |   |   |   |   |   |   |   |   start <= 355383: nucleus_
(59.5/13.98)
|   |   |   |   |   |   |   |   |   |   start > 355383
|   |   |   |   |   |   |   |   |   |   |   start <= 363063:
cytoplasm_ (10.92)
|   |   |   |   |   |   |   |   |   |   |   start > 363063: nucleus_
(23.45)
|   |   |   |   start > 366980
|   |   |   |   |   start <= 401540
|   |   |   |   |   |   start <= 387020
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 383302
|   |   |   |   |   |   |   |   |   start <= 370516: nucleus_
(28.8/13.51)
|   |   |   |   |   |   |   |   |   start > 370516
|   |   |   |   |   |   |   |   |   |   start <= 379585: cytoplasm_
(18.88)
|   |   |   |   |   |   |   |   |   |   start > 379585: nucleus_
(15.35)
|   |   |   |   |   |   |   |   start > 383302:
microtubule_organizing_center_ (19.24)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 379585:
endoplasmic_reticulum_ (6.41)
|   |   |   |   |   |   |   |   start > 379585: Golgi_apparatus_
(14.33)
|   |   |   |   |   |   start > 387020
|   |   |   |   |   |   |   start <= 391098
|   |   |   |   |   |   |   |   strand = C: mitochondrion_ (17.78)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 388821:
plasma_membrane_ (14.54)
|   |   |   |   |   |   |   |   |   start > 388821: nucleus_
(33.47/15.83)
|   |   |   |   |   |   |   start > 391098
|   |   |   |   |   |   |   |   start <= 397076
```

```
|   |   |   |   |   |   |   |   |   start <= 396378: mitochondrion_
(82.65/14.85)
|   |   |   |   |   |   |   |   |   start > 396378:
cellular_component_ (13.79)
|   |   |   |   |   |   |   |   start > 397076: mitochondrion_
(49.07)
|   |   |   |   |   start > 401540
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 411568
|   |   |   |   |   |   |   |   start <= 407708: cytoplasm_
(40.67/12.44)
|   |   |   |   |   |   |   |   start > 407708:
cytoplasmic_membrane-bound_vesicle_ (16.42)
|   |   |   |   |   |   |   start > 411568: cytoplasm_ (41.35/9.89)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 407708
|   |   |   |   |   |   |   |   start <= 406303: cytoplasm_ (20.99)
|   |   |   |   |   |   |   |   start > 406303
|   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(17.03/3.45)
|   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(30.36/12.66)
|   |   |   |   |   |   |   start > 407708
|   |   |   |   |   |   |   |   distance <= 841: mitochondrion_
(10.4/0.48)
|   |   |   |   |   |   |   |   distance > 841
|   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
mitochondrion_ (5.81/0.83)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(22.2/4.25)
|   |   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(17.32)
|   start > 413981
|   |   start <= 610364
|   |   |   start <= 573330
|   |   |   |   start <= 558523
|   |   |   |   |   start <= 502733
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   stop <= 499455
|   |   |   |   |   |   |   |   start <= 449244
|   |   |   |   |   |   |   |   |   start <= 420028: chromosome_
(18.25)
|   |   |   |   |   |   |   |   |   start > 420028
|   |   |   |   |   |   |   |   |   |   start <= 437490
|   |   |   |   |   |   |   |   |   |   |   start <= 429626
|   |   |   |   |   |   |   |   |   |   |   |   start <= 422148:
cytoplasm_ (26.95)
|   |   |   |   |   |   |   |   |   |   |   |   start > 422148
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 424988:
mitochondrion_ (17.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 424988:
cytoplasm_ (9.91)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 429626:
cellular_component_ (17.07)
|   |   |   |   |   |   |   |   |   |   start > 437490
|   |   |   |   |   |   |   |   |   |   |   start <= 445101:
membrane_ (22.33/10.91)
|   |   |   |   |   |   |   |   |   |   |   start > 445101:
cytoplasm_ (34.09/11.47)
|   |   |   |   |   |   |   |   start > 449244
|   |   |   |   |   |   |   |   |   start <= 491991
|   |   |   |   |   |   |   |   |   |   start <= 480189
|   |   |   |   |   |   |   |   |   |   |   start <= 463553
|   |   |   |   |   |   |   |   |   |   |   |   start <= 458407
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 451364:
nucleus_ (15.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 451364
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
454014
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: nucleus_ (20.19/7.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: cytoplasm_ (17.57/5.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
454014: cytoplasm_ (17.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 458407:
mitochondrion_ (28.91)
|   |   |   |   |   |   |   |   |   |   |   start > 463553
|   |   |   |   |   |   |   |   |   |   |   |   start <= 478063
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 475452
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
469475
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
466299
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: nucleus_ (10.6/4.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: cytoplasm_ (17.66/7.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
466299: cytoplasm_ (12.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
469475
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
472351: cellular_component_ (12.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
472351
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance <= 6654: cytoplasm_ (15.43/6.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
distance > 6654: nucleus_ (3.54/0.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 475452:
cytoplasm_ (19.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 478063:
nucleus_ (18.89)
|   |   |   |   |   |   |   |   |   |   start > 480189:
mitochondrion_ (28.31)
```

```
|   |   |   |   |   |   |   |   |   start > 491991
|   |   |   |   |   |   |   |   |   |   start <= 497703: nucleus_
(97.01/36.91)
|   |   |   |   |   |   |   |   |   |   start > 497703: cytoplasm_
(10.24)
|   |   |   |   |   |   |   stop > 499455
|   |   |   |   |   |   |   |   start <= 500687: nucleolus_ (24.62)
|   |   |   |   |   |   |   |   start > 500687
|   |   |   |   |   |   |   |   |   start <= 501890: chromosome_
(10.15)
|   |   |   |   |   |   |   |   |   start > 501890:
cellular_component_ (21.39)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 483013
|   |   |   |   |   |   |   |   start <= 434787
|   |   |   |   |   |   |   |   |   start <= 429626: cytoplasm_
(39.27/15.33)
|   |   |   |   |   |   |   |   |   start > 429626: mitochondrion_
(8.81)
|   |   |   |   |   |   |   |   start > 434787
|   |   |   |   |   |   |   |   |   start <= 454014
|   |   |   |   |   |   |   |   |   |   start <= 451364
|   |   |   |   |   |   |   |   |   |   |   start <= 437490:
cellular_component_ (21.95)
|   |   |   |   |   |   |   |   |   |   |   start > 437490
|   |   |   |   |   |   |   |   |   |   |   |   start <= 439207:
ribosome_ (23.09/8.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 439207
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 445101:
cellular_component_ (12.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 445101:
cytoplasm_ (14.58)
|   |   |   |   |   |   |   |   |   |   start > 451364: nucleolus_
(18.56)
|   |   |   |   |   |   |   |   |   start > 454014
|   |   |   |   |   |   |   |   |   |   start <= 455824: chromosome_
(13.68)
|   |   |   |   |   |   |   |   |   |   start > 455824
|   |   |   |   |   |   |   |   |   |   |   start <= 464826
|   |   |   |   |   |   |   |   |   |   |   |   start <= 460526:
cellular_component_ (17.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 460526:
cytoplasm_ (18.92)
|   |   |   |   |   |   |   |   |   |   |   start > 464826:
cellular_component_ (43.47)
|   |   |   |   |   |   |   start > 483013
|   |   |   |   |   |   |   |   start <= 486586
|   |   |   |   |   |   |   |   |   start <= 484083: mitochondrion_
(12.06)
|   |   |   |   |   |   |   |   |   start > 484083: cytoskeleton_
(29.91/10.85)
|   |   |   |   |   |   |   |   start > 486586
|   |   |   |   |   |   |   |   |   start <= 494998: cytoplasm_
(24.9)
```

```
|   |   |   |   |   |   |   |   |   start > 494998: mitochondrion_
(15.76)
|   |   |   |   |   start > 502733
|   |   |   |   |   |   start <= 513592
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 509279: cytoplasm_ (8.23)
|   |   |   |   |   |   |   |   start > 509279: ribosome_ (20.07)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 504894: cytoplasm_ (16.83)
|   |   |   |   |   |   |   |   start > 504894
|   |   |   |   |   |   |   |   |   start <= 505332
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   distance <= 641:
endoplasmic_reticulum_ (5.64/2.79)
|   |   |   |   |   |   |   |   |   |   |   distance > 641:
membrane_ (20.67/6.82)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   distance <= 2974:
endomembrane_system_ (12.77/6.92)
|   |   |   |   |   |   |   |   |   |   |   distance > 2974:
endoplasmic_reticulum_ (7.8/3.27)
|   |   |   |   |   |   |   |   |   start > 505332
|   |   |   |   |   |   |   |   |   |   start <= 511314: cytoplasm_
(28.4/10.29)
|   |   |   |   |   |   |   |   |   |   start > 511314
|   |   |   |   |   |   |   |   |   |   |   distance <= 2214:
membrane_ (14.64/7.91)
|   |   |   |   |   |   |   |   |   |   |   distance > 2214:
endomembrane_system_ (30.55/18.27)
|   |   |   |   |   |   start > 513592
|   |   |   |   |   |   |   start <= 536206
|   |   |   |   |   |   |   |   start <= 523344
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 521788:
cellular_component_ (9.25)
|   |   |   |   |   |   |   |   |   |   start > 521788: nucleus_
(24.14/12.03)
|   |   |   |   |   |   |   |   |   strand = W: cytoplasm_
(29.06/7.51)
|   |   |   |   |   |   |   |   start > 523344
|   |   |   |   |   |   |   |   |   start <= 534697
|   |   |   |   |   |   |   |   |   |   start <= 527803
|   |   |   |   |   |   |   |   |   |   |   start <= 523695
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleolus_ (10.22/3.47)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
mitochondrion_ (18.46/5.23)
|   |   |   |   |   |   |   |   |   |   |   start > 523695:
mitochondrion_ (15.65)
|   |   |   |   |   |   |   |   |   |   start > 527803
|   |   |   |   |   |   |   |   |   |   |   start <= 532118:
cellular_component_ (13.04)
|   |   |   |   |   |   |   |   |   |   |   start > 532118:
nucleolus_ (17.22)
```

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|   |   |   |   |   |   |   |   |   start > 534697
|   |   |   |   |   |   |   |   |   |   start <= 535569: cytoplasm_
(19.15)
|   |   |   |   |   |   |   |   |   |   start > 535569: chromosome_
(22.93)
|   |   |   |   |   |   |   start > 536206
|   |   |   |   |   |   |   |   start <= 547713
|   |   |   |   |   |   |   |   |   start <= 537837
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
endoplasmic_reticulum_ (14.08/4.6)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(12.45/4.77)
|   |   |   |   |   |   |   |   |   start > 537837
|   |   |   |   |   |   |   |   |   |   start <= 544962
|   |   |   |   |   |   |   |   |   |   |   start <= 540055:
cytoplasm_ (45.71/14.05)
|   |   |   |   |   |   |   |   |   |   |   start > 540055: nucleus_
(28.0)
|   |   |   |   |   |   |   |   |   |   start > 544962: cytoplasm_
(27.22)
|   |   |   |   |   |   |   |   start > 547713
|   |   |   |   |   |   |   |   |   start <= 553361
|   |   |   |   |   |   |   |   |   |   start <= 551927: ribosome_
(21.77)
|   |   |   |   |   |   |   |   |   |   start > 551927: nucleus_
(8.96)
|   |   |   |   |   |   |   |   |   start > 553361
|   |   |   |   |   |   |   |   |   |   start <= 556474:
mitochondrion_ (9.41)
|   |   |   |   |   |   |   |   |   |   start > 556474: cytoplasm_
(18.24)
|   |   |   |   start > 558523
|   |   |   |   |   start <= 564434
|   |   |   |   |   |   start <= 563095
|   |   |   |   |   |   |   start <= 560995
|   |   |   |   |   |   |   |   start <= 559198: cellular_component_
(14.31)
|   |   |   |   |   |   |   |   start > 559198: membrane_
(39.47/8.38)
|   |   |   |   |   |   |   start > 560995
|   |   |   |   |   |   |   |   start <= 562527: mitochondrion_
(8.87)
|   |   |   |   |   |   |   |   start > 562527
|   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: cytoplasm_ (2.59/0.5)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: cytoplasm_ (5.75/1.13)
|   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
mitochondrion_ (2.79/0.56)
```

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|   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = transcription_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
cytoplasm_ (8.05/2.69)
|   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: mitochondrion_ (10.2/4.35)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: mitochondrion_ (0.36/0.17)
|   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
mitochondrion_ (3.67/1.39)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: mitochondrion_ (3.85/0.58)
|   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   start > 563095: nucleus_ (63.84/32.98)
|   |   |   |   |   start > 564434
|   |   |   |   |   |   start <= 571015: cellular_component_ (64.44)
|   |   |   |   |   |   start > 571015
|   |   |   |   |   |   |   start <= 572247: mitochondrion_ (36.19)
|   |   |   |   |   |   |   start > 572247
|   |   |   |   |   |   |   |   start <= 572954: cytoplasm_ (13.48)
|   |   |   |   |   |   |   |   start > 572954: cellular_component_
(16.71)
|   |   |   start > 573330
|   |   |   |   start <= 583920
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 577717: membrane_fraction_ (12.67)
|   |   |   |   |   |   start > 577717: cytoplasmic_membrane-
bound_vesicle_ (26.83)
|   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   start <= 575065
|   |   |   |   |   |   |   neigh_strand = W: membrane_ (12.51/3.22)
|   |   |   |   |   |   |   neigh_strand = C: vacuole_ (17.21/6.78)
|   |   |   |   |   |   start > 575065: endoplasmic_reticulum_
(24.65)
|   |   |   |   start > 583920
|   |   |   |   |   start <= 594885
|   |   |   |   |   |   start <= 586708
|   |   |   |   |   |   |   start <= 586387: peroxisome_
(45.57/15.71)
|   |   |   |   |   |   |   start > 586387: cytoplasm_ (24.81)
|   |   |   |   |   |   start > 586708
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 592627
|   |   |   |   |   |   |   |   |   start <= 589549: nucleus_
(18.59)
|   |   |   |   |   |   |   |   |   start > 589549:
membrane_fraction_ (43.08/18.51)
|   |   |   |   |   |   |   |   start > 592627:
mitochondrial_envelope_ (29.71)
|   |   |   |   |   |   |   strand = W: nucleus_ (56.35/33.43)
|   |   |   |   |   start > 594885
|   |   |   |   |   |   start <= 599157: chromosome_ (19.36)
|   |   |   |   |   |   start > 599157
|   |   |   |   |   |   |   strand = C: cytoplasm_ (70.45)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 605980: chromosome_ (13.46)
|   |   |   |   |   |   |   |   start > 605980: cytoplasm_ (8.92)
|   |   start > 610364
|   |   |   start <= 806422
|   |   |   |   start <= 721402
|   |   |   |   |   start <= 655075
|   |   |   |   |   |   start <= 625810
|   |   |   |   |   |   |   start <= 616565
|   |   |   |   |   |   |   |   start <= 611313: cellular_component_
(23.85)
|   |   |   |   |   |   |   |   start > 611313
|   |   |   |   |   |   |   |   |   start <= 611739: nucleus_
(16.17)
|   |   |   |   |   |   |   |   |   start > 611739: mitochondrion_
(16.6)
|   |   |   |   |   |   |   start > 616565
|   |   |   |   |   |   |   |   start <= 623212
|   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(26.34/9.8)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 618478: cytoplasm_
(28.87/12.25)
|   |   |   |   |   |   |   |   |   |   start > 618478: nucleus_
(20.12)
|   |   |   |   |   |   |   |   start > 623212
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 624079:
cellular_component_ (19.92)
```

```
|   |   |   |   |   |   |   |   |   |   start > 624079: nucleus_
(18.01)
|   |   |   |   |   |   |   |   |   strand = W: cellular_component_
(20.3)
|   |   |   |   |   |   start > 625810
|   |   |   |   |   |   |   start <= 628188
|   |   |   |   |   |   |   |   start <= 626348: nucleolus_ (17.94)
|   |   |   |   |   |   |   |   start > 626348
|   |   |   |   |   |   |   |   |   start <= 627807
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
endoplasmic_reticulum_ (18.47/9.36)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
membrane_fraction_ (32.64/17.15)
|   |   |   |   |   |   |   |   |   start > 627807: cytoplasm_
(22.7)
|   |   |   |   |   |   |   start > 628188
|   |   |   |   |   |   |   |   start <= 652886
|   |   |   |   |   |   |   |   |   start <= 635983
|   |   |   |   |   |   |   |   |   |   start <= 629024:
cellular_component_ (17.62)
|   |   |   |   |   |   |   |   |   |   start > 629024
|   |   |   |   |   |   |   |   |   |   |   start <= 632354:
cytoplasm_ (33.38/9.11)
|   |   |   |   |   |   |   |   |   |   |   start > 632354:
cellular_component_ (13.87)
|   |   |   |   |   |   |   |   |   start > 635983
|   |   |   |   |   |   |   |   |   |   start <= 650035
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 637499:
mitochondrion_ (13.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 637499:
nucleolus_ (18.12)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 645655
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 637499:
mitochondrion_ (12.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 637499:
cellular_component_ (11.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 645655:
mitochondrion_ (63.43/32.49)
|   |   |   |   |   |   |   |   |   |   start > 650035
|   |   |   |   |   |   |   |   |   |   |   strand = C:
cellular_component_ (15.52)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 651144:
ribosome_ (7.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 651144:
nucleolus_ (11.71)
|   |   |   |   |   |   |   |   start > 652886
|   |   |   |   |   |   |   |   |   start <= 654033: membrane_
(33.35/13.05)
|   |   |   |   |   |   |   |   |   start > 654033: cytoplasm_
(14.9)
|   |   |   |   |   start > 655075
```

```
|   |   |   |   |   |   start <= 659744
|   |   |   |   |   |   |   start <= 659197: Golgi_apparatus_
(36.96/13.28)
|   |   |   |   |   |   |   start > 659197:
microtubule_organizing_center_ (23.37)
|   |   |   |   |   |   start > 659744
|   |   |   |   |   |   |   start <= 667536
|   |   |   |   |   |   |   |   start <= 667043
|   |   |   |   |   |   |   |   |   start <= 662643: nucleus_
(39.59/17.32)
|   |   |   |   |   |   |   |   |   start > 662643
|   |   |   |   |   |   |   |   |   |   start <= 664751:
endoplasmic_reticulum_ (16.23)
|   |   |   |   |   |   |   |   |   |   start > 664751: nucleus_
(20.88)
|   |   |   |   |   |   |   |   start > 667043
|   |   |   |   |   |   |   |   |   start <= 667455:
cellular_component_ (19.95)
|   |   |   |   |   |   |   |   |   start > 667455:
endoplasmic_reticulum_ (13.92)
|   |   |   |   |   |   |   start > 667536
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 671324: peroxisome_
(18.38)
|   |   |   |   |   |   |   |   |   start > 671324
|   |   |   |   |   |   |   |   |   |   start <= 716714
|   |   |   |   |   |   |   |   |   |   |   start <= 696795
|   |   |   |   |   |   |   |   |   |   |   |   start <= 689082
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 684466:
mitochondrion_ (40.58/13.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 684466:
cellular_component_ (10.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 689082:
mitochondrion_ (22.39)
|   |   |   |   |   |   |   |   |   |   |   start > 696795
|   |   |   |   |   |   |   |   |   |   |   |   start <= 707132
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 701789:
cytoplasm_ (12.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 701789:
Golgi_apparatus_ (20.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 707132
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 715444:
mitochondrion_ (17.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 715444:
cytoplasm_ (20.88)
|   |   |   |   |   |   |   |   |   |   start > 716714
|   |   |   |   |   |   |   |   |   |   |   start <= 720652:
nucleus_ (39.13/16.59)
|   |   |   |   |   |   |   |   |   |   |   start > 720652:
mitochondrion_ (24.02)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 689082
|   |   |   |   |   |   |   |   |   |   start <= 687515
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 671324:
mitochondrion_ (12.94)
|   |   |   |   |   |   |   |   |   |   |   start > 671324
|   |   |   |   |   |   |   |   |   |   |   |   start <= 684466
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 675895:
cellular_component_ (14.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 675895:
cytoplasm_ (15.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 684466:
cellular_component_ (16.78)
|   |   |   |   |   |   |   |   |   |   start > 687515:
mitochondrion_ (31.61/15.67)
|   |   |   |   |   |   |   |   |   start > 689082
|   |   |   |   |   |   |   |   |   |   start <= 696795
|   |   |   |   |   |   |   |   |   |   |   start <= 693380:
nucleus_ (18.91)
|   |   |   |   |   |   |   |   |   |   |   start > 693380
|   |   |   |   |   |   |   |   |   |   |   |   start <= 695349:
endoplasmic_reticulum_ (12.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 695349:
membrane_fraction_ (12.39)
|   |   |   |   |   |   |   |   |   |   start > 696795
|   |   |   |   |   |   |   |   |   |   |   start <= 701789:
cellular_component_ (14.37)
|   |   |   |   |   |   |   |   |   |   |   start > 701789
|   |   |   |   |   |   |   |   |   |   |   |   start <= 712315
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 707132:
nucleus_ (18.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 707132:
cytoplasm_ (11.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 712315:
cellular_component_ (34.96/15.07)
|   |   |   |   start > 721402
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 768038
|   |   |   |   |   |   |   start <= 763112
|   |   |   |   |   |   |   |   start <= 754296
|   |   |   |   |   |   |   |   |   start <= 751960
|   |   |   |   |   |   |   |   |   |   start <= 724625
|   |   |   |   |   |   |   |   |   |   |   start <= 722395:
cytoplasm_ (41.37/26.66)
|   |   |   |   |   |   |   |   |   |   |   start > 722395: nucleus_
(14.15)
|   |   |   |   |   |   |   |   |   |   start > 724625
|   |   |   |   |   |   |   |   |   |   |   start <= 736925:
nucleolus_ (20.53)
|   |   |   |   |   |   |   |   |   |   |   start > 736925
|   |   |   |   |   |   |   |   |   |   |   |   start <= 747962
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 743748:
nucleus_ (15.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 743748:
cytoplasm_ (12.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 747962
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 749676:
nucleolus_ (23.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 749676:
nucleus_ (12.21)
|   |   |   |   |   |   |   |   |   start > 751960: ribosome_
(12.58)
|   |   |   |   |   |   |   |   start > 754296
|   |   |   |   |   |   |   |   |   start <= 757249: vacuole_
(17.12)
|   |   |   |   |   |   |   |   |   start > 757249
|   |   |   |   |   |   |   |   |   |   start <= 759806: cytoplasm_
(28.9/9.15)
|   |   |   |   |   |   |   |   |   |   start > 759806: nucleolus_
(12.47)
|   |   |   |   |   |   |   start > 763112
|   |   |   |   |   |   |   |   distance <= 3051: nucleus_
(13.26/2.18)
|   |   |   |   |   |   |   |   distance > 3051: ribosome_
(22.14/7.28)
|   |   |   |   |   |   start > 768038
|   |   |   |   |   |   |   start <= 794918
|   |   |   |   |   |   |   |   start <= 782030
|   |   |   |   |   |   |   |   |   start <= 778000
|   |   |   |   |   |   |   |   |   |   start <= 770800: cytoplasm_
(26.97)
|   |   |   |   |   |   |   |   |   |   start > 770800
|   |   |   |   |   |   |   |   |   |   |   start <= 775718:
mitochondrion_ (11.41)
|   |   |   |   |   |   |   |   |   |   |   start > 775718:
cytoplasm_ (21.1)
|   |   |   |   |   |   |   |   |   start > 778000: mitochondrion_
(28.7)
|   |   |   |   |   |   |   |   start > 782030
|   |   |   |   |   |   |   |   |   start <= 784280
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: nucleus_
(27.78/9.96)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: cytoplasm_
(15.52/5.37)
|   |   |   |   |   |   |   |   |   start > 784280
|   |   |   |   |   |   |   |   |   |   start <= 789838
|   |   |   |   |   |   |   |   |   |   |   start <= 788882:
cytoplasm_ (18.7)
|   |   |   |   |   |   |   |   |   |   |   start > 788882:
ribosome_ (24.79)
|   |   |   |   |   |   |   |   |   |   start > 789838: cytoplasm_
(26.51)
|   |   |   |   |   |   |   start > 794918
|   |   |   |   |   |   |   |   start <= 798517: cellular_component_
(16.66)
|   |   |   |   |   |   |   |   start > 798517
|   |   |   |   |   |   |   |   |   start <= 804455: nucleus_
(21.08)
|   |   |   |   |   |   |   |   |   start > 804455: nucleolus_
(13.78)
```

```
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 736925
|   |   |   |   |   |   |   start <= 733267
|   |   |   |   |   |   |   |   start <= 732413
|   |   |   |   |   |   |   |   |   start <= 724625: mitochondrion_
(15.31)
|   |   |   |   |   |   |   |   |   start > 724625: ribosome_ (9.69)
|   |   |   |   |   |   |   |   start > 732413: cellular_component_
(16.55)
|   |   |   |   |   |   |   start > 733267
|   |   |   |   |   |   |   |   start <= 733544: vacuole_
(41.6/19.71)
|   |   |   |   |   |   |   |   start > 733544: mitochondrion_
(31.47)
|   |   |   |   |   |   start > 736925
|   |   |   |   |   |   |   start <= 794918
|   |   |   |   |   |   |   |   start <= 743748
|   |   |   |   |   |   |   |   |   start <= 739184: nucleolus_
(49.56/29.54)
|   |   |   |   |   |   |   |   |   start > 739184
|   |   |   |   |   |   |   |   |   |   start <= 742970
|   |   |   |   |   |   |   |   |   |   |   start <= 740265:
nucleus_ (20.81)
|   |   |   |   |   |   |   |   |   |   |   start > 740265:
cellular_component_ (36.03/16.01)
|   |   |   |   |   |   |   |   |   |   start > 742970: ribosome_
(18.72)
|   |   |   |   |   |   |   |   start > 743748
|   |   |   |   |   |   |   |   |   start <= 784280
|   |   |   |   |   |   |   |   |   |   start <= 769282
|   |   |   |   |   |   |   |   |   |   |   start <= 751960
|   |   |   |   |   |   |   |   |   |   |   |   start <= 747962:
plasma_membrane_ (15.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 747962:
mitochondrion_ (16.44)
|   |   |   |   |   |   |   |   |   |   |   start > 751960
|   |   |   |   |   |   |   |   |   |   |   |   start <= 757249:
cellular_component_ (42.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 757249
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 763112:
cytoplasm_ (15.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 763112:
cellular_component_ (15.66)
|   |   |   |   |   |   |   |   |   |   start > 769282
|   |   |   |   |   |   |   |   |   |   |   start <= 772914:
cytoplasm_ (33.25)
|   |   |   |   |   |   |   |   |   |   |   start > 772914
|   |   |   |   |   |   |   |   |   |   |   |   start <= 775718:
membrane_fraction_ (41.91/25.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 775718:
cytoplasm_ (16.87)
|   |   |   |   |   |   |   |   |   start > 784280
|   |   |   |   |   |   |   |   |   |   start <= 793725:
cellular_component_ (26.21)
```

```
|   |   |   |   |   |   |   |   |   |   start > 793725
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleus_ (20.37/3.89)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cellular_component_ (17.19/7.05)
|   |   |   |   |   |   |   start > 794918
|   |   |   |   |   |   |   |   start <= 801771
|   |   |   |   |   |   |   |   |   start <= 795804: mitochondrion_
(19.59)
|   |   |   |   |   |   |   |   |   start > 795804
|   |   |   |   |   |   |   |   |   |   start <= 798517: membrane_
(15.8)
|   |   |   |   |   |   |   |   |   |   start > 798517:
mitochondrion_ (16.42)
|   |   |   |   |   |   |   |   start > 801771
|   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
nucleolus_ (9.08/2.16)
|   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: ribosome_ (1.74/0.43)
|   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = transcription_:
nucleolus_ (9.61/4.31)
|   |   |   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
nucleolus_ (2.94/1.01)
|   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: nucleolus_ (2.42/0.46)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: nucleolus_ (1.44/0.59)
|   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = protein_binding_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
ribosome_ (4.66/1.7)
|   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: ribosome_ (3.51/0.55)
|   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: ribosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
ribosome_ (7.69/1.05)
|   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_budding_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = motor_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: ribosome_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: ribosome_ (0.0)
|   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: ribosome_ (0.0)
|   |   |   start > 806422
|   |   |   |   start <= 887002
|   |   |   |   |   start <= 854794
|   |   |   |   |   |   start <= 832338
|   |   |   |   |   |   |   start <= 818580
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 815310
|   |   |   |   |   |   |   |   |   |   start <= 808316: cytoplasm_
(21.22)
|   |   |   |   |   |   |   |   |   |   start > 808316
|   |   |   |   |   |   |   |   |   |   |   start <= 811088:
endoplasmic_reticulum_ (32.39/11.21)
|   |   |   |   |   |   |   |   |   |   |   start > 811088
|   |   |   |   |   |   |   |   |   |   |   |   start <= 813979:
cytoplasm_ (19.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 813979:
endoplasmic_reticulum_ (16.86)
|   |   |   |   |   |   |   |   |   start > 815310: plasma_membrane_
(9.7)
|   |   |   |   |   |   |   |   strand = W: cellular_component_
(12.44)
|   |   |   |   |   |   |   start > 818580
|   |   |   |   |   |   |   |   start <= 831328
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 826350:
cellular_component_ (19.3)
|   |   |   |   |   |   |   |   |   |   start > 826350: nucleus_
(11.25)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 820255: nucleus_
(28.99)
|   |   |   |   |   |   |   |   |   |   start > 820255: cytoplasm_
(29.06/9.64)
|   |   |   |   |   |   |   |   start > 831328: endomembrane_system_
(31.63/19.73)
|   |   |   |   |   |   start > 832338
|   |   |   |   |   |   |   start <= 845344
|   |   |   |   |   |   |   |   start <= 837927
|   |   |   |   |   |   |   |   |   start <= 835097: mitochondrion_
(21.8)
|   |   |   |   |   |   |   |   |   start > 835097: cytoplasm_
(30.72)
|   |   |   |   |   |   |   |   start > 837927
|   |   |   |   |   |   |   |   |   start <= 841690
```

```
|   |   |   |   |   |   |   |   |   |   start <= 838186:
endomembrane_system_ (16.58)
|   |   |   |   |   |   |   |   |   |   start > 838186:
cellular_component_ (17.12)
|   |   |   |   |   |   |   |   |   start > 841690: mitochondrion_
(28.41)
|   |   |   |   |   |   |   start > 845344
|   |   |   |   |   |   |   |   strand = C: nucleolus_ (15.66)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 852629
|   |   |   |   |   |   |   |   |   |   start <= 845570: nucleus_
(15.62)
|   |   |   |   |   |   |   |   |   |   start > 845570
|   |   |   |   |   |   |   |   |   |   |   start <= 848684:
cytoplasm_ (18.38)
|   |   |   |   |   |   |   |   |   |   |   start > 848684: nucleus_
(26.24/10.15)
|   |   |   |   |   |   |   |   |   start > 852629:
endomembrane_system_ (9.6)
|   |   |   |   |   start > 854794
|   |   |   |   |   |   start <= 858889
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 856965: mitochondrion_
(15.5)
|   |   |   |   |   |   |   |   start > 856965: ribosome_
(37.54/17.16)
|   |   |   |   |   |   |   strand = W: cytoskeleton_ (11.75)
|   |   |   |   |   |   start > 858889
|   |   |   |   |   |   |   start <= 880231
|   |   |   |   |   |   |   |   start <= 865349
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 861921:
membrane_fraction_ (14.47)
|   |   |   |   |   |   |   |   |   |   start > 861921:
cytoskeleton_ (15.72)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 861921: cytoplasm_
(33.91/16.32)
|   |   |   |   |   |   |   |   |   |   start > 861921:
endoplasmic_reticulum_ (13.51)
|   |   |   |   |   |   |   |   start > 865349
|   |   |   |   |   |   |   |   |   start <= 872624
|   |   |   |   |   |   |   |   |   |   start <= 867090: cytoplasm_
(9.12)
|   |   |   |   |   |   |   |   |   |   start > 867090:
mitochondrion_ (31.12)
|   |   |   |   |   |   |   |   |   start > 872624
|   |   |   |   |   |   |   |   |   |   start <= 874986: cytoplasm_
(18.42)
|   |   |   |   |   |   |   |   |   |   start > 874986:
endoplasmic_reticulum_ (22.36/8.41)
|   |   |   |   |   |   |   start > 880231
|   |   |   |   |   |   |   |   start <= 881158: mitochondrion_
(16.2)
```

```
|   |   |   |   |   |   |   |   start > 881158
|   |   |   |   |   |   |   |   |   neigh_num <= 1: mitochondrion_
(10.45/4.29)
|   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
mitochondrion_ (16.73/9.31)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   distance <= 738:
plasma_membrane_ (5.06/1.54)
|   |   |   |   |   |   |   |   |   |   |   distance > 738:
membrane_fraction_ (8.76/1.94)
|   |   |   |   start > 887002
|   |   |   |   |   start <= 902799
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 898404
|   |   |   |   |   |   |   |   start <= 895425
|   |   |   |   |   |   |   |   |   start <= 892220: nucleus_
(33.13/14.66)
|   |   |   |   |   |   |   |   |   start > 892220: cytoplasm_
(21.81)
|   |   |   |   |   |   |   |   start > 895425: nucleus_
(35.76/6.24)
|   |   |   |   |   |   |   start > 898404: cytoplasm_ (16.02)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 901708
|   |   |   |   |   |   |   |   start <= 898404: nucleus_
(24.83/11.55)
|   |   |   |   |   |   |   |   start > 898404: cellular_component_
(11.6)
|   |   |   |   |   |   |   start > 901708: nucleus_ (19.34/9.28)
|   |   |   |   |   start > 902799
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 914536
|   |   |   |   |   |   |   |   start <= 912141: cellular_component_
(8.83)
|   |   |   |   |   |   |   |   start > 912141: plasma_membrane_
(13.87)
|   |   |   |   |   |   |   start > 914536: cellular_component_
(24.79)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 904285: cellular_component_
(19.32)
|   |   |   |   |   |   |   start > 904285
|   |   |   |   |   |   |   |   start <= 904823: cytoplasm_ (11.42)
|   |   |   |   |   |   |   |   start > 904823
|   |   |   |   |   |   |   |   |   start <= 912141:
cellular_component_ (14.5)
|   |   |   |   |   |   |   |   |   start > 912141
|   |   |   |   |   |   |   |   |   |   start <= 920086: cytoplasm_
(9.97)
|   |   |   |   |   |   |   |   |   |   start > 920086:
cellular_component_ (7.21)
```

For Molecular Function

```
|   start <= 858889
|   |   start <= 445101
|   |   |   start <= 298553
|   |   |   |   start <= 296737
|   |   |   |   |   start <= 181474
|   |   |   |   |   |   start <= 67549
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 13175
|   |   |   |   |   |   |   |   |   start <= 7244:
helicase_activity_ (11.17)
|   |   |   |   |   |   |   |   |   start > 7244:
oxidoreductase_activity_ (12.35)
|   |   |   |   |   |   |   |   start > 13175
|   |   |   |   |   |   |   |   |   start <= 58687
|   |   |   |   |   |   |   |   |   |   start <= 26930
|   |   |   |   |   |   |   |   |   |   |   start <= 21700
|   |   |   |   |   |   |   |   |   |   |   |   start <= 17065:
molecular_function_ (34.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 17065
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 20536:
transferase_activity_ (19.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 20536:
molecular_function_ (18.62)
|   |   |   |   |   |   |   |   |   |   |   start > 21700
|   |   |   |   |   |   |   |   |   |   |   |   start <= 23684:
structural_molecule_activity_ (21.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 23684:
transporter_activity_ (12.54)
|   |   |   |   |   |   |   |   |   |   start > 26930
|   |   |   |   |   |   |   |   |   |   |   start <= 51640
|   |   |   |   |   |   |   |   |   |   |   |   start <= 34243:
oxidoreductase_activity_ (11.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 34243
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 41794:
transferase_activity_ (15.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 41794
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
46942: transcription_regulator_activity_ (11.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
46942: transferase_activity_ (11.77)
|   |   |   |   |   |   |   |   |   |   |   start > 51640:
molecular_function_ (43.95)
|   |   |   |   |   |   |   |   |   start > 58687:
structural_molecule_activity_ (29.63)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 34243
|   |   |   |   |   |   |   |   |   start <= 7244: protein_binding_
(14.89)
|   |   |   |   |   |   |   |   |   start > 7244
|   |   |   |   |   |   |   |   |   |   start <= 21700:
molecular_function_ (29.12)
|   |   |   |   |   |   |   |   |   |   start > 21700
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 26930:
hydrolase_activity_ (11.11)
|   |   |   |   |   |   |   |   |   |   |   start > 26930
|   |   |   |   |   |   |   |   |   |   |   |   start <= 30611:
molecular_function_ (22.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 30611
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 32334:
hydrolase_activity_ (17.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 32334:
molecular_function_ (12.49)
|   |   |   |   |   |   |   |   start > 34243
|   |   |   |   |   |   |   |   |   start <= 45063
|   |   |   |   |   |   |   |   |   |   start <= 44045
|   |   |   |   |   |   |   |   |   |   |   start <= 38196:
transporter_activity_ (9.74)
|   |   |   |   |   |   |   |   |   |   |   start > 38196:
DNA_binding_ (14.92)
|   |   |   |   |   |   |   |   |   |   start > 44045:
protein_kinase_activity_ (21.99)
|   |   |   |   |   |   |   |   |   start > 45063
|   |   |   |   |   |   |   |   |   |   start <= 54793
|   |   |   |   |   |   |   |   |   |   |   start <= 46942:
protein_binding_ (13.18)
|   |   |   |   |   |   |   |   |   |   |   start > 46942:
molecular_function_ (24.51)
|   |   |   |   |   |   |   |   |   |   start > 54793:
transferase_activity_ (17.16)
|   |   |   |   |   |   start > 67549
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 115347
|   |   |   |   |   |   |   |   |   start <= 79909
|   |   |   |   |   |   |   |   |   |   start <= 70624
|   |   |   |   |   |   |   |   |   |   |   start <= 68294:
RNA_binding_ (24.89)
|   |   |   |   |   |   |   |   |   |   |   start > 68294:
molecular_function_ (6.77)
|   |   |   |   |   |   |   |   |   |   start > 70624
|   |   |   |   |   |   |   |   |   |   |   start <= 77267:
transcription_regulator_activity_ (15.5)
|   |   |   |   |   |   |   |   |   |   |   start > 77267:
enzyme_regulator_activity_ (13.66)
|   |   |   |   |   |   |   |   |   start > 79909
|   |   |   |   |   |   |   |   |   |   start <= 101862
|   |   |   |   |   |   |   |   |   |   |   start <= 92235
|   |   |   |   |   |   |   |   |   |   |   |   start <= 83090:
DNA_binding_ (15.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 83090
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 86739:
peptidase_activity_ (10.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 86739:
transcription_regulator_activity_ (13.57)
|   |   |   |   |   |   |   |   |   |   |   start > 92235
|   |   |   |   |   |   |   |   |   |   |   |   start <= 97371
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 95369:
molecular_function_ (11.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 95369:
oxidoreductase_activity_ (12.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 97371
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 99400:
structural_molecule_activity_ (6.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 99400:
molecular_function_ (15.97)
|   |   |   |   |   |   |   |   |   |   start > 101862
|   |   |   |   |   |   |   |   |   |   |   start <= 108806:
transporter_activity_ (29.38)
|   |   |   |   |   |   |   |   |   |   |   start > 108806:
DNA_binding_ (36.54/16.1)
|   |   |   |   |   |   |   |   start > 115347
|   |   |   |   |   |   |   |   |   start <= 121324
|   |   |   |   |   |   |   |   |   |   start <= 118898:
oxidoreductase_activity_ (22.44)
|   |   |   |   |   |   |   |   |   |   start > 118898:
isomerase_activity_ (15.02)
|   |   |   |   |   |   |   |   |   start > 121324
|   |   |   |   |   |   |   |   |   |   start <= 151871
|   |   |   |   |   |   |   |   |   |   |   start <= 148683
|   |   |   |   |   |   |   |   |   |   |   |   start <= 124172:
RNA_binding_ (12.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 124172
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 142210:
molecular_function_ (62.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 142210
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
146482: protein_binding_ (12.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
146482: molecular_function_ (15.71)
|   |   |   |   |   |   |   |   |   |   |   start > 148683:
helicase_activity_ (15.34)
|   |   |   |   |   |   |   |   |   |   start > 151871
|   |   |   |   |   |   |   |   |   |   |   start <= 167308
|   |   |   |   |   |   |   |   |   |   |   |   start <= 163620
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 160180:
hydrolase_activity_ (18.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 160180:
RNA_binding_ (14.63)
|   |   |   |   |   |   |   |   |   |   |   |   start > 163620:
oxidoreductase_activity_ (37.14)
|   |   |   |   |   |   |   |   |   |   |   start > 167308
|   |   |   |   |   |   |   |   |   |   |   |   start <= 173139:
molecular_function_ (28.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 173139
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 178426:
RNA_binding_ (19.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 178426:
molecular_function_ (9.34)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 159383
```

```
|   |   |   |   |   |   |   |   |   start <= 95369
|   |   |   |   |   |   |   |   |   |   start <= 79909
|   |   |   |   |   |   |   |   |   |   |   start <= 77267
|   |   |   |   |   |   |   |   |   |   |   |   start <= 70138
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 68294:
transcription_regulator_activity_ (16.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 68294:
molecular_function_ (19.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 70138
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 70624:
enzyme_regulator_activity_ (11.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 70624:
transcription_regulator_activity_ (18.25)
|   |   |   |   |   |   |   |   |   |   |   start > 77267:
molecular_function_ (20.13)
|   |   |   |   |   |   |   |   |   |   start > 79909
|   |   |   |   |   |   |   |   |   |   |   start <= 82275:
protein_binding_ (13.67)
|   |   |   |   |   |   |   |   |   |   |   start > 82275
|   |   |   |   |   |   |   |   |   |   |   |   start <= 86739:
RNA_binding_ (11.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 86739:
protein_binding_ (8.66)
|   |   |   |   |   |   |   |   |   start > 95369
|   |   |   |   |   |   |   |   |   |   start <= 111002
|   |   |   |   |   |   |   |   |   |   |   start <= 110247
|   |   |   |   |   |   |   |   |   |   |   |   start <= 101862:
lyase_activity_ (7.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 101862:
molecular_function_ (53.32)
|   |   |   |   |   |   |   |   |   |   |   start > 110247:
isomerase_activity_ (18.14)
|   |   |   |   |   |   |   |   |   |   start > 111002
|   |   |   |   |   |   |   |   |   |   |   start <= 133475
|   |   |   |   |   |   |   |   |   |   |   |   start <= 121324:
enzyme_regulator_activity_ (17.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 121324:
transferase_activity_ (14.46)
|   |   |   |   |   |   |   |   |   |   |   start > 133475
|   |   |   |   |   |   |   |   |   |   |   |   start <= 158760
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 142210:
molecular_function_ (55.32/11.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 142210
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
148683: structural_molecule_activity_ (10.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
148683
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
151871: lyase_activity_ (15.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
151871: molecular_function_ (9.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 158760:
enzyme_regulator_activity_ (20.47)
|   |   |   |   |   |   |   |   start > 159383
```

```
|   |   |   |   |   |   |   |   |   start <= 164790
|   |   |   |   |   |   |   |   |   |   start <= 160180:
phosphoprotein_phosphatase_activity_ (17.68)
|   |   |   |   |   |   |   |   |   |   start > 160180:
protein_binding_ (19.04)
|   |   |   |   |   |   |   |   |   start > 164790
|   |   |   |   |   |   |   |   |   |   start <= 178426
|   |   |   |   |   |   |   |   |   |   |   start <= 170402:
molecular_function_ (31.58)
|   |   |   |   |   |   |   |   |   |   |   start > 170402
|   |   |   |   |   |   |   |   |   |   |   |   start <= 171594:
transcription_regulator_activity_ (17.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 171594:
molecular_function_ (29.42)
|   |   |   |   |   |   |   |   |   |   start > 178426: RNA_binding_
(12.67)
|   |   |   |   |   start > 181474
|   |   |   |   |   |   start <= 253848
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 236588
|   |   |   |   |   |   |   |   |   start <= 205642
|   |   |   |   |   |   |   |   |   |   start <= 192788
|   |   |   |   |   |   |   |   |   |   |   start <= 183968:
molecular_function_ (17.22)
|   |   |   |   |   |   |   |   |   |   |   start > 183968:
transcription_regulator_activity_ (21.48)
|   |   |   |   |   |   |   |   |   |   start > 192788
|   |   |   |   |   |   |   |   |   |   |   start <= 196170:
molecular_function_ (32.58)
|   |   |   |   |   |   |   |   |   |   |   start > 196170
|   |   |   |   |   |   |   |   |   |   |   |   start <= 204103:
transporter_activity_ (12.42)
|   |   |   |   |   |   |   |   |   |   |   |   start > 204103:
molecular_function_ (9.2)
|   |   |   |   |   |   |   |   |   start > 205642
|   |   |   |   |   |   |   |   |   |   start <= 225889
|   |   |   |   |   |   |   |   |   |   |   start <= 217362
|   |   |   |   |   |   |   |   |   |   |   |   start <= 209525:
hydrolase_activity_ (27.38/9.84)
|   |   |   |   |   |   |   |   |   |   |   |   start > 209525:
molecular_function_ (10.57)
|   |   |   |   |   |   |   |   |   |   |   start > 217362:
structural_molecule_activity_ (29.77)
|   |   |   |   |   |   |   |   |   |   start > 225889
|   |   |   |   |   |   |   |   |   |   |   start <= 231149
|   |   |   |   |   |   |   |   |   |   |   |   start <= 228937:
molecular_function_ (18.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 228937:
hydrolase_activity_ (20.06)
|   |   |   |   |   |   |   |   |   |   |   start > 231149:
molecular_function_ (22.03)
|   |   |   |   |   |   |   |   start > 236588
|   |   |   |   |   |   |   |   |   start <= 244149
```

```
|   |   |   |   |   |   |   |   |   |   start <= 241536:
phosphoprotein_phosphatase_activity_ (21.07)
|   |   |   |   |   |   |   |   |   |   start > 241536:
transcription_regulator_activity_ (13.53)
|   |   |   |   |   |   |   |   |   start > 244149
|   |   |   |   |   |   |   |   |   |   start <= 251516
|   |   |   |   |   |   |   |   |   |   |   start <= 247677:
molecular_function_ (18.74)
|   |   |   |   |   |   |   |   |   |   |   start > 247677:
structural_molecule_activity_ (11.81)
|   |   |   |   |   |   |   |   |   |   start > 251516
|   |   |   |   |   |   |   |   |   |   |   start <= 252990:
transferase_activity_ (24.85)
|   |   |   |   |   |   |   |   |   |   |   start > 252990:
molecular_function_ (11.62)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 246116
|   |   |   |   |   |   |   |   |   start <= 225889
|   |   |   |   |   |   |   |   |   |   start <= 217362
|   |   |   |   |   |   |   |   |   |   |   start <= 196170:
transferase_activity_ (10.23)
|   |   |   |   |   |   |   |   |   |   |   start > 196170
|   |   |   |   |   |   |   |   |   |   |   |   start <= 214189
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 209525:
molecular_function_ (21.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 209525:
structural_molecule_activity_ (7.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 214189:
molecular_function_ (33.27)
|   |   |   |   |   |   |   |   |   |   start > 217362
|   |   |   |   |   |   |   |   |   |   |   start <= 220138:
protein_binding_ (14.04)
|   |   |   |   |   |   |   |   |   |   |   start > 220138
|   |   |   |   |   |   |   |   |   |   |   |   start <= 221406:
DNA_binding_ (14.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 221406:
structural_molecule_activity_ (9.95)
|   |   |   |   |   |   |   |   |   start > 225889
|   |   |   |   |   |   |   |   |   |   start <= 243225
|   |   |   |   |   |   |   |   |   |   |   start <= 236588
|   |   |   |   |   |   |   |   |   |   |   |   start <= 228937:
transferase_activity_ (13.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 228937
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 231149:
molecular_function_ (15.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 231149
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
233457: transferase_activity_ (14.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
233457: molecular_function_ (12.8)
|   |   |   |   |   |   |   |   |   |   |   start > 236588:
transferase_activity_ (23.32)
|   |   |   |   |   |   |   |   |   |   start > 243225
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 244149:
protein_binding_ (15.9)
|   |   |   |   |   |   |   |   |   |   |   start > 244149:
molecular_function_ (9.99)
|   |   |   |   |   |   |   |   start > 246116:
transcription_regulator_activity_ (37.33/11.57)
|   |   |   |   |   |   start > 253848
|   |   |   |   |   |   |   start <= 291133
|   |   |   |   |   |   |   |   start <= 264541
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 260221:
molecular_function_ (46.33)
|   |   |   |   |   |   |   |   |   |   start > 260221:
lyase_activity_ (17.42)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 260221:
transferase_activity_ (11.74)
|   |   |   |   |   |   |   |   |   |   start > 260221:
molecular_function_ (37.29)
|   |   |   |   |   |   |   |   start > 264541
|   |   |   |   |   |   |   |   |   start <= 271136
|   |   |   |   |   |   |   |   |   |   start <= 267174:
hydrolase_activity_ (15.66)
|   |   |   |   |   |   |   |   |   |   start > 267174:
protein_kinase_activity_ (16.74)
|   |   |   |   |   |   |   |   |   start > 271136
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 274017:
molecular_function_ (11.23)
|   |   |   |   |   |   |   |   |   |   |   start > 274017:
hydrolase_activity_ (18.06)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 279681
|   |   |   |   |   |   |   |   |   |   |   |   start <= 274017:
molecular_function_ (39.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 274017:
transcription_regulator_activity_ (14.08)
|   |   |   |   |   |   |   |   |   |   |   start > 279681
|   |   |   |   |   |   |   |   |   |   |   |   start <= 284101:
oxidoreductase_activity_ (8.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 284101
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 288078
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
285099: molecular_function_ (15.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
285099: transporter_activity_ (11.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 288078:
molecular_function_ (23.07)
|   |   |   |   |   |   |   start > 291133: transferase_activity_
(30.41)
|   |   |   |   start > 296737: RNA_binding_ (128.77)
|   |   |   start > 298553
|   |   |   |   start <= 382897
|   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   start <= 337312
|   |   |   |   |   |   |   start <= 318679
|   |   |   |   |   |   |   |   start <= 302484: molecular_function_
(21.96)
|   |   |   |   |   |   |   |   start > 302484:
transcription_regulator_activity_ (59.33/20.03)
|   |   |   |   |   |   |   start > 318679
|   |   |   |   |   |   |   |   start <= 327481
|   |   |   |   |   |   |   |   |   start <= 323299:
molecular_function_ (26.24)
|   |   |   |   |   |   |   |   |   start > 323299: protein_binding_
(21.07)
|   |   |   |   |   |   |   |   start > 327481: molecular_function_
(34.65)
|   |   |   |   |   |   start > 337312
|   |   |   |   |   |   |   start <= 348259
|   |   |   |   |   |   |   |   start <= 343519
|   |   |   |   |   |   |   |   |   start <= 341141:
transporter_activity_ (23.67)
|   |   |   |   |   |   |   |   |   start > 341141:
phosphoprotein_phosphatase_activity_ (13.33)
|   |   |   |   |   |   |   |   start > 343519
|   |   |   |   |   |   |   |   |   start <= 346516: DNA_binding_
(37.55/18.13)
|   |   |   |   |   |   |   |   |   start > 346516:
transporter_activity_ (34.36/13.78)
|   |   |   |   |   |   |   start > 348259
|   |   |   |   |   |   |   |   start <= 366980
|   |   |   |   |   |   |   |   |   start <= 350380:
transcription_regulator_activity_ (19.87)
|   |   |   |   |   |   |   |   |   start > 350380
|   |   |   |   |   |   |   |   |   |   start <= 355383:
oxidoreductase_activity_ (10.57)
|   |   |   |   |   |   |   |   |   |   start > 355383:
structural_molecule_activity_ (9.57)
|   |   |   |   |   |   |   |   start > 366980
|   |   |   |   |   |   |   |   |   start <= 379585:
molecular_function_ (36.64)
|   |   |   |   |   |   |   |   |   start > 379585:
transcription_regulator_activity_ (13.51)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 321874
|   |   |   |   |   |   |   start <= 312155
|   |   |   |   |   |   |   |   start <= 310207
|   |   |   |   |   |   |   |   |   start <= 302484:
molecular_function_ (26.83)
|   |   |   |   |   |   |   |   |   start > 302484
|   |   |   |   |   |   |   |   |   |   start <= 307488:
protein_binding_ (12.61)
|   |   |   |   |   |   |   |   |   |   start > 307488:
molecular_function_ (12.63)
|   |   |   |   |   |   |   |   start > 310207: DNA_binding_ (21.37)
|   |   |   |   |   |   |   start > 312155
```

```
|   |   |   |   |   |   |   |   start <= 315376:
oxidoreductase_activity_ (26.44)
|   |   |   |   |   |   |   |   start > 315376
|   |   |   |   |   |   |   |   |   start <= 318679:
molecular_function_ (13.53)
|   |   |   |   |   |   |   |   |   start > 318679:
structural_molecule_activity_ (13.73)
|   |   |   |   |   |   start > 321874
|   |   |   |   |   |   |   start <= 337787
|   |   |   |   |   |   |   |   start <= 337312
|   |   |   |   |   |   |   |   |   start <= 325876:
molecular_function_ (38.26)
|   |   |   |   |   |   |   |   |   start > 325876
|   |   |   |   |   |   |   |   |   |   start <= 335297
|   |   |   |   |   |   |   |   |   |   |   start <= 330792
|   |   |   |   |   |   |   |   |   |   |   |   start <= 327481:
protein_binding_ (17.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 327481:
molecular_function_ (18.35)
|   |   |   |   |   |   |   |   |   |   |   start > 330792:
protein_binding_ (23.47)
|   |   |   |   |   |   |   |   |   |   start > 335297:
molecular_function_ (12.55)
|   |   |   |   |   |   |   |   start > 337312:
transcription_regulator_activity_ (12.3)
|   |   |   |   |   |   |   start > 337787
|   |   |   |   |   |   |   |   start <= 343519: peptidase_activity_
(14.69)
|   |   |   |   |   |   |   |   start > 343519
|   |   |   |   |   |   |   |   |   start <= 353870
|   |   |   |   |   |   |   |   |   |   start <= 352279:
molecular_function_ (32.26)
|   |   |   |   |   |   |   |   |   |   start > 352279: DNA_binding_
(27.21)
|   |   |   |   |   |   |   |   |   start > 353870
|   |   |   |   |   |   |   |   |   |   start <= 355383:
protein_binding_ (11.72)
|   |   |   |   |   |   |   |   |   |   start > 355383:
molecular_function_ (41.37)
|   |   |   |   start > 382897
|   |   |   |   |   start <= 392754
|   |   |   |   |   |   start <= 391098
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 387020:
enzyme_regulator_activity_ (19.5)
|   |   |   |   |   |   |   |   start > 387020:
transporter_activity_ (19.66)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 383302:
transporter_activity_ (40.92/18.79)
|   |   |   |   |   |   |   |   start > 383302
|   |   |   |   |   |   |   |   |   start <= 388821:
oxidoreductase_activity_ (14.38)
```

```
|   |   |   |   |   |   |   |   |   start > 388821:
hydrolase_activity_ (20.91)
|   |   |   |   |   |   start > 391098
|   |   |   |   |   |   |   start <= 392514: protein_binding_
(17.48)
|   |   |   |   |   |   |   start > 392514: RNA_binding_ (12.03)
|   |   |   |   |   start > 392754
|   |   |   |   |   |   start <= 413472
|   |   |   |   |   |   |   start <= 407708
|   |   |   |   |   |   |   |   start <= 396378:
transferase_activity_ (15.9)
|   |   |   |   |   |   |   |   start > 396378
|   |   |   |   |   |   |   |   |   start <= 406303:
molecular_function_ (111.9)
|   |   |   |   |   |   |   |   |   start > 406303:
transferase_activity_ (15.62)
|   |   |   |   |   |   |   start > 407708
|   |   |   |   |   |   |   |   strand = C: molecular_function_
(45.41)
|   |   |   |   |   |   |   |   strand = W: DNA_binding_ (39.62)
|   |   |   |   |   |   start > 413472
|   |   |   |   |   |   |   start <= 420028
|   |   |   |   |   |   |   |   start <= 413981: hydrolase_activity_
(17.59)
|   |   |   |   |   |   |   |   start > 413981:
structural_molecule_activity_ (18.43)
|   |   |   |   |   |   |   start > 420028
|   |   |   |   |   |   |   |   start <= 439207
|   |   |   |   |   |   |   |   |   start <= 424988
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 422148
|   |   |   |   |   |   |   |   |   |   |   |   start <= 420660:
molecular_function_ (16.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 420660:
protein_binding_ (18.95)
|   |   |   |   |   |   |   |   |   |   |   start > 422148:
molecular_function_ (19.19)
|   |   |   |   |   |   |   |   |   |   strand = W:
transporter_activity_ (16.43)
|   |   |   |   |   |   |   |   |   start > 424988
|   |   |   |   |   |   |   |   |   |   start <= 429626
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
molecular_function_ (9.78/2.44)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
helicase_activity_ (7.99/1.31)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
molecular_function_ (9.36/3.57)
|   |   |   |   |   |   |   |   |   |   start > 429626
|   |   |   |   |   |   |   |   |   |   |   start <= 434787
|   |   |   |   |   |   |   |   |   |   |   |   start <= 431094:
molecular_function_ (20.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 431094:
oxidoreductase_activity_ (9.77)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 434787:
molecular_function_ (36.87)
|   |   |   |   |   |   |   |   start > 439207
|   |   |   |   |   |   |   |   |   start <= 442526:
hydrolase_activity_ (18.37)
|   |   |   |   |   |   |   |   |   start > 442526:
transporter_activity_ (9.64)
|   |   start > 445101
|   |   |   strand = C
|   |   |   |   start <= 583920
|   |   |   |   |   start <= 478063
|   |   |   |   |   |   start <= 460526
|   |   |   |   |   |   |   start <= 449244: peptidase_activity_
(21.9)
|   |   |   |   |   |   |   start > 449244
|   |   |   |   |   |   |   |   start <= 454014
|   |   |   |   |   |   |   |   |   start <= 451364:
hydrolase_activity_ (23.0)
|   |   |   |   |   |   |   |   |   start > 451364: protein_binding_
(11.59)
|   |   |   |   |   |   |   |   start > 454014
|   |   |   |   |   |   |   |   |   start <= 458407:
molecular_function_ (14.52)
|   |   |   |   |   |   |   |   |   start > 458407:
hydrolase_activity_ (19.79)
|   |   |   |   |   |   start > 460526
|   |   |   |   |   |   |   start <= 472351
|   |   |   |   |   |   |   |   start <= 466299
|   |   |   |   |   |   |   |   |   start <= 463553:
molecular_function_ (13.15)
|   |   |   |   |   |   |   |   |   start > 463553:
isomerase_activity_ (17.59)
|   |   |   |   |   |   |   |   start > 466299
|   |   |   |   |   |   |   |   |   start <= 469475:
transferase_activity_ (10.77)
|   |   |   |   |   |   |   |   |   start > 469475:
molecular_function_ (7.74)
|   |   |   |   |   |   |   start > 472351
|   |   |   |   |   |   |   |   start <= 475452:
protein_kinase_activity_ (7.44)
|   |   |   |   |   |   |   |   start > 475452: isomerase_activity_
(9.96)
|   |   |   |   |   start > 478063
|   |   |   |   |   |   start <= 556474
|   |   |   |   |   |   |   start <= 480189: DNA_binding_
(37.37/16.83)
|   |   |   |   |   |   |   start > 480189
|   |   |   |   |   |   |   |   start <= 541198
|   |   |   |   |   |   |   |   |   start <= 514455
|   |   |   |   |   |   |   |   |   |   start <= 497703
|   |   |   |   |   |   |   |   |   |   |   start <= 491991
|   |   |   |   |   |   |   |   |   |   |   |   start <= 484083:
molecular_function_ (7.74)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 484083:
oxidoreductase_activity_ (12.06)
|   |   |   |   |   |   |   |   |   |   |   start > 491991
|   |   |   |   |   |   |   |   |   |   |   |   start <= 493791:
molecular_function_ (21.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 493791
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 494998:
structural_molecule_activity_ (16.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 494998:
molecular_function_ (14.06)
|   |   |   |   |   |   |   |   |   |   start > 497703
|   |   |   |   |   |   |   |   |   |   |   start <= 501890
|   |   |   |   |   |   |   |   |   |   |   |   start <= 500071:
RNA_binding_ (16.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 500071
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 500687:
signal_transducer_activity_ (7.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 500687:
structural_molecule_activity_ (10.03)
|   |   |   |   |   |   |   |   |   |   |   start > 501890
|   |   |   |   |   |   |   |   |   |   |   |   start <= 505332:
molecular_function_ (13.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 505332
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 509279:
hydrolase_activity_ (11.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 509279:
RNA_binding_ (8.77)
|   |   |   |   |   |   |   |   |   start > 514455
|   |   |   |   |   |   |   |   |   |   start <= 527803
|   |   |   |   |   |   |   |   |   |   |   start <= 521788:
molecular_function_ (11.14)
|   |   |   |   |   |   |   |   |   |   |   start > 521788:
transferase_activity_ (14.87)
|   |   |   |   |   |   |   |   |   |   start > 527803:
molecular_function_ (47.87)
|   |   |   |   |   |   |   |   start > 541198
|   |   |   |   |   |   |   |   |   start <= 553361
|   |   |   |   |   |   |   |   |   |   start <= 547713:
DNA_binding_ (14.12)
|   |   |   |   |   |   |   |   |   |   start > 547713:
structural_molecule_activity_ (10.57)
|   |   |   |   |   |   |   |   |   start > 553361:
oxidoreductase_activity_ (14.3)
|   |   |   |   |   |   start > 556474
|   |   |   |   |   |   |   start <= 568550
|   |   |   |   |   |   |   |   start <= 560365:
translation_regulator_activity_ (20.15)
|   |   |   |   |   |   |   |   start > 560365: peptidase_activity_
(21.92)
|   |   |   |   |   |   |   start > 568550
|   |   |   |   |   |   |   |   start <= 577717
|   |   |   |   |   |   |   |   |   start <= 571015:
hydrolase_activity_ (15.49)
```

```
|   |   |   |   |   |   |   |   |   start > 571015:
molecular_function_ (65.74)
|   |   |   |   |   |   |   |   start > 577717: hydrolase_activity_
(19.08)
|   |   |   |   start > 583920
|   |   |   |   |   start <= 724625
|   |   |   |   |   |   start <= 720652
|   |   |   |   |   |   |   start <= 626348
|   |   |   |   |   |   |   |   start <= 586708
|   |   |   |   |   |   |   |   |   start <= 586387:
protein_binding_ (21.7)
|   |   |   |   |   |   |   |   |   start > 586387:
molecular_function_ (27.08)
|   |   |   |   |   |   |   |   start > 586708
|   |   |   |   |   |   |   |   |   start <= 603081
|   |   |   |   |   |   |   |   |   |   start <= 594885
|   |   |   |   |   |   |   |   |   |   |   start <= 589549:
transcription_regulator_activity_ (27.26)
|   |   |   |   |   |   |   |   |   |   |   start > 589549
|   |   |   |   |   |   |   |   |   |   |   |   start <= 592627:
hydrolase_activity_ (17.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 592627:
transporter_activity_ (13.44)
|   |   |   |   |   |   |   |   |   |   start > 594885
|   |   |   |   |   |   |   |   |   |   |   start <= 599157:
DNA_binding_ (13.56)
|   |   |   |   |   |   |   |   |   |   |   start > 599157:
oxidoreductase_activity_ (34.33)
|   |   |   |   |   |   |   |   |   start > 603081
|   |   |   |   |   |   |   |   |   |   start <= 624079
|   |   |   |   |   |   |   |   |   |   |   start <= 616565
|   |   |   |   |   |   |   |   |   |   |   |   start <= 605980:
molecular_function_ (16.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 605980:
enzyme_regulator_activity_ (16.34)
|   |   |   |   |   |   |   |   |   |   |   start > 616565
|   |   |   |   |   |   |   |   |   |   |   |   start <= 623212:
hydrolase_activity_ (11.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 623212:
molecular_function_ (14.99)
|   |   |   |   |   |   |   |   |   |   start > 624079:
transcription_regulator_activity_ (14.86)
|   |   |   |   |   |   |   start > 626348
|   |   |   |   |   |   |   |   start <= 667043
|   |   |   |   |   |   |   |   |   start <= 655075
|   |   |   |   |   |   |   |   |   |   start <= 629024:
protein_binding_ (10.45)
|   |   |   |   |   |   |   |   |   |   start > 629024
|   |   |   |   |   |   |   |   |   |   |   start <= 637499
|   |   |   |   |   |   |   |   |   |   |   |   start <= 635983:
molecular_function_ (17.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 635983:
structural_molecule_activity_ (16.71)
|   |   |   |   |   |   |   |   |   |   |   start > 637499
```

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|   |   |   |   |   |   |   |   |   |   |   |   start <= 647117:
helicase_activity_ (14.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 647117:
molecular_function_ (10.02)
|   |   |   |   |   |   |   |   |   start > 655075
|   |   |   |   |   |   |   |   |   |   start <= 662643:
protein_binding_ (20.05)
|   |   |   |   |   |   |   |   |   |   start > 662643: DNA_binding_
(17.35)
|   |   |   |   |   |   |   |   start > 667043
|   |   |   |   |   |   |   |   |   start <= 715444
|   |   |   |   |   |   |   |   |   |   start <= 696795
|   |   |   |   |   |   |   |   |   |   |   distance <= 3665
|   |   |   |   |   |   |   |   |   |   |   |   start <= 671324:
molecular_function_ (30.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 671324
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 684466:
transferase_activity_ (5.43/0.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 684466:
molecular_function_ (23.86)
|   |   |   |   |   |   |   |   |   |   |   distance > 3665
|   |   |   |   |   |   |   |   |   |   |   |   start <= 675895
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 671324:
molecular_function_ (2.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 671324:
transferase_activity_ (7.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 675895
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 684466:
ligase_activity_ (20.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 684466:
molecular_function_ (10.11)
|   |   |   |   |   |   |   |   |   |   start > 696795
|   |   |   |   |   |   |   |   |   |   |   start <= 701789:
protein_kinase_activity_ (20.06)
|   |   |   |   |   |   |   |   |   |   |   start > 701789
|   |   |   |   |   |   |   |   |   |   |   |   start <= 707132:
enzyme_regulator_activity_ (13.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 707132:
molecular_function_ (19.17)
|   |   |   |   |   |   |   |   |   start > 715444
|   |   |   |   |   |   |   |   |   |   start <= 716714:
hydrolase_activity_ (15.96)
|   |   |   |   |   |   |   |   |   |   start > 716714:
protein_binding_ (18.33)
|   |   |   |   |   |   start > 720652
|   |   |   |   |   |   |   start <= 722395
|   |   |   |   |   |   |   |   start <= 721402:
structural_molecule_activity_ (16.84)
|   |   |   |   |   |   |   |   start > 721402:
oxidoreductase_activity_ (18.03)
|   |   |   |   |   |   |   start > 722395:
transcription_regulator_activity_ (31.55)
|   |   |   |   |   start > 724625
|   |   |   |   |   |   start <= 804455
```

```
|   |   |   |   |   |   |   start <= 757249
|   |   |   |   |   |   |   |   start <= 751960
|   |   |   |   |   |   |   |   |   start <= 747962
|   |   |   |   |   |   |   |   |   |   start <= 743748
|   |   |   |   |   |   |   |   |   |   |   start <= 736925:
RNA_binding_ (14.43)
|   |   |   |   |   |   |   |   |   |   |   start > 736925:
enzyme_regulator_activity_ (19.08)
|   |   |   |   |   |   |   |   |   |   start > 743748:
molecular_function_ (16.53)
|   |   |   |   |   |   |   |   |   start > 747962
|   |   |   |   |   |   |   |   |   |   start <= 749676:
hydrolase_activity_ (25.21)
|   |   |   |   |   |   |   |   |   |   start > 749676: RNA_binding_
(21.06/8.37)
|   |   |   |   |   |   |   |   start > 751960
|   |   |   |   |   |   |   |   |   start <= 754296:
structural_molecule_activity_ (20.54)
|   |   |   |   |   |   |   |   |   start > 754296:
transporter_activity_ (19.33)
|   |   |   |   |   |   |   start > 757249
|   |   |   |   |   |   |   |   start <= 788882
|   |   |   |   |   |   |   |   |   start <= 778000
|   |   |   |   |   |   |   |   |   |   start <= 763112
|   |   |   |   |   |   |   |   |   |   |   start <= 759806:
molecular_function_ (12.65)
|   |   |   |   |   |   |   |   |   |   |   start > 759806:
RNA_binding_ (15.3)
|   |   |   |   |   |   |   |   |   |   start > 763112:
molecular_function_ (89.18)
|   |   |   |   |   |   |   |   |   start > 778000
|   |   |   |   |   |   |   |   |   |   start <= 782030
|   |   |   |   |   |   |   |   |   |   |   start <= 779126:
oxidoreductase_activity_ (14.79)
|   |   |   |   |   |   |   |   |   |   |   start > 779126:
translation_regulator_activity_ (16.51)
|   |   |   |   |   |   |   |   |   |   start > 782030:
molecular_function_ (34.97)
|   |   |   |   |   |   |   |   start > 788882
|   |   |   |   |   |   |   |   |   start <= 794918
|   |   |   |   |   |   |   |   |   |   start <= 789838:
RNA_binding_ (16.68)
|   |   |   |   |   |   |   |   |   |   start > 789838:
enzyme_regulator_activity_ (11.09)
|   |   |   |   |   |   |   |   |   start > 794918
|   |   |   |   |   |   |   |   |   |   start <= 798517:
molecular_function_ (14.96)
|   |   |   |   |   |   |   |   |   |   start > 798517: RNA_binding_
(10.59)
|   |   |   |   |   |   start > 804455
|   |   |   |   |   |   |   start <= 838186
|   |   |   |   |   |   |   |   start <= 820255
|   |   |   |   |   |   |   |   |   start <= 811088
|   |   |   |   |   |   |   |   |   |   start <= 807547
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 806422:
transcription_regulator_activity_ (14.67)
|   |   |   |   |   |   |   |   |   |   |   start > 806422:
transferase_activity_ (14.99)
|   |   |   |   |   |   |   |   |   |   start > 807547
|   |   |   |   |   |   |   |   |   |   |   start <= 808316:
molecular_function_ (8.37)
|   |   |   |   |   |   |   |   |   |   |   start > 808316:
oxidoreductase_activity_ (8.89)
|   |   |   |   |   |   |   |   |   start > 811088
|   |   |   |   |   |   |   |   |   |   start <= 813979:
protein_binding_ (14.43)
|   |   |   |   |   |   |   |   |   |   start > 813979
|   |   |   |   |   |   |   |   |   |   |   start <= 815310:
peptidase_activity_ (12.74)
|   |   |   |   |   |   |   |   |   |   |   start > 815310:
protein_binding_ (13.53)
|   |   |   |   |   |   |   |   start > 820255
|   |   |   |   |   |   |   |   |   start <= 835097
|   |   |   |   |   |   |   |   |   |   start <= 832338
|   |   |   |   |   |   |   |   |   |   |   start <= 826350:
molecular_function_ (18.85)
|   |   |   |   |   |   |   |   |   |   |   start > 826350:
transcription_regulator_activity_ (17.76)
|   |   |   |   |   |   |   |   |   |   start > 832338:
molecular_function_ (23.85)
|   |   |   |   |   |   |   |   |   start > 835097:
transferase_activity_ (17.13)
|   |   |   |   |   |   |   start > 838186
|   |   |   |   |   |   |   |   start <= 856965
|   |   |   |   |   |   |   |   |   start <= 845570:
hydrolase_activity_ (33.56)
|   |   |   |   |   |   |   |   |   start > 845570
|   |   |   |   |   |   |   |   |   |   start <= 852629:
RNA_binding_ (15.51)
|   |   |   |   |   |   |   |   |   |   start > 852629:
hydrolase_activity_ (14.39)
|   |   |   |   |   |   |   |   start > 856965: molecular_function_
(16.16)
|   |   |   strand = W
|   |   |   |   start <= 675895
|   |   |   |   |   start <= 629024
|   |   |   |   |   |   start <= 523695
|   |   |   |   |   |   |   start <= 460526
|   |   |   |   |   |   |   |   start <= 454014
|   |   |   |   |   |   |   |   |   start <= 451364:
molecular_function_ (17.24)
|   |   |   |   |   |   |   |   |   start > 451364: RNA_binding_
(18.64)
|   |   |   |   |   |   |   |   start > 454014
|   |   |   |   |   |   |   |   |   start <= 455824: DNA_binding_
(20.53)
|   |   |   |   |   |   |   |   |   start > 455824: protein_binding_
(11.9)
```

```
|   |   |   |   |   |   |   start > 460526
|   |   |   |   |   |   |   |   start <= 514455
|   |   |   |   |   |   |   |   |   start <= 486586
|   |   |   |   |   |   |   |   |   |   start <= 483013:
molecular_function_ (59.52)
|   |   |   |   |   |   |   |   |   |   start > 483013
|   |   |   |   |   |   |   |   |   |   |   start <= 484083:
transferase_activity_ (8.88)
|   |   |   |   |   |   |   |   |   |   |   start > 484083:
motor_activity_ (16.59)
|   |   |   |   |   |   |   |   |   start > 486586
|   |   |   |   |   |   |   |   |   |   start <= 494998:
ligase_activity_ (18.21)
|   |   |   |   |   |   |   |   |   |   start > 494998:
molecular_function_ (78.88)
|   |   |   |   |   |   |   |   start > 514455
|   |   |   |   |   |   |   |   |   start <= 517538: RNA_binding_
(16.9)
|   |   |   |   |   |   |   |   |   start > 517538:
helicase_activity_ (8.05)
|   |   |   |   |   |   start > 523695
|   |   |   |   |   |   |   start <= 605980
|   |   |   |   |   |   |   |   start <= 583920
|   |   |   |   |   |   |   |   |   start <= 546124
|   |   |   |   |   |   |   |   |   |   start <= 537837
|   |   |   |   |   |   |   |   |   |   |   start <= 527803:
structural_molecule_activity_ (14.68)
|   |   |   |   |   |   |   |   |   |   |   start > 527803:
molecular_function_ (42.67)
|   |   |   |   |   |   |   |   |   |   start > 537837
|   |   |   |   |   |   |   |   |   |   |   start <= 541198
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
transcription_regulator_activity_ (2.32/0.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_binding_ (3.84/0.91)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: transcription_regulator_activity_ (5.63/2.06)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: DNA_binding_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: DNA_binding_ (2.11/0.9)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: DNA_binding_ (5.91/1.11)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: DNA_binding_ (3.31/0.71)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: transcription_regulator_activity_ (4.6/1.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: DNA_binding_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
transcription_regulator_activity_ (1.36/0.47)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: DNA_binding_ (0.0)
```

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|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: transcription_regulator_activity_
(2.68/0.63)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: DNA_binding_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   start > 541198
|   |   |   |   |   |   |   |   |   |   |   |   start <= 545154:
molecular_function_ (10.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 545154:
protein_kinase_activity_ (13.46)
|   |   |   |   |   |   |   |   |   start > 546124
|   |   |   |   |   |   |   |   |   |   start <= 573330
|   |   |   |   |   |   |   |   |   |   |   start <= 563095
|   |   |   |   |   |   |   |   |   |   |   |   start <= 551927
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 547713:
molecular_function_ (12.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 547713:
structural_molecule_activity_ (14.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 551927
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 560365:
molecular_function_ (57.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 560365
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
560995: transferase_activity_ (12.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
560995: molecular_function_ (14.05)
```

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|   |   |   |   |   |   |   |   |   |   start > 563095
|   |   |   |   |   |   |   |   |   |   |   start <= 564434:
structural_molecule_activity_ (20.36)
|   |   |   |   |   |   |   |   |   |   |   start > 564434
|   |   |   |   |   |   |   |   |   |   |   |   start <= 568550:
molecular_function_ (13.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 568550:
structural_molecule_activity_ (14.45)
|   |   |   |   |   |   |   |   |   |   start > 573330:
molecular_function_ (40.33)
|   |   |   |   |   |   |   |   start > 583920
|   |   |   |   |   |   |   |   |   start <= 599157: DNA_binding_
(25.86)
|   |   |   |   |   |   |   |   |   start > 599157:
transcription_regulator_activity_ (20.64)
|   |   |   |   |   |   |   start > 605980
|   |   |   |   |   |   |   |   start <= 608688: hydrolase_activity_
(5.77)
|   |   |   |   |   |   |   |   start > 608688
|   |   |   |   |   |   |   |   |   start <= 625810:
molecular_function_ (114.85)
|   |   |   |   |   |   |   |   |   start > 625810
|   |   |   |   |   |   |   |   |   |   start <= 626348:
RNA_binding_ (17.58)
|   |   |   |   |   |   |   |   |   |   start > 626348:
molecular_function_ (35.08)
|   |   |   |   |   start > 629024
|   |   |   |   |   |   start <= 652886
|   |   |   |   |   |   |   start <= 647117
|   |   |   |   |   |   |   |   start <= 637499
|   |   |   |   |   |   |   |   |   start <= 632354:
protein_binding_ (19.43)
|   |   |   |   |   |   |   |   |   start > 632354:
oxidoreductase_activity_ (14.27)
|   |   |   |   |   |   |   |   start > 637499
|   |   |   |   |   |   |   |   |   start <= 645655:
molecular_function_ (12.46)
|   |   |   |   |   |   |   |   |   start > 645655: protein_binding_
(18.04)
|   |   |   |   |   |   |   start > 647117
|   |   |   |   |   |   |   |   start <= 650035:
structural_molecule_activity_ (8.68)
|   |   |   |   |   |   |   |   start > 650035: RNA_binding_ (21.63)
|   |   |   |   |   |   start > 652886
|   |   |   |   |   |   |   start <= 662643
|   |   |   |   |   |   |   |   start <= 655075: molecular_function_
(32.69)
|   |   |   |   |   |   |   |   start > 655075
|   |   |   |   |   |   |   |   |   start <= 659744: motor_activity_
(27.37)
|   |   |   |   |   |   |   |   |   start > 659744:
enzyme_regulator_activity_ (16.53)
|   |   |   |   |   |   |   start > 662643
|   |   |   |   |   |   |   |   start <= 667536
```

```
|   |   |   |   |   |   |   |   |   start <= 664751:
molecular_function_ (16.38)
|   |   |   |   |   |   |   |   |   start > 664751:
isomerase_activity_ (15.56)
|   |   |   |   |   |   |   |   start > 667536
|   |   |   |   |   |   |   |   |   start <= 671324:
transporter_activity_ (12.73)
|   |   |   |   |   |   |   |   |   start > 671324:
molecular_function_ (20.5)
|   |   |   |   start > 675895
|   |   |   |   |   start <= 732413
|   |   |   |   |   |   start <= 712315
|   |   |   |   |   |   |   start <= 693380
|   |   |   |   |   |   |   |   start <= 687515:
transferase_activity_ (31.99)
|   |   |   |   |   |   |   |   start > 687515
|   |   |   |   |   |   |   |   |   start <= 689082:
structural_molecule_activity_ (23.05)
|   |   |   |   |   |   |   |   |   start > 689082: RNA_binding_
(17.79)
|   |   |   |   |   |   |   start > 693380
|   |   |   |   |   |   |   |   start <= 695349: protein_binding_
(17.93)
|   |   |   |   |   |   |   |   start > 695349
|   |   |   |   |   |   |   |   |   start <= 701789
|   |   |   |   |   |   |   |   |   |   start <= 696795:
transferase_activity_ (20.65)
|   |   |   |   |   |   |   |   |   |   start > 696795:
ligase_activity_ (12.06)
|   |   |   |   |   |   |   |   |   start > 701789
|   |   |   |   |   |   |   |   |   |   start <= 707132:
molecular_function_ (18.41)
|   |   |   |   |   |   |   |   |   |   start > 707132:
transferase_activity_ (11.7)
|   |   |   |   |   |   start > 712315
|   |   |   |   |   |   |   start <= 724625
|   |   |   |   |   |   |   |   start <= 720652: peptidase_activity_
(17.5)
|   |   |   |   |   |   |   |   start > 720652:
transcription_regulator_activity_ (13.46)
|   |   |   |   |   |   |   start > 724625:
structural_molecule_activity_ (18.35)
|   |   |   |   |   start > 732413
|   |   |   |   |   |   start <= 837927
|   |   |   |   |   |   |   start <= 793725
|   |   |   |   |   |   |   |   start <= 747962
|   |   |   |   |   |   |   |   |   start <= 739184:
molecular_function_ (82.43)
|   |   |   |   |   |   |   |   |   start > 739184
|   |   |   |   |   |   |   |   |   |   start <= 742970
|   |   |   |   |   |   |   |   |   |   |   start <= 740265:
hydrolase_activity_ (24.83)
|   |   |   |   |   |   |   |   |   |   |   start > 740265:
transcription_regulator_activity_ (23.63)
```

```
|   |   |   |   |   |   |   |   |   |   start > 742970
|   |   |   |   |   |   |   |   |   |   |   start <= 743748:
molecular_function_ (18.76)
|   |   |   |   |   |   |   |   |   |   |   start > 743748:
hydrolase_activity_ (18.25)
|   |   |   |   |   |   |   |   start > 747962
|   |   |   |   |   |   |   |   |   start <= 751960: DNA_binding_
(13.68)
|   |   |   |   |   |   |   |   |   start > 751960
|   |   |   |   |   |   |   |   |   |   start <= 770800
|   |   |   |   |   |   |   |   |   |   |   start <= 769282
|   |   |   |   |   |   |   |   |   |   |   |   start <= 757249:
molecular_function_ (34.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 757249
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 763112:
ligase_activity_ (12.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 763112:
molecular_function_ (15.61)
|   |   |   |   |   |   |   |   |   |   |   start > 769282:
lyase_activity_ (10.25)
|   |   |   |   |   |   |   |   |   |   start > 770800
|   |   |   |   |   |   |   |   |   |   |   start <= 772914:
transferase_activity_ (15.04)
|   |   |   |   |   |   |   |   |   |   |   start > 772914:
molecular_function_ (65.19)
|   |   |   |   |   |   |   start > 793725
|   |   |   |   |   |   |   |   start <= 818826
|   |   |   |   |   |   |   |   |   start <= 813979
|   |   |   |   |   |   |   |   |   |   start <= 795804
|   |   |   |   |   |   |   |   |   |   |   start <= 794918:
hydrolase_activity_ (14.66)
|   |   |   |   |   |   |   |   |   |   |   start > 794918:
protein_binding_ (13.41)
|   |   |   |   |   |   |   |   |   |   start > 795804
|   |   |   |   |   |   |   |   |   |   |   start <= 801771
|   |   |   |   |   |   |   |   |   |   |   |   start <= 798517:
molecular_function_ (15.94)
|   |   |   |   |   |   |   |   |   |   |   |   start > 798517:
hydrolase_activity_ (17.35)
|   |   |   |   |   |   |   |   |   |   |   start > 801771:
molecular_function_ (22.3)
|   |   |   |   |   |   |   |   |   start > 813979: protein_binding_
(15.54)
|   |   |   |   |   |   |   |   start > 818826
|   |   |   |   |   |   |   |   |   start <= 820255:
phosphoprotein_phosphatase_activity_ (14.13)
|   |   |   |   |   |   |   |   |   start > 820255
|   |   |   |   |   |   |   |   |   |   start <= 826350:
molecular_function_ (19.05)
|   |   |   |   |   |   |   |   |   |   start > 826350
|   |   |   |   |   |   |   |   |   |   |   start <= 835097:
hydrolase_activity_ (18.97)
|   |   |   |   |   |   |   |   |   |   |   start > 835097:
molecular_function_ (13.68)
```

```
|   |   |   |   |   |   start > 837927
|   |   |   |   |   |   |   start <= 848684
|   |   |   |   |   |   |   |   start <= 845570
|   |   |   |   |   |   |   |   |   start <= 841941
|   |   |   |   |   |   |   |   |   |   start <= 838186:
RNA_binding_ (6.51)
|   |   |   |   |   |   |   |   |   |   start > 838186:
structural_molecule_activity_ (9.61)
|   |   |   |   |   |   |   |   |   start > 841941: RNA_binding_
(19.39)
|   |   |   |   |   |   |   |   start > 845570: lyase_activity_
(7.96)
|   |   |   |   |   |   |   start > 848684
|   |   |   |   |   |   |   |   start <= 852629:
protein_kinase_activity_ (15.04)
|   |   |   |   |   |   |   |   start > 852629
|   |   |   |   |   |   |   |   |   start <= 854794:
molecular_function_ (12.52)
|   |   |   |   |   |   |   |   |   start > 854794:
structural_molecule_activity_ (12.85)
|   start > 858889
|   |   start <= 887002
|   |   |   strand = C
|   |   |   |   start <= 867090
|   |   |   |   |   start <= 861921: transferase_activity_ (17.81)
|   |   |   |   |   start > 861921
|   |   |   |   |   |   start <= 865349: motor_activity_ (14.61)
|   |   |   |   |   |   start > 865349: transferase_activity_
(13.68)
|   |   |   |   start > 867090
|   |   |   |   |   start <= 872624
|   |   |   |   |   |   start <= 869626: hydrolase_activity_ (15.2)
|   |   |   |   |   |   start > 869626: molecular_function_ (19.89)
|   |   |   |   |   start > 872624
|   |   |   |   |   |   start <= 874986: oxidoreductase_activity_
(12.18)
|   |   |   |   |   |   start > 874986: hydrolase_activity_ (8.78)
|   |   |   strand = W
|   |   |   |   start <= 874986
|   |   |   |   |   start <= 867090: transferase_activity_
(52.75/12.61)
|   |   |   |   |   start > 867090: peptidase_activity_ (21.95)
|   |   |   |   start > 874986: transferase_activity_ (30.26)
|   |   start > 887002
|   |   |   strand = C
|   |   |   |   start <= 904823
|   |   |   |   |   start <= 896668
|   |   |   |   |   |   start <= 895425
|   |   |   |   |   |   |   start <= 892220: protein_binding_
(14.12)
|   |   |   |   |   |   |   start > 892220:
translation_regulator_activity_ (22.46)
|   |   |   |   |   |   start > 895425: molecular_function_ (15.89)
|   |   |   |   |   start > 896668
```

```
|   |   |   |   |   |   start <= 898404: enzyme_regulator_activity_
(24.79)
|   |   |   |   |   |   start > 898404: hydrolase_activity_ (23.23)
|   |   |   |   start > 904823
|   |   |   |   |   start <= 917894
|   |   |   |   |   |   start <= 912141: oxidoreductase_activity_
(18.05)
|   |   |   |   |   |   start > 912141
|   |   |   |   |   |   |   start <= 914536: transporter_activity_
(12.65)
|   |   |   |   |   |   |   start > 914536: molecular_function_
(14.63)
|   |   |   |   |   start > 917894: protein_binding_ (34.83/13.48)
|   |   |   strand = W
|   |   |   |   start <= 901708
|   |   |   |   |   start <= 898404: molecular_function_ (19.21)
|   |   |   |   |   start > 898404: peptidase_activity_ (15.35)
|   |   |   |   start > 901708
|   |   |   |   |   start <= 912141: molecular_function_ (68.61)
|   |   |   |   |   start > 912141
|   |   |   |   |   |   start <= 920086: lyase_activity_ (11.05)
|   |   |   |   |   |   start > 920086: molecular_function_ (12.6)
```

For Biological Process

```
|   start <= 845570
|   |   start <= 448085
|   |   |   start <= 288078
|   |   |   |   start <= 50954
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 26930
|   |   |   |   |   |   |   start <= 14754
|   |   |   |   |   |   |   |   start <= 13175
|   |   |   |   |   |   |   |   |   start <= 7244:
biological_process_ (7.34)
|   |   |   |   |   |   |   |   |   start > 7244:
protein_modification_process_ (20.65)
|   |   |   |   |   |   |   |   start > 13175: cellular_respiration_
(25.52)
|   |   |   |   |   |   |   start > 14754
|   |   |   |   |   |   |   |   start <= 20536
|   |   |   |   |   |   |   |   |   start <= 17065
|   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 3595:
meiosis_ (19.65/8.2)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 3595:
cell_cycle_ (4.08/0.98)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cell_cycle_ (7.23/3.56)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
3595: DNA_metabolic_process_ (2.28/1.07)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 3595:
meiosis_ (2.35/0.51)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cell_cycle_ (1.25/0.76)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (22.4/10.98)
|   |   |   |   |   |   |   |   |   start > 17065:
lipid_metabolic_process_ (23.26)
|   |   |   |   |   |   |   |   start > 20536
|   |   |   |   |   |   |   |   |   start <= 23684
|   |   |   |   |   |   |   |   |   |   start <= 21700: transport_
(18.8)
|   |   |   |   |   |   |   |   |   |   start > 21700
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cell_cycle_ (10.08/2.35)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cell_cycle_ (5.02/2.1)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
meiosis_ (11.63/2.84)
|   |   |   |   |   |   |   |   |   start > 23684: transport_
(18.87)
|   |   |   |   |   |   start > 26930
|   |   |   |   |   |   |   start <= 41794
|   |   |   |   |   |   |   |   start <= 34243: electron_transport_
(14.42)
|   |   |   |   |   |   |   |   start > 34243:
protein_modification_process_ (17.52)
|   |   |   |   |   |   |   start > 41794
|   |   |   |   |   |   |   |   start <= 46942: transcription_
(19.32)
|   |   |   |   |   |   |   |   start > 46942: cellular_respiration_
(20.66)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 32334
|   |   |   |   |   |   |   start <= 21700
|   |   |   |   |   |   |   |   start <= 13175
|   |   |   |   |   |   |   |   |   start <= 7244:
cellular_homeostasis_ (9.62)
|   |   |   |   |   |   |   |   |   start > 7244:
biological_process_ (10.7)
|   |   |   |   |   |   |   |   start > 13175: response_to_stress_
(16.87)
|   |   |   |   |   |   |   start > 21700
|   |   |   |   |   |   |   |   start <= 26930:
DNA_metabolic_process_ (32.12/10.85)
|   |   |   |   |   |   |   |   start > 26930: biological_process_
(24.12)
|   |   |   |   |   |   start > 32334
|   |   |   |   |   |   |   start <= 44045
|   |   |   |   |   |   |   |   start <= 38196
|   |   |   |   |   |   |   |   |   start <= 34243:
RNA_metabolic_process_ (16.56)
|   |   |   |   |   |   |   |   |   start > 34243: transport_
(14.91)
```

```
|   |   |   |   |   |   |   |   start > 38196: transcription_
(17.91)
|   |   |   |   |   |   |   start > 44045:
protein_modification_process_ (32.74)
|   |   |   |   start > 50954
|   |   |   |   |   start <= 111002
|   |   |   |   |   |   start <= 67549
|   |   |   |   |   |   |   start <= 58687
|   |   |   |   |   |   |   |   start <= 56773
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: transport_
(24.41/10.95)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
biological_process_ (16.13/3.36)
|   |   |   |   |   |   |   |   |   strand = W: biological_process_
(40.52)
|   |   |   |   |   |   |   |   start > 56773: transport_ (21.49)
|   |   |   |   |   |   |   start > 58687
|   |   |   |   |   |   |   |   start <= 62322:
organelle_organization_and_biogenesis_ (16.33)
|   |   |   |   |   |   |   |   start > 62322:
nuclear_organization_and_biogenesis_ (14.79)
|   |   |   |   |   |   start > 67549
|   |   |   |   |   |   |   start <= 99400
|   |   |   |   |   |   |   |   start <= 83090
|   |   |   |   |   |   |   |   |   start <= 67938:
RNA_metabolic_process_ (33.34/15.25)
|   |   |   |   |   |   |   |   |   start > 67938
|   |   |   |   |   |   |   |   |   |   start <= 77040
|   |   |   |   |   |   |   |   |   |   |   start <= 68294:
DNA_metabolic_process_ (19.7)
|   |   |   |   |   |   |   |   |   |   |   start > 68294
|   |   |   |   |   |   |   |   |   |   |   |   start <= 70138:
biological_process_ (48.17)
|   |   |   |   |   |   |   |   |   |   |   |   start > 70138
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 70624:
response_to_stress_ (13.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 70624:
amino_acid_and_derivative_metabolic_process_ (30.39/14.98)
|   |   |   |   |   |   |   |   |   |   start > 77040
|   |   |   |   |   |   |   |   |   |   |   stop <= 81481
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 79909:
DNA_metabolic_process_ (21.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 79909:
cell_cycle_ (22.66/7.73)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cell_cycle_ (13.0)
|   |   |   |   |   |   |   |   |   |   |   stop > 81481
|   |   |   |   |   |   |   |   |   |   |   |   start <= 82275:
biological_process_ (20.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 82275:
ribosome_biogenesis_and_assembly_ (9.92)
|   |   |   |   |   |   |   |   start > 83090
```

```
|   |   |   |   |   |   |   |   |   start <= 90731
|   |   |   |   |   |   |   |   |   |   start <= 86739:
protein_catabolic_process_ (26.21)
|   |   |   |   |   |   |   |   |   |   start > 86739: translation_
(11.62)
|   |   |   |   |   |   |   |   |   start > 90731
|   |   |   |   |   |   |   |   |   |   start <= 97371
|   |   |   |   |   |   |   |   |   |   |   distance <= 3508:
response_to_stress_ (22.19/2.75)
|   |   |   |   |   |   |   |   |   |   |   distance > 3508:
biological_process_ (3.84)
|   |   |   |   |   |   |   |   |   |   start > 97371: cell_cycle_
(22.97/8.07)
|   |   |   |   |   |   |   start > 99400
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 101862:
biological_process_ (10.99)
|   |   |   |   |   |   |   |   |   start > 101862:
generation_of_precursor_metabolites_and_energy_ (14.26)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 108806
|   |   |   |   |   |   |   |   |   |   start <= 104777:
biological_process_ (29.88)
|   |   |   |   |   |   |   |   |   |   start > 104777:
RNA_metabolic_process_ (20.39)
|   |   |   |   |   |   |   |   |   start > 108806:
biological_process_ (37.31)
|   |   |   |   |   start > 111002
|   |   |   |   |   |   start <= 159383
|   |   |   |   |   |   |   start <= 140214
|   |   |   |   |   |   |   |   start <= 131572
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 129367
|   |   |   |   |   |   |   |   |   |   |   start <= 118898
|   |   |   |   |   |   |   |   |   |   |   |   start <= 115347:
biological_process_ (17.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 115347:
lipid_metabolic_process_ (15.85)
|   |   |   |   |   |   |   |   |   |   |   start > 118898
|   |   |   |   |   |   |   |   |   |   |   |   start <= 121324:
meiosis_ (22.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 121324
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 124172:
translation_ (9.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 124172:
biological_process_ (15.28)
|   |   |   |   |   |   |   |   |   |   start > 129367: transport_
(29.41/14.43)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: transport_
(20.04/6.42)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: vesicle-
mediated_transport_ (15.81/5.88)
|   |   |   |   |   |   |   |   start > 131572
```

```
|   |   |   |   |   |   |   |   |   start <= 137550
|   |   |   |   |   |   |   |   |   |   start <= 133475
|   |   |   |   |   |   |   |   |   |   |   start <= 131896:
translation_ (14.82)
|   |   |   |   |   |   |   |   |   |   |   start > 131896:
response_to_stress_ (15.73)
|   |   |   |   |   |   |   |   |   |   start > 133475
|   |   |   |   |   |   |   |   |   |   |   start <= 135500:
RNA_metabolic_process_ (20.43/9.97)
|   |   |   |   |   |   |   |   |   |   |   start > 135500:
translation_ (15.09)
|   |   |   |   |   |   |   |   |   start > 137550: transport_
(22.97/9.39)
|   |   |   |   |   |   |   start > 140214
|   |   |   |   |   |   |   |   start <= 151871
|   |   |   |   |   |   |   |   |   start <= 141533: sporulation_
(29.37/8.07)
|   |   |   |   |   |   |   |   |   start > 141533
|   |   |   |   |   |   |   |   |   |   start <= 146482
|   |   |   |   |   |   |   |   |   |   |   strand = C: cell_cycle_
(22.33)
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 142210:
DNA_metabolic_process_ (12.46)
|   |   |   |   |   |   |   |   |   |   |   |   start > 142210:
translation_ (30.97)
|   |   |   |   |   |   |   |   |   |   start > 146482:
DNA_metabolic_process_ (59.02)
|   |   |   |   |   |   |   |   start > 151871
|   |   |   |   |   |   |   |   |   strand = C:
lipid_metabolic_process_ (19.89)
|   |   |   |   |   |   |   |   |   strand = W: response_to_stress_
(45.58/15.47)
|   |   |   |   |   |   start > 159383
|   |   |   |   |   |   |   start <= 204103
|   |   |   |   |   |   |   |   start <= 181474
|   |   |   |   |   |   |   |   |   stop <= 161994:
cellular_homeostasis_ (34.99/16.01)
|   |   |   |   |   |   |   |   |   stop > 161994
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 173139
|   |   |   |   |   |   |   |   |   |   |   |   start <= 163620
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: RNA_metabolic_process_ (5.34/0.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: ribosome_biogenesis_and_assembly_ (4.49/1.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: ribosome_biogenesis_and_assembly_ (16.07/4.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 163620
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 167308
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
164790: biological_process_ (21.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
164790: electron_transport_ (7.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 167308:
biological_process_ (35.75)
|   |   |   |   |   |   |   |   |   |   |   start > 173139
|   |   |   |   |   |   |   |   |   |   |   |   start <= 178426:
RNA_metabolic_process_ (15.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 178426:
conjugation_ (12.3)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 171594
|   |   |   |   |   |   |   |   |   |   |   |   start <= 168795
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 164790:
transport_ (6.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 164790:
translation_ (19.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 168795
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 170402:
vesicle-mediated_transport_ (13.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 170402:
carbohydrate_metabolic_process_ (15.89)
|   |   |   |   |   |   |   |   |   |   |   start > 171594
|   |   |   |   |   |   |   |   |   |   |   |   start <= 173139:
biological_process_ (22.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 173139
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 178426:
transport_ (15.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 178426:
biological_process_ (13.12)
|   |   |   |   |   |   |   |   start > 181474
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 192788
|   |   |   |   |   |   |   |   |   |   |   start <= 183968:
translation_ (9.44)
|   |   |   |   |   |   |   |   |   |   |   start > 183968:
transcription_ (15.55)
|   |   |   |   |   |   |   |   |   |   start > 192788
|   |   |   |   |   |   |   |   |   |   |   start <= 195755:
transport_ (17.79)
|   |   |   |   |   |   |   |   |   |   |   start > 195755
|   |   |   |   |   |   |   |   |   |   |   |   start <= 196170:
translation_ (18.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 196170:
transport_ (10.73)
|   |   |   |   |   |   |   |   |   strand = W:
vitamin_metabolic_process_ (15.45)
|   |   |   |   |   |   |   start > 204103
|   |   |   |   |   |   |   |   start <= 273118
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 247677
|   |   |   |   |   |   |   |   |   |   |   start <= 236588
|   |   |   |   |   |   |   |   |   |   |   |   start <= 209525:
biological_process_ (35.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 209525
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 231149
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
225889
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
217362
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: DNA_metabolic_process_ (17.22/7.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: cell_cycle_ (6.55/0.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
217362: translation_ (16.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
225889: DNA_metabolic_process_ (29.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 231149:
biological_process_ (27.75)
|   |   |   |   |   |   |   |   |   |   |   start > 236588
|   |   |   |   |   |   |   |   |   |   |   |   start <= 244149
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 241536:
cellular_homeostasis_ (15.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 241536:
cell_cycle_ (11.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 244149:
DNA_metabolic_process_ (20.04)
|   |   |   |   |   |   |   |   |   |   start > 247677
|   |   |   |   |   |   |   |   |   |   |   start <= 260221
|   |   |   |   |   |   |   |   |   |   |   |   start <= 253848
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 251516:
translation_ (17.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 251516
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
252990: lipid_metabolic_process_ (10.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
252990: biological_process_ (9.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 253848
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 258416:
signal_transduction_ (15.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 258416:
translation_ (19.06)
|   |   |   |   |   |   |   |   |   |   |   start > 260221
|   |   |   |   |   |   |   |   |   |   |   |   start <= 271136
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 264541:
biological_process_ (14.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 264541
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
2169: protein_modification_process_ (18.89/5.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
2169: DNA_metabolic_process_ (20.02/7.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 271136:
biological_process_ (16.57)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 214189
|   |   |   |   |   |   |   |   |   |   |   start <= 205642:
DNA_metabolic_process_ (14.62)
|   |   |   |   |   |   |   |   |   |   |   start > 205642
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 209525:
cell_cycle_ (9.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 209525
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: cytoskeleton_organization_and_biogenesis_ (16.35/9.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: cell_cycle_ (21.68/12.54)
|   |   |   |   |   |   |   |   |   |   start > 214189
|   |   |   |   |   |   |   |   |   |   |   start <= 244149
|   |   |   |   |   |   |   |   |   |   |   |   start <= 225889
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 217362
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
216435: biological_process_ (19.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
216435: RNA_metabolic_process_ (12.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 217362
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
220138: response_to_stress_ (15.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
220138
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
221406: cell_cycle_ (12.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
221406: translation_ (10.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 225889
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 236588
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
231149: biological_process_ (46.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
231149
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
233457: protein_modification_process_ (16.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
233457: biological_process_ (17.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 236588
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
243225: response_to_stress_ (13.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
243225: biological_process_ (11.64)
|   |   |   |   |   |   |   |   |   |   |   start > 244149
|   |   |   |   |   |   |   |   |   |   |   |   start <= 260221
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 246116:
transport_ (26.81/13.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 246116
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
247677
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: transcription_ (33.5/19.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: RNA_metabolic_process_ (12.07/7.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
247677
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
253848: response_to_stress_ (12.26)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
253848: RNA_metabolic_process_ (10.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 260221
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 264541:
biological_process_ (36.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 264541
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
267174: vesicle-mediated_transport_ (18.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
267174: biological_process_ (35.95)
|   |   |   |   |   |   |   |   start > 273118
|   |   |   |   |   |   |   |   |   strand = C:
lipid_metabolic_process_ (30.01)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 279681
|   |   |   |   |   |   |   |   |   |   |   start <= 274017:
transport_ (16.98)
|   |   |   |   |   |   |   |   |   |   |   start > 274017:
transcription_ (17.7)
|   |   |   |   |   |   |   |   |   |   start > 279681
|   |   |   |   |   |   |   |   |   |   |   start <= 284101:
amino_acid_and_derivative_metabolic_process_ (11.92)
|   |   |   |   |   |   |   |   |   |   |   start > 284101
|   |   |   |   |   |   |   |   |   |   |   |   start <= 285099:
biological_process_ (9.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 285099:
transport_ (8.45)
|   |   |   start > 288078
|   |   |   |   start <= 305592
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 298867:
protein_modification_process_ (22.08)
|   |   |   |   |   |   start > 298867
|   |   |   |   |   |   |   start <= 302484:
lipid_metabolic_process_ (21.12)
|   |   |   |   |   |   |   start > 302484: pseudohyphal_growth_
(12.56)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 291133: translation_ (43.12/11.27)
|   |   |   |   |   |   start > 291133:
ribosome_biogenesis_and_assembly_ (282.84/128.12)
|   |   |   |   start > 305592
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 379585
|   |   |   |   |   |   |   start <= 348259
|   |   |   |   |   |   |   |   start <= 323299
|   |   |   |   |   |   |   |   |   start <= 318679:
protein_catabolic_process_ (19.78)
|   |   |   |   |   |   |   |   |   start > 318679: translation_
(32.9)
|   |   |   |   |   |   |   |   start > 323299
|   |   |   |   |   |   |   |   |   start <= 330792
|   |   |   |   |   |   |   |   |   |   start <= 327481:
organelle_organization_and_biogenesis_ (40.49/19.85)
```

```
|   |   |   |   |   |   |   |   |   |   start > 327481: conjugation_
(28.04)
|   |   |   |   |   |   |   |   |   start > 330792
|   |   |   |   |   |   |   |   |   |   start <= 343519
|   |   |   |   |   |   |   |   |   |   |   start <= 341141:
biological_process_ (33.06)
|   |   |   |   |   |   |   |   |   |   |   start > 341141:
cell_cycle_ (13.17)
|   |   |   |   |   |   |   |   |   |   start > 343519
|   |   |   |   |   |   |   |   |   |   |   start <= 346516:
response_to_stress_ (17.98)
|   |   |   |   |   |   |   |   |   |   |   start > 346516:
transport_ (18.91)
|   |   |   |   |   |   |   start > 348259
|   |   |   |   |   |   |   |   start <= 366980
|   |   |   |   |   |   |   |   |   start <= 350380: transcription_
(25.43)
|   |   |   |   |   |   |   |   |   start > 350380
|   |   |   |   |   |   |   |   |   |   start <= 355383:
vitamin_metabolic_process_ (11.98)
|   |   |   |   |   |   |   |   |   |   start > 355383:
nuclear_organization_and_biogenesis_ (14.68)
|   |   |   |   |   |   |   |   start > 366980
|   |   |   |   |   |   |   |   |   start <= 370516:
ribosome_biogenesis_and_assembly_ (16.73)
|   |   |   |   |   |   |   |   |   start > 370516: translation_
(23.1)
|   |   |   |   |   |   start > 379585
|   |   |   |   |   |   |   start <= 424988
|   |   |   |   |   |   |   |   start <= 407708
|   |   |   |   |   |   |   |   |   start <= 387020
|   |   |   |   |   |   |   |   |   |   start <= 383302:
protein_modification_process_ (15.96)
|   |   |   |   |   |   |   |   |   |   start > 383302: cell_cycle_
(22.62)
|   |   |   |   |   |   |   |   |   start > 387020
|   |   |   |   |   |   |   |   |   |   start <= 392754
|   |   |   |   |   |   |   |   |   |   |   start <= 388821:
cellular_respiration_ (18.79)
|   |   |   |   |   |   |   |   |   |   |   start > 388821:
membrane_organization_and_biogenesis_ (10.76)
|   |   |   |   |   |   |   |   |   |   start > 392754
|   |   |   |   |   |   |   |   |   |   |   start <= 399701:
cell_wall_organization_and_biogenesis_ (12.62)
|   |   |   |   |   |   |   |   |   |   |   start > 399701:
sporulation_ (14.84)
|   |   |   |   |   |   |   |   start > 407708
|   |   |   |   |   |   |   |   |   start <= 413981
|   |   |   |   |   |   |   |   |   |   start <= 411568: vesicle-
mediated_transport_ (19.72)
|   |   |   |   |   |   |   |   |   |   start > 411568:
biological_process_ (30.1)
|   |   |   |   |   |   |   |   |   start > 413981
|   |   |   |   |   |   |   |   |   |   start <= 420660
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 420028:
cell_cycle_ (15.24)
|   |   |   |   |   |   |   |   |   |   |   start > 420028:
translation_ (14.7)
|   |   |   |   |   |   |   |   |   |   start > 420660
|   |   |   |   |   |   |   |   |   |   |   start <= 422148:
vesicle-mediated_transport_ (22.21)
|   |   |   |   |   |   |   |   |   |   |   start > 422148:
cell_cycle_ (23.69)
|   |   |   |   |   |   |   start > 424988
|   |   |   |   |   |   |   |   start <= 429626:
RNA_metabolic_process_ (38.25/21.59)
|   |   |   |   |   |   |   |   start > 429626
|   |   |   |   |   |   |   |   |   start <= 445101
|   |   |   |   |   |   |   |   |   |   start <= 437490:
cellular_respiration_ (14.56)
|   |   |   |   |   |   |   |   |   |   start > 437490: transport_
(15.54)
|   |   |   |   |   |   |   |   |   start > 445101:
protein_modification_process_ (20.91)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 372517
|   |   |   |   |   |   |   start <= 315376
|   |   |   |   |   |   |   |   start <= 312155: biological_process_
(64.48/14.38)
|   |   |   |   |   |   |   |   start > 312155:
amino_acid_and_derivative_metabolic_process_ (15.02)
|   |   |   |   |   |   |   start > 315376
|   |   |   |   |   |   |   |   start <= 343519
|   |   |   |   |   |   |   |   |   start <= 323299
|   |   |   |   |   |   |   |   |   |   start <= 321874
|   |   |   |   |   |   |   |   |   |   |   start <= 318679:
DNA_metabolic_process_ (15.39)
|   |   |   |   |   |   |   |   |   |   |   start > 318679:
translation_ (15.54)
|   |   |   |   |   |   |   |   |   |   start > 321874
|   |   |   |   |   |   |   |   |   |   |   distance <= 538:
conjugation_ (4.34/0.0)
|   |   |   |   |   |   |   |   |   |   |   distance > 538:
protein_modification_process_ (30.26/11.27)
|   |   |   |   |   |   |   |   |   start > 323299
|   |   |   |   |   |   |   |   |   |   start <= 337312
|   |   |   |   |   |   |   |   |   |   |   start <= 330792
|   |   |   |   |   |   |   |   |   |   |   |   start <= 327481
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 325876:
biological_process_ (11.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 325876:
signal_transduction_ (17.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 327481:
cellular_respiration_ (15.36)
|   |   |   |   |   |   |   |   |   |   |   start > 330792
|   |   |   |   |   |   |   |   |   |   |   |   start <= 335297:
cytokinesis_ (17.02)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 335297:
biological_process_ (15.57)
|   |   |   |   |   |   |   |   |   |   start > 337312
|   |   |   |   |   |   |   |   |   |   |   start <= 337787:
RNA_metabolic_process_ (22.66/10.08)
|   |   |   |   |   |   |   |   |   |   |   start > 337787:
protein_modification_process_ (21.42)
|   |   |   |   |   |   |   |   start > 343519
|   |   |   |   |   |   |   |   |   start <= 352602
|   |   |   |   |   |   |   |   |   |   start <= 352279
|   |   |   |   |   |   |   |   |   |   |   start <= 350380:
biological_process_ (24.59)
|   |   |   |   |   |   |   |   |   |   |   start > 350380:
translation_ (18.81)
|   |   |   |   |   |   |   |   |   |   start > 352279
|   |   |   |   |   |   |   |   |   |   |   distance <= 2848:
amino_acid_and_derivative_metabolic_process_ (18.55/7.67)
|   |   |   |   |   |   |   |   |   |   |   distance > 2848:
biological_process_ (7.1/2.08)
|   |   |   |   |   |   |   |   |   start > 352602
|   |   |   |   |   |   |   |   |   |   start <= 355383:
DNA_metabolic_process_ (24.42)
|   |   |   |   |   |   |   |   |   |   start > 355383
|   |   |   |   |   |   |   |   |   |   |   start <= 363063:
translation_ (10.58)
|   |   |   |   |   |   |   |   |   |   |   start > 363063: meiosis_
(17.42)
|   |   |   |   |   |   start > 372517
|   |   |   |   |   |   |   start <= 399701
|   |   |   |   |   |   |   |   start <= 392754
|   |   |   |   |   |   |   |   |   start <= 388821
|   |   |   |   |   |   |   |   |   |   start <= 383302
|   |   |   |   |   |   |   |   |   |   |   start <= 379585:
conjugation_ (11.86)
|   |   |   |   |   |   |   |   |   |   |   start > 379585:
organelle_organization_and_biogenesis_ (15.68)
|   |   |   |   |   |   |   |   |   |   start > 383302
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
transport_ (8.34/2.15)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 1876:
biological_process_ (9.26/2.06)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 1876:
transport_ (8.26/3.13)
|   |   |   |   |   |   |   |   |   start > 388821:
RNA_metabolic_process_ (44.29)
|   |   |   |   |   |   |   |   start > 392754
|   |   |   |   |   |   |   |   |   start <= 397902
|   |   |   |   |   |   |   |   |   |   start <= 397076:
sporulation_ (22.48)
|   |   |   |   |   |   |   |   |   |   start > 397076: translation_
(22.81)
|   |   |   |   |   |   |   |   |   start > 397902
```

```
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
conjugation_ (13.55/4.47)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
nuclear_organization_and_biogenesis_ (28.0/9.63)
|   |   |   |   |   |   |   start > 399701
|   |   |   |   |   |   |   |   start <= 413981
|   |   |   |   |   |   |   |   |   start <= 406303
|   |   |   |   |   |   |   |   |   |   start <= 401540:
biological_process_ (23.91)
|   |   |   |   |   |   |   |   |   |   start > 401540:
cell_wall_organization_and_biogenesis_ (23.99)
|   |   |   |   |   |   |   |   |   start > 406303
|   |   |   |   |   |   |   |   |   |   start <= 409153
|   |   |   |   |   |   |   |   |   |   |   start <= 407708:
protein_modification_process_ (18.06)
|   |   |   |   |   |   |   |   |   |   |   start > 407708:
transcription_ (23.86)
|   |   |   |   |   |   |   |   |   |   start > 409153
|   |   |   |   |   |   |   |   |   |   |   start <= 411568:
organelle_organization_and_biogenesis_ (17.26)
|   |   |   |   |   |   |   |   |   |   |   start > 411568:
protein_modification_process_ (23.32)
|   |   |   |   |   |   |   |   start > 413981
|   |   |   |   |   |   |   |   |   start <= 434787
|   |   |   |   |   |   |   |   |   |   start <= 429626: transport_
(36.46/13.65)
|   |   |   |   |   |   |   |   |   |   start > 429626:
generation_of_precursor_metabolites_and_energy_ (7.62)
|   |   |   |   |   |   |   |   |   start > 434787
|   |   |   |   |   |   |   |   |   |   start <= 439207:
biological_process_ (32.39)
|   |   |   |   |   |   |   |   |   |   start > 439207:
RNA_metabolic_process_ (15.39)
|   |   start > 448085
|   |   |   start <= 577717
|   |   |   |   start <= 477605
|   |   |   |   |   start <= 458407
|   |   |   |   |   |   start <= 454014
|   |   |   |   |   |   |   strand = C: response_to_stress_ (28.8)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 451364: biological_process_
(19.67)
|   |   |   |   |   |   |   |   start > 451364:
ribosome_biogenesis_and_assembly_ (20.85)
|   |   |   |   |   |   start > 454014
|   |   |   |   |   |   |   start <= 455824:
cytoskeleton_organization_and_biogenesis_ (39.07/11.77)
|   |   |   |   |   |   |   start > 455824:
vitamin_metabolic_process_ (36.07)
|   |   |   |   |   start > 458407
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 475452
|   |   |   |   |   |   |   |   start <= 466299
```

```
|   |   |   |   |   |   |   |   |   start <= 460526: translation_
(13.29)
|   |   |   |   |   |   |   |   |   start > 460526
|   |   |   |   |   |   |   |   |   |   start <= 463553:
biological_process_ (7.54)
|   |   |   |   |   |   |   |   |   |   start > 463553:
carbohydrate_metabolic_process_ (12.22)
|   |   |   |   |   |   |   |   start > 466299
|   |   |   |   |   |   |   |   |   start <= 469475:
protein_modification_process_ (15.26)
|   |   |   |   |   |   |   |   |   start > 469475
|   |   |   |   |   |   |   |   |   |   start <= 472351:
biological_process_ (17.53)
|   |   |   |   |   |   |   |   |   |   start > 472351:
protein_modification_process_ (10.49)
|   |   |   |   |   |   |   start > 475452
|   |   |   |   |   |   |   |   distance <= 2401:
carbohydrate_metabolic_process_ (17.47/5.42)
|   |   |   |   |   |   |   |   distance > 2401:
cellular_homeostasis_ (10.7/2.74)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 464826: translation_ (12.86)
|   |   |   |   |   |   |   start > 464826: cell_budding_ (21.77)
|   |   |   |   start > 477605
|   |   |   |   |   start <= 544962
|   |   |   |   |   |   start <= 535569
|   |   |   |   |   |   |   start <= 523344
|   |   |   |   |   |   |   |   start <= 486586
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 480189:
DNA_metabolic_process_ (10.32)
|   |   |   |   |   |   |   |   |   |   start > 480189: translation_
(10.65)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 483013:
biological_process_ (24.6)
|   |   |   |   |   |   |   |   |   |   start > 483013
|   |   |   |   |   |   |   |   |   |   |   start <= 484083:
amino_acid_and_derivative_metabolic_process_ (17.12)
|   |   |   |   |   |   |   |   |   |   |   start > 484083:
cell_wall_organization_and_biogenesis_ (15.46)
|   |   |   |   |   |   |   |   start > 486586
|   |   |   |   |   |   |   |   |   start <= 500071
|   |   |   |   |   |   |   |   |   |   start <= 497703
|   |   |   |   |   |   |   |   |   |   |   start <= 494494
|   |   |   |   |   |   |   |   |   |   |   |   start <= 493791:
biological_process_ (35.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 493791:
transcription_ (24.49)
|   |   |   |   |   |   |   |   |   |   |   start > 494494:
biological_process_ (40.15)
|   |   |   |   |   |   |   |   |   |   start > 497703:
RNA_metabolic_process_ (32.41/13.47)
|   |   |   |   |   |   |   |   |   start > 500071
```

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|   |   |   |   |   |   |   |   |   |   start <= 510347
|   |   |   |   |   |   |   |   |   |   |   start <= 500687:
DNA_metabolic_process_ (23.96/10.93)
|   |   |   |   |   |   |   |   |   |   |   start > 500687
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 509279:
biological_process_ (43.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 509279:
translation_ (14.06)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 504894:
translation_ (9.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 504894:
protein_catabolic_process_ (9.27)
|   |   |   |   |   |   |   |   |   |   start > 510347
|   |   |   |   |   |   |   |   |   |   |   start <= 514455:
biological_process_ (64.99)
|   |   |   |   |   |   |   |   |   |   |   start > 514455
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 521788:
biological_process_ (8.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 521788:
transcription_ (10.71)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
DNA_metabolic_process_ (15.06)
|   |   |   |   |   |   |   start > 523344
|   |   |   |   |   |   |   |   start <= 527803
|   |   |   |   |   |   |   |   |   start <= 523695:
ribosome_biogenesis_and_assembly_ (17.35)
|   |   |   |   |   |   |   |   |   start > 523695:
nuclear_organization_and_biogenesis_ (13.42)
|   |   |   |   |   |   |   |   start > 527803
|   |   |   |   |   |   |   |   |   start <= 534697
|   |   |   |   |   |   |   |   |   |   start <= 532118:
biological_process_ (14.9)
|   |   |   |   |   |   |   |   |   |   start > 532118:
ribosome_biogenesis_and_assembly_ (14.55)
|   |   |   |   |   |   |   |   |   start > 534697:
biological_process_ (19.08)
|   |   |   |   |   |   start > 535569
|   |   |   |   |   |   |   start <= 540055
|   |   |   |   |   |   |   |   start <= 536206: cell_cycle_
(49.02/31.18)
|   |   |   |   |   |   |   |   start > 536206
|   |   |   |   |   |   |   |   |   start <= 537837:
organelle_organization_and_biogenesis_ (8.4)
|   |   |   |   |   |   |   |   |   start > 537837: cell_cycle_
(19.02/8.93)
|   |   |   |   |   |   |   start > 540055
|   |   |   |   |   |   |   |   start <= 541198: transcription_
(13.99)
|   |   |   |   |   |   |   |   start > 541198:
DNA_metabolic_process_ (11.37)
|   |   |   |   |   start > 544962
```

```
|   |   |   |   |   |   start <= 558523
|   |   |   |   |   |   |   start <= 547713
|   |   |   |   |   |   |   |   start <= 545154:
cytoskeleton_organization_and_biogenesis_ (16.29)
|   |   |   |   |   |   |   |   start > 545154: response_to_stress_
(23.95)
|   |   |   |   |   |   |   start > 547713
|   |   |   |   |   |   |   |   start <= 551927: translation_
(26.18)
|   |   |   |   |   |   |   |   start > 551927
|   |   |   |   |   |   |   |   |   start <= 556474
|   |   |   |   |   |   |   |   |   |   start <= 553361:
biological_process_ (8.44)
|   |   |   |   |   |   |   |   |   |   start > 553361:
generation_of_precursor_metabolites_and_energy_ (29.75/10.84)
|   |   |   |   |   |   |   |   |   start > 556474: translation_
(23.84)
|   |   |   |   |   |   start > 558523
|   |   |   |   |   |   |   start <= 568181
|   |   |   |   |   |   |   |   start <= 560365: biological_process_
(33.11)
|   |   |   |   |   |   |   |   start > 560365
|   |   |   |   |   |   |   |   |   start <= 562527:
protein_modification_process_ (28.85)
|   |   |   |   |   |   |   |   |   start > 562527
|   |   |   |   |   |   |   |   |   |   strand = C:
protein_modification_process_ (10.26)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 563095:
response_to_stress_ (8.58)
|   |   |   |   |   |   |   |   |   |   |   start > 563095:
nuclear_organization_and_biogenesis_ (15.14)
|   |   |   |   |   |   |   start > 568181
|   |   |   |   |   |   |   |   start <= 575065
|   |   |   |   |   |   |   |   |   start <= 571015
|   |   |   |   |   |   |   |   |   |   start <= 568550:
biological_process_ (20.98)
|   |   |   |   |   |   |   |   |   |   start > 568550:
DNA_metabolic_process_ (19.39)
|   |   |   |   |   |   |   |   |   start > 571015
|   |   |   |   |   |   |   |   |   |   start <= 572954
|   |   |   |   |   |   |   |   |   |   |   start <= 572043:
biological_process_ (12.27)
|   |   |   |   |   |   |   |   |   |   |   start > 572043:
translation_ (24.59)
|   |   |   |   |   |   |   |   |   |   start > 572954:
biological_process_ (39.0)
|   |   |   |   |   |   |   |   start > 575065:
protein_catabolic_process_ (20.61)
|   |   |   start > 577717
|   |   |   |   start <= 740265
|   |   |   |   |   start <= 599157
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 586708
```

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|   |   |   |   |   |   |   |   start <= 583920:
membrane_organization_and_biogenesis_ (19.6)
|   |   |   |   |   |   |   |   start > 583920
|   |   |   |   |   |   |   |   |   start <= 586387:
organelle_organization_and_biogenesis_ (21.34)
|   |   |   |   |   |   |   |   |   start > 586387: translation_
(19.55)
|   |   |   |   |   |   |   start > 586708
|   |   |   |   |   |   |   |   start <= 592627
|   |   |   |   |   |   |   |   |   start <= 589549:
pseudohyphal_growth_ (24.14)
|   |   |   |   |   |   |   |   |   start > 589549:
cellular_respiration_ (16.8)
|   |   |   |   |   |   |   |   start > 592627
|   |   |   |   |   |   |   |   |   start <= 594885: transport_
(20.33)
|   |   |   |   |   |   |   |   |   start > 594885:
cytoskeleton_organization_and_biogenesis_ (15.71)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   neigh_num <= 1: meiosis_ (18.87/8.71)
|   |   |   |   |   |   |   neigh_num > 1: DNA_metabolic_process_
(21.7/12.26)
|   |   |   |   |   start > 599157
|   |   |   |   |   |   start <= 659744
|   |   |   |   |   |   |   start <= 619857
|   |   |   |   |   |   |   |   start <= 611313
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 600871:
response_to_stress_ (16.42)
|   |   |   |   |   |   |   |   |   |   start > 600871
|   |   |   |   |   |   |   |   |   |   |   start <= 605980:
biological_process_ (37.86)
|   |   |   |   |   |   |   |   |   |   |   start > 605980:
protein_catabolic_process_ (13.4)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 611015
|   |   |   |   |   |   |   |   |   |   |   start <= 608688
|   |   |   |   |   |   |   |   |   |   |   |   start <= 605980:
response_to_stress_ (11.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 605980:
DNA_metabolic_process_ (13.94)
|   |   |   |   |   |   |   |   |   |   |   start > 608688:
response_to_stress_ (21.51)
|   |   |   |   |   |   |   |   |   |   start > 611015:
biological_process_ (15.06)
|   |   |   |   |   |   |   |   start > 611313
|   |   |   |   |   |   |   |   |   start <= 616565
|   |   |   |   |   |   |   |   |   |   start <= 611739:
cell_wall_organization_and_biogenesis_ (14.41)
|   |   |   |   |   |   |   |   |   |   start > 611739:
cellular_homeostasis_ (17.28)
|   |   |   |   |   |   |   |   |   start > 616565
|   |   |   |   |   |   |   |   |   |   start <= 618478:
biological_process_ (23.28)
```

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|   |   |   |   |   |   |   |   |   |   start > 618478:
DNA_metabolic_process_ (21.48)
|   |   |   |   |   |   |   start > 619857
|   |   |   |   |   |   |   |   start <= 626348
|   |   |   |   |   |   |   |   |   start <= 625810
|   |   |   |   |   |   |   |   |   |   start <= 623212:
RNA_metabolic_process_ (16.64)
|   |   |   |   |   |   |   |   |   |   start > 623212
|   |   |   |   |   |   |   |   |   |   |   start <= 624079:
biological_process_ (18.15)
|   |   |   |   |   |   |   |   |   |   |   start > 624079
|   |   |   |   |   |   |   |   |   |   |   |   start <= 625166:
transcription_ (13.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 625166:
biological_process_ (13.52)
|   |   |   |   |   |   |   |   |   start > 625810:
RNA_metabolic_process_ (37.92/16.06)
|   |   |   |   |   |   |   |   start > 626348
|   |   |   |   |   |   |   |   |   start <= 651144
|   |   |   |   |   |   |   |   |   |   start <= 628188
|   |   |   |   |   |   |   |   |   |   |   start <= 627807:
vesicle-mediated_transport_ (19.14)
|   |   |   |   |   |   |   |   |   |   |   start > 627807:
protein_catabolic_process_ (10.49)
|   |   |   |   |   |   |   |   |   |   start > 628188
|   |   |   |   |   |   |   |   |   |   |   start <= 645655
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 637499
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
635983: biological_process_ (11.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
635983: translation_ (15.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 637499
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: response_to_stress_ (10.79/2.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: meiosis_ (14.13/4.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: response_to_stress_ (6.5/1.22)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 632354
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
629024: biological_process_ (16.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
629024: response_to_stress_ (19.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 632354:
biological_process_ (34.47)
|   |   |   |   |   |   |   |   |   |   |   start > 645655
|   |   |   |   |   |   |   |   |   |   |   |   start <= 647117:
vesicle-mediated_transport_ (26.54/13.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 647117:
translation_ (15.12)
```

```
|   |   |   |   |   |   |   |   |   start > 651144
|   |   |   |   |   |   |   |   |   |   start <= 655075
|   |   |   |   |   |   |   |   |   |   |   start <= 652274:
ribosome_biogenesis_and_assembly_ (25.85/9.35)
|   |   |   |   |   |   |   |   |   |   |   start > 652274:
biological_process_ (42.66)
|   |   |   |   |   |   |   |   |   |   start > 655075
|   |   |   |   |   |   |   |   |   |   |   start <= 659197:
vesicle-mediated_transport_ (21.54)
|   |   |   |   |   |   |   |   |   |   |   start > 659197: meiosis_
(16.8)
|   |   |   |   |   |   start > 659744
|   |   |   |   |   |   |   start <= 720652
|   |   |   |   |   |   |   |   start <= 674765
|   |   |   |   |   |   |   |   |   start <= 664751
|   |   |   |   |   |   |   |   |   |   start <= 662643: cell_cycle_
(17.64)
|   |   |   |   |   |   |   |   |   |   start > 662643:
cell_wall_organization_and_biogenesis_ (18.49)
|   |   |   |   |   |   |   |   |   start > 664751
|   |   |   |   |   |   |   |   |   |   start <= 667536
|   |   |   |   |   |   |   |   |   |   |   start <= 667043
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (21.8/9.17)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (11.39/4.72)
|   |   |   |   |   |   |   |   |   |   |   start > 667043
|   |   |   |   |   |   |   |   |   |   |   |   start <= 667455:
biological_process_ (11.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 667455:
DNA_metabolic_process_ (17.39)
|   |   |   |   |   |   |   |   |   |   start > 667536
|   |   |   |   |   |   |   |   |   |   |   start <= 671324
|   |   |   |   |   |   |   |   |   |   |   |   start <= 668491
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
transport_ (18.75/3.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
organelle_organization_and_biogenesis_ (17.56/8.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 668491:
organelle_organization_and_biogenesis_ (12.98)
|   |   |   |   |   |   |   |   |   |   |   start > 671324:
carbohydrate_metabolic_process_ (15.1)
|   |   |   |   |   |   |   |   start > 674765
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 716714
|   |   |   |   |   |   |   |   |   |   |   start <= 701789
|   |   |   |   |   |   |   |   |   |   |   |   start <= 684466:
lipid_metabolic_process_ (14.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 684466
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 696795
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
689082: biological_process_ (18.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
689082: anatomical_structure_morphogenesis_ (17.92)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 696795:
cellular_homeostasis_ (27.52/12.77)
|   |   |   |   |   |   |   |   |   |   |   start > 701789
|   |   |   |   |   |   |   |   |   |   |   |   start <= 707132
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
7354: vesicle-mediated_transport_ (30.63/12.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 7354:
transport_ (9.16/3.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 707132:
biological_process_ (40.75)
|   |   |   |   |   |   |   |   |   |   start > 716714:
DNA_metabolic_process_ (28.31/12.46)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 701789
|   |   |   |   |   |   |   |   |   |   |   start <= 689082
|   |   |   |   |   |   |   |   |   |   |   |   start <= 687515
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 675895:
biological_process_ (13.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 675895:
lipid_metabolic_process_ (37.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 687515:
organelle_organization_and_biogenesis_ (34.71/13.36)
|   |   |   |   |   |   |   |   |   |   |   start > 689082
|   |   |   |   |   |   |   |   |   |   |   |   start <= 695349
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 693380:
RNA_metabolic_process_ (21.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 693380:
response_to_stress_ (17.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 695349:
biological_process_ (36.19)
|   |   |   |   |   |   |   |   |   |   start > 701789
|   |   |   |   |   |   |   |   |   |   |   start <= 712315
|   |   |   |   |   |   |   |   |   |   |   |   start <= 707132:
transcription_ (14.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 707132:
lipid_metabolic_process_ (20.45)
|   |   |   |   |   |   |   |   |   |   |   start > 712315:
protein_modification_process_ (18.59)
|   |   |   |   |   |   |   start > 720652
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 722395
|   |   |   |   |   |   |   |   |   |   start <= 721402:
translation_ (14.07)
|   |   |   |   |   |   |   |   |   |   start > 721402:
biological_process_ (16.72)
|   |   |   |   |   |   |   |   |   start > 722395
|   |   |   |   |   |   |   |   |   |   start <= 724625: cell_cycle_
(20.83)
|   |   |   |   |   |   |   |   |   |   start > 724625:
ribosome_biogenesis_and_assembly_ (15.29)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 736925
|   |   |   |   |   |   |   |   |   |   start <= 733267
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 724625:
transcription_ (32.6/16.24)
|   |   |   |   |   |   |   |   |   |   |   start > 724625
|   |   |   |   |   |   |   |   |   |   |   |   start <= 732413:
translation_ (13.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 732413:
biological_process_ (14.12)
|   |   |   |   |   |   |   |   |   |   start > 733267
|   |   |   |   |   |   |   |   |   |   |   distance <= 863:
organelle_organization_and_biogenesis_ (11.8/2.85)
|   |   |   |   |   |   |   |   |   |   |   distance > 863:
membrane_organization_and_biogenesis_ (75.51/30.5)
|   |   |   |   |   |   |   |   |   start > 736925
|   |   |   |   |   |   |   |   |   |   start <= 739184:
biological_process_ (18.68)
|   |   |   |   |   |   |   |   |   |   start > 739184:
cell_wall_organization_and_biogenesis_ (33.4)
|   |   |   |   start > 740265
|   |   |   |   |   start <= 746352
|   |   |   |   |   |   strand = C:
ribosome_biogenesis_and_assembly_ (46.46/19.1)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 742970: cell_cycle_
(68.15/39.12)
|   |   |   |   |   |   |   start > 742970
|   |   |   |   |   |   |   |   start <= 743748
|   |   |   |   |   |   |   |   |   distance <= 1915: transport_
(18.7/4.46)
|   |   |   |   |   |   |   |   |   distance > 1915: vesicle-
mediated_transport_ (27.78/9.1)
|   |   |   |   |   |   |   |   start > 743748: pseudohyphal_growth_
(20.11)
|   |   |   |   |   start > 746352
|   |   |   |   |   |   start <= 826350
|   |   |   |   |   |   |   start <= 804455
|   |   |   |   |   |   |   |   start <= 797924
|   |   |   |   |   |   |   |   |   start <= 763112
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 754296
|   |   |   |   |   |   |   |   |   |   |   |   start <= 749676
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 747962:
translation_ (15.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 747962:
ribosome_biogenesis_and_assembly_ (12.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 749676
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 751960:
RNA_metabolic_process_ (11.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 751960:
translation_ (17.91)
|   |   |   |   |   |   |   |   |   |   |   start > 754296
|   |   |   |   |   |   |   |   |   |   |   |   start <= 759806
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 757249:
transport_ (26.75/9.08)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 757249:
biological_process_ (13.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 759806:
ribosome_biogenesis_and_assembly_ (34.94/16.74)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 751960:
organelle_organization_and_biogenesis_ (16.48)
|   |   |   |   |   |   |   |   |   |   |   start > 751960
|   |   |   |   |   |   |   |   |   |   |   |   start <= 757249:
biological_process_ (29.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 757249:
lipid_metabolic_process_ (11.77)
|   |   |   |   |   |   |   |   |   start > 763112
|   |   |   |   |   |   |   |   |   |   start <= 768038:
protein_modification_process_ (31.81/15.54)
|   |   |   |   |   |   |   |   |   |   start > 768038
|   |   |   |   |   |   |   |   |   |   |   start <= 793368
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 789838
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
788882
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
782030
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 778000
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 770800: translation_ (12.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 770800: biological_process_ (30.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 778000
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 779126: electron_transport_ (10.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 779126: translation_ (15.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
782030: biological_process_ (32.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
788882: translation_ (16.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 789838:
response_to_stress_ (13.14)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 775718
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
769282: biological_process_ (11.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
769282
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
772914
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 770800: response_to_stress_ (15.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 770800: biological_process_ (10.74)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
772914: response_to_stress_ (19.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 775718:
biological_process_ (34.99/13.64)
|   |   |   |   |   |   |   |   |   |   |   start > 793368
|   |   |   |   |   |   |   |   |   |   |   |   start <= 794918
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 793725:
biological_process_ (14.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 793725:
DNA_metabolic_process_ (24.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 794918:
biological_process_ (37.1)
|   |   |   |   |   |   |   |   start > 797924
|   |   |   |   |   |   |   |   |   strand = C:
RNA_metabolic_process_ (22.71)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 798517
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
transport_ (8.96/2.61)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: vesicle-
mediated_transport_ (17.96/6.67)
|   |   |   |   |   |   |   |   |   |   start > 798517
|   |   |   |   |   |   |   |   |   |   |   start <= 801771:
cellular_respiration_ (14.69)
|   |   |   |   |   |   |   |   |   |   |   start > 801771:
ribosome_biogenesis_and_assembly_ (14.38)
|   |   |   |   |   |   |   start > 804455
|   |   |   |   |   |   |   |   start <= 815310
|   |   |   |   |   |   |   |   |   start <= 813979
|   |   |   |   |   |   |   |   |   |   start <= 806422:
transcription_ (12.72)
|   |   |   |   |   |   |   |   |   |   start > 806422
|   |   |   |   |   |   |   |   |   |   |   start <= 810776
|   |   |   |   |   |   |   |   |   |   |   |   start <= 807547:
biological_process_ (9.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 807547
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 808316:
translation_ (9.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 808316:
lipid_metabolic_process_ (8.96)
|   |   |   |   |   |   |   |   |   |   |   start > 810776:
biological_process_ (34.1)
|   |   |   |   |   |   |   |   |   start > 813979:
protein_modification_process_ (22.01)
|   |   |   |   |   |   |   |   start > 815310
|   |   |   |   |   |   |   |   |   start <= 820255
|   |   |   |   |   |   |   |   |   |   strand = C:
organelle_organization_and_biogenesis_ (12.17)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 818826:
cell_cycle_ (8.76)
|   |   |   |   |   |   |   |   |   |   |   start > 818826:
transcription_ (23.91)
```

```
|   |   |   |   |   |   |   |   |   start > 820255:
biological_process_ (34.15)
|   |   |   |   |   |   start > 826350
|   |   |   |   |   |   |   start <= 837927
|   |   |   |   |   |   |   |   start <= 831328:
carbohydrate_metabolic_process_ (14.78)
|   |   |   |   |   |   |   |   start > 831328
|   |   |   |   |   |   |   |   |   start <= 832338:
protein_modification_process_ (20.96)
|   |   |   |   |   |   |   |   |   start > 832338: translation_
(53.55/13.75)
|   |   |   |   |   |   |   start > 837927
|   |   |   |   |   |   |   |   start <= 841690
|   |   |   |   |   |   |   |   |   start <= 838186:
DNA_metabolic_process_ (28.87)
|   |   |   |   |   |   |   |   |   start > 838186:
ribosome_biogenesis_and_assembly_ (17.21)
|   |   |   |   |   |   |   |   start > 841690
|   |   |   |   |   |   |   |   |   start <= 841941: translation_
(13.4)
|   |   |   |   |   |   |   |   |   start > 841941:
RNA_metabolic_process_ (33.36)
|   start > 845570
|   |   strand = C
|   |   |   start <= 896668
|   |   |   |   start <= 869626
|   |   |   |   |   start <= 856965
|   |   |   |   |   |   start <= 852629:
ribosome_biogenesis_and_assembly_ (14.33)
|   |   |   |   |   |   start > 852629: cellular_respiration_
(12.65)
|   |   |   |   |   start > 856965
|   |   |   |   |   |   start <= 867090
|   |   |   |   |   |   |   start <= 861921
|   |   |   |   |   |   |   |   start <= 858889: biological_process_
(10.96)
|   |   |   |   |   |   |   |   start > 858889:
lipid_metabolic_process_ (16.94)
|   |   |   |   |   |   |   start > 861921
|   |   |   |   |   |   |   |   start <= 865349:
cytoskeleton_organization_and_biogenesis_ (15.51)
|   |   |   |   |   |   |   |   start > 865349: biological_process_
(21.24)
|   |   |   |   |   |   start > 867090: cellular_homeostasis_
(12.48)
|   |   |   |   start > 869626
|   |   |   |   |   start <= 881158
|   |   |   |   |   |   start <= 872624:
ribosome_biogenesis_and_assembly_ (18.41)
|   |   |   |   |   |   start > 872624
|   |   |   |   |   |   |   start <= 874986:
generation_of_precursor_metabolites_and_energy_ (15.23)
|   |   |   |   |   |   |   start > 874986: conjugation_ (13.72)
|   |   |   |   |   start > 881158
```

```
|   |   |   |   |   |   start <= 892220: transport_ (22.11)
|   |   |   |   |   |   start > 892220:
ribosome_biogenesis_and_assembly_ (44.46)
|   |   |   start > 896668
|   |   |   |   start <= 917894
|   |   |   |   |   start <= 912141
|   |   |   |   |   |   start <= 898404: biological_process_ (22.62)
|   |   |   |   |   |   start > 898404
|   |   |   |   |   |   |   start <= 904823:
lipid_metabolic_process_ (15.6)
|   |   |   |   |   |   |   start > 904823: biological_process_
(10.75)
|   |   |   |   |   start > 912141
|   |   |   |   |   |   start <= 914536: transport_ (15.53)
|   |   |   |   |   |   start > 914536: biological_process_ (19.14)
|   |   |   |   start > 917894: vitamin_metabolic_process_ (17.84)
|   |   strand = W
|   |   |   start <= 901708
|   |   |   |   start <= 858889
|   |   |   |   |   start <= 848684: vitamin_metabolic_process_
(12.95)
|   |   |   |   |   start > 848684
|   |   |   |   |   |   start <= 852629: biological_process_ (15.29)
|   |   |   |   |   |   start > 852629
|   |   |   |   |   |   |   start <= 854794: transport_ (25.3/11.48)
|   |   |   |   |   |   |   start > 854794: biological_process_
(10.91)
|   |   |   |   start > 858889
|   |   |   |   |   start <= 874986
|   |   |   |   |   |   start <= 867090
|   |   |   |   |   |   |   start <= 861921:
protein_catabolic_process_ (14.68)
|   |   |   |   |   |   |   start > 861921: lipid_metabolic_process_
(20.45)
|   |   |   |   |   |   start > 867090:
protein_modification_process_ (17.54)
|   |   |   |   |   start > 874986
|   |   |   |   |   |   start <= 892220
|   |   |   |   |   |   |   start <= 881158
|   |   |   |   |   |   |   |   distance <= 1267:
cell_wall_organization_and_biogenesis_ (5.03/0.21)
|   |   |   |   |   |   |   |   distance > 1267: sporulation_
(27.0/10.97)
|   |   |   |   |   |   |   start > 881158:
cell_wall_organization_and_biogenesis_ (14.37)
|   |   |   |   |   |   start > 892220
|   |   |   |   |   |   |   start <= 898404: RNA_metabolic_process_
(13.46)
|   |   |   |   |   |   |   start > 898404:
protein_catabolic_process_ (15.63)
|   |   |   start > 901708
|   |   |   |   start <= 904823
|   |   |   |   |   start <= 904285: biological_process_ (23.65)
|   |   |   |   |   start > 904285: pseudohyphal_growth_ (21.17)
```

```
|   |   |   |   start > 904823: biological_process_ (36.77)
```

Decision Tree Generated for Chromosome Fourteen:
For Cellular Component

```
|   start <= 155101
|   |   strand = W
|   |   |   start <= 117349
|   |   |   |   start <= 82806
|   |   |   |   |   start <= 34695
|   |   |   |   |   |   start <= 19302
|   |   |   |   |   |   |   start <= 8330: vacuole_ (20.54)
|   |   |   |   |   |   |   start > 8330: cellular_component_
(67.89)
|   |   |   |   |   |   start > 19302
|   |   |   |   |   |   |   start <= 24047: cellular_bud_ (24.5)
|   |   |   |   |   |   |   start > 24047
|   |   |   |   |   |   |   |   start <= 31943: cytoplasm_
(55.87/33.32)
|   |   |   |   |   |   |   |   start > 31943: vacuole_ (20.68)
|   |   |   |   |   start > 34695
|   |   |   |   |   |   start <= 58155
|   |   |   |   |   |   |   start <= 44446
|   |   |   |   |   |   |   |   start <= 37699: mitochondrion_
(30.97)
|   |   |   |   |   |   |   |   start > 37699: nucleus_
(76.19/24.83)
|   |   |   |   |   |   |   start > 44446
|   |   |   |   |   |   |   |   start <= 52661
|   |   |   |   |   |   |   |   |   start <= 48286: chromosome_
(28.44)
|   |   |   |   |   |   |   |   |   start > 48286: nucleus_
(37.15/16.51)
|   |   |   |   |   |   |   |   start > 52661: mitochondrion_
(31.66)
|   |   |   |   |   |   start > 58155
|   |   |   |   |   |   |   start <= 68915
|   |   |   |   |   |   |   |   start <= 65744
|   |   |   |   |   |   |   |   |   start <= 62943:
site_of_polarized_growth_ (39.87/18.89)
|   |   |   |   |   |   |   |   |   start > 62943: cell_wall_
(32.21)
|   |   |   |   |   |   |   |   start > 65744
|   |   |   |   |   |   |   |   |   start <= 66517: nucleus_
(50.51/20.46)
|   |   |   |   |   |   |   |   |   start > 66517: cell_cortex_
(48.41/17.92)
|   |   |   |   |   |   |   start > 68915
|   |   |   |   |   |   |   |   start <= 80640
|   |   |   |   |   |   |   |   |   start <= 76946:
cellular_component_ (26.39)
|   |   |   |   |   |   |   |   |   start > 76946: cellular_bud_
(60.28/22.26)
```

```
|   |   |   |   |   |   |   |   start > 80640: nucleus_
(41.18/17.49)
|   |   |   |   start > 82806
|   |   |   |   |   distance <= 43061
|   |   |   |   |   |   start <= 108467
|   |   |   |   |   |   |   start <= 90303
|   |   |   |   |   |   |   |   start <= 86218: nucleus_ (28.32)
|   |   |   |   |   |   |   |   start > 86218
|   |   |   |   |   |   |   |   |   start <= 87897:
cellular_component_ (29.86)
|   |   |   |   |   |   |   |   |   start > 87897: nucleus_
(50.96/24.99)
|   |   |   |   |   |   |   start > 90303
|   |   |   |   |   |   |   |   start <= 91994
|   |   |   |   |   |   |   |   |   distance <= 2389: cytoplasm_
(6.34/1.8)
|   |   |   |   |   |   |   |   |   distance > 2389:
Golgi_apparatus_ (41.2/18.09)
|   |   |   |   |   |   |   |   start > 91994
|   |   |   |   |   |   |   |   |   start <= 107687
|   |   |   |   |   |   |   |   |   |   start <= 96312: nucleus_
(19.44)
|   |   |   |   |   |   |   |   |   |   start > 96312: nucleolus_
(31.12)
|   |   |   |   |   |   |   |   |   start > 107687: nucleus_
(66.4/26.3)
|   |   |   |   |   |   start > 108467
|   |   |   |   |   |   |   start <= 110917:
site_of_polarized_growth_ (28.8)
|   |   |   |   |   |   |   start > 110917
|   |   |   |   |   |   |   |   start <= 116679
|   |   |   |   |   |   |   |   |   start <= 113271: nucleus_
(51.34/21.67)
|   |   |   |   |   |   |   |   |   start > 113271:
cellular_component_ (54.61)
|   |   |   |   |   |   |   |   start > 116679: cytoplasm_ (25.12)
|   |   |   |   |   distance > 43061
|   |   |   |   |   |   start <= 95223: nucleolus_ (24.23)
|   |   |   |   |   |   start > 95223: cytoplasm_ (45.14)
|   |   |   start > 117349
|   |   |   |   start <= 138551
|   |   |   |   |   start <= 129084
|   |   |   |   |   |   start <= 119268
|   |   |   |   |   |   |   neigh_strand = W: plasma_membrane_
(20.78/5.78)
|   |   |   |   |   |   |   neigh_strand = C: membrane_fraction_
(23.9/9.24)
|   |   |   |   |   |   start > 119268: chromosome_ (21.69)
|   |   |   |   |   start > 129084
|   |   |   |   |   |   start <= 137700: cellular_component_ (27.81)
|   |   |   |   |   |   start > 137700: plasma_membrane_
(43.37/19.35)
|   |   |   |   start > 138551
|   |   |   |   |   start <= 140879: Golgi_apparatus_ (47.62/19.21)
```

```
|   |   |   |   |   start > 140879: chromosome_ (131.21/59.38)
|   |   strand = C
|   |   |   start <= 82806
|   |   |   |   start <= 24047
|   |   |   |   |   start <= 19302
|   |   |   |   |   |   start <= 8330: nucleus_ (7.26)
|   |   |   |   |   |   start > 8330
|   |   |   |   |   |   |   start <= 17248: cellular_component_
(51.33)
|   |   |   |   |   |   |   start > 17248
|   |   |   |   |   |   |   |   neigh_strand = W:
cellular_component_ (13.42/5.9)
|   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(26.54/11.57)
|   |   |   |   |   start > 19302
|   |   |   |   |   |   start <= 22633: peroxisome_ (55.08/23.06)
|   |   |   |   |   |   start > 22633: mitochondrial_envelope_
(26.93)
|   |   |   |   start > 24047
|   |   |   |   |   start <= 48286
|   |   |   |   |   |   start <= 34695
|   |   |   |   |   |   |   start <= 28346: vacuole_ (28.79)
|   |   |   |   |   |   |   start > 28346
|   |   |   |   |   |   |   |   start <= 31943: membrane_ (28.18)
|   |   |   |   |   |   |   |   start > 31943: cell_wall_ (24.23)
|   |   |   |   |   |   start > 34695
|   |   |   |   |   |   |   start <= 44446
|   |   |   |   |   |   |   |   start <= 40618: plasma_membrane_
(57.25/24.54)
|   |   |   |   |   |   |   |   start > 40618
|   |   |   |   |   |   |   |   |   start <= 43074: cytoplasm_
(26.14)
|   |   |   |   |   |   |   |   |   start > 43074: mitochondrion_
(25.15)
|   |   |   |   |   |   |   start > 44446: nucleus_ (60.28/24.68)
|   |   |   |   |   start > 48286
|   |   |   |   |   |   start <= 68915
|   |   |   |   |   |   |   start <= 58155
|   |   |   |   |   |   |   |   start <= 52661
|   |   |   |   |   |   |   |   |   start <= 51687: ribosome_
(25.94)
|   |   |   |   |   |   |   |   |   start > 51687: mitochondrion_
(17.78)
|   |   |   |   |   |   |   |   start > 52661
|   |   |   |   |   |   |   |   |   start <= 55896: nucleolus_
(25.95)
|   |   |   |   |   |   |   |   |   start > 55896:
cellular_component_ (29.56)
|   |   |   |   |   |   |   start > 58155
|   |   |   |   |   |   |   |   start <= 60297: vacuole_ (19.34)
|   |   |   |   |   |   |   |   start > 60297: ribosome_ (59.63)
|   |   |   |   |   |   start > 68915
|   |   |   |   |   |   |   start <= 76946: cytoplasm_ (58.41/25.42)
```

```
|   |   |   |   |   |   |   start > 76946: cellular_component_
(21.73)
|   |   |   start > 82806
|   |   |   |   start <= 146616
|   |   |   |   |   start <= 135384
|   |   |   |   |   |   start <= 122883
|   |   |   |   |   |   |   start <= 113271
|   |   |   |   |   |   |   |   start <= 104805
|   |   |   |   |   |   |   |   |   start <= 90303: plasma_membrane_
(41.66/20.63)
|   |   |   |   |   |   |   |   |   start > 90303
|   |   |   |   |   |   |   |   |   |   start <= 96312: cytoplasm_
(13.61)
|   |   |   |   |   |   |   |   |   |   start > 96312:
mitochondrion_ (20.93)
|   |   |   |   |   |   |   |   start > 104805
|   |   |   |   |   |   |   |   |   start <= 108467
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
membrane_fraction_ (15.58/9.13)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
site_of_polarized_growth_ (4.03/1.03)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: site_of_polarized_growth_ (3.06/1.21)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: site_of_polarized_growth_
(4.87/2.21)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
membrane_fraction_ (7.49/3.41)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: site_of_polarized_growth_ (6.77/3.92)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
membrane_fraction_ (6.41/4.56)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
site_of_polarized_growth_ (3.02/0.64)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: cytoplasm_ (3.91/1.33)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: cellular_bud_ (1.55/0.76)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: membrane_fraction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: site_of_polarized_growth_ (3.19/1.76)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: site_of_polarized_growth_ (6.97/3.54)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: cytoplasm_ (4.81/2.86)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
membrane_fraction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: cytoplasm_ (3.1/1.97)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: membrane_fraction_ (2.79/0.85)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: membrane_fraction_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: membrane_fraction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   start > 108467:
endoplasmic_reticulum_ (35.53)
|   |   |   |   |   |   |   start > 113271: nucleus_ (72.69/45.37)
|   |   |   |   |   |   start > 122883
|   |   |   |   |   |   |   start <= 129084: cytoplasmic_membrane-
bound_vesicle_ (22.76)
|   |   |   |   |   |   |   start > 129084
|   |   |   |   |   |   |   |   neigh_num <= 1:
site_of_polarized_growth_ (26.16/9.42)
|   |   |   |   |   |   |   |   neigh_num > 1: cellular_bud_
(29.91/14.1)
|   |   |   |   |   start > 135384
|   |   |   |   |   |   start <= 140879: plasma_membrane_ (30.07)
|   |   |   |   |   |   start > 140879: cytoplasm_ (85.99)
|   |   |   |   start > 146616
|   |   |   |   |   neigh_num <= 1: endoplasmic_reticulum_
(47.45/30.85)
|   |   |   |   |   neigh_num > 1: membrane_ (64.13/41.8)
|   start > 155101
|   |   start <= 726218
|   |   |   start <= 614822
|   |   |   |   start <= 531726
|   |   |   |   |   start <= 269594
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 206931
|   |   |   |   |   |   |   |   start <= 200570
|   |   |   |   |   |   |   |   |   start <= 185461
|   |   |   |   |   |   |   |   |   |   start <= 164624: cytoplasm_
(90.72/56.33)
|   |   |   |   |   |   |   |   |   |   start > 164624
|   |   |   |   |   |   |   |   |   |   |   start <= 175411:
nucleus_ (85.01/17.19)
|   |   |   |   |   |   |   |   |   |   |   start > 175411
|   |   |   |   |   |   |   |   |   |   |   |   start <= 182876:
ribosome_ (60.51/28.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 182876:
nucleus_ (32.82)
|   |   |   |   |   |   |   |   |   start > 185461
|   |   |   |   |   |   |   |   |   |   start <= 188052:
cell_cortex_ (32.99/15.68)
|   |   |   |   |   |   |   |   |   |   start > 188052
|   |   |   |   |   |   |   |   |   |   |   start <= 191325:
cytoplasm_ (28.24)
|   |   |   |   |   |   |   |   |   |   |   start > 191325:
mitochondrion_ (42.18/15.56)
|   |   |   |   |   |   |   |   start > 200570
```

```
|   |   |   |   |   |   |   |   |   start <= 205189
|   |   |   |   |   |   |   |   |   |   start <= 202429:
Golgi_apparatus_ (27.09)
|   |   |   |   |   |   |   |   |   |   start > 202429: membrane_
(20.09)
|   |   |   |   |   |   |   |   |   start > 205189:
cellular_component_ (37.55/18.08)
|   |   |   |   |   |   |   start > 206931
|   |   |   |   |   |   |   |   start <= 244469
|   |   |   |   |   |   |   |   |   start <= 211923
|   |   |   |   |   |   |   |   |   |   start <= 210234: cytoplasm_
(24.98)
|   |   |   |   |   |   |   |   |   |   start > 210234:
cellular_bud_ (40.85/19.13)
|   |   |   |   |   |   |   |   |   start > 211923
|   |   |   |   |   |   |   |   |   |   start <= 238239: cytoplasm_
(160.53/66.47)
|   |   |   |   |   |   |   |   |   |   start > 238239
|   |   |   |   |   |   |   |   |   |   |   start <= 240332:
vacuole_ (23.96)
|   |   |   |   |   |   |   |   |   |   |   start > 240332: nucleus_
(52.78)
|   |   |   |   |   |   |   |   start > 244469
|   |   |   |   |   |   |   |   |   start <= 255354
|   |   |   |   |   |   |   |   |   |   start <= 245618: peroxisome_
(27.28)
|   |   |   |   |   |   |   |   |   |   start > 245618
|   |   |   |   |   |   |   |   |   |   |   start <= 252060
|   |   |   |   |   |   |   |   |   |   |   |   start <= 247462:
cytoplasm_ (28.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 247462
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 250932:
nucleus_ (20.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 250932:
cytoplasm_ (27.01)
|   |   |   |   |   |   |   |   |   |   |   start > 252060
|   |   |   |   |   |   |   |   |   |   |   |   start <= 254419:
ribosome_ (46.34/22.84)
|   |   |   |   |   |   |   |   |   |   |   |   start > 254419:
cytoplasm_ (42.58/18.97)
|   |   |   |   |   |   |   |   |   start > 255354: peroxisome_
(27.66)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 170019
|   |   |   |   |   |   |   |   start <= 160374
|   |   |   |   |   |   |   |   |   start <= 157866: cytoplasm_
(108.68/34.2)
|   |   |   |   |   |   |   |   |   start > 157866:
endoplasmic_reticulum_ (38.18)
|   |   |   |   |   |   |   |   start > 160374
|   |   |   |   |   |   |   |   |   start <= 164624: nucleus_ (33.7)
|   |   |   |   |   |   |   |   |   start > 164624
|   |   |   |   |   |   |   |   |   |   start <= 167791: cytoplasm_
(27.89)
```

```
|   |   |   |   |   |   |   |   |   |   start > 167791: nucleus_
(68.86/28.58)
|   |   |   |   |   |   |   start > 170019
|   |   |   |   |   |   |   |   start <= 234414
|   |   |   |   |   |   |   |   |   start <= 186886
|   |   |   |   |   |   |   |   |   |   start <= 181023
|   |   |   |   |   |   |   |   |   |   |   start <= 172287:
mitochondrion_ (33.33)
|   |   |   |   |   |   |   |   |   |   |   start > 172287
|   |   |   |   |   |   |   |   |   |   |   |   start <= 175411:
nucleus_ (25.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 175411:
mitochondrion_ (23.06)
|   |   |   |   |   |   |   |   |   |   start > 181023
|   |   |   |   |   |   |   |   |   |   |   start <= 182876:
nucleolus_ (29.43)
|   |   |   |   |   |   |   |   |   |   |   start > 182876: nucleus_
(33.49)
|   |   |   |   |   |   |   |   |   start > 186886
|   |   |   |   |   |   |   |   |   |   start <= 230673
|   |   |   |   |   |   |   |   |   |   |   start <= 217043
|   |   |   |   |   |   |   |   |   |   |   |   start <= 197944:
cytoplasm_ (54.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 197944
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 206931:
membrane_ (15.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 206931:
cytoplasm_ (15.32)
|   |   |   |   |   |   |   |   |   |   |   start > 217043
|   |   |   |   |   |   |   |   |   |   |   |   start <= 218663
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: nucleus_ (17.46/6.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1577: nucleus_ (6.65/1.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
1577: cellular_component_ (27.67/12.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 218663
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 222432
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
220202: cytoplasm_ (29.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
220202: mitochondrion_ (45.19/21.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 222432
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
224470: microtubule_organizing_center_ (21.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
224470
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
227371: cytoplasm_ (50.72/22.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
227371: nucleus_ (21.26)
|   |   |   |   |   |   |   |   |   |   start > 230673: nucleolus_
(37.04)
```

```
|   |   |   |   |   |   |   |   start > 234414
|   |   |   |   |   |   |   |   |   start <= 252060
|   |   |   |   |   |   |   |   |   |   start <= 241690:
endoplasmic_reticulum_ (28.94)
|   |   |   |   |   |   |   |   |   |   start > 241690:
mitochondrion_ (64.76)
|   |   |   |   |   |   |   |   |   start > 252060
|   |   |   |   |   |   |   |   |   |   start <= 263204
|   |   |   |   |   |   |   |   |   |   |   start <= 259579
|   |   |   |   |   |   |   |   |   |   |   |   start <= 258156:
nucleus_ (26.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 258156:
cellular_component_ (27.93)
|   |   |   |   |   |   |   |   |   |   |   start > 259579: nucleus_
(28.4)
|   |   |   |   |   |   |   |   |   |   start > 263204
|   |   |   |   |   |   |   |   |   |   |   start <= 264454:
mitochondrion_ (53.55/24.03)
|   |   |   |   |   |   |   |   |   |   |   start > 264454
|   |   |   |   |   |   |   |   |   |   |   |   start <= 266531:
nucleus_ (27.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 266531:
cytoplasm_ (20.75)
|   |   |   |   |   start > 269594
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 372228
|   |   |   |   |   |   |   |   start <= 348523
|   |   |   |   |   |   |   |   |   start <= 276503
|   |   |   |   |   |   |   |   |   |   start <= 274369:
cellular_component_ (33.61)
|   |   |   |   |   |   |   |   |   |   start > 274369:
plasma_membrane_ (39.49/18.28)
|   |   |   |   |   |   |   |   |   start > 276503
|   |   |   |   |   |   |   |   |   |   start <= 298337
|   |   |   |   |   |   |   |   |   |   |   start <= 284261
|   |   |   |   |   |   |   |   |   |   |   |   start <= 282396
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 280433:
cytoplasm_ (21.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 280433:
cell_wall_ (31.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 282396:
cytoplasm_ (60.43/29.07)
|   |   |   |   |   |   |   |   |   |   |   start > 284261
|   |   |   |   |   |   |   |   |   |   |   |   start <= 286309
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: cytoskeleton_ (30.31/9.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: microtubule_organizing_center_ (23.66/6.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 286309
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 292671:
nucleus_ (60.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 292671:
endoplasmic_reticulum_ (30.56)
|   |   |   |   |   |   |   |   |   |   start > 298337
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 331324
|   |   |   |   |   |   |   |   |   |   |   |   start <= 330331
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 326322
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
310638
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
304617: ribosome_ (16.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
304617: nucleus_ (35.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
310638: cellular_component_ (26.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 326322:
cytoplasm_ (54.74/23.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 330331:
ribosome_ (33.59)
|   |   |   |   |   |   |   |   |   |   |   start > 331324
|   |   |   |   |   |   |   |   |   |   |   |   start <= 339614
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 332599
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleolus_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_binding_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_biogenesis_and_assembly_: cellular_bud_ (1.33/0.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleus_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 6554: nucleus_ (2.46/1.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 6554: cytoplasm_ (4.07/0.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_component_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= hydrolase_activity_: cellular_bud_ (2.4/0.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasm_: cytoplasm_ (5.59/0.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= molecular_function_: cytoplasm_ (12.16/5.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_: nucleus_ (5.29/1.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= meiosis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= pseudohyphal_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= biological_process_: cellular_bud_ (1.15/0.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transport_: cellular_bud_ (1.42/0.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrion_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transporter_activity_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= structural_molecule_activity_: cellular_bud_ (3.48/0.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endomembrane_system_: cellular_bud_ (2.98/0.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_fraction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_binding_: nucleus_ (1.92/1.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transduction_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_: cellular_bud_ (3.53/1.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peroxisome_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= oxidoreductase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= carbohydrate_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endoplasmic_reticulum_: nucleus_ (2.63/0.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_: nucleus_ (1.78/0.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_catabolic_process_: cellular_bud_ (1.3/0.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= enzyme_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= organelle_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_modification_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cortex_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_kinase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytokinesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_binding_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_regulator_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transferase_activity_: cytoplasm_ (1.97/0.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= Golgi_apparatus_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= chromosome_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= phosphoprotein_phosphatase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= response_to_stress_: cellular_bud_ (0.94/0.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lyase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_respiration_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vesicle-mediated_transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peptidase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lipid_metabolic_process_: cytoplasm_ (3.7/2.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= plasma_membrane_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= electron_transport_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= conjugation_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vacuole_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= helicase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_: cytoplasm_ (4.43/2.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ligase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_bud_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= site_of_polarized_growth_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cycle_: nucleus_ (3.33/1.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= isomerase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transducer_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= amino_acid_and_derivative_metabolic_process_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleotidyltransferase_activity_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= microtubule_organizing_center_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= sporulation_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vitamin_metabolic_process_: cytoplasm_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= extracellular_region_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nuclear_organization_and_biogenesis_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_budding_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrial_envelope_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasmic_membrane-bound_vesicle_: cytoplasm_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 332599
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
336547: cell_wall_ (25.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
336547: endomembrane_system_ (25.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 339614
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 342518:
nucleus_ (123.57/59.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 342518:
cytoplasm_ (35.17)
|   |   |   |   |   |   |   |   start > 348523
|   |   |   |   |   |   |   |   |   start <= 357455
|   |   |   |   |   |   |   |   |   |   start <= 351717
|   |   |   |   |   |   |   |   |   |   |   start <= 350942:
nucleolus_ (21.97)
|   |   |   |   |   |   |   |   |   |   |   start > 350942:
endoplasmic_reticulum_ (19.75)
|   |   |   |   |   |   |   |   |   |   start > 351717
|   |   |   |   |   |   |   |   |   |   |   start <= 352416:
extracellular_region_ (15.79)
|   |   |   |   |   |   |   |   |   |   |   start > 352416:
plasma_membrane_ (21.24)
|   |   |   |   |   |   |   |   |   start > 357455
|   |   |   |   |   |   |   |   |   |   start <= 366035: nucleus_
(55.31/11.25)
|   |   |   |   |   |   |   |   |   |   start > 366035
|   |   |   |   |   |   |   |   |   |   |   start <= 366743:
cytoskeleton_ (58.44/26.67)
|   |   |   |   |   |   |   |   |   |   |   start > 366743: nucleus_
(25.85)
|   |   |   |   |   |   |   start > 372228
|   |   |   |   |   |   |   |   start <= 499418
|   |   |   |   |   |   |   |   |   distance <= 19559
|   |   |   |   |   |   |   |   |   |   start <= 387229
|   |   |   |   |   |   |   |   |   |   |   start <= 381482
|   |   |   |   |   |   |   |   |   |   |   |   start <= 375323:
nucleolus_ (24.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 375323
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 378769:
mitochondrion_ (20.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 378769:
cytoplasm_ (23.3)
|   |   |   |   |   |   |   |   |   |   |   start > 381482
```

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|   |   |   |   |   |   |   |   |   |   |   |   start <= 383989:
cellular_component_ (51.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 383989:
cytoskeleton_ (43.87/17.63)
|   |   |   |   |   |   |   |   |   |   start > 387229
|   |   |   |   |   |   |   |   |   |   |   start <= 427737
|   |   |   |   |   |   |   |   |   |   |   |   start <= 394687:
nucleus_ (75.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 394687
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 412773
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
408343: cytoplasm_ (65.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
408343: nucleolus_ (33.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 412773
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
413641: cytoplasm_ (79.49/44.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
413641
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
420100: cytoplasm_ (40.17/16.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
420100: nucleus_ (13.3)
|   |   |   |   |   |   |   |   |   |   |   start > 427737
|   |   |   |   |   |   |   |   |   |   |   |   start <= 447613
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 442360
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
430089: mitochondrion_ (26.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
430089
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
435001: vacuole_ (10.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
435001: mitochondrion_ (22.84)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 442360:
cytoskeleton_ (15.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 447613
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 456567
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
452410
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
450873
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 449870: cytoplasm_ (17.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 449870: cellular_component_ (23.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
450873: cytoplasm_ (22.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
452410: cellular_component_ (42.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 456567
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
481392
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
462413
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 457706: nucleus_ (53.44/22.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 457706: cellular_bud_ (22.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
462413
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 467133: cytoplasm_ (45.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 467133
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 471379: mitochondrion_ (31.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 471379
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start <= 479769: nucleus_ (87.42/24.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start > 479769: mitochondrion_ (82.25/46.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
481392
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
485608
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 483557: cellular_component_ (38.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 483557: nucleolus_ (21.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
485608
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 495002
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 490318
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start <= 488387: mitochondrion_ (29.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
|   start > 488387: nucleus_ (27.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 490318: mitochondrion_ (41.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 495002: cellular_component_ (24.11)
|   |   |   |   |   |   |   |   |   distance > 19559
|   |   |   |   |   |   |   |   |   |   start <= 444317: cytoplasm_
(65.0)
|   |   |   |   |   |   |   |   |   |   start > 444317
|   |   |   |   |   |   |   |   |   |   |   start <= 447613:
cytoskeleton_ (4.0)
|   |   |   |   |   |   |   |   |   |   |   start > 447613:
cytoplasm_ (16.62)
|   |   |   |   |   |   |   |   start > 499418
|   |   |   |   |   |   |   |   |   start <= 503725
|   |   |   |   |   |   |   |   |   |   start <= 499682: ribosome_
(30.75)
```

```
|   |   |   |   |   |   |   |   |   |   start > 499682
|   |   |   |   |   |   |   |   |   |   |   start <= 501516:
cell_wall_ (26.04)
|   |   |   |   |   |   |   |   |   |   |   start > 501516:
plasma_membrane_ (29.01)
|   |   |   |   |   |   |   |   |   start > 503725
|   |   |   |   |   |   |   |   |   |   start <= 510541
|   |   |   |   |   |   |   |   |   |   |   start <= 507759:
mitochondrion_ (25.63)
|   |   |   |   |   |   |   |   |   |   |   start > 507759:
nucleolus_ (20.37)
|   |   |   |   |   |   |   |   |   |   start > 510541
|   |   |   |   |   |   |   |   |   |   |   start <= 529943:
cytoplasm_ (58.36)
|   |   |   |   |   |   |   |   |   |   |   start > 529943:
mitochondrion_ (32.53)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 443008
|   |   |   |   |   |   |   |   start <= 295511
|   |   |   |   |   |   |   |   |   start <= 272309
|   |   |   |   |   |   |   |   |   |   start <= 271172:
cellular_component_ (26.18)
|   |   |   |   |   |   |   |   |   |   start > 271172:
mitochondrion_ (21.78)
|   |   |   |   |   |   |   |   |   start > 272309
|   |   |   |   |   |   |   |   |   |   start <= 282396:
endoplasmic_reticulum_ (75.54/46.18)
|   |   |   |   |   |   |   |   |   |   start > 282396
|   |   |   |   |   |   |   |   |   |   |   start <= 292671:
mitochondrion_ (17.0)
|   |   |   |   |   |   |   |   |   |   |   start > 292671
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (22.89/6.85)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
Golgi_apparatus_ (23.32/9.52)
|   |   |   |   |   |   |   |   start > 295511
|   |   |   |   |   |   |   |   |   start <= 326322
|   |   |   |   |   |   |   |   |   |   start <= 318811
|   |   |   |   |   |   |   |   |   |   |   start <= 300651
|   |   |   |   |   |   |   |   |   |   |   |   start <= 298337:
nucleus_ (26.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 298337:
cytoplasm_ (58.82/23.81)
|   |   |   |   |   |   |   |   |   |   |   start > 300651
|   |   |   |   |   |   |   |   |   |   |   |   start <= 310638
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 306982
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
304617: mitochondrion_ (14.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
304617: vacuole_ (11.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 306982
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
308614: nucleolus_ (19.23)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
308614: plasma_membrane_ (17.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 310638:
mitochondrion_ (48.39)
|   |   |   |   |   |   |   |   |   |   start > 318811
|   |   |   |   |   |   |   |   |   |   |   start <= 321361:
nucleus_ (27.03)
|   |   |   |   |   |   |   |   |   |   |   start > 321361
|   |   |   |   |   |   |   |   |   |   |   |   start <= 323834:
site_of_polarized_growth_ (48.04/22.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 323834:
nucleus_ (21.59)
|   |   |   |   |   |   |   |   |   start > 326322
|   |   |   |   |   |   |   |   |   |   start <= 350942
|   |   |   |   |   |   |   |   |   |   |   start <= 340354
|   |   |   |   |   |   |   |   |   |   |   |   start <= 332599:
cytoplasm_ (28.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 332599
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: nucleus_ (5.56/3.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
3429: nucleus_ (6.45/2.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
3429: endomembrane_system_ (4.93/1.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: nucleus_ (4.02/1.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: membrane_ (11.4/6.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: nucleus_ (4.29/1.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: endomembrane_system_ (3.72/0.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: endomembrane_system_ (6.25/3.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: endomembrane_system_ (1.28/0.59)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: membrane_ (4.59/1.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: endomembrane_system_ (4.47/1.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: membrane_ (6.78/1.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: endomembrane_system_ (6.03/2.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: endomembrane_system_ (5.85/0.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: endomembrane_system_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: nucleus_ (2.04/0.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: nucleus_ (2.56/1.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: membrane_ (5.3/2.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: membrane_ (4.43/1.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: endomembrane_system_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: endomembrane_system_ (1.35/0.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: membrane_ (3.53/1.78)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: nucleus_ (2.77/1.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: membrane_ (3.82/2.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: endomembrane_system_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: endomembrane_system_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   start > 340354
|   |   |   |   |   |   |   |   |   |   |   |   start <= 345278
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 342518:
endoplasmic_reticulum_ (32.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 342518:
plasma_membrane_ (27.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 345278
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 346315:
cytoplasm_ (22.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 346315
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
349758
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
348523: nucleus_ (25.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
348523: endoplasmic_reticulum_ (20.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
349758: nucleus_ (50.07/19.95)
|   |   |   |   |   |   |   |   |   |   start > 350942
|   |   |   |   |   |   |   |   |   |   |   start <= 408343
|   |   |   |   |   |   |   |   |   |   |   |   start <= 375323
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 370370
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
352416: cellular_component_ (8.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
352416
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
366743
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 359598: mitochondrion_ (18.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 359598: nucleus_ (27.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
366743: mitochondrion_ (32.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 370370
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
373583
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
372228
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleolus_: mitochondrion_ (0.85/0.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = RNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_biogenesis_and_assembly_: nucleus_
(1.8/0.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleus_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: cytoplasm_ (2.98/0.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: nucleus_ (11.67/7.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_component_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = hydrolase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasm_: mitochondrion_ (5.57/2.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = molecular_function_: mitochondrion_ (11.63/6.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_: mitochondrion_ (3.65/1.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = meiosis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = pseudohyphal_growth_: nucleus_ (4.73/1.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = biological_process_: nucleus_ (1.4/0.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transport_: nucleus_ (9.43/4.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrion_: cytoplasm_ (5.21/2.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transporter_activity_: mitochondrion_ (1.43/0.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = structural_molecule_activity_: nucleus_ (1.34/0.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endomembrane_system_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_fraction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_binding_: cytoplasm_ (3.24/1.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transduction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ribosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peroxisome_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = oxidoreductase_activity_: nucleus_ (3.52/0.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = endoplasmic_reticulum_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = enzyme_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = organelle_organization_and_biogenesis_:
mitochondrion_ (4.52/2.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_metabolic_process_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: nucleus_ (4.57/2.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: cytoplasm_ (5.87/2.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_modification_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cortex_: cytoplasm_ (7.3/1.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_: mitochondrion_ (2.66/0.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = protein_kinase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytokinesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = DNA_binding_: mitochondrion_ (1.71/0.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transcription_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = transferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = Golgi_apparatus_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_organization_and_biogenesis_: nucleus_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = chromosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = phosphoprotein_phosphatase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = response_to_stress_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lyase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_respiration_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vesicle-mediated_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = peptidase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = lipid_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = plasma_membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoskeleton_organization_and_biogenesis_: nucleus_
(2.62/1.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = electron_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = conjugation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vacuole_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = helicase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_wall_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = ligase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cellular_bud_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = site_of_polarized_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_cycle_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = isomerase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = amino_acid_and_derivative_metabolic_process_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = microtubule_organizing_center_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = sporulation_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = vitamin_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = extracellular_region_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cell_budding_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = mitochondrial_envelope_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
NeighGO_term = cytoplasmic_membrane-bound_vesicle_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
372228
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: cytoplasm_ (35.57/14.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: nucleus_ (26.59/11.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
373583: nucleus_ (34.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 375323
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 383989
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
380833: endoplasmic_reticulum_ (23.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
380833: cellular_component_ (34.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 383989
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
401042
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
394687
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: mitochondrion_ (36.86/14.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: membrane_ (22.9/9.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
394687: mitochondrion_ (51.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
401042: nucleus_ (52.34/22.52)
|   |   |   |   |   |   |   |   |   |   |   start > 408343
|   |   |   |   |   |   |   |   |   |   |   |   start <= 417304
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 413641:
vacuole_ (20.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 413641
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleolus_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: endomembrane_system_ (2.08/0.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: membrane_fraction_ (8.55/3.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_binding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= RNA_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_biogenesis_and_assembly_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: membrane_ (4.16/2.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: endomembrane_system_ (4.42/2.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleus_
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 3204: endomembrane_system_ (17.09/11.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 3204: membrane_fraction_ (4.41/2.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_component_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= hydrolase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasm_: endomembrane_system_ (7.94/4.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= molecular_function_
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: endomembrane_system_ (3.55/1.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: membrane_ (11.94/6.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= meiosis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= pseudohyphal_growth_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= biological_process_: endoplasmic_reticulum_ (7.91/4.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transport_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrion_: endomembrane_system_ (3.51/2.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transporter_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= structural_molecule_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endomembrane_system_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_fraction_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_binding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transduction_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ribosome_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peroxisome_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= oxidoreductase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= carbohydrate_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= endoplasmic_reticulum_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_catabolic_process_: endoplasmic_reticulum_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= translation_regulator_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= enzyme_regulator_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= membrane_organization_and_biogenesis_: endoplasmic_reticulum_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= organelle_organization_and_biogenesis_: endoplasmic_reticulum_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_metabolic_process_: endomembrane_system_ (10.2/6.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_modification_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cortex_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= protein_kinase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytokinesis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= DNA_binding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transcription_regulator_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= transferase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= Golgi_apparatus_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_organization_and_biogenesis_: endoplasmic_reticulum_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= chromosome_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= phosphoprotein_phosphatase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= response_to_stress_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lyase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_respiration_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vesicle-mediated_transport_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= peptidase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= lipid_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= plasma_membrane_: endoplasmic_reticulum_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoskeleton_organization_and_biogenesis_: endoplasmic_reticulum_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= electron_transport_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= conjugation_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vacuole_: membrane_fraction_ (3.8/2.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= helicase_activity_: endoplasmic_reticulum_ (3.81/1.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_wall_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= ligase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cellular_bud_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= site_of_polarized_growth_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_cycle_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= isomerase_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= signal_transducer_activity_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= amino_acid_and_derivative_metabolic_process_:
endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nucleotidyltransferase_activity_: endoplasmic_reticulum_
(6.21/1.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= microtubule_organizing_center_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= sporulation_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= vitamin_metabolic_process_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= extracellular_region_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= nuclear_organization_and_biogenesis_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cell_budding_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= mitochondrial_envelope_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term
= cytoplasmic_membrane-bound_vesicle_: endoplasmic_reticulum_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 417304
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 439285
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
420100: nucleus_ (111.91/50.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
420100
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
424497: membrane_fraction_ (21.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
424497
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 430089: mitochondrion_ (37.94/15.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 430089: cytoplasm_ (24.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 439285
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
440572: plasma_membrane_ (23.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
440572
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
440921: cellular_component_ (34.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
440921: nucleus_ (19.37)
|   |   |   |   |   |   |   start > 443008
|   |   |   |   |   |   |   |   start <= 495002
|   |   |   |   |   |   |   |   |   start <= 473392
|   |   |   |   |   |   |   |   |   |   start <= 457706
|   |   |   |   |   |   |   |   |   |   |   start <= 444317
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
nucleolus_ (24.21/9.71)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
ribosome_ (19.83/7.06)
|   |   |   |   |   |   |   |   |   |   |   start > 444317:
membrane_ (20.48)
|   |   |   |   |   |   |   |   |   |   start > 457706:
cytoskeleton_ (55.64/24.96)
|   |   |   |   |   |   |   |   |   start > 473392
|   |   |   |   |   |   |   |   |   |   start <= 478033
|   |   |   |   |   |   |   |   |   |   |   start <= 476620:
cytoplasm_ (56.64/24.63)
|   |   |   |   |   |   |   |   |   |   |   start > 476620:
membrane_ (27.56)
|   |   |   |   |   |   |   |   |   |   start > 478033
|   |   |   |   |   |   |   |   |   |   |   start <= 483557
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
site_of_polarized_growth_ (29.11/11.9)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_bud_ (23.14/10.0)
|   |   |   |   |   |   |   |   |   |   |   start > 483557
|   |   |   |   |   |   |   |   |   |   |   |   start <= 491524:
cytoplasm_ (30.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 491524:
ribosome_ (26.52)
|   |   |   |   |   |   |   |   start > 495002
|   |   |   |   |   |   |   |   |   start <= 514936
|   |   |   |   |   |   |   |   |   |   start <= 507759
|   |   |   |   |   |   |   |   |   |   |   start <= 501516:
nucleus_ (18.46)
|   |   |   |   |   |   |   |   |   |   |   start > 501516
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: membrane_fraction_ (0.17/0.04)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
membrane_fraction_ (5.75/0.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (5.43/1.14)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: cytoplasm_ (4.24/0.57)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: membrane_fraction_ (4.61/1.67)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: cytoplasm_ (0.32/0.02)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: membrane_fraction_ (2.5/0.69)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: membrane_fraction_ (1.97/0.51)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: cytoplasm_ (6.21/1.93)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: membrane_fraction_ (2.47/0.86)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: membrane_fraction_ (0.82/0.04)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: cytoplasm_ (3.66/0.83)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: membrane_fraction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: membrane_fraction_
(2.22/0.41)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: cytoplasm_ (1.46/0.19)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: membrane_fraction_ (5.14/1.16)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: membrane_fraction_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: cytoplasm_ (3.94/0.37)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: cytoplasm_ (3.56/1.48)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: membrane_fraction_ (4.95/0.22)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: membrane_fraction_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: membrane_fraction_ (0.0)
|   |   |   |   |   |   |   |   |   |   start > 507759: nucleus_
(57.49)
|   |   |   |   |   |   |   |   |   start > 514936
|   |   |   |   |   |   |   |   |   |   start <= 517250: vacuole_
(20.58)
```

```
|   |   |   |   |   |   |   |   |   |   start > 517250
|   |   |   |   |   |   |   |   |   |   |   start <= 518846:
mitochondrion_ (25.94)
|   |   |   |   |   |   |   |   |   |   |   start > 518846:
cytoplasm_ (17.11)
|   |   |   |   start > 531726
|   |   |   |   |   start <= 542305
|   |   |   |   |   |   start <= 537912
|   |   |   |   |   |   |   strand = W: Golgi_apparatus_ (25.37)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 534983: cellular_component_
(43.03)
|   |   |   |   |   |   |   |   start > 534983: Golgi_apparatus_
(21.13)
|   |   |   |   |   |   start > 537912
|   |   |   |   |   |   |   strand = W: endoplasmic_reticulum_
(75.7/21.54)
|   |   |   |   |   |   |   strand = C: plasma_membrane_ (21.81)
|   |   |   |   |   start > 542305
|   |   |   |   |   |   distance <= 20940
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 574507
|   |   |   |   |   |   |   |   |   start <= 547095
|   |   |   |   |   |   |   |   |   |   start <= 542964: cytoplasm_
(54.8/23.82)
|   |   |   |   |   |   |   |   |   |   start > 542964:
Golgi_apparatus_ (39.35/17.49)
|   |   |   |   |   |   |   |   |   start > 547095
|   |   |   |   |   |   |   |   |   |   start <= 560766
|   |   |   |   |   |   |   |   |   |   |   start <= 547114:
cellular_component_ (43.27)
|   |   |   |   |   |   |   |   |   |   |   start > 547114
|   |   |   |   |   |   |   |   |   |   |   |   start <= 555049
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 553381
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
548101: nucleus_ (58.5/22.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
548101: cytoplasm_ (31.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 553381
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: cellular_component_ (32.62/11.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: nucleus_ (24.3/7.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 555049
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 557021:
endoplasmic_reticulum_ (35.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 557021:
nucleus_ (57.83/27.09)
|   |   |   |   |   |   |   |   |   |   start > 560766
|   |   |   |   |   |   |   |   |   |   |   start <= 573000:
cellular_component_ (61.57/1.03)
|   |   |   |   |   |   |   |   |   |   |   start > 573000:
cytoplasm_ (24.55)
|   |   |   |   |   |   |   |   start > 574507
```

```
|   |   |   |   |   |   |   |   |   start <= 613636
|   |   |   |   |   |   |   |   |   |   start <= 597540
|   |   |   |   |   |   |   |   |   |   |   start <= 579581
|   |   |   |   |   |   |   |   |   |   |   |   start <= 576728
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= C: chromosome_ (26.15/8.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= F: nucleus_ (17.05/5.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= P: nucleus_ (17.5/4.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 576728
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cytoplasm_ (26.37/12.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
nucleus_ (32.99/7.61)
|   |   |   |   |   |   |   |   |   |   |   start > 579581
|   |   |   |   |   |   |   |   |   |   |   |   start <= 586821:
mitochondrion_ (27.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 586821:
nucleus_ (63.51/20.34)
|   |   |   |   |   |   |   |   |   |   start > 597540
|   |   |   |   |   |   |   |   |   |   |   start <= 606320
|   |   |   |   |   |   |   |   |   |   |   |   start <= 605385:
cytoplasm_ (66.88/20.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 605385:
ribosome_ (27.39)
|   |   |   |   |   |   |   |   |   |   |   start > 606320: nucleus_
(97.2/46.88)
|   |   |   |   |   |   |   |   |   start > 613636: peroxisome_
(84.58/52.91)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 581921
|   |   |   |   |   |   |   |   |   start <= 560766
|   |   |   |   |   |   |   |   |   |   start <= 555049:
Golgi_apparatus_ (22.98)
|   |   |   |   |   |   |   |   |   |   start > 555049
|   |   |   |   |   |   |   |   |   |   |   start <= 559815:
mitochondrion_ (25.3)
|   |   |   |   |   |   |   |   |   |   |   start > 559815:
cytoplasm_ (3.62)
|   |   |   |   |   |   |   |   |   start > 560766
|   |   |   |   |   |   |   |   |   |   start <= 576728: nucleus_
(73.99/17.93)
|   |   |   |   |   |   |   |   |   |   start > 576728:
Golgi_apparatus_ (24.33)
|   |   |   |   |   |   |   |   start > 581921
|   |   |   |   |   |   |   |   |   start <= 593228
|   |   |   |   |   |   |   |   |   |   start <= 591161
|   |   |   |   |   |   |   |   |   |   |   start <= 585588:
nucleus_ (66.96/28.81)
|   |   |   |   |   |   |   |   |   |   |   start > 585588
|   |   |   |   |   |   |   |   |   |   |   |   start <= 587848
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 586821:
cellular_component_ (31.54)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 586821:
cytoplasm_ (24.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 587848:
cellular_component_ (32.01)
|   |   |   |   |   |   |   |   |   |   start > 591161: nucleus_
(36.48)
|   |   |   |   |   |   |   |   |   start > 593228
|   |   |   |   |   |   |   |   |   |   start <= 597540:
cell_cortex_ (58.46/26.31)
|   |   |   |   |   |   |   |   |   |   start > 597540:
cellular_component_ (96.91)
|   |   |   |   |   |   distance > 20940
|   |   |   |   |   |   |   start <= 576728: cytoplasm_ (99.44)
|   |   |   |   |   |   |   start > 576728
|   |   |   |   |   |   |   |   start <= 593228
|   |   |   |   |   |   |   |   |   start <= 585588:
cellular_component_ (13.25)
|   |   |   |   |   |   |   |   |   start > 585588: nucleolus_
(28.18)
|   |   |   |   |   |   |   |   start > 593228: cytoplasm_ (21.36)
|   |   |   start > 614822
|   |   |   |   start <= 620069
|   |   |   |   |   start <= 618221
|   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   NeighGO_term = nucleolus_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
endomembrane_system_ (10.51/2.44)
|   |   |   |   |   |   |   NeighGO_term = RNA_metabolic_process_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = nucleus_:
endomembrane_system_ (9.03/3.83)
|   |   |   |   |   |   |   NeighGO_term = cellular_component_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
endoplasmic_reticulum_ (8.92/2.9)
|   |   |   |   |   |   |   NeighGO_term = molecular_function_:
endoplasmic_reticulum_ (2.63/0.83)
|   |   |   |   |   |   |   NeighGO_term = translation_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = meiosis_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = biological_process_:
endoplasmic_reticulum_ (11.45/6.01)
|   |   |   |   |   |   |   NeighGO_term = transport_:
endoplasmic_reticulum_ (5.78/1.32)
|   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
endomembrane_system_ (3.2/1.67)
```

```
|   |   |   |   |   |   |   NeighGO_term = transporter_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
endoplasmic_reticulum_ (1.33/0.49)
|   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
endomembrane_system_ (4.6/1.54)
|   |   |   |   |   |   |   NeighGO_term = protein_binding_:
endoplasmic_reticulum_ (1.65/0.55)
|   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
endoplasmic_reticulum_ (6.15/3.27)
|   |   |   |   |   |   |   NeighGO_term = ribosome_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = peroxisome_:
endomembrane_system_ (3.94/1.93)
|   |   |   |   |   |   |   NeighGO_term = oxidoreductase_activity_:
membrane_ (1.45/0.49)
|   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: membrane_ (3.22/1.62)
|   |   |   |   |   |   |   NeighGO_term = endoplasmic_reticulum_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = membrane_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = DNA_metabolic_process_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transcription_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cytoskeleton_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = protein_kinase_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transferase_activity_:
endomembrane_system_ (0.0)
```

```
|   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = chromosome_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = lyase_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cellular_respiration_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = lipid_metabolic_process_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: endomembrane_system_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = electron_transport_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = conjugation_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = vacuole_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_wall_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cellular_bud_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: endomembrane_system_
(0.0)
|   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: endomembrane_system_ (0.0)
```

```
|   |   |   |   |   |   |   NeighGO_term = sporulation_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = extracellular_region_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_budding_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = mitochondrial_envelope_:
endomembrane_system_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: endomembrane_system_ (0.0)
|   |   |   |   |   |   neigh_strand = C: membrane_ (36.23/16.18)
|   |   |   |   |   start > 618221
|   |   |   |   |   |   start <= 619567: ribosome_ (41.58)
|   |   |   |   |   |   start > 619567: membrane_fraction_
(68.09/33.74)
|   |   |   |   start > 620069
|   |   |   |   |   start <= 706141
|   |   |   |   |   |   start <= 692563
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 670420
|   |   |   |   |   |   |   |   |   start <= 653389
|   |   |   |   |   |   |   |   |   |   start <= 640398
|   |   |   |   |   |   |   |   |   |   |   start <= 636988
|   |   |   |   |   |   |   |   |   |   |   |   start <= 622917:
nucleus_ (61.65/28.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 622917
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 633858:
cytoplasm_ (51.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 633858
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
635945: nucleolus_ (15.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
635945: cytoplasm_ (17.86)
|   |   |   |   |   |   |   |   |   |   |   start > 636988:
endoplasmic_reticulum_ (21.66)
|   |   |   |   |   |   |   |   |   |   start > 640398
|   |   |   |   |   |   |   |   |   |   |   start <= 643746:
nucleus_ (78.32/36.22)
|   |   |   |   |   |   |   |   |   |   |   start > 643746:
cytoplasm_ (144.47/56.45)
|   |   |   |   |   |   |   |   |   start > 653389
|   |   |   |   |   |   |   |   |   |   start <= 664272:
mitochondrion_ (49.58)
|   |   |   |   |   |   |   |   |   |   start > 664272
|   |   |   |   |   |   |   |   |   |   |   start <= 668379:
endoplasmic_reticulum_ (43.23)
|   |   |   |   |   |   |   |   |   |   |   start > 668379: nucleus_
(45.07/20.06)
|   |   |   |   |   |   |   |   start > 670420
|   |   |   |   |   |   |   |   |   start <= 678801
```

```
|   |   |   |   |   |   |   |   |   |   start <= 674925: nucleus_
(107.87/45.94)
|   |   |   |   |   |   |   |   |   |   start > 674925
|   |   |   |   |   |   |   |   |   |   |   start <= 676179:
vacuole_ (27.88)
|   |   |   |   |   |   |   |   |   |   |   start > 676179:
endoplasmic_reticulum_ (25.17)
|   |   |   |   |   |   |   |   |   start > 678801: cytoplasm_
(179.07/50.92)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 672411
|   |   |   |   |   |   |   |   |   start <= 631063
|   |   |   |   |   |   |   |   |   |   start <= 625831:
mitochondrion_ (58.07)
|   |   |   |   |   |   |   |   |   |   start > 625831
|   |   |   |   |   |   |   |   |   |   |   start <= 627458:
nucleolus_ (46.82)
|   |   |   |   |   |   |   |   |   |   |   start > 627458:
mitochondrion_ (15.45)
|   |   |   |   |   |   |   |   |   start > 631063
|   |   |   |   |   |   |   |   |   |   start <= 647434
|   |   |   |   |   |   |   |   |   |   |   start <= 642692
|   |   |   |   |   |   |   |   |   |   |   |   start <= 632601:
cytoplasm_ (28.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 632601
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 633858:
mitochondrion_ (34.52/15.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 633858:
cytoplasm_ (65.04/27.47)
|   |   |   |   |   |   |   |   |   |   |   start > 642692: nucleus_
(24.41)
|   |   |   |   |   |   |   |   |   |   start > 647434
|   |   |   |   |   |   |   |   |   |   |   start <= 653389:
membrane_ (26.88)
|   |   |   |   |   |   |   |   |   |   |   start > 653389
|   |   |   |   |   |   |   |   |   |   |   |   start <= 668379
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 664272:
mitochondrion_ (28.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 664272:
mitochondrial_envelope_ (17.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 668379:
mitochondrion_ (29.49)
|   |   |   |   |   |   |   |   start > 672411
|   |   |   |   |   |   |   |   |   start <= 678801
|   |   |   |   |   |   |   |   |   |   start <= 676179:
membrane_fraction_ (25.13)
|   |   |   |   |   |   |   |   |   |   start > 676179: cytoplasm_
(37.45)
|   |   |   |   |   |   |   |   |   start > 678801
|   |   |   |   |   |   |   |   |   |   start <= 686012:
site_of_polarized_growth_ (58.36/27.71)
|   |   |   |   |   |   |   |   |   |   start > 686012:
cellular_component_ (27.3)
|   |   |   |   |   |   start > 692563
```

```
|   |   |   |   |   |   |   start <= 694049: cytoskeleton_
(51.19/18.95)
|   |   |   |   |   |   |   start > 694049
|   |   |   |   |   |   |   |   start <= 701661
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 695597: nucleolus_
(17.44)
|   |   |   |   |   |   |   |   |   |   start > 695597:
mitochondrion_ (24.0)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 694824
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
ribosome_ (22.68/9.57)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
mitochondrion_ (30.25/10.61)
|   |   |   |   |   |   |   |   |   |   start > 694824
|   |   |   |   |   |   |   |   |   |   |   start <= 695597:
mitochondrion_ (32.22)
|   |   |   |   |   |   |   |   |   |   |   start > 695597
|   |   |   |   |   |   |   |   |   |   |   |   start <= 699692:
endoplasmic_reticulum_ (18.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 699692:
mitochondrion_ (21.22)
|   |   |   |   |   |   |   |   start > 701661
|   |   |   |   |   |   |   |   |   start <= 703701
|   |   |   |   |   |   |   |   |   |   start <= 701897: cytoplasm_
(19.46)
|   |   |   |   |   |   |   |   |   |   start > 701897: cell_wall_
(25.09)
|   |   |   |   |   |   |   |   |   start > 703701: mitochondrion_
(31.31)
|   |   |   |   |   start > 706141
|   |   |   |   |   |   start <= 713657
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 708525
|   |   |   |   |   |   |   |   |   start <= 707790: nucleus_
(73.02/46.77)
|   |   |   |   |   |   |   |   |   start > 707790: cytoplasm_
(24.0)
|   |   |   |   |   |   |   |   start > 708525: membrane_ (28.64)
|   |   |   |   |   |   |   strand = C: membrane_fraction_ (26.23)
|   |   |   |   |   |   start > 713657
|   |   |   |   |   |   |   strand = W: nucleolus_ (21.23)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 720649: cytoplasm_ (90.22)
|   |   |   |   |   |   |   |   start > 720649
|   |   |   |   |   |   |   |   |   start <= 724307: nucleolus_
(116.53/44.39)
|   |   |   |   |   |   |   |   |   start > 724307: cytoplasm_
(29.04)
|   |   start > 726218
|   |   |   start <= 743540
|   |   |   |   start <= 733303
|   |   |   |   |   start <= 730187: mitochondrion_ (49.43/20.59)
```

```
|   |   |   |   |   start > 730187: plasma_membrane_ (25.12)
|   |   |   |   start > 733303
|   |   |   |   |   start <= 736803
|   |   |   |   |   |   start <= 734291: cytoplasm_ (42.63)
|   |   |   |   |   |   start > 734291: cellular_component_ (11.78)
|   |   |   |   |   start > 736803
|   |   |   |   |   |   start <= 739951: plasma_membrane_ (24.09)
|   |   |   |   |   |   start > 739951: vacuole_ (26.42)
|   |   |   start > 743540
|   |   |   |   start <= 771468
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 755035: cellular_component_ (24.94)
|   |   |   |   |   |   start > 755035: membrane_ (48.22/20.52)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 746943: membrane_ (23.31)
|   |   |   |   |   |   start > 746943
|   |   |   |   |   |   |   start <= 759099
|   |   |   |   |   |   |   |   start <= 753700: cellular_component_
(47.08)
|   |   |   |   |   |   |   |   start > 753700
|   |   |   |   |   |   |   |   |   start <= 755035:
membrane_fraction_ (21.71)
|   |   |   |   |   |   |   |   |   start > 755035:
extracellular_region_ (25.35)
|   |   |   |   |   |   |   start > 759099: cellular_component_
(81.22)
|   |   |   |   start > 771468
|   |   |   |   |   start <= 778738
|   |   |   |   |   |   start <= 776300
|   |   |   |   |   |   |   start <= 772657: plasma_membrane_
(23.39)
|   |   |   |   |   |   |   start > 772657: cellular_component_
(25.74)
|   |   |   |   |   |   start > 776300
|   |   |   |   |   |   |   NeighGO_term = nucleolus_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = RNA_binding_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = RNA_metabolic_process_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = nucleus_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cellular_component_
|   |   |   |   |   |   |   |   neigh_strand = W: plasma_membrane_
(2.52/0.52)
|   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   distance <= 3003:
plasma_membrane_ (4.29/0.91)
|   |   |   |   |   |   |   |   |   distance > 3003: nucleus_
(5.58/2.06)
|   |   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
mitochondrion_ (2.01/0.29)
```

```
|   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
mitochondrion_ (1.2/0.47)
|   |   |   |   |   |   |   NeighGO_term = molecular_function_:
nucleus_ (7.91/4.07)
|   |   |   |   |   |   |   NeighGO_term = translation_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = meiosis_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = biological_process_
|   |   |   |   |   |   |   |   neigh_strand = W: plasma_membrane_
(3.59/1.58)
|   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   distance <= 3003:
mitochondrion_ (2.37/0.96)
|   |   |   |   |   |   |   |   |   |   distance > 3003:
plasma_membrane_ (4.59/1.86)
|   |   |   |   |   |   |   |   |   neigh_num > 1: mitochondrion_
(5.07/2.21)
|   |   |   |   |   |   |   NeighGO_term = transport_:
mitochondrion_ (6.77/1.75)
|   |   |   |   |   |   |   NeighGO_term = mitochondrion_:
plasma_membrane_ (2.87/0.53)
|   |   |   |   |   |   |   NeighGO_term = transporter_activity_:
plasma_membrane_ (0.81/0.41)
|   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = endomembrane_system_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = membrane_fraction_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = protein_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = signal_transduction_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = ribosome_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = peroxisome_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = oxidoreductase_activity_:
mitochondrion_ (5.51/2.98)
|   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = endoplasmic_reticulum_:
mitochondrion_ (3.15/1.24)
|   |   |   |   |   |   |   NeighGO_term = membrane_: nucleus_
(1.62/0.71)
|   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = DNA_metabolic_process_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transcription_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_cortex_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = cytoskeleton_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = protein_kinase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cytokinesis_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = DNA_binding_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = transferase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = Golgi_apparatus_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = chromosome_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = response_to_stress_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = lyase_activity_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = cellular_respiration_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: nucleus_ (4.73/1.4)
|   |   |   |   |   |   |   NeighGO_term = peptidase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = lipid_metabolic_process_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = plasma_membrane_:
nucleus_ (4.31/0.7)
|   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = electron_transport_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = conjugation_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = vacuole_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   NeighGO_term = helicase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_wall_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = ligase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cellular_bud_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_cycle_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = isomerase_activity_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = sporulation_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = extracellular_region_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cell_budding_: nucleus_
(0.0)
|   |   |   |   |   |   |   NeighGO_term = mitochondrial_envelope_:
nucleus_ (0.0)
|   |   |   |   |   |   |   NeighGO_term = cytoplasmic_membrane-
bound_vesicle_: nucleus_ (0.0)
|   |   |   |   |   start > 778738
|   |   |   |   |   |   start <= 779916
|   |   |   |   |   |   |   distance <= 8008: cytoplasm_
(22.23/8.83)
|   |   |   |   |   |   |   distance > 8008: endoplasmic_reticulum_
(16.23/3.78)
|   |   |   |   |   |   start > 779916: cellular_component_ (42.79)
```

For Molecular Function

```
|   start <= 703701
|   |   start <= 646952
|   |   |   start <= 87897
|   |   |   |   start <= 52661
|   |   |   |   |   start <= 40328
|   |   |   |   |   |   start <= 22633
|   |   |   |   |   |   |   start <= 14832
```

```
|   |   |   |   |   |   |   |   start <= 6098: helicase_activity_
(12.72)
|   |   |   |   |   |   |   |   start > 6098
|   |   |   |   |   |   |   |   |   start <= 12876:
molecular_function_ (56.18)
|   |   |   |   |   |   |   |   |   start > 12876
|   |   |   |   |   |   |   |   |   |   start <= 13267:
protein_binding_ (35.13)
|   |   |   |   |   |   |   |   |   |   start > 13267:
molecular_function_ (27.86)
|   |   |   |   |   |   |   start > 14832
|   |   |   |   |   |   |   |   start <= 17248:
oxidoreductase_activity_ (31.95)
|   |   |   |   |   |   |   |   start > 17248
|   |   |   |   |   |   |   |   |   start <= 19302:
transcription_regulator_activity_ (30.21)
|   |   |   |   |   |   |   |   |   start > 19302: protein_binding_
(25.75)
|   |   |   |   |   |   start > 22633
|   |   |   |   |   |   |   start <= 31943
|   |   |   |   |   |   |   |   start <= 23274:
transporter_activity_ (63.81/23.69)
|   |   |   |   |   |   |   |   start > 23274
|   |   |   |   |   |   |   |   |   start <= 28346
|   |   |   |   |   |   |   |   |   |   start <= 24047:
hydrolase_activity_ (30.41)
|   |   |   |   |   |   |   |   |   |   start > 24047:
transferase_activity_ (22.01)
|   |   |   |   |   |   |   |   |   start > 28346:
hydrolase_activity_ (64.05)
|   |   |   |   |   |   |   start > 31943
|   |   |   |   |   |   |   |   start <= 34234:
structural_molecule_activity_ (21.46)
|   |   |   |   |   |   |   |   start > 34234
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 34695:
transporter_activity_ (28.08)
|   |   |   |   |   |   |   |   |   |   start > 34695:
molecular_function_ (31.17)
|   |   |   |   |   |   |   |   |   strand = C:
transporter_activity_ (29.3)
|   |   |   |   |   start > 40328
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 40618: RNA_binding_ (22.24)
|   |   |   |   |   |   |   start > 40618
|   |   |   |   |   |   |   |   start <= 44446:
transcription_regulator_activity_ (27.14)
|   |   |   |   |   |   |   |   start > 44446
|   |   |   |   |   |   |   |   |   start <= 48286: DNA_binding_
(36.17)
|   |   |   |   |   |   |   |   |   start > 48286:
transcription_regulator_activity_ (21.23)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 43074: lyase_activity_ (29.49)
```

```
|   |   |   |   |   |   |   start > 43074
|   |   |   |   |   |   |   |   start <= 48286
|   |   |   |   |   |   |   |   |   start <= 44446: protein_binding_
(29.27)
|   |   |   |   |   |   |   |   |   start > 44446:
molecular_function_ (21.98)
|   |   |   |   |   |   |   |   start > 48286: protein_binding_
(49.53)
|   |   |   |   start > 52661
|   |   |   |   |   start <= 80260
|   |   |   |   |   |   start <= 64562
|   |   |   |   |   |   |   start <= 59791
|   |   |   |   |   |   |   |   strand = W:
structural_molecule_activity_ (24.85)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 58155
|   |   |   |   |   |   |   |   |   |   start <= 55896:
molecular_function_ (20.02)
|   |   |   |   |   |   |   |   |   |   start > 55896:
protein_kinase_activity_ (27.95)
|   |   |   |   |   |   |   |   |   start > 58155:
molecular_function_ (24.24)
|   |   |   |   |   |   |   start > 59791
|   |   |   |   |   |   |   |   strand = W: hydrolase_activity_
(30.67)
|   |   |   |   |   |   |   |   strand = C:
structural_molecule_activity_ (59.14)
|   |   |   |   |   |   start > 64562
|   |   |   |   |   |   |   start <= 68915
|   |   |   |   |   |   |   |   start <= 65744: molecular_function_
(31.67)
|   |   |   |   |   |   |   |   start > 65744
|   |   |   |   |   |   |   |   |   start <= 66517:
nucleotidyltransferase_activity_ (27.43)
|   |   |   |   |   |   |   |   |   start > 66517:
protein_kinase_activity_ (29.09)
|   |   |   |   |   |   |   start > 68915
|   |   |   |   |   |   |   |   start <= 76583:
enzyme_regulator_activity_ (19.5)
|   |   |   |   |   |   |   |   start > 76583: molecular_function_
(62.75)
|   |   |   |   |   start > 80260
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 82806
|   |   |   |   |   |   |   |   start <= 80640:
enzyme_regulator_activity_ (29.12)
|   |   |   |   |   |   |   |   start > 80640: isomerase_activity_
(33.16)
|   |   |   |   |   |   |   start > 82806
|   |   |   |   |   |   |   |   start <= 86218: DNA_binding_ (21.52)
|   |   |   |   |   |   |   |   start > 86218:
enzyme_regulator_activity_ (28.66)
|   |   |   |   |   |   strand = C: transporter_activity_ (23.03)
|   |   |   start > 87897
```

```
|   |   |   |   strand = W
|   |   |   |   |   start <= 503725
|   |   |   |   |   |   start <= 408343
|   |   |   |   |   |   |   start <= 241690
|   |   |   |   |   |   |   |   start <= 172287
|   |   |   |   |   |   |   |   |   start <= 116679
|   |   |   |   |   |   |   |   |   |   start <= 96312
|   |   |   |   |   |   |   |   |   |   |   start <= 91994
|   |   |   |   |   |   |   |   |   |   |   |   start <= 89210:
RNA_binding_ (16.36)
|   |   |   |   |   |   |   |   |   |   |   |   start > 89210:
molecular_function_ (42.07)
|   |   |   |   |   |   |   |   |   |   |   start > 91994:
RNA_binding_ (34.61)
|   |   |   |   |   |   |   |   |   |   start > 96312
|   |   |   |   |   |   |   |   |   |   |   start <= 107687
|   |   |   |   |   |   |   |   |   |   |   |   start <= 104805:
molecular_function_ (51.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 104805:
hydrolase_activity_ (28.11)
|   |   |   |   |   |   |   |   |   |   |   start > 107687
|   |   |   |   |   |   |   |   |   |   |   |   start <= 108467:
protein_binding_ (24.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 108467:
molecular_function_ (77.15)
|   |   |   |   |   |   |   |   |   start > 116679
|   |   |   |   |   |   |   |   |   |   start <= 138551
|   |   |   |   |   |   |   |   |   |   |   start <= 117349:
transferase_activity_ (28.77)
|   |   |   |   |   |   |   |   |   |   |   start > 117349
|   |   |   |   |   |   |   |   |   |   |   |   start <= 137700
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 119268:
transporter_activity_ (52.38/25.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 119268:
molecular_function_ (64.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 137700:
transporter_activity_ (17.06)
|   |   |   |   |   |   |   |   |   |   start > 138551
|   |   |   |   |   |   |   |   |   |   |   start <= 148213
|   |   |   |   |   |   |   |   |   |   |   |   start <= 140879:
transferase_activity_ (23.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 140879:
nucleotidyltransferase_activity_ (43.72)
|   |   |   |   |   |   |   |   |   |   |   start > 148213
|   |   |   |   |   |   |   |   |   |   |   |   start <= 157866:
DNA_binding_ (36.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 157866
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 164624:
transferase_activity_ (25.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 164624:
molecular_function_ (27.26)
|   |   |   |   |   |   |   |   start > 172287
|   |   |   |   |   |   |   |   |   start <= 211923
|   |   |   |   |   |   |   |   |   |   start <= 188052
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 182876
|   |   |   |   |   |   |   |   |   |   |   |   start <= 175411:
protein_binding_ (33.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 175411:
ligase_activity_ (23.41)
|   |   |   |   |   |   |   |   |   |   |   start > 182876:
protein_binding_ (52.04)
|   |   |   |   |   |   |   |   |   |   start > 188052
|   |   |   |   |   |   |   |   |   |   |   start <= 210234
|   |   |   |   |   |   |   |   |   |   |   |   start <= 202429
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 200570
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
191325: molecular_function_ (25.12)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
191325: transcription_regulator_activity_ (18.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 200570:
peptidase_activity_ (27.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 202429
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 206931
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
205189: molecular_function_ (22.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
205189: transcription_regulator_activity_ (16.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 206931:
molecular_function_ (27.4)
|   |   |   |   |   |   |   |   |   |   |   start > 210234:
protein_binding_ (16.65)
|   |   |   |   |   |   |   |   |   start > 211923
|   |   |   |   |   |   |   |   |   |   start <= 230673
|   |   |   |   |   |   |   |   |   |   |   start <= 227371
|   |   |   |   |   |   |   |   |   |   |   |   start <= 220202:
hydrolase_activity_ (18.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 220202:
peptidase_activity_ (21.77)
|   |   |   |   |   |   |   |   |   |   |   start > 227371:
phosphoprotein_phosphatase_activity_ (41.25/19.57)
|   |   |   |   |   |   |   |   |   |   start > 230673
|   |   |   |   |   |   |   |   |   |   |   start <= 234414:
ligase_activity_ (51.31/23.79)
|   |   |   |   |   |   |   |   |   |   |   start > 234414
|   |   |   |   |   |   |   |   |   |   |   |   start <= 238239:
enzyme_regulator_activity_ (35.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 238239
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 240332:
hydrolase_activity_ (19.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 240332:
DNA_binding_ (26.58)
|   |   |   |   |   |   |   start > 241690
|   |   |   |   |   |   |   |   start <= 332599
|   |   |   |   |   |   |   |   |   start <= 287996
|   |   |   |   |   |   |   |   |   |   start <= 255354
|   |   |   |   |   |   |   |   |   |   |   start <= 254419
|   |   |   |   |   |   |   |   |   |   |   |   start <= 252060
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 247462
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <=
245618
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
244469: molecular_function_ (22.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
244469: protein_binding_ (25.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   start >
245618: molecular_function_ (30.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 247462
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
250932: RNA_binding_ (22.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
250932: protein_binding_ (31.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 252060:
molecular_function_ (28.73)
|   |   |   |   |   |   |   |   |   |   |   start > 254419:
protein_kinase_activity_ (28.24)
|   |   |   |   |   |   |   |   |   |   start > 255354
|   |   |   |   |   |   |   |   |   |   |   start <= 280433
|   |   |   |   |   |   |   |   |   |   |   |   start <= 274369
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 266531:
oxidoreductase_activity_ (35.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 266531:
molecular_function_ (18.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 274369
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 276503:
transferase_activity_ (22.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 276503:
ligase_activity_ (24.6)
|   |   |   |   |   |   |   |   |   |   |   start > 280433
|   |   |   |   |   |   |   |   |   |   |   |   start <= 286309
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 282396:
molecular_function_ (33.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 282396:
protein_binding_ (53.4)
|   |   |   |   |   |   |   |   |   |   |   |   start > 286309:
molecular_function_ (33.58)
|   |   |   |   |   |   |   |   |   start > 287996
|   |   |   |   |   |   |   |   |   |   start <= 298337
|   |   |   |   |   |   |   |   |   |   |   start <= 292671:
peptidase_activity_ (28.21)
|   |   |   |   |   |   |   |   |   |   |   start > 292671:
oxidoreductase_activity_ (14.2)
|   |   |   |   |   |   |   |   |   |   start > 298337
|   |   |   |   |   |   |   |   |   |   |   start <= 330331
|   |   |   |   |   |   |   |   |   |   |   |   start <= 310638
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 304617:
structural_molecule_activity_ (15.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 304617:
protein_binding_ (19.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 310638:
molecular_function_ (43.33)
|   |   |   |   |   |   |   |   |   |   |   start > 330331
```

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|   |   |   |   |   |   |   |   |   |   |   |   start <= 331324:
structural_molecule_activity_ (30.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 331324:
protein_kinase_activity_ (15.63)
|   |   |   |   |   |   |   |   start > 332599
|   |   |   |   |   |   |   |   |   start <= 383989
|   |   |   |   |   |   |   |   |   |   start <= 351717
|   |   |   |   |   |   |   |   |   |   |   start <= 348523
|   |   |   |   |   |   |   |   |   |   |   |   start <= 339614
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 336547:
molecular_function_ (37.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 336547:
transferase_activity_ (24.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 339614:
molecular_function_ (75.68)
|   |   |   |   |   |   |   |   |   |   |   start > 348523
|   |   |   |   |   |   |   |   |   |   |   |   start <= 350942:
RNA_binding_ (22.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 350942:
molecular_function_ (17.53)
|   |   |   |   |   |   |   |   |   |   start > 351717
|   |   |   |   |   |   |   |   |   |   |   start <= 378769
|   |   |   |   |   |   |   |   |   |   |   |   start <= 357455
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 352416:
protein_binding_ (24.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 352416:
transporter_activity_ (22.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 357455
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 375323
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
359598
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num <= 1: molecular_function_ (26.37/12.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_num > 1: hydrolase_activity_ (18.31/5.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
359598
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
366743
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 366035: molecular_function_ (27.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 366035: protein_binding_ (27.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
366743: molecular_function_ (74.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 375323:
transporter_activity_ (20.06)
|   |   |   |   |   |   |   |   |   |   |   start > 378769
|   |   |   |   |   |   |   |   |   |   |   |   start <= 382361
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 381482:
transferase_activity_ (24.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 381482:
hydrolase_activity_ (25.34)
```

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|   |   |   |   |   |   |   |   |   |   |   |   start > 382361:
molecular_function_ (28.27)
|   |   |   |   |   |   |   |   |   start > 383989
|   |   |   |   |   |   |   |   |   |   start <= 394687
|   |   |   |   |   |   |   |   |   |   |   start <= 392894
|   |   |   |   |   |   |   |   |   |   |   |   start <= 387229:
structural_molecule_activity_ (33.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 387229:
RNA_binding_ (25.5)
|   |   |   |   |   |   |   |   |   |   |   start > 392894:
peptidase_activity_ (35.5)
|   |   |   |   |   |   |   |   |   |   start > 394687
|   |   |   |   |   |   |   |   |   |   |   start <= 406360
|   |   |   |   |   |   |   |   |   |   |   |   start <= 401042:
molecular_function_ (25.79)
|   |   |   |   |   |   |   |   |   |   |   |   start > 401042:
transferase_activity_ (16.56)
|   |   |   |   |   |   |   |   |   |   |   start > 406360:
molecular_function_ (28.18)
|   |   |   |   |   |   start > 408343
|   |   |   |   |   |   |   start <= 479769
|   |   |   |   |   |   |   |   start <= 430089
|   |   |   |   |   |   |   |   |   start <= 413641
|   |   |   |   |   |   |   |   |   |   start <= 412773:
nucleotidyltransferase_activity_ (29.6)
|   |   |   |   |   |   |   |   |   |   start > 412773:
helicase_activity_ (30.46)
|   |   |   |   |   |   |   |   |   start > 413641
|   |   |   |   |   |   |   |   |   |   start <= 420100:
molecular_function_ (19.58)
|   |   |   |   |   |   |   |   |   |   start > 420100
|   |   |   |   |   |   |   |   |   |   |   start <= 427737:
transcription_regulator_activity_ (21.3)
|   |   |   |   |   |   |   |   |   |   |   start > 427737:
nucleotidyltransferase_activity_ (17.25)
|   |   |   |   |   |   |   |   start > 430089
|   |   |   |   |   |   |   |   |   start <= 456567
|   |   |   |   |   |   |   |   |   |   start <= 435001:
transporter_activity_ (26.2)
|   |   |   |   |   |   |   |   |   |   start > 435001
|   |   |   |   |   |   |   |   |   |   |   start <= 452410
|   |   |   |   |   |   |   |   |   |   |   |   start <= 447613:
molecular_function_ (68.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 447613
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 450873
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
449870: hydrolase_activity_ (15.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
449870: transferase_activity_ (18.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 450873:
molecular_function_ (22.86)
|   |   |   |   |   |   |   |   |   |   |   start > 452410:
signal_transducer_activity_ (25.06)
|   |   |   |   |   |   |   |   |   start > 456567
```

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|   |   |   |   |   |   |   |   |   |   start <= 457706:
DNA_binding_ (48.13/21.01)
|   |   |   |   |   |   |   |   |   |   start > 457706
|   |   |   |   |   |   |   |   |   |   |   start <= 467133
|   |   |   |   |   |   |   |   |   |   |   |   start <= 466336:
molecular_function_ (51.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 466336:
hydrolase_activity_ (24.94)
|   |   |   |   |   |   |   |   |   |   |   start > 467133
|   |   |   |   |   |   |   |   |   |   |   |   start <= 473392
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 471379:
transporter_activity_ (27.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 471379:
DNA_binding_ (26.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 473392:
molecular_function_ (29.02)
|   |   |   |   |   |   |   start > 479769
|   |   |   |   |   |   |   |   start <= 488387
|   |   |   |   |   |   |   |   |   start <= 483557
|   |   |   |   |   |   |   |   |   |   start <= 481392:
protein_binding_ (24.51)
|   |   |   |   |   |   |   |   |   |   start > 481392:
transcription_regulator_activity_ (35.79)
|   |   |   |   |   |   |   |   |   start > 483557
|   |   |   |   |   |   |   |   |   |   start <= 485608:
RNA_binding_ (29.74)
|   |   |   |   |   |   |   |   |   |   start > 485608:
ligase_activity_ (22.86)
|   |   |   |   |   |   |   |   start > 488387
|   |   |   |   |   |   |   |   |   start <= 491524
|   |   |   |   |   |   |   |   |   |   start <= 490318:
hydrolase_activity_ (22.61)
|   |   |   |   |   |   |   |   |   |   start > 490318:
transferase_activity_ (28.76)
|   |   |   |   |   |   |   |   |   start > 491524
|   |   |   |   |   |   |   |   |   |   start <= 499418
|   |   |   |   |   |   |   |   |   |   |   start <= 495002:
transporter_activity_ (27.03)
|   |   |   |   |   |   |   |   |   |   |   start > 495002:
molecular_function_ (20.14)
|   |   |   |   |   |   |   |   |   |   start > 499418
|   |   |   |   |   |   |   |   |   |   |   start <= 501516
|   |   |   |   |   |   |   |   |   |   |   |   start <= 499682:
structural_molecule_activity_ (13.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 499682:
hydrolase_activity_ (17.4)
|   |   |   |   |   |   |   |   |   |   |   start > 501516:
transporter_activity_ (21.12)
|   |   |   |   |   start > 503725
|   |   |   |   |   |   start <= 581921
|   |   |   |   |   |   |   start <= 538174
|   |   |   |   |   |   |   |   start <= 510541:
transferase_activity_ (47.28)
|   |   |   |   |   |   |   |   start > 510541
```

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|   |   |   |   |   |   |   |   |   start <= 529943
|   |   |   |   |   |   |   |   |   |   start <= 526087
|   |   |   |   |   |   |   |   |   |   |   start <= 519170:
molecular_function_ (18.32)
|   |   |   |   |   |   |   |   |   |   |   start > 519170:
enzyme_regulator_activity_ (24.14)
|   |   |   |   |   |   |   |   |   |   start > 526087:
phosphoprotein_phosphatase_activity_ (27.96)
|   |   |   |   |   |   |   |   |   start > 529943
|   |   |   |   |   |   |   |   |   |   start <= 531726:
oxidoreductase_activity_ (23.75)
|   |   |   |   |   |   |   |   |   |   start > 531726
|   |   |   |   |   |   |   |   |   |   |   start <= 534983:
molecular_function_ (31.22)
|   |   |   |   |   |   |   |   |   |   |   start > 534983:
transferase_activity_ (22.22)
|   |   |   |   |   |   |   start > 538174
|   |   |   |   |   |   |   |   start <= 573000
|   |   |   |   |   |   |   |   |   start <= 553381
|   |   |   |   |   |   |   |   |   |   start <= 542964
|   |   |   |   |   |   |   |   |   |   |   start <= 542305:
molecular_function_ (33.57)
|   |   |   |   |   |   |   |   |   |   |   start > 542305:
peptidase_activity_ (24.82)
|   |   |   |   |   |   |   |   |   |   start > 542964:
molecular_function_ (132.35)
|   |   |   |   |   |   |   |   |   start > 553381
|   |   |   |   |   |   |   |   |   |   start <= 560766
|   |   |   |   |   |   |   |   |   |   |   start <= 555049:
transcription_regulator_activity_ (35.22)
|   |   |   |   |   |   |   |   |   |   |   start > 555049
|   |   |   |   |   |   |   |   |   |   |   |   start <= 557021:
transferase_activity_ (22.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 557021:
lyase_activity_ (27.39)
|   |   |   |   |   |   |   |   |   |   start > 560766:
molecular_function_ (82.62)
|   |   |   |   |   |   |   |   start > 573000
|   |   |   |   |   |   |   |   |   start <= 579581
|   |   |   |   |   |   |   |   |   |   start <= 574507:
phosphoprotein_phosphatase_activity_ (23.21)
|   |   |   |   |   |   |   |   |   |   start > 574507
|   |   |   |   |   |   |   |   |   |   |   start <= 576728:
DNA_binding_ (36.46)
|   |   |   |   |   |   |   |   |   |   |   start > 576728:
transcription_regulator_activity_ (52.12/23.38)
|   |   |   |   |   |   |   |   |   start > 579581:
molecular_function_ (26.05)
|   |   |   |   |   |   start > 581921
|   |   |   |   |   |   |   start <= 635945
|   |   |   |   |   |   |   |   start <= 609687
|   |   |   |   |   |   |   |   |   start <= 602908
|   |   |   |   |   |   |   |   |   |   start <= 597540
|   |   |   |   |   |   |   |   |   |   |   start <= 587848
```

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|   |   |   |   |   |   |   |   |   |   |   |   start <= 585588:
hydrolase_activity_ (13.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 585588:
RNA_binding_ (28.11)
|   |   |   |   |   |   |   |   |   |   |   start > 587848:
hydrolase_activity_ (28.53)
|   |   |   |   |   |   |   |   |   |   start > 597540
|   |   |   |   |   |   |   |   |   |   |   start <= 602313:
molecular_function_ (21.36)
|   |   |   |   |   |   |   |   |   |   |   start > 602313:
RNA_binding_ (15.63)
|   |   |   |   |   |   |   |   |   start > 602908
|   |   |   |   |   |   |   |   |   |   start <= 606320
|   |   |   |   |   |   |   |   |   |   |   start <= 605385:
enzyme_regulator_activity_ (26.98)
|   |   |   |   |   |   |   |   |   |   |   start > 605385:
translation_regulator_activity_ (25.07)
|   |   |   |   |   |   |   |   |   |   start > 606320:
hydrolase_activity_ (27.86)
|   |   |   |   |   |   |   |   start > 609687
|   |   |   |   |   |   |   |   |   start <= 620069
|   |   |   |   |   |   |   |   |   |   start <= 614822
|   |   |   |   |   |   |   |   |   |   |   start <= 613636:
molecular_function_ (22.14)
|   |   |   |   |   |   |   |   |   |   |   start > 613636:
oxidoreductase_activity_ (30.69)
|   |   |   |   |   |   |   |   |   |   start > 614822:
protein_binding_ (35.78)
|   |   |   |   |   |   |   |   |   start > 620069
|   |   |   |   |   |   |   |   |   |   start <= 627458
|   |   |   |   |   |   |   |   |   |   |   start <= 622917:
RNA_binding_ (29.77)
|   |   |   |   |   |   |   |   |   |   |   start > 622917:
hydrolase_activity_ (28.67)
|   |   |   |   |   |   |   |   |   |   start > 627458:
molecular_function_ (46.68)
|   |   |   |   |   |   |   start > 635945
|   |   |   |   |   |   |   |   start <= 640398
|   |   |   |   |   |   |   |   |   start <= 636988:
protein_binding_ (26.59)
|   |   |   |   |   |   |   |   |   start > 636988:
transferase_activity_ (25.02)
|   |   |   |   |   |   |   |   start > 640398:
transcription_regulator_activity_ (35.7)
|   |   |   |   strand = C
|   |   |   |   |   start <= 224470
|   |   |   |   |   |   start <= 135384
|   |   |   |   |   |   |   start <= 108467
|   |   |   |   |   |   |   |   start <= 104805
|   |   |   |   |   |   |   |   |   start <= 96312:
molecular_function_ (21.17)
|   |   |   |   |   |   |   |   |   start > 96312:
structural_molecule_activity_ (32.39)
```

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|   |   |   |   |   |   |   |   start > 104805:
signal_transducer_activity_ (21.9)
|   |   |   |   |   |   |   start > 108467
|   |   |   |   |   |   |   |   start <= 122883:
oxidoreductase_activity_ (77.72)
|   |   |   |   |   |   |   |   start > 122883
|   |   |   |   |   |   |   |   |   start <= 129084:
enzyme_regulator_activity_ (26.05)
|   |   |   |   |   |   |   |   |   start > 129084: protein_binding_
(25.17)
|   |   |   |   |   |   start > 135384
|   |   |   |   |   |   |   start <= 186886
|   |   |   |   |   |   |   |   start <= 160374
|   |   |   |   |   |   |   |   |   start <= 140879:
transporter_activity_ (22.12)
|   |   |   |   |   |   |   |   |   start > 140879
|   |   |   |   |   |   |   |   |   |   start <= 145282:
molecular_function_ (31.49)
|   |   |   |   |   |   |   |   |   |   start > 145282
|   |   |   |   |   |   |   |   |   |   |   start <= 146616:
transporter_activity_ (26.31)
|   |   |   |   |   |   |   |   |   |   |   start > 146616
|   |   |   |   |   |   |   |   |   |   |   |   start <= 157456:
molecular_function_ (84.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 157456
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 157866:
transporter_activity_ (74.85/33.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 157866:
molecular_function_ (26.39)
|   |   |   |   |   |   |   |   start > 160374
|   |   |   |   |   |   |   |   |   start <= 164624:
transcription_regulator_activity_ (33.96)
|   |   |   |   |   |   |   |   |   start > 164624
|   |   |   |   |   |   |   |   |   |   start <= 175411
|   |   |   |   |   |   |   |   |   |   |   start <= 170019:
molecular_function_ (61.83)
|   |   |   |   |   |   |   |   |   |   |   start > 170019
|   |   |   |   |   |   |   |   |   |   |   |   start <= 172287:
structural_molecule_activity_ (26.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 172287:
RNA_binding_ (28.08)
|   |   |   |   |   |   |   |   |   |   start > 175411
|   |   |   |   |   |   |   |   |   |   |   start <= 181023:
molecular_function_ (37.45)
|   |   |   |   |   |   |   |   |   |   |   start > 181023
|   |   |   |   |   |   |   |   |   |   |   |   start <= 182876:
nucleotidyltransferase_activity_ (24.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 182876:
molecular_function_ (33.01)
|   |   |   |   |   |   |   start > 186886
|   |   |   |   |   |   |   |   start <= 218663
|   |   |   |   |   |   |   |   |   start <= 206931
|   |   |   |   |   |   |   |   |   |   start <= 191325:
translation_regulator_activity_ (23.11)
```

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|   |   |   |   |   |   |   |   |   |   start > 191325:
oxidoreductase_activity_ (52.95)
|   |   |   |   |   |   |   |   |   start > 206931
|   |   |   |   |   |   |   |   |   |   start <= 217043:
transporter_activity_ (20.9)
|   |   |   |   |   |   |   |   |   |   start > 217043:
transcription_regulator_activity_ (26.3)
|   |   |   |   |   |   |   |   start > 218663
|   |   |   |   |   |   |   |   |   start <= 222432
|   |   |   |   |   |   |   |   |   |   start <= 220202:
protein_binding_ (20.36)
|   |   |   |   |   |   |   |   |   |   start > 220202
|   |   |   |   |   |   |   |   |   |   |   distance <= 6366:
enzyme_regulator_activity_ (38.57/15.78)
|   |   |   |   |   |   |   |   |   |   |   distance > 6366:
molecular_function_ (6.68/2.62)
|   |   |   |   |   |   |   |   |   start > 222432:
structural_molecule_activity_ (32.33)
|   |   |   |   |   start > 224470
|   |   |   |   |   |   start <= 340354
|   |   |   |   |   |   |   start <= 308614
|   |   |   |   |   |   |   |   start <= 282396
|   |   |   |   |   |   |   |   |   start <= 241690
|   |   |   |   |   |   |   |   |   |   start <= 230673
|   |   |   |   |   |   |   |   |   |   |   start <= 227371:
molecular_function_ (18.83)
|   |   |   |   |   |   |   |   |   |   |   start > 227371:
RNA_binding_ (20.93)
|   |   |   |   |   |   |   |   |   |   start > 230673
|   |   |   |   |   |   |   |   |   |   |   start <= 234414:
hydrolase_activity_ (29.68)
|   |   |   |   |   |   |   |   |   |   |   start > 234414:
transferase_activity_ (32.87)
|   |   |   |   |   |   |   |   |   start > 241690
|   |   |   |   |   |   |   |   |   |   start <= 264454
|   |   |   |   |   |   |   |   |   |   |   start <= 258156
|   |   |   |   |   |   |   |   |   |   |   |   start <= 252060:
molecular_function_ (57.21)
|   |   |   |   |   |   |   |   |   |   |   |   start > 252060:
protein_binding_ (21.75)
|   |   |   |   |   |   |   |   |   |   |   start > 258156:
molecular_function_ (76.57)
|   |   |   |   |   |   |   |   |   |   start > 264454
|   |   |   |   |   |   |   |   |   |   |   start <= 269594
|   |   |   |   |   |   |   |   |   |   |   |   start <= 266531:
transcription_regulator_activity_ (28.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 266531:
RNA_binding_ (18.51)
|   |   |   |   |   |   |   |   |   |   |   start > 269594:
molecular_function_ (94.48)
|   |   |   |   |   |   |   |   start > 282396
|   |   |   |   |   |   |   |   |   start <= 295511
|   |   |   |   |   |   |   |   |   |   start <= 292671:
structural_molecule_activity_ (18.34)
```

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|   |   |   |   |   |   |   |   |   |   start > 292671:
transferase_activity_ (24.02)
|   |   |   |   |   |   |   |   |   start > 295511
|   |   |   |   |   |   |   |   |   |   start <= 306982
|   |   |   |   |   |   |   |   |   |   |   start <= 300651
|   |   |   |   |   |   |   |   |   |   |   |   start <= 298337:
molecular_function_ (20.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 298337:
hydrolase_activity_ (28.48)
|   |   |   |   |   |   |   |   |   |   |   start > 300651
|   |   |   |   |   |   |   |   |   |   |   |   start <= 304617:
structural_molecule_activity_ (21.79)
|   |   |   |   |   |   |   |   |   |   |   |   start > 304617:
molecular_function_ (23.06)
|   |   |   |   |   |   |   |   |   |   start > 306982: RNA_binding_
(21.29)
|   |   |   |   |   |   |   start > 308614
|   |   |   |   |   |   |   |   start <= 321361
|   |   |   |   |   |   |   |   |   start <= 318811
|   |   |   |   |   |   |   |   |   |   start <= 310638:
molecular_function_ (20.09)
|   |   |   |   |   |   |   |   |   |   start > 310638
|   |   |   |   |   |   |   |   |   |   |   start <= 317673:
lyase_activity_ (25.22)
|   |   |   |   |   |   |   |   |   |   |   start > 317673:
molecular_function_ (17.53)
|   |   |   |   |   |   |   |   |   start > 318811:
transcription_regulator_activity_ (32.66)
|   |   |   |   |   |   |   |   start > 321361
|   |   |   |   |   |   |   |   |   start <= 326322:
molecular_function_ (55.16)
|   |   |   |   |   |   |   |   |   start > 326322
|   |   |   |   |   |   |   |   |   |   start <= 332599:
hydrolase_activity_ (19.42)
|   |   |   |   |   |   |   |   |   |   start > 332599:
molecular_function_ (23.59)
|   |   |   |   |   |   start > 340354
|   |   |   |   |   |   |   start <= 483557
|   |   |   |   |   |   |   |   start <= 372228
|   |   |   |   |   |   |   |   |   start <= 359598
|   |   |   |   |   |   |   |   |   |   start <= 346315
|   |   |   |   |   |   |   |   |   |   |   start <= 342518:
protein_binding_ (32.49)
|   |   |   |   |   |   |   |   |   |   |   start > 342518
|   |   |   |   |   |   |   |   |   |   |   |   start <= 345278:
protein_kinase_activity_ (20.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 345278:
protein_binding_ (31.31)
|   |   |   |   |   |   |   |   |   |   start > 346315
|   |   |   |   |   |   |   |   |   |   |   start <= 348523:
nucleotidyltransferase_activity_ (23.72)
|   |   |   |   |   |   |   |   |   |   |   start > 348523
|   |   |   |   |   |   |   |   |   |   |   |   start <= 350942
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 349758:
molecular_function_ (24.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 349758:
protein_binding_ (14.94)
|   |   |   |   |   |   |   |   |   |   |   |   start > 350942:
molecular_function_ (41.66)
|   |   |   |   |   |   |   |   |   start > 359598
|   |   |   |   |   |   |   |   |   |   start <= 370370
|   |   |   |   |   |   |   |   |   |   |   start <= 366743:
DNA_binding_ (26.7)
|   |   |   |   |   |   |   |   |   |   |   start > 366743:
structural_molecule_activity_ (26.35)
|   |   |   |   |   |   |   |   |   |   start > 370370:
isomerase_activity_ (32.22)
|   |   |   |   |   |   |   |   start > 372228
|   |   |   |   |   |   |   |   |   start <= 440921
|   |   |   |   |   |   |   |   |   |   start <= 420100
|   |   |   |   |   |   |   |   |   |   |   start <= 380833
|   |   |   |   |   |   |   |   |   |   |   |   start <= 373583:
oxidoreductase_activity_ (28.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 373583
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 375323:
molecular_function_ (26.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 375323:
transferase_activity_ (19.88)
|   |   |   |   |   |   |   |   |   |   |   start > 380833
|   |   |   |   |   |   |   |   |   |   |   |   start <= 401042
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 383989:
molecular_function_ (33.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 383989
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
394687: transporter_activity_ (27.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
394687
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
398372: molecular_function_ (20.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
398372: transporter_activity_ (23.95)
|   |   |   |   |   |   |   |   |   |   |   |   start > 401042
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 408343:
hydrolase_activity_ (14.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 408343
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
417304
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
413641: molecular_function_ (22.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
413641: oxidoreductase_activity_ (24.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
417304: molecular_function_ (46.45)
|   |   |   |   |   |   |   |   |   |   start > 420100
|   |   |   |   |   |   |   |   |   |   |   start <= 440572
|   |   |   |   |   |   |   |   |   |   |   |   start <= 430089
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 424497:
hydrolase_activity_ (23.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 424497:
transferase_activity_ (19.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 430089
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 439285:
phosphoprotein_phosphatase_activity_ (20.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 439285:
hydrolase_activity_ (28.61)
|   |   |   |   |   |   |   |   |   |   |   start > 440572:
molecular_function_ (27.66)
|   |   |   |   |   |   |   |   |   start > 440921
|   |   |   |   |   |   |   |   |   |   start <= 476620
|   |   |   |   |   |   |   |   |   |   |   start <= 473392
|   |   |   |   |   |   |   |   |   |   |   |   start <= 444317
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 443008:
protein_binding_ (19.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 443008:
structural_molecule_activity_ (19.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 444317
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 457706:
molecular_function_ (18.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 457706:
protein_binding_ (25.9)
|   |   |   |   |   |   |   |   |   |   |   start > 473392:
structural_molecule_activity_ (30.86)
|   |   |   |   |   |   |   |   |   |   start > 476620
|   |   |   |   |   |   |   |   |   |   |   start <= 478033:
molecular_function_ (32.8)
|   |   |   |   |   |   |   |   |   |   |   start > 478033:
protein_binding_ (31.27)
|   |   |   |   |   |   |   start > 483557
|   |   |   |   |   |   |   |   start <= 620069
|   |   |   |   |   |   |   |   |   start <= 518846
|   |   |   |   |   |   |   |   |   |   start <= 510541
|   |   |   |   |   |   |   |   |   |   |   start <= 501516
|   |   |   |   |   |   |   |   |   |   |   |   start <= 495002
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 491524:
molecular_function_ (23.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 491524:
RNA_binding_ (26.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 495002:
DNA_binding_ (24.66)
|   |   |   |   |   |   |   |   |   |   |   start > 501516
|   |   |   |   |   |   |   |   |   |   |   |   start <= 507759:
protein_binding_ (51.55/23.44)
|   |   |   |   |   |   |   |   |   |   |   |   start > 507759:
RNA_binding_ (26.38)
|   |   |   |   |   |   |   |   |   |   start > 510541
|   |   |   |   |   |   |   |   |   |   |   start <= 514936:
helicase_activity_ (31.11)
|   |   |   |   |   |   |   |   |   |   |   start > 514936
|   |   |   |   |   |   |   |   |   |   |   |   start <= 517250:
molecular_function_ (17.87)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 517250:
transporter_activity_ (16.34)
|   |   |   |   |   |   |   |   |   start > 518846
|   |   |   |   |   |   |   |   |   |   start <= 570478
|   |   |   |   |   |   |   |   |   |   |   start <= 555049:
molecular_function_ (147.47)
|   |   |   |   |   |   |   |   |   |   |   start > 555049
|   |   |   |   |   |   |   |   |   |   |   |   start <= 559815:
oxidoreductase_activity_ (32.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 559815:
molecular_function_ (81.85)
|   |   |   |   |   |   |   |   |   |   start > 570478
|   |   |   |   |   |   |   |   |   |   |   start <= 591161
|   |   |   |   |   |   |   |   |   |   |   |   start <= 587848
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 576728:
DNA_binding_ (21.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 576728
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
585588
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
581921: transferase_activity_ (27.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
581921: transcription_regulator_activity_ (26.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
585588
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
586821: molecular_function_ (21.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
586821: transferase_activity_ (21.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 587848:
transcription_regulator_activity_ (76.31/37.6)
|   |   |   |   |   |   |   |   |   |   |   start > 591161
|   |   |   |   |   |   |   |   |   |   |   |   start <= 618221
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 597540
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
593228: molecular_function_ (29.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
593228: protein_kinase_activity_ (27.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 597540:
molecular_function_ (107.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 618221:
protein_binding_ (73.55/31.85)
|   |   |   |   |   |   |   |   start > 620069
|   |   |   |   |   |   |   |   |   start <= 625831
|   |   |   |   |   |   |   |   |   |   start <= 622917:
structural_molecule_activity_ (26.26)
|   |   |   |   |   |   |   |   |   |   start > 622917:
transporter_activity_ (29.41)
|   |   |   |   |   |   |   |   |   start > 625831
|   |   |   |   |   |   |   |   |   |   start <= 631063
|   |   |   |   |   |   |   |   |   |   |   start <= 627458:
RNA_binding_ (36.86)
|   |   |   |   |   |   |   |   |   |   |   start > 627458:
transferase_activity_ (13.46)
```

```
|   |   |   |   |   |   |   |   |   |   start > 631063
|   |   |   |   |   |   |   |   |   |   |   start <= 642692
|   |   |   |   |   |   |   |   |   |   |   |   start <= 633858
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 632601:
molecular_function_ (24.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 632601:
transporter_activity_ (17.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 633858
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 636988:
nucleotidyltransferase_activity_ (17.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 636988:
molecular_function_ (22.01)
|   |   |   |   |   |   |   |   |   |   |   start > 642692:
RNA_binding_ (19.33)
|   |   start > 646952
|   |   |   start <= 692563
|   |   |   |   strand = W
|   |   |   |   |   start <= 678801
|   |   |   |   |   |   start <= 674925
|   |   |   |   |   |   |   start <= 665341
|   |   |   |   |   |   |   |   start <= 647434:
transferase_activity_ (35.56)
|   |   |   |   |   |   |   |   start > 647434
|   |   |   |   |   |   |   |   |   start <= 664272
|   |   |   |   |   |   |   |   |   |   start <= 653389:
molecular_function_ (48.89)
|   |   |   |   |   |   |   |   |   |   start > 653389
|   |   |   |   |   |   |   |   |   |   |   start <= 662915:
transporter_activity_ (23.74)
|   |   |   |   |   |   |   |   |   |   |   start > 662915:
molecular_function_ (19.22)
|   |   |   |   |   |   |   |   |   start > 664272:
transferase_activity_ (28.9)
|   |   |   |   |   |   |   start > 665341
|   |   |   |   |   |   |   |   start <= 670420
|   |   |   |   |   |   |   |   |   start <= 668379:
molecular_function_ (25.24)
|   |   |   |   |   |   |   |   |   start > 668379:
transcription_regulator_activity_ (25.41)
|   |   |   |   |   |   |   |   start > 670420: molecular_function_
(55.96)
|   |   |   |   |   |   start > 674925
|   |   |   |   |   |   |   start <= 676179: isomerase_activity_
(36.3)
|   |   |   |   |   |   |   start > 676179: transferase_activity_
(23.2)
|   |   |   |   |   start > 678801
|   |   |   |   |   |   start <= 687637
|   |   |   |   |   |   |   start <= 686012:
phosphoprotein_phosphatase_activity_ (20.68)
|   |   |   |   |   |   |   start > 686012: ligase_activity_ (33.92)
|   |   |   |   |   |   start > 687637: molecular_function_ (73.43)
|   |   |   |   strand = C
|   |   |   |   |   start <= 676179
```

```
|   |   |   |   |   |   start <= 664272
|   |   |   |   |   |   |   start <= 653389: transporter_activity_
(30.64)
|   |   |   |   |   |   |   start > 653389: ligase_activity_ (34.83)
|   |   |   |   |   |   start > 664272
|   |   |   |   |   |   |   start <= 668379: peptidase_activity_
(23.35)
|   |   |   |   |   |   |   start > 668379
|   |   |   |   |   |   |   |   start <= 672411:
structural_molecule_activity_ (29.13)
|   |   |   |   |   |   |   |   start > 672411:
enzyme_regulator_activity_ (14.52)
|   |   |   |   |   start > 676179
|   |   |   |   |   |   start <= 686012
|   |   |   |   |   |   |   start <= 678801: molecular_function_
(26.62)
|   |   |   |   |   |   |   start > 678801: protein_kinase_activity_
(61.87/26.19)
|   |   |   |   |   |   start > 686012: molecular_function_ (29.87)
|   |   |   start > 692563
|   |   |   |   start <= 695597
|   |   |   |   |   strand = W: helicase_activity_ (25.71)
|   |   |   |   |   strand = C: structural_molecule_activity_
(94.86)
|   |   |   |   start > 695597
|   |   |   |   |   start <= 701661
|   |   |   |   |   |   start <= 699692: molecular_function_ (36.12)
|   |   |   |   |   |   start > 699692: transferase_activity_
(21.42)
|   |   |   |   |   start > 701661
|   |   |   |   |   |   start <= 701897: lyase_activity_ (26.87)
|   |   |   |   |   |   start > 701897: protein_binding_ (29.5)
|   start > 703701
|   |   start <= 736803
|   |   |   start <= 726218
|   |   |   |   start <= 708525
|   |   |   |   |   start <= 706141: translation_regulator_activity_
(27.27)
|   |   |   |   |   start > 706141
|   |   |   |   |   |   start <= 707790: transferase_activity_
(29.7)
|   |   |   |   |   |   start > 707790: protein_kinase_activity_
(22.5)
|   |   |   |   start > 708525
|   |   |   |   |   start <= 723113
|   |   |   |   |   |   start <= 718329
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 713657: hydrolase_activity_
(22.01)
|   |   |   |   |   |   |   |   start > 713657: RNA_binding_ (22.46)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 716122
|   |   |   |   |   |   |   |   |   start <= 713657:
molecular_function_ (17.9)
```

```
|   |   |   |   |   |   |   |   |   start > 713657:
oxidoreductase_activity_ (19.44)
|   |   |   |   |   |   |   |   start > 716122: molecular_function_
(23.19)
|   |   |   |   |   |   start > 718329
|   |   |   |   |   |   |   stop <= 721122: hydrolase_activity_
(52.87)
|   |   |   |   |   |   |   stop > 721122: RNA_binding_ (17.03)
|   |   |   |   |   start > 723113
|   |   |   |   |   |   start <= 724307:
transcription_regulator_activity_ (25.83)
|   |   |   |   |   |   start > 724307: molecular_function_ (18.63)
|   |   |   start > 726218
|   |   |   |   strand = W: transferase_activity_ (68.31)
|   |   |   |   strand = C
|   |   |   |   |   start <= 733303: transporter_activity_ (48.23)
|   |   |   |   |   start > 733303: ligase_activity_ (27.02)
|   |   start > 736803
|   |   |   start <= 771468
|   |   |   |   start <= 739951: oxidoreductase_activity_ (34.89)
|   |   |   |   start > 739951
|   |   |   |   |   start <= 746943: molecular_function_ (73.78)
|   |   |   |   |   start > 746943
|   |   |   |   |   |   strand = W: hydrolase_activity_ (27.19)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 750008: hydrolase_activity_
(28.96)
|   |   |   |   |   |   |   start > 750008
|   |   |   |   |   |   |   |   start <= 759099
|   |   |   |   |   |   |   |   |   start <= 755035:
molecular_function_ (37.49)
|   |   |   |   |   |   |   |   |   start > 755035:
hydrolase_activity_ (24.05)
|   |   |   |   |   |   |   |   start > 759099: molecular_function_
(57.38)
|   |   |   start > 771468
|   |   |   |   start <= 778738
|   |   |   |   |   strand = W: transporter_activity_ (27.15)
|   |   |   |   |   strand = C: oxidoreductase_activity_ (40.83)
|   |   |   |   start > 778738: molecular_function_ (64.73)
```

For Biological Process

```
|   distance <= 26345
|   |   start <= 643746
|   |   |   start <= 44279
|   |   |   |   start <= 19302
|   |   |   |   |   start <= 17248
|   |   |   |   |   |   start <= 11452
|   |   |   |   |   |   |   strand = W: biological_process_ (24.74)
|   |   |   |   |   |   |   strand = C: DNA_metabolic_process_
(7.91)
|   |   |   |   |   |   start > 11452
```

```
|   |   |   |   |   |   |   start <= 14832:
vitamin_metabolic_process_ (76.66)
|   |   |   |   |   |   |   start > 14832: biological_process_
(17.68)
|   |   |   |   |   start > 17248: protein_modification_process_
(37.76/16.31)
|   |   |   |   start > 19302
|   |   |   |   |   start <= 31943
|   |   |   |   |   |   start <= 24047
|   |   |   |   |   |   |   strand = W: cytokinesis_ (36.52)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 22633: signal_transduction_
(29.37)
|   |   |   |   |   |   |   |   start > 22633
|   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (15.63/3.91)
|   |   |   |   |   |   |   |   |   neigh_strand = C: transport_
(36.7/13.93)
|   |   |   |   |   |   start > 24047
|   |   |   |   |   |   |   start <= 28346:
membrane_organization_and_biogenesis_ (67.92/23.83)
|   |   |   |   |   |   |   start > 28346
|   |   |   |   |   |   |   |   start <= 31377: conjugation_ (28.48)
|   |   |   |   |   |   |   |   start > 31377:
membrane_organization_and_biogenesis_ (37.99/18.36)
|   |   |   |   |   start > 31943
|   |   |   |   |   |   start <= 40328
|   |   |   |   |   |   |   start <= 34234:
cell_wall_organization_and_biogenesis_ (17.53)
|   |   |   |   |   |   |   start > 34234
|   |   |   |   |   |   |   |   start <= 34695: transport_ (35.64)
|   |   |   |   |   |   |   |   start > 34695
|   |   |   |   |   |   |   |   |   start <= 37699:
biological_process_ (25.54)
|   |   |   |   |   |   |   |   |   start > 37699: transport_
(19.37)
|   |   |   |   |   |   start > 40328
|   |   |   |   |   |   |   strand = W: RNA_metabolic_process_
(26.13)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 43074:
amino_acid_and_derivative_metabolic_process_ (32.86)
|   |   |   |   |   |   |   |   start > 43074:
organelle_organization_and_biogenesis_ (20.59)
|   |   |   start > 44279
|   |   |   |   start <= 491524
|   |   |   |   |   start <= 350673
|   |   |   |   |   |   start <= 258156
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 117349
|   |   |   |   |   |   |   |   |   start <= 96312
|   |   |   |   |   |   |   |   |   |   start <= 62943
|   |   |   |   |   |   |   |   |   |   |   start <= 48286
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 44446:
transcription_ (24.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 44446:
DNA_metabolic_process_ (29.03)
|   |   |   |   |   |   |   |   |   |   |   start > 48286
|   |   |   |   |   |   |   |   |   |   |   |   start <= 58155
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 52661:
cell_cycle_ (19.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 52661:
translation_ (26.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 58155:
organelle_organization_and_biogenesis_ (20.33)
|   |   |   |   |   |   |   |   |   |   start > 62943
|   |   |   |   |   |   |   |   |   |   |   start <= 76946
|   |   |   |   |   |   |   |   |   |   |   |   start <= 66517
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 65744:
biological_process_ (23.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 65744:
RNA_metabolic_process_ (43.5/18.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 66517
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 68915:
cytokinesis_ (23.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 68915:
biological_process_ (28.8)
|   |   |   |   |   |   |   |   |   |   |   start > 76946
|   |   |   |   |   |   |   |   |   |   |   |   start <= 87897
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 82806
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
80640: vesicle-mediated_transport_ (22.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
80640: RNA_metabolic_process_ (24.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 82806
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
86218: DNA_metabolic_process_ (15.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
86218: cell_cycle_ (18.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 87897
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 90303:
transcription_ (29.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 90303
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
91994: vesicle-mediated_transport_ (42.55/19.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
91994: RNA_metabolic_process_ (24.52)
|   |   |   |   |   |   |   |   |   start > 96312
|   |   |   |   |   |   |   |   |   |   start <= 110917
|   |   |   |   |   |   |   |   |   |   |   start <= 108467
|   |   |   |   |   |   |   |   |   |   |   |   start <= 107687:
ribosome_biogenesis_and_assembly_ (20.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 107687:
response_to_stress_ (29.88)
|   |   |   |   |   |   |   |   |   |   |   start > 108467:
membrane_organization_and_biogenesis_ (85.0/53.01)
|   |   |   |   |   |   |   |   |   |   start > 110917
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 116679
|   |   |   |   |   |   |   |   |   |   |   |   start <= 113271:
transcription_ (32.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 113271:
biological_process_ (31.87)
|   |   |   |   |   |   |   |   |   |   |   start > 116679:
amino_acid_and_derivative_metabolic_process_ (40.38)
|   |   |   |   |   |   |   |   start > 117349
|   |   |   |   |   |   |   |   |   start <= 172287
|   |   |   |   |   |   |   |   |   |   start <= 157866
|   |   |   |   |   |   |   |   |   |   |   start <= 140879
|   |   |   |   |   |   |   |   |   |   |   |   start <= 138551
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 129084
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
119268: transport_ (22.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
119268: DNA_metabolic_process_ (19.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 129084
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
137700: biological_process_ (33.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
137700: transport_ (18.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 138551:
cytokinesis_ (21.7)
|   |   |   |   |   |   |   |   |   |   |   start > 140879
|   |   |   |   |   |   |   |   |   |   |   |   start <= 148213:
cell_cycle_ (75.53/35.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 148213:
DNA_metabolic_process_ (27.35)
|   |   |   |   |   |   |   |   |   |   start > 157866:
biological_process_ (91.22/30.04)
|   |   |   |   |   |   |   |   |   start > 172287
|   |   |   |   |   |   |   |   |   |   start <= 247462
|   |   |   |   |   |   |   |   |   |   |   start <= 188052
|   |   |   |   |   |   |   |   |   |   |   |   start <= 182876
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 175411:
meiosis_ (26.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 175411:
ribosome_biogenesis_and_assembly_ (28.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 182876
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 185461:
DNA_metabolic_process_ (25.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 185461:
cell_wall_organization_and_biogenesis_ (27.07)
|   |   |   |   |   |   |   |   |   |   |   start > 188052
|   |   |   |   |   |   |   |   |   |   |   |   start <= 230673
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 205189
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
200570: biological_process_ (84.7/28.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
200570
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
202429: protein_modification_process_ (28.04)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
202429: biological_process_ (24.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 205189
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
211923
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
206931: transcription_ (19.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
206931
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 210234: response_to_stress_ (21.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 210234: cytokinesis_ (14.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
211923
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
227371
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 220202: ribosome_biogenesis_and_assembly_ (16.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 220202: organelle_organization_and_biogenesis_ (29.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
227371: ribosome_biogenesis_and_assembly_ (24.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 230673
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 238239:
DNA_metabolic_process_ (69.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 238239
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
244469
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
240332: biological_process_ (32.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
240332
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 241690: transcription_ (24.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 241690: biological_process_ (28.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
244469
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
245618: transport_ (49.73/21.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
245618: biological_process_ (24.09)
|   |   |   |   |   |   |   |   |   |   start > 247462
|   |   |   |   |   |   |   |   |   |   |   start <= 250932
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_metabolic_process_ (53.58/28.64)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cell_cycle_ (34.32/17.5)
|   |   |   |   |   |   |   |   |   |   |   start > 250932
|   |   |   |   |   |   |   |   |   |   |   |   start <= 252060:
translation_ (32.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 252060
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 254419:
biological_process_ (17.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 254419:
ribosome_biogenesis_and_assembly_ (25.13)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 160374
|   |   |   |   |   |   |   |   |   start <= 60297
|   |   |   |   |   |   |   |   |   |   start <= 51687
|   |   |   |   |   |   |   |   |   |   |   start <= 48286:
biological_process_ (21.85)
|   |   |   |   |   |   |   |   |   |   |   start > 48286:
protein_catabolic_process_ (21.14)
|   |   |   |   |   |   |   |   |   |   start > 51687
|   |   |   |   |   |   |   |   |   |   |   start <= 55896
|   |   |   |   |   |   |   |   |   |   |   |   start <= 52661:
response_to_stress_ (38.71/18.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 52661:
ribosome_biogenesis_and_assembly_ (29.48)
|   |   |   |   |   |   |   |   |   |   |   start > 55896
|   |   |   |   |   |   |   |   |   |   |   |   start <= 58155:
response_to_stress_ (58.24/27.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 58155:
biological_process_ (21.47)
|   |   |   |   |   |   |   |   |   start > 60297
|   |   |   |   |   |   |   |   |   |   start <= 113271
|   |   |   |   |   |   |   |   |   |   |   start <= 108467
|   |   |   |   |   |   |   |   |   |   |   |   start <= 68915:
translation_ (57.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 68915
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 91994
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
76946: transport_ (21.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
76946
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
82806: sporulation_ (59.65/23.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
82806: transport_ (20.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 91994
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
104805: translation_ (17.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
104805: cell_wall_organization_and_biogenesis_ (15.89)
|   |   |   |   |   |   |   |   |   |   |   start > 108467:
lipid_metabolic_process_ (36.1)
|   |   |   |   |   |   |   |   |   |   start > 113271
|   |   |   |   |   |   |   |   |   |   |   start <= 135384
|   |   |   |   |   |   |   |   |   |   |   |   start <= 129084
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 122883:
biological_process_ (28.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 122883:
vesicle-mediated_transport_ (25.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 129084:
pseudohyphal_growth_ (33.74)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 135384
|   |   |   |   |   |   |   |   |   |   |   |   start <= 146616
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 140879:
transport_ (31.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 140879
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
145282: translation_ (31.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
145282: transport_ (28.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 146616
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 157456
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
148213: vesicle-mediated_transport_ (51.78/22.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
148213: biological_process_ (32.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 157456
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
157866: response_to_stress_ (31.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
157866: transport_ (53.99/25.17)
|   |   |   |   |   |   |   |   start > 160374
|   |   |   |   |   |   |   |   |   start <= 206931
|   |   |   |   |   |   |   |   |   |   start <= 175411
|   |   |   |   |   |   |   |   |   |   |   start <= 167791
|   |   |   |   |   |   |   |   |   |   |   |   start <= 164624:
transcription_ (32.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 164624:
signal_transduction_ (28.95)
|   |   |   |   |   |   |   |   |   |   |   start > 167791
|   |   |   |   |   |   |   |   |   |   |   |   start <= 172287
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 170019:
biological_process_ (27.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 170019:
translation_ (24.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 172287:
transcription_ (28.32)
|   |   |   |   |   |   |   |   |   |   start > 175411
|   |   |   |   |   |   |   |   |   |   |   start <= 186886
|   |   |   |   |   |   |   |   |   |   |   |   start <= 182876
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 181023:
biological_process_ (25.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 181023:
ribosome_biogenesis_and_assembly_ (26.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 182876:
RNA_metabolic_process_ (27.22)
|   |   |   |   |   |   |   |   |   |   |   start > 186886
|   |   |   |   |   |   |   |   |   |   |   |   start <= 197944
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 191325:
translation_ (27.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 191325:
response_to_stress_ (25.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 197944:
biological_process_ (30.68)
|   |   |   |   |   |   |   |   |   start > 206931
```

```
|   |   |   |   |   |   |   |   |   |   start <= 234414
|   |   |   |   |   |   |   |   |   |   |   start <= 220202
|   |   |   |   |   |   |   |   |   |   |   |   start <= 218663
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 217043:
transport_ (18.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 217043:
RNA_metabolic_process_ (21.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 218663:
DNA_metabolic_process_ (27.62)
|   |   |   |   |   |   |   |   |   |   |   start > 220202
|   |   |   |   |   |   |   |   |   |   |   |   start <= 224470
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 222432
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: vesicle-mediated_transport_ (16.97/7.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: ribosome_biogenesis_and_assembly_ (28.91/10.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 222432:
cell_cycle_ (25.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 224470
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 229095:
RNA_metabolic_process_ (24.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 229095:
ribosome_biogenesis_and_assembly_ (24.09)
|   |   |   |   |   |   |   |   |   |   start > 234414
|   |   |   |   |   |   |   |   |   |   |   start <= 247462
|   |   |   |   |   |   |   |   |   |   |   |   start <= 241690:
protein_modification_process_ (32.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 241690:
organelle_organization_and_biogenesis_ (24.33)
|   |   |   |   |   |   |   |   |   |   |   start > 247462
|   |   |   |   |   |   |   |   |   |   |   |   start <= 252060:
biological_process_ (26.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 252060:
DNA_metabolic_process_ (19.31)
|   |   |   |   |   |   start > 258156
|   |   |   |   |   |   |   start <= 282396
|   |   |   |   |   |   |   |   start <= 259579: sporulation_
(46.26)
|   |   |   |   |   |   |   |   start > 259579
|   |   |   |   |   |   |   |   |   start <= 269594
|   |   |   |   |   |   |   |   |   |   start <= 264454
|   |   |   |   |   |   |   |   |   |   |   start <= 263204:
response_to_stress_ (25.44)
|   |   |   |   |   |   |   |   |   |   |   start > 263204:
biological_process_ (21.57)
|   |   |   |   |   |   |   |   |   |   start > 264454
|   |   |   |   |   |   |   |   |   |   |   start <= 266531:
carbohydrate_metabolic_process_ (24.01)
|   |   |   |   |   |   |   |   |   |   |   start > 266531:
pseudohyphal_growth_ (22.85)
|   |   |   |   |   |   |   |   |   start > 269594
|   |   |   |   |   |   |   |   |   |   start <= 280433
|   |   |   |   |   |   |   |   |   |   |   start <= 274369
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 272309:
biological_process_ (50.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 272309
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 273616:
sporulation_ (20.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 273616:
biological_process_ (31.78)
|   |   |   |   |   |   |   |   |   |   |   start > 274369
|   |   |   |   |   |   |   |   |   |   |   |   start <= 276503:
cell_budding_ (27.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 276503:
biological_process_ (25.16)
|   |   |   |   |   |   |   |   |   |   start > 280433:
response_to_stress_ (33.76)
|   |   |   |   |   |   |   start > 282396
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 292671
|   |   |   |   |   |   |   |   |   |   start <= 287996
|   |   |   |   |   |   |   |   |   |   |   start <= 284261:
transport_ (29.97)
|   |   |   |   |   |   |   |   |   |   |   start > 284261
|   |   |   |   |   |   |   |   |   |   |   |   start <= 286309:
nuclear_organization_and_biogenesis_ (48.02/21.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 286309:
transport_ (18.61)
|   |   |   |   |   |   |   |   |   |   start > 287996:
protein_modification_process_ (25.03)
|   |   |   |   |   |   |   |   |   start > 292671
|   |   |   |   |   |   |   |   |   |   start <= 332599
|   |   |   |   |   |   |   |   |   |   |   start <= 331324
|   |   |   |   |   |   |   |   |   |   |   |   start <= 330331
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 304617
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
298337: biological_process_ (34.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
298337: translation_ (18.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 304617
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
310638: cell_cycle_ (18.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
310638: biological_process_ (51.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 330331:
translation_ (23.48)
|   |   |   |   |   |   |   |   |   |   |   start > 331324
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
conjugation_ (27.41/9.93)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
biological_process_ (31.28/9.52)
|   |   |   |   |   |   |   |   |   |   start > 332599
|   |   |   |   |   |   |   |   |   |   |   start <= 339614
|   |   |   |   |   |   |   |   |   |   |   |   start <= 336547:
response_to_stress_ (30.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 336547:
transport_ (41.65)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 339614:
biological_process_ (72.7)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 310638
|   |   |   |   |   |   |   |   |   |   start <= 308614
|   |   |   |   |   |   |   |   |   |   |   start <= 292671:
translation_ (31.32)
|   |   |   |   |   |   |   |   |   |   |   start > 292671
|   |   |   |   |   |   |   |   |   |   |   |   start <= 295511:
biological_process_ (20.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 295511
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 304617
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
298337: ribosome_biogenesis_and_assembly_ (27.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
298337
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
300651: signal_transduction_ (13.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
300651: translation_ (19.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 304617
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
306982: biological_process_ (23.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
306982: ribosome_biogenesis_and_assembly_ (23.36)
|   |   |   |   |   |   |   |   |   |   start > 308614
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
signal_transduction_ (20.4/6.83)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
conjugation_ (22.43/6.92)
|   |   |   |   |   |   |   |   |   start > 310638
|   |   |   |   |   |   |   |   |   |   start <= 345278
|   |   |   |   |   |   |   |   |   |   |   start <= 321361
|   |   |   |   |   |   |   |   |   |   |   |   start <= 318811
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 317673:
lipid_metabolic_process_ (22.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 317673:
biological_process_ (27.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 318811:
transcription_ (26.38)
|   |   |   |   |   |   |   |   |   |   |   start > 321361
|   |   |   |   |   |   |   |   |   |   |   |   start <= 332599
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 326322
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
323834: cytokinesis_ (23.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
323834: cell_cycle_ (27.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 326322:
ribosome_biogenesis_and_assembly_ (34.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 332599
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 340354:
protein_catabolic_process_ (33.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 340354
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
342518: lipid_metabolic_process_ (37.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
342518: cytokinesis_ (23.29)
|   |   |   |   |   |   |   |   |   |   start > 345278
|   |   |   |   |   |   |   |   |   |   |   start <= 348523
|   |   |   |   |   |   |   |   |   |   |   |   start <= 346315:
biological_process_ (36.49)
|   |   |   |   |   |   |   |   |   |   |   |   start > 346315:
transcription_ (35.34)
|   |   |   |   |   |   |   |   |   |   |   start > 348523
|   |   |   |   |   |   |   |   |   |   |   |   start <= 349758:
organelle_organization_and_biogenesis_ (52.84/24.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 349758:
biological_process_ (20.51)
|   |   |   |   |   start > 350673
|   |   |   |   |   |   start <= 418490
|   |   |   |   |   |   |   start <= 374871
|   |   |   |   |   |   |   |   start <= 355044
|   |   |   |   |   |   |   |   |   start <= 350942:
DNA_metabolic_process_ (57.91/25.08)
|   |   |   |   |   |   |   |   |   start > 350942
|   |   |   |   |   |   |   |   |   |   start <= 351717:
biological_process_ (49.61)
|   |   |   |   |   |   |   |   |   |   start > 351717
|   |   |   |   |   |   |   |   |   |   |   start <= 352416:
conjugation_ (34.75/14.17)
|   |   |   |   |   |   |   |   |   |   |   start > 352416:
biological_process_ (18.08)
|   |   |   |   |   |   |   |   start > 355044
|   |   |   |   |   |   |   |   |   start <= 366743
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 366035
|   |   |   |   |   |   |   |   |   |   |   |   start <= 359598
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 357455:
pseudohyphal_growth_ (20.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 357455:
ribosome_biogenesis_and_assembly_ (24.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 359598:
biological_process_ (28.51)
|   |   |   |   |   |   |   |   |   |   |   start > 366035
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
pseudohyphal_growth_ (24.52/9.45)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
pseudohyphal_growth_ (18.38/6.83)
|   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cytoskeleton_organization_and_biogenesis_ (12.93/4.13)
|   |   |   |   |   |   |   |   |   |   strand = C:
DNA_metabolic_process_ (23.98)
|   |   |   |   |   |   |   |   |   start > 366743
|   |   |   |   |   |   |   |   |   |   start <= 370057:
translation_ (27.54)
|   |   |   |   |   |   |   |   |   |   start > 370057
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 372228:
DNA_metabolic_process_ (48.24)
|   |   |   |   |   |   |   |   |   |   |   start > 372228
|   |   |   |   |   |   |   |   |   |   |   |   start <= 373583:
biological_process_ (23.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 373583:
DNA_metabolic_process_ (31.34)
|   |   |   |   |   |   |   start > 374871
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 383989
|   |   |   |   |   |   |   |   |   |   start <= 381482
|   |   |   |   |   |   |   |   |   |   |   start <= 378769
|   |   |   |   |   |   |   |   |   |   |   |   start <= 375323:
ribosome_biogenesis_and_assembly_ (16.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 375323:
transport_ (45.13/16.7)
|   |   |   |   |   |   |   |   |   |   |   start > 378769:
vitamin_metabolic_process_ (36.57)
|   |   |   |   |   |   |   |   |   |   start > 381482
|   |   |   |   |   |   |   |   |   |   |   start <= 382361:
cell_wall_organization_and_biogenesis_ (59.32/25.3)
|   |   |   |   |   |   |   |   |   |   |   start > 382361:
conjugation_ (39.3)
|   |   |   |   |   |   |   |   |   start > 383989
|   |   |   |   |   |   |   |   |   |   start <= 394687
|   |   |   |   |   |   |   |   |   |   |   start <= 387229:
cytoskeleton_organization_and_biogenesis_ (47.05/22.83)
|   |   |   |   |   |   |   |   |   |   |   start > 387229
|   |   |   |   |   |   |   |   |   |   |   |   start <= 392894:
RNA_metabolic_process_ (24.59)
|   |   |   |   |   |   |   |   |   |   |   |   start > 392894:
lipid_metabolic_process_ (33.21)
|   |   |   |   |   |   |   |   |   |   start > 394687
|   |   |   |   |   |   |   |   |   |   |   start <= 406360
|   |   |   |   |   |   |   |   |   |   |   |   start <= 401042:
ribosome_biogenesis_and_assembly_ (59.38/38.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 401042:
carbohydrate_metabolic_process_ (19.44)
|   |   |   |   |   |   |   |   |   |   |   start > 406360
|   |   |   |   |   |   |   |   |   |   |   |   start <= 408343:
cytoskeleton_organization_and_biogenesis_ (56.91/19.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 408343:
ribosome_biogenesis_and_assembly_ (45.55)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 413641
|   |   |   |   |   |   |   |   |   |   start <= 398372
|   |   |   |   |   |   |   |   |   |   |   start <= 380833:
lipid_metabolic_process_ (22.6)
|   |   |   |   |   |   |   |   |   |   |   start > 380833
|   |   |   |   |   |   |   |   |   |   |   |   start <= 383989:
biological_process_ (34.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 383989
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 394687:
transport_ (34.47)
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   start > 394687:
biological_process_ (29.17)
|   |   |   |   |   |   |   |   |   |   start > 398372
|   |   |   |   |   |   |   |   |   |   |   start <= 408343
|   |   |   |   |   |   |   |   |   |   |   |   start <= 401042:
membrane_organization_and_biogenesis_ (22.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 401042:
RNA_metabolic_process_ (25.95)
|   |   |   |   |   |   |   |   |   |   |   start > 408343:
biological_process_ (24.29)
|   |   |   |   |   |   |   |   |   start > 413641
|   |   |   |   |   |   |   |   |   |   start <= 417304:
electron_transport_ (24.32)
|   |   |   |   |   |   |   |   |   |   start > 417304:
ribosome_biogenesis_and_assembly_ (25.59)
|   |   |   |   |   |   start > 418490
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 457706
|   |   |   |   |   |   |   |   |   start <= 435001
|   |   |   |   |   |   |   |   |   |   start <= 430089
|   |   |   |   |   |   |   |   |   |   |   start <= 427737
|   |   |   |   |   |   |   |   |   |   |   |   start <= 420100:
DNA_metabolic_process_ (23.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 420100:
amino_acid_and_derivative_metabolic_process_ (21.56)
|   |   |   |   |   |   |   |   |   |   |   start > 427737:
DNA_metabolic_process_ (32.67)
|   |   |   |   |   |   |   |   |   |   start > 430089: transport_
(27.21)
|   |   |   |   |   |   |   |   |   start > 435001
|   |   |   |   |   |   |   |   |   |   start <= 450873
|   |   |   |   |   |   |   |   |   |   |   start <= 447613
|   |   |   |   |   |   |   |   |   |   |   |   start <= 442360:
biological_process_ (23.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 442360:
cytoskeleton_organization_and_biogenesis_ (18.35)
|   |   |   |   |   |   |   |   |   |   |   start > 447613
|   |   |   |   |   |   |   |   |   |   |   |   start <= 449870:
vesicle-mediated_transport_ (19.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 449870:
biological_process_ (28.07)
|   |   |   |   |   |   |   |   |   |   start > 450873
|   |   |   |   |   |   |   |   |   |   |   start <= 452410:
response_to_stress_ (23.86)
|   |   |   |   |   |   |   |   |   |   |   start > 452410
|   |   |   |   |   |   |   |   |   |   |   |   start <= 456567:
cell_wall_organization_and_biogenesis_ (22.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 456567:
DNA_metabolic_process_ (18.62)
|   |   |   |   |   |   |   |   start > 457706
|   |   |   |   |   |   |   |   |   start <= 471379
|   |   |   |   |   |   |   |   |   |   start <= 467133
|   |   |   |   |   |   |   |   |   |   |   start <= 466336:
biological_process_ (45.26)
```

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|   |   |   |   |   |   |   |   |   |   |   start > 466336:
translation_ (44.9/20.73)
|   |   |   |   |   |   |   |   |   |   start > 467133: transport_
(27.66)
|   |   |   |   |   |   |   |   |   start > 471379
|   |   |   |   |   |   |   |   |   |   start <= 479769
|   |   |   |   |   |   |   |   |   |   |   start <= 473392
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 12622:
cell_cycle_ (41.53/16.05)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 12622:
DNA_metabolic_process_ (6.04/0.2)
|   |   |   |   |   |   |   |   |   |   |   start > 473392:
cell_cycle_ (23.15)
|   |   |   |   |   |   |   |   |   |   start > 479769
|   |   |   |   |   |   |   |   |   |   |   start <= 485608
|   |   |   |   |   |   |   |   |   |   |   |   start <= 483557
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 481392:
biological_process_ (20.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 481392:
signal_transduction_ (22.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 483557:
ribosome_biogenesis_and_assembly_ (31.84)
|   |   |   |   |   |   |   |   |   |   |   start > 485608
|   |   |   |   |   |   |   |   |   |   |   |   start <= 490318
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 488387:
translation_ (20.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 488387:
DNA_metabolic_process_ (25.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 490318:
biological_process_ (21.62)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 443008
|   |   |   |   |   |   |   |   |   start <= 440921
|   |   |   |   |   |   |   |   |   |   start <= 430089
|   |   |   |   |   |   |   |   |   |   |   start <= 420100:
biological_process_ (23.64)
|   |   |   |   |   |   |   |   |   |   |   start > 420100
|   |   |   |   |   |   |   |   |   |   |   |   start <= 424497:
cell_wall_organization_and_biogenesis_ (24.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 424497:
amino_acid_and_derivative_metabolic_process_ (15.98)
|   |   |   |   |   |   |   |   |   |   start > 430089
|   |   |   |   |   |   |   |   |   |   |   start <= 439285:
response_to_stress_ (34.96)
|   |   |   |   |   |   |   |   |   |   |   start > 439285
|   |   |   |   |   |   |   |   |   |   |   |   start <= 440572:
pseudohyphal_growth_ (20.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 440572:
biological_process_ (18.36)
|   |   |   |   |   |   |   |   |   start > 440921:
DNA_metabolic_process_ (46.89/21.04)
|   |   |   |   |   |   |   |   start > 443008
|   |   |   |   |   |   |   |   |   start <= 476620
|   |   |   |   |   |   |   |   |   |   start <= 457706
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 444317:
translation_ (13.54)
|   |   |   |   |   |   |   |   |   |   |   start > 444317:
biological_process_ (26.88)
|   |   |   |   |   |   |   |   |   |   start > 457706
|   |   |   |   |   |   |   |   |   |   |   start <= 473392:
cytokinesis_ (22.41)
|   |   |   |   |   |   |   |   |   |   |   start > 473392:
translation_ (34.95)
|   |   |   |   |   |   |   |   |   start > 476620
|   |   |   |   |   |   |   |   |   |   start <= 478033:
response_to_stress_ (29.35)
|   |   |   |   |   |   |   |   |   |   start > 478033
|   |   |   |   |   |   |   |   |   |   |   start <= 483557:
pseudohyphal_growth_ (61.29/26.79)
|   |   |   |   |   |   |   |   |   |   |   start > 483557:
biological_process_ (25.86)
|   |   |   |   start > 491524
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 605385
|   |   |   |   |   |   |   start <= 547095
|   |   |   |   |   |   |   |   start <= 526087
|   |   |   |   |   |   |   |   |   start <= 499418
|   |   |   |   |   |   |   |   |   |   start <= 495002:
membrane_organization_and_biogenesis_ (32.04)
|   |   |   |   |   |   |   |   |   |   start > 495002:
biological_process_ (22.19)
|   |   |   |   |   |   |   |   |   start > 499418
|   |   |   |   |   |   |   |   |   |   start <= 507759
|   |   |   |   |   |   |   |   |   |   |   start <= 501516
|   |   |   |   |   |   |   |   |   |   |   |   start <= 499682:
translation_ (30.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 499682:
organelle_organization_and_biogenesis_ (20.32)
|   |   |   |   |   |   |   |   |   |   |   start > 501516
|   |   |   |   |   |   |   |   |   |   |   |   start <= 503725:
transport_ (22.65)
|   |   |   |   |   |   |   |   |   |   |   |   start > 503725:
translation_ (18.1)
|   |   |   |   |   |   |   |   |   |   start > 507759
|   |   |   |   |   |   |   |   |   |   |   start <= 519170
|   |   |   |   |   |   |   |   |   |   |   |   start <= 510541:
ribosome_biogenesis_and_assembly_ (15.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 510541:
biological_process_ (18.0)
|   |   |   |   |   |   |   |   |   |   |   start > 519170:
organelle_organization_and_biogenesis_ (29.06)
|   |   |   |   |   |   |   |   start > 526087
|   |   |   |   |   |   |   |   |   start <= 538174
|   |   |   |   |   |   |   |   |   |   start <= 531726
|   |   |   |   |   |   |   |   |   |   |   start <= 529943:
protein_modification_process_ (59.12/26.87)
|   |   |   |   |   |   |   |   |   |   |   start > 529943:
electron_transport_ (24.29)
```

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|   |   |   |   |   |   |   |   |   |   start > 531726
|   |   |   |   |   |   |   |   |   |   |   start <= 534983:
vesicle-mediated_transport_ (54.56/23.37)
|   |   |   |   |   |   |   |   |   |   |   start > 534983:
protein_modification_process_ (34.35)
|   |   |   |   |   |   |   |   |   start > 538174
|   |   |   |   |   |   |   |   |   |   start <= 542964
|   |   |   |   |   |   |   |   |   |   |   start <= 542305:
biological_process_ (33.86)
|   |   |   |   |   |   |   |   |   |   |   start > 542305:
lipid_metabolic_process_ (75.02/33.8)
|   |   |   |   |   |   |   |   |   |   start > 542964
|   |   |   |   |   |   |   |   |   |   |   start <= 545269:
vesicle-mediated_transport_ (56.02/26.86)
|   |   |   |   |   |   |   |   |   |   |   start > 545269:
translation_ (2.64)
|   |   |   |   |   |   |   start > 547095
|   |   |   |   |   |   |   |   start <= 574507
|   |   |   |   |   |   |   |   |   start <= 557021
|   |   |   |   |   |   |   |   |   |   start <= 553381:
biological_process_ (81.16)
|   |   |   |   |   |   |   |   |   |   start > 553381
|   |   |   |   |   |   |   |   |   |   |   start <= 555049:
transcription_ (29.2)
|   |   |   |   |   |   |   |   |   |   |   start > 555049:
protein_modification_process_ (19.95)
|   |   |   |   |   |   |   |   |   start > 557021
|   |   |   |   |   |   |   |   |   |   start <= 568116
|   |   |   |   |   |   |   |   |   |   |   start <= 560766:
response_to_stress_ (27.2)
|   |   |   |   |   |   |   |   |   |   |   start > 560766:
translation_ (6.21)
|   |   |   |   |   |   |   |   |   |   start > 568116
|   |   |   |   |   |   |   |   |   |   |   start <= 573000:
biological_process_ (58.0)
|   |   |   |   |   |   |   |   |   |   |   start > 573000:
response_to_stress_ (20.06)
|   |   |   |   |   |   |   |   start > 574507
|   |   |   |   |   |   |   |   |   start <= 597540
|   |   |   |   |   |   |   |   |   |   start <= 586821
|   |   |   |   |   |   |   |   |   |   |   start <= 579581
|   |   |   |   |   |   |   |   |   |   |   |   start <= 576728:
DNA_metabolic_process_ (23.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 576728:
transcription_ (23.15)
|   |   |   |   |   |   |   |   |   |   |   start > 579581:
membrane_organization_and_biogenesis_ (37.15)
|   |   |   |   |   |   |   |   |   |   start > 586821:
transcription_ (95.43/58.68)
|   |   |   |   |   |   |   |   |   start > 597540
|   |   |   |   |   |   |   |   |   |   start <= 602908:
RNA_metabolic_process_ (22.95)
|   |   |   |   |   |   |   |   |   |   start > 602908
```

```
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
organelle_organization_and_biogenesis_ (21.56/6.47)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
membrane_organization_and_biogenesis_ (30.56/11.39)
|   |   |   |   |   |   start > 605385
|   |   |   |   |   |   |   start <= 635945
|   |   |   |   |   |   |   |   start <= 614822
|   |   |   |   |   |   |   |   |   start <= 609687
|   |   |   |   |   |   |   |   |   |   start <= 606320:
translation_ (22.85)
|   |   |   |   |   |   |   |   |   |   start > 606320: meiosis_
(22.47)
|   |   |   |   |   |   |   |   |   start > 609687
|   |   |   |   |   |   |   |   |   |   start <= 613636:
biological_process_ (26.69)
|   |   |   |   |   |   |   |   |   |   start > 613636:
carbohydrate_metabolic_process_ (41.13)
|   |   |   |   |   |   |   |   start > 614822
|   |   |   |   |   |   |   |   |   start <= 622917: transport_
(124.34/61.93)
|   |   |   |   |   |   |   |   |   start > 622917
|   |   |   |   |   |   |   |   |   |   start <= 633858:
translation_ (57.74/30.55)
|   |   |   |   |   |   |   |   |   |   start > 633858:
biological_process_ (13.73)
|   |   |   |   |   |   |   start > 635945
|   |   |   |   |   |   |   |   start <= 640398
|   |   |   |   |   |   |   |   |   start <= 636988: vesicle-
mediated_transport_ (29.57)
|   |   |   |   |   |   |   |   |   start > 636988:
lipid_metabolic_process_ (28.89)
|   |   |   |   |   |   |   |   start > 640398
|   |   |   |   |   |   |   |   |   start <= 642692: transcription_
(27.2)
|   |   |   |   |   |   |   |   |   start > 642692: cell_cycle_
(57.85/26.21)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 559815
|   |   |   |   |   |   |   start <= 534983
|   |   |   |   |   |   |   |   start <= 501516
|   |   |   |   |   |   |   |   |   start <= 495002: translation_
(37.4)
|   |   |   |   |   |   |   |   |   start > 495002:
pseudohyphal_growth_ (30.13)
|   |   |   |   |   |   |   |   start > 501516
|   |   |   |   |   |   |   |   |   start <= 514936
|   |   |   |   |   |   |   |   |   |   start <= 507759: transport_
(34.0)
|   |   |   |   |   |   |   |   |   |   start > 507759
|   |   |   |   |   |   |   |   |   |   |   start <= 510541:
ribosome_biogenesis_and_assembly_ (22.17)
|   |   |   |   |   |   |   |   |   |   |   start > 510541:
transport_ (24.47)
|   |   |   |   |   |   |   |   |   start > 514936
```

```
|   |   |   |   |   |   |   |   |   |   start <= 526087
|   |   |   |   |   |   |   |   |   |   |   start <= 517250:
biological_process_ (22.64)
|   |   |   |   |   |   |   |   |   |   |   start > 517250
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleolus_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_binding_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleus_: transport_ (8.76/0.94)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: cellular_respiration_ (3.23/1.83)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasm_: transport_ (4.9/2.4)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1285: transport_ (3.03/0.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
1285: organelle_organization_and_biogenesis_ (2.11/0.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: organelle_organization_and_biogenesis_ (17.19/8.89)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
meiosis_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: transport_ (3.89/2.24)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transport_: cellular_respiration_ (4.79/1.91)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: organelle_organization_and_biogenesis_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peroxisome_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cortex_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytokinesis_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_binding_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: organelle_organization_and_biogenesis_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: transport_ (1.57/0.52)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
chromosome_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vesicle-mediated_transport_: transport_ (2.72/1.41)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
conjugation_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vacuole_: organelle_organization_and_biogenesis_ (2.37/0.76)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: organelle_organization_and_biogenesis_
(6.72/1.39)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_cycle_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: organelle_organization_and_biogenesis_
(0.0)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
sporulation_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: organelle_organization_and_biogenesis_
(0.0)
|   |   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_:
organelle_organization_and_biogenesis_ (0.0)
|   |   |   |   |   |   |   |   |   |   start > 526087:
biological_process_ (26.63)
|   |   |   |   |   |   |   start > 534983
|   |   |   |   |   |   |   |   start <= 555049
|   |   |   |   |   |   |   |   |   start <= 538174: transport_
(57.24/24.42)
|   |   |   |   |   |   |   |   |   start > 538174
|   |   |   |   |   |   |   |   |   |   start <= 545269:
signal_transduction_ (54.05/20.99)
|   |   |   |   |   |   |   |   |   |   start > 545269: vesicle-
mediated_transport_ (42.78/17.4)
|   |   |   |   |   |   |   |   start > 555049
|   |   |   |   |   |   |   |   |   neigh_strand = W:
carbohydrate_metabolic_process_ (26.54/10.13)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
cellular_respiration_ (30.58/12.15)
|   |   |   |   |   |   start > 559815
|   |   |   |   |   |   |   start <= 614822
|   |   |   |   |   |   |   |   start <= 585588
|   |   |   |   |   |   |   |   |   start <= 576728
|   |   |   |   |   |   |   |   |   |   start <= 570478
|   |   |   |   |   |   |   |   |   |   |   start <= 560766:
translation_ (2.44)
|   |   |   |   |   |   |   |   |   |   |   start > 560766:
biological_process_ (34.34)
|   |   |   |   |   |   |   |   |   |   start > 570478:
DNA_metabolic_process_ (30.87)
```

```
|   |   |   |   |   |   |   |   |   start > 576728
|   |   |   |   |   |   |   |   |   |   start <= 581921:
cell_wall_organization_and_biogenesis_ (22.54)
|   |   |   |   |   |   |   |   |   |   start > 581921: meiosis_
(29.78)
|   |   |   |   |   |   |   |   start > 585588
|   |   |   |   |   |   |   |   |   start <= 593228
|   |   |   |   |   |   |   |   |   |   start <= 591161:
biological_process_ (99.58)
|   |   |   |   |   |   |   |   |   |   start > 591161:
ribosome_biogenesis_and_assembly_ (36.2)
|   |   |   |   |   |   |   |   |   start > 593228
|   |   |   |   |   |   |   |   |   |   start <= 597540:
cytokinesis_ (31.44)
|   |   |   |   |   |   |   |   |   |   start > 597540:
biological_process_ (81.45)
|   |   |   |   |   |   |   start > 614822
|   |   |   |   |   |   |   |   start <= 625831
|   |   |   |   |   |   |   |   |   start <= 618221:
protein_catabolic_process_ (26.56)
|   |   |   |   |   |   |   |   |   start > 618221
|   |   |   |   |   |   |   |   |   |   start <= 622917:
translation_ (76.62)
|   |   |   |   |   |   |   |   |   |   start > 622917: transport_
(20.76)
|   |   |   |   |   |   |   |   start > 625831
|   |   |   |   |   |   |   |   |   start <= 636988
|   |   |   |   |   |   |   |   |   |   start <= 631063
|   |   |   |   |   |   |   |   |   |   |   start <= 627458:
ribosome_biogenesis_and_assembly_ (20.85)
|   |   |   |   |   |   |   |   |   |   |   start > 627458:
cellular_respiration_ (21.16/10.48)
|   |   |   |   |   |   |   |   |   |   start > 631063
|   |   |   |   |   |   |   |   |   |   |   start <= 633858
|   |   |   |   |   |   |   |   |   |   |   |   start <= 632601:
translation_ (7.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 632601:
biological_process_ (13.43)
|   |   |   |   |   |   |   |   |   |   |   start > 633858:
ribosome_biogenesis_and_assembly_ (15.33)
|   |   |   |   |   |   |   |   |   start > 636988:
organelle_organization_and_biogenesis_ (27.37)
|   |   start > 643746
|   |   |   start <= 662915
|   |   |   |   start <= 653389
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 652467
|   |   |   |   |   |   |   start <= 647434:
ribosome_biogenesis_and_assembly_ (27.38)
|   |   |   |   |   |   |   start > 647434: biological_process_
(22.7)
|   |   |   |   |   |   start > 652467: RNA_metabolic_process_
(33.32)
|   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   start <= 647434: RNA_metabolic_process_
(37.13)
|   |   |   |   |   |   start > 647434: transport_ (34.69)
|   |   |   |   start > 653389
|   |   |   |   |   start <= 661376:
nuclear_organization_and_biogenesis_ (49.35/20.27)
|   |   |   |   |   start > 661376:
organelle_organization_and_biogenesis_ (67.27/28.72)
|   |   |   start > 662915
|   |   |   |   start <= 726218
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 686012
|   |   |   |   |   |   |   start <= 676179
|   |   |   |   |   |   |   |   start <= 672411
|   |   |   |   |   |   |   |   |   start <= 668379
|   |   |   |   |   |   |   |   |   |   start <= 665341
|   |   |   |   |   |   |   |   |   |   |   start <= 664272:
biological_process_ (25.25)
|   |   |   |   |   |   |   |   |   |   |   start > 664272:
lipid_metabolic_process_ (18.72)
|   |   |   |   |   |   |   |   |   |   start > 665341:
biological_process_ (26.92)
|   |   |   |   |   |   |   |   |   start > 668379
|   |   |   |   |   |   |   |   |   |   start <= 670420:
DNA_metabolic_process_ (24.29)
|   |   |   |   |   |   |   |   |   |   start > 670420:
biological_process_ (27.27)
|   |   |   |   |   |   |   |   start > 672411
|   |   |   |   |   |   |   |   |   start <= 674925: cytokinesis_
(27.93)
|   |   |   |   |   |   |   |   |   start > 674925:
biological_process_ (23.41)
|   |   |   |   |   |   |   start > 676179:
protein_modification_process_ (58.52)
|   |   |   |   |   |   start > 686012
|   |   |   |   |   |   |   start <= 699692
|   |   |   |   |   |   |   |   start <= 690323
|   |   |   |   |   |   |   |   |   start <= 687637:
biological_process_ (31.13)
|   |   |   |   |   |   |   |   |   start > 687637:
RNA_metabolic_process_ (34.98)
|   |   |   |   |   |   |   |   start > 690323
|   |   |   |   |   |   |   |   |   start <= 695597
|   |   |   |   |   |   |   |   |   |   start <= 694049:
biological_process_ (26.43)
|   |   |   |   |   |   |   |   |   |   start > 694049:
ribosome_biogenesis_and_assembly_ (21.91)
|   |   |   |   |   |   |   |   |   start > 695597:
biological_process_ (26.58)
|   |   |   |   |   |   |   start > 699692
|   |   |   |   |   |   |   |   start <= 706141
|   |   |   |   |   |   |   |   |   start <= 703701
|   |   |   |   |   |   |   |   |   |   start <= 701897:
lipid_metabolic_process_ (14.22)
```

```
|   |   |   |   |   |   |   |   |   |   start > 701897: conjugation_
(20.65)
|   |   |   |   |   |   |   |   |   start > 703701: translation_
(28.56)
|   |   |   |   |   |   |   |   start > 706141
|   |   |   |   |   |   |   |   |   start <= 707790:
RNA_metabolic_process_ (15.61)
|   |   |   |   |   |   |   |   |   start > 707790
|   |   |   |   |   |   |   |   |   |   start <= 713657:
biological_process_ (65.59)
|   |   |   |   |   |   |   |   |   |   start > 713657:
RNA_metabolic_process_ (7.42/1.3)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 706141
|   |   |   |   |   |   |   start <= 690323
|   |   |   |   |   |   |   |   start <= 676179
|   |   |   |   |   |   |   |   |   start <= 672411
|   |   |   |   |   |   |   |   |   |   start <= 668379:
protein_modification_process_ (17.53)
|   |   |   |   |   |   |   |   |   |   start > 668379: translation_
(23.36)
|   |   |   |   |   |   |   |   |   start > 672411: vesicle-
mediated_transport_ (48.65/23.83)
|   |   |   |   |   |   |   |   start > 676179
|   |   |   |   |   |   |   |   |   start <= 686012
|   |   |   |   |   |   |   |   |   |   start <= 678801:
biological_process_ (27.68)
|   |   |   |   |   |   |   |   |   |   start > 678801:
response_to_stress_ (32.15)
|   |   |   |   |   |   |   |   |   start > 686012:
protein_modification_process_ (30.27)
|   |   |   |   |   |   |   start > 690323
|   |   |   |   |   |   |   |   start <= 694049:
cytoskeleton_organization_and_biogenesis_ (67.32/38.53)
|   |   |   |   |   |   |   |   start > 694049
|   |   |   |   |   |   |   |   |   start <= 695597: translation_
(39.07)
|   |   |   |   |   |   |   |   |   start > 695597
|   |   |   |   |   |   |   |   |   |   start <= 699692: transport_
(27.13)
|   |   |   |   |   |   |   |   |   |   start > 699692:
biological_process_ (29.41)
|   |   |   |   |   |   start > 706141
|   |   |   |   |   |   |   start <= 716122
|   |   |   |   |   |   |   |   start <= 713657: sporulation_
(56.89/25.79)
|   |   |   |   |   |   |   |   start > 713657:
amino_acid_and_derivative_metabolic_process_ (24.2)
|   |   |   |   |   |   |   start > 716122
|   |   |   |   |   |   |   |   start <= 718329:
protein_modification_process_ (24.05)
|   |   |   |   |   |   |   |   start > 718329
|   |   |   |   |   |   |   |   |   start <= 722212:
RNA_metabolic_process_ (24.27/3.08)
```

```
|   |   |   |   |   |   |   |   |   start > 722212:
ribosome_biogenesis_and_assembly_ (37.59)
|   |   |   |   start > 726218
|   |   |   |   |   start <= 739951
|   |   |   |   |   |   start <= 733303: transport_ (48.09)
|   |   |   |   |   |   start > 733303
|   |   |   |   |   |   |   start <= 734291:
vitamin_metabolic_process_ (36.23)
|   |   |   |   |   |   |   start > 734291
|   |   |   |   |   |   |   |   start <= 736803:
protein_modification_process_ (25.71)
|   |   |   |   |   |   |   |   start > 736803: transport_ (21.48)
|   |   |   |   |   start > 739951
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 772657
|   |   |   |   |   |   |   |   start <= 755035: biological_process_
(21.5)
|   |   |   |   |   |   |   |   start > 755035: transport_ (51.45)
|   |   |   |   |   |   |   start > 772657
|   |   |   |   |   |   |   |   start <= 779916: vesicle-
mediated_transport_ (25.03)
|   |   |   |   |   |   |   |   start > 779916: biological_process_
(8.68)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 776300
|   |   |   |   |   |   |   |   start <= 755035: biological_process_
(123.1)
|   |   |   |   |   |   |   |   start > 755035
|   |   |   |   |   |   |   |   |   start <= 759099: cytokinesis_
(23.33)
|   |   |   |   |   |   |   |   |   start > 759099:
biological_process_ (99.71)
|   |   |   |   |   |   |   start > 776300
|   |   |   |   |   |   |   |   start <= 779916: response_to_stress_
(28.75)
|   |   |   |   |   |   |   |   start > 779916: biological_process_
(21.45)
|   distance > 26345
|   |   start <= 576728
|   |   |   start <= 91994
|   |   |   |   strand = W: RNA_metabolic_process_ (38.87/13.81)
|   |   |   |   strand = C: DNA_metabolic_process_ (5.23/1.93)
|   |   |   start > 91994
|   |   |   |   start <= 302682
|   |   |   |   |   start <= 164624: translation_ (64.47)
|   |   |   |   |   start > 164624: RNA_metabolic_process_ (25.47)
|   |   |   |   start > 302682: translation_ (151.37)
|   |   start > 576728
|   |   |   start <= 593228
|   |   |   |   start <= 585588: ribosome_biogenesis_and_assembly_
(29.98)
|   |   |   |   start > 585588
|   |   |   |   |   neigh_strand = W: RNA_metabolic_process_
(18.73/4.69)
```

```
|   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   neigh_num <= 1: RNA_metabolic_process_
(17.17/5.07)
|   |   |   |   |   |   neigh_num > 1:
ribosome_biogenesis_and_assembly_ (7.08/1.89)
|   |   |   start > 593228
|   |   |   |   start <= 633858
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 622917
|   |   |   |   |   |   |   start <= 609687: translation_ (26.54)
|   |   |   |   |   |   |   start > 609687: transport_ (6.83/2.6)
|   |   |   |   |   |   start > 622917
|   |   |   |   |   |   |   start <= 627458
|   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
pseudohyphal_growth_ (5.78/0.59)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
translation_ (4.44/1.97)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
translation_ (6.69/3.14)
|   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
translation_ (5.98/3.38)
|   |   |   |   |   |   |   |   neigh_num > 1: meiosis_ (7.62/2.52)
|   |   |   |   |   |   |   start > 627458: translation_ (18.3)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 631063
|   |   |   |   |   |   |   start <= 627458
|   |   |   |   |   |   |   |   start <= 625831: transport_ (5.4)
|   |   |   |   |   |   |   |   start > 625831:
ribosome_biogenesis_and_assembly_ (7.23)
|   |   |   |   |   |   |   start > 627458: cellular_respiration_
(6.8/1.84)
|   |   |   |   |   |   start > 631063: translation_ (15.9/0.81)
|   |   |   |   start > 633858
|   |   |   |   |   start <= 723113
|   |   |   |   |   |   neigh_strand = W:
ribosome_biogenesis_and_assembly_ (43.72/14.62)
|   |   |   |   |   |   neigh_strand = C: RNA_metabolic_process_
(25.4/11.01)
|   |   |   |   |   start > 723113: translation_ (25.34/1.38)
```

Decision Tree Generated for Chromosome Fifteen:
For Cellular Component

```
start <= 104326
|   |   start <= 53097
|   |   |   start <= 40747
|   |   |   |   start <= 24293
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 6175: cellular_component_ (23.13)
|   |   |   |   |   |   start > 6175: membrane_ (22.91)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 17795
```

```
|   |   |   |   |   |   |   start <= 11910: cellular_component_
(26.35)
|   |   |   |   |   |   |   start > 11910
|   |   |   |   |   |   |   |   start <= 15504: cytoplasm_ (12.47)
|   |   |   |   |   |   |   |   start > 15504: cellular_component_
(13.83)
|   |   |   |   |   |   start > 17795
|   |   |   |   |   |   |   start <= 21310: cytoplasmic_membrane-
bound_vesicle_ (15.31)
|   |   |   |   |   |   |   start > 21310: cellular_component_
(17.15)
|   |   |   |   start > 24293
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 27083
|   |   |   |   |   |   |   start <= 25272: plasma_membrane_ (17.73)
|   |   |   |   |   |   |   start > 25272: cellular_component_
(11.01)
|   |   |   |   |   |   start > 27083
|   |   |   |   |   |   |   start <= 34657: cell_wall_ (14.65)
|   |   |   |   |   |   |   start > 34657: plasma_membrane_ (7.14)
|   |   |   |   |   strand = C: extracellular_region_ (14.6)
|   |   |   start > 40747
|   |   |   |   start <= 52787
|   |   |   |   |   start <= 44937
|   |   |   |   |   |   start <= 43693
|   |   |   |   |   |   |   neigh_strand = C: cytoplasm_ (8.34/3.08)
|   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(5.24/2.04)
|   |   |   |   |   |   |   |   neigh_num > 1: nucleus_ (9.06/2.03)
|   |   |   |   |   |   start > 43693: cytoplasm_ (15.36)
|   |   |   |   |   start > 44937
|   |   |   |   |   |   strand = W: cellular_component_
(63.87/41.52)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 47573: cellular_component_
(45.16/20.76)
|   |   |   |   |   |   |   start > 47573
|   |   |   |   |   |   |   |   start <= 48863: peroxisome_ (14.86)
|   |   |   |   |   |   |   |   start > 48863: nucleus_ (21.41)
|   |   |   |   start > 52787: nucleolus_ (20.37)
|   |   start > 53097
|   |   |   start <= 87844
|   |   |   |   start <= 58759
|   |   |   |   |   start <= 55557: nucleus_ (82.89/38.2)
|   |   |   |   |   start > 55557: mitochondrion_ (57.93/15.71)
|   |   |   |   start > 58759
|   |   |   |   |   start <= 65621
|   |   |   |   |   |   strand = W: cytoplasmic_membrane-
bound_vesicle_ (17.04)
|   |   |   |   |   |   strand = C: ribosome_ (70.08/30.09)
|   |   |   |   |   start > 65621
|   |   |   |   |   |   start <= 79479
|   |   |   |   |   |   |   start <= 70325
```

```
|   |   |   |   |   |   |   |   start <= 68754: cytoplasm_ (16.73)
|   |   |   |   |   |   |   |   start > 68754
|   |   |   |   |   |   |   |   |   start <= 70044: nucleus_
(30.42/14.42)
|   |   |   |   |   |   |   |   |   start > 70044
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(6.12/1.63)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cytoplasm_
(23.74/5.99)
|   |   |   |   |   |   |   start > 70325
|   |   |   |   |   |   |   |   start <= 71300: cell_wall_ (8.79)
|   |   |   |   |   |   |   |   start > 71300
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 74400
|   |   |   |   |   |   |   |   |   |   |   start <= 73031:
cellular_component_ (11.83)
|   |   |   |   |   |   |   |   |   |   |   start > 73031:
plasma_membrane_ (4.33)
|   |   |   |   |   |   |   |   |   |   start > 74400:
mitochondrion_ (13.72)
|   |   |   |   |   |   |   |   |   strand = C: cellular_component_
(20.5)
|   |   |   |   |   |   start > 79479
|   |   |   |   |   |   |   start <= 80348: ribosome_ (18.87)
|   |   |   |   |   |   |   start > 80348: cytoplasm_ (86.32/21.38)
|   |   |   start > 87844
|   |   |   |   strand = W
|   |   |   |   |   start <= 101475: nucleus_ (49.47)
|   |   |   |   |   start > 101475: plasma_membrane_ (23.57)
|   |   |   |   strand = C
|   |   |   |   |   start <= 94402
|   |   |   |   |   |   start <= 91419: plasma_membrane_ (23.83)
|   |   |   |   |   |   start > 91419: ribosome_ (30.79)
|   |   |   |   |   start > 94402
|   |   |   |   |   |   start <= 99809
|   |   |   |   |   |   |   neigh_num <= 1: membrane_ (11.87/2.58)
|   |   |   |   |   |   |   neigh_num > 1: vacuole_ (15.65/4.08)
|   |   |   |   |   |   start > 99809: cellular_component_ (26.07)
|   start > 104326
|   |   start <= 1043040
|   |   |   start <= 755010
|   |   |   |   start <= 679358
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 274958
|   |   |   |   |   |   |   start <= 124001
|   |   |   |   |   |   |   |   start <= 106710:
site_of_polarized_growth_ (45.5/20.53)
|   |   |   |   |   |   |   |   start > 106710
|   |   |   |   |   |   |   |   |   start <= 109176:
endoplasmic_reticulum_ (47.33/23.13)
|   |   |   |   |   |   |   |   |   start > 109176
|   |   |   |   |   |   |   |   |   |   start <= 111033:
mitochondrion_ (19.02)
```

```
|   |   |   |   |   |   |   |   |   |   start > 111033: membrane_
(52.65/32.04)
|   |   |   |   |   |   |   start > 124001
|   |   |   |   |   |   |   |   start <= 265430
|   |   |   |   |   |   |   |   |   start <= 228330
|   |   |   |   |   |   |   |   |   |   start <= 165714
|   |   |   |   |   |   |   |   |   |   |   start <= 147382:
cytoplasm_ (120.93/74.73)
|   |   |   |   |   |   |   |   |   |   |   start > 147382:
cellular_component_ (29.33/6.1)
|   |   |   |   |   |   |   |   |   |   start > 165714
|   |   |   |   |   |   |   |   |   |   |   start <= 196507
|   |   |   |   |   |   |   |   |   |   |   |   start <= 194970
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 187024:
cytoplasm_ (89.35/23.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 187024:
endomembrane_system_ (19.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 194970:
mitochondrion_ (18.18)
|   |   |   |   |   |   |   |   |   |   |   start > 196507
|   |   |   |   |   |   |   |   |   |   |   |   start <= 204471:
microtubule_organizing_center_ (20.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 204471:
cytoplasm_ (109.8/36.35)
|   |   |   |   |   |   |   |   |   start > 228330
|   |   |   |   |   |   |   |   |   |   start <= 238618
|   |   |   |   |   |   |   |   |   |   |   start <= 228613:
nucleus_ (15.29)
|   |   |   |   |   |   |   |   |   |   |   start > 228613:
cellular_component_ (94.07/42.22)
|   |   |   |   |   |   |   |   |   |   start > 238618
|   |   |   |   |   |   |   |   |   |   |   start <= 256744:
mitochondrion_ (116.17/62.74)
|   |   |   |   |   |   |   |   |   |   |   start > 256744
|   |   |   |   |   |   |   |   |   |   |   |   start <= 259490:
nucleolus_ (12.13)
|   |   |   |   |   |   |   |   |   |   |   |   start > 259490:
nucleus_ (65.62/25.07)
|   |   |   |   |   |   |   |   start > 265430
|   |   |   |   |   |   |   |   |   start <= 271371:
membrane_fraction_ (27.81)
|   |   |   |   |   |   |   |   |   start > 271371
|   |   |   |   |   |   |   |   |   |   start <= 274674: cytoplasm_
(20.49)
|   |   |   |   |   |   |   |   |   |   start > 274674:
mitochondrion_ (14.4)
|   |   |   |   |   |   start > 274958
|   |   |   |   |   |   |   start <= 307939
|   |   |   |   |   |   |   |   stop <= 303580
|   |   |   |   |   |   |   |   |   start <= 288899
|   |   |   |   |   |   |   |   |   |   start <= 278057
|   |   |   |   |   |   |   |   |   |   |   start <= 277087:
cellular_component_ (17.07)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 277087:
mitochondrion_ (19.65)
|   |   |   |   |   |   |   |   |   |   start > 278057
|   |   |   |   |   |   |   |   |   |   |   start <= 288193:
cytoplasm_ (45.2/17.87)
|   |   |   |   |   |   |   |   |   |   |   start > 288193
|   |   |   |   |   |   |   |   |   |   |   |   start <= 288421:
cellular_component_ (17.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 288421:
plasma_membrane_ (13.29)
|   |   |   |   |   |   |   |   |   start > 288899
|   |   |   |   |   |   |   |   |   |   start <= 301048:
cellular_component_ (73.07/14.62)
|   |   |   |   |   |   |   |   |   |   start > 301048: cytoplasm_
(17.29)
|   |   |   |   |   |   |   |   stop > 303580
|   |   |   |   |   |   |   |   |   start <= 305350:
plasma_membrane_ (38.15/17.21)
|   |   |   |   |   |   |   |   |   start > 305350: nucleolus_
(21.39)
|   |   |   |   |   |   |   start > 307939
|   |   |   |   |   |   |   |   start <= 632165
|   |   |   |   |   |   |   |   |   start <= 578565
|   |   |   |   |   |   |   |   |   |   start <= 449438
|   |   |   |   |   |   |   |   |   |   |   start <= 349679
|   |   |   |   |   |   |   |   |   |   |   |   start <= 312368:
mitochondrion_ (19.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 312368
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 326833:
cellular_component_ (69.08/31.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 326833:
mitochondrion_ (107.52/77.88)
|   |   |   |   |   |   |   |   |   |   |   start > 349679
|   |   |   |   |   |   |   |   |   |   |   |   start <= 356543:
cellular_component_ (26.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 356543
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 364369
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
357674: cytoplasm_ (19.25/7.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
357674
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
361412: mitochondrion_ (32.29/14.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
361412: plasma_membrane_ (18.41)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 364369
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
441536
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
379781: nucleus_ (69.06/35.36)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
379781
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 405768
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 389213: cytoplasm_ (50.14/14.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 389213: nucleus_ (66.53/46.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 405768
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 421651: mitochondrion_ (97.81/58.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 421651: cellular_component_ (51.66/12.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
441536
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
444688: ribosome_ (21.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
444688: cellular_component_ (55.68/27.57)
|   |   |   |   |   |   |   |   |   |   start > 449438
|   |   |   |   |   |   |   |   |   |   |   start <= 519122
|   |   |   |   |   |   |   |   |   |   |   |   start <= 482035
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 464773
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
464452: endomembrane_system_ (25.78/7.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
464452: nucleus_ (25.68/11.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 464773:
nucleus_ (195.82/159.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 482035
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 493434
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
487709: vacuole_ (33.21/16.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
487709: ribosome_ (34.41/15.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 493434
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
507506: cellular_bud_ (81.04/63.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
507506: plasma_membrane_ (73.58/55.34)
|   |   |   |   |   |   |   |   |   |   |   start > 519122
|   |   |   |   |   |   |   |   |   |   |   |   start <= 571959
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 530430:
cellular_component_ (89.5/59.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 530430
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
534076: cytoplasm_ (28.26/12.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
534076
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
545030: cellular_component_ (25.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
545030: cytoplasm_ (88.23/40.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 571959
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 573176:
endomembrane_system_ (10.18)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 573176:
ribosome_ (32.84/12.78)
|   |   |   |   |   |   |   |   |   start > 578565
|   |   |   |   |   |   |   |   |   |   start <= 612000:
mitochondrion_ (85.12/19.56)
|   |   |   |   |   |   |   |   |   |   start > 612000
|   |   |   |   |   |   |   |   |   |   |   start <= 619841:
plasma_membrane_ (33.57/9.46)
|   |   |   |   |   |   |   |   |   |   |   start > 619841
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 3078:
mitochondrion_ (22.07/6.69)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 3078:
cellular_component_ (12.81/0.86)
|   |   |   |   |   |   |   |   start > 632165
|   |   |   |   |   |   |   |   |   start <= 642742: nucleus_
(61.8/28.3)
|   |   |   |   |   |   |   |   |   start > 642742: cytoplasm_
(190.23/103.56)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 569559
|   |   |   |   |   |   |   start <= 356543
|   |   |   |   |   |   |   |   start <= 303036
|   |   |   |   |   |   |   |   |   start <= 271371
|   |   |   |   |   |   |   |   |   |   start <= 153490
|   |   |   |   |   |   |   |   |   |   |   start <= 111033:
cytoplasm_ (80.73/36.12)
|   |   |   |   |   |   |   |   |   |   |   start > 111033
|   |   |   |   |   |   |   |   |   |   |   |   start <= 126689:
nucleus_ (69.61/23.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 126689
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 137825:
cytoplasm_ (55.66/21.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 137825:
mitochondrion_ (71.94/24.32)
|   |   |   |   |   |   |   |   |   |   start > 153490
|   |   |   |   |   |   |   |   |   |   |   start <= 243496
|   |   |   |   |   |   |   |   |   |   |   |   start <= 210265
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 207176:
cytoplasm_ (244.44/154.59)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 207176:
cellular_component_ (21.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 210265
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 220766:
vacuole_ (47.38/28.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 220766:
cytoplasm_ (84.84/9.15)
|   |   |   |   |   |   |   |   |   |   |   start > 243496: nucleus_
(112.14/75.57)
|   |   |   |   |   |   |   |   |   start > 271371
|   |   |   |   |   |   |   |   |   |   start <= 288421
|   |   |   |   |   |   |   |   |   |   |   start <= 277087
|   |   |   |   |   |   |   |   |   |   |   |   start <= 273725:
mitochondrion_ (14.91)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 273725:
mitochondrial_envelope_ (10.36)
|   |   |   |   |   |   |   |   |   |   |   start > 277087
|   |   |   |   |   |   |   |   |   |   |   |   start <= 282165:
cytoplasm_ (26.94)
|   |   |   |   |   |   |   |   |   |   |   |   start > 282165:
mitochondrion_ (17.25)
|   |   |   |   |   |   |   |   |   |   start > 288421
|   |   |   |   |   |   |   |   |   |   |   start <= 292530:
Golgi_apparatus_ (20.25)
|   |   |   |   |   |   |   |   |   |   |   start > 292530
|   |   |   |   |   |   |   |   |   |   |   |   start <= 297079:
cytoplasm_ (15.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 297079:
membrane_ (28.6/17.47)
|   |   |   |   |   |   |   |   start > 303036
|   |   |   |   |   |   |   |   |   start <= 337344
|   |   |   |   |   |   |   |   |   |   start <= 310313
|   |   |   |   |   |   |   |   |   |   |   start <= 305350:
chromosome_ (32.56/10.87)
|   |   |   |   |   |   |   |   |   |   |   start > 305350:
mitochondrion_ (15.08)
|   |   |   |   |   |   |   |   |   |   start > 310313
|   |   |   |   |   |   |   |   |   |   |   start <= 312368:
site_of_polarized_growth_ (37.29/15.16)
|   |   |   |   |   |   |   |   |   |   |   start > 312368
|   |   |   |   |   |   |   |   |   |   |   |   start <= 316939:
nucleus_ (57.18/14.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 316939:
plasma_membrane_ (58.83/43.67)
|   |   |   |   |   |   |   |   |   start > 337344: cytoplasm_
(106.36/48.54)
|   |   |   |   |   |   |   start > 356543
|   |   |   |   |   |   |   |   start <= 375857
|   |   |   |   |   |   |   |   |   start <= 364369: membrane_
(12.14)
|   |   |   |   |   |   |   |   |   start > 364369: mitochondrion_
(47.89/15.7)
|   |   |   |   |   |   |   |   start > 375857
|   |   |   |   |   |   |   |   |   start <= 449438
|   |   |   |   |   |   |   |   |   |   start <= 410870
|   |   |   |   |   |   |   |   |   |   |   start <= 397668
|   |   |   |   |   |   |   |   |   |   |   |   start <= 394524:
nucleus_ (93.74/32.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 394524:
cellular_component_ (28.62)
|   |   |   |   |   |   |   |   |   |   |   start > 397668:
nucleolus_ (52.98/26.63)
|   |   |   |   |   |   |   |   |   |   start > 410870: nucleus_
(398.93/209.07)
|   |   |   |   |   |   |   |   |   start > 449438
|   |   |   |   |   |   |   |   |   |   start <= 495128
|   |   |   |   |   |   |   |   |   |   |   start <= 482035
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 461278:
membrane_ (133.71/81.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 461278:
cytoplasm_ (74.32/29.85)
|   |   |   |   |   |   |   |   |   |   |   start > 482035:
mitochondrion_ (52.91)
|   |   |   |   |   |   |   |   |   |   start > 495128
|   |   |   |   |   |   |   |   |   |   |   start <= 551115:
nucleus_ (238.48/159.78)
|   |   |   |   |   |   |   |   |   |   |   start > 551115
|   |   |   |   |   |   |   |   |   |   |   |   start <= 554571:
nucleus_ (79.35/57.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 554571:
cytoplasm_ (93.62/39.66)
|   |   |   |   |   |   start > 569559
|   |   |   |   |   |   |   start <= 570808: mitochondrial_envelope_
(21.62)
|   |   |   |   |   |   |   start > 570808
|   |   |   |   |   |   |   |   start <= 648503
|   |   |   |   |   |   |   |   |   distance <= 5303: nucleus_
(396.36/238.99)
|   |   |   |   |   |   |   |   |   distance > 5303:
cellular_component_ (33.19/17.65)
|   |   |   |   |   |   |   |   start > 648503
|   |   |   |   |   |   |   |   |   start <= 662402
|   |   |   |   |   |   |   |   |   |   start <= 649304: ribosome_
(14.52)
|   |   |   |   |   |   |   |   |   |   start > 649304:
endoplasmic_reticulum_ (111.88/66.72)
|   |   |   |   |   |   |   |   |   start > 662402
|   |   |   |   |   |   |   |   |   |   start <= 672412: cytoplasm_
(43.92/22.28)
|   |   |   |   |   |   |   |   |   |   start > 672412: peroxisome_
(34.48/15.1)
|   |   |   |   start > 679358
|   |   |   |   |   start <= 741570
|   |   |   |   |   |   start <= 722912
|   |   |   |   |   |   |   start <= 700568
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 685768
|   |   |   |   |   |   |   |   |   |   start <= 683112:
cellular_component_ (8.13)
|   |   |   |   |   |   |   |   |   |   start > 683112:
mitochondrion_ (34.82)
|   |   |   |   |   |   |   |   |   start > 685768
|   |   |   |   |   |   |   |   |   |   start <= 690696
|   |   |   |   |   |   |   |   |   |   |   start <= 689625:
nucleus_ (19.41)
|   |   |   |   |   |   |   |   |   |   |   start > 689625:
cell_wall_ (11.73)
|   |   |   |   |   |   |   |   |   |   start > 690696: nucleus_
(29.1/11.29)
|   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   start <= 680867: nucleolus_
(19.59)
|   |   |   |   |   |   |   |   |   start > 680867
|   |   |   |   |   |   |   |   |   |   start <= 690696: nucleus_
(12.63)
|   |   |   |   |   |   |   |   |   |   start > 690696: membrane_
(9.45)
|   |   |   |   |   |   |   start > 700568
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 710447
|   |   |   |   |   |   |   |   |   |   start <= 710202: cytoplasm_
(15.03)
|   |   |   |   |   |   |   |   |   |   start > 710202: peroxisome_
(16.76)
|   |   |   |   |   |   |   |   |   start > 710447
|   |   |   |   |   |   |   |   |   |   start <= 712867: chromosome_
(28.72/13.18)
|   |   |   |   |   |   |   |   |   |   start > 712867
|   |   |   |   |   |   |   |   |   |   |   start <= 721947
|   |   |   |   |   |   |   |   |   |   |   |   start <= 717087:
nucleus_ (8.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 717087:
cellular_component_ (13.66)
|   |   |   |   |   |   |   |   |   |   |   start > 721947:
cytoplasm_ (9.86)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 712867
|   |   |   |   |   |   |   |   |   |   start <= 704225:
cellular_component_ (8.83)
|   |   |   |   |   |   |   |   |   |   start > 704225
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cellular_component_ (11.65/4.99)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cellular_component_ (6.6/1.12)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
nucleus_ (12.49/4.03)
|   |   |   |   |   |   |   |   |   start > 712867
|   |   |   |   |   |   |   |   |   |   start <= 717087:
mitochondrion_ (18.58)
|   |   |   |   |   |   |   |   |   |   start > 717087
|   |   |   |   |   |   |   |   |   |   |   start <= 720066:
endomembrane_system_ (15.4)
|   |   |   |   |   |   |   |   |   |   |   start > 720066:
mitochondrion_ (15.75)
|   |   |   |   |   |   start > 722912
|   |   |   |   |   |   |   start <= 737727
|   |   |   |   |   |   |   |   start <= 727513: mitochondrion_
(49.68/15.64)
|   |   |   |   |   |   |   |   start > 727513: nucleus_ (52.24)
|   |   |   |   |   |   |   start > 737727
|   |   |   |   |   |   |   |   start <= 738321: nucleolus_ (24.0)
|   |   |   |   |   |   |   |   start > 738321: mitochondrion_
(16.25)
|   |   |   |   |   start > 741570
```

```
|   |   |   |   |   |   start <= 746304
|   |   |   |   |   |   |   strand = W: plasma_membrane_ (7.57)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 745282: nucleus_
(28.72/12.03)
|   |   |   |   |   |   |   |   start > 745282: cell_wall_ (22.6)
|   |   |   |   |   |   start > 746304
|   |   |   |   |   |   |   strand = W: chromosome_ (18.71)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 747283: mitochondrion_
(15.09)
|   |   |   |   |   |   |   |   start > 747283: Golgi_apparatus_
(36.62)
|   |   |   start > 755010
|   |   |   |   start <= 826384
|   |   |   |   |   start <= 780108
|   |   |   |   |   |   start <= 767778
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 755329: cytoplasm_ (17.2)
|   |   |   |   |   |   |   |   start > 755329
|   |   |   |   |   |   |   |   |   start <= 761266
|   |   |   |   |   |   |   |   |   |   start <= 758331:
mitochondrion_ (17.07)
|   |   |   |   |   |   |   |   |   |   start > 758331:
cellular_component_ (20.09)
|   |   |   |   |   |   |   |   |   start > 761266
|   |   |   |   |   |   |   |   |   |   distance <= 2733: cytoplasm_
(15.68/8.73)
|   |   |   |   |   |   |   |   |   |   distance > 2733
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cytoplasm_ (4.39/0.73)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
mitochondrion_ (7.17/1.9)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
mitochondrion_ (14.24/5.27)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 761266
|   |   |   |   |   |   |   |   |   start <= 758331: mitochondrion_
(16.75)
|   |   |   |   |   |   |   |   |   start > 758331: nucleolus_
(32.49)
|   |   |   |   |   |   |   |   start > 761266: mitochondrion_
(26.94)
|   |   |   |   |   |   start > 767778
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 772602
|   |   |   |   |   |   |   |   |   start <= 770801: nucleus_
(31.38)
|   |   |   |   |   |   |   |   |   start > 770801: cellular_bud_
(30.27/10.37)
|   |   |   |   |   |   |   |   start > 772602
|   |   |   |   |   |   |   |   |   start <= 775847
```

```
|   |   |   |   |   |   |   |   |   |   start <= 774574:
mitochondrion_ (11.36)
|   |   |   |   |   |   |   |   |   |   start > 774574: cell_cortex_
(10.62)
|   |   |   |   |   |   |   |   |   start > 775847: nucleolus_
(12.54)
|   |   |   |   |   |   |   strand = C: ribosome_ (13.31)
|   |   |   |   |   start > 780108
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 811008
|   |   |   |   |   |   |   |   start <= 797677
|   |   |   |   |   |   |   |   |   start <= 786996
|   |   |   |   |   |   |   |   |   |   start <= 783678
|   |   |   |   |   |   |   |   |   |   |   start <= 780907:
cytoplasm_ (17.08)
|   |   |   |   |   |   |   |   |   |   |   start > 780907
|   |   |   |   |   |   |   |   |   |   |   |   start <= 781995:
cellular_component_ (8.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 781995:
cytoplasm_ (11.89)
|   |   |   |   |   |   |   |   |   |   start > 783678
|   |   |   |   |   |   |   |   |   |   |   start <= 784858:
cytoskeleton_ (13.72)
|   |   |   |   |   |   |   |   |   |   |   start > 784858:
mitochondrion_ (27.97/13.92)
|   |   |   |   |   |   |   |   |   start > 786996
|   |   |   |   |   |   |   |   |   |   start <= 792532:
cellular_component_ (33.87/15.72)
|   |   |   |   |   |   |   |   |   |   start > 792532: cytoplasm_
(12.21)
|   |   |   |   |   |   |   |   start > 797677
|   |   |   |   |   |   |   |   |   start <= 807272
|   |   |   |   |   |   |   |   |   |   start <= 804378: ribosome_
(36.83/8.06)
|   |   |   |   |   |   |   |   |   |   start > 804378: membrane_
(11.95)
|   |   |   |   |   |   |   |   |   start > 807272:
microtubule_organizing_center_ (39.65/13.87)
|   |   |   |   |   |   |   start > 811008
|   |   |   |   |   |   |   |   start <= 817291: cytoplasm_
(76.49/18.78)
|   |   |   |   |   |   |   |   start > 817291
|   |   |   |   |   |   |   |   |   start <= 818865: cellular_bud_
(28.71/11.39)
|   |   |   |   |   |   |   |   |   start > 818865
|   |   |   |   |   |   |   |   |   |   start <= 821022
|   |   |   |   |   |   |   |   |   |   |   start <= 820453:
cytoplasm_ (17.22)
|   |   |   |   |   |   |   |   |   |   |   start > 820453:
mitochondrion_ (13.27)
|   |   |   |   |   |   |   |   |   |   start > 821022: cytoplasm_
(35.57/15.47)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 800732
```

```
|   |   |   |   |   |   |   |   start <= 789858: cell_wall_ (14.91)
|   |   |   |   |   |   |   |   start > 789858
|   |   |   |   |   |   |   |   |   start <= 797677
|   |   |   |   |   |   |   |   |   |   start <= 792532: nucleus_
(21.01)
|   |   |   |   |   |   |   |   |   |   start > 792532: cytoplasm_
(29.79)
|   |   |   |   |   |   |   |   |   start > 797677: nucleus_ (27.88)
|   |   |   |   |   |   |   start > 800732
|   |   |   |   |   |   |   |   start <= 807272
|   |   |   |   |   |   |   |   |   start <= 802308:
cellular_component_ (21.94/8.2)
|   |   |   |   |   |   |   |   |   start > 802308
|   |   |   |   |   |   |   |   |   |   start <= 804378: cytoplasm_
(22.9)
|   |   |   |   |   |   |   |   |   |   start > 804378:
mitochondrion_ (20.26)
|   |   |   |   |   |   |   |   start > 807272
|   |   |   |   |   |   |   |   |   start <= 820453
|   |   |   |   |   |   |   |   |   |   start <= 813984
|   |   |   |   |   |   |   |   |   |   |   start <= 811671:
cellular_component_ (17.04)
|   |   |   |   |   |   |   |   |   |   |   start > 811671: nucleus_
(13.37)
|   |   |   |   |   |   |   |   |   |   start > 813984:
cellular_component_ (17.23)
|   |   |   |   |   |   |   |   |   start > 820453
|   |   |   |   |   |   |   |   |   |   start <= 824866: cytoplasm_
(17.04)
|   |   |   |   |   |   |   |   |   |   start > 824866:
cellular_component_ (17.07)
|   |   |   |   start > 826384
|   |   |   |   |   start <= 960984
|   |   |   |   |   |   start <= 877684
|   |   |   |   |   |   |   start <= 837673
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 832331: nucleolus_
(14.09)
|   |   |   |   |   |   |   |   |   start > 832331
|   |   |   |   |   |   |   |   |   |   distance <= 1506: nucleus_
(24.35/7.16)
|   |   |   |   |   |   |   |   |   |   distance > 1506: nucleolus_
(66.45/36.51)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 832812
|   |   |   |   |   |   |   |   |   |   start <= 830573: vacuole_
(15.65)
|   |   |   |   |   |   |   |   |   |   start > 830573:
mitochondrion_ (13.3)
|   |   |   |   |   |   |   |   |   start > 832812: plasma_membrane_
(26.86)
|   |   |   |   |   |   |   start > 837673
|   |   |   |   |   |   |   |   start <= 848477
|   |   |   |   |   |   |   |   |   start <= 845791
```

```
|   |   |   |   |   |   |   |   |   |   start <= 841068: cytoplasm_
(34.74/12.68)
|   |   |   |   |   |   |   |   |   |   start > 841068
|   |   |   |   |   |   |   |   |   |   |   start <= 842402
|   |   |   |   |   |   |   |   |   |   |   |   start <= 841332:
cellular_component_ (23.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 841332:
nucleolus_ (29.06)
|   |   |   |   |   |   |   |   |   |   |   start > 842402
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (16.81)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 844629:
nucleus_ (14.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 844629:
cellular_component_ (15.87)
|   |   |   |   |   |   |   |   |   start > 845791: cytoplasm_
(61.68/14.4)
|   |   |   |   |   |   |   |   start > 848477
|   |   |   |   |   |   |   |   |   start <= 850279: mitochondrion_
(58.05/12.11)
|   |   |   |   |   |   |   |   |   start > 850279
|   |   |   |   |   |   |   |   |   |   start <= 870201
|   |   |   |   |   |   |   |   |   |   |   start <= 868339
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 854258:
nucleus_ (31.26/13.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 854258
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
861174: membrane_ (17.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
861174
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
867097: ribosome_ (13.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
867097: nucleus_ (13.71)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 851838:
cellular_component_ (17.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 851838
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
854258
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
853356: vacuole_ (19.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
853356: cytoplasm_ (15.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
854258
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
861174: nucleus_ (18.71/8.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
861174
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 867097: vacuole_ (13.19)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 867097: cellular_component_ (11.69)
|   |   |   |   |   |   |   |   |   |   |   start > 868339
|   |   |   |   |   |   |   |   |   |   |   |   start <= 869207:
nucleolus_ (16.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 869207:
cytoplasm_ (14.61)
|   |   |   |   |   |   |   |   |   |   start > 870201
|   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (13.63)
|   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (70.05/19.77)
|   |   |   |   |   |   start > 877684
|   |   |   |   |   |   |   start <= 931800
|   |   |   |   |   |   |   |   start <= 888748
|   |   |   |   |   |   |   |   |   start <= 880963
|   |   |   |   |   |   |   |   |   |   start <= 878433:
cytoplasmic_membrane-bound_vesicle_ (11.31)
|   |   |   |   |   |   |   |   |   |   start > 878433
|   |   |   |   |   |   |   |   |   |   |   distance <= 1027:
cellular_bud_ (7.75/2.0)
|   |   |   |   |   |   |   |   |   |   |   distance > 1027:
site_of_polarized_growth_ (16.99/4.5)
|   |   |   |   |   |   |   |   |   start > 880963
|   |   |   |   |   |   |   |   |   |   start <= 882897: cytoplasm_
(44.23)
|   |   |   |   |   |   |   |   |   |   start > 882897
|   |   |   |   |   |   |   |   |   |   |   start <= 884512:
nucleus_ (20.71)
|   |   |   |   |   |   |   |   |   |   |   start > 884512:
cytoplasm_ (39.95/13.97)
|   |   |   |   |   |   |   |   start > 888748
|   |   |   |   |   |   |   |   |   start <= 925037
|   |   |   |   |   |   |   |   |   |   start <= 901191
|   |   |   |   |   |   |   |   |   |   |   strand = W:
mitochondrion_ (10.18)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 898357
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 894089
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
891430: plasma_membrane_ (12.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
891430: endoplasmic_reticulum_ (14.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 894089
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
896384: nucleus_ (12.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
896384: nucleolus_ (16.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 898357
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 899925
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: membrane_ (6.7/2.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: endoplasmic_reticulum_ (22.07/6.67)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 899925:
ribosome_ (14.71)
|   |   |   |   |   |   |   |   |   |   start > 901191
|   |   |   |   |   |   |   |   |   |   |   start <= 912819
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 904757
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: nucleus_ (13.82/3.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: cytoplasm_ (10.2/3.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 904757
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
909340: mitochondrion_ (9.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
909340: nucleus_ (15.12)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 907552
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
904757: cellular_component_ (8.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
904757: mitochondrion_ (8.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 907552:
cellular_component_ (13.01)
|   |   |   |   |   |   |   |   |   |   |   start > 912819
|   |   |   |   |   |   |   |   |   |   |   |   start <= 915091:
Golgi_apparatus_ (19.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 915091
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
endoplasmic_reticulum_ (16.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
922902
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
921059: cytoplasm_ (13.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
921059
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: nucleus_ (17.72/7.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: cytoplasm_ (13.98/4.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
922902: endoplasmic_reticulum_ (8.88)
|   |   |   |   |   |   |   |   |   start > 925037
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 925718:
site_of_polarized_growth_ (29.28/12.55)
|   |   |   |   |   |   |   |   |   |   |   start > 925718:
plasma_membrane_ (18.03)
|   |   |   |   |   |   |   |   |   |   strand = C:
cytoplasmic_membrane-bound_vesicle_ (10.67)
|   |   |   |   |   |   |   |   start > 931800
|   |   |   |   |   |   |   |   |   start <= 949106
|   |   |   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   |   start <= 943653: vacuole_
(38.99/13.51)
|   |   |   |   |   |   |   |   |   |   start > 943653:
mitochondrion_ (11.41)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 939346:
membrane_fraction_ (14.23)
|   |   |   |   |   |   |   |   |   |   start > 939346:
mitochondrion_ (45.58/12.82)
|   |   |   |   |   |   |   |   start > 949106
|   |   |   |   |   |   |   |   |   start <= 956895
|   |   |   |   |   |   |   |   |   |   start <= 954341
|   |   |   |   |   |   |   |   |   |   |   start <= 949770:
endoplasmic_reticulum_ (7.01)
|   |   |   |   |   |   |   |   |   |   |   start > 949770: nucleus_
(16.2)
|   |   |   |   |   |   |   |   |   |   start > 954341:
cellular_component_ (16.46)
|   |   |   |   |   |   |   |   |   start > 956895
|   |   |   |   |   |   |   |   |   |   start <= 958829: cytoplasm_
(15.87)
|   |   |   |   |   |   |   |   |   |   start > 958829: nucleolus_
(38.02)
|   |   |   |   |   start > 960984
|   |   |   |   |   |   start <= 1025570
|   |   |   |   |   |   |   start <= 1017650
|   |   |   |   |   |   |   |   start <= 996508
|   |   |   |   |   |   |   |   |   start <= 980680
|   |   |   |   |   |   |   |   |   |   strand = W: cytoplasm_
(18.5)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 967622:
cytoplasm_ (18.0/7.28)
|   |   |   |   |   |   |   |   |   |   |   start > 967622: nucleus_
(20.55)
|   |   |   |   |   |   |   |   |   start > 980680
|   |   |   |   |   |   |   |   |   |   start <= 994852
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 981825
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: nucleus_ (6.82/1.89)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: mitochondrion_ (6.19/1.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: nucleus_ (6.44/2.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 981825:
cellular_component_ (18.11)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 989786
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 986459:
mitochondrion_ (15.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 986459:
plasma_membrane_ (16.69)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 989786:
mitochondrion_ (17.83)
|   |   |   |   |   |   |   |   |   |   start > 994852: nucleus_
(15.46)
|   |   |   |   |   |   |   |   start > 996508
|   |   |   |   |   |   |   |   |   start <= 1000825: cytoplasm_
(70.22/32.03)
|   |   |   |   |   |   |   |   |   start > 1000825
|   |   |   |   |   |   |   |   |   |   start <= 1007219
|   |   |   |   |   |   |   |   |   |   |   start <= 1005135
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1003222:
mitochondrion_ (11.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1003222:
nucleus_ (38.12/22.98)
|   |   |   |   |   |   |   |   |   |   |   start > 1005135:
mitochondrion_ (24.69)
|   |   |   |   |   |   |   |   |   |   start > 1007219
|   |   |   |   |   |   |   |   |   |   |   start <= 1009710:
cytoplasm_ (15.41)
|   |   |   |   |   |   |   |   |   |   |   start > 1009710
|   |   |   |   |   |   |   |   |   |   |   |   start <= 1010159:
nucleus_ (16.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 1010159
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cytoplasm_ (14.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
1014819: nucleus_ (26.08/10.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
1014819: cytoplasm_ (12.91)
|   |   |   |   |   |   |   start > 1017650
|   |   |   |   |   |   |   |   start <= 1023210
|   |   |   |   |   |   |   |   |   start <= 1018744:
cellular_component_ (10.55)
|   |   |   |   |   |   |   |   |   start > 1018744: nucleus_ (7.71)
|   |   |   |   |   |   |   |   start > 1023210: cellular_component_
(14.87)
|   |   |   |   |   |   start > 1025570
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 1030992
|   |   |   |   |   |   |   |   |   start <= 1026005
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
cell_cortex_ (8.34/2.74)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cell_cortex_ (10.03/2.85)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cytoskeleton_ (11.52/3.66)
|   |   |   |   |   |   |   |   |   start > 1026005: nucleus_
(12.95)
|   |   |   |   |   |   |   |   start > 1030992
|   |   |   |   |   |   |   |   |   start <= 1036832:
microtubule_organizing_center_ (15.63)
|   |   |   |   |   |   |   |   |   start > 1036832: mitochondrion_
(20.24)
```

```
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 1034180
|   |   |   |   |   |   |   |   |   start <= 1028623: ribosome_
(17.13)
|   |   |   |   |   |   |   |   |   start > 1028623: cytoplasm_
(86.2/39.66)
|   |   |   |   |   |   |   |   start > 1034180: nucleus_
(53.52/14.7)
|   |   start > 1043040
|   |   |   start <= 1066837
|   |   |   |   start <= 1058421
|   |   |   |   |   start <= 1049509
|   |   |   |   |   |   start <= 1045194: cellular_component_
(14.49)
|   |   |   |   |   |   start > 1045194
|   |   |   |   |   |   |   start <= 1046224: endomembrane_system_
(13.1)
|   |   |   |   |   |   |   start > 1046224: cellular_component_
(13.26)
|   |   |   |   |   start > 1049509
|   |   |   |   |   |   start <= 1055543
|   |   |   |   |   |   |   start <= 1051288: nucleus_ (12.7)
|   |   |   |   |   |   |   start > 1051288: plasma_membrane_
(22.64)
|   |   |   |   |   |   start > 1055543: cellular_component_ (13.67)
|   |   |   |   start > 1058421
|   |   |   |   |   start <= 1061053: cell_wall_ (28.44)
|   |   |   |   |   start > 1061053
|   |   |   |   |   |   start <= 1065041
|   |   |   |   |   |   |   start <= 1061562: mitochondrion_ (22.92)
|   |   |   |   |   |   |   start > 1061562: cytoplasm_ (11.24)
|   |   |   |   |   |   start > 1065041: mitochondrion_
(34.92/15.86)
|   |   |   start > 1066837
|   |   |   |   start <= 1072921
|   |   |   |   |   start <= 1070239: cellular_component_ (19.73)
|   |   |   |   |   start > 1070239: cytoplasm_ (9.86)
|   |   |   |   start > 1072921: cellular_component_ (103.76)
```

For Molecular Function

```
|   start <= 1017650
|   |   start <= 160594
|   |   |   start <= 43693
|   |   |   |   start <= 34657
|   |   |   |   |   start <= 6175
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 4130: molecular_function_
(12.95)
|   |   |   |   |   |   |   start > 4130: hydrolase_activity_
(14.81)
|   |   |   |   |   |   strand = C: oxidoreductase_activity_ (12.96)
|   |   |   |   |   start > 6175
|   |   |   |   |   |   start <= 10118: transporter_activity_ (29.9)
```

```
|   |   |   |   |   |   start > 10118
|   |   |   |   |   |   |   start <= 27083
|   |   |   |   |   |   |   |   start <= 17795: molecular_function_
(35.23)
|   |   |   |   |   |   |   |   start > 17795
|   |   |   |   |   |   |   |   |   start <= 21310:
transporter_activity_ (13.76)
|   |   |   |   |   |   |   |   |   start > 21310
|   |   |   |   |   |   |   |   |   |   start <= 25272
|   |   |   |   |   |   |   |   |   |   |   start <= 24293:
molecular_function_ (15.65)
|   |   |   |   |   |   |   |   |   |   |   start > 24293:
transporter_activity_ (10.25)
|   |   |   |   |   |   |   |   |   |   start > 25272:
molecular_function_ (17.65)
|   |   |   |   |   |   |   start > 27083
|   |   |   |   |   |   |   |   start <= 31605: hydrolase_activity_
(12.86)
|   |   |   |   |   |   |   |   start > 31605: molecular_function_
(9.44)
|   |   |   |   start > 34657: oxidoreductase_activity_ (34.88)
|   |   |   start > 43693
|   |   |   |   start <= 136220
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 97551
|   |   |   |   |   |   |   start <= 44937:
enzyme_regulator_activity_ (32.41/12.56)
|   |   |   |   |   |   |   start > 44937
|   |   |   |   |   |   |   |   start <= 53097: molecular_function_
(46.71)
|   |   |   |   |   |   |   |   start > 53097
|   |   |   |   |   |   |   |   |   start <= 61024
|   |   |   |   |   |   |   |   |   |   start <= 55557: RNA_binding_
(21.55)
|   |   |   |   |   |   |   |   |   |   start > 55557:
transferase_activity_ (40.23)
|   |   |   |   |   |   |   |   |   start > 61024
|   |   |   |   |   |   |   |   |   |   start <= 77560
|   |   |   |   |   |   |   |   |   |   |   start <= 70325:
molecular_function_ (35.41)
|   |   |   |   |   |   |   |   |   |   |   start > 70325
|   |   |   |   |   |   |   |   |   |   |   |   start <= 71300:
transferase_activity_ (10.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 71300
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 74400
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
73031: molecular_function_ (9.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
73031: transporter_activity_ (6.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 74400:
molecular_function_ (12.15)
|   |   |   |   |   |   |   |   |   |   start > 77560
|   |   |   |   |   |   |   |   |   |   |   start <= 91419
|   |   |   |   |   |   |   |   |   |   |   |   start <= 83834
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 80348:
RNA_binding_ (12.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 80348:
transferase_activity_ (7.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 83834:
RNA_binding_ (21.71)
|   |   |   |   |   |   |   |   |   |   |   start > 91419:
molecular_function_ (14.34)
|   |   |   |   |   |   start > 97551
|   |   |   |   |   |   |   start <= 109176
|   |   |   |   |   |   |   |   start <= 104326
|   |   |   |   |   |   |   |   |   start <= 101475
|   |   |   |   |   |   |   |   |   |   start <= 99809:
transcription_regulator_activity_ (18.71)
|   |   |   |   |   |   |   |   |   |   start > 99809:
nucleotidyltransferase_activity_ (19.19)
|   |   |   |   |   |   |   |   |   start > 101475:
protein_kinase_activity_ (19.64)
|   |   |   |   |   |   |   |   start > 104326
|   |   |   |   |   |   |   |   |   start <= 106710:
enzyme_regulator_activity_ (33.96)
|   |   |   |   |   |   |   |   |   start > 106710:
transferase_activity_ (17.97)
|   |   |   |   |   |   |   start > 109176
|   |   |   |   |   |   |   |   start <= 117454: molecular_function_
(57.4)
|   |   |   |   |   |   |   |   start > 117454
|   |   |   |   |   |   |   |   |   start <= 124001:
transporter_activity_ (21.76)
|   |   |   |   |   |   |   |   |   start > 124001
|   |   |   |   |   |   |   |   |   |   start <= 129237:
protein_kinase_activity_ (17.13)
|   |   |   |   |   |   |   |   |   |   start > 129237:
molecular_function_ (13.68)
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 83834
|   |   |   |   |   |   |   start <= 65621
|   |   |   |   |   |   |   |   start <= 53097
|   |   |   |   |   |   |   |   |   start <= 48863
|   |   |   |   |   |   |   |   |   |   start <= 47573:
transcription_regulator_activity_ (18.66)
|   |   |   |   |   |   |   |   |   |   start > 47573:
molecular_function_ (19.33)
|   |   |   |   |   |   |   |   |   start > 48863
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
transcription_regulator_activity_ (16.36/6.95)
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_binding_ (12.17/4.98)
|   |   |   |   |   |   |   |   start > 53097
|   |   |   |   |   |   |   |   |   start <= 56451:
isomerase_activity_ (19.7)
|   |   |   |   |   |   |   |   |   start > 56451
|   |   |   |   |   |   |   |   |   |   start <= 61024:
translation_regulator_activity_ (13.06)
```

```
|   |   |   |   |   |   |   |   |   |   start > 61024:
molecular_function_ (18.21)
|   |   |   |   |   |   |   start > 65621
|   |   |   |   |   |   |   |   start <= 74400
|   |   |   |   |   |   |   |   |   start <= 68754:
transferase_activity_ (17.4)
|   |   |   |   |   |   |   |   |   start > 68754:
transcription_regulator_activity_ (8.92)
|   |   |   |   |   |   |   |   start > 74400
|   |   |   |   |   |   |   |   |   start <= 80348:
protein_kinase_activity_ (12.9)
|   |   |   |   |   |   |   |   |   start > 80348:
oxidoreductase_activity_ (13.12)
|   |   |   |   |   |   start > 83834
|   |   |   |   |   |   |   start <= 99809
|   |   |   |   |   |   |   |   start <= 87844: RNA_binding_ (8.02)
|   |   |   |   |   |   |   |   start > 87844
|   |   |   |   |   |   |   |   |   start <= 91419:
transporter_activity_ (17.68)
|   |   |   |   |   |   |   |   |   start > 91419
|   |   |   |   |   |   |   |   |   |   start <= 94402:
structural_molecule_activity_ (23.91)
|   |   |   |   |   |   |   |   |   |   start > 94402:
transporter_activity_ (11.88)
|   |   |   |   |   |   |   start > 99809
|   |   |   |   |   |   |   |   start <= 135838
|   |   |   |   |   |   |   |   |   start <= 111033:
molecular_function_ (73.34)
|   |   |   |   |   |   |   |   |   start > 111033
|   |   |   |   |   |   |   |   |   |   start <= 126689
|   |   |   |   |   |   |   |   |   |   |   start <= 117454
|   |   |   |   |   |   |   |   |   |   |   |   start <= 113802:
DNA_binding_ (12.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 113802
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 115808:
signal_transducer_activity_ (11.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 115808:
DNA_binding_ (8.01)
|   |   |   |   |   |   |   |   |   |   |   start > 117454:
transferase_activity_ (16.35)
|   |   |   |   |   |   |   |   |   |   start > 126689:
molecular_function_ (36.64)
|   |   |   |   |   |   |   |   start > 135838: RNA_binding_ (14.32)
|   |   |   |   start > 136220
|   |   |   |   |   start <= 142815
|   |   |   |   |   |   start <= 137825: ligase_activity_ (12.1)
|   |   |   |   |   |   start > 137825
|   |   |   |   |   |   |   start <= 141347
|   |   |   |   |   |   |   |   start <= 139045:
transferase_activity_ (18.75)
|   |   |   |   |   |   |   |   start > 139045: helicase_activity_
(15.26)
|   |   |   |   |   |   |   start > 141347
```

```
|   |   |   |   |   |   |   |   start <= 142555: DNA_binding_
(20.19)
|   |   |   |   |   |   |   |   start > 142555:
transferase_activity_ (16.85)
|   |   |   |   |   start > 142815
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 145334
|   |   |   |   |   |   |   |   start <= 144204: molecular_function_
(17.61)
|   |   |   |   |   |   |   |   start > 144204:
structural_molecule_activity_ (13.3)
|   |   |   |   |   |   |   start > 145334
|   |   |   |   |   |   |   |   start <= 147382: DNA_binding_
(18.52)
|   |   |   |   |   |   |   |   start > 147382: molecular_function_
(10.28)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 153490:
transcription_regulator_activity_ (16.95)
|   |   |   |   |   |   |   start > 153490
|   |   |   |   |   |   |   |   start <= 154745:
oxidoreductase_activity_ (17.65)
|   |   |   |   |   |   |   |   start > 154745
|   |   |   |   |   |   |   |   |   start <= 159173:
molecular_function_ (8.58)
|   |   |   |   |   |   |   |   |   start > 159173:
oxidoreductase_activity_ (13.73)
|   |   start > 160594
|   |   |   start <= 539466
|   |   |   |   start <= 368127
|   |   |   |   |   start <= 286173
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 217126
|   |   |   |   |   |   |   |   start <= 196507
|   |   |   |   |   |   |   |   |   distance <= 4919
|   |   |   |   |   |   |   |   |   |   start <= 165714:
molecular_function_ (28.07)
|   |   |   |   |   |   |   |   |   |   start > 165714
|   |   |   |   |   |   |   |   |   |   |   start <= 194970
|   |   |   |   |   |   |   |   |   |   |   |   start <= 185438
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 181682:
protein_binding_ (16.2/1.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 181682:
transporter_activity_ (14.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 185438
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 187024:
transferase_activity_ (7.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 187024:
protein_binding_ (14.45)
|   |   |   |   |   |   |   |   |   |   |   start > 194970:
molecular_function_ (23.15)
|   |   |   |   |   |   |   |   |   distance > 4919
|   |   |   |   |   |   |   |   |   |   start <= 171070
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 168727:
protein_binding_ (7.25)
|   |   |   |   |   |   |   |   |   |   |   start > 168727:
enzyme_regulator_activity_ (20.56)
|   |   |   |   |   |   |   |   |   |   start > 171070
|   |   |   |   |   |   |   |   |   |   |   start <= 187024:
transferase_activity_ (2.32)
|   |   |   |   |   |   |   |   |   |   |   start > 187024:
protein_binding_ (4.94)
|   |   |   |   |   |   |   |   start > 196507
|   |   |   |   |   |   |   |   |   start <= 212244
|   |   |   |   |   |   |   |   |   |   start <= 204471:
structural_molecule_activity_ (12.54)
|   |   |   |   |   |   |   |   |   |   start > 204471:
transferase_activity_ (16.55)
|   |   |   |   |   |   |   |   |   start > 212244:
oxidoreductase_activity_ (15.73)
|   |   |   |   |   |   |   start > 217126
|   |   |   |   |   |   |   |   start <= 263476
|   |   |   |   |   |   |   |   |   start <= 231754
|   |   |   |   |   |   |   |   |   |   start <= 219210:
ligase_activity_ (16.92)
|   |   |   |   |   |   |   |   |   |   start > 219210:
molecular_function_ (81.39)
|   |   |   |   |   |   |   |   |   start > 231754
|   |   |   |   |   |   |   |   |   |   start <= 249824
|   |   |   |   |   |   |   |   |   |   |   start <= 238618
|   |   |   |   |   |   |   |   |   |   |   |   start <= 234939
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 234345:
RNA_binding_ (17.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 234345:
transcription_regulator_activity_ (14.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 234939:
ligase_activity_ (18.96)
|   |   |   |   |   |   |   |   |   |   |   start > 238618
|   |   |   |   |   |   |   |   |   |   |   |   start <= 247149
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 243496:
protein_kinase_activity_ (11.3)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 243496:
protein_binding_ (14.66)
|   |   |   |   |   |   |   |   |   |   |   |   start > 247149:
hydrolase_activity_ (15.67)
|   |   |   |   |   |   |   |   |   |   start > 249824
|   |   |   |   |   |   |   |   |   |   |   start <= 255336
|   |   |   |   |   |   |   |   |   |   |   |   start <= 254296:
structural_molecule_activity_ (21.44)
|   |   |   |   |   |   |   |   |   |   |   |   start > 254296:
peptidase_activity_ (12.44)
|   |   |   |   |   |   |   |   |   |   |   start > 255336
|   |   |   |   |   |   |   |   |   |   |   |   start <= 259924
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 256744:
molecular_function_ (11.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 256744
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
259490: RNA_binding_ (14.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
259490: molecular_function_ (9.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 259924:
ligase_activity_ (20.13)
|   |   |   |   |   |   |   |   start > 263476
|   |   |   |   |   |   |   |   |   start <= 282165
|   |   |   |   |   |   |   |   |   |   start <= 271371
|   |   |   |   |   |   |   |   |   |   |   start <= 265430:
molecular_function_ (9.65)
|   |   |   |   |   |   |   |   |   |   |   start > 265430:
transferase_activity_ (20.85)
|   |   |   |   |   |   |   |   |   |   start > 271371
|   |   |   |   |   |   |   |   |   |   |   start <= 277087:
molecular_function_ (58.18)
|   |   |   |   |   |   |   |   |   |   |   start > 277087
|   |   |   |   |   |   |   |   |   |   |   |   start <= 278057:
RNA_binding_ (23.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 278057:
molecular_function_ (15.87)
|   |   |   |   |   |   |   |   |   start > 282165:
transporter_activity_ (27.26)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 207176
|   |   |   |   |   |   |   |   start <= 198942
|   |   |   |   |   |   |   |   |   start <= 193542
|   |   |   |   |   |   |   |   |   |   start <= 187024
|   |   |   |   |   |   |   |   |   |   |   start <= 181682:
hydrolase_activity_ (9.9)
|   |   |   |   |   |   |   |   |   |   |   start > 181682:
RNA_binding_ (20.73)
|   |   |   |   |   |   |   |   |   |   start > 187024:
hydrolase_activity_ (16.51)
|   |   |   |   |   |   |   |   |   start > 193542:
molecular_function_ (37.33)
|   |   |   |   |   |   |   |   start > 198942
|   |   |   |   |   |   |   |   |   start <= 202518
|   |   |   |   |   |   |   |   |   |   start <= 201879:
hydrolase_activity_ (17.59)
|   |   |   |   |   |   |   |   |   |   start > 201879:
transcription_regulator_activity_ (16.98)
|   |   |   |   |   |   |   |   |   start > 202518
|   |   |   |   |   |   |   |   |   |   start <= 204471:
isomerase_activity_ (11.08)
|   |   |   |   |   |   |   |   |   |   start > 204471:
hydrolase_activity_ (23.69)
|   |   |   |   |   |   |   start > 207176
|   |   |   |   |   |   |   |   start <= 282165
|   |   |   |   |   |   |   |   |   start <= 249824
|   |   |   |   |   |   |   |   |   |   start <= 231754
|   |   |   |   |   |   |   |   |   |   |   start <= 220766:
molecular_function_ (69.52)
|   |   |   |   |   |   |   |   |   |   |   start > 220766
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 226074:
hydrolase_activity_ (12.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 226074:
molecular_function_ (30.97)
|   |   |   |   |   |   |   |   |   |   start > 231754
|   |   |   |   |   |   |   |   |   |   |   start <= 234939:
lyase_activity_ (14.28)
|   |   |   |   |   |   |   |   |   |   |   start > 234939
|   |   |   |   |   |   |   |   |   |   |   |   start <= 243496:
molecular_function_ (28.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 243496:
lyase_activity_ (10.39)
|   |   |   |   |   |   |   |   |   start > 249824
|   |   |   |   |   |   |   |   |   |   start <= 254296
|   |   |   |   |   |   |   |   |   |   |   start <= 252645:
RNA_binding_ (22.16)
|   |   |   |   |   |   |   |   |   |   |   start > 252645:
structural_molecule_activity_ (9.09)
|   |   |   |   |   |   |   |   |   |   start > 254296
|   |   |   |   |   |   |   |   |   |   |   start <= 270421:
molecular_function_ (47.98)
|   |   |   |   |   |   |   |   |   |   |   start > 270421
|   |   |   |   |   |   |   |   |   |   |   |   start <= 271371:
transcription_regulator_activity_ (11.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 271371:
molecular_function_ (44.28)
|   |   |   |   |   |   |   |   start > 282165: hydrolase_activity_
(20.6)
|   |   |   |   |   start > 286173
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 325250
|   |   |   |   |   |   |   |   start <= 312368
|   |   |   |   |   |   |   |   |   start <= 303036:
molecular_function_ (114.06)
|   |   |   |   |   |   |   |   |   start > 303036
|   |   |   |   |   |   |   |   |   |   start <= 305350:
hydrolase_activity_ (16.01)
|   |   |   |   |   |   |   |   |   |   start > 305350:
molecular_function_ (29.58)
|   |   |   |   |   |   |   |   start > 312368
|   |   |   |   |   |   |   |   |   start <= 316939:
transcription_regulator_activity_ (11.11)
|   |   |   |   |   |   |   |   |   start > 316939:
enzyme_regulator_activity_ (14.79)
|   |   |   |   |   |   |   start > 325250
|   |   |   |   |   |   |   |   start <= 331456
|   |   |   |   |   |   |   |   |   start <= 329418
|   |   |   |   |   |   |   |   |   |   start <= 326833:
hydrolase_activity_ (18.15)
|   |   |   |   |   |   |   |   |   |   start > 326833:
transferase_activity_ (15.73)
|   |   |   |   |   |   |   |   |   start > 329418:
peptidase_activity_ (24.63)
|   |   |   |   |   |   |   |   start > 331456
```

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|   |   |   |   |   |   |   |   |   start <= 349679
|   |   |   |   |   |   |   |   |   |   start <= 346950:
molecular_function_ (28.35)
|   |   |   |   |   |   |   |   |   |   start > 346950:
hydrolase_activity_ (15.29)
|   |   |   |   |   |   |   |   |   start > 349679
|   |   |   |   |   |   |   |   |   |   start <= 357674
|   |   |   |   |   |   |   |   |   |   |   start <= 356543:
molecular_function_ (23.08)
|   |   |   |   |   |   |   |   |   |   |   start > 356543:
phosphoprotein_phosphatase_activity_ (18.89)
|   |   |   |   |   |   |   |   |   |   start > 357674:
molecular_function_ (46.64)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 329418
|   |   |   |   |   |   |   |   start <= 312368
|   |   |   |   |   |   |   |   |   start <= 297079
|   |   |   |   |   |   |   |   |   |   start <= 292530:
protein_binding_ (10.78)
|   |   |   |   |   |   |   |   |   |   start > 292530:
protein_kinase_activity_ (13.5)
|   |   |   |   |   |   |   |   |   start > 297079:
molecular_function_ (58.82)
|   |   |   |   |   |   |   |   start > 312368
|   |   |   |   |   |   |   |   |   start <= 316939
|   |   |   |   |   |   |   |   |   |   start <= 315388:
isomerase_activity_ (35.03/16.75)
|   |   |   |   |   |   |   |   |   |   start > 315388:
nucleotidyltransferase_activity_ (15.12)
|   |   |   |   |   |   |   |   |   start > 316939
|   |   |   |   |   |   |   |   |   |   start <= 322995:
transferase_activity_ (30.13)
|   |   |   |   |   |   |   |   |   |   start > 322995:
protein_binding_ (13.82)
|   |   |   |   |   |   |   start > 329418
|   |   |   |   |   |   |   |   start <= 337344: ligase_activity_
(10.54)
|   |   |   |   |   |   |   |   start > 337344
|   |   |   |   |   |   |   |   |   start <= 342415
|   |   |   |   |   |   |   |   |   |   start <= 340372:
molecular_function_ (38.68)
|   |   |   |   |   |   |   |   |   |   start > 340372:
signal_transducer_activity_ (5.73)
|   |   |   |   |   |   |   |   |   start > 342415:
molecular_function_ (56.09)
|   |   |   |   start > 368127
|   |   |   |   |   start <= 472727
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 413007
|   |   |   |   |   |   |   |   start <= 400348
|   |   |   |   |   |   |   |   |   start <= 394524
|   |   |   |   |   |   |   |   |   |   start <= 378219
|   |   |   |   |   |   |   |   |   |   |   start <= 373439:
molecular_function_ (10.59)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 373439:
DNA_binding_ (16.54)
|   |   |   |   |   |   |   |   |   |   start > 378219:
molecular_function_ (126.81/28.51)
|   |   |   |   |   |   |   |   |   start > 394524: protein_binding_
(21.4)
|   |   |   |   |   |   |   |   start > 400348
|   |   |   |   |   |   |   |   |   start <= 401555:
oxidoreductase_activity_ (19.58)
|   |   |   |   |   |   |   |   |   start > 401555
|   |   |   |   |   |   |   |   |   |   start <= 407064
|   |   |   |   |   |   |   |   |   |   |   start <= 405768:
enzyme_regulator_activity_ (12.18)
|   |   |   |   |   |   |   |   |   |   |   start > 405768:
hydrolase_activity_ (13.45)
|   |   |   |   |   |   |   |   |   |   start > 407064
|   |   |   |   |   |   |   |   |   |   |   start <= 408425:
molecular_function_ (15.72)
|   |   |   |   |   |   |   |   |   |   |   start > 408425
|   |   |   |   |   |   |   |   |   |   |   |   start <= 410870:
enzyme_regulator_activity_ (10.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 410870:
molecular_function_ (12.53)
|   |   |   |   |   |   |   start > 413007
|   |   |   |   |   |   |   |   start <= 447441
|   |   |   |   |   |   |   |   |   start <= 438645
|   |   |   |   |   |   |   |   |   |   start <= 421651:
transporter_activity_ (26.02)
|   |   |   |   |   |   |   |   |   |   start > 421651
|   |   |   |   |   |   |   |   |   |   |   start <= 432188:
protein_binding_ (15.56)
|   |   |   |   |   |   |   |   |   |   |   start > 432188:
molecular_function_ (9.16)
|   |   |   |   |   |   |   |   |   start > 438645
|   |   |   |   |   |   |   |   |   |   start <= 444688
|   |   |   |   |   |   |   |   |   |   |   start <= 441536:
protein_kinase_activity_ (13.63)
|   |   |   |   |   |   |   |   |   |   |   start > 441536:
structural_molecule_activity_ (17.73)
|   |   |   |   |   |   |   |   |   |   start > 444688:
oxidoreductase_activity_ (23.58)
|   |   |   |   |   |   |   |   start > 447441
|   |   |   |   |   |   |   |   |   start <= 464773
|   |   |   |   |   |   |   |   |   |   start <= 457822
|   |   |   |   |   |   |   |   |   |   |   start <= 449438:
molecular_function_ (19.6)
|   |   |   |   |   |   |   |   |   |   |   start > 449438:
transporter_activity_ (21.53)
|   |   |   |   |   |   |   |   |   |   start > 457822:
molecular_function_ (31.96)
|   |   |   |   |   |   |   |   |   start > 464773
|   |   |   |   |   |   |   |   |   |   start <= 468214:
protein_binding_ (17.86)
|   |   |   |   |   |   |   |   |   |   start > 468214
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 471901:
molecular_function_ (22.7)
|   |   |   |   |   |   |   |   |   |   |   start > 471901:
RNA_binding_ (11.28)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 423733
|   |   |   |   |   |   |   |   start <= 405768
|   |   |   |   |   |   |   |   |   start <= 373439
|   |   |   |   |   |   |   |   |   |   start <= 371685:
protein_binding_ (21.65)
|   |   |   |   |   |   |   |   |   |   start > 371685:
molecular_function_ (14.68)
|   |   |   |   |   |   |   |   |   start > 373439
|   |   |   |   |   |   |   |   |   |   start <= 397086
|   |   |   |   |   |   |   |   |   |   |   start <= 392176
|   |   |   |   |   |   |   |   |   |   |   |   start <= 381053
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 375857:
hydrolase_activity_ (10.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 375857:
transferase_activity_ (12.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 381053:
DNA_binding_ (42.9/12.24)
|   |   |   |   |   |   |   |   |   |   |   start > 392176
|   |   |   |   |   |   |   |   |   |   |   |   start <= 394524:
hydrolase_activity_ (24.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 394524:
transferase_activity_ (20.06)
|   |   |   |   |   |   |   |   |   |   start > 397086
|   |   |   |   |   |   |   |   |   |   |   start <= 401555
|   |   |   |   |   |   |   |   |   |   |   |   start <= 397668:
molecular_function_ (12.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 397668:
protein_binding_ (16.49)
|   |   |   |   |   |   |   |   |   |   |   start > 401555:
transcription_regulator_activity_ (12.66)
|   |   |   |   |   |   |   |   start > 405768
|   |   |   |   |   |   |   |   |   start <= 415908
|   |   |   |   |   |   |   |   |   |   start <= 410870:
RNA_binding_ (27.21)
|   |   |   |   |   |   |   |   |   |   start > 410870:
helicase_activity_ (15.43)
|   |   |   |   |   |   |   |   |   start > 415908
|   |   |   |   |   |   |   |   |   |   start <= 417682:
enzyme_regulator_activity_ (14.88)
|   |   |   |   |   |   |   |   |   |   start > 417682:
hydrolase_activity_ (31.79)
|   |   |   |   |   |   |   start > 423733
|   |   |   |   |   |   |   |   start <= 429859
|   |   |   |   |   |   |   |   |   start <= 427226:
molecular_function_ (19.74)
|   |   |   |   |   |   |   |   |   start > 427226
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
lyase_activity_ (22.49/5.58)
```

```
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
enzyme_regulator_activity_ (21.8/7.05)
|   |   |   |   |   |   |   |   start > 429859
|   |   |   |   |   |   |   |   |   start <= 449438
|   |   |   |   |   |   |   |   |   |   start <= 436347:
protein_binding_ (49.7/18.37)
|   |   |   |   |   |   |   |   |   |   start > 436347
|   |   |   |   |   |   |   |   |   |   |   start <= 444688:
molecular_function_ (40.96)
|   |   |   |   |   |   |   |   |   |   |   start > 444688:
protein_binding_ (16.42)
|   |   |   |   |   |   |   |   |   start > 449438
|   |   |   |   |   |   |   |   |   |   start <= 468214
|   |   |   |   |   |   |   |   |   |   |   start <= 457822
|   |   |   |   |   |   |   |   |   |   |   |   start <= 453770:
transferase_activity_ (18.1)
|   |   |   |   |   |   |   |   |   |   |   |   start > 453770
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 454215:
molecular_function_ (10.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 454215:
enzyme_regulator_activity_ (13.4)
|   |   |   |   |   |   |   |   |   |   |   start > 457822
|   |   |   |   |   |   |   |   |   |   |   |   start <= 461278:
transporter_activity_ (19.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 461278:
transferase_activity_ (10.97)
|   |   |   |   |   |   |   |   |   |   start > 468214:
protein_binding_ (20.14)
|   |   |   |   |   start > 472727
|   |   |   |   |   |   start <= 525279
|   |   |   |   |   |   |   start <= 502796
|   |   |   |   |   |   |   |   start <= 482035
|   |   |   |   |   |   |   |   |   start <= 474554
|   |   |   |   |   |   |   |   |   |   start <= 474418:
transporter_activity_ (18.72)
|   |   |   |   |   |   |   |   |   |   start > 474418: DNA_binding_
(19.29)
|   |   |   |   |   |   |   |   |   start > 474554
|   |   |   |   |   |   |   |   |   |   start <= 480589
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 479535:
transcription_regulator_activity_ (11.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 479535:
hydrolase_activity_ (15.15)
|   |   |   |   |   |   |   |   |   |   |   strand = C:
hydrolase_activity_ (16.97)
|   |   |   |   |   |   |   |   |   |   start > 480589:
transferase_activity_ (15.2)
|   |   |   |   |   |   |   |   start > 482035
|   |   |   |   |   |   |   |   |   start <= 487709
|   |   |   |   |   |   |   |   |   |   start <= 487441:
molecular_function_ (21.74)
|   |   |   |   |   |   |   |   |   |   start > 487441:
transporter_activity_ (20.01)
```

```
|   |   |   |   |   |   |   |   |   start > 487709
|   |   |   |   |   |   |   |   |   |   start <= 492843
|   |   |   |   |   |   |   |   |   |   |   start <= 490830:
hydrolase_activity_ (16.53)
|   |   |   |   |   |   |   |   |   |   |   start > 490830:
phosphoprotein_phosphatase_activity_ (18.4)
|   |   |   |   |   |   |   |   |   |   start > 492843
|   |   |   |   |   |   |   |   |   |   |   start <= 493434:
molecular_function_ (17.65)
|   |   |   |   |   |   |   |   |   |   |   start > 493434
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
hydrolase_activity_ (29.35)
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (15.82)
|   |   |   |   |   |   |   start > 502796
|   |   |   |   |   |   |   |   start <= 511179
|   |   |   |   |   |   |   |   |   start <= 504329:
isomerase_activity_ (21.39)
|   |   |   |   |   |   |   |   |   start > 504329
|   |   |   |   |   |   |   |   |   |   start <= 507506
|   |   |   |   |   |   |   |   |   |   |   start <= 505795:
structural_molecule_activity_ (22.03)
|   |   |   |   |   |   |   |   |   |   |   start > 505795:
molecular_function_ (16.49)
|   |   |   |   |   |   |   |   |   |   start > 507506
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
structural_molecule_activity_ (17.55/5.01)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
protein_binding_ (10.89/3.0)
|   |   |   |   |   |   |   |   start > 511179
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 511826:
transferase_activity_ (21.02)
|   |   |   |   |   |   |   |   |   |   start > 511826
|   |   |   |   |   |   |   |   |   |   |   start <= 519122
|   |   |   |   |   |   |   |   |   |   |   |   start <= 515245:
hydrolase_activity_ (20.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 515245
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 517643:
molecular_function_ (14.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 517643:
protein_binding_ (10.8)
|   |   |   |   |   |   |   |   |   |   |   start > 519122
|   |   |   |   |   |   |   |   |   |   |   |   start <= 523028
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 521354:
enzyme_regulator_activity_ (17.18)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 521354:
transferase_activity_ (14.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 523028:
hydrolase_activity_ (18.68)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 515245:
transporter_activity_ (19.3)
```

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|   |   |   |   |   |   |   |   |   |   start > 515245:
transferase_activity_ (17.27)
|   |   |   |   |   |   start > 525279
|   |   |   |   |   |   |   start <= 528942:
transcription_regulator_activity_ (14.09)
|   |   |   |   |   |   |   start > 528942
|   |   |   |   |   |   |   |   start <= 534076
|   |   |   |   |   |   |   |   |   start <= 531509
|   |   |   |   |   |   |   |   |   |   start <= 530430:
molecular_function_ (14.96)
|   |   |   |   |   |   |   |   |   |   start > 530430: RNA_binding_
(11.14)
|   |   |   |   |   |   |   |   |   start > 531509: DNA_binding_
(18.54)
|   |   |   |   |   |   |   |   start > 534076: molecular_function_
(38.58)
|   |   |   start > 539466
|   |   |   |   start <= 742911
|   |   |   |   |   start <= 580251
|   |   |   |   |   |   start <= 559732
|   |   |   |   |   |   |   start <= 550247
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 545030:
peptidase_activity_ (18.9)
|   |   |   |   |   |   |   |   |   start > 545030:
molecular_function_ (19.7)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 546858:
nucleotidyltransferase_activity_ (28.23)
|   |   |   |   |   |   |   |   |   start > 546858:
protein_kinase_activity_ (13.45)
|   |   |   |   |   |   |   start > 550247
|   |   |   |   |   |   |   |   start <= 554571
|   |   |   |   |   |   |   |   |   strand = W:
oxidoreductase_activity_ (14.23)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 552888:
protein_binding_ (11.98)
|   |   |   |   |   |   |   |   |   |   start > 552888:
transcription_regulator_activity_ (17.13)
|   |   |   |   |   |   |   |   start > 554571
|   |   |   |   |   |   |   |   |   start <= 558643:
peptidase_activity_ (17.93)
|   |   |   |   |   |   |   |   |   start > 558643:
oxidoreductase_activity_ (17.86)
|   |   |   |   |   |   start > 559732
|   |   |   |   |   |   |   start <= 569559
|   |   |   |   |   |   |   |   strand = W:
enzyme_regulator_activity_ (14.39)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 561171:
hydrolase_activity_ (16.43)
|   |   |   |   |   |   |   |   |   start > 561171
```

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|   |   |   |   |   |   |   |   |   |   start <= 566192:
lyase_activity_ (12.27)
|   |   |   |   |   |   |   |   |   |   start > 566192:
structural_molecule_activity_ (12.47)
|   |   |   |   |   |   |   start > 569559
|   |   |   |   |   |   |   |   start <= 573176
|   |   |   |   |   |   |   |   |   start <= 570808:
transporter_activity_ (16.33)
|   |   |   |   |   |   |   |   |   start > 570808
|   |   |   |   |   |   |   |   |   |   start <= 572839:
molecular_function_ (28.45)
|   |   |   |   |   |   |   |   |   |   start > 572839:
transporter_activity_ (15.61)
|   |   |   |   |   |   |   |   start > 573176
|   |   |   |   |   |   |   |   |   start <= 578565
|   |   |   |   |   |   |   |   |   |   start <= 575099:
translation_regulator_activity_ (11.48)
|   |   |   |   |   |   |   |   |   |   start > 575099:
enzyme_regulator_activity_ (20.64)
|   |   |   |   |   |   |   |   |   start > 578565:
oxidoreductase_activity_ (13.0)
|   |   |   |   |   start > 580251
|   |   |   |   |   |   start <= 727513
|   |   |   |   |   |   |   start <= 624730
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 594426
|   |   |   |   |   |   |   |   |   |   start <= 586982:
transcription_regulator_activity_ (18.85)
|   |   |   |   |   |   |   |   |   |   start > 586982:
ligase_activity_ (16.55)
|   |   |   |   |   |   |   |   |   start > 594426
|   |   |   |   |   |   |   |   |   |   start <= 612000
|   |   |   |   |   |   |   |   |   |   |   start <= 609198:
molecular_function_ (13.22)
|   |   |   |   |   |   |   |   |   |   |   start > 609198:
structural_molecule_activity_ (19.49)
|   |   |   |   |   |   |   |   |   |   start > 612000
|   |   |   |   |   |   |   |   |   |   |   start <= 619841:
transporter_activity_ (22.26)
|   |   |   |   |   |   |   |   |   |   |   start > 619841:
molecular_function_ (16.93)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 612000
|   |   |   |   |   |   |   |   |   |   start <= 609198
|   |   |   |   |   |   |   |   |   |   |   start <= 593058
|   |   |   |   |   |   |   |   |   |   |   |   start <= 583682:
molecular_function_ (23.54)
|   |   |   |   |   |   |   |   |   |   |   |   start > 583682
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 586982:
protein_binding_ (11.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 586982:
helicase_activity_ (10.94)
|   |   |   |   |   |   |   |   |   |   |   start > 593058
|   |   |   |   |   |   |   |   |   |   |   |   start <= 605093
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 602343
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
594426: molecular_function_ (14.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
594426: transferase_activity_ (6.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 602343:
molecular_function_ (15.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 605093
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 606608:
protein_binding_ (15.32)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 606608:
molecular_function_ (30.17)
|   |   |   |   |   |   |   |   |   |   start > 609198:
transferase_activity_ (16.32)
|   |   |   |   |   |   |   |   |   start > 612000
|   |   |   |   |   |   |   |   |   |   start <= 616672:
nucleotidyltransferase_activity_ (30.49)
|   |   |   |   |   |   |   |   |   |   start > 616672:
molecular_function_ (21.26)
|   |   |   |   |   |   |   start > 624730
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 658748
|   |   |   |   |   |   |   |   |   |   start <= 644567
|   |   |   |   |   |   |   |   |   |   |   start <= 632165:
structural_molecule_activity_ (18.74)
|   |   |   |   |   |   |   |   |   |   |   start > 632165
|   |   |   |   |   |   |   |   |   |   |   |   start <= 642742
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 633840:
molecular_function_ (8.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 633840:
hydrolase_activity_ (12.11)
|   |   |   |   |   |   |   |   |   |   |   |   start > 642742:
molecular_function_ (14.89)
|   |   |   |   |   |   |   |   |   |   start > 644567
|   |   |   |   |   |   |   |   |   |   |   start <= 649304:
ligase_activity_ (8.62)
|   |   |   |   |   |   |   |   |   |   |   start > 649304
|   |   |   |   |   |   |   |   |   |   |   |   start <= 654211:
transcription_regulator_activity_ (19.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 654211
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 657265:
hydrolase_activity_ (15.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 657265:
transcription_regulator_activity_ (16.03)
|   |   |   |   |   |   |   |   |   start > 658748
|   |   |   |   |   |   |   |   |   |   start <= 680867
|   |   |   |   |   |   |   |   |   |   |   start <= 675940
|   |   |   |   |   |   |   |   |   |   |   |   start <= 667180:
lyase_activity_ (14.42)
|   |   |   |   |   |   |   |   |   |   |   |   start > 667180:
protein_binding_ (13.37)
|   |   |   |   |   |   |   |   |   |   |   start > 675940
|   |   |   |   |   |   |   |   |   |   |   |   start <= 678873:
molecular_function_ (6.03)
```

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|   |   |   |   |   |   |   |   |   |   |   |   start > 678873:
transferase_activity_ (14.25)
|   |   |   |   |   |   |   |   |   |   start > 680867
|   |   |   |   |   |   |   |   |   |   |   start <= 712867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 689625
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 684031
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
683112: molecular_function_ (15.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
683112: translation_regulator_activity_ (12.42)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 684031:
molecular_function_ (39.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 689625
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 700568:
hydrolase_activity_ (21.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 700568:
molecular_function_ (37.03)
|   |   |   |   |   |   |   |   |   |   |   start > 712867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 721947
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 717087:
peptidase_activity_ (10.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 717087:
lyase_activity_ (13.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 721947
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 722912:
helicase_activity_ (12.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 722912:
molecular_function_ (11.48)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 632165
|   |   |   |   |   |   |   |   |   |   start <= 630541
|   |   |   |   |   |   |   |   |   |   |   start <= 627981:
hydrolase_activity_ (13.88)
|   |   |   |   |   |   |   |   |   |   |   start > 627981:
ligase_activity_ (14.46)
|   |   |   |   |   |   |   |   |   |   start > 630541:
peptidase_activity_ (27.34)
|   |   |   |   |   |   |   |   |   start > 632165
|   |   |   |   |   |   |   |   |   |   start <= 648503
|   |   |   |   |   |   |   |   |   |   |   start <= 633840:
RNA_binding_ (21.05)
|   |   |   |   |   |   |   |   |   |   |   start > 633840
|   |   |   |   |   |   |   |   |   |   |   |   start <= 642742
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 639268:
molecular_function_ (22.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 639268:
transcription_regulator_activity_ (11.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 642742:
molecular_function_ (38.98)
|   |   |   |   |   |   |   |   |   |   start > 648503
|   |   |   |   |   |   |   |   |   |   |   start <= 679358
|   |   |   |   |   |   |   |   |   |   |   |   start <= 663886
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 662402
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
649304: structural_molecule_activity_ (6.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
649304: transferase_activity_ (35.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 662402:
molecular_function_ (19.22)
|   |   |   |   |   |   |   |   |   |   |   |   start > 663886
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 672412
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
670242: structural_molecule_activity_ (29.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
670242: RNA_binding_ (16.91)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 672412
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
675940: isomerase_activity_ (11.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
675940: structural_molecule_activity_ (20.58)
|   |   |   |   |   |   |   |   |   |   |   start > 679358
|   |   |   |   |   |   |   |   |   |   |   |   start <= 700568
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 680867:
RNA_binding_ (15.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 680867
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
690696: hydrolase_activity_ (12.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
690696: transporter_activity_ (9.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 700568
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 717087
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
704225: molecular_function_ (14.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
704225
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
712867: transcription_regulator_activity_ (10.65)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
712867: molecular_function_ (11.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 717087
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
722912
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
720066: RNA_binding_ (16.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
720066: transferase_activity_ (13.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
722912: molecular_function_ (20.94)
|   |   |   |   |   |   start > 727513
|   |   |   |   |   |   |   start <= 738321
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 733926:
phosphoprotein_phosphatase_activity_ (15.24)
|   |   |   |   |   |   |   |   |   start > 733926:
nucleotidyltransferase_activity_ (23.1)
|   |   |   |   |   |   |   |   strand = C
```

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|   |   |   |   |   |   |   |   |   start <= 733926:
nucleotidyltransferase_activity_ (15.02)
|   |   |   |   |   |   |   |   |   start > 733926:
transferase_activity_ (15.38)
|   |   |   |   |   |   |   start > 738321
|   |   |   |   |   |   |   |   start <= 741570: hydrolase_activity_
(19.01)
|   |   |   |   |   |   |   |   start > 741570:
signal_transducer_activity_ (21.23)
|   |   |   |   start > 742911
|   |   |   |   |   start <= 925037
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 784858
|   |   |   |   |   |   |   |   start <= 770801
|   |   |   |   |   |   |   |   |   start <= 749302: DNA_binding_
(21.46)
|   |   |   |   |   |   |   |   |   start > 749302
|   |   |   |   |   |   |   |   |   |   start <= 762826
|   |   |   |   |   |   |   |   |   |   |   start <= 758331
|   |   |   |   |   |   |   |   |   |   |   |   start <= 755329:
molecular_function_ (15.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 755329:
transporter_activity_ (16.78)
|   |   |   |   |   |   |   |   |   |   |   start > 758331:
molecular_function_ (34.11)
|   |   |   |   |   |   |   |   |   |   start > 762826:
transcription_regulator_activity_ (20.21)
|   |   |   |   |   |   |   |   start > 770801
|   |   |   |   |   |   |   |   |   start <= 780108
|   |   |   |   |   |   |   |   |   |   start <= 775847
|   |   |   |   |   |   |   |   |   |   |   start <= 774574
|   |   |   |   |   |   |   |   |   |   |   |   start <= 772602:
protein_kinase_activity_ (11.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 772602:
protein_binding_ (11.46)
|   |   |   |   |   |   |   |   |   |   |   start > 774574:
protein_kinase_activity_ (18.39)
|   |   |   |   |   |   |   |   |   |   start > 775847: RNA_binding_
(8.1)
|   |   |   |   |   |   |   |   |   start > 780108
|   |   |   |   |   |   |   |   |   |   start <= 780907:
oxidoreductase_activity_ (17.56)
|   |   |   |   |   |   |   |   |   |   start > 780907
|   |   |   |   |   |   |   |   |   |   |   start <= 783678:
molecular_function_ (21.41)
|   |   |   |   |   |   |   |   |   |   |   start > 783678:
protein_binding_ (10.98)
|   |   |   |   |   |   |   start > 784858
|   |   |   |   |   |   |   |   start <= 882763
|   |   |   |   |   |   |   |   |   start <= 826384
|   |   |   |   |   |   |   |   |   |   start <= 811671
|   |   |   |   |   |   |   |   |   |   |   start <= 792532
|   |   |   |   |   |   |   |   |   |   |   |   start <= 786996:
ligase_activity_ (11.69)
```

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|   |   |   |   |   |   |   |   |   |   |   |   start > 786996:
transferase_activity_ (21.79)
|   |   |   |   |   |   |   |   |   |   |   start > 792532
|   |   |   |   |   |   |   |   |   |   |   |   start <= 807272
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 803668:
molecular_function_ (41.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 803668
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
804378: transferase_activity_ (19.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
804378: molecular_function_ (17.9)
|   |   |   |   |   |   |   |   |   |   |   |   start > 807272
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 811008:
structural_molecule_activity_ (15.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 811008:
molecular_function_ (17.85)
|   |   |   |   |   |   |   |   |   |   start > 811671
|   |   |   |   |   |   |   |   |   |   |   start <= 813984
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 785:
enzyme_regulator_activity_ (3.1/0.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 785:
translation_regulator_activity_ (13.53/3.11)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
enzyme_regulator_activity_ (19.04/5.99)
|   |   |   |   |   |   |   |   |   |   |   start > 813984
|   |   |   |   |   |   |   |   |   |   |   |   start <= 821022
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 818865:
molecular_function_ (22.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 818865
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
820453: protein_binding_ (10.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
820453: molecular_function_ (18.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 821022:
protein_binding_ (15.23)
|   |   |   |   |   |   |   |   |   start > 826384
|   |   |   |   |   |   |   |   |   |   start <= 844629
|   |   |   |   |   |   |   |   |   |   |   start <= 837673
|   |   |   |   |   |   |   |   |   |   |   |   start <= 832331:
RNA_binding_ (23.42)
|   |   |   |   |   |   |   |   |   |   |   |   start > 832331
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 832812:
molecular_function_ (13.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 832812:
transferase_activity_ (22.89)
|   |   |   |   |   |   |   |   |   |   |   start > 837673
|   |   |   |   |   |   |   |   |   |   |   |   start <= 842402
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 841332:
translation_regulator_activity_ (19.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 841332:
RNA_binding_ (16.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 842402:
lyase_activity_ (19.74)
```

```
|   |   |   |   |   |   |   |   |   |   start > 844629
|   |   |   |   |   |   |   |   |   |   |   start <= 880963
|   |   |   |   |   |   |   |   |   |   |   |   start <= 868339
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 861174:
molecular_function_ (93.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 861174
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
867097: structural_molecule_activity_ (7.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
867097: molecular_function_ (8.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 868339
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 869207:
transcription_regulator_activity_ (17.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 869207
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
875598
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
870201: molecular_function_ (17.4)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
870201: transferase_activity_ (21.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
875598: molecular_function_ (24.22)
|   |   |   |   |   |   |   |   |   |   |   start > 880963:
translation_regulator_activity_ (24.02)
|   |   |   |   |   |   |   |   start > 882763
|   |   |   |   |   |   |   |   |   start <= 909340
|   |   |   |   |   |   |   |   |   |   start <= 884512
|   |   |   |   |   |   |   |   |   |   |   start <= 882897:
ligase_activity_ (21.45)
|   |   |   |   |   |   |   |   |   |   |   start > 882897:
hydrolase_activity_ (20.96)
|   |   |   |   |   |   |   |   |   |   start > 884512
|   |   |   |   |   |   |   |   |   |   |   start <= 896384:
molecular_function_ (16.61)
|   |   |   |   |   |   |   |   |   |   |   start > 896384
|   |   |   |   |   |   |   |   |   |   |   |   start <= 904757:
transcription_regulator_activity_ (11.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 904757:
ligase_activity_ (14.09)
|   |   |   |   |   |   |   |   |   start > 909340
|   |   |   |   |   |   |   |   |   |   start <= 912819:
RNA_binding_ (9.98)
|   |   |   |   |   |   |   |   |   |   start > 912819:
transferase_activity_ (12.04)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 795333
|   |   |   |   |   |   |   |   start <= 789858
|   |   |   |   |   |   |   |   |   start <= 758331
|   |   |   |   |   |   |   |   |   |   start <= 749302
|   |   |   |   |   |   |   |   |   |   |   start <= 745282:
transferase_activity_ (16.72)
|   |   |   |   |   |   |   |   |   |   |   start > 745282:
molecular_function_ (61.6)
|   |   |   |   |   |   |   |   |   |   start > 749302
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 755329:
peptidase_activity_ (10.41)
|   |   |   |   |   |   |   |   |   |   |   start > 755329:
transferase_activity_ (21.57)
|   |   |   |   |   |   |   |   |   start > 758331
|   |   |   |   |   |   |   |   |   |   start <= 761266
|   |   |   |   |   |   |   |   |   |   |   start <= 759783:
RNA_binding_ (13.06)
|   |   |   |   |   |   |   |   |   |   |   start > 759783:
nucleotidyltransferase_activity_ (17.31)
|   |   |   |   |   |   |   |   |   |   start > 761266
|   |   |   |   |   |   |   |   |   |   |   start <= 772602:
molecular_function_ (27.76)
|   |   |   |   |   |   |   |   |   |   |   start > 772602
|   |   |   |   |   |   |   |   |   |   |   |   start <= 783678:
structural_molecule_activity_ (10.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 783678:
molecular_function_ (24.86)
|   |   |   |   |   |   |   |   start > 789858
|   |   |   |   |   |   |   |   |   start <= 792532:
isomerase_activity_ (14.75)
|   |   |   |   |   |   |   |   |   start > 792532:
transferase_activity_ (16.06)
|   |   |   |   |   |   |   start > 795333
|   |   |   |   |   |   |   |   start <= 848477
|   |   |   |   |   |   |   |   |   start <= 804378
|   |   |   |   |   |   |   |   |   |   start <= 800732
|   |   |   |   |   |   |   |   |   |   |   start <= 797677:
oxidoreductase_activity_ (22.22)
|   |   |   |   |   |   |   |   |   |   |   start > 797677:
protein_binding_ (10.8)
|   |   |   |   |   |   |   |   |   |   start > 800732
|   |   |   |   |   |   |   |   |   |   |   start <= 802308:
RNA_binding_ (12.39)
|   |   |   |   |   |   |   |   |   |   |   start > 802308:
transferase_activity_ (13.06)
|   |   |   |   |   |   |   |   |   start > 804378
|   |   |   |   |   |   |   |   |   |   start <= 841332
|   |   |   |   |   |   |   |   |   |   |   start <= 826384
|   |   |   |   |   |   |   |   |   |   |   |   start <= 807272:
transporter_activity_ (22.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 807272
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 813984
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
811671: molecular_function_ (25.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
811671: peptidase_activity_ (17.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 813984
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
824866
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
820453: molecular_function_ (8.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
820453: protein_kinase_activity_ (11.07)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
824866: molecular_function_ (21.54)
|   |   |   |   |   |   |   |   |   |   |   start > 826384
|   |   |   |   |   |   |   |   |   |   |   |   start <= 830573
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
3343: transporter_activity_ (24.03/10.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 3343:
hydrolase_activity_ (9.2/2.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 830573
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 837673
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
832812: molecular_function_ (18.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
832812: transporter_activity_ (29.85)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 837673:
molecular_function_ (20.39)
|   |   |   |   |   |   |   |   |   |   start > 841332
|   |   |   |   |   |   |   |   |   |   |   start <= 842816:
RNA_binding_ (12.4)
|   |   |   |   |   |   |   |   |   |   |   start > 842816
|   |   |   |   |   |   |   |   |   |   |   |   start <= 844629:
protein_binding_ (16.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 844629
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 845791:
hydrolase_activity_ (11.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 845791:
protein_binding_ (14.6)
|   |   |   |   |   |   |   |   start > 848477
|   |   |   |   |   |   |   |   |   start <= 891430
|   |   |   |   |   |   |   |   |   |   start <= 854258
|   |   |   |   |   |   |   |   |   |   |   start <= 853356
|   |   |   |   |   |   |   |   |   |   |   |   start <= 851838:
molecular_function_ (11.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 851838:
oxidoreductase_activity_ (18.96)
|   |   |   |   |   |   |   |   |   |   |   start > 853356:
molecular_function_ (21.03)
|   |   |   |   |   |   |   |   |   |   start > 854258
|   |   |   |   |   |   |   |   |   |   |   start <= 870201
|   |   |   |   |   |   |   |   |   |   |   |   start <= 861174:
transcription_regulator_activity_ (12.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 861174:
molecular_function_ (27.06)
|   |   |   |   |   |   |   |   |   |   |   start > 870201
|   |   |   |   |   |   |   |   |   |   |   |   start <= 882897
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 875598:
transporter_activity_ (16.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 875598:
transcription_regulator_activity_ (16.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 882897
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 889020:
molecular_function_ (13.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 889020:
transporter_activity_ (12.85)
```

```
|   |   |   |   |   |   |   |   |   start > 891430
|   |   |   |   |   |   |   |   |   |   start <= 901191
|   |   |   |   |   |   |   |   |   |   |   start <= 899925
|   |   |   |   |   |   |   |   |   |   |   |   start <= 896384
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 894089:
molecular_function_ (5.93)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 894089:
RNA_binding_ (16.18)
|   |   |   |   |   |   |   |   |   |   |   |   start > 896384:
molecular_function_ (27.26)
|   |   |   |   |   |   |   |   |   |   |   start > 899925:
structural_molecule_activity_ (17.94)
|   |   |   |   |   |   |   |   |   |   start > 901191
|   |   |   |   |   |   |   |   |   |   |   start <= 916027
|   |   |   |   |   |   |   |   |   |   |   |   start <= 909340
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 907552
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
904757: molecular_function_ (10.57)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
904757: transporter_activity_ (13.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 907552:
molecular_function_ (12.84)
|   |   |   |   |   |   |   |   |   |   |   |   start > 909340:
transferase_activity_ (11.23)
|   |   |   |   |   |   |   |   |   |   |   start > 916027
|   |   |   |   |   |   |   |   |   |   |   |   start <= 922902
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 921059:
molecular_function_ (17.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 921059:
oxidoreductase_activity_ (13.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 922902:
molecular_function_ (21.01)
|   |   |   |   |   start > 925037
|   |   |   |   |   |   start <= 949106
|   |   |   |   |   |   |   start <= 939346
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 925718
|   |   |   |   |   |   |   |   |   |   distance <= 3047:
protein_binding_ (11.6/2.17)
|   |   |   |   |   |   |   |   |   |   distance > 3047:
motor_activity_ (24.49/8.45)
|   |   |   |   |   |   |   |   |   start > 925718:
hydrolase_activity_ (8.92)
|   |   |   |   |   |   |   |   strand = C: protein_binding_ (43.53)
|   |   |   |   |   |   |   start > 939346
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 943653
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
hydrolase_activity_ (13.66/5.03)
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
transporter_activity_ (11.96/4.07)
|   |   |   |   |   |   |   |   |   start > 943653:
transporter_activity_ (12.38)
|   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   start <= 944593:
nucleotidyltransferase_activity_ (11.53)
|   |   |   |   |   |   |   |   |   start > 944593: ligase_activity_
(11.19)
|   |   |   |   |   |   start > 949106
|   |   |   |   |   |   |   start <= 1005135
|   |   |   |   |   |   |   |   start <= 986459
|   |   |   |   |   |   |   |   |   start <= 954341
|   |   |   |   |   |   |   |   |   |   start <= 949770:
transferase_activity_ (9.59)
|   |   |   |   |   |   |   |   |   |   start > 949770: DNA_binding_
(20.77)
|   |   |   |   |   |   |   |   |   start > 954341
|   |   |   |   |   |   |   |   |   |   start <= 976418
|   |   |   |   |   |   |   |   |   |   |   start <= 958829:
molecular_function_ (49.87)
|   |   |   |   |   |   |   |   |   |   |   start > 958829
|   |   |   |   |   |   |   |   |   |   |   |   start <= 960984:
nucleotidyltransferase_activity_ (25.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 960984:
molecular_function_ (27.99)
|   |   |   |   |   |   |   |   |   |   start > 976418
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 980680:
molecular_function_ (15.86)
|   |   |   |   |   |   |   |   |   |   |   |   start > 980680:
nucleotidyltransferase_activity_ (12.55)
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 981825
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 583:
DNA_binding_ (3.47/0.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 583
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1983: transcription_regulator_activity_ (7.19/0.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
1983
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 6197: DNA_binding_ (15.01/5.88)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 6197: transcription_regulator_activity_ (4.4/0.38)
|   |   |   |   |   |   |   |   |   |   |   |   start > 981825:
transferase_activity_ (15.1)
|   |   |   |   |   |   |   |   start > 986459
|   |   |   |   |   |   |   |   |   start <= 989786
|   |   |   |   |   |   |   |   |   |   start <= 988779:
transporter_activity_ (23.61)
|   |   |   |   |   |   |   |   |   |   start > 988779:
protein_binding_ (13.58)
|   |   |   |   |   |   |   |   |   start > 989786
|   |   |   |   |   |   |   |   |   |   start <= 996508
|   |   |   |   |   |   |   |   |   |   |   start <= 994852:
molecular_function_ (15.59)
|   |   |   |   |   |   |   |   |   |   |   start > 994852:
protein_kinase_activity_ (23.63)
```

```
|   |   |   |   |   |   |   |   |   |   start > 996508:
molecular_function_ (68.35)
|   |   |   |   |   |   |   start > 1005135
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 1010159
|   |   |   |   |   |   |   |   |   |   start <= 1007219:
oxidoreductase_activity_ (18.68)
|   |   |   |   |   |   |   |   |   |   start > 1007219:
DNA_binding_ (15.4)
|   |   |   |   |   |   |   |   |   start > 1010159: RNA_binding_
(19.84)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 1011187:
protein_binding_ (19.18)
|   |   |   |   |   |   |   |   |   start > 1011187
|   |   |   |   |   |   |   |   |   |   start <= 1014819:
hydrolase_activity_ (12.96)
|   |   |   |   |   |   |   |   |   |   start > 1014819:
translation_regulator_activity_ (10.94)
|   start > 1017650
|   |   start <= 1036832
|   |   |   start <= 1026841
|   |   |   |   strand = W
|   |   |   |   |   start <= 1026005: protein_binding_ (15.37)
|   |   |   |   |   start > 1026005: DNA_binding_ (20.17)
|   |   |   |   strand = C
|   |   |   |   |   start <= 1018744: peptidase_activity_ (20.81)
|   |   |   |   |   start > 1018744
|   |   |   |   |   |   start <= 1023210:
transcription_regulator_activity_ (17.75)
|   |   |   |   |   |   start > 1023210: molecular_function_ (19.29)
|   |   |   start > 1026841
|   |   |   |   start <= 1034180
|   |   |   |   |   start <= 1028623: structural_molecule_activity_
(18.69)
|   |   |   |   |   start > 1028623
|   |   |   |   |   |   start <= 1030992: enzyme_regulator_activity_
(13.78)
|   |   |   |   |   |   start > 1030992: signal_transducer_activity_
(15.97)
|   |   |   |   start > 1034180
|   |   |   |   |   start <= 1036469:
transcription_regulator_activity_ (23.21)
|   |   |   |   |   start > 1036469: structural_molecule_activity_
(19.76)
|   |   start > 1036832
|   |   |   start <= 1076782
|   |   |   |   start <= 1055543
|   |   |   |   |   start <= 1049509
|   |   |   |   |   |   start <= 1043040: oxidoreductase_activity_
(21.41)
|   |   |   |   |   |   start > 1043040
|   |   |   |   |   |   |   start <= 1046224
```

```
|   |   |   |   |   |   |   |   start <= 1045194:
molecular_function_ (12.03)
|   |   |   |   |   |   |   |   start > 1045194:
transferase_activity_ (15.42)
|   |   |   |   |   |   |   start > 1046224: molecular_function_
(15.16)
|   |   |   |   |   start > 1049509
|   |   |   |   |   |   start <= 1051288:
transcription_regulator_activity_ (27.72/12.21)
|   |   |   |   |   |   start > 1051288: oxidoreductase_activity_
(9.96)
|   |   |   |   start > 1055543
|   |   |   |   |   start <= 1061053: molecular_function_ (42.23)
|   |   |   |   |   start > 1061053
|   |   |   |   |   |   start <= 1072921
|   |   |   |   |   |   |   start <= 1070239
|   |   |   |   |   |   |   |   start <= 1061562:
oxidoreductase_activity_ (11.87)
|   |   |   |   |   |   |   |   start > 1061562
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 1065041:
molecular_function_ (17.23)
|   |   |   |   |   |   |   |   |   |   start > 1065041:
lyase_activity_ (16.12)
|   |   |   |   |   |   |   |   |   strand = C: molecular_function_
(18.12)
|   |   |   |   |   |   |   start > 1070239:
oxidoreductase_activity_ (18.17)
|   |   |   |   |   |   start > 1072921: molecular_function_ (33.04)
|   |   |   start > 1076782
|   |   |   |   start <= 1080274
|   |   |   |   |   start <= 1079256
|   |   |   |   |   |   distance <= 5959: protein_binding_
(24.19/6.26)
|   |   |   |   |   |   distance > 5959: peptidase_activity_
(7.32/0.67)
|   |   |   |   |   start > 1079256: lyase_activity_ (17.9)
|   |   |   |   start > 1080274
|   |   |   |   |   start <= 1084367: molecular_function_ (25.6)
|   |   |   |   |   start > 1084367: helicase_activity_ (12.33)
```

For Biological Process

```
|   start <= 981825
|   |   start <= 252645
|   |   |   start <= 193542
|   |   |   |   start <= 96361
|   |   |   |   |   start <= 73031
|   |   |   |   |   |   start <= 43693
|   |   |   |   |   |   |   start <= 40747
|   |   |   |   |   |   |   |   start <= 27083
|   |   |   |   |   |   |   |   |   start <= 6175:
biological_process_ (33.39)
|   |   |   |   |   |   |   |   |   start > 6175
```

```
|   |   |   |   |   |   |   |   |   |   start <= 10118: transport_
(23.87)
|   |   |   |   |   |   |   |   |   |   start > 10118
|   |   |   |   |   |   |   |   |   |   |   start <= 17795:
biological_process_ (25.2)
|   |   |   |   |   |   |   |   |   |   |   start > 17795
|   |   |   |   |   |   |   |   |   |   |   |   start <= 25272
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = W:
transport_ (10.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
21310: transport_ (8.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
21310: biological_process_ (11.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 25272:
biological_process_ (21.27)
|   |   |   |   |   |   |   |   start > 27083
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 34657:
biological_process_ (14.02)
|   |   |   |   |   |   |   |   |   |   start > 34657: transport_
(10.5)
|   |   |   |   |   |   |   |   |   strand = C:
cell_wall_organization_and_biogenesis_ (12.73)
|   |   |   |   |   |   |   start > 40747: response_to_stress_
(10.88)
|   |   |   |   |   |   start > 43693
|   |   |   |   |   |   |   start <= 56451
|   |   |   |   |   |   |   |   start <= 48863
|   |   |   |   |   |   |   |   |   start <= 44937:
RNA_metabolic_process_ (22.58)
|   |   |   |   |   |   |   |   |   start > 44937
|   |   |   |   |   |   |   |   |   |   start <= 47573
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
protein_modification_process_ (15.06/5.19)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (15.08/4.79)
|   |   |   |   |   |   |   |   |   |   start > 47573
|   |   |   |   |   |   |   |   |   |   |   start <= 48642:
organelle_organization_and_biogenesis_ (23.8)
|   |   |   |   |   |   |   |   |   |   |   start > 48642:
DNA_metabolic_process_ (22.01)
|   |   |   |   |   |   |   |   start > 48863
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 55557:
ribosome_biogenesis_and_assembly_ (53.05)
|   |   |   |   |   |   |   |   |   |   start > 55557:
RNA_metabolic_process_ (24.05)
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 53097
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 2327:
biological_process_ (9.58/2.18)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   distance > 2327:
RNA_metabolic_process_ (5.91/2.31)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
transcription_ (38.19/20.54)
|   |   |   |   |   |   |   |   |   |   start > 53097:
vitamin_metabolic_process_ (16.92)
|   |   |   |   |   |   |   start > 56451
|   |   |   |   |   |   |   |   start <= 68754
|   |   |   |   |   |   |   |   |   start <= 65350
|   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (29.07/12.34)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 61024:
translation_ (15.8)
|   |   |   |   |   |   |   |   |   |   |   start > 61024:
DNA_metabolic_process_ (19.25)
|   |   |   |   |   |   |   |   |   start > 65350:
biological_process_ (44.96)
|   |   |   |   |   |   |   |   start > 68754
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 71300
|   |   |   |   |   |   |   |   |   |   |   start <= 70325:
cell_cycle_ (8.98)
|   |   |   |   |   |   |   |   |   |   |   start > 70325:
cell_wall_organization_and_biogenesis_ (31.51/15.19)
|   |   |   |   |   |   |   |   |   |   start > 71300:
biological_process_ (11.68)
|   |   |   |   |   |   |   |   |   strand = C: transcription_
(10.47)
|   |   |   |   |   start > 73031
|   |   |   |   |   |   start <= 87844
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 80348
|   |   |   |   |   |   |   |   |   start <= 77560: transport_
(19.24)
|   |   |   |   |   |   |   |   |   start > 77560: translation_
(12.64)
|   |   |   |   |   |   |   |   start > 80348:
RNA_metabolic_process_ (24.04)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 83834
|   |   |   |   |   |   |   |   |   start <= 80348:
response_to_stress_ (9.55)
|   |   |   |   |   |   |   |   |   start > 80348:
carbohydrate_metabolic_process_ (11.62)
|   |   |   |   |   |   |   |   start > 83834:
ribosome_biogenesis_and_assembly_ (13.6)
|   |   |   |   |   |   start > 87844
|   |   |   |   |   |   |   start <= 91419: transport_ (21.83)
|   |   |   |   |   |   |   start > 91419
|   |   |   |   |   |   |   |   start <= 94402: translation_ (37.71)
|   |   |   |   |   |   |   |   start > 94402: transport_ (14.26)
|   |   |   |   start > 96361
|   |   |   |   |   start <= 109176
```

```
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 104326
|   |   |   |   |   |   |   |   start <= 101475
|   |   |   |   |   |   |   |   |   start <= 97551: conjugation_
(27.07/12.41)
|   |   |   |   |   |   |   |   |   start > 97551
|   |   |   |   |   |   |   |   |   |   start <= 99809:
response_to_stress_ (14.11)
|   |   |   |   |   |   |   |   |   |   start > 99809:
DNA_metabolic_process_ (17.67)
|   |   |   |   |   |   |   |   start > 101475:
protein_modification_process_ (47.36/22.0)
|   |   |   |   |   |   |   start > 104326
|   |   |   |   |   |   |   |   start <= 106710:
cytoskeleton_organization_and_biogenesis_ (24.59)
|   |   |   |   |   |   |   |   start > 106710
|   |   |   |   |   |   |   |   |   neigh_strand = C:
signal_transduction_ (38.52/21.62)
|   |   |   |   |   |   |   |   |   neigh_strand = W:
protein_modification_process_ (33.58/17.13)
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 104326: biological_process_
(19.62)
|   |   |   |   |   |   |   start > 104326: conjugation_ (24.11)
|   |   |   |   |   start > 109176
|   |   |   |   |   |   start <= 147382
|   |   |   |   |   |   |   start <= 129237
|   |   |   |   |   |   |   |   start <= 115808
|   |   |   |   |   |   |   |   |   start <= 110297
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cell_wall_organization_and_biogenesis_ (18.0/6.29)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
response_to_stress_ (35.27/14.65)
|   |   |   |   |   |   |   |   |   start > 110297
|   |   |   |   |   |   |   |   |   |   start <= 111886
|   |   |   |   |   |   |   |   |   |   |   start <= 111033:
translation_ (21.34)
|   |   |   |   |   |   |   |   |   |   |   start > 111033:
transcription_ (29.71/12.76)
|   |   |   |   |   |   |   |   |   |   start > 111886
|   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   start <= 112102:
biological_process_ (17.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 112102:
translation_ (14.88)
|   |   |   |   |   |   |   |   |   |   |   strand = C:
cell_wall_organization_and_biogenesis_ (13.84)
|   |   |   |   |   |   |   |   start > 115808
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 124001: transport_
(12.63)
|   |   |   |   |   |   |   |   |   |   start > 124001:
cell_wall_organization_and_biogenesis_ (10.16)
|   |   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   |   start <= 126689
|   |   |   |   |   |   |   |   |   |   |   start <= 117454:
meiosis_ (12.01)
|   |   |   |   |   |   |   |   |   |   |   start > 117454:
RNA_metabolic_process_ (25.68)
|   |   |   |   |   |   |   |   |   |   start > 126689:
lipid_metabolic_process_ (16.95)
|   |   |   |   |   |   |   start > 129237
|   |   |   |   |   |   |   |   start <= 139045
|   |   |   |   |   |   |   |   |   start <= 136183
|   |   |   |   |   |   |   |   |   |   start <= 135838:
biological_process_ (16.92)
|   |   |   |   |   |   |   |   |   |   start > 135838:
ribosome_biogenesis_and_assembly_ (29.69/13.67)
|   |   |   |   |   |   |   |   |   start > 136183
|   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (13.23)
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 137825:
translation_ (13.52)
|   |   |   |   |   |   |   |   |   |   |   start > 137825:
biological_process_ (14.04)
|   |   |   |   |   |   |   |   start > 139045
|   |   |   |   |   |   |   |   |   start <= 142815
|   |   |   |   |   |   |   |   |   |   strand = W:
RNA_metabolic_process_ (18.96)
|   |   |   |   |   |   |   |   |   |   strand = C:
DNA_metabolic_process_ (43.3)
|   |   |   |   |   |   |   |   |   start > 142815
|   |   |   |   |   |   |   |   |   |   start <= 144204:
biological_process_ (19.63)
|   |   |   |   |   |   |   |   |   |   start > 144204
|   |   |   |   |   |   |   |   |   |   |   start <= 145334:
meiosis_ (17.92)
|   |   |   |   |   |   |   |   |   |   |   start > 145334:
DNA_metabolic_process_ (19.55)
|   |   |   |   |   |   start > 147382
|   |   |   |   |   |   |   start <= 171070
|   |   |   |   |   |   |   |   start <= 165714
|   |   |   |   |   |   |   |   |   start <= 153490:
response_to_stress_ (18.24)
|   |   |   |   |   |   |   |   |   start > 153490
|   |   |   |   |   |   |   |   |   |   start <= 159173:
biological_process_ (53.48)
|   |   |   |   |   |   |   |   |   |   start > 159173
|   |   |   |   |   |   |   |   |   |   |   strand = W:
biological_process_ (18.47)
|   |   |   |   |   |   |   |   |   |   |   strand = C:
generation_of_precursor_metabolites_and_energy_ (8.46)
|   |   |   |   |   |   |   |   start > 165714
|   |   |   |   |   |   |   |   |   start <= 168727: transport_
(14.39)
|   |   |   |   |   |   |   |   |   start > 168727:
response_to_stress_ (11.29)
```

```
|   |   |   |   |   |   |   start > 171070
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 181682:
cell_wall_organization_and_biogenesis_ (19.78)
|   |   |   |   |   |   |   |   |   start > 181682
|   |   |   |   |   |   |   |   |   |   start <= 185438:
generation_of_precursor_metabolites_and_energy_ (15.94)
|   |   |   |   |   |   |   |   |   |   start > 185438:
cytoskeleton_organization_and_biogenesis_ (18.74)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 187024:
ribosome_biogenesis_and_assembly_ (30.22)
|   |   |   |   |   |   |   |   |   start > 187024: transport_
(12.0)
|   |   |   start > 193542
|   |   |   |   start <= 226074
|   |   |   |   |   start <= 212244
|   |   |   |   |   |   start <= 202518
|   |   |   |   |   |   |   start <= 201879
|   |   |   |   |   |   |   |   start <= 198942
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 194970:
DNA_metabolic_process_ (16.33)
|   |   |   |   |   |   |   |   |   |   start > 194970
|   |   |   |   |   |   |   |   |   |   |   start <= 196507:
sporulation_ (17.26)
|   |   |   |   |   |   |   |   |   |   |   start > 196507:
biological_process_ (12.49)
|   |   |   |   |   |   |   |   |   strand = C: biological_process_
(31.51)
|   |   |   |   |   |   |   |   start > 198942:
DNA_metabolic_process_ (16.22)
|   |   |   |   |   |   |   start > 201879: signal_transduction_
(14.95)
|   |   |   |   |   |   start > 202518
|   |   |   |   |   |   |   strand = W: DNA_metabolic_process_
(13.6)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 204471:
RNA_metabolic_process_ (32.82/15.98)
|   |   |   |   |   |   |   |   start > 204471
|   |   |   |   |   |   |   |   |   start <= 210265
|   |   |   |   |   |   |   |   |   |   start <= 205885: vesicle-
mediated_transport_ (15.34)
|   |   |   |   |   |   |   |   |   |   start > 205885
|   |   |   |   |   |   |   |   |   |   |   start <= 207176:
biological_process_ (31.5/13.23)
|   |   |   |   |   |   |   |   |   |   |   start > 207176:
response_to_stress_ (20.56)
|   |   |   |   |   |   |   |   |   start > 210265: vesicle-
mediated_transport_ (15.82)
|   |   |   |   |   start > 212244
|   |   |   |   |   |   start <= 216137:
organelle_organization_and_biogenesis_ (12.86)
```

```
|   |   |   |   |   |   start > 216137
|   |   |   |   |   |   |   strand = W: biological_process_
(97.92/28.78)
|   |   |   |   |   |   |   strand = C: vitamin_metabolic_process_
(16.42)
|   |   |   |   start > 226074
|   |   |   |   |   start <= 238618
|   |   |   |   |   |   start <= 230084
|   |   |   |   |   |   |   start <= 228330: translation_ (25.62)
|   |   |   |   |   |   |   start > 228330
|   |   |   |   |   |   |   |   start <= 228613:
RNA_metabolic_process_ (6.88)
|   |   |   |   |   |   |   |   start > 228613: biological_process_
(15.07)
|   |   |   |   |   |   start > 230084
|   |   |   |   |   |   |   start <= 234345
|   |   |   |   |   |   |   |   strand = W: RNA_metabolic_process_
(27.72/12.83)
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 231754:
response_to_stress_ (20.6)
|   |   |   |   |   |   |   |   |   start > 231754:
amino_acid_and_derivative_metabolic_process_ (9.68)
|   |   |   |   |   |   |   start > 234345
|   |   |   |   |   |   |   |   start <= 234939:
DNA_metabolic_process_ (29.32/14.05)
|   |   |   |   |   |   |   |   start > 234939: response_to_stress_
(19.98)
|   |   |   |   |   start > 238618
|   |   |   |   |   |   start <= 249824
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 247149
|   |   |   |   |   |   |   |   |   start <= 243496:
protein_modification_process_ (10.93)
|   |   |   |   |   |   |   |   |   start > 243496:
signal_transduction_ (20.12)
|   |   |   |   |   |   |   |   start > 247149: biological_process_
(19.92)
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 243496: biological_process_
(25.2)
|   |   |   |   |   |   |   |   start > 243496:
DNA_metabolic_process_ (11.34)
|   |   |   |   |   |   start > 249824: RNA_metabolic_process_
(15.99)
|   |   start > 252645
|   |   |   strand = W
|   |   |   |   start <= 654211
|   |   |   |   |   start <= 378219
|   |   |   |   |   |   start <= 303036
|   |   |   |   |   |   |   start <= 265430
|   |   |   |   |   |   |   |   start <= 256744
|   |   |   |   |   |   |   |   |   start <= 254296: translation_
(21.32)
```

```
|   |   |   |   |   |   |   |   |   start > 254296
|   |   |   |   |   |   |   |   |   |   start <= 255336:
protein_catabolic_process_ (14.36)
|   |   |   |   |   |   |   |   |   |   start > 255336:
biological_process_ (11.67)
|   |   |   |   |   |   |   |   start > 256744
|   |   |   |   |   |   |   |   |   start <= 259924
|   |   |   |   |   |   |   |   |   |   start <= 259490:
ribosome_biogenesis_and_assembly_ (22.35/8.67)
|   |   |   |   |   |   |   |   |   |   start > 259490:
DNA_metabolic_process_ (17.14)
|   |   |   |   |   |   |   |   |   start > 259924
|   |   |   |   |   |   |   |   |   |   start <= 263476:
translation_ (15.22)
|   |   |   |   |   |   |   |   |   |   start > 263476:
carbohydrate_metabolic_process_ (13.76)
|   |   |   |   |   |   |   start > 265430
|   |   |   |   |   |   |   |   start <= 288193
|   |   |   |   |   |   |   |   |   start <= 277087
|   |   |   |   |   |   |   |   |   |   start <= 274674
|   |   |   |   |   |   |   |   |   |   |   start <= 271371:
biological_process_ (17.12)
|   |   |   |   |   |   |   |   |   |   |   start > 271371:
translation_ (11.9)
|   |   |   |   |   |   |   |   |   |   start > 274674:
biological_process_ (29.69)
|   |   |   |   |   |   |   |   |   start > 277087
|   |   |   |   |   |   |   |   |   |   start <= 282165:
translation_ (27.55)
|   |   |   |   |   |   |   |   |   |   start > 282165
|   |   |   |   |   |   |   |   |   |   |   start <= 286173:
DNA_metabolic_process_ (12.86)
|   |   |   |   |   |   |   |   |   |   |   start > 286173:
translation_ (6.92)
|   |   |   |   |   |   |   |   start > 288193
|   |   |   |   |   |   |   |   |   start <= 301048
|   |   |   |   |   |   |   |   |   |   start <= 292530
|   |   |   |   |   |   |   |   |   |   |   start <= 288899:
biological_process_ (38.86)
|   |   |   |   |   |   |   |   |   |   |   start > 288899:
transcription_ (15.96)
|   |   |   |   |   |   |   |   |   |   start > 292530:
biological_process_ (49.52)
|   |   |   |   |   |   |   |   |   start > 301048: translation_
(13.39)
|   |   |   |   |   |   start > 303036
|   |   |   |   |   |   |   start <= 338622
|   |   |   |   |   |   |   |   start <= 326833
|   |   |   |   |   |   |   |   |   start <= 312368
|   |   |   |   |   |   |   |   |   |   start <= 307939
|   |   |   |   |   |   |   |   |   |   |   start <= 305350:
lipid_metabolic_process_ (16.49)
|   |   |   |   |   |   |   |   |   |   |   start > 305350:
ribosome_biogenesis_and_assembly_ (17.79)
```

```
|   |   |   |   |   |   |   |   |   |   start > 307939:
cellular_respiration_ (16.86)
|   |   |   |   |   |   |   |   |   start > 312368
|   |   |   |   |   |   |   |   |   |   start <= 325250:
DNA_metabolic_process_ (33.76)
|   |   |   |   |   |   |   |   |   |   start > 325250:
ribosome_biogenesis_and_assembly_ (8.72)
|   |   |   |   |   |   |   |   start > 326833
|   |   |   |   |   |   |   |   |   start <= 329418:
protein_modification_process_ (29.75/13.72)
|   |   |   |   |   |   |   |   |   start > 329418
|   |   |   |   |   |   |   |   |   |   start <= 331456:
protein_catabolic_process_ (15.82)
|   |   |   |   |   |   |   |   |   |   start > 331456:
ribosome_biogenesis_and_assembly_ (9.5)
|   |   |   |   |   |   |   start > 338622
|   |   |   |   |   |   |   |   start <= 373439
|   |   |   |   |   |   |   |   |   start <= 356543
|   |   |   |   |   |   |   |   |   |   start <= 349679
|   |   |   |   |   |   |   |   |   |   |   start <= 346950:
biological_process_ (21.76)
|   |   |   |   |   |   |   |   |   |   |   start > 346950:
transport_ (11.92)
|   |   |   |   |   |   |   |   |   |   start > 349679:
biological_process_ (27.0)
|   |   |   |   |   |   |   |   |   start > 356543
|   |   |   |   |   |   |   |   |   |   start <= 361412
|   |   |   |   |   |   |   |   |   |   |   start <= 357674:
translation_ (11.65)
|   |   |   |   |   |   |   |   |   |   |   start > 357674:
RNA_metabolic_process_ (11.16)
|   |   |   |   |   |   |   |   |   |   start > 361412:
biological_process_ (45.23)
|   |   |   |   |   |   |   |   start > 373439:
lipid_metabolic_process_ (34.07/14.68)
|   |   |   |   |   start > 378219
|   |   |   |   |   |   start <= 482035
|   |   |   |   |   |   |   start <= 421651
|   |   |   |   |   |   |   |   start <= 394524
|   |   |   |   |   |   |   |   |   start <= 379781: cell_cycle_
(19.39)
|   |   |   |   |   |   |   |   |   start > 379781
|   |   |   |   |   |   |   |   |   |   start <= 386825
|   |   |   |   |   |   |   |   |   |   |   start <= 381053:
biological_process_ (10.32)
|   |   |   |   |   |   |   |   |   |   |   start > 381053:
pseudohyphal_growth_ (16.68)
|   |   |   |   |   |   |   |   |   |   start > 386825:
biological_process_ (24.97)
|   |   |   |   |   |   |   |   start > 394524
|   |   |   |   |   |   |   |   |   start <= 401555
|   |   |   |   |   |   |   |   |   |   start <= 400348: transport_
(43.28/19.15)
```

```
|   |   |   |   |   |   |   |   |   |   start > 400348:
membrane_organization_and_biogenesis_ (20.16)
|   |   |   |   |   |   |   |   |   start > 401555
|   |   |   |   |   |   |   |   |   |   start <= 413007
|   |   |   |   |   |   |   |   |   |   |   start <= 407064
|   |   |   |   |   |   |   |   |   |   |   |   start <= 405768:
response_to_stress_ (17.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 405768:
carbohydrate_metabolic_process_ (16.56)
|   |   |   |   |   |   |   |   |   |   |   start > 407064
|   |   |   |   |   |   |   |   |   |   |   |   start <= 410870
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 408425:
biological_process_ (11.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 408425:
response_to_stress_ (15.31)
|   |   |   |   |   |   |   |   |   |   |   |   start > 410870:
biological_process_ (20.22)
|   |   |   |   |   |   |   |   |   |   start > 413007
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
transport_ (19.53/6.0)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (10.5/4.6)
|   |   |   |   |   |   |   start > 421651
|   |   |   |   |   |   |   |   start <= 447441
|   |   |   |   |   |   |   |   |   start <= 432188
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
organelle_organization_and_biogenesis_ (20.85/11.21)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: cell_cycle_
(22.61/12.5)
|   |   |   |   |   |   |   |   |   start > 432188
|   |   |   |   |   |   |   |   |   |   start <= 444688
|   |   |   |   |   |   |   |   |   |   |   start <= 441536
|   |   |   |   |   |   |   |   |   |   |   |   start <= 438645:
translation_ (10.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 438645:
response_to_stress_ (13.23)
|   |   |   |   |   |   |   |   |   |   |   start > 441536:
translation_ (21.05)
|   |   |   |   |   |   |   |   |   |   start > 444688:
electron_transport_ (40.6/16.18)
|   |   |   |   |   |   |   |   start > 447441
|   |   |   |   |   |   |   |   |   start <= 471901
|   |   |   |   |   |   |   |   |   |   start <= 464471
|   |   |   |   |   |   |   |   |   |   |   start <= 457822
|   |   |   |   |   |   |   |   |   |   |   |   start <= 449438:
biological_process_ (22.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 449438:
vesicle-mediated_transport_ (13.98)
|   |   |   |   |   |   |   |   |   |   |   start > 457822
|   |   |   |   |   |   |   |   |   |   |   |   start <= 464452:
translation_ (12.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 464452:
biological_process_ (14.98)
|   |   |   |   |   |   |   |   |   |   start > 464471
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 464773
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 553:
meiosis_ (3.67/0.13)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 553:
cell_cycle_ (28.78/9.55)
|   |   |   |   |   |   |   |   |   |   |   start > 464773
|   |   |   |   |   |   |   |   |   |   |   |   start <= 468214:
vesicle-mediated_transport_ (8.51)
|   |   |   |   |   |   |   |   |   |   |   |   start > 468214:
biological_process_ (13.44)
|   |   |   |   |   |   |   |   |   start > 471901
|   |   |   |   |   |   |   |   |   |   start <= 479535
|   |   |   |   |   |   |   |   |   |   |   start <= 474554:
DNA_metabolic_process_ (23.12)
|   |   |   |   |   |   |   |   |   |   |   start > 474554:
cell_cycle_ (15.46)
|   |   |   |   |   |   |   |   |   |   start > 479535
|   |   |   |   |   |   |   |   |   |   |   start <= 480589:
organelle_organization_and_biogenesis_ (23.42)
|   |   |   |   |   |   |   |   |   |   |   start > 480589:
protein_modification_process_ (15.94)
|   |   |   |   |   |   start > 482035
|   |   |   |   |   |   |   start <= 511826
|   |   |   |   |   |   |   |   start <= 495128
|   |   |   |   |   |   |   |   |   start <= 487709
|   |   |   |   |   |   |   |   |   |   start <= 487441:
translation_ (25.87)
|   |   |   |   |   |   |   |   |   |   start > 487441:
cellular_homeostasis_ (23.04)
|   |   |   |   |   |   |   |   |   start > 487709
|   |   |   |   |   |   |   |   |   |   start <= 493434:
ribosome_biogenesis_and_assembly_ (9.2)
|   |   |   |   |   |   |   |   |   |   start > 493434:
cell_wall_organization_and_biogenesis_ (20.23)
|   |   |   |   |   |   |   |   start > 495128
|   |   |   |   |   |   |   |   |   start <= 502796: transport_
(36.01/16.35)
|   |   |   |   |   |   |   |   |   start > 502796
|   |   |   |   |   |   |   |   |   |   start <= 507506:
translation_ (15.97)
|   |   |   |   |   |   |   |   |   |   start > 507506:
protein_modification_process_ (13.15)
|   |   |   |   |   |   |   start > 511826
|   |   |   |   |   |   |   |   start <= 566192
|   |   |   |   |   |   |   |   |   start <= 525279
|   |   |   |   |   |   |   |   |   |   start <= 519122
|   |   |   |   |   |   |   |   |   |   |   start <= 517643:
biological_process_ (23.92)
|   |   |   |   |   |   |   |   |   |   |   start > 517643: vesicle-
mediated_transport_ (10.78)
|   |   |   |   |   |   |   |   |   |   start > 519122
|   |   |   |   |   |   |   |   |   |   |   start <= 521354:
signal_transduction_ (10.95)
|   |   |   |   |   |   |   |   |   |   |   start > 521354
```

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|   |   |   |   |   |   |   |   |   |   |   |   start <= 523028:
amino_acid_and_derivative_metabolic_process_ (11.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 523028:
cell_wall_organization_and_biogenesis_ (10.78)
|   |   |   |   |   |   |   |   |   start > 525279
|   |   |   |   |   |   |   |   |   |   start <= 546858
|   |   |   |   |   |   |   |   |   |   |   start <= 534076
|   |   |   |   |   |   |   |   |   |   |   |   start <= 528942:
transcription_ (19.27)
|   |   |   |   |   |   |   |   |   |   |   |   start > 528942
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 531509:
biological_process_ (51.06/16.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 531509:
transcription_ (16.47)
|   |   |   |   |   |   |   |   |   |   |   start > 534076
|   |   |   |   |   |   |   |   |   |   |   |   start <= 545030
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 539466:
biological_process_ (12.64)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 539466:
protein_catabolic_process_ (15.19)
|   |   |   |   |   |   |   |   |   |   |   |   start > 545030:
biological_process_ (18.46)
|   |   |   |   |   |   |   |   |   |   start > 546858
|   |   |   |   |   |   |   |   |   |   |   start <= 554571:
response_to_stress_ (10.87)
|   |   |   |   |   |   |   |   |   |   |   start > 554571:
pseudohyphal_growth_ (11.24)
|   |   |   |   |   |   |   |   start > 566192
|   |   |   |   |   |   |   |   |   start <= 612000
|   |   |   |   |   |   |   |   |   |   start <= 578565
|   |   |   |   |   |   |   |   |   |   |   start <= 575099
|   |   |   |   |   |   |   |   |   |   |   |   start <= 571959:
translation_ (19.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 571959
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 573176:
vesicle-mediated_transport_ (18.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 573176:
translation_ (16.61)
|   |   |   |   |   |   |   |   |   |   |   start > 575099:
signal_transduction_ (13.74)
|   |   |   |   |   |   |   |   |   |   start > 578565
|   |   |   |   |   |   |   |   |   |   |   start <= 594426
|   |   |   |   |   |   |   |   |   |   |   |   start <= 586982
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 580251
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: cellular_respiration_ (5.51/0.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: carbohydrate_metabolic_process_ (21.05/7.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 580251:
transcription_ (19.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 586982
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 972:
carbohydrate_metabolic_process_ (14.46/4.39)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 972:
cellular_respiration_ (22.29/5.51)
|   |   |   |   |   |   |   |   |   |   |   start > 594426
|   |   |   |   |   |   |   |   |   |   |   |   start <= 609198:
organelle_organization_and_biogenesis_ (15.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 609198:
translation_ (15.17)
|   |   |   |   |   |   |   |   |   start > 612000
|   |   |   |   |   |   |   |   |   |   start <= 642742
|   |   |   |   |   |   |   |   |   |   |   start <= 619841:
transport_ (15.81)
|   |   |   |   |   |   |   |   |   |   |   start > 619841
|   |   |   |   |   |   |   |   |   |   |   |   start <= 632165
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 627981:
biological_process_ (11.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 627981:
translation_ (17.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 632165
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 633840
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = C: transport_ (9.48/2.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = F: transport_ (16.46/6.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   |
Neigh_GO_aspect = P: biological_process_ (7.67/2.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 633840:
biological_process_ (14.61)
|   |   |   |   |   |   |   |   |   |   start > 642742
|   |   |   |   |   |   |   |   |   |   |   start <= 649304
|   |   |   |   |   |   |   |   |   |   |   |   start <= 644567:
membrane_organization_and_biogenesis_ (17.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 644567:
translation_ (10.05)
|   |   |   |   |   |   |   |   |   |   |   start > 649304:
transport_ (26.92)
|   |   |   |   start > 654211
|   |   |   |   |   start <= 868339
|   |   |   |   |   |   start <= 774574
|   |   |   |   |   |   |   start <= 738321
|   |   |   |   |   |   |   |   start <= 722912
|   |   |   |   |   |   |   |   |   start <= 678873
|   |   |   |   |   |   |   |   |   |   start <= 658748
|   |   |   |   |   |   |   |   |   |   |   start <= 657265:
RNA_metabolic_process_ (19.91)
|   |   |   |   |   |   |   |   |   |   |   start > 657265:
transcription_ (19.63)
|   |   |   |   |   |   |   |   |   |   start > 658748
|   |   |   |   |   |   |   |   |   |   |   start <= 667180:
biological_process_ (20.33)
|   |   |   |   |   |   |   |   |   |   |   start > 667180
|   |   |   |   |   |   |   |   |   |   |   |   start <= 675940:
cytokinesis_ (12.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 675940:
biological_process_ (14.71)
```

```
|   |   |   |   |   |   |   |   |   start > 678873
|   |   |   |   |   |   |   |   |   |   start <= 690696
|   |   |   |   |   |   |   |   |   |   |   start <= 685768
|   |   |   |   |   |   |   |   |   |   |   |   start <= 680867:
amino_acid_and_derivative_metabolic_process_ (14.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 680867
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 684031
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
683112: biological_process_ (14.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
683112: translation_ (16.83)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 684031:
biological_process_ (15.94)
|   |   |   |   |   |   |   |   |   |   |   start > 685768
|   |   |   |   |   |   |   |   |   |   |   |   start <= 689625:
response_to_stress_ (14.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 689625:
sporulation_ (16.78)
|   |   |   |   |   |   |   |   |   |   start > 690696
|   |   |   |   |   |   |   |   |   |   |   start <= 712867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 710202
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 700568:
DNA_metabolic_process_ (16.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 700568:
translation_ (9.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 710202
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 710447:
organelle_organization_and_biogenesis_ (11.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 710447:
meiosis_ (14.41)
|   |   |   |   |   |   |   |   |   |   |   start > 712867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 717087:
biological_process_ (13.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 717087
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 721947:
amino_acid_and_derivative_metabolic_process_ (14.04)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 721947:
translation_ (12.95)
|   |   |   |   |   |   |   |   |   start > 722912
|   |   |   |   |   |   |   |   |   |   start <= 733926
|   |   |   |   |   |   |   |   |   |   |   start <= 727513:
ribosome_biogenesis_and_assembly_ (8.52)
|   |   |   |   |   |   |   |   |   |   |   start > 727513:
protein_modification_process_ (41.75/24.63)
|   |   |   |   |   |   |   |   |   |   start > 733926: transcription_
(23.61)
|   |   |   |   |   |   |   |   start > 738321
|   |   |   |   |   |   |   |   |   start <= 755329
|   |   |   |   |   |   |   |   |   |   start <= 745282
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: conjugation_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: biological_process_ (3.01/1.6)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
signal_transduction_ (2.43/1.22)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: biological_process_ (1.0/0.34)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
signal_transduction_ (19.78/9.73)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
signal_transduction_ (1.57/0.78)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_
|   |   |   |   |   |   |   |   |   |   |   distance <= 2327:
biological_process_ (3.06/0.55)
|   |   |   |   |   |   |   |   |   |   |   distance > 2327:
conjugation_ (2.28/0.93)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
conjugation_ (1.32/0.27)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
conjugation_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoplasmic_membrane-bound_vesicle_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: biological_process_ (5.45/1.95)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
conjugation_ (2.57/0.97)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: conjugation_ (6.3/3.09)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: biological_process_
(4.21/2.53)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: conjugation_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: conjugation_ (1.96/0.48)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: conjugation_ (0.0)
|   |   |   |   |   |   |   |   |   start > 745282
|   |   |   |   |   |   |   |   |   |   start <= 749302
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (11.12/3.96)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cell_cycle_ (12.05/3.45)
```

```
|   |   |   |   |   |   |   |   |   |   start > 749302:
biological_process_ (24.9)
|   |   |   |   |   |   |   |   start > 755329
|   |   |   |   |   |   |   |   |   start <= 770801
|   |   |   |   |   |   |   |   |   |   start <= 758331:
organelle_organization_and_biogenesis_ (27.05/11.71)
|   |   |   |   |   |   |   |   |   |   start > 758331
|   |   |   |   |   |   |   |   |   |   |   start <= 762826:
biological_process_ (27.64)
|   |   |   |   |   |   |   |   |   |   |   start > 762826: meiosis_
(22.36)
|   |   |   |   |   |   |   |   |   start > 770801
|   |   |   |   |   |   |   |   |   |   start <= 772602:
signal_transduction_ (24.62)
|   |   |   |   |   |   |   |   |   |   start > 772602:
organelle_organization_and_biogenesis_ (31.84/13.85)
|   |   |   |   |   |   start > 774574
|   |   |   |   |   |   |   start <= 811008
|   |   |   |   |   |   |   |   start <= 804378
|   |   |   |   |   |   |   |   |   start <= 784858
|   |   |   |   |   |   |   |   |   |   start <= 780108
|   |   |   |   |   |   |   |   |   |   |   start <= 775847:
protein_modification_process_ (12.1)
|   |   |   |   |   |   |   |   |   |   |   start > 775847:
ribosome_biogenesis_and_assembly_ (11.68)
|   |   |   |   |   |   |   |   |   |   start > 780108
|   |   |   |   |   |   |   |   |   |   |   start <= 783678
|   |   |   |   |   |   |   |   |   |   |   |   start <= 780907:
biological_process_ (15.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 780907
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 781995:
vesicle-mediated_transport_ (11.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 781995:
biological_process_ (8.53)
|   |   |   |   |   |   |   |   |   |   |   start > 783678:
cytoskeleton_organization_and_biogenesis_ (13.19)
|   |   |   |   |   |   |   |   |   start > 784858
|   |   |   |   |   |   |   |   |   |   start <= 792532
|   |   |   |   |   |   |   |   |   |   |   start <= 786996:
DNA_metabolic_process_ (11.27)
|   |   |   |   |   |   |   |   |   |   |   start > 786996
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
1732: RNA_metabolic_process_ (13.8/3.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 1732:
DNA_metabolic_process_ (5.59/1.57)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (24.07/5.17)
|   |   |   |   |   |   |   |   |   |   start > 792532
|   |   |   |   |   |   |   |   |   |   |   start <= 803668:
biological_process_ (30.44)
|   |   |   |   |   |   |   |   |   |   |   start > 803668:
protein_modification_process_ (20.09)
|   |   |   |   |   |   |   |   start > 804378
```

```
|   |   |   |   |   |   |   |   |   start <= 807272
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
sporulation_ (14.62/2.74)
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cell_wall_organization_and_biogenesis_ (23.77/9.36)
|   |   |   |   |   |   |   |   |   start > 807272
|   |   |   |   |   |   |   |   |   |   distance <= 2679:
cytoskeleton_organization_and_biogenesis_ (32.5/13.11)
|   |   |   |   |   |   |   |   |   |   distance > 2679: cell_cycle_
(15.05/2.42)
|   |   |   |   |   |   |   start > 811008
|   |   |   |   |   |   |   |   start <= 826384
|   |   |   |   |   |   |   |   |   start <= 818865
|   |   |   |   |   |   |   |   |   |   distance <= 1480:
biological_process_ (44.99/0.1)
|   |   |   |   |   |   |   |   |   |   distance > 1480
|   |   |   |   |   |   |   |   |   |   |   start <= 813984
|   |   |   |   |   |   |   |   |   |   |   |   start <= 811671:
biological_process_ (8.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 811671:
translation_ (12.09)
|   |   |   |   |   |   |   |   |   |   |   start > 813984:
biological_process_ (12.16)
|   |   |   |   |   |   |   |   |   start > 818865
|   |   |   |   |   |   |   |   |   |   start <= 821022
|   |   |   |   |   |   |   |   |   |   |   start <= 820453:
cytoskeleton_organization_and_biogenesis_ (14.94)
|   |   |   |   |   |   |   |   |   |   |   start > 820453:
membrane_organization_and_biogenesis_ (11.07)
|   |   |   |   |   |   |   |   |   |   start > 821022:
cytoskeleton_organization_and_biogenesis_ (15.66)
|   |   |   |   |   |   |   |   start > 826384
|   |   |   |   |   |   |   |   |   start <= 842402
|   |   |   |   |   |   |   |   |   |   start <= 832812:
ribosome_biogenesis_and_assembly_ (60.16/15.73)
|   |   |   |   |   |   |   |   |   |   start > 832812
|   |   |   |   |   |   |   |   |   |   |   start <= 841332
|   |   |   |   |   |   |   |   |   |   |   |   start <= 837673:
RNA_metabolic_process_ (13.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 837673:
translation_ (14.43)
|   |   |   |   |   |   |   |   |   |   |   start > 841332:
RNA_metabolic_process_ (32.65/13.68)
|   |   |   |   |   |   |   |   |   start > 842402
|   |   |   |   |   |   |   |   |   |   start <= 861174
|   |   |   |   |   |   |   |   |   |   |   start <= 848477
|   |   |   |   |   |   |   |   |   |   |   |   start <= 847452:
biological_process_ (26.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 847452:
cytoskeleton_organization_and_biogenesis_ (17.66)
|   |   |   |   |   |   |   |   |   |   |   start > 848477:
biological_process_ (70.2)
|   |   |   |   |   |   |   |   |   |   start > 861174
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 867097:
translation_ (15.16)
|   |   |   |   |   |   |   |   |   |   |   start > 867097:
ribosome_biogenesis_and_assembly_ (14.59)
|   |   |   |   |   start > 868339
|   |   |   |   |   |   start <= 925718
|   |   |   |   |   |   |   start <= 882763
|   |   |   |   |   |   |   |   start <= 875598
|   |   |   |   |   |   |   |   |   start <= 870201
|   |   |   |   |   |   |   |   |   |   start <= 869207:
transcription_ (23.04)
|   |   |   |   |   |   |   |   |   |   start > 869207:
biological_process_ (13.29)
|   |   |   |   |   |   |   |   |   start > 870201: sporulation_
(28.03/13.91)
|   |   |   |   |   |   |   |   start > 875598
|   |   |   |   |   |   |   |   |   start <= 880963: cytokinesis_
(57.63/23.3)
|   |   |   |   |   |   |   |   |   start > 880963: translation_
(15.67)
|   |   |   |   |   |   |   start > 882763
|   |   |   |   |   |   |   |   start <= 896384
|   |   |   |   |   |   |   |   |   start <= 882897
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
biological_process_ (11.84/4.85)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
biological_process_ (5.98/1.62)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
amino_acid_and_derivative_metabolic_process_ (11.48/4.92)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
amino_acid_and_derivative_metabolic_process_ (17.81/3.81)
|   |   |   |   |   |   |   |   |   start > 882897
|   |   |   |   |   |   |   |   |   |   start <= 884512:
DNA_metabolic_process_ (20.47)
|   |   |   |   |   |   |   |   |   |   start > 884512:
biological_process_ (17.28)
|   |   |   |   |   |   |   |   start > 896384
|   |   |   |   |   |   |   |   |   start <= 912819
|   |   |   |   |   |   |   |   |   |   start <= 909340
|   |   |   |   |   |   |   |   |   |   |   start <= 904757:
pseudohyphal_growth_ (14.17)
|   |   |   |   |   |   |   |   |   |   |   start > 904757:
lipid_metabolic_process_ (7.78)
|   |   |   |   |   |   |   |   |   |   start > 909340:
RNA_metabolic_process_ (15.27)
|   |   |   |   |   |   |   |   |   start > 912819
|   |   |   |   |   |   |   |   |   |   start <= 916027:
protein_modification_process_ (17.33)
|   |   |   |   |   |   |   |   |   |   start > 916027: vesicle-
mediated_transport_ (13.73)
|   |   |   |   |   |   start > 925718
|   |   |   |   |   |   |   start <= 949770
|   |   |   |   |   |   |   |   start <= 944593
```

```
|   |   |   |   |   |   |   |   |   start <= 931800: transport_
(19.04)
|   |   |   |   |   |   |   |   |   start > 931800:
organelle_organization_and_biogenesis_ (45.25/9.86)
|   |   |   |   |   |   |   |   start > 944593:
cell_wall_organization_and_biogenesis_ (24.76/10.59)
|   |   |   |   |   |   |   start > 949770
|   |   |   |   |   |   |   |   start <= 967622
|   |   |   |   |   |   |   |   |   start <= 954341: transcription_
(14.81)
|   |   |   |   |   |   |   |   |   start > 954341
|   |   |   |   |   |   |   |   |   |   start <= 958829:
sporulation_ (17.83)
|   |   |   |   |   |   |   |   |   |   start > 958829:
transcription_ (10.34)
|   |   |   |   |   |   |   |   start > 967622
|   |   |   |   |   |   |   |   |   start <= 980680: translation_
(24.5)
|   |   |   |   |   |   |   |   |   start > 980680:
DNA_metabolic_process_ (6.86)
|   |   |   strand = C
|   |   |   |   start <= 593058
|   |   |   |   |   start <= 421651
|   |   |   |   |   |   start <= 397668
|   |   |   |   |   |   |   start <= 316939
|   |   |   |   |   |   |   |   start <= 282165
|   |   |   |   |   |   |   |   |   start <= 271371
|   |   |   |   |   |   |   |   |   |   start <= 270421
|   |   |   |   |   |   |   |   |   |   |   start <= 254296:
translation_ (14.14)
|   |   |   |   |   |   |   |   |   |   |   start > 254296
|   |   |   |   |   |   |   |   |   |   |   |   start <= 268188
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 259924:
biological_process_ (13.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 259924:
transport_ (13.58)
|   |   |   |   |   |   |   |   |   |   |   |   start > 268188:
biological_process_ (14.39)
|   |   |   |   |   |   |   |   |   |   start > 270421:
transcription_ (20.62)
|   |   |   |   |   |   |   |   |   start > 271371
|   |   |   |   |   |   |   |   |   |   start <= 277087
|   |   |   |   |   |   |   |   |   |   |   start <= 273725:
organelle_organization_and_biogenesis_ (12.58)
|   |   |   |   |   |   |   |   |   |   |   start > 273725:
transport_ (44.11/16.87)
|   |   |   |   |   |   |   |   |   |   start > 277087:
biological_process_ (18.17)
|   |   |   |   |   |   |   |   start > 282165
|   |   |   |   |   |   |   |   |   start <= 303036
|   |   |   |   |   |   |   |   |   |   start <= 292530
|   |   |   |   |   |   |   |   |   |   |   start <= 288421:
ribosome_biogenesis_and_assembly_ (14.11)
```

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|   |   |   |   |   |   |   |   |   |   |   start > 288421: vesicle-
mediated_transport_ (17.88)
|   |   |   |   |   |   |   |   |   |   start > 292530
|   |   |   |   |   |   |   |   |   |   |   start <= 297079:
signal_transduction_ (15.18)
|   |   |   |   |   |   |   |   |   |   |   start > 297079:
protein_catabolic_process_ (21.68)
|   |   |   |   |   |   |   |   |   start > 303036
|   |   |   |   |   |   |   |   |   |   start <= 312368
|   |   |   |   |   |   |   |   |   |   |   start <= 305350:
transcription_ (15.72)
|   |   |   |   |   |   |   |   |   |   |   start > 305350
|   |   |   |   |   |   |   |   |   |   |   |   start <= 310313:
organelle_organization_and_biogenesis_ (15.32)
|   |   |   |   |   |   |   |   |   |   |   |   start > 310313:
biological_process_ (14.79)
|   |   |   |   |   |   |   |   |   |   start > 312368
|   |   |   |   |   |   |   |   |   |   |   start <= 315388:
DNA_metabolic_process_ (11.61)
|   |   |   |   |   |   |   |   |   |   |   start > 315388:
transcription_ (23.2)
|   |   |   |   |   |   |   start > 316939
|   |   |   |   |   |   |   |   start <= 386825
|   |   |   |   |   |   |   |   |   start <= 356543
|   |   |   |   |   |   |   |   |   |   start <= 338622
|   |   |   |   |   |   |   |   |   |   |   start <= 329418
|   |   |   |   |   |   |   |   |   |   |   |   start <= 322995:
protein_modification_process_ (18.56)
|   |   |   |   |   |   |   |   |   |   |   |   start > 322995:
lipid_metabolic_process_ (8.95)
|   |   |   |   |   |   |   |   |   |   |   start > 329418
|   |   |   |   |   |   |   |   |   |   |   |   start <= 337344:
DNA_metabolic_process_ (9.01)
|   |   |   |   |   |   |   |   |   |   |   |   start > 337344:
biological_process_ (10.53)
|   |   |   |   |   |   |   |   |   |   start > 338622
|   |   |   |   |   |   |   |   |   |   |   start <= 349679
|   |   |   |   |   |   |   |   |   |   |   |   start <= 342415
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 339979:
response_to_stress_ (17.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 339979
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
340372: translation_ (10.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
340372: cell_wall_organization_and_biogenesis_ (7.98)
|   |   |   |   |   |   |   |   |   |   |   |   start > 342415
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 344335:
DNA_metabolic_process_ (12.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 344335:
response_to_stress_ (21.1)
|   |   |   |   |   |   |   |   |   |   |   start > 349679:
translation_ (16.35)
|   |   |   |   |   |   |   |   |   start > 356543
|   |   |   |   |   |   |   |   |   |   start <= 375857
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 364369:
transport_ (15.34)
|   |   |   |   |   |   |   |   |   |   |   start > 364369
|   |   |   |   |   |   |   |   |   |   |   |   start <= 371685:
biological_process_ (23.64)
|   |   |   |   |   |   |   |   |   |   |   |   start > 371685
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 373439:
ribosome_biogenesis_and_assembly_ (12.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 373439:
biological_process_ (17.47)
|   |   |   |   |   |   |   |   |   |   start > 375857
|   |   |   |   |   |   |   |   |   |   |   start <= 381053:
protein_modification_process_ (9.21)
|   |   |   |   |   |   |   |   |   |   |   start > 381053:
response_to_stress_ (16.74)
|   |   |   |   |   |   |   |   start > 386825
|   |   |   |   |   |   |   |   |   start <= 394524
|   |   |   |   |   |   |   |   |   |   start <= 392176:
pseudohyphal_growth_ (18.06)
|   |   |   |   |   |   |   |   |   |   start > 392176:
DNA_metabolic_process_ (30.12)
|   |   |   |   |   |   |   |   |   start > 394524
|   |   |   |   |   |   |   |   |   |   start <= 397086: vesicle-
mediated_transport_ (18.09)
|   |   |   |   |   |   |   |   |   |   start > 397086:
biological_process_ (13.96)
|   |   |   |   |   |   start > 397668
|   |   |   |   |   |   |   start <= 401555:
cytoskeleton_organization_and_biogenesis_ (20.59)
|   |   |   |   |   |   |   start > 401555
|   |   |   |   |   |   |   |   start <= 410870
|   |   |   |   |   |   |   |   |   start <= 405768:
RNA_metabolic_process_ (9.9)
|   |   |   |   |   |   |   |   |   start > 405768:
ribosome_biogenesis_and_assembly_ (55.14/23.1)
|   |   |   |   |   |   |   |   start > 410870
|   |   |   |   |   |   |   |   |   start <= 415908: translation_
(31.17)
|   |   |   |   |   |   |   |   |   start > 415908
|   |   |   |   |   |   |   |   |   |   start <= 417682:
signal_transduction_ (17.49)
|   |   |   |   |   |   |   |   |   |   start > 417682:
RNA_metabolic_process_ (26.55/12.92)
|   |   |   |   |   start > 421651
|   |   |   |   |   |   start <= 515245
|   |   |   |   |   |   |   start <= 454215
|   |   |   |   |   |   |   |   start <= 444688
|   |   |   |   |   |   |   |   |   start <= 427226
|   |   |   |   |   |   |   |   |   |   start <= 423733:
membrane_organization_and_biogenesis_ (17.67)
|   |   |   |   |   |   |   |   |   |   start > 423733:
biological_process_ (27.29)
|   |   |   |   |   |   |   |   |   start > 427226
|   |   |   |   |   |   |   |   |   |   start <= 436347
```

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|   |   |   |   |   |   |   |   |   |   |   start <= 432188
|   |   |   |   |   |   |   |   |   |   |   |   start <= 429859:
cell_cycle_ (14.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 429859:
ribosome_biogenesis_and_assembly_ (18.12)
|   |   |   |   |   |   |   |   |   |   |   start > 432188:
cytokinesis_ (39.16/12.99)
|   |   |   |   |   |   |   |   |   |   start > 436347
|   |   |   |   |   |   |   |   |   |   |   start <= 441536
|   |   |   |   |   |   |   |   |   |   |   |   start <= 440260:
biological_process_ (8.68)
|   |   |   |   |   |   |   |   |   |   |   |   start > 440260:
organelle_organization_and_biogenesis_ (13.02)
|   |   |   |   |   |   |   |   |   |   |   start > 441536:
biological_process_ (16.01)
|   |   |   |   |   |   |   |   start > 444688
|   |   |   |   |   |   |   |   |   start <= 453770
|   |   |   |   |   |   |   |   |   |   start <= 449438:
protein_modification_process_ (47.0/22.73)
|   |   |   |   |   |   |   |   |   |   start > 449438:
lipid_metabolic_process_ (42.42/17.22)
|   |   |   |   |   |   |   |   |   start > 453770:
membrane_organization_and_biogenesis_ (31.81/10.8)
|   |   |   |   |   |   |   start > 454215
|   |   |   |   |   |   |   |   start <= 474554
|   |   |   |   |   |   |   |   |   start <= 468214
|   |   |   |   |   |   |   |   |   |   start <= 461278
|   |   |   |   |   |   |   |   |   |   |   start <= 457822:
vesicle-mediated_transport_ (9.69)
|   |   |   |   |   |   |   |   |   |   |   start > 457822:
transport_ (14.96)
|   |   |   |   |   |   |   |   |   |   start > 461278:
DNA_metabolic_process_ (12.94)
|   |   |   |   |   |   |   |   |   start > 468214
|   |   |   |   |   |   |   |   |   |   start <= 472727:
RNA_metabolic_process_ (18.58)
|   |   |   |   |   |   |   |   |   |   start > 472727:
cellular_homeostasis_ (22.51)
|   |   |   |   |   |   |   |   start > 474554
|   |   |   |   |   |   |   |   |   start <= 507506
|   |   |   |   |   |   |   |   |   |   start <= 490830
|   |   |   |   |   |   |   |   |   |   |   start <= 487709
|   |   |   |   |   |   |   |   |   |   |   |   start <= 482035:
lipid_metabolic_process_ (10.49)
|   |   |   |   |   |   |   |   |   |   |   |   start > 482035:
biological_process_ (21.84)
|   |   |   |   |   |   |   |   |   |   |   start > 487709: vesicle-
mediated_transport_ (20.88)
|   |   |   |   |   |   |   |   |   |   start > 490830
|   |   |   |   |   |   |   |   |   |   |   start <= 502796:
biological_process_ (45.8)
|   |   |   |   |   |   |   |   |   |   |   start > 502796
|   |   |   |   |   |   |   |   |   |   |   |   start <= 505795:
ribosome_biogenesis_and_assembly_ (16.29)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 505795:
biological_process_ (15.34)
|   |   |   |   |   |   |   |   |   start > 507506
|   |   |   |   |   |   |   |   |   |   start <= 511826:
nuclear_organization_and_biogenesis_ (27.73/13.36)
|   |   |   |   |   |   |   |   |   |   start > 511826:
lipid_metabolic_process_ (33.54)
|   |   |   |   |   |   start > 515245
|   |   |   |   |   |   |   start <= 554571
|   |   |   |   |   |   |   |   start <= 552888
|   |   |   |   |   |   |   |   |   start <= 546858
|   |   |   |   |   |   |   |   |   |   start <= 539466
|   |   |   |   |   |   |   |   |   |   |   start <= 525279:
protein_modification_process_ (7.06)
|   |   |   |   |   |   |   |   |   |   |   start > 525279:
transport_ (33.19/11.79)
|   |   |   |   |   |   |   |   |   |   start > 539466:
transcription_ (22.3)
|   |   |   |   |   |   |   |   |   start > 546858
|   |   |   |   |   |   |   |   |   |   start <= 551115:
ribosome_biogenesis_and_assembly_ (32.08/11.05)
|   |   |   |   |   |   |   |   |   |   start > 551115:
response_to_stress_ (41.49/24.41)
|   |   |   |   |   |   |   |   start > 552888
|   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   distance <= 549:
transcription_ (3.25/0.96)
|   |   |   |   |   |   |   |   |   |   |   distance > 549:
RNA_metabolic_process_ (2.46/0.95)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (18.0/7.33)
|   |   |   |   |   |   |   |   |   neigh_strand = W:
RNA_metabolic_process_ (30.98/14.82)
|   |   |   |   |   |   |   start > 554571
|   |   |   |   |   |   |   |   start <= 569559
|   |   |   |   |   |   |   |   |   start <= 558643:
protein_modification_process_ (17.78)
|   |   |   |   |   |   |   |   |   start > 558643
|   |   |   |   |   |   |   |   |   |   start <= 566192:
biological_process_ (56.23)
|   |   |   |   |   |   |   |   |   |   start > 566192
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
biological_process_ (12.43/2.16)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_homeostasis_ (15.74/5.49)
|   |   |   |   |   |   |   |   start > 569559
|   |   |   |   |   |   |   |   |   start <= 583682
|   |   |   |   |   |   |   |   |   |   start <= 570808: transport_
(27.93/13.11)
|   |   |   |   |   |   |   |   |   |   start > 570808
|   |   |   |   |   |   |   |   |   |   |   start <= 575099:
biological_process_ (14.73)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 575099:
transport_ (17.7)
|   |   |   |   |   |   |   |   |   start > 583682
|   |   |   |   |   |   |   |   |   |   start <= 586982:
protein_modification_process_ (15.08)
|   |   |   |   |   |   |   |   |   |   start > 586982:
response_to_stress_ (21.56)
|   |   |   |   start > 593058
|   |   |   |   |   start <= 842816
|   |   |   |   |   |   start <= 761266
|   |   |   |   |   |   |   start <= 679358
|   |   |   |   |   |   |   |   start <= 644567
|   |   |   |   |   |   |   |   |   start <= 609198
|   |   |   |   |   |   |   |   |   |   start <= 605093
|   |   |   |   |   |   |   |   |   |   |   start <= 594426:
translation_ (15.84)
|   |   |   |   |   |   |   |   |   |   |   start > 594426
|   |   |   |   |   |   |   |   |   |   |   |   start <= 602343:
vitamin_metabolic_process_ (10.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 602343:
DNA_metabolic_process_ (11.22)
|   |   |   |   |   |   |   |   |   |   start > 605093
|   |   |   |   |   |   |   |   |   |   |   start <= 606608:
ribosome_biogenesis_and_assembly_ (15.56)
|   |   |   |   |   |   |   |   |   |   |   start > 606608:
RNA_metabolic_process_ (23.34)
|   |   |   |   |   |   |   |   |   start > 609198
|   |   |   |   |   |   |   |   |   |   start <= 630541
|   |   |   |   |   |   |   |   |   |   |   start <= 616672
|   |   |   |   |   |   |   |   |   |   |   |   start <= 612000:
protein_modification_process_ (35.75/15.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 612000:
transcription_ (12.15)
|   |   |   |   |   |   |   |   |   |   |   start > 616672
|   |   |   |   |   |   |   |   |   |   |   |   start <= 627981:
biological_process_ (36.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 627981
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
3516: DNA_metabolic_process_ (11.98/5.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
3516: organelle_organization_and_biogenesis_ (2.82/0.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
biological_process_ (32.26/18.63)
|   |   |   |   |   |   |   |   |   |   start > 630541
|   |   |   |   |   |   |   |   |   |   |   start <= 633840
|   |   |   |   |   |   |   |   |   |   |   |   start <= 632165:
protein_catabolic_process_ (22.09)
|   |   |   |   |   |   |   |   |   |   |   |   start > 632165:
RNA_metabolic_process_ (18.43)
|   |   |   |   |   |   |   |   |   |   |   start > 633840
|   |   |   |   |   |   |   |   |   |   |   |   start <= 639268:
biological_process_ (27.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 639268
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 642742:
transport_ (14.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 642742:
biological_process_ (24.07)
|   |   |   |   |   |   |   |   start > 644567
|   |   |   |   |   |   |   |   |   start <= 662402
|   |   |   |   |   |   |   |   |   |   start <= 649304
|   |   |   |   |   |   |   |   |   |   |   start <= 648503:
transcription_ (14.61)
|   |   |   |   |   |   |   |   |   |   |   start > 648503:
translation_ (9.74)
|   |   |   |   |   |   |   |   |   |   start > 649304:
lipid_metabolic_process_ (53.18/16.03)
|   |   |   |   |   |   |   |   |   start > 662402
|   |   |   |   |   |   |   |   |   |   start <= 670242
|   |   |   |   |   |   |   |   |   |   |   start <= 667180
|   |   |   |   |   |   |   |   |   |   |   |   start <= 663886:
translation_ (9.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 663886
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= C: cell_wall_organization_and_biogenesis_ (7.56/2.53)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= F: cell_wall_organization_and_biogenesis_ (4.34/1.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect
= P: sporulation_ (13.99/4.1)
|   |   |   |   |   |   |   |   |   |   |   start > 667180: meiosis_
(13.47)
|   |   |   |   |   |   |   |   |   |   start > 670242
|   |   |   |   |   |   |   |   |   |   |   start <= 675940
|   |   |   |   |   |   |   |   |   |   |   |   start <= 672412:
transcription_ (11.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 672412:
lipid_metabolic_process_ (13.11)
|   |   |   |   |   |   |   |   |   |   |   start > 675940:
translation_ (20.51)
|   |   |   |   |   |   |   start > 679358
|   |   |   |   |   |   |   |   start <= 747283
|   |   |   |   |   |   |   |   |   start <= 722912
|   |   |   |   |   |   |   |   |   |   start <= 700568
|   |   |   |   |   |   |   |   |   |   |   start <= 680867:
ribosome_biogenesis_and_assembly_ (27.56/10.34)
|   |   |   |   |   |   |   |   |   |   |   start > 680867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 690696:
nuclear_organization_and_biogenesis_ (8.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 690696:
transport_ (17.09)
|   |   |   |   |   |   |   |   |   |   start > 700568
|   |   |   |   |   |   |   |   |   |   |   start <= 717087
|   |   |   |   |   |   |   |   |   |   |   |   start <= 712867
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 704225:
biological_process_ (11.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 704225:
transcription_ (24.13)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 712867:
biological_process_ (15.28)
|   |   |   |   |   |   |   |   |   |   |   start > 717087
|   |   |   |   |   |   |   |   |   |   |   |   start <= 720066:
meiosis_ (10.54)
|   |   |   |   |   |   |   |   |   |   |   |   start > 720066:
ribosome_biogenesis_and_assembly_ (28.03/11.06)
|   |   |   |   |   |   |   |   |   start > 722912
|   |   |   |   |   |   |   |   |   |   start <= 745282
|   |   |   |   |   |   |   |   |   |   |   start <= 738321
|   |   |   |   |   |   |   |   |   |   |   |   start <= 733926
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 727513:
biological_process_ (11.61)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 727513:
transcription_ (13.15)
|   |   |   |   |   |   |   |   |   |   |   |   start > 733926:
biological_process_ (38.53/17.7)
|   |   |   |   |   |   |   |   |   |   |   start > 738321
|   |   |   |   |   |   |   |   |   |   |   |   start <= 742911:
organelle_organization_and_biogenesis_ (25.2)
|   |   |   |   |   |   |   |   |   |   |   |   start > 742911:
transcription_ (17.32)
|   |   |   |   |   |   |   |   |   |   start > 745282:
biological_process_ (34.04)
|   |   |   |   |   |   |   |   start > 747283
|   |   |   |   |   |   |   |   |   start <= 755329
|   |   |   |   |   |   |   |   |   |   start <= 749302: transport_
(37.84/13.38)
|   |   |   |   |   |   |   |   |   |   start > 749302:
protein_modification_process_ (14.19)
|   |   |   |   |   |   |   |   |   start > 755329
|   |   |   |   |   |   |   |   |   |   start <= 759783
|   |   |   |   |   |   |   |   |   |   |   start <= 758331:
cellular_respiration_ (11.41)
|   |   |   |   |   |   |   |   |   |   |   start > 758331:
ribosome_biogenesis_and_assembly_ (31.99/15.02)
|   |   |   |   |   |   |   |   |   |   start > 759783:
transcription_ (16.21)
|   |   |   |   |   |   start > 761266
|   |   |   |   |   |   |   start <= 800732
|   |   |   |   |   |   |   |   start <= 789858
|   |   |   |   |   |   |   |   |   start <= 772602:
biological_process_ (39.03/11.38)
|   |   |   |   |   |   |   |   |   start > 772602
|   |   |   |   |   |   |   |   |   |   start <= 783678:
translation_ (9.24)
|   |   |   |   |   |   |   |   |   |   start > 783678:
cell_wall_organization_and_biogenesis_ (35.88/15.58)
|   |   |   |   |   |   |   |   start > 789858
|   |   |   |   |   |   |   |   |   start <= 795333
|   |   |   |   |   |   |   |   |   |   start <= 792532:
ribosome_biogenesis_and_assembly_ (25.38)
|   |   |   |   |   |   |   |   |   |   start > 792532:
lipid_metabolic_process_ (21.48)
```

```
|   |   |   |   |   |   |   |   |   start > 795333
|   |   |   |   |   |   |   |   |   |   start <= 797677:
biological_process_ (13.56)
|   |   |   |   |   |   |   |   |   |   start > 797677: cell_cycle_
(14.36)
|   |   |   |   |   |   |   start > 800732
|   |   |   |   |   |   |   |   start <= 837673
|   |   |   |   |   |   |   |   |   start <= 820453
|   |   |   |   |   |   |   |   |   |   start <= 807272
|   |   |   |   |   |   |   |   |   |   |   start <= 802308:
RNA_metabolic_process_ (15.94)
|   |   |   |   |   |   |   |   |   |   |   start > 802308
|   |   |   |   |   |   |   |   |   |   |   |   start <= 804378:
biological_process_ (13.88)
|   |   |   |   |   |   |   |   |   |   |   |   start > 804378:
transport_ (15.41)
|   |   |   |   |   |   |   |   |   |   start > 807272:
protein_catabolic_process_ (62.62)
|   |   |   |   |   |   |   |   |   start > 820453
|   |   |   |   |   |   |   |   |   |   start <= 824866:
cellular_homeostasis_ (21.76)
|   |   |   |   |   |   |   |   |   |   start > 824866
|   |   |   |   |   |   |   |   |   |   |   start <= 832812
|   |   |   |   |   |   |   |   |   |   |   |   start <= 826384:
biological_process_ (15.73)
|   |   |   |   |   |   |   |   |   |   |   |   start > 826384
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 830573:
organelle_organization_and_biogenesis_ (19.95)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 830573:
biological_process_ (10.96)
|   |   |   |   |   |   |   |   |   |   |   start > 832812:
transport_ (19.98)
|   |   |   |   |   |   |   |   start > 837673
|   |   |   |   |   |   |   |   |   start <= 841332: sporulation_
(14.97)
|   |   |   |   |   |   |   |   |   start > 841332:
RNA_metabolic_process_ (33.21/15.94)
|   |   |   |   |   start > 842816
|   |   |   |   |   |   start <= 909340
|   |   |   |   |   |   |   start <= 889020
|   |   |   |   |   |   |   |   start <= 861174
|   |   |   |   |   |   |   |   |   start <= 853356
|   |   |   |   |   |   |   |   |   |   start <= 844629:
DNA_metabolic_process_ (19.71)
|   |   |   |   |   |   |   |   |   |   start > 844629
|   |   |   |   |   |   |   |   |   |   |   start <= 848477
|   |   |   |   |   |   |   |   |   |   |   |   start <= 845791:
biological_process_ (15.84)
|   |   |   |   |   |   |   |   |   |   |   |   start > 845791:
transcription_ (12.57)
|   |   |   |   |   |   |   |   |   |   |   start > 848477
|   |   |   |   |   |   |   |   |   |   |   |   start <= 851838:
ribosome_biogenesis_and_assembly_ (19.14)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 851838:
biological_process_ (15.54)
|   |   |   |   |   |   |   |   |   start > 853356
|   |   |   |   |   |   |   |   |   |   start <= 854258:
translation_ (17.36)
|   |   |   |   |   |   |   |   |   |   start > 854258:
DNA_metabolic_process_ (13.79)
|   |   |   |   |   |   |   |   start > 861174
|   |   |   |   |   |   |   |   |   start <= 870201:
biological_process_ (41.03)
|   |   |   |   |   |   |   |   |   start > 870201
|   |   |   |   |   |   |   |   |   |   start <= 875598:
response_to_stress_ (19.25)
|   |   |   |   |   |   |   |   |   |   start > 875598
|   |   |   |   |   |   |   |   |   |   |   start <= 882897:
transcription_ (27.39)
|   |   |   |   |   |   |   |   |   |   |   start > 882897:
biological_process_ (12.56)
|   |   |   |   |   |   |   start > 889020
|   |   |   |   |   |   |   |   start <= 896384
|   |   |   |   |   |   |   |   |   start <= 894089: transport_
(33.95/8.51)
|   |   |   |   |   |   |   |   |   start > 894089:
RNA_metabolic_process_ (11.32)
|   |   |   |   |   |   |   |   start > 896384
|   |   |   |   |   |   |   |   |   start <= 901191
|   |   |   |   |   |   |   |   |   |   start <= 899925
|   |   |   |   |   |   |   |   |   |   |   start <= 898357:
ribosome_biogenesis_and_assembly_ (13.39)
|   |   |   |   |   |   |   |   |   |   |   start > 898357:
biological_process_ (22.85)
|   |   |   |   |   |   |   |   |   |   start > 899925: translation_
(21.36/8.47)
|   |   |   |   |   |   |   |   |   start > 901191
|   |   |   |   |   |   |   |   |   |   start <= 907552
|   |   |   |   |   |   |   |   |   |   |   start <= 904757:
sporulation_ (11.42)
|   |   |   |   |   |   |   |   |   |   |   start > 904757:
transport_ (13.54)
|   |   |   |   |   |   |   |   |   |   start > 907552:
biological_process_ (15.51)
|   |   |   |   |   |   start > 909340
|   |   |   |   |   |   |   start <= 944593
|   |   |   |   |   |   |   |   start <= 925718
|   |   |   |   |   |   |   |   |   start <= 921059
|   |   |   |   |   |   |   |   |   |   start <= 916027:
protein_modification_process_ (15.32)
|   |   |   |   |   |   |   |   |   |   start > 916027:
DNA_metabolic_process_ (17.02)
|   |   |   |   |   |   |   |   |   start > 921059
|   |   |   |   |   |   |   |   |   |   start <= 922902:
amino_acid_and_derivative_metabolic_process_ (19.6)
|   |   |   |   |   |   |   |   |   |   start > 922902:
response_to_stress_ (11.86)
```

```
|   |   |   |   |   |   |   |   start > 925718
|   |   |   |   |   |   |   |   |   start <= 939346: vesicle-
mediated_transport_ (43.25)
|   |   |   |   |   |   |   |   |   start > 939346:
DNA_metabolic_process_ (16.22)
|   |   |   |   |   |   |   start > 944593
|   |   |   |   |   |   |   |   start <= 960984
|   |   |   |   |   |   |   |   |   start <= 958829
|   |   |   |   |   |   |   |   |   |   start <= 949770:
translation_ (11.29)
|   |   |   |   |   |   |   |   |   |   start > 949770:
protein_modification_process_ (15.16)
|   |   |   |   |   |   |   |   |   start > 958829:
ribosome_biogenesis_and_assembly_ (18.42)
|   |   |   |   |   |   |   |   start > 960984
|   |   |   |   |   |   |   |   |   start <= 967622:
biological_process_ (18.52)
|   |   |   |   |   |   |   |   |   start > 967622: transcription_
(8.52)
|   start > 981825
|   |   start <= 1036832
|   |   |   strand = W
|   |   |   |   start <= 1010159
|   |   |   |   |   start <= 1000825: biological_process_ (43.83)
|   |   |   |   |   start > 1000825
|   |   |   |   |   |   start <= 1005135: cellular_respiration_
(20.69)
|   |   |   |   |   |   start > 1005135
|   |   |   |   |   |   |   start <= 1007219:
vitamin_metabolic_process_ (18.18)
|   |   |   |   |   |   |   start > 1007219: transcription_ (12.15)
|   |   |   |   start > 1010159
|   |   |   |   |   start <= 1017650: RNA_metabolic_process_ (12.04)
|   |   |   |   |   start > 1017650
|   |   |   |   |   |   start <= 1030992
|   |   |   |   |   |   |   start <= 1026005:
cytoskeleton_organization_and_biogenesis_ (13.84)
|   |   |   |   |   |   |   start > 1026005
|   |   |   |   |   |   |   |   distance <= 6792
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
DNA_metabolic_process_ (14.86/7.52)
|   |   |   |   |   |   |   |   |   neigh_num > 1: cell_cycle_
(23.66/12.96)
|   |   |   |   |   |   |   |   distance > 6792: meiosis_
(14.65/6.62)
|   |   |   |   |   |   start > 1030992:
cytoskeleton_organization_and_biogenesis_ (21.98)
|   |   |   strand = C
|   |   |   |   start <= 1011187
|   |   |   |   |   start <= 994852
|   |   |   |   |   |   start <= 989786
|   |   |   |   |   |   |   start <= 986459: biological_process_
(13.85)
|   |   |   |   |   |   |   start > 986459: transport_ (14.49)
```

```
|   |   |   |   |   |   start > 989786: biological_process_ (13.92)
|   |   |   |   |   start > 994852
|   |   |   |   |   |   start <= 1005135
|   |   |   |   |   |   |   start <= 1000825
|   |   |   |   |   |   |   |   start <= 997210: meiosis_ (21.42)
|   |   |   |   |   |   |   |   start > 997210: signal_transduction_
(18.17)
|   |   |   |   |   |   |   start > 1000825
|   |   |   |   |   |   |   |   neigh_num <= 1: meiosis_
(23.39/11.07)
|   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   distance <= 3140: meiosis_
(9.18/4.37)
|   |   |   |   |   |   |   |   |   distance > 3140: cell_cycle_
(25.46/14.48)
|   |   |   |   |   |   start > 1005135: biological_process_ (13.94)
|   |   |   |   start > 1011187
|   |   |   |   |   start <= 1028623
|   |   |   |   |   |   start <= 1018744
|   |   |   |   |   |   |   start <= 1017650
|   |   |   |   |   |   |   |   start <= 1014819:
signal_transduction_ (12.6)
|   |   |   |   |   |   |   |   start > 1014819: translation_
(13.09)
|   |   |   |   |   |   |   start > 1017650:
protein_catabolic_process_ (21.49)
|   |   |   |   |   |   start > 1018744
|   |   |   |   |   |   |   start <= 1026841
|   |   |   |   |   |   |   |   start <= 1023210:
organelle_organization_and_biogenesis_ (14.12)
|   |   |   |   |   |   |   |   start > 1023210: biological_process_
(12.19)
|   |   |   |   |   |   |   start > 1026841: translation_ (22.46)
|   |   |   |   |   start > 1028623
|   |   |   |   |   |   start <= 1030992: transport_ (23.09)
|   |   |   |   |   |   start > 1030992
|   |   |   |   |   |   |   start <= 1034180: signal_transduction_
(18.49)
|   |   |   |   |   |   |   start > 1034180: cell_cycle_ (17.05)
|   |   start > 1036832
|   |   |   start <= 1061053
|   |   |   |   start <= 1051288
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 1046224
|   |   |   |   |   |   |   start <= 1045194: biological_process_
(31.93)
|   |   |   |   |   |   |   start > 1045194:
generation_of_precursor_metabolites_and_energy_ (29.24/12.8)
|   |   |   |   |   |   start > 1046224: biological_process_ (33.31)
|   |   |   |   |   strand = C:
amino_acid_and_derivative_metabolic_process_ (10.23)
|   |   |   |   start > 1051288
|   |   |   |   |   start <= 1058421
|   |   |   |   |   |   start <= 1055543: transport_ (16.38)
```

```
|   |   |   |   |   |   start > 1055543: biological_process_ (13.51)
|   |   |   |   |   start > 1058421: transport_ (28.64)
|   |   |   start > 1061053
|   |   |   |   strand = W
|   |   |   |   |   start <= 1070239
|   |   |   |   |   |   start <= 1065041: biological_process_
(26.02)
|   |   |   |   |   |   start > 1065041: DNA_metabolic_process_
(7.94)
|   |   |   |   |   start > 1070239: biological_process_ (71.16)
|   |   |   |   strand = C: biological_process_ (68.75/13.95)
```

Decision Tree Generated for Chromosome Sixteen:
For Cellular Component

```
|   start <= 688169
|   |   start <= 96258
|   |   |   start <= 44344
|   |   |   |   start <= 38169
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 15355
|   |   |   |   |   |   |   start <= 6007: mitochondrion_ (3.03)
|   |   |   |   |   |   |   start > 6007: cellular_component_
(59.39)
|   |   |   |   |   |   start > 15355
|   |   |   |   |   |   |   start <= 16868: membrane_fraction_
(15.96)
|   |   |   |   |   |   |   start > 16868: cellular_component_
(15.2)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 30482
|   |   |   |   |   |   |   start <= 25087
|   |   |   |   |   |   |   |   start <= 22938
|   |   |   |   |   |   |   |   |   start <= 16868:
cellular_component_ (12.17)
|   |   |   |   |   |   |   |   |   start > 16868: plasma_membrane_
(9.72)
|   |   |   |   |   |   |   |   start > 22938: nucleus_ (21.21/8.74)
|   |   |   |   |   |   |   start > 25087: mitochondrion_ (32.44)
|   |   |   |   |   |   start > 30482
|   |   |   |   |   |   |   start <= 33013: cell_cortex_ (22.46)
|   |   |   |   |   |   |   start > 33013
|   |   |   |   |   |   |   |   start <= 35236: nucleus_ (19.42)
|   |   |   |   |   |   |   |   start > 35236: cellular_component_
(14.54)
|   |   |   |   start > 38169
|   |   |   |   |   strand = C: membrane_ (13.58)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 39121: nucleolus_ (14.46)
|   |   |   |   |   |   start > 39121: plasma_membrane_ (14.62)
|   |   |   start > 44344
|   |   |   |   start <= 88517
|   |   |   |   |   start <= 74719
|   |   |   |   |   |   start <= 66614
```

```
|   |   |   |   |   |   |   start <= 52671
|   |   |   |   |   |   |   |   start <= 49303
|   |   |   |   |   |   |   |   |   start <= 47336
|   |   |   |   |   |   |   |   |   |   start <= 46506: cytoplasm_
(13.47)
|   |   |   |   |   |   |   |   |   |   start > 46506:
mitochondrion_ (10.32)
|   |   |   |   |   |   |   |   |   start > 47336: nucleus_
(39.6/19.71)
|   |   |   |   |   |   |   |   start > 49303: Golgi_apparatus_
(8.13)
|   |   |   |   |   |   |   start > 52671
|   |   |   |   |   |   |   |   start <= 63279
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 55153:
cellular_component_ (17.51)
|   |   |   |   |   |   |   |   |   |   start > 55153: cytoplasm_
(11.01)
|   |   |   |   |   |   |   |   |   strand = W: cellular_component_
(17.94)
|   |   |   |   |   |   |   |   start > 63279: nucleus_
(24.47/10.94)
|   |   |   |   |   |   start > 66614
|   |   |   |   |   |   |   start <= 73006
|   |   |   |   |   |   |   |   start <= 67725:
microtubule_organizing_center_ (17.1)
|   |   |   |   |   |   |   |   start > 67725
|   |   |   |   |   |   |   |   |   start <= 69485
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
cellular_component_ (6.24/0.95)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
nucleus_ (2.12/0.59)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: nucleus_ (14.45/4.91)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
cellular_component_ (2.51/1.17)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: cellular_component_ (4.35/0.84)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: nucleus_ (1.51/0.28)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
nucleus_ (2.45/0.37)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: cellular_component_
(2.54/1.24)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: cellular_component_ (2.04/1.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: nucleus_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: nucleus_ (0.0)
|   |   |   |   |   |   |   |   |   start > 69485:
microtubule_organizing_center_ (14.41)
|   |   |   |   |   |   |   start > 73006
|   |   |   |   |   |   |   |   start <= 73881: mitochondrion_
(9.04)
|   |   |   |   |   |   |   |   start > 73881: cellular_component_
(10.0)
|   |   |   |   |   start > 74719
|   |   |   |   |   |   start <= 79353
|   |   |   |   |   |   |   start <= 76239: ribosome_ (18.44)
|   |   |   |   |   |   |   start > 76239
|   |   |   |   |   |   |   |   distance <= 889: plasma_membrane_
(3.77/0.06)
|   |   |   |   |   |   |   |   distance > 889: membrane_fraction_
(23.51/9.47)
|   |   |   |   |   |   start > 79353
|   |   |   |   |   |   |   start <= 85586
|   |   |   |   |   |   |   |   start <= 84196
|   |   |   |   |   |   |   |   |   start <= 82356: nucleus_ (17.82)
|   |   |   |   |   |   |   |   |   start > 82356
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
nucleus_ (10.68/4.17)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cytoplasm_ (20.45/5.15)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
nucleus_ (4.67/1.74)
|   |   |   |   |   |   |   |   start > 84196
|   |   |   |   |   |   |   |   |   start <= 85297: Golgi_apparatus_
(16.16)
```

```
|   |   |   |   |   |   |   |   |   start > 85297: nucleus_
(25.75/12.53)
|   |   |   |   |   |   |   start > 85586
|   |   |   |   |   |   |   |   start <= 88033: cellular_component_
(10.83)
|   |   |   |   |   |   |   |   start > 88033: cytoplasm_ (16.3)
|   |   |   |   start > 88517
|   |   |   |   |   start <= 95109: site_of_polarized_growth_
(29.02/12.38)
|   |   |   |   |   start > 95109: cellular_component_ (17.89)
|   |   start > 96258
|   |   |   start <= 450374
|   |   |   |   start <= 321629
|   |   |   |   |   start <= 218629
|   |   |   |   |   |   start <= 107275
|   |   |   |   |   |   |   start <= 105440
|   |   |   |   |   |   |   |   start <= 100496
|   |   |   |   |   |   |   |   |   start <= 99484: cytoplasm_
(17.16)
|   |   |   |   |   |   |   |   |   start > 99484: ribosome_ (17.72)
|   |   |   |   |   |   |   |   start > 100496
|   |   |   |   |   |   |   |   |   strand = C: vacuole_
(49.59/12.44)
|   |   |   |   |   |   |   |   |   strand = W: nucleus_ (13.21)
|   |   |   |   |   |   |   start > 105440
|   |   |   |   |   |   |   |   start <= 106172: chromosome_
(41.04/19.12)
|   |   |   |   |   |   |   |   start > 106172: plasma_membrane_
(16.26)
|   |   |   |   |   |   start > 107275
|   |   |   |   |   |   |   start <= 191405
|   |   |   |   |   |   |   |   start <= 163596
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 121767:
endomembrane_system_ (52.21/30.83)
|   |   |   |   |   |   |   |   |   |   start > 121767
|   |   |   |   |   |   |   |   |   |   |   start <= 156211
|   |   |   |   |   |   |   |   |   |   |   |   start <= 128087:
mitochondrion_ (18.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 128087
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 150613
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
143820
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
135789: cytoplasm_ (15.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
135789: nucleolus_ (33.2/20.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
143820: cytoplasm_ (17.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 150613
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
153494: nucleus_ (24.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
153494: cytoplasm_ (17.84)
```

```
|   |   |   |   |   |   |   |   |   |   start > 156211
|   |   |   |   |   |   |   |   |   |   |   start <= 159908:
cytoskeleton_ (23.93)
|   |   |   |   |   |   |   |   |   |   |   start > 159908:
mitochondrion_ (50.44/29.48)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 147415
|   |   |   |   |   |   |   |   |   |   |   start <= 126006
|   |   |   |   |   |   |   |   |   |   |   |   start <= 115312
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 108652:
mitochondrion_ (35.03/13.21)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 108652:
cellular_component_ (21.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 115312
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 118382
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
117067: cytoplasm_ (19.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
117067: nucleus_ (30.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 118382:
cytoplasm_ (75.01/31.03)
|   |   |   |   |   |   |   |   |   |   |   start > 126006
|   |   |   |   |   |   |   |   |   |   |   |   start <= 135789
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 133042
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
130161: mitochondrion_ (14.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
130161: endoplasmic_reticulum_ (18.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 133042:
ribosome_ (25.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 135789
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 143820
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
138697
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
136749: cellular_component_ (13.74)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
136749: Golgi_apparatus_ (15.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
138697: cellular_component_ (14.11)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 143820:
mitochondrion_ (18.1)
|   |   |   |   |   |   |   |   |   |   start > 147415
|   |   |   |   |   |   |   |   |   |   |   start <= 157841
|   |   |   |   |   |   |   |   |   |   |   |   start <= 153494
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 150613:
cytoplasm_ (14.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 150613:
nucleolus_ (12.35)
|   |   |   |   |   |   |   |   |   |   |   |   start > 153494:
cytoplasm_ (30.47/13.41)
|   |   |   |   |   |   |   |   |   |   |   start > 157841:
endoplasmic_reticulum_ (22.05)
|   |   |   |   |   |   |   |   start > 163596
```

```
|   |   |   |   |   |   |   |   |   start <= 171154
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 169337:
mitochondrion_ (30.88/13.87)
|   |   |   |   |   |   |   |   |   |   |   start > 169337: nucleus_
(19.35)
|   |   |   |   |   |   |   |   |   |   strand = W: nucleus_
(47.73/13.24)
|   |   |   |   |   |   |   |   |   start > 171154
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 184678
|   |   |   |   |   |   |   |   |   |   |   |   start <= 183055
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 176222:
cytoplasm_ (14.58)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 176222:
endomembrane_system_ (12.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 183055:
cytoplasm_ (17.39)
|   |   |   |   |   |   |   |   |   |   |   start > 184678
|   |   |   |   |   |   |   |   |   |   |   |   start <= 187724:
nucleus_ (14.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 187724:
cellular_component_ (20.37)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 173826
|   |   |   |   |   |   |   |   |   |   |   |   start <= 171483:
membrane_ (45.18/24.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 171483
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 173151:
ribosome_ (14.0)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 173151:
nucleolus_ (8.51)
|   |   |   |   |   |   |   |   |   |   |   start > 173826
|   |   |   |   |   |   |   |   |   |   |   |   start <= 179276
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 175042:
mitochondrion_ (19.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 175042
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
176222: membrane_ (25.55/10.07)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
176222: chromosome_ (16.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 179276
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 189153
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
184678: nucleus_ (15.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
184678: membrane_ (19.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 189153:
mitochondrion_ (23.29)
|   |   |   |   |   |   |   |   start > 191405
|   |   |   |   |   |   |   |   |   start <= 213961
|   |   |   |   |   |   |   |   |   |   start <= 195425
|   |   |   |   |   |   |   |   |   |   |   start <= 193647:
extracellular_region_ (16.49)
```

```
|   |   |   |   |   |   |   |   |   |   start > 193647:
endoplasmic_reticulum_ (16.36)
|   |   |   |   |   |   |   |   |   start > 195425
|   |   |   |   |   |   |   |   |   |   start <= 202535
|   |   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(26.07)
|   |   |   |   |   |   |   |   |   |   |   strand = W:
mitochondrion_ (11.37)
|   |   |   |   |   |   |   |   |   |   start > 202535
|   |   |   |   |   |   |   |   |   |   |   start <= 205247
|   |   |   |   |   |   |   |   |   |   |   |   start <= 203420:
nucleus_ (13.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 203420:
vacuole_ (16.05)
|   |   |   |   |   |   |   |   |   |   |   start > 205247
|   |   |   |   |   |   |   |   |   |   |   |   start <= 210262:
cytoplasm_ (38.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 210262
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 212157
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W: cytoplasm_ (9.41/2.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 1637: nucleus_ (7.26/2.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 1637: cytoplasm_ (7.15/2.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 212157:
nucleus_ (11.28)
|   |   |   |   |   |   |   |   start > 213961
|   |   |   |   |   |   |   |   |   start <= 218362:
plasma_membrane_ (22.42)
|   |   |   |   |   |   |   |   |   start > 218362:
endoplasmic_reticulum_ (14.98)
|   |   |   |   |   start > 218629
|   |   |   |   |   |   start <= 273254
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 239076
|   |   |   |   |   |   |   |   |   start <= 223142:
microtubule_organizing_center_ (17.78)
|   |   |   |   |   |   |   |   |   start > 223142
|   |   |   |   |   |   |   |   |   |   start <= 237337
|   |   |   |   |   |   |   |   |   |   |   start <= 231216
|   |   |   |   |   |   |   |   |   |   |   |   start <= 228313
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 225740:
mitochondrion_ (7.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 225740:
cellular_component_ (11.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 228313:
cytoplasm_ (20.05)
|   |   |   |   |   |   |   |   |   |   |   start > 231216:
mitochondrion_ (24.39)
|   |   |   |   |   |   |   |   |   |   start > 237337:
cellular_component_ (20.12)
```

```
|   |   |   |   |   |   |   |   start > 239076
|   |   |   |   |   |   |   |   |   start <= 246989
|   |   |   |   |   |   |   |   |   |   start <= 242699
|   |   |   |   |   |   |   |   |   |   |   start <= 241496:
nucleus_ (19.46)
|   |   |   |   |   |   |   |   |   |   |   start > 241496:
cell_wall_ (25.34)
|   |   |   |   |   |   |   |   |   |   start > 242699
|   |   |   |   |   |   |   |   |   |   |   start <= 244026:
membrane_ (27.45/10.94)
|   |   |   |   |   |   |   |   |   |   |   start > 244026: nucleus_
(28.97/13.4)
|   |   |   |   |   |   |   |   |   start > 246989
|   |   |   |   |   |   |   |   |   |   start <= 256766
|   |   |   |   |   |   |   |   |   |   |   start <= 254813
|   |   |   |   |   |   |   |   |   |   |   |   start <= 251667:
mitochondrion_ (15.87)
|   |   |   |   |   |   |   |   |   |   |   |   start > 251667:
site_of_polarized_growth_ (28.52/12.89)
|   |   |   |   |   |   |   |   |   |   |   start > 254813:
membrane_ (21.24)
|   |   |   |   |   |   |   |   |   |   start > 256766
|   |   |   |   |   |   |   |   |   |   |   start <= 260930:
mitochondrion_ (41.04)
|   |   |   |   |   |   |   |   |   |   |   start > 260930
|   |   |   |   |   |   |   |   |   |   |   |   start <= 268187:
nucleus_ (29.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 268187:
mitochondrion_ (15.02)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 231216
|   |   |   |   |   |   |   |   |   start <= 223142: mitochondrion_
(11.45)
|   |   |   |   |   |   |   |   |   start > 223142
|   |   |   |   |   |   |   |   |   |   start <= 228313: membrane_
(22.26)
|   |   |   |   |   |   |   |   |   |   start > 228313:
mitochondrion_ (11.0)
|   |   |   |   |   |   |   |   start > 231216
|   |   |   |   |   |   |   |   |   start <= 268187
|   |   |   |   |   |   |   |   |   |   start <= 259335
|   |   |   |   |   |   |   |   |   |   |   start <= 246989:
cytoplasm_ (43.1)
|   |   |   |   |   |   |   |   |   |   |   start > 246989:
nucleolus_ (15.04)
|   |   |   |   |   |   |   |   |   |   start > 259335:
cellular_component_ (58.76/12.8)
|   |   |   |   |   |   |   |   |   start > 268187
|   |   |   |   |   |   |   |   |   |   start <= 271309: vacuole_
(13.45)
|   |   |   |   |   |   |   |   |   |   start > 271309: peroxisome_
(19.08)
|   |   |   |   |   |   start > 273254
|   |   |   |   |   |   |   start <= 313387
```

```
|   |   |   |   |   |   |   |   start <= 286060
|   |   |   |   |   |   |   |   |   start <= 277528
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleolus_
(8.51/2.9)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(11.36/3.35)
|   |   |   |   |   |   |   |   |   start > 277528
|   |   |   |   |   |   |   |   |   |   start <= 280479: cytoplasm_
(33.97)
|   |   |   |   |   |   |   |   |   |   start > 280479
|   |   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   |   start <= 282121:
nucleolus_ (16.77)
|   |   |   |   |   |   |   |   |   |   |   |   start > 282121:
cytoplasm_ (10.08)
|   |   |   |   |   |   |   |   |   |   |   strand = W: ribosome_
(4.1)
|   |   |   |   |   |   |   |   start > 286060
|   |   |   |   |   |   |   |   |   start <= 303120
|   |   |   |   |   |   |   |   |   |   start <= 292426
|   |   |   |   |   |   |   |   |   |   |   start <= 289033:
cellular_component_ (6.61)
|   |   |   |   |   |   |   |   |   |   |   start > 289033
|   |   |   |   |   |   |   |   |   |   |   |   start <= 291050:
nucleus_ (19.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 291050
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: nucleus_ (8.24/1.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: cellular_component_ (20.46/8.76)
|   |   |   |   |   |   |   |   |   |   start > 292426
|   |   |   |   |   |   |   |   |   |   |   start <= 301227
|   |   |   |   |   |   |   |   |   |   |   |   start <= 299502
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 296646
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
2928: ribosome_ (31.32/19.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   distance >
2928: endoplasmic_reticulum_ (19.34/13.44)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 296646:
mitochondrion_ (32.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 299502:
nucleus_ (40.82/9.55)
|   |   |   |   |   |   |   |   |   |   |   start > 301227
|   |   |   |   |   |   |   |   |   |   |   |   start <= 301715:
mitochondrial_envelope_ (42.62/15.63)
|   |   |   |   |   |   |   |   |   |   |   |   start > 301715:
ribosome_ (16.61)
|   |   |   |   |   |   |   |   |   start > 303120
|   |   |   |   |   |   |   |   |   |   start <= 309603
|   |   |   |   |   |   |   |   |   |   |   start <= 304386:
cell_wall_ (17.75)
|   |   |   |   |   |   |   |   |   |   |   start > 304386
|   |   |   |   |   |   |   |   |   |   |   |   strand = C: nucleus_
(33.01)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   strand = W:
cellular_component_ (38.48/16.42)
|   |   |   |   |   |   |   |   |   |   start > 309603
|   |   |   |   |   |   |   |   |   |   |   start <= 310209:
nucleolus_ (14.79)
|   |   |   |   |   |   |   |   |   |   |   start > 310209:
cytoplasm_ (19.64)
|   |   |   |   |   |   |   start > 313387
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 320766
|   |   |   |   |   |   |   |   |   |   start <= 318944:
extracellular_region_ (11.4)
|   |   |   |   |   |   |   |   |   |   start > 318944: nucleus_
(45.31/14.15)
|   |   |   |   |   |   |   |   |   start > 320766: chromosome_
(11.97)
|   |   |   |   |   |   |   |   strand = W:
microtubule_organizing_center_ (37.34/14.56)
|   |   |   |   start > 321629
|   |   |   |   |   start <= 364949
|   |   |   |   |   |   start <= 338619
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 329605
|   |   |   |   |   |   |   |   |   start <= 324286:
cellular_component_ (12.97)
|   |   |   |   |   |   |   |   |   start > 324286: cytoplasm_
(38.78)
|   |   |   |   |   |   |   |   start > 329605
|   |   |   |   |   |   |   |   |   start <= 337142:
cellular_component_ (41.16)
|   |   |   |   |   |   |   |   |   start > 337142: peroxisome_
(15.05)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 326627
|   |   |   |   |   |   |   |   |   start <= 324286:
membrane_fraction_ (18.13)
|   |   |   |   |   |   |   |   |   start > 324286: mitochondrion_
(19.89)
|   |   |   |   |   |   |   |   start > 326627
|   |   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_
(11.94/3.38)
|   |   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(17.08/6.07)
|   |   |   |   |   |   start > 338619
|   |   |   |   |   |   |   start <= 361869
|   |   |   |   |   |   |   |   start <= 344738
|   |   |   |   |   |   |   |   |   start <= 339943: cytoplasm_
(27.38)
|   |   |   |   |   |   |   |   |   start > 339943: ribosome_
(39.22/14.27)
|   |   |   |   |   |   |   |   start > 344738
|   |   |   |   |   |   |   |   |   start <= 359403
|   |   |   |   |   |   |   |   |   |   start <= 355409
|   |   |   |   |   |   |   |   |   |   |   start <= 349116
```

```
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
mitochondrion_ (24.11)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 348443:
cytoplasm_ (13.17)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 348443:
mitochondrion_ (18.75)
|   |   |   |   |   |   |   |   |   |   |   start > 349116
|   |   |   |   |   |   |   |   |   |   |   |   start <= 352272:
cytoplasm_ (20.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 352272
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <=
4602: ribosome_ (26.28/12.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 4602:
cytoplasm_ (12.8/6.58)
|   |   |   |   |   |   |   |   |   |   start > 355409:
mitochondrion_ (37.99)
|   |   |   |   |   |   |   |   |   start > 359403: cytoplasm_
(33.52)
|   |   |   |   |   |   |   start > 361869
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 364065: mitochondrion_
(11.14)
|   |   |   |   |   |   |   |   |   start > 364065:
cellular_component_ (16.61)
|   |   |   |   |   |   |   |   strand = W: mitochondrion_ (15.76)
|   |   |   |   |   start > 364949
|   |   |   |   |   |   start <= 387064
|   |   |   |   |   |   |   start <= 370660
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 366924: membrane_
(61.32/36.62)
|   |   |   |   |   |   |   |   |   start > 366924
|   |   |   |   |   |   |   |   |   |   start <= 369438:
cellular_component_ (22.29)
|   |   |   |   |   |   |   |   |   |   start > 369438:
endoplasmic_reticulum_ (49.08/29.16)
|   |   |   |   |   |   |   |   strand = W: nucleus_ (38.13/17.72)
|   |   |   |   |   |   |   start > 370660
|   |   |   |   |   |   |   |   start <= 378392
|   |   |   |   |   |   |   |   |   strand = C: ribosome_
(37.18/10.09)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 373790
|   |   |   |   |   |   |   |   |   |   |   start <= 370975:
nucleolus_ (12.41)
|   |   |   |   |   |   |   |   |   |   |   start > 370975:
plasma_membrane_ (28.14)
|   |   |   |   |   |   |   |   |   |   start > 373790:
mitochondrion_ (64.48/36.46)
|   |   |   |   |   |   |   |   start > 378392
|   |   |   |   |   |   |   |   |   strand = C: nucleus_
(58.28/22.79)
|   |   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   |   start <= 381962:
cellular_component_ (17.0)
|   |   |   |   |   |   |   |   |   |   start > 381962
|   |   |   |   |   |   |   |   |   |   |   start <= 383452:
endoplasmic_reticulum_ (11.3)
|   |   |   |   |   |   |   |   |   |   |   start > 383452:
endomembrane_system_ (65.85/44.11)
|   |   |   |   |   |   start > 387064
|   |   |   |   |   |   |   start <= 410440
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 408741: mitochondrion_
(52.45)
|   |   |   |   |   |   |   |   |   start > 408741:
cellular_component_ (6.48)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 404947
|   |   |   |   |   |   |   |   |   |   start <= 398102
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
membrane_fraction_ (13.5/3.97)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
cytoplasm_ (10.42/3.1)
|   |   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
cytoplasm_ (9.99/4.57)
|   |   |   |   |   |   |   |   |   |   start > 398102: cytoplasm_
(12.5)
|   |   |   |   |   |   |   |   |   start > 404947
|   |   |   |   |   |   |   |   |   |   start <= 406633: ribosome_
(6.83)
|   |   |   |   |   |   |   |   |   |   start > 406633:
endoplasmic_reticulum_ (15.7)
|   |   |   |   |   |   |   start > 410440
|   |   |   |   |   |   |   |   start <= 429613
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 426230
|   |   |   |   |   |   |   |   |   |   |   start <= 425093
|   |   |   |   |   |   |   |   |   |   |   |   start <= 420945:
nucleus_ (27.32/10.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 420945
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 423889:
mitochondrion_ (15.81)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 423889:
nucleus_ (11.36)
|   |   |   |   |   |   |   |   |   |   |   start > 425093:
cytoplasm_ (8.72)
|   |   |   |   |   |   |   |   |   |   start > 426230: nucleus_
(24.78)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 415760
|   |   |   |   |   |   |   |   |   |   |   start <= 412251:
nucleus_ (12.16)
|   |   |   |   |   |   |   |   |   |   |   start > 412251:
cell_cortex_ (8.55)
|   |   |   |   |   |   |   |   |   |   start > 415760
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 426230:
cytoplasm_ (54.59)
|   |   |   |   |   |   |   |   |   |   |   start > 426230:
membrane_ (35.66/16.07)
|   |   |   |   |   |   |   |   start > 429613
|   |   |   |   |   |   |   |   |   start <= 444576
|   |   |   |   |   |   |   |   |   |   strand = C: cytoplasm_
(7.03)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 432585
|   |   |   |   |   |   |   |   |   |   |   |   start <= 429936:
mitochondrion_ (23.62)
|   |   |   |   |   |   |   |   |   |   |   |   start > 429936:
cytoplasm_ (36.37/16.11)
|   |   |   |   |   |   |   |   |   |   |   start > 432585
|   |   |   |   |   |   |   |   |   |   |   |   start <= 435961:
mitochondrial_envelope_ (12.37)
|   |   |   |   |   |   |   |   |   |   |   |   start > 435961:
mitochondrion_ (12.61)
|   |   |   |   |   |   |   |   |   start > 444576: plasma_membrane_
(14.61)
|   |   |   start > 450374
|   |   |   |   start <= 480179
|   |   |   |   |   start <= 467257
|   |   |   |   |   |   start <= 459960
|   |   |   |   |   |   |   start <= 455756
|   |   |   |   |   |   |   |   start <= 453732: cellular_component_
(34.02)
|   |   |   |   |   |   |   |   start > 453732
|   |   |   |   |   |   |   |   |   start <= 454987: nucleus_
(21.78)
|   |   |   |   |   |   |   |   |   start > 454987:
cellular_component_ (16.77)
|   |   |   |   |   |   |   start > 455756
|   |   |   |   |   |   |   |   strand = C: membrane_fraction_
(20.1)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 458796:
cellular_component_ (18.78)
|   |   |   |   |   |   |   |   |   start > 458796: Golgi_apparatus_
(12.31)
|   |   |   |   |   |   start > 459960
|   |   |   |   |   |   |   start <= 466940
|   |   |   |   |   |   |   |   start <= 461963: membrane_ (15.26)
|   |   |   |   |   |   |   |   start > 461963
|   |   |   |   |   |   |   |   |   start <= 465959: nucleus_ (57.9)
|   |   |   |   |   |   |   |   |   start > 465959
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1: nucleus_
(21.69/6.8)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cellular_component_ (23.5/8.42)
|   |   |   |   |   |   |   start > 466940: vacuole_ (29.24/11.95)
|   |   |   |   |   start > 467257
|   |   |   |   |   |   start <= 469936: nucleolus_ (21.89)
```

```
|   |   |   |   |   |   start > 469936
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 475738: cellular_component_
(50.31/14.97)
|   |   |   |   |   |   |   |   start > 475738: mitochondrion_
(17.55)
|   |   |   |   |   |   |   strand = W: cellular_component_ (41.9)
|   |   |   |   start > 480179
|   |   |   |   |   start <= 543845
|   |   |   |   |   |   start <= 529347
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 488205
|   |   |   |   |   |   |   |   |   start <= 482841: ribosome_
(21.09)
|   |   |   |   |   |   |   |   |   start > 482841:
cellular_component_ (20.09)
|   |   |   |   |   |   |   |   start > 488205
|   |   |   |   |   |   |   |   |   start <= 527544
|   |   |   |   |   |   |   |   |   |   start <= 495504
|   |   |   |   |   |   |   |   |   |   |   start <= 491362:
cellular_bud_ (30.47/14.98)
|   |   |   |   |   |   |   |   |   |   |   start > 491362: nucleus_
(11.96)
|   |   |   |   |   |   |   |   |   |   start > 495504
|   |   |   |   |   |   |   |   |   |   |   start <= 517649
|   |   |   |   |   |   |   |   |   |   |   |   start <= 506695:
cytoplasm_ (27.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 506695
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 514176:
endomembrane_system_ (16.15)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 514176:
endoplasmic_reticulum_ (22.77)
|   |   |   |   |   |   |   |   |   |   |   start > 517649:
cytoplasm_ (48.26)
|   |   |   |   |   |   |   |   |   start > 527544: mitochondrion_
(19.57)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 498094
|   |   |   |   |   |   |   |   |   start <= 480532: cytoplasm_
(36.47/16.09)
|   |   |   |   |   |   |   |   |   start > 480532
|   |   |   |   |   |   |   |   |   |   start <= 488205
|   |   |   |   |   |   |   |   |   |   |   start <= 482841
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
mitochondrion_ (13.72/5.14)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
plasma_membrane_ (13.65/3.89)
|   |   |   |   |   |   |   |   |   |   |   start > 482841:
cellular_component_ (15.33)
|   |   |   |   |   |   |   |   |   |   start > 488205
|   |   |   |   |   |   |   |   |   |   |   start <= 493541:
cytoplasm_ (15.76)
|   |   |   |   |   |   |   |   |   |   |   start > 493541
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 495504: 
mitochondrion_ (15.54)
|   |   |   |   |   |   |   |   |   |   |   |   start > 495504: 
cytoplasm_ (15.27)
|   |   |   |   |   |   |   |   start > 498094
|   |   |   |   |   |   |   |   |   start <= 521011
|   |   |   |   |   |   |   |   |   |   start <= 503515
|   |   |   |   |   |   |   |   |   |   |   start <= 499663: 
cellular_component_ (9.79)
|   |   |   |   |   |   |   |   |   |   |   start > 499663: nucleus_ 
(32.48/15.53)
|   |   |   |   |   |   |   |   |   |   start > 503515
|   |   |   |   |   |   |   |   |   |   |   start <= 506695: 
nucleus_ (16.48)
|   |   |   |   |   |   |   |   |   |   |   start > 506695
|   |   |   |   |   |   |   |   |   |   |   |   start <= 514176: 
cellular_component_ (19.84)
|   |   |   |   |   |   |   |   |   |   |   |   start > 514176
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 517649: 
nucleus_ (14.76)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 517649
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 
1: cellular_component_ (12.93/4.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 
1: nucleus_ (26.94/7.67)
|   |   |   |   |   |   |   |   |   start > 521011: nucleus_ 
(42.11/19.48)
|   |   |   |   |   |   start > 529347
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 535015: cellular_component_ 
(43.85/20.26)
|   |   |   |   |   |   |   |   start > 535015
|   |   |   |   |   |   |   |   |   start <= 539382: ribosome_ 
(33.6/16.48)
|   |   |   |   |   |   |   |   |   start > 539382: nucleus_ 
(40.29/18.12)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 529720: ribosome_ 
(34.9/14.78)
|   |   |   |   |   |   |   |   start > 529720
|   |   |   |   |   |   |   |   |   start <= 535015: 
Golgi_apparatus_ (21.69)
|   |   |   |   |   |   |   |   |   start > 535015: nucleus_ (13.81)
|   |   |   |   |   start > 543845
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 568993
|   |   |   |   |   |   |   |   start <= 560286
|   |   |   |   |   |   |   |   |   start <= 552017: cytoplasm_ 
(49.98/18.6)
|   |   |   |   |   |   |   |   |   start > 552017
|   |   |   |   |   |   |   |   |   |   start <= 556374: membrane_ 
(15.82)
|   |   |   |   |   |   |   |   |   |   start > 556374: cytoplasm_ 
(10.47)
```

```
|   |   |   |   |   |   |   |   start > 560286
|   |   |   |   |   |   |   |   |   start <= 563765:
endoplasmic_reticulum_ (11.53)
|   |   |   |   |   |   |   |   |   start > 563765
|   |   |   |   |   |   |   |   |   |   start <= 565038:
mitochondrion_ (15.7)
|   |   |   |   |   |   |   |   |   |   start > 565038
|   |   |   |   |   |   |   |   |   |   |   start <= 566668:
cytoplasm_ (13.83)
|   |   |   |   |   |   |   |   |   |   |   start > 566668:
mitochondrion_ (11.47)
|   |   |   |   |   |   |   start > 568993
|   |   |   |   |   |   |   |   start <= 648701
|   |   |   |   |   |   |   |   |   start <= 581193
|   |   |   |   |   |   |   |   |   |   start <= 573015
|   |   |   |   |   |   |   |   |   |   |   distance <= 1791:
chromosome_ (6.25/0.21)
|   |   |   |   |   |   |   |   |   |   |   distance > 1791:
nucleus_ (15.05/5.58)
|   |   |   |   |   |   |   |   |   |   start > 573015: nucleolus_
(19.54)
|   |   |   |   |   |   |   |   |   start > 581193
|   |   |   |   |   |   |   |   |   |   start <= 621255
|   |   |   |   |   |   |   |   |   |   |   start <= 610478
|   |   |   |   |   |   |   |   |   |   |   |   start <= 603354
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 591023
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
584039
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
582731: cellular_component_ (11.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
582731: mitochondrion_ (11.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
584039: cellular_component_ (16.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 591023
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
593066: nucleolus_ (28.69/16.01)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
593066
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
596747: membrane_fraction_ (18.27)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
596747: mitochondrion_ (10.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 603354
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 607309
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: cytoplasm_ (9.88/2.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: nucleus_ (21.16/9.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 607309
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <=
1: nucleus_ (18.34/7.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num >
1: cellular_component_ (22.13/8.12)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 610478
|   |   |   |   |   |   |   |   |   |   |   |   start <= 615376:
mitochondrion_ (27.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 615376:
cellular_component_ (13.7)
|   |   |   |   |   |   |   |   |   |   start > 621255
|   |   |   |   |   |   |   |   |   |   |   start <= 642205
|   |   |   |   |   |   |   |   |   |   |   |   start <= 631512
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 623524:
cytoplasm_ (9.67)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 623524:
Golgi_apparatus_ (8.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 631512:
cytoplasm_ (44.88/20.92)
|   |   |   |   |   |   |   |   |   |   |   start > 642205:
membrane_fraction_ (12.18)
|   |   |   |   |   |   |   |   start > 648701
|   |   |   |   |   |   |   |   |   start <= 675628
|   |   |   |   |   |   |   |   |   |   distance <= 2204
|   |   |   |   |   |   |   |   |   |   |   distance <= 88:
cytoplasm_ (6.3/1.53)
|   |   |   |   |   |   |   |   |   |   |   distance > 88: nucleus_
(65.65/23.75)
|   |   |   |   |   |   |   |   |   |   distance > 2204
|   |   |   |   |   |   |   |   |   |   |   start <= 659179
|   |   |   |   |   |   |   |   |   |   |   |   start <= 654163:
cytoplasm_ (13.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 654163:
nucleus_ (3.72)
|   |   |   |   |   |   |   |   |   |   |   start > 659179:
membrane_ (23.79/8.77)
|   |   |   |   |   |   |   |   |   start > 675628
|   |   |   |   |   |   |   |   |   |   start <= 681210
|   |   |   |   |   |   |   |   |   |   |   start <= 677162:
mitochondrion_ (25.39)
|   |   |   |   |   |   |   |   |   |   |   start > 677162:
endoplasmic_reticulum_ (17.32)
|   |   |   |   |   |   |   |   |   |   start > 681210
|   |   |   |   |   |   |   |   |   |   |   start <= 684350:
nucleus_ (37.05/15.15)
|   |   |   |   |   |   |   |   |   |   |   start > 684350
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
nucleus_ (18.0/6.07)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cytoplasm_ (23.49/8.22)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 643833
|   |   |   |   |   |   |   |   start <= 544628: membrane_
(49.51/23.25)
|   |   |   |   |   |   |   |   start > 544628
|   |   |   |   |   |   |   |   |   start <= 610478
|   |   |   |   |   |   |   |   |   |   start <= 552017
|   |   |   |   |   |   |   |   |   |   |   start <= 548483:
cytoplasm_ (45.14/22.24)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 548483:
cellular_component_ (21.92)
|   |   |   |   |   |   |   |   |   |   start > 552017
|   |   |   |   |   |   |   |   |   |   |   start <= 596747
|   |   |   |   |   |   |   |   |   |   |   |   start <= 572266
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 554602
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= W
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
<= 1642: cytoplasm_ (4.47/1.55)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   distance
> 1642: nucleus_ (8.4/1.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand
= C: cytoplasm_ (14.37/5.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 554602
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
565038: mitochondrion_ (36.48/12.05)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
565038: cytoplasm_ (11.99)
|   |   |   |   |   |   |   |   |   |   |   |   start > 572266
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 576549:
nucleus_ (25.54)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 576549
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
585582: mitochondrion_ (15.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
585582: nucleus_ (52.46/18.38)
|   |   |   |   |   |   |   |   |   |   |   start > 596747:
mitochondrion_ (34.11)
|   |   |   |   |   |   |   |   |   start > 610478
|   |   |   |   |   |   |   |   |   |   start <= 642205
|   |   |   |   |   |   |   |   |   |   |   start <= 623524
|   |   |   |   |   |   |   |   |   |   |   |   start <= 615376:
cell_wall_ (16.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 615376:
membrane_ (10.87)
|   |   |   |   |   |   |   |   |   |   |   start > 623524
|   |   |   |   |   |   |   |   |   |   |   |   start <= 639522
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 631512
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
627877: nucleus_ (15.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
627877: cytoplasm_ (31.59/14.8)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 631512
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
634120: plasma_membrane_ (13.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
634120: nucleus_ (19.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 639522:
cytoplasm_ (19.77)
|   |   |   |   |   |   |   |   |   |   start > 642205: vacuole_
(33.83/14.46)
|   |   |   |   |   |   |   start > 643833
|   |   |   |   |   |   |   |   start <= 654163
```

```
|   |   |   |   |   |   |   |   |   start <= 645947:
cellular_component_ (18.61)
|   |   |   |   |   |   |   |   |   start > 645947
|   |   |   |   |   |   |   |   |   |   start <= 648701: cytoplasm_
(59.79/26.01)
|   |   |   |   |   |   |   |   |   |   start > 648701: ribosome_
(14.3)
|   |   |   |   |   |   |   |   start > 654163
|   |   |   |   |   |   |   |   |   start <= 685895
|   |   |   |   |   |   |   |   |   |   start <= 656796: nucleus_
(40.89/17.46)
|   |   |   |   |   |   |   |   |   |   start > 656796
|   |   |   |   |   |   |   |   |   |   |   start <= 667673
|   |   |   |   |   |   |   |   |   |   |   |   start <= 659179
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 657526:
mitochondrion_ (18.71)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 657526:
cellular_component_ (27.85)
|   |   |   |   |   |   |   |   |   |   |   |   start > 659179
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 664957:
cytoplasm_ (19.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 664957
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
666277: mitochondrion_ (9.13)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
666277: site_of_polarized_growth_ (10.69)
|   |   |   |   |   |   |   |   |   |   |   start > 667673
|   |   |   |   |   |   |   |   |   |   |   |   start <= 672468
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 671123:
cellular_component_ (30.85/14.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 671123:
nucleus_ (12.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 672468
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 682217
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
681210
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
673748: mitochondrion_ (12.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
673748
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 678317: nucleus_ (25.89/12.66)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 678317
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 679690: chromosome_ (15.43)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 679690: cytoplasm_ (18.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
681210: mitochondrion_ (17.47)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 682217:
nucleus_ (27.39/11.03)
|   |   |   |   |   |   |   |   |   start > 685895: membrane_
(16.46)
```

```
|   start > 688169
|   |   start <= 828136
|   |   |   strand = C
|   |   |   |   start <= 824922
|   |   |   |   |   start <= 732347
|   |   |   |   |   |   start <= 713273
|   |   |   |   |   |   |   start <= 696816
|   |   |   |   |   |   |   |   start <= 692415: nucleus_
(28.38/12.09)
|   |   |   |   |   |   |   |   start > 692415: cytoplasm_
(37.96/8.6)
|   |   |   |   |   |   |   start > 696816
|   |   |   |   |   |   |   |   start <= 703968
|   |   |   |   |   |   |   |   |   start <= 700592:
cellular_component_ (8.56)
|   |   |   |   |   |   |   |   |   start > 700592: cytoplasm_
(21.33)
|   |   |   |   |   |   |   |   start > 703968
|   |   |   |   |   |   |   |   |   start <= 706970: nucleus_
(19.16)
|   |   |   |   |   |   |   |   |   start > 706970
|   |   |   |   |   |   |   |   |   |   start <= 710099:
cellular_component_ (12.25)
|   |   |   |   |   |   |   |   |   |   start > 710099: cytoplasm_
(13.86)
|   |   |   |   |   |   start > 713273
|   |   |   |   |   |   |   start <= 719240
|   |   |   |   |   |   |   |   start <= 718466: ribosome_
(21.5/10.3)
|   |   |   |   |   |   |   |   start > 718466: nucleolus_ (52.53)
|   |   |   |   |   |   |   start > 719240
|   |   |   |   |   |   |   |   start <= 720635
|   |   |   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_
(9.93/3.71)
|   |   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: cytoplasm_
(6.03/2.2)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(14.24/3.32)
|   |   |   |   |   |   |   |   start > 720635
|   |   |   |   |   |   |   |   |   start <= 724715: mitochondrion_
(26.37)
|   |   |   |   |   |   |   |   |   start > 724715
|   |   |   |   |   |   |   |   |   |   start <= 730490
|   |   |   |   |   |   |   |   |   |   |   start <= 725392:
ribosome_ (12.46)
|   |   |   |   |   |   |   |   |   |   |   start > 725392:
mitochondrion_ (13.65)
|   |   |   |   |   |   |   |   |   |   start > 730490: ribosome_
(17.36)
|   |   |   |   |   start > 732347
|   |   |   |   |   |   start <= 760023
|   |   |   |   |   |   |   start <= 744282
|   |   |   |   |   |   |   |   start <= 740059
```

```
|   |   |   |   |   |   |   |   |   start <= 736431
|   |   |   |   |   |   |   |   |   |   neigh_strand = W: nucleolus_
(14.71/5.79)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C: nucleus_
(15.32/4.0)
|   |   |   |   |   |   |   |   |   start > 736431: Golgi_apparatus_
(15.02)
|   |   |   |   |   |   |   |   start > 740059: cellular_component_
(39.21/14.8)
|   |   |   |   |   |   |   start > 744282: nucleolus_ (41.49)
|   |   |   |   |   |   start > 760023
|   |   |   |   |   |   |   start <= 814387
|   |   |   |   |   |   |   |   start <= 794961
|   |   |   |   |   |   |   |   |   start <= 775180
|   |   |   |   |   |   |   |   |   |   start <= 771651: cytoplasm_
(11.56)
|   |   |   |   |   |   |   |   |   |   start > 771651: nucleus_
(8.2)
|   |   |   |   |   |   |   |   |   start > 775180: cytoplasm_
(45.83)
|   |   |   |   |   |   |   |   start > 794961
|   |   |   |   |   |   |   |   |   start <= 802355
|   |   |   |   |   |   |   |   |   |   distance <= 4185:
cellular_component_ (19.57/6.51)
|   |   |   |   |   |   |   |   |   |   distance > 4185: nucleus_
(3.83/0.28)
|   |   |   |   |   |   |   |   |   start > 802355
|   |   |   |   |   |   |   |   |   |   start <= 812449:
plasma_membrane_ (14.18)
|   |   |   |   |   |   |   |   |   |   start > 812449: cytoplasm_
(15.07)
|   |   |   |   |   |   |   start > 814387
|   |   |   |   |   |   |   |   start <= 822616
|   |   |   |   |   |   |   |   |   start <= 819525:
microtubule_organizing_center_ (12.68)
|   |   |   |   |   |   |   |   |   start > 819525: nucleolus_
(28.26/13.08)
|   |   |   |   |   |   |   |   start > 822616: cellular_component_
(22.15)
|   |   |   |   start > 824922
|   |   |   |   |   start <= 826555: cytoplasm_ (11.4)
|   |   |   |   |   start > 826555
|   |   |   |   |   |   NeighGO_term = cellular_component_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = peptidase_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = protein_binding_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term = biological_process_:
cytoplasm_ (3.31/1.13)
|   |   |   |   |   |   NeighGO_term = molecular_function_
|   |   |   |   |   |   |   neigh_num <= 1: cytoplasm_ (12.21/4.63)
|   |   |   |   |   |   |   neigh_num > 1: ribosome_ (2.08/0.44)
```

```
|   |   |   |   |   |   NeighGO_term = mitochondrion_: cytoplasm_
(2.3/0.32)
|   |   |   |   |   |   NeighGO_term = transporter_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = membrane_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = lyase_activity_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cellular_respiration_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cytoplasm_
|   |   |   |   |   |   |   neigh_strand = W: ribosome_ (6.31/1.54)
|   |   |   |   |   |   |   neigh_strand = C: cytoplasm_ (9.58/2.12)
|   |   |   |   |   |   NeighGO_term = nucleus_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = enzyme_regulator_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = conjugation_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cell_cycle_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = motor_activity_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term = transport_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cellular_bud_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term = site_of_polarized_growth_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cytokinesis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = response_to_stress_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = helicase_activity_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term = RNA_metabolic_process_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = vacuole_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = hydrolase_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = chromosome_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cytoskeleton_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term = endomembrane_system_:
ribosome_ (0.0)
```

```
|   |   |   |   |   |   NeighGO_term = endoplasmic_reticulum_:
cytoplasm_ (0.62/0.24)
|   |   |   |   |   |   NeighGO_term = transferase_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
protein_modification_process_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cellular_homeostasis_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = nucleolus_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = vitamin_metabolic_process_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = RNA_binding_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = DNA_metabolic_process_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = isomerase_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = lipid_metabolic_process_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = plasma_membrane_: ribosome_
(3.21/0.8)
|   |   |   |   |   |   NeighGO_term = protein_kinase_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = DNA_binding_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = meiosis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = ribosome_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = translation_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = transcription_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = ligase_activity_: ribosome_
(1.57/0.35)
|   |   |   |   |   |   NeighGO_term = peroxisome_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = mitochondrial_envelope_:
ribosome_ (8.65/1.09)
|   |   |   |   |   |   NeighGO_term = extracellular_region_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = membrane_fraction_: ribosome_
(10.01/0.47)
|   |   |   |   |   |   NeighGO_term = pseudohyphal_growth_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: cytoplasm_ (2.49/0.35)
|   |   |   |   |   |   NeighGO_term = protein_catabolic_process_:
ribosome_ (1.08/0.46)
|   |   |   |   |   |   NeighGO_term = oxidoreductase_activity_:
ribosome_ (0.0)
```

```
|   |   |   |   |   |   NeighGO_term = Golgi_apparatus_: ribosome_
(0.0)
|   |   |   |   |   |   NeighGO_term = vesicle-mediated_transport_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cell_wall_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = signal_transduction_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = signal_transducer_activity_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = sporulation_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = electron_transport_:
ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cell_cortex_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: ribosome_ (0.0)
|   |   |   |   |   |   NeighGO_term = cell_budding_: ribosome_
(0.0)
|   |   |   strand = W
|   |   |   |   start <= 778579
|   |   |   |   |   start <= 700592
|   |   |   |   |   |   start <= 698867: cytoplasm_ (42.85)
|   |   |   |   |   |   start > 698867: ribosome_ (39.15/19.27)
|   |   |   |   |   start > 700592
|   |   |   |   |   |   start <= 744173
|   |   |   |   |   |   |   start <= 730490
|   |   |   |   |   |   |   |   start <= 713273
|   |   |   |   |   |   |   |   |   start <= 706970:
cellular_component_ (40.74)
|   |   |   |   |   |   |   |   |   start > 706970
|   |   |   |   |   |   |   |   |   |   start <= 710099: nucleus_
(13.9)
|   |   |   |   |   |   |   |   |   |   start > 710099:
cellular_component_ (8.93)
|   |   |   |   |   |   |   |   start > 713273
|   |   |   |   |   |   |   |   |   start <= 729789
|   |   |   |   |   |   |   |   |   |   start <= 720635: nucleus_
(14.53)
|   |   |   |   |   |   |   |   |   |   start > 720635:
mitochondrion_ (24.07)
|   |   |   |   |   |   |   |   |   start > 729789: nucleus_ (15.78)
|   |   |   |   |   |   |   start > 730490: cellular_component_
(66.82)
|   |   |   |   |   |   start > 744173
|   |   |   |   |   |   |   start <= 758646
|   |   |   |   |   |   |   |   start <= 747304
|   |   |   |   |   |   |   |   |   start <= 744282: cytoplasm_
(23.87)
|   |   |   |   |   |   |   |   |   start > 744282
```

```
|   |   |   |   |   |   |   |   |   |   start <= 744687:
cellular_component_ (19.13)
|   |   |   |   |   |   |   |   |   |   start > 744687: cytoplasm_
(16.77)
|   |   |   |   |   |   |   |   start > 747304
|   |   |   |   |   |   |   |   |   start <= 753299
|   |   |   |   |   |   |   |   |   |   start <= 752255:
mitochondrion_ (30.85/12.72)
|   |   |   |   |   |   |   |   |   |   start > 752255:
endoplasmic_reticulum_ (15.48)
|   |   |   |   |   |   |   |   |   start > 753299
|   |   |   |   |   |   |   |   |   |   start <= 754875: cytoplasm_
(16.41)
|   |   |   |   |   |   |   |   |   |   start > 754875:
mitochondrion_ (17.87)
|   |   |   |   |   |   |   start > 758646
|   |   |   |   |   |   |   |   start <= 760023: cellular_component_
(15.93)
|   |   |   |   |   |   |   |   start > 760023
|   |   |   |   |   |   |   |   |   start <= 771651: nucleus_
(53.32/25.74)
|   |   |   |   |   |   |   |   |   start > 771651:
cellular_component_ (12.16)
|   |   |   |   start > 778579
|   |   |   |   |   start <= 786204
|   |   |   |   |   |   start <= 782041: cellular_bud_ (21.88/10.21)
|   |   |   |   |   |   start > 782041: plasma_membrane_
(34.82/14.91)
|   |   |   |   |   start > 786204
|   |   |   |   |   |   start <= 818319
|   |   |   |   |   |   |   start <= 798047
|   |   |   |   |   |   |   |   start <= 792683
|   |   |   |   |   |   |   |   |   start <= 787957: mitochondrion_
(8.24)
|   |   |   |   |   |   |   |   |   start > 787957
|   |   |   |   |   |   |   |   |   |   start <= 790079: nucleus_
(28.2/13.25)
|   |   |   |   |   |   |   |   |   |   start > 790079: cytoplasm_
(14.91)
|   |   |   |   |   |   |   |   start > 792683
|   |   |   |   |   |   |   |   |   start <= 794961: ribosome_
(10.44)
|   |   |   |   |   |   |   |   |   start > 794961: mitochondrion_
(34.97)
|   |   |   |   |   |   |   start > 798047
|   |   |   |   |   |   |   |   start <= 802355
|   |   |   |   |   |   |   |   |   start <= 799230: nucleus_ (18.7)
|   |   |   |   |   |   |   |   |   start > 799230: nucleolus_
(33.29/14.73)
|   |   |   |   |   |   |   |   start > 802355
|   |   |   |   |   |   |   |   |   start <= 814387
|   |   |   |   |   |   |   |   |   |   start <= 812449: cytoplasm_
(15.62)
```

```
|   |   |   |   |   |   |   |   |   |   start > 812449:
mitochondrion_ (17.51)
|   |   |   |   |   |   |   |   |   start > 814387: nucleus_
(29.61/12.29)
|   |   |   |   |   |   start > 818319
|   |   |   |   |   |   |   start <= 819525: cytoplasm_ (17.4)
|   |   |   |   |   |   |   start > 819525
|   |   |   |   |   |   |   |   start <= 821728: cellular_component_
(17.51)
|   |   |   |   |   |   |   |   start > 821728: cytoplasm_ (12.43)
|   |   start > 828136
|   |   |   start <= 911018
|   |   |   |   start <= 883824
|   |   |   |   |   start <= 839773
|   |   |   |   |   |   start <= 831671
|   |   |   |   |   |   |   start <= 829914
|   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   neigh_strand = W:
endoplasmic_reticulum_ (10.28/6.84)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
plasma_membrane_ (26.57/13.89)
|   |   |   |   |   |   |   |   neigh_num > 1
|   |   |   |   |   |   |   |   |   distance <= 1939: cytoplasm_
(10.62/4.18)
|   |   |   |   |   |   |   |   |   distance > 1939: mitochondrion_
(35.07/26.03)
|   |   |   |   |   |   |   start > 829914: mitochondrial_envelope_
(9.72)
|   |   |   |   |   |   start > 831671
|   |   |   |   |   |   |   start <= 834561
|   |   |   |   |   |   |   |   start <= 833685
|   |   |   |   |   |   |   |   |   start <= 833454: nucleus_
(13.88)
|   |   |   |   |   |   |   |   |   start > 833454:
cellular_component_ (14.21)
|   |   |   |   |   |   |   |   start > 833685: nucleus_
(32.84/13.69)
|   |   |   |   |   |   |   start > 834561
|   |   |   |   |   |   |   |   start <= 837409: mitochondrion_
(14.64)
|   |   |   |   |   |   |   |   start > 837409
|   |   |   |   |   |   |   |   |   distance <= 7683:
plasma_membrane_ (30.15/10.74)
|   |   |   |   |   |   |   |   |   distance > 7683:
membrane_fraction_ (4.34/0.43)
|   |   |   |   |   start > 839773
|   |   |   |   |   |   start <= 870699
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 868300
|   |   |   |   |   |   |   |   |   start <= 861302:
cellular_component_ (18.38)
|   |   |   |   |   |   |   |   |   start > 861302
|   |   |   |   |   |   |   |   |   |   start <= 866418: nucleus_
(16.52)
```

```
|   |   |   |   |   |   |   |   |   |   start > 866418:
cellular_component_ (43.45/23.03)
|   |   |   |   |   |   |   |   start > 868300: ribosome_ (15.98)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 843258: cellular_component_
(25.27)
|   |   |   |   |   |   |   |   start > 843258
|   |   |   |   |   |   |   |   |   start <= 861302
|   |   |   |   |   |   |   |   |   |   start <= 857579
|   |   |   |   |   |   |   |   |   |   |   start <= 856898:
cytoplasm_ (8.47)
|   |   |   |   |   |   |   |   |   |   |   start > 856898:
membrane_ (14.38)
|   |   |   |   |   |   |   |   |   |   start > 857579: cytoplasm_
(19.2)
|   |   |   |   |   |   |   |   |   start > 861302:
cellular_component_ (11.5)
|   |   |   |   |   |   start > 870699
|   |   |   |   |   |   |   start <= 876625
|   |   |   |   |   |   |   |   start <= 875364: peroxisome_
(41.89/26.02)
|   |   |   |   |   |   |   |   start > 875364: mitochondrion_
(17.3)
|   |   |   |   |   |   |   start > 876625
|   |   |   |   |   |   |   |   strand = C: cytoplasm_ (31.65)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 880365
|   |   |   |   |   |   |   |   |   |   start <= 878072
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
cellular_component_ (11.48/4.37)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1: nucleus_
(36.7/12.13)
|   |   |   |   |   |   |   |   |   |   start > 878072: nucleolus_
(32.23/14.94)
|   |   |   |   |   |   |   |   |   start > 880365:
membrane_fraction_ (18.48)
|   |   |   |   start > 883824
|   |   |   |   |   start <= 888704
|   |   |   |   |   |   start <= 887833: cytoplasm_ (55.87/26.93)
|   |   |   |   |   |   start > 887833:
microtubule_organizing_center_ (44.31/20.6)
|   |   |   |   |   start > 888704
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 892328: cellular_component_
(19.88)
|   |   |   |   |   |   |   start > 892328
|   |   |   |   |   |   |   |   start <= 902040
|   |   |   |   |   |   |   |   |   start <= 895957: nucleus_
(16.75)
|   |   |   |   |   |   |   |   |   start > 895957: cytoplasm_
(15.05)
|   |   |   |   |   |   |   |   start > 902040: nucleus_
(33.38/15.72)
|   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   start <= 900190
|   |   |   |   |   |   |   |   start <= 888970: cytoplasm_
(32.24/13.27)
|   |   |   |   |   |   |   |   start > 888970: nucleus_ (61.97)
|   |   |   |   |   |   |   start > 900190
|   |   |   |   |   |   |   |   start <= 902040
|   |   |   |   |   |   |   |   |   start <= 900751: mitochondrion_
(38.81/16.95)
|   |   |   |   |   |   |   |   |   start > 900751: cytoplasm_
(33.38/9.78)
|   |   |   |   |   |   |   |   start > 902040: membrane_ (22.98)
|   |   |   start > 911018
|   |   |   |   start <= 912475
|   |   |   |   |   start <= 911253: nucleolus_ (19.07)
|   |   |   |   |   start > 911253: cellular_bud_ (31.22/14.06)
|   |   |   |   start > 912475
|   |   |   |   |   start <= 919377
|   |   |   |   |   |   strand = C: nucleus_ (20.05)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 912660: cytoplasm_ (11.62)
|   |   |   |   |   |   |   start > 912660: mitochondrion_ (24.05)
|   |   |   |   |   start > 919377
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 939028
|   |   |   |   |   |   |   |   start <= 931372
|   |   |   |   |   |   |   |   |   start <= 923375: cytoplasm_
(10.31)
|   |   |   |   |   |   |   |   |   start > 923375: plasma_membrane_
(14.78)
|   |   |   |   |   |   |   |   start > 931372: nucleus_
(24.03/10.02)
|   |   |   |   |   |   |   start > 939028: cellular_component_
(11.0)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 939918
|   |   |   |   |   |   |   |   start <= 931372
|   |   |   |   |   |   |   |   |   start <= 923375:
plasma_membrane_ (19.51)
|   |   |   |   |   |   |   |   |   start > 923375:
cellular_component_ (10.48)
|   |   |   |   |   |   |   |   start > 931372: plasma_membrane_
(22.66)
|   |   |   |   |   |   |   start > 939918: cellular_component_
(22.95)
```

For Molecular Function

```
|   start <= 634120
|   |   stop <= 518732
|   |   |   start <= 138697
|   |   |   |   start <= 63279
|   |   |   |   |   start <= 11887
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 8427
```

```
|   |   |   |   |   |   |   |   start <= 6007: helicase_activity_
(6.64)
|   |   |   |   |   |   |   |   start > 6007: molecular_function_
(14.75)
|   |   |   |   |   |   |   start > 8427: lyase_activity_ (14.43)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   neigh_strand = W: protein_binding_
(7.61/1.83)
|   |   |   |   |   |   |   neigh_strand = C: peptidase_activity_
(14.99/5.15)
|   |   |   |   |   start > 11887
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 49303: molecular_function_
(91.19)
|   |   |   |   |   |   |   start > 49303
|   |   |   |   |   |   |   |   start <= 52671: protein_binding_
(8.59)
|   |   |   |   |   |   |   |   start > 52671
|   |   |   |   |   |   |   |   |   start <= 55153:
transferase_activity_ (7.06)
|   |   |   |   |   |   |   |   |   start > 55153:
molecular_function_ (7.33)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 41043
|   |   |   |   |   |   |   |   start <= 30079
|   |   |   |   |   |   |   |   |   start <= 25087
|   |   |   |   |   |   |   |   |   |   start <= 22938:
transporter_activity_ (11.4)
|   |   |   |   |   |   |   |   |   |   start > 22938:
transferase_activity_ (14.85)
|   |   |   |   |   |   |   |   |   start > 25087:
transporter_activity_ (17.3)
|   |   |   |   |   |   |   |   start > 30079
|   |   |   |   |   |   |   |   |   start <= 38169
|   |   |   |   |   |   |   |   |   |   start <= 35236
|   |   |   |   |   |   |   |   |   |   |   start <= 33013
|   |   |   |   |   |   |   |   |   |   |   |   start <= 30482:
hydrolase_activity_ (9.16)
|   |   |   |   |   |   |   |   |   |   |   |   start > 30482:
molecular_function_ (11.86)
|   |   |   |   |   |   |   |   |   |   |   start > 33013:
hydrolase_activity_ (17.45)
|   |   |   |   |   |   |   |   |   |   start > 35236:
molecular_function_ (19.07)
|   |   |   |   |   |   |   |   |   start > 38169
|   |   |   |   |   |   |   |   |   |   start <= 39121:
transferase_activity_ (13.84)
|   |   |   |   |   |   |   |   |   |   start > 39121:
transporter_activity_ (17.95)
|   |   |   |   |   |   |   start > 41043
|   |   |   |   |   |   |   |   start <= 47336: lyase_activity_
(15.81)
|   |   |   |   |   |   |   |   start > 47336: molecular_function_
(28.42)
```

```
|   |   |   |   start > 63279
|   |   |   |   |   start <= 82356
|   |   |   |   |   |   start <= 79353
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   distance <= 1665
|   |   |   |   |   |   |   |   |   start <= 73881
|   |   |   |   |   |   |   |   |   |   start <= 73006:
motor_activity_ (3.87/0.14)
|   |   |   |   |   |   |   |   |   |   start > 73006:
oxidoreductase_activity_ (15.05)
|   |   |   |   |   |   |   |   |   start > 73881
|   |   |   |   |   |   |   |   |   |   start <= 74719:
molecular_function_ (7.4)
|   |   |   |   |   |   |   |   |   |   start > 74719: RNA_binding_
(9.21/1.32)
|   |   |   |   |   |   |   |   distance > 1665
|   |   |   |   |   |   |   |   |   distance <= 1860:
motor_activity_ (10.14/1.24)
|   |   |   |   |   |   |   |   |   distance > 1860:
enzyme_regulator_activity_ (37.19/3.42)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 67725:
structural_molecule_activity_ (20.24)
|   |   |   |   |   |   |   |   start > 67725:
transcription_regulator_activity_ (11.01)
|   |   |   |   |   |   start > 79353: DNA_binding_ (39.08/17.84)
|   |   |   |   |   start > 82356
|   |   |   |   |   |   start <= 107275
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 100496
|   |   |   |   |   |   |   |   |   start <= 88517
|   |   |   |   |   |   |   |   |   |   start <= 85586:
molecular_function_ (24.06)
|   |   |   |   |   |   |   |   |   |   start > 85586:
transporter_activity_ (18.84)
|   |   |   |   |   |   |   |   |   start > 88517
|   |   |   |   |   |   |   |   |   |   start <= 96258
|   |   |   |   |   |   |   |   |   |   |   start <= 95109:
protein_binding_ (17.95)
|   |   |   |   |   |   |   |   |   |   |   start > 95109:
molecular_function_ (18.56)
|   |   |   |   |   |   |   |   |   |   start > 96258:
protein_binding_ (18.79)
|   |   |   |   |   |   |   |   start > 100496
|   |   |   |   |   |   |   |   |   start <= 103232:
protein_kinase_activity_ (9.25)
|   |   |   |   |   |   |   |   |   start > 103232:
transporter_activity_ (35.14/14.59)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 106172
|   |   |   |   |   |   |   |   |   start <= 99484:
molecular_function_ (38.2)
|   |   |   |   |   |   |   |   |   start > 99484
|   |   |   |   |   |   |   |   |   |   start <= 103232
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 100496:
translation_regulator_activity_ (11.2)
|   |   |   |   |   |   |   |   |   |   |   start > 100496:
helicase_activity_ (21.98)
|   |   |   |   |   |   |   |   |   |   start > 103232:
molecular_function_ (15.24)
|   |   |   |   |   |   |   |   start > 106172: protein_binding_
(19.29)
|   |   |   |   |   |   start > 107275
|   |   |   |   |   |   |   start <= 130161
|   |   |   |   |   |   |   |   start <= 108652:
transferase_activity_ (41.39/20.65)
|   |   |   |   |   |   |   |   start > 108652
|   |   |   |   |   |   |   |   |   start <= 121767
|   |   |   |   |   |   |   |   |   |   strand = C:
transferase_activity_ (20.81)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 117067:
molecular_function_ (29.65)
|   |   |   |   |   |   |   |   |   |   |   start > 117067:
hydrolase_activity_ (56.58)
|   |   |   |   |   |   |   |   |   start > 121767:
molecular_function_ (67.4)
|   |   |   |   |   |   |   start > 130161
|   |   |   |   |   |   |   |   start <= 135789
|   |   |   |   |   |   |   |   |   start <= 133042:
transporter_activity_ (18.3)
|   |   |   |   |   |   |   |   |   start > 133042:
structural_molecule_activity_ (21.08)
|   |   |   |   |   |   |   |   start > 135789
|   |   |   |   |   |   |   |   |   start <= 136749:
enzyme_regulator_activity_ (16.69)
|   |   |   |   |   |   |   |   |   start > 136749:
hydrolase_activity_ (20.77)
|   |   |   start > 138697
|   |   |   |   start <= 289033
|   |   |   |   |   start <= 230837
|   |   |   |   |   |   start <= 169337
|   |   |   |   |   |   |   start <= 159908
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 156211
|   |   |   |   |   |   |   |   |   |   start <= 150613
|   |   |   |   |   |   |   |   |   |   |   start <= 143820:
molecular_function_ (9.18)
|   |   |   |   |   |   |   |   |   |   |   start > 143820:
transferase_activity_ (16.55)
|   |   |   |   |   |   |   |   |   |   start > 150613
|   |   |   |   |   |   |   |   |   |   |   start <= 153494:
isomerase_activity_ (13.75)
|   |   |   |   |   |   |   |   |   |   |   start > 153494:
molecular_function_ (17.64)
|   |   |   |   |   |   |   |   |   start > 156211:
protein_kinase_activity_ (21.48)
|   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   start <= 153494
|   |   |   |   |   |   |   |   |   |   start <= 147415:
molecular_function_ (36.54)
|   |   |   |   |   |   |   |   |   |   start > 147415
|   |   |   |   |   |   |   |   |   |   |   start <= 150613:
RNA_binding_ (18.4)
|   |   |   |   |   |   |   |   |   |   |   start > 150613:
molecular_function_ (21.95)
|   |   |   |   |   |   |   |   |   start > 153494
|   |   |   |   |   |   |   |   |   |   start <= 157841:
transferase_activity_ (15.73)
|   |   |   |   |   |   |   |   |   |   start > 157841:
molecular_function_ (20.52)
|   |   |   |   |   |   |   start > 159908
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 166255:
hydrolase_activity_ (14.91)
|   |   |   |   |   |   |   |   |   start > 166255
|   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
transcription_regulator_activity_ (20.19/6.93)
|   |   |   |   |   |   |   |   |   |   neigh_num > 1: DNA_binding_
(20.99/6.68)
|   |   |   |   |   |   |   |   strand = W: protein_kinase_activity_
(33.93)
|   |   |   |   |   |   start > 169337
|   |   |   |   |   |   |   start <= 218362
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 210262
|   |   |   |   |   |   |   |   |   |   start <= 184678:
molecular_function_ (78.33)
|   |   |   |   |   |   |   |   |   |   start > 184678
|   |   |   |   |   |   |   |   |   |   |   start <= 187724:
RNA_binding_ (19.19)
|   |   |   |   |   |   |   |   |   |   |   start > 187724:
molecular_function_ (71.03)
|   |   |   |   |   |   |   |   |   start > 210262
|   |   |   |   |   |   |   |   |   |   start <= 213961:
transcription_regulator_activity_ (19.66)
|   |   |   |   |   |   |   |   |   |   start > 213961:
molecular_function_ (23.8)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 205247
|   |   |   |   |   |   |   |   |   |   start <= 184678
|   |   |   |   |   |   |   |   |   |   |   start <= 173826
|   |   |   |   |   |   |   |   |   |   |   |   stop <= 173903
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 171483:
molecular_function_ (10.19)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 171483:
RNA_binding_ (9.27)
|   |   |   |   |   |   |   |   |   |   |   |   stop > 173903:
structural_molecule_activity_ (12.62)
|   |   |   |   |   |   |   |   |   |   |   start > 173826
|   |   |   |   |   |   |   |   |   |   |   |   start <= 176222
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 175042:
molecular_function_ (12.63)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 175042:
protein_binding_ (18.07)
|   |   |   |   |   |   |   |   |   |   |   |   start > 176222:
molecular_function_ (31.05)
|   |   |   |   |   |   |   |   |   |   start > 184678
|   |   |   |   |   |   |   |   |   |   |   start <= 191405:
transferase_activity_ (27.51)
|   |   |   |   |   |   |   |   |   |   |   start > 191405
|   |   |   |   |   |   |   |   |   |   |   |   start <= 203420
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 195425:
protein_binding_ (18.69)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 195425
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
199094: structural_molecule_activity_ (13.08)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
199094: protein_binding_ (7.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 203420:
molecular_function_ (13.63)
|   |   |   |   |   |   |   |   |   start > 205247
|   |   |   |   |   |   |   |   |   |   start <= 208156:
phosphoprotein_phosphatase_activity_ (11.02)
|   |   |   |   |   |   |   |   |   |   start > 208156: RNA_binding_
(17.83)
|   |   |   |   |   |   |   start > 218362
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 225740
|   |   |   |   |   |   |   |   |   |   start <= 223142:
protein_binding_ (20.9)
|   |   |   |   |   |   |   |   |   |   start > 223142:
transferase_activity_ (14.28)
|   |   |   |   |   |   |   |   |   start > 225740
|   |   |   |   |   |   |   |   |   |   start <= 228313:
oxidoreductase_activity_ (26.4)
|   |   |   |   |   |   |   |   |   |   start > 228313:
protein_binding_ (27.25/11.63)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 223142
|   |   |   |   |   |   |   |   |   |   start <= 218629:
transferase_activity_ (11.78)
|   |   |   |   |   |   |   |   |   |   start > 218629:
structural_molecule_activity_ (19.9)
|   |   |   |   |   |   |   |   |   start > 223142:
molecular_function_ (14.87)
|   |   |   |   |   start > 230837
|   |   |   |   |   |   start <= 254309
|   |   |   |   |   |   |   start <= 237106
|   |   |   |   |   |   |   |   start <= 231216: molecular_function_
(24.08)
|   |   |   |   |   |   |   |   start > 231216:
nucleotidyltransferase_activity_ (20.93)
|   |   |   |   |   |   |   start > 237106
```

```
|   |   |   |   |   |   |   |   strand = C: molecular_function_
(113.31)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 241496:
molecular_function_ (20.37)
|   |   |   |   |   |   |   |   |   start > 241496: ligase_activity_
(14.55)
|   |   |   |   |   |   start > 254309
|   |   |   |   |   |   |   start <= 272814
|   |   |   |   |   |   |   |   start <= 260930
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 256766:
molecular_function_ (23.53)
|   |   |   |   |   |   |   |   |   |   start > 256766
|   |   |   |   |   |   |   |   |   |   |   start <= 259335:
motor_activity_ (11.0)
|   |   |   |   |   |   |   |   |   |   |   start > 259335:
peptidase_activity_ (18.99)
|   |   |   |   |   |   |   |   |   strand = W:
transferase_activity_ (23.4)
|   |   |   |   |   |   |   |   start > 260930
|   |   |   |   |   |   |   |   |   start <= 271309
|   |   |   |   |   |   |   |   |   |   start <= 264191:
protein_kinase_activity_ (15.49)
|   |   |   |   |   |   |   |   |   |   start > 264191
|   |   |   |   |   |   |   |   |   |   |   start <= 267534
|   |   |   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (22.2)
|   |   |   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 264601:
molecular_function_ (15.94)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 264601:
isomerase_activity_ (15.14)
|   |   |   |   |   |   |   |   |   |   |   start > 267534
|   |   |   |   |   |   |   |   |   |   |   |   start <= 268187:
protein_kinase_activity_ (18.96)
|   |   |   |   |   |   |   |   |   |   |   |   start > 268187:
molecular_function_ (14.45)
|   |   |   |   |   |   |   |   |   start > 271309:
transferase_activity_ (20.6)
|   |   |   |   |   |   |   start > 272814
|   |   |   |   |   |   |   |   start <= 281516
|   |   |   |   |   |   |   |   |   start <= 273254:
hydrolase_activity_ (15.38)
|   |   |   |   |   |   |   |   |   start > 273254
|   |   |   |   |   |   |   |   |   |   start <= 277528:
RNA_binding_ (22.06)
|   |   |   |   |   |   |   |   |   |   start > 277528
|   |   |   |   |   |   |   |   |   |   |   start <= 280479:
molecular_function_ (31.75)
|   |   |   |   |   |   |   |   |   |   |   start > 280479:
RNA_binding_ (11.81)
|   |   |   |   |   |   |   |   start > 281516
```

```
|   |   |   |   |   |   |   |   |   strand = C:
protein_kinase_activity_ (25.03)
|   |   |   |   |   |   |   |   |   strand = W:
structural_molecule_activity_ (7.57)
|   |   |   |   start > 289033
|   |   |   |   |   start <= 335485
|   |   |   |   |   |   start <= 310209
|   |   |   |   |   |   |   start <= 301227
|   |   |   |   |   |   |   |   start <= 297552
|   |   |   |   |   |   |   |   |   start <= 291050:
transcription_regulator_activity_ (21.51)
|   |   |   |   |   |   |   |   |   start > 291050
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 292426:
protein_binding_ (14.57)
|   |   |   |   |   |   |   |   |   |   |   start > 292426:
enzyme_regulator_activity_ (13.67)
|   |   |   |   |   |   |   |   |   |   strand = W: protein_binding_
(17.41)
|   |   |   |   |   |   |   |   start > 297552
|   |   |   |   |   |   |   |   |   start <= 299502:
transporter_activity_ (18.52)
|   |   |   |   |   |   |   |   |   start > 299502:
transcription_regulator_activity_ (20.09)
|   |   |   |   |   |   |   start > 301227
|   |   |   |   |   |   |   |   strand = C: DNA_binding_ (28.96)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 304386
|   |   |   |   |   |   |   |   |   |   start <= 301715:
molecular_function_ (25.18)
|   |   |   |   |   |   |   |   |   |   start > 301715
|   |   |   |   |   |   |   |   |   |   |   start <= 303120:
RNA_binding_ (17.21)
|   |   |   |   |   |   |   |   |   |   |   start > 303120:
molecular_function_ (17.65)
|   |   |   |   |   |   |   |   |   start > 304386
|   |   |   |   |   |   |   |   |   |   start <= 305297:
transcription_regulator_activity_ (11.35)
|   |   |   |   |   |   |   |   |   |   start > 305297: RNA_binding_
(20.9)
|   |   |   |   |   |   start > 310209
|   |   |   |   |   |   |   start <= 326627
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 320766
|   |   |   |   |   |   |   |   |   |   start <= 318944:
hydrolase_activity_ (17.94)
|   |   |   |   |   |   |   |   |   |   start > 318944:
transcription_regulator_activity_ (14.39)
|   |   |   |   |   |   |   |   |   start > 320766
|   |   |   |   |   |   |   |   |   |   start <= 324286:
molecular_function_ (30.61)
|   |   |   |   |   |   |   |   |   |   start > 324286:
helicase_activity_ (14.91)
|   |   |   |   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   |   |   |   start <= 318944:
structural_molecule_activity_ (30.87)
|   |   |   |   |   |   |   |   |   start > 318944
|   |   |   |   |   |   |   |   |   |   start <= 324286:
molecular_function_ (15.43)
|   |   |   |   |   |   |   |   |   |   start > 324286:
structural_molecule_activity_ (14.36)
|   |   |   |   |   |   |   start > 326627
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 329605:
isomerase_activity_ (11.57)
|   |   |   |   |   |   |   |   |   start > 329605:
enzyme_regulator_activity_ (20.12)
|   |   |   |   |   |   |   |   strand = W: hydrolase_activity_
(22.26)
|   |   |   |   |   start > 335485
|   |   |   |   |   |   start <= 459960
|   |   |   |   |   |   |   start <= 369438
|   |   |   |   |   |   |   |   start <= 364724
|   |   |   |   |   |   |   |   |   start <= 344738
|   |   |   |   |   |   |   |   |   |   start <= 338918
|   |   |   |   |   |   |   |   |   |   |   start <= 337142:
oxidoreductase_activity_ (16.21)
|   |   |   |   |   |   |   |   |   |   |   start > 337142:
molecular_function_ (31.82)
|   |   |   |   |   |   |   |   |   |   start > 338918:
hydrolase_activity_ (23.26)
|   |   |   |   |   |   |   |   |   start > 344738
|   |   |   |   |   |   |   |   |   |   strand = C:
molecular_function_ (102.95)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 355697
|   |   |   |   |   |   |   |   |   |   |   |   start <= 352272:
molecular_function_ (24.05)
|   |   |   |   |   |   |   |   |   |   |   |   start > 352272:
ligase_activity_ (13.99)
|   |   |   |   |   |   |   |   |   |   |   start > 355697:
molecular_function_ (26.07)
|   |   |   |   |   |   |   |   start > 364724
|   |   |   |   |   |   |   |   |   start <= 366732
|   |   |   |   |   |   |   |   |   |   start <= 364949:
ligase_activity_ (16.04)
|   |   |   |   |   |   |   |   |   |   start > 364949:
enzyme_regulator_activity_ (15.22)
|   |   |   |   |   |   |   |   |   start > 366732:
hydrolase_activity_ (40.69)
|   |   |   |   |   |   |   start > 369438
|   |   |   |   |   |   |   |   start <= 418509
|   |   |   |   |   |   |   |   |   start <= 381962
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 373790:
protein_binding_ (21.52)
|   |   |   |   |   |   |   |   |   |   |   start > 373790
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 378392:
structural_molecule_activity_ (19.66)
|   |   |   |   |   |   |   |   |   |   |   |   start > 378392:
DNA_binding_ (20.35)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 373790
|   |   |   |   |   |   |   |   |   |   |   |   start <= 370975:
molecular_function_ (16.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 370975:
transporter_activity_ (20.27)
|   |   |   |   |   |   |   |   |   |   |   start > 373790:
oxidoreductase_activity_ (63.97/15.99)
|   |   |   |   |   |   |   |   |   start > 381962
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 398102
|   |   |   |   |   |   |   |   |   |   |   |   start <= 387064:
transferase_activity_ (24.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 387064:
hydrolase_activity_ (19.52)
|   |   |   |   |   |   |   |   |   |   |   start > 398102
|   |   |   |   |   |   |   |   |   |   |   |   start <= 404947:
protein_binding_ (12.78)
|   |   |   |   |   |   |   |   |   |   |   |   start > 404947
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 408741:
transporter_activity_ (10.73)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 408741:
molecular_function_ (7.51)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 406633
|   |   |   |   |   |   |   |   |   |   |   |   start <= 383452:
hydrolase_activity_ (13.17)
|   |   |   |   |   |   |   |   |   |   |   |   start > 383452
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 398102
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
387064: structural_molecule_activity_ (15.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
387064: peptidase_activity_ (17.97)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 398102:
structural_molecule_activity_ (27.08)
|   |   |   |   |   |   |   |   |   |   |   start > 406633
|   |   |   |   |   |   |   |   |   |   |   |   start <= 412251
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 410440:
transferase_activity_ (15.24)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 410440:
DNA_binding_ (11.83)
|   |   |   |   |   |   |   |   |   |   |   |   start > 412251
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 415760:
hydrolase_activity_ (9.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 415760:
peptidase_activity_ (13.6)
|   |   |   |   |   |   |   |   start > 418509
|   |   |   |   |   |   |   |   |   start <= 455756
|   |   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   |   start <= 423889
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 420945:
molecular_function_ (16.23)
|   |   |   |   |   |   |   |   |   |   |   |   start > 420945:
transferase_activity_ (19.17)
|   |   |   |   |   |   |   |   |   |   |   start > 423889
|   |   |   |   |   |   |   |   |   |   |   |   start <= 435961:
molecular_function_ (69.43)
|   |   |   |   |   |   |   |   |   |   |   |   start > 435961
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 453054
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
450374: transporter_activity_ (11.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
450374: transferase_activity_ (12.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 453054:
molecular_function_ (42.09)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 429936
|   |   |   |   |   |   |   |   |   |   |   |   start <= 426230:
molecular_function_ (33.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 426230
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 427924:
protein_binding_ (20.02)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 427924:
molecular_function_ (19.76)
|   |   |   |   |   |   |   |   |   |   |   start > 429936
|   |   |   |   |   |   |   |   |   |   |   |   start <= 444576
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 432585:
oxidoreductase_activity_ (13.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 432585
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
435961: transporter_activity_ (17.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
435961: oxidoreductase_activity_ (6.55)
|   |   |   |   |   |   |   |   |   |   |   |   start > 444576:
molecular_function_ (20.25)
|   |   |   |   |   |   |   |   |   start > 455756
|   |   |   |   |   |   |   |   |   |   strand = C:
transferase_activity_ (18.29)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 458796:
enzyme_regulator_activity_ (15.72)
|   |   |   |   |   |   |   |   |   |   |   start > 458796:
hydrolase_activity_ (13.06)
|   |   |   |   |   |   start > 459960
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 474704
|   |   |   |   |   |   |   |   |   start <= 464398
|   |   |   |   |   |   |   |   |   |   start <= 461963:
transferase_activity_ (16.29)
|   |   |   |   |   |   |   |   |   |   start > 461963: DNA_binding_
(12.84)
|   |   |   |   |   |   |   |   |   start > 464398:
transcription_regulator_activity_ (45.7/15.38)
|   |   |   |   |   |   |   |   start > 474704
```

```
|   |   |   |   |   |   |   |   |   start <= 491362
|   |   |   |   |   |   |   |   |   |   start <= 480179
|   |   |   |   |   |   |   |   |   |   |   start <= 475738:
molecular_function_ (22.5)
|   |   |   |   |   |   |   |   |   |   |   start > 475738:
ligase_activity_ (20.8)
|   |   |   |   |   |   |   |   |   |   start > 480179
|   |   |   |   |   |   |   |   |   |   |   start <= 482841:
protein_binding_ (16.87)
|   |   |   |   |   |   |   |   |   |   |   start > 482841:
molecular_function_ (32.06)
|   |   |   |   |   |   |   |   |   start > 491362
|   |   |   |   |   |   |   |   |   |   start <= 506695
|   |   |   |   |   |   |   |   |   |   |   start <= 503515:
protein_kinase_activity_ (29.52)
|   |   |   |   |   |   |   |   |   |   |   start > 503515:
oxidoreductase_activity_ (14.22)
|   |   |   |   |   |   |   |   |   |   start > 506695
|   |   |   |   |   |   |   |   |   |   |   start <= 517649
|   |   |   |   |   |   |   |   |   |   |   |   start <= 514176:
peptidase_activity_ (17.8)
|   |   |   |   |   |   |   |   |   |   |   |   start > 514176:
molecular_function_ (13.7)
|   |   |   |   |   |   |   |   |   |   |   start > 517649:
transferase_activity_ (25.77)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 480179
|   |   |   |   |   |   |   |   |   start <= 464398:
transcription_regulator_activity_ (13.34)
|   |   |   |   |   |   |   |   |   start > 464398
|   |   |   |   |   |   |   |   |   |   start <= 467257:
molecular_function_ (41.04)
|   |   |   |   |   |   |   |   |   |   start > 467257
|   |   |   |   |   |   |   |   |   |   |   start <= 469936:
RNA_binding_ (14.34)
|   |   |   |   |   |   |   |   |   |   |   start > 469936:
molecular_function_ (34.72)
|   |   |   |   |   |   |   |   start > 480179
|   |   |   |   |   |   |   |   |   start <= 482841
|   |   |   |   |   |   |   |   |   |   start <= 480532:
DNA_binding_ (24.53)
|   |   |   |   |   |   |   |   |   |   start > 480532:
transporter_activity_ (34.18/16.63)
|   |   |   |   |   |   |   |   |   start > 482841
|   |   |   |   |   |   |   |   |   |   start <= 499663
|   |   |   |   |   |   |   |   |   |   |   start <= 495504
|   |   |   |   |   |   |   |   |   |   |   |   start <= 493541:
molecular_function_ (32.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 493541:
helicase_activity_ (16.98)
|   |   |   |   |   |   |   |   |   |   |   start > 495504
|   |   |   |   |   |   |   |   |   |   |   |   start <= 498094:
transferase_activity_ (19.92)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 498094:
molecular_function_ (12.45)
|   |   |   |   |   |   |   |   |   |   start > 499663
|   |   |   |   |   |   |   |   |   |   |   start <= 506695:
DNA_binding_ (39.78)
|   |   |   |   |   |   |   |   |   |   |   start > 506695:
molecular_function_ (13.15)
|   |   stop > 518732
|   |   |   start <= 607309
|   |   |   |   strand = C
|   |   |   |   |   start <= 544628
|   |   |   |   |   |   start <= 529720
|   |   |   |   |   |   |   start <= 527544: hydrolase_activity_
(18.04)
|   |   |   |   |   |   |   start > 527544:
structural_molecule_activity_ (18.74)
|   |   |   |   |   |   start > 529720
|   |   |   |   |   |   |   start <= 539382
|   |   |   |   |   |   |   |   start <= 535015:
transcription_regulator_activity_ (18.21)
|   |   |   |   |   |   |   |   start > 535015: molecular_function_
(18.43)
|   |   |   |   |   |   |   start > 539382:
transcription_regulator_activity_ (19.63)
|   |   |   |   |   start > 544628
|   |   |   |   |   |   start <= 556374
|   |   |   |   |   |   |   start <= 552017:
enzyme_regulator_activity_ (14.2)
|   |   |   |   |   |   |   start > 552017: protein_binding_ (19.92)
|   |   |   |   |   |   start > 556374
|   |   |   |   |   |   |   start <= 582731
|   |   |   |   |   |   |   |   start <= 566668: molecular_function_
(48.39)
|   |   |   |   |   |   |   |   start > 566668
|   |   |   |   |   |   |   |   |   start <= 568993: lyase_activity_
(13.5)
|   |   |   |   |   |   |   |   |   start > 568993
|   |   |   |   |   |   |   |   |   |   start <= 581193
|   |   |   |   |   |   |   |   |   |   |   start <= 573015:
molecular_function_ (5.46)
|   |   |   |   |   |   |   |   |   |   |   start > 573015:
nucleotidyltransferase_activity_ (17.66)
|   |   |   |   |   |   |   |   |   |   start > 581193:
molecular_function_ (12.42)
|   |   |   |   |   |   |   start > 582731
|   |   |   |   |   |   |   |   start <= 603354
|   |   |   |   |   |   |   |   |   start <= 593066
|   |   |   |   |   |   |   |   |   |   start <= 584039:
transporter_activity_ (9.91)
|   |   |   |   |   |   |   |   |   |   start > 584039:
molecular_function_ (22.68)
|   |   |   |   |   |   |   |   |   start > 593066
|   |   |   |   |   |   |   |   |   |   start <= 596747:
enzyme_regulator_activity_ (19.26)
```

```
|   |   |   |   |   |   |   |   |   |   start > 596747:
transporter_activity_ (12.16)
|   |   |   |   |   |   |   |   start > 603354: molecular_function_
(21.87)
|   |   |   |   strand = W
|   |   |   |   |   start <= 594473
|   |   |   |   |   |   start <= 554602
|   |   |   |   |   |   |   start <= 521011
|   |   |   |   |   |   |   |   start <= 517649: protein_binding_
(19.05)
|   |   |   |   |   |   |   |   start > 517649:
transcription_regulator_activity_ (18.43)
|   |   |   |   |   |   |   start > 521011
|   |   |   |   |   |   |   |   start <= 552017
|   |   |   |   |   |   |   |   |   start <= 539382
|   |   |   |   |   |   |   |   |   |   start <= 529720:
molecular_function_ (37.62)
|   |   |   |   |   |   |   |   |   |   start > 529720
|   |   |   |   |   |   |   |   |   |   |   start <= 535015:
protein_binding_ (18.25)
|   |   |   |   |   |   |   |   |   |   |   start > 535015:
helicase_activity_ (22.66)
|   |   |   |   |   |   |   |   |   start > 539382
|   |   |   |   |   |   |   |   |   |   start <= 544628:
transporter_activity_ (27.53)
|   |   |   |   |   |   |   |   |   |   start > 544628:
molecular_function_ (44.97)
|   |   |   |   |   |   |   |   start > 552017: protein_binding_
(23.16)
|   |   |   |   |   |   start > 554602
|   |   |   |   |   |   |   start <= 572266
|   |   |   |   |   |   |   |   start <= 556374:
transferase_activity_ (10.63)
|   |   |   |   |   |   |   |   start > 556374: molecular_function_
(26.65)
|   |   |   |   |   |   |   start > 572266
|   |   |   |   |   |   |   |   start <= 576549:
transcription_regulator_activity_ (26.74)
|   |   |   |   |   |   |   |   start > 576549
|   |   |   |   |   |   |   |   |   start <= 585582:
molecular_function_ (12.15)
|   |   |   |   |   |   |   |   |   start > 585582:
transcription_regulator_activity_ (14.67)
|   |   |   |   |   start > 594473
|   |   |   |   |   |   start <= 596747: DNA_binding_ (40.23/14.41)
|   |   |   |   |   |   start > 596747:
structural_molecule_activity_ (18.12)
|   |   |   start > 607309
|   |   |   |   start <= 615376
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 610478: hydrolase_activity_ (8.02)
|   |   |   |   |   |   start > 610478:
transcription_regulator_activity_ (13.31)
|   |   |   |   |   strand = W
```

```
|   |   |   |   |   |   start <= 610478: peptidase_activity_ (9.23)
|   |   |   |   |   |   start > 610478: hydrolase_activity_ (19.88)
|   |   |   |   start > 615376
|   |   |   |   |   start <= 622628: molecular_function_ (26.8)
|   |   |   |   |   start > 622628
|   |   |   |   |   |   start <= 627877
|   |   |   |   |   |   |   start <= 626964: protein_binding_
(26.02)
|   |   |   |   |   |   |   start > 626964: molecular_function_
(16.6)
|   |   |   |   |   |   start > 627877: protein_binding_ (31.2)
|   start > 634120
|   |   start <= 900190
|   |   |   start <= 648701
|   |   |   |   start <= 643833
|   |   |   |   |   start <= 642205
|   |   |   |   |   |   start <= 639522
|   |   |   |   |   |   |   start <= 639016: ligase_activity_
(17.52)
|   |   |   |   |   |   |   start > 639016:
transcription_regulator_activity_ (19.32)
|   |   |   |   |   |   start > 639522: ligase_activity_ (22.62)
|   |   |   |   |   start > 642205
|   |   |   |   |   |   neigh_strand = W: transporter_activity_
(16.71/3.3)
|   |   |   |   |   |   neigh_strand = C: hydrolase_activity_
(19.22/7.24)
|   |   |   |   start > 643833
|   |   |   |   |   strand = C: oxidoreductase_activity_ (20.08)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 647302: molecular_function_ (33.57)
|   |   |   |   |   |   start > 647302: enzyme_regulator_activity_
(47.87/21.52)
|   |   |   start > 648701
|   |   |   |   start <= 856898
|   |   |   |   |   start <= 782041
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 703968
|   |   |   |   |   |   |   |   start <= 681210
|   |   |   |   |   |   |   |   |   start <= 654163: RNA_binding_
(20.43)
|   |   |   |   |   |   |   |   |   start > 654163
|   |   |   |   |   |   |   |   |   |   start <= 667673:
molecular_function_ (40.54)
|   |   |   |   |   |   |   |   |   |   start > 667673
|   |   |   |   |   |   |   |   |   |   |   start <= 675628:
isomerase_activity_ (18.91)
|   |   |   |   |   |   |   |   |   |   |   start > 675628:
molecular_function_ (26.48)
|   |   |   |   |   |   |   |   start > 681210
|   |   |   |   |   |   |   |   |   start <= 694835
|   |   |   |   |   |   |   |   |   |   start <= 684350:
hydrolase_activity_ (12.63)
|   |   |   |   |   |   |   |   |   |   start > 684350
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 688169:
transferase_activity_ (27.08)
|   |   |   |   |   |   |   |   |   |   |   start > 688169
|   |   |   |   |   |   |   |   |   |   |   |   start <= 692415:
phosphoprotein_phosphatase_activity_ (20.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 692415:
transferase_activity_ (11.59)
|   |   |   |   |   |   |   |   |   start > 694835
|   |   |   |   |   |   |   |   |   |   start <= 700592:
molecular_function_ (27.59)
|   |   |   |   |   |   |   |   |   |   start > 700592:
ligase_activity_ (14.31)
|   |   |   |   |   |   |   start > 703968
|   |   |   |   |   |   |   |   start <= 720635
|   |   |   |   |   |   |   |   |   start <= 718466
|   |   |   |   |   |   |   |   |   |   start <= 706970:
RNA_binding_ (13.59)
|   |   |   |   |   |   |   |   |   |   start > 706970:
molecular_function_ (49.74)
|   |   |   |   |   |   |   |   |   start > 718466
|   |   |   |   |   |   |   |   |   |   start <= 719240:
RNA_binding_ (54.73)
|   |   |   |   |   |   |   |   |   |   start > 719240:
molecular_function_ (10.89)
|   |   |   |   |   |   |   |   start > 720635
|   |   |   |   |   |   |   |   |   start <= 740059
|   |   |   |   |   |   |   |   |   |   start <= 724715:
enzyme_regulator_activity_ (19.92)
|   |   |   |   |   |   |   |   |   |   start > 724715
|   |   |   |   |   |   |   |   |   |   |   start <= 732347
|   |   |   |   |   |   |   |   |   |   |   |   start <= 730490:
molecular_function_ (22.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 730490:
structural_molecule_activity_ (9.09)
|   |   |   |   |   |   |   |   |   |   |   start > 732347
|   |   |   |   |   |   |   |   |   |   |   |   start <= 736431:
transcription_regulator_activity_ (10.24)
|   |   |   |   |   |   |   |   |   |   |   |   start > 736431:
molecular_function_ (14.62)
|   |   |   |   |   |   |   |   |   start > 740059
|   |   |   |   |   |   |   |   |   |   start <= 760023
|   |   |   |   |   |   |   |   |   |   |   start <= 744282:
RNA_binding_ (26.3)
|   |   |   |   |   |   |   |   |   |   |   start > 744282
|   |   |   |   |   |   |   |   |   |   |   |   start <= 747304:
nucleotidyltransferase_activity_ (18.91)
|   |   |   |   |   |   |   |   |   |   |   |   start > 747304:
RNA_binding_ (12.13)
|   |   |   |   |   |   |   |   |   |   start > 760023
|   |   |   |   |   |   |   |   |   |   |   start <= 771651:
molecular_function_ (13.55)
|   |   |   |   |   |   |   |   |   |   |   start > 771651
|   |   |   |   |   |   |   |   |   |   |   |   start <= 775180:
enzyme_regulator_activity_ (12.49)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 775180:
molecular_function_ (13.42)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 679690
|   |   |   |   |   |   |   |   start <= 667673
|   |   |   |   |   |   |   |   |   start <= 659179
|   |   |   |   |   |   |   |   |   |   start <= 656796
|   |   |   |   |   |   |   |   |   |   |   start <= 654163:
structural_molecule_activity_ (17.11)
|   |   |   |   |   |   |   |   |   |   |   start > 654163:
protein_binding_ (13.93)
|   |   |   |   |   |   |   |   |   |   start > 656796
|   |   |   |   |   |   |   |   |   |   |   start <= 657526:
ligase_activity_ (14.28)
|   |   |   |   |   |   |   |   |   |   |   start > 657526:
molecular_function_ (17.79)
|   |   |   |   |   |   |   |   |   start > 659179
|   |   |   |   |   |   |   |   |   |   start <= 666277
|   |   |   |   |   |   |   |   |   |   |   start <= 664957:
transferase_activity_ (13.32)
|   |   |   |   |   |   |   |   |   |   |   start > 664957:
signal_transducer_activity_ (22.8/9.18)
|   |   |   |   |   |   |   |   |   |   start > 666277:
protein_binding_ (17.6)
|   |   |   |   |   |   |   |   start > 667673
|   |   |   |   |   |   |   |   |   start <= 673748
|   |   |   |   |   |   |   |   |   |   start <= 671123:
transcription_regulator_activity_ (7.99)
|   |   |   |   |   |   |   |   |   |   start > 671123
|   |   |   |   |   |   |   |   |   |   |   start <= 672468:
RNA_binding_ (13.62)
|   |   |   |   |   |   |   |   |   |   |   start > 672468:
transporter_activity_ (7.65)
|   |   |   |   |   |   |   |   |   start > 673748
|   |   |   |   |   |   |   |   |   |   start <= 678317:
hydrolase_activity_ (34.31/13.11)
|   |   |   |   |   |   |   |   |   |   start > 678317: DNA_binding_
(15.08)
|   |   |   |   |   |   |   start > 679690
|   |   |   |   |   |   |   |   start <= 725392
|   |   |   |   |   |   |   |   |   start <= 706970
|   |   |   |   |   |   |   |   |   |   start <= 685895
|   |   |   |   |   |   |   |   |   |   |   start <= 682217:
molecular_function_ (32.06)
|   |   |   |   |   |   |   |   |   |   |   start > 682217:
transcription_regulator_activity_ (17.81)
|   |   |   |   |   |   |   |   |   |   start > 685895
|   |   |   |   |   |   |   |   |   |   |   start <= 698867:
molecular_function_ (69.34)
|   |   |   |   |   |   |   |   |   |   |   start > 698867
|   |   |   |   |   |   |   |   |   |   |   |   start <= 700592:
translation_regulator_activity_ (16.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 700592:
molecular_function_ (31.55)
```

```
|   |   |   |   |   |   |   |   |   start > 706970
|   |   |   |   |   |   |   |   |   |   start <= 720635
|   |   |   |   |   |   |   |   |   |   |   start <= 713273
|   |   |   |   |   |   |   |   |   |   |   |   start <= 710099:
transcription_regulator_activity_ (9.45)
|   |   |   |   |   |   |   |   |   |   |   |   start > 710099:
molecular_function_ (12.57)
|   |   |   |   |   |   |   |   |   |   |   start > 713273:
transcription_regulator_activity_ (16.41)
|   |   |   |   |   |   |   |   |   |   start > 720635:
molecular_function_ (16.61)
|   |   |   |   |   |   |   |   start > 725392
|   |   |   |   |   |   |   |   |   start <= 742452
|   |   |   |   |   |   |   |   |   |   start <= 732347
|   |   |   |   |   |   |   |   |   |   |   start <= 730490
|   |   |   |   |   |   |   |   |   |   |   |   start <= 729789:
structural_molecule_activity_ (8.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 729789:
protein_binding_ (8.61)
|   |   |   |   |   |   |   |   |   |   |   start > 730490:
peptidase_activity_ (12.51)
|   |   |   |   |   |   |   |   |   |   start > 732347
|   |   |   |   |   |   |   |   |   |   |   start <= 740059:
protein_kinase_activity_ (14.1)
|   |   |   |   |   |   |   |   |   |   |   start > 740059:
structural_molecule_activity_ (13.94)
|   |   |   |   |   |   |   |   |   start > 742452
|   |   |   |   |   |   |   |   |   |   start <= 760023
|   |   |   |   |   |   |   |   |   |   |   start <= 747304
|   |   |   |   |   |   |   |   |   |   |   |   start <= 744687:
molecular_function_ (56.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 744687:
protein_kinase_activity_ (10.46)
|   |   |   |   |   |   |   |   |   |   |   start > 747304
|   |   |   |   |   |   |   |   |   |   |   |   start <= 752255:
transferase_activity_ (11.41)
|   |   |   |   |   |   |   |   |   |   |   |   start > 752255:
molecular_function_ (64.32)
|   |   |   |   |   |   |   |   |   |   start > 760023
|   |   |   |   |   |   |   |   |   |   |   start <= 771651
|   |   |   |   |   |   |   |   |   |   |   |   start <= 769300:
isomerase_activity_ (12.72)
|   |   |   |   |   |   |   |   |   |   |   |   start > 769300:
enzyme_regulator_activity_ (6.73)
|   |   |   |   |   |   |   |   |   |   |   start > 771651
|   |   |   |   |   |   |   |   |   |   |   |   start <= 778579:
transferase_activity_ (18.25)
|   |   |   |   |   |   |   |   |   |   |   |   start > 778579:
peptidase_activity_ (13.26)
|   |   |   |   |   start > 782041
|   |   |   |   |   |   start <= 817919
|   |   |   |   |   |   |   start <= 814054
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 812449
```

```
|   |   |   |   |   |   |   |   |   |   start <= 794961
|   |   |   |   |   |   |   |   |   |   |   start <= 792683:
transporter_activity_ (13.16)
|   |   |   |   |   |   |   |   |   |   |   start > 792683:
transferase_activity_ (12.06)
|   |   |   |   |   |   |   |   |   |   start > 794961
|   |   |   |   |   |   |   |   |   |   |   start <= 802355:
transcription_regulator_activity_ (11.62)
|   |   |   |   |   |   |   |   |   |   |   start > 802355:
transporter_activity_ (23.26)
|   |   |   |   |   |   |   |   |   start > 812449:
molecular_function_ (16.03)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 797553
|   |   |   |   |   |   |   |   |   |   start <= 790079
|   |   |   |   |   |   |   |   |   |   |   start <= 786204:
transporter_activity_ (20.83)
|   |   |   |   |   |   |   |   |   |   |   start > 786204:
molecular_function_ (22.68)
|   |   |   |   |   |   |   |   |   |   start > 790079
|   |   |   |   |   |   |   |   |   |   |   start <= 792683:
RNA_binding_ (18.72)
|   |   |   |   |   |   |   |   |   |   |   start > 792683
|   |   |   |   |   |   |   |   |   |   |   |   start <= 794961:
structural_molecule_activity_ (14.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 794961:
transporter_activity_ (14.81)
|   |   |   |   |   |   |   |   |   start > 797553
|   |   |   |   |   |   |   |   |   |   start <= 799230
|   |   |   |   |   |   |   |   |   |   |   start <= 798047:
molecular_function_ (17.04)
|   |   |   |   |   |   |   |   |   |   |   start > 798047:
DNA_binding_ (14.38)
|   |   |   |   |   |   |   |   |   |   start > 799230
|   |   |   |   |   |   |   |   |   |   |   start <= 802355:
RNA_binding_ (9.97)
|   |   |   |   |   |   |   |   |   |   |   start > 802355:
molecular_function_ (25.37)
|   |   |   |   |   |   |   start > 814054
|   |   |   |   |   |   |   |   start <= 814387:
transferase_activity_ (12.32)
|   |   |   |   |   |   |   |   start > 814387: motor_activity_
(14.53)
|   |   |   |   |   |   start > 817919
|   |   |   |   |   |   |   start <= 822616
|   |   |   |   |   |   |   |   strand = C: RNA_binding_ (12.0)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 821728:
molecular_function_ (48.29)
|   |   |   |   |   |   |   |   |   start > 821728: ligase_activity_
(18.48)
|   |   |   |   |   |   |   start > 822616
|   |   |   |   |   |   |   |   start <= 837409: molecular_function_
(145.66)
```

```
|   |   |   |   |   |   |   |   start > 837409
|   |   |   |   |   |   |   |   |   strand = C:
transporter_activity_ (14.53)
|   |   |   |   |   |   |   |   |   strand = W: molecular_function_
(45.12)
|   |   |   |   start > 856898
|   |   |   |   |   start <= 878072
|   |   |   |   |   |   start <= 870699
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 866418
|   |   |   |   |   |   |   |   |   start <= 861302:
molecular_function_ (14.63)
|   |   |   |   |   |   |   |   |   start > 861302:
protein_kinase_activity_ (12.84)
|   |   |   |   |   |   |   |   start > 866418
|   |   |   |   |   |   |   |   |   start <= 868300: DNA_binding_
(18.11)
|   |   |   |   |   |   |   |   |   start > 868300:
translation_regulator_activity_ (13.45)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 857579: hydrolase_activity_
(18.55)
|   |   |   |   |   |   |   |   start > 857579
|   |   |   |   |   |   |   |   |   start <= 861302
|   |   |   |   |   |   |   |   |   |   start <= 860411:
molecular_function_ (8.6)
|   |   |   |   |   |   |   |   |   |   start > 860411:
transferase_activity_ (14.89)
|   |   |   |   |   |   |   |   |   start > 861302:
molecular_function_ (16.81)
|   |   |   |   |   |   start > 870699
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 876625:
structural_molecule_activity_ (25.77)
|   |   |   |   |   |   |   |   start > 876625:
oxidoreductase_activity_ (14.28)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 876625:
signal_transducer_activity_ (17.45)
|   |   |   |   |   |   |   |   start > 876625:
transcription_regulator_activity_ (19.65)
|   |   |   |   |   start > 878072
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 888970
|   |   |   |   |   |   |   |   start <= 883824: molecular_function_
(24.29)
|   |   |   |   |   |   |   |   start > 883824
|   |   |   |   |   |   |   |   |   start <= 887833:
hydrolase_activity_ (22.54)
|   |   |   |   |   |   |   |   |   start > 887833:
molecular_function_ (19.4)
|   |   |   |   |   |   |   start > 888970
|   |   |   |   |   |   |   |   start <= 892328:
transferase_activity_ (17.76)
```

```
|   |   |   |   |   |   |   |   start > 892328
|   |   |   |   |   |   |   |   |   start <= 895957:
hydrolase_activity_ (17.81)
|   |   |   |   |   |   |   |   |   start > 895957:
enzyme_regulator_activity_ (16.76)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 888970
|   |   |   |   |   |   |   |   start <= 885792
|   |   |   |   |   |   |   |   |   start <= 880365:
molecular_function_ (22.21)
|   |   |   |   |   |   |   |   |   start > 880365
|   |   |   |   |   |   |   |   |   |   start <= 883824:
protein_binding_ (13.39)
|   |   |   |   |   |   |   |   |   |   start > 883824:
molecular_function_ (15.08)
|   |   |   |   |   |   |   |   start > 885792:
nucleotidyltransferase_activity_ (17.14)
|   |   |   |   |   |   |   start > 888970
|   |   |   |   |   |   |   |   start <= 895957
|   |   |   |   |   |   |   |   |   start <= 892328: RNA_binding_
(14.96)
|   |   |   |   |   |   |   |   |   start > 892328:
molecular_function_ (17.15)
|   |   |   |   |   |   |   |   start > 895957: RNA_binding_ (23.77)
|   |   start > 900190
|   |   |   start <= 919037
|   |   |   |   start <= 902040: transferase_activity_ (60.17/17.59)
|   |   |   |   start > 902040
|   |   |   |   |   start <= 911018
|   |   |   |   |   |   start <= 907214: protein_binding_ (16.81)
|   |   |   |   |   |   start > 907214:
transcription_regulator_activity_ (19.14)
|   |   |   |   |   start > 911018
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 912660: protein_binding_
(18.97)
|   |   |   |   |   |   |   start > 912660:
nucleotidyltransferase_activity_ (22.44)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 911253:
nucleotidyltransferase_activity_ (22.59)
|   |   |   |   |   |   |   start > 911253: molecular_function_
(13.75)
|   |   |   start > 919037
|   |   |   |   strand = C
|   |   |   |   |   start <= 931372
|   |   |   |   |   |   start <= 923375: transferase_activity_
(18.24)
|   |   |   |   |   |   start > 923375: transporter_activity_
(12.76)
|   |   |   |   |   start > 931372
|   |   |   |   |   |   start <= 939028:
transcription_regulator_activity_ (20.18)
```

```
|   |   |   |   |   |   start > 939028: oxidoreductase_activity_
(12.57)
|   |   |   |   strand = W
|   |   |   |   |   start <= 919377: oxidoreductase_activity_
(20.91)
|   |   |   |   |   start > 919377
|   |   |   |   |   |   start <= 939918
|   |   |   |   |   |   |   start <= 931372
|   |   |   |   |   |   |   |   start <= 923375:
transporter_activity_ (9.77)
|   |   |   |   |   |   |   |   start > 923375: molecular_function_
(10.22)
|   |   |   |   |   |   |   start > 931372: transporter_activity_
(16.7)
|   |   |   |   |   |   start > 939918
|   |   |   |   |   |   |   start <= 943876: molecular_function_
(15.82)
|   |   |   |   |   |   |   start > 943876: helicase_activity_
(6.54)
```

For Biological Process

```
|   start <= 96258
|   |   strand = C
|   |   |   start <= 85586
|   |   |   |   start <= 49303
|   |   |   |   |   start <= 6007: DNA_metabolic_process_ (5.36)
|   |   |   |   |   start > 6007: biological_process_ (119.55)
|   |   |   |   start > 49303
|   |   |   |   |   start <= 73006
|   |   |   |   |   |   start <= 56274
|   |   |   |   |   |   |   start <= 55153
|   |   |   |   |   |   |   |   start <= 52671: vesicle-
mediated_transport_ (11.56)
|   |   |   |   |   |   |   |   start > 52671:
vitamin_metabolic_process_ (24.26)
|   |   |   |   |   |   |   start > 55153: translation_ (11.58)
|   |   |   |   |   |   start > 56274
|   |   |   |   |   |   |   start <= 69485: conjugation_ (19.55)
|   |   |   |   |   |   |   start > 69485:
cytoskeleton_organization_and_biogenesis_ (24.34)
|   |   |   |   |   start > 73006
|   |   |   |   |   |   start <= 79353
|   |   |   |   |   |   |   start <= 74719: biological_process_
(24.58)
|   |   |   |   |   |   |   start > 74719
|   |   |   |   |   |   |   |   start <= 76239: translation_ (10.79)
|   |   |   |   |   |   |   |   start > 76239: vesicle-
mediated_transport_ (12.32)
|   |   |   |   |   |   start > 79353
|   |   |   |   |   |   |   start <= 82356:
carbohydrate_metabolic_process_ (10.52)
|   |   |   |   |   |   |   start > 82356: biological_process_
(29.68)
```

```
|   |   |   start > 85586
|   |   |   |   start <= 95109
|   |   |   |   |   start <= 88517: transport_ (20.09)
|   |   |   |   |   start > 88517: cytokinesis_ (15.81)
|   |   |   |   start > 95109:
cytoskeleton_organization_and_biogenesis_ (21.37)
|   |   strand = W
|   |   |   start <= 35236
|   |   |   |   start <= 30079
|   |   |   |   |   start <= 22938
|   |   |   |   |   |   start <= 16868: biological_process_ (15.3)
|   |   |   |   |   |   start > 16868: transport_ (18.95)
|   |   |   |   |   start > 22938
|   |   |   |   |   |   start <= 25087:
amino_acid_and_derivative_metabolic_process_ (24.46)
|   |   |   |   |   |   start > 25087:
generation_of_precursor_metabolites_and_energy_ (20.57)
|   |   |   |   start > 30079
|   |   |   |   |   start <= 33013
|   |   |   |   |   |   start <= 30482: cellular_respiration_
(24.59)
|   |   |   |   |   |   start > 30482:
cytoskeleton_organization_and_biogenesis_ (20.87)
|   |   |   |   |   start > 33013: pseudohyphal_growth_ (29.75/9.3)
|   |   |   start > 35236
|   |   |   |   start <= 47336
|   |   |   |   |   start <= 41043
|   |   |   |   |   |   start <= 39121
|   |   |   |   |   |   |   start <= 38169: cell_cycle_ (17.3)
|   |   |   |   |   |   |   start > 38169:
ribosome_biogenesis_and_assembly_ (9.29)
|   |   |   |   |   |   start > 39121: transport_ (19.18)
|   |   |   |   |   start > 41043
|   |   |   |   |   |   neigh_num <= 1: cellular_respiration_
(9.66/3.19)
|   |   |   |   |   |   neigh_num > 1:
carbohydrate_metabolic_process_ (22.19/8.52)
|   |   |   |   start > 47336
|   |   |   |   |   start <= 85586
|   |   |   |   |   |   start <= 67725
|   |   |   |   |   |   |   start <= 63279: biological_process_
(28.93)
|   |   |   |   |   |   |   start > 63279:
cytoskeleton_organization_and_biogenesis_ (31.86/15.34)
|   |   |   |   |   |   start > 67725
|   |   |   |   |   |   |   start <= 76239: DNA_metabolic_process_
(31.92/15.31)
|   |   |   |   |   |   |   start > 76239: biological_process_
(13.25)
|   |   |   |   |   start > 85586: transport_ (29.14)
|   start > 96258
|   |   start <= 696816
|   |   |   start <= 593914
|   |   |   |   start <= 193647
```

```
|   |   |   |   |   start <= 166255
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 135789
|   |   |   |   |   |   |   |   start <= 108652
|   |   |   |   |   |   |   |   |   start <= 103232
|   |   |   |   |   |   |   |   |   |   start <= 100496:
response_to_stress_ (12.48)
|   |   |   |   |   |   |   |   |   |   start > 100496:
biological_process_ (19.01)
|   |   |   |   |   |   |   |   |   start > 103232:
organelle_organization_and_biogenesis_ (21.2)
|   |   |   |   |   |   |   |   start > 108652
|   |   |   |   |   |   |   |   |   start <= 121767:
protein_modification_process_ (26.52)
|   |   |   |   |   |   |   |   |   start > 121767
|   |   |   |   |   |   |   |   |   |   start <= 128087:
cellular_homeostasis_ (16.09)
|   |   |   |   |   |   |   |   |   |   start > 128087:
response_to_stress_ (24.38)
|   |   |   |   |   |   |   start > 135789
|   |   |   |   |   |   |   |   start <= 153494
|   |   |   |   |   |   |   |   |   start <= 143820:
ribosome_biogenesis_and_assembly_ (18.7)
|   |   |   |   |   |   |   |   |   start > 143820
|   |   |   |   |   |   |   |   |   |   start <= 150613:
vitamin_metabolic_process_ (28.27)
|   |   |   |   |   |   |   |   |   |   start > 150613:
ribosome_biogenesis_and_assembly_ (14.66)
|   |   |   |   |   |   |   |   start > 153494
|   |   |   |   |   |   |   |   |   start <= 159908
|   |   |   |   |   |   |   |   |   |   start <= 156211: transport_
(14.17)
|   |   |   |   |   |   |   |   |   |   start > 156211: cytokinesis_
(18.38)
|   |   |   |   |   |   |   |   |   start > 159908:
lipid_metabolic_process_ (16.14)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 143820
|   |   |   |   |   |   |   |   start <= 130161
|   |   |   |   |   |   |   |   |   start <= 103232
|   |   |   |   |   |   |   |   |   |   start <= 100496
|   |   |   |   |   |   |   |   |   |   |   start <= 99484
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
ribosome_biogenesis_and_assembly_ (9.25/3.79)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
response_to_stress_ (11.23/3.77)
|   |   |   |   |   |   |   |   |   |   |   start > 99484:
translation_ (17.86)
|   |   |   |   |   |   |   |   |   |   start > 100496:
ribosome_biogenesis_and_assembly_ (34.86/14.03)
|   |   |   |   |   |   |   |   |   start > 103232
|   |   |   |   |   |   |   |   |   |   start <= 108652
|   |   |   |   |   |   |   |   |   |   |   start <= 106172:
biological_process_ (24.57)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 106172
|   |   |   |   |   |   |   |   |   |   |   |   start <= 107275:
membrane_organization_and_biogenesis_ (15.39)
|   |   |   |   |   |   |   |   |   |   |   |   start > 107275:
lipid_metabolic_process_ (21.77)
|   |   |   |   |   |   |   |   |   |   start > 108652
|   |   |   |   |   |   |   |   |   |   |   start <= 118382
|   |   |   |   |   |   |   |   |   |   |   |   start <= 117067:
biological_process_ (43.33)
|   |   |   |   |   |   |   |   |   |   |   |   start > 117067:
RNA_metabolic_process_ (26.27)
|   |   |   |   |   |   |   |   |   |   |   start > 118382
|   |   |   |   |   |   |   |   |   |   |   |   start <= 121767:
ribosome_biogenesis_and_assembly_ (15.28)
|   |   |   |   |   |   |   |   |   |   |   |   start > 121767:
biological_process_ (38.45)
|   |   |   |   |   |   |   |   start > 130161
|   |   |   |   |   |   |   |   |   start <= 135789
|   |   |   |   |   |   |   |   |   |   start <= 133042
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = W:
cell_wall_organization_and_biogenesis_ (19.67/6.55)
|   |   |   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   |   |   distance <= 4695:
transport_ (3.29/0.4)
|   |   |   |   |   |   |   |   |   |   |   |   distance > 4695:
cell_wall_organization_and_biogenesis_ (20.54/9.42)
|   |   |   |   |   |   |   |   |   |   start > 133042: translation_
(23.41)
|   |   |   |   |   |   |   |   |   start > 135789
|   |   |   |   |   |   |   |   |   |   start <= 138697
|   |   |   |   |   |   |   |   |   |   |   start <= 136749:
carbohydrate_metabolic_process_ (10.83)
|   |   |   |   |   |   |   |   |   |   |   start > 136749:
transport_ (22.67/11.18)
|   |   |   |   |   |   |   |   |   |   start > 138697:
biological_process_ (27.37)
|   |   |   |   |   |   |   start > 143820
|   |   |   |   |   |   |   |   start <= 157841
|   |   |   |   |   |   |   |   |   start <= 150613
|   |   |   |   |   |   |   |   |   |   start <= 147415:
organelle_organization_and_biogenesis_ (15.15)
|   |   |   |   |   |   |   |   |   |   start > 147415:
DNA_metabolic_process_ (11.05)
|   |   |   |   |   |   |   |   |   start > 150613
|   |   |   |   |   |   |   |   |   |   start <= 153494:
ribosome_biogenesis_and_assembly_ (13.99)
|   |   |   |   |   |   |   |   |   |   start > 153494:
biological_process_ (22.03)
|   |   |   |   |   |   |   |   start > 157841
|   |   |   |   |   |   |   |   |   start <= 159908:
RNA_metabolic_process_ (27.12)
|   |   |   |   |   |   |   |   |   start > 159908
|   |   |   |   |   |   |   |   |   |   start <= 164275:
ribosome_biogenesis_and_assembly_ (30.83/11.5)
```

```
|   |   |   |   |   |   |   |   |   |   start > 164275:
protein_modification_process_ (16.9)
|   |   |   |   |   start > 166255
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 171483
|   |   |   |   |   |   |   |   start <= 169337: response_to_stress_
(14.87)
|   |   |   |   |   |   |   |   start > 169337:
generation_of_precursor_metabolites_and_energy_ (11.06)
|   |   |   |   |   |   |   start > 171483
|   |   |   |   |   |   |   |   start <= 183055
|   |   |   |   |   |   |   |   |   start <= 176222:
biological_process_ (16.98)
|   |   |   |   |   |   |   |   |   start > 176222
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = C:
nuclear_organization_and_biogenesis_ (11.19/4.08)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = F:
nuclear_organization_and_biogenesis_ (4.71/2.04)
|   |   |   |   |   |   |   |   |   |   Neigh_GO_aspect = P:
conjugation_ (11.28/1.48)
|   |   |   |   |   |   |   |   start > 183055
|   |   |   |   |   |   |   |   |   start <= 184678:
biological_process_ (15.04)
|   |   |   |   |   |   |   |   |   start > 184678
|   |   |   |   |   |   |   |   |   |   start <= 187724:
transcription_ (7.33)
|   |   |   |   |   |   |   |   |   |   start > 187724:
biological_process_ (12.43)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 184678
|   |   |   |   |   |   |   |   start <= 179276
|   |   |   |   |   |   |   |   |   start <= 173826
|   |   |   |   |   |   |   |   |   |   start <= 173151
|   |   |   |   |   |   |   |   |   |   |   start <= 171483:
meiosis_ (16.62)
|   |   |   |   |   |   |   |   |   |   |   start > 171483:
translation_ (9.02)
|   |   |   |   |   |   |   |   |   |   start > 173151:
ribosome_biogenesis_and_assembly_ (26.34/12.46)
|   |   |   |   |   |   |   |   |   start > 173826
|   |   |   |   |   |   |   |   |   |   start <= 176222
|   |   |   |   |   |   |   |   |   |   |   start <= 175042:
response_to_stress_ (11.23)
|   |   |   |   |   |   |   |   |   |   |   start > 175042: vesicle-
mediated_transport_ (10.77)
|   |   |   |   |   |   |   |   |   |   start > 176222: meiosis_
(25.13)
|   |   |   |   |   |   |   |   start > 179276
|   |   |   |   |   |   |   |   |   neigh_strand = W:
DNA_metabolic_process_ (11.61/3.75)
|   |   |   |   |   |   |   |   |   neigh_strand = C
|   |   |   |   |   |   |   |   |   |   distance <= 4146:
DNA_metabolic_process_ (6.78/2.87)
```

```
|   |   |   |   |   |   |   |   |   |   distance > 4146:
ribosome_biogenesis_and_assembly_ (3.46/0.18)
|   |   |   |   |   |   |   start > 184678
|   |   |   |   |   |   |   |   start <= 191405
|   |   |   |   |   |   |   |   |   start <= 189153: transport_
(10.18)
|   |   |   |   |   |   |   |   |   start > 189153:
response_to_stress_ (14.74)
|   |   |   |   |   |   |   |   start > 191405: conjugation_
(37.65/17.12)
|   |   |   |   start > 193647
|   |   |   |   |   start <= 264601
|   |   |   |   |   |   start <= 223142
|   |   |   |   |   |   |   start <= 213961
|   |   |   |   |   |   |   |   start <= 202535
|   |   |   |   |   |   |   |   |   strand = C: biological_process_
(43.53)
|   |   |   |   |   |   |   |   |   strand = W: translation_ (17.12)
|   |   |   |   |   |   |   |   start > 202535
|   |   |   |   |   |   |   |   |   start <= 205247
|   |   |   |   |   |   |   |   |   |   start <= 203420:
transcription_ (10.11)
|   |   |   |   |   |   |   |   |   |   start > 203420:
cell_wall_organization_and_biogenesis_ (17.33)
|   |   |   |   |   |   |   |   |   start > 205247
|   |   |   |   |   |   |   |   |   |   start <= 210262:
translation_ (17.42)
|   |   |   |   |   |   |   |   |   |   start > 210262
|   |   |   |   |   |   |   |   |   |   |   start <= 212157:
DNA_metabolic_process_ (13.75)
|   |   |   |   |   |   |   |   |   |   |   start > 212157:
transcription_ (12.74)
|   |   |   |   |   |   |   start > 213961
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 218629:
protein_catabolic_process_ (21.35)
|   |   |   |   |   |   |   |   |   start > 218629: cell_cycle_
(11.56)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 218629:
protein_modification_process_ (14.12)
|   |   |   |   |   |   |   |   |   start > 218629: translation_
(8.35)
|   |   |   |   |   |   start > 223142
|   |   |   |   |   |   |   start <= 244026
|   |   |   |   |   |   |   |   start <= 230837
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 228313:
biological_process_ (35.94)
|   |   |   |   |   |   |   |   |   |   start > 228313:
ribosome_biogenesis_and_assembly_ (17.85)
|   |   |   |   |   |   |   |   |   strand = W:
lipid_metabolic_process_ (14.82)
|   |   |   |   |   |   |   |   start > 230837
```

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|   |   |   |   |   |   |   |   |   start <= 241496
|   |   |   |   |   |   |   |   |   |   start <= 239076
|   |   |   |   |   |   |   |   |   |   |   start <= 237106
|   |   |   |   |   |   |   |   |   |   |   |   start <= 231216:
biological_process_ (16.26)
|   |   |   |   |   |   |   |   |   |   |   |   start > 231216:
DNA_metabolic_process_ (15.13)
|   |   |   |   |   |   |   |   |   |   |   start > 237106:
biological_process_ (39.23)
|   |   |   |   |   |   |   |   |   |   start > 239076
|   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1: meiosis_
(15.89/5.45)
|   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (24.34/12.18)
|   |   |   |   |   |   |   |   |   start > 241496:
biological_process_ (52.2)
|   |   |   |   |   |   |   start > 244026
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 259335
|   |   |   |   |   |   |   |   |   |   start <= 251667
|   |   |   |   |   |   |   |   |   |   |   start <= 246989:
DNA_metabolic_process_ (39.11/18.79)
|   |   |   |   |   |   |   |   |   |   |   start > 246989:
cellular_respiration_ (22.93)
|   |   |   |   |   |   |   |   |   |   start > 251667
|   |   |   |   |   |   |   |   |   |   |   start <= 256766
|   |   |   |   |   |   |   |   |   |   |   |   start <= 254813:
biological_process_ (12.52)
|   |   |   |   |   |   |   |   |   |   |   |   start > 254813:
conjugation_ (15.15)
|   |   |   |   |   |   |   |   |   |   |   start > 256766:
cytoskeleton_organization_and_biogenesis_ (14.2)
|   |   |   |   |   |   |   |   |   start > 259335
|   |   |   |   |   |   |   |   |   |   start <= 260930:
sporulation_ (18.07)
|   |   |   |   |   |   |   |   |   |   start > 260930:
DNA_metabolic_process_ (16.26)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 246989: translation_
(14.25)
|   |   |   |   |   |   |   |   |   start > 246989
|   |   |   |   |   |   |   |   |   |   start <= 259335:
ribosome_biogenesis_and_assembly_ (10.4)
|   |   |   |   |   |   |   |   |   |   start > 259335:
biological_process_ (13.11)
|   |   |   |   |   start > 264601
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 474704
|   |   |   |   |   |   |   |   start <= 322070
|   |   |   |   |   |   |   |   |   start <= 289033
|   |   |   |   |   |   |   |   |   |   start <= 273254
|   |   |   |   |   |   |   |   |   |   |   start <= 268187:
RNA_metabolic_process_ (14.14)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 268187:
protein_modification_process_ (11.39)
|   |   |   |   |   |   |   |   |   |   start > 273254
|   |   |   |   |   |   |   |   |   |   |   start <= 282121
|   |   |   |   |   |   |   |   |   |   |   |   start <= 277528:
ribosome_biogenesis_and_assembly_ (12.89)
|   |   |   |   |   |   |   |   |   |   |   |   start > 277528
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 280479:
vesicle-mediated_transport_ (18.9)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 280479:
ribosome_biogenesis_and_assembly_ (10.85)
|   |   |   |   |   |   |   |   |   |   |   start > 282121
|   |   |   |   |   |   |   |   |   |   |   |   start <= 286060:
biological_process_ (7.08)
|   |   |   |   |   |   |   |   |   |   |   |   start > 286060:
signal_transduction_ (13.8)
|   |   |   |   |   |   |   |   |   start > 289033
|   |   |   |   |   |   |   |   |   |   start <= 313387
|   |   |   |   |   |   |   |   |   |   |   start <= 291050:
meiosis_ (16.87)
|   |   |   |   |   |   |   |   |   |   |   start > 291050
|   |   |   |   |   |   |   |   |   |   |   |   start <= 304386
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 292426:
transcription_ (14.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 292426
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
299502
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
297552: biological_process_ (18.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
297552: transport_ (31.24/14.62)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
299502
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = W: biological_process_ (23.13/7.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |
neigh_strand = C: carbohydrate_metabolic_process_ (12.08/4.5)
|   |   |   |   |   |   |   |   |   |   |   |   start > 304386:
transcription_ (25.82)
|   |   |   |   |   |   |   |   |   |   start > 313387
|   |   |   |   |   |   |   |   |   |   |   start <= 318944:
anatomical_structure_morphogenesis_ (15.77)
|   |   |   |   |   |   |   |   |   |   |   start > 318944
|   |   |   |   |   |   |   |   |   |   |   |   start <= 320766:
DNA_metabolic_process_ (17.6)
|   |   |   |   |   |   |   |   |   |   |   |   start > 320766:
meiosis_ (57.89/28.09)
|   |   |   |   |   |   |   |   start > 322070
|   |   |   |   |   |   |   |   |   start <= 453732
|   |   |   |   |   |   |   |   |   |   start <= 378392
|   |   |   |   |   |   |   |   |   |   |   start <= 364949
|   |   |   |   |   |   |   |   |   |   |   |   start <= 344738
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 337142
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
326627
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
324286: biological_process_ (16.98)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
324286: translation_ (15.06)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
326627
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
329605: lipid_metabolic_process_ (19.75)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
329605
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start <= 335485: pseudohyphal_growth_ (15.56)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
start > 335485: biological_process_ (11.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 337142
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
338619: organelle_organization_and_biogenesis_ (15.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
338619
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
339943: translation_ (19.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
339943: lipid_metabolic_process_ (10.34)
|   |   |   |   |   |   |   |   |   |   |   |   start > 344738
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 364065
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
352272
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
349116: biological_process_ (18.33)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
349116: DNA_metabolic_process_ (15.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
352272: biological_process_ (43.09)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 364065:
organelle_organization_and_biogenesis_ (20.67)
|   |   |   |   |   |   |   |   |   |   |   start > 364949
|   |   |   |   |   |   |   |   |   |   |   |   start <= 369438
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 366924:
protein_modification_process_ (14.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 366924:
lipid_metabolic_process_ (17.7)
|   |   |   |   |   |   |   |   |   |   |   |   start > 369438
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 373790:
transport_ (13.96)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 373790:
translation_ (22.72)
|   |   |   |   |   |   |   |   |   |   start > 378392
|   |   |   |   |   |   |   |   |   |   |   start <= 408741
|   |   |   |   |   |   |   |   |   |   |   |   start <= 383452:
cell_wall_organization_and_biogenesis_ (42.39/18.75)
|   |   |   |   |   |   |   |   |   |   |   |   start > 383452
```

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|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 398102:
RNA_metabolic_process_ (40.31)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 398102
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
404947: ribosome_biogenesis_and_assembly_ (12.82)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
404947: generation_of_precursor_metabolites_and_energy_ (12.74)
|   |   |   |   |   |   |   |   |   |   |   start > 408741
|   |   |   |   |   |   |   |   |   |   |   |   start <= 432585:
biological_process_ (122.89/13.81)
|   |   |   |   |   |   |   |   |   |   |   |   start > 432585
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 450374
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
435961: translation_ (11.72)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
435961: transport_ (11.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 450374
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
453054: lipid_metabolic_process_ (23.5)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
453054: biological_process_ (18.73)
|   |   |   |   |   |   |   |   |   start > 453732
|   |   |   |   |   |   |   |   |   |   start <= 461963
|   |   |   |   |   |   |   |   |   |   |   start <= 455756:
protein_modification_process_ (46.02/28.47)
|   |   |   |   |   |   |   |   |   |   |   start > 455756
|   |   |   |   |   |   |   |   |   |   |   |   start <= 459960:
cell_wall_organization_and_biogenesis_ (17.17)
|   |   |   |   |   |   |   |   |   |   |   |   start > 459960:
cytokinesis_ (24.98/8.35)
|   |   |   |   |   |   |   |   |   |   start > 461963
|   |   |   |   |   |   |   |   |   |   |   start <= 464398:
DNA_metabolic_process_ (15.31)
|   |   |   |   |   |   |   |   |   |   |   start > 464398
|   |   |   |   |   |   |   |   |   |   |   |   start <= 469936:
RNA_metabolic_process_ (13.93)
|   |   |   |   |   |   |   |   |   |   |   |   start > 469936:
meiosis_ (14.06)
|   |   |   |   |   |   |   start > 474704
|   |   |   |   |   |   |   |   start <= 560286
|   |   |   |   |   |   |   |   |   start <= 539382
|   |   |   |   |   |   |   |   |   |   start <= 514176
|   |   |   |   |   |   |   |   |   |   |   start <= 491362
|   |   |   |   |   |   |   |   |   |   |   |   start <= 480179
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 475738:
DNA_metabolic_process_ (20.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 475738:
translation_ (12.44)
|   |   |   |   |   |   |   |   |   |   |   |   start > 480179
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 488205:
biological_process_ (35.26)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 488205:
vesicle-mediated_transport_ (18.84)
|   |   |   |   |   |   |   |   |   |   |   start > 491362
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start <= 495504:
cell_cycle_ (12.53)
|   |   |   |   |   |   |   |   |   |   |   |   start > 495504
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 506695
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
503515: protein_modification_process_ (14.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
503515: amino_acid_and_derivative_metabolic_process_ (13.23)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 506695:
cell_cycle_ (38.07/14.53)
|   |   |   |   |   |   |   |   |   |   start > 514176
|   |   |   |   |   |   |   |   |   |   |   start <= 517649:
transport_ (47.79/29.11)
|   |   |   |   |   |   |   |   |   |   |   start > 517649
|   |   |   |   |   |   |   |   |   |   |   |   start <= 527544:
biological_process_ (60.55/15.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 527544
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 535015
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
529720: translation_ (15.51)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
529720: cell_cycle_ (19.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 535015:
biological_process_ (18.61)
|   |   |   |   |   |   |   |   |   start > 539382
|   |   |   |   |   |   |   |   |   |   start <= 552017
|   |   |   |   |   |   |   |   |   |   |   start <= 544628:
transcription_ (12.75)
|   |   |   |   |   |   |   |   |   |   |   start > 544628: vesicle-
mediated_transport_ (28.43/7.35)
|   |   |   |   |   |   |   |   |   |   start > 552017
|   |   |   |   |   |   |   |   |   |   |   start <= 556374:
DNA_metabolic_process_ (15.12)
|   |   |   |   |   |   |   |   |   |   |   start > 556374:
translation_ (11.73)
|   |   |   |   |   |   |   |   start > 560286
|   |   |   |   |   |   |   |   |   start <= 573015
|   |   |   |   |   |   |   |   |   |   start <= 566668
|   |   |   |   |   |   |   |   |   |   |   start <= 565038:
biological_process_ (25.62)
|   |   |   |   |   |   |   |   |   |   |   start > 565038:
response_to_stress_ (12.54)
|   |   |   |   |   |   |   |   |   |   start > 566668
|   |   |   |   |   |   |   |   |   |   |   start <= 568993:
amino_acid_and_derivative_metabolic_process_ (14.27)
|   |   |   |   |   |   |   |   |   |   |   start > 568993: meiosis_
(12.16)
|   |   |   |   |   |   |   |   |   start > 573015
|   |   |   |   |   |   |   |   |   |   start <= 593066
|   |   |   |   |   |   |   |   |   |   |   start <= 581193:
ribosome_biogenesis_and_assembly_ (11.11)
|   |   |   |   |   |   |   |   |   |   |   start > 581193
|   |   |   |   |   |   |   |   |   |   |   |   start <= 591023
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 584039
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
582731: biological_process_ (10.86)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
582731: transport_ (13.46)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 584039:
biological_process_ (22.29)
|   |   |   |   |   |   |   |   |   |   |   |   start > 591023:
ribosome_biogenesis_and_assembly_ (4.79)
|   |   |   |   |   |   |   |   |   |   start > 593066: transport_
(19.96)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 364949
|   |   |   |   |   |   |   |   start <= 318944
|   |   |   |   |   |   |   |   |   start <= 303120
|   |   |   |   |   |   |   |   |   |   start <= 280479
|   |   |   |   |   |   |   |   |   |   |   start <= 271309
|   |   |   |   |   |   |   |   |   |   |   |   start <= 265027:
response_to_stress_ (20.03)
|   |   |   |   |   |   |   |   |   |   |   |   start > 265027:
biological_process_ (40.33)
|   |   |   |   |   |   |   |   |   |   |   start > 271309
|   |   |   |   |   |   |   |   |   |   |   |   start <= 273254:
transport_ (13.97)
|   |   |   |   |   |   |   |   |   |   |   |   start > 273254:
DNA_metabolic_process_ (11.73)
|   |   |   |   |   |   |   |   |   |   start > 280479
|   |   |   |   |   |   |   |   |   |   |   start <= 299502
|   |   |   |   |   |   |   |   |   |   |   |   start <= 289033:
translation_ (13.74)
|   |   |   |   |   |   |   |   |   |   |   |   start > 289033
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: cellular_homeostasis_ (15.51/6.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: biological_process_ (20.77/5.76)
|   |   |   |   |   |   |   |   |   |   |   start > 299502
|   |   |   |   |   |   |   |   |   |   |   |   start <= 301715:
cellular_respiration_ (20.61)
|   |   |   |   |   |   |   |   |   |   |   |   start > 301715:
translation_ (23.29)
|   |   |   |   |   |   |   |   |   start > 303120
|   |   |   |   |   |   |   |   |   |   start <= 313387
|   |   |   |   |   |   |   |   |   |   |   start <= 305297
|   |   |   |   |   |   |   |   |   |   |   |   start <= 304386:
meiosis_ (16.12)
|   |   |   |   |   |   |   |   |   |   |   |   start > 304386:
cell_cycle_ (8.59)
|   |   |   |   |   |   |   |   |   |   |   start > 305297
|   |   |   |   |   |   |   |   |   |   |   |   start <= 310209:
ribosome_biogenesis_and_assembly_ (12.92)
|   |   |   |   |   |   |   |   |   |   |   |   start > 310209:
transport_ (20.52)
|   |   |   |   |   |   |   |   |   |   start > 313387: cell_cycle_
(44.69/14.36)
|   |   |   |   |   |   |   |   start > 318944
```

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|   |   |   |   |   |   |   |   |   start <= 352272
|   |   |   |   |   |   |   |   |   |   start <= 329605
|   |   |   |   |   |   |   |   |   |   |   start <= 324286:
biological_process_ (17.25)
|   |   |   |   |   |   |   |   |   |   |   start > 324286
|   |   |   |   |   |   |   |   |   |   |   |   start <= 326627:
translation_ (18.3)
|   |   |   |   |   |   |   |   |   |   |   |   start > 326627:
protein_modification_process_ (12.55)
|   |   |   |   |   |   |   |   |   |   start > 329605
|   |   |   |   |   |   |   |   |   |   |   start <= 339943:
amino_acid_and_derivative_metabolic_process_ (29.73/11.85)
|   |   |   |   |   |   |   |   |   |   |   start > 339943:
biological_process_ (22.44)
|   |   |   |   |   |   |   |   |   start > 352272
|   |   |   |   |   |   |   |   |   |   start <= 360206
|   |   |   |   |   |   |   |   |   |   |   start <= 355697:
translation_ (19.05)
|   |   |   |   |   |   |   |   |   |   |   start > 355697:
RNA_metabolic_process_ (12.35)
|   |   |   |   |   |   |   |   |   |   start > 360206
|   |   |   |   |   |   |   |   |   |   |   start <= 361869:
biological_process_ (22.18)
|   |   |   |   |   |   |   |   |   |   |   start > 361869:
translation_ (28.86)
|   |   |   |   |   |   |   start > 364949
|   |   |   |   |   |   |   |   start <= 493541
|   |   |   |   |   |   |   |   |   start <= 406633
|   |   |   |   |   |   |   |   |   |   start <= 370975
|   |   |   |   |   |   |   |   |   |   |   start <= 366924:
protein_catabolic_process_ (26.85)
|   |   |   |   |   |   |   |   |   |   |   start > 366924:
ribosome_biogenesis_and_assembly_ (14.79)
|   |   |   |   |   |   |   |   |   |   start > 370975
|   |   |   |   |   |   |   |   |   |   |   start <= 383452
|   |   |   |   |   |   |   |   |   |   |   |   start <= 373790:
transport_ (20.57)
|   |   |   |   |   |   |   |   |   |   |   |   start > 373790
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 378392:
response_to_stress_ (17.52)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 378392
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
381962: biological_process_ (12.25)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
381962: response_to_stress_ (12.46)
|   |   |   |   |   |   |   |   |   |   |   start > 383452
|   |   |   |   |   |   |   |   |   |   |   |   start <= 398102
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 387064:
vesicle-mediated_transport_ (14.92)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 387064:
DNA_metabolic_process_ (34.03/13.06)
|   |   |   |   |   |   |   |   |   |   |   |   start > 398102:
translation_ (20.13)
|   |   |   |   |   |   |   |   |   start > 406633
```

```
|   |   |   |   |   |   |   |   |   |   start <= 427924
|   |   |   |   |   |   |   |   |   |   |   start <= 418509
|   |   |   |   |   |   |   |   |   |   |   |   start <= 412251
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 410440:
protein_modification_process_ (7.37)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 410440:
carbohydrate_metabolic_process_ (12.82)
|   |   |   |   |   |   |   |   |   |   |   |   start > 412251
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 415760:
biological_process_ (10.14)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 415760:
protein_modification_process_ (8.31)
|   |   |   |   |   |   |   |   |   |   |   start > 418509
|   |   |   |   |   |   |   |   |   |   |   |   start <= 420945:
transcription_ (18.47)
|   |   |   |   |   |   |   |   |   |   |   |   start > 420945
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 426230:
biological_process_ (15.77)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 426230:
DNA_metabolic_process_ (10.81)
|   |   |   |   |   |   |   |   |   |   start > 427924
|   |   |   |   |   |   |   |   |   |   |   start <= 461963
|   |   |   |   |   |   |   |   |   |   |   |   start <= 455756
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 435961
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
429936: transport_ (27.72/10.45)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
429936
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
432585: biological_process_ (12.2)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
432585: organelle_organization_and_biogenesis_ (20.12/8.16)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 435961
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
444576: response_to_stress_ (9.68)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
444576: biological_process_ (18.04)
|   |   |   |   |   |   |   |   |   |   |   |   start > 455756
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 458796:
protein_catabolic_process_ (14.49)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 458796:
transport_ (12.11)
|   |   |   |   |   |   |   |   |   |   |   start > 461963
|   |   |   |   |   |   |   |   |   |   |   |   start <= 469936
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 465959
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
464398: ribosome_biogenesis_and_assembly_ (24.28)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
464398: transcription_ (37.02/14.03)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 465959
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
467257: organelle_organization_and_biogenesis_ (27.6)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
467257: ribosome_biogenesis_and_assembly_ (19.29)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   start > 469936
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 480532
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
480179: biological_process_ (26.99)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
480179: transcription_ (20.7)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 480532
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
482841: transport_ (12.39)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
482841: biological_process_ (25.82)
|   |   |   |   |   |   |   |   start > 493541
|   |   |   |   |   |   |   |   |   start <= 514176
|   |   |   |   |   |   |   |   |   |   start <= 503515
|   |   |   |   |   |   |   |   |   |   |   start <= 498094
|   |   |   |   |   |   |   |   |   |   |   |   start <= 495504:
RNA_metabolic_process_ (8.71)
|   |   |   |   |   |   |   |   |   |   |   |   start > 495504:
lipid_metabolic_process_ (12.18)
|   |   |   |   |   |   |   |   |   |   |   start > 498094
|   |   |   |   |   |   |   |   |   |   |   |   start <= 499663
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
W: sporulation_ (11.48/4.87)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_strand =
C: cell_wall_organization_and_biogenesis_ (11.51/3.67)
|   |   |   |   |   |   |   |   |   |   |   |   start > 499663:
response_to_stress_ (18.1)
|   |   |   |   |   |   |   |   |   |   start > 503515
|   |   |   |   |   |   |   |   |   |   |   start <= 506695
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = W
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1:
DNA_metabolic_process_ (8.37/1.22)
|   |   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
cell_cycle_ (7.52/2.93)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_strand = C:
cell_cycle_ (15.71/4.49)
|   |   |   |   |   |   |   |   |   |   |   start > 506695:
pseudohyphal_growth_ (12.94)
|   |   |   |   |   |   |   |   |   start > 514176
|   |   |   |   |   |   |   |   |   |   start <= 539382
|   |   |   |   |   |   |   |   |   |   |   start <= 527544
|   |   |   |   |   |   |   |   |   |   |   |   start <= 517649:
biological_process_ (41.54/18.76)
|   |   |   |   |   |   |   |   |   |   |   |   start > 517649
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 521011:
transcription_ (12.79)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 521011:
biological_process_ (17.05)
|   |   |   |   |   |   |   |   |   |   |   start > 527544
|   |   |   |   |   |   |   |   |   |   |   |   start <= 535015
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 529720:
ribosome_biogenesis_and_assembly_ (22.35)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 529720:
vesicle-mediated_transport_ (35.82/13.69)
```

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|   |   |   |   |   |   |   |   |   |   |   |   start > 535015:
cell_cycle_ (35.49/17.25)
|   |   |   |   |   |   |   |   |   |   start > 539382
|   |   |   |   |   |   |   |   |   |   |   start <= 556374
|   |   |   |   |   |   |   |   |   |   |   |   start <= 548483
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 544628:
lipid_metabolic_process_ (15.48)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 544628:
RNA_metabolic_process_ (19.69)
|   |   |   |   |   |   |   |   |   |   |   |   start > 548483
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 554602:
protein_modification_process_ (24.38)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 554602:
cellular_respiration_ (21.93/9.94)
|   |   |   |   |   |   |   |   |   |   |   start > 556374
|   |   |   |   |   |   |   |   |   |   |   |   start <= 565038:
biological_process_ (11.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 565038
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 573015
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
572266: translation_ (10.29)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
572266: transcription_ (8.1)
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 573015
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start <=
576549: transport_ (17.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   |   start >
576549: translation_ (13.69)
|   |   |   start > 593914
|   |   |   |   start <= 673748
|   |   |   |   |   start <= 621255
|   |   |   |   |   |   start <= 610028
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 607309: biological_process_
(52.4)
|   |   |   |   |   |   |   |   start > 607309:
DNA_metabolic_process_ (11.03)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 596747:
DNA_metabolic_process_ (68.07/31.14)
|   |   |   |   |   |   |   |   start > 596747:
generation_of_precursor_metabolites_and_energy_ (16.47)
|   |   |   |   |   |   start > 610028
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 615376: transcription_
(35.74/14.94)
|   |   |   |   |   |   |   |   start > 615376: biological_process_
(14.34)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 610478:
organelle_organization_and_biogenesis_ (15.54)
|   |   |   |   |   |   |   |   start > 610478: response_to_stress_
(15.31)
|   |   |   |   |   start > 621255
```

```
|   |   |   |   |   |   start <= 659179
|   |   |   |   |   |   |   start <= 639522
|   |   |   |   |   |   |   |   start <= 639016
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 631512
|   |   |   |   |   |   |   |   |   |   |   start <= 623524:
translation_ (11.36)
|   |   |   |   |   |   |   |   |   |   |   start > 623524: vesicle-
mediated_transport_ (13.63)
|   |   |   |   |   |   |   |   |   |   start > 631512: translation_
(21.53)
|   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   start <= 627877
|   |   |   |   |   |   |   |   |   |   |   start <= 623524:
vesicle-mediated_transport_ (16.81)
|   |   |   |   |   |   |   |   |   |   |   start > 623524:
cell_wall_organization_and_biogenesis_ (12.86)
|   |   |   |   |   |   |   |   |   |   start > 627877
|   |   |   |   |   |   |   |   |   |   |   start <= 631512:
protein_modification_process_ (13.25)
|   |   |   |   |   |   |   |   |   |   |   start > 631512: vesicle-
mediated_transport_ (20.43)
|   |   |   |   |   |   |   |   start > 639016
|   |   |   |   |   |   |   |   |   distance <= 3542
|   |   |   |   |   |   |   |   |   |   distance <= 2282:
DNA_metabolic_process_ (10.31/3.49)
|   |   |   |   |   |   |   |   |   |   distance > 2282:
RNA_metabolic_process_ (10.39/3.17)
|   |   |   |   |   |   |   |   |   distance > 3542:
DNA_metabolic_process_ (19.04/3.19)
|   |   |   |   |   |   |   start > 639522
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 648701:
protein_modification_process_ (22.81)
|   |   |   |   |   |   |   |   |   start > 648701
|   |   |   |   |   |   |   |   |   |   start <= 654163:
RNA_metabolic_process_ (15.68)
|   |   |   |   |   |   |   |   |   |   start > 654163:
biological_process_ (18.13)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 647302
|   |   |   |   |   |   |   |   |   |   start <= 645947
|   |   |   |   |   |   |   |   |   |   |   start <= 642205:
biological_process_ (34.58)
|   |   |   |   |   |   |   |   |   |   |   start > 642205
|   |   |   |   |   |   |   |   |   |   |   |   start <= 643833:
organelle_organization_and_biogenesis_ (21.02)
|   |   |   |   |   |   |   |   |   |   |   |   start > 643833:
biological_process_ (13.08)
|   |   |   |   |   |   |   |   |   |   start > 645947:
signal_transduction_ (16.05)
|   |   |   |   |   |   |   |   |   start > 647302
|   |   |   |   |   |   |   |   |   |   start <= 654163:
translation_ (58.79/15.47)
```

```
|   |   |   |   |   |   |   |   |   |   start > 654163
|   |   |   |   |   |   |   |   |   |   |   start <= 657526
|   |   |   |   |   |   |   |   |   |   |   |   start <= 656796:
biological_process_ (20.48)
|   |   |   |   |   |   |   |   |   |   |   |   start > 656796:
translation_ (17.56)
|   |   |   |   |   |   |   |   |   |   |   start > 657526:
biological_process_ (22.63)
|   |   |   |   |   |   start > 659179
|   |   |   |   |   |   |   start <= 671123
|   |   |   |   |   |   |   |   start <= 665971
|   |   |   |   |   |   |   |   |   start <= 664670
|   |   |   |   |   |   |   |   |   |   neigh_strand = W:
organelle_organization_and_biogenesis_ (13.63/3.06)
|   |   |   |   |   |   |   |   |   |   neigh_strand = C:
DNA_metabolic_process_ (15.02/6.44)
|   |   |   |   |   |   |   |   |   start > 664670:
DNA_metabolic_process_ (37.81)
|   |   |   |   |   |   |   |   start > 665971
|   |   |   |   |   |   |   |   |   start <= 666277:
protein_modification_process_ (35.8/20.86)
|   |   |   |   |   |   |   |   |   start > 666277
|   |   |   |   |   |   |   |   |   |   start <= 667673:
cytokinesis_ (20.07)
|   |   |   |   |   |   |   |   |   |   start > 667673:
DNA_metabolic_process_ (16.25)
|   |   |   |   |   |   |   start > 671123
|   |   |   |   |   |   |   |   start <= 672468:
RNA_metabolic_process_ (11.81)
|   |   |   |   |   |   |   |   start > 672468:
organelle_organization_and_biogenesis_ (19.06/8.63)
|   |   |   |   start > 673748
|   |   |   |   |   start <= 688169
|   |   |   |   |   |   start <= 678317
|   |   |   |   |   |   |   start <= 675628:
amino_acid_and_derivative_metabolic_process_ (16.64)
|   |   |   |   |   |   |   start > 675628: biological_process_
(55.11)
|   |   |   |   |   |   start > 678317
|   |   |   |   |   |   |   start <= 684350
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
protein_modification_process_ (13.29/4.18)
|   |   |   |   |   |   |   |   |   neigh_num > 1: transcription_
(42.91/25.26)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 681210
|   |   |   |   |   |   |   |   |   |   start <= 679690:
transcription_ (15.1)
|   |   |   |   |   |   |   |   |   |   start > 679690:
protein_modification_process_ (25.88)
|   |   |   |   |   |   |   |   |   start > 681210:
vitamin_metabolic_process_ (32.21/13.09)
|   |   |   |   |   |   |   start > 684350
```

```
|   |   |   |   |   |   |   |   strand = C:
amino_acid_and_derivative_metabolic_process_ (17.84)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 685895: transcription_
(24.67/11.58)
|   |   |   |   |   |   |   |   |   start > 685895:
biological_process_ (19.35)
|   |   |   |   |   start > 688169
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 694835
|   |   |   |   |   |   |   |   start <= 692415:
protein_modification_process_ (15.01)
|   |   |   |   |   |   |   |   start > 692415
|   |   |   |   |   |   |   |   |   neigh_num <= 1:
vitamin_metabolic_process_ (11.18/2.63)
|   |   |   |   |   |   |   |   |   neigh_num > 1:
carbohydrate_metabolic_process_ (25.32/10.99)
|   |   |   |   |   |   |   start > 694835: response_to_stress_
(28.96/10.86)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 689562: translation_ (20.39)
|   |   |   |   |   |   |   start > 689562: RNA_metabolic_process_
(12.95)
|   |   start > 696816
|   |   |   start <= 833685
|   |   |   |   start <= 814054
|   |   |   |   |   start <= 760023
|   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   start <= 732347
|   |   |   |   |   |   |   |   start <= 719240
|   |   |   |   |   |   |   |   |   start <= 718466
|   |   |   |   |   |   |   |   |   |   start <= 706970
|   |   |   |   |   |   |   |   |   |   |   start <= 700592:
biological_process_ (16.3)
|   |   |   |   |   |   |   |   |   |   |   start > 700592
|   |   |   |   |   |   |   |   |   |   |   |   start <= 703968:
translation_ (16.14)
|   |   |   |   |   |   |   |   |   |   |   |   start > 703968:
RNA_metabolic_process_ (14.36)
|   |   |   |   |   |   |   |   |   |   start > 706970
|   |   |   |   |   |   |   |   |   |   |   start <= 713273
|   |   |   |   |   |   |   |   |   |   |   |   start <= 710099:
biological_process_ (12.0)
|   |   |   |   |   |   |   |   |   |   |   |   start > 710099:
transport_ (7.77)
|   |   |   |   |   |   |   |   |   |   |   start > 713273:
biological_process_ (18.45)
|   |   |   |   |   |   |   |   |   start > 718466:
ribosome_biogenesis_and_assembly_ (110.23/52.49)
|   |   |   |   |   |   |   |   start > 719240
|   |   |   |   |   |   |   |   |   start <= 730490
|   |   |   |   |   |   |   |   |   |   start <= 724715
|   |   |   |   |   |   |   |   |   |   |   start <= 720635:
biological_process_ (12.65)
```

```
|   |   |   |   |   |   |   |   |   |   |   start > 720635: vesicle-
mediated_transport_ (16.68)
|   |   |   |   |   |   |   |   |   |   start > 724715:
biological_process_ (30.83)
|   |   |   |   |   |   |   |   |   start > 730490: translation_
(13.97)
|   |   |   |   |   |   |   start > 732347
|   |   |   |   |   |   |   |   start <= 740059
|   |   |   |   |   |   |   |   |   start <= 736431:
ribosome_biogenesis_and_assembly_ (13.71)
|   |   |   |   |   |   |   |   |   start > 736431
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_component_: transport_ (5.42/2.47)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
peptidase_activity_: transport_ (11.75/2.15)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_binding_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
biological_process_: vesicle-mediated_transport_ (1.19/0.46)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
molecular_function_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrion_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transporter_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
generation_of_precursor_metabolites_and_energy_: vesicle-
mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = membrane_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lyase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
carbohydrate_metabolic_process_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_respiration_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytoplasm_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleus_:
vesicle-mediated_transport_ (4.94/1.78)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
enzyme_regulator_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = conjugation_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
microtubule_organizing_center_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
structural_molecule_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cycle_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_organization_and_biogenesis_: vesicle-
mediated_transport_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
motor_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = transport_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_bud_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
site_of_polarized_growth_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cytokinesis_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
response_to_stress_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ribosome_biogenesis_and_assembly_: vesicle-mediated_transport_
(4.7/0.55)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
helicase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
RNA_metabolic_process_: vesicle-mediated_transport_ (3.85/1.32)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vacuole_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
hydrolase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
organelle_organization_and_biogenesis_: vesicle-mediated_transport_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = chromosome_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cytoskeleton_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endomembrane_system_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
endoplasmic_reticulum_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transferase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_modification_process_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cellular_homeostasis_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = nucleolus_:
vesicle-mediated_transport_ (2.51/0.98)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
vitamin_metabolic_process_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = RNA_binding_:
vesicle-mediated_transport_ (2.6/0.18)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
DNA_metabolic_process_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
isomerase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
lipid_metabolic_process_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
plasma_membrane_: vesicle-mediated_transport_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_kinase_activity_: vesicle-mediated_transport_ (1.64/0.7)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = DNA_binding_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_regulator_activity_: transport_ (4.43/1.63)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = meiosis_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = ribosome_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = translation_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nuclear_organization_and_biogenesis_: vesicle-mediated_transport_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
transcription_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
nucleotidyltransferase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
ligase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = peroxisome_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
mitochondrial_envelope_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
extracellular_region_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
anatomical_structure_morphogenesis_: vesicle-mediated_transport_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_fraction_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
pseudohyphal_growth_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
amino_acid_and_derivative_metabolic_process_: vesicle-
mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
protein_catabolic_process_: vesicle-mediated_transport_ (1.03/0.45)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
oxidoreductase_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
Golgi_apparatus_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = vesicle-
mediated_transport_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_wall_organization_and_biogenesis_: vesicle-mediated_transport_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_wall_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transduction_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
signal_transducer_activity_: vesicle-mediated_transport_ (0.0)
```

```
|   |   |   |   |   |   |   |   |   |   NeighGO_term = sporulation_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
phosphoprotein_phosphatase_activity_: vesicle-mediated_transport_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
electron_transport_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
membrane_organization_and_biogenesis_: vesicle-mediated_transport_
(0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term = cell_cortex_:
vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
translation_regulator_activity_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   |   |   NeighGO_term =
cell_budding_: vesicle-mediated_transport_ (0.0)
|   |   |   |   |   |   |   |   start > 740059
|   |   |   |   |   |   |   |   |   start <= 744282:
RNA_metabolic_process_ (17.6)
|   |   |   |   |   |   |   |   |   start > 744282:
ribosome_biogenesis_and_assembly_ (34.32)
|   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   start <= 704852
|   |   |   |   |   |   |   |   start <= 700592
|   |   |   |   |   |   |   |   |   start <= 698867: transport_
(8.65)
|   |   |   |   |   |   |   |   |   start > 698867: translation_
(11.57)
|   |   |   |   |   |   |   |   start > 700592:
organelle_organization_and_biogenesis_ (16.7)
|   |   |   |   |   |   |   start > 704852
|   |   |   |   |   |   |   |   stop <= 744353
|   |   |   |   |   |   |   |   |   start <= 725392
|   |   |   |   |   |   |   |   |   |   start <= 710099
|   |   |   |   |   |   |   |   |   |   |   start <= 706970:
biological_process_ (12.97)
|   |   |   |   |   |   |   |   |   |   |   start > 706970:
transcription_ (11.31)
|   |   |   |   |   |   |   |   |   |   start > 710099:
biological_process_ (53.35/7.42)
|   |   |   |   |   |   |   |   |   start > 725392
|   |   |   |   |   |   |   |   |   |   start <= 730490
|   |   |   |   |   |   |   |   |   |   |   start <= 729789:
translation_ (8.41)
|   |   |   |   |   |   |   |   |   |   |   start > 729789:
RNA_metabolic_process_ (15.18)
|   |   |   |   |   |   |   |   |   |   start > 730490
|   |   |   |   |   |   |   |   |   |   |   start <= 742452
|   |   |   |   |   |   |   |   |   |   |   |   start <= 732347:
protein_catabolic_process_ (19.79)
|   |   |   |   |   |   |   |   |   |   |   |   start > 732347
|   |   |   |   |   |   |   |   |   |   |   |   |   start <= 740059:
biological_process_ (13.55)
```

```
|   |   |   |   |   |   |   |   |   |   |   |   |   start > 740059:
protein_catabolic_process_ (16.26)
|   |   |   |   |   |   |   |   |   |   |   start > 742452:
translation_ (21.12)
|   |   |   |   |   |   |   |   stop > 744353
|   |   |   |   |   |   |   |   |   start <= 752255
|   |   |   |   |   |   |   |   |   |   start <= 744687:
biological_process_ (30.49)
|   |   |   |   |   |   |   |   |   |   start > 744687: cell_cycle_
(22.33)
|   |   |   |   |   |   |   |   |   start > 752255:
biological_process_ (67.99)
|   |   |   |   |   start > 760023
|   |   |   |   |   |   start <= 782041
|   |   |   |   |   |   |   start <= 775834
|   |   |   |   |   |   |   |   start <= 767750:
amino_acid_and_derivative_metabolic_process_ (12.42)
|   |   |   |   |   |   |   |   start > 767750
|   |   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   |   start <= 771651:
translation_ (18.78)
|   |   |   |   |   |   |   |   |   |   start > 771651
|   |   |   |   |   |   |   |   |   |   |   start <= 775180
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num <= 1
|   |   |   |   |   |   |   |   |   |   |   |   |   distance <= 858:
DNA_metabolic_process_ (2.58/0.34)
|   |   |   |   |   |   |   |   |   |   |   |   |   distance > 858:
cell_cycle_ (5.8/0.5)
|   |   |   |   |   |   |   |   |   |   |   |   neigh_num > 1:
DNA_metabolic_process_ (17.1/6.53)
|   |   |   |   |   |   |   |   |   |   |   start > 775180:
translation_ (13.4)
|   |   |   |   |   |   |   |   |   strand = W: cell_cycle_ (9.86)
|   |   |   |   |   |   |   start > 775834
|   |   |   |   |   |   |   |   start <= 778579:
vitamin_metabolic_process_ (13.64)
|   |   |   |   |   |   |   |   start > 778579
|   |   |   |   |   |   |   |   |   neigh_num <= 1: conjugation_
(9.68/1.83)
|   |   |   |   |   |   |   |   |   neigh_num > 1: cell_budding_
(9.08/2.47)
|   |   |   |   |   |   start > 782041
|   |   |   |   |   |   |   start <= 798047
|   |   |   |   |   |   |   |   start <= 790079
|   |   |   |   |   |   |   |   |   start <= 786204: transport_
(13.84)
|   |   |   |   |   |   |   |   |   start > 786204
|   |   |   |   |   |   |   |   |   |   start <= 787957:
membrane_organization_and_biogenesis_ (17.73)
|   |   |   |   |   |   |   |   |   |   start > 787957:
biological_process_ (10.81)
|   |   |   |   |   |   |   |   start > 790079
|   |   |   |   |   |   |   |   |   start <= 794961
|   |   |   |   |   |   |   |   |   |   strand = C
```

```
|   |   |   |   |   |   |   |   |   |   |   start <= 792683:
organelle_organization_and_biogenesis_ (9.85)
|   |   |   |   |   |   |   |   |   |   |   start > 792683:
cytoskeleton_organization_and_biogenesis_ (10.09)
|   |   |   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   |   |   start <= 792683:
RNA_metabolic_process_ (10.75)
|   |   |   |   |   |   |   |   |   |   |   start > 792683:
translation_ (15.41)
|   |   |   |   |   |   |   |   |   start > 794961
|   |   |   |   |   |   |   |   |   |   start <= 797553
|   |   |   |   |   |   |   |   |   |   |   start <= 797206:
RNA_metabolic_process_ (14.41)
|   |   |   |   |   |   |   |   |   |   |   start > 797206:
transport_ (28.52/11.54)
|   |   |   |   |   |   |   |   |   |   start > 797553:
RNA_metabolic_process_ (17.78)
|   |   |   |   |   |   |   start > 798047
|   |   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   |   start <= 812449:
biological_process_ (10.69)
|   |   |   |   |   |   |   |   |   start > 812449: transport_
(14.95)
|   |   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   |   start <= 802355
|   |   |   |   |   |   |   |   |   |   start <= 799230:
DNA_metabolic_process_ (11.33)
|   |   |   |   |   |   |   |   |   |   start > 799230:
ribosome_biogenesis_and_assembly_ (13.02)
|   |   |   |   |   |   |   |   |   start > 802355: translation_
(12.01)
|   |   |   |   start > 814054
|   |   |   |   |   start <= 821419
|   |   |   |   |   |   start <= 814387: electron_transport_
(40.87/13.53)
|   |   |   |   |   |   start > 814387
|   |   |   |   |   |   |   start <= 817919: meiosis_ (18.02)
|   |   |   |   |   |   |   start > 817919
|   |   |   |   |   |   |   |   distance <= 1187: translation_
(15.38/2.4)
|   |   |   |   |   |   |   |   distance > 1187:
ribosome_biogenesis_and_assembly_ (15.1/1.07)
|   |   |   |   |   start > 821419
|   |   |   |   |   |   start <= 822616
|   |   |   |   |   |   |   start <= 821728: biological_process_
(14.3)
|   |   |   |   |   |   |   start > 821728:
amino_acid_and_derivative_metabolic_process_ (34.32)
|   |   |   |   |   |   start > 822616
|   |   |   |   |   |   |   start <= 829914: biological_process_
(77.96)
|   |   |   |   |   |   |   start > 829914
|   |   |   |   |   |   |   |   start <= 831671:
protein_catabolic_process_ (12.28)
```

```
|   |   |   |   |   |   |   |   start > 831671: biological_process_
(27.01)
|   |   |   start > 833685
|   |   |   |   start <= 912660
|   |   |   |   |   strand = C
|   |   |   |   |   |   start <= 883824
|   |   |   |   |   |   |   start <= 843258
|   |   |   |   |   |   |   |   start <= 837409:
RNA_metabolic_process_ (39.1/15.19)
|   |   |   |   |   |   |   |   start > 837409: transport_ (16.05)
|   |   |   |   |   |   |   start > 843258
|   |   |   |   |   |   |   |   start <= 868300
|   |   |   |   |   |   |   |   |   start <= 866418
|   |   |   |   |   |   |   |   |   |   start <= 861302:
biological_process_ (7.73)
|   |   |   |   |   |   |   |   |   |   start > 861302:
transcription_ (8.13)
|   |   |   |   |   |   |   |   |   start > 866418:
DNA_metabolic_process_ (18.78)
|   |   |   |   |   |   |   |   start > 868300
|   |   |   |   |   |   |   |   |   start <= 876625: translation_
(40.65)
|   |   |   |   |   |   |   |   |   start > 876625
|   |   |   |   |   |   |   |   |   |   start <= 878686:
biological_process_ (37.86/17.51)
|   |   |   |   |   |   |   |   |   |   start > 878686: translation_
(15.4)
|   |   |   |   |   |   start > 883824
|   |   |   |   |   |   |   start <= 902040
|   |   |   |   |   |   |   |   start <= 895957
|   |   |   |   |   |   |   |   |   start <= 888970
|   |   |   |   |   |   |   |   |   |   start <= 887833: vesicle-
mediated_transport_ (15.43)
|   |   |   |   |   |   |   |   |   |   start > 887833:
biological_process_ (14.0)
|   |   |   |   |   |   |   |   |   start > 888970
|   |   |   |   |   |   |   |   |   |   start <= 892328:
protein_modification_process_ (16.73)
|   |   |   |   |   |   |   |   |   |   start > 892328:
transcription_ (16.79)
|   |   |   |   |   |   |   |   start > 895957: vesicle-
mediated_transport_ (48.04/30.19)
|   |   |   |   |   |   |   start > 902040
|   |   |   |   |   |   |   |   start <= 911253: transcription_
(16.36)
|   |   |   |   |   |   |   |   start > 911253: cytokinesis_ (19.36)
|   |   |   |   |   strand = W
|   |   |   |   |   |   start <= 888970
|   |   |   |   |   |   |   start <= 861302
|   |   |   |   |   |   |   |   start <= 843258
|   |   |   |   |   |   |   |   |   start <= 837409:
cytoskeleton_organization_and_biogenesis_ (17.39)
|   |   |   |   |   |   |   |   |   start > 837409:
biological_process_ (34.85)
```

```
|   |   |   |   |   |   |   |   start > 843258
|   |   |   |   |   |   |   |   |   start <= 860411
|   |   |   |   |   |   |   |   |   |   start <= 856898:
translation_ (14.1)
|   |   |   |   |   |   |   |   |   |   start > 856898
|   |   |   |   |   |   |   |   |   |   |   start <= 857579:
cell_wall_organization_and_biogenesis_ (9.86)
|   |   |   |   |   |   |   |   |   |   |   start > 857579:
translation_ (7.3)
|   |   |   |   |   |   |   |   |   start > 860411:
generation_of_precursor_metabolites_and_energy_ (14.46)
|   |   |   |   |   |   |   start > 861302
|   |   |   |   |   |   |   |   start <= 880365
|   |   |   |   |   |   |   |   |   start <= 876625
|   |   |   |   |   |   |   |   |   |   start <= 870699:
DNA_metabolic_process_ (11.12)
|   |   |   |   |   |   |   |   |   |   start > 870699:
cell_wall_organization_and_biogenesis_ (19.46)
|   |   |   |   |   |   |   |   |   start > 876625
|   |   |   |   |   |   |   |   |   |   start <= 878072:
transcription_ (16.43)
|   |   |   |   |   |   |   |   |   |   start > 878072:
protein_modification_process_ (14.96)
|   |   |   |   |   |   |   |   start > 880365
|   |   |   |   |   |   |   |   |   start <= 883824:
cytoskeleton_organization_and_biogenesis_ (18.12)
|   |   |   |   |   |   |   |   |   start > 883824
|   |   |   |   |   |   |   |   |   |   start <= 885792:
biological_process_ (18.5)
|   |   |   |   |   |   |   |   |   |   start > 885792:
DNA_metabolic_process_ (13.27)
|   |   |   |   |   |   start > 888970
|   |   |   |   |   |   |   start <= 900751
|   |   |   |   |   |   |   |   start <= 900190
|   |   |   |   |   |   |   |   |   start <= 895957
|   |   |   |   |   |   |   |   |   |   start <= 892328:
RNA_metabolic_process_ (15.26)
|   |   |   |   |   |   |   |   |   |   start > 892328:
protein_modification_process_ (17.69)
|   |   |   |   |   |   |   |   |   start > 895957:
RNA_metabolic_process_ (18.78)
|   |   |   |   |   |   |   |   start > 900190:
protein_modification_process_ (22.63)
|   |   |   |   |   |   |   start > 900751
|   |   |   |   |   |   |   |   start <= 907214
|   |   |   |   |   |   |   |   |   start <= 902040:
generation_of_precursor_metabolites_and_energy_ (21.35)
|   |   |   |   |   |   |   |   |   start > 902040:
biological_process_ (17.64)
|   |   |   |   |   |   |   |   start > 907214
|   |   |   |   |   |   |   |   |   start <= 911253: transcription_
(16.18)
|   |   |   |   |   |   |   |   |   start > 911253:
RNA_metabolic_process_ (25.99/12.19)
```

```
|   |   |   |   start > 912660
|   |   |   |   |   start <= 919377
|   |   |   |   |   |   start <= 919037:
ribosome_biogenesis_and_assembly_ (15.75)
|   |   |   |   |   |   start > 919037: cellular_respiration_
(39.29/17.53)
|   |   |   |   |   start > 919377
|   |   |   |   |   |   start <= 926933
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 923375:
protein_modification_process_ (10.99)
|   |   |   |   |   |   |   |   start > 923375: transport_ (14.88)
|   |   |   |   |   |   |   strand = W: transport_ (25.49/8.66)
|   |   |   |   |   |   start > 926933
|   |   |   |   |   |   |   strand = C
|   |   |   |   |   |   |   |   start <= 939028
|   |   |   |   |   |   |   |   |   neigh_strand = W: transcription_
(16.79/4.61)
|   |   |   |   |   |   |   |   |   neigh_strand = C:
biological_process_ (8.96/3.22)
|   |   |   |   |   |   |   |   start > 939028: biological_process_
(15.22)
|   |   |   |   |   |   |   strand = W
|   |   |   |   |   |   |   |   start <= 939918
|   |   |   |   |   |   |   |   |   start <= 931372:
biological_process_ (16.89)
|   |   |   |   |   |   |   |   |   start > 931372: transport_
(21.06)
|   |   |   |   |   |   |   |   start > 939918: biological_process_
(22.91)
```

Decision Tree Generated for Mitochondrial Chromosome:
For Cellular Component

```
mitochondrion_ (451.08)
```

For Molecular Function

```
|   start <= 61022
|   |   start <= 48201
|   |   |   stop <= 25255
|   |   |   |   stop <= 18830
|   |   |   |   |   stop <= 16322
|   |   |   |   |   |   start <= 6546
|   |   |   |   |   |   |   start <= 731: molecular_function_ (8.76)
|   |   |   |   |   |   |   start > 731:
structural_molecule_activity_ (5.03)
|   |   |   |   |   |   start > 6546: molecular_function_ (19.53)
|   |   |   |   |   stop > 16322: RNA_binding_ (12.48)
|   |   |   |   stop > 18830
|   |   |   |   |   start <= 13818: hydrolase_activity_ (40.54)
|   |   |   |   |   start > 13818: molecular_function_ (6.2)
|   |   |   stop > 25255
|   |   |   |   start <= 28487
|   |   |   |   |   start <= 13818: oxidoreductase_activity_ (5.62)
```

```
|   |   |   |   |   start > 13818: transporter_activity_ (19.99)
|   |   |   |   start > 28487
|   |   |   |   |   stop <= 42251
|   |   |   |   |   |   start <= 35373: molecular_function_ (16.9)
|   |   |   |   |   |   start > 35373
|   |   |   |   |   |   |   stop <= 38579: hydrolase_activity_ (5.7)
|   |   |   |   |   |   |   stop > 38579: RNA_binding_ (14.91)
|   |   |   |   |   stop > 42251
|   |   |   |   |   |   start <= 36540: oxidoreductase_activity_
(16.32)
|   |   |   |   |   |   start > 36540
|   |   |   |   |   |   |   start <= 46723: transporter_activity_
(6.17)
|   |   |   |   |   |   |   start > 46723: molecular_function_
(12.67)
|   |   start > 48201
|   |   |   start <= 58009: structural_molecule_activity_ (23.14)
|   |   |   start > 58009: hydrolase_activity_ (6.39)
|   start > 61022
|   |   start <= 85035
|   |   |   start <= 72630: molecular_function_ (219.09)
|   |   |   start > 72630
|   |   |   |   start <= 73758: oxidoreductase_activity_ (8.38)
|   |   |   |   start > 73758
|   |   |   |   |   start <= 78533: molecular_function_ (42.26)
|   |   |   |   |   start > 78533
|   |   |   |   |   |   start <= 79213: oxidoreductase_activity_
(11.15)
|   |   |   |   |   |   start > 79213: molecular_function_ (10.32)
|   |   start > 85035: hydrolase_activity_ (15.6)
```

For Biological Process

```
|   start <= 46723
|   |   start <= 9374: translation_ (33.44)
|   |   start > 9374
|   |   |   stop <= 25255
|   |   |   |   stop <= 16322: cellular_respiration_ (6.45)
|   |   |   |   stop > 16322
|   |   |   |   |   start <= 13818
|   |   |   |   |   |   stop <= 19996
|   |   |   |   |   |   |   stop <= 18830: RNA_metabolic_process_
(5.97)
|   |   |   |   |   |   |   stop > 18830: biological_process_
(11.35)
|   |   |   |   |   |   stop > 19996
|   |   |   |   |   |   |   stop <= 21935: RNA_metabolic_process_
(10.58/2.68)
|   |   |   |   |   |   |   stop > 21935: DNA_metabolic_process_
(8.34)
|   |   |   |   |   start > 13818: biological_process_ (6.09)
|   |   |   stop > 25255
|   |   |   |   start <= 35373
|   |   |   |   |   start <= 28487
```

```
|   |   |   |   |   |   start <= 13818: cellular_respiration_
(9.02/3.03)
|   |   |   |   |   |   start > 13818:
generation_of_precursor_metabolites_and_energy_ (24.65)
|   |   |   |   |   start > 28487: translation_ (9.57)
|   |   |   |   start > 35373
|   |   |   |   |   start <= 36540
|   |   |   |   |   |   stop <= 42251: RNA_metabolic_process_
(17.57)
|   |   |   |   |   |   stop > 42251: electron_transport_
(18.14/7.95)
|   |   |   |   |   start > 36540:
generation_of_precursor_metabolites_and_energy_ (6.14)
|   start > 46723
|   |   start <= 72630
|   |   |   stop <= 61729
|   |   |   |   start <= 48901: translation_ (20.25)
|   |   |   |   start > 48901: DNA_metabolic_process_ (9.91)
|   |   |   stop > 61729: translation_ (195.92)
|   |   start > 72630
|   |   |   start <= 85035
|   |   |   |   start <= 74495
|   |   |   |   |   start <= 73758: cellular_respiration_
(22.53/9.96)
|   |   |   |   |   start > 73758: biological_process_ (10.03)
|   |   |   |   start > 74495
|   |   |   |   |   start <= 78533: translation_ (21.32)
|   |   |   |   |   start > 78533
|   |   |   |   |   |   start <= 79213
|   |   |   |   |   |   |   neigh_num <= 1: cellular_respiration_
(8.28/2.69)
|   |   |   |   |   |   |   neigh_num > 1: electron_transport_
(29.25/11.23)
|   |   |   |   |   |   start > 79213: translation_ (13.98)
|   |   |   start > 85035: RNA_metabolic_process_ (12.98)
```