



ORIGINAL ARTICLE

Improving Interpretation of Cardiac Phenotypes and Enhancing Discovery With Expanded Knowledge in the Gene Ontology

BACKGROUND: A systems biology approach to cardiac physiology requires a comprehensive representation of how coordinated processes operate in the heart, as well as the ability to interpret relevant transcriptomic and proteomic experiments. The Gene Ontology (GO) Consortium provides structured, controlled vocabularies of biological terms that can be used to summarize and analyze functional knowledge for gene products.

METHODS AND RESULTS: In this study, we created a computational resource to facilitate genetic studies of cardiac physiology by integrating literature curation with attention to an improved and expanded ontological representation of heart processes in the Gene Ontology. As a result, the Gene Ontology now contains terms that comprehensively describe the roles of proteins in cardiac muscle cell action potential, electrical coupling, and the transmission of the electrical impulse from the sinoatrial node to the ventricles. Evaluating the effectiveness of this approach to inform data analysis demonstrated that Gene Ontology annotations, analyzed within an expanded ontological context of heart processes, can help to identify candidate genes associated with arrhythmic disease risk loci.

CONCLUSIONS: We determined that a combination of curation and ontology development for heart-specific genes and processes supports the identification and downstream analysis of genes responsible for the spread of the cardiac action potential through the heart. Annotating these genes and processes in a structured format facilitates data analysis and supports effective retrieval of gene-centric information about cardiac defects.

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Clinical Perspective

Identification of critical proteins and RNAs as potential drug targets requires computationally accessible descriptors, both in terms of their roles in biological pathways and the molecules they interact with to fulfill their actions. This information is also vital in choosing prognostic and diagnostic biomarkers, particularly for multifactorial diseases such as heart disease that might benefit from measurement of multiple biomarkers. Recent improvements in omic technologies have led to projects such as the 100 000 Genomes Project and genome-wide association studies, which are producing vast amounts of genetic data pertinent to human health. Furthermore, it is now possible to catalog which proteins or RNAs are present in normal or disease tissues, or individual cells. Understanding the molecular network or biological processes associated with a drug target can help predict off-target effects or the potential for drug repurposing because many gene products are active in multiple pathways. In addition, these networks can be used to predict the most efficacious molecules within the networks, through the identification of key positions at which the whole networks may be perturbed; these molecules are often associated with disease-causing mutations or identified as drug targets. One of the major resources used by omic researchers is the Gene Ontology. This article explains the considerable improvements made by the Gene Ontology Consortium in the bioinformatic description of cardiac physiology. These new descriptions are all based on published data and are now included in all major biological databases, thus available for use by the global scientific community to enhance the understanding of cardiovascular-relevant data.

Cardiac electrical conduction systems enable coordinated regulation of heart contraction in metazoans, ranging from fly to human. Disturbances of normal heart rhythm can occur de novo, but, more critically and commonly, they are an important feature of many cardiac diseases, and have substantial impacts on patient morbidity and mortality. To gain insight into the mechanisms of arrhythmia, high-throughput genome-scale methodologies (including genome-wide association studies [GWAS], transcriptomics, exon sequencing, and proteomics) are being used.^{1–3} However, interpretation of these high-throughput experiments relying on descriptions of the cellular and physiological roles of gene products, and a computational approach to interrogation of cardiac gene function, is a bottleneck in these analyses. Our work aims to fill this gap by capturing information

in the Gene Ontology (GO) resource in a structured way, thus integrating knowledge about genes, cells, tissues and organs. To support data interpretation, the GO Consortium (GOC) provides a freely available, structured, controlled vocabulary, the ontology,⁴ that enables association of defined terms, describing cellular roles and locations, with a protein or RNA. This association process, called GO annotation, provides a computer-interpretable summary of the results of many independent experiments. GO terms describe Molecular Functions (molecular activities of a gene product), Biological Processes (the broader context in which a gene product acts), and Cellular Components (the subcellular location of a gene product). Some examples of GO terms relevant to cardiac research are, respectively, *voltage-gated sodium channel activity*, *Purkinje myocyte action potential*, and *Z disc*.

GO provides users with a summary of experimentally verified or predicted functions of genes, proteins, and RNAs.^{3,5} Because of this high-impact information, GO data are incorporated into over 50 functional analysis tools and is routinely used to analyze large data sets.⁶ The coordinated action of gene products involved in cardiac conduction at the cellular level results in proper heart functioning at the organ level and in healthy conditions at the whole organism level. Therefore, detailed and interoperable knowledge about gene products' roles is essential to better analyze heart failure phenotypes and ultimately to address potentially fatal conditions. The features listed above make GO an ideal resource to aid the interpretation of large-scale cardiac physiology investigations.

Before our expansion of the cardiac function domain, there were only 3 GO terms to describe how the cardiac cycle is coordinated: *cardiac conduction*, *membrane depolarization during atrial cardiac muscle cell action potential*, and *membrane repolarization during atrial cardiac muscle cell action potential*. In this article, we detail how GO editors and biocurators worked together with experimental researchers to ensure provision of accurate structured terminology⁷ that describes features of gene products involved in cardiac physiology, and to generate GO annotations⁸ that capture those roles based on published literature, thereby improving representation of this area of biology. In particular, we focused on processes involved in and regulating the coordinated contraction of the heart. We also show that our effort improves the investigation of heart-related GWAS and transcriptomic data sets.

METHODS

The data, analytic methods, and study materials have been made available to other researchers for purposes of reproducing the results or replicating the procedure. Protein, RNA, and macromolecular complex GO annotations are available from the UniProt GO annotation and GOC sites (<https://www.ebi.ac.uk/GOA/downloads>, <http://www.geneontology.org/gene-associations/>) and searchable in the AmiGO2⁷ and QuickGO⁹ browsers; GO

terms are downloadable from the GOC site (<http://www.geneontology.org/ontology/>) and searchable in AmiGO2 and QuickGO. The annotations have also been incorporated into many biological knowledge bases, including Ensembl,¹⁰ UniProtKB,¹¹ and NCBI-Gene,¹² and exploited by numerous freely available functional analysis tools, including Database for Annotation, Visualization and Integrated Discovery,¹³ g:profiler,¹⁴ Protein Analysis Through Evolutionary Relationships (PANTHER),¹⁵ and Visual Annotation Display (VLAD).¹⁶ Full methods are available in the [Data Supplement](#).

Generation of a Prioritized List of Cardiac Physiology-Relevant Gene Products

A list of 88 human proteins known to be required for normal cardiac function was compiled based on 8 literature reviews^{17–24} (Table I in the [Data Supplement](#)). To keep the focus more specifically on ion channels, the following were not retained in the prioritized list of genes: ATPases, ATPase regulatory proteins, hormones, hormone receptors, and proteins required for normal heart development. However, angiotensinogen and 2 angiotensin I-converting enzymes were included in the prioritized protein list to ensure that the ontology was sufficiently developed to enable future projects to capture the role of gene products that regulate heart rate and contraction.²⁵ Orthologs of these 88 human proteins were identified in mouse, rat, zebrafish, and *Drosophila* using the Protein Analysis Through Evolutionary Relationships orthology prediction tool.¹⁵ In addition, a list of 7 human microRNAs (miRNAs) identified as key players in modulating cardiac excitability at the time we started our curation effort was determined from 3 reviews^{26–28}; literature available for these miRNAs was curated up to March 2016. Prioritized human gene products described above are listed in Table I in the [Data Supplement](#), and for all of them, GO annotations supported by experimental data were included in the GO database according to established procedural guidelines^{8,29,30} (details are given in Methods in the [Data Supplement](#)).

Identification of Candidate Genes Associated With Arrhythmia Risk Loci

We compiled a list of Mendelian inherited arrhythmia disorder genes associated with atrial fibrillation, long-QT syndrome, short-QT syndrome, catecholaminergic polymorphic ventricular tachycardia, and Brugada syndrome^{1,31,32} and candidate genes associated with GWAS risk loci for these disorders^{2,31} (literature search February 2016; Table II in the [Data Supplement](#)). Nine GO terms relevant to normal cardiac physiology (such as *cardiac conduction*, *muscle contraction*, and *response to oxygen levels*) were selected to investigate whether gene annotations to these normal processes could be correlated with arrhythmia candidate genes (Table III in the [Data Supplement](#)), and the associated annotations were downloaded on March 11, 2016 using the QuickGO browser⁹ (<http://www.ebi.ac.uk/QuickGO/>; Methods in the [Data Supplement](#)).

GO Functional Analysis of Transcriptomic Data Sets

A ventricular cardiomyocyte (VCM) data set³ was analyzed using the BinGO plugin³³ within the Cytoscape v3.3.0 tool,³⁴ applying

the recommended hypergeometric test and Benjamini and Hochberg False Discovery Rate correction, and a *P* value <0.05 (full details in Methods in the [Data Supplement](#)). To determine the impact of this focused project, we used gene association files from November 2011 (ie, the start of this project) and February 2016 (ie, the end of the project; files available from <ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/>). For both analyses, the ontology version March 7, 2016 was included (available from <http://geneontology.org/page/download-ontology>).

RESULTS

Representation of Cardiac-Relevant Gene Products' Features Via Ontology Development

A coordinated working group of GO editors, GO biocurators, and field experts expanded the cardiac physiology domain by adding 197 new cardiac-relevant GO terms (Methods and Table IV in the [Data Supplement](#)). Of these, 87 refer to processes that contribute to cardiac conduction and thus describe the propagation of the action potential through the conduction system and cardiac chambers. An example of an ontology branch representing cardiac-relevant GO terms is shown in Figure.

The expansion of the cardiac-related processes in GO describes events that occur at 3 key biological levels: the single cell, the tissue (multicellular), and the organ. In addition to these biological levels, the ontology was expanded to cover generic processes (such as *regulation of potassium ion export*) or developmental processes (such as *cardiac pacemaker cell differentiation*) required for the annotation of cardiac-relevant gene products. These new ontology terms enable biocurators to capture the role of gene products in specific tissues of the heart (by applying GO terms such as *adrenergic receptor signaling pathway involved in cardiac muscle relaxation*), specific cell types (eg, *atrioventricular (AV) node cell to bundle of His cell communication*), and the whole organ (eg, *regulation of the force of heart contraction by cardiac conduction*). The addition of both generic terms, and terms that reference specific anatomical structures, allowed us to overcome challenges with respect to granularity of organism specificity. For example, the term *cell communication involved in cardiac conduction* can be used for any organism with a cardiac organ, and a child term like *AV node cell to bundle of His cell communication* can be used specifically for species that have the relevant anatomical structures, in this case AV node and bundle of His. By describing processes at the various levels, curators can choose appropriate terms with respect to the experiments and organisms they are curating. Where possible, terms were defined by creating necessary and sufficient statements using relationships between GO terms and terms from cross-referenced external ontologies, such as Uberon for anatomical structures, the Cell Ontol-

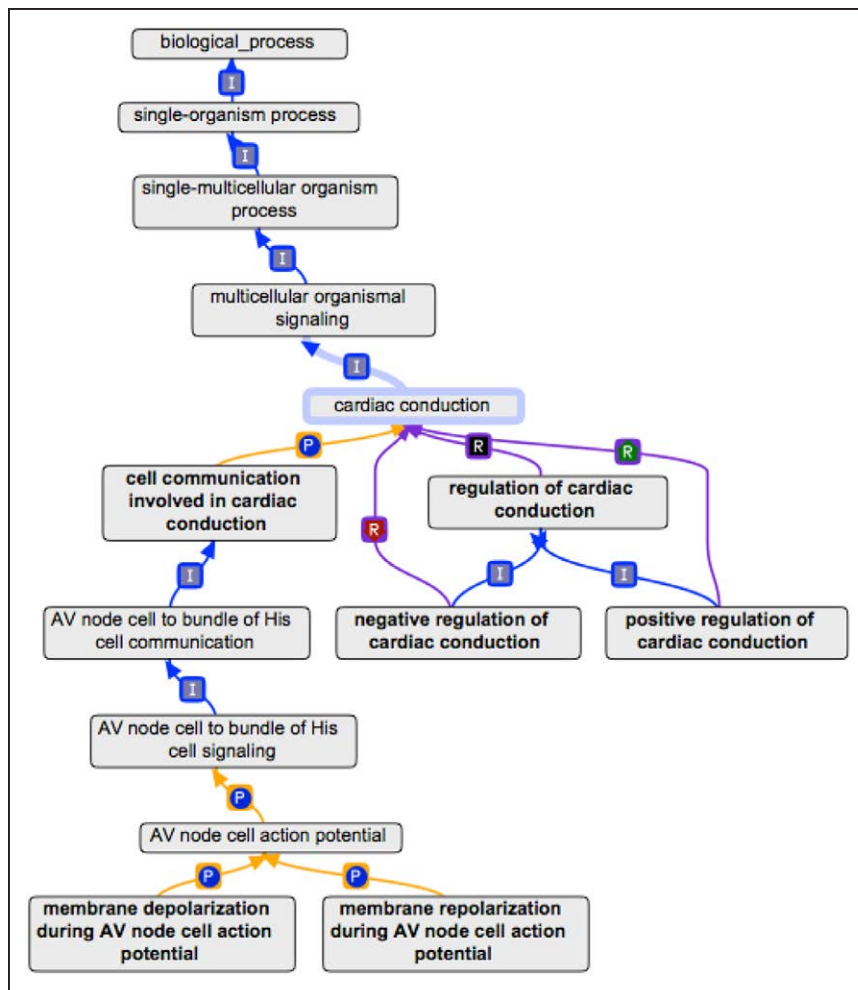


Figure. Part of the ontology describing AV node cell action potential and the regulation of ventricular cardiac muscle cell action potential.

The entire model is not shown; this portion graphically illustrates how ontology terms relate to each other. Blue lines marked with I indicate the child term is a type of its parent, and orange lines marked with P indicate that child term is always a part of its parent. Purple lines marked with R indicate regulates, positively regulates, or negatively regulates relations.

ogy for cell types, and Chemicals of Biological Interest for chemicals (ChEBI), taking advantage of their species interoperability and thus making the terms accessible to computational reasoning.³⁵

Cell-to-Cell Communication in the Heart

Cell communication is a key aspect of the coordinated activity of the heart. We created new terms, such as *cell communication involved in cardiac conduction*, to bring together all processes that mediate interactions between a cell and its surroundings and that also contribute to the process of cardiac conduction. This part of the ontology now includes terms to describe cell-to-cell impulse propagation by means of cardiac action potentials and electrical coupling (such as *AV node cell to bundle of His cell communication by electrical coupling*), as well as terms to describe the attachment of one cell to another or to the extracellular matrix (such as *bundle of His cell-Purkinje myocyte adhesion involved in cell communication*). In addition, many of the 22 new cardiac conduction-relevant Molecular Function terms describe channel or transporter activities that are necessary to propagate the electrical signals between specific cells and across the heart (eg, *gap*

junction channel activity involved in cardiac conduction electric coupling).

The cardiac action potential branch of GO includes terms referring to a variety of cell types within the heart (Figure), such as *AV node cell action potential*, *membrane depolarization during AV node cell action potential* and *membrane repolarization during AV node cell action potential*, as well as terms that describe the regulation of the action potential (not shown). Similar terms also describe action potentials in SA node cells, bundle of His cells, and Purkinje myocytes (not shown).

Ensuring Capture of Robust Information About Genetic Contributions to Cardiac Physiology via GO Annotation

There is a considerable volume of literature describing the physiological characterization of the heart. This project brought together expertise from University College London,³⁶ Queen Mary University of London, University of Oxford, Mouse Genome Informatics,³⁷ the Rat Genome Database,³⁸ the Zebrafish Information Network,³⁹ and FlyBase.⁴⁰ It was unrealistic for the information from all

cardiac physiology research papers to be captured during this project; however, over 500 papers have been reviewed and used to annotate cardiac-relevant gene products with the expanded GO structure. A key aspect of gene product GO annotation is the recognition that a single gene product may have several functions, may participate in multiple processes, and can be found in a variety of subcellular locations. Consequently, fully describing how a gene functions typically results in >1 GO term associated with a single gene product⁴ (Table 1).

The aim of creating multiple statements (annotations) about a single gene product is to comprehensively capture the knowledge about its biological role, as supported by published experimental data. For example, over 30 papers were curated to provide information about the human sodium channel SCN5A (Q14524). Individual experiments, such as immunostaining, expression of various sodium channel constructs in *Xenopus* oocytes or rat cardiomyocytes, combined with descriptions of cardiac disease associated with the protein, such as long-QT and Brugada syndromes, have provided evidence that this protein is found in the *Z disk*,⁴¹ has *voltage-gated sodium channel activity involved in cardiac muscle cell action potential*,⁴² and is involved in *membrane depolarization during Purkinje myocyte cell action potential*.⁴³ In contrast, the experimental data described in a single paper⁴⁴ supported 9 annotations

for the human protein RNF207 (Q6ZRF8). This article also resulted in 18 experimentally supported annotations to 5 other human proteins (DNAJA1, P31689; HSPA1A, P0DMV8; HSPA1B, P0DMV9; HSPA8, P11142; KCNH2, Q12809) and 1 zebrafish protein (Rnf207b, E9QHE3).

There is increasing evidence for the role of miRNAs in controlling cardiac physiology, particularly in the regulation of potassium and calcium ion channel function, where dysregulation can lead to aberrant action potential duration and cardiac conduction.^{27,28} For this project, 7 miRNAs were prioritized for annotation (Methods and Table I in the [Data Supplement](#)), resulting in 27 annotations with relevance to cardiac function. For example, Li et al⁴⁵ demonstrated that miR-1 (URS00001DC04F_9606) and miR-133a (URS00004C9052_9606) could regulate the slow delayed rectifier potassium current (I_{Ks}) in human cells during simulated hyperglycemia. Furthermore, they showed that this was because of their ability to regulate the expression of 2 potassium channel proteins, KCNE1 (P15382) and KCNQ1 (P51787), which mediate I_{Ks} . These roles of miR-1 and miR-133a have been captured by the terms *negative regulation of membrane repolarization during cardiac muscle cell action potential* and *negative regulation of delayed rectifier potassium channel activity*, as well as *gene silencing by miRNA*, with KCNE1 included as the target of miR-1 and KCNQ1 as the target of miR-133a in annotation extensions (Methods in the [Data Supplement](#)).

Table 1. Selection of GO Annotations Associated With Human ACE2

| GO Identifier | GO Term Name | Code | Reference | With |
|--------------------|---|------|----------------|--------------------------------|
| Biological process | | | | |
| GO:0002005 | Angiotensin catabolic process in blood | IC | PMID:10924499 | GO:0004180 |
| GO:0003081 | Regulation of systemic arterial blood pressure by renin-angiotensin | IMP | PMID:18258853 | ... |
| GO:0019229 | Regulation of vasoconstriction | IC | PMID:15380922 | GO:0004180 |
| GO:0046813 | Receptor-mediated virion attachment to host cell | IDA | PMID:18343844 | ... |
| GO:0060452 | Positive regulation of cardiac muscle contraction | IEA | GO_REF:0000019 | Ensembl: ENSMUSP00000107890 |
| GO:1903598 | Positive regulation of gap junction assembly | IMP | PMID:12967627 | ... |
| GO:1903779 | Regulation of cardiac conduction | IMP | PMID:12967627 | ... |
| Molecular function | | | | |
| GO:0004175 | Endopeptidase activity | IDA | PMID:15283675 | ... |
| GO:0004180 | Carboxypeptidase activity | IDA | PMID:10969042 | ... |
| GO:0005515 | Protein binding | IPI | PMID:21068237 | UniProtKB:O15393 |
| Cellular component | | | | |
| GO:0005576 | Extracellular region | IEA | GO_REF:0000037 | UniProtKB-KW:KW-0964 |
| GO:0070062 | Extracellular exosome | IDA | PMID:19056867 | ... |
| GO:0016020 | Membrane | IEA | GO_REF:0000002 | InterPro:IPR001548 |

A selection of the 61 annotations associated with human ACE2 (Q9BYF1) illustrates the range of annotations associated with a single protein. Code indicates the evidence code used to support the annotation (www.geneontology.org/GO.evidence.shtml)⁸; Reference lists the source of the data supporting the annotation, this may be the curated article or information about the electronic annotation pipeline; and the With field provides additional information to support the annotation, such as the Gene Ontology (GO) identifier which supports an IC annotation or the Ensembl identifier from which the annotation is propagated.⁸

IC indicates Inferred by Curator; IMP, Inferred from Mutant Phenotype; IDA, Inferred from Direct Assay; IEA, Inferred from Electronic Annotation; IPI, Inferred from Physical Interaction.

The Application of Information Derived From Orthologs

Experimental data to support GO annotations are not always available for human proteins and especially not for miRNAs, but may be obtainable for model organism orthologs. Inferential assertions about the roles of human gene products can be achieved by mapping annotations from their orthologous gene products. The electronic pipeline Ensembl Compara ensures that experimentally supported annotations associated with those proteins that have a 1-to-1 ortholog across human, mouse, and rat are applied to all orthologs.¹⁰ For example, the predicted 1-to-1 orthology between the mouse ACE2 (Q8R0I0) and human ACE2 (Q9BYF1) proteins as defined by Compara has enabled 3 experimentally supported mouse ACE2 annotations (including *positive regulation of cardiac muscle contraction*) to be associated with human ACE2. The GOC also provides an expert curation tool, called Phylogenetic Annotation and Inference Tool,⁴⁶ that enables biocurators to infer annotations across many species based on phylogenetic relationships and protein family membership. In addition, in some cases where knowledge from Compara and Phylogenetic Annotation and Inference Tool was not available, orthology was reviewed on a case-by-case basis and used to support transfer of annotations to the orthologous proteins⁴⁷ (see next section and Methods in the [Data Supplement](#)).

Comprehensive Capture of Information About Prioritized Gene Products Through Annotation

The manual annotation of the 88 heart-relevant human proteins that were prioritized in this effort (Table I in the [Data Supplement](#)) led to the submission of over 3100 annotations to the GO database. This represents a 4-fold increase in the number of manual annotations associated with these proteins. Furthermore, annotation of model organism experimental data has provided a further 2000 annotations to 82 of these proteins through the transfer of experimentally supported annotations to orthologous human proteins via the Ensembl Compara pipeline,¹⁰ Phylogenetic Annotation and Inference Tool,⁴⁶ and other expert curation methods.⁴⁷ To supplement the orthology-based curation, we manually transferred 50 relevant biological process annotations from mouse or rat to human, using the Inferred From Sequence or Structural Similarity evidence code.⁸ When annotations provided through other electronic pipelines⁴⁷ (such as mappings between UniProtKB Keywords and InterPro) are included, the 88 prioritized human proteins have a total of 7263 annotations (as of March 2017). The number of annotations per protein ranges from 20 associated with RNF207 (Q6ZRF8) to 272 associated with CAV1 (Q03135), with an average of 82 annotations per protein. Over 140 annotations

are associated with the 7 prioritized human miRNAs. Therefore, this curation effort allowed bioinformatic capture of knowledge of genes that were not represented before, and it enables more informative data analysis, as shown below.

Using GO to Interpret GWAS

GWAS have identified many risk loci associated with cardiac disorders.^{1,31} In some cases, the impact of a variant on a protein-coding gene is relatively easy to identify because of predicted, and often experimentally verified, deleterious nonsynonymous substitutions. However, often risk variants identified in a genomic area fall within an intronic, intergenic, or regulatory region, making it difficult to identify the true causative variant(s) associated with the risk, and which protein-coding genes or functional RNA genes should be considered as candidates contributing to a disease.^{2,31} The cost of investigating a candidate gene's role in a disease is considerable. Consequently, before experimental investigation, various *in silico* approaches are generally undertaken to try to narrow down the choice of which gene in a gene-rich region is involved in a disease. If nonsynonymous deleterious gene variants in a gene in the same region have already been associated with a similar phenotype, this is good supporting evidence for candidate gene choice. However, other approaches, such as those described by MacArthur et al,⁴⁸ may also be valuable. These include considering whether any of the potential candidate genes encode a protein that interacts with proteins previously implicated in the disease (either using *in silico* network analysis or through coimmunoprecipitation experiments), or if the gene is expressed in tissues relevant to the disease (eg, by using expression quantitative trait loci data³¹).

MacArthur et al⁴⁸ also describe selecting candidate genes based on a known function or role which is shared with other genes established as associated with the disease of interest or is consistent with their mutant phenotype. This approach can be easily undertaken using GO annotation data, and yet it is rarely included in the *in silico* investigations of GWAS results. After our focused annotation effort, the ability to use GO annotations to identify candidate genes associated with arrhythmia disorders was evaluated. Human proteins associated with 9 GO terms that are relevant to normal cardiac physiology were downloaded using QuickGO⁹ (GO terms are shown in Table IV in the [Data Supplement](#)). The corresponding genes were then compared with Mendelian genes for arrhythmia disorders (atrial fibrillation, long-QT syndrome, short-QT syndrome, catecholaminergic polymorphic ventricular tachycardia, Brugada syndrome^{1,31,32}) and with GWAS candidate variants associated with QT interval length and atrial fibrillation risk loci, described by Tucker et al² and Arking

et al.³¹ Of 45 Mendelian arrhythmia-associated genes (described in 3 reviews to 2015^{1,31,32}), 43 were annotated with ≥1 of the cardiac-relevant GO terms (Table II in the [Data Supplement](#)), with *SRL* and *GREM2* being the exceptions. The GO annotations associated with the 83 GWAS-identified candidate genes (associated with 48 risk loci) suggest that GO data can contribute to prioritization of candidate risk genes. Cardiac physiology-relevant GO terms suggest the prioritization of 36 of the 83 candidate genes. This selection approach compares favorably with that taken by Arking et al.³¹ In that study, authors identified 35 common variant QT interval loci and used expression quantitative trait loci, protein interaction, and coimmunoprecipitation data to identify 70 candidate genes associated with these loci (Table II in the [Data Supplement](#)). Both the GO and the expression quantitative trait loci approaches suggest 27 QT interval candidate genes, whereas coimmunoprecipitation suggests 12 genes and in silico protein interaction networks 15 genes. For example, GO annotations hint that *RNF207*, at 1p36, is a good candidate for variations in QT interval length, with annotations to 6 of the key GO terms, and that potassium transport-associated *KCNAB2* is a good alternative candidate. In contrast, in silico protein interaction data support 3 other genes at this locus (*ACOT7*, *KCNAB2*, and *RPL22*; Table 2). Similarly, GO annotation information narrows the candidates at the 3p21 locus to 3 genes (*MYL3*, *SCAP*, and *SETD2*; Table 2), with *MYL3* having the strongest anno-

tation support, because of its role in muscle contraction and heart development; the analysis provided by Arking et al.³¹ suggested 5 candidate genes at this locus. Notably, at the 1q24 risk locus, GO annotations, expression quantitative trait loci, and coimmunoprecipitation data all suggest *ATP1B1* as the candidate gene (Table 2). This illustrates that GO annotations can provide additional data to either support the choice of candidate genes or suggest alternative candidates.

Functional Analysis of Atrial and Ventricular High-Throughput Data Sets

To provide a measure of the impact of our cardiac-focused annotation project on data interpretation, we compared the functional analysis of a specific heart transcriptomic data set using GO annotations available in November 2016 to an equivalent analysis using GO annotation data available in February 2011. A VCM transcriptomic data set³ was used to investigate this, as we anticipated that a ventricular-specific transcriptome was likely to include the ion channels, and their regulators, required for cardiac repolarization and depolarization. Poon et al.³ profiled the transcriptome of human embryonic stem cells and compared this to the transcriptome of adult human VCMs, after filtering out the transcripts that were not significantly differentially expressed between the 2 cell types.³ Poon et al.³ found that GO terms describing translation elongation,

Table 2. Using GO to Support the Identification of the Likely Causative Gene Associated With 3 QT Interval Risk Loci³¹

| QT Interval Risk | rs846111 | | | rs10919070 | | rs17784882 | | | | | | |
|---------------------------------------|---------------|--------------|---------------|---------------|---------------|-------------|--|---------------|-------------|---------------|-------------|--------------|
| Nearest Gene | <i>RNF207</i> | | | <i>ATP1B1</i> | | <i>ELP6</i> | | | | | | |
| GWAS Candidate Gene | | <i>ACOT7</i> | <i>KCNAB2</i> | <i>RPL22</i> | | <i>NME7</i> | | <i>KLHL18</i> | <i>MYL3</i> | <i>PTPN23</i> | <i>SCAP</i> | <i>SETD2</i> |
| GO term name | | | | | | | | | | | | |
| Cardiac conduction | * | | | | * | | | | | | | |
| Regulation of membrane potential | * | | | | * | | | | | | | |
| Actin filament-based process | * | | | | | | | * | | | | |
| Potassium ion transmembrane transport | * | | * | | * | | | | | | | |
| Sodium ion transmembrane transport | | | | | * | | | | | | | |
| Calcium ion transmembrane transport | | | | | * | | | | | | | |
| Muscle contraction | * | | | | * | | | | * | | | |
| Heart development | * | | | | | | | | * | | | * |
| Response to oxygen levels | | | | | * | | | | | | * | |
| Candidate gene predicted by | | | | | | | | | | | | |
| GO annotation data | <i>RNF207</i> | | <i>KCNAB2</i> | | <i>ATP1B1</i> | | | | <i>MYL3</i> | | <i>SCAP</i> | <i>SETD2</i> |
| eQTL or protein interaction data | | <i>ACOT7</i> | <i>KCNAB2</i> | <i>RPL22</i> | <i>ATP1B1</i> | <i>NME7</i> | | <i>KLHL18</i> | <i>MYL3</i> | <i>PTPN23</i> | <i>SCAP</i> | <i>SETD2</i> |

Gene Ontology (GO) annotation data can be used to provide additional information about candidate genes, located close to the risk loci, and add to the information provided by expression quantitative trait loci data (eQTL) or protein interaction data (full list of arrhythmia associated genes in Table II in the [Data Supplement](#)). Association of these terms with the genes in close proximity to the QT interval risk loci suggests that these are candidate causative genes. At the bottom of the table, the candidate gene predicted by either GO annotation, eQTL, or protein interaction data is listed: GO annotation data (based on the annotations listed in the table); eQTL or protein interaction data (based on eQTL, in silico QT interval loci protein network analysis or coimmunoprecipitation with 1 of 5 LQTS Mendelian proteins³¹).

*The association of 1 of the 9 selected GO terms with a listed gene.

as well as muscle system, contraction, and energy generation (their wording), were enriched within the 200 most abundant transcripts in adult human VCMs. Our analysis using the 2011 and 2016 GO annotation data sets confirms findings of Poon et al,³ with the majority of these proteins annotated to either *muscle contraction*, *mitochondrion organization*, *respiratory electron transport chain*, *gene expression*, or *developmental process* terms. Notably, our analysis also demonstrates that the terms *cardiac conduction*, *regulation of cardiac conduction*, and *regulation of the force of heart contraction* (among others) were significantly enriched in the 2016 analysis. Although VCMs are not involved in cardiac conduction, it is not unexpected that *cardiac conduction* and child terms will be enriched in a ventricular data set, because many of the same action potential-associated proteins are present in ventricular, atrial, and conduction tissues.²³ The identification of the cardiac-specific terms within this data set does, however, confirm that the GO terms and annotations created by this focused project are sufficient to enable the identification of the increased expression of genes involved in these processes. In 2011, many of the cardiac physiology GO terms did not exist, and consequently, these terms are (understandably) not enriched using the 2011 annotation data set (Table 3; Table V in the Data Supplement).

DISCUSSION

In this article, we describe work to improve the GO resource in representing relevant cardiac processes, and in capturing roles of gene products from published literature through GO annotation. The majority of publications describing heart or cardiomyocyte transcriptomic and proteomic data sets use GO annotations

to investigate the pathways associated with this important organ.^{3,5} We tested whether our recent cardiac-relevant annotations could be used to support a more informative interpretation of high-throughput studies. Our reanalysis of the top 200 differentially expressed transcripts in adult human VCMs³ (compared with the human embryonic stem cells transcriptome; Table V in the Data Supplement) confirms the original findings of Poon et al³ and, in addition, shows that the transcriptome of these cells is enriched for GO terms referring to cardiac physiology, including *cardiac conduction*, *regulation of cardiac conduction*, *regulation of cardiac muscle contraction by calcium ion signaling*, and *regulation of the force of heart contraction*. Notably, the enrichment of these terms is only possible because of the expansion of the GO resource in this area. These cardiac-relevant terms are identified despite more than half of these highly expressed proteins being associated with protein synthesis, mitochondrial respiratory systems, or having a structural cellular role. The significance of our work lies in the enhanced ability to identify cardiac-relevant genes within cardiac tissue; cardiac physiologists can now use the GO to test genomic profiles and confirm the presence of relevant genes. For example, researchers who are using in vitro cardiac cell differentiation systems can now test the profiles of gene expression in their cells to examine and confirm progression toward mature cardiomyocytes. This has potential application in the field of heart cell regeneration.

Furthermore, our analysis of QT interval length and atrial fibrillation risk loci, described by Tucker et al² and Arking et al,³¹ demonstrates that our focused GO annotation of cardiac physiological processes provides an enhanced GO resource that can be used, in combination with other experimental and in silico approaches, to suggest candidate genes associated with cardiac dis-

Table 3. Comparison of Functional Analysis of Adult Ventricular Cardiomyocyte Data³ Using Gene Ontology (Full List of Enriched Terms in Table V in the Data Supplement)

| GO Identifier | GO Term Name | 2011 | | | 2016 | | |
|---------------|--|------|-------------------|------|------|-------------------|----|
| | | n | Corrected P Value | x | n | Corrected P Value | x |
| GO:0007005 | Mitochondrion organization | #N/A | #N/A | #N/A | 679 | 4.56E-12 | 24 |
| GO:0022904 | Respiratory electron transport chain | 135 | 5.48E-34 | 29 | 157 | 1.67E-34 | 29 |
| GO:0010467 | Gene expression | 2206 | 4.58E-11 | 45 | 5483 | 1.09E-13 | 73 |
| GO:0032502 | Developmental process | 5680 | 4.09E-12 | 80 | 6093 | 1.82E-07 | 64 |
| GO:0061337 | Cardiac conduction | #N/A | #N/A | #N/A | 126 | 1.71E-02 | 4 |
| GO:1903779 | Regulation of cardiac conduction | #N/A | #N/A | #N/A | 68 | 1.57E-05 | 6 |
| GO:0002026 | Regulation of the force of heart contraction | #N/A | #N/A | #N/A | 31 | 5.93E-06 | 5 |

A selection of Biological Process terms extracted from 2 analyses of the top 200 differentially expressed transcripts in hA-VCMs (adult human ventricular cardiomyocytes; compared with the human embryonic stem cells [hESCs] transcriptome³). Terms selected are either cardiac physiology relevant or align with terms identified by Poon et al.³ Analyses were conducted using the BinGO plugin³³ within the Cytoscape v3.3.0 tool³⁴ using either the 2011 or 2016 Gene Ontology (GO) annotation data set. n indicates the number of protein IDs associated with the GO term, and x is the number of IDs in both the submitted list and associated with the GO term. The inclusion of only the most abundant VCM transcripts probably accounts for the low number of genes in this data set associated with the cardiac terms. #N/A indicates term was not significantly enriched in the data set.

ease. In particular, our results suggest that *ATP1B1*, a Na⁺/K⁺-ATPase β-subunit, is the most likely candidate gene for further study at the 1q24 risk locus because it is associated with cardiac-relevant GO annotations. Another potential use of cardiac GO annotations is to extend protein network analysis. Overlaying proteins with relevant annotations (and hence known cardiac role) onto an existing network would highlight their interacting partners, and these could be explored as candidate genes.

With researchers turning to *Drosophila* and zebrafish as model systems for heart disease,^{49,50} there is a requirement for GO to represent cardiac physiology using terms that are species independent.⁶ The *Drosophila* pulsatile heart tube, with its anterior aorta, looks structurally very distinct from the zebrafish 2-chambered and the mammalian 4-chambered hearts. However, despite this, many of the new GO terms created during this project can be applied across all species because many orthologous genes have similar functions. The major limiting factor to the GO annotation of nonmammalian systems is the paucity of research describing the roles of individual gene products in the cardiac cycle in those species, as the majority of these data relate to mammals. Indeed, the curation effort described in this article focuses on improving analysis tools for human cardiovascular research.

Our results show that collaboration between members of relevant model organism databases and focused curation groups can improve and extend the capture of information about physiological processes in GO, in this particular study, cardiac processes. This effort was enhanced by the collaboration with experts in the cardiac research field who helped us identify key aspects of the process, key genes, and key publications on which to focus. As knowledge of the cardiac system continues to advance, there will be opportunities to capture additional cardiac information in GO. We have provided a structured framework for the addition of new knowledge to the resource, for example, to better describe information about the proteins involved in the mechanical aspect of the heart, and to fully capture roles of gene products and hormones in regulating cardiac physiology. Our work also shows that collaboration between groups developing ontologies and creating biological annotations and scientists and clinicians engaged in active research can lead to substantial improvements in the computational representation of biological knowledge. The GOC welcomes input from researchers about any aspect of our work, including changes to the ontology and suggestions of papers and gene products to annotate (goannotation@ucl.ac.uk, <http://geneontology.org/page/contributing-go>). A variety of GitHub repositories with issue trackers are in place for specific queries: for general inquiries about GO (<https://github.com/geneontology/helpdesk>), for specific questions

about annotations or annotation-related topics (<https://github.com/geneontology/go-annotation/>), and for specific questions or suggestions about the content and structure of the ontology (<https://github.com/geneontology/go-ontology/>). Such collaborations improve the value of the GO resource for the benefit of the entire cardiovascular research community and facilitate the interpretation of high-throughput data sets, toward the identification of dysregulated cardiac pathways, as well as variants and risk alleles, associated with cardiovascular diseases. This has important implications for cardiovascular physicians needing to interpret potentially pathological variants in their patients as a resource for the most up-to-date bioinformatic data to inform diagnosis and cascade screening in families.

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None.

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FOOTNOTES

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**Improving Interpretation of Cardiac Phenotypes and Enhancing Discovery With
Expanded Knowledge in the Gene Ontology**

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SUPPLEMENTAL MATERIAL

Methods

Ontology engineering

GO provides more than a simple flat list of terms. Instead, the terms have defined relations between each other, which can be represented in a graphical view (see Figure 1, which is a view of the ontology created with the OBO-Edit tool Graph Editor function using the public OBO release of GO on April 26, 2017, <http://purl.obolibrary.org/obo/go.obo>).¹ Each GO term can have multiple, more general, ‘parent’ terms and multiple, more specific, ‘child’ terms. Different relations are available to define the connection between two GO terms². Five core relations have been applied to the cardiac physiology part of the ontology: *is_a*, *part_of*, *regulates*, *positively_regulates* and *negatively_regulates*. The *is_a* relation denotes that the child term has all the characteristics of its parent but is a more specific term, with differences that distinguish it from other *is_a* children, for example ‘AV node cell to bundle of His cell communication’ is a subtype of ‘cell communication involved in cardiac conduction’ and is distinguished by the cells that are communicating. The *part_of* relation denotes that the child term is always a part of the parent term and together with additional parts make up the parent. For example, ‘AV node cell action potential’ is part of the process of ‘AV node cell to bundle of His cell signaling’ because it is required to propagate the electrical signal along the AV node cell. Another example is that GO Molecular Function terms describing channel activities required for the changes in membrane potential that are associated with an action potential have ‘*part_of*’ relationships with the relevant membrane depolarization and repolarization terms. Coupling the channel activities with the processes that regulate membrane potential in these sections of the ontology provides a good example of how the Molecular Function and Biological Process branches can be integrated. The various types of regulation relations describe when a process has a regulatory or controlling effect on another process, for example ‘regulation of cardiac conduction’ describes a type of process that has a regulatory effect on ‘cardiac conduction’. The development of the ontology to describe cardiac-related processes involved more than placing the new GO terms in the ontology. Each GO term was assigned a unique GO identifier (ID), a descriptive definition and synonyms used in the literature. Synonyms and definitions facilitate the curation of a gene product’s role by allowing easier retrieval of appropriate GO terms when searching the ontology. They also provide a clear, human-readable meaning of the term. Additionally, where applicable, GO terms are defined computationally by creating necessary and sufficient statements using relationships between GO terms and terms from cross-referenced external ontologies^{3,4}.

Expert curation using Gene Ontology

To create GO annotations supported by experimental data, expert GO curators read publications and summarised the data in annotations⁵. There is a vast number of publications describing the function of the gene products we have prioritized, therefore only a fraction of the available literature was curated. Because the curators are based at different institutes, different strategies were taken to identify the appropriate papers to annotate^{6,7}. Since the focus of this project was to capture the role of specific gene products in cardiac physiology, the papers selected usually contained experimental data describing the prioritized proteins and their role in cardiac systems.

Whenever possible, annotations also specify additional contextual information, such as the location of a function or process in a ‘regular ventricular cardiac myocyte’ or ‘heart left ventricle’, by using

annotation extensions⁴ that refer to external ontologies such as the Cell Ontology (CL)⁸⁻¹⁰ or the Uberon multi-species anatomy ontology^{11,12}. For example, human SCN5A is associated with the GO term ‘Z disc’ with the annotation extension ‘part_of’ ‘cardiac muscle cell’⁴. Thus, this annotation specifies the cell, as well as the cellular, location of this protein.

Each annotation includes the gene product identifier, a GO term, an evidence code, and a reference². The QuickGO browser (<http://www.ebi.ac.uk/QuickGO/>)¹³ or the AmiGO2 browser (<http://amigo.geneontology.org/amigo/search/ontology>)¹⁴ were used to search for the most specific GO terms to ‘capture’ the experimental data presented in each paper. Appropriate evidence codes were given to each annotation based on the type of experimental data presented in the published papers (www.geneontology.org/GO.evidence.shtml)¹⁵. The evidence code ‘Inferred by Curator’ (IC) was applied when a combination of experimental data from more than one paper supported the annotation. To ensure full annotation of the human, mouse and rat proteomes, experimentally supported annotations associated with model organism and human gene products are automatically transferred to the orthologous mammalian gene products via the Ensembl Compara pipeline¹⁶. However, 13 of the 88 prioritized proteins are members of highly conserved protein families and therefore do not have 1-to-1 orthologs in human, mouse and rat, as defined by Ensembl Compara. In these cases, GO annotations with experimental evidence codes were associated to orthologous human, mouse and rat proteins, by the expert curators, using the evidence code ISS (Inferred from Sequence Similarity), or ISO (Inferred from Orthology) based on confirmation of predicted orthology by the HUGO Gene Nomenclature Committee (<http://www.genenames.org/>) ortholog prediction tool (HCOP)¹⁷. The procedure for curation of miRNAs is detailed in Huntley et al. 2016⁵.

Identifying experimental data to annotate

The PubMed database¹⁸ was used to locate recent papers reviewing the literature for cardiac electrophysiology and channelopathies. Gene products with a known role in the cardiac cycle were identified from these reviews. PubMed searches, with each individual gene symbol, name or synonym and additional filters, were conducted to provide a comprehensive coverage of the role of these proteins with respect to the cardiac physiology. These searches included specific filters, in addition to the relevant gene-symbol and name: ‘AND cardiac’, ‘AND heart’, or ‘AND conduction’. The selection of papers to curate was then based on whether: 1) they contained experimental data; 2) new information would be added to the current GO annotation data associated with the protein; 3) it was possible to identify the species the protein or expression construct was derived from. Only papers that met all three criteria were curated. The choice of papers curated was, therefore, influenced by the information captured previously (i.e. papers already annotated with existing cardiac terms were excluded). While human gene products were the main focus of this annotation project, other species gene products were also curated where information was available.

Identification of candidate genes associated with arrhythmia risk loci

The QuickGO browser¹³, with ‘taxon’ and ‘GO term’ filters applied, was used to download all human proteins associated with nine GO terms that are relevant to normal cardiac physiology (these nine GO terms are listed in Supplemental Table IV). The Microsoft Excel VLOOKUP function was used to identify the Mendelian genes and the candidate genes (listed in Supplemental Table III) that were associated with the selected GO terms.

GO functional analysis of transcriptomic datasets

A ventricular cardiomyocyte dataset¹⁹ was analysed using the BinGO plugin²⁰ within the Cytoscape v3.3.0 tool²¹, according to the tools recommended procedure. BinGO has the facility to choose which GO annotation dataset to include in the analysis, allowing 2011 and 2016 annotation datasets to be compared. The ontology go-basic.obo (dated 7/03/2016) was downloaded from the GO Consortium website (<http://geneontology.org/page/download-ontology>), and the gene association files (containing the annotation datasets) gene_association.goa_human.104.gz (dated 14/11/2011) and gene_association.goa_human.154.gz (dated 16/02/2016), were downloaded from <ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/old/HUMAN/> and <ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/HUMAN/> respectively. For the analysis UniProtKB accessions were submitted with the following settings: assess overrepresentation; hypergeometric test; Benjamini & Hochberg False Discovery Rate correction; $p < 0.05$ significance level; 'whole annotation' was used as reference set, leading to a comparison of the GO terms associated with the ventricular cardiomyocyte dataset¹⁹ with the GO terms associated with the human proteome.

Supplemental Tables

Supplemental Table I. 88 Cardiac physiology gene products prioritized for annotation. Human proteins with a role in cardiac excitability were compiled based on the description of proteins listed in eleven cardiac physiology reviews²²⁻³². This list was then filtered to remove hormones and hormone receptors involved in regulating the heart rate (with the exception of AGT, ACE and ACE2) and proteins involved in regulating heart development. This enabled us to focus more specifically on ion channels and ATPases and the proteins directly regulating their activity.

| Approved symbol | Approved name | UniProt ID/RNA central ID | Link to QuickGO or AmiGO annotation record |
|-----------------|---|---------------------------|---|
| ACE | angiotensin I converting enzyme | P12821 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P12821 |
| ACE2 | angiotensin I converting enzyme 2 | Q9BYF1 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9BYF1 |
| AGT | angiotensinogen | P01019 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P01019 |
| AKAP6 | A-kinase anchoring protein 6 | Q13023 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q13023 |
| AKAP9 | A-kinase anchoring protein 9 | Q99966 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q99966 |
| ANK2 | ankyrin 2 | Q01484 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q01484 |
| ANK3 | ankyrin 3 | Q12955 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q12955 |
| ASPH | aspartate beta-hydroxylase | Q12797 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q12797 |
| ATP1A1 | ATPase Na ⁺ /K ⁺ transporting subunit alpha 1 | P05023 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P05023 |
| ATP1A2 | ATPase Na ⁺ /K ⁺ transporting subunit alpha 2 | P50993 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P50993 |
| ATP1A3 | ATPase Na ⁺ /K ⁺ transporting subunit alpha 3 | P13637 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P13637 |
| ATP1B1 | ATPase Na ⁺ /K ⁺ transporting subunit beta 1 | P05026 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P05026 |
| ATP2A2 | ATPase sarcoplasmic/endoplasmic reticulum Ca ²⁺ transporting 2 | P16815 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P16815 |
| ATP2B4 | ATPase plasma membrane Ca ²⁺ transporting 4 | P23634 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P23634 |
| CACNA1C | calcium voltage-gated channel subunit alpha1 C | Q13936 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q13936 |
| CACNA1D | calcium voltage-gated channel subunit alpha1 D | Q01668 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q01668 |
| CACNA1G | calcium voltage-gated channel subunit alpha1 G | O43497 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O43497 |
| CACNAZD1 | calcium voltage-gated channel auxiliary subunit alpha2delta 1 | P54289 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P54289 |
| CACNB2 | calcium voltage-gated channel auxiliary subunit beta 2 | O08289 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O08289 |
| CALM1 | calmodulin 1 | P62158 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P62158 |
| CAMK2D | calcium/calmodulin dependent protein kinase II delta | Q13557 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q13557 |
| CASQ2 | calsequestrin 2 | O14958 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O14958 |
| CAV1 | caveolin 1 | O03135 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O03135 |
| CAV2 | caveolin 2 | P51636 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P51636 |
| CAV3 | caveolin 3 | P56539 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P56539 |
| CLIC2 | chloride intracellular channel 2 | O15247 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O15247 |
| CNOT1 | CCR4-NOT transcription complex subunit 1 | AS5YK6 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=AS5YK6 |
| DLG1 | discs large MAGUK scaffold protein 1 | Q12959 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q12959 |
| DMD | dystrophin | P11532 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P11532 |
| DSG2 | desmoglein 2 | O14126 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O14126 |
| FGF12 | fibroblast growth factor 12 | P61328 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P61328 |
| FGF13 | fibroblast growth factor 13 | Q92913 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q92913 |
| FKBP1B | FK506 binding protein 1B | P68106 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P68106 |
| FLNA | filamin A | P21333 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P21333 |
| FXD1 | FXD domain containing ion transport regulator 1 | O00168 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O00168 |
| GJA1 | gap junction protein alpha 1 | P17302 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P17302 |
| GJA5 | gap junction protein alpha 5 | P36382 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P36382 |
| GPDI1 | glycerol-3-phosphate dehydrogenase 1 like | O8N335 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O8N335 |
| GSTM2 | glutathione S-transferase mu 2 | P28161 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P28161 |
| HCN4 | hyperpolarization activated cyclic nucleotide gated potassium channel 4 | Q9Y304 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9Y304 |
| HRC | histidine rich calcium binding protein | P23327 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P23327 |
| KCN5A | potassium voltage-gated channel subfamily A member 5 | P22460 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P22460 |
| KCN3D | potassium voltage-gated channel subfamily D member 3 | O9UK17 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O9UK17 |
| KCNE1 | potassium voltage-gated channel subfamily E regulatory subunit 1 | P15382 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P15382 |
| KCNE2 | potassium voltage-gated channel subfamily E regulatory subunit 2 | Q9Y6J6 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9Y6J6 |
| KCNE3 | potassium voltage-gated channel subfamily E regulatory subunit 3 | Q9Y6H6 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9Y6H6 |
| KCNE5 | potassium voltage-gated channel subfamily E regulatory subunit 5 | Q9UJ90 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9UJ90 |
| KCNH2 | potassium voltage-gated channel subfamily H member 2 | Q12809 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q12809 |
| KCNJ2 | potassium voltage-gated channel subfamily J member 2 | P63252 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P63252 |
| KCNJ5 | potassium voltage-gated channel subfamily J member 5 | P48544 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P48544 |
| KCNJ8 | potassium voltage-gated channel subfamily J member 8 | Q15842 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q15842 |
| KCNQ1 | potassium voltage-gated channel subfamily Q member 1 | P51787 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P51787 |
| LIG3 | DNA ligase 3 | P49916 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P49916 |
| LITAF | lipopolysaccharide induced TNF factor | Q99732 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q99732 |
| NDRG4 | NDRG family member 4 | Q9ULP0 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9ULP0 |
| NEDD4L | neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase | Q96PU5 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q96PU5 |
| NOS1 | nitric oxide synthase 1 | P29475 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P29475 |
| NOS1AP | nitric oxide synthase 1 adaptor protein | Q75052 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q75052 |
| NPPA | natriuretic peptide A | P01160 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P01160 |
| NUP155 | nucleoporin 155 | O75694 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O75694 |
| PDE4B | phosphodiesterase 4B | Q07343 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q07343 |
| PDE4D | phosphodiesterase 4D | O08499 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O08499 |
| PKP2 | plakophilin 2 | Q99559 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q99559 |
| PLN | phospholamban | P26678 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P26678 |
| PRKACA | protein kinase cAMP-activated catalytic subunit alpha | P17612 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P17612 |
| PTPN3 | protein tyrosine phosphatase, non-receptor type 3 | P26045 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P26045 |
| RANGRF | RAN guanine nucleotide release factor | Q9HD47 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9HD47 |
| RNF207 | ring finger protein 207 | Q6ZRF8 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q6ZRF8 |
| RYR2 | ryanodine receptor 2 | Q92736 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q92736 |
| SCN10A | sodium voltage-gated channel alpha subunit 10 | Q9Y5Y9 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9Y5Y9 |
| SCN1B | sodium voltage-gated channel beta subunit 1 | O07699 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O07699 |
| SCN2B | sodium voltage-gated channel beta subunit 2 | O60939 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O60939 |
| SCN3B | sodium voltage-gated channel beta subunit 3 | O9NY72 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O9NY72 |
| SCN4B | sodium voltage-gated channel beta subunit 4 | O8IWT1 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O8IWT1 |
| SCN5A | sodium voltage-gated channel alpha subunit 5 | Q14524 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q14524 |
| SLC8A1 | solute carrier family 8 member A1 | P32418 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P32418 |
| SLC8B1 | solute carrier family 8 member B1 | O6J4K2 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O6J4K2 |
| SLC9A1 | solute carrier family 9 member A1 | P19634 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P19634 |
| SLMAP | sarcolemma associated protein | Q14BN4 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q14BN4 |
| SNTA1 | syntrophin alpha 1 | Q13424 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q13424 |
| SPTBN4 | spectrin beta, non-erythrocytic 4 | Q9H254 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q9H254 |
| SRI | sorcin | P30626 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P30626 |
| TCAP | titin-cap | O15273 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=O15273 |
| TRDN | triadin | Q13061 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q13061 |
| TRPM4 | transient receptor potential cation channel subfamily M member 4 | Q8TD43 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q8TD43 |
| YWHAE | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon | P62258 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=P62258 |
| YWHAH | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta | Q04917 | http://www.ebi.ac.uk/QuickGO/GProtein?ac=Q04917 |
| hsa-miR-1-3p | miR-1 | URS00001DC04F_9606 | http://amigo.geneontology.org/amigo/gene_product/RNACentral:URS00001DC04F_9606 |
| hsa-miR-26a-5p | miR-26 | URS000019B0F7_9606 | http://amigo.geneontology.org/amigo/gene_product/RNACentral:URS000019B0F7_9606 |
| hsa-miR-133a-3p | miR-133a | URS00004C9052_9606 | http://amigo.geneontology.org/amigo/gene_product/RNACentral:URS00004C9052_9606 |
| hsa-miR-208a-3p | miR-208a | URS00000E5433_9606 | http://amigo.geneontology.org/amigo/gene_product/RNACentral:URS00000E5433_9606 |
| hsa-miR-212-3p | miR-212 | URS00001D68AE_9606 | http://amigo.geneontology.org/amigo/gene_product/RNACentral:URS00001D68AE_9606 |
| hsa-miR-328-3p | miR-328 | URS00005FDE70_9606 | http://amigo.geneontology.org/amigo/gene_product/RNACentral:URS00005FDE70_9606 |
| hsa-miR-499-5p | miR-499 | URS00000C7662_9606 | http://amigo.geneontology.org/amigo/gene_product/RNACentral:URS00000C7662_9606 |

Supplemental Table II. Using Gene Ontology to support the identification of the likely causative gene associated with QT interval length and AF risk loci. 117 genes identified as either a known Mendelian gene associated with AF, LQTS, SQTS, CPVT or BrS^{33,34}, or a candidate gene associated with AF risk loci or loci associated with QT interval length, by GWAS^{33,35,36}. Nine GO terms were selected based on their potential relevance to cardiac physiology (Supplemental Table III). QuickGO¹³ was used to download all human proteins associated with these terms either directly or to a child term with one of the following relations: part_of, is_a, regulates, negatively_regulates, positively_regulates (11 March 2016). The association of these 9 GO terms with each of the AF or QT interval-associated genes was then determined, indicated by solid filled cell. Candidate genes identified by annotation to a relevant GO term were then compared with arrhythmia disorder Mendelian genes and candidate genes identified using eQTL, *in silico* QT interval loci protein network analysis (PPI-QT) or co-immunoprecipitation with one of 5 LQTS Mendelian proteins (CoIP)³³. ELP6 is the approved symbol for C3orf75.

Supplemental Table III. Cardiac physiology relevant *Biological Process* GO terms. Nine GO terms were selected based on their potential relevance to cardiac physiology.

| GO identifier | GO term name |
|----------------------|---------------------------------------|
| GO:0061337 | cardiac conduction |
| GO:0042391 | regulation of membrane potential |
| GO:0030029 | actin filament-based process |
| GO:0071805 | potassium ion transmembrane transport |
| GO:0035725 | sodium ion transmembrane transport |
| GO:0070588 | calcium ion transmembrane transport |
| GO:0006936 | muscle contraction |
| GO:0007507 | heart development |
| GO:0070482 | response to oxygen levels |

Supplemental Table IV. List of new cardiac physiology relevant GO terms.

197 new GO terms were created to support the annotation of 88 prioritized proteins and 7 miRNAs and their role in cardiac processes. These were created by the GO editors following an ontology development meeting in November 2011 and individual requests by GO curators. Table IV lists 200 GO terms as it includes 3 terms, 'membrane depolarization during atrial cardiac muscle cell action potential' and 'membrane repolarization during atrial cardiac muscle cell action potential', as well as 'cardiac conduction', indicated by *, that were already in the ontology). The column header 'Aspect' lists the ontology to which the GO term belongs, either Molecular Function or Biological Process. Information about the number of annotations associated with each GO term is provided (based on data available 18 October 2017) in two ways: as the number of direct annotations (number of times each GO term has been associated with a gene product from any species) and number of annotations to child term/s (number of times a child term for each GO term has been associated with a gene product from any species). Terms were considered as child terms if they had an is_a, part_of, occurs_in, regulates, positively_regulates or negatively_regulates relation to the parent term. The graph nature of the ontology means that some annotations will be represented more than once in this table.

Of the 197 new GO terms created, 136 have been directly associated with a gene product. Of the 63 terms without direct annotations, 22 provide a parent GO term that will facilitate gene grouping during functional analyses using GO datasets. For example, 'atrial cardiac muscle cell membrane repolarization' has no direct annotations, but its child terms have been used in 226 annotations. 41 terms, mostly leaf nodes, have not yet been associated with any gene product either directly or via child terms; many of these refer either to processes occurring in specific cell types, such as 'negative regulation of AV node cell action potential', or describe very specific functions, e.g. 'stretch-activated, cation-selective, calcium channel activity involved in regulation of action potential'. Some of these areas of study did not fall under the focus of this project, and relevant literature was not examined in detail. Future annotation projects, for example looking at signaling pathways that regulate both the rate and strength of heart contractions, may lead to the association of proteins or RNAs with these terms.

| Aspect | GO ID | GO term name | Number of annotations using term listed | Number of annotations using child term |
|---|------------|--|---|--|
| Child terms of GO term cardiac conduction*, GO:0061337 | | | | |
| Biological Process | GO:0086014 | atrial cardiac muscle cell action potential | 215 | |
| Biological Process | GO:0099624 | atrial cardiac muscle cell membrane repolarization | 0 | 226 |
| Biological Process | GO:0086066 | atrial cardiac muscle cell to AV node cell communication | 13 | |
| Biological Process | GO:0086044 | atrial cardiac muscle cell to AV node cell communication by electrical coupling | 76 | |
| Biological Process | GO:0086026 | atrial cardiac muscle cell to AV node cell signaling | 0 | 604 |
| Biological Process | GO:0086071 | atrial cardiac muscle cell-AV node cell adhesion involved in cell communication | 0 | 0 |
| Biological Process | GO:0086016 | AV node cell action potential | 112 | |
| Biological Process | GO:0086067 | AV node cell to bundle of His cell communication | 52 | |
| Biological Process | GO:0086053 | AV node cell to bundle of His cell communication by electrical coupling | 121 | |
| Biological Process | GO:0086027 | AV node cell to bundle of His cell signaling | 44 | |
| Biological Process | GO:0086072 | AV node cell-bundle of His cell adhesion involved in cell communication | 4 | |
| Biological Process | GO:0086043 | bundle of His cell action potential | 32 | |
| Biological Process | GO:0086069 | bundle of His cell to Purkinje myocyte communication | 4 | |
| Biological Process | GO:0086054 | bundle of His cell to Purkinje myocyte communication by electrical coupling | 35 | |
| Biological Process | GO:0086028 | bundle of His cell to Purkinje myocyte signaling | 0 | 285 |
| Biological Process | GO:0086073 | bundle of His cell-Purkinje myocyte adhesion involved in cell communication | 181 | |
| Biological Process | GO:0086064 | cell communication by electrical coupling involved in cardiac conduction | 91 | |
| Biological Process | GO:0086065 | cell communication involved in cardiac conduction | 39 | |
| Biological Process | GO:0086019 | cell-cell signaling involved in cardiac conduction | 40 | |
| Biological Process | GO:0098912 | membrane depolarization during atrial cardiac muscle cell action potential* | 71 | |
| Biological Process | GO:0086045 | membrane depolarization during AV node cell action potential | 140 | |
| Biological Process | GO:0086048 | membrane depolarization during bundle of His cell action potential | 62 | |
| Biological Process | GO:0086047 | membrane depolarization during Purkinje myocyte cell action potential | 60 | |
| Biological Process | GO:0086046 | membrane depolarization during SA node cell action potential | 138 | |
| Biological Process | GO:0098914 | membrane repolarization during atrial cardiac muscle cell action potential* | 93 | |
| Biological Process | GO:0086049 | membrane repolarization during AV node cell action potential | 0 | 0 |
| Biological Process | GO:0086050 | membrane repolarization during bundle of His cell action potential | 27 | |
| Biological Process | GO:0086051 | membrane repolarization during Purkinje myocyte action potential | 0 | 0 |
| Biological Process | GO:0086052 | membrane repolarization during SA node cell action potential | 29 | |
| Biological Process | GO:1903948 | negative regulation of atrial cardiac muscle cell action potential | 0 | 0 |
| Biological Process | GO:1903950 | negative regulation of AV node cell action potential | 0 | 0 |
| Biological Process | GO:1903780 | negative regulation of cardiac conduction | 0 | 0 |
| Biological Process | GO:1901845 | negative regulation of cell communication by electrical coupling involved in cardiac conduction | 0 | 0 |
| Biological Process | GO:1905028 | negative regulation of membrane depolarization during AV node cell action potential | 0 | 0 |
| Biological Process | GO:1905001 | negative regulation of membrane repolarization during atrial cardiac muscle cell action potential | 0 | 0 |
| Biological Process | GO:1903953 | negative regulation of voltage-gated potassium channel activity involved in atrial cardiac muscle cell action potential repolarization | 0 | 0 |
| Biological Process | GO:1903949 | positive regulation of atrial cardiac muscle cell action potential | 3 | |
| Biological Process | GO:1903951 | positive regulation of AV node cell action potential | 0 | 0 |
| Biological Process | GO:1903781 | positive regulation of cardiac conduction | 0 | 8 |
| Biological Process | GO:1901846 | positive regulation of cell communication by electrical coupling involved in cardiac conduction | 2 | |
| Biological Process | GO:1905029 | positive regulation of membrane depolarization during AV node cell action potential | 0 | 0 |
| Biological Process | GO:1905002 | positive regulation of membrane repolarization during atrial cardiac muscle cell action potential | 0 | 0 |
| Biological Process | GO:1903954 | positive regulation of voltage-gated potassium channel activity involved in atrial cardiac muscle cell action potential repolarization | 3 | |
| Biological Process | GO:0086017 | Purkinje myocyte action potential | 0 | 131 |
| Biological Process | GO:0086068 | Purkinje myocyte to ventricular cardiac muscle cell communication | 0 | 160 |
| Biological Process | GO:0086055 | Purkinje myocyte to ventricular cardiac muscle cell communication by electrical coupling | 1 | |
| Biological Process | GO:0086029 | Purkinje myocyte to ventricular cardiac muscle cell signaling | 27 | |
| Biological Process | GO:0086074 | Purkinje myocyte-ventricular cardiac muscle cell adhesion involved in cell communication | 0 | 0 |
| Biological Process | GO:0098910 | regulation of atrial cardiac muscle cell action potential | 127 | |
| Biological Process | GO:0098904 | regulation of AV node cell action potential | 113 | |
| Biological Process | GO:0098905 | regulation of bundle of His cell action potential | 99 | |
| Biological Process | GO:1903779 | regulation of cardiac conduction | 447 | |

| | | | | |
|--|------------|---|------|------|
| <i>Biological Process</i> | GO:1901844 | regulation of cell communication by electrical coupling involved in cardiac conduction | 106 | |
| <i>Biological Process</i> | GO:0086091 | regulation of heart rate by cardiac conduction | 1171 | |
| <i>Biological Process</i> | GO:1905027 | regulation of membrane depolarization during AV node cell action potential | 0 | 0 |
| <i>Biological Process</i> | GO:1905000 | regulation of membrane repolarization during atrial cardiac muscle cell action potential | 2 | |
| <i>Biological Process</i> | GO:0098906 | regulation of Purkinje myocyte action potential | 35 | |
| <i>Biological Process</i> | GO:0098907 | regulation of SA node cell action potential | 84 | |
| <i>Biological Process</i> | GO:0086092 | regulation of the force of heart contraction by cardiac conduction | 68 | |
| <i>Biological Process</i> | GO:1903952 | regulation of voltage-gated potassium channel activity involved in atrial cardiac muscle cell action potential repolarization | 0 | 3 |
| <i>Biological Process</i> | GO:0086015 | SA node cell action potential | 165 | |
| <i>Biological Process</i> | GO:0086070 | SA node cell to atrial cardiac muscle cell communication | 70 | |
| <i>Biological Process</i> | GO:0086021 | SA node cell to atrial cardiac muscle cell communication by electrical coupling | 3 | |
| <i>Biological Process</i> | GO:0086018 | SA node cell to atrial cardiac muscle cell signalling | 44 | |
| <i>Biological Process</i> | GO:0086022 | SA node cell-atrial cardiac muscle cell adhesion involved in cell communication | 0 | 0 |
| <i>Molecular Function</i> | GO:0086082 | cell adhesive protein binding involved in AV node cell-bundle of His cell communication | 2 | |
| <i>Molecular Function</i> | GO:0086083 | cell adhesive protein binding involved in bundle of His cell-Purkinje myocyte communication | 17 | |
| <i>Molecular Function</i> | GO:0086076 | gap junction channel activity involved in atrial cardiac muscle cell-AV node cell electrical coupling | 40 | |
| <i>Molecular Function</i> | GO:0086077 | gap junction channel activity involved in AV node cell-bundle of His cell electrical coupling | 85 | |
| <i>Molecular Function</i> | GO:0086078 | gap junction channel activity involved in bundle of His cell-Purkinje myocyte electrical coupling | 35 | |
| <i>Molecular Function</i> | GO:0086075 | gap junction channel activity involved in cardiac conduction electrical coupling | 40 | |
| <i>Molecular Function</i> | GO:0086079 | gap junction channel activity involved in Purkinje myocyte-ventricular cardiac muscle cell electrical coupling | 1 | |
| <i>Molecular Function</i> | GO:0086020 | gap junction channel activity involved in SA node cell-atrial cardiac muscle cell electrical coupling | 3 | |
| <i>Molecular Function</i> | GO:0086056 | voltage-gated calcium channel activity involved in AV node cell action potential | 112 | |
| <i>Molecular Function</i> | GO:0086057 | voltage-gated calcium channel activity involved in bundle of His cell action potential | 34 | |
| <i>Molecular Function</i> | GO:0086058 | voltage-gated calcium channel activity involved in Purkinje myocyte cell action potential | 0 | 0 |
| <i>Molecular Function</i> | GO:0086059 | voltage-gated calcium channel activity involved SA node cell action potential | 104 | |
| <i>Molecular Function</i> | GO:0086089 | voltage-gated potassium channel activity involved in atrial cardiac muscle cell action potential repolarization | 90 | |
| <i>Molecular Function</i> | GO:0086086 | voltage-gated potassium channel activity involved in AV node cell action potential repolarization | 0 | 0 |
| <i>Molecular Function</i> | GO:0086087 | voltage-gated potassium channel activity involved in bundle of His cell action potential repolarization | 27 | |
| <i>Molecular Function</i> | GO:0086088 | voltage-gated potassium channel activity involved in Purkinje myocyte action potential repolarization | 0 | 0 |
| <i>Molecular Function</i> | GO:0086041 | voltage-gated potassium channel activity involved in SA node cell action potential depolarization | 29 | |
| <i>Molecular Function</i> | GO:0086090 | voltage-gated potassium channel activity involved in SA node cell action potential repolarization | 29 | |
| <i>Molecular Function</i> | GO:0086060 | voltage-gated sodium channel activity involved in AV node cell action potential | 4 | |
| <i>Molecular Function</i> | GO:0086061 | voltage-gated sodium channel activity involved in bundle of His cell action potential | 4 | |
| <i>Molecular Function</i> | GO:0086062 | voltage-gated sodium channel activity involved in Purkinje myocyte action potential | 36 | |
| <i>Molecular Function</i> | GO:0086063 | voltage-gated sodium channel activity involved in SA node cell action potential | 6 | |
| Other cardiac-relevant GO terms | | | | |
| <i>Biological Process</i> | GO:0086096 | adenylate cyclase-inhibiting adrenergic receptor signaling pathway involved in heart process | 0 | 0 |
| <i>Biological Process</i> | GO:0086102 | adenylate cyclase-inhibiting G-protein coupled acetylcholine receptor signaling pathway involved in negative regulation of heart rate | 0 | 0 |
| <i>Biological Process</i> | GO:0086030 | adrenergic receptor signaling pathway involved in cardiac muscle relaxation | 3 | |
| <i>Biological Process</i> | GO:0086023 | adrenergic receptor signaling pathway involved in heart process | 62 | |
| <i>Biological Process</i> | GO:0086024 | adrenergic receptor signaling pathway involved in positive regulation of heart rate | 2 | |
| <i>Biological Process</i> | GO:0038166 | angiotensin-activated signaling pathway | 784 | |
| <i>Biological Process</i> | GO:0086098 | angiotensin-activated signaling pathway involved in heart process | 73 | |
| <i>Biological Process</i> | GO:0090662 | ATP hydrolysis coupled transmembrane transport | 2577 | |
| <i>Biological Process</i> | GO:1903515 | calcium ion transport from cytosol to endoplasmic reticulum | 56 | |
| <i>Biological Process</i> | GO:1903514 | calcium ion transport from endoplasmic reticulum to cytosol | 36 | |
| <i>Biological Process</i> | GO:0086001 | cardiac muscle cell action potential | 65 | |
| <i>Biological Process</i> | GO:0086002 | cardiac muscle cell action potential involved in contraction | 436 | |
| <i>Biological Process</i> | GO:0086003 | cardiac muscle cell contraction | 12 | |
| <i>Biological Process</i> | GO:0086042 | cardiac muscle cell-cardiac muscle cell adhesion | 63 | |
| <i>Biological Process</i> | GO:0014898 | cardiac muscle hypertrophy in response to stress | 440 | |
| <i>Biological Process</i> | GO:0060926 | cardiac pacemaker cell development | 0 | 100 |
| <i>Biological Process</i> | GO:0060920 | cardiac pacemaker cell differentiation | 0 | 150 |
| <i>Biological Process</i> | GO:0060927 | cardiac pacemaker cell fate commitment | 0 | 33 |
| <i>Biological Process</i> | GO:1903513 | endoplasmic reticulum to cytosol transport | 0 | 1787 |
| <i>Biological Process</i> | GO:0086100 | endothelin receptor signaling pathway | 561 | |
| <i>Biological Process</i> | GO:0086101 | endothelin receptor signaling pathway involved in heart process | 0 | 0 |
| <i>Biological Process</i> | GO:0086093 | G-protein coupled acetylcholine receptor signaling pathway involved in involved in heart process | 0 | 0 |
| <i>Biological Process</i> | GO:0086033 | G-protein coupled acetylcholine receptor signaling pathway involved in negative regulation of heart rate | 0 | 0 |
| <i>Biological Process</i> | GO:0086103 | G-protein coupled receptor signaling pathway involved in heart process | 35 | |
| <i>Biological Process</i> | GO:0086010 | membrane depolarization during action potential | 757 | |
| <i>Biological Process</i> | GO:0086012 | membrane depolarization during cardiac muscle cell action potential | 183 | |
| <i>Biological Process</i> | GO:0098913 | membrane depolarization during ventricular cardiac muscle cell action potential | 0 | 0 |
| <i>Biological Process</i> | GO:0086009 | membrane repolarization | 310 | |
| <i>Biological Process</i> | GO:0086011 | membrane repolarization during action potential | 142 | |
| <i>Biological Process</i> | GO:0086013 | membrane repolarization during cardiac muscle cell action potential | 143 | |

| | | | | |
|--------------------|------------|--|-----|-----|
| Biological Process | GO:0098915 | membrane repolarization during ventricular cardiac muscle cell action potential | 156 | |
| Biological Process | GO:1901205 | negative regulation of adrenergic receptor signaling pathway involved in heart process | 32 | |
| Biological Process | GO:1903246 | negative regulation of adrenergic receptor signaling pathway involved in positive regulation of heart rate | 0 | 0 |
| Biological Process | GO:1903280 | negative regulation of calcium:sodium antiporter activity | 6 | |
| Biological Process | GO:1902260 | negative regulation of delayed rectifier potassium channel activity | 182 | |
| Biological Process | GO:1903597 | negative regulation of gap junction assembly | 36 | |
| Biological Process | GO:1903609 | negative regulation of inward rectifier potassium channel activity | 36 | |
| Biological Process | GO:1900826 | negative regulation of membrane depolarization during cardiac muscle cell action potential | 34 | |
| Biological Process | GO:1905032 | negative regulation of membrane repolarization during cardiac muscle cell action potential | 0 | 36 |
| Biological Process | GO:1905025 | negative regulation of membrane repolarization during ventricular cardiac muscle cell action potential | 36 | |
| Biological Process | GO:1902309 | negative regulation of peptidyl-serine dephosphorylation | 102 | |
| Biological Process | GO:1902303 | negative regulation of potassium ion export | 28 | |
| Biological Process | GO:1903765 | negative regulation of potassium ion export across plasma membrane | 36 | |
| Biological Process | GO:1903287 | negative regulation of potassium ion import | 0 | 0 |
| Biological Process | GO:1903783 | negative regulation of sodium ion import across plasma membrane | 0 | 0 |
| Biological Process | GO:1902306 | negative regulation of sodium ion transmembrane transport | 95 | |
| Biological Process | GO:0098736 | negative regulation of the force of heart contraction | 31 | |
| Biological Process | GO:1903946 | negative regulation of ventricular cardiac muscle cell action potential | 0 | 36 |
| Biological Process | GO:1903761 | negative regulation of voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization | 0 | 0 |
| Biological Process | GO:0086097 | phospholipase C-activating angiotensin-activated signaling pathway | 44 | |
| Biological Process | GO:0086099 | phospholipase C-activating angiotensin-activated signaling pathway involved in heart process | 0 | 0 |
| Biological Process | GO:0003301 | physiological cardiac muscle hypertrophy | 13 | |
| Biological Process | GO:1901206 | positive regulation of adrenergic receptor signaling pathway involved in heart process | 29 | |
| Biological Process | GO:1903247 | positive regulation of adrenergic receptor signaling pathway involved in positive regulation of heart rate | 0 | 0 |
| Biological Process | GO:1903281 | positive regulation of calcium:sodium antiporter activity | 75 | |
| Biological Process | GO:1903598 | positive regulation of gap junction assembly | 114 | |
| Biological Process | GO:0086095 | positive regulation of IKACH channel activity by G-protein coupled acetylcholine receptor signaling pathway involved in negative regulation of heart rate | 0 | 0 |
| Biological Process | GO:1900827 | positive regulation of membrane depolarization during cardiac muscle cell action potential | 3 | |
| Biological Process | GO:1905033 | positive regulation of membrane repolarization during cardiac muscle cell action potential | 0 | 40 |
| Biological Process | GO:1905026 | positive regulation of membrane repolarization during ventricular cardiac muscle cell action potential | 0 | 37 |
| Biological Process | GO:1902310 | positive regulation of peptidyl-serine dephosphorylation | 85 | |
| Biological Process | GO:1902304 | positive regulation of potassium ion export | 6 | |
| Biological Process | GO:1903766 | positive regulation of potassium ion export across plasma membrane | 34 | |
| Biological Process | GO:1903288 | positive regulation of potassium ion import | 138 | |
| Biological Process | GO:0086094 | positive regulation of ryanodine-sensitive calcium-release channel activity by adrenergic receptor signaling pathway involved in positive regulation of cardiac muscle contraction | 0 | 0 |
| Biological Process | GO:1903784 | positive regulation of sodium ion import across plasma membrane | 0 | 0 |
| Biological Process | GO:1902307 | positive regulation of sodium ion transmembrane transport | 6 | |
| Biological Process | GO:0098735 | positive regulation of the force of heart contraction | 161 | |
| Biological Process | GO:1903947 | positive regulation of ventricular cardiac muscle cell action potential | 0 | 37 |
| Biological Process | GO:1903762 | positive regulation of voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization | 37 | |
| Biological Process | GO:0003165 | Purkinje myocyte development | 34 | |
| Biological Process | GO:0003168 | Purkinje myocyte differentiation | 33 | |
| Biological Process | GO:1901204 | regulation of adrenergic receptor signaling pathway involved in heart process | 0 | 61 |
| Biological Process | GO:1903245 | regulation of adrenergic receptor signaling pathway involved in positive regulation of heart rate | 0 | 0 |
| Biological Process | GO:1903279 | regulation of calcium:sodium antiporter activity | 0 | 81 |
| Biological Process | GO:0098901 | regulation of cardiac muscle cell action potential | 20 | |
| Biological Process | GO:0098909 | regulation of cardiac muscle cell action potential involved in regulation of contraction | 163 | |
| Biological Process | GO:0086004 | regulation of cardiac muscle cell contraction | 262 | |
| Biological Process | GO:0086036 | regulation of cardiac muscle cell membrane potential | 200 | |
| Biological Process | GO:1903596 | regulation of gap junction assembly | 0 | 150 |
| Biological Process | GO:1900825 | regulation of membrane depolarization during cardiac muscle cell action potential | 133 | |
| Biological Process | GO:0060306 | regulation of membrane repolarization | 341 | |
| Biological Process | GO:1905031 | regulation of membrane repolarization during cardiac muscle cell action potential | 3 | |
| Biological Process | GO:1905024 | regulation of membrane repolarization during ventricular cardiac muscle cell action potential | 0 | 104 |
| Biological Process | GO:1902308 | regulation of peptidyl-serine dephosphorylation | 0 | 187 |
| Biological Process | GO:1902302 | regulation of potassium ion export | 0 | 135 |
| Biological Process | GO:1903764 | regulation of potassium ion export across plasma membrane | 31 | |
| Biological Process | GO:1903286 | regulation of potassium ion import | 31 | |
| Biological Process | GO:0014861 | regulation of skeletal muscle contraction via regulation of action potential | 43 | |
| Biological Process | GO:1903782 | regulation of sodium ion import across plasma membrane | 0 | 0 |
| Biological Process | GO:1902305 | regulation of sodium ion transmembrane transport | 167 | |
| Biological Process | GO:0098911 | regulation of ventricular cardiac muscle cell action potential | 337 | |
| Biological Process | GO:0060307 | regulation of ventricular cardiac muscle cell membrane repolarization | 461 | |
| Biological Process | GO:1903760 | regulation of voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization | 31 | |
| Biological Process | GO:1903416 | response to glycoside | 78 | |
| Biological Process | GO:0086005 | ventricular cardiac muscle cell action potential | 392 | |
| Biological Process | GO:0099625 | ventricular cardiac muscle cell membrane repolarization | 34 | |
| Molecular Function | GO:0086039 | calcium-transporting ATPase activity involved in regulation of cardiac muscle cell membrane potential | 10 | |
| Molecular Function | GO:0086038 | calcium:sodium antiporter activity involved in regulation of cardiac muscle cell membrane potential | 42 | |

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|---------------------------------|------------|--|---------------|---|
| <i>Molecular Function</i> | GO:0086081 | cell adhesive protein binding involved in atrial cardiac muscle cell-AV node cell communication | 0 | 0 |
| <i>Molecular Function</i> | GO:0086084 | cell adhesive protein binding involved in Purkinje myocyte-ventricular cardiac muscle cell communication | 0 | 0 |
| <i>Molecular Function</i> | GO:0086085 | cell adhesive protein binding involved in SA cardiac muscle cell-atrial cardiac muscle cell communication | 0 | 0 |
| <i>Molecular Function</i> | GO:1903763 | gap junction channel activity involved in cell communication by electrical coupling | 150 | |
| <i>Molecular Function</i> | GO:0086080 | protein binding involved in heterotypic cell-cell adhesion | 123 | |
| <i>Molecular Function</i> | GO:0086037 | sodium:potassium-exchanging ATPase activity involved in regulation of cardiac muscle cell membrane potential | 26 | |
| <i>Molecular Function</i> | GO:0086040 | sodium:proton antiporter activity involved in regulation of cardiac muscle cell membrane potential | 1 | |
| <i>Molecular Function</i> | GO:0097364 | stretch-activated, cation-selective, calcium channel activity involved in regulation of action potential | 0 | 0 |
| <i>Molecular Function</i> | GO:0097365 | stretch-activated, cation-selective, calcium channel activity involved in regulation of cardiac muscle cell action potential | 0 | 0 |
| <i>Molecular Function</i> | GO:0086007 | voltage-gated calcium channel activity involved in cardiac muscle cell action potential | 76 | |
| <i>Molecular Function</i> | GO:0086008 | voltage-gated potassium channel activity involved in cardiac muscle cell action potential repolarization | 89 | |
| <i>Molecular Function</i> | GO:1902282 | voltage-gated potassium channel activity involved in ventricular cardiac muscle cell action potential repolarization | 157 | |
| <i>Molecular Function</i> | GO:0086006 | voltage-gated sodium channel activity involved in cardiac muscle cell action potential | 225 | |
| Total direct annotations | | | 16,935 | |

Supplemental Table Vi. hA-VCMs protein list. The 200 most abundant transcripts in hA-VCMs, as compared to hESCs transcripts, as listed by Poon et al.¹⁹

| HGNC Symbol | EntrezGene ID | UniProtKB ID | comments |
|-------------|---------------|--------------|---|
| MYL2 | 4633 | P10916 | |
| MYH7 | 4625 | P12883 | |
| MYL3 | 4634 | P08590 | |
| ACTC1 | 70 | P68032 | |
| HS.508682 | | | Not available |
| CRYAB | 1410 | P02511 | |
| ACTA1 | 58 | P68133 | |
| CKM | 1158 | P06732 | |
| ATP5B | 506 | P06576 | |
| COX4I1 | 1327 | P13073 | |
| FARSB | 10056 | Q9NSD9 | |
| TNNC1 | 7134 | P63316 | |
| RPS16 | 6217 | P62249 | |
| HSPB7 | 27129 | Q9UBY9 | |
| RN7SL1 | 6029 | | RNA, 7SL, cytoplasmic 1 |
| MYOM1 | 8736 | P52179 | |
| HSPB1 | 3315 | P04792 | |
| MYBPC3 | 4607 | Q14896 | |
| TMSB4XP8 | 7117 | | thymosin beta 4, X-linked pseudogene 8 |
| MYL12A | 10627 | P19105 | |
| COX7C | 1350 | P15954 | |
| SLC25A4 | 291 | P12235 | |
| RPLP2 | 6181 | P05387 | |
| DES | 1674 | P17661 | |
| NDUFA1 | 4694 | O15239 | |
| EEF1A2 | 1917 | Q05639 | |
| ATP5A1 | 498 | P25705 | |
| OAZ1 | 4946 | P54368 | |
| COX7A1 | 1346 | P24310 | |
| MDH1 | 4190 | P40925 | |
| TPT1 | 7178 | P13693 | |
| NDUFA4 | 4697 | O00483 | |
| ATP5E | 514 | P56381 | |
| RPS25 | 6230 | P62851 | |
| CD81 | 975 | P60033 | |
| MYH6 | 4624 | P13533 | |
| COX5B | 1329 | P10606 | |
| TCAP | 8557 | O15273 | |
| MYOM2 | 9172 | P54296 | |
| RPS27 | 6232 | P42677 | |
| UQCRQ | 27089 | O14949 | |
| TNNI3 | 7137 | P19429 | |
| MDH2 | 4191 | P40926 | |
| CHCHD10 | 400916 | Q8WYQ3 | |
| COX5A | 9377 | P20674 | |
| CASQ2 | 845 | O14958 | |
| UBC | 7316 | P0CG48 | |
| LAIR1 | 3903 | Q6GTX8 | |
| CKMT2 | 1160 | P17540 | |
| MB | 4151 | P02144 | |
| TPM1 | 7168 | P09493 | |
| RPL38 | 6169 | P63173 | |
| SLC7A5P2 | 387254 | | solute carrier family 7 member 5 pseudogene 2 |
| TOMM7 | 54543 | Q9P0U1 | |
| FLNC | 2318 | Q14315 | |
| PSAP | 5660 | P07602 | |
| TNNT2 | 7139 | P45379 | |
| RPS10 | 6204 | P46783 | |
| CDH2 | 1000 | P19022 | |
| F2R | 2149 | P25116 | |
| C19ORF31 | 404664 | | HGNC listed as a cloning artifact |
| RACK1 | 10399 | P63244 | |
| PTGDS | 5730 | P41222 | |
| HRC | 3270 | P23327 | |
| EEF2 | 1938 | P13639 | |
| RPS19 | 6223 | P39019 | |
| YBX3 | 8531 | P16989 | |
| RPL11 | 6135 | P62913 | |

| | | | |
|---------|--------|--------|-----------------------------|
| COX6C | 1345 | P09669 | |
| RPL18A | 6142 | Q02543 | |
| NDUFB8 | 4714 | O95169 | |
| GPX3 | 2878 | P22352 | |
| PAM | 5066 | P19021 | |
| MFGE8 | 4240 | Q08431 | |
| ATP5H | 10476 | O75947 | |
| EEF1A1 | 1915 | P68104 | |
| IL18 | 3606 | Q14116 | |
| NDUFAB1 | 4706 | O14561 | |
| ECH1 | 1891 | Q13011 | |
| CMYA5 | 202333 | Q8N3K9 | |
| GAPDH | 2597 | P04406 | |
| RPS29 | 6235 | P62273 | |
| FTL | 2512 | P02792 | |
| SRL | 6345 | Q86TD4 | |
| SYNPO2L | 79933 | Q9H987 | |
| APOD | 347 | P05090 | |
| MYL7 | 58498 | Q01449 | |
| COX7A2 | 1347 | P14406 | |
| RPS27A | 6233 | P62979 | |
| ORC6 | 23594 | Q9Y5N6 | |
| FHL2 | 2274 | Q14192 | |
| RPS20 | 6224 | P60866 | |
| RPLP1 | 6176 | P05386 | |
| UBB | 7314 | P0CG47 | |
| COX8A | 1351 | P10176 | |
| TUBA1B | 10376 | P68363 | |
| CST3 | 1471 | P01034 | |
| RPL41 | 6171 | P62945 | |
| NAG18 | 57051 | | withdrawn by NCBI |
| EIF4A2 | 1974 | Q14240 | |
| HBB | 3043 | P68871 | |
| HSPA1A | 3303 | P0DMV8 | |
| ROCK2 | 9475 | O75116 | |
| RPL19 | 6143 | P84098 | |
| MSH3 | 4437 | P20585 | |
| NPPB | 4879 | P16860 | |
| ZNF486 | 90649 | Q96H40 | |
| HBA1 | 3039 | P69905 | |
| UQCRFS1 | 7386 | P47985 | |
| CCNI | 10983 | Q14094 | |
| RPL24 | 6152 | P83731 | |
| TUBA3FP | 113691 | | tubulin alpha 3f pseudogene |
| RPL27 | 6155 | P61353 | |
| ATP2A2 | 488 | P16615 | |
| HSPB3 | 8988 | Q12988 | |
| LILRB3 | 11025 | Q6PI73 | |
| RPS11 | 6205 | P62280 | |
| NDUFS5 | 4725 | O43920 | |
| SOD1 | 6647 | P00441 | |
| CHCHD2 | 51142 | Q9Y6H1 | |
| JUND | 3727 | P17535 | |
| ENO3 | 2027 | P13929 | |
| CYC1 | 1537 | P08574 | |
| H3F3A | 3020 | P84243 | |
| RPS2 | 6187 | P15880 | |
| NDUFS8 | 4728 | O00217 | |
| PDK4 | 5166 | Q16654 | |
| ATP5O | 539 | P48047 | |
| RPL35A | 6165 | P18077 | |
| LDHB | 3945 | P07195 | |
| RPS3A | 6189 | P61247 | |
| NUCB1 | 4924 | Q02818 | |
| IDH2 | 3418 | P48735 | |
| EIF3E | 3646 | P60228 | |
| RPS6 | 6194 | P62753 | |
| GOT2 | 2806 | P00505 | |
| NDUFA3 | 4696 | O95167 | |

| | | |
|----------|--------|--------|
| RHOQ | 23433 | P17081 |
| VDAC3 | 7419 | Q9Y277 |
| VWF | 7450 | P04275 |
| COX6B1 | 1340 | P14854 |
| MGST3 | 4259 | O14880 |
| RPL18 | 6141 | Q07020 |
| RBPMS2 | 348093 | Q6ZRY4 |
| HSPA1B | 3304 | P0DMV9 |
| GOT1 | 2805 | P17174 |
| RPS12 | 6206 | P25398 |
| SRP14 | 6727 | P37108 |
| RPL6 | 6128 | Q02878 |
| RPL39 | 6170 | P62891 |
| IFITM3 | 10410 | Q01628 |
| NDUFB10 | 4716 | O96000 |
| RPS17 | 6218 | P08708 |
| NDUFA8 | 4702 | P51970 |
| TMSB10 | 9168 | P63313 |
| ATP5J | 522 | P18859 |
| AURKAIP1 | 54998 | Q9NWT8 |
| ATP5C1 | 509 | P36542 |
| GHITM | 27069 | Q9H3K2 |
| UBA52 | 7311 | P62987 |
| SPARCL1 | 8404 | Q14515 |
| RPL35 | 11224 | P42766 |
| RPS14 | 6208 | P62263 |
| DUSP3 | 1845 | P51452 |
| LGALS1 | 3956 | P09382 |
| NACA | 4666 | Q13765 |
| RPL27A | 6157 | P46776 |
| NMRK2 | 27231 | Q9NPI5 |
| FAU | 2197 | P35544 |
| NPPA | 4878 | P01160 |
| NCOA4 | 8031 | Q13772 |
| RPL3 | 6122 | P39023 |
| PCLAF | 9768 | Q15004 |
| GABPB2 | 126626 | Q8TAK5 |
| MGP | 4256 | P08493 |
| NDUFB5 | 4711 | O43674 |
| PDE4C | 5143 | Q08493 |
| MT1X | 4501 | P80297 |
| ALKBH5 | 54890 | Q6P6C2 |
| RPL10A | 4736 | P62906 |
| AKR1D1 | 6718 | P51857 |
| RPS28 | 6234 | P62857 |
| HSPB6 | 126393 | O14558 |
| GPD1L | 23171 | Q8N335 |
| PDCD7 | 10081 | Q8N8D1 |
| WBP2 | 23558 | Q969T9 |
| RPL5 | 6125 | P46777 |
| ACAT1 | 38 | P24752 |
| NDUFB2 | 4708 | O95178 |
| COX7B | 1349 | P24311 |
| CCR6 | 1235 | P51684 |
| MYL6 | 4637 | P60660 |
| BSG | 682 | P35613 |
| DECR1 | 1666 | Q16698 |
| TIMP1 | 7076 | P01033 |
| MSRB2 | 22921 | Q9Y3D2 |
| CALM2 | 805 | P62158 |
| TSPAN9 | 10867 | O75954 |
| RPS18 | 6222 | P62269 |
| SLC25A3 | 5250 | Q00325 |

Supplemental Table VII. hA-VCMs BinGO 2016. BinGO analysis of the adult ventricular cardiomyocyte (hA-VCMs) data¹⁹ using the 2016 GO annotation dataset. **x** is the number of IDs in both the submitted list and associated with the GO term, **n** indicates the number of protein IDs associated with the GO term, **X** is the number of protein IDs submitted for analysis, **N** is the number of protein IDs used as the background set.

| GO-ID | GO term | p-value | corr p-value | x | n | X | N | Proteins submitted in analysis that are associated with the GO term |
|------------|--|----------|--------------|----|------|-----|-------|---|
| GO:000027 | ribosomal large subunit assembly | 2.49E-09 | 3.37E-08 | 6 | 24 | 190 | 35980 | Q02878 P63173 P39023 P83731 P62913 P46777 |
| GO:000028 | ribosomal small subunit assembly | 5.13E-10 | 7.26E-09 | 6 | 19 | 190 | 35980 | P42677 P63173 P08708 P62263 P46783 P39019 |
| GO:000075 | cell cycle checkpoint | 1.57E-02 | 4.33E-02 | 5 | 275 | 190 | 35980 | POCCG47 P62987 P83731 P62979 POCCG48 |
| GO:000077 | DNA damage checkpoint | 1.28E-02 | 3.77E-02 | 4 | 170 | 190 | 35980 | POCCG47 P62987 P62979 POCCG48 |
| GO:000082 | G1/S transition of mitotic cell cycle | 2.50E-03 | 1.02E-02 | 5 | 176 | 190 | 35980 | POCCG47 P62987 Q9Y5N6 P62979 POCCG48 |
| GO:000086 | G2/M transition of mitotic cell cycle | 6.95E-03 | 2.33E-02 | 4 | 142 | 190 | 35980 | POCCG47 P62987 P62979 POCCG48 |
| GO:000165 | MAPK cascade | 1.39E-03 | 6.35E-03 | 8 | 401 | 190 | 35980 | POCCG47 P51452 Q14116 P62987 P62979 P02511 P62158 POCCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P6 1247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P629 06 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:000184 | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 6.70E-55 | 3.32E-57 | 37 | 125 | 190 | 35980 | POCCG47 P62987 P62979 POCCG48 |
| GO:000186 | activation of MAPKK activity | 1.96E-03 | 8.37E-03 | 6 | 244 | 190 | 35980 | POCCG47 P62987 P62979 P62158 P25116 POCCG48 |
| GO:000187 | activation of MAPK activity | 1.32E-04 | 8.21E-04 | 6 | 146 | 190 | 35980 | POCCG47 P60033 P62987 P62979 P00441 POCCG48 |
| GO:000271 | polysaccharide biosynthetic process | 1.13E-04 | 7.13E-04 | 4 | 47 | 190 | 35980 | POCCG47 P62987 P62979 POCCG48 |
| GO:000302 | response to reactive oxygen species | 1.97E-07 | 2.07E-06 | 10 | 210 | 190 | 35980 | P02144 P05090 P13639 P68871 P09493 P22352 P02511 P69905 P00441 P0 1034 |
| GO:000422 | mitophagy | 6.34E-06 | 5.43E-05 | 8 | 183 | 190 | 35980 | POCCG47 P52179 Q9P0U1 P40925 P62987 P62979 P10176 POCCG48 |
| GO:000423 | macromitophagy | 1.68E-06 | 1.57E-05 | 8 | 153 | 190 | 35980 | POCCG47 P52179 Q9P0U1 P40925 P62987 P62979 P10176 POCCG48 |
| GO:000462 | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 3.45E-04 | 1.91E-03 | 3 | 26 | 190 | 35980 | P62263 P62249 P39019 |
| GO:000715 | nucleotide-excision repair, DNA damage recognition | 5.12E-06 | 4.49E-05 | 4 | 22 | 190 | 35980 | POCCG47 P62987 P62979 POCCG48 |
| GO:000724 | double-strand break repair via homologous recombination | 8.20E-03 | 2.68E-02 | 4 | 149 | 190 | 35980 | POCCG47 P62987 P62979 POCCG48 |
| GO:000725 | recombinational repair | 8.39E-03 | 2.72E-02 | 4 | 150 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P6 1247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P629 06 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P6 62249 |
| GO:000956 | nuclear-transcribed mRNA catabolic process | 3.50E-48 | 6.12E-46 | 38 | 200 | 190 | 35980 | P63244 P63173 P08493 Q14192 P62280 P17535 P06576 P63244 Q14192 P62280 P17535 P06576 POCCG47 P02144 P01160 P19021 P62987 P62979 P02511 Q6P6C2 POCCG48 P01034 P07602 P01033 Q14116 P09382 P68871 P04275 P62158 P04792 P19105 P2 5116 P00441 P01034 POCCG47 Q14116 P05090 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 POCCG47 P05090 P62987 P62979 POCCG48 POCCG47 Q14116 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P6 1247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P629 06 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 P07602 POCCG47 P51452 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P23327 P62979 P62158 P04792 P25116 Q8N335 P00441 P07602 POCCG47 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P62979 P62158 P25116 P00441 |
| GO:0001503 | ossification | 5.25E-04 | 2.73E-03 | 7 | 263 | 190 | 35980 | P63244 P63173 P08493 Q14192 P62280 P17535 P06576 |
| GO:0001649 | osteoblast differentiation | 6.10E-04 | 3.10E-03 | 5 | 128 | 190 | 35980 | P63244 Q14192 P62280 P17535 P06576 |
| GO:0001666 | response to hypoxia | 5.41E-06 | 4.72E-05 | 10 | 303 | 190 | 35980 | POCCG47 P02144 P01160 P19021 P62987 P62979 P02511 Q6P6C2 POCCG48 P01034 P07602 P01033 Q14116 P09382 P68871 P04275 P62158 P04792 P19105 P2 5116 P00441 P01034 POCCG47 Q14116 P05090 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 POCCG47 P05090 P62987 P62979 POCCG48 POCCG47 Q14116 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P6 1247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P629 06 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 P07602 POCCG47 P51452 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P23327 P62979 P62158 P04792 P25116 Q8N335 P00441 P07602 POCCG47 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P62979 P62158 P25116 P00441 |
| GO:0001817 | regulation of cytokine production | 4.56E-04 | 2.43E-03 | 11 | 614 | 190 | 35980 | POCCG47 P63244 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 POCCG47 P05090 P62987 P62979 POCCG48 POCCG47 Q14116 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P6 1247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P629 06 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 P07602 POCCG47 P51452 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P23327 P62979 P62158 P04792 P25116 Q8N335 P00441 P07602 POCCG47 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P62979 P62158 P25116 P00441 |
| GO:0001818 | negative regulation of cytokine production | 7.43E-03 | 2.45E-02 | 5 | 228 | 190 | 35980 | POCCG47 P05090 P62987 P62979 POCCG48 |
| GO:0001819 | positive regulation of cytokine production | 5.02E-05 | 3.54E-04 | 10 | 393 | 190 | 35980 | POCCG47 Q14116 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P6 1247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P629 06 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 P07602 POCCG47 P51452 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P23327 P62979 P62158 P04792 P25116 Q8N335 P00441 P07602 POCCG47 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P62979 P62158 P25116 P00441 |
| GO:0001887 | selenium compound metabolic process | 2.79E-54 | 8.29E-52 | 36 | 116 | 190 | 35980 | P07602 P01033 Q14116 P09382 P68871 P04275 P62158 P04792 P19105 P2 5116 P00441 P01034 POCCG47 Q14116 P05090 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 POCCG47 P05090 P62987 P62979 POCCG48 POCCG47 Q14116 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P6 1247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P629 06 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 P07602 POCCG47 P51452 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P23327 P62979 P62158 P04792 P25116 Q8N335 P00441 P07602 POCCG47 Q14116 O75116 P19022 POCCG48 P63244 P60033 P62987 P62979 P62158 P25116 P00441 |
| GO:0001932 | regulation of protein phosphorylation | 2.73E-03 | 1.09E-02 | 17 | 1505 | 190 | 35980 | POCCG47 P63244 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P10916 P08590 P16615 P13533 P12883 Q14896 Q14958 P01160 P09493 P16615 P23327 P62158 P13533 Q8N335 P 12883 POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0001934 | positive regulation of protein phosphorylation | 4.24E-03 | 1.61E-02 | 13 | 1057 | 190 | 35980 | POCCG47 P63244 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P10916 P08590 P16615 P13533 P12883 Q14896 Q14958 P01160 P09493 P16615 P23327 P62158 P13533 Q8N335 P 12883 POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0001959 | regulation of cytokine-mediated signaling pathway | 1.12E-05 | 9.10E-05 | 7 | 142 | 190 | 35980 | POCCG47 P63244 P0DMV8 P0DMV9 P62987 P62979 P04792 P25116 P00441 POCCG48 P10916 P08590 P16615 P13533 P12883 Q14896 Q14958 P01160 P09493 P16615 P23327 P62158 P13533 Q8N335 P 12883 POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002026 | regulation of the force of heart contraction | 5.92E-07 | 5.93E-06 | 5 | 31 | 190 | 35980 | Q14896 Q14958 P01160 P09493 P16615 P23327 P62158 P13533 Q8N335 P 12883 POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002027 | regulation of heart rate | 5.27E-11 | 7.84E-10 | 10 | 90 | 190 | 35980 | Q14896 Q14958 P01160 P09493 P16615 P23327 P62158 P13533 Q8N335 P 12883 POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002218 | activation of innate immune response | 2.58E-03 | 1.05E-02 | 6 | 258 | 190 | 35980 | POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002220 | innate immune response activating cell surface receptor | 5.09E-04 | 2.65E-03 | 5 | 123 | 190 | 35980 | POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002221 | pattern recognition receptor signaling pathway | 1.48E-03 | 6.64E-03 | 5 | 156 | 190 | 35980 | POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002223 | stimulatory C-type lectin receptor signaling pathway | 4.54E-04 | 2.43E-03 | 5 | 120 | 190 | 35980 | POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002224 | toil-like receptor signaling pathway | 8.29E-04 | 4.08E-03 | 5 | 137 | 190 | 35980 | POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 P52179 P40925 P62987 Q16654 Q6P6C2 P10176 P02144 P08708 P62263 P00441 P39019 |
| GO:0002230 | positive regulation of defense response to virus by host | 3.67E-05 | 2.69E-04 | 6 | 116 | 190 | 35980 | POCCG47 P51452 P62987 P62979 P62158 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 POCCG48 POCCG47 P62987 P62979 P62158 POCCG48 POCCG47 P51452 P62987 P62979 P62158 POCCG48 |

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|------------|---|----------|----------|-----|------|-----|-------|---|
| GO:0006753 | nucleoside phosphate metabolic process | 6.37E-24 | 2.06E-22 | 37 | 809 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 P01160 O43674 P40926 P40925 O00483 P36542 P10176 O95178 O96000 P16860 P13073 P25705 P18859 Q9NP15 P07195 P56381 Q8WYQ3 O15239 P20674 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 Q43920 P13533 O95167 P12883 P17081 Q8N335 P06576 |
| GO:0006754 | ATP biosynthetic process | 5.96E-10 | 8.36E-09 | 8 | 56 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P0CCG47 O75947 P06732 P0DMV8 P0DMV9 P01160 O43674 P40926 P40925 P36542 P0CCG48 O96000 P16860 P13073 P07195 P62158 Q8WYQ3 O15239 P20674 O95169 P48047 P04406 O14561 Q43920 O95167 P02511 P17081 Q8N335 P13929 O00483 P10176 O95178 P25705 P18859 Q9NP15 Q16654 P62979 P56381 P51452 O00217 Q14116 Q08493 P51970 O75116 P13533 P12883 P17540 P62987 P25116 P06576 |
| GO:0006793 | phosphorus metabolic process | 6.88E-09 | 8.78E-08 | 50 | 4056 | 190 | 35980 | P0CCG47 O75947 P06732 P0DMV8 P0DMV9 P01160 O43674 P40926 P40925 P36542 P0CCG48 O96000 P16860 P13073 P07195 P62158 Q8WYQ3 O15239 P20674 O95169 P48047 P04406 O14561 Q43920 O95167 P02511 P17081 Q8N335 P13929 O00483 P10176 O95178 P25705 P18859 Q9NP15 Q16654 P62979 P56381 P51452 O00217 Q14116 Q08493 P51970 O75116 P13533 P12883 P17540 P62987 P25116 P06576 |
| GO:0006796 | phosphate-containing compound metabolic process | 3.67E-09 | 4.78E-08 | 50 | 3980 | 190 | 35980 | P0CCG47 O75947 P06732 P0DMV8 P0DMV9 P01160 O43674 P40926 P40925 P36542 P0CCG48 O96000 P16860 P13073 P07195 P62158 Q8WYQ3 O15239 P20674 O95169 P48047 P04406 O14561 Q43920 O95167 P02511 P17081 Q8N335 P13929 O00483 P10176 O95178 P25705 P18859 Q9NP15 Q16654 P62979 P56381 P51452 O00217 Q14116 Q08493 P51970 O75116 P13533 P12883 P17540 P62987 P25116 P06576 |
| GO:0006807 | nitrogen compound metabolic process | 5.01E-27 | 2.26E-25 | 115 | 8603 | 190 | 35980 | O75947 O43674 O96000 P16860 P13073 P07195 P46783 P83731 P62913 P62753 P24752 O15239 P20674 Q13765 O95169 P13639 P48047 P04406 O14561 Q8Y5N6 P16989 Q8Y6H1 O95167 P84099 P63173 P68104 P46777 Q13772 P06866 P46776 P62289 P62249 Q8N335 P07602 P22538 P10176 O95178 P12235 P62891 P25705 P18859 O14192 P56381 P00441 P54368 O00217 Q08493 P08708 P18077 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P1588 O1P17540 Q02543 Q9NWT8 P62263 Q12420 P62945 P62289 P0CCG47 P06732 Q8N5D9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 Q8TAK5 P36542 P0CCG48 P39019 P00505 P39023 P62273 P62158 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O14880 P19021 P37108 Q43920 O05639 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P17174 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 Q00325 P62987 P20585 P06576 |
| GO:0006810 | transport | 1.36E-18 | 3.12E-17 | 90 | 6916 | 190 | 35980 | P0CCG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CCG48 P39019 P16860 P00509 P13073 P00505 O14949 P39023 P62273 P46783 P83731 P62913 P24310 P69905 P62158 P24311 P62753 P20674 Q13765 Q07020 P01033 P10606 P48047 Q9Y277 P19021 P14406 P37108 Q9Y6H1 Q08431 P84098 O14958 P63173 P61353 P47985 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P2398 P09669 P68363 O00483 P14854 P10176 P12235 P13693 P62891 P42766 Q02878 P25705 P18859 P60033 P68871 P61247 P62857 P62979 P56381 P62851 P00441 P54368 P02144 Q9P0U1 P08708 P62906 P18077 P15954 Q6P6C2 P42677 P41222 P15880 Q02543 Q00325 P62263 P62987 P62945 P04275 P62289 P25116 P06576 |
| GO:0006811 | ion transport | 1.47E-07 | 1.56E-06 | 34 | 2414 | 190 | 35980 | P0CCG47 O75947 P02792 P09669 O00483 P14854 P16615 P36542 P10176 P0CCG48 P13693 P13073 P25705 P00505 P18859 O14949 P68871 P62979 P56381 P24310 P69905 P24311 P20674 P10606 P48047 Q9Y277 P14406 P15954 O14958 Q00325 P62987 P47985 P25116 P06576 |
| GO:0006812 | cation transport | 1.49E-06 | 1.41E-05 | 24 | 1503 | 190 | 35980 | O75947 P10606 P02792 P09669 P48047 P14406 O00483 P14854 P16615 P36542 P15954 P10176 P13693 P13073 P25705 P18859 O14949 P47985 P56381 P24310 P24311 P25116 P06576 P20674 |
| GO:0006818 | hydrogen transport | 1.88E-16 | 3.89E-15 | 20 | 298 | 190 | 35980 | O75947 P10606 P09669 P48047 P14406 O00483 P14854 P36542 P15954 P10176 P13073 P25705 P18859 O14949 P47985 P56381 P24310 P24311 P06576 P20674 |
| GO:0006839 | mitochondrial transport | 2.45E-07 | 2.54E-06 | 10 | 215 | 190 | 35980 | O75947 P0DMV8 P25705 Q9P0U1 P48047 P18859 P36542 Q9Y6H1 P56381 P06576 |
| GO:0006873 | cellular ion homeostasis | 5.79E-04 | 2.96E-03 | 10 | 533 | 190 | 35980 | P13693 P02792 P51684 O14958 P19429 P16615 P23327 P25116 P00441 P06576 |
| GO:0006874 | cellular calcium ion homeostasis | 1.67E-03 | 7.33E-03 | 7 | 321 | 190 | 35980 | P13693 P51684 O14958 P19429 P16615 P23327 P25116 P00441 P25398 P62280 P35613 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q9P0U1 P08708 P62906 P18077 P37108 Q9Y6H1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62289 P05387 P25116 P62249 |
| GO:0006875 | cellular metal ion homeostasis | 9.41E-04 | 4.57E-03 | 9 | 470 | 190 | 35980 | P0CCG47 P52179 Q9P0U1 P40925 P62987 Q16654 P62979 Q6P6C2 P10176 P0CCG48 |
| GO:0006886 | intracellular protein transport | 7.28E-23 | 2.14E-21 | 41 | 1120 | 190 | 35980 | P0CCG47 P04406 Q9H3K2 P68032 P12235 P0CCG48 Q8N8D1 P63244 P09382 P62987 P62979 P02511 P25116 P071034 |
| GO:0006914 | autophagy | 1.02E-04 | 6.52E-04 | 10 | 428 | 190 | 35980 | P0CCG47 P10916 P051684 P35613 P0CCG48 P39019 P19429 P09493 P83731 P62979 P62158 P45379 P00441 O15273 Q14896 O75116 P19022 P68133 P17661 P68032 P13533 P19105 P12883 P60660 P08590 P62987 P04792 Q8N335 P06576 P63316 |
| GO:0006915 | apoptotic process | 4.33E-03 | 1.64E-02 | 14 | 1185 | 190 | 35980 | P0CCG47 P04406 Q9H3K2 P68032 P12235 P0CCG48 Q8N8D1 P63244 P09382 P62987 P62979 P02511 P25116 P071034 |
| GO:0006928 | movement of cell or subcellular component | 6.42E-08 | 7.07E-07 | 30 | 1882 | 190 | 35980 | P0CCG47 P10916 P051684 P35613 P0CCG48 P39019 P19429 P09493 P83731 P62979 P62158 P45379 P00441 O15273 Q14896 O75116 P19022 P68133 P17661 P68032 P13533 P19105 P12883 P60660 P08590 P62987 P04792 Q8N335 P06576 P63316 |
| GO:0006935 | chemotaxis | 7.38E-03 | 2.44E-02 | 11 | 880 | 190 | 35980 | P0CCG47 P51684 P60660 O75116 P62987 P83731 P62979 P62158 P19105 P0CCG48 P39019 |
| GO:0006936 | muscle contraction | 9.35E-27 | 4.09E-25 | 27 | 264 | 190 | 35980 | P52179 P10916 P54296 Q01449 P19429 P09493 P23327 P62158 P45379 P02144 Q15273 Q14896 P13639 O75116 P68133 P17661 P68032 P13533 P19105 P12883 O14958 P17540 P60660 P08590 P02511 Q8N335 P63316 Q14896 P10916 P01160 P16615 P12883 O14958 P19429 P08590 P09493 P23327 P62158 P45379 P25116 O14558 P00441 P63316 |
| GO:0006937 | regulation of muscle contraction | 2.42E-15 | 4.80E-14 | 16 | 179 | 190 | 35980 | P19429 P25116 P00441 |
| GO:0006940 | regulation of smooth muscle contraction | 6.62E-03 | 2.24E-02 | 3 | 72 | 190 | 35980 | P02144 O15273 Q14896 P10916 P13639 P68032 P13533 P12883 O14958 P19429 P08590 P09493 P23327 P62158 P45379 P25116 O14558 P00441 P63316 |
| GO:0006941 | striated muscle contraction | 7.91E-18 | 1.74E-16 | 15 | 101 | 190 | 35980 | P19429 P08590 P09493 P45379 Q8N335 P63316 |
| GO:0006942 | regulation of striated muscle contraction | 6.20E-10 | 8.65E-09 | 9 | 83 | 190 | 35980 | Q14896 P10916 O14958 P01160 P08590 P16615 P23327 P62158 P12883 P0CCG47 P0DMV8 P0DMV9 Q12988 P01160 P40925 P16615 P35613 P0CCG48 P05090 P09493 P69905 P62158 P24752 P01034 Q13765 P01033 P13639 P04406 P19021 P16989 P19105 P09382 P02511 P07602 P52179 P13929 P51684 P10176 P62891 P84243 P60033 P68871 Q9Y6H1 Q16654 P22352 P62979 Q15004 Q01628 P00441 P51452 O00217 P02144 Q14116 O15273 Q9P0U1 Q6P6C2 Q9Y3D2 P62987 P04275 P04792 P25116 P20585 |
| GO:0006952 | defense response | 1.52E-02 | 4.33E-02 | 18 | 1947 | 190 | 35980 | P0CCG47 P51452 P52179 Q14116 P51684 P04406 P40925 Q6P6C2 P10176 P0CCG48 P62891 P62987 Q16654 P62979 P62158 Q01628 P25116 P01034 |
| GO:0006977 | DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest | 4.20E-04 | 2.27E-03 | 4 | 66 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0006979 | response to oxidative stress | 2.80E-08 | 3.27E-07 | 15 | 461 | 190 | 35980 | O00217 P02144 P0DMV8 P13639 P0DMV9 P16615 P05090 Q9Y3D2 P68871 P09493 P22352 P02511 P69905 P00441 P01034 |
| GO:0006996 | organelle organization | 3.70E-11 | 5.62E-10 | 58 | 4481 | 190 | 35980 | P0CCG47 P10916 P0DMV8 O43674 P40925 P16615 P0CCG48 P39019 O96000 P39023 P09493 P46783 P83731 P62913 P45379 Q8WYQ3 O15239 Q14896 O95169 P04406 O14561 Q43920 Q9Y6H1 P68032 O95167 O14958 P63173 P46777 P02511 P17081 P52179 P68363 P68871 P17661 P12235 Q02878 P84243 P62979 Q15004 P00441 O00217 O15273 P51970 Q9P0U1 P08708 O75116 P68133 P17661 P13533 P42677 Q9NWT8 Q9Y3D2 P62263 P62987 P63313 P25116 P20585 P06576 |
| GO:0007005 | mitochondrion organization | 2.58E-13 | 4.56E-12 | 24 | 679 | 190 | 35980 | P0CCG47 P52179 O00217 O95169 P0DMV8 P51970 Q9P0U1 O43674 O14561 P40925 Q43920 Q9Y6H1 O95167 P10176 O95178 P12235 P0CCG48 O96000 Q9NWT8 P62987 P62979 Q8WYQ3 P06576 O15239 |
| GO:0007009 | plasma membrane organization | 1.28E-02 | 3.76E-02 | 5 | 261 | 190 | 35980 | O75116 P19022 P16615 P35613 P00441 |
| GO:0007010 | cytoskeleton organization | 3.37E-04 | 1.88E-03 | 19 | 1479 | 190 | 35980 | O15273 Q14896 P10916 P04406 O75116 P68363 P68133 P17661 P68032 P13533 O14958 Q9Y3D2 P09493 P02511 Q15004 P63313 P17081 P45379 P0441 |
| GO:0007015 | actin filament organization | 1.28E-02 | 3.77E-02 | 6 | 362 | 190 | 35980 | O15273 Q9Y3D2 P68133 P68032 P63313 P45379 |
| GO:0007093 | mitotic cell cycle checkpoint | 3.47E-03 | 1.35E-02 | 5 | 190 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 7.18E-04 | 3.62E-03 | 16 | 1207 | 190 | 35980 | P0CCG47 P51452 P01160 P051684 P35613 P0CCG48 P19105 P0CCG48 P16860 P06660 P62987 Q16654 P62979 P62158 P17081 P04792 P62753 |
| GO:0007169 | transmembrane receptor protein tyrosine kinase signaling pathway | 1.33E-03 | 6.10E-03 | 13 | 923 | 190 | 35980 | P0CCG47 P51452 P01160 P051684 P35613 P0CCG48 P19105 P0CCG48 P16860 P06660 P62987 P51452 O75116 P17081 P04792 P62753 |
| GO:0007179 | transforming growth factor beta receptor signaling | 1.31E-02 | 3.82E-02 | 4 | 171 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0007219 | Notch signaling pathway | 3.61E-04 | 1.99E-03 | 6 | 176 | 190 | 35980 | P0CCG47 P17174 P62887 P62979 P0CCG48 P39019 |
| GO:0007220 | Notch receptor processing | 6.17E-06 | 5.31E-05 | 4 | 23 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 4.37E-05 | 3.12E-04 | 5 | 73 | 190 | 35980 | P0CCG47 O75116 P62887 P62979 P0CCG48 |
| GO:0007254 | JNK cascade | 1.30E-03 | 6.00E-03 | 4 | 89 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0007265 | Ras protein signal transduction | 1.18E-02 | 3.48E-02 | 6 | 355 | 190 | 35980 | P0CCG47 O75116 P62887 P62979 P62158 P0CCG48 |

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|------------|--|----------|----------|-----|------|-----|-------|---|
| GO:0007275 | multicellular organism development | 1.72E-07 | 1.82E-06 | 55 | 5183 | 190 | 35980 | P0CG47 P10916 P01160 P35613 P0CG48 P39019 P63244 P05090 O14949 P09493 P83731 P62158 P45379 P24311 P24752 P01034 Q13765 P01033 P14896 P13639 P19021 P19022 P16989 P68032 Q08431 P19105 P63173 P08493 P06060 P09382 P02511 Q13772 P07602 P14854 P19429 P25705 P84243 P18859 Q14192 P62979 P00441 P02144 Q14116 O15273 O75116 P68133 P13533 P12883 P08590 P62263 P62987 P04275 P20585 P06576 P63316 |
| GO:0007399 | nervous system development | 1.81E-02 | 4.91E-02 | 22 | 2582 | 190 | 35980 | P0CG47 P13639 O75116 P19021 P19022 P14854 P19105 P0CG48 P05090 P84243 P18859 O14949 P06060 P0382 P62987 P83731 P62979 P62158 P24311 P24752 P00441 P01034 |
| GO:0007409 | axonogenesis | 1.30E-02 | 3.82E-02 | 9 | 705 | 190 | 35980 | P0CG47 P06060 O75116 P62987 P83731 P62979 P62158 P19105 P0CG48 |
| GO:0007411 | central nervous system development | 5.11E-03 | 1.85E-02 | 12 | 957 | 190 | 35980 | P0CG47 P06060 O75116 P62987 P83731 P62979 P62158 P19105 P0CG48 |
| GO:0007420 | brain development | 6.06E-03 | 2.07E-02 | 10 | 737 | 190 | 35980 | P0CG47 P05090 P84243 P18859 O14949 P19022 P14854 P62158 P24752 P01034 |
| GO:0007507 | heart development | 3.22E-08 | 3.74E-07 | 16 | 537 | 190 | 35980 | Q13765 P02144 O15273 Q14896 P10916 P01160 P19021 P68032 P13533 P12883 P19429 Q14192 P08590 P09493 P45379 P63316 |
| GO:0007512 | adult heart development | 7.72E-05 | 5.20E-04 | 3 | 16 | 190 | 35980 | O15273 Q14896 P10916 P13639 P68133 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P02511 P45379 P63316 |
| GO:0007517 | muscle organ development | 8.22E-11 | 1.22E-09 | 15 | 300 | 190 | 35980 | O15273 Q14896 P10916 P13639 P68133 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P02511 P45379 P63316 |
| GO:0007519 | skeletal muscle tissue development | 5.83E-03 | 2.01E-02 | 4 | 135 | 190 | 35980 | P13639 P06060 P08590 P68133 |
| GO:0007565 | female pregnancy | 4.40E-03 | 1.68E-02 | 5 | 201 | 190 | 35980 | P01160 P19021 P35613 P00441 P01034 |
| GO:0007566 | embryo implantation | 1.86E-03 | 8.00E-03 | 3 | 46 | 190 | 35980 | P35613 P00441 P01034 |
| GO:0007568 | aging | 7.91E-04 | 3.92E-03 | 7 | 282 | 190 | 35980 | P01033 P13929 P05090 P13639 P02511 P17535 P00441 |
| GO:0007596 | blood coagulation | 3.41E-05 | 2.54E-04 | 12 | 541 | 190 | 35980 | P07602 P01033 P84243 P68871 P16615 P04275 P62158 P04792 P35613 P19105 P25116 P00441 |
| GO:0007599 | hemostasis | 3.73E-05 | 2.73E-04 | 12 | 546 | 190 | 35980 | P07602 P01033 P84243 P68871 P16615 P04275 P62158 P04792 P35613 P19105 P25116 P00441 |
| GO:0007623 | circadian rhythm | 2.24E-04 | 1.30E-03 | 6 | 161 | 190 | 35980 | P0CG47 P62987 P62979 P17535 P0CG48 P01034 |
| GO:0008015 | blood circulation | 5.95E-12 | 9.50E-11 | 18 | 401 | 190 | 35980 | O15273 Q14896 P10916 P01160 P68032 P13533 P12883 P16860 Q14958 P19429 P68871 P08590 P09493 P45379 P25116 Q8N335 P00441 P63316 |
| GO:0008016 | regulation of heart contraction | 2.90E-13 | 5.04E-12 | 16 | 243 | 190 | 35980 | Q14896 P10916 P01160 P16615 P17661 P13533 P12883 O14958 P19429 Q9UB9Y P08590 P09493 P23327 P62158 P45379 Q8N335 |
| GO:0008104 | protein localization | 2.01E-14 | 3.83E-13 | 46 | 2432 | 190 | 35980 | P25398 Q969T9 P62280 P35613 P39019 P62891 P42766 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 Q9P0U1 P08708 O75116 P62906 P19022 P18077 P37108 Q9Y6H1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P762945 P46777 P05386 P60866 P46776 P62269 P05387 P25116 P62249 |
| GO:0008152 | metabolic process | 1.65E-10 | 2.39E-09 | 148 | 2093 | 190 | 35980 | O75947 Q43674 P16615 O96000 P16860 P13073 O14949 P07195 P46783 P83731 P62913 P62753 P24752 O15239 P20674 Q13765 O95169 P13639 P48047 P04406 O14561 P08297 Q9Y5N6 P16989 Q9Y6H1 O95167 Q08431 P84098 P63173 P68104 P08574 P47985 P46777 Q13772 P60866 P46776 P6022 P62249 Q13011 Q8N335 P07602 P52179 P25398 P68363 P01176 O95178 P12235 P62891 P25705 P18859 Q14192 P68871 Q16654 P65381 P00441 P54368 Q00217 Q14116 Q08493 P08708 O75116 P18077 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9NWT8 Q9Y3D2 P62263 Q14240 P62945 P62269 P0CG47 P06732 Q8NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 Q8TAK5 P36542 P35613 P0CG48 P39019 P63244 P05090 P00505 P39023 P62273 P24311 P69905 P62158 P24311 Q8WYQ3 P01034 Q07020 P10606 Q96H40 O14880 P19021 P37108 Q43920 Q05639 P61353 P02511 P05386 P17081 P05387 P13929 P09669 Q00483 P14854 P42766 Q02878 P84243 P60033 Q9N51P P17174 P61247 P62857 P22352 Q16698 P62979 Q15004 P62851 P51970 Q9P0U1 P62906 P15954 P51857 P13533 Q00325 P08590 P62987 P04275 P04792 P25116 P20585 P06576 P48735 |
| GO:0008217 | regulation of blood pressure | 7.43E-06 | 6.20E-05 | 8 | 187 | 190 | 35980 | P16860 P19429 P01160 P68871 P09493 P13533 P25116 P00441 |
| GO:0008219 | cell death | 7.25E-03 | 2.41E-02 | 14 | 1259 | 190 | 35980 | P0CG47 P04406 Q9H3K2 P68032 P12235 P0CG48 Q8N8D1 P63244 P09382 P62987 P62979 P02511 P25116 P01034 |
| GO:0008286 | insulin receptor signaling pathway | 2.33E-04 | 1.35E-03 | 8 | 305 | 190 | 35980 | P0CG47 P62987 Q16654 P62979 P62158 P17081 P62753 P0CG48 |
| GO:0008406 | gonad development | 7.84E-03 | 2.57E-02 | 5 | 231 | 190 | 35980 | P0CG47 P16989 Q13772 P00441 P01034 |
| GO:0008584 | male gonad development | 6.29E-03 | 2.14E-02 | 4 | 138 | 190 | 35980 | P0CG47 P16989 Q13772 P01034 |
| GO:0009056 | catabolic process | 3.68E-24 | 1.24E-22 | 58 | 2321 | 190 | 35980 | P0CG47 P40925 P62280 P0CG48 P39019 P00505 P39023 P62273 P46783 P83731 P62913 P69905 P62158 P62753 P24752 Q07020 P04406 P64098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 Q13011 Q8N335 P52179 P13929 P25398 P10176 P62891 P42766 Q02878 P68871 P17174 P61247 P62857 P22352 Q16698 P62979 P62851 Q08493 Q9P0U1 P08708 P62906 P18077 P51857 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 |
| GO:0009057 | macromolecule catabolic process | 7.48E-22 | 2.04E-20 | 41 | 1193 | 190 | 35980 | P0CG47 P25398 P62280 P0CG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62158 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0009058 | biosynthetic process | 8.64E-21 | 2.25E-19 | 94 | 6964 | 190 | 35980 | P0CG47 O75947 P06732 Q8NSD9 P01160 P40926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P00505 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P24752 P02674 Q13765 Q07020 P10606 Q96H40 P13639 P48047 P04406 O14561 Q14880 Q9Y5N6 P37108 P16989 Q9Y6H1 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 Q13772 P60866 P46776 P60228 P62249 P25398 P09669 Q00483 P14854 P10176 P12235 P62891 P42766 Q02878 P25705 P18859 Q14192 Q9N51P P17174 P61247 P62857 P62979 P6381 Q15004 P62851 P00441 P54368 Q14116 P08708 P62906 P18077 P15954 P51857 P17535 P42677 P41222 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:0009059 | macromolecule biosynthetic process | 5.89E-13 | 1.01E-11 | 68 | 5325 | 190 | 35980 | P0CG47 Q9NSD9 P01160 P62280 Q8TAK5 P0CG48 P39019 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 P20674 Q13765 Q07020 P10606 Q96H40 P13639 P48047 P04406 O14561 Q14880 Q9Y5N6 P37108 P16989 Q9Y6H1 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 Q13772 P60866 P46776 P60228 P62249 P25398 P09669 Q00483 P14854 P10176 P12235 P62891 P42766 Q02878 P25705 P18859 Q14192 Q9N51P P17174 P61247 P62857 P62979 P6381 Q15004 P62851 P00441 P54368 Q14116 P08708 P62906 P18077 P15954 P51857 P17535 P42677 P41222 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:0009060 | aerobic respiration | 8.71E-04 | 4.27E-03 | 4 | 80 | 190 | 35980 | P13073 P40926 P40925 P48735 |
| GO:0009069 | serine family amino acid metabolic process | 3.86E-51 | 8.83E-49 | 36 | 138 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62158 P62851 P62753 P08708 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0009116 | nucleoside metabolic process | 1.22E-20 | 3.16E-19 | 29 | 545 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 Q43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 Q15239 P20674 Q00217 O95169 P51970 P48047 P04406 O14561 Q43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0009117 | nucleotide metabolic process | 3.06E-24 | 1.07E-22 | 37 | 792 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 Q43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 Q15239 P20674 Q00217 O95169 P51970 P48047 P04406 O14561 Q43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0009119 | ribonucleoside metabolic process | 1.50E-21 | 4.05E-20 | 29 | 505 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 Q43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 Q15239 P20674 Q00217 O95169 P51970 P48047 P04406 O14561 Q43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0009123 | nucleoside monophosphate metabolic process | 4.63E-23 | 1.38E-21 | 28 | 403 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 Q43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 Q15239 P20674 Q00217 O95169 P51970 P48047 P04406 O14561 Q43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0009124 | nucleoside monophosphate biosynthetic process | 4.61E-07 | 4.65E-06 | 8 | 129 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 |
| GO:0009126 | purine nucleoside monophosphate metabolic process | 4.48E-24 | 1.48E-22 | 28 | 370 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 Q43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 Q15239 P20674 Q00217 O95169 P51970 P48047 P04406 O14561 Q43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0009127 | purine nucleoside monophosphate biosynthetic process | 6.41E-08 | 7.07E-07 | 8 | 100 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 |
| GO:0009141 | nucleoside triphosphate metabolic process | 1.00E-24 | 3.68E-23 | 29 | 389 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 Q43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 Q15239 P20674 Q00217 O95169 P51970 P48047 P04406 O14561 Q43920 P13533 O95167 P12883 P17081 P06576 |

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|------------|---|----------|----------|----|------|-----|-------|--|
| GO:0009142 | nucleoside triphosphate biosynthetic process | 1.55E-07 | 1.65E-06 | 8 | 112 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009144 | purine nucleoside triphosphate metabolic process | 1.10E-25 | 4.48E-24 | 29 | 360 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009145 | purine nucleoside triphosphate biosynthetic process | 3.94E-08 | 4.50E-07 | 8 | 94 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009150 | purine ribonucleotide metabolic process | 1.75E-24 | 6.25E-23 | 32 | 526 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009152 | purine ribonucleotide biosynthetic process | 1.73E-07 | 1.82E-06 | 10 | 207 | 190 | 35980 | O75947 P18660 P25705 P48047 P18859 P01160 P36542 P56381 Q8WYQ3 P06576 |
| GO:0009156 | ribonucleoside monophosphate biosynthetic process | 2.18E-07 | 2.27E-06 | 8 | 117 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009161 | ribonucleoside monophosphate metabolic process | 1.43E-23 | 4.52E-22 | 28 | 386 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009163 | nucleoside biosynthetic process | 7.43E-06 | 6.20E-05 | 8 | 187 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009165 | nucleotide biosynthetic process | 2.47E-06 | 2.28E-05 | 11 | 344 | 190 | 35980 | O75947 P18660 P25705 P48047 P18859 P01160 Q9NP15 P36542 P56381 Q 8WYQ3 P06576 |
| GO:0009167 | purine ribonucleoside monophosphate metabolic process | 4.16E-24 | 1.39E-22 | 28 | 369 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009168 | purine ribonucleoside monophosphate biosynthetic | 6.41E-08 | 7.07E-07 | 8 | 100 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P18660 Q08493 P01160 |
| GO:0009187 | cyclic nucleotide metabolic process | 1.29E-02 | 3.78E-02 | 3 | 92 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P18660 Q08493 P01160 |
| GO:0009199 | ribonucleoside triphosphate metabolic process | 1.02E-25 | 4.20E-24 | 29 | 359 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009201 | ribonucleoside triphosphate biosynthetic process | 5.92E-08 | 6.60E-07 | 8 | 99 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009205 | purine ribonucleoside triphosphate metabolic process | 6.27E-26 | 2.63E-24 | 29 | 353 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009206 | purine ribonucleoside triphosphate biosynthetic process | 3.62E-08 | 4.17E-07 | 8 | 93 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009250 | glucan biosynthetic process | 1.85E-05 | 1.45E-04 | 4 | 30 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009259 | ribonucleotide metabolic process | 4.63E-24 | 1.51E-22 | 32 | 543 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P 17081 P06576 |
| GO:0009260 | ribonucleotide biosynthetic process | 3.30E-07 | 3.37E-06 | 10 | 222 | 190 | 35980 | O75947 P18660 P25705 P48047 P18859 P01160 P36542 P56381 Q8WYQ3 P06576 |
| GO:0009266 | response to temperature stimulus | 2.58E-03 | 1.05E-02 | 6 | 258 | 190 | 35980 | P0DMV8 P0DMV9 Q9UB9Y P16989 P02511 P00441 P0DMV8 P0DMV9 Q9UB9Y P02511 P00441 |
| GO:0009408 | response to heat | 2.63E-03 | 1.06E-02 | 5 | 178 | 190 | 35980 | P0DMV8 P0DMV9 Q9UB9Y P02511 P00441 P0DMV8 P0DMV9 Q9UB9Y P02511 P00441 |
| GO:0009605 | response to external stimulus | 3.25E-06 | 2.92E-05 | 31 | 2393 | 190 | 35980 | P0CG47 P52179 P51684 P01160 P40925 P10176 P0CG48 P39019 P13693 P 62891 P13073 P8373 Q16654 P62979 P62158 P24752 P01628 P00441 P01 034 Q14116 O15273 P13639 O75116 P68133 Q6P6C2 P17535 P19105 P606 60 P62987 P04792 P25116 P52179 Q14116 P40925 Q6P6C2 P10176 P17535 P13693 P62891 P62987 Q 16654 P04792 Q01628 P25116 P07602 Q13765 P01033 P13929 P16615 P35613 P19105 P05090 P84243 P6 0033 P09382 P68871 P09493 P04275 P62158 P04792 P25116 P00441 P010 34 |
| GO:0009607 | response to biotic stimulus | 2.11E-03 | 8.89E-03 | 13 | 973 | 190 | 35980 | P52179 Q14116 P40925 Q6P6C2 P10176 P17535 P13693 P62891 P62987 Q 16654 P04792 Q01628 P25116 P07602 Q13765 P01033 P13929 P16615 P35613 P19105 P05090 P84243 P6 0033 P09382 P68871 P09493 P04275 P62158 P04792 P25116 P00441 P010 34 |
| GO:0009611 | response to wounding | 5.60E-08 | 6.28E-07 | 19 | 798 | 190 | 35980 | P0CG47 P02144 O15273 P0DMV8 P0DMV9 P01160 P19021 P68133 P16989 Q6P6C2 P17535 P0CG48 Q05639 Q9UB9Y P62987 P62979 P02511 Q1500 4 P62158 P00441 P01034 P68871 O14880 P47985 P22352 P69905 P00441 P01034 P0CG47 P10916 P35613 P0CG48 P63244 P05090 P19429 Q14192 P09493 P8373 P62979 P62158 P45379 P00441 Q13765 Q14116 O15273 Q14896 O 75116 P19021 P19022 P68133 P68032 P13533 Q0843 P19105 P12883 O14 958 P63173 P08493 P60660 P08590 P62987 P02511 P25116 P06576 P6331 6 P0CG47 Q969T9 P01160 P16615 P35613 P0CG48 P84243 P60033 Q14192 P17174 Q16654 P62979 P62158 P62752 P24752 P00441 P101034 P1033 P0 2144 P13639 O75116 O14880 P19021 P68133 P13533 Q0843 P19105 P17535 Q8N 801 P41222 O14958 P68104 P08574 P62987 P47985 P02511 Q13772 P170 81 |
| GO:0009719 | response to endogenous stimulus | 2.39E-12 | 3.94E-11 | 37 | 1852 | 190 | 35980 | P0CG47 Q969T9 P01160 P16615 P35613 P0CG48 P84243 Q14192 P17174 Q16654 P62979 P62158 P62752 P24752 P00441 P101034 P1033 P02144 P13639 O 75116 P19021 P68133 Q0843 P17535 Q8N801 P41222 P08574 P62987 P47 985 P02511 Q13772 P17081 O15273 Q14896 P10916 P19021 P19022 P68133 P68032 P13533 P35613 P1 2883 P19429 P63173 P08493 Q14192 P08590 P09493 P45379 P00441 P633 16 P07602 P0CG47 P13929 P10916 P01160 P16615 P35613 P05090 P19429 Q 14192 P09493 P45379 P24752 P00441 P101034 Q13765 P01033 O15273 Q14 896 P13639 P19022 P68133 P68032 P13533 P12883 P63173 P08493 P6066 0 P08590 P63316 P0CG47 Q13765 P0DMV8 P13639 P0DMV9 Q969T9 P16989 Q8TAK5 Q9Y6 H1 P17535 P0CG48 P63244 P60033 Q14192 P68871 P62987 P62979 Q1377 2 P62158 P17081 P04792 P25116 P01034 P0CG47 P0DMV8 P0DMV9 Q8N3K9 P0CG48 P39019 P63244 P05090 P194 29 P84243 Q14192 P62979 P62158 P45379 Q8WYQ3 Q01628 P00441 P010 34 P51452 Q13765 P54368 P01033 P04406 O75116 P16989 P17535 P62263 P62987 Q14240 P02511 P04792 P60228 P20585 Q8N335 P07602 P0CG47 P0DMV8 P0DMV9 Q969T9 Q8TAK5 P0CG48 P39019 P632 44 P84243 P60033 Q14192 P68871 P09493 P62979 P62158 P45379 P00441 P01034 Q13765 P54368 Q14116 Q14896 P13639 O75116 P19022 P68133 P 16989 Q9Y6H1 P68032 P17535 P15880 Q05639 Q9NWT8 P08590 P62987 Q 13772 P17081 P04792 P25116 P20585 P0CG47 P54368 P01033 P63244 Q05639 P68104 P60033 P62987 P62979 P 0CG48 P01034 P0CG47 P54368 P63244 P60033 P62987 P62979 P0CG48 P07602 P0CG47 P0DMV8 P0DMV9 Q8N3K9 P0CG48 P13693 P63244 P050 90 P60033 P23227 P62979 P62158 P00441 P51452 P01033 Q14116 P19022 P16989 Q8N8D1 O14958 P09382 P62987 P17081 P04792 P25116 Q8N335 P07602 P0CG47 Q14116 P0DMV8 P0DMV9 P19022 P0CG48 Q8N8D1 P632 44 P60033 P09382 P62987 P62979 P62158 P25116 P00441 P0CG47 P51452 P0DMV8 P0DMV9 P19022 P16989 Q8N3K9 P0CG48 P136 93 P63244 P05090 O14958 P62987 P62979 P62158 P04792 Q8N335 O75947 P10916 Q969T9 O43674 Q9H3K2 P16615 O96000 P18660 P13073 O14949 P09493 P07195 P46783 P8373 P62913 P62753 P24752 O15239 P2 0674 Q13765 O95169 P13639 P48047 Q9Y277 P04406 O14561 P080297 Q9Y 5N6 P16989 Q9Y6H1 O95167 Q0843 P19105 P84098 O14958 P63173 P681 04 P09382 P08574 P47985 P46777 Q13772 P60866 P46776 P60228 P62249 Q13011 Q8N335 P07602 P52179 P25398 P68363 P10176 O95178 P12235 P 13693 P62891 P19429 P25705 P18859 Q14192 P68871 Q16654 P56381 Q01 628 P00441 P54368 O00217 Q14116 O15273 Q08493 P08708 Q14515 O751 16 P68133 P18077 P1761 Q9P6C2 P17535 P12883 Q8N8D1 P42677 P4122 2 P15880 P17540 Q02543 Q9NWT8 Q9Y2D2 P62263 Q14240 P62945 P6226 9 P0CG47 P62987 P62989 P0DMV8 P0DMV9 P01160 P40925 P40925 P62 280 Q8TAK5 P36542 P36543 P0CG48 P39019 P63244 P05090 P00505 P390 23 P62273 P24310 P68905 P62158 P45379 P24311 Q8WYQ3 P01034 Q070 20 P01033 P10606 Q14896 Q9H40 O14880 P19021 P19022 P14406 P3710 8 O43920 P68032 Q05639 P08493 P61353 P60660 P02511 P05386 P17081 P05387 P13929 P02792 P09669 P51684 O00483 P14854 P42766 Q002878 P8 4243 P60033 Q9NP15 P17174 P61247 P62857 P23327 P22352 Q16698 P629 79 Q15004 P62851 P51452 P02144 Q14315 P51970 Q9P0U1 O175954 P6290 6 P15954 P51857 P13533 Q00325 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P06576 P63316 P48735 P13073 P13639 P68133 Q16654 P24752 P00441 P39019 P01034 |
| GO:0009605 | response to external stimulus | 3.25E-06 | 2.92E-05 | 31 | 2393 | 190 | 35980 | P0CG47 P52179 P51684 P01160 P40925 P10176 P0CG48 P39019 P13693 P 62891 P13073 P8373 Q16654 P62979 P62158 P24752 P01628 P00441 P01 034 Q14116 O15273 P13639 O75116 P68133 Q6P6C2 P17535 P19105 P606 60 P62987 P04792 P25116 P52179 Q14116 P40925 Q6P6C2 P10176 P17535 P13693 P62891 P62987 Q 16654 P04792 Q01628 P25116 P07602 Q13765 P01033 P13929 P16615 P35613 P19105 P05090 P84243 P6 0033 P09382 P68871 P09493 P04275 P62158 P04792 P25116 P00441 P010 34 |
| GO:0009607 | response to biotic stimulus | 2.11E-03 | 8.89E-03 | 13 | 973 | 190 | 35980 | P52179 Q14116 P40925 Q6P6C2 P10176 P17535 P13693 P62891 P62987 Q 16654 P04792 Q01628 P25116 P07602 Q13765 P01033 P13929 P16615 P35613 P19105 P05090 P84243 P6 0033 P09382 P68871 P09493 P04275 P62158 P04792 P25116 P00441 P010 34 |
| GO:0009611 | response to wounding | 5.60E-08 | 6.28E-07 | 19 | | | | |

| | | | | | | | | |
|------------|--|----------|----------|-----|------|-----|-------|--|
| GO:0010033 | response to organic substance | 1.37E-16 | 2.87E-15 | 57 | 3237 | 190 | 35980 | P0CG47 Q12988 Q969T9 P01160 P16615 P35613 P0CG48 P63244 P00505 P39023 P62158 P62753 P24752 P01034 P01033 P13639 P04406 O14880 P80297 P19021 P16989 P68032 Q08431 O14958 P68104 P09382 P08574 P4795 P02511 Q13772 P17081 P07602 P51684 P68363 P84243 P60303 Q14192 Q09UB9 P1714 Q16654 P22352 P62979 Q01628 P00441 P51452 P02144 Q14116 O75116 P68133 P13533 P17535 Q8N8D1 P41222 P62987 Q14240 P04792 P25116 |
| GO:0010035 | response to inorganic substance | 2.74E-09 | 3.68E-08 | 17 | 517 | 190 | 35980 | P02144 P13639 P80297 P19021 P68133 P35613 P17535 O14958 Q05639 P68871 P02511 P69905 P62158 P45379 P00441 P63316 P01034 O14958 P80297 P19021 P68133 P62158 P45379 P35613 P17535 P00441 P63316 |
| GO:0010038 | response to metal ion | 2.03E-05 | 1.58E-04 | 10 | 353 | 190 | 35980 | P0CG47 P01033 P13639 P01160 O14880 P16615 P35613 P17535 P0CG48 O14958 P17174 P08574 P62987 Q16654 P62979 P62158 P17081 P62753 P0441 O00217 O95169 P51970 O43674 O14561 O43920 O95167 O95178 O96000 O15239 |
| GO:0010243 | response to organonitrogen compound | 1.74E-06 | 1.63E-05 | 19 | 1002 | 190 | 35980 | P01160 P09493 P16615 P23327 |
| GO:0010257 | NADH dehydrogenase complex assembly | 1.13E-12 | 1.88E-11 | 10 | 62 | 190 | 35980 | P0CG47 Q9NSD9 P0DMV8 P01160 P62280 Q8TAK5 P0CG48 P39019 P63244 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 P20674 Q13765 Q07020 P10606 Q96H40 P13639 P37108 P16989 Q9Y6H1 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 Q13772 P60866 P46776 P05387 P60228 P62249 P25389 P09669 O00483 P14854 P10176 P12235 P62891 P42766 Q02878 P84243 Q14192 P61247 P62857 P62979 P62851 P08708 P62906 P18077 P15954 Q6P6C2 P17535 Q8N8D1 P42677 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P04792 P62269 P25116 |
| GO:0010522 | regulation of calcium ion transport into cytosol | 1.65E-03 | 7.26E-03 | 4 | 95 | 190 | 35980 | O14958 P23327 P62158 P25116 |
| GO:0010557 | positive regulation of macromolecule biosynthetic process | 1.56E-03 | 6.94E-03 | 20 | 1815 | 190 | 35980 | P0CG47 Q13765 P0DMV8 P13639 P0DMV9 Q969T9 P16989 Q8TAK5 Q9Y6H1 P17535 P0CG48 P60033 Q14192 P62987 P62979 Q13772 P17081 P04792 P25116 P01034 |
| GO:0010562 | positive regulation of phosphorus metabolic process | 5.72E-03 | 1.98E-02 | 14 | 1224 | 190 | 35980 | P07602 P0CG47 Q14116 O75116 P19022 P0CG48 P63244 Q05639 P60033 P62987 P62979 P62158 P25116 P00441 |
| GO:0010604 | positive regulation of macromolecule metabolic process | 2.15E-04 | 1.26E-03 | 32 | 3122 | 190 | 35980 | P07602 P0CG47 P0DMV8 P0DMV9 Q969T9 Q8TAK5 P0CG48 P63244 P84243 P60033 Q14192 P62979 P62158 P00441 P01034 Q13765 P54368 Q14116 P13639 O75116 P19022 P68133 P16989 Q9Y6H1 P68032 P17535 Q9NWT8 P62987 Q13772 P17081 P04792 P25116 |
| GO:0010605 | negative regulation of macromolecule metabolic process | 5.64E-04 | 2.90E-03 | 28 | 2733 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 Q8N3K9 P0CG48 P63244 P05090 P84243 Q14192 P62979 P62158 Q01628 P01034 P17535 P01033 P04406 O75116 P16989 P17535 P62263 P62987 Q14240 P02511 P04792 P60228 P0585 Q8N335 |
| GO:0010608 | posttranscriptional regulation of gene expression | 2.08E-06 | 1.93E-05 | 14 | 564 | 190 | 35980 | P0CG47 P0DMV8 P13639 P04406 P16989 P0CG48 P63244 P61373 P62263 P62987 Q14240 P62979 P04792 P60228 |
| GO:0010628 | positive regulation of gene expression | 1.83E-04 | 1.10E-03 | 23 | 1898 | 190 | 35980 | P0CG47 Q13765 Q14116 P0DMV8 P13639 P0DMV9 Q969T9 O75116 P68133 P16989 Q8TAK5 Q9Y6H1 P68032 P17535 P0CG48 P84243 P60033 Q14192 P62987 P62979 Q13772 P17081 P25116 |
| GO:0010634 | positive regulation of epithelial cell migration | 1.79E-02 | 4.86E-02 | 3 | 104 | 190 | 35980 | P51684 O75116 P04792 |
| GO:0010646 | regulation of cell communication | 5.42E-03 | 1.90E-02 | 30 | 3496 | 190 | 35980 | P07602 P0CG47 P0DMV8 P0DMV9 P16615 Q8N3K9 P12235 P0CG48 P13693 P63244 P05090 P60033 P23327 P62979 P62158 P00441 P51452 P01033 Q14116 Q08493 P19022 P16989 Q8N8D1 O14958 P09382 P62987 P17081 P04792 P25116 Q8N335 |
| GO:0010648 | negative regulation of cell communication | 2.32E-04 | 1.34E-03 | 18 | 1317 | 190 | 35980 | P0CG47 P51452 Q08493 P0DMV8 P0DMV9 P19022 P16989 Q8N3K9 P0CG48 P13693 P63244 P05090 O14958 P62987 P62979 P62158 P04792 Q8N335 |
| GO:0010649 | regulation of cell communication by electrical coupling | 1.69E-05 | 1.33E-04 | 3 | 10 | 190 | 35980 | O14958 P23327 P62158 |
| GO:0010803 | regulation of tumor necrosis factor-mediated signaling | 8.45E-09 | 1.07E-07 | 7 | 50 | 190 | 35980 | P0CG47 P63244 P0DMV8 P0DMV9 P62987 P62979 P0CG48 |
| GO:0010880 | regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum | 3.45E-04 | 1.91E-03 | 3 | 26 | 190 | 35980 | O14958 P23327 P62158 |
| GO:0010881 | regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion | 1.55E-04 | 9.48E-04 | 3 | 20 | 190 | 35980 | O14958 P16615 P23327 P62158 |
| GO:0010882 | regulation of cardiac muscle contraction by calcium ion | 7.37E-06 | 6.19E-05 | 4 | 24 | 190 | 35980 | O14958 P16615 P23327 P62158 |
| GO:0010927 | cellular component assembly involved in morphogenesis | 4.27E-05 | 3.07E-04 | 9 | 309 | 190 | 35980 | O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 |
| GO:0010939 | regulation of necrotic cell death | 7.72E-08 | 8.36E-07 | 6 | 41 | 190 | 35980 | P0CG47 P62987 P16989 P62979 P12235 P0CG48 |
| GO:0010941 | regulation of cell death | 8.76E-08 | 9.40E-07 | 29 | 1800 | 190 | 35980 | O14958 P23327 P62158 |
| GO:0010942 | positive regulation of cell death | 3.84E-04 | 2.11E-03 | 12 | 702 | 190 | 35980 | O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 |
| GO:0010959 | regulation of metal ion transport | 1.18E-02 | 3.48E-02 | 6 | 355 | 190 | 35980 | P0CG47 P62987 P16989 P62979 P12235 P0CG48 P13693 P63244 Q14192 P68871 P61247 Q16654 P62979 P69905 P62753 P00441 P01034 Q13765 P01033 P16989 P68032 P17535 Q8N8D1 Q05639 P09382 P62987 P02511 P04792 P25116 |
| GO:0012501 | programmed cell death | 4.97E-03 | 1.83E-02 | 14 | 1204 | 190 | 35980 | P0CG47 P63244 Q05639 P68871 P62987 P62979 P69905 P62753 P25116 P00441 P0CG48 Q8N8D1 |
| GO:0014070 | response to organic cyclic compound | 2.18E-07 | 2.27E-06 | 21 | 1055 | 190 | 35980 | O14958 P01160 P62987 P62158 P25116 Q8N335 |
| GO:0014074 | response to purine-containing compound | 1.61E-02 | 4.41E-02 | 4 | 182 | 190 | 35980 | P0CG47 P04406 Q09H3K2 P68032 P12235 P0CG48 Q8N8D1 P63244 P09382 P62987 P62979 P02511 P25116 P01034 |
| GO:0014706 | striated muscle tissue development | 5.02E-12 | 8.07E-11 | 16 | 293 | 190 | 35980 | O14958 P35613 P17535 P00441 |
| GO:0014733 | regulation of skeletal muscle adaptation | 1.30E-06 | 1.27E-05 | 4 | 16 | 190 | 35980 | O15273 Q14896 P10916 P13639 P01160 P68133 P68032 P13533 P12883 P19429 Q14192 P60660 P08590 P09493 P45379 P63316 |
| GO:0014866 | skeletal myofibril assembly | 4.99E-06 | 4.39E-05 | 3 | 7 | 190 | 35980 | P16615 Q8N3K9 P12883 P63316 |
| GO:0014883 | transition between fast and slow fiber | 1.19E-05 | 9.64E-05 | 3 | 9 | 190 | 35980 | O15273 P68133 P68032 |
| GO:0014888 | striated muscle adaptation | 3.45E-04 | 1.91E-03 | 3 | 26 | 190 | 35980 | P16615 P12883 P63316 |
| GO:0015031 | protein transport | 7.63E-16 | 1.53E-14 | 42 | 1852 | 190 | 35980 | O15273 P01160 P68133 |
| GO:0015669 | gas transport | 1.24E-03 | 5.79E-03 | 3 | 40 | 190 | 35980 | P25398 P62280 P35613 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 Q9POU1 P08708 P62906 P18077 P37108 Q9Y6H1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P46776 P62269 P05387 P25116 P62249 |
| GO:0015671 | oxygen transport | 9.10E-04 | 4.44E-03 | 3 | 36 | 190 | 35980 | P02144 P68871 P69905 |
| GO:0015672 | monovalent inorganic cation transport | 1.90E-08 | 2.29E-07 | 20 | 827 | 190 | 35980 | P02144 P68871 P69905 |
| GO:0015980 | energy derivation by oxidation of organic compounds | 3.54E-36 | 2.92E-34 | 38 | 402 | 190 | 35980 | O75947 P10606 P09669 P48047 P14406 O00483 P14854 P36542 P15954 P10176 P13073 P25705 P18859 O14949 P47985 P56381 P24310 P24311 P06576 P20674 |
| GO:0015985 | energy coupled proton transport, down electrochemical | 3.33E-09 | 4.40E-08 | 7 | 44 | 190 | 35980 | P0CG47 O75947 P09669 O43674 P40926 P40925 O00483 P14854 P36542 P10176 O95178 P12235 P0CG48 O96000 P13073 P25705 P18859 O14949 P62979 P56381 P62158 P24311 O15239 O95169 P51970 P48047 O14561 O43920 P15954 O95167 P08574 P62987 P47985 P06576 P48735 |
| GO:0015986 | ATP synthesis coupled proton transport | 3.33E-09 | 4.40E-08 | 7 | 44 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 P06576 |
| GO:0015992 | proton transport | 1.65E-16 | 3.44E-15 | 20 | 296 | 190 | 35980 | O75947 P10606 P09669 P48047 P14406 O00483 P14854 P36542 P15954 P10176 P13073 P25705 P18859 O14949 P47985 P56381 P24310 P24311 P06576 P20674 |
| GO:0016032 | viral process | 1.56E-34 | 1.05E-32 | 46 | 783 | 190 | 35980 | P0CG47 P25398 P0DMV8 P0DMV9 P62280 P12235 P0CG48 P39019 P62891 P42766 P63244 Q02878 P60033 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P08708 P62906 P18077 Q08431 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0016043 | cellular component organization | 3.35E-24 | 1.14E-22 | 101 | 7195 | 190 | 35980 | P10916 O43674 P16615 O96000 P09493 P46783 P83731 P62913 P62753 P24752 O15239 O95169 P04406 O14561 Q9Y6H1 O95167 Q08431 P19105 P84098 O14958 P61373 P46777 P60866 P46776 P60228 P62249 P52179 P25398 P68363 P10176 O95178 P12235 P62891 P68871 P00441 O00217 O15273 P08708 O75116 P68133 P18077 P17661 P42677 P15880 Q02543 Q9NWT8 Q9Y3D2 P62263 P62945 P62269 P0CG47 P0DMV8 P40925 P62280 P35613 P0CG48 P39019 P05090 P39023 P62273 P69905 P62158 P45379 Q8YWC3 P01034 Q07020 P01033 Q14896 P19021 P19022 P37108 O43920 P68032 P61353 P60660 P02511 P05386 P17081 P05387 P02792 P42766 Q02878 P84243 P61247 P62857 P22352 Q16698 P62979 Q15004 P62851 Q14315 P51970 Q9POU1 P62906 P13533 P62987 P04275 P63313 P25116 P20585 P06576 |
| GO:0016051 | carbohydrate biosynthetic process | 4.20E-08 | 4.78E-07 | 10 | 178 | 190 | 35980 | P0CG47 P13929 P00505 P40926 P04406 P40925 P17174 P62987 P62979 P0CG48 |
| GO:0016054 | organic acid catabolic process | 2.39E-03 | 9.85E-03 | 6 | 254 | 190 | 35980 | P00505 P17174 Q16698 P51857 P24752 Q13011 |

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| GO:0016070 | RNA metabolic process | 7.22E-13 | 1.23E-11 | 62 | 4569 | 190 | 35980 | P0CG47 Q9NSD9 P01160 P62280 Q8TAK5 P0CG48 P39019 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 P20674 Q13765 Q07020 P10606 Q96H40 P16989 Q9Y6H1 P84098 P63173 P68104 P61353 P46777 P05386 Q13772 P06086 P46776 P05387 P60228 P62249 P25398 P06669 Q00483 P14854 P10176 P62891 P42766 Q02878 Q14192 P61247 P62857 P62979 P62851 P08708 P62906 P18077 P15954 Q6P6C2 P17535 Q8N8D1 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P46777 P05386 P06866 P46776 P62269 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 Q6P6C2 Q8N8D1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P06866 P46776 P62269 P05387 P60228 P62249 |
| GO:0016071 | mRNA metabolic process | 1.60E-28 | 7.53E-27 | 40 | 743 | 190 | 35980 | P42766 P08708 P62263 P18077 P62857 P62913 P46777 P62753 P62249 P39019 |
| GO:0016072 | rRNA metabolic process | 7.76E-08 | 8.36E-07 | 10 | 190 | 190 | 35980 | P0CG47 P52179 Q9P0U1 P40925 P62987 Q16654 P62979 Q6P6C2 P10176 P0CG48 |
| GO:0016236 | macroautophagy | 1.82E-06 | 1.70E-05 | 10 | 268 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P05387 P60228 P62249 |
| GO:0016259 | selenocysteine metabolic process | 4.22E-59 | 6.27E-56 | 36 | 90 | 190 | 35980 | P0CG47 P52179 Q9P0U1 P40925 P62987 Q16654 P62979 Q6P6C2 P10176 P0CG48 |
| GO:0016265 | death | 7.25E-03 | 2.41E-02 | 14 | 1259 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P05387 P60228 P62249 |
| GO:0016310 | phosphorylation | 6.95E-06 | 5.88E-05 | 32 | 2611 | 190 | 35980 | P0CG47 P13829 P06732 Q43674 O00483 P36542 P10176 O95178 P0CG48 Q96000 P13073 Q8N8D1 Q16654 P62979 P62158 Q8WYQ3 O15239 P20674 P51452 O00217 Q14116 O95169 P51970 P04406 O14561 O75116 Q043920 O95167 P17540 P62987 P02511 P25116 |
| GO:0016482 | cytoplasmic transport | 3.21E-25 | 1.26E-23 | 42 | 1030 | 190 | 35980 | P25398 P16615 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q9P0U1 P08708 P62906 P18077 P3108 Q9Y6H1 Q6P6C2 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P06866 P46776 P62269 P05387 P25116 P62249 |
| GO:0016485 | protein processing | 5.21E-03 | 1.85E-02 | 6 | 298 | 190 | 35980 | P0CG47 P63244 P62987 P62979 P25116 P0CG48 |
| GO:0017015 | regulation of transforming growth factor beta receptor | 3.30E-03 | 1.29E-02 | 4 | 115 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0018130 | heterocycle biosynthetic process | 2.81E-19 | 6.63E-18 | 68 | 3999 | 190 | 35980 | P0CG47 O75947 P01160 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P20674 Q13765 Q07020 P10606 Q96H40 P48047 P16989 Q9Y6H1 P84098 P63173 P68104 P61353 P46777 P05386 Q13772 P06086 P46776 P05387 P62249 P25398 P09669 O00483 P14854 P10176 P62891 P42766 Q02878 P25705 P18859 Q14192 Q8N8D1 P61247 P62857 P62979 P56381 Q15004 P62851 P08708 P62906 P18077 P15954 P17535 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 P06576 |
| GO:0019058 | viral life cycle | 1.56E-46 | 2.31E-44 | 41 | 288 | 190 | 35980 | P0CG47 P25398 P0DMV8 P0DMV9 P62280 P0CG48 P39019 P62891 P42766 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0019068 | virion assembly | 4.83E-05 | 3.41E-04 | 4 | 38 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0019080 | viral gene expression | 4.65E-57 | 4.60E-54 | 38 | 124 | 190 | 35980 | P0CG47 P25398 P62280 P0CG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P06866 P46776 P62269 P05387 P62249 |
| GO:0019082 | viral protein processing | 3.61E-07 | 3.67E-06 | 4 | 12 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0019083 | viral transcription | 9.15E-55 | 3.51E-52 | 36 | 113 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P05387 P60228 P62249 |
| GO:0019216 | regulation of lipid metabolic process | 1.50E-03 | 6.70E-03 | 7 | 315 | 190 | 35980 | P07602 P63244 P05090 Q05639 P00333 Q16654 P00441 |
| GO:0019220 | regulation of phosphate metabolic process | 5.96E-03 | 2.04E-02 | 19 | 1904 | 190 | 35980 | P07602 P0CG47 P51452 Q14116 O75116 P19022 Q8N3K9 P0CG48 P63244 Q05639 P60033 P62987 P23327 P23327 P62158 P04792 P25116 Q8N335 P00441 |
| GO:0019318 | hexose metabolic process | 1.11E-09 | 1.53E-08 | 13 | 253 | 190 | 35980 | P0CG47 P13929 P40926 P04406 P40925 P0CG48 P05090 P00505 P17174 P62987 Q16654 P62979 P62158 |
| GO:0019319 | hexose biosynthetic process | 3.48E-06 | 3.11E-05 | 6 | 77 | 190 | 35980 | P13929 P00505 P40926 P04406 P40925 P17174 |
| GO:0019362 | pyridine nucleotide metabolic process | 2.23E-04 | 1.30E-03 | 7 | 228 | 190 | 35980 | P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0019438 | aromatic compound biosynthetic process | 1.93E-19 | 4.62E-18 | 68 | 3971 | 190 | 35980 | P0CG47 O75947 P01160 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P20674 Q13765 Q07020 P10606 Q96H40 P48047 P16989 Q9Y6H1 P84098 P63173 P68104 P61353 P46777 P05386 Q13772 P06086 P46776 P05387 P62249 P25398 P09669 O00483 P14854 P10176 P62891 P42766 Q02878 P25705 P18859 Q14192 Q8N8D1 P61247 P62857 P62979 P56381 Q15004 P62851 P08708 P62906 P18077 P15954 P17535 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 P06576 |
| GO:0019439 | aromatic compound catabolic process | 2.91E-34 | 1.88E-32 | 39 | 489 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P06866 P46776 P62269 P05387 P60228 P62249 |
| GO:0019538 | protein metabolic process | 6.70E-06 | 5.72E-05 | 70 | 8155 | 190 | 35980 | P0CG47 Q9NSD9 P01160 P40926 P62280 P0CG48 P39019 P63244 P39023 P62273 P46783 P83731 P62913 P62158 P62753 P01034 Q13765 Q07020 P13639 P04406 O14561 P19021 P37108 Q9Y6H1 Q08431 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P06866 P46776 P05387 P60228 P62249 P25398 P6363 P12235 P62891 P42766 Q02878 P64243 P61247 P62857 Q16654 P62979 P62851 P51452 Q14116 Q9P0U1 P08708 O75116 P62906 P18077 P42677 P15880 Q02543 Q9NP15 Q9Y3D2 Q00325 P62263 P62987 Q14240 P62945 P04275 P62269 P25116 |
| GO:0019637 | organophosphate metabolic process | 1.77E-17 | 3.82E-16 | 39 | 1418 | 190 | 35980 | P13929 O75947 P06732 P0DMV8 P0DMV9 P01160 Q43674 P40926 P40925 O00483 P36542 P10176 O95178 Q96000 P16860 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 Q00217 Q08493 O95169 P51970 P04406 O14561 O43920 P13533 O95167 P12883 P17081 Q8N335 P06576 |
| GO:0019674 | NAD metabolic process | 3.03E-07 | 3.12E-06 | 7 | 83 | 190 | 35980 | P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0019693 | ribose phosphate metabolic process | 1.83E-23 | 5.72E-22 | 32 | 568 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 P01160 Q43674 O00483 P36542 P10176 O95178 Q96000 P16860 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 Q00217 Q08493 O95169 P51970 P04406 O14561 O43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0019722 | calcium-mediated signaling | 1.99E-03 | 8.47E-03 | 4 | 100 | 190 | 35980 | O14958 P16615 P23327 P62158 |
| GO:0019725 | cellular homeostasis | 1.47E-04 | 9.03E-04 | 14 | 831 | 190 | 35980 | P0CG47 P02792 P51684 P16615 P0CG48 P13693 P63244 O14958 P19429 P09382 P23327 P25116 P00441 P06576 |
| GO:0019752 | carboxylic acid metabolic process | 2.19E-32 | 1.30E-30 | 56 | 1471 | 190 | 35980 | P06732 Q9NSD9 P40926 P40925 P62280 P35613 P39019 P00505 P39023 P62273 P07195 P46783 P83731 P62913 P62753 P24752 Q07020 P04406 O14561 P19021 P84098 P63173 P61353 P46777 P05386 P06866 P46776 P05387 P60228 P62249 Q13011 P13929 P25398 P62891 P42766 Q02878 P17174 P61247 P62857 Q16654 Q16698 P62979 P62851 P08708 P62906 P18077 P51857 P42677 P41222 P15880 Q02543 P62263 P62987 P62945 P62269 P46783 |
| GO:0019932 | second-messenger-mediated signaling | 1.41E-02 | 4.06E-02 | 4 | 175 | 190 | 35980 | O14958 P16615 P23327 P62158 |
| GO:0019985 | translesion synthesis | 7.51E-06 | 6.26E-05 | 5 | 41 | 190 | 35980 | P0CG47 P62987 P62979 Q15004 P0CG48 |
| GO:0021762 | substantia nigra development | 1.86E-03 | 8.00E-03 | 3 | 56 | 190 | 35980 | P18859 P14854 P62158 |
| GO:0022411 | cellular component disassembly | 3.25E-36 | 2.76E-34 | 45 | 673 | 190 | 35980 | P0CG47 P52179 P25398 P40925 P62280 P01160 P35613 P0CG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 Q8N8D1 P61353 P62263 P62987 P62945 P46777 P05386 P06866 P46776 P62269 P05387 P62249 |
| GO:0022607 | cellular component assembly | 1.54E-14 | 2.96E-13 | 47 | 2516 | 190 | 35980 | P0CG47 P10816 Q43674 O95178 P0CG48 P39019 Q96000 Q02878 P84243 P39023 P68871 P00493 P46783 P83731 P62913 P22352 Q16698 P62979 P905 P45379 P24752 O15239 O00217 Q14315 O15273 Q14896 O95169 P51970 P08708 O14561 P19021 P19022 P68133 O43920 P8032 P13533 O95167 P42677 O14958 P63173 Q9Y3D2 P62263 P62987 P46777 P02511 P04275 P60228 |
| GO:0022613 | ribonucleoprotein complex biogenesis | 8.20E-10 | 1.13E-08 | 17 | 477 | 190 | 35980 | P08708 P18077 P39019 P42677 P42766 Q02878 P63173 P39023 P62263 P46783 P83731 P62857 P62913 P46777 P62753 P60228 P62249 |
| GO:0022618 | ribonucleoprotein complex assembly | 1.06E-08 | 1.33E-07 | 12 | 250 | 190 | 35980 | P42677 Q02878 P63173 P08708 P39023 P62263 P46783 P83731 P62913 P46777 P60228 P39019 |

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| GO:0022898 | regulation of transmembrane transporter activity | 5.08E-03 | 1.85E-02 | 5 | 208 | 190 | 35980 | O14958 P01160 P23327 P62158 Q8N335 O75947 P09669 O43674 O00483 P14854 P36542 P10176 O95178 O96000 P13073 P25705 P18859 O14949 P56381 P24311 O15239 P20674 O00217 P1606 O95169 P51970 P48047 O14561 O43920 P15954 O95167 P08574 P47985 P06576 |
| GO:0022900 | electron transport chain | 3.89E-35 | 2.82E-33 | 29 | 173 | 190 | 35980 | O75947 P09669 O43674 O00483 P14854 P36542 P10176 O95178 O96000 P13073 P25705 P18859 O14949 P56381 P24311 O15239 P20674 O00217 P1606 O95169 P51970 P48047 O14561 O43920 P15954 O95167 P08574 P47985 P06576 |
| GO:0022904 | respiratory electron transport chain | 1.90E-36 | 1.67E-34 | 29 | 157 | 190 | 35980 | O75947 P09669 O43674 O00483 P14854 P36542 P10176 O95178 O96000 P13073 P25705 P18859 O14949 P56381 P24311 O15239 P20674 O00217 P1606 O95169 P51970 P48047 O14561 O43920 P15954 O95167 P08574 P47985 P06576 |
| GO:0023014 | signal transduction by protein phosphorylation | 3.68E-03 | 1.41E-02 | 8 | 470 | 190 | 35980 | POCG47 P51452 Q14116 P62987 P62979 P02511 P62158 POCG48 P07602 POCG47 P0DMV8 P0DMV9 P01160 P16615 Q8N3K9 P12235 POCG48 P13693 P63244 P05090 P19429 P60033 P23327 P62979 P62158 P00441 P51452 P01033 Q14116 P08493 P19022 P16989 Q8N801 O14958 P09382 P62987 P17081 P04792 P25116 Q8N335 |
| GO:0023051 | regulation of signaling | 1.51E-03 | 6.76E-03 | 32 | 3500 | 190 | 35980 | P07602 POCG47 Q14116 P62987 P62979 P02511 P62158 POCG48 P07602 POCG47 Q14116 P62987 P62979 P02511 P62158 POCG48 P39019 P63244 P60033 P09382 P62987 P62979 P62158 P25116 P00441 POCG47 P51452 Q08493 P0DMV8 P0DMV9 P19022 P16989 Q8N3K9 POCG48 P13693 P63244 P05090 O14958 P62987 P62979 P62158 P04792 Q8N335 |
| GO:0023056 | positive regulation of signaling | 1.83E-02 | 4.94E-02 | 16 | 1696 | 190 | 35980 | P13693 P02792 P51684 O14958 P19429 P16615 P23327 P25116 P00441 P06576 O15273 Q14896 P10916 O75116 P68133 P17661 P68032 P13533 P12883 O14958 P19429 Q9Y3D2 P06060 P08590 P09493 P63313 P17081 P45379 Q8N335 P63316 |
| GO:0023057 | negative regulation of signaling | 2.08E-04 | 1.23E-03 | 18 | 1305 | 190 | 35980 | O15273 Q14896 P10916 O75116 P68133 P17661 P68032 P13533 O14958 Q9Y3D2 P09493 P63313 P17081 P45379 O15273 Q14896 P10916 O75116 P68133 P17661 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P45379 Q8N335 P63316 |
| GO:0030003 | cellular cation homeostasis | 4.72E-04 | 2.49E-03 | 10 | 519 | 190 | 35980 | O15273 Q14896 P10916 O75116 P68133 P17661 P68032 P13533 O14958 Q9Y3D2 P09493 P63313 P17081 P45379 O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P45379 P63316 |
| GO:0030029 | actin filament-based process | 1.75E-08 | 2.13E-07 | 20 | 823 | 190 | 35980 | O15273 Q14896 P10916 O75116 P68133 P17661 P68032 P13533 O14958 Q9Y3D2 P09493 P63313 P17081 P45379 O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P45379 P63316 |
| GO:0030036 | actin cytoskeleton organization | 1.95E-04 | 1.16E-03 | 13 | 751 | 190 | 35980 | O15273 Q14896 P10916 O75116 P68133 P17661 P68032 P13533 O14958 Q9Y3D2 P09493 P63313 P17081 P45379 O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P45379 P63316 |
| GO:0030048 | actin filament-based movement | 3.01E-18 | 6.74E-17 | 15 | 95 | 190 | 35980 | O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P45379 P63316 |
| GO:0030049 | muscle filament sliding | 1.08E-22 | 3.13E-21 | 14 | 39 | 190 | 35980 | O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P45379 P63316 |
| GO:0030111 | regulation of Wnt signaling pathway | 1.01E-02 | 3.16E-02 | 6 | 343 | 190 | 35980 | POCG47 P63244 P19022 P62987 P62979 POCG48 P07602 POCG47 P10916 P01160 P16615 P62280 POCG48 P39019 P63244 P05090 P19429 O14949 Q14192 P09493 P61247 P8373 P62979 P62158 P45379 P00441 P01034 P02144 Q14135 Q15273 Q14896 P13639 O75116 P19022 P68133 P68032 Q6P6C2 P13533 P17535 P19105 O14958 Q08493 P06060 P09382 P62263 P62987 P02511 P06576 |
| GO:0030154 | cell differentiation | 1.41E-06 | 1.36E-05 | 42 | 3701 | 190 | 35980 | POCG47 P01033 P63244 Q8NWT8 P62987 P62979 P02511 P25116 POCG48 P01034 P07602 P01033 P68871 P04275 P62158 P04792 P19105 P25116 P00441 POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030162 | regulation of proteolysis | 1.37E-02 | 3.97E-02 | 10 | 835 | 190 | 35980 | POCG47 P01033 P63244 Q8NWT8 P62987 P62979 P02511 P25116 POCG48 P01034 P07602 P01033 P68871 P04275 P62158 P04792 P19105 P25116 P00441 POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030168 | platelet activation | 8.58E-06 | 7.11E-05 | 9 | 252 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030177 | positive regulation of Wnt signaling pathway | 1.33E-02 | 3.87E-02 | 4 | 172 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030178 | negative regulation of Wnt signaling pathway | 1.03E-03 | 4.92E-03 | 6 | 215 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030218 | erythrocyte differentiation | 7.41E-03 | 2.45E-02 | 3 | 75 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030239 | myofibril assembly | 2.25E-11 | 3.46E-10 | 9 | 58 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030240 | skeletal muscle thin filament assembly | 1.44E-06 | 1.38E-05 | 3 | 5 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030260 | entry into host cell | 1.11E-02 | 3.31E-02 | 3 | 87 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030308 | negative regulation of cell growth | 2.32E-03 | 9.60E-03 | 5 | 173 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030330 | DNA damage response, signal transduction by p53 class | 1.53E-03 | 6.79E-03 | 4 | 93 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030490 | maturation of SSU-rRNA | 6.42E-04 | 3.25E-03 | 3 | 32 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030512 | negative regulation of transforming growth factor beta receptor signaling pathway | 9.13E-04 | 4.44E-03 | 4 | 81 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030522 | intracellular receptor signaling pathway | 1.52E-03 | 6.78E-03 | 6 | 232 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0030901 | midbrain development | 1.30E-03 | 6.00E-03 | 4 | 89 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0031032 | actomyosin structure organization | 2.77E-09 | 3.70E-08 | 9 | 98 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0031098 | stress-activated protein kinase signaling cascade | 2.39E-04 | 1.38E-03 | 6 | 163 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0031145 | anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process | 1.14E-03 | 5.40E-03 | 4 | 86 | 190 | 35980 | POCG47 P62987 P62979 POCG48 POCG47 P63244 P19022 P62987 P62979 POCG48 P02144 P62263 P39019 O15273 Q14896 P10916 O14958 P09493 P68133 P68032 P45379 P13533 O15273 P68133 P68032 PDMV8 P0DMV9 P60033 P63244 P18660 P10916 P01160 P02511 POCG47 P62987 P62979 POCG48 P62263 P62249 P39019 |
| GO:0031324 | negative regulation of cellular metabolic process | 4.85E-04 | 2.55E-03 | 28 | 2707 | 190 | 35980 | POCG47 P0DMV8 P0DMV9 Q8N3K9 POCG48 P63244 P05090 P84243 Q14192 P62979 P62158 Q01628 P01034 P01034 P13765 P01033 P04060 O75116 P16989 P17535 P62263 P62987 Q14240 P02511 P04792 P60228 P20585 Q8N335 P07602 POCG47 P0DMV8 P0DMV9 Q969T9 Q8TAK5 POCG48 P63244 P60033 Q14192 P68871 P62979 P62158 P00441 P01034 Q13765 Q14116 P13639 O75116 P19022 P16989 Q9Y6H1 P17535 Q05639 Q8NWT8 P62987 Q13772 P17081 P04792 P25116 POCG47 Q13765 P0DMV8 P13639 P0DMV9 Q969T9 P16989 Q8TAK5 Q9Y6H1 P17535 POCG48 P63244 P60033 Q14192 P68871 P62979 P62158 P00441 P01034 P13765 P01033 P04060 O75116 P19022 P16989 Q9Y6H1 P17535 Q05639 Q8NWT8 P62987 Q13772 P17081 P04792 P25116 POCG47 Q13765 P0DMV8 P13639 P0DMV9 Q969T9 P16989 Q8TAK5 Q9Y6H1 P17535 POCG48 P63244 P60033 Q14192 P68871 P62979 P62158 P00441 P01034 P13765 P01033 P04060 O75116 P19022 P16989 Q9Y6H1 P17535 Q05639 Q8NWT8 P62987 Q13772 P17081 P04792 P25116 POCG47 P17081 P04792 P25116 POCG47 Q13765 P0DMV8 P13639 P0DMV9 Q969T9 P16989 Q8TAK5 Q9Y6H1 P17535 POCG48 P63244 P60033 Q14192 P68871 P62979 P62158 P00441 P01034 P13765 P01033 P04060 O75116 P19022 P16989 Q9Y6H1 P17535 Q05639 Q8NWT8 P62987 Q13772 P17081 P04792 P25116 POCG47 P17081 P04792 P25116 POCG47 Q13765 P0 |

| | | | | | | | | |
|------------|--|----------|----------|----|------|-----|-------|---|
| GO:0034654 | nucleobase-containing compound biosynthetic process | 3.06E-20 | 7.71E-19 | 68 | 3838 | 190 | 35980 | P0CG47 O75947 P01160 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P20674 Q13765 Q07020 P10606 Q96H40 P48047 P16989 Q9Y6H1 P84098 P63173 P68104 P61353 P46777 P05386 Q13772 P08066 P46776 P05387 P62249 P25398 P09669 O00483 P14854 P10176 P62891 P42766 Q02878 P25705 P18859 Q14192 Q9NP15 P61247 P62857 P62979 P56381 Q15004 P62851 P08708 P62906 P18077 P15954 P17535 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 P06576 |
| GO:0034655 | nucleobase-containing compound catabolic process | 1.28E-37 | 1.27E-35 | 39 | 401 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0034660 | ncRNA metabolic process | 1.70E-03 | 7.46E-03 | 11 | 723 | 190 | 35980 | P42766 Q9NSD9 P08708 P62263 P18077 P62857 P62913 P46777 P62753 P62249 P39019 |
| GO:0034762 | regulation of transmembrane transport | 9.86E-03 | 3.11E-02 | 8 | 557 | 190 | 35980 | P54368 O14958 Q9Y277 P01160 P23327 P62158 P25116 Q8N335 |
| GO:0034763 | negative regulation of transmembrane transport | 1.22E-02 | 3.60E-02 | 3 | 90 | 190 | 35980 | P54368 O14958 P62158 |
| GO:0035051 | cardiocyte differentiation | 3.85E-05 | 2.81E-04 | 6 | 117 | 190 | 35980 | O15273 P109116 Q14192 P01160 P68032 P13533 |
| GO:0035150 | regulation of tube size | 1.99E-03 | 8.47E-03 | 5 | 167 | 190 | 35980 | P16860 P01160 P68871 P25116 P00441 |
| GO:0035637 | multicellular organismal signaling | 2.26E-03 | 9.40E-03 | 5 | 172 | 190 | 35980 | O14958 P19429 P01160 P16615 P00441 |
| GO:0035666 | TRIF-dependent toll-like receptor signaling pathway | 7.21E-05 | 4.89E-04 | 5 | 81 | 190 | 35980 | P0CG47 P51452 P62987 P62979 P0CG48 |
| GO:0035872 | nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway | 1.03E-04 | 6.61E-04 | 4 | 46 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0036293 | response to decreased oxygen levels | 6.99E-06 | 5.91E-05 | 10 | 312 | 190 | 35980 | P0CG47 P02144 P01160 P19021 P62987 P62979 P02511 Q6P6C2 P0CG48 P1034 |
| GO:0036294 | cellular response to decreased oxygen levels | 6.78E-03 | 2.28E-02 | 4 | 141 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0036297 | interstrand cross-link repair | 7.21E-05 | 4.89E-04 | 4 | 42 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0038061 | NIK/NF-kappaB signaling | 1.92E-03 | 8.23E-03 | 4 | 99 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0038123 | toll-like receptor TLR1:TLR2 signaling pathway | 5.31E-05 | 3.71E-04 | 5 | 76 | 190 | 35980 | P0CG47 P51452 P62987 P62979 P0CG48 |
| GO:0038124 | toll-like receptor TLR6:TLR2 signaling pathway | 5.31E-05 | 3.71E-04 | 5 | 76 | 190 | 35980 | P0CG47 P51452 P62987 P62979 P0CG48 |
| GO:0040008 | regulation of growth | 3.51E-04 | 1.94E-03 | 12 | 695 | 190 | 35980 | Q13765 P63244 P16860 P109116 P84243 P60033 P01160 P80297 P16989 P02511 P13533 P00441 |
| GO:0040011 | locomotion | 4.58E-03 | 1.71E-02 | 17 | 1585 | 190 | 35980 | P0CG47 P51684 P0DMV8 P0DMV9 O75116 P19022 P35613 P19105 P0CG48 P39019 P60033 P60660 P62987 P83731 P62979 P62158 P06576 |
| GO:0040012 | regulation of locomotion | 4.51E-03 | 1.69E-02 | 11 | 822 | 190 | 35980 | P01033 P63244 P05090 P51684 P60033 P09382 P09493 O75116 P04792 Q01628 P25116 |
| GO:0042058 | regulation of epidermal growth factor receptor signaling | 9.56E-04 | 4.63E-03 | 4 | 82 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0042059 | negative regulation of epidermal growth factor receptor | 7.21E-05 | 4.89E-04 | 4 | 42 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0042060 | wound healing | 1.32E-06 | 1.28E-05 | 16 | 709 | 190 | 35980 | P07602 Q13765 P01033 P13929 P16615 P35613 P19105 P05090 P84243 P68871 P09493 P04275 P62158 P04792 P25116 P00441 |
| GO:0042176 | regulation of protein catabolic process | 4.17E-04 | 2.26E-03 | 9 | 419 | 190 | 35980 | P0CG47 P54368 P01033 P63244 P60033 P62987 P62979 P0CG48 P1034 |
| GO:0042221 | response to chemical | 1.53E-18 | 3.47E-17 | 74 | 4840 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 Q12988 Q96919 P01160 P16615 P35613 P0CG48 P39019 P63244 P05090 P13073 P00505 P39023 P09493 Q02818 P83731 P69905 P62158 P45379 P62753 P24752 P01034 P01033 P13639 P04406 O14880 P80297 P19021 P37108 P16989 P68032 Q08431 P19105 O14958 Q05639 P68104 P60660 P09382 P08574 P47985 P02511 Q13772 P17081 P07602 P13929 P51684 P68363 P84243 P60033 Q14192 P68871 Q9UB9Y P17174 Q16654 P22352 P62979 Q01628 P00441 P51452 P02144 Q14116 O75116 P68133 P13533 P17535 Q8N8D1 P41222 P62987 Q14240 P04792 P25116 P63316 |
| GO:0042246 | tissue regeneration | 3.98E-03 | 1.51E-02 | 3 | 60 | 190 | 35980 | Q13765 P13929 P05090 |
| GO:0042254 | ribosome biogenesis | 5.02E-12 | 8.07E-11 | 16 | 293 | 190 | 35980 | P08708 P18077 P39019 P42677 P42766 Q02878 P63173 P39023 P62263 P46783 P83731 P62857 P62913 P46777 P62753 P62249 |
| GO:0042255 | ribosome assembly | 3.22E-14 | 6.07E-13 | 11 | 63 | 190 | 35980 | P42677 Q02878 P63173 P08708 P39023 P62263 P46783 P83731 P62913 P46777 P39019 |
| GO:0042273 | ribosomal large subunit biogenesis | 2.32E-10 | 3.34E-09 | 8 | 50 | 190 | 35980 | P42766 Q02878 P63173 P39023 P18077 P83731 P62913 P46777 |
| GO:0042274 | ribosomal small subunit biogenesis | 6.63E-12 | 1.05E-10 | 9 | 51 | 190 | 35980 | P42677 P63173 P08708 P62263 P46783 P62857 P62753 P62249 P39019 |
| GO:0042276 | error-prone translation synthesis | 2.74E-06 | 2.52E-05 | 4 | 19 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0042278 | purine nucleoside metabolic process | 2.17E-22 | 6.15E-21 | 29 | 471 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 Q15239 P20674 Q00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0042325 | regulation of phosphorylation | 2.58E-03 | 1.05E-02 | 18 | 1628 | 190 | 35980 | P07602 P0CG47 P51452 Q14116 O75116 P19022 P0CG48 P63244 Q05639 P60033 P62987 P23327 P62979 P62158 P04792 P25116 Q8N335 P00441 |
| GO:0042327 | positive regulation of phosphorylation | 2.24E-03 | 9.31E-03 | 14 | 1100 | 190 | 35980 | P07602 P0CG47 Q14116 O75116 P19022 P0CG48 P63244 Q05639 P60033 P62987 P62979 P62158 P25116 P00441 |
| GO:0042330 | taxis | 7.38E-03 | 2.44E-02 | 11 | 880 | 190 | 35980 | P0CG47 P51684 P60660 O75116 P62987 P83731 P62979 P62158 P19105 P0CG48 P39019 |
| GO:0042391 | regulation of membrane potential | 3.72E-03 | 1.43E-02 | 7 | 371 | 190 | 35980 | P0CG47 P63244 O14958 P01160 P16615 Q8N335 P00441 |
| GO:0042451 | purine nucleoside biosynthetic process | 1.45E-06 | 1.38E-05 | 8 | 150 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 |
| GO:0042455 | ribonucleoside biosynthetic process | 4.96E-06 | 4.38E-05 | 8 | 177 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 |
| GO:0042493 | response to drug | 3.57E-05 | 2.63E-04 | 11 | 458 | 190 | 35980 | P13929 P05090 P13639 P09382 P19021 P47985 P37108 P68032 P17535 P00441 P1034 |
| GO:0042542 | response to hydrogen peroxide | 2.78E-06 | 2.53E-05 | 7 | 115 | 190 | 35980 | P02144 P13639 P68871 P02511 P69905 P00441 P1034 |
| GO:0042590 | antigen processing and presentation of exogenous peptide antigen via MHC class I | 7.65E-03 | 2.52E-02 | 4 | 146 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0042592 | homeostatic process | 1.25E-05 | 1.00E-04 | 23 | 1590 | 190 | 35980 | P0CG47 P02144 P02792 P51684 P08708 P19022 P16615 P0CG48 P39019 P13693 P63244 O14958 P19429 P09382 P62263 P17174 Q16654 P23327 P04792 P62753 P25116 P00441 P06576 |
| GO:0042692 | muscle cell differentiation | 5.11E-11 | 7.63E-10 | 15 | 290 | 190 | 35980 | Q14315 O15273 Q14896 P109116 P01160 P19022 P68133 P16615 P68032 P13533 O14958 Q14192 P09382 P09493 P45379 |
| GO:0042743 | hydrogen peroxide metabolic process | 2.41E-05 | 1.85E-04 | 4 | 32 | 190 | 35980 | P68871 P22352 P69905 P00441 |
| GO:0042744 | hydrogen peroxide catabolic process | 1.32E-04 | 8.21E-04 | 3 | 19 | 190 | 35980 | P68871 P22352 P69905 |
| GO:0042769 | DNA damage response, detection of DNA damage | 3.89E-05 | 2.81E-04 | 4 | 36 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0042770 | signal transduction in response to DNA damage | 2.63E-03 | 1.06E-02 | 4 | 108 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0042773 | ATP synthesis coupled electron transport | 1.55E-17 | 3.37E-16 | 14 | 83 | 190 | 35980 | O00217 O95169 P51970 O43674 O14561 O00483 O43920 O95167 P10176 O95178 O96000 P13073 O15239 P20674 |
| GO:0042775 | mitochondrial ATP synthesis coupled electron transport | 5.07E-18 | 1.12E-16 | 14 | 77 | 190 | 35980 | O00217 O95169 P51970 O43674 O14561 O00483 O43920 O95167 P10176 O95178 O96000 P13073 O15239 P20674 |
| GO:0042776 | mitochondrial ATP synthesis coupled proton transport | 4.89E-12 | 7.99E-11 | 7 | 19 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 P06576 |
| GO:0042981 | regulation of apoptotic process | 3.10E-05 | 2.32E-04 | 23 | 1685 | 190 | 35980 | P0CG47 Q13765 P01033 P0DMV8 P0DMV9 P16989 P68032 P0CG48 Q8N8D1 P13693 P63244 Q05639 Q14192 P09382 P62987 P61247 Q16654 P62979 P02511 P04792 P62753 P25116 P00441 |
| GO:0043043 | peptide biosynthetic process | 1.35E-30 | 7.32E-29 | 47 | 1020 | 190 | 35980 | P25398 Q9NSD9 P62280 P12235 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P13639 P08708 P62906 P18077 P37108 P42677 P84098 P15880 Q05639 P63173 P68104 Q02543 Q9NW8T P61353 Q00325 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0043065 | positive regulation of apoptotic process | 2.73E-03 | 1.09E-02 | 10 | 657 | 190 | 35980 | P0CG47 P63244 Q05639 P62987 P62979 P62753 P25116 P00441 P0CG48 Q8N8D1 |
| GO:0043066 | negative regulation of apoptotic process | 2.93E-06 | 2.66E-05 | 18 | 941 | 190 | 35980 | P0CG47 Q13765 P01033 P0DMV8 P0DMV9 P16989 P68032 P0CG48 P13693 Q14192 P62987 P61247 Q16654 P62979 P02511 P04792 P25116 P00441 |
| GO:0043067 | regulation of programmed cell death | 3.72E-06 | 3.31E-05 | 25 | 1698 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 P12235 P0CG48 P13693 P63244 Q14192 P61247 Q16654 P62979 P62753 P00441 P1034 Q13765 P01033 P16989 P68032 Q8N8D1 Q05639 P09382 P62987 P02511 P04792 P25116 |
| GO:0043068 | positive regulation of programmed cell death | 2.88E-03 | 1.14E-02 | 10 | 662 | 190 | 35980 | P0CG47 P63244 Q05639 P62987 P62979 P62753 P25116 P00441 P0CG48 Q8N8D1 |
| GO:0043069 | negative regulation of programmed cell death | 8.07E-07 | 7.97E-06 | 19 | 951 | 190 | 35980 | P0CG47 Q13765 P01033 P0DMV8 P0DMV9 P16989 P68032 P12235 P0CG48 P13693 Q14192 P62987 P61247 Q16654 P62979 P02511 P04792 P25116 P00441 |
| GO:0043086 | negative regulation of catalytic activity | 4.54E-05 | 3.23E-04 | 17 | 1048 | 190 | 35980 | P0CG47 P51452 P54368 P01033 O75116 Q8N335 P0CG48 P63244 P19429 P62987 Q14240 P62979 P02511 P04792 P45379 Q8WYQ3 P1034 |
| GO:0043122 | regulation of I-kappaB kinase/NF-kappaB signaling | 5.62E-05 | 3.89E-04 | 8 | 248 | 190 | 35980 | P0CG47 Q14116 P09382 P62987 P62979 P04792 P25116 P0CG48 |
| GO:0043123 | positive regulation of I-kappaB kinase/NF-kappaB | 7.95E-05 | 5.33E-04 | 7 | 193 | 190 | 35980 | P0CG47 Q14116 P09382 P62987 P62979 P25116 P0CG48 |

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|------------|---|----------|----------|-----|-------|-----|-------|---|
| GO:0043170 | macromolecule metabolic process | 2.06E-04 | 1.22E-03 | 93 | 13022 | 190 | 35980 | P0CG47 Q9NSD9 P0DMV8 P01160 P40926 P62280 Q8TAK5 P0CG48 P39019 P63244 P13073 P39023 P62273 P46783 P83731 P62913 P62158 P24311 P62753 P20674 P01034 Q13765 Q07020 P10606 Q96H40 P13639 P04406 O14561 P19021 Q9Y5N6 P37108 P16989 Q9Y6H1 Q08431 P84098 Q05639 P63173 P68104 P61353 P46777 P02511 P05386 Q13772 P60866 P46776 P05387 P60228 P62249 P25398 P09669 P68363 O00483 P14854 P10176 P12235 P62891 P42766 Q02878 P84243 P60033 Q14192 P61247 P62857 P16654 P62979 Q15004 P62851 P51452 Q14116 Q9POU1 P08708 O75116 P62906 P18077 P15954 Q6P6C2 P17535 Q8N8D1 P42677 P15880 Q02543 Q9NWT8 Q9Y3D2 Q00325 P62263 P62987 Q14240 P62945 P04275 P04792 P62269 P25116 P20585 |
| GO:0043207 | response to external biotic stimulus | 1.43E-03 | 6.49E-03 | 13 | 931 | 190 | 35980 | P52179 Q14116 P40925 Q6P6C2 P10176 P17535 P13693 P62891 P62987 Q16654 P04792 Q01628 P25116 |
| GO:0043241 | protein complex disassembly | 2.00E-42 | 2.48E-40 | 37 | 253 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 Q9NWT8 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0043405 | regulation of MAP kinase activity | 1.31E-03 | 6.05E-03 | 9 | 493 | 190 | 35980 | P0CG47 P51452 P60033 P62987 P62979 P62158 P25116 P00441 P0CG48 |
| GO:0043406 | positive regulation of MAP kinase activity | 1.05E-03 | 5.03E-03 | 6 | 216 | 190 | 35980 | P0CG47 P60033 P62987 P62979 P00441 P0CG48 |
| GO:0043408 | regulation of MAPK cascade | 5.56E-03 | 1.93E-02 | 11 | 846 | 190 | 35980 | P07602 P0CG47 P51452 P60033 P19022 P62987 P62979 P62158 P25116 P00441 P0CG48 |
| GO:0043410 | positive regulation of MAPK cascade | 2.31E-03 | 9.57E-03 | 10 | 642 | 190 | 35980 | P07602 P0CG47 P60033 P19022 P62987 P62979 P62158 P25116 P00441 P0CG48 |
| GO:0043434 | response to peptide hormone | 6.75E-07 | 6.71E-06 | 15 | 591 | 190 | 35980 | P0CG47 P01033 P01160 P16615 P35613 P17535 P0CG48 P17174 P08574 P62987 Q16654 P62979 P62158 P17081 P62753 |
| GO:0043436 | oxoacid metabolic process | 1.89E-30 | 1.01E-28 | 56 | 1605 | 190 | 35980 | P06732 Q9NSD9 P40926 P40925 P62280 P35613 P39019 P00505 P39023 P62273 P07195 P46783 P83731 P62913 P62753 P24752 Q07020 P04406 Q14561 P19021 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 Q13011 P13929 P25398 P62891 P42766 Q02878 P17174 P61247 P62857 Q16654 Q16698 P62979 P62851 P08708 P62906 P18077 P51857 P42677 P41222 P15880 P17540 Q02543 P62263 P62987 P62945 P62269 P48735 |
| GO:0043462 | regulation of ATPase activity | 5.51E-08 | 6.20E-07 | 7 | 65 | 190 | 35980 | Q14896 P19429 P08590 P09493 P45379 P13533 P63316 |
| GO:0043487 | regulation of RNA stability | 1.22E-05 | 9.89E-05 | 7 | 144 | 190 | 35980 | P0CG47 P0DMV8 P62987 P16989 P62979 P04792 P0CG48 |
| GO:0043488 | regulation of mRNA stability | 1.02E-05 | 8.39E-05 | 7 | 140 | 190 | 35980 | P0CG47 P0DMV8 P62987 P16989 P62979 P04792 P0CG48 |
| GO:0043500 | muscle adaptation | 6.42E-04 | 3.25E-03 | 3 | 32 | 190 | 35980 | O15273 P01160 P68133 |
| GO:0043502 | regulation of muscle adaptation | 5.55E-04 | 2.86E-03 | 4 | 71 | 190 | 35980 | P16615 Q8N3K9 P12883 P63316 |
| GO:0043549 | regulation of kinase activity | 8.60E-03 | 2.76E-02 | 12 | 1025 | 190 | 35980 | P0CG47 P51452 P63244 Q05639 P60033 P62987 P62979 P62158 P04792 P25116 P00441 P0CG48 |
| GO:0043603 | cellular amide metabolic process | 1.34E-26 | 5.76E-25 | 49 | 1396 | 190 | 35980 | Q9NSD9 P62280 P39019 P39023 P62273 P46783 P83731 P62913 P62753 Q13765 Q07020 P13639 P19021 P37108 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P12235 P62891 P42766 Q02878 P61247 P62857 P62979 P62851 P00441 P08708 P62906 P18077 P42677 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 |
| GO:0043604 | amide biosynthetic process | 7.21E-29 | 3.57E-27 | 47 | 1117 | 190 | 35980 | P25398 Q9NSD9 P62280 P12235 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P13639 P08708 P62906 P18077 P37108 P42677 P84098 P15880 Q05639 P63173 P68104 Q02543 Q9NWT8 P61353 Q00325 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0043618 | regulation of transcription from RNA polymerase II promoter in response to stress | 3.31E-04 | 1.86E-03 | 4 | 62 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0043620 | regulation of DNA-templated transcription in response to stress | 4.45E-04 | 2.39E-03 | 4 | 67 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0043623 | cellular protein complex assembly | 1.61E-08 | 1.99E-07 | 15 | 442 | 190 | 35980 | O00217 O15273 Q14896 O95169 P51970 O43674 O14561 O43920 O95167 O95178 O96000 O14958 Q9Y3D2 P02511 O15239 |
| GO:0043624 | cellular protein complex disassembly | 1.71E-44 | 2.31E-42 | 37 | 224 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P13639 P08708 P62906 P18077 P37108 P42677 P84098 P15880 Q05639 P63173 P68104 Q02543 Q9NWT8 P61353 Q00325 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0043627 | response to estrogen | 1.39E-03 | 6.35E-03 | 6 | 228 | 190 | 35980 | P13639 Q96979 P19021 P02511 Q08431 P01034 |
| GO:0043648 | dicarboxylic acid metabolic process | 3.45E-04 | 1.91E-03 | 5 | 113 | 190 | 35980 | P00505 P40926 P40925 P17174 P48735 |
| GO:0043666 | regulation of phosphoprotein phosphatase activity | 1.37E-02 | 3.96E-02 | 3 | 94 | 190 | 35980 | O75116 Q8N3K9 P62158 |
| GO:0043900 | regulation of multi-organism process | 3.47E-04 | 1.92E-03 | 10 | 499 | 190 | 35980 | P52179 P01033 P41222 P09382 P40925 P62987 Q16654 Q6P6C2 P10176 Q1628 |
| GO:0043933 | macromolecular complex subunit organization | 2.72E-25 | 1.08E-23 | 67 | 3020 | 190 | 35980 | Q43674 P62280 P39019 O96000 P39023 P62273 P46783 P83731 P62913 P6905 P45379 P62753 P24752 Q15239 Q07020 Q14896 O95169 O14561 P19021 P19022 Q43920 P68032 O95167 P84098 O14958 P63173 P61353 P46777 P02511 P05386 P60866 P46776 P05387 P60228 P62249 P25398 O95178 P62891 P42766 Q02878 P84243 P68871 P61247 P62857 P22352 Q16698 P62979 P62851 O00217 O15273 P51970 P08708 P62906 P68133 P18077 P17661 P42677 P15880 Q02543 Q9NWT8 Q9Y3D2 P62263 P62987 P62945 P04275 P63313 P62269 |
| GO:0044033 | multi-organism metabolic process | 3.79E-56 | 2.82E-53 | 38 | 130 | 190 | 35980 | P0CG47 P25398 P62280 P0CG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0044042 | glucan metabolic process | 2.88E-05 | 2.17E-04 | 5 | 67 | 190 | 35980 | P0CG47 P62987 P62979 P62158 P0CG48 |
| GO:0044057 | regulation of system process | 4.48E-13 | 7.75E-12 | 22 | 568 | 190 | 35980 | Q14896 P10916 P01160 P16615 P17661 Q8N3K9 P13533 P12883 P16860 O14958 P19429 Q9UB9 P08590 P09493 P23327 P62158 P45379 P25116 O14558 Q8N335 P00441 P63316 |
| GO:0044085 | cellular component biogenesis | 2.53E-16 | 5.18E-15 | 52 | 2752 | 190 | 35980 | P0CG47 P10916 O43674 P0CG48 P39019 O96000 P39023 P09493 P46783 P83731 P62913 P69905 P45379 P62753 P24752 Q15239 Q14896 O95169 O14561 P19021 P19022 Q43920 P68032 O95167 O14958 P63173 P46777 P02511 P06228 P62249 O95178 P42766 Q02878 P84243 P68871 P62857 P22352 Q16698 P62979 Q00217 Q14315 O15273 P51970 P08708 P68133 P18077 P13533 P42677 Q9Y3D2 P62263 P62987 P04275 |
| GO:0044092 | negative regulation of molecular function | 7.18E-05 | 4.89E-04 | 19 | 1310 | 190 | 35980 | P0CG47 P51452 P54368 P01033 O75116 Q8N3K9 P0CG48 P63244 O14958 P19429 P62987 Q14240 P62979 P02511 P62158 P04792 P45379 Q8WYQ3 P01034 |
| GO:0044237 | cellular metabolic process | 5.94E-21 | 1.56E-19 | 140 | 14451 | 190 | 35980 | O75947 O43674 O96000 P16860 P13073 O14949 P07195 P46783 P83731 P62913 P62753 P24752 Q15239 P20674 Q13765 O95169 P13639 P48047 P04406 O14561 Q9Y5N6 P16989 Q9Y6H1 O95167 Q08431 P84098 P63173 P68104 P104 P08574 P47985 P46777 Q13772 P60866 P46776 P60228 P62249 Q13011 Q8N335 P07602 P25398 P68363 P01176 O95178 P12235 P62891 P25705 P18859 Q14192 P68871 Q16654 P56381 P00441 P54368 O00217 Q14116 Q08493 P08708 O75116 P18077 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P15880 P17540 Q02543 Q9NWT8 Q9Y3D2 P62263 Q14240 P62945 P62280 P0CG47 P06732 Q9NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 Q8TAK5 P36542 P35613 P0CG48 P39019 P00505 P39023 P62273 P24310 P69905 P62158 P24311 Q8WYQ3 P01034 Q07020 P10606 Q96H40 O14880 P19021 P37108 O43920 Q05639 P61353 P02511 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 P60033 Q9NPI5 P17174 P61247 P62857 P22352 Q16698 P62979 Q15004 P62851 P51452 P51970 Q9POU1 P62906 P15954 P51857 P13533 Q00325 P62987 P25116 P20585 P06576 P48735 |
| GO:0044238 | primary metabolic process | 2.73E-13 | 4.81E-12 | 132 | 15593 | 190 | 35980 | O75947 O43674 O96000 P16860 P13073 P07195 P46783 P83731 P62913 P62753 P24752 Q15239 P20674 Q13765 O95169 P13639 P48047 O14561 Q9Y5N6 P16989 Q9Y6H1 O95167 Q08431 P84098 P63173 P68104 P46777 Q13772 P60866 P46776 P60228 P62249 Q13011 Q8N335 P07602 P25398 P68363 P01176 O95178 P12235 P62891 P25705 P18859 Q14192 Q16654 P56381 P01176 Q08493 P08708 O75116 P18077 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9NWT8 Q9Y3D2 P62263 Q14240 P62945 P62280 P0CG47 P06732 Q9NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P00505 P00505 P39023 P62273 P24310 P09605 P62158 P24311 Q8WYQ3 P01034 Q07020 P10606 Q96H40 O14880 P19021 P37108 O43920 Q05639 P61353 P02511 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 P60033 Q9NPI5 P17174 P61247 P62857 P22352 Q16698 P62979 Q15004 P62851 P51452 P51970 Q9POU1 P62906 P15954 P51857 P13533 Q00325 P62987 P25116 P20585 P06576 P48735 |

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|------------|--|----------|----------|-----|-------|-----|-------|---|
| GO:0044248 | cellular catabolic process | 8.42E-25 | 3.13E-23 | 51 | 1684 | 190 | 35980 | P0CG47 P62280 P0CG48 P39019 P00505 P39023 P62273 P46783 P83731 P62913 P69905 P62158 P62753 P24752 Q07020 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60288 P62249 Q13011 P25398 P62891 P42766 Q02878 P68871 P11714 P61247 P62857 P22352 Q16698 P62979 P62851 Q08493 P08708 P62906 P18077 P51857 P42677 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:0044249 | cellular biosynthetic process | 1.09E-18 | 2.51E-17 | 88 | 6618 | 190 | 35980 | P0CG47 Q75947 Q9NSD9 P01160 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P00505 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P24752 P20674 Q13765 Q07020 P10606 Q96H40 P13639 P48047 Q14561 Q14880 Q9Y5N6 P37108 P16989 Q9Y6H1 P84098 Q05639 P63173 P68104 P63173 P68104 P61353 P46777 P02511 P05386 Q13772 P60866 P46776 P05387 P60288 P62249 Q8N335 P25398 P09669 Q00483 P14854 P10176 P12235 P62857 P42766 Q02878 P25705 P18859 Q14192 Q9NPI5 P17174 P61247 P62857 P62979 P56381 Q15004 P62851 P00441 P54368 P08708 P62906 P18077 P15954 P51857 P17535 P42677 P41222 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:0044260 | cellular macromolecule metabolic process | 4.88E-06 | 4.32E-05 | 89 | 11251 | 190 | 35980 | P0CG47 Q9NSD9 P01160 P40926 P62280 Q8TAK5 P0CG48 P39019 P13073 P39023 P62273 P46783 P83731 P62913 P62158 P24311 P62753 P20674 P1034 Q13765 Q07020 P10606 Q96H40 P13639 P04406 Q14561 P19021 Q9Y5N6 P37108 P16989 Q9Y6H1 Q08431 P84098 Q05639 P63173 P68104 P61353 P46777 P02511 P05386 Q13772 P60866 P46776 P05387 P60288 P62249 P25398 P09669 P68363 Q00483 P14854 P10176 P12235 P62857 P42766 Q02878 P84243 P60033 Q14192 P61247 P62857 Q16654 P62979 Q15004 P62851 P51452 Q14116 Q9P0U1 P08708 Q75116 P62906 P18077 P15954 Q6P6C2 P17535 Q8N8D1 P42677 P15880 Q02543 Q9NWT8 Q9Y3D2 Q00325 P62263 P62987 Q14240 P62945 P62269 P25116 P20585 |
| GO:0044262 | cellular carbohydrate metabolic process | 1.19E-04 | 7.49E-04 | 7 | 206 | 190 | 35980 | P0CG47 P17174 P62887 P62979 P62158 P0CG48 P48735 |
| GO:0044264 | cellular polysaccharide metabolic process | 8.10E-05 | 5.40E-04 | 5 | 83 | 190 | 35980 | P0CG47 P62987 P62979 P62158 P0CG48 |
| GO:0044265 | cellular macromolecule catabolic process | 2.97E-23 | 8.93E-22 | 40 | 1029 | 190 | 35980 | P0CG47 P25398 P62280 P0CG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P63173 P62857 P62913 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60288 P62249 |
| GO:0044267 | cellular protein metabolic process | 3.63E-09 | 4.75E-08 | 68 | 6461 | 190 | 35980 | P0CG47 Q9NSD9 P01160 P40926 P62280 P0CG48 P39019 P39023 P62273 P46783 P83731 P62913 P62158 P24311 P62753 P20674 P1034 Q13765 Q07020 P10606 Q96H40 P13639 P04406 Q14561 P19021 P37108 Q9Y6H1 Q08431 P84098 Q05639 P63173 P68104 P61353 P46777 P02511 P05386 P60866 P46776 P05387 P60288 P62249 P25398 P68363 P12235 P62891 P42766 Q02878 P25705 P18859 Q14192 Q9NPI5 P61247 P62857 Q16654 P62979 P62851 P51452 Q14116 Q9P0U1 P08708 Q75116 P62906 P18077 P42677 P15880 Q02543 Q9NWT8 Q9Y3D2 Q00325 P62263 P62987 Q14240 P62945 P62269 P25116 |
| GO:0044270 | cellular nitrogen compound catabolic process | 8.72E-35 | 6.17E-33 | 39 | 474 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60288 P62249 |
| GO:0044271 | cellular nitrogen compound biosynthetic process | 1.96E-20 | 5.03E-19 | 78 | 4964 | 190 | 35980 | P0CG47 Q75947 Q9NSD9 P01160 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P20674 Q13765 Q07020 P10606 Q96H40 P13639 P48047 P37108 P16989 Q9Y6H1 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 Q13772 P60866 P46776 P05387 P60288 P62249 P25398 P09669 Q00483 P14854 P10176 P12235 P62857 P42766 Q02878 P25705 P18859 Q14192 Q9NPI5 P61247 P62857 P62979 P56381 Q15004 P62851 P54368 P08708 P62906 P18077 P15954 P17535 P42677 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:0044281 | small molecule metabolic process | 2.67E-59 | 6.27E-56 | 107 | 3389 | 190 | 35980 | O75947 Q43674 Q96000 P16860 P13073 Q14949 P07195 P46783 P83731 P62913 P62753 P24752 Q15239 P20674 Q95169 P48047 P04406 Q14561 P80297 Q95167 P84098 P63173 P08574 P47985 P46777 P60866 P46776 P62249 Q13011 Q8N335 P60760 P25398 P10176 Q95178 P12235 P62891 P25705 P18859 Q14192 P68871 Q16654 P56381 P54368 Q00217 Q08493 P08708 P18077 P12883 P42677 P41222 P15880 P17540 Q02543 P62263 P62945 P62269 P0CG47 P06732 Q9NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 P36542 P35613 P0CG48 P39019 P05090 P00505 P39023 P62273 P69905 P62158 P24311 Q8WYQ3 Q07020 P10606 Q14880 P19021 Q43920 P61353 P05386 P17081 P05387 P13929 P09669 Q00483 P14854 P42766 Q02878 Q9NPI5 P17174 P61247 P62857 Q16698 P62979 P62851 P51970 P62906 P15954 P51857 P13533 P62987 P06576 P48735 |
| GO:0044282 | small molecule catabolic process | 1.02E-03 | 4.89E-03 | 8 | 382 | 190 | 35980 | P13929 P00505 P04406 P17174 Q16698 P51857 P24752 Q13011 |
| GO:0044283 | small molecule biosynthetic process | 1.58E-03 | 6.98E-03 | 10 | 609 | 190 | 35980 | P13929 P41222 P00505 P40926 P04406 Q14561 P40925 P17174 P51857 P24752 |
| GO:0044403 | symbiosis, encompassing mutualism through parasitism | 2.04E-33 | 1.26E-31 | 46 | 830 | 190 | 35980 | P0CG47 P25398 P0DMV8 P0DMV9 P62280 P12235 P0CG48 P39019 P62891 P42766 P63244 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P08708 P62906 P18077 Q08431 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0044409 | entry into host | 1.11E-02 | 3.31E-02 | 3 | 87 | 190 | 35980 | P0DMV8 P0DMV9 P60033 |
| GO:0044419 | interspecies interaction between organisms | 2.04E-33 | 1.26E-31 | 46 | 830 | 190 | 35980 | P0CG47 P25398 P0DMV8 P0DMV9 P62280 P12235 P0CG48 P39019 P62891 P42766 P63244 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P08708 P62906 P18077 Q08431 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0044699 | single-organism process | 3.25E-21 | 8.72E-20 | 174 | 22141 | 190 | 35980 | O75947 P10916 Q43674 Q9H3K2 P16615 Q96000 P16860 P13073 Q14949 P09493 P07195 P46783 P83731 P62913 P62753 P24752 Q15239 P20674 Q13765 Q95169 P13639 P48047 Q9Y277 P04406 Q14561 P08297 Q9Y5N6 P16989 Q9Y6H1 Q95167 Q08431 P19105 P84098 Q14958 P63173 P09382 P08574 P47985 P46777 Q13772 P60866 P46776 P62249 Q13011 Q8N335 P0760 P25179 P25398 P68363 P10176 Q95178 P12235 P13639 P62891 P19429 P25705 P18859 Q14192 P68871 Q16654 P56381 Q01628 P00441 P54368 Q00217 Q14116 Q15273 Q08493 P08708 Q14515 Q75116 P68133 P18077 P17661 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9NWT8 Q9Y3D2 P62263 Q14240 P62945 P62269 P0CG47 P6732 Q9NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 P36542 P35613 P0CG48 P39019 P63244 P05090 Q14094 P00505 P39023 P62273 P24310 P69905 P62158 P45379 P24311 Q8WYQ3 P1034 Q07020 P1033 P10606 Q14896 Q14880 P19021 P19022 P14406 P37108 Q43920 P68032 P08493 P61353 P06606 P02511 P05386 P17081 P05387 P13929 P02792 P09669 P51684 Q00483 P14854 P42766 Q02878 P84243 P60033 Q9NPI5 P17174 P61247 P62857 P23327 P22352 Q16698 P62979 Q15004 P62851 P51452 P02144 Q14315 P51970 Q9P0U1 Q75954 P62906 P15954 P51857 P13533 Q00325 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P06576 P63316 P48735 |
| GO:0044706 | multi-multicellular organism process | 1.10E-02 | 3.29E-02 | 5 | 251 | 190 | 35980 | P01160 P19021 P35613 P00441 P101034 |
| GO:0044707 | single-multicellular organism process | 1.97E-08 | 2.37E-07 | 64 | 6139 | 190 | 35980 | P0CG47 P10916 P01160 P16615 P62280 P35613 P0CG48 P39019 P63244 P05090 Q14949 P09493 P83731 P62158 P45379 P24311 P24752 P01034 Q13765 P01033 P10606 Q14896 P13639 P19021 P19022 P13639 P16989 P68032 Q08431 P19105 Q14958 P63173 P08493 P60660 P09382 P02511 Q13772 P07602 P14854 P19429 P25705 P62857 P84243 P18859 Q14192 P68871 P62979 P00441 P02144 Q14116 Q15273 Q75116 P68133 P51857 P13533 P17535 P12883 P08590 P62263 P62987 P04275 P04792 P25116 P20585 P06576 P63316 |

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|------------|---|----------|----------|-----|-------|-----|-------|---|
| GO:0044710 | single-organism metabolic process | 2.89E-35 | 2.15E-33 | 122 | 8018 | 190 | 35980 | O75947 O43674 O96000 P16860 P13073 O14949 P07195 P46783 P83731 P62913 P62753 P24752 O15239 P20674 O95169 P13639 P48047 P04406 O14561 P0297 O95167 P84098 P63173 P08574 P47985 P46777 P60866 P46776 P62249 Q13011 Q8N335 P07602 P52179 P25398 P10176 O95178 P12235 P62891 P25705 P18859 Q14192 P68871 Q16654 P56381 P00441 P54368 O00217 Q14116 Q08493 P08708 P18077 Q6P6C2 P12883 P42677 P41222 P15880 P17540 Q02543 Q9NWT8 Q9Y3D2 P62263 P62945 P62269 P0CCG47 P06732 Q9NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 P36542 P35613 P0CCG48 P39019 P05090 P00505 P39023 P62273 P69905 P62158 P24311 Q8WYQ3 Q07020 P10606 O14880 P19021 O43920 P61353 P02511 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P60033 Q9NP15 P1714 P61247 P62857 P23232 Q16698 P62979 Q15004 P62851 P51452 P51970 Q9P0U1 P62906 P15954 P51857 P13533 P62987 P04275 P20585 P06576 P48735 |
| GO:0044711 | single-organism biosynthetic process | 1.32E-07 | 1.42E-06 | 30 | 1946 | 190 | 35980 | P0CCG47 P13929 O75947 P01160 P40926 P40925 P36542 P0CCG48 P16860 P25705 P00505 P18859 Q9NP15 P1714 P62979 P56381 Q15004 Q8WYQ3 P24752 P13639 P48047 P04406 O14561 O14880 P51857 P41222 Q9NWT8 P62987 Q8N335 P06576 |
| GO:0044712 | single-organism catabolic process | 2.34E-06 | 2.17E-05 | 21 | 1224 | 190 | 35980 | P0CCG47 P52179 P13929 Q08493 Q9P0U1 P04406 P40925 P51857 P10176 P0CCG48 P00505 P68871 P17174 P62987 P22352 Q16698 P62979 P69905 P62158 P24752 Q13011 |
| GO:0044723 | single-organism carbohydrate metabolic process | 1.26E-03 | 5.88E-03 | 14 | 1034 | 190 | 35980 | P0CCG47 P13929 P40926 P04406 P40925 P0CCG48 P05090 P00505 P17174 P62987 Q16654 P62979 P62158 P48735 |
| GO:0044763 | single-organism cellular process | 2.58E-25 | 1.04E-23 | 168 | 19209 | 190 | 35980 | O75947 P10916 O43674 Q9H3K2 P16615 O96000 P16860 P13073 O14949 P09493 P07195 P46783 P83731 P62913 P62753 P24752 O15239 P20674 O95169 P13639 P48047 Q9Y277 P04406 O14561 Q9Y5N6 O95167 Q08431 P19105 P84098 O14958 P63173 P09382 P08574 P47985 P46777 Q13772 P60866 P46776 P62249 Q13011 Q8N335 P07602 P52179 P25398 P68363 P10176 Q95178 P12235 P13639 P62891 P19429 P25705 P18859 Q14192 P68871 Q16654 P56381 Q01628 P00441 O00217 Q14116 O15273 Q08493 P08708 Q14515 O75116 P68133 P18077 P17661 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9NWT8 Q9Y3D2 P62263 Q14240 P62945 P62269 P0CCG47 P06732 Q9NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 P36542 P35613 P0CCG48 P39019 P63244 P05090 P39023 P62273 P24310 P69905 P62158 P45379 P24311 Q8WYQ3 P101034 Q07020 P01033 P10606 Q14896 Q14880 P19021 P19022 P14406 P37108 Q043920 P68032 P08493 P61353 P60660 P02511 P05386 P17081 P05387 P13929 P02792 P09669 P51684 O00483 P14854 P42766 Q02878 P84243 P60033 Q9NP15 P1714 P61247 P62857 P23232 Q16698 P62979 Q15004 P62851 P51452 P51970 Q9P0U1 Q14315 P51970 Q9P0U1 O75954 P62906 P15954 P51857 P13533 Q00325 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P06576 P63316 P48735 |
| GO:0044764 | multi-organism cellular process | 1.95E-34 | 1.29E-32 | 46 | 787 | 190 | 35980 | P0CCG47 P25398 P0DMV8 P0DMV9 P62280 P12235 P0CCG48 P39019 P62991 P42766 P63244 Q02878 P60033 P39023 P62273 P46783 P61247 P63731 P62857 P62913 P62753 P62851 P62753 Q13765 Q07020 P08708 P62906 P18077 Q08431 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0044765 | single-organism transport | 7.96E-25 | 3.00E-23 | 87 | 5265 | 190 | 35980 | P0CCG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CCG48 P39019 P16860 P05090 P13073 P00505 O14949 P39023 P62273 P46783 P83731 P62913 P24310 P69905 P62158 P24311 P62753 P20674 Q07020 P01033 P10606 P48047 Q9Y277 P19021 P14406 P37108 Q9Y6H1 Q08431 P84098 O14958 P63173 P61353 P47985 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P02792 P25398 P09669 P68363 O00483 P14854 P10176 P12235 P13639 P62891 P42766 Q02878 P25705 P18859 P60033 P68871 P61247 P62857 P62979 P56381 P62851 P00441 P02144 Q9P0U1 P08708 P62906 P18077 P15954 Q6P6C2 P42677 P15880 Q02543 Q00325 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:0044766 | multi-organism transport | 3.89E-05 | 2.81E-04 | 4 | 36 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0044767 | single-organism developmental process | 2.08E-08 | 2.47E-07 | 63 | 6002 | 190 | 35980 | P0CCG47 P10916 P01160 P16615 P62280 P35613 P0CCG48 P39019 P63244 P05090 O14949 P09493 P83731 P62158 P45379 P24311 P24752 P01034 Q13765 P01033 Q14896 P13639 P19021 P19022 P16989 P68032 Q08431 P19105 P14958 P63173 P08493 P60660 P09382 P02511 Q13772 P07602 P13929 P14854 P19429 P25705 P84243 P18859 Q14192 P61247 P62979 P00441 P02144 Q14315 Q14116 O15273 O75116 P68133 Q6P6C2 P13533 P17535 P12883 P08590 P62263 P62987 P04275 P20585 P06576 P63316 |
| GO:0044770 | cell cycle phase transition | 6.77E-03 | 2.28E-02 | 6 | 315 | 190 | 35980 | P0CCG47 P62987 Q9Y5N6 P83731 P62979 P0CCG48 |
| GO:0044772 | mitotic cell cycle phase transition | 6.38E-03 | 2.17E-02 | 6 | 311 | 190 | 35980 | P0CCG47 P62987 Q9Y5N6 P83731 P62979 P0CCG48 |
| GO:0044773 | mitotic DNA damage checkpoint | 2.22E-03 | 9.26E-03 | 4 | 103 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0044774 | mitotic DNA integrity checkpoint | 2.81E-03 | 1.12E-02 | 4 | 110 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0044783 | G1 DNA damage checkpoint | 8.31E-04 | 4.08E-03 | 4 | 79 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0044802 | single-organism membrane organization | 1.46E-28 | 7.10E-27 | 44 | 957 | 190 | 35980 | P25398 P0DMV8 P16615 P62280 P35613 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62753 P00441 Q07020 Q9P0U1 P08708 O75116 P62906 P19022 P18077 P37108 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0044819 | mitotic G1/S transition checkpoint | 8.31E-04 | 4.08E-03 | 4 | 79 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0044839 | cell cycle G2/M phase transition | 6.95E-03 | 2.33E-02 | 4 | 142 | 190 | 35980 | P0CCG47 P62987 P62979 P0CCG48 |
| GO:0044843 | cell cycle G1/S phase transition | 2.50E-03 | 1.02E-02 | 5 | 176 | 190 | 35980 | P0CCG47 P62987 Q9Y5N6 P62979 P0CCG48 |
| GO:0045047 | protein targeting to ER | 1.33E-54 | 4.39E-52 | 37 | 127 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62753 Q07020 P08708 P62906 P18077 P37108 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0045088 | regulation of innate immune response | 5.02E-04 | 2.62E-03 | 9 | 430 | 190 | 35980 | P0CCG47 P51452 P0DMV8 P0DMV9 P62987 P62979 P62158 P0CCG48 P39019 |
| GO:0045089 | positive regulation of innate immune response | 1.34E-03 | 6.17E-03 | 7 | 309 | 190 | 35980 | P0CCG47 P16989 Q13772 P00441 P01034 |
| GO:0045137 | development of primary sexual characteristics | 8.55E-03 | 2.76E-02 | 5 | 236 | 190 | 35980 | P25398 Q96979 P62280 P35613 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62753 Q13765 Q07020 Q9P0U1 P08708 O75116 P62906 P19022 P18077 P37108 Q9Y6H1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P25116 P62249 |
| GO:0045184 | establishment of protein localization | 4.30E-17 | 9.13E-16 | 45 | 1970 | 190 | 35980 | O15273 Q14896 O14958 P09493 P45379 P13533 |
| GO:0045214 | sarcomere organization | 3.42E-08 | 3.96E-07 | 6 | 36 | 190 | 35980 | O75947 P09669 O43674 P40926 P40925 O00483 P14854 P36542 P10176 O95178 O96000 P13073 P25705 P18859 O14949 P56381 P24311 O15239 P20674 O00217 P10606 O95169 P51970 P48047 O14561 O43920 P15954 O95167 P08574 P47985 P06576 P48735 |
| GO:0045333 | cellular respiration | 6.27E-36 | 5.04E-34 | 32 | 231 | 190 | 35980 | P13639 P00505 P68032 P00441 |
| GO:0045471 | response to ethanol | 6.95E-03 | 2.33E-02 | 4 | 142 | 190 | 35980 | P0CCG47 P54368 P63244 P60033 P62987 P62979 P0CCG48 |
| GO:0045732 | positive regulation of protein catabolic process | 4.90E-04 | 2.57E-03 | 7 | 260 | 190 | 35980 | P0CCG47 P51452 O75116 P62987 P62979 P0CCG48 |
| GO:0045787 | positive regulation of cell cycle | 1.40E-02 | 4.02E-02 | 6 | 369 | 190 | 35980 | P01160 P09493 P16615 P23327 |
| GO:0045823 | positive regulation of heart contraction | 3.89E-05 | 2.81E-04 | 4 | 36 | 190 | 35980 | P0CCG47 P51452 P63244 P60033 P62987 P62979 P62158 P0CCG48 P00441 P0CCG48 |
| GO:0045859 | regulation of protein kinase activity | 1.29E-02 | 3.79E-02 | 11 | 954 | 190 | 35980 | P0CCG47 P63244 Q9NWT8 P62987 P62979 P25116 P0CCG48 |
| GO:0045862 | positive regulation of proteolysis | 3.72E-03 | 1.43E-02 | 7 | 371 | 190 | 35980 | P0CCG47 Q13765 P0DMV8 P0DMV9 Q96979 Q8TAK5 Q9Y6H1 P17535 P0CCG48 P60033 Q14192 P62987 P62979 Q13772 P17081 P25116 |
| GO:0045893 | positive regulation of transcription, DNA-templated | 9.65E-03 | 3.05E-02 | 16 | 1575 | 190 | 35980 | P63244 P16860 P10916 P01160 P80297 P02511 |
| GO:0045926 | negative regulation of growth | 2.04E-03 | 8.66E-03 | 6 | 246 | 190 | 35980 | P0CCG47 Q9NWT8 P62987 P83731 P62979 P0CCG48 |
| GO:0045930 | negative regulation of mitotic cell cycle | 3.17E-03 | 1.25E-02 | 6 | 269 | 190 | 35980 | P0CCG47 Q13765 P0DMV8 P0DMV9 Q96979 Q8TAK5 Q9Y6H1 P17535 P0CCG48 P63244 P60033 Q14192 P62987 P62979 Q13772 P62158 P17081 P25116 P01034 |
| GO:0045932 | positive regulation of nucleobase-containing compound metabolic process | 4.94E-03 | 1.83E-02 | 19 | 1870 | 190 | 35980 | P07602 P0CCG47 Q14116 O75116 P10606 P0CCG48 P63244 Q05639 P60033 P62987 P62979 P62158 P1600441 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0046034 | ATP metabolic process | 3.65E-26 | 1.55E-24 | 28 | 311 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 O95178 O96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0046128 | purine ribonucleoside metabolic process | 1.82E-22 | 5.20E-21 | 29 | 468 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 |
| GO:0046129 | purine ribonucleoside biosynthetic process | 1.45E-06 | 1.38E-05 | 8 | 150 | 190 | 35980 | P13929 P00505 P40926 P04406 P40925 P17174 |
| GO:0046364 | monosaccharide biosynthetic process | 5.79E-06 | 5.02E-05 | 6 | 84 | 190 | 35980 | |

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|------------|---|----------|----------|----|------|-----|-------|---|
| GO:0046390 | ribose phosphate biosynthetic process | 3.73E-07 | 3.78E-06 | 10 | 225 | 190 | 35980 | O75947 P16860 P25705 P48047 P18859 P01160 P36544 P5638 I Q8WYQ3 P06576 |
| GO:0046395 | carboxylic acid catabolic process | 2.39E-03 | 9.85E-03 | 6 | 254 | 190 | 35980 | P00505 P17174 Q16698 P51857 P24752 Q13011 O75947 O43674 O96000 P16860 P13073 P07195 P46783 P8373 P62913 P62753 O15239 P20674 Q13765 O95169 P48047 P04406 O14561 Q9Y5N6 P16989 Q9Y6H1 O95167 P84098 P63173 P68104 P46777 Q13772 P06086 P46776 P60228 P62249 Q8N335 P25398 P01176 O95178 P62891 P25705 P18859 Q14192 P56381 O00217 Q08493 P08708 P18077 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P15880 Q02543 P62263 Q14240 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P04926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 P62987 P20585 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0046483 | heterocycle metabolic process | 2.66E-24 | 9.40E-23 | 99 | 6901 | 190 | 35980 | P06989 P13533 P00441 P0CG47 P16989 Q13772 P01034 P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P46783 P61247 P62857 P62913 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P62263 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P04926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 P62987 P20585 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0046496 | nicotinamide nucleotide metabolic process | 2.23E-04 | 1.30E-03 | 7 | 228 | 190 | 35980 | P0CG47 P16989 Q13772 P01034 P16989 P13533 P00441 P0CG47 P16989 Q13772 P01034 P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P46783 P61247 P62857 P62913 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P62263 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P04926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 P62987 P20585 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0046546 | development of primary male sexual characteristics | 6.29E-03 | 2.14E-02 | 4 | 138 | 190 | 35980 | P0CG47 P16989 Q13772 P01034 P16989 P13533 P00441 P0CG47 P16989 Q13772 P01034 P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P46783 P61247 P62857 P62913 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P62263 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P04926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 P62987 P20585 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0046620 | regulation of organ growth | 1.01E-02 | 3.17E-02 | 3 | 84 | 190 | 35980 | P0CG47 P16989 Q13772 P01034 P16989 P13533 P00441 P0CG47 P16989 Q13772 P01034 P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P46783 P61247 P62857 P62913 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P62263 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P04926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 P62987 P20585 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0046661 | male sex differentiation | 1.11E-02 | 3.32E-02 | 4 | 163 | 190 | 35980 | P0CG47 P16989 Q13772 P01034 P16989 P13533 P00441 P0CG47 P16989 Q13772 P01034 P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P46783 P61247 P62857 P62913 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P62263 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P04926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 P62987 P20585 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0046700 | heterocycle catabolic process | 6.67E-36 | 5.22E-34 | 40 | 480 | 190 | 35980 | P0CG47 P16989 Q13772 P01034 P16989 P13533 P00441 P0CG47 P16989 Q13772 P01034 P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P46783 P61247 P62857 P62913 P62753 Q07020 Q08493 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P62263 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P04926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9NP15 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P13533 P62987 P20585 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 Q8N335 |
| GO:0046718 | viral entry into host cell | 1.08E-02 | 3.25E-02 | 3 | 86 | 190 | 35980 | P0DMV8 P0DMV9 P60033 P0CG47 P62987 P62979 P0CG48 P0CG47 O75947 P0DMV8 P16815 P62280 P36544 P35613 P0CG48 P39019 P39023 P62273 P46783 P8373 P162913 P62753 Q07020 P48047 P37108 Q9Y6H1 P84098 P63173 P68104 P46777 P05386 P06086 P46776 P05387 P62249 P02792 P25398 P68363 P62891 P42766 Q02878 P25705 P18859 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 P62906 P18077 Q6P6C2 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 P25116 P06576 |
| GO:0046794 | transport of virus | 3.47E-05 | 2.57E-04 | 4 | 35 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 P0CG47 O75947 P0DMV8 P16815 P62280 P36544 P35613 P0CG48 P39019 P39023 P62273 P46783 P8373 P162913 P62753 Q07020 P48047 P37108 Q9Y6H1 P84098 P63173 P68104 P46777 P05386 P06086 P46776 P05387 P62249 P02792 P25398 P68363 P62891 P42766 Q02878 P25705 P18859 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 P62906 P18077 Q6P6C2 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 P25116 P06576 |
| GO:0046907 | intracellular transport | 4.79E-25 | 1.83E-23 | 56 | 2060 | 190 | 35980 | P0CG47 O75116 P62987 P62979 P62158 P04792 P0CG48 P0CG47 O10916 P01160 P16615 P0CG48 P05090 O14949 Q14192 P09493 P8373 P162913 P62158 P45379 P01034 Q14315 O15273 Q14896 Q75116 P68133 P68032 P13533 P17535 P19105 O14958 P60680 P62987 P02511 P0CG47 P63244 O75116 P19021 P62987 P62979 P17535 P00441 P0CG48 P01034 P07602 P0CG47 P10916 P01160 P14854 P35613 P39019 P05090 P19429 P84243 P18859 Q14949 Q14192 P09493 P8373 P162158 P45379 P24752 P00441 P01034 Q13765 P01033 P02144 Q15273 Q14896 P13639 P19021 P19021 P268133 P16989 P68032 P13533 P12883 P63173 P08493 P60660 P09382 P08590 P62263 P02511 P04275 Q13772 P63316 P0CG47 P0DMV8 P0DMV9 P09691 P01160 P16615 Q8TAK5 P0CG48 P39019 P16860 P09493 P69905 P62158 P45379 P62753 P01034 Q13765 P01033 Q14896 P13639 P19021 P16989 Q9Y6H1 P68032 Q08431 O14958 Q05639 Q9NP15 P61247 P17081 Q8N335 P07602 P51684 P84243 P60033 Q14192 P6887 P23327 P62979 P00441 P51452 P54368 Q14116 Q9P0U1 O75116 P68133 P17535 Q8N8D1 P15880 Q9NWT8 P08590 P62987 P04792 P25116 P20585 |
| GO:0048010 | vascular endothelial growth factor receptor signaling | 9.88E-04 | 4.75E-03 | 7 | 293 | 190 | 35980 | P0CG47 P10916 P01160 P16615 P0CG48 P05090 O14949 Q14192 P09493 P8373 P162913 P62158 P45379 P01034 Q14315 O15273 Q14896 Q75116 P68133 P68032 P13533 P17535 P19105 O14958 P60680 P62987 P02511 P0CG47 P63244 O75116 P19021 P62987 P62979 P17535 P00441 P0CG48 P01034 P07602 P0CG47 P10916 P01160 P14854 P35613 P39019 P05090 P19429 P84243 P18859 Q14949 Q14192 P09493 P8373 P162158 P45379 P24752 P00441 P01034 Q13765 P01033 P02144 Q15273 Q14896 P13639 P19021 P19021 P268133 P16989 P68032 P13533 P12883 P63173 P08493 P60660 P09382 P08590 P62263 P02511 P04275 Q13772 P63316 P0CG47 P0DMV8 P0DMV9 P09691 P01160 P16615 Q8TAK5 P0CG48 P39019 P16860 P09493 P69905 P62158 P45379 P62753 P01034 Q13765 P01033 Q14896 P13639 P19021 P16989 Q9Y6H1 P68032 Q08431 O14958 Q05639 Q9NP15 P61247 P17081 Q8N335 P07602 P51684 P84243 P60033 Q14192 P6887 P23327 P62979 P00441 P51452 P54368 Q14116 Q9P0U1 O75116 P68133 P17535 Q8N8D1 P15880 Q9NWT8 P08590 P62987 P04792 P25116 P20585 |
| GO:0048468 | cell development | 9.22E-07 | 9.01E-06 | 28 | 1903 | 190 | 35980 | P0CG47 P10916 P01160 P16615 P0CG48 P05090 O14949 Q14192 P09493 P8373 P162913 P62158 P45379 P01034 Q14315 O15273 Q14896 Q75116 P68133 P68032 P13533 P17535 P19105 O14958 P60680 P62987 P02511 P0CG47 P63244 O75116 P19021 P62987 P62979 P17535 P00441 P0CG48 P01034 P07602 P0CG47 P10916 P01160 P14854 P35613 P39019 P05090 P19429 P84243 P18859 Q14949 Q14192 P09493 P8373 P162158 P45379 P24752 P00441 P01034 Q13765 P01033 P02144 Q15273 Q14896 P13639 P19021 P19021 P268133 P16989 P68032 P13533 P12883 P63173 P08493 P60660 P09382 P08590 P62263 P02511 P04275 Q13772 P63316 P0CG47 P0DMV8 P0DMV9 P09691 P01160 P16615 Q8TAK5 P0CG48 P39019 P16860 P09493 P69905 P62158 P45379 P62753 P01034 Q13765 P01033 Q14896 P13639 P19021 P16989 Q9Y6H1 P68032 Q08431 O14958 Q05639 Q9NP15 P61247 P17081 Q8N335 P07602 P51684 P84243 P60033 Q14192 P6887 P23327 P62979 P00441 P51452 P54368 Q14116 Q9P0U1 O75116 P68133 P17535 Q8N8D1 P15880 Q9NWT8 P08590 P62987 P04792 P25116 P20585 |
| GO:0048511 | rhythmic process | 1.02E-05 | 8.41E-05 | 10 | 326 | 190 | 35980 | P0CG47 P10916 P01160 P16615 P0CG48 P05090 O14949 Q14192 P09493 P8373 P162913 P62158 P45379 P01034 Q14315 O15273 Q14896 Q75116 P68133 P68032 P13533 P17535 P19105 O14958 P60680 P62987 P02511 P0CG47 P63244 O75116 P19021 P62987 P62979 P17535 P00441 P0CG48 P01034 P07602 P0CG47 P10916 P01160 P14854 P35613 P39019 P05090 P19429 P84243 P18859 Q14949 Q14192 P09493 P8373 P162158 P45379 P24752 P00441 P01034 Q13765 P01033 P02144 Q15273 Q14896 P13639 P19021 P19021 P268133 P16989 P68032 P13533 P12883 P63173 P08493 P60660 P09382 P08590 P62263 P02511 P04275 Q13772 P63316 P0CG47 P0DMV8 P0DMV9 P09691 P01160 P16615 Q8TAK5 P0CG48 P39019 P16860 P09493 P69905 P62158 P45379 P62753 P01034 Q13765 P01033 Q14896 P13639 P19021 P16989 Q9Y6H1 P68032 Q08431 O14958 Q05639 Q9NP15 P61247 P17081 Q8N335 P07602 P51684 P84243 P60033 Q14192 P6887 P23327 P62979 P00441 P51452 P54368 Q14116 Q9P0U1 O75116 P68133 P17535 Q8N8D1 P15880 Q9NWT8 P08590 P62987 P04792 P25116 P20585 |
| GO:0048519 | negative regulation of biological process | 6.46E-09 | 8.28E-08 | 59 | 5261 | 190 | 35980 | P0CG47 P10916 P01160 P16615 P0CG48 P05090 O14949 Q14192 P09493 P8373 P162913 P62158 P45379 P01034 Q14315 O15273 Q14896 Q75116 P68133 P68032 P13533 P17535 P19105 O14958 P60680 P62987 P02511 P0CG47 P63244 O75116 P19021 P62987 P62979 P17535 P00441 P0CG48 P01034 P07602 P0CG47 P10916 P01160 P14854 P35613 P39019 P05090 P19429 P84243 P18859 Q14949 Q14192 P09493 P8373 P162158 P45379 P24752 P00441 P01034 Q13765 P01033 P02144 Q15273 Q14896 P13639 P19021 P19021 P268133 P16989 P68032 P13533 P12883 P63173 P08493 P60660 P09382 P08590 P62263 P02511 P04275 Q13772 P63316 P0CG47 P0DMV8 P0DMV9 P09691 P01160 P16615 Q8TAK5 P0CG48 P39019 P16860 P09493 P69905 P62158 P45379 P62753 P01034 Q13765 P01033 Q14896 P13639 P19021 P16989 Q9Y6H1 P68032 Q08431 O14958 Q05639 Q9NP15 P61247 P17081 Q8N335 P07602 P51684 P84243 P60033 Q14192 P6887 P23327 P62979 P00441 P51452 P54368 Q14116 Q9P0U1 O75116 P68133 P17535 Q8N8D1 P15880 Q9NWT8 P08590 P62987 P04792 P25116 P20585 |
| GO:0048522 | positive regulation of biological process | 7.64E-04 | 3.82E-03 | 45 | 5319 | 190 | 35980 | P07602 P0CG47 P10916 P01160 P14854 P35613 P39019 P05090 P19429 P84243 P18859 Q14949 Q14192 P09493 P8373 P162158 P45379 P24752 P00441 P01034 Q13765 P01033 P02144 Q15273 Q14896 P13639 P19021 P19021 P268133 P16989 P68032 P13533 P12883 P63173 P08493 P60660 P09382 P08590 P62263 P02511 P04275 Q13772 P63316 P0CG47 P0DMV8 P0DMV9 P09691 P01160 P16615 Q8TAK5 P0CG48 P39019 P16860 P09493 P69905 P62158 P45379 P62753 P01034 Q13765 P01033 Q14896 P13639 P19021 P16989 Q9Y6H1 P68032 Q08431 O14958 Q05639 Q9NP15 P61247 P17081 Q8N335 P07602 P51684 P84243 P60033 Q14192 P6887 P23327 P62979 P00441 P51452 P54368 Q14116 Q9P0U1 O75116 P68133 P17535 Q8N |

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|------------|--|----------|----------|-----|-------|-----|-------|---|
| GO:0050789 | regulation of biological process | 1.24E-02 | 3.66E-02 | 108 | 17440 | 190 | 35980 | P10916 Q96979 P16615 P16860 P09493 P83731 P62753 Q13765 P13639 Q9Y27 P04406 P80297 P16989 Q9Y6H1 Q08431 P19105 Q14958 P63173 P68104 P09382 Q13772 P60228 O14558 Q8N335 P07602 P52179 Q6GTX8 Q8N3K9 P10176 P12235 P13693 P19429 P25705 Q14192 P68871 Q16654 Q01628 P00441 P54368 Q14116 Q08493 Q14515 O75116 P68133 P17661 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P41222 P15880 Q9NWT8 Q9Y3D2 P62263 Q14240 P0CG47 P0DMV8 P0DMV9 P01160 P40925 Q8TAK5 P5613 P0CG48 P39019 P63244 P05090 Q14094 Q02818 P69905 P62158 P45379 Q8WYQ3 P01034 P01033 Q14896 Q96H40 O14880 P19021 P19022 P68032 Q05639 P08493 P60660 P02511 P17081 P51684 Q02878 P84243 P60033 Q9UB9Y Q9NPI5 P17174 P61247 P23327 P62979 Q15004 P51452 Q9P0U1 Q75954 P13533 P08590 P62987 P04792 P25116 P20585 P06576 P63316 |
| GO:0050790 | regulation of catalytic activity | 7.58E-04 | 3.80E-03 | 31 | 3212 | 190 | 35980 | P07602 P0CG47 P0DMV8 Q8N3K9 P0CG48 P63244 P19429 P60033 P09493 P62979 P62158 P45379 Q8WYQ3 P00441 P01034 P51452 P54368 P01033 Q14896 O75116 P13533 P15880 Q05639 P08590 P62987 Q14240 P02511 P04792 P25116 P20585 P63316 |
| GO:0050801 | ion homeostasis | 1.79E-04 | 1.07E-03 | 12 | 645 | 190 | 35980 | P13693 P02792 P51684 O14958 P19429 P17174 P16615 Q16654 P23327 P25116 P00441 P06576 |
| GO:0050817 | coagulation | 3.54E-05 | 2.62E-04 | 12 | 543 | 190 | 35980 | P07602 P01033 P84243 P68871 P16615 P04275 P62158 P04792 P35613 P9105 P25116 P00441 |
| GO:0050848 | regulation of calcium-mediated signaling | 9.13E-04 | 4.44E-03 | 4 | 81 | 190 | 35980 | Q14958 P23327 Q8N3K9 P62158 |
| GO:0050849 | negative regulation of calcium-mediated signaling | 1.32E-04 | 8.21E-04 | 3 | 19 | 190 | 35980 | O14958 Q8N3K9 P62158 |
| GO:0050852 | T cell receptor signaling pathway | 1.52E-02 | 4.33E-02 | 4 | 179 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0050878 | regulation of body fluid levels | 4.33E-05 | 3.10E-04 | 14 | 740 | 190 | 35980 | P07602 P01033 P19021 P16615 P35613 P19105 P16860 P84243 P68871 P04275 P62158 P04792 P25116 P00441 |
| GO:0050879 | multicellular organismal movement | 7.72E-08 | 8.36E-07 | 6 | 41 | 190 | 35980 | P02144 O15273 P19429 P13639 P12883 P63316 |
| GO:0050880 | regulation of blood vessel size | 1.94E-03 | 8.31E-03 | 5 | 166 | 190 | 35980 | P16860 P01160 P68871 P25116 P00441 |
| GO:0050881 | musculoskeletal movement | 7.72E-08 | 8.36E-07 | 6 | 41 | 190 | 35980 | P02144 O15273 P19429 P13639 P12883 P63316 |
| GO:0050896 | response to stimulus | 5.92E-08 | 6.60E-07 | 96 | 11437 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 Q12988 Q96979 P01160 P40925 P16615 P35613 P0CG48 P39019 P63244 P16860 P05090 P13073 P00505 P39023 P09493 Q02818 P6373 P69905 P62158 P45379 P62753 P24752 P01034 Q13765 P01033 P13639 P04406 O14880 P80297 P19021 P37108 P16989 P68032 Q08431 P19105 O14958 Q05639 P68104 P06660 P09382 P08574 P47985 P02511 Q13772 P17081 P07602 P52179 P19329 Q6GTX8 P51684 P68363 Q6P173 P10176 P13693 P62828 P84243 P60033 Q14192 P68871 Q9UB9Y P17174 Q16654 P23327 P23252 P62979 Q15004 Q01628 P00441 P51452 O00217 P02144 Q14116 O15273 Q08493 Q9P0U1 O75954 Q14515 O75116 P68133 Q6P6C2 P13533 P17535 Q8N8D1 P42677 P41222 Q9Y3D2 P62987 Q14240 P04275 P04792 P25116 P20585 P63316 |
| GO:0051049 | regulation of transport | 5.36E-05 | 3.72E-04 | 25 | 1991 | 190 | 35980 | P0DMV8 P01160 P16615 P12235 P63244 P16860 P05090 Q02818 P23327 P62158 P45379 P54368 Q14116 Q08493 Q14896 Q9P0U1 Q9Y277 P19021 Q08431 O14958 P02511 P17081 P25116 Q8N335 P63316 |
| GO:0051050 | positive regulation of transport | 1.31E-02 | 3.83E-02 | 11 | 956 | 190 | 35980 | P54368 Q14116 P63244 P16860 Q9P0U1 P01160 P62158 P17081 Q08431 P25116 Q8N335 |
| GO:0051051 | negative regulation of transport | 1.15E-03 | 5.45E-03 | 9 | 484 | 190 | 35980 | P54368 P63244 Q08493 P05090 O14958 P0DMV8 P02511 P62158 P25116 |
| GO:0051091 | positive regulation of sequence-specific DNA binding transcription factor activity | 2.49E-03 | 1.02E-02 | 6 | 256 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 P62987 P62979 P0CG48 |
| GO:0051092 | positive regulation of NF-kappaB transcription factor | 1.58E-04 | 9.68E-04 | 6 | 151 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 P62987 P62979 P0CG48 |
| GO:0051129 | negative regulation of cellular component organization | 1.37E-02 | 3.97E-02 | 9 | 711 | 190 | 35980 | P63244 P05090 P0DMV8 P0DMV9 Q9NWT8 P09382 O75116 P17081 P01034 |
| GO:0051146 | striated muscle cell differentiation | 1.19E-10 | 1.74E-09 | 13 | 211 | 190 | 35980 | Q14315 O15273 Q14896 P10916 P01160 P19022 P68133 P68032 P13533 Q14958 Q14192 P09493 P45379 |
| GO:0051147 | regulation of muscle cell differentiation | 1.16E-02 | 3.45E-02 | 4 | 165 | 190 | 35980 | Q13765 Q14116 Q9NPI5 P19022 |
| GO:0051173 | positive regulation of nitrogen compound metabolic process | 7.49E-04 | 3.76E-03 | 22 | 1967 | 190 | 35980 | P0CG47 Q13765 P0DMV8 P13639 P0DMV9 Q96979 P16989 Q8TAK5 Q9Y6H1 P17535 P0CG48 P63244 P60033 Q14192 P68871 P62987 P62979 Q13772 P62158 P17081 P25116 P01034 |
| GO:0051174 | regulation of phosphorus metabolic process | 2.94E-03 | 1.16E-02 | 20 | 1917 | 190 | 35980 | P07602 P0CG47 P51452 Q14116 O75116 P19022 Q8N3K9 P0CG48 P63244 Q05639 P60033 P62987 Q16654 P23327 P62979 P62158 P04792 P25116 Q8N335 P00441 |
| GO:0051179 | localization | 3.78E-16 | 7.65E-15 | 94 | 8120 | 190 | 35980 | P0CG47 Q75947 P0DMV8 Q96979 P16615 P62280 P36542 P35613 P0CG48 P39019 P16860 P05090 P13073 P00505 Q14949 P39023 P62273 P46783 P83731 P62913 P24310 P69905 P62158 P24311 P62753 P20674 Q13765 Q07020 P01033 P10606 P48047 Q9Y277 P19021 P19022 P14406 P37108 Q9Y6H1 Q08431 P84098 O14958 P63173 P61353 P47985 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P02792 P25398 P09669 P51684 P68363 Q00483 P14854 P10176 P12235 P13693 P62891 P42766 Q02878 P25705 P18559 P60033 P68871 P61247 P62857 P62979 P63581 P62851 P00441 P54368 P02144 Q9P0U1 P08708 O75116 P62906 P18077 P15954 Q6P6C2 P42677 P41222 P15880 Q02543 Q00325 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:0051223 | regulation of protein transport | 1.07E-02 | 3.23E-02 | 10 | 803 | 190 | 35980 | P54368 Q14116 P63244 Q08493 P05090 Q9P0U1 P19021 Q02818 P12235 P25116 |
| GO:0051234 | establishment of localization | 1.06E-19 | 2.56E-18 | 93 | 7073 | 190 | 35980 | P0CG47 Q75947 P0DMV8 Q96979 P16615 P62280 P36542 P35613 P0CG48 P39019 P16860 P05090 P13073 P00505 Q14949 P39023 P62273 P46783 P83731 P62913 P24310 P69905 P62158 P24311 P62753 P20674 Q13765 Q07020 P01033 P10606 P48047 Q9Y277 P19021 P19022 P14406 P37108 Q9Y6H1 Q08431 P84098 O14958 P63173 P61353 P47985 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P02792 P25398 P09669 P68363 Q00483 P14854 P10176 P12235 P13693 P62891 P42766 Q02878 P25705 P18559 P60033 P68871 P61247 P62857 P62979 P63581 P62851 P00441 P54368 P02144 Q9P0U1 P08708 O75116 P62906 P18077 P15954 Q6P6C2 P42677 P41222 P15880 Q02543 Q00325 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:0051239 | regulation of multicellular organismal process | 1.13E-11 | 1.76E-10 | 45 | 2789 | 190 | 35980 | P0CG47 P10916 P51684 P0DMV8 P0DMV9 P01160 P16615 Q8N3K9 P0CG48 P39019 P63244 P16860 P05090 P19429 Q9UB9Y P09493 Q16654 P23327 P62979 P62158 P45379 P00441 P01034 Q13765 P01033 Q14116 Q14896 O75116 P19022 P16989 P17661 P13533 P17535 P12883 P41222 O14958 P08493 P09382 P08590 P62987 P04792 P25116 O14558 Q8N335 P63316 |
| GO:0051240 | positive regulation of multicellular organismal process | 1.55E-05 | 1.23E-04 | 22 | 1498 | 190 | 35980 | P0CG47 Q13765 Q14116 P51684 P0DMV8 P0DMV9 P01160 O75116 P16615 P16989 P17535 P0CG48 P39019 P63244 P16860 P09493 P62987 P23327 P62979 P04792 P25116 P00441 |
| GO:0051241 | negative regulation of multicellular organismal process | 4.59E-05 | 3.26E-04 | 17 | 1049 | 190 | 35980 | P0CG47 P01033 P01160 O75116 P16615 P16989 P0CG48 P39019 P16860 P41222 P05090 P09382 P62987 P62979 P25116 P00441 P01034 |
| GO:0051246 | regulation of protein metabolic process | 3.23E-06 | 2.92E-05 | 36 | 3024 | 190 | 35980 | P07602 P0CG47 P0DMV8 P0DMV9 Q96979 Q8N3K9 P0CG48 P63244 P05090 P60033 P23327 P62979 P62158 P00441 P01034 P51452 P54368 P01033 Q14116 P13639 P04406 O75116 P19022 P16989 Q05639 P63173 P68104 Q9NWT8 P62263 P62987 Q14240 P02511 P04792 P60228 P25116 Q8N335 |
| GO:0051247 | positive regulation of protein metabolic process | 1.30E-03 | 6.03E-03 | 19 | 1657 | 190 | 35980 | P07602 P0CG47 P54368 Q14116 P13639 Q96979 O75116 P19022 P16989 P0CG48 P63244 Q9NWT8 P60033 P62987 P62979 P62158 P04792 P25116 P00441 |
| GO:0051248 | negative regulation of protein metabolic process | 6.43E-05 | 4.41E-04 | 19 | 1299 | 190 | 35980 | P0CG47 P51452 P01033 P0DMV8 P0DMV9 P04406 O75116 Q8N3K9 P0CG48 P63244 P05090 P62987 P62979 P02511 P62158 P04792 P60228 Q8N335 P01034 |
| GO:0051254 | positive regulation of RNA metabolic process | 1.40E-02 | 4.03E-02 | 16 | 1644 | 190 | 35980 | P0CG47 Q13765 P0DMV8 P0DMV9 Q96979 Q8TAK5 Q9Y6H1 P17535 P0CG48 P60033 Q14192 P62987 P62979 Q13772 P17081 P25116 |
| GO:0051259 | protein oligomerization | 6.08E-05 | 4.19E-04 | 11 | 486 | 190 | 35980 | P68871 P19021 P19022 P23252 Q16698 P02511 P04275 P24752 |
| GO:0051260 | protein homooligomerization | 5.55E-03 | 1.93E-02 | 6 | 302 | 190 | 35980 | P19021 P23252 Q16698 P02511 P04275 P24752 |
| GO:0051270 | regulation of cellular component movement | 1.26E-04 | 7.90E-04 | 14 | 819 | 190 | 35980 | P01033 Q14896 P51684 O75116 P16615 P39019 P63244 P05090 P60033 P09493 P04792 P45379 P25116 P63316 |
| GO:0051279 | regulation of release of sequestered calcium ion into | 7.92E-04 | 3.92E-03 | 4 | 78 | 190 | 35980 | Q14958 P23327 P62158 P25116 |
| GO:0051282 | regulation of sequestering of calcium ion | 3.51E-03 | 1.36E-02 | 4 | 117 | 190 | 35980 | O14958 P23327 P62158 P25116 |
| GO:0051291 | protein heterooligomerization | 1.41E-03 | 6.42E-03 | 4 | 91 | 190 | 35980 | P68871 P19022 P69905 P45379 |
| GO:0051336 | regulation of hydrolase activity | 8.67E-03 | 2.78E-02 | 18 | 1834 | 190 | 35980 | P01033 Q14896 P0DMV8 O75116 Q8N3K9 P13533 P63244 P19429 P08590 P09493 P02511 P62158 P45379 P25116 P20585 P00441 P6316 P01034 |
| GO:0051338 | regulation of transferase activity | 1.49E-03 | 6.66E-03 | 15 | 1172 | 190 | 35980 | P0CG47 P51452 P0CG48 P63244 P16860 Q05639 P62987 P62979 Q14240 P62979 P62158 P04792 Q9WYQ3 P25116 P00441 |
| GO:0051340 | regulation of ligase activity | 1.00E-02 | 3.16E-02 | 4 | 158 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0051346 | negative regulation of hydrolase activity | 1.63E-02 | 4.45E-02 | 7 | 493 | 190 | 35980 | P01033 P19429 O75116 Q8N3K9 P02511 P45379 P01034 |
| GO:0051347 | positive regulation of transferase activity | 6.94E-03 | 2.33E-02 | 10 | 752 | 190 | 35980 | P0CG47 P15880 Q05639 P60033 P62987 P62979 P62158 P25116 P00441 P0CG48 |
| GO:0051348 | negative regulation of transferase activity | 2.77E-04 | 1.58E-03 | 9 | 396 | 190 | 35980 | P0CG47 P51452 P63244 P62987 Q14240 P62979 P04792 Q8WYQ3 P0CG48 |
| GO:0051351 | positive regulation of ligase activity | 2.22E-03 | 9.26E-03 | 4 | 103 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |

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|------------|--|----------|----------|----|------|-----|-------|---|
| GO:0051352 | negative regulation of ligase activity | 2.55E-03 | 1.04E-02 | 4 | 107 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0051384 | response to glucocorticoid | 1.99E-03 | 8.47E-03 | 5 | 167 | 190 | 35980 | P41222 P19021 P171174 P62158 Q8N8D1 |
| GO:0051403 | stress-activated MAPK cascade | 7.56E-05 | 5.12E-03 | 6 | 132 | 190 | 35980 | POCG47 P51452 P62987 P62979 P02511 POCG48 |
| GO:0051436 | negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 1.85E-03 | 7.97E-03 | 4 | 98 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0051437 | positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition | 6.50E-04 | 3.28E-03 | 4 | 74 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0051438 | regulation of ubiquitin-protein transferase activity | 9.81E-03 | 3.10E-02 | 4 | 157 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0051439 | regulation of ubiquitin-protein ligase activity involved in | 2.63E-03 | 1.06E-02 | 4 | 108 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0051443 | positive regulation of ubiquitin-protein transferase activity | 1.85E-03 | 7.97E-03 | 4 | 98 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0051444 | negative regulation of ubiquitin-protein transferase activity | 2.38E-03 | 9.82E-03 | 4 | 105 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0051592 | response to calcium ion | 3.62E-03 | 1.39E-02 | 4 | 118 | 190 | 35980 | O14958 P62158 P45379 P17535 |
| GO:0051604 | protein maturation | 7.62E-03 | 2.51E-02 | 6 | 323 | 190 | 35980 | POCG47 P63244 P62987 P62979 P25116 POCG48 |
| | | | | | | | | POCG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P39023 P62273 P46783 P63731 P62913 P62158 P62753 Q07020 P01033 P48047 P19022 P37108 Q9Y6H1 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P02792 P25398 P68363 P62891 P42766 Q02878 P25705 P18859 P60033 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 O75116 P62906 P18077 Q6P6C2 P42677 P15880 Q02543 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:0051641 | cellular localization | 6.56E-22 | 1.81E-20 | 63 | 3063 | 190 | 35980 | POCG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P39023 P62273 P46783 P63731 P62913 P62158 P62753 Q07020 P01033 P48047 P19022 P37108 Q9Y6H1 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P02792 P25398 P68363 P62891 P42766 Q02878 P25705 P18859 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 P62906 P18077 Q6P6C2 P42677 P15880 Q02543 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:0051649 | establishment of localization in cell | 2.66E-23 | 8.07E-22 | 60 | 2598 | 190 | 35980 | POCG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P39023 P62273 P46783 P63731 P62913 P62158 P62753 Q07020 P01033 P48047 P19022 P37108 Q9Y6H1 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P02792 P25398 P68363 P62891 P42766 Q02878 P25705 P18859 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 P62906 P18077 Q6P6C2 P42677 P15880 Q02543 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:0051704 | multi-organism process | 7.81E-27 | 3.46E-25 | 64 | 2565 | 190 | 35980 | POCG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P39023 P62273 P46783 P63731 P62913 P62158 P62753 Q07020 P01033 P48047 P19022 P37108 Q9Y6H1 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 P52179 P25398 P10176 P12235 P13693 P62891 P42766 Q02878 P60033 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 P62906 P18077 Q6P6C2 P17535 P42677 P15880 Q02543 P62263 P62987 P14240 P62945 P04792 P62269 P25116 P52179 Q14116 P08708 P62906 P18077 Q6P6C2 P17535 P13693 P62891 P62987 Q16654 P04792 Q01628 P25116 |
| GO:0051707 | response to other organism | 1.43E-03 | 6.49E-03 | 13 | 931 | 190 | 35980 | POCG47 P51452 Q15004 P62158 |
| GO:0051726 | regulation of cell cycle | 1.68E-02 | 4.58E-02 | 13 | 1260 | 190 | 35980 | POCG47 P51452 Q15004 P62158 |
| GO:0051806 | entry into cell of other organism involved in symbiotic | 1.11E-02 | 3.31E-02 | 3 | 87 | 190 | 35980 | P0DMV8 P0DMV9 P60033 |
| GO:0051828 | entry into other organism involved in symbiotic interaction | 1.11E-02 | 3.31E-02 | 3 | 87 | 190 | 35980 | P0DMV8 P0DMV9 P60033 |
| GO:0051881 | regulation of mitochondrial membrane potential | 3.61E-03 | 1.39E-02 | 3 | 58 | 190 | 35980 | POCG47 P63244 P00441 |
| GO:0051924 | regulation of calcium ion transport | 8.55E-03 | 2.76E-02 | 5 | 236 | 190 | 35980 | O14958 P01160 P23272 P62158 P25116 |
| GO:0052126 | movement in host environment | 1.11E-02 | 3.31E-02 | 3 | 87 | 190 | 35980 | P0DMV8 P0DMV9 P60033 |
| GO:0052192 | movement in environment of other organism involved in | 1.11E-02 | 3.31E-02 | 3 | 87 | 190 | 35980 | P0DMV8 P0DMV9 P60033 |
| GO:0055001 | muscle cell development | 2.06E-12 | 3.42E-11 | 13 | 153 | 190 | 35980 | Q14315 O15273 Q14896 P10916 P01160 P68133 P16615 P68032 P13533 O14958 Q14192 P09493 P45379 |
| GO:0055002 | striated muscle cell development | 1.34E-11 | 2.09E-10 | 12 | 140 | 190 | 35980 | Q14315 O15273 Q14896 P10916 O14958 Q14192 P01160 P09493 P68133 P68032 P45379 P13533 |
| GO:0055003 | cardiac myofibril assembly | 7.72E-05 | 5.20E-04 | 3 | 16 | 190 | 35980 | O15273 P10916 P68032 |
| GO:0055006 | cardiac cell development | 1.16E-06 | 1.14E-05 | 6 | 64 | 190 | 35980 | O15273 P10916 Q14192 P01160 P68032 P13533 |
| GO:0055007 | cardiac muscle cell differentiation | 1.04E-05 | 8.52E-05 | 6 | 93 | 190 | 35980 | O15273 P10916 Q14192 P01160 P68032 P13533 |
| GO:0055008 | cardiac muscle tissue morphogenesis | 9.93E-15 | 1.92E-13 | 11 | 57 | 190 | 35980 | O15273 Q14896 P10916 P19429 P08590 P09493 P68032 P45379 P13533 P12883 P63316 |
| GO:0055010 | ventricular cardiac muscle tissue morphogenesis | 7.99E-13 | 1.36E-11 | 9 | 41 | 190 | 35980 | Q14896 P10916 P19429 P08590 P09493 P45379 P13533 P12883 P63316 |
| GO:0055013 | cardiac muscle cell development | 8.74E-07 | 8.60E-06 | 6 | 61 | 190 | 35980 | O15273 P10916 Q14192 P01160 P68032 P13533 |
| GO:0055065 | metal ion homeostasis | 2.28E-03 | 9.45E-03 | 9 | 535 | 190 | 35980 | P13693 P02792 P51684 O14958 P19429 P16615 P23327 P25116 P00441 |
| GO:0055074 | calcium ion homeostasis | 2.15E-03 | 9.05E-03 | 7 | 336 | 190 | 35980 | P13693 P51684 O14958 P19429 P16615 P23327 P25116 |
| GO:0055080 | cation homeostasis | 3.81E-04 | 2.10E-03 | 11 | 601 | 190 | 35980 | P13693 P02792 P51684 O14958 P19429 P16615 P23327 P25116 P00441 P06576 |
| GO:0055082 | cellular chemical homeostasis | 1.36E-04 | 8.43E-04 | 12 | 626 | 190 | 35980 | P13693 P02792 P63244 P51684 O14958 P19429 P09382 P16615 P23327 P25116 P00441 P06576 |
| GO:0055085 | transmembrane transport | 1.58E-06 | 1.49E-05 | 32 | 2432 | 190 | 35980 | POCG47 O75947 P02792 P09669 O00483 P14854 P16615 P36542 P10176 P12235 P0CG48 P13073 P25705 P18859 Q14949 P62979 P56381 P24310 P24311 P20674 P10606 Q9P0U1 P48047 Q9Y77 P14406 P15954 O14958 Q00325 P62987 P47985 P25116 P06576 |
| GO:0055086 | nucleobase-containing small molecule metabolic process | 3.05E-22 | 8.48E-21 | 37 | 906 | 190 | 35980 | P13929 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P39023 P62273 P46783 P63731 P62913 P62158 P62753 Q07020 P01033 P48047 P19022 P37108 Q9Y6H1 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 P07602 P02792 P25398 P68363 P62891 P42766 Q02878 P25705 P18859 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 O75116 P62906 P18077 Q6P6C2 P17535 P42677 P15880 Q02543 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:0055114 | oxidation-reduction process | 9.69E-20 | 2.36E-18 | 51 | 2195 | 190 | 35980 | POCG47 O75947 Q43674 P40928 P40925 P36542 P0CG48 O96000 P13073 O14949 P07195 P62158 P24311 O15239 P20674 P10606 O95169 P48047 O4406 O14561 O14880 P19021 Q43920 O95167 P08574 P47985 Q13011 Q8N35 P13929 P09669 O00483 P14854 P10176 O95178 P12235 P25705 P18859 P23252 Q16698 P62979 P56381 P00441 O00217 P51970 P15954 P51857 Q6P6C2 Q9Y3D2 P62987 P06576 P48735 |
| GO:0055117 | regulation of cardiac muscle contraction | 2.68E-05 | 2.05E-04 | 5 | 66 | 190 | 35980 | O14958 P01160 P16615 P23327 P25116 |
| GO:0060047 | heart contraction | 8.97E-18 | 1.96E-16 | 14 | 80 | 190 | 35980 | O15273 Q14896 P10916 P68032 P13533 P12883 O14958 P19429 P08590 P09493 P45379 Q8N335 P00441 P63316 |
| GO:0060048 | cardiac muscle contraction | 4.89E-17 | 1.03E-15 | 13 | 69 | 190 | 35980 | O15273 Q14896 P10916 P68032 P13533 P12883 O14958 P19429 P08590 P09493 P45379 Q8N335 P63316 |
| GO:0060314 | regulation of ryanodine-sensitive calcium-release channel | 3.45E-04 | 1.91E-03 | 3 | 26 | 190 | 35980 | O14958 P23327 P62158 |
| GO:0060322 | head development | 8.84E-03 | 2.83E-02 | 10 | 780 | 190 | 35980 | POCG47 P05090 P84243 P18859 O14949 P19022 P14854 P62158 P24752 P10134 |
| GO:0060341 | regulation of cellular localization | 3.42E-06 | 3.07E-05 | 22 | 1360 | 190 | 35980 | P54368 Q14116 Q08493 Q14896 P0DMV8 Q9P0U1 P19021 P19022 P16615 P12235 P63244 P05090 O14958 Q02818 P23327 P02511 P62158 P17081 P45379 P25116 Q8N335 P63316 |
| GO:0060415 | muscle tissue morphogenesis | 9.29E-14 | 1.69E-12 | 11 | 69 | 190 | 35980 | O15273 Q14896 P10916 P19429 P08590 P09493 P68032 P45379 P13533 P12883 P63316 |
| GO:0060537 | muscle tissue development | 1.12E-11 | 1.76E-10 | 16 | 309 | 190 | 35980 | O15273 Q14896 P10916 P13639 P01160 P68133 P68032 P13533 P12883 P19429 Q14192 P60660 P08590 P09493 P45379 P63316 |
| GO:0060538 | skeletal muscle organ development | 8.39E-03 | 2.72E-02 | 4 | 150 | 190 | 35980 | P13639 P60660 P08590 P68133 |
| GO:0060548 | negative regulation of cell death | 2.58E-08 | 3.02E-07 | 22 | 1017 | 190 | 35980 | P07602 POCG47 Q13765 P01033 P0DMV8 P0DMV9 P16989 P68032 P12235 P0CG48 P13693 P63244 Q14192 P62987 P61247 Q16654 P62979 P02511 P04792 P25116 P00441 P01034 |
| GO:0060759 | regulation of response to cytokine stimulus | 1.46E-05 | 1.17E-04 | 7 | 148 | 190 | 35980 | POCG47 P63244 P0DMV8 P0DMV9 P62987 P62979 P0CG48 |
| GO:0060828 | regulation of canonical Wnt signaling pathway | 1.17E-02 | 3.46E-02 | 5 | 255 | 190 | 35980 | POCG47 P19022 P62987 P62979 POCG48 |
| GO:0061024 | membrane organization | 2.31E-29 | 1.16E-27 | 49 | 1211 | 190 | 35980 | POCG47 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P39023 P62273 P46783 P63731 P62913 P62158 P62753 Q07020 P19022 P37108 Q8431 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P62249 P02792 P25398 P62891 P42766 Q02878 P61247 P62857 P62979 P62851 P00441 Q9P0U1 P08708 O75116 P62906 P18077 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 |
| GO:0061061 | muscle structure development | 3.78E-14 | 6.98E-13 | 22 | 502 | 190 | 35980 | Q14315 O15273 Q14896 P10916 P13639 P01160 P19022 P68133 P16615 P68032 P13533 P12883 O14958 P19429 Q14192 P60660 P09382 P08590 P09493 P25116 P45379 P63316 |
| GO:0061337 | cardiac conduction | 4.57E-03 | 1.71E-02 | 4 | 126 | 190 | 35980 | O14958 P19429 P01160 P16615 |
| GO:0061418 | regulation of transcription from RNA polymerase II promoter in response to hypoxia | 2.73E-05 | 2.08E-04 | 4 | 33 | 190 | 35980 | POCG47 P62987 P62979 POCG48 |
| GO:0061458 | reproductive system development | 2.80E-03 | 1.11E-02 | 8 | 449 | 190 | 35980 | P07602 POCG47 P16989 P04275 Q13772 P35613 P00441 P01034 |
| GO:0061564 | axon development | 5.84E-03 | 2.01E-02 | 10 | 733 | 190 | 35980 | POCG47 P05090 P60660 O75116 P62987 P83731 P62979 P62158 P19105 P0CG48 |
| GO:0061726 | mitochondrion disassembly | 6.34E-06 | 5.43E-05 | 8 | 183 | 190 | 35980 | POCG47 P52179 Q9P0U1 P40925 P62987 P62979 P10176 P0CG48 O43674 O95178 P39019 O96000 Q02878 P84243 P39023 P6887 P46783 P83731 P62913 P62158 P62753 P69905 P45379 P24752 O15239 O00217 O15273 Q14896 O95169 P51970 P08708 O14561 P19021 P19022 Q43920 O95167 P42677 O14958 P63173 Q9Y3D2 P62263 P46777 P02511 P04275 P60228 |
| GO:0065003 | macromolecular complex assembly | 1.27E-13 | 2.30E-12 | 37 | 1678 | 190 | 35980 | |

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|------------|--|----------|----------|-----|-------|-----|-------|---|
| GO:0065007 | biological regulation | 8.63E-03 | 2.77E-02 | 113 | 18213 | 190 | 35980 | P10916 Q96979 P16615 P16860 P09493 P83731 P62753 Q13765 P13639 Q9Y277 P04406 P80297 P16989 Q9Y6H1 Q08431 P19105 Q14958 P63173 P68104 P09382 Q13772 P60228 Q14558 Q8N335 P07602 P52179 Q6GT8 Q8N3K9 P10176 P12235 P13693 P19429 P25705 Q14192 P68871 Q16654 Q01628 P00441 P54368 Q14116 Q08493 P08708 Q14515 O75116 P68133 P17661 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P41222 P15880 Q9NWT8 Q9Y3D2 P62263 Q14240 P0C47 P0DMV8 P0DMV9 P01160 P40926 P06228 P35613 P0C48 P39019 P05090 Q14094 Q02818 P69905 P62158 P45379 Q8WYQ3 P01034 P01033 Q14896 Q96H40 Q14880 P19021 P19022 P68032 Q05639 P08493 P06660 P02511 P17081 P02792 P51684 Q02878 P64243 P60033 Q9UB9 Q9NP15 P17174 P61247 P23327 P62979 Q15004 P51452 P02144 Q9P0U1 O75954 P51857 P13533 P08590 P62987 P04275 P04792 P25116 P20585 P06576 P63316 |
| GO:0065008 | regulation of biological quality | 1.17E-10 | 1.72E-09 | 55 | 4225 | 190 | 35980 | P0C47 P10916 P0DMV8 P0DMV9 P01160 P16615 P35613 P0C48 P39019 P63244 P16860 P09493 P62158 P45379 P62753 P01033 Q14896 P04406 P19021 P19022 P16989 P19105 Q14958 P09382 P17081 Q8N335 P07602 Q02792 P51684 P12235 P13693 P19429 P25705 Q14192 P68871 P17174 Q16654 P23327 P62979 P00441 P02144 Q08493 Q9P0U1 P08708 P51857 P13533 P12883 P08590 P62263 P62987 P04275 P04792 P25116 P06576 P63316 P07602 P0C47 P0DMV8 P0DMV9 P01160 Q8N3K9 P0C48 P63244 P19429 P60033 P09493 P23327 P62979 P62158 P45379 Q8WYQ3 P00441 P01033 P145379 P54368 P01033 Q14896 Q75116 P13533 Q14958 P15880 Q05639 P08590 P62987 Q14240 P02511 P04792 P25116 P20585 Q8N335 P63316 P54368 Q14116 P63244 Q08493 P05090 Q9P0U1 P19021 Q02818 P17081 P12235 P25116 |
| GO:0065009 | regulation of molecular function | 3.10E-04 | 1.74E-03 | 36 | 3759 | 190 | 35980 | O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P6060 P08590 P09493 P45379 Q8N335 P63316 |
| GO:0070201 | regulation of establishment of protein localization | 7.26E-03 | 2.41E-02 | 11 | 878 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0070252 | actin-mediated cell contraction | 8.46E-20 | 2.08E-18 | 15 | 76 | 190 | 35980 | Q43674 Q95178 P39019 Q96000 P84243 P68871 P22352 Q16698 P69905 P45379 P24752 Q15239 Q00217 Q15273 Q14896 Q095169 P51970 Q14561 P19021 P19022 Q43920 Q95167 Q14958 Q9Y3D2 P02511 P04275 |
| GO:0070265 | nerotic cell death | 4.83E-05 | 3.41E-04 | 4 | 38 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0070266 | neuroptotic process | 1.61E-05 | 1.28E-04 | 4 | 29 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0070271 | protein complex biogenesis | 1.70E-08 | 2.08E-07 | 26 | 1366 | 190 | 35980 | O43674 Q95178 P39019 Q96000 P84243 P68871 P22352 Q16698 P69905 P45379 P24752 Q15239 Q00217 Q15273 Q14896 Q095169 P51970 Q14561 P19021 P19022 Q43920 Q95167 Q14958 Q9Y3D2 P02511 P04275 |
| GO:0070423 | nucleotide-binding oligomerization domain containing | 1.40E-05 | 1.12E-04 | 4 | 28 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0070482 | response to oxygen levels | 1.14E-05 | 9.25E-05 | 10 | 330 | 190 | 35980 | P0C47 P02144 P01160 P19021 P62987 P62979 P02511 Q6P6C2 P0C48 P01034 |
| GO:0070527 | platelet aggregation | 1.43E-03 | 6.49E-03 | 3 | 42 | 190 | 35980 | P88871 P04792 P19105 |
| GO:0070727 | cellular macromolecule localization | 3.47E-19 | 8.12E-18 | 44 | 1652 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62857 P07020 P08708 P62906 P18077 P37108 P42677 P84098 P15880 P63173 Q02543 P61302 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P25116 P62249 |
| GO:0070848 | response to growth factor | 8.00E-03 | 2.62E-02 | 11 | 890 | 190 | 35980 | P0C47 P51452 P63244 P13693 P68104 P62987 P62979 P62158 P04792 P13533 P0C48 |
| GO:0070887 | cellular response to chemical stimulus | 2.34E-08 | 2.76E-07 | 41 | 3060 | 190 | 35980 | P07602 P0C47 P51684 Q96979 P68363 P0C48 P63244 P60033 Q14192 P39023 P17174 Q16654 P62979 P62158 P62753 Q01628 P00441 P51452 Q14116 P13639 P04406 P08708 P19021 P19022 Q43920 Q95167 Q14958 P15880 Q05639 P08590 P62987 Q14240 Q13772 P17081 P04792 |
| GO:0070911 | global genome nucleotide-excision repair | 3.31E-04 | 1.86E-03 | 4 | 62 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0070925 | organelle assembly | 3.32E-10 | 4.72E-09 | 20 | 651 | 190 | 35980 | O15273 Q14896 P10916 P08708 P68133 P68032 P13533 P39019 P42677 Q02878 Q14958 P63173 P39023 P09493 P62263 P46783 P83731 P62913 P46777 P45379 |
| GO:0070972 | protein localization to endoplasmic reticulum | 2.64E-51 | 6.55E-49 | 37 | 152 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62857 P07020 P08708 P62906 P18077 P37108 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P25116 P62249 |
| GO:0070987 | error-free translesion synthesis | 2.74E-06 | 2.52E-05 | 4 | 19 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0071156 | regulation of cell cycle arrest | 4.57E-03 | 1.71E-02 | 4 | 126 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0071158 | positive regulation of cell cycle arrest | 1.35E-03 | 6.20E-03 | 4 | 90 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0071310 | cellular response to organic substance | 4.16E-07 | 4.21E-06 | 34 | 2525 | 190 | 35980 | P07602 P0C47 P51684 Q96979 P68363 P0C48 P63244 P60033 Q14192 P39023 P17174 Q16654 P62979 P62158 P62753 Q01628 P00441 P51452 Q14116 P13639 P04406 P08708 P19021 P19022 Q43920 Q95167 Q14958 P15880 Q05639 P08590 P62987 Q14240 Q13772 P17081 P04792 |
| GO:0071345 | cellular response to cytokine stimulus | 7.78E-04 | 3.88E-03 | 13 | 870 | 190 | 35980 | P0C47 P51684 P04406 P08708 P62979 P68363 P16989 P0C48 P63244 P39023 P62987 Q14240 P62979 Q01628 |
| GO:0071356 | cellular response to tumor necrosis factor | 2.21E-03 | 9.25E-03 | 6 | 250 | 190 | 35980 | P0C47 P63244 P62987 P16989 P62979 P0C48 |
| GO:0071363 | cellular response to growth factor stimulus | 6.53E-03 | 2.21E-02 | 11 | 865 | 190 | 35980 | P0C47 P51452 P63244 P13693 P68104 P62987 P62979 P62158 P04792 P13533 P0C48 |
| GO:0071375 | cellular response to peptide hormone stimulus | 1.06E-03 | 5.04E-03 | 9 | 478 | 190 | 35980 | P0C47 P17174 P62987 Q16654 P62979 P62158 P17081 P62753 P0C48 |
| GO:0071407 | cellular response to organic cyclic compound | 1.17E-02 | 3.46E-02 | 8 | 574 | 190 | 35980 | Q14116 Q14958 Q96979 Q14192 P09382 O75116 Q13772 P00441 |
| GO:0071417 | cellular response to organonitrogen compound | 7.94E-04 | 3.92E-03 | 11 | 657 | 190 | 35980 | P0C47 Q14958 P17174 P62987 Q16654 P62979 P62158 P17081 P62753 P00441 P0C48 |
| GO:0071453 | cellular response to oxygen levels | 8.39E-03 | 2.72E-02 | 4 | 150 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0071456 | cellular response to hypoxia | 5.68E-03 | 1.97E-02 | 4 | 134 | 190 | 35980 | P0C47 P62987 P62979 P0C48 |
| GO:0071495 | cellular response to endogenous stimulus | 5.29E-05 | 3.71E-04 | 20 | 1393 | 190 | 35980 | P0C47 P13639 Q96979 Q75116 P13533 P17535 P0C48 Q14958 P68104 P60033 Q14192 P17174 P62987 Q16654 P62979 Q13772 P62158 P17081 P62753 P00441 |
| GO:0071702 | organic substance transport | 3.46E-14 | 6.43E-13 | 50 | 2889 | 190 | 35980 | P62280 P35613 P39019 P05090 P00505 P39023 P62273 P46783 P83731 P62913 P62913 P69905 P62753 Q13765 Q07020 Q9Y277 P37108 Q9Y6H1 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P62249 P07602 P25398 P12235 P62891 P42766 Q02878 P68871 P61247 P62857 P62979 P62851 Q9P0U1 P08708 P62906 P18077 Q6P6C2 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 P25116 |
| GO:0071704 | organic substance metabolic process | 3.03E-14 | 5.73E-13 | 137 | 16191 | 190 | 35980 | O75947 Q43674 Q96000 P16860 P13073 P07195 P46783 P83731 P62913 P62753 P24752 Q15239 P20674 Q13765 Q95169 P13639 P48047 P04406 Q14561 Q9Y5N6 P16989 Q9Y6H1 Q95167 Q08431 P84098 P63173 P68104 P46777 Q13772 P60866 P46776 P60228 P62249 Q13011 Q8N335 P07602 P25398 P68363 P10176 Q95178 P12235 P62891 P25705 P18859 Q14192 Q16654 P56381 P00441 P54368 Q00217 Q14116 Q08493 P08708 O75116 P18077 Q6P6C2 P17535 P12883 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9NWT8 Q9Y3D2 P62263 Q14240 P62945 P62269 P0C47 P6732 Q9N8D1 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 Q8TAK5 P35642 P35613 P0C48 P39019 P63244 P05090 P00505 P39023 P62273 P62158 P2431 Q18WYQ3 P01034 Q07020 P10606 Q96H40 Q14880 P19021 P37108 Q04392 Q05639 P61353 P02511 P05386 P17081 P05387 P13929 P09669 Q00483 P14854 P42766 Q02878 P84243 P60033 Q9NP15 P17174 P61247 P62857 Q16698 P62979 Q15004 P62851 P51452 P51970 Q9P0U1 P62906 P15954 P51857 P13533 Q00325 P62987 P04275 P04792 P25116 P20585 P06576 P46735 |
| GO:0071822 | protein complex subunit organization | 1.39E-34 | 9.58E-33 | 66 | 2022 | 190 | 35980 | O43674 P62280 P39019 Q96000 P39023 P62273 P46783 P83731 P62913 P69905 P45379 P62753 P24752 Q15239 Q07020 Q14896 Q95169 Q14561 P19021 P19022 Q43920 P68032 Q95167 P84098 Q14958 P63173 P61353 P46777 P02511 P05386 P60866 P46776 P05387 P62249 P25398 Q95178 P62891 P42766 Q02878 P84243 P68871 P61247 P62857 P22352 Q16698 P62979 P62851 Q00217 Q15273 P51970 P08708 P62906 P68133 P18077 P17661 P42677 P15880 Q02543 Q9NWT8 Q9Y3D2 P62263 P62987 P62945 P04275 P63313 P62269 |
| GO:0071826 | ribonucleoprotein complex subunit organization | 1.64E-08 | 2.01E-07 | 12 | 260 | 190 | 35980 | P42677 Q02878 P63173 P08708 P39023 P62263 P46783 P83731 P62913 P46777 P60228 P39019 |
| GO:0071840 | cellular component organization or biogenesis | 2.36E-23 | 7.22E-22 | 101 | 7374 | 190 | 35980 | P10916 Q43674 P16615 Q96000 P09493 P46783 P83731 P62913 P62753 P24752 Q15239 Q95169 P04406 Q14561 Q9Y6H1 Q95167 Q08431 P19105 P84098 Q14958 P63173 P46777 P60866 P46776 P60228 P62249 P52179 P25398 P68363 P10176 Q95178 P12235 P62891 P68871 P00441 Q00217 Q15273 P08708 O75116 P68133 P18077 P17661 P42677 P15880 Q02543 Q9NWT8 Q9Y3D2 P62263 P62945 P62269 P0C47 P0DMV8 P40925 P62280 P35613 P0C48 P39019 P05090 P39023 P62273 P69905 P62158 P45379 Q8WYQ3 P01034 Q07020 P01033 Q14896 P19021 P19022 P37108 Q43920 P68032 P61353 P60660 P02511 P05386 P17081 P05387 P02792 P42766 Q02878 P84243 P61247 P62857 P22352 Q16698 P62979 Q15004 P62851 Q14315 P51970 Q9P0U1 P62906 P13533 P62987 P04275 P63313 P25116 P20585 P06576 |
| GO:0071897 | DNA biosynthetic process | 7.01E-04 | 3.54E-03 | 5 | 132 | 190 | 35980 | P0C47 P62987 P62979 Q15004 P0C48 |
| GO:0071900 | regulation of protein serine/threonine kinase activity | 3.07E-03 | 1.21E-02 | 10 | 668 | 190 | 35980 | P0C47 P51452 P60033 P62987 P62979 P62158 P04792 P25116 P00441 P0C48 |

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|------------|---|----------|----------|-----|------|-----|-------|---|
| GO:0071902 | positive regulation of protein serine/threonine kinase | 1.47E-03 | 6.62E-03 | 7 | 314 | 190 | 35980 | P0CG47 P60033 P62987 P62979 P62158 P00441 P0CG48 |
| GO:0072329 | monocarboxylic acid catabolic process | 2.72E-03 | 1.09E-02 | 4 | 109 | 190 | 35980 | P00505 Q16698 P51857 Q13011 |
| GO:0072331 | signal transduction by p53 class mediator | 6.45E-03 | 2.19E-02 | 4 | 139 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0072350 | tricarboxylic acid metabolic process | 4.77E-03 | 1.77E-02 | 3 | 64 | 190 | 35980 | P40926 P40925 P48735 |
| GO:0072358 | cardiovascular system development | 2.01E-08 | 2.40E-07 | 21 | 915 | 190 | 35980 | Q13765 P02144 Q14116 O15273 Q14896 P10916 P01160 P19021 P19022 P68032 P13533 Q08431 P12883 P05090 P19429 Q14192 P08590 P09493 P45379 P06576 P63316 |
| GO:0072359 | circulatory system development | 2.01E-08 | 2.40E-07 | 21 | 915 | 190 | 35980 | Q13765 P02144 Q14116 O15273 Q14896 P10916 P01160 P19021 P19022 P68032 P13533 Q08431 P12883 P05090 P19429 Q14192 P08590 P09493 P45379 P06576 P63316 |
| GO:0072395 | signal transduction involved in cell cycle checkpoint | 5.55E-04 | 2.86E-03 | 4 | 71 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0072401 | signal transduction involved in DNA integrity checkpoint | 5.26E-04 | 2.73E-03 | 4 | 70 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0072413 | signal transduction involved in mitotic cell cycle | 4.71E-04 | 2.49E-03 | 4 | 68 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0072422 | signal transduction involved in DNA damage checkpoint | 5.26E-04 | 2.73E-03 | 4 | 70 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0072431 | signal transduction involved in mitotic G1 DNA damage | 4.45E-04 | 2.39E-03 | 4 | 67 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0072503 | cellular divalent inorganic cation homeostasis | 2.23E-03 | 9.29E-03 | 7 | 338 | 190 | 35980 | P13693 P51684 O14958 P19429 P16615 P23327 P25116 |
| GO:0072507 | divalent inorganic cation homeostasis | 3.21E-03 | 1.26E-02 | 7 | 361 | 190 | 35980 | P13693 P51684 O14958 P19429 P16615 P23327 P25116 |
| GO:0072521 | purine-containing compound metabolic process | 2.48E-22 | 6.94E-21 | 32 | 619 | 190 | 35980 | P13929 O75947 P0DMV8 P0DMV9 P01160 O43674 O00483 P36542 P10176 O95178 O96000 P16860 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P17081 P06576 |
| GO:0072524 | pyridine-containing compound metabolic process | 2.89E-04 | 1.64E-03 | 7 | 238 | 190 | 35980 | O75947 P16860 P25705 P48047 P18859 P01160 P36542 P56381 Q8WYQ3 P06576 |
| GO:0072593 | reactive oxygen species metabolic process | 8.92E-05 | 5.80E-04 | 6 | 136 | 190 | 35980 | P13929 P40926 P04406 Q8N815 P07195 P40925 Q8N335 |
| GO:0072594 | establishment of protein localization to organelle | 9.04E-38 | 9.27E-36 | 40 | 431 | 190 | 35980 | P68871 Q16654 P22352 P69905 P62158 P00441 |
| GO:0072599 | establishment of protein localization to endoplasmic reticulum | 5.02E-54 | 1.36E-51 | 37 | 131 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q9P01 P08708 P62906 P18077 P31708 Q09Y6H1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P25116 P62249 |
| GO:0072657 | protein localization to membrane | 8.43E-40 | 9.29E-38 | 41 | 416 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q9P01 P08708 P62906 P18077 P31708 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0075733 | intracellular transport of virus | 2.41E-05 | 1.85E-04 | 4 | 32 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0080134 | regulation of response to stress | 6.52E-07 | 6.50E-06 | 25 | 1540 | 190 | 35980 | P07602 P0CG47 P52179 P0DMV8 P0DMV9 P40925 P10176 P0CG48 P39019 P13693 P63244 P05090 Q16654 P62979 P62158 P00441 P51452 Q14116 P16989 Q9Y6H1 Q6P6C2 P62987 P02511 P04792 P25116 |
| GO:0080135 | regulation of cellular response to stress | 1.14E-03 | 5.39E-03 | 11 | 689 | 190 | 35980 | P07602 P51452 P13693 P63244 P0DMV8 P0DMV9 P16989 Q9Y6H1 P02511 P04792 P00441 |
| GO:0090002 | establishment of protein localization to plasma membrane | 1.33E-02 | 3.86E-02 | 3 | 93 | 190 | 35980 | O75116 P19022 P35613 |
| GO:0090068 | positive regulation of cell cycle process | 1.44E-02 | 4.13E-02 | 5 | 269 | 190 | 35980 | P0CG47 O75116 P62987 P62979 P0CG48 |
| GO:0090090 | negative regulation of canonical Wnt signaling pathway | 2.15E-03 | 9.05E-03 | 5 | 170 | 190 | 35980 | P0CG47 P19022 P62987 P62979 P0CG48 |
| GO:0090101 | negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 4.08E-03 | 1.55E-02 | 4 | 122 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0090150 | establishment of protein localization to membrane | 7.76E-46 | 1.10E-43 | 41 | 299 | 190 | 35980 | P25398 P62280 P35613 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q9P01 P108708 O75116 P62906 P19022 P18077 P31708 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0090257 | regulation of muscle system process | 7.59E-15 | 1.48E-13 | 17 | 230 | 190 | 35980 | Q14896 P10916 P01160 P16615 Q8N3K9 P12883 O14958 P19429 P08590 P09493 P23327 P62158 P45379 P25116 O14558 P00441 P63316 |
| GO:0090263 | positive regulation of canonical Wnt signaling pathway | 6.29E-03 | 2.14E-02 | 4 | 138 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0090279 | regulation of calcium ion import | 2.63E-03 | 1.06E-02 | 4 | 108 | 190 | 35980 | O14958 P23327 P62158 P25116 |
| GO:0090288 | negative regulation of cellular response to growth factor | 8.59E-03 | 2.76E-02 | 4 | 151 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0090304 | nucleic acid metabolic process | 9.55E-11 | 1.41E-09 | 66 | 5665 | 190 | 35980 | P0CG47 Q9NSD9 P01160 P62280 Q8TAK5 P0CG48 P39019 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 P20674 Q13765 Q07020 P10606 Q96H40 Q9Y5N6 P16989 Q9Y6H1 P84098 P63173 P68104 P61353 P46777 P05386 Q13772 P60866 P46776 P05387 P60229 P62249 P25398 P09699 O00483 P14854 P10176 P62891 P42766 Q02878 P84243 Q14192 P61247 P62857 P62979 Q15004 P62851 P08708 P62906 P18077 P15954 Q6P6C2 P17535 Q8N815 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P20685 |
| GO:0090407 | organophosphate biosynthetic process | 8.01E-05 | 5.35E-04 | 13 | 686 | 190 | 35980 | O75947 P66732 P48047 P01160 P36542 P16860 P25705 P18859 Q9N1P5 P56381 Q8WYQ3 Q8N335 P06576 |
| GO:0097031 | mitochondrial respiratory chain complex I biogenesis | 1.13E-12 | 1.88E-11 | 10 | 62 | 190 | 35980 | Q00217 O95169 P51970 O43674 O14561 O43920 O95176 O95178 O96000 O15239 |
| GO:0097300 | programmed necrotic cell death | 4.34E-05 | 3.10E-04 | 4 | 37 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:0097305 | response to alcohol | 1.96E-04 | 1.17E-03 | 9 | 378 | 190 | 35980 | P13693 P00505 O75116 P19021 P68032 P02511 P62158 P00441 P01034 |
| GO:0097485 | neuron projection guidance | 4.57E-03 | 1.71E-02 | 9 | 595 | 190 | 35980 | P0CG47 P60660 O75116 P62987 P83731 P62979 P62158 P19105 P0CG48 |
| GO:0098542 | defense response to other organism | 8.90E-03 | 2.84E-02 | 8 | 547 | 190 | 35980 | P52179 P62891 P40925 P62987 Q16654 Q6P6C2 P10176 Q01628 |
| GO:0098655 | cation transmembrane transport | 7.73E-08 | 8.36E-07 | 22 | 1083 | 190 | 35980 | O75947 P10606 P09669 P48047 P14406 O00483 P14854 P16615 P36542 P15954 P10176 P13073 P25705 P18859 O14949 P47985 P56381 P24310 P24311 P25116 P06576 P20674 |
| GO:0098660 | inorganic ion transmembrane transport | 2.08E-08 | 2.47E-07 | 23 | 1095 | 190 | 35980 | O75947 P10606 P09669 P48047 P14406 O00483 P14854 P16615 P36542 P15954 P10176 P13073 P25705 P18859 O14949 Q00325 P47985 P56381 P24310 P24311 P25116 P06576 P20674 |
| GO:0098662 | inorganic cation transmembrane transport | 5.46E-09 | 7.02E-08 | 22 | 932 | 190 | 35980 | O75947 P10606 P09669 P48047 P14406 O00483 P14854 P16615 P36542 P15954 P10176 P13073 P25705 P18859 O14949 P47985 P56381 P24310 P24311 P25116 P06576 P20674 |
| GO:0098754 | detoxification | 1.44E-03 | 6.49E-03 | 5 | 155 | 190 | 35980 | P68871 O14880 P22352 P69905 P00441 |
| GO:0098771 | inorganic ion homeostasis | 4.62E-04 | 2.46E-03 | 11 | 615 | 190 | 35980 | P13693 P02792 P51684 O14958 P19429 P16615 Q16654 P23327 P25116 P00441 P06576 |
| GO:0098779 | mitophagy in response to mitochondrial depolarization | 5.83E-03 | 2.01E-02 | 4 | 135 | 190 | 35980 | P52179 Q9P0U1 P40925 P10176 |
| GO:0098780 | response to mitochondrial depolarisation | 5.83E-03 | 2.01E-02 | 4 | 135 | 190 | 35980 | P52179 Q9P0U1 P40925 P10176 |
| GO:0098792 | xenophagy | 1.33E-05 | 1.06E-04 | 6 | 97 | 190 | 35980 | P52179 P40925 P62987 Q16654 Q6P6C2 P10176 |
| GO:0098869 | cellular oxidant detoxification | 1.21E-03 | 5.67E-03 | 5 | 149 | 190 | 35980 | P68871 O14880 P22352 P69905 P00441 |
| GO:1900034 | regulation of cellular response to heat | 7.68E-03 | 2.52E-02 | 3 | 76 | 190 | 35980 | P0DMV8 P0DMV9 P02511 |
| GO:1900407 | regulation of cellular response to oxidative stress | 2.92E-04 | 1.65E-03 | 4 | 60 | 190 | 35980 | P07602 P63244 P04792 P00441 |
| GO:1900408 | negative regulation of cellular response to oxidative stress | 9.87E-04 | 4.75E-03 | 3 | 37 | 190 | 35980 | P07602 P63244 P04792 |
| GO:1901019 | regulation of calcium ion transmembrane transporter | 9.13E-04 | 4.44E-03 | 4 | 81 | 190 | 35980 | O14958 P01160 P23327 P62158 |
| GO:1901135 | carbohydrate derivative metabolic process | 3.37E-11 | 5.14E-10 | 34 | 1731 | 190 | 35980 | P07602 P13929 O75947 P0DMV8 P0DMV9 P01160 O43674 O00483 P36542 P10176 O95178 O96000 P16860 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 P13533 O95167 P12883 P17081 Q8N335 P06576 |
| GO:1901184 | regulation of ERBB signaling pathway | 1.09E-03 | 5.20E-03 | 4 | 85 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1901185 | negative regulation of ERBB signaling pathway | 7.91E-05 | 5.31E-04 | 4 | 43 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1901293 | nucleoside phosphate biosynthetic process | 3.25E-06 | 2.92E-05 | 11 | 354 | 190 | 35980 | O75947 P16860 P25705 P48047 P18859 P01160 Q9N1P5 P36542 P56381 Q8WYQ3 P06576 |
| GO:1901360 | organic cyclic compound metabolic process | 2.05E-23 | 6.35E-22 | 100 | 7222 | 190 | 35980 | O75947 O43674 O96000 P16860 P13073 P07195 P46783 P83731 P62913 P62753 O15239 P20674 Q13765 O95169 P48047 P04406 O14561 Q9Y5N6 P16989 Q9Y6H1 O95167 P84098 P63173 P68104 P46777 Q13772 P60866 P46776 P60228 P62249 Q8N335 P25398 P10176 O95178 P62891 P25705 P18859 Q14192 P56381 O00217 Q08493 P08708 P18077 Q6P6C2 P17535 P12883 Q8N815 P42677 P15880 Q02543 P62263 Q14240 P62945 P62269 P0CG47 Q9NSD9 P0DMV8 P0DMV9 P01160 P40926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P00505 P39023 P62273 P24311 Q8WYQ3 Q07020 P10606 Q96H40 O43920 P61353 P05386 P17081 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P84243 Q9N1P5 P61247 P62857 P62979 Q15004 P62851 P51970 P62906 P15954 P51857 P13533 P62987 P20585 P06576 |
| GO:1901361 | organic cyclic compound catabolic process | 1.35E-35 | 1.03E-33 | 41 | 527 | 190 | 35980 | P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q9P01 P08708 P62906 P18077 P51857 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |

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|------------|---|----------|----------|----|------|-----|-------|--|
| GO:1901362 | organic cyclic compound biosynthetic process | 4.07E-19 | 9.46E-18 | 69 | 4141 | 190 | 35980 | P0CG47 O75947 P01160 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P20674 Q13765 Q07020 P10606 Q96H40 P48047 P16989 Q9Y6H1 P84098 P63173 P68104 P61353 P46777 P05386 Q13772 P06866 P46776 P05387 P62249 P25398 P09669 O00483 P14854 P10176 P62891 P42766 Q02878 P25705 P18859 Q14192 Q9NP15 P61247 P62857 P62979 P56381 Q15004 P62851 P08708 P62906 P18077 P15954 P51857 P17535 P42677 P15880 Q02543 P62263 P62987 P62945 P62269 P06576 |
| GO:1901564 | organonitrogen compound metabolic process | 5.24E-49 | 9.74E-47 | 94 | 3102 | 190 | 35980 | O75947 P06732 Q9NSD9 P0DMV8 P0DMV9 P01160 Q43674 P40926 P40925 P62280 P36542 P39019 P16860 P13073 P00505 P39023 P62273 P07195 P46783 P83731 P62913 P62753 Q8WYQ3 P24752 O15239 P20674 Q13765 Q07020 Q95169 P13639 P48047 P04406 O14561 O14880 P19021 P37108 Q43920 Q95167 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P17081 P06866 P46776 P05387 P60228 P62249 Q8N335 P07602 P13929 P25398 O00483 P10176 Q95178 P12235 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P00441 P54368 O00217 Q08493 P51970 P08708 P62906 P18077 P13533 P12883 P42677 P15880 P17540 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:1901566 | organonitrogen compound biosynthetic process | 2.34E-33 | 1.42E-31 | 63 | 1893 | 190 | 35980 | O75947 P06732 Q9NSD9 P01160 P62280 P36542 P39019 P16860 P00505 P39023 P62273 P46783 P83731 P62913 P62753 Q8WYQ3 Q13765 Q07020 P13639 P48047 P14880 P37108 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P06866 P46776 P05387 P60228 P62249 P25398 P12235 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P54368 P08708 P62906 P18077 P42677 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:1901575 | organic substance catabolic process | 4.99E-21 | 1.33E-19 | 51 | 2049 | 190 | 35980 | P0CG47 P62280 P0CG48 P39019 P00505 P39023 P62273 P46783 P83731 P62913 P62158 P62753 P24752 Q07020 P04406 P84098 P63173 P61353 P46777 P05386 P06866 P46776 P05387 P60228 P62249 Q13011 Q8N335 P13929 P25398 P62891 P42766 Q02878 P17174 P61247 P62857 P16989 P62979 P62851 Q08493 P08708 P62906 P18077 P51857 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 |
| GO:1901576 | organic substance biosynthetic process | 2.09E-20 | 5.31E-19 | 92 | 6775 | 190 | 35980 | P0CG47 O75947 P06732 Q9NSD9 P01160 P40926 P40925 P62280 Q8TAK5 P36542 P0CG48 P39019 P16860 P13073 P00505 P39023 P62273 P46783 P83731 P62913 P24311 P62753 Q8WYQ3 P24752 P20674 Q13765 Q07020 P10606 Q96H40 P13639 P48047 P04406 O14561 O14880 Q9Y6H1 P37108 P16989 Q9Y6H1 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 Q13772 P06866 P46776 P05387 P60228 P62249 Q8N335 P13929 P25398 P09669 Q00483 P14854 P10176 P12235 P62891 P42766 Q02878 P25705 P18859 Q14192 Q9NP15 P17174 P61247 P62857 P62979 P56381 Q15004 P62851 P54368 P08708 P62906 P18077 P15954 P51857 P17535 P42677 P14222 P15880 Q02543 Q9NWT8 Q00325 P62263 P62987 Q14240 P62945 P62269 P06576 |
| GO:1901605 | alpha-amino acid metabolic process | 7.25E-37 | 6.74E-35 | 40 | 454 | 190 | 35980 | P06732 P25398 P62280 P39019 P62891 P42766 Q02878 P00505 P39023 P62273 P17174 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P17540 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P06866 P46776 P62269 P05387 P62249 |
| GO:1901652 | response to peptide | 1.40E-06 | 1.35E-05 | 15 | 627 | 190 | 35980 | P0CG47 P01033 P01160 P16615 P35613 P17535 P0CG48 P17174 P08574 P62987 Q16654 P62979 P62158 P17081 P62753 |
| GO:1901653 | cellular response to peptide | 1.37E-03 | 6.26E-03 | 9 | 496 | 190 | 35980 | P0CG47 P17174 P62987 Q16654 P62979 P62158 P17081 P62753 P0CG48 P13929 O75947 P0DMV8 P0DMV9 O43674 O00483 P36542 P10176 Q95178 Q96000 P13073 P25705 P18859 P56381 Q8WYQ3 O15239 P20674 Q00217 Q95169 P51970 P48047 P04406 O14561 O43920 P13533 Q95167 P12883 P17081 P06576 |
| GO:1901659 | glycosyl compound biosynthetic process | 8.35E-06 | 6.93E-05 | 8 | 190 | 190 | 35980 | O75947 P25705 P48047 P18859 P36542 P56381 Q8WYQ3 P06576 |
| GO:1901698 | response to nitrogen compound | 6.90E-06 | 5.86E-05 | 19 | 1103 | 190 | 35980 | P0CG47 P01033 P13639 P01160 O14880 P16615 P35613 P17535 P0CG48 O14958 P17174 P08574 P62987 Q16654 P62979 P62158 P17081 P62753 P0441 |
| GO:1901699 | cellular response to nitrogen compound | 1.72E-03 | 7.52E-03 | 11 | 724 | 190 | 35980 | P0CG47 O14958 P17174 P62987 Q16654 P62979 P62158 P17081 P62753 P0441 P0CG48 |
| GO:1901700 | response to oxygen-containing compound | 2.74E-11 | 4.20E-10 | 33 | 1622 | 190 | 35980 | P0CG47 P01160 P16615 P35613 P0CG48 P63244 P05090 P00505 P68871 P09493 P17174 Q16654 P22352 P62979 P69905 P62158 P62753 P00441 P01034 P01033 P02144 Q14116 P13639 O75116 P19021 P68032 P17535 P09382 P08574 P62987 P02511 P17081 P25116 |
| GO:1901701 | cellular response to oxygen-containing compound | 1.15E-04 | 7.28E-04 | 16 | 1022 | 190 | 35980 | P0CG47 Q14116 O75116 P0CG48 P63244 P09382 P09493 P17174 P62987 Q16654 P62979 P62158 P17081 P62753 P00441 P01034 |
| GO:1902400 | intracellular signal transduction involved in G1 DNA signal transduction involved in mitotic DNA damage | 4.45E-04 | 2.39E-03 | 4 | 67 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1902402 | signal transduction involved in mitotic DNA damage | 4.71E-04 | 2.49E-03 | 4 | 68 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1902403 | signal transduction involved in mitotic DNA integrity | 4.71E-04 | 2.49E-03 | 4 | 68 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1902531 | regulation of intracellular signal transduction | 8.47E-05 | 5.54E-04 | 24 | 1924 | 190 | 35980 | P07602 P0CG47 P51452 Q14116 P0DMV8 P0DMV9 P19022 P16989 Q8N3K9 P0CG48 P13693 P63244 O14958 P60033 P09382 P62987 P23327 P62979 P62158 P17081 P04792 P25116 Q8N335 P00441 P51452 P13693 P63244 O14958 P0DMV8 P16989 Q8N3K9 P62158 P04792 Q8N335 |
| GO:1902532 | negative regulation of intracellular signal transduction | 2.24E-04 | 1.30E-03 | 10 | 472 | 190 | 35980 | P07602 P0CG47 Q14116 P0DMV8 P0DMV9 P19022 P0CG48 P63244 P60033 P09382 P62987 P62979 P62158 P16989 P62158 P00441 |
| GO:1902533 | positive regulation of intracellular signal transduction | 5.14E-04 | 2.67E-03 | 15 | 1054 | 190 | 35980 | P0CG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P16860 P05090 P13073 P00505 O14949 P39023 P62273 P46783 P83731 P62913 P24310 P69905 P62158 P24311 P62753 P20674 Q07020 P1033 P10606 P48047 Q9Y277 P19021 P19022 P14406 P37108 Q9Y6H1 Q08431 P84098 P14958 P63173 P61353 P47985 P46777 P05386 P06866 P46776 P05387 P62249 P07602 P07602 P02792 P25398 P25398 P68363 Q00483 P14854 P10176 P12235 P13693 P62891 P42766 Q02878 P25705 P18859 P06033 P68871 P1247 P62857 P62979 P56381 P62851 P00441 P02144 Q9P0U1 P08708 O75116 P62906 P18077 P15954 Q6P6C2 P42677 P15880 Q02543 Q00325 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:1902579 | multi-organism localization | 3.89E-05 | 2.81E-04 | 4 | 36 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1902580 | single-organism cellular localization | 1.56E-27 | 7.13E-26 | 44 | 1014 | 190 | 35980 | P0CG47 P25398 P62280 P35613 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 Q9P0U1 P08708 O75116 P62906 P19022 P18077 P37108 Q9Y6H1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P06866 P46776 P62269 P05387 P25116 P62249 |
| GO:1902582 | single-organism intracellular transport | 7.99E-31 | 4.40E-29 | 56 | 1578 | 190 | 35980 | P0CG47 O75947 P0DMV8 P16615 P62280 P36542 P35613 P0CG48 P39019 P39023 P62273 P46783 P83731 P62913 P62753 Q07020 P48047 P37108 Q9Y6H1 P84098 P63173 P61353 P46777 P05386 P06866 P46776 P05387 P62249 P07602 P25398 P68363 P62891 P42766 Q02878 P25705 P18859 P61247 P62857 P62979 P56381 P62851 P00441 Q9P0U1 P08708 P62906 P18077 Q6P6C2 P42677 P15880 Q02543 P62263 P62987 P62945 P04275 P62269 P25116 P06576 |
| GO:1902583 | multi-organism intracellular transport | 2.41E-05 | 1.85E-04 | 4 | 32 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1902589 | single-organism organelle organization | 4.88E-04 | 2.56E-03 | 31 | 3128 | 190 | 35980 | P0CG47 P52179 P10916 P0DMV8 P40925 P68363 P10176 P0CG48 P09493 P83731 P62979 Q15004 P45379 P00441 O15273 Q14896 Q9P0U1 P04406 O75116 P68133 P17661 P68032 P13533 O14958 Q9NWT8 Q9Y3D2 P62987 P02511 P63313 P17081 P20585 |
| GO:1902600 | hydrogen ion transmembrane transport | 1.97E-18 | 4.44E-17 | 20 | 236 | 190 | 35980 | O75947 P10606 P09669 P48047 P14406 O00483 P14854 P36542 P15954 P01176 P13073 P25705 P18859 O14949 P47985 P56381 P24310 P24311 P06576 P20674 |
| GO:1902680 | positive regulation of RNA biosynthetic process | 1.13E-02 | 3.36E-02 | 16 | 1603 | 190 | 35980 | P0CG47 Q13765 P0DMV8 P0DMV9 Q96979 Q8TAK5 Q9Y6H1 P17535 P0CG48 P60033 Q14192 P62979 P2979 P17081 P25116 |
| GO:1902806 | regulation of cell cycle G1/S phase transition | 1.31E-02 | 3.82E-02 | 4 | 171 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1902807 | negative regulation of cell cycle G1/S phase transition | 3.96E-03 | 1.51E-02 | 4 | 121 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1902882 | regulation of response to oxidative stress | 4.20E-04 | 2.27E-03 | 4 | 66 | 190 | 35980 | P07602 P63244 P04792 P00441 |
| GO:1902883 | negative regulation of response to oxidative stress | 9.87E-04 | 4.75E-03 | 3 | 37 | 190 | 35980 | P07602 P63244 P04792 |
| GO:1903008 | organelle disassembly | 1.26E-05 | 1.01E-04 | 8 | 201 | 190 | 35980 | P0CG47 P52179 Q9P0U1 P40925 P62987 P62979 P10176 P0CG48 |
| GO:1903050 | regulation of proteolysis involved in cellular protein | 1.05E-02 | 4.29E-02 | 5 | 272 | 190 | 35980 | P0CG47 P63244 P62987 P62979 P0CG48 |
| GO:1903052 | positive regulation of proteolysis involved in cellular | 2.15E-03 | 9.05E-03 | 5 | 170 | 190 | 35980 | P0CG47 P63244 P62987 P62979 P0CG48 |
| GO:1903115 | regulation of actin filament-based movement | 2.12E-05 | 1.65E-04 | 4 | 31 | 190 | 35980 | Q14896 P16615 P45379 P63316 |
| GO:1903169 | regulation of calcium ion transmembrane transport | 7.25E-04 | 3.65E-03 | 5 | 133 | 190 | 35980 | O14958 P01160 P23327 P62158 P25116 |
| GO:1903201 | regulation of oxidative stress-induced cell death | 1.13E-04 | 7.13E-04 | 4 | 47 | 190 | 35980 | P07602 P63244 P04792 P00441 |
| GO:1903202 | negative regulation of oxidative stress-induced cell death | 7.69E-04 | 3.84E-03 | 3 | 34 | 190 | 35980 | P07602 P63244 P04792 |
| GO:1903220 | regulation of protein modification by small protein | 7.19E-03 | 2.39E-02 | 6 | 319 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 P62987 P62979 P0CG48 |
| GO:1903321 | negative regulation of protein modification by small protein conjugation or removal | 2.47E-04 | 1.42E-03 | 6 | 164 | 190 | 35980 | P0CG47 P0DMV8 P0DMV9 P62987 P62979 P0CG48 |

| | | | | | | | | |
|------------|---|----------|----------|----|------|-----|-------|---|
| GO:1903362 | regulation of cellular protein catabolic process | 4.80E-03 | 1.79E-02 | 6 | 293 | 190 | 35980 | P0CG47 P63244 P60033 P62987 P62979 P0CG48 |
| GO:1903364 | positive regulation of cellular protein catabolic process | 4.70E-04 | 2.49E-03 | 6 | 185 | 190 | 35980 | P0CG47 P63244 P60033 P62987 P62979 P0CG48 |
| GO:1903508 | positive regulation of nucleic acid-templated transcription | 9.65E-03 | 3.05E-02 | 16 | 1575 | 190 | 35980 | P0CG47 Q13765 P0DMV8 P0DMV9 Q969T9 Q8TAK5 Q9Y6H1 P17535 P0CG48 P60033 Q14192 P62987 P62979 Q13772 P17081 P25116 |
| GO:1903522 | regulation of blood circulation | 1.84E-13 | 3.31E-12 | 18 | 326 | 190 | 35980 | Q14896 P10916 P01160 P16615 P17661 P13533 P12883 P16860 O14958 P19429 Q9UBY9 P08590 P09493 P23327 P62158 P45379 P25116 Q8N335 |
| GO:1903524 | positive regulation of blood circulation | 1.69E-04 | 1.02E-03 | 5 | 97 | 190 | 35980 | P01160 P09493 P16615 P23327 P25116 |
| GO:1903649 | regulation of cytoplasmic transport | 3.32E-03 | 1.30E-02 | 8 | 462 | 190 | 35980 | Q14116 P63244 P05090 O14958 Q9P0U1 P23327 P62158 P25116 |
| GO:1903651 | positive regulation of cytoplasmic transport | 1.50E-02 | 4.29E-02 | 5 | 272 | 190 | 35980 | Q14116 P63244 Q9P0U1 P62158 P25116 |
| GO:1903779 | regulation of cardiac conduction | 1.67E-06 | 1.57E-05 | 6 | 68 | 190 | 35980 | O14958 P19429 P01160 P16615 P23327 P62158 |
| GO:1903827 | regulation of cellular protein localization | 3.12E-03 | 1.23E-02 | 9 | 561 | 190 | 35980 | P54368 Q14116 P63244 P05090 Q9P0U1 Q02818 P19022 P17081 Q8N335 |
| GO:1903844 | regulation of cellular response to transforming growth factor beta stimulus | 3.41E-03 | 1.33E-02 | 4 | 116 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1903845 | negative regulation of cellular response to transforming growth factor beta stimulus | 9.56E-04 | 4.63E-03 | 4 | 82 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:1904062 | regulation of cation transmembrane transport | 1.45E-03 | 6.56E-03 | 6 | 230 | 190 | 35980 | O14958 P01160 P23327 P62158 P25116 Q8N335 |
| GO:1990267 | response to transition metal nanoparticle | 1.61E-03 | 7.10E-03 | 5 | 159 | 190 | 35980 | P80297 P19021 Q02818 P35613 P00441 |
| GO:1990542 | mitochondrial transmembrane transport | 1.79E-09 | 2.44E-08 | 8 | 64 | 190 | 35980 | O75947 P25705 Q9P0U1 P48047 P18859 P36542 P56381 P06576 |
| GO:1990748 | cellular detoxification | 1.32E-03 | 6.07E-03 | 5 | 152 | 190 | 35980 | P68871 O14880 P22352 P69905 P00441 |
| GO:2000021 | regulation of ion homeostasis | 1.38E-04 | 8.56E-04 | 7 | 211 | 190 | 35980 | P63244 P16860 O14958 P23327 P62158 P25116 Q8N335 |
| GO:2000045 | regulation of G1/S transition of mitotic cell cycle | 1.07E-02 | 3.23E-02 | 4 | 161 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:2000058 | regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process | 1.78E-03 | 7.70E-03 | 4 | 97 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:2000060 | positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process | 1.24E-03 | 5.79E-03 | 4 | 88 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:2000134 | negative regulation of G1/S transition of mitotic cell cycle | 3.51E-03 | 1.36E-02 | 4 | 117 | 190 | 35980 | P0CG47 P62987 P62979 P0CG48 |
| GO:2001233 | regulation of apoptotic signaling pathway | 3.09E-04 | 1.74E-03 | 9 | 402 | 190 | 35980 | P0CG47 P13693 P63244 P0DMV8 P0DMV9 P16989 P04792 P00441 Q8N8D1 |
| GO:2001234 | negative regulation of apoptotic signaling pathway | 5.83E-03 | 2.01E-02 | 5 | 215 | 190 | 35980 | P13693 P0DMV8 P0DMV9 P16989 P04792 |
| GO:2001242 | regulation of intrinsic apoptotic signaling pathway | 1.97E-05 | 1.54E-04 | 7 | 155 | 190 | 35980 | P0CG47 P13693 P63244 P0DMV8 P16989 P04792 P00441 |
| GO:2001243 | negative regulation of intrinsic apoptotic signaling pathway | 1.65E-03 | 7.26E-03 | 4 | 95 | 190 | 35980 | P13693 P0DMV8 P16989 P04792 |
| GO:2001244 | positive regulation of intrinsic apoptotic signaling pathway | 3.79E-03 | 1.45E-02 | 3 | 59 | 190 | 35980 | P0CG47 P63244 P00441 |
| GO:2001257 | regulation of cation channel activity | 2.14E-03 | 9.02E-03 | 4 | 102 | 190 | 35980 | O14958 P01160 P23327 P62158 |

Supplemental Table VIII. hA-VCMs BinGO 2011. BinGO analysis of the adult ventricular cardiomyocyte (hA-VCMs) data¹⁹ using the 2011 GO annotation dataset. **x** is the number of IDs in both the submitted list and associated with the GO term, **n** indicates the number of protein IDs associated with the GO term, **X** is the number of protein IDs submitted for analysis, **N** is the number of protein IDs used as the background set.

| GO-ID | Description | p-value | corr p-value | x | n | X | N | Proteins submitted in analysis that are associated with the GO term |
|------------|--|----------|--------------|----|------|-----|-------|--|
| GO:000028 | ribosomal small subunit assembly | 5.69E-08 | 8.67E-07 | 4 | 7 | 178 | 27688 | P08708 P62263 P62851 P62753 |
| GO:000075 | cell cycle checkpoint | 5.93E-03 | 2.83E-02 | 6 | 252 | 178 | 27688 | POCG47 P62987 Q9Y5N6 P83731 P62979 POCG48 |
| GO:000082 | G1/S transition of mitotic cell cycle | 4.58E-03 | 2.28E-02 | 5 | 167 | 178 | 27688 | POCG47 P62987 Q9Y5N6 P62979 POCG48 |
| GO:000084 | mitotic S phase | 1.13E-03 | 7.77E-03 | 5 | 121 | 178 | 27688 | POCG47 P62987 Q9Y5N6 P62979 POCG48 |
| GO:000165 | MAPK cascade | 9.25E-03 | 3.89E-02 | 5 | 198 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:000187 | activation of MAPK activity | 3.35E-04 | 2.84E-03 | 6 | 143 | 178 | 27688 | POCG47 P60033 P62987 P62979 P00441 POCG48 |
| GO:000302 | response to reactive oxygen species | 7.31E-05 | 7.33E-04 | 7 | 157 | 178 | 27688 | P02144 Q14116 P68871 P09493 P69905 P00441 P12883 |
| GO:0001817 | regulation of cytokine production | 4.05E-03 | 2.09E-02 | 8 | 393 | 178 | 27688 | POCG47 Q14116 P62987 P62979 P04792 P25116 P00441 POCG48 |
| GO:0002027 | regulation of heart rate | 2.01E-03 | 1.19E-02 | 3 | 39 | 178 | 27688 | P09493 P13533 P12883 |
| GO:0002218 | activation of innate immune response | 1.66E-03 | 1.03E-02 | 5 | 132 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0002221 | pattern recognition receptor signaling pathway | 5.71E-04 | 4.50E-03 | 5 | 104 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0002224 | toll-like receptor signaling pathway | 3.59E-04 | 3.02E-03 | 5 | 94 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0002262 | myeloid cell homeostasis | 3.31E-05 | 3.53E-04 | 6 | 94 | 178 | 27688 | P01033 P02144 P08708 P62263 P00441 P39019 |
| GO:0002576 | platelet degranulation | 1.79E-04 | 1.61E-03 | 5 | 81 | 178 | 27688 | P07602 P01033 P04275 P62158 P00441 |
| GO:0002753 | cytoplasmic pattern recognition receptor signaling | 2.58E-05 | 2.84E-04 | 4 | 27 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0002755 | MyD88-dependent toll-like receptor signaling | 1.09E-04 | 1.06E-03 | 5 | 73 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0002756 | MyD88-independent toll-like receptor signaling | 6.27E-05 | 6.35E-04 | 5 | 65 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0002758 | innate immune response-activating signal | 7.37E-04 | 5.59E-03 | 5 | 110 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0003007 | heart morphogenesis | 2.38E-09 | 4.02E-08 | 12 | 181 | 178 | 27688 | O15273 Q14896 P10916 P19429 Q14192 P08590 P09493 P68032 P45379 P13533 P12883 P63316 |
| GO:0003008 | system process | 1.08E-09 | 1.94E-08 | 30 | 1297 | 178 | 27688 | P52179 P10916 P01160 P54296 P16860 Q01449 P19429 P68871 P09493 P23327 P62158 P45379 P00441 P02144 Q14116 O15273 Q14896 O75116 P68133 P17661 P68032 P13533 P12883 O14958 P17540 P60660 P08590 P02511 P25116 P63316 |
| GO:0003012 | muscle system process | 2.35E-23 | 1.38E-21 | 25 | 233 | 178 | 27688 | P52179 P10916 P54296 Q01449 P19429 P09493 P23327 P62158 P45379 P00441 P02144 O15273 Q14896 O75116 P68133 P17661 P68032 P13533 P12883 O14958 P17540 P60660 P08590 P02511 P63316 |
| GO:0003013 | circulatory system process | 2.76E-09 | 4.59E-08 | 15 | 320 | 178 | 27688 | Q14116 O15273 Q14896 P10916 P01160 P68032 P13533 P16860 P19429 P68871 P08590 P09493 P25116 P00441 P63316 |
| GO:0003015 | heart process | 2.75E-12 | 5.64E-11 | 9 | 39 | 178 | 27688 | O15273 Q14896 P10916 P19429 P08590 P09493 P68032 P00441 P63316 |
| GO:0003018 | vascular process in circulatory system | 6.07E-04 | 4.74E-03 | 6 | 160 | 178 | 27688 | Q14116 P16860 P01160 P68871 P25116 P00441 |
| GO:0003205 | cardiac chamber development | 1.08E-09 | 1.94E-08 | 10 | 101 | 178 | 27688 | Q14896 P10916 P19429 Q14192 P08590 P09493 P45379 P13533 P12883 P63316 |
| GO:0003206 | cardiac chamber morphogenesis | 4.77E-10 | 8.79E-09 | 10 | 93 | 178 | 27688 | Q14896 P10916 P19429 Q14192 P08590 P09493 P45379 P13533 P12883 P63316 |
| GO:0003208 | cardiac ventricle morphogenesis | 1.99E-10 | 3.80E-09 | 9 | 61 | 178 | 27688 | Q14896 P10916 P19429 P08590 P09493 P45379 P13533 P12883 P63316 |
| GO:0003229 | ventricular cardiac muscle tissue development | 1.11E-11 | 2.22E-10 | 9 | 45 | 178 | 27688 | Q14896 P10916 P19429 P08590 P09493 P45379 P13533 P12883 P63316 |
| GO:0003231 | cardiac ventricle development | 3.34E-09 | 5.52E-08 | 9 | 83 | 178 | 27688 | Q14896 P10916 P19429 P08590 P09493 P45379 P13533 P12883 P63316 |
| GO:0005996 | monosaccharide metabolic process | 3.09E-04 | 2.63E-03 | 8 | 262 | 178 | 27688 | P13929 P00505 P40926 P04406 P40925 P17174 Q16654 P62158 |
| GO:0006006 | glucose metabolic process | 1.38E-05 | 1.58E-04 | 8 | 168 | 178 | 27688 | P13929 P06732 Q9NSD9 P40926 P04406 O14561 P40925 O14880 P51857 P35613 P41222 P17540 P00505 P07195 P17174 Q16654 Q16698 P24752 Q13011 P48735 |
| GO:0006082 | organic acid metabolic process | 8.24E-04 | 6.19E-03 | 20 | 1417 | 178 | 27688 | P13929 P04406 P07195 Q16654 P35613 |
| GO:0006090 | pyruvate metabolic process | 2.29E-03 | 1.31E-02 | 5 | 142 | 178 | 27688 | P13929 O75947 P09669 O43674 P40926 P40925 O00483 P14854 P36542 P10176 O95178 P12235 O96000 P13073 P25705 P18859 O14949 P07195 P56381 P24310 P62158 P24311 O15239 P20674 O00217 P16066 O95169 P51970 P48047 P04406 O14561 O43920 P15954 O95167 Q00325 P08574 P47985 Q13011 P06576 P48735 |
| GO:0006091 | generation of precursor metabolites and energy | 2.08E-30 | 1.89E-28 | 40 | 552 | 178 | 27688 | P13929 O75947 P09669 O43674 P40926 P40925 O00483 P14854 P36542 P10176 O95178 P12235 O96000 P13073 P25705 P18859 O14949 P07195 P56381 P24310 P62158 P24311 O15239 P20674 O00217 P16066 O95169 P51970 P48047 P04406 O14561 O43920 P15954 O95167 Q00325 P08574 P47985 Q13011 P06576 P48735 |
| GO:0006094 | gluconeogenesis | 1.79E-06 | 2.40E-05 | 6 | 57 | 178 | 27688 | P13929 P00505 P40926 P04406 P40925 P17174 |
| GO:0006099 | tricarboxylic acid cycle | 6.52E-03 | 2.87E-02 | 3 | 59 | 178 | 27688 | P40926 P40925 P48735 |
| GO:0006101 | citrate metabolic process | 8.17E-03 | 3.49E-02 | 3 | 64 | 178 | 27688 | P40926 P40925 P48735 |
| GO:0006103 | 2-oxoglutarate metabolic process | 4.79E-04 | 3.87E-03 | 3 | 24 | 178 | 27688 | P00505 P17174 P48735 |
| GO:0006107 | oxaloacetate metabolic process | 1.12E-04 | 1.08E-03 | 3 | 15 | 178 | 27688 | P00505 P40926 P40925 |
| GO:0006119 | oxidative phosphorylation | 2.59E-13 | 6.19E-12 | 12 | 84 | 178 | 27688 | O00217 O95169 P51970 O43674 O14561 O00483 O43920 P36542 O95167 O95178 O96000 O15239 |
| GO:0006120 | mitochondrial electron transport, NADH to ubiquinone | 1.34E-14 | 3.69E-13 | 11 | 49 | 178 | 27688 | O00217 O95169 P51970 O43674 O14561 O00483 O43920 O95167 O95178 O96000 O15239 |
| GO:0006139 | nucleobase-containing compound metabolic process | 1.07E-21 | 5.27E-20 | 75 | 3654 | 178 | 27688 | POCG47 O75947 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 POCG48 P39019 O96000 P16860 P39023 P62273 P07195 P46783 P83731 P62913 P62753 O15239 Q13765 Q07020 O95169 P48047 P04406 O14561 Q9Y5N6 O43920 O95167 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P13929 P25398 O00483 O95178 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P61247 P62857 P62979 P56381 P62851 P00441 O00217 Q08493 P51970 P08708 P62906 P18077 Q8N8D1 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P04792 P62269 P20585 P06576 |
| GO:0006163 | purine nucleotide metabolic process | 6.01E-15 | 1.79E-13 | 25 | 522 | 178 | 27688 | P13929 O75947 P01160 O43674 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 P06576 |
| GO:0006164 | purine nucleotide biosynthetic process | 2.80E-06 | 3.61E-05 | 10 | 232 | 178 | 27688 | O75947 P16860 P25705 P48047 P18859 P01160 P16615 P36542 P56381 P06576 |
| GO:0006364 | rRNA processing | 9.33E-08 | 1.36E-06 | 9 | 121 | 178 | 27688 | P08708 P62263 P18077 P62857 P62913 P46777 P62753 P62249 P39019 P25398 Q9NSD9 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62857 P62979 P62851 P62753 Q13765 Q07020 P13639 P08708 P62906 P18077 P42677 P84098 P15880 P63173 P61353 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0006412 | translation | 3.88E-31 | 4.02E-29 | 43 | 648 | 178 | 27688 | P08708 Q14240 P61247 P60228 |
| GO:0006413 | translational initiation | 2.58E-04 | 2.23E-03 | 4 | 48 | 178 | 27688 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P13639 P08708 P62906 P18077 P42677 P84098 P15880 P63173 P68104 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 |
| GO:0006414 | translational elongation | 2.57E-56 | 1.40E-53 | 38 | 110 | 178 | 27688 | P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P13639 P08708 P62906 P18077 P42677 P84098 P15880 P63173 P68104 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 |
| GO:0006415 | translational termination | 4.21E-55 | 1.83E-52 | 36 | 95 | 178 | 27688 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0006417 | regulation of translation | 3.36E-03 | 1.79E-02 | 6 | 224 | 178 | 27688 | P63244 P62263 Q14240 P37108 P04792 P60228 |
| GO:0006446 | regulation of translational initiation | 4.83E-03 | 2.38E-02 | 3 | 53 | 178 | 27688 | Q14240 P04792 P60228 |
| GO:0006518 | peptide metabolic process | 6.77E-31 | 6.41E-29 | 46 | 789 | 178 | 27688 | P25398 Q9NSD9 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P22352 P62979 P62851 P62753 P00441 Q13765 Q07020 P13639 P08708 P62906 P19021 P18077 P42677 P84098 P15880 Q05639 P63173 P68104 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0006725 | cellular aromatic compound metabolic process | 9.69E-20 | 3.98E-18 | 75 | 3941 | 178 | 27688 | POCG47 O75947 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 POCG48 P39019 O96000 P16860 P39023 P62273 P07195 P46783 P83731 P62913 P62753 O15239 Q13765 Q07020 O95169 P48047 P04406 O14561 Q9Y5N6 O43920 O95167 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 |
| GO:0006733 | oxidoreduction coenzyme metabolic process | 2.17E-03 | 1.26E-02 | 6 | 205 | 178 | 27688 | P13929 P40926 P04406 Q9NP15 P07195 P40925 |

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| GO:0006753 | nucleoside phosphate metabolic process | 5.62E-14 | 1.46E-12 | 28 | 747 | 178 | 27688 | P13929 O75947 P01160 O43674 P40926 P40925 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 Q9NP15 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 P06576 |
| GO:0006754 | ATP biosynthetic process | 5.08E-07 | 7.08E-06 | 8 | 108 | 178 | 27688 | O75947 P25705 P48047 P18859 P16615 P36542 P56381 P06576 P0CG47 P13929 O75947 P06732 P01160 O43674 P40926 P40925 O00483 P16615 P36542 O95178 P0CG48 O96000 P16860 P25705 P18859 P60033 Q9NP15 P07195 Q16654 P62979 P56381 O15239 P51452 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O75116 O43920 O95167 P62987 P25116 Q8N335 P06576 |
| GO:0006793 | phosphorus metabolic process | 8.59E-09 | 1.37E-07 | 39 | 2244 | 178 | 27688 | P0CG47 P13929 O75947 P06732 P01160 O43674 P40926 P40925 O00483 P16615 P36542 O95178 P0CG48 O96000 P16860 P25705 P18859 P60033 Q9NP15 P07195 Q16654 P62979 P56381 O15239 P51452 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O75116 O43920 O95167 P62987 P25116 Q8N335 P06576 |
| GO:0006796 | phosphate-containing compound metabolic process | 3.96E-09 | 6.43E-08 | 39 | 2182 | 178 | 27688 | P0CG47 P13929 O75947 P06732 P01160 O43674 P40926 P40925 O00483 P16615 P36542 O95178 P0CG48 O96000 P16860 P25705 P18859 P60033 Q9NP15 P07195 Q16654 P62979 P56381 O15239 P51452 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O75116 O43920 O95167 P62987 P25116 Q8N335 P06576 |
| GO:0006807 | nitrogen compound metabolic process | 9.93E-21 | 4.60E-19 | 88 | 5152 | 178 | 27688 | P0CG47 O75947 P06732 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 P0CG48 P39019 O96000 P16860 P00505 P39023 P62273 P07195 P46783 P83731 P62913 P62158 P62753 P24752 O15239 Q13765 Q07020 O95169 P13639 P48047 P04406 O14561 P19021 Q9Y5N6 O43920 O95167 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P07602 P13929 P25398 O00483 O95178 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P22352 P62979 P56381 P62851 P00441 P54368 O00217 Q08493 P51970 P08708 P62906 P18077 Q8N8D1 P42677 P15880 P17540 Q02543 P62263 P62987 Q14240 P62945 P04792 P62269 P20585 P06576 |
| GO:0006810 | transport | 1.02E-04 | 1.00E-03 | 53 | 5023 | 178 | 27688 | P0CG47 O75947 O43674 P16615 P36542 P35613 P0CG48 P39019 O96000 P16860 P05090 P00505 O14949 P62913 P69905 P62158 O15239 Q13765 P01033 O95169 P48047 Q9Y277 O14561 P37108 O43920 O95167 Q08431 P19105 P08574 P47985 P07602 P02792 P68363 O00483 O95178 P12235 P13693 P25705 P18859 P68871 P62979 P56381 P00441 O00217 P02144 P51970 Q9P0U1 P41222 Q00325 P62987 P04275 P25116 P06576 |
| GO:0006818 | hydrogen transport | 4.23E-05 | 4.44E-04 | 7 | 144 | 178 | 27688 | O75947 P25705 P48047 P18859 P36542 P56381 P06576 |
| GO:0006839 | mitochondrial transport | 1.74E-06 | 2.34E-05 | 8 | 127 | 178 | 27688 | O75947 P25705 Q9P0U1 P48047 P18859 P36542 P56381 P06576 |
| GO:0006928 | movement of cell or subcellular component | 3.21E-05 | 3.44E-04 | 23 | 1392 | 178 | 27688 | O15273 Q14896 P10916 P51684 O75116 P68363 P19022 P68133 P17661 P68032 P13533 P35613 P12883 Q01449 P19429 P60660 P08590 P09493 P83731 P04792 P45379 P06576 P63316 |
| GO:0006936 | muscle contraction | 2.25E-23 | 1.36E-21 | 24 | 205 | 178 | 27688 | P52179 P02144 O15273 Q14896 P10916 P54296 O75116 P68133 P17661 P68032 P13533 P12883 Q01449 O14958 P19429 P17540 P60660 P08590 P09493 P23327 P02511 P62158 P45379 P63316 |
| GO:0006937 | regulation of muscle contraction | 1.47E-08 | 2.31E-07 | 9 | 98 | 178 | 27688 | Q14896 P10916 P19429 P08590 P09493 P25116 O14558 P00441 P63316 |
| GO:0006940 | regulation of smooth muscle contraction | 3.87E-03 | 2.02E-02 | 3 | 49 | 178 | 27688 | P19429 P25116 P00441 |
| GO:0006941 | striated muscle contraction | 6.35E-12 | 1.28E-10 | 10 | 61 | 178 | 27688 | P02144 O15273 Q14896 O14958 P19429 P08590 P09493 P68032 P13533 P63316 |
| GO:0006942 | regulation of striated muscle contraction | 1.87E-03 | 1.14E-02 | 3 | 38 | 178 | 27688 | Q14896 P10916 P08590 |
| GO:0006950 | response to stress | 7.81E-04 | 5.91E-03 | 39 | 3628 | 178 | 27688 | P07602 P0CG47 P13929 P51684 Q12988 P16615 P35613 P0CG48 P16860 P84243 P60033 P68871 Q9UBV9 P09493 P22352 P62979 P69905 P62158 P24752 Q01628 P00441 P01034 P51452 O00217 P01033 P02144 Q14116 O15273 Q14880 P19021 P16989 P12883 P09382 P62987 P04275 P04792 P25116 P20585 O14558 |
| GO:0006977 | DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest | 8.72E-04 | 6.35E-03 | 4 | 66 | 178 | 27688 | P0CG47 P62987 P62979 P0CG48 |
| GO:0006979 | response to oxidative stress | 5.01E-04 | 4.02E-03 | 9 | 354 | 178 | 27688 | O00217 P02144 Q14116 P68871 P09493 P22352 P69905 P00441 P12883 |
| GO:0006986 | response to unfolded protein | 1.30E-02 | 4.95E-02 | 3 | 76 | 178 | 27688 | Q12988 Q9UBV9 P04792 |
| GO:0007093 | mitotic cell cycle checkpoint | 2.74E-03 | 1.52E-02 | 5 | 148 | 178 | 27688 | P0CG47 P62987 P83731 P62979 P0CG48 |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 9.64E-03 | 4.01E-02 | 11 | 752 | 178 | 27688 | P0CG47 P51452 P16860 P01160 P62987 P62979 P62158 P17081 P13533 P62753 P0CG48 |
| GO:0007173 | epidermal growth factor receptor signaling | 2.04E-03 | 1.20E-02 | 4 | 83 | 178 | 27688 | P0CG47 P62987 P62979 P0CG48 |
| GO:0007249 | I-kappaB kinase/NF-kappaB signaling | 4.67E-04 | 3.80E-03 | 4 | 56 | 178 | 27688 | P0CG47 P62987 P62979 P0CG48 |
| GO:0007254 | JNK cascade | 3.09E-03 | 1.66E-02 | 4 | 93 | 178 | 27688 | P0CG47 P62987 P62979 P0CG48 |
| GO:0007275 | multicellular organism development | 2.80E-14 | 7.62E-13 | 76 | 5038 | 178 | 27688 | P10916 P62280 P35613 P39019 P63244 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P45379 P62753 P24752 Q07020 P01033 Q14896 P19021 P19022 P16989 P68032 Q08431 P84098 O14958 P63173 P08493 P61353 P60660 P09382 P46777 P05386 Q13772 P60866 P46776 P05387 P62249 P07602 P25398 P62891 P42766 Q02878 P19429 P25705 P84243 Q14192 P61247 P62857 P62979 P62851 P00441 P51452 P02144 Q14116 O15273 P08708 O75116 P62906 P68133 P18077 P13533 P12883 P42677 P15880 Q02543 P08590 P62263 P62987 P62945 P04275 P04792 P62269 P20585 P06576 P63316 |
| GO:0007346 | regulation of mitotic cell cycle | 4.19E-03 | 2.12E-02 | 7 | 312 | 178 | 27688 | P0CG47 P51452 Q9NWT8 P62987 P83731 P62979 P0CG48 |
| GO:0007507 | heart development | 1.24E-07 | 1.78E-06 | 16 | 489 | 178 | 27688 | P02144 O15273 Q14896 P10916 P19021 P68032 P13533 P12883 P16860 O14958 P19429 Q14192 P08590 P09493 P45379 P63316 |
| GO:0007512 | adult heart development | 1.38E-04 | 1.28E-03 | 3 | 16 | 178 | 27688 | O15273 P13533 P12883 |
| GO:0007517 | muscle organ development | 2.19E-08 | 3.40E-07 | 13 | 268 | 178 | 27688 | O15273 Q14896 P10916 P68133 P68032 P13533 P12883 P19429 P60660 P08590 P09493 P45379 P63316 |
| GO:0007596 | blood coagulation | 2.00E-03 | 1.19E-02 | 10 | 518 | 178 | 27688 | P07602 P01033 P84243 P68871 P16615 P04275 P62158 P35613 P25116 P00441 |
| GO:0007599 | hemostasis | 2.18E-03 | 1.26E-02 | 10 | 524 | 178 | 27688 | P07602 P01033 P84243 P68871 P16615 P04275 P62158 P35613 P25116 P00441 |
| GO:0008015 | blood circulation | 2.65E-09 | 4.44E-08 | 15 | 319 | 178 | 27688 | Q14116 O15273 Q14896 P10916 P01160 P68032 P13533 P16860 P19429 P68871 P08590 P09493 P25116 P00441 P63316 |
| GO:0008016 | regulation of heart contraction | 1.04E-05 | 1.22E-04 | 7 | 116 | 178 | 27688 | Q9UBV9 P08590 P09493 P17661 P45379 P13533 P12883 |
| GO:0008063 | Toll signaling pathway | 1.41E-04 | 1.30E-03 | 5 | 77 | 178 | 27688 | P0CG47 P51452 P62987 P62979 P0CG48 |
| GO:0008152 | metabolic process | 8.85E-14 | 2.24E-12 | 123 | 11504 | 178 | 27688 | O75947 O43674 P16615 O96000 P16860 P13073 O14949 P07195 P46783 P83731 P62913 P62753 P24752 P20674 Q13765 O95169 P13639 P48047 P04406 O14561 Q9Y5N6 O95167 P84098 P63173 P68104 P08574 P47985 P46777 P60866 P46776 P60228 P62249 Q13011 Q8N335 P07602 P25398 P68363 P10176 O95178 P12235 P62891 P25705 P18859 Q14192 P68871 Q16654 P56381 P00441 P54368 O00217 Q14116 Q08493 P08708 O75116 P18077 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9Y3D2 P62263 Q14240 P62945 P62269 P0CG47 P06732 Q9NSD9 P01160 P40926 P40925 P62280 P36542 P35613 P0CG48 P39019 P05090 P00505 P39023 P62273 P24310 P69905 P62158 P24311 Q07020 P10606 O14880 P19021 O43920 Q05639 P61353 P05386 P05387 P13929 P09669 O00483 P14854 P42766 Q02878 P60033 Q9NP15 P17174 P61247 P62857 P22352 Q16698 P62979 P62851 P51452 P51970 P62906 P15954 P51857 Q00325 P62987 P04275 P04792 P25116 P20585 P06576 P48735 |
| GO:0008217 | regulation of blood pressure | 5.48E-05 | 5.65E-04 | 7 | 150 | 178 | 27688 | P16860 P19429 P01160 P68871 P09493 P13533 P00441 |
| GO:0008219 | cell death | 1.13E-02 | 4.59E-02 | 15 | 1206 | 178 | 27688 | P0CG47 P02792 Q12988 P04406 Q9H3K2 P68032 P0CG48 Q8N8D1 P09382 P62987 P61247 P62979 P04792 P25116 P00441 |
| GO:0009056 | catabolic process | 1.09E-03 | 7.56E-03 | 22 | 1668 | 178 | 27688 | P0CG47 P13929 Q08493 P04406 P51857 P0CG48 P00505 P68871 P07195 P17174 P62987 Q14240 P22352 Q16698 P62979 P69905 P62158 P60228 P24752 Q13011 Q8N335 P00441 |

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| GO:0009987 | cellular process | 1.03E-14 | 2.94E-13 | 163 | 18611 | 178 | 27688 | O75947 P10916 O43674 Q9H3K2 P16615 O96000 P16860 P13073 O1494 9 P09493 P07195 P46783 P83731 P62913 P62753 P24752 O15239 P2067 4 Q13765 O95169 P13639 P48047 Q9Y277 P04406 O14561 P80297 Q9Y5 N6 O95167 Q08431 P19105 P84098 P63173 P68104 P09382 P08574 P47 985 P46777 Q13772 P60866 P46776 P60228 P62249 Q13011 Q8N335 P0 7602 P25398 P68363 P10176 O95178 P12235 P13693 P62891 P19429 P2 5705 P18859 Q14192 P68871 Q16654 P56381 Q01628 P00441 P54368 O 00217 Q14116 O15273 Q08493 P08708 Q14515 O75116 P68133 P18077 P17661 P17535 P12883 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9Y3D2 P62263 Q14240 P62945 P62269 P0C647 P06732 Q9NSD9 Q129 88 P01160 P40926 P40925 P62280 P36542 P35613 P0C648 P39019 Q014 49 P00505 P39023 P62273 P24310 P69905 P62158 P45379 P24311 P010 34 Q07020 P01033 P10606 Q14896 O14880 P19021 P19022 P37108 O43 920 P68032 Q05639 P08493 P61353 P60660 P02511 P05386 P17081 P05 387 P13929 P02792 P09669 P51684 O00483 P14854 P42766 Q02878 P84 243 P60033 Q9NPIS P17174 P61247 P62857 P22352 Q16698 P62979 P62 851 P51452 P02144 Q14315 P51970 Q9POU1 P62906 P15954 P51857 P1 3533 Q00325 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P0 6576 P63316 P48735 P0C647 Q12988 P01160 P35613 P0C648 P16860 P84243 P00505 Q14192 Q9UB9Y P17174 P22352 P62979 P62158 P62753 P24752 Q01628 P0044 1 P51452 P01033 P02144 Q14116 P80297 P19021 P68133 P68032 P1353 3 Q08431 Q8N8D1 P41222 P08493 P09382 P08574 P62987 P47985 Q137 72 P17081 P04792 P25116 P02144 Q14116 P80297 P19021 P68133 P35613 P17535 P16860 Q05639 P08493 P68871 P22352 P69905 P62158 P45379 P00441 P16860 P08493 P80297 P19021 P68133 P62158 P45379 P35613 P17535 P00441 P25398 Q9NSD9 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P13639 P08708 P62906 P18077 Q8N8D1 P42677 P84098 P1588 0 Q05639 P63173 P68104 Q02543 P61353 P62263 P62987 Q14240 P629 45 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P25116 P622 49 P0C647 Q9NWT8 O75116 P62987 P62979 P62158 P0C648 P63244 P62263 Q14240 P37108 P04792 P60228 Q14116 P25116 P01034 O15273 P10916 P09493 P68133 P68032 P13533 P0C647 P01033 Q14116 P16989 P12235 P0C648 P13693 P63244 Q05639 Q14192 P09382 P68871 P62987 P62979 P02511 P69905 P04792 P62753 P25116 P00441 P0C647 Q9NWT8 P62987 P62979 P0C648 Q14116 P19021 P68133 P35613 Q08431 Q8N8D1 P16860 P41222 Q1419 2 P09382 P17174 P22352 Q13772 P24752 O15273 Q14896 P10916 P68133 P68032 P13533 P12883 P19429 Q14192 P60660 P08590 P09493 P45379 P63316 O15273 P68133 P68032 P68871 P69905 P39019 O75947 P09669 O43674 P40926 P40925 O00483 P14854 P36542 P10176 O95178 P12235 O96000 P13073 P25705 P18859 O14949 P56381 P6215 8 P24311 O15239 P20674 O00217 P10606 O95169 P51970 P48047 O145 61 O43920 P15954 O95167 P08574 P47985 P06576 P48735 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 P0C647 P25398 P62280 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P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P08708 P62906 P18077 Q8N8D1 P42677 P8409 8 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P4677 7 P05386 P04792 P60866 P46776 P62269 P05387 P60228 P62249 P0C647 P25398 P62280 P0C648 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P04792 P60866 P46776 P62269 P05387 P60228 P62249 P08708 P62263 P18077 P62857 P62913 P46777 P62753 P62249 P39019 P0C647 P62987 P62979 P0C648 P0C647 P02792 Q12988 P04406 Q9H3K2 P68032 P0C648 Q8N8D1 P0938 2 P62987 P61247 P62979 P04792 P25116 P00441 P0C647 P51452 O00217 P13929 O95169 P51970 O43674 P04406 O14561 O75116 O00483 O43920 P36542 O95167 O95178 P0C648 O96000 P071 95 P62987 Q16654 P62979 P25116 O15239 P63244 P37108 P60228 O75947 P25398 P01160 P16615 P62280 P36542 P39019 P62891 P42766 Q02878 P16860 P25705 P18859 P39023 P62273 Q9NPIS P46783 P61247 P83731 P62857 P62913 P62979 P56381 P62851 P62753 Q13765 Q07020 P48047 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P06576 P25398 P62280 P39019 P62891 P42766 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0010033 | response to organic substance | 7.05E-08 | 1.06E-06 | 39 | 2426 | 178 | 27688 | |
| GO:0010035 | response to inorganic substance | 6.06E-08 | 9.16E-07 | 16 | 464 | 178 | 27688 | |
| GO:0010038 | response to metal ion | 3.57E-05 | 3.80E-04 | 10 | 311 | 178 | 27688 | |
| GO:0010467 | gene expression | 2.14E-12 | 4.58E-11 | 45 | 2206 | 178 | 27688 | |
| GO:0010564 | regulation of cell cycle process | 7.94E-03 | 3.42E-02 | 7 | 352 | 178 | 27688 | |
| GO:0010608 | posttranscriptional regulation of gene expression | 7.12E-03 | 3.11E-02 | 6 | 262 | 178 | 27688 | |
| GO:0010712 | regulation of collagen metabolic process | 1.99E-04 | 1.76E-03 | 3 | 18 | 178 | 27688 | |
| GO:0010927 | cellular component assembly involved in | 4.47E-04 | 3.65E-03 | 6 | 151 | 178 | 27688 | |
| GO:0010941 | regulation of cell death | 4.11E-04 | 3.38E-03 | 20 | 1340 | 178 | 27688 | |
| GO:0010948 | negative regulation of cell cycle process | 5.70E-03 | 2.73E-02 | 5 | 176 | 178 | 27688 | |
| GO:0014070 | response to organic cyclic compound | 3.88E-03 | 2.02E-02 | 14 | 963 | 178 | 27688 | |
| GO:0014706 | striated muscle tissue development | 5.13E-10 | 9.38E-09 | 14 | 238 | 178 | 27688 | |
| GO:0014866 | skeletal myofibril assembly | 1.43E-05 | 1.62E-04 | 3 | 8 | 178 | 27688 | |
| GO:0015669 | gas transport | 1.12E-04 | 1.08E-03 | 3 | 15 | 178 | 27688 | |
| GO:0015980 | energy derivation by oxidation of organic compounds | 1.47E-29 | 1.23E-27 | 34 | 363 | 178 | 27688 | |
| GO:0015985 | energy coupled proton transport, down | 1.50E-09 | 2.63E-08 | 7 | 33 | 178 | 27688 | |
| GO:0015986 | ATP synthase coupled proton transport | 1.50E-09 | 2.63E-08 | 7 | 33 | 178 | 27688 | |
| GO:0015992 | proton transport | 3.87E-05 | 4.08E-04 | 7 | 142 | 178 | 27688 | |
| GO:0016032 | viral process | 1.39E-33 | 1.79E-31 | 40 | 458 | 178 | 27688 | |
| GO:0016043 | cellular component organization | 3.41E-14 | 9.05E-13 | 72 | 4606 | 178 | 27688 | |
| GO:0016051 | carbohydrate biosynthetic process | 1.06E-03 | 7.37E-03 | 6 | 178 | 178 | 27688 | |
| GO:0016053 | organic acid biosynthetic process | 9.71E-03 | 4.03E-02 | 7 | 366 | 178 | 27688 | |
| GO:0016054 | organic acid catabolic process | 4.16E-03 | 2.11E-02 | 6 | 234 | 178 | 27688 | |
| GO:0016070 | RNA metabolic process | 3.19E-15 | 1.01E-13 | 44 | 1755 | 178 | 27688 | |
| GO:0016071 | mRNA metabolic process | 8.91E-29 | 6.93E-27 | 41 | 651 | 178 | 27688 | |
| GO:0016072 | rRNA metabolic process | 1.73E-07 | 2.48E-06 | 9 | 130 | 178 | 27688 | |
| GO:0016197 | endosomal transport | 9.25E-03 | 3.89E-02 | 4 | 127 | 178 | 27688 | |
| GO:0016265 | death | 1.18E-02 | 4.76E-02 | 15 | 1212 | 178 | 27688 | |
| GO:0016310 | phosphorylation | 7.16E-07 | 9.86E-06 | 23 | 1103 | 178 | 27688 | |
| GO:0017148 | negative regulation of translation | 1.26E-02 | 4.91E-02 | 3 | 75 | 178 | 27688 | |
| GO:0018130 | heterocycle biosynthetic process | 9.73E-25 | 6.23E-23 | 48 | 1218 | 178 | 27688 | |
| GO:0019058 | viral life cycle | 1.56E-49 | 4.24E-47 | 37 | 142 | 178 | 27688 | |
| GO:0019080 | viral gene expression | 1.60E-57 | 1.74E-54 | 36 | 84 | 178 | 27688 | |
| GO:0019083 | viral transcription | 1.60E-57 | 1.74E-54 | 36 | 84 | 178 | 27688 | |

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|------------|--|----------|----------|----|------|-----|-------|---|
| GO:0019318 | hexose metabolic process | 1.28E-04 | 1.20E-03 | 8 | 230 | 178 | 27688 | P13929 P00505 P40926 P04406 P40925 P17174 Q16654 P62158 |
| GO:0019319 | hexose biosynthetic process | 2.96E-06 | 3.79E-05 | 6 | 62 | 178 | 27688 | P13929 P00505 P40926 P04406 P40925 P17174 |
| GO:0019362 | pyridine nucleotide metabolic process | 1.52E-03 | 9.70E-03 | 6 | 191 | 178 | 27688 | P13929 P40926 P04406 P0406 Q9NP15 P07195 P40925 O75947 P25398 P01160 P16615 P62280 P36542 P39019 P62891 P42766 Q02878 P16860 P25705 P18859 P39023 P62273 Q9NP15 P46783 P61247 P83731 P62857 P62913 P62979 P56381 P62851 P62753 Q13765 Q07020 P48047 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P06576 POCG47 Q9NSD9 P40926 P62280 POCG48 P39019 P39023 P62273 P46783 P83731 P62913 P62753 Q13765 Q07020 P13639 P04406 P19021 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P68363 P62891 P42766 Q02878 P61247 P62857 Q16654 P62979 P62851 P51452 Q14116 P08708 O75116 P62906 P1807 7 P42677 P15880 Q02543 Q9Y3D2 P62263 P62987 Q14240 P62945 P042 75 P62269 P25116 P13929 O75947 P06732 P01160 O43674 P40926 P40925 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P60033 Q9NP15 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O1456 1 O43920 O95167 Q8N335 P06576 P40926 P07195 P40925 P13929 O75947 P01160 O43674 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P07195 P56381 O15239 O00217 Q08493 O9516 9 P51970 P48047 P04406 O14561 O43920 O95167 P06576 P13929 P06732 Q9NSD9 P40926 P04406 O14561 P40925 O14880 P51857 P35613 P41222 P17540 P00505 P07195 P17174 Q16654 Q16698 P24752 Q13011 P48735 POCG47 P42677 P62987 Q9Y5N6 P62979 POCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 P00441 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 O00217 Q14315 O15273 P10916 P08708 P68363 P19022 P68133 O43920 P68032 P13533 P84243 P68871 P029493 P62263 P83731 P22352 Q16698 P02511 P04275 P69905 P62851 P62753 P24752 P08708 P62263 P18077 P83731 P62857 P62913 P46777 P62851 P62269 P62753 P62249 P39019 P08708 P62263 P83731 P62851 P62753 O75947 P09669 O43674 O00483 P14854 P36542 P10176 O95178 O96000 P13073 P25705 P18859 O14949 P56381 P24311 O15239 P20674 O0021 7 P10606 O95169 P51970 P48047 O14561 O43920 P15954 O95167 P085 74 P47985 P06576 O75947 P09669 O43674 O00483 P14854 P36542 P10176 O95178 O96000 P13073 P25705 P18859 O14949 P56381 P24311 O15239 P20674 O0021 7 P10606 O95169 P51970 P48047 O14561 O43920 P15954 O95167 P085 74 P47985 P06576 POCG47 P51452 P62987 P62979 POCG48 O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 Q01449 P19429 P60660 P08590 P09493 P63313 P17081 P45379 P63316 O15273 P10916 P09493 P68133 P68032 P63313 P17081 P13533 O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 Q01449 P19429 P60660 P08590 P09493 P45379 P63316 O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P60660 P08590 P09493 P45379 P63316 POCG47 P01033 P63244 Q9NWT8 P62987 P62979 P25116 POCG48 P0103 4 P07602 P01033 P16615 P04275 P62158 P25116 P00441 P01033 P02144 P62263 P39019 O15273 P10916 P09493 P68133 P68032 P13533 O15273 P68133 P68032 POCG47 P62987 P62979 POCG48 POCG47 Q14192 P62987 P62979 Q13772 POCG48 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 O15273 P10916 P09493 P68133 P68032 P13533 POCG47 P51452 P62987 P62979 POCG48 POCG47 P62987 P62979 POCG48 POCG47 P01033 P63244 P62987 P62979 POCG48 P01034 P10916 P01160 P54296 P16615 P62280 P35613 P39019 P63244 P16860 Q01449 Q14094 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P62158 P45379 P62753 P24752 Q07020 P01033 P10606 Q14896 O1488 O P19021 P19022 P16989 P68032 Q08431 P84098 O14958 P63173 P0849 3 P61353 P60660 P09382 P46777 P02511 P05386 Q13772 P60866 P4677 6 P05387 P62249 P07602 P52179 P25398 P62891 P42766 Q02878 P1942 9 P25705 P84243 Q14192 P68871 P61247 P62857 P23327 P22352 P6297 9 P62851 P00441 P51452 P02144 Q14116 O15273 P08708 O75116 P629 06 P68133 P18077 P17661 P51857 P13533 P17535 P12883 P42677 P158 80 P17540 Q02543 P08590 P62263 P62987 P62945 P04275 P04792 P622 69 P25116 P20585 P06576 P63316 P10916 P16615 P62280 P35613 P39019 P63244 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P45379 P62753 P24752 Q07020 P01033 Q14896 P19021 P19022 P16989 P68032 Q08431 P84098 O14958 P63173 P08493 P61353 P60660 P09382 P46777 P05386 Q13772 P60866 P63173 P08493 P61353 P60660 P09382 P46777 P05386 Q13772 P60866 P46776 P05387 P62249 P07602 P13929 P25398 P62891 P42766 Q02878 P19429 P25705 P84243 Q14192 P61247 P62857 P62979 P62851 P00441 P51452 P02144 Q14116 O15273 P08708 O75116 P62906 P68133 P1807 7 P13533 P17535 P12883 P42677 P15880 Q02543 P08590 P62263 P6298 7 P62945 P04275 P04792 P62269 P25116 P20585 P06576 P63316 Q14116 P04792 P25116 Q14116 P04792 P25116 |
| GO:0019438 | aromatic compound biosynthetic process | 9.06E-25 | 5.98E-23 | 48 | 1216 | 178 | 27688 | |
| GO:0019538 | protein metabolic process | 1.05E-05 | 1.22E-04 | 56 | 5004 | 178 | 27688 | |
| GO:0019637 | organophosphate metabolic process | 1.41E-11 | 2.79E-10 | 31 | 1156 | 178 | 27688 | |
| GO:0019674 | NAD metabolic process | 3.87E-03 | 2.02E-02 | 3 | 49 | 178 | 27688 | |
| GO:0019693 | ribose phosphate metabolic process | 3.09E-15 | 9.89E-14 | 25 | 507 | 178 | 27688 | |
| GO:0019752 | carboxylic acid metabolic process | 4.15E-04 | 3.39E-03 | 20 | 1341 | 178 | 27688 | |
| GO:0022403 | cell cycle phase | 1.31E-02 | 4.96E-02 | 6 | 299 | 178 | 27688 | |
| GO:0022411 | cellular component disassembly | 9.54E-42 | 1.73E-39 | 37 | 221 | 178 | 27688 | |
| GO:0022607 | cellular component assembly | 1.37E-04 | 1.28E-03 | 24 | 1636 | 178 | 27688 | |
| GO:0022613 | ribonucleoprotein complex biogenesis | 2.43E-07 | 3.44E-06 | 12 | 275 | 178 | 27688 | |
| GO:0022618 | ribonucleoprotein complex assembly | 1.01E-03 | 7.10E-03 | 5 | 118 | 178 | 27688 | |
| GO:0022900 | electron transport chain | 2.50E-32 | 2.72E-30 | 29 | 179 | 178 | 27688 | |
| GO:0022904 | respiratory electron transport chain | 3.78E-36 | 5.48E-34 | 29 | 135 | 178 | 27688 | |
| GO:0023014 | signal transduction by protein phosphorylation | 9.25E-03 | 3.89E-02 | 5 | 198 | 178 | 27688 | |
| GO:0030029 | actin filament-based process | 3.25E-08 | 5.02E-07 | 17 | 505 | 178 | 27688 | |
| GO:0030036 | actin cytoskeleton organization | 9.83E-03 | 4.07E-02 | 8 | 458 | 178 | 27688 | |
| GO:0030048 | actin filament-based movement | 3.00E-20 | 1.33E-18 | 15 | 60 | 178 | 27688 | |
| GO:0030049 | muscle filament sliding | 1.04E-21 | 5.24E-20 | 14 | 38 | 178 | 27688 | |
| GO:0030162 | regulation of proteolysis | 4.30E-03 | 2.17E-02 | 9 | 485 | 178 | 27688 | |
| GO:0030168 | platelet activation | 1.36E-03 | 9.02E-03 | 7 | 255 | 178 | 27688 | |
| GO:0030218 | erythrocyte differentiation | 1.15E-03 | 7.85E-03 | 4 | 71 | 178 | 27688 | |
| GO:0030239 | myofibril assembly | 4.91E-07 | 6.89E-06 | 6 | 46 | 178 | 27688 | |
| GO:0030240 | skeletal muscle thin filament assembly | 8.97E-06 | 1.07E-04 | 3 | 7 | 178 | 27688 | |
| GO:0030330 | DNA damage response, signal transduction by p53 | 2.14E-03 | 1.25E-02 | 4 | 84 | 178 | 27688 | |
| GO:0030522 | intracellular receptor signaling pathway | 5.50E-04 | 4.35E-03 | 6 | 157 | 178 | 27688 | |
| GO:0031016 | pancreas development | 3.90E-43 | 7.71E-41 | 36 | 185 | 178 | 27688 | |
| GO:0031018 | endocrine pancreas development | 1.05E-47 | 2.29E-45 | 36 | 142 | 178 | 27688 | |
| GO:0031032 | actomyosin structure organization | 1.05E-05 | 1.23E-04 | 6 | 77 | 178 | 27688 | |
| GO:0031098 | stress-activated protein kinase signaling cascade | 1.96E-03 | 1.17E-02 | 5 | 137 | 178 | 27688 | |
| GO:0031145 | anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein | 2.04E-03 | 1.20E-02 | 4 | 83 | 178 | 27688 | |
| GO:0031329 | regulation of cellular catabolic process | 1.45E-03 | 9.50E-03 | 7 | 258 | 178 | 27688 | |
| GO:0031331 | positive regulation of cellular catabolic process | 4.58E-03 | 2.28E-02 | 5 | 167 | 178 | 27688 | |
| GO:0031349 | positive regulation of defense response | 4.60E-03 | 2.28E-02 | 6 | 239 | 178 | 27688 | |
| GO:0031397 | negative regulation of protein ubiquitination | 4.01E-03 | 2.07E-02 | 4 | 100 | 178 | 27688 | |
| GO:0031398 | positive regulation of protein ubiquitination | 7.39E-03 | 3.22E-02 | 4 | 119 | 178 | 27688 | |
| GO:0031571 | mitotic G1 DNA damage checkpoint | 1.27E-03 | 8.50E-03 | 4 | 73 | 178 | 27688 | |
| GO:0032147 | activation of protein kinase activity | 1.42E-03 | 9.32E-03 | 7 | 257 | 178 | 27688 | |
| GO:0032269 | negative regulation of cellular protein metabolic process | 5.22E-03 | 2.53E-02 | 11 | 690 | 178 | 27688 | |
| GO:0032479 | regulation of type I interferon production | 5.34E-04 | 4.28E-03 | 4 | 58 | 178 | 27688 | |
| GO:0032480 | negative regulation of type I interferon | 5.16E-05 | 5.37E-04 | 4 | 32 | 178 | 27688 | |
| GO:0032501 | multicellular organismal process | 3.81E-17 | 1.43E-15 | 94 | 6554 | 178 | 27688 | |
| GO:0032502 | developmental process | 1.69E-13 | 4.09E-12 | 80 | 5680 | 178 | 27688 | |
| GO:0032651 | regulation of interleukin-1 beta production | 2.33E-03 | 1.33E-02 | 3 | 41 | 178 | 27688 | |
| GO:0032652 | regulation of interleukin-1 production | 2.85E-03 | 1.57E-02 | 3 | 44 | 178 | 27688 | |

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| GO:0032774 | RNA biosynthetic process | 5.54E-24 | 3.45E-22 | 37 | 669 | 178 | 27688 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0032781 | positive regulation of ATPase activity | 2.13E-06 | 2.78E-05 | 4 | 15 | 178 | 27688 | Q14896 P08590 P09493 P45379 |
| GO:0032787 | monocarboxylic acid metabolic process | 1.62E-04 | 1.48E-03 | 13 | 607 | 178 | 27688 | P13929 P04406 O14561 O14880 P51857 P35613 P41222 P07195 Q16654 Q16698 P24752 Q13011 P48735 |
| GO:0032970 | regulation of actin filament-based process | 1.91E-03 | 1.16E-02 | 6 | 200 | 178 | 27688 | Q14896 P09493 O75116 P63313 P17081 P63316 |
| GO:0032984 | macromolecular complex disassembly | 2.05E-49 | 4.96E-47 | 36 | 129 | 178 | 27688 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0033275 | actin-myosin filament sliding | 1.04E-21 | 5.24E-20 | 14 | 38 | 178 | 27688 | O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P06660 P08590 P09493 P45379 P63316 |
| GO:0034101 | erythrocyte homeostasis | 1.41E-04 | 1.30E-03 | 5 | 77 | 178 | 27688 | P01033 P02144 P08708 P62263 P39019 |
| GO:0034130 | toll-like receptor 1 signaling pathway | 8.36E-05 | 8.24E-04 | 5 | 69 | 178 | 27688 | POC647 P51452 P62987 P62979 POC648 |
| GO:0034134 | toll-like receptor 2 signaling pathway | 8.36E-05 | 8.24E-04 | 5 | 69 | 178 | 27688 | POC647 P51452 P62987 P62979 POC648 |
| GO:0034138 | toll-like receptor 3 signaling pathway | 5.40E-05 | 5.59E-04 | 5 | 63 | 178 | 27688 | POC647 P51452 P62987 P62979 POC648 |
| GO:0034142 | toll-like receptor 4 signaling pathway | 1.33E-04 | 1.24E-03 | 5 | 76 | 178 | 27688 | POC647 P51452 P62987 P62979 POC648 |
| GO:0034220 | ion transmembrane transport | 3.44E-04 | 2.90E-03 | 9 | 336 | 178 | 27688 | O75947 P25705 P48047 P18859 P16615 P36542 P56381 P35613 P06576 |
| GO:0034248 | regulation of cellular amide metabolic process | 3.90E-03 | 2.03E-02 | 6 | 231 | 178 | 27688 | P63244 P62263 Q14240 P37108 P04792 P60228 |
| GO:0034249 | negative regulation of cellular amide metabolic process | 1.30E-02 | 4.95E-02 | 3 | 76 | 178 | 27688 | P63244 P37108 P60228 |
| GO:0034470 | ncRNA processing | 5.64E-05 | 5.79E-04 | 9 | 264 | 178 | 27688 | P08708 P62263 P18077 P62857 P62913 P46777 P62753 P62249 P39019 |
| GO:0034614 | cellular response to reactive oxygen species | 4.83E-03 | 2.38E-02 | 3 | 53 | 178 | 27688 | Q14116 P09493 P00441 |
| GO:0034622 | cellular macromolecular complex assembly | 6.37E-03 | 2.83E-02 | 10 | 611 | 178 | 27688 | O00217 O15273 P84243 P08708 P62263 P68363 P83731 O43920 P62851 P62753 |
| GO:0034641 | cellular nitrogen compound metabolic process | 1.36E-22 | 7.57E-21 | 86 | 4630 | 178 | 27688 | POC647 O75947 P06732 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 POC648 P39019 O96000 P16860 P00505 P39023 P62273 P07195 P46783 P83731 P62913 P62753 P24752 O15239 Q13765 Q07020 O95169 P13639 P48047 P04406 O14561 P19021 Q9Y5N6 O43920 O95167 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P13929 P25398 O00483 O95178 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P22352 P62979 P56381 P00441 P54368 O00217 Q08493 P51970 P08708 P62906 P18077 Q8N8D1 P42677 P15880 P17540 Q02543 P62263 P62987 Q14240 P62945 P04792 P62269 P20585 P06576 |
| GO:0034645 | cellular macromolecule biosynthetic process | 3.69E-13 | 8.64E-12 | 44 | 2010 | 178 | 27688 | P25398 Q9NSD9 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P13639 P08708 P62906 Q9Y5N6 P18077 P42677 P84098 P15880 Q05639 P63173 P68104 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0034654 | nucleobase-containing compound biosynthetic process | 4.24E-27 | 3.08E-25 | 48 | 1075 | 178 | 27688 | O75947 P25398 P01160 P16615 P62280 P36542 P39019 P62891 P42766 Q02878 P16860 P25705 P18859 P39023 P62273 Q9NP15 P46783 P61247 P83731 P62857 P62913 P62979 P56381 P62851 P62753 Q13765 Q07020 P48047 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P06576 |
| GO:0034660 | ncRNA metabolic process | 1.62E-03 | 1.02E-02 | 10 | 503 | 178 | 27688 | Q9NSD9 P08708 P62263 P18077 P62857 P62913 P46777 P62753 P62249 P39019 |
| GO:0035051 | cardiocyte differentiation | 7.07E-04 | 5.38E-03 | 5 | 109 | 178 | 27688 | O15273 P10916 Q14192 P68032 P13533 |
| GO:0035150 | regulation of tube size | 2.36E-03 | 1.34E-02 | 5 | 143 | 178 | 27688 | P16860 P01160 P68871 P25116 P00441 |
| GO:0035270 | endocrine system development | 8.16E-38 | 1.27E-35 | 36 | 255 | 178 | 27688 | P25398 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 |
| GO:0035872 | nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway | 2.58E-05 | 2.84E-04 | 4 | 27 | 178 | 27688 | POC647 P62987 P62979 POC648 |
| GO:0038127 | ERBB signaling pathway | 2.04E-03 | 1.20E-02 | 4 | 83 | 178 | 27688 | POC647 P62987 P62979 POC648 |
| GO:0038179 | neurotrophin signaling pathway | 2.87E-03 | 1.58E-02 | 6 | 217 | 178 | 27688 | POC647 P51452 P62987 P62979 P62158 POC648 |
| GO:0042058 | regulation of epidermal growth factor receptor negative regulation of epidermal growth factor receptor signaling pathway | 1.48E-03 | 9.54E-03 | 4 | 76 | 178 | 27688 | POC647 P62987 P62979 POC648 |
| GO:0042059 | negative regulation of epidermal growth factor receptor signaling pathway | 1.53E-04 | 1.40E-03 | 4 | 42 | 178 | 27688 | POC647 P62987 P62979 POC648 |
| GO:0042060 | wound healing | 1.51E-03 | 9.68E-03 | 12 | 677 | 178 | 27688 | P07602 P01033 P13929 P84243 P68871 P09493 P16615 P04275 P62158 P35613 P25116 P00441 |
| GO:0042176 | regulation of protein catabolic process | 1.24E-03 | 8.37E-03 | 7 | 251 | 178 | 27688 | POC647 P01033 P63244 P62987 P62979 POC648 P01034 |
| GO:0042221 | response to chemical | 4.01E-10 | 7.45E-09 | 54 | 3507 | 178 | 27688 | POC647 Q12988 P01160 P35613 POC648 P16860 P13073 P00505 P09493 P83731 P69905 P62158 P45379 P62753 P24752 P01033 O14880 P80297 P19021 P37108 P68032 Q08431 Q05639 P08493 P06660 P09382 P08574 P47985 Q13772 P17081 P13929 P51684 P84243 Q14192 P68871 Q9UB9 P17174 P22352 P62979 Q01628 P00441 P51452 P02144 Q14116 O75116 P68133 P13533 P17535 P12883 Q8N8D1 P41222 P62987 P04792 P25116 P08708 P62263 P18077 P83731 P62851 P62753 P62269 P62753 P62249 P39019 |
| GO:0042254 | ribosome biogenesis | 2.23E-09 | 3.80E-08 | 12 | 180 | 178 | 27688 | P08708 P62263 P18077 P83731 P62857 P62913 P46777 P62851 P62269 P62753 P62249 P39019 |
| GO:0042255 | ribosome assembly | 1.94E-07 | 2.76E-06 | 5 | 21 | 178 | 27688 | P08708 P62263 P83731 P62851 P62753 |
| GO:0042273 | ribosomal large subunit biogenesis | 7.85E-07 | 1.08E-05 | 4 | 12 | 178 | 27688 | P18077 P83731 P62913 P46777 |
| GO:0042274 | ribosomal small subunit biogenesis | 1.90E-11 | 3.73E-10 | 7 | 19 | 178 | 27688 | P08708 P62263 P62857 P62851 P62753 P62249 P39019 |
| GO:0042278 | purine nucleoside metabolic process | 1.58E-13 | 3.87E-12 | 22 | 446 | 178 | 27688 | O00217 P13929 O75947 O95169 P51970 P48047 O43674 P04406 O14561 O00483 P16615 O43920 P36542 O95167 O95178 O96000 P25705 P18859 P07195 P56381 P06576 O15239 |
| GO:0042451 | purine nucleoside biosynthetic process | 2.66E-05 | 2.90E-04 | 8 | 184 | 178 | 27688 | O75947 P25705 P48047 P18859 P16615 P36542 P56381 P06576 |
| GO:0042455 | ribonucleoside biosynthetic process | 4.65E-05 | 4.86E-04 | 8 | 199 | 178 | 27688 | O75947 P25705 P48047 P18859 P16615 P36542 P56381 P06576 |
| GO:0042493 | response to drug | 8.47E-03 | 3.60E-02 | 9 | 540 | 178 | 27688 | P13929 P16860 P09382 P19021 P47985 P37108 P22352 P68032 P00441 |
| GO:0042542 | response to hydrogen peroxide | 5.46E-04 | 4.34E-03 | 5 | 103 | 178 | 27688 | P02144 Q14116 P68871 P69905 P00441 |
| GO:0042692 | muscle cell differentiation | 3.16E-05 | 3.41E-04 | 9 | 245 | 178 | 27688 | O15273 P10916 Q14192 P09382 P09493 P19022 P68133 P68032 P13533 |
| GO:0042743 | hydrogen peroxide metabolic process | 1.26E-04 | 1.19E-03 | 4 | 40 | 178 | 27688 | P68871 P22352 P69905 P00441 |
| GO:0042744 | hydrogen peroxide catabolic process | 6.82E-04 | 5.23E-03 | 3 | 27 | 178 | 27688 | P68871 P22352 P69905 |
| GO:0042770 | signal transduction in response to DNA damage | 3.60E-03 | 1.89E-02 | 4 | 97 | 178 | 27688 | POC647 P62987 P62979 POC648 |
| GO:0042773 | ATP synthesis coupled electron transport | 1.67E-12 | 3.60E-11 | 11 | 74 | 178 | 27688 | O00217 O95169 P51970 O43674 O14561 O00483 O43920 O95167 O95178 O96000 O15239 |
| GO:0042775 | mitochondrial ATP synthesis coupled electron transport | 6.33E-13 | 1.45E-11 | 11 | 68 | 178 | 27688 | O00217 O95169 P51970 O43674 O14561 O00483 O43920 O95167 O95178 O96000 O15239 |
| GO:0042776 | mitochondrial ATP synthesis coupled proton transport | 2.48E-12 | 5.20E-11 | 7 | 15 | 178 | 27688 | O75947 P25705 P48047 P18859 P36542 P56381 P06576 |
| GO:0042981 | regulation of apoptotic process | 3.51E-03 | 1.85E-02 | 17 | 1270 | 178 | 27688 | POC647 P01033 Q14116 P16989 POC648 P13693 P63244 Q05639 Q14192 P09382 P62987 P62979 P02511 P04792 P62753 P25116 P00441 |
| GO:0043043 | peptide biosynthetic process | 2.35E-30 | 2.05E-28 | 43 | 677 | 178 | 27688 | P25398 Q9NSD9 P62280 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 Q13765 Q07020 P13639 P08708 P62906 P18077 P42677 P84098 P15880 Q05639 P63173 P68104 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P60228 P62249 |
| GO:0043066 | negative regulation of apoptotic process | 9.84E-04 | 6.93E-03 | 13 | 735 | 178 | 27688 | POC647 P01033 P16989 POC648 P13693 Q05639 Q14192 P62987 P62979 P02511 P04792 P25116 P00441 |
| GO:0043067 | regulation of programmed cell death | 3.88E-03 | 2.02E-02 | 17 | 1283 | 178 | 27688 | POC647 P01033 Q14116 P16989 POC648 P13693 P63244 Q05639 Q14192 P09382 P62987 P62979 P02511 P04792 P62753 P25116 P00441 |
| GO:0043069 | negative regulation of programmed cell death | 1.06E-03 | 7.37E-03 | 13 | 741 | 178 | 27688 | POC647 P01033 P16989 POC648 P13693 Q05639 Q14192 P62987 P62979 P02511 P04792 P25116 P00441 |
| GO:0043085 | positive regulation of catalytic activity | 6.42E-04 | 4.95E-03 | 15 | 887 | 178 | 27688 | P07602 POC647 Q14896 POC648 P63244 P60033 P08590 P09493 P62987 P62979 P62158 P45379 P25116 P20585 P00441 |

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| GO:0044267 | cellular protein metabolic process | 2.11E-10 | 4.00E-09 | 54 | 3447 | 178 | 27688 | POCG47 Q9NSD9 P40926 P62280 POCG48 P39019 P39023 P62273 P46783 P83731 P62913 P62753 Q13765 Q07020 P13639 P04406 P19021 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P68363 P62891 P42766 Q02878 P61247 P62857 Q16654 P62979 P62851 P51452 P08708 O75116 P62906 P18077 P42677 P15880 Q02543 Q9Y3D2 P62263 P62987 Q14240 P62945 P62269 P25116 P05947 Q9NSD9 P01160 P16615 P62280 P36542 P39019 P16860 P39023 P62273 P46783 P83731 P62913 P62753 Q13765 Q07020 P13639 P48047 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P61247 P62857 P62979 P56381 P62851 P54368 P08708 P62906 P18077 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P06576 P13929 O75947 P06732 Q9NSD9 P01160 O43674 P40926 P40925 O00483 P16615 P36542 O95178 P35613 O96000 P16860 P25705 P00505 P18859 Q9NP15 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P62906 P15954 P51857 P13533 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P06576 P63316 P48735 P10916 P16615 P62280 P35613 P39019 P63244 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P62158 P45379 P62753 P24752 Q07020 P01033 P10606 Q14896 O14880 P19021 P19022 P16989 P68032 Q08431 P84098 O14958 P63173 P08493 P61353 P60660 P09382 P46777 P05386 Q13772 P60866 P46776 P05387 P62249 P07602 P25398 P62891 P42766 Q02878 P19429 P25705 P84243 Q14192 P68871 P61247 P62857 P62979 P62851 P00441 P51452 P02144 Q14116 O15273 P08708 O75116 P62906 P68133 P18077 P51857 P13533 P17535 P12883 P42677 P15880 O Q02543 P08590 P62263 P62987 P62945 P04275 P04792 P62269 P25116 P20585 P06576 P63316 POCG47 O75947 P06732 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P36542 P35613 POCG48 O96000 P16860 P05090 P13073 P00505 O14949 P07195 P69905 P62158 P24311 P24752 O15239 P20674 P10606 O95169 P48047 P04406 O14561 O14880 O43920 O95167 P08574 P47985 Q13011 P07602 P13929 P09669 O00483 P14854 P10176 O95178 P12235 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P01160 P40926 P40925 P62280 P36542 P35613 POCG48 P39019 Q01449 P00505 P39023 P62273 P69905 P62158 P45379 P24311 P01034 Q07020 P01033 P10606 Q14896 O14880 P19022 P37108 O43920 P68032 P08493 P61353 P60660 P05386 P17081 P05387 P13929 P07292 P09669 P51684 O00483 P14854 P42766 Q02878 P84243 P60033 Q9NP15 P17174 P61247 P62857 P22352 Q16698 P62979 P62851 P51452 P02144 Q14315 P51970 Q9POU1 P62906 P15954 P51857 P13533 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P06576 P63316 P48735 POCG47 P25398 P62280 P12235 POCG48 P39019 P62891 P42766 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62851 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P07602 POCG47 O75947 P02792 P68363 P16615 P36542 P35613 P12235 POCG48 P39019 P13693 P16860 P05090 P25705 P00505 P18859 P68871 P62913 P62979 P56381 P69905 P62158 P00441 P01033 Q9POU1 P48047 Q9Y277 P37108 Q08431 P19105 P62987 P04275 P25116 P06576 P10916 P62280 P35613 P39019 P63244 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P45379 P62753 P24752 Q07020 P01033 Q14896 P19021 P19022 P37108 O43920 P68032 P08493 P61353 P60660 P05388 P17081 P05387 P13929 P07292 P09669 P51684 O00483 P14854 P42766 Q02878 P60033 Q9NP15 P17174 P61247 P62851 P22352 Q16698 P62979 P62851 P51452 P02144 Q14315 P51970 Q9POU1 P62906 P15954 P51857 P13533 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P06576 P63316 P48735 POCG47 P25398 P62280 P12235 POCG48 P39019 P62891 P42766 Q02878 P60033 P39023 P62273 P46783 P61247 P83731 P62851 P62913 P62979 P62851 P62753 Q07020 P08708 P62906 P18077 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 P62945 P46777 P05386 P60866 P46776 P62269 P05387 P62249 P07602 POCG47 O75947 P02792 P68363 P16615 P36542 P35613 P12235 POCG48 P39019 P13693 P16860 P05090 P25705 P00505 P18859 P68871 P62913 P62979 P56381 P69905 P62158 P00441 P01033 Q9POU1 P48047 Q9Y277 P37108 Q08431 P19105 P62987 P04275 P25116 P06576 P10916 P62280 P35613 P39019 P63244 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P45379 P62753 P24752 Q07020 P01033 Q14896 P19021 P19022 P37108 O43920 P68032 P08493 P61353 P60660 P05388 P17081 P05387 P13929 P07292 P09669 P51684 O00483 P14854 P42766 Q02878 P60033 Q9NP15 P17174 P61247 P62851 P22352 Q16698 P62979 P62851 P51452 P02144 Q14315 P51970 Q9POU1 P62906 P15954 P51857 P13533 P08590 P62987 P04275 P63313 P04792 P25116 P20585 P06576 P63316 P48735 POCG47 P62987 Q9Y5N6 P83731 P62979 POCG48 |
| GO:0044271 | cellular nitrogen compound biosynthetic process | 2.76E-22 | 1.49E-20 | 55 | 1879 | 178 | 27688 | |
| GO:0044281 | small molecule metabolic process | 5.11E-09 | 8.24E-08 | 43 | 2596 | 178 | 27688 | |
| GO:0044283 | small molecule biosynthetic process | 8.96E-04 | 6.50E-03 | 11 | 549 | 178 | 27688 | |
| GO:0044403 | symbiosis, encompassing mutualism through parasitism | 2.34E-32 | 2.68E-30 | 40 | 492 | 178 | 27688 | |
| GO:0044419 | interspecies interaction between organisms | 6.70E-29 | 5.40E-27 | 44 | 781 | 178 | 27688 | |
| GO:0044699 | single-organism process | 1.49E-12 | 3.27E-11 | 155 | 17596 | 178 | 27688 | |
| GO:0044707 | single-multicellular organism process | 6.41E-15 | 1.89E-13 | 84 | 5832 | 178 | 27688 | |
| GO:0044710 | single-organism metabolic process | 1.74E-09 | 3.00E-08 | 70 | 5507 | 178 | 27688 | |
| GO:0044711 | single-organism biosynthetic process | 1.01E-04 | 9.86E-04 | 23 | 1501 | 178 | 27688 | |
| GO:0044712 | single-organism catabolic process | 9.51E-04 | 6.74E-03 | 14 | 826 | 178 | 27688 | |
| GO:0044763 | single-organism cellular process | 8.67E-17 | 3.15E-15 | 147 | 14664 | 178 | 27688 | |
| GO:0044764 | multi-organism cellular process | 2.14E-33 | 2.59E-31 | 40 | 463 | 178 | 27688 | |
| GO:0044765 | single-organism transport | 1.12E-02 | 4.54E-02 | 35 | 3688 | 178 | 27688 | |
| GO:0044767 | single-organism developmental process | 6.84E-13 | 1.55E-11 | 78 | 5585 | 178 | 27688 | |
| GO:0044770 | cell cycle phase transition | 1.16E-02 | 4.67E-02 | 6 | 291 | 178 | 27688 | |
| GO:0044772 | mitotic cell cycle phase transition | 1.16E-02 | 4.67E-02 | 6 | 291 | 178 | 27688 | |

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|------------|--|----------|----------|----|------|-----|-------|---|
| GO:0044773 | mitotic DNA damage checkpoint | 2.97E-03 | 1.62E-02 | 4 | 92 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0044774 | mitotic DNA integrity checkpoint | 3.60E-03 | 1.89E-02 | 4 | 97 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0044783 | G1 DNA damage checkpoint | 1.27E-03 | 8.50E-03 | 4 | 73 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0044819 | mitotic G1/S transition checkpoint | 1.27E-03 | 8.50E-03 | 4 | 73 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0044843 | cell cycle G1/S phase transition | 4.58E-03 | 2.28E-02 | 5 | 167 | 178 | 27688 | POCG47 P62987 Q9Y5N6 P62979 POCG48 |
| GO:0045089 | positive regulation of innate immune response | 4.70E-03 | 2.32E-02 | 5 | 168 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0045214 | sarcomere organization | 6.09E-04 | 4.74E-03 | 3 | 26 | 178 | 27688 | O15273 P09493 P13533 O75947 P09669 O43674 P40926 P40925 O00483 P14854 P36542 P10176 O95178 O96000 P13073 P25705 P18859 O14949 P56381 P24311 O1523 9 P02674 O00217 P10606 O95169 P51970 P48047 O14561 O43920 P159 54 O95167 P08574 P47985 P06576 P48735 POCG47 P63244 P62987 P62979 POCG48 POCG47 P51452 O75116 P62987 P62979 POCG48 POCG47 P51452 P63244 P60033 P62987 P62979 P04792 P25116 P00441 POCG48 POCG47 P60033 P62987 P62979 P25116 P00441 POCG48 POCG47 P63244 Q9NWT8 P62987 P62979 P25116 POCG48 POCG47 Q9NWT8 P62987 P83731 P62979 POCG48 P13929 P25705 P04406 P07195 P06576 O00217 P13929 O75947 O95169 P51970 P48047 O43674 P04406 O14561 O00483 P16615 O43920 P36542 O95167 O95178 O96000 P25705 P1885 9 P07195 P56381 P06576 O15239 O00217 P13929 O75947 O95169 P51970 P48047 O43674 P04406 O14561 O00483 P16615 O43920 P36542 O95167 O95178 O96000 P25705 P1885 9 P07195 P56381 P06576 O15239 O75947 P25705 P48047 P18859 P16615 P36542 P56381 P06576 P13929 P00505 P40926 P04406 P40925 P17174 O75947 P16860 P25705 P48047 P18859 P01160 P16615 P36542 P56381 P06576 P41222 P00505 O14561 O14880 P17174 P51857 P24752 P00505 P17174 Q16698 P51857 P24752 Q13011 POCG47 O75947 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 POCG48 P39019 O96000 P16860 P39023 P62273 P07195 P46783 P83731 P62913 P62753 O15239 Q13765 Q07020 O95169 P48047 P0440 6 O14561 Q9Y5N6 O43920 O95167 P84098 P63173 P61353 P46777 P053 86 P60866 P46776 P05387 P60228 P62249 P13929 P25398 O00483 O951 78 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P61247 P62857 P629 79 P56381 P62851 P00441 O00217 Q08493 P51970 P08708 P62906 P180 77 Q8N8D1 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P04 792 P62269 P20585 P06576 P13929 P40926 P04406 P07195 P40925 POCG47 O75947 P02792 Q9POU1 P48047 P68363 P37108 P16615 P36542 P19105 POCG48 P25705 P18859 P62987 P62913 P62979 P56381 P25116 P06576 POCG47 P51452 P62987 P62979 P62158 POCG48 P10916 P62280 P35613 P39019 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P45379 P62753 P24752 Q07020 P01033 Q14896 P19021 P16989 P68032 P84098 O14958 P63173 P08493 P61353 P60660 P46777 P05386 Q13772 P60866 P46776 P05387 P62249 P07602 P25398 P62891 P42766 Q02878 P19429 P84243 Q14192 P61247 P62857 P62979 P62851 P00441 P02144 Q14116 O15273 P08708 P62906 P68133 P18077 P13533 P12883 P42677 P15880 Q02543 P08590 P62263 P62987 P62945 P04275 P62269 P63316 POCG47 P10916 P01160 P12235 POCG48 P13693 P63244 P16860 P19429 P25705 Q14192 Q9NP15 P09493 P83731 P62979 P62158 P00441 P54379 P00441 P01034 P51452 P01033 Q08493 O75116 P80297 P37108 P16989 Q05639 Q9NWT8 P09382 P62263 P62987 P02511 P63313 P17081 P04792 P6022 8 P25116 P20585 P06576 POCG47 P10916 P01160 P12235 POCG48 P13693 P63244 P16860 P25705 Q14192 Q9NP15 P09493 P83731 P62979 P62158 P00441 P01034 P51452 P01033 Q08493 P37108 P16989 Q05639 Q9NWT8 P09382 P62263 P6298 7 P02511 P63313 P17081 P04792 P60228 P25116 P20585 P06576 P41222 Q14192 P19021 P17174 P68133 P22352 Q13772 Q08431 Q8N8D 1 O15273 Q14896 P10916 P19429 P08590 P09493 P68032 P45379 P13533 P12883 P63316 O15273 Q14896 P10916 P19429 P08493 P08590 P09493 P68032 P45379 P13533 P12883 P63316 P10916 P62280 P35613 P39019 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P45379 P62753 P24752 Q07020 P01033 Q14896 P19021 P19022 P16989 P68032 Q08431 P84098 O14958 P63173 P08493 P61353 P60660 P09382 P46777 P05386 Q13772 P60866 P46776 P05387 P62249 P07602 P25398 P62891 P42766 Q02878 P19429 P84243 Q14192 P61247 P62857 P62979 P62851 P00441 P02144 Q14116 O15273 P08708 O75116 P62906 P68133 P18077 P13533 P12883 P42677 P15880 Q02543 P08590 P62263 P62987 P62945 P04275 P04792 P62269 P20585 P06576 P63316 O15273 Q14896 P10916 P19429 Q14192 P08590 P09493 P68032 P45379 P13533 P12883 P63316 O15273 P68133 P13533 P10916 P16615 P62280 P35613 P39019 P16860 O14949 P39023 P62273 P09493 P46783 P83731 P62913 P45379 P62753 P24752 Q07020 P01033 Q14896 P19021 P19022 P16989 P68032 Q08431 P84098 O14958 P63173 P08493 P61353 P60660 P09382 P46777 P05386 Q13772 P60866 P46776 P05387 P62249 P07602 P13929 P25398 P62891 P42766 Q02878 P19429 P25705 P84243 Q14192 P61247 P62857 P62979 P62851 P00441 P51452 P02144 Q14116 O15273 P08708 O75116 P62906 P68133 P18077 P1353 3 P17535 P12883 P42677 P15880 Q02543 P08590 P62263 P62987 P6294 5 P04275 P04792 P62269 P25116 P20585 P06576 P63316 P01033 P02144 P08708 P62263 P25116 P00441 P39019 P07602 POCG47 P51452 Q14896 P13533 POCG48 P63244 P19429 P60033 P08590 P09493 P62987 P62979 P62158 P04792 P45379 P25116 P20585 P00441 P63316 P01034 P07602 P01033 P84243 P68871 P16615 P04275 P62158 P35613 P25116 P00441 POCG47 P62987 P62979 POCG48 POCG47 P62987 P62979 POCG48 P07602 P01033 P16860 P84243 P68871 P16615 P04275 P62158 P35613 P25116 P00441 P16860 P01160 P68871 P25116 P00441 POCG47 P62987 P62979 POCG48 O15273 P10916 Q14192 P09493 P68133 P68032 P13533 POCG47 O75947 O43674 P16615 P36542 P35613 POCG48 P39019 O96000 P16860 P05090 P00505 O14949 P62913 P69905 P62158 O15239 Q1376 5 P01033 O95169 P48047 Q9Y27 O14561 P19022 P37108 O43920 O951 67 Q08431 P19105 P08574 P47985 P07602 P02792 P51684 P68363 O004 83 O95178 P12235 P13693 P25705 P18859 P60033 P68871 P62979 P563 81 P00441 O00217 P02144 P51970 Q9POU1 P41222 Q00325 P62987 P04 275 P63313 P04792 P25116 P06576 |
| GO:0045333 | cellular respiration | 5.13E-35 | 6.99E-33 | 32 | 206 | 178 | 27688 | |
| GO:0045732 | positive regulation of protein catabolic process | 2.82E-03 | 1.56E-02 | 5 | 149 | 178 | 27688 | |
| GO:0045787 | positive regulation of cell cycle | 4.89E-03 | 2.40E-02 | 6 | 242 | 178 | 27688 | |
| GO:0045859 | regulation of protein kinase activity | 9.52E-03 | 3.98E-02 | 10 | 649 | 178 | 27688 | |
| GO:0045860 | positive regulation of protein kinase activity | 9.85E-03 | 4.07E-02 | 7 | 367 | 178 | 27688 | |
| GO:0045862 | positive regulation of proteolysis | 1.52E-03 | 9.70E-03 | 7 | 260 | 178 | 27688 | |
| GO:0045930 | negative regulation of mitotic cell cycle | 8.59E-04 | 6.34E-03 | 6 | 171 | 178 | 27688 | |
| GO:0046031 | ADP metabolic process | 1.40E-03 | 9.28E-03 | 5 | 127 | 178 | 27688 | |
| GO:0046034 | ATP metabolic process | 2.22E-16 | 7.81E-15 | 22 | 324 | 178 | 27688 | |
| GO:0046128 | purine ribonucleoside metabolic process | 1.38E-13 | 3.46E-12 | 22 | 443 | 178 | 27688 | |
| GO:0046129 | purine ribonucleoside biosynthetic process | 2.66E-05 | 2.90E-04 | 8 | 184 | 178 | 27688 | |
| GO:0046364 | monosaccharide biosynthetic process | 7.73E-06 | 9.35E-05 | 6 | 73 | 178 | 27688 | |
| GO:0046390 | ribose phosphate biosynthetic process | 2.31E-06 | 2.99E-05 | 10 | 227 | 178 | 27688 | |
| GO:0046394 | carboxylic acid biosynthetic process | 9.71E-03 | 4.03E-02 | 7 | 366 | 178 | 27688 | |
| GO:0046395 | carboxylic acid catabolic process | 4.16E-03 | 2.11E-02 | 6 | 234 | 178 | 27688 | |
| GO:0046483 | heterocycle metabolic process | 5.23E-20 | 2.28E-18 | 75 | 3900 | 178 | 27688 | |
| GO:0046496 | nicotinamide nucleotide metabolic process | 7.49E-03 | 3.25E-02 | 5 | 188 | 178 | 27688 | |
| GO:0046907 | intracellular transport | 1.88E-03 | 1.14E-02 | 19 | 1409 | 178 | 27688 | |
| GO:0048011 | neurotrophin TRK receptor signaling pathway | 2.87E-03 | 1.58E-02 | 6 | 217 | 178 | 27688 | |
| GO:0048513 | animal organ development | 4.79E-21 | 2.27E-19 | 66 | 2908 | 178 | 27688 | |
| GO:0048519 | negative regulation of biological process | 1.80E-03 | 1.10E-02 | 39 | 3792 | 178 | 27688 | |
| GO:0048523 | negative regulation of cellular process | 4.42E-03 | 2.22E-02 | 35 | 3471 | 178 | 27688 | |
| GO:0048545 | response to steroid hormone | 1.07E-02 | 4.37E-02 | 9 | 561 | 178 | 27688 | |
| GO:0048644 | muscle organ morphogenesis | 2.62E-13 | 6.19E-12 | 11 | 63 | 178 | 27688 | |
| GO:0048729 | tissue morphogenesis | 5.42E-04 | 4.33E-03 | 12 | 601 | 178 | 27688 | |
| GO:0048731 | system development | 6.13E-17 | 2.26E-15 | 73 | 4195 | 178 | 27688 | |
| GO:0048738 | cardiac muscle tissue development | 1.03E-10 | 1.99E-09 | 12 | 138 | 178 | 27688 | |
| GO:0048747 | muscle fiber development | 9.33E-04 | 6.64E-03 | 3 | 30 | 178 | 27688 | |
| GO:0048856 | anatomical structure development | 1.15E-16 | 4.09E-15 | 79 | 4893 | 178 | 27688 | |
| GO:0048872 | homeostasis of number of cells | 1.71E-04 | 1.54E-03 | 7 | 180 | 178 | 27688 | |
| GO:0050790 | regulation of catalytic activity | 1.54E-03 | 9.78E-03 | 21 | 1602 | 178 | 27688 | |
| GO:0050817 | coagulation | 2.00E-03 | 1.19E-02 | 10 | 518 | 178 | 27688 | |
| GO:0050851 | antigen receptor-mediated signaling pathway | 1.17E-02 | 4.71E-02 | 4 | 136 | 178 | 27688 | |
| GO:0050852 | T cell receptor signaling pathway | 5.62E-03 | 2.70E-02 | 4 | 110 | 178 | 27688 | |
| GO:0050878 | regulation of body fluid levels | 5.22E-03 | 2.53E-02 | 11 | 690 | 178 | 27688 | |
| GO:0050880 | regulation of blood vessel size | 2.29E-03 | 1.31E-02 | 5 | 142 | 178 | 27688 | |
| GO:0051092 | positive regulation of NF-kappaB transcription | 2.43E-03 | 1.37E-02 | 4 | 87 | 178 | 27688 | |
| GO:0051146 | striated muscle cell differentiation | 5.96E-05 | 6.09E-04 | 7 | 152 | 178 | 27688 | |
| GO:0051179 | localization | 2.83E-04 | 2.42E-03 | 58 | 5886 | 178 | 27688 | |

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|------------|---|----------|----------|-----|-------|-----|-------|--|
| GO:0051234 | establishment of localization | 1.66E-04 | 1.50E-03 | 53 | 5116 | 178 | 27688 | POCG47 O75947 O43674 P16615 P36542 P35613 POCG48 P39019 O96000 P16860 P05090 P00505 O14949 P62913 P69905 P62158 O15239 Q13765 P01033 O95169 P48047 Q92777 O14561 P37108 O43920 O95167 Q08431 P19105 P08574 P47985 P07602 P02792 P68363 O00483 O95178 P12235 P13693 P25705 P18859 P68871 P62979 P56381 P00441 O00217 P02144 P51970 Q9P0U1 P41222 Q00325 P62987 P04275 P25116 P06576 POCG47 P10916 POCG48 P63244 P16860 P19429 Q9UB9Y P09493 P62979 P45379 P00441 P01034 Q14116 Q14896 O75116 P19022 P16989 P17661 P13533 P17535 P12883 P41222 P08493 P09382 P08590 P62987 P04792 P25116 Q14558 P63316 |
| GO:0051239 | regulation of multicellular organismal process | 1.52E-05 | 1.71E-04 | 30 | 2027 | 178 | 27688 | POCG47 P51452 P01033 P63244 P62987 P37108 P62979 P04792 P60228 POCG48 P01034 |
| GO:0051248 | negative regulation of protein metabolic process | 9.20E-03 | 3.89E-02 | 11 | 747 | 178 | 27688 | P68871 P22352 Q16698 P02511 P04275 P69905 P24752 |
| GO:0051259 | protein oligomerization | 3.97E-03 | 2.06E-02 | 7 | 309 | 178 | 27688 | P22352 Q16698 P02511 P04275 P24752 |
| GO:0051260 | protein homooligomerization | 8.16E-03 | 3.49E-02 | 5 | 192 | 178 | 27688 | POCG47 P62987 Q9Y5N6 P62979 POCG48 |
| GO:0051320 | S phase | 1.17E-03 | 7.98E-03 | 5 | 122 | 178 | 27688 | POCG47 P62987 Q9Y5N6 P62979 POCG48 |
| GO:0051325 | interphase | 3.34E-03 | 1.79E-02 | 5 | 155 | 178 | 27688 | POCG47 P62987 Q9Y5N6 P62979 POCG48 |
| GO:0051329 | mitotic interphase | 2.90E-03 | 1.59E-02 | 5 | 150 | 178 | 27688 | P63244 Q14896 P19429 P08590 P09493 P62158 P45379 P13533 P25116 P20585 P63316 P01034 |
| GO:0051336 | regulation of hydrolase activity | 4.46E-03 | 2.23E-02 | 12 | 774 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051340 | regulation of ligase activity | 4.93E-03 | 2.41E-02 | 4 | 106 | 178 | 27688 | P63244 Q14896 P08590 P09493 P62158 P45379 P25116 P20585 |
| GO:0051345 | positive regulation of hydrolase activity | 4.43E-03 | 2.22E-02 | 8 | 399 | 178 | 27688 | POCG47 P51452 P63244 P62987 P62979 P04792 POCG48 |
| GO:0051348 | negative regulation of transferase activity | 2.22E-03 | 1.28E-02 | 7 | 278 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051351 | positive regulation of ligase activity | 2.14E-03 | 1.25E-02 | 4 | 84 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051352 | negative regulation of ligase activity | 1.96E-03 | 1.17E-02 | 4 | 82 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051384 | response to glucocorticoid | 1.19E-02 | 4.79E-02 | 5 | 211 | 178 | 27688 | P41222 P19021 P17174 P22352 Q8N8D1 |
| GO:0051403 | stress-activated MAPK cascade | 1.61E-03 | 1.01E-02 | 5 | 131 | 178 | 27688 | POCG47 P51452 P62987 P62979 POCG48 |
| GO:0051436 | negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 1.48E-03 | 9.54E-03 | 4 | 76 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051437 | positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle | 1.21E-03 | 8.17E-03 | 4 | 72 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051438 | regulation of ubiquitin-protein transferase activity | 4.93E-03 | 2.41E-02 | 4 | 106 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051439 | regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 2.43E-03 | 1.37E-02 | 4 | 87 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051443 | positive regulation of ubiquitin-protein | 1.79E-03 | 1.10E-02 | 4 | 80 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051444 | negative regulation of ubiquitin-protein | 1.96E-03 | 1.17E-02 | 4 | 82 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0051592 | response to calcium ion | 5.97E-04 | 4.67E-03 | 5 | 105 | 178 | 27688 | P16860 P08493 P62158 P45379 P17535 |
| GO:0051641 | cellular localization | 6.34E-04 | 4.91E-03 | 26 | 2041 | 178 | 27688 | O7602 POCG47 O75947 P02792 P68363 P16615 P36542 P12235 POCG48 P25705 P18859 P62913 P62979 P56381 P62158 P00441 P01033 Q9P0U1 P48047 P37108 P19105 P62987 P04275 P63316 P25116 P06576 |
| GO:0051649 | establishment of localization in cell | 2.60E-04 | 2.24E-03 | 25 | 1816 | 178 | 27688 | O7602 POCG47 O75947 P02792 P68363 P16615 P36542 P12235 POCG48 P25705 P18859 P62913 P62979 P56381 P62158 P00441 P01033 Q9P0U1 P48047 P37108 P19105 P62987 P04275 P25116 P06576 |
| GO:0051704 | multi-organism process | 2.54E-18 | 9.87E-17 | 54 | 2209 | 178 | 27688 | POCG47 P62280 P35613 POCG48 P39019 P63244 Q14094 P39023 P62273 P46783 P83731 P62913 P62753 Q13765 Q07020 P16989 Q08431 P84098 P63173 P16353 P46777 P05386 P60866 P46776 P05387 P62249 P25398 P12235 P13693 P62891 P42766 Q002878 P60033 P61247 P62857 P22352 P62979 P62851 Q01628 P00441 Q14116 P08708 P62906 P18077 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P04792 P62269 P25116 |
| GO:0055001 | muscle cell development | 3.41E-06 | 4.34E-05 | 7 | 98 | 178 | 27688 | O15273 P10916 Q14192 P09493 P68133 P68032 P13533 |
| GO:0055002 | striated muscle cell development | 2.07E-06 | 2.72E-05 | 7 | 91 | 178 | 27688 | O15273 P10916 Q14192 P09493 P68133 P68032 P13533 |
| GO:0055003 | cardiac myofibril assembly | 2.35E-04 | 2.08E-03 | 3 | 19 | 178 | 27688 | O15273 P10916 P68032 |
| GO:0055006 | cardiac cell development | 9.20E-06 | 1.09E-04 | 5 | 44 | 178 | 27688 | O15273 P10916 Q14192 P68032 P13533 |
| GO:0055007 | cardiac muscle cell differentiation | 2.37E-04 | 2.09E-03 | 5 | 86 | 178 | 27688 | O15273 P10916 Q14192 P68032 P13533 |
| GO:0055008 | cardiac muscle tissue morphogenesis | 1.34E-14 | 3.69E-13 | 11 | 49 | 178 | 27688 | O15273 Q14896 P10916 P19429 P08590 P09493 P68032 P45379 P13533 P12883 P63316 |
| GO:0055010 | ventricular cardiac muscle tissue morphogenesis | 1.63E-12 | 3.55E-11 | 9 | 37 | 178 | 27688 | Q14896 P10916 P19429 P08590 P09493 P45379 P13533 P12883 P63316 |
| GO:0055013 | cardiac muscle cell development | 9.20E-06 | 1.09E-04 | 5 | 44 | 178 | 27688 | O15273 P10916 Q14192 P68032 P13533 |
| GO:0055082 | cellular chemical homeostasis | 1.01E-02 | 4.15E-02 | 8 | 460 | 178 | 27688 | P13693 P02792 P51684 P19429 P09382 P25116 P00441 P06576 |
| GO:0055086 | nucleobase-containing small molecule metabolic process | 8.87E-13 | 1.97E-11 | 28 | 837 | 178 | 27688 | P13929 O75947 P01160 O43674 P40926 P40925 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 Q9NPI5 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 P06576 |
| GO:0055114 | oxidation-reduction process | 1.59E-20 | 7.20E-19 | 37 | 845 | 178 | 27688 | O75947 P09669 O43674 P40926 P40925 O00483 P14854 P36542 P10176 O95178 P12235 O96000 P13073 P25705 P18859 O14949 Q16698 P56381 P62158 P24311 O15239 P20674 O00217 P10606 O95169 P51970 P48047 O14561 O43920 P15954 P51857 O95167 P08574 P47985 Q13011 P06576 P48735 |
| GO:0060047 | heart contraction | 2.75E-12 | 5.64E-11 | 9 | 39 | 178 | 27688 | O15273 Q14896 P10916 P19429 P08590 P09493 P68032 P00441 P63316 |
| GO:0060048 | cardiac muscle contraction | 7.24E-10 | 1.31E-08 | 7 | 30 | 178 | 27688 | O15273 Q14896 P19429 P08590 P09493 P68032 P63316 |
| GO:0060415 | muscle tissue morphogenesis | 5.31E-14 | 1.39E-12 | 11 | 55 | 178 | 27688 | O15273 Q14896 P10916 P19429 P08590 P09493 P68032 P45379 P13533 P12883 P63316 |
| GO:0060537 | muscle tissue development | 1.70E-09 | 2.96E-08 | 14 | 261 | 178 | 27688 | O15273 Q14896 P10916 P68133 P68032 P13533 P12883 P19429 Q14192 P06060 P08590 P09493 P45379 P63316 |
| GO:0060548 | negative regulation of cell death | 5.75E-04 | 4.52E-03 | 14 | 784 | 178 | 27688 | POCG47 P01033 P16989 P12235 POCG48 P13693 Q05639 Q14192 P62987 P62979 P02511 P04792 P25116 P00441 |
| GO:0061024 | membrane organization | 2.41E-03 | 1.37E-02 | 9 | 444 | 178 | 27688 | POCG47 P02792 P62987 P37108 P62979 Q08431 P19105 P00441 POCG48 |
| GO:0061061 | muscle structure development | 3.86E-08 | 5.91E-07 | 16 | 449 | 178 | 27688 | O15273 Q14896 P10916 P19022 P68133 P68032 P13533 P12883 P19429 Q14192 P06060 P09382 P08590 P09493 P45379 P63316 |
| GO:0065003 | macromolecular complex assembly | 6.70E-04 | 5.15E-03 | 17 | 1086 | 178 | 27688 | O00217 O15273 P08708 P68363 O43920 P84243 P68871 P62263 P83731 P22352 Q16698 P02511 P04275 P69905 P62851 P62753 P24752 |
| GO:0065008 | regulation of biological quality | 2.65E-04 | 2.27E-03 | 36 | 3074 | 178 | 27688 | P07602 P02792 P51684 P01160 P16615 P35613 P12235 P39019 P13693 P16860 P19429 P84243 P68871 P09493 P62158 P62753 P00441 P01033 P02144 Q14116 Q08493 P08708 P04406 P51857 P13533 P19105 P12883 P09382 P08590 P62263 P04275 P63313 P17081 P25116 P06576 P63316 |
| GO:0070252 | actin-mediated cell contraction | 2.46E-21 | 1.19E-19 | 14 | 40 | 178 | 27688 | O15273 Q14896 P10916 P68133 P17661 P68032 P13533 P12883 P19429 P06060 P08590 P09493 P45379 P63316 |
| GO:0070423 | nucleotide-binding oligomerization domain containing signaling pathway | 2.58E-05 | 2.84E-04 | 4 | 27 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0070887 | cellular response to chemical stimulus | 2.74E-03 | 1.52E-02 | 22 | 1795 | 178 | 27688 | POCG47 P51452 Q14116 P51684 O14880 P08297 P13533 P17535 POCG48 Q14192 P09382 P09493 P17174 P62987 P62979 Q13772 P62158 P17081 P04792 P62753 Q01628 P00441 |
| GO:0070925 | organelle assembly | 8.42E-07 | 1.15E-05 | 11 | 254 | 178 | 27688 | O15273 P10916 P08708 P09493 P62263 P68133 P83731 P68032 P62851 P13533 P62753 |
| GO:0071156 | regulation of cell cycle arrest | 5.27E-03 | 2.54E-02 | 4 | 108 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0071158 | positive regulation of cell cycle arrest | 1.79E-03 | 1.10E-02 | 4 | 80 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0071704 | organic substance metabolic process | 3.42E-09 | 5.60E-08 | 107 | 10632 | 178 | 27688 | O75947 O43674 P16615 O96000 P16860 P07195 P46783 P83731 P62913 P62753 P24752 O15239 Q13765 O95169 P13639 P48047 P04406 O14561 Q9Y5N6 O95167 P84098 P63173 P68104 P46777 P60866 P46776 P60228 P62249 Q13011 Q8N335 P07602 P25398 P68363 O95178 P62891 P25705 P18859 Q14192 Q16654 P56381 P00441 P54368 O00217 Q14116 Q08493 P08708 O75116 P18077 Q8N8D1 P42677 P41222 P15880 P17540 Q02543 Q9Y3D2 P62263 Q14240 P62945 P62269 POCG47 P06732 Q9N5D9 P01160 P40926 P40925 P62280 P36542 P35613 POCG48 P39019 P05090 P00505 P39023 P62273 P62158 Q07020 O14880 P19021 O43920 Q05639 P61353 P05386 P05387 P13929 O00483 P42766 Q02878 P60033 Q9NPI5 P17174 P61247 P62857 P22352 Q16698 P62979 P62851 P51452 P51970 P62906 P51857 P62987 P04275 P04792 P25116 P20585 P06576 P48735 |

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|------------|--|----------|----------|----|------|-----|-------|---|
| GO:0071822 | protein complex subunit organization | 5.81E-26 | 3.95E-24 | 50 | 1259 | 178 | 27688 | P62280 P39019 P39023 P62273 P46783 P83731 P62913 P69905 P62753 P24752 Q07020 O43920 P68032 P84098 P63173 P61353 P46777 P02511 P05386 P60866 P46776 P05387 P62249 P25398 P68363 P62891 P42766 Q02878 P84243 P68871 P61247 P62857 P22352 Q16698 P62979 P62851 O00217 O15273 P08708 P62906 P68133 P18077 P42677 P15880 Q02543 P62263 P62987 P62945 P04275 P62269 |
| GO:0071826 | ribonucleoprotein complex subunit organization | 1.31E-03 | 8.70E-03 | 5 | 125 | 178 | 27688 | P08708 P62263 P83731 P62851 P62753 POCG47 P10916 P62280 POCG48 P39019 P39023 P62273 P09493 P46783 P83731 P62913 P69905 P62753 P24752 P01034 Q07020 P19022 P37108 O43920 P68032 Q08431 P19105 P84098 P63173 P61353 P60660 P46777 P02511 P05386 P17081 P60866 P46776 P05387 P62249 P02792 P25398 P68363 P12235 P62891 P42766 Q02878 P84243 P68871 P61247 P62857 P22352 Q16698 P62979 P62851 P00441 O00217 Q14315 O15273 Q9P001 P08708 O75116 P62906 P68133 P18077 P17661 P13533 P42677 P15880 Q02543 P62263 P62987 P62945 P04275 P63313 P62269 P25116 P20585 |
| GO:0071840 | cellular component organization or biogenesis | 1.43E-13 | 3.53E-12 | 72 | 4736 | 178 | 27688 | POCG47 P51452 P60033 P62987 P62979 P25116 P00441 POCG48 POCG47 P60033 P62987 P62979 P00441 POCG48 P41222 O14561 O14880 P51857 P24752 POCG47 P62987 P62979 POCG48 P40926 P40925 P48735 P02144 Q14116 O15273 Q14896 P10916 P19021 P19022 P68032 P13533 Q08431 P12883 P16860 O14958 P19429 Q14192 P08590 P09493 P04792 P45379 P06576 P63316 P02144 Q14116 O15273 Q14896 P10916 P19021 P19022 P68032 P13533 Q08431 P12883 P16860 O14958 P19429 Q14192 P08590 P09493 P04792 P45379 P06576 P63316 |
| GO:0071900 | regulation of protein serine/threonine kinase | 1.26E-02 | 4.91E-02 | 8 | 479 | 178 | 27688 | POCG47 P51452 P60033 P62987 P62979 P25116 P00441 POCG48 |
| GO:0071902 | positive regulation of protein serine/threonine | 5.71E-03 | 2.73E-02 | 6 | 250 | 178 | 27688 | POCG47 P60033 P62987 P62979 P00441 POCG48 |
| GO:0072330 | monocarboxylic acid biosynthetic process | 1.04E-02 | 4.27E-02 | 5 | 204 | 178 | 27688 | P41222 O14561 O14880 P51857 P24752 |
| GO:0072331 | signal transduction by p53 class mediator | 4.15E-03 | 2.11E-02 | 4 | 101 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0072350 | tricarboxylic acid metabolic process | 1.04E-02 | 4.27E-02 | 3 | 70 | 178 | 27688 | P40926 P40925 P48735 P02144 Q14116 O15273 Q14896 P10916 P19021 P19022 P68032 P13533 Q08431 P12883 P16860 O14958 P19429 Q14192 P08590 P09493 P04792 P45379 P06576 P63316 |
| GO:0072358 | cardiovascular system development | 8.45E-08 | 1.25E-06 | 21 | 822 | 178 | 27688 | P02144 Q14116 O15273 Q14896 P10916 P19021 P19022 P68032 P13533 Q08431 P12883 P16860 O14958 P19429 Q14192 P08590 P09493 P04792 P45379 P06576 P63316 |
| GO:0072359 | circulatory system development | 8.45E-08 | 1.25E-06 | 21 | 822 | 178 | 27688 | P02144 Q14116 O15273 Q14896 P10916 P19021 P19022 P68032 P13533 Q08431 P12883 P16860 O14958 P19429 Q14192 P08590 P09493 P04792 P45379 P06576 P63316 |
| GO:0072395 | signal transduction involved in cell cycle | 9.76E-04 | 6.90E-03 | 4 | 68 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0072401 | signal transduction involved in DNA integrity | 9.23E-04 | 6.59E-03 | 4 | 67 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0072413 | signal transduction involved in mitotic cell cycle | 9.23E-04 | 6.59E-03 | 4 | 67 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0072422 | signal transduction involved in DNA damage | 9.23E-04 | 6.59E-03 | 4 | 67 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0072431 | signal transduction involved in mitotic G1 DNA | 8.72E-04 | 6.35E-03 | 4 | 66 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:0072521 | purine-containing compound metabolic process | 6.75E-14 | 1.73E-12 | 25 | 581 | 178 | 27688 | P13929 O75947 P01160 O43674 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 P06576 O75947 P16860 P25705 P48047 P18859 P01160 P16615 P36542 P56381 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 P68871 P22352 P69905 P62158 P00441 POCG47 O75116 P62987 P62979 POCG48 Q14896 P10916 P19429 P08590 P09493 P25116 O14558 P00441 P63316 POCG47 P25398 Q9NSD9 P62280 POCG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 P00441 Q13765 Q07020 P08708 P62906 Q9Y5N6 P18077 Q8N8D1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P04792 P60866 P46776 P62269 P05387 P60228 P20585 P62249 O75947 P06732 P48047 P01160 P16615 P36542 P16860 P25705 P18859 P60033 Q9NP15 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 POCG47 P42677 P62987 Q9Y5N6 P62979 POCG48 P07602 P13929 O75947 P01160 O43674 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 Q8N335 P06576 POCG47 P62987 P62979 POCG48 POCG47 P62987 P62979 POCG48 O75947 P16860 P25705 P48047 P18859 P01160 Q9NP15 P16615 P36542 P56381 P06576 POCG47 O75947 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 POCG48 P39019 O96000 P16860 P39023 P62273 P07195 P46783 P83731 P62913 P62753 O15239 Q13765 Q07020 O95169 P48047 P04406 O14561 Q9Y5N6 O43920 O95167 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P13929 P25398 O00483 O95178 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P61247 P62857 P62979 P56381 P62851 P08708 P62906 P18077 P51857 P15880 Q02543 P62263 P62987 Q14240 P62945 P04792 P62269 P06576 O75947 P01160 P16615 P62280 P36542 P39019 P16860 P39023 P62273 P46783 P83731 P62913 P62753 Q13765 Q07020 P48047 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P08708 P62906 P18077 P51857 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P06576 O75947 P06732 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 P39019 O96000 P16860 P00505 P39023 P62273 P07195 P46783 P83731 P62913 P62753 P24752 O15239 Q13765 Q07020 O95169 P13639 P48047 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P54368 P08708 P62906 P18077 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P06576 POCG47 P13929 Q08493 P04406 P51857 POCG48 P00505 P07195 P17174 P62987 Q14240 Q16698 P62979 P62158 P60228 P24752 Q13011 Q8N335 P00441 O75947 P06732 Q9NSD9 P01160 P40926 P40925 P16615 P62280 P36542 P39019 P16860 P00505 P39023 P62273 P46783 P83731 P62913 P62753 P24752 Q13765 Q07020 P13639 P48047 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P54368 P08708 P62906 P18077 P51857 P42677 P41222 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P06576 P01033 Q14116 P16860 P01160 P17174 P08574 P17081 P62753 P35613 O00217 P13929 O75947 O95169 P51970 P48047 O43674 P04406 O14561 O00483 P16615 O43920 P36542 O95178 O96000 P25705 P18859 P07195 P56381 P06576 O15239 O75947 P25705 P48047 P18859 P16615 P36542 P56381 P06576 |
| GO:0072522 | purine-containing compound biosynthetic process | 7.41E-06 | 9.01E-05 | 10 | 259 | 178 | 27688 | P13929 O75947 P01160 O43674 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 P06576 O75947 P16860 P25705 P48047 P18859 P01160 P16615 P36542 P56381 P06576 P13929 P40926 P04406 Q9NP15 P07195 P40925 P68871 P22352 P69905 P62158 P00441 POCG47 O75116 P62987 P62979 POCG48 Q14896 P10916 P19429 P08590 P09493 P25116 O14558 P00441 P63316 POCG47 P25398 Q9NSD9 P62280 POCG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 P00441 Q13765 Q07020 P08708 P62906 Q9Y5N6 P18077 Q8N8D1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P04792 P60866 P46776 P62269 P05387 P60228 P20585 P62249 O75947 P06732 P48047 P01160 P16615 P36542 P16860 P25705 P18859 P60033 Q9NP15 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 POCG47 P42677 P62987 Q9Y5N6 P62979 POCG48 P07602 P13929 O75947 P01160 O43674 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 Q8N335 P06576 POCG47 P62987 P62979 POCG48 POCG47 P62987 P62979 POCG48 O75947 P16860 P25705 P48047 P18859 P01160 Q9NP15 P16615 P36542 P56381 P06576 POCG47 O75947 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 POCG48 P39019 O96000 P16860 P39023 P62273 P07195 P46783 P83731 P62913 P62753 O15239 Q13765 Q07020 O95169 P48047 P04406 O14561 Q9Y5N6 O43920 O95167 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P13929 P25398 O00483 O95178 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P61247 P62857 P62979 P56381 P62851 P08708 P62906 P18077 P51857 P15880 Q02543 P62263 P62987 Q14240 P62945 P04792 P62269 P06576 O75947 P01160 P16615 P62280 P36542 P39019 P16860 P39023 P62273 P46783 P83731 P62913 P62753 Q13765 Q07020 P48047 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P08708 P62906 P18077 P51857 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P06576 O75947 P06732 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 P39019 O96000 P16860 P00505 P39023 P62273 P07195 P46783 P83731 P62913 P62753 P24752 O15239 Q13765 Q07020 O95169 P13639 P48047 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P54368 P08708 P62906 P18077 P42677 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P06576 POCG47 P13929 Q08493 P04406 P51857 POCG48 P00505 P07195 P17174 P62987 Q14240 Q16698 P62979 P62158 P60228 P24752 Q13011 Q8N335 P00441 O75947 P06732 Q9NSD9 P01160 P40926 P40925 P16615 P62280 P36542 P39019 P16860 P00505 P39023 P62273 P46783 P83731 P62913 P62753 P24752 Q13765 Q07020 P13639 P48047 P84098 Q05639 P63173 P68104 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P25398 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P17174 P61247 P62857 P62979 P56381 P62851 P54368 P08708 P62906 P18077 P51857 P42677 P41222 P15880 Q02543 P62263 P62987 Q14240 P62945 P62269 P06576 P01033 Q14116 P16860 P01160 P17174 P08574 P17081 P62753 P35613 O00217 P13929 O75947 O95169 P51970 P48047 O43674 P04406 O14561 O00483 P16615 O43920 P36542 O95178 O96000 P25705 P18859 P07195 P56381 P06576 O15239 O75947 P25705 P48047 P18859 P16615 P36542 P56381 P06576 |
| GO:0072524 | pyridine-containing compound metabolic process | 2.01E-03 | 1.19E-02 | 6 | 202 | 178 | 27688 | P13929 P40926 P04406 Q9NP15 P07195 P40925 P68871 P22352 P69905 P62158 P00441 POCG47 O75116 P62987 P62979 POCG48 Q14896 P10916 P19429 P08590 P09493 P25116 O14558 P00441 P63316 POCG47 P25398 Q9NSD9 P62280 POCG48 P39019 P62891 P42766 Q02878 P39023 P62273 P46783 P61247 P83731 P62857 P62913 P62979 P62851 P62753 P00441 Q13765 Q07020 P08708 P62906 Q9Y5N6 P18077 Q8N8D1 P42677 P84098 P15880 P63173 Q02543 P61353 P62263 P62987 Q14240 P62945 P46777 P05386 P04792 P60866 P46776 P62269 P05387 P60228 P20585 P62249 O75947 P06732 P48047 P01160 P16615 P36542 P16860 P25705 P18859 P60033 Q9NP15 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 O75947 P25705 P48047 P18859 P36542 P56381 P06576 POCG47 P42677 P62987 Q9Y5N6 P62979 POCG48 P07602 P13929 O75947 P01160 O43674 O00483 P16615 P36542 O95178 O96000 P16860 P25705 P18859 P07195 P56381 O15239 O00217 Q08493 O95169 P51970 P48047 P04406 O14561 O43920 O95167 Q8N335 P06576 POCG47 P62987 P62979 POCG48 POCG47 P62987 P62979 POCG48 O75947 P16860 P25705 P48047 P18859 P01160 Q9NP15 P16615 P36542 P56381 P06576 POCG47 O75947 Q9NSD9 P01160 O43674 P40926 P40925 P16615 P62280 P36542 POCG48 P39019 O96000 P16860 P39023 P62273 P07195 P46783 P83731 P62913 P62753 O15239 Q13765 Q07020 O95169 P48047 P04406 O14561 Q9Y5N6 O43920 O95167 P84098 P63173 P61353 P46777 P05386 P60866 P46776 P05387 P60228 P62249 P13929 P25398 O00483 O95178 P62891 P42766 Q02878 P25705 P18859 Q9NP15 P61247 P62857 P62979 P56381 P62851 P08708 P6 |

| | | | | | | | | |
|------------|---|----------|----------|----|------|-----|-------|---|
| GO:1901700 | response to oxygen-containing compound | 1.64E-04 | 1.49E-03 | 21 | 1348 | 178 | 27688 | P01033 P02144 Q14116 P01160 P19021 P68032 P35613 P12883 P16860 P00505 P09382 P68871 P09493 P17174 P08574 P22352 P69905 P17081 P62753 P25116 P00441 |
| GO:1901988 | negative regulation of cell cycle phase transition | 8.29E-03 | 3.54E-02 | 4 | 123 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1901991 | negative regulation of mitotic cell cycle phase | 7.61E-03 | 3.29E-02 | 4 | 120 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1902400 | intracellular signal transduction involved in G1 | 8.72E-04 | 6.35E-03 | 4 | 66 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1902402 | signal transduction involved in mitotic DNA | 9.23E-04 | 6.59E-03 | 4 | 67 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1902403 | signal transduction involved in mitotic DNA | 9.23E-04 | 6.59E-03 | 4 | 67 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1902578 | single-organism localization | 1.20E-02 | 4.81E-02 | 36 | 3840 | 178 | 27688 | P07602 POCG47 O75947 P02792 P68363 P16615 P36542 P35613 P12235 POCG48 P39019 P13693 P16860 P05090 P25705 P00505 P18859 P68871 P62913 P62979 P56381 P69905 P62158 P00441 P01033 Q9POU1 P48047 Q9V277 P37108 Q08431 P19105 P62987 P04275 P63313 P25116 P06576 |
| GO:1902582 | single-organism intracellular transport | 1.83E-05 | 2.05E-04 | 19 | 975 | 178 | 27688 | POCG47 O75947 P02792 Q9POU1 P48047 P68363 P37108 P16615 P36542 P19105 POCG48 P25705 P18859 P62987 P62913 P62979 P56381 P25116 P06576 |
| GO:1902600 | hydrogen ion transmembrane transport | 8.78E-06 | 1.06E-04 | 7 | 113 | 178 | 27688 | O75947 P25705 P48047 P18859 P36542 P56381 P06576 |
| GO:1902806 | regulation of cell cycle G1/S phase transition | 3.09E-03 | 1.66E-02 | 4 | 93 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1902807 | negative regulation of cell cycle G1/S phase | 1.63E-03 | 1.02E-02 | 4 | 78 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1903050 | regulation of proteolysis involved in cellular | 2.82E-03 | 1.56E-02 | 5 | 149 | 178 | 27688 | POCG47 P63244 P62987 P62979 POCG48 |
| GO:1903052 | positive regulation of proteolysis involved in cellular protein catabolic process | 7.99E-04 | 6.02E-03 | 5 | 112 | 178 | 27688 | POCG47 P63244 P62987 P62979 POCG48 |
| GO:1903321 | negative regulation of protein modification by small protein conjugation or removal | 4.30E-03 | 2.17E-02 | 4 | 102 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1903322 | positive regulation of protein modification by small protein conjugation or removal | 9.50E-03 | 3.98E-02 | 4 | 128 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:1903362 | regulation of cellular protein catabolic process | 3.25E-03 | 1.74E-02 | 5 | 154 | 178 | 27688 | POCG47 P63244 P62987 P62979 POCG48 |
| GO:1903364 | positive regulation of cellular protein catabolic | 8.32E-04 | 6.23E-03 | 5 | 113 | 178 | 27688 | POCG47 P63244 P62987 P62979 POCG48 |
| GO:1903522 | regulation of blood circulation | 4.52E-06 | 5.62E-05 | 9 | 192 | 178 | 27688 | P16860 Q9UBV9 P08590 P09493 P17661 P45379 P13533 P25116 P12883 |
| GO:1990267 | response to transition metal nanoparticle | 9.25E-03 | 3.89E-02 | 4 | 127 | 178 | 27688 | P80297 P19021 P35613 P00441 |
| GO:1990542 | mitochondrial transmembrane transport | 6.28E-09 | 1.01E-07 | 7 | 40 | 178 | 27688 | O75947 P25705 P48047 P18859 P36542 P56381 P06576 |
| GO:2000045 | regulation of G1/S transition of mitotic cell cycle | 3.09E-03 | 1.66E-02 | 4 | 93 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:2000058 | regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic process | 1.79E-03 | 1.10E-02 | 4 | 80 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:2000060 | positive regulation of protein ubiquitination involved in ubiquitin-dependent protein catabolic | 1.48E-03 | 9.54E-03 | 4 | 76 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |
| GO:2000134 | negative regulation of G1/S transition of mitotic | 1.63E-03 | 1.02E-02 | 4 | 78 | 178 | 27688 | POCG47 P62987 P62979 POCG48 |

Supplemental Table Viv. 2011 v 2016 comparison. A selection of *Biological Process* GO terms extracted from two BinGO analyses, using either the 2016 or the 2011 GO annotation dataset and adult ventricular cardiomyocyte data¹⁹ (2016-hA-VCMs and 2011-hA-VCMs, respectively). GO terms selected either align with the GO terms identified by Poon et al., 2013, or a descriptive GO term associated with a large proportion of the analysed dataset, or are terms from the ‘*cardiac conduction*’ domain of the ontology. **n** indicates the number of protein IDs associated with the GO term, **corr p-value** is the p-value after Benjamini & Hochberg False Discovery Rate correction, **x** is the number of IDs in both the submitted list and associated with the GO term, #N/A indicates that this term was not significantly enriched in the dataset. The corrected p-values in the 2016 analysis are highlighted in green if the p-value is more significant in the 2016 analysis, and orange if the p-value is more significant in the 2011 analysis.

| Description | n | 2016-hA-VCMS | | 2011-hA-VCMS | | |
|---|-------|--------------|----|--------------|--------------|------|
| | | corr p-value | x | n | corr p-value | x |
| GO:0006614 SRP-dependent cotranslational protein targeting to membrane | 123 | 1.98E-52 | 37 | | #N/A | #N/A |
| GO:0045047 protein targeting to ER | 127 | 4.39E-52 | 37 | | #N/A | #N/A |
| GO:0072599 establishment of protein localization to endoplasmic reticulum | 131 | 1.36E-51 | 37 | | #N/A | #N/A |
| GO:0006414 translational elongation | 223 | 2.52E-47 | 40 | 110 | 1.40E-53 | 38 |
| GO:0006091 generation of precursor metabolites and energy | 574 | 1.06E-34 | 43 | 552 | 1.89E-28 | 40 |
| GO:0022904 respiratory electron transport chain | 157 | 1.67E-34 | 29 | 135 | 5.48E-34 | 29 |
| GO:0022411 cellular component disassembly | 673 | 2.76E-34 | 45 | 221 | 1.73E-39 | 37 |
| GO:0045333 cellular respiration | 231 | 5.04E-34 | 32 | 206 | 6.99E-33 | 32 |
| GO:0044419 interspecies interaction between organisms | 830 | 1.26E-31 | 46 | 781 | 5.40E-27 | 44 |
| GO:0061024 membrane organization | 1211 | 1.16E-27 | 49 | 444 | 1.37E-02 | 9 |
| GO:0003012 muscle system process | 319 | 7.11E-27 | 30 | 233 | 1.38E-21 | 25 |
| GO:0016071 mRNA metabolic process | 743 | 7.53E-27 | 40 | 651 | 6.93E-27 | 41 |
| GO:0006936 muscle contraction | 264 | 4.09E-25 | 27 | 205 | 1.36E-21 | 24 |
| GO:0033275 actin-myosin filament sliding | 39 | 3.13E-21 | 14 | 38 | 5.24E-20 | 14 |
| GO:0070252 actin-mediated cell contraction | 76 | 2.08E-18 | 15 | 40 | 1.19E-19 | 14 |
| GO:0051234 establishment of localization | 7073 | 2.56E-18 | 93 | 5116 | 1.50E-03 | 53 |
| GO:0006810 transport | 6916 | 3.12E-17 | 90 | 5023 | 1.00E-03 | 53 |
| GO:0042775 mitochondrial ATP synthesis coupled electron transport | 77 | 1.12E-16 | 14 | 68 | 1.45E-11 | 11 |
| GO:0006941 striated muscle contraction | 101 | 1.74E-16 | 15 | 61 | 1.28E-10 | 10 |
| GO:0060047 heart contraction | 80 | 1.96E-16 | 14 | 39 | 5.64E-11 | 9 |
| GO:0060048 cardiac muscle contraction | 69 | 1.03E-15 | 13 | 30 | 1.31E-08 | 7 |
| GO:0032774 RNA biosynthetic process | 3310 | 7.53E-15 | 57 | 669 | 3.45E-22 | 37 |
| GO:0006937 regulation of muscle contraction | 179 | 4.80E-14 | 16 | 98 | 2.31E-07 | 9 |
| GO:0010467 gene expression | 5483 | 1.09E-13 | 73 | 2206 | 4.58E-11 | 45 |
| GO:0090257 regulation of muscle system process | 230 | 1.48E-13 | 17 | 122 | 1.45E-06 | 9 |
| GO:0061061 muscle structure development | 502 | 6.98E-13 | 22 | 449 | 5.91E-07 | 16 |
| GO:1903522 regulation of blood circulation | 326 | 3.31E-12 | 18 | 192 | 5.62E-05 | 9 |
| GO:0009725 response to hormone | 1187 | 3.76E-12 | 31 | 1086 | 2.69E-05 | 22 |
| GO:0007005 mitochondrion organization | 679 | 4.56E-12 | 24 | | #N/A | #N/A |
| GO:0008016 regulation of heart contraction | 243 | 5.04E-12 | 16 | 116 | 1.22E-04 | 7 |
| GO:0055001 muscle cell development | 153 | 3.42E-11 | 13 | 98 | 4.34E-05 | 7 |
| GO:0048738 cardiac muscle tissue development | 164 | 8.07E-11 | 13 | 138 | 1.99E-09 | 12 |
| GO:0008015 blood circulation | 401 | 9.50E-11 | 18 | 319 | 4.44E-08 | 15 |
| GO:0042692 muscle cell differentiation | 290 | 7.63E-10 | 15 | 245 | 3.41E-04 | 9 |
| GO:0002027 regulation of heart rate | 90 | 7.84E-10 | 10 | 39 | 1.19E-02 | 3 |
| GO:0051146 striated muscle cell differentiation | 211 | 1.74E-09 | 13 | 152 | 6.09E-04 | 7 |
| GO:0044267 cellular protein metabolic process | 6461 | 4.75E-08 | 68 | 3447 | 4.00E-09 | 54 |
| GO:0009888 tissue development | 1677 | 6.35E-08 | 30 | 1526 | 6.26E-03 | 21 |
| GO:0032502 developmental process | 6093 | 1.82E-07 | 64 | 5680 | 4.09E-12 | 80 |
| GO:0030029 actin filament-based process | 823 | 2.13E-07 | 20 | 505 | 5.02E-07 | 17 |
| GO:0072358 cardiovascular system development | 915 | 2.40E-07 | 21 | 822 | 1.25E-06 | 21 |
| GO:0006950 response to stress | 4615 | 2.77E-07 | 53 | 3628 | 5.91E-03 | 39 |
| GO:0007507 heart development | 537 | 3.74E-07 | 16 | 489 | 1.78E-06 | 16 |
| GO:0009653 anatomical structure morphogenesis | 2626 | 4.21E-07 | 37 | 2300 | 1.82E-02 | 26 |
| GO:0034220 ion transmembrane transport | 1636 | 4.90E-07 | 28 | 336 | 2.90E-03 | 9 |
| GO:0009611 response to wounding | 798 | 6.28E-07 | 19 | 835 | 7.37E-03 | 14 |
| GO:0050896 response to stimulus | 11437 | 6.60E-07 | 96 | | #N/A | #N/A |
| GO:0010941 regulation of cell death | 1800 | 9.40E-07 | 29 | 1340 | 3.38E-03 | 20 |
| GO:0006811 ion transport | 2414 | 1.56E-06 | 34 | | #N/A | #N/A |
| GO:0002026 regulation of the force of heart contraction | 31 | 5.93E-06 | 5 | | #N/A | #N/A |
| GO:0043434 response to peptide hormone | 591 | 6.71E-06 | 15 | 527 | 3.18E-02 | 9 |
| GO:0048468 cell development | 1903 | 9.01E-06 | 28 | | #N/A | #N/A |
| GO:0030154 cell differentiation | 3701 | 1.36E-05 | 42 | | #N/A | #N/A |
| GO:1903779 regulation of cardiac conduction | 68 | 1.57E-05 | 6 | | #N/A | #N/A |
| GO:0048869 cellular developmental process | 3946 | 6.01E-05 | 42 | | #N/A | #N/A |
| GO:0010882 regulation of cardiac muscle contraction by calcium ion signaling | 24 | 6.19E-05 | 4 | | #N/A | #N/A |
| GO:0007596 blood coagulation | 541 | 2.54E-04 | 12 | 518 | 1.19E-02 | 10 |
| GO:0006366 transcription from RNA polymerase II promoter | 833 | 2.90E-04 | 15 | | #N/A | #N/A |
| GO:0010881 regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion | 20 | 9.48E-04 | 3 | | #N/A | #N/A |
| GO:0007010 cytoskeleton organization | 1479 | 1.88E-03 | 19 | | #N/A | #N/A |
| GO:1902533 positive regulation of intracellular signal transduction | 1054 | 2.67E-03 | 15 | | #N/A | #N/A |
| GO:0033554 cellular response to stress | 2165 | 1.02E-02 | 22 | | #N/A | #N/A |
| GO:0061337 cardiac conduction | 126 | 1.71E-02 | 4 | | #N/A | #N/A |
| GO:0012501 programmed cell death | 1204 | 1.83E-02 | 14 | | #N/A | #N/A |
| GO:0045893 positive regulation of transcription, DNA-templated | 1575 | 3.05E-02 | 16 | | #N/A | #N/A |

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