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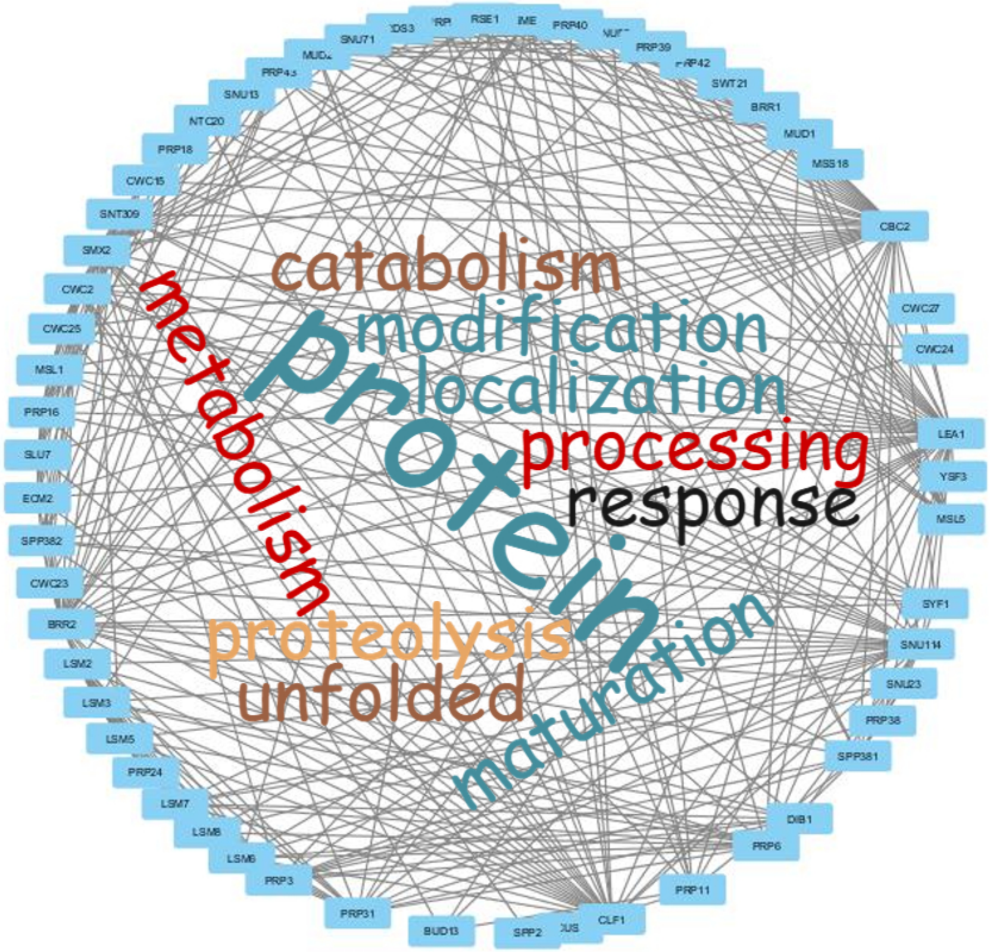

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Transcriptional regulation of the genes involved in protein metabolism and processing in *Saccharomyces cerevisiae*

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Abstract

Topological analysis of large networks, which focus on a specific biological process or on related biological processes, where functional coherence exists among the interacting members, may provide a wealth of insight into cellular functionality. This work presents an unbiased systems approach to analyze genetic, transcriptional regulatory, and physical interaction networks of yeast genes possessing such functional coherence to gain novel biological insight. The present analysis identified only a few transcriptional regulators amongst a large gene cohort associated with the protein metabolism and processing in yeast. These transcription factors are not functionally required for the maintenance of these tasks in growing cells. Rather, they are involved in rewiring gene transcription in response to such major challenges as starvation, hypoxia, DNA damage, heat shock, or the accumulation of unfolded proteins. Indeed, only a subset of these proteins were captured empirically in the nuclear-enriched fraction of non-stressed yeast cells, suggesting that the transcriptional regulation of protein metabolism and processing in yeast is primarily concerned with maintaining cellular robustness in the face of threat by either internal or external stressors.

INTRODUCTION

Biological activities at the cellular level are not isolated but are governed by a set of concerted interactions between the functional molecules responsible for performing a given task. For this reason, network analysis is often employed to elucidate how these coordinated interactions facilitate the functioning of an entire biological system (Ma and Gao 2012). The connectivity graph of a cellular network, in which biological entities such as genes, proteins, or metabolites are connected through edges that represent interactions such as reactions or structural relationships, is often employed to identify the topological features of a network (Barabási and Oltvai 2004a; Meyers 2009). Examples of the theoretical analysis of such graphs were reported by Erdös and Rényi as early as in the 1960s, in a study of large random networks (Erdös and Rényi 1960).

In the early days of network biology, it became immediately apparent that the topological structure of biological networks were different from that of random networks. Interactions described in biological networks were found to follow a power law degree distribution, and these networks were shown to exhibit properties such as a scale-free nature, 'small-world' properties, high tolerance to random attacks and low tolerance to targeted attacks, growth by preferential attachment, and the manifestation of distinct motif signatures and dense modules (Siegal, Promislow and Bergman 2006; Lima-Mendez and van Helden 2009; Winterbach *et al.* 2013; Hu, Thomas and Brunak 2016). Nonconformities from these characteristics were usually attributed to the use of incomplete or poor-quality data (Siegal, Promislow and Bergman 2006; Lima-Mendez and van Helden 2009; Michailidis 2012; Mitra *et al.* 2013). However, some of these nonconforming observations persisted even after large numbers of high-quality interaction datasets became available, and advanced network analysis tools emerged. Existing characterization of biological networks needed to be modified and adapted accordingly, thus considering some of these conventional features as mere artefacts of biological graph representation (Winterbach *et al.* 2013). The analysis of biological networks then became increasingly focused, not on the investigation of the global network properties, but on the identification of functionally relevant sub-structures (Milo *et al.* 2002; Mitra *et al.* 2013; Winterbach *et al.* 2013). Identification of tightly interconnected substructures called modules became a valuable concept for exploring the workings of both control or healthy cellular systems as well as those of modified or diseased states of the system (Spirin and Mirny 2003; Barabási and Oltvai 2004b; Ideker and Sharan 2008). The study of even smaller local substructures comprised only of a few nodes has allowed the identification of recurrent patterns, called the motifs, within and across different cellular networks. These patterns were deemed useful in predicting novel interactions between nodes that are evolutionarily conserved across organisms or systems (Schwikowski, Uetz and Fields 2000).

In this paper, we introduce the term “functional homogeneity”, by which we mean the consideration of a specific biological process, or a group of related biological processes in the identification of the network components, to be considered as a criterion in the reconstruction of cellular networks. We explore its impact on the extent of biological insight that can be gained by the topological analysis of molecular networks. Using the yeast *Saccharomyces cerevisiae* as our model system, we have compiled sets of genes, each of which could be attributed to a single broad biological process or a broad group of functionally linked biological processes in the cell: (i) protein metabolic process, protein folding and localization, and unfolded protein response; (ii) gene expression (including both transcription and translation); (iii) cell cycle; or (iv) small molecule metabolism. We adopted an unbiased systems approach to study them by constructing the genetic, transcriptional regulatory, and physical interaction networks of the genes in these four sets, and analyzed their topological properties. We investigated whether the large size of these networks would be a factor limiting the extent of biological information we can extract from these sets. We then explored the potential of maintaining functional homogeneity within network components as a criterion in constructing biological networks, and how it impacts the topological properties of the network. As a final exercise, we aimed to extract biologically relevant insight from these networks, and analytically focused on transcriptional regulation mechanisms governing protein metabolism and processing (PT) in yeast. We carried out an in-depth investigation of the nuclear proteome to confirm the inferences made from our topological analysis. Our analysis showed that protein metabolism and processing in yeast are self-governed by a very small number of transcription factors, whose activities are not required during normal growth, but which elicit a major re-wiring of the transcription network of PT genes in response to stress conditions.

MATERIALS AND METHODS

Gene and annotation datasets

Seven different gene product sets were investigated in the study. Gene Ontology (GO) Biological Process terms were employed to compile the function-specific sets (Ashburner *et al.* 2000) of *Saccharomyces cerevisiae* gene products associated with the following GO IDs: (i) protein metabolism and processing (PT) (GO:0006457, GO:0008104, GO:0019538, GO:0006986), (ii) gene expression (GE) (GO:0010467), (iii) cell cycle (CC) (GO:0007049), and (iv) small molecule metabolism (SMM) (GO:0044281). Adopting GO annotations allowed us (i) to conduct a global search and avoid context specificity, as frequently encountered in hypothesis-driven studies, and thus refrain from potential bias in both analysis and interpretation, and (ii) to capture "practically" true functional specificity, since *S. cerevisiae* is one of the best-annotated organisms available to date as the collective result of extensive curation coupled with continuous influx of a large amount of high-quality empirical data. The hierarchy of the GO terms included in the analysis was selected such that the level of detail of information included in individual subsets, hence their granularity, would not compromise the observations made on the networks constructed from these subsets. The GO term association data for these four sets and for the global set (Biological Process root node GO: 0008150) (6447 genes) were accessed from http://www.geneontology.org/ (access date 03/03/2017) (Consortium 2015). A pool of 1000 random sets, with equal size to that of PT (2533 gene products), was constructed by randomly selecting entries from the global set. Average parameter values of these random sets were used for further analyses (average of 100 random networks for the investigation of the genetic interactions), and the significance of the difference between PT and random proportions were evaluated by the z-statistic. The PT-C (complement of PT) set was constructed from all the non-PT gene products of the global set (3914 gene products). Signaling-associated gene products were identified using the GO signaling term (GO:0023046). Haplosufficiency, essentiality, Gene Ontology associations, and human protein functional homology information was retrieved from the Saccharomyces Genome Database (SGD) accessed on 22/03/2017 (Cherry *et al.* 2012). Node data (i.e. gene sets) are provided in Supplementary Data 1. Data on protein phosphorylation were taken both from SGD and from Vlastaridis *et al.* (Vlastaridis *et al.* 2017).

Network reconstruction

Curated physical and genetic interactions documented for *S. cerevisiae* were retrieved from BIOGRID (Stark *et al.* 2006) on 22/02/2017 (release 3.4.145). A dataset by Jansen *et al.* (Jansen, Greenbaum and Gerstein 2002), where the authors used 10 permanent complexes as a basis for the classification of most *S. cerevisiae* complexes as permanent or transient based on correlations with gene expression, was used to distinguish between the permanent and transient physical interactions. Dosage rescue, synthetic rescue, phenotypic suppression and positive genetic interactions were classified as "alleviating" responses, whereas synthetic growth defect, phenotypic enhancement, synthetic lethality, dosage growth defect, dosage lethality, synthetic haploinsufficiency, and negative genetic interactions were classified as "aggravating" phenotypic responses in the analysis of genetic interaction networks. Physical and genetic interactions were both regarded as bidirectional and the graph edges were of uniform weight. A genetically interacting pair was double-counted only when evidence for both aggravating and alleviating effects on the phenotype were documented. Self-loops (e.g. homodimers) were excluded from the analyses. Transcriptional regulatory network interactions were accessed from YEASTRACT (Teixeira *et al.* 2014) (access date 22/02/2017). Transcription factor targets were used only when both DNA binding and expression evidence were documented. Transcription factors that do not have any curated targets were excluded from analysis. Regulatory evidence under all reported environmental conditions was included to avoid context-specific bias. The majority of the documented interactions employed in the study, extracted from the databases detailed above, are sourced from high-quality interactome datasets generated by empirical genome-scale studies on yeast, thereby avoiding any potential bias imposed by limited availability of data on specific subsets of genes. Furthermore, for all documented interactions included in the study, multiple instances of experimental evidence for a single interacting pair from one or more independent resources (experimental types, different studies, different experimental conditions) were scaled down to a single instance in order to avoid any potential bias in network reconstruction created by disproportionately available data on different biological processes. Essentially, any empirically documented interaction was included in the analysis to avoid context specificity in this global analysis. Yeast, being a model organism that has been extensively studied at the genome scale, does not suffer from lack of genome-wide high quality interaction data availability, therefore, interaction data inferred from indirect evidence or computational studies were excluded purposefully to avoid potentially misleading outcomes. Protein-protein, genetic and transcriptional regulatory networks (abbreviated from this point forward as PINs, GINs, and TRNs, respectively) were constructed and investigated separately for each gene product set (global, random, PT, PT-C, GE, CC, SMM), and the results of the analysis of each of these 21 networks constructed are also reported separately. Edge (interaction) data are available in Supplementary Data 1.

Network and data analysis

Cytoscape v3.5.0 was employed for the removal of duplicate interaction pairs and self-loops, and for topological network analysis (Cline *et al.* 2007). Statistical analyses and network randomization were conducted in MATLAB R2016b. Hubs were defined as nodes connected to at least 10% of the other nodes in the network and degree centrality was adopted as the hub-metric. Out-degree was employed as the characteristic parameter for the identification of principal transcription factors; i.e. the hub-like nodes in the bi-partite graph of the transcriptional regulatory network. Networks were normalized against the total number of nodes that they contained as reference. Dissimilarities in structural properties that could not be explained by the size effect were then determined by a "difference" metric, where a numerical network property was identified to be different from those for other networks only if the following relationship held true:

For any numerically representable network property a_i for any network i = 1…n and where $j \neq i$

$$a_i + 0.2a_i > a_j \quad or \quad a_i - 0.2a_i < a_j$$

indicating that a property must differ by at least 20% from its peers in order to be identified as distinctly different.

A hypergeometric distribution was used to evaluate the statistical significance of functional enrichments (Bardsley 2016). The background and sample populations for each analysis is explained in the text as required. Princeton GO tools were employed for Gene Ontology Enrichment Analysis (http://go.princeton.edu/cgi-bin/GOTermFinder) accessed on (19/05/2017) (Boyle *et al.* 2004). The p-values used to evaluate the significance of the enrichment were Bonferroni corrected. False discovery rates of these enrichments were also calculated, and those with $q > 0.05$ were rejected. GO terms that were classified as "Inferred from Electronic Annotation" were excluded from analysis. The background for the analyses was the complete genome. The GO terms that were reported in the text are the top hits. MeV: MultiExperiment Viewer was used for integrative data analysis (Howe *et al.* 2010). k-means clustering was employed for data classification (K = 2, distance metric = Pearson correlation, maximum number of instances to test all elements in the data set for cluster fit = 10000). The z-statistic was employed in evaluating the significance of proportional differences. Standard protocols were followed for multiple linear regression (MLR) and the determination of data normality (Lai, Robbins and Wei 1979). Symbolic regression (SR) was employed as described by (Oliver Morales and Rodríguez Vázquez 2004; Cankorur-Cetinkaya *et al.* 2017). The gene expression data (Gene Expression Omnibus accession number GSE41094) was adopted from Rodríguez-Lombardero *et al.* (Rodriguez-Lombardero *et al.* 2014a). Rank correlations were employed in evaluating the emPAI values that correspond to protein abundance (Ishihama *et al.* 2005).

Cell culture and pre-treatment for sub-cellular fractionation

The *S. cerevisiae* strain used in this study was BY4741 harboring GFP-tagged Hsp82p (*MAT***a** *HSP82-GFP::HIS3 his3Δ1 leu2Δ0 met15Δ0 ura3Δ0*) (Huh *et al.* 2003). Two separate cultures were grown to an OD_{600} of 0.6 at 30°C in SD-His media with shaking. In total, 120

OD units were used for the nuclear preparation and 240 OD units were used for the chromatin preparation.

Pre-treatment of cells prior to lysis was based on (Rieder and Emr 2001). Cells were incubated at 5 OD units per mL of 25 mM Tris-HCl, pH 7.5, 10 mM TCEP for 10 minutes at room temperature. Cells were subsequently treated for 10 minutes at 30°C with 1 µg zymolyase 100-T (Nacalai Tesque) per OD unit of yeast, in spheroplasting medium (SD-His supplemented with 25 mM Tris-HCl, pH 7.5 and 1.3 M sorbitol), at 20 OD units per mL. Spheroplasts were washed once in SD-His, supplemented with 1.2 M sorbitol, at 5 OD units per mL.

Sub-cellular fractionation

Nuclei were prepared according to (Kizer, Xiao and Strahl 2006), with the modification that lysis was carried out at 20 OD units/mL lysis buffer. This yielded a supernatant (S_{NUC}) and a nuclear pellet (P_{NUC}).

Chromatin was prepared according to (Kim *et al.* 2011), but in the absence of thiodiglycol. This yielded a supernatant (S_{CHROMA}) and chromatin pellet (P_{CHROMA}). The pellet was additionally treated with 500 U benzonase nuclease (Merck Millipore) for 30 minutes on ice and resolubilized in 30 mM Tris-HCl, pH 6.8, 2% (w/v) SDS.

Sample preparation for mass spectrometry

Protein concentrations were estimated and aliquots representing 75 µg total protein per sample were resolved on 4-15% linear gradient polyacrylamide gels (Bio-Rad) which were stained with Coomassie brilliant blue. Gel lanes were cut into equally sized bands (16 bands for S_{NUC} and P_{NUC}; eight bands for S_{CHROMA} and P_{CHROMA}). Bands were destained, reduced (dithiothreitol), alkylated (iodoacetamide) and subjected to tryptic digest at 37°C for 16 hours.

Mass spectrometric analysis of samples

In all cases, approximately 1 μg of sample was injected on-column per mass spectrometry run. The tryptic digests from bands corresponding to S_{NUC} and P_{NUC} were analyzed using a Dionex Ultimate 3000 RSLCnano UPLC (Thermo Fisher Scientific) system coupled in-line to a Q Exactive Hybrid Quadrupole-Orbitrap mass spectrometer (Thermo Fisher Scientific). The mass spectrometry method used was the same as described in (Mata *et al.* 2017), but with the modification that fragmentation was carried out on the twenty most intense ions per survey scan with charge state of 2+ and above.

The tryptic digests from bands corresponding to S_{CHROMA} and P_{CHROMA} were analyzed using a nanoAcquity UPLC system (Waters) coupled in-line to an LTQ Orbitrap Velos Hybrid Ion Trap mass spectrometer (Thermo Fisher Scientific). The mass spectrometry method used was the same as described in (Chen *et al.* 2015), but the Orbitrap was operated at a resolution of 30,000 and fragmentation was carried out on the twenty most intense ions per survey scan with charge state of 2+ and above. The details of the proteomics analysis are provided in Supplementary Data 2.

Mass spectrometry data processing and data availability

Files of raw mass spectrometry data were converted to Mascot Generic Format (MGF) using MSConvert (version 3.0.9283, Proteowizard). MGF files were searched using an in-house Mascot server (version 2.6.0, Matrix Science) against a canonical *S. cerevisiae* database, downloaded from UniProt (March 2017; 6,749 sequences). Samples corresponding to each gel lane were merged for searching, yielding a combined results file of mass spectrometry runs for a given sample. Carbamidomethylation of cysteine was specified as a fixed modification and oxidation of methionine as a variable modification. A 1% FDR threshold for protein identifications was imposed, based on the search of a decoy database of reversed protein entries. Relative protein quantification was inferred using the built-in emPAI score (Ishihama *et al.* 2005) feature of Mascot (Supplementary Data 3). The proteome data are available via ProteomeXchange with identifier PXD007525.

RESULTS AND DISCUSSION

We investigated the network organization and transcriptional regulation of the genes and their products involved in protein metabolism and processing (PT). We define PT as comprising the biosynthesis, modification, localization, and degradation of proteins. This set of processes is orchestrated by 2533 gene products in the yeast *Saccharomyces cerevisiae*, approximately 38% of the genes encoding protein, rRNA, snRNA, snoRNA or tRNA molecules. The physical, genetic and transcriptional regulatory interaction networks of this set of genes and gene products were constructed, and these networks were topologically investigated (each one separately) to identify whether network topology could alone be used to provide further biological insight into this system. We investigated the effects of both the size of the network and the functional relatedness between interacting nodes on these findings, and further evaluated their ubiquity by analyzing other large networks of gene sets dedicated to specific functions in yeast; gene expression (GE, 2128 gene products), cell cycle (CC, 786 gene products), and small molecule metabolism (SMM, 835 gene products). A summary of the biological networks constructed for all sub-systems and for the whole cell (6447 gene products) are provided in Supplementary Table 1 and in Figure 1A. We present here what we identify as the necessary and sufficient criteria to be met for gaining biological insight from the topological analysis of these large networks under investigation, and then move on to discuss our findings on the unusual properties regarding transcriptional regulation of the protein metabolism and processing in yeast, and the potential implications thereof.

Transcriptional regulation of protein metabolism and processing in yeast

The topological analysis (Supplementary Table 1) of the transcriptional regulatory network (TRN) of PT yielded a small repertoire of only 17 gene products out of the 2533, to encode transcription factors (TFs), indicating their significant under-representation in this subset ($p-value < 10^{-15}$). Either these TFs had a direct role in the transcriptional regulation of protein metabolism and processing, or they were involved in regulating a transcription factor by a transaction concerning these processes.

These TFs were determined to be involved in significantly fewer epistatic or physical interactions with the remaining members of the PT subset than what was observed for TFs in general at the whole cell level; the underrepresentation was by 2.98-fold and 2.78-fold, respectively, in comparison to that of the whole cell networks ($p-value < 10^{-20}$ for both analyses). Interestingly, despite their modest interaction profile within the PT network, these TFs were documented to be involved in significantly higher number of epsitatic or physical interactions at the whole cell level than other yeast TFs; that were empirically reported as an interaction partner in 1.9-fold and 1.8-fold more physical and epistatic interactions than what would be expected as in the case of other yeast TFs, respectively ($p-value < 0.005$ for both analyses). This could indicate that the specific roles of these TFs in protein metabolism and processing was strictly defined, and did not demand extensive communication (i.e. interactions) with the non-TF members of the network. Limited number of interactions indicated that they were not identified as hubs in either the GIN or the PIN of protein metabolism and processing, however they all were first neighbors to at least two hubs in both GIN and PIN, thus acting as facilitators of information flow in both networks. In other words, despite their relatively low degree, the strength of these TF nodes (see Barrat *et al.* 2004 for a formal description) was very high indicating the importance, or rather the centrality of these TFs within these networks.

Furthermore, only Hsf1p, a heat shock protein regulating gene transcription in response to stress, was shown empirically to complement the function of its cognate human gene among these PT TFs. However, we observed that a significantly higher fraction of the non-TF genes in the PT subset, which are binding targets of these TFs, were able to complement human gene function than the fraction of those, which are the binding targets of all yeast TFs at the whole cell level (11% vs 8.5%, indicating 1.3-fold over-enrichment, $p-value < 10^{-09}$). This could hint at the possibility of those genes that were involved in protein metabolism and processing to be conserved across the domain of Eukarya.

Hubs in the PT networks

Seven genes (*VAM6*, *RPN11*, *HSP82*, *CDC28*, *UBP3*, *RPN10* and *BRE5*) were identified as hubs in both the physical and the genetic interaction networks of PT, whereas the global PIN and GIN did not share any hubs. These hubs were tightly connected to other gene or gene products through both physical and genetic interactions in their respective networks, and possibly played a pivotal role in protein metabolism and processing. They exclusively had aggravating genetic interactions with other PT genes. Indeed, synthetic-lethal genetic interactions were previously reported to significantly overlap with protein–protein interactions, and were reported to be largely confined to genes within pathways that contain at least one essential gene (Boone, Bussey and Andrews 2007), providing further support for the present findings. Although these seven hubs are not themselves TFs, their transcription was regulated by the principal TFs of the PT TRN (Rap1p, Yap1p, Rpn4p, Hsf1p), stressing their topological importance further, as given by a node-based measure; the degree connectivity, in the context of protein metabolism and processing networks. Essential genes (43% vs. 15% for the global TRN) and functional orthologs of human genes (14% vs. 1% for the global TRN) were significantly overrepresented $(p - value < 0.01)$ among the principal TFs of the PT TRN (Supplementary Table 2).

Small network size is neither necessary nor a sufficient criterion for reconstructing biologically meaningful cellular networks

The topological differences between the PT interaction networks and the global interaction networks evoked two related questions regarding this analysis: (i) Did these biologically relevant differences arise only because the global set of the yeast coding genome was reduced down to 38% of its original size, which would be in line with earlier arguments stating that it was necessary to work with small networks to achieve biological insight (Hakes *et al.* 2008)? (ii) Did functional coherence among its gene members contribute to the understanding of the PT subset? We addressed these questions by generating and investigating 1000 randomly selected sub-sets of the global yeast gene set that comprised 2533 genes (the node size of the PT set). On average, $39.30 \pm 0.79\%$ of these random sets were associated with genes from the PT set. Since, the PT set itself constituted 38% of the global set in yeast, we concluded that this randomization was both a robust and realistic downsizing of the global set. The genetic interaction, protein interaction, and transcription regulatory networks of these random sets were then constructed. The characteristics of these networks were compared to those of both the global set and the *bona fide* PT set (Table 1). Although the node size of the random sets were equivalent to that of PT, PT was significantly enriched for signaling-associated or essential genes $(p - value < 0.01)$. Although both the random and the PT subset had a higher number of nodes identified as hubs, this was considerably more prominent in the physical and genetic interaction networks of PT, and was only a slight increase for the random subsets.

Scaling down reduced the available information at the interaction level for both random and PT networks since only the interactions between the genes of a given set were considered in the analysis. The random GIN and PIN were more severely affected, having fewer interactions, than PT GIN and PIN, and this difference was significant ($p-value < 0.01$). The functional homogeneity among the members of the PT subset produced higher within-graph connectivity than that of random graphs characterized by high network density by 45% and 40%, and shortened characteristic path lengths by 10% and 8% for PIN and GIN, respectively. In contrast to these observations on the physical and genetic interaction networks, the transcriptional regulatory events, at both the node and interaction levels, were significantly underrepresented in PT ($p-value < 0.01$), indicating that there were (i) fewer nodes identified as TFs, (ii) fewer nodes identified as target genes of these TFs, and (iii) fewer TF-gene binding interactions between (i) and (ii). As these characteristics and features could not be attributed to the expected topological measures of the TRN, they emerge as novel biological insight, rather than an inherent artefact of topological network analysis.

The analysis of random networks along with the PT networks revealed that investigating the cellular networks of genes involved in protein metabolism and processing had a substantial (and significant) impact on network topology, allowing the identification of unexpected structural features and differences, which could potentially lead to novel biological insight, whereas the arbitrary reduction of the node (and consequently network) size did not markedly affect the topological characteristics of cellular networks in comparison to what would be expected of the global networks.

Functional specificity is necessary but not sufficient to explain the unique transcriptional regulatory signature of protein metabolism and processing

The next question to be explored was whether these unexpected topological features identified for PT were unique to protein metabolism and processing, or ubiquitously observed in many “functionally homogeneous” subsets. For this purpose, three other functionally homogeneous subsets were selected: gene expression (GE), cell cycle (CC), and small molecule metabolism (SMM). GE was of comparable size to PT, and the nodes of the two sets had 47% overlap, resulting from the sharing of the translation process between the two sets. The CC and SMM subsets shared fewer nodes with PT than GE, and were smaller than both PT and GE, although the size reduction remained within a single order of magnitude. The overlaps between the subsets (Figure 1B) allowed us to address the problem of ubiquity: If the unique nodes of these subsets did not contribute to their respective network topology substantially, the analyses conducted on GE, CC, and SMM networks would likely yield similar observations to those obtained from the analysis of the PT networks.

In contrast to what we observed in the case of PT, genes encoding TFs were not significantly under-represented in neither GE, SMM, nor CC sets ($p-value > 0.1$). The topological features of the PINS, GINS and TRNS of these subsets were investigated (Supplementary Tables 1, 2). The set of all topological properties determined for the TRNs, GINs and PINs constituted a unique topological profile for each of PT, GE, CC, SMM, random, and PT-C subsets. We then asked the question of whether the topological profile of PT was similar to or different from the others and conducted k-means clustering to classify these profiles into two clusters. As expected, the topological profiles of subsets of randomly selected nodes and that of PT clustered separately. The topological profiles of CC and GE were more like that of PT, leading them to cluster together. The PT-C topological profile was similar to that of random subsets, as was the SMM profile (Figure 1C).

Despite being functionally well defined and thus “homogeneous”, the network topology of SMM was different from those of the other functional networks. The gene products of the members of SMM are most frequently involved in metabolic routes in the cell or in the regulatory events controlling these metabolic pathways. The flow and exchange of information often takes place through the small molecules, themselves, rather than the genes or gene products in the metabolic network. In contrast, the expression of genes or proteins, or the cell cycle, where the genes or gene products themselves undergo changes, relay or exchange information. This could have resulted in the topological properties of the SMM being different to those of PT, GE and CC. Parallel linear cascades of information flow with fewer connections are common in metabolic networks, and this was observable at the level of network connectivity. SMM gene and/or gene product networks were sparser and less connected than those of PT, GE or CC. The SMM PIN had the largest diameter (d = 11) among all PINs, and by 37.5% larger than that of the subsequent network. Significant differences were also observed in network hubs; although PT, GE, and CC PIN hubs were enriched for essential genes or genes whose absence impairs growth (45%, 48%, and 52%, respectively, vs. 21% for global, $p-value < 0.01$), this was not observed for SMM PIN. In contrast, SMM GIN hubs comprised significantly fewer such genes (8% vs. 52% for global, $p-value < 0.01$) (Supplementary Table 2). In line with these results, Szappanos *et al.* reported a unique property of yeast metabolic networks (SMM), too, highlighting the underrepresentation of genetic interactions, specifically of those that take place between pathways (Szappanos *et al.* 2011).

Networks of PT, GE, CC, and SMM comprised fewer interactions, even after normalizing the networks with respect to the number of nodes that they possess (Table 2). This down-sizing effect was considered as an artefact of the network reconstruction process, due to the consideration of interactions existing only within the members of each set, and is not discussed further. GE and SMM networks were enriched for the number of TFs that are present among the participating genes/gene products; this contrasts with the PT, in which the TFs, and consequently the transcriptional regulatory interactions involving those TFs were significantly underrepresented ($p-value < 0.01$). As a result, fewer nodes were identified as principal TFs (by out degree) in the TRN of PT than of GE, SMM, or CC. On the other hand, more hubs were identified in the GINs and PINs of all “functionally homogeneous” sets, with CC networks possessing more hubs than the others (Supplementary Table 1, Figure 2).

As discussed above, the underrepresentation of TFs within the PT subset was still remarkable and unique, even after the analysis of the GE, CC, and SMM sets. The subsequent question to address was whether the expression of the PT genes would be dominantly regulated by non-PT TFs, and that would be the typical transcriptional regulatory route for PT genes or not. This analysis was conducted on the PT subset, as well as on the GE, SMM, and CC subsets, for comparison. The number of non-subset TFs regulating the expression of the genes in the subset (to regulate their auxiliary roles to that of the subset) was 1-2 fold higher than the number of subset TFs, regardless of the specific biological role of the subset. However, there were no significant differences between the PT, GC, CC, and SMM subsets ($p-value > 0.1$), and thus did not contribute to elucidating the unique transcriptional regulatory signature of PT (Figure 2).

We investigated the PT specificity of this phenomenon further by artificially replacing a fraction of the PT nodes by those that were known not to have any role in protein metabolism and processing (i.e. introducing false positives). Even upon the random replacement of only 10% of the nodes, the reconstructed PT TRN had up to 75% more transcription factors and 63% more interactions. If 40% of the nodes were randomly replaced by those that are known not to be involved with protein metabolism and processing, the reconstructed TRN had 237% more TFs and 257% more interactions.

Since 17% of the protein-coding genes in *S. cerevisiae* are still not assigned to known biological processes (Cherry *et al.* 2012), we investigated the possibility of the presence of false negatives in our current analysis due to missing information on yet functionally unassinged genes of the protein metabolism and processing. We artificially introduced nodes with no known biological process associations into PT so as to increase its size by 10%; this was accompanied by only 13% increase in the number of TFs, and 11% increase in the transcriptional regulatory interactions. Increasing the node size by 40% was accompanied by an increase of 39% and 49% in the same parameters, respectively, indicating a roughly linear trend between node size and network expansion, so the possible future inclusion of genes with yet non-assigned PT functionality is unlikely to change the transcriptional regulatory landscape either.

Functional homogeneity is necessary

The final question we addressed was: (i) Could the specific differences in PT network topology be attributed to the employment of a functionally coherent set that focuses on a single broad biological process? Or (ii) Would the topological network analysis of a set of gene products that can be attributed to different and marginally related biological processes be as informative? For this purpose, the "functionally non-homogeneous" PT-C set was investigated. The analysis of the PT-C networks indicated that the topological features of these networks were similar to those of the random networks. Higher number of transient protein-protein interactions and aggravating genetic interactions were identified among the members of the PT-C subset than within randomly selected genes/gene products, but this difference was not statistically significant ($p - value > 0.05$). Despite higher number of interactions reported within the subset, the connectivity of the GIN and PIN were significantly impaired, as implicated by 17% and 8% longer characteristic path lengths than random networks, and 57% and 71% fewer hubs, respectively (p-value<0.01) (Supplementary Table 1). The weak connectivity, possibly caused by the functional heterogeneity observed among PT-C members, constrained the topological analysis providing biologically relevant insight.

Proteomic localization of PT transcription factors in non-stressed yeast cells

The subcellular compartments where the proteins constituting PT, CC and GE dominantly localized to, as given by their GO Cellular Component identifications, were investigated, and different subcellular compartments were identified as particularly prominent for each subset. CC proteins were significantly and solely localized in the nucleus $\left(p-value<10^{-20}\right)$, and GE proteins in both the nucleus and the cytosol $(p-value<10^{-20})$ (Figure 3). Despite the substantial overlap between GE and PT components, the enriched GO Cellular Component terms for the two subsets were different, and the PT set was not significantly enriched for nuclearly located proteins. Considering the unusual transcriptional regulatory features of the PT subset implicated by network analysis, we carried out an in-depth investigation of the proteomic landscape of yeast in the nuclear-enriched and the chromatin-enriched fractions as well as in the remaining components with a specific focus on PT proteins, and in particular, the PT TFs (Supplementary Data 3). In order to provide context specificity for our findings on the generalized network analysis, we investigated the yeast cells grown in rich medium under optimal growth conditions, without any particular limitations, thus providing the yeast population a non-stressed environment.

In total 1572 and 3272 proteins were captured in the chromatin-enriched and nuclear-enriched subcellular fractions, respectively. In order to simplify the description, we will refer to these two independent experiments as CHROMA and NUCLEA, respectively. CHROMA and NUCLEA had identified 1541 proteins in common. The proteins that were exclusively detected in the chromatin were involved in chromatin-remodeling processes ($p - value < 10^{-9}$), and those identified in the non-chromatin fraction were significantly associated with small molecule, oxidation-reduction, and nitrogen compound metabolic processes ($p - value < 10^{-7}$). Proteins specific to the nuclear-enriched fraction were associated with the cellular component organization or biogenesis process term ($p - value < 10^{-31}$). In contrast, proteins detected exclusively in the supernatant of NUCLEA were enriched for small molecule metabolic process ($p - value < 10^{-18}$). Our analysis of the shotgun proteome of the nucleus (specifically, that of the non-chromatin fraction) was highly specific, with only a few proteins ubiquitously detected in more than one enriched fraction (Supplementary Data 3).

CHROMA and NUCLEA datasets were both significantly enriched for the components of the PT TRN ($p - value < 10^{-13}$) indicating that the empirical data would satisfactorily cover our domain of interest. Furthermore, the PT TRN components were significantly overrepresented in the supernatant data from CHROMA, which is enriched with the non-chromatin fraction of the nucleus ($p - value < 10^{-4}$). This could possibly indicate a role for the PT proteins in the regulation of nuclear processes. Despite this high coverage, only seven of the 17 TFs in the PT were identified in the proteomic analysis; Gzf3p, Hsf1p, Rap1p, Rlm1p, Rtg3p, Skn7p, and Mot2p (Supplementary Data 3). This could indicate that the remaining 10 TFs could have roles in regulation of protein metabolism and processing under different conditions, possibly in the presence of an internal or an external stress factor.

This proteomics dataset demonstrated that the products of 27% of the protein-encoding genes in the yeast genome were located in the nucleus. Within this nuclearly localated subset, 23% of all reported yeast TFs was captured. Although the TFs were slightly underrepresented in the nuclearly located proteome dataset, this was statistically insignificant ($p-value = 0.12$). A similar exercise conducted for the PT components indicated that 30% of the PT genes were captured in this dataset, and 41% of all PT TFs were identified in the nuclear proteome. This showed that, in fact, a higher fraction of the PT TFs were captured in the nuclear proteome than would be expected, and this overrepresentation was significant ($p-value = 0.0016$).

These seven TFs were responsible for the transcriptional regulation of only 16 genes in the PT TRN. In a final approach to analyzing our findings and revealing biological insights, we constructed a non-parametric model to describe the expression of these 16 genes making use of the protein expression data on their regulator TFs. The gene expression data under similar conditions as those for the proteomic analysis were obtained from (Rodriguez-Lombardero *et al.* 2014b). We constructed a matrix describing the relationship between the TF protein abundance and target gene expression levels, and used this mathematical abstraction to formulate a predictive model of target gene expression based on the availability (given by abundance) of their transcription factors (Figure 4 A). The non-normality of the data (fat-tailed, with excess kurtosis = 2.4, positively skewed = 1.5) was accounted for by constructing a non-linear regression model employing symbolic regression. The model was able to describe the data with a satisfactory goodness-of-fit ($R^2 = 0.82$ vs. MLR $R^2 = 0.66$) (Figure 4 B, Supplementary Data 3). This regression model allowed us to describe the transcription of 16 gene targets of these seven TFs with reasonable accuracy. Protein metabolism and processing are closely related to the growth and proliferation of the cell. The precise level control over transcription of growth-associated processes (see Hallikas *et al.* 2006) as implicated by this model describing the transcriptional regulation of PT in a context-dependent manner (i.e. steady growth of non-stressed yeast cells) could have contributed to the reasonably high level of its descriptive success, in defiance of size limitations on the data.

Despite its small size, this model comprises all empirically identified transcriptional regulatory events by PT TFs under the stated non-stressed conditions. That being said, this final analysis rests on model construction that employs learning algorithms, and the relationship between model performance and data size should be taken into consideration in evaluation of the results.

Final remarks

Through a systematically conducted topological analysis of yeast, we identified that there were only a small number of transcription factors annotated to protein metabolism and processing despite the high number of genes involved in these processes, which comprised of nearly 38% of the gene products of *Saccharomyces cerevisiae*. Transcription factors are only annotated to the regulation of a process, if that process is directly initiated/activated by that target gene's transcription, and not if the process is activated by an independent mechanism following the biosynthesis of the participating gene products. Transcription factors annotated in the PT network were therefore i) directly regulating the process performed by the PT gene or ii) represent an instance where a PT regulates the transcription factor. Although the TFs identified (see Table 3) were highly interactive nodes, their specific role in protein metabolism and processing was tightly defined, and allowed less interaction (i.e. communication) with other nodes in the network. This reduced interactivity of the identified TFs makes it more likely that they represent instances described as (ii) above.

Nine of these TFs identified protein metabolism and processing functionalities regulating transcription (usually *via* protein recruitment to chromatin; Gis1p, Gzf3p, Hap1p, Hsf1p, Mac1p, Mot2p, Rap1p, Rph1p, and Xbp1p), and three represented TFs directly regulating processes performed by the PT (Hac1p, Skn7p, and Yap1p; all related to the Unfolded Protein Response). The fact that only a small number of TFs regulate PT genes does not necessarily imply that the transcriptional response is devoid of flexibility. At least 11 (92%), and possibly all (see Table 3), of the 12 TFs involved are subject to post-translational modification by phosphorylation. This compares to 114/177 (64%) for all yeast TFs, which represents a statistically significant difference ($p = 0.03$ for 11 or $p = 0.004$ for 12); moreover, a much larger proportion of the PT TFs have a high number (>7) of phosphorylation sites than to the bulk of TFs (42% versus 20%; $p = 0.06$). Even when considering TFs regulating PT genes, which were not themselves in the PT set, the network still had a reduced number of TFs indicating that the transcription of these genes is also orchestrated by a smaller set of TFs.

This analysis has demonstrated that the "execution" of the processes associated with protein metabolism and processing is rarely directly transcriptionally regulated, unlike the execution of metabolic processes, for example. Pathways in the small molecule metabolism are often activated by direct and specific transcriptional activation in response to nutrient and environmental conditions. Gene products are often functional as expressed, and the metabolic pathway is fine-tuned by "within pathway" rate-limiting steps executed by substrate activation and inhibition when nutrients are replete or limited. The large number of transcription factors controlling the processes encoded by this network (see Supplementary Table 1) is a consequence of the need to respond rapidly and specifically to the external environment and express pathway components to utilize available nutrients. The "regulation" discussed in this context remains strictly "hierarchical" (Rossell *et al.* 2006) restricted to epigenetic, transcriptional, translational or post-translational control, as metabolic regulation information at the global scale is rarely available.

Our findings on the small number of transcription factors involved in the direct regulation of the PT network were supported by the identification of a relatively low number of transcription factors (7) in the nuclear-enriched fraction of the proteome, which were responsible for the transcriptional regulation of protein metabolism and processing in yeast under normal (non-stressed) growth conditions. PT events, because they are mainly relevant to large numbers of proteins (e.g. translation relating to all proteins), or proteins always required at least once every cell cycle, are not transcriptionally regulated in growing cells; rather, they are post-transcriptionally regulated. Many transcription factors involved in the regulation of protein metabolism and processing only come into play in response to external (starvation, heat shock, oxidative stress, hypoxia, glucose repression) or internal (unfolded proteins, ER stress, DNA damage) stresses and effect a major rewiring of the transcriptional network.

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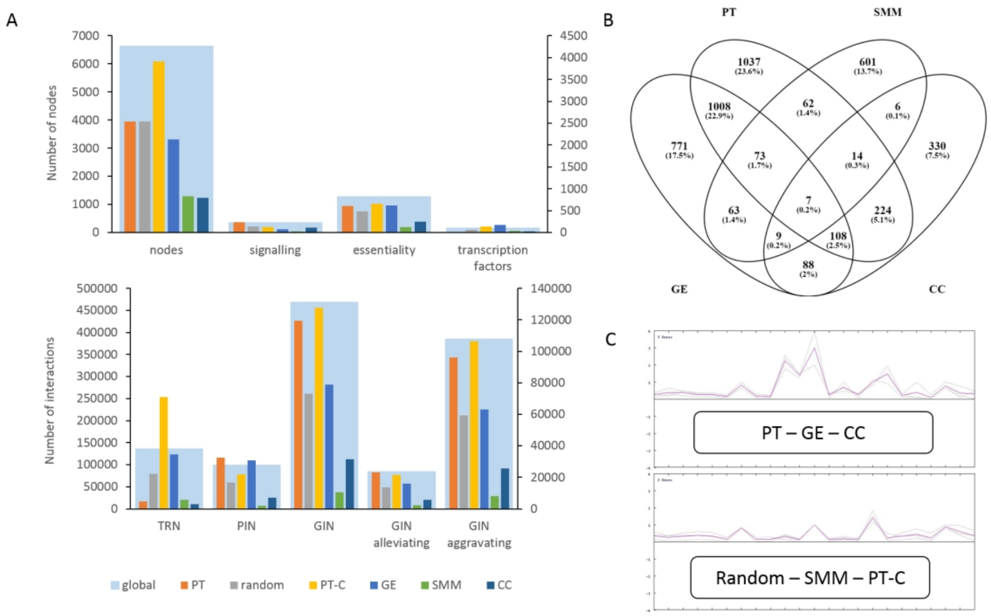

Figure 1. Summary of network properties of the systems under investigation.
(A) The number of nodes and interactions for each system under investigation; the global network, PT, the random network, PT-C, GE, CC, and SMM are provided in two plots. In both plots, the sub-systems are compared against the global network denoted by the light blue bar in the background. The primary vertical axis on the left hand side represents the values for the global network; whereas the secondary vertical axis on the right is used for the sub-systems. (B) The overlap of nodes amongst different sub-systems with defined biological functionality. The percentage values given in parentheses denote the relative proportion of the numbers among the total number of unique nodes from all four sub-systems. (C) Classification of the sub-networks by K-means clustering based on the topological properties summarized in Supplementary Table 1. Different attributes, on which clustering is based, are represented on the horizontal axis, and the vertical axis represents and arbitrary distance metric for the attribute profiles. The two main classes of sub-networks are highlighted in the rounded boxes on their respective similarity profiles. Note that the abbreviations adopted in the Figure are consistent throughout the article.

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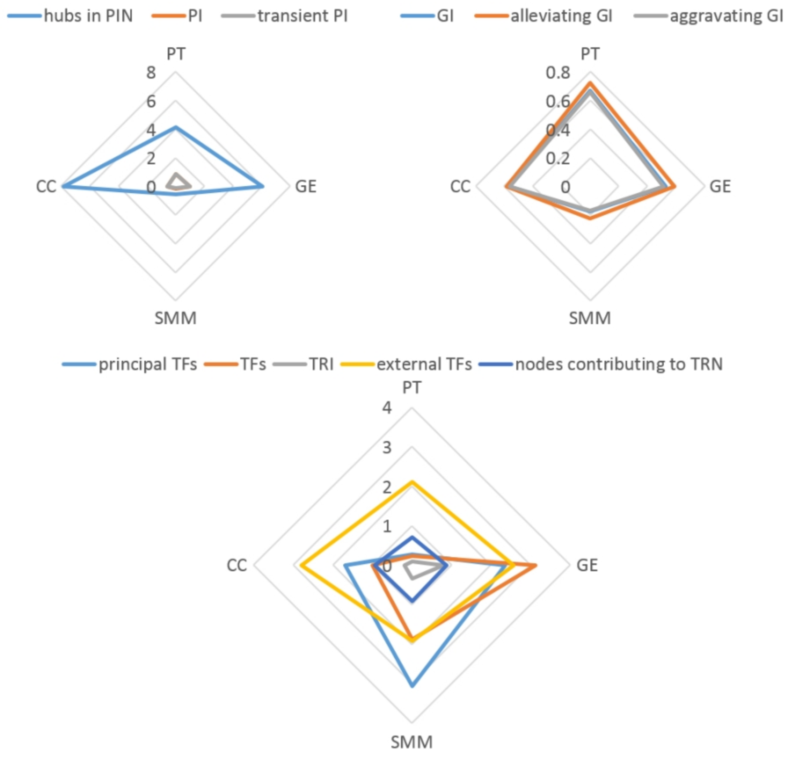

Figure 2. Relative differences in topological parameters about functionally defined subsystems. Radar plots were employed to highlight the relative differences between PT, GE, SMM, and CC. The size of each subnetwork is normalized against that of the global network and the topological properties displayed in the Figure represent the ratio of the numerical value for that property to that of the global network.

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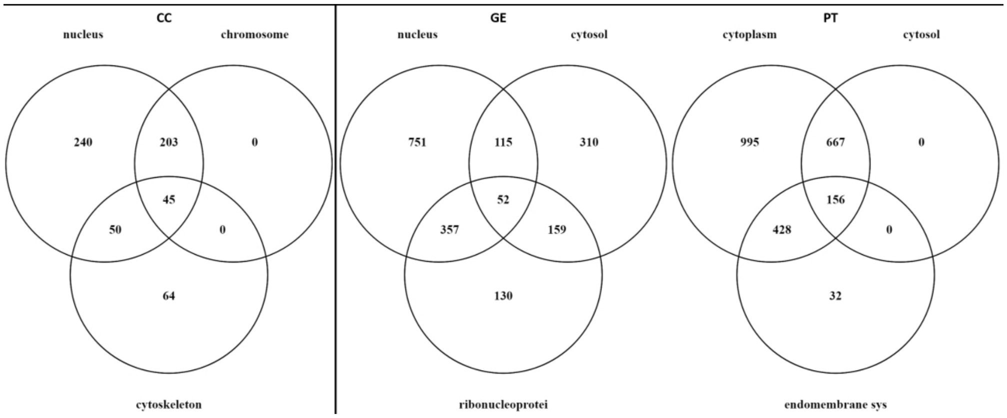

Figure 3. Principal subcellular locations for the genes in the subnetworks of the PT-GE-CC class. The main subcellular components were identified by the Gene Ontology Component and only components populated by at least 30% of the nodes constituting a subsystem are displayed. NB: Cytoplasm, as defined by the Gene Ontology, is comprised of all of the contents of a cell excluding the plasma membrane and nucleus, but including other subcellular structures. Cytosol, on the other hand, defines the part of the cytoplasm that does not contain organelles, but which does contain other particulate matter, such as protein complexes.

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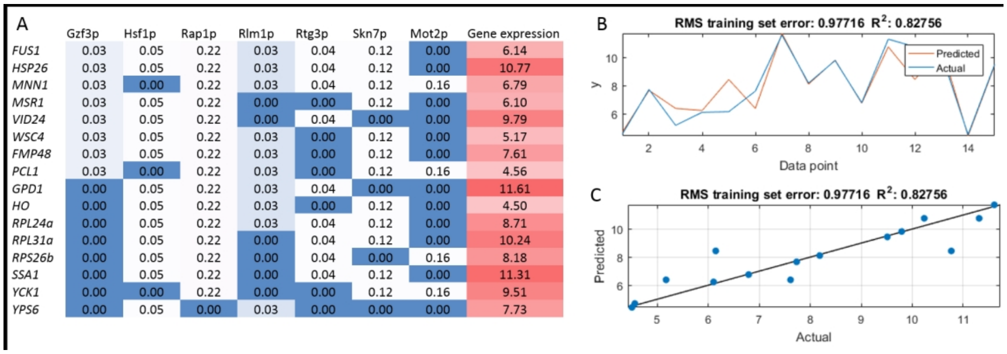
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	Gzf3p	Hsf1p	Rap1p	Rlm1p	Rtg3p	Skn7p	Mot2p	Gene expression
FUS1	0.03	0.05	0.22	0.03	0.04	0.12	0.00	6.14
HSP26	0.03	0.05	0.22	0.03	0.04	0.12	0.00	10.77
MNN1	0.03	0.00	0.22	0.03	0.04	0.12	0.16	6.79
MSR1	0.03	0.05	0.22	0.00	0.00	0.12	0.00	6.10
VID24	0.03	0.05	0.22	0.00	0.04	0.00	0.00	9.79
WSC4	0.03	0.05	0.22	0.03	0.00	0.12	0.00	5.17
FMP48	0.03	0.05	0.22	0.03	0.00	0.12	0.00	7.61
PCL1	0.03	0.00	0.22	0.03	0.00	0.12	0.16	4.56
GPD1	0.00	0.05	0.22	0.03	0.04	0.00	0.00	11.61
HO	0.00	0.05	0.22	0.03	0.00	0.12	0.00	4.50
RPL24a	0.00	0.05	0.22	0.03	0.04	0.12	0.00	8.71
RPL31a	0.00	0.05	0.22	0.00	0.04	0.12	0.00	10.24
RPS26b	0.00	0.05	0.22	0.00	0.04	0.00	0.16	8.18
SSA1	0.00	0.05	0.22	0.00	0.04	0.12	0.00	11.31
YCK1	0.00	0.00	0.22	0.00	0.00	0.12	0.16	9.51
YPS6	0.00	0.05	0.00	0.03	0.00	0.00	0.00	7.73

Figure 4. Transcription factor abundance as a proxy for target gene mRNA expression. (A) Nuclear abundance patterns of the transcription factors from PT quantified in the proteomics study. The mRNA levels for their target genes were adopted from a study conducted under similar conditions (Rodriguez-Lombardero *et al*. 2014b). The TF profile for each target gene is provided in separate rows, and each TF's contribution to the expression of these 16 genes is provided in separate columns. The colour coding denotes the strength of the contribution in terms of relative protein abundance (shades of blue) or the gene expression level (shades of red). The lighter blue colour denotes more prominent contribution by that TF to the gene expression level, with dark blue indication no contribution. The darker red colour indicates higher gene expression. (B) and (C) The goodness of fit measures for the non-linear model predicting target gene mRNA expression levels utilizing transcription factor protein abundance. The abscissa denotes different genes, for which a model was constructed, and the ordinate displays the unitless gene expression values in (B). Both the abscissa and the ordinate denote the unitless gene expression values in the plot shown in (C), which displays the variation between the model predictions from the actual expression values.

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FIGURE LEGENDS

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Table 1. A network-based comparison of the protein metabolism and processing *gene set* against 1000 randomly generated gene sets of the same size

Fraction of the feature calculated as a ratio of that in the subset to that in the global set	$\frac{PT}{global}$	$\frac{random}{global}$ *(average ± standard deviation)*	*PT different from random Y/N [p-value]*
node size of network used in analysis	0.38	0.38 ± 0.00	N [1.00]
signaling-associated genes	0.65	0.39 ± 0.02	Y [< 0.01]
essential genes	0.47	0.35± 0.01	Y [< 0.01]
hubs in PIN	1.57	0.37±0.12	Y [N/A][a]
hubs in GIN	2.39	0.46±0.04	Y [N/A][a]
TFs	0.09	0.37± 0.04	Y [< 0.01]
principal TFs by outdegree	0.11	0.73± 0.08	Y [< 0.01]
interactions in TRN	0.03	0.14 ± 0.02	Y [< 0.01]
interactions in PIN	0.33	0.15± 0.01	Y [< 0.01]
interactions in permanent protein complexes	0.64	0.16± 0.04	Y [< 0.01]
interactions in transient protein complexes	0.33	0.15± 0.01	Y [< 0.01]
interactions in GIN	0.25	0.15± 0.01	Y [< 0.01]
alleviating genetic interactions	0.28	0.15± 0.01	Y [< 0.01]
aggravating genetic interactions	0.25	0.17± 0.00	Y [< 0.01]

[a] N/A: not applicable

Table 2. Distinct network properties of PT, GE, and CC that cannot be explained by a size effect[a,b]

	$\frac{PT}{global}$	$\frac{GE}{global}$	$\frac{CCN}{global}$
fraction of genes contributing to TRN	0.27	0.28	0.11
fraction of principal transcription factors by out-degree	0.11	0.75	0.20
fraction of TFs	0.09	1.00	0.12
fraction of interactions in TRN	0.03	0.26	0.02
fraction of genes that are not a target for any TF	0.45	0.48	0.02
signaling	0.65	0.21	0.31
fraction of interactions in PIN	0.33	0.31	0.07
fraction of interactions in permanent protein complexes	0.64	0.47	0.00
fraction of interactions in transient protein complexes	0.33	0.31	0.07
fraction of signaling-associated genes	0.65	0.21	0.31

[a] Red and blue denote the underrepresentation and overrepresentation of the property relative to that of the global system, respectively.

[b] Network features were normalized relative to node size to facilitate comparison.

Table 3. Transcription factors involved in the regulation of the expression of the protein metabolism and processing gene set

TF[a]	*Systematic name*	*Mode of Action*	*Number of Phosphorylation Sites from SGD*	*Number of Phosphorylation Sites from (Vlastaridis et al. 2017)*	*Cognate Kinase(s)*	*Inducing Stressor(s)*
Gis1p	*YDR096w*	Activator Repressor	7	12		Starvation Hypoxia
Gzf3p	*YJL110c*	Repressor	8	4	Kdx1p, Snf1p, Tor1p	
Hac1p	*YFL031c*	Activator	4	0[c]		Unfolded proteins ER Stress
Hap1p	*YLR256w*	Activator	8	5	Yak1p	Heat shock Diauxie
Hsf1p	*YGL073w*	Activator	7	9	Snf1p, Tra1p	DNA damage
Mac1p	*YMR021c*	Activator	2	1		Oxidative stress DNA damage
Mot2p	*YER068w*	?[b]	1	8		

Rap1p	*YNL216w*	Activator Repressor	8	5	Tra1p	Hypoxia Starvation
Rph1p	*YER169w*		7	15		Starvation DNA damage
Skn7p	*YHR206w*	Activator	4	0		Oxidative stress Osmotic stress
Xbp1p	*YIL101c*	Activator	3	3		Starvation DNA replication stress
Yap1p	*YML007w*	Activator	4	14		Oxidative stress Starvation DNA replication stress

[a] Rlm1p, Rpn4p, Rtg3p, and Smp1p were identified as PT TFs in our analyses, but found to represent mis-annotations. They were either annotated by computational inference (IMP-type annotation), incorrectly mapped, or their function was not correctly described. For example, Rpn4p has a role in regulating the transcription of the proteasome, but is not involved in the positive regulation of proteasomal ubiquitin-dependent protein catabolic process, as previously

annotated. These annotation errors were reported to the Saccharomyces Genome Database and have now been corrected.

[b] Mot2p/Not4p/Sig1p is most likely to regulate transcription via its activity as a ubiquitin-protein ligase as part of the CCR4-NOT complex. However, a binding site has been defined for it (Badis *et al.* 2008; de Boer and Hughes 2012) and may bind to single-stranded DNA and act as a transcriptional activator –T.D. Hughes, personal communication).

[c] The expression of *HAC1* is post-transcriptionally regulated by the induction, by ER stress, of the splicing of an intron from its pre-mRNA (Kawahara *et al.* 1997).

Table S1. Summary of the topological analysis of the networks[a]

Feature	*global*	*PT*	*random*[b]	*PT-C*	*GE*	*SMM*	*CC*
system size (nodes)	6647	2533	2533	3914	2128	835	786
signalling-associated genes	368	241	133	127	76	27	113
essential genes	1295	610	481	655	620	129	249
genes contributing to aggravating GI	5770	2146	2204	3467	1694	777	778
genes contributing to alleviating GI	5715	2101	2051	3187	1651	643	746
interactions in GIN	468792	119421	72931	127841	78941	10402	31386
GIN diameter	6	6	5	5	5	5	4
alleviating interactions in GIN	84522	23334	13697	21614	15870	2360	5812
aggravating interactions in GIN	384270	96087	59234	106227	63071	8041	25573
Interaction ratio (alleviating : aggravating)	0.22	0.24	0.23	0.20	0.25	0.29	0.23
hubs in GIN	101	241	42	14	181	37	261
hubs in aggravating GIN	153	230	26	11	190	23	218
aggravating GIN : GIN hub ratio	1.51	0.95	0.62	0.79	1.05	0.62	0.84
hubs in alleviating GIN	1	2	1	0	0	1	4

alleviating GIN : GIN hub ratio	0.01	0.01	0.02	0	0.00	0.03	0.02
interactions in PIN	98944	32611	16840	21848	30664	1801	7180
interactions in permanent protein complexes	1424	906	221	449	663	165	0
interactions in transient protein complexes	97520	31705	16619	21399	30001	1636	7180
% interactions in permanent protein complexes	1.44%	2.78%	1.31%	2.06%	2.16%	9.16%	0.00%
PIN diameter	6	6	7	8	5	11	7
hubs in PIN	14	22	7	2	27	1	13
genes contributing to TRN	6647	1871	2334	3666	1930	785	755
transcription factors	179	16	66	135	179	42	21
interactions in TRN	135091	4596	22020	70903	34688	5755	2984
undirected TRN diameter	6	4	5	6	6	5	4
principal transcription factors by out-degree	65	7	30	62	49	25	13
not a target for any transcription factor	435	197	173	273	208	25	7
% non-transcription factor target genes	6.75%	7.78%	6.83%	6.97%	9.77%	2.99%	0.89%

[a] Network features were normalized relative to node size to facilitate comparison.

[b] Results are presented from the analysis of a randomly selected random network selected at random among the population of 1000 random networks.

Table S2. Essentiality and human functional complementarity of the network hubs[a]

		fraction of hubs whose null mutants have impaired viability (%)	*fraction of hubs that can complement human gene function (%)*
PIN hubs	global	21.43	14.29
	PT	45.45	27.27
	random[b]	14.29	28.57
	PT-C	0.00	0.00
	GE	48.15	14.81
	SMM	0.00	100.00
	CC	61.54	38.46
GIN hubs	global	51.49	22.77
	PT	46.47	22.82
	random[b]	64.29	33.33
	PT-C	35.71	14.29
	GE	34.81	14.92
	SMM	8.11	24.32
	CC	49.43	13.41
aggravating GIN hubs	global	45.75	22.88
	PT	48.26	23.48
	random[b]	65.38	42.31
	PT-C	27.27	18.18
	GE	35.79	14.74
	SMM	8.70	21.74

	CC	50.92	12.39
alleviating GIN hubs	global	100.00	0.00
	PT	100.00	0.00
	random[b]	100.00	0.00
	PT-C	N/A	N/A
	GE	N/A	N/A
	SMM	0.00	0.00
	CC	100.00	50.00
TRN principal TFs	global	15.38	1.54
	PT	42.86	14.29
	random[b]	13.33	0.00
	PT-C	15.38	0.00
	GE	20.41	2.04
	SMM	20.00	0.00
	CC	7.69	0.00

[a] Network features were normalized relative to node size to facilitate comparison.

[b] Results are presented from the analysis of a randomly selected random network selected at random among the population of 1000 random networks.

SUPPLEMENTARY INFORMATION

Supplementary Data 1. This document includes the node information, the genetic interaction network (GIN), physical interaction network (PIN), transcriptional regulatory network (TRN), and the permanent protein complexes for the global network, PT, the random network, the PT-C, GE, CCN, and SMM. The file also includes miscellaneous data on signaling-associated proteins, gene essentiality, human functional homology, haplosufficiency, and permanent protein complex information (format: .xlsx).

Supplementary Data 2. This document details out the experimental protocols employed in the proteomics analysis. (format: .docx).

Supplementary Data 3. This document includes the relative abundance (provided as emPAI scores) of the proteins identified in the mass spectrometric analysis of the chromatin enriched and nuclear enriched subcellular fractions along with the details on the statistical and model-based analyses of the datasets in the subsequent worksheets (format: .xlsx).

Supplementary Table 1. Summary of the topological analysis of the networks re-constructed in this study for of the systems under investigation; the global network, PT, the random network, PT-C, GE, CCN, and SMM (format: .docx).

Supplementary Table 2. Summary of the analysis of the hubs in the genetic (alleviating and aggravating genetic interaction networks also investigated separately) and physical interaction networks as well as the principal TFs in the transcriptional regulatory network of the systems under investigation; the global network, PT, the random network, PT-C, GE, CCN, and SMM. The fraction of the hubs whose null mutants are reported to have impaired viability, and those that can complement human gene functionality are provided in the Table.

Proteomics analysis detailed protocol

Cell culture and pre-treatment for sub-cellular fractionation:

The S. cerevisiae strain used in this study was BY4741 harbouring GFP-tagged Hsp82p (*MAT***a** *HSP82-GFP::HIS3 his3Δ1 leu2Δ0 met15Δ0 ura3Δ0*) (28). Two separate cultures were grown at 30°C in SD-His media with shaking to an OD600 of 0.6. In total, 120 OD units (200 mL cells) were used for a nuclear preparation and 240 OD units (400 mL cells) were used for a chromatin preparation.

Pre-treatment of cells prior to lysis was based on (29). The cells were incubated at 5 OD units per mL of 25 mM Tris-HCl, pH 7.5, 10 mM TCEP for 10 minutes at room temperature. Cells were harvested, resuspended in spheroplasting medium A (SD-His supplemented with 25 mM Tris-HCl, pH 7.5 and 1.2 M sorbitol) at 20 OD units per mL and treated for 10 minutes at 30°C with 1 µg zymolyase 100-T (Nacalai Tesque) per OD unit of yeast. Spheroplasts were harvested, washed once in spheroplasting medium B (SD-His supplemented with 1.2 M sorbitol) at 5 OD units per mL and pelleted.

Nuclear preparation:

The nuclear preparation was carried out according to (30), with modifications. The spheroplast pellet was resuspended in 6 mL of lysis buffer (18% (w/v) Ficoll PM 400 (Sigma Aldrich), 20 mM K_2HPO_4, pH 6.8, 1 mM $MgCl_2$, 0.5 mM EDTA, pH 8.0, complete protease inhibitor (Roche)) and lysed by 20 up-down strokes with the tight pestle of a 7 mL Dounce homogeniser (Wheaton). The sample was centrifuged at 3,220 × g for 10 minutes at 4°C. The supernatant was subsequently ultracentrifuged, using a Type 70 Ti rotor, in an Optima LE-80K ultracentrifuge (Beckman Coulter) at 26,000 RPM, 4°C. Ultracentrifugation was carried out for

35 minutes using fast acceleration and deceleration settings and yielded a supernatant (S_{50}) and a nuclear pellet (P_{50}). The pellet was resuspended in buffer NP (340 mM sucrose, 20 mM Tris-HCl, pH 7.4, 50 mM KCl, 5 mM $MgCl_2$, complete protease inhibitor tablet (Roche)).

Chromatin preparation:

The chromatin preparation was carried out according to (31), but in the absence of thiodiglycol. Briefly, spheroplasts were lysed at 130 OD units per mL of lysis buffer (5 mM Tris-HCl, pH 7.4, 20 mM KCl, 2 mM EDTA, 120 nM spermidine, 50 nM spermine, 400 mM sorbitol, 1% (v/v) Triton X-100, complete protease inhibitor tablet (Roche)) for 10 minutes on ice. The sample was centrifuged for 10 minutes at 16,000 × g, 4°C, yielding a supernatant (S_{16}) and chromatin pellet (P_{16}). The pellet was treated with 500 U benzonase nuclease (Merck Millipore) for 30 minutes on ice and resolubilised in 30 mM Tris-HCl, pH 6.8, 2% (w/v) SDS.

Sample preparation for mass spectrometry:

Samples were prepared for mass spectrometry using in-gel digestion. Protein concentrations were estimated using a BCA assay (Pierce) for the S_{50} and P_{50} samples, and a Detergent Compatible assay (Bio-Rad) for the S_{16} and P_{16} samples. Aliquots representing 75 µg total protein per sample were resolved on 4-15% linear gradient polyacrylamide gels (Bio-Rad), which were stained with colloidal Coomassie brilliant blue. Gel lanes were excised, cut into equally sized bands (16 for the nuclear preparation samples and 8 for the chromatin preparation samples) and each band was further cut into 1 mm cubes. The gel cubes were destained to completion using 50 mM ammonium bicarbonate in 50% (v/v) acetonitrile. Samples were reduced with 10 mM dithiothreitol at 56°C for 1 hour and subsequently alkylated with 5 mM iodoacetamide for 45 minutes at room temperature in the dark. Gel cubes were dehydrated in acetonitrile and dried. Sequencing grade modified trypsin (Promega) in 50 mM ammonium bicarbonate, was added to each gel band (1:50 (w/w) protease:protein) and digestion was allowed to proceed at 37°C for 16 hours.

Mass spectrometric analysis of samples:

In all cases, approximately 1 µg of sample was injected on-column per mass spectrometry run. The tryptic digests from bands corresponding to S_{50} and P_{50} were analysed using a Dionex Ultimate 3000 RSLCnano UPLC (Thermo Fisher Scientific) system coupled in-line to a Q Exactive Hybrid Quadrupole-Orbitrap mass spectrometer (Thermo Fisher Scientific). The mass spectrometry method used was the same as described in (Mata *et al.* 2017), but with the modification that fragmentation, using higher energy collisional dissociation (HCD – NCE: 25%), was carried out on the twenty most intense ions per survey scan with charge state of 2+ and above.

The tryptic digests from bands corresponding to S_{16} and P_{16} were analysed using a nanoAcquity UPLC system (Waters) coupled in-line to an LTQ Orbitrap Velos Hybrid Ion Trap mass spectrometer (Thermo Fisher Scientific). The mass spectrometry method used was the same as described in (Chen *et al.* 2015), but the Orbitrap was operated at a resolution of 30,000 and fragmentation, using collision-induced dissociation (CID – NCE: 30%), was carried out on the twenty most intense ions per survey scan with charge state of 2+ and above.

Mass spectrometry data processing:

Mass spectrometry raw data files were converted to Mascot Generic Format (MGF) using MSConvert (version 3.0.9283, Proteowizard). MGF files were searched using an in-house

Mascot server (version 2.6.0, Matrix Science) against a canonical Saccharomyces cerevisiae database, downloaded from UniProt (March 2017; 6,749 sequences). Samples corresponding to each original gel lane were merged for searching, yielding a "master" results file of mass spectrometry runs for a given sample. Precursor ion tolerance was set to ±25 ppm for all experiments. For LTQ Orbitrap Velos experiments the fragment ion tolerance was set to ±0.6 Da and for Q Exactive experiments it was set to ±0.1 Da. In all cases carbamidomethylation of cysteine was included as a fixed modification and oxidation of methionine was included as a variable modification. A 1% FDR threshold for protein identifications was imposed using a target-decoy approach, based on a search of a decoy database of reversed protein entries. Relative protein quantification was inferred using the built-in emPAI score (32) feature of Mascot (Supplementary Material 2).

References

Chen, C., E. Buhl, M. Xu, V. Croset, J. S. Rees *et al.*, 2015 Drosophila Ionotropic Receptor 25a mediates circadian clock resetting by temperature. Nature 527: 516–520.

Mata, C. I., B. Fabre, M. L. A. T. M. Hertog, H. T. Parsons, M. J. Deery *et al.*, 2017 In-depth characterization of the tomato fruit pericarp proteome. Proteomics 17: 1600406.

Filtered Pellet

protein access ID	protein description	emPAI	relative abundance
P19097	Fatty acid synthase subunit	1.88	0.46
P32324	Elongation factor 2 OS=Sacc	7.88	0.95
P00560	Phosphoglycerate kinase OS	28.68	1.47
P07149	Fatty acid synthase subunit	1.07	0.32
P00925	Enolase 2 OS=Saccharomyce	29.98	1.49
P00549	Pyruvate kinase 1 OS=Sacch	16.29	1.24
P15108	ATP-dependent molecular c	4.84	0.77
P02829	ATP-dependent molecular c	4.44	0.74
P10592	Heat shock protein SSA2 OS	8.52	0.98
P16521	Elongation factor 3A OS=Sa	3.90	0.69
P11484	Ribosome-associated molec	6.89	0.90
P10591	Heat shock protein SSA1 OS	8.45	0.98
P40150	Ribosome-associated molec	6.89	0.90
P00924	Enolase 1 OS=Saccharomyce	14.38	1.19
P17255	V-type proton ATPase cataly	3.56	0.66
P05030	Plasma membrane ATPase 1	3.16	0.62
P02994	Elongation factor 1-alpha O	17.50	1.27
P00359	Glyceraldehyde-3-phosphat	67.23	1.83
Q00955	Acetyl-CoA carboxylase OS=	0.77	0.25
P05694	5-methyltetrahydropteroylt	2.98	0.60
P09624	Dihydrolipoyl dehydrogenas	9.60	1.03
P07259	Protein URA2 OS=Saccharo	0.65	0.22
P06169	Pyruvate decarboxylase isoz	5.34	0.80
P32589	Heat shock protein homolog	4.23	0.72
P00358	Glyceraldehyde-3-phosphat	29.59	1.49
P10081	ATP-dependent RNA helicas	8.20	0.96
P00330	Alcohol dehydrogenase 1 O	10.15	1.05
P09436	Isoleucine--tRNA ligase, cyt	1.08	0.32
P37291	Serine hydroxymethyltransf	6.30	0.86
P38720	6-phosphogluconate dehyd	5.34	0.80
P14540	Fructose-bisphosphate aldo	6.54	0.88
Q12460	Nucleolar protein 56 OS=Sa	3.47	0.65
P04807	Hexokinase-2 OS=Saccharo	3.06	0.61
P15019	Transaldolase OS=Saccharo	11.85	1.11
P0C2I9	Transposon Ty1-PR1 Gag-Po	0.65	0.22
P14126	60S ribosomal protein L3 O	7.69	0.94
P06634	ATP-dependent RNA helicas	2.42	0.53
P04840	Mitochondrial outer membr	9.19	1.01
P29453	60S ribosomal protein L8-B	23.07	1.38
P00360	Glyceraldehyde-3-phosphat	8.43	0.97
P16861	ATP-dependent 6-phosphof	1.30	0.36
P04147	Polyadenylate-binding prote	2.25	0.51
P21576	Vacuolar protein sorting-ass	2.15	0.50
P26637	Leucine--tRNA ligase, cytopl	0.84	0.26
P54115	Magnesium-activated aldeh	3.35	0.64
P23248	40S ribosomal protein S1-B	18.00	1.28
P60010	Actin OS=Saccharomyces ce	11.07	1.08
P39954	Adenosylhomocysteinase O	4.57	0.75
P06168	Ketol-acid reductoisomeras	2.99	0.60
P0CS90	Heat shock protein SSC1, mi	1.74	0.44

P07262	NADP-specific glutamate de	3.17	0.62
P17076	60S ribosomal protein L8-A	16.22	1.24
P16140	V-type proton ATPase subu	2.43	0.54
P33442	40S ribosomal protein S1-A	15.31	1.21
P31539	Heat shock protein 104 OS=	1.10	0.32
P0CX35	40S ribosomal protein S4-A	16.99	1.26
P04802	Aspartate--tRNA ligase, cyt	2.30	0.52
P04050	DNA-directed RNA polymer	0.56	0.19
P07267	Saccharopepsin OS=Sacchar	2.57	0.55
P48570	Homocitrate synthase, cyto	3.04	0.61
P26783	40S ribosomal protein S5 O	15.75	1.22
P19882	Heat shock protein 60, mito	1.54	0.40
Q12122	Homocitrate synthase, mito	2.87	0.59
P00927	Threonine dehydratase, mit	1.82	0.45
Q12213	60S ribosomal protein L7-B	11.95	1.11
Q12499	Nucleolar protein 58 OS=Sa	1.72	0.43
P0CX37	40S ribosomal protein S6-A	7.09	0.91
P40825	Alanine--tRNA ligase, mitoc	0.83	0.26
P32473	Pyruvate dehydrogenase E1	2.67	0.56
P05737	60S ribosomal protein L7-A	11.95	1.11
P00830	ATP synthase subunit beta,	2.36	0.53
P12709	Glucose-6-phosphate isome	2.46	0.54
P19414	Aconitate hydratase, mitoc	1.17	0.34
P46655	Glutamate--tRNA ligase, cyt	1.27	0.36
P32599	Fimbrin OS=Saccharomyces	1.36	0.37
P05750	40S ribosomal protein S3 O	7.44	0.93
P00950	Phosphoglycerate mutase 1	8.20	0.96
P23254	Transketolase 1 OS=Sacchar	1.80	0.45
P00942	Triosephosphate isomerase	7.23	0.92
P38631	1,3-beta-glucan synthase co	0.39	0.14
P09440	C-1-tetrahydrofolate syntha	1.04	0.31
P38011	Guanine nucleotide-binding	4.10	0.71
O13516	40S ribosomal protein S9-A	14.31	1.18
P04801	Threonine--tRNA ligase, cyt	1.19	0.34
P32563	V-type proton ATPase subu	0.91	0.28
P0CX82	60S ribosomal protein L19-	12.57	1.13
P38934	Nuclear segregation protein	2.09	0.49
P16862	ATP-dependent 6-phosphof	0.80	0.26
P53252	Sphingolipid long chain base	2.90	0.59
P05755	40S ribosomal protein S9-B	14.52	1.19
P33892	eIF-2-alpha kinase activator	0.23	0.09
P06105	Protein SCP160 OS=Sacchar	0.53	0.18
P10964	DNA-directed RNA polymer	0.46	0.16
P10664	60S ribosomal protein L4-A	3.28	0.63
P18239	ADP,ATP carrier protein 2 O	5.77	0.83
P11076	ADP-ribosylation factor 1 O	11.40	1.09
P16387	Pyruvate dehydrogenase E1	3.58	0.66
P05317	60S acidic ribosomal protei	4.37	0.73
P38249	Eukaryotic translation initia	0.75	0.24
P04806	Hexokinase-1 OS=Saccharo	1.63	0.42
P38088	Glycine--tRNA ligase 1, mito	0.83	0.26
P23641	Mitochondrial phosphate ca	3.20	0.62

P32468	Cell division control protein	2.38	0.53
P19146	ADP-ribosylation factor 2 O	11.08	1.08
P02309	Histone H4 OS=Saccharomy	59.38	1.78
P00815	Histidine biosynthesis trifun	0.71	0.23
P33302	Pleiotropic ABC efflux trans	0.36	0.13
P36008	Elongation factor 1-gamma	1.76	0.44
P07806-2	Isoform Cytoplasmic of Vali	0.54	0.19
P32582	Cystathionine beta-synthas	0.97	0.29
P22137	Clathrin heavy chain OS=Sa	0.36	0.13
P20447	ATP-dependent RNA helicas	1.63	0.42
P34760	Peroxiredoxin TSA1 OS=Sac	4.69	0.76
P10659	S-adenosylmethionine synt	1.76	0.44
Q03690	Clustered mitochondria pro	0.43	0.16
P25694	Cell division control protein	0.68	0.23
P0CX55	40S ribosomal protein S18-	19.40	1.31
P06367	40S ribosomal protein S14-	23.84	1.40
P16474	78 kDa glucose-regulated pr	0.78	0.25
P19358	S-adenosylmethionine synt	1.73	0.44
P41807	V-type proton ATPase subu	1.38	0.38
P31116	Homoserine dehydrogenase	2.42	0.53
P07245	C-1-tetrahydrofolate syntha	0.67	0.22
P07251	ATP synthase subunit alpha,	1.07	0.32
P0C0W1	40S ribosomal protein S22-	23.25	1.38
P32558	FACT complex subunit SPT1	0.43	0.16
P29311	Protein BMH1 OS=Saccharo	5.54	0.82
P38788	Ribosome-associated compl	1.26	0.35
P48164	40S ribosomal protein S7-B	7.79	0.94
P17709	Glucokinase-1 OS=Saccharo	0.98	0.30
P53221	60S ribosomal protein L26-	25.74	1.43
Q07551	NADPH-dependent alpha-ke	2.30	0.52
P38013	Peroxiredoxin type-2 OS=Sa	5.99	0.84
P38219	Obg-like ATPase 1 OS=Sacch	1.61	0.42
P53978	Elongation factor 3B OS=Sa	0.57	0.20
P0CX45	60S ribosomal protein L2-A	2.96	0.60
P0CX84	60S ribosomal protein L35-	13.43	1.16
P06786	DNA topoisomerase 2 OS=S	0.30	0.11
P26786	40S ribosomal protein S7-A	9.92	1.04
P32327	Pyruvate carboxylase 2 OS=	0.29	0.11
P41805	60S ribosomal protein L10	6.62	0.88
P07284	Serine--tRNA ligase, cytopla	1.21	0.34
Q12230	Sphingolipid long chain base	2.47	0.54
P32368	Phosphoinositide phosphat	0.70	0.23
P03965	Carbamoyl-phosphate synt	0.47	0.17
P15180	Lysine--tRNA ligase, cytopla	1.30	0.36
O14455	60S ribosomal protein L36-	42.05	1.63
P05740	60S ribosomal protein L17-	3.96	0.70
P0CX53	60S ribosomal protein L12-	5.28	0.80
P38972	Phosphoribosylformylglycin	0.33	0.12
P38701	40S ribosomal protein S20	19.63	1.31
P46990	60S ribosomal protein L17-	3.96	0.70
P32466	Low-affinity glucose transp	1.28	0.36
Q3E757	60S ribosomal protein L11-	7.50	0.93

P0CX23	60S ribosomal protein L20-A	6.93	0.90
P32497	Eukaryotic translation initiat	0.43	0.16
P0CX49	60S ribosomal protein L18-A	5.18	0.79
P0CX41	60S ribosomal protein L23-A	46.22	1.67
P46367	Potassium-activated aldehy	0.79	0.25
P14832	Peptidyl-prolyl cis-trans isor	5.50	0.81
P38707	Asparagine--tRNA ligase, cyt	0.58	0.20
P15646	rRNA 2~-O-methyltransferas	2.92	0.59
P0CX51	40S ribosomal protein S16-A	9.57	1.02
P34730	Protein BMH2 OS=Saccharo	3.57	0.66
P05743	60S ribosomal protein L26-A	18.25	1.28
P05745	60S ribosomal protein L36-A	27.34	1.45
P48589	40S ribosomal protein S12 C	7.35	0.92
P05756	40S ribosomal protein S13 C	5.90	0.84
P49090	Asparagine synthetase [glut	1.23	0.35
P07283	Phosphomannomutase OS=	3.29	0.63
P15703	Glucan 1,3-beta-glucosidase	1.63	0.42
P22146	1,3-beta-glucanosyltransfera	0.73	0.24
P40024	ABC transporter ATP-binding	0.74	0.24
P39004	High-affinity hexose transpo	0.97	0.29
P50095	Inosine-5~-monophosphate	0.79	0.25
Q02486	ARS-binding factor 2, mitoch	10.05	1.04
P39076	T-complex protein 1 subunit	0.64	0.21
P23542	Aspartate aminotransferase	1.05	0.31
P05738	60S ribosomal protein L9-A	6.07	0.85
P54839	Hydroxymethylglutaryl-CoA	0.67	0.22
P49089	Asparagine synthetase [glut	1.08	0.32
P0CX31	40S ribosomal protein S24-A	7.47	0.93
Q05506	Arginine--tRNA ligase, cytop	0.85	0.27
P39003	High-affinity hexose transpo	0.97	0.29
P07342	Acetolactate synthase cataly	0.56	0.19
P00817	Inorganic pyrophosphatase	1.79	0.45
P11412	Glucose-6-phosphate 1-deh	0.64	0.21
P26785	60S ribosomal protein L16-B	5.74	0.83
P36105	60S ribosomal protein L14-A	14.91	1.20
P02407	40S ribosomal protein S17-A	6.87	0.90
Q05022	rRNA biogenesis protein RRP	0.22	0.09
P32481	Eukaryotic translation initiat	0.77	0.25
P35691	Translationally-controlled tu	6.40	0.87
P12385	Eukaryotic peptide chain rel	1.16	0.33
P32449	Phospho-2-dehydro-3-deoxy	1.04	0.31
P28241	Isocitrate dehydrogenase [N	1.30	0.36
P05748	60S ribosomal protein L15-A	3.68	0.67
P00931	Tryptophan synthase OS=Sa	0.54	0.19
P41277	Glycerol-1-phosphate phosp	2.24	0.51
P12695	Dihydrolipoyllysine-residue	0.73	0.24
P22138	DNA-directed RNA polymera	0.28	0.11
P0CX43	60S ribosomal protein L1-A	2.79	0.58
Q06639	Chromatin structure-remod	0.38	0.14
Q03940	RuvB-like protein 1 OS=Sacc	0.93	0.29
P39676	Flavohemoprotein OS=Sacch	1.10	0.32
Q03532	ATP-dependent RNA helicas	0.79	0.25

P10127	Alcohol dehydrogenase 4 O	0.77	0.25
P38708	Putative proline--tRNA ligas	0.44	0.16
P34167	Eukaryotic translation initiat	1.19	0.34
P38891	Branched-chain-amino-acid	0.91	0.28
P25443	40S ribosomal protein S2 O	2.32	0.52
P04456	60S ribosomal protein L25	6.99	0.90
P11986	Inositol-3-phosphate syntha	0.74	0.24
P26321	60S ribosomal protein L5 O	1.67	0.43
Q03195	Translation initiation factor	0.51	0.18
Q05911	Adenylosuccinate lyase OS=	1.00	0.30
Q12159	RNA annealing protein YRA1	2.75	0.57
P29704	Squalene synthase OS=Sacc	0.89	0.28
P80210	Adenylosuccinate synthetas	0.63	0.21
Q04013	Citrate/oxoglutarate carrier	1.63	0.42
P32905	40S ribosomal protein S0-A	1.32	0.37
P02293	Histone H2B.1 OS=Saccharo	8.98	1.00
P49723	Ribonucleoside-diphosphat	0.80	0.26
P07991	Ornithine aminotransferase	0.84	0.26
P0CX39	40S ribosomal protein S8-A	1.30	0.36
P41911	Glycerol-3-phosphate dehy	0.61	0.21
P38626	NADH-cytochrome b5 reduc	1.45	0.39
P26784	60S ribosomal protein L16-	3.41	0.64
P43609	Chromatin structure-remod	0.35	0.13
Q03558	NADPH dehydrogenase 2 O	1.09	0.32
P04911	Histone H2A.1 OS=Saccharo	4.30	0.72
P33775	Dolichyl-phosphate-mannos	0.36	0.13
P0C2H6	60S ribosomal protein L27-	5.09	0.78
P22768	Argininosuccinate synthase	0.82	0.26
P31373	Cystathionine gamma-lyase	0.95	0.29
P32465	Low-affinity glucose transp	0.81	0.26
P08518	DNA-directed RNA polymer	0.23	0.09
P38988	Mitochondrial GTP/GDP car	1.70	0.43
P32835	GTP-binding nuclear protei	2.10	0.49
P38625	GMP synthase [glutamine-h	0.76	0.25
P28834	Isocitrate dehydrogenase [	1.06	0.31
P53090	Aromatic/aminoadipate am	0.52	0.18
P40069	Importin subunit beta-4 OS	0.21	0.08
Q02326	60S ribosomal protein L6-A	2.24	0.51
P02406	60S ribosomal protein L28	4.35	0.73
P20081	FK506-binding protein 1 OS	8.84	0.99
P29547	Elongation factor 1-gamma	0.65	0.22
P07280	40S ribosomal protein S19-	4.86	0.77
P21954	Isocitrate dehydrogenase [	1.19	0.34
P30624	Long-chain-fatty-acid--CoA	0.44	0.16
P32288	Glutamine synthetase OS=S	0.96	0.29
P06780	GTP-binding protein RHO1	1.23	0.35
Q12672	60S ribosomal protein L21-	2.60	0.56
P14742	Glutamine--fructose-6-phos	0.42	0.15
P33767	Dolichyl-diphosphooligosac	0.61	0.21
Q12680	Glutamate synthase [NADH]	0.15	0.06
P41338	Acetyl-CoA acetyltransferas	0.76	0.25
Q02753	60S ribosomal protein L21-	2.60	0.56

P0C0V8	40S ribosomal protein S21-A	9.66	1.03
P41056	60S ribosomal protein L33-B	5.72	0.83
P26263	Pyruvate decarboxylase isoz	0.36	0.13
Q12690	60S ribosomal protein L13-A	1.84	0.45
P05739	60S ribosomal protein L6-B	2.24	0.51
P54838	Dihydroxyacetone kinase 1	0.46	0.16
P13188	Glutamine--tRNA ligase OS=	0.36	0.13
Q12512	Protein ZPS1 OS=Saccharom	1.76	0.44
P29509	Thioredoxin reductase 1 OS	0.73	0.24
P39015	Suppressor protein STM1 O	1.20	0.34
P05744	60S ribosomal protein L33-A	5.83	0.83
P08566	Pentafunctional AROM poly	0.15	0.06
P32454	Aminopeptidase 2, mitocho	0.30	0.11
P09457	ATP synthase subunit 5, mit	1.80	0.45
P14120	60S ribosomal protein L30	4.08	0.71
P32861	UTP--glucose-1-phosphate	0.66	0.22
P38085	Valine/tyrosine/tryptophan	0.41	0.15
P32804	Zinc-regulated transporter 1	0.76	0.25
P36010	Nucleoside diphosphate kin	2.90	0.59
P38998	Saccharopine dehydrogenas	0.77	0.25
P53551	Histone H1 OS=Saccharomy	0.97	0.29
P08524	Farnesyl pyrophosphate syn	0.59	0.20
P04449	60S ribosomal protein L24-A	2.77	0.58
P32380	Spindle pole body compone	0.24	0.09
P00958	Methionine--tRNA ligase, cy	0.32	0.12
P52910	Acetyl-coenzyme A syntheta	0.46	0.16
P27616	Phosphoribosylaminoimidaz	0.98	0.30
Q03048	Cofilin OS=Saccharomyces c	2.23	0.51
P09064	Eukaryotic translation initiat	1.10	0.32
P09734	Tubulin alpha-3 chain OS=Sa	0.60	0.20
P32527	Zuotin OS=Saccharomyces c	0.47	0.17
P07170	Adenylate kinase OS=Saccha	1.64	0.42
P07246	Alcohol dehydrogenase 3, m	0.79	0.25
P32445	Single-stranded DNA-bindin	2.36	0.53
P02992	Elongation factor Tu, mitoch	0.64	0.21
P47075	Vacuolar transporter chape	0.33	0.12
P47143	Adenosine kinase OS=Sacch	0.68	0.23
P39727	ER-derived vesicles protein	0.50	0.18
P30902	ATP synthase subunit d, mit	1.59	0.41
P00890	Citrate synthase, mitochonc	0.43	0.16
P36421	Tyrosine--tRNA ligase, cytop	0.71	0.23
P0CX25	60S ribosomal protein L43-A	5.02	0.78
P52286	Suppressor of kinetochore p	1.86	0.46
P25491	Mitochondrial protein impo	0.87	0.27
Q03973	High mobility group protein	0.99	0.30
P54837	Endoplasmic reticulum vesic	1.18	0.34
P05759	Ubiquitin-40S ribosomal prc	1.93	0.47
P09733	Tubulin alpha-1 chain OS=Sa	0.60	0.20
P16120	Threonine synthase OS=Sac	0.39	0.14
P06208	2-isopropylmalate synthase	0.41	0.15
P41940	Mannose-1-phosphate guar	0.81	0.26
P38264	SRP-independent targeting	2.78	0.58

P0C0T4	40S ribosomal protein S25-E	3.72	0.67
P15303	Protein transport protein SE	0.25	0.10
P38144	ISWI chromatin-remodeling	0.24	0.09
P53131	Pre-mRNA-splicing factor AT	0.31	0.12
P04076	Argininosuccinate lyase OS=	0.73	0.24
P38286	Very-long-chain 3-oxoacyl-C	0.63	0.21
P00445	Superoxide dismutase [Cu-Z	3.32	0.64
P47133	ER membrane protein comp	0.74	0.24
P0C2H8	60S ribosomal protein L31-A	5.01	0.78
P32568	Protein SNQ2 OS=Saccharon	0.15	0.06
P31412	V-type proton ATPase subun	0.71	0.23
P0CX47	40S ribosomal protein S11-A	2.71	0.57
P05374	Phosphatidylethanolamine I	0.26	0.10
P24783	ATP-dependent RNA helicas	0.47	0.17
P41810	Coatomer subunit beta OS=	0.19	0.08
P39007	Dolichyl-diphosphooligosacc	0.42	0.15
Q02725	Vacuolar transporter chaper	0.22	0.09
Q12692	Histone H2A.Z OS=Saccharo	2.69	0.57
P53742	Nucleolar GTP-binding prote	0.53	0.18
P07256	Cytochrome b-c1 complex s	0.33	0.12
P23301	Eukaryotic translation initiat	2.90	0.59
P37012	Phosphoglucomutase 2 OS=	0.35	0.13
P33330	Phosphoserine aminotransfe	0.55	0.19
Q07478	ATP-dependent RNA helicas	0.60	0.20
P39533	Homocitrate dehydratase, n	0.31	0.12
P40961	Prohibitin-1 OS=Saccharomy	0.83	0.26
P19524	Myosin-2 OS=Saccharomyce	0.11	0.05
P37292	Serine hydroxymethyltransf	0.55	0.19
P27810	Alpha-1,2 mannosyltransfer	0.67	0.22
P0C0X0	40S ribosomal protein S28-E	19.78	1.32
P29952	Mannose-6-phosphate isom	0.48	0.17
Q00055	Glycerol-3-phosphate dehyc	0.39	0.14
P39976	D-2-hydroxyglutarate--pyru	0.29	0.11
P40302	Proteasome subunit alpha t	1.08	0.32
P36015	Synaptobrevin homolog YKT	1.80	0.45
P22336	Replication factor A protein	0.31	0.12
P50085	Prohibitin-2 OS=Saccharomy	0.73	0.24
P38009	Bifunctional purine biosynth	0.34	0.13
P40106	Glycerol-1-phosphate phosp	0.96	0.29
P14906	Protein translocation protei	0.37	0.14
P39986	Manganese-transporting AT	0.19	0.08
P02557	Tubulin beta chain OS=Sacch	0.32	0.12
P01123	GTP-binding protein YPT1 O	1.73	0.44
P15992	Heat shock protein 26 OS=S	0.81	0.26
P53731	Actin-related protein 2/3 co	0.61	0.21
P49167	60S ribosomal protein L38 C	3.83	0.68
P43603	LAS seventeen-binding prote	0.47	0.17
P07244	Bifunctional purine biosynth	0.18	0.07
P35723	Endoplasmic reticulum trans	1.23	0.35
P11745	Ran GTPase-activating prote	0.36	0.13
P25294	Protein SIS1 OS=Saccharomy	0.66	0.22
P37303	Low specificity L-threonine a	0.55	0.19

P54885	Gamma-glutamyl phosphate	0.33	0.12
P14020	Dolichol-phosphate mannos	0.86	0.27
P39077	T-complex protein 1 subunit	0.38	0.14
P53622	Coatomer subunit alpha OS=	0.15	0.06
P38911	FK506-binding nuclear prote	0.36	0.13
P05626	ATP synthase subunit 4, mit	1.01	0.30
P32915	Protein transport protein SE	0.43	0.16
P09938	Ribonucleoside-diphosphate	0.36	0.13
P0CX29	40S ribosomal protein S23-A	2.20	0.51
P53335	Protein PXR1 OS=Saccharom	0.83	0.26
P32614	Fumarate reductase 1 OS=Sa	0.45	0.16
P22515	Ubiquitin-activating enzyme	0.18	0.07
P32074	Coatomer subunit gamma C	0.20	0.08
P11632	Non-histone chromosomal p	1.37	0.37
P17967	Protein disulfide-isomerase	0.50	0.18
Q08972	[NU+] prion formation prote	0.11	0.05
P40531	Protein GVP36 OS=Saccharo	0.47	0.17
P07257	Cytochrome b-c1 complex s	0.42	0.15
P40185	Protein MMF1, mitochondri	1.41	0.38
P23585	High-affinity glucose transpo	0.27	0.10
P47154	CAAX prenyl protease 1 OS=	0.44	0.16
Q00764	Alpha,alpha-trehalose-phos	0.52	0.18
Q01560	Nucleolar protein 3 OS=Sacc	0.37	0.14
P22147	5~-3~ exoribonuclease 1 OS	0.11	0.05
P00447	Superoxide dismutase [Mn],	0.44	0.16
P32366	V-type proton ATPase subur	0.43	0.16
P39107	Mannan polymerase comple	0.36	0.13
P33322	H/ACA ribonucleoprotein cc	0.41	0.15
Q06689	Cell membrane protein YLR4	0.38	0.14
P47018	Maintenance of telomere ca	0.31	0.12
P39517	ATP-dependent RNA helicas	0.39	0.14
P35844	Oxysterol-binding protein h	0.47	0.17
Q04439	Myosin-5 OS=Saccharomyce	0.11	0.05
Q12464	RuvB-like protein 2 OS=Sacc	0.32	0.12
Q01855	40S ribosomal protein S15 C	2.23	0.51
Q12125	Golgi to ER traffic protein 4	0.68	0.23
P39744	Nucleolar complex protein 2	0.26	0.10
P53261	Pescadillo homolog OS=Sacc	0.31	0.12
P25087	Sterol 24-C-methyltransfera	0.39	0.14
P23292	Casein kinase I homolog 2 O	0.36	0.13
P38879	Nascent polypeptide-associa	1.13	0.33
P32598	Serine/threonine-protein ph	0.68	0.23
P53278	Uncharacterized protein YG	0.23	0.09
P33399	La protein homolog OS=Sacc	0.55	0.19
P36049	rRNA-processing protein EB	0.33	0.12
Q3E841	Uncharacterized protein YN	4.60	0.75
P07260	Eukaryotic translation initiat	0.79	0.25
P38077	ATP synthase subunit gamm	0.32	0.12
P38999	Saccharopine dehydrogenas	0.47	0.17
P17106	Centromere-binding protein	0.27	0.10
P13663	Aspartate-semialdehyde del	0.43	0.16
Q12404	Protein disulfide-isomerase	0.68	0.23

P25342	Cell division control protein	0.47	0.17
P28274	CTP synthase 1 OS=Saccharc	0.24	0.09
P31382	Dolichyl-phosphate-mannos	0.18	0.07
P53254	U3 small nucleolar RNA-assc	0.11	0.05
P42945	U3 small nucleolar RNA-assc	0.10	0.04
P48837	Nucleoporin NUP57 OS=Sac	0.28	0.11
Q01939	26S protease regulatory sub	0.23	0.09
Q03640	Tricalbin-3 OS=Saccharomyc	0.09	0.04
Q12377	26S proteasome regulatory	0.33	0.12
Q08745	40S ribosomal protein S10-A	1.99	0.48
P27692	Transcription elongation fac	0.13	0.05
P32419	Malate dehydrogenase, per	0.46	0.16
P22203	V-type proton ATPase subur	0.71	0.23
Q04373	Pumilio homology domain fa	0.21	0.08
Q99207	Nucleolar complex protein 1	0.22	0.09
Q12447	Polyamine N-acetyltransfera	1.34	0.37
P38353	Sec sixty-one protein homol	0.30	0.11
Q08421	Enhancer of translation tern	0.35	0.13
P39522	Dihydroxy-acid dehydratase	0.16	0.06
P16622	Ferrochelatase, mitochondr	0.53	0.18
P40525	60S ribosomal protein L34-E	1.74	0.44
P39938	40S ribosomal protein S26-A	0.97	0.29
P40037	Protein HMF1 OS=Saccharor	0.95	0.29
P00128	Cytochrome b-c1 complex s	1.60	0.41
P38061	60S ribosomal protein L32 C	2.55	0.55
Q04894	NADP-dependent alcohol de	0.42	0.15
P21965	Protein kinase MCK1 OS=Sa	0.39	0.14
P27809	Glycolipid 2-alpha-mannosy	0.44	0.16
P32495	H/ACA ribonucleoprotein cc	1.26	0.35
Q12074	Spermidine synthase OS=Sa	0.53	0.18
Q04697	Glucose-signaling factor 2 O	0.51	0.18
P33307	Importin alpha re-exporter (	0.14	0.06
P32478	Cell wall mannoprotein HSP	0.41	0.15
P14904	Vacuolar aminopeptidase 1	0.28	0.11
P47117	Actin-related protein 3 OS=S	0.33	0.12
P46982	Alpha-1,2-mannosyltransfer	0.15	0.06
P53235	Eukaryotic translation initiat	0.22	0.09
P40510	D-3-phosphoglycerate dehy	0.32	0.12
Q08208	Nucleolar protein 12 OS=Sac	0.20	0.08
Q03103	Endoplasmic oxidoreductin-	0.24	0.09
P32471	Elongation factor 1-beta OS	0.87	0.27
P33201	Ribosome assembly factor M	0.41	0.15
P40010	Nuclear GTP-binding proteir	0.18	0.07
P49166	60S ribosomal protein L37-A	2.95	0.60
P20433	DNA-directed RNA polymera	0.74	0.24
P37838	Nucleolar protein 4 OS=Sacc	0.20	0.08
P38755	Oxysterol-binding protein h	0.33	0.12
P39685	Nucleoporin POM152 OS=Sa	0.10	0.04
Q03921	Protein dopey OS=Saccharo	0.10	0.04
P39078	T-complex protein 1 subunit	0.18	0.07
P35997	40S ribosomal protein S27-A	3.49	0.65
P53927	Ribosome biogenesis protei	0.45	0.16

P40482	Protein transport protein SE	0.10	0.04
P28272	Dihydroorotate dehydrogen	0.50	0.18
P53633	Prenylated Rab acceptor 1 C	1.06	0.31
P38912	Eukaryotic translation initiat	1.23	0.35
P13298	Orotate phosphoribosyltran	0.46	0.16
P02400	60S acidic ribosomal proteir	1.33	0.37
Q06631	Protein BFR2 OS=Saccharom	0.17	0.07
P38840	Aromatic amino acid aminot	0.18	0.07
P07263	Histidine--tRNA ligase, mito	0.27	0.10
P21538	DNA-binding protein REB1 C	0.17	0.07
P53721	Respiratory supercomplex fa	0.74	0.24
O14467	Multiprotein-bridging factor	1.35	0.37
P07278	cAMP-dependent protein ki	0.35	0.13
P32381	Actin-related protein 2 OS=S	0.24	0.09
P53145	Large subunit GTPase 1 OS=	0.22	0.09
P32657	Chromo domain-containing	0.09	0.04
P00431	Cytochrome c peroxidase, m	0.42	0.15
P37302	Aminopeptidase Y OS=Sacch	0.27	0.10
P25293	Nucleosome assembly prote	0.22	0.09
P43585	Vacuolar transporter chaper	0.16	0.06
P19454	Casein kinase II subunit alph	0.43	0.16
P39730	Eukaryotic translation initiat	0.14	0.06
P38764	26S proteasome regulatory	0.09	0.04
P39985	DNA polymerase V OS=Sacc	0.13	0.05
P36112	MICOS complex subunit MIC	0.26	0.10
P39101	Protein CAJ1 OS=Saccharom	0.24	0.09
P15891	Actin-binding protein OS=Sa	0.24	0.09
P32521	Actin cytoskeleton-regulato	0.06	0.03
P39079	T-complex protein 1 subunit	0.27	0.10
P05453	Eukaryotic peptide chain rel	0.20	0.08
Q12000	Translation machinery-asso	0.27	0.10
P53040	Transcription initiation facto	0.18	0.07
P33299	26S protease regulatory sub	0.20	0.08
Q6Q547	H/ACA ribonucleoprotein co	2.93	0.59
P25605	Acetolactate synthase small	0.32	0.12
P29468	Poly(A) polymerase OS=Sacc	0.25	0.10
Q06218	ATP-dependent RNA helicas	0.23	0.09
Q03655	Probable 1,3-beta-glucanosy	0.18	0.07
Q06488	Chromatin structure-remod	0.15	0.06
P00498	ATP phosphoribosyltransfer	0.34	0.13
P27472	Glycogen [starch] synthase i	0.13	0.05
Q04491	Protein transport protein SE	0.33	0.12
Q06505	Transcription factor SPN1 O	0.23	0.09
Q06440	Coronin-like protein OS=Sac	0.14	0.06
P39729	Ribosome-interacting GTPas	0.26	0.10
P38993	Iron transport multicopper c	0.22	0.09
P53723	UPF0674 endoplasmic reticu	0.22	0.09
P40032	Prolyl 3,4-dihydroxylase TPA	0.14	0.06
P15624	Phenylalanine--tRNA ligase I	0.15	0.06
P12612	T-complex protein 1 subunit	0.17	0.07
P33416	Heat shock protein 78, mito	0.11	0.05
Q05905	Protein HRI1 OS=Saccharom	0.41	0.15

P34077	Nucleoporin NIC96 OS=Sacc	0.10	0.04
P07560	Ras-related protein SEC4 OS	0.49	0.17
P21147	Acyl-CoA desaturase 1 OS=S	0.28	0.11
P54003	Protein SUR7 OS=Saccharon	0.32	0.12
P22217	Thioredoxin-1 OS=Saccharo	1.27	0.36
Q04067	Eukaryotic translation initiat	0.36	0.13
P17883	Superkiller protein 3 OS=Sac	0.06	0.03
P36148	Glycerol-3-phosphate O-acy	0.12	0.05
Q10740	Leukotriene A-4 hydrolase h	0.13	0.05
Q12250	26S proteasome regulatory	0.20	0.08
P20435	DNA-directed RNA polymera	0.69	0.23
P30605	Myo-inositol transporter 1 (	0.16	0.06
P14164	ARS-binding factor 1 OS=Sac	0.19	0.08
P00410	Cytochrome c oxidase subu	0.39	0.14
P32476	Squalene monooxygenase C	0.19	0.08
Q05775	Eukaryotic translation initiat	0.38	0.14
P38137	Peroxisomal-coenzyme A sy	0.17	0.07
P06738	Glycogen phosphorylase OS	0.10	0.04
P32588	Nuclear and cytoplasmic po	0.20	0.08
P41921	Glutathione reductase OS=S	0.19	0.08
Q06511	Ribosomal RNA-processing p	0.40	0.15
P53337	ER-derived vesicles protein	0.31	0.12
P32352	C-8 sterol isomerase OS=Sac	0.46	0.16
P38555	GTP-binding protein YPT31/	0.47	0.17
P38250	Increased sodium tolerance	0.09	0.04
P40693	Ribosome biogenesis protei	0.29	0.11
Q12746	Plasma membrane-associate	0.31	0.12
P47079	T-complex protein 1 subunit	0.26	0.10
Q12211	tRNA pseudouridine syntha	0.16	0.06
P04786	DNA topoisomerase 1 OS=S	0.11	0.05
P00729	Carboxypeptidase Y OS=Sac	0.17	0.07
P35194	U3 small nucleolar RNA-asso	0.03	0.01
P00044	Cytochrome c iso-1 OS=Sacc	1.13	0.33
P20107	Zinc/cadmium resistance pr	0.10	0.04
P38688	Signal recognition particle s	0.14	0.06
Q04947	Reticulon-like protein 1 OS=	0.33	0.12
P34163	Sterol esterase TGL1 OS=Sa	0.16	0.06
Q12359	Ammonia transport outwar	0.36	0.13
P38715	NADPH-dependent aldose r	0.29	0.11
P38174	Methionine aminopeptidase	0.22	0.09
Q08773	ISWI chromatin-remodeling	0.08	0.03
Q06205	FK506-binding protein 4 OS	0.24	0.09
Q12117	Protein MRH1 OS=Saccharo	0.47	0.17
P28777	Chorismate synthase OS=Sa	0.26	0.10
Q08548	Lysophospholipid acyltransf	0.14	0.06
Q12118	Small glutamine-rich tetratr	0.29	0.11
Q06168	Chromatin structure-remod	0.10	0.04
P38075	Pyridoxamine 5~-phosphate	0.42	0.15
Q07623	Nucleolar protein 6 OS=Sacc	0.45	0.16
P36060	NADH-cytochrome b5 reduc	0.32	0.12
P36013	NAD-dependent malic enzy	0.14	0.06
P40485	Phosphatidylinositol 4,5-bis	0.13	0.05

Q08723	26S proteasome regulatory	0.28	0.11
P40495	Homoisocitrate dehydrogen	0.26	0.10
P22696	Peptidyl-prolyl cis-trans isor	0.62	0.21
Q12452	3-keto-steroid reductase OS	0.27	0.10
P16603	NADPH--cytochrome P450 r	0.13	0.05
P05749	60S ribosomal protein L22-	0.98	0.30
P47001	Cell wall mannoprotein CIS	0.49	0.17
Q04636	FACT complex subunit POB	0.08	0.03
P27476	Nuclear localization sequen	0.24	0.09
Q06078	U3 small nucleolar RNA-ass	0.09	0.04
P15496	Isopentenyl-diphosphate De	0.32	0.12
P38115	D-arabinose dehydrogenase	0.27	0.10
Q99316	Protein disulfide isomerase	0.33	0.12
P39940	E3 ubiquitin-protein ligase	0.11	0.05
Q12434	Rho GDP-dissociation inhibi	0.50	0.18
P25349	Flavoprotein-like protein YC	0.19	0.08
P32660	Phospholipid-transporting	0.05	0.02
P38248	Cell wall protein ECM33 OS=	0.11	0.05
P08417	Fumarate hydratase, mitoc	0.09	0.04
P53184	Nicotinamidase OS=Sacchar	0.46	0.16
Q07915	Ribosome biogenesis protei	0.48	0.17
P10622	60S acidic ribosomal protei	0.54	0.19
P11633	Non-histone chromosomal	0.50	0.18
P15705	Heat shock protein STI1 OS=	0.15	0.06
P06103	Eukaryotic translation initia	0.11	0.05
P32457	Cell division control protein	0.17	0.07
P32386	ATP-dependent bile acid pe	0.05	0.02
Q05123	Actin-like protein ARP9 OS=	0.19	0.08
Q05359	Protein ERP1 OS=Saccharom	0.46	0.16
P25340	Delta(24(24(1)))-sterol redu	0.18	0.07
P22139	DNA-directed RNA polymer	0.71	0.23
Q12306	Ubiquitin-like protein SMT3	0.50	0.18
P47190	Dolichyl-phosphate-mannos	0.12	0.05
Q07657	Seventh homolog of septin	0.16	0.06
P32787	Mitochondrial genome mai	0.36	0.13
P21827	Guanine nucleotide exchan	0.19	0.08
P40030	Ergosterol biosynthetic prot	0.31	0.12
P40029	Peptide methionine sulfoxid	0.55	0.19
P52871	Protein transport protein SE	0.62	0.21
P38858	6-phosphogluconolactonase	0.40	0.15
P20436	DNA-directed RNA polymer	0.76	0.25
P25719	Peptidyl-prolyl cis-trans isor	0.27	0.10
P20606	Small COPII coat GTPase SA	0.55	0.19
P18900	Hexaprenyl pyrophosphate	0.20	0.08
P38787	2-dehydropantoate 2-reduc	0.12	0.05
P33754	Translocation protein SEC6	0.47	0.17
P36161	Nucleoporin NUP133 OS=Sa	0.07	0.03
P36051	GPI ethanolamine phosphat	0.09	0.04
Q05933	Actin-related protein 2/3 co	0.58	0.20
P15700	Uridylate kinase OS=Sacchar	0.50	0.18
Q02969	Peroxisomal membrane pro	0.23	0.09
P28007	H/ACA ribonucleoprotein c	0.24	0.09

P32500	Nucleoporin NDC1 OS=Saccl	0.14	0.06
P32458	Cell division control protein	0.22	0.09
P0CX27	60S ribosomal protein L42-A	1.10	0.32
P33417	Intrastrand cross-link recogr	0.07	0.03
P38427	Trehalose synthase complex	0.08	0.03
P35179	Protein transport protein SS	0.67	0.22
P40897	Oligopeptide transporter 1 (	0.05	0.02
P32913	Vacuolar protein sorting-ass	0.16	0.06
P32583	Suppressor protein SRP40 O	0.12	0.05
Q02821	Importin subunit alpha OS=S	0.17	0.07
P23180	Probable oxidoreductase AI	0.09	0.04
P40474	Quinidine resistance proteir	0.17	0.07
Q02892	Nucleolar GTP-binding prote	0.14	0.06
P00401	Cytochrome c oxidase subur	0.08	0.03
P40581	Peroxiredoxin HYR1 OS=Sac	0.28	0.11
P53852	Cysteine--tRNA ligase OS=Sa	0.11	0.05
P24280	SEC14 cytosolic factor OS=S	0.31	0.12
P38689	Ribose-phosphate pyrophos	0.31	0.12
P32597	Nuclear protein STH1/NPS1	0.06	0.03
Q02642	Nascent polypeptide-associ	0.32	0.12
P15454	Guanylate kinase OS=Saccha	0.58	0.20
P40518	Actin-related protein 2/3 co	0.32	0.12
Q03161	Glucose-6-phosphate 1-epir	0.15	0.06
P37898	Alanine/arginine aminopept	0.10	0.04
P40548	HSP70 co-chaperone SNL1 C	0.29	0.11
P08536	Sulfate adenylyltransferase	0.09	0.04
P07264	3-isopropylmalate dehydrat	0.12	0.05
P43621	Coatomer subunit delta OS=	0.17	0.07
P38234	Protein RFS1 OS=Saccharom	0.23	0.09
P38152	Tricarboxylate transport prc	0.16	0.06
P25358	Elongation of fatty acids prc	0.12	0.05
Q01080	DNA-directed RNA polymera	0.11	0.05
P43639	Casein kinase II subunit beta	0.16	0.06
P35178	Ribosomal RNA-processing p	0.33	0.12
P32832	Chromatin structure-remod	0.21	0.08
P33314	Inhibitory regulator protein	0.08	0.03
P46956	Inorganic phosphate transp	0.14	0.06
Q99190	Very-long-chain enoyl-CoA r	0.29	0.11
P39683	Nicotinate phosphoribosyltr	0.10	0.04
P20967	2-oxoglutarate dehydrogena	0.09	0.04
P46992	Cell wall protein YJL171C OS	0.12	0.05
P53154	Glycerol uptake protein 1 O	0.08	0.03
P53163	54S ribosomal protein L12, r	0.26	0.10
P38781	Chromatin structure-remod	0.05	0.02
P00899	Anthranilate synthase comp	0.09	0.04
P40540	ER membrane protein comp	0.34	0.13
P32379	Proteasome subunit alpha t	0.18	0.07
P52553	Prefoldin subunit 6 OS=Sacc	0.42	0.15
P53914	RNA cytidine acetyltransfera	0.04	0.02
P40557	ER-retained PMA1-suppress	0.06	0.03
P38968	Protein transport protein SE	0.03	0.01
P61830	Histone H3 OS=Saccharomy	0.36	0.13

P36091	Mannan endo-1,6-alpha-ma	0.10	0.04
P00937	Multifunctional tryptophan	0.09	0.04
Q12363	Transcriptional modulator V	0.22	0.09
P47124	Putative glycosyltransferase	0.11	0.05
Q06408	Transaminated amino acid c	0.07	0.03
P39929	Vacuolar-sorting protein SN	0.19	0.08
Q12040	Broad-specificity phosphata	0.20	0.08
Q06685	Inositol hexakisphosphate a	0.08	0.03
P32911	Eukaryotic translation initiat	0.45	0.16
Q08023	Protein FMP25, mitochondr	0.07	0.03
P21801	Succinate dehydrogenase [u	0.16	0.06
P53981	Uncharacterized phosphata	0.19	0.08
P33331	Nuclear transport factor 2 C	0.38	0.14
P08067	Cytochrome b-c1 complex s	0.22	0.09
P39926	Protein SSO2 OS=Saccharon	0.15	0.06
P25303	DnaJ-related protein SCJ1 O	0.12	0.05
Q12233	ATP synthase subunit g, mit	0.43	0.16
Q12136	Something about silencing p	0.07	0.03
Q06344	Pre-rRNA-processing protei	0.07	0.03
P22289	Cytochrome b-c1 complex s	0.85	0.27
P32892	ATP-dependent RNA helicas	0.06	0.03
P19881	4-nitrophenylphosphatase C	0.15	0.06
P53173	ER-derived vesicles protein	0.34	0.13
P69771	Vacuolar protein-sorting-ass	0.23	0.09
P41811	Coatomer subunit beta~ OS	0.05	0.02
P41733	GPI transamidase compone	0.11	0.05
P39935	Eukaryotic initiation factor 4	0.05	0.02
O13329	DNA replication fork-blocki	0.07	0.03
P40319	Elongation of fatty acids pro	0.27	0.10
Q00684	Tyrosine-protein phosphata	0.08	0.03
P32337	Importin subunit beta-3 OS=	0.04	0.02
Q12160	Uncharacterized protein YP	0.82	0.26
Q02795	Dolichyl-diphosphooligosacc	0.16	0.06
P53322	High-affinity nicotinic acid t	0.08	0.03
P32178	Chorismate mutase OS=Sacc	0.17	0.07
P37263	UPF0743 protein YCR087C-A	0.30	0.11
Q03862	Probable metalloprotease A	0.07	0.03
Q04869	Uncharacterized protein YM	0.13	0.05
P41920	Ran-specific GTPase-activati	0.50	0.18
P00546	Cyclin-dependent kinase 1 C	0.15	0.06
P40088	Plasma membrane iron per	0.23	0.09
Q92317	Negative cofactor 2 comple	0.32	0.12
P50108	Probable alpha-1,6-mannos	0.11	0.05
P40160	Serine/threonine-protein ki	0.10	0.04
P40008	Protein FMP52, mitochondr	0.21	0.08
P42943	T-complex protein 1 subuni	0.08	0.03
Q08965	Ribosome biogenesis protei	0.04	0.02
P39006	Phosphatidylserine decarbo	0.09	0.04
Q08601	Metacaspase-1 OS=Sacchar	0.10	0.04
P36080	Ribosomal RNA-processing p	0.10	0.04
P25618	Protein CWH43 OS=Sacchar	0.04	0.02
P32331	Carrier protein YMC1, mitoc	0.15	0.06

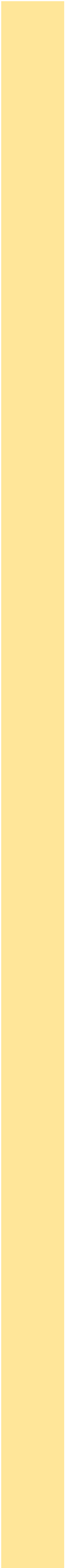
P89886	Translation machinery-asso	0.26	0.10
Q08826	Sorting nexin-3 OS=Sacchar	0.28	0.11
Q03435	Non-histone protein 10 OS=	0.22	0.09
Q12445	Nucleoporin POM34 OS=Sa	0.15	0.06
P46971	Dolichyl-phosphate-mannos	0.06	0.03
Q96VH5	MICOS complex subunit MI	0.56	0.19
P47077	Nucleolar protein 9 OS=Sac	0.06	0.03
P36016	Heat shock protein 70 hom	0.05	0.02
Q05785	Epsin-2 OS=Saccharomyces	0.07	0.03
P32333	TATA-binding protein-associ	0.02	0.01
P21524	Ribonucleoside-diphosphat	0.05	0.02
P32377	Diphosphomevalonate deca	0.11	0.05
Q04305	U3 small nucleolar RNA-ass	0.09	0.04
Q12386	Actin-like protein ARP8 OS=	0.05	0.02
P32796	Carnitine O-acetyltransferas	0.06	0.03
Q12263	Serine/threonine-protein ki	0.04	0.02
P23615	Transcription elongation fac	0.03	0.01
P07703	DNA-directed RNA polymer	0.13	0.05
Q03880	V-type ATPase assembly fac	0.40	0.15
P38902	DNA-directed RNA polymer	0.41	0.15
P53206	Putative cysteine synthase	0.12	0.05
P23638	Proteasome subunit alpha t	0.18	0.07
Q05926	Glutaredoxin-8 OS=Sacchar	0.44	0.16
P36160	Ribosome biogenesis protei	0.13	0.05
P27929	37S ribosomal protein NAM	0.09	0.04
P0CX33	40S ribosomal protein S30-	0.90	0.28
P53834	Hsp90 co-chaperone HCH1	0.31	0.12
P38624	Proteasome subunit beta ty	0.22	0.09
Q12335	Protoplast secreted protein	0.25	0.10
P38112	ATP-dependent RNA helicas	0.06	0.03
P42846	Protein KRI1 OS=Saccharom	0.07	0.03
P30656	Proteasome subunit beta ty	0.16	0.06
P36101	tRNA threonylcarbamoylad	0.10	0.04
P25582	27S pre-rRNA (guanosine(2	0.05	0.02
P09950	5-aminolevulinate synthase,	0.08	0.03
P25567	RNA-binding protein SRO9	0.10	0.04
P14843	Phospho-2-dehydro-3-deox	0.12	0.05
P47096	3-hydroxyanthranilate 3,4-d	0.26	0.10
Q08193	1,3-beta-glucanosyltransfer	0.09	0.04
Q00245	GTP-binding protein RHO3	0.20	0.08
P38295	Medium-chain fatty acid et	0.10	0.04
P48836	V-type proton ATPase subu	0.44	0.16
P40053	Altered inheritance of mito	0.07	0.03
P38798	Nonsense-mediated mRNA	0.04	0.02
P08456	CDP-diacylglycerol--serine C	0.16	0.06
Q3E756	UPF0768 protein YBL029C-	0.50	0.18
Q01662	Methionine aminopeptidas	0.11	0.05
P38165	Retrograde regulation prot	0.09	0.04
Q12168	Endo-1,3(4)-beta-glucanase	0.06	0.03
P49954	Probable hydrolase NIT3 OS	0.16	0.06
P38230	Probable quinone oxidored	0.14	0.06
P38221	Phosphatidate cytidylyltran	0.09	0.04

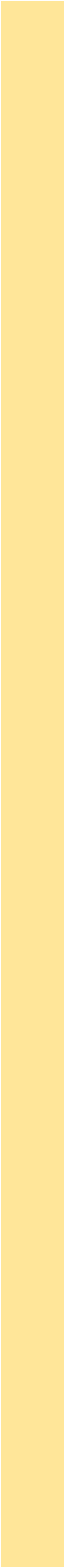
P31380	ATP-dependent helicase FUI	0.04	0.02
P38910	10 kDa heat shock protein, r	0.51	0.18
P23291	Casein kinase I homolog 1 O	0.08	0.03
P30822	Exportin-1 OS=Saccharomyc	0.04	0.02
P40075	Vesicle-associated membrar	0.19	0.08
P18759	Vesicular-fusion protein SEC	0.06	0.03
P39012	GPI transamidase componei	0.07	0.03
P53011	Nucleoporin SEH1 OS=Sacch	0.13	0.05
P48231	Tricalbin-2 OS=Saccharomyc	0.04	0.02
Q08986	S-adenosylmethionine perm	0.08	0.03
P48412	Nonsense-mediated mRNA (	0.11	0.05
Q02776	Mitochondrial import inner	0.09	0.04
P31383	Protein phosphatase PP2A r	0.07	0.03
Q12466	Tricalbin-1 OS=Saccharomyc	0.04	0.02
P32895	Ribose-phosphate pyrophos	0.10	0.04
P34241	Nucleolar pre-ribosomal-ass	0.02	0.01
P04046	Amidophosphoribosyltransf	0.09	0.04
P40002	Transcriptional regulator MI	0.07	0.03
Q08760	Bud site selection protein R/	0.10	0.04
P39990	13 kDa ribonucleoprotein-as	0.40	0.15
P17423	Homoserine kinase OS=Sacc	0.13	0.05
P36094	Spindle pole body compone	0.12	0.05
P25297	Inorganic phosphate transpo	0.08	0.03
P35719	Uncharacterized protein MF	0.21	0.08
Q08732	Serine/threonine-protein kii	0.06	0.03
P47054	Nucleoporin NUP192 OS=Sa	0.03	0.01
P39998	Enhancer of mRNA-decappii	0.08	0.03
P40303	Proteasome subunit alpha t	0.18	0.07
P21243	Proteasome subunit alpha t	0.18	0.07
Q06678	54S ribosomal protein L35, r	0.12	0.05
P53075	Outer spore wall assembly p	0.07	0.03
P32351	Sugar utilization regulatory	0.13	0.05
P0CT04	Protease B inhibitor 2 OS=S	0.71	0.23
P40471	NADPH-dependent 1-acyldil	0.15	0.06
P46995	Histone-lysine N-methyltrar	0.06	0.03
P41057	40S ribosomal protein S29-/	0.94	0.29
P53125	Imitation switch two comple	0.03	0.01
P46989	Autophagy-related protein 2	0.17	0.07
Q99385	Vacuolar calcium ion transp	0.11	0.05
P01120	Ras-like protein 2 OS=Sacch	0.15	0.06
P25644	DNA topoisomerase 2-assoc	0.06	0.03
P32803	Endosomal protein P24B OS	0.22	0.09
P49095	Glycine dehydrogenase (dec	0.04	0.02
Q05016	NADP-dependent 3-hydroxy	0.18	0.07
Q08960	S-adenosyl-L-methionine-de	0.05	0.02
Q01532	Cysteine proteinase 1, mito	0.09	0.04
Q00711	Succinate dehydrogenase [u	0.07	0.03
Q08977	UPF0662 protein YPL260W (	0.08	0.03
P46151	Methylenetetrahydrofolate	0.07	0.03
Q12446	Proline-rich protein LAS17 C	0.07	0.03
Q99297	Mitochondrial 2-oxodicarbo	0.15	0.06
P21264	Phosphoribosylaminoimidaz	0.08	0.03

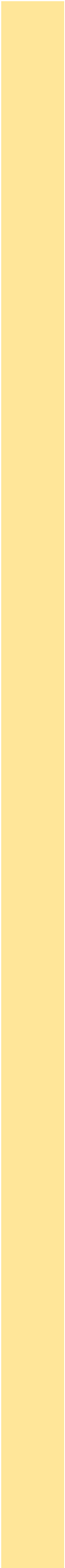
P10080	Single-stranded nucleic acid	0.15	0.06
Q12402	Protein YOP1 OS=Saccharon	0.26	0.10
P48439	Dolichyl-diphosphooligosac	0.13	0.05
P38079	Protein YRO2 OS=Saccharon	0.13	0.05
P20448	ATP-dependent RNA helicas	0.06	0.03
P17649	4-aminobutyrate aminotran	0.09	0.04
P33333	Probable 1-acyl-sn-glycerol-	0.15	0.06
P47169	Sulfite reductase [NADPH] s	0.03	0.01
P33204	Actin-related protein 2/3 co	0.27	0.10
P28321	Monoglyceride lipase OS=Sa	0.14	0.06
P36136	Sedoheptulose 1,7-bisphosp	0.16	0.06
Q03761	Transcription initiation facto	0.08	0.03
P53883	Nucleolar protein 13 OS=Sa	0.11	0.05
P53388	Dicarboxylic amino acid peri	0.07	0.03
P47006	DNA-directed RNA polymera	0.19	0.08
P53829	Protein CAF40 OS=Saccharo	0.12	0.05
Q06132	Suppressor of glycerol defe	0.05	0.02
P40541	Cohesin subunit SCC3 OS=Sa	0.04	0.02
Q06156	Condensin complex subunit	0.04	0.02
Q02792	5~-3~ exoribonuclease 2 OS	0.04	0.02
P53297	PAB1-binding protein 1 OS=	0.06	0.03
Q07979	Chromatin structure-remod	0.09	0.04
P15625	Phenylalanine--tRNA ligase	0.09	0.04
P38861	60S ribosomal export protei	0.08	0.03
P38333	Essential nuclear protein 1	0.09	0.04
Q02959	Histone deacetylase HOS3	0.06	0.03
P23644	Mitochondrial import recep	0.12	0.05
Q02206	Chromatin structure-remod	0.07	0.03
P38086	DNA repair and recombinati	0.04	0.02
Q12019	Midasin OS=Saccharomyces	0.01	0.00
Q03124	Chromatin structure-remod	0.07	0.03
P45818	ATP-dependent RNA helicas	0.08	0.03
Q06252	Uncharacterized protein YL	0.24	0.09
P46964	Dolichyl-diphosphooligosac	0.37	0.14
P30657	Proteasome subunit beta ty	0.17	0.07
P38817	ADP-ribosylation factor-bin	0.08	0.03
Q12099	ATP-dependent RNA helicas	0.11	0.05
P38122	3-methyl-2-oxobutanoate h	0.15	0.06
P40986	Cell division control protein	0.09	0.04
P24276	Protein SSD1 OS=Saccharon	0.03	0.01
P40096	Negative cofactor 2 comple	0.35	0.13
P53860	Phosphatidylinositol transfe	0.12	0.05
Q12164	Pore membrane protein of	0.16	0.06
P39106	Alpha-1,3-mannosyltransfer	0.05	0.02
P34248	Probable intramembrane pr	0.07	0.03
Q86ZR7	Putative uncharacterized hy	0.20	0.08
P40215	External NADH-ubiquinone	0.08	0.03
P22276	DNA-directed RNA polymera	0.04	0.02
P33339	Transcription factor tau 131	0.04	0.02
P32356	Neutral trehalase OS=Sacch	0.06	0.03
P34237	Protein CASP OS=Saccharon	0.06	0.03
Q02209	Uncharacterized protein YK	0.12	0.05

P39540	Elongation of fatty acids pr	0.14	0.06
Q07729	Probable guanine deaminas	0.09	0.04
P54783	D-arabinono-1,4-lactone oxi	0.08	0.03
P38811	Transcription-associated pr	0.01	0.00
P89105	RNA polymerase-associated	0.04	0.02
P50861	6,7-dimethyl-8-ribityllumazi	0.29	0.11
Q04080	GPI transamidase compone	0.08	0.03
P05319	60S acidic ribosomal protei	0.54	0.19
P89102	Exocyst complex componen	0.04	0.02
P40422	DNA-directed RNA polymer	0.78	0.25
P32908	Structural maintenance of c	0.03	0.01
Q05050	Eisosome protein 1 OS=Sacc	0.05	0.02
P23724	Proteasome subunit beta ty	0.19	0.08
P05375	Phosphatidyl-N-methyletha	0.22	0.09
Q08299	Siderophore iron transporte	0.07	0.03
P04650	60S ribosomal protein L39	1.05	0.31
Q06188	PWWP domain-containing p	0.14	0.06
P38962	Golgi apparatus membrane	0.22	0.09
P38280	Spore-specific protein YSW1	0.07	0.03
P07274	Profilin OS=Saccharomyces	0.40	0.15
P38856	Clathrin coat assembly prot	0.07	0.03
P34087	DNA-directed RNA polymer	0.28	0.11
P47082	Vacuolar amino acid transp	0.07	0.03
P53049	Oligomycin resistance ATP-	0.03	0.01
Q06630	Mitochondrial homologous	0.19	0.08
P27514	Low-affinity phosphate tran	0.05	0.02
P14737	DNA repair protein RAD9 O	0.03	0.01
Q12154	ATPase GET3 OS=Saccharo	0.13	0.05
P40035	Mitochondrial phosphate ca	0.15	0.06
P25367	[PIN+] prion protein RNQ1	0.12	0.05
P10962	Protein MAK16 OS=Sacchar	0.14	0.06
P07172	Histidinol-phosphate amino	0.12	0.05
P19073	Cell division control protein	0.24	0.09
Q96VH4	Putative nitroreductase HB	0.25	0.10
Q12109	Tryptophan--tRNA ligase, cy	0.10	0.04
P32341	Vacuolar ATPase assembly i	0.20	0.08
P40318	ERAD-associated E3 ubiquiti	0.03	0.01
P53141	Myosin light chain 1 OS=Sac	0.33	0.12
P51402	60S ribosomal protein L37-	0.58	0.20
Q12207	Non-classical export protein	0.28	0.11
P32565	26S proteasome regulatory	0.05	0.02
Q03774	tRNA (guanine-N(7)-)-methy	0.10	0.04
P30665	DNA replication licensing fa	0.05	0.02
P32906	Endoplasmic reticulum man	0.08	0.03
P53617	Protein NRD1 OS=Saccharo	0.08	0.03
Q07897	Protein CMS1 OS=Saccharo	0.15	0.06
Q08235	Ribosome biogenesis protei	0.15	0.06
P43123	UDP-N-acetylglucosamine p	0.09	0.04
P43535	Protein GCN20 OS=Sacchar	0.06	0.03
P10614	Lanosterol 14-alpha demet	0.08	0.03
P38869	Protein SVP26 OS=Saccharo	0.19	0.08
P11938	DNA-binding protein RAP1	0.05	0.02

P27614	Carboxypeptidase S OS=Sac	0.08	0.03
P12688	Serine/threonine-protein ki	0.06	0.03
P06197	CDP-diacylglycerol--inositol	0.21	0.08
Q06385	Vacuolar protein sorting-ass	0.13	0.05
P53903	Processing of GAS1 and ALP	0.36	0.13
P15565	tRNA (guanine(26)-N(2))-dir	0.08	0.03
P25382	Ribosome assembly protein	0.09	0.04
Q06405	ATP synthase subunit f, mit	0.51	0.18
P47037	Structural maintenance of c	0.03	0.01
P81449	ATP synthase subunit e, mit	0.53	0.18
P00425	Cytochrome c oxidase polyp	0.31	0.12
P54861	Dynamin-related protein D	0.06	0.03
Q08561	Ino eighty subunit 4 OS=Sac	0.43	0.16
P05318	60S acidic ribosomal protei	0.53	0.18
P08679	Citrate synthase, peroxisom	0.10	0.04
Q02774	Secretory component prote	0.22	0.09
P15873	Proliferating cell nuclear an	0.18	0.07
Q03941	Dephospho-CoA kinase CAB	0.19	0.08
P38719	ATP-dependent RNA helicas	0.10	0.04
Q04264	Sister chromatid cohesion p	0.03	0.01
Q12176	Ribosome biogenesis protei	0.04	0.02
P53912	Uncharacterized protein YN	0.12	0.05
P19807	Choline transport protein O	0.08	0.03
Q12449	Hsp90 co-chaperone AHA1	0.13	0.05
P20459	Eukaryotic translation initia	0.14	0.06
P40355	Uncharacterized protein YJ	0.04	0.02
Q06287	Ribosomal RNA small subun	0.18	0.07
P32629	Mannan polymerase II comp	0.09	0.04







Filtered Supernatant

protein access ID	protein description	emPAI	relative abundance
P19097	Fatty acid synthase su	15.48	1.22
Q00955	Acetyl-CoA carboxylase	7.39	0.92
P07149	Fatty acid synthase su	8.03	0.96
P07259	Protein URA2 OS=Sacc	4.28	0.72
P16521	Elongation factor 3A O	19.38	1.31
P06105	Protein SCP160 OS=Sa	9.25	1.01
Q12680	Glutamate synthase [N	2.35	0.53
P32324	Elongation factor 2 OS=	24.73	1.41
P15108	ATP-dependent molec	19.06	1.30
P33892	eIF-2-alpha kinase acti	1.37	0.37
P16861	ATP-dependent 6-phos	10.63	1.07
P10592	Heat shock protein SSA	33.73	1.54
P05694	5-methyltetrahydropte	13.98	1.18
P40150	Ribosome-associated	23.59	1.39
P11484	Ribosome-associated	23.59	1.39
P09436	Isoleucine--tRNA ligase	6.42	0.87
P02829	ATP-dependent molec	14.56	1.19
P32589	Heat shock protein ho	40.88	1.62
P10591	Heat shock protein SSA	25.17	1.42
P31539	Heat shock protein 104	10.20	1.05
P22137	Clathrin heavy chain O	2.46	0.54
P00549	Pyruvate kinase 1 OS=	67.68	1.84
P17255	V-type proton ATPase	7.29	0.92
P08566	Pentafunctional AROM	2.98	0.60
P03965	Carbamoyl-phosphate	5.03	0.78
P00925	Enolase 2 OS=Sacchar	68.28	1.84
P00560	Phosphoglycerate kina	39.69	1.61
P07245	C-1-tetrahydrofolate sy	5.10	0.79
P16862	ATP-dependent 6-phos	5.98	0.84
P05030	Plasma membrane ATP	4.80	0.76
P19882	Heat shock protein 60,	14.19	1.18
P00359	Glyceraldehyde-3-phos	289.26	2.46
P25694	Cell division control pr	9.19	1.01
P0CS90	Heat shock protein SSC	12.78	1.14
P07806-2	Isoform Cytoplasmic o	4.04	0.70
P38972	Phosphoribosylformylg	2.34	0.52
P00924	Enolase 1 OS=Sacchar	27.16	1.45
P26637	Leucine--tRNA ligase, c	3.60	0.66
P40825	Alanine--tRNA ligase,	3.51	0.65
P06169	Pyruvate decarboxylas	19.06	1.30
Q03690	Clustered mitochondri	2.36	0.53
P04801	Threonine--tRNA ligase	7.82	0.95
P32327	Pyruvate carboxylase 2	3.45	0.65
P07262	NADP-specific glutama	14.77	1.20
P16140	V-type proton ATPase	12.87	1.14
Q05022	rRNA biogenesis protei	1.55	0.41
P00815	Histidine biosynthesis	5.59	0.82
P38088	Glycine--tRNA ligase 1,	7.32	0.92
P32582	Cystathionine beta-syn	13.99	1.18
Q12019	Midasin OS=Sacchar	0.38	0.14

P11154	Pyruvate carboxylase 1	3.14	0.62
P54115	Magnesium-activated a	13.60	1.16
P19414	Aconitate hydratase, m	7.23	0.92
P10081	ATP-dependent RNA he	28.37	1.47
P07702	L-2-aminoadipate redu	2.00	0.48
P32454	Aminopeptidase 2, mit	2.58	0.55
P16474	78 kDa glucose-regulat	5.77	0.83
P00358	Glyceraldehyde-3-phos	128.61	2.11
P46655	Glutamate--tRNA ligase	5.51	0.81
P10964	DNA-directed RNA poly	1.20	0.34
P37291	Serine hydroxymethylt	22.59	1.37
P38631	1,3-beta-glucan syntha	1.16	0.33
P04147	Polyadenylate-binding	7.45	0.93
P00360	Glyceraldehyde-3-phos	58.63	1.78
Q08972	[NU+] prion formation	1.88	0.46
P04807	Hexokinase-2 OS=Saccl	16.98	1.25
P15019	Transaldolase OS=Sacc	30.33	1.50
P23254	Transketolase 1 OS=Sa	5.87	0.84
P12709	Glucose-6-phosphate is	6.49	0.87
P07244	Bifunctional purine bio	3.67	0.67
P49090	Asparagine synthetase	6.72	0.89
P32528	Urea amidolyase OS=Sa	1.02	0.31
P22515	Ubiquitin-activating en	2.61	0.56
P16120	Threonine synthase OS	6.87	0.90
P22147	5~-3~ exoribonuclease	1.38	0.38
P19358	S-adenosylmethionine	21.61	1.35
P38720	6-phosphogluconate de	9.73	1.03
P06634	ATP-dependent RNA he	9.09	1.00
P40024	ABC transporter ATP-b	5.97	0.84
P07284	Serine--tRNA ligase, cy	8.92	1.00
Q05506	Arginine--tRNA ligase,	7.29	0.92
P06168	Ketol-acid reductoisom	8.34	0.97
P38009	Bifunctional purine bio	5.56	0.82
P02994	Elongation factor 1-alp	11.68	1.10
P14540	Fructose-bisphosphate	34.26	1.55
P53622	Coatomer subunit alph	1.57	0.41
P38788	Ribosome-associated c	5.50	0.81
P60010	Actin OS=Saccharomyc	36.34	1.57
P38707	Asparagine--tRNA ligas	5.15	0.79
P07251	ATP synthase subunit a	5.44	0.81
P04806	Hexokinase-1 OS=Saccl	6.55	0.88
P04840	Mitochondrial outer m	21.05	1.34
P46367	Potassium-activated al	5.25	0.80
P32558	FACT complex subunit	1.71	0.43
P41811	Coatomer subunit beta	1.86	0.46
P04802	Aspartate--tRNA ligase	4.56	0.75
P13188	Glutamine--tRNA ligase	3.15	0.62
P39954	Adenosylhomocysteina	10.92	1.08
P38011	Guanine nucleotide-bir	21.63	1.35
P15705	Heat shock protein STI	4.18	0.71
P29453	60S ribosomal protein	38.68	1.60
P06738	Glycogen phosphorylas	2.01	0.48

P05750	40S ribosomal protein	40.74	1.62
P49089	Asparagine synthetase	5.69	0.83
P00931	Tryptophan synthase C	2.23	0.51
P52910	Acetyl-coenzyme A syn	4.10	0.71
P40069	Importin subunit beta-	1.09	0.32
P00330	Alcohol dehydrogenase	11.63	1.10
P17076	60S ribosomal protein	38.68	1.60
P32074	Coatomer subunit gam	1.58	0.41
P50095	Inosine-5~-monophosp	4.29	0.72
P14126	60S ribosomal protein	12.36	1.13
Q05911	Adenylosuccinate lyase	5.73	0.83
P22138	DNA-directed RNA poly	1.08	0.32
P29311	Protein BMH1 OS=Sacc	35.45	1.56
P38764	26S proteasome regula	1.48	0.39
P38249	Eukaryotic translation i	1.81	0.45
P33442	40S ribosomal protein	42.58	1.64
P22202	Heat shock protein SSA	2.41	0.53
P04050	DNA-directed RNA poly	0.72	0.24
P10659	S-adenosylmethionine	10.89	1.08
P15180	Lysine--tRNA ligase, cyt	4.67	0.75
P12385	Eukaryotic peptide cha	5.24	0.80
Q03195	Translation initiation fa	3.54	0.66
P15624	Phenylalanine--tRNA lig	4.00	0.70
P00958	Methionine--tRNA ligas	2.36	0.53
P41810	Coatomer subunit beta	1.60	0.41
P32563	V-type proton ATPase s	1.56	0.41
P23248	40S ribosomal protein	35.48	1.56
P31116	Homoserine dehydroge	8.12	0.96
P09624	Dihydrolipoyl dehydrog	5.84	0.84
P39730	Eukaryotic translation i	1.64	0.42
P06208	2-isopropylmalate synt	3.88	0.69
P00942	Triosephosphate isome	12.91	1.14
P49626	60S ribosomal protein	5.94	0.84
P10664	60S ribosomal protein	5.94	0.84
P32861	UTP--glucose-1-phosph	3.98	0.70
P00830	ATP synthase subunit b	4.17	0.71
P17967	Protein disulfide-isome	3.67	0.67
P24783	ATP-dependent RNA he	4.09	0.71
P54113	Bifunctional purine bio	3.25	0.63
P32497	Eukaryotic translation i	1.50	0.40
P30624	Long-chain-fatty-acid--	2.35	0.53
Q03558	NADPH dehydrogenase	6.40	0.87
P09440	C-1-tetrahydrofolate sy	1.44	0.39
P38625	GMP synthase [glutam	4.03	0.70
Q12213	60S ribosomal protein	20.57	1.33
P31688	Trehalose-phosphatase	1.62	0.42
P00817	Inorganic pyrophospha	17.63	1.27
Q02725	Vacuolar transporter cl	1.68	0.43
P05737	60S ribosomal protein	20.57	1.33
P40989	1,3-beta-glucan syntha	0.61	0.21
P32565	26S proteasome regula	1.27	0.36
P07263	Histidine--tRNA ligase,	3.14	0.62

Q12460	Nucleolar protein 56 O	3.11	0.61
P39676	Flavohemoprotein OS=	4.42	0.73
P00950	Phosphoglycerate mut	14.33	1.19
P16603	NADPH--cytochrome P	1.69	0.43
P21954	Isocitrate dehydrogen	6.12	0.85
P34730	Protein BMH2 OS=Sacc	16.93	1.25
P53978	Elongation factor 3B O	1.35	0.37
P36008	Elongation factor 1-ga	4.63	0.75
P38934	Nuclear segregation pr	4.21	0.72
P38427	Trehalose synthase co	1.00	0.30
P41277	Glycerol-1-phosphate	19.56	1.31
P0CX37	40S ribosomal protein	12.62	1.13
P06367	40S ribosomal protein	233.65	2.37
P0CX35	40S ribosomal protein	20.08	1.32
P10127	Alcohol dehydrogenas	4.56	0.75
P15625	Phenylalanine--tRNA li	3.07	0.61
Q12122	Homocitrate synthase,	3.69	0.67
P34760	Peroxiredoxin TSA1 OS	12.55	1.13
P29509	Thioredoxin reductase	4.96	0.78
P26783	40S ribosomal protein	23.34	1.39
P07283	Phosphomannomutase	14.61	1.19
P26263	Pyruvate decarboxylas	1.94	0.47
P23542	Aspartate aminotransf	4.14	0.71
P38999	Saccharopine dehydro	4.17	0.71
P53852	Cysteine--tRNA ligase	1.80	0.45
P20967	2-oxoglutarate dehydr	1.11	0.32
P07264	3-isopropylmalate deh	1.85	0.45
P32527	Zuotin OS=Saccharomy	3.69	0.67
P31412	V-type proton ATPase	3.49	0.65
P53252	Sphingolipid long chain	3.98	0.70
P07257	Cytochrome b-c1 comp	4.13	0.71
P48570	Homocitrate synthase,	3.04	0.61
P80210	Adenylosuccinate synt	3.34	0.64
Q07551	NADPH-dependent alp	6.32	0.86
P0C2I9	Transposon Ty1-PR1 G	0.61	0.21
P11412	Glucose-6-phosphate 1	2.17	0.50
P11986	Inositol-3-phosphate s	2.84	0.58
P49367	Homoaconitase, mitoc	1.41	0.38
P39986	Manganese-transporti	0.88	0.27
P26321	60S ribosomal protein	6.10	0.85
P23301	Eukaryotic translation i	101.33	2.01
P38968	Protein transport prot	0.61	0.21
P27616	Phosphoribosylaminoi	7.88	0.95
P50094	Inosine-5~-monophosp	2.22	0.51
P38219	Obg-like ATPase 1 OS=	5.79	0.83
P37012	Phosphoglucomutase	2.07	0.49
P54839	Hydroxymethylglutaryl	2.61	0.56
P22768	Argininosuccinate synt	5.05	0.78
P32368	Phosphoinositide phos	1.72	0.43
P00498	ATP phosphoribosyltra	9.22	1.01
P32599	Fimbrin OS=Saccharom	1.52	0.40
P32481	Eukaryotic translation i	1.88	0.46

P17505	Malate dehydrogenase	7.36	0.92
P08524	Farnesyl pyrophosphat	3.51	0.65
P25087	Sterol 24-C-methyltran	4.68	0.75
P53090	Aromatic/aminoadipat	1.98	0.47
P38013	Peroxiredoxin type-2 O	22.55	1.37
P13663	Aspartate-semialdehyd	4.88	0.77
P14742	Glutamine--fructose-6-	1.15	0.33
P47169	Sulfite reductase [NAD	0.51	0.18
O13516	40S ribosomal protein	17.86	1.28
P07342	Acetolactate synthase	1.43	0.39
P15303	Protein transport prot	1.29	0.36
P38708	Putative proline--tRNA	1.21	0.34
P05755	40S ribosomal protein	18.13	1.28
P41338	Acetyl-CoA acetyltrans	2.45	0.54
P38891	Branched-chain-amino	2.28	0.52
P06103	Eukaryotic translation i	1.24	0.35
P08518	DNA-directed RNA pol	0.73	0.24
P37292	Serine hydroxymethylt	3.88	0.69
P47143	Adenosine kinase OS=S	5.13	0.79
P31373	Cystathionine gamma-l	2.40	0.53
P41940	Mannose-1-phosphate	3.17	0.62
P54838	Dihydroxyacetone kina	1.49	0.40
P33416	Heat shock protein 78,	0.96	0.29
P49723	Ribonucleoside-diphos	5.58	0.82
P54885	Gamma-glutamyl phos	1.85	0.45
P0CX53	60S ribosomal protein	12.77	1.14
P16387	Pyruvate dehydrogena	4.60	0.75
P32473	Pyruvate dehydrogena	2.26	0.51
P43585	Vacuolar transporter c	1.11	0.32
Q12499	Nucleolar protein 58 O	1.50	0.40
Q01532	Cysteine proteinase 1,	1.56	0.41
P0CX45	60S ribosomal protein	6.88	0.90
P09938	Ribonucleoside-diphos	2.78	0.58
P41805	60S ribosomal protein	14.93	1.20
P27476	Nuclear localization se	2.99	0.60
Q00764	Alpha,alpha-trehalose-	1.98	0.47
P32614	Fumarate reductase 1	2.34	0.52
Q07478	ATP-dependent RNA he	2.38	0.53
P38115	D-arabinose dehydroge	3.83	0.68
Q12230	Sphingolipid long chain	3.44	0.65
P29547	Elongation factor 1-ga	2.69	0.57
P23641	Mitochondrial phospha	3.19	0.62
P33734	Imidazole glycerol pho	1.34	0.37
P26786	40S ribosomal protein	19.92	1.32
P32288	Glutamine synthetase	2.85	0.59
P40495	Homoisocitrate dehydr	4.18	0.71
P07256	Cytochrome b-c1 comp	2.10	0.49
P07991	Ornithine aminotransf	2.40	0.53
P24280	SEC14 cytosolic factor	4.77	0.76
P07280	40S ribosomal protein	45.08	1.66
P23615	Transcription elongati	0.40	0.15
P05743	60S ribosomal protein	50.48	1.71

P02407	40S ribosomal protein	24.56	1.41
P21264	Phosphoribosylaminoi	1.48	0.39
P18239	ADP,ATP carrier protei	6.75	0.89
Q04728	Arginine biosynthesis b	2.59	0.56
P02557	Tubulin beta chain OS=	2.33	0.52
P32449	Phospho-2-dehydro-3-	3.14	0.62
P28241	Isocitrate dehydrogena	2.28	0.52
P53221	60S ribosomal protein	50.48	1.71
P0CX82	60S ribosomal protein	9.91	1.04
P11076	ADP-ribosylation facto	11.38	1.09
P38701	40S ribosomal protein	55.46	1.75
P26785	60S ribosomal protein	9.28	1.01
P46990	60S ribosomal protein	8.85	0.99
P17709	Glucokinase-1 OS=Sacc	1.78	0.44
P19146	ADP-ribosylation facto	11.06	1.08
Q05016	NADP-dependent 3-hy	3.28	0.63
P39077	T-complex protein 1 su	1.83	0.45
P05740	60S ribosomal protein	8.85	0.99
P26784	60S ribosomal protein	9.28	1.01
P0CX55	40S ribosomal protein	34.23	1.55
P32590	Heat shock protein ho	1.08	0.32
P41807	V-type proton ATPase	1.82	0.45
P39015	Suppressor protein ST	4.65	0.75
Q04062	26S proteasome regula	3.25	0.63
P47075	Vacuolar transporter c	0.87	0.27
P05317	60S acidic ribosomal p	5.18	0.79
P25443	40S ribosomal protein	6.81	0.89
P39533	Homocitrate dehydrata	0.73	0.24
P0CX84	60S ribosomal protein	27.09	1.45
Q12363	Transcriptional modula	1.41	0.38
P21576	Vacuolar protein sortin	0.94	0.29
P39522	Dihydroxy-acid dehydr	1.11	0.32
P13298	Orotate phosphoribos	4.54	0.74
P40016	26S proteasome regula	1.02	0.31
P0CX43	60S ribosomal protein	10.86	1.07
P28834	Isocitrate dehydrogena	2.76	0.58
P48164	40S ribosomal protein	12.55	1.13
P23638	Proteasome subunit al	4.16	0.71
P36016	Heat shock protein 70	0.69	0.23
P15646	rRNA 2~-O-methyltran	3.49	0.65
P33330	Phosphoserine aminot	3.12	0.61
P46672	tRNA-aminoacylation c	2.07	0.49
P0CX51	40S ribosomal protein	18.04	1.28
P40217	Eukaryotic translation i	2.36	0.53
P0CX23	60S ribosomal protein	14.80	1.20
P32471	Elongation factor 1-bet	11.10	1.08
P47120	Deoxyhypusine hydrox	2.68	0.57
P38077	ATP synthase subunit g	2.44	0.54
Q12154	ATPase GET3 OS=Sacch	2.29	0.52
P35691	Translationally-control	11.19	1.09
P39976	D-2-hydroxyglutarate--	1.56	0.41
P48589	40S ribosomal protein	19.69	1.32

P04076	Argininosuccinate lyase	1.98	0.47
P43616	Cys-Gly metallodipepti	1.92	0.47
P07170	Adenylate kinase OS=S	9.22	1.01
P0C0W1	40S ribosomal protein	32.30	1.52
P14832	Peptidyl-prolyl cis-tran	10.07	1.04
P53598	Succinate--CoA ligase [	3.38	0.64
P40212	60S ribosomal protein	5.55	0.82
Q12690	60S ribosomal protein	5.55	0.82
P33302	Pleiotropic ABC efflux t	0.32	0.12
P22146	1,3-beta-glucanosyltra	0.88	0.27
P38791	Deoxyhypusine syntha	3.15	0.62
P37303	Low specificity L-threo	1.40	0.38
Q03048	Cofilin OS=Saccharomy	6.76	0.89
Q06408	Transaminated amino	0.93	0.29
P07267	Saccharopepsin OS=Sa	1.10	0.32
P40302	Proteasome subunit al	4.19	0.72
P05738	60S ribosomal protein	7.78	0.94
P34167	Eukaryotic translation i	1.66	0.42
P38555	GTP-binding protein YF	4.58	0.75
P49095	Glycine dehydrogenase	0.64	0.21
P40482	Protein transport prote	0.58	0.20
P0CX31	40S ribosomal protein	14.58	1.19
Q12166	2-isopropylmalate synt	1.32	0.37
Q12118	Small glutamine-rich te	3.58	0.66
P54783	D-arabinono-1,4-lactor	1.21	0.34
Q3E757	60S ribosomal protein	7.49	0.93
P20449	ATP-dependent RNA he	1.40	0.38
P00890	Citrate synthase, mitoc	1.04	0.31
P01120	Ras-like protein 2 OS=S	2.90	0.59
P40531	Protein GVP36 OS=Sac	1.79	0.45
P25386	Intracellular protein tra	0.29	0.11
Q05905	Protein HRI1 OS=Sacch	3.67	0.67
P51996	GTP-binding protein YF	3.61	0.66
P39935	Eukaryotic initiation fa	0.49	0.17
Q06252	Uncharacterized protei	9.28	1.01
P36010	Nucleoside diphosphat	10.59	1.06
P07560	Ras-related protein SE	3.03	0.61
P15992	Heat shock protein 26	4.90	0.77
P40106	Glycerol-1-phosphate p	4.40	0.73
P0CX39	40S ribosomal protein	4.27	0.72
Q02326	60S ribosomal protein	7.29	0.92
P29952	Mannose-6-phosphate	1.66	0.42
P15873	Proliferating cell nucle	3.31	0.63
P0CX41	60S ribosomal protein	63.97	1.81
P39076	T-complex protein 1 su	0.78	0.25
P38840	Aromatic amino acid a	1.07	0.32
P28777	Chorismate synthase C	1.82	0.45
P38426	Trehalose synthase cor	0.49	0.17
P0C2H8	60S ribosomal protein	50.64	1.71
P02406	60S ribosomal protein	20.60	1.33
P36421	Tyrosine--tRNA ligase,	1.62	0.42
P41911	Glycerol-3-phosphate	1.35	0.37

P05756	40S ribosomal protein	8.08	0.96
Q04894	NADP-dependent alcoh	2.65	0.56
P47079	T-complex protein 1 su	1.15	0.33
P38075	Pyridoxamine 5~-phos	3.82	0.68
P40510	D-3-phosphoglycerate	1.29	0.36
Q03640	Tricalbin-3 OS=Sacchar	0.28	0.11
P04456	60S ribosomal protein	18.43	1.29
P25375	Saccharolysin OS=Sacch	0.68	0.23
P12945	N-terminal acetyltrans	0.54	0.19
P42945	U3 small nucleolar RNA	0.30	0.11
P0C2H9	60S ribosomal protein	35.08	1.56
Q04491	Protein transport prote	2.60	0.56
P20459	Eukaryotic translation i	2.38	0.53
P53131	Pre-mRNA-splicing fact	0.63	0.21
P22203	V-type proton ATPase	3.17	0.62
P37302	Aminopeptidase Y OS=	1.03	0.31
P00812	Arginase OS=Saccharor	2.72	0.57
P00445	Superoxide dismutase	12.93	1.14
P40053	Altered inheritance of	0.80	0.26
P14906	Protein translocation p	0.55	0.19
P38264	SRP-independent targe	13.30	1.16
P22803	Thioredoxin-2 OS=Sacc	16.62	1.25
P38205	Multisite-specific tRNA	0.72	0.24
Q08971	Protein PBDC1 homolo	13.46	1.16
P40185	Protein MMF1, mitoch	6.76	0.89
P35194	U3 small nucleolar RNA	0.16	0.06
P43593	Ubiquitin carboxyl-terr	0.94	0.29
P01123	GTP-binding protein YF	5.10	0.79
P51401	60S ribosomal protein	5.99	0.84
P36105	60S ribosomal protein	20.60	1.33
P16550	Protein APA1 OS=Sacch	3.10	0.61
P38144	ISWI chromatin-remod	0.38	0.14
P00899	Anthranilate synthase	0.94	0.29
Q12159	RNA annealing protein	5.59	0.82
P36015	Synaptobrevin homolo	5.37	0.80
Q04869	Uncharacterized protei	1.37	0.37
Q04178	Hypoxanthine-guanine	4.34	0.73
Q04947	Reticulon-like protein 1	2.14	0.50
P38912	Eukaryotic translation i	13.46	1.16
P43535	Protein GCN20 OS=Sac	0.75	0.24
P38626	NADH-cytochrome b5 r	2.83	0.58
Q02455	Protein MLP1 OS=Sacch	0.24	0.09
Q12074	Spermidine synthase O	2.09	0.49
Q04409	Putative glucokinase-2	0.96	0.29
P0CX49	60S ribosomal protein	3.92	0.69
P21524	Ribonucleoside-diphos	0.39	0.14
P0C2H6	60S ribosomal protein	13.99	1.18
P32377	Diphosphomevalonate	1.61	0.42
P17555	Adenylyl cyclase-associ	0.78	0.25
P05748	60S ribosomal protein	3.68	0.67
P53235	Eukaryotic translation i	0.70	0.23
Q02753	60S ribosomal protein	6.75	0.89

Q12754	Ribosomal RNA-proces	0.32	0.12
P20606	Small COPII coat GTPas	3.61	0.66
P11745	Ran GTPase-activating	0.85	0.27
P05319	60S acidic ribosomal pr	7.60	0.93
P47176	Branched-chain-amino	1.47	0.39
P53691	Peptidyl-prolyl cis-tran	1.73	0.44
P47117	Actin-related protein 3	0.95	0.29
P39517	ATP-dependent RNA he	0.77	0.25
P09064	Eukaryotic translation i	1.82	0.45
P41921	Glutathione reductase	0.85	0.27
P27614	Carboxypeptidase S OS	0.93	0.29
P04046	Amidophosphoribosylt	1.10	0.32
O14455	60S ribosomal protein	64.27	1.81
Q03940	RuvB-like protein 1 OS	1.55	0.41
P05739	60S ribosomal protein	4.18	0.71
Q00055	Glycerol-3-phosphate	1.67	0.43
P02400	60S acidic ribosomal pr	7.25	0.92
P25605	Acetolactate synthase	1.62	0.42
P38715	NADPH-dependent ald	1.42	0.38
P15891	Actin-binding protein	0.92	0.28
P07260	Eukaryotic translation i	3.74	0.68
P33299	26S protease regulator	1.26	0.35
P32379	Proteasome subunit al	1.68	0.43
P38858	6-phosphogluconolact	3.56	0.66
P40054	D-3-phosphoglycerate	0.91	0.28
Q08162	Exosome complex exor	0.39	0.14
P14020	Dolichol-phosphate ma	4.48	0.74
P38754	60S ribosomal protein	14.89	1.20
P39078	T-complex protein 1 su	0.77	0.25
P27472	Glycogen [starch] synth	0.80	0.26
P07246	Alcohol dehydrogenase	1.53	0.40
Q04067	Eukaryotic translation i	1.93	0.47
P09733	Tubulin alpha-1 chain	1.12	0.33
Q03532	ATP-dependent RNA he	0.79	0.25
P32381	Actin-related protein 2	1.92	0.47
P32905	40S ribosomal protein	1.74	0.44
Q12447	Polyamine N-acetyltrar	4.49	0.74
P05453	Eukaryotic peptide cha	0.64	0.21
Q12458	Putative reductase 1 O	1.96	0.47
P25294	Protein SIS1 OS=Sacch	1.74	0.44
P32891	D-lactate dehydrogena	0.66	0.22
P38998	Saccharopine dehydrog	1.48	0.39
Q03161	Glucose-6-phosphate 1	1.64	0.42
P07213	Mitochondrial import r	0.72	0.24
P42943	T-complex protein 1 su	0.74	0.24
P15703	Glucan 1,3-beta-glucos	1.29	0.36
Q05515	Survival factor 1 OS=Sa	0.84	0.26
P25343	Reduced viability upon	2.46	0.54
Q06685	Inositol hexakisphosph	0.39	0.14
P05745	60S ribosomal protein	41.98	1.63
P19881	4-nitrophenylphosphat	1.26	0.35
P32939	GTP-binding protein Y	2.36	0.53

P14904	Vacuolar aminopeptida	0.64	0.21
P14120	60S ribosomal protein	16.15	1.23
Q01560	Nucleolar protein 3 OS	0.87	0.27
P23639	Proteasome subunit al	2.37	0.53
P32602	Alpha-soluble NSF atta	1.35	0.37
P02992	Elongation factor Tu, m	1.20	0.34
P38069	Alpha-1,2-mannosyltra	0.75	0.24
Q12466	Tricalbin-1 OS=Sacchar	0.28	0.11
P54837	Endoplasmic reticulum	2.21	0.51
Q04013	Citrate/oxoglutarate ca	1.29	0.36
Q04175	Importin beta SMX1 OS	0.30	0.11
Q01939	26S protease regulator	0.87	0.27
P53912	Uncharacterized protei	0.99	0.30
P24276	Protein SSD1 OS=Sacch	0.31	0.12
P38689	Ribose-phosphate pyro	1.55	0.41
P39079	T-complex protein 1 su	0.74	0.24
P05626	ATP synthase subunit 4	1.40	0.38
P18562	Uracil phosphoribosyltr	3.55	0.66
P0C0V8	40S ribosomal protein	16.09	1.23
P09734	Tubulin alpha-3 chain	0.93	0.29
P08536	Sulfate adenylyltransfe	0.78	0.25
Q06010	A-factor-processing en	0.38	0.14
Q12335	Protoplast secreted pro	3.80	0.68
P38687	Signal recognition part	0.51	0.18
P38911	FK506-binding nuclear	1.04	0.31
P05744	60S ribosomal protein	9.03	1.00
P41056	60S ribosomal protein	8.82	0.99
Q04660	Ribosome biogenesis p	0.44	0.16
Q03862	Probable metalloprote	0.66	0.22
P15454	Guanylate kinase OS=S	5.17	0.79
P43123	UDP-N-acetylglucosam	0.55	0.19
Q04439	Myosin-5 OS=Saccharo	0.27	0.10
Q3E754	40S ribosomal protein	16.09	1.23
P53920	Pro-apoptotic serine pr	0.41	0.15
P20081	FK506-binding protein	8.82	0.99
P0CX47	40S ribosomal protein	3.82	0.68
P43588	Ubiquitin carboxyl-term	2.00	0.48
P18759	Vesicular-fusion protei	0.57	0.20
P37898	Alanine/arginine amino	0.41	0.15
P40032	Prolyl 3,4-dihydroxylas	0.56	0.19
P09457	ATP synthase subunit 5	2.44	0.54
P12695	Dihydrolipoyllysine-res	0.73	0.24
P40961	Prohibitin-1 OS=Saccha	1.12	0.33
P40462	Protein TMA108 OS=Sa	0.30	0.11
P53981	Uncharacterized phosp	1.78	0.44
Q04636	FACT complex subunit	0.57	0.20
P38861	60S ribosomal export p	0.61	0.21
P29704	Squalene synthase OS=	0.89	0.28
P04449	60S ribosomal protein	5.41	0.81
Q02892	Nucleolar GTP-binding	0.56	0.19
P12612	T-complex protein 1 su	0.72	0.24
P32501	Translation initiation fa	0.50	0.18

Q04373	Pumilio homology dom	0.55	0.19
P22217	Thioredoxin-1 OS=Sacc	6.76	0.89
P89105	RNA polymerase-assoc	0.26	0.10
P33322	H/ACA ribonucleoprote	0.83	0.26
P30902	ATP synthase subunit c	2.28	0.52
P36018	GTP-binding protein YF	1.45	0.39
P36013	NAD-dependent malic	0.46	0.16
P21243	Proteasome subunit al	1.73	0.44
P16622	Ferrochelatase, mitoch	0.89	0.28
P07703	DNA-directed RNA poly	0.86	0.27
P46680	Actin-interacting prote	0.42	0.15
Q06706	Elongator complex pro	0.24	0.09
Q05933	Actin-related protein 2	3.92	0.69
P07172	Histidinol-phosphate a	0.93	0.29
P38431-2	Isoform Short of Eukar	1.15	0.33
P40093	UPF0160 protein YER1	1.09	0.32
P47133	ER membrane protein	1.30	0.36
P14843	Phospho-2-dehydro-3-	1.22	0.35
P00447	Superoxide dismutase	1.49	0.40
P48836	V-type proton ATPase	5.29	0.80
P36136	Sedoheptulose 1,7-bis	1.89	0.46
P38295	Medium-chain fatty ac	0.90	0.28
P47912	Long-chain-fatty-acid--	0.53	0.18
P35719	Uncharacterized protei	2.09	0.49
Q02642	Nascent polypeptide-a	2.97	0.60
Q06205	FK506-binding protein	0.71	0.23
P22336	Replication factor A pr	0.50	0.18
Q04697	Glucose-signaling facto	1.06	0.31
P33775	Dolichyl-phosphate-ma	0.43	0.16
P25719	Peptidyl-prolyl cis-tran	3.10	0.61
P06780	GTP-binding protein RH	1.72	0.43
P17423	Homoserine kinase OS	0.83	0.26
P49954	Probable hydrolase NIT	0.78	0.25
Q12480	Probable electron tran	1.15	0.33
P25635	Periodic tryptophan pr	0.38	0.14
Q08686	Thiosulfate sulfurtrans	1.28	0.36
P32178	Chorismate mutase OS	1.58	0.41
Q04344	Hit family protein 1 OS	5.34	0.80
P32835	GTP-binding nuclear pr	1.57	0.41
Q12449	Hsp90 co-chaperone A	1.05	0.31
P38879	Nascent polypeptide-a	3.52	0.66
P32319	Vacuolar protein sortin	0.17	0.07
P30656	Proteasome subunit be	1.10	0.32
Q06142	Importin subunit beta-	0.35	0.13
P28274	CTP synthase 1 OS=Sac	0.55	0.19
P36017	Vacuolar protein sortin	1.76	0.44
P25491	Mitochondrial protein	0.87	0.27
Q07878	Vacuolar protein sortin	0.07	0.03
P39683	Nicotinate phosphoribo	0.62	0.21
Q04371	Protein-glutamate O-m	0.69	0.23
P25349	Flavoprotein-like prote	1.90	0.46
P32804	Zinc-regulated transpo	0.76	0.25

P22696	Peptidyl-prolyl cis-tran	3.23	0.63
P40047	Aldehyde dehydrogena	0.52	0.18
P39744	Nucleolar complex pro	0.42	0.15
P40215	External NADH-ubiquir	0.57	0.20
Q02821	Importin subunit alpha	0.48	0.17
P17649	4-aminobutyrate amin	0.70	0.23
Q12068	NADPH-dependent me	0.85	0.27
P32179	3~(2~),5~-bisphosphat	1.05	0.31
P89886	Translation machinery-	2.16	0.50
P53081	NGG1-interacting facto	1.08	0.32
P24000	60S ribosomal protein	3.97	0.70
P0CX29	40S ribosomal protein	3.28	0.63
P40518	Actin-related protein 2	2.93	0.59
P36060	NADH-cytochrome b5 r	1.00	0.30
P31382	Dolichyl-phosphate-ma	0.31	0.12
Q12746	Plasma membrane-ass	0.95	0.29
Q06151	m7GpppX diphosphata	0.78	0.25
P32598	Serine/threonine-prote	0.91	0.28
O13563	26S proteasome regula	2.68	0.57
P27809	Glycolipid 2-alpha-man	0.90	0.28
Q12109	Tryptophan--tRNA ligas	0.77	0.25
Q04225	Ribosome assembly pr	0.39	0.14
Q02931	NET1-associated nucle	0.21	0.08
P53184	Nicotinamidase OS=Sa	1.56	0.41
P23724	Proteasome subunit be	1.40	0.38
P35844	Oxysterol-binding prot	0.77	0.25
P40037	Protein HMF1 OS=Sacc	2.80	0.58
P39966	Protein phosphatase 2	0.59	0.20
P0C0T4	40S ribosomal protein	3.72	0.67
P19812	E3 ubiquitin-protein lig	0.11	0.05
P17883	Superkiller protein 3 O	0.19	0.08
P40413	T-complex protein 1 su	0.36	0.13
P53199	Sterol-4-alpha-carboxy	0.44	0.16
P52488	Ubiquitin-activating en	0.39	0.14
P53731	Actin-related protein 2	0.81	0.26
P40303	Proteasome subunit al	0.93	0.29
P34160	Nuclear cap-binding pr	0.27	0.10
P53633	Prenylated Rab accept	3.23	0.63
P39985	DNA polymerase V OS=	0.23	0.09
P25567	RNA-binding protein S	0.64	0.21
P25293	Nucleosome assembly	0.48	0.17
P31383	Protein phosphatase P	0.40	0.15
Q01476	Ubiquitin carboxyl-terr	0.18	0.07
P54861	Dynamin-related prote	0.32	0.12
P19524	Myosin-2 OS=Saccharo	0.14	0.06
P38817	ADP-ribosylation facto	0.34	0.13
P05749	60S ribosomal protein	1.79	0.45
Q86ZR7	Putative uncharacteriz	1.44	0.39
P36049	rRNA-processing prote	0.61	0.21
P05759	Ubiquitin-40S ribosom	1.93	0.47
P00410	Cytochrome c oxidase	1.27	0.36
P40075	Vesicle-associated mer	1.01	0.30

P47018	Maintenance of telome	0.43	0.16
Q03280	E3 ubiquitin-protein lig	0.08	0.03
Q12452	3-keto-steroid reducta:	0.43	0.16
P38688	Signal recognition part	0.38	0.14
P16649	General transcriptional	0.27	0.10
P10614	Lanosterol 14-alpha de	0.48	0.17
P27810	Alpha-1,2 mannosyltra	0.85	0.27
P35723	Endoplasmic reticulum	1.72	0.43
Q01662	Methionine aminopept	0.71	0.23
Q00245	GTP-binding protein RH	1.08	0.32
P54860	E4 ubiquitin-protein lig	0.24	0.09
P32263	Pyrroline-5-carboxylate	0.86	0.27
Q07505	Putative carboxymethy	0.83	0.26
P39940	E3 ubiquitin-protein lig	0.29	0.11
Q12250	26S proteasome regula	0.44	0.16
P53254	U3 small nucleolar RNA	0.14	0.06
P53261	Pescadillo homolog OS	0.50	0.18
P33767	Dolichyl-diphosphoolig	0.61	0.21
P09232	Cerevisin OS=Saccharo	0.31	0.12
P38988	Mitochondrial GTP/GD	1.03	0.31
P21304	Periodic tryptophan pr	0.45	0.16
P38061	60S ribosomal protein	3.86	0.69
P14065	Glycerol 2-dehydrogen	0.71	0.23
P25655	General negative regul	0.10	0.04
Q12178	Cytosine deaminase OS	1.86	0.46
P53008	Mannosyl-oligosacchar	0.22	0.09
P32352	C-8 sterol isomerase O:	0.76	0.25
P32476	Squalene monooxygen	0.67	0.22
P32356	Neutral trehalase OS=S	0.32	0.12
Q12377	26S proteasome regula	0.46	0.16
P36047	Protein phosphatase 1	0.44	0.16
Q08220	Glutathione synthetase	0.53	0.18
P19454	Casein kinase II subunit	0.82	0.26
P32790	Actin cytoskeleton-regu	0.19	0.08
P38260	Hsp70 nucleotide exch	1.06	0.31
P38737	Proteasome componer	0.12	0.05
P09950	5-aminolevulinate synt	0.37	0.14
P53834	Hsp90 co-chaperone H	1.25	0.35
Q05359	Protein ERP1 OS=Sacch	1.13	0.33
P21965	Protein kinase MCK1 O	0.55	0.19
P52489	Pyruvate kinase 2 OS=S	0.41	0.15
Q12532	Ribosome quality contr	0.22	0.09
Q99287	Protein SEY1 OS=Sacch	0.24	0.09
Q06705	Phosphatidylinositol tra	0.49	0.17
P47089	Translation machinery-	0.86	0.27
P32445	Single-stranded DNA-b	1.48	0.39
P51601	GTP cyclohydrolase 1 C	1.32	0.37
Q05775	Eukaryotic translation i	0.62	0.21
P47039	Probable kynurenine--c	0.46	0.16
P28000	DNA-directed RNA poly	1.38	0.38
P23180	Probable oxidoreducta	0.30	0.11
P08417	Fumarate hydratase, m	0.42	0.15

P46992	Cell wall protein YJL17	0.39	0.14
P32568	Protein SNQ2 OS=Sacc	0.12	0.05
Q06631	Protein BFR2 OS=Sacch	0.26	0.10
P52286	Suppressor of kinetoch	0.88	0.27
P32495	H/ACA ribonucleoprot	1.97	0.47
P21242	Probable proteasome	0.82	0.26
P38694	Putative aldehyde deh	0.30	0.11
P20436	DNA-directed RNA pol	2.08	0.49
P35997	40S ribosomal protein	6.41	0.87
P50085	Prohibitin-2 OS=Sacch	0.99	0.30
P53312	Succinate--CoA ligase [	0.49	0.17
P41920	Ran-specific GTPase-ac	2.40	0.53
P39727	ER-derived vesicles pr	0.36	0.13
P38286	Very-long-chain 3-oxo	0.44	0.16
P39958	Rab GDP-dissociation i	0.58	0.20
Q03103	Endoplasmic oxidored	0.24	0.09
P56628	60S ribosomal protein	1.76	0.44
Q12189	Ribose-5-phosphate is	0.95	0.29
P38624	Proteasome subunit be	1.21	0.34
P0C0X0	40S ribosomal protein	10.32	1.05
Q06078	U3 small nucleolar RN	0.20	0.08
Q08647	Multisubstrate pseudo	0.28	0.11
P34241	Nucleolar pre-ribosom	0.12	0.05
P38166	Protein transport prot	1.16	0.33
P48015	Aminomethyltransfera	0.70	0.23
P36114	Mitochondrial outer m	0.34	0.13
Q08723	26S proteasome regul	0.64	0.21
P42842	Essential for maintena	0.26	0.10
P21306	ATP synthase subunit	6.53	0.88
Q12125	Golgi to ER traffic prot	0.68	0.23
Q12211	tRNA pseudouridine sy	0.26	0.10
P32496	26S proteasome regul	0.81	0.26
P49167	60S ribosomal protein	3.83	0.68
P15565	tRNA (guanine(26)-N(2	0.34	0.13
P39990	13 kDa ribonucleoprot	2.88	0.59
P32386	ATP-dependent bile ac	0.11	0.05
P39938	40S ribosomal protein	1.76	0.44
P32457	Cell division control pr	0.37	0.14
P40202	Superoxide dismutase	0.97	0.29
Q12009	tRNA (guanine-N(7)-)-	0.52	0.18
Q08985	Homocysteine S-methy	0.67	0.22
P25373	Glutaredoxin-1 OS=Sac	2.07	0.49
P53839	Glyoxylate reductase 1	0.44	0.16
P40581	Peroxiredoxin HYR1 O	1.12	0.33
P30822	Exportin-1 OS=Sacchar	0.21	0.08
P38795	Glutamine-dependent	0.26	0.10
P28272	Dihydroorotate dehyd	0.72	0.24
P40319	Elongation of fatty aci	0.43	0.16
P33204	Actin-related protein 2	1.03	0.31
P30771	ATP-dependent helica	0.24	0.09
Q01855	40S ribosomal protein	3.32	0.64
P04911	Histone H2A.1 OS=Sac	1.72	0.43

P28495	F-actin-capping protei	0.85	0.27
P32898	Mitochondrial presequ	0.18	0.07
P19262	Dihydrolipoyllysine-res	0.33	0.12
P32337	Importin subunit beta-	0.12	0.05
Q01852	Mitochondrial import i	0.47	0.17
P07275	Delta-1-pyrroline-5-car	0.34	0.13
P50861	6,7-dimethyl-8-ribityllu	3.52	0.66
P53900	Prefoldin subunit 4 OS	1.51	0.40
P30657	Proteasome subunit be	0.62	0.21
P43603	LAS seventeen-binding	0.33	0.12
P33399	La protein homolog OS	0.55	0.19
P14306	Carboxypeptidase Y in	1.16	0.33
Q12522	Eukaryotic translation i	0.42	0.15
Q08745	40S ribosomal protein	1.99	0.48
P21734	Ubiquitin-conjugating	0.79	0.25
P05375	Phosphatidyl-N-methyl	0.83	0.26
P33297	26S protease regulator	0.63	0.21
P00425	Cytochrome c oxidase	1.97	0.47
P13517	F-actin-capping protei	0.54	0.19
Q12306	Ubiquitin-like protein	4.00	0.70
P04161	Phosphoribosylglycina	1.20	0.34
P20051	Dihydroorotase OS=Sa	0.79	0.25
P38116	ADP-ribosylation facto	0.99	0.30
P38810	SED5-binding protein 3	0.15	0.06
P41057	40S ribosomal protein	13.17	1.15
P33307	Importin alpha re-expo	0.19	0.08
P02293	Histone H2B.1 OS=Sac	2.72	0.57
P53303	Zinc finger protein ZPR	0.40	0.15
P53200	Protein-lysine N-methy	0.92	0.28
P22276	DNA-directed RNA pol	0.16	0.06
Q12207	Non-classical export pr	1.08	0.32
P39968	Vacuolar protein 8 OS=	0.25	0.10
P18962	Dipeptidyl aminopepti	0.17	0.07
P53111	NADPH-dependent ald	0.45	0.16
Q04336	Uncharacterized prote	0.12	0.05
P41058	40S ribosomal protein	12.61	1.13
Q10740	Leukotriene A-4 hydrol	0.28	0.11
Q08601	Metacaspase-1 OS=Sac	0.34	0.13
P53914	RNA cytidine acetyltra	0.13	0.05
P38071	Enoyl-[acyl-carrier prot	0.57	0.20
P32468	Cell division control pr	0.50	0.18
Q08225	Probable dipeptidyl pe	0.19	0.08
P47037	Structural maintenanc	0.14	0.06
P38777	Family of serine hydrol	0.68	0.23
Q12133	Signal peptidase compl	1.42	0.38
P39685	Nucleoporin POM152	0.10	0.04
P53145	Large subunit GTPase 1	0.22	0.09
P32366	V-type proton ATPase	0.43	0.16
P38248	Cell wall protein ECM3	0.24	0.09
P38993	Iron transport multico	0.30	0.11
P12688	Serine/threonine-prot	0.20	0.08
P40414	Tropomyosin-2 OS=Sac	1.67	0.43

P38143	Glutathione peroxidas	1.13	0.33
P32915	Protein transport prote	0.31	0.12
Q07381	Ribosome biogenesis p	0.17	0.07
P02309	Histone H4 OS=Sacchar	2.42	0.53
P49166	60S ribosomal protein	2.95	0.60
P07347	N-terminal acetyltrans	0.97	0.29
Q12464	RuvB-like protein 2 OS	0.32	0.12
P32803	Endosomal protein P2	1.23	0.35
P48231	Tricalbin-2 OS=Sacchar	0.15	0.06
P39729	Ribosome-interacting	0.41	0.15
Q12692	Histone H2A.Z OS=Sac	1.66	0.42
P05373	Delta-aminolevulinic a	0.64	0.21
Q08641	tRNA(Thr) (cytosine(32	0.30	0.11
Q08235	Ribosome biogenesis p	0.52	0.18
P33331	Nuclear transport fact	2.65	0.56
P47771	Aldehyde dehydrogena	0.41	0.15
P38199	Heterogeneous nuclea	0.41	0.15
P38986	L-asparaginase 1 OS=S	0.40	0.15
Q08208	Nucleolar protein 12 O	0.20	0.08
P00927	Threonine dehydratase	0.25	0.10
P33298	26S protease regulator	0.35	0.13
Q12434	Rho GDP-dissociation i	0.84	0.26
P22141	Proteasome subunit be	0.87	0.27
P00729	Carboxypeptidase Y OS	0.27	0.10
P06782	Carbon catabolite-dere	0.30	0.11
O14467	Multiprotein-bridging f	1.35	0.37
P40525	60S ribosomal protein	1.74	0.44
Q12675	Phospholipid-transport	0.05	0.02
P15700	Uridylate kinase OS=Sa	0.84	0.26
Q99260	GTP-binding protein YF	0.47	0.17
Q96VH4	Putative nitroreductas	0.96	0.29
P10080	Single-stranded nuclei	0.77	0.25
P38910	10 kDa heat shock prot	2.42	0.53
P38886	26S proteasome regula	0.89	0.28
P06115	Catalase T OS=Sacchar	0.24	0.09
Q12220	U3 small nucleolar RN	0.19	0.08
P32892	ATP-dependent RNA he	0.18	0.07
P25342	Cell division control pr	0.47	0.17
P47119	Inosine triphosphate p	0.89	0.28
P31384	Glucose-repressible alc	0.11	0.05
Q12314	Protein arginine N-met	0.77	0.25
Q12305	Thiosulfate sulfurtrans	1.48	0.39
Q12265	Ribose-phosphate pyro	0.30	0.11
Q04304	UPF0659 protein YMR	0.46	0.16
P32419	Malate dehydrogenase	0.46	0.16
Q06625	Glycogen debranching	0.08	0.03
P33338	Protein SLA2 OS=Sacch	0.14	0.06
P46681	D-2-hydroxyglutarate--	0.27	0.10
Q03219	Uncharacterized protei	0.57	0.20
P10869	Aspartokinase OS=Sac	0.27	0.10
P53723	UPF0674 endoplasmic	0.35	0.13
P53228	Transaldolase NQM1 O	0.46	0.16

P47108	Nucleolar pre-ribosoma	0.11	0.05
Q08977	UPF0662 protein YPL26	0.35	0.13
P50086	Probable 26S proteaso	0.44	0.16
Q08951	AP-3 complex subunit	0.14	0.06
Q04458	Fatty aldehyde dehydr	0.17	0.07
P39726	Glycine cleavage syster	0.65	0.22
P39101	Protein CAJ1 OS=Sacch	0.37	0.14
P46956	Inorganic phosphate tr	0.50	0.18
P00937	Multifunctional tryptop	0.30	0.11
P53883	Nucleolar protein 13 O	0.36	0.13
P38225	Very long-chain fatty a	0.13	0.05
P05374	Phosphatidylethanolan	0.15	0.06
P42935	Elongator complex pro	0.17	0.07
P40469	DNA repair/transcriptio	0.13	0.05
P15424	ATP-dependent RNA he	0.20	0.08
P40509	Coatomer subunit epsi	0.32	0.12
Q08421	Enhancer of translatior	0.22	0.09
Q99321	Diphosphoinositol poly	0.91	0.28
Q99258	3,4-dihydroxy-2-butan	0.85	0.27
P36775	Lon protease homolog,	0.12	0.05
P47077	Nucleolar protein 9 OS	0.20	0.08
P20107	Zinc/cadmium resistan	0.34	0.13
P36048	Pre-mRNA-splicing fact	0.13	0.05
P00424	Cytochrome c oxidase	0.73	0.24
Q06494	Putative pyridoxal redu	0.28	0.11
Q07527	tRNA (guanosine(18)-2	0.09	0.04
Q06489	Methylthioribose-1-ph	0.37	0.14
P53860	Phosphatidylinositol tr	0.42	0.15
P23644	Mitochondrial import r	0.25	0.10
P0CX25	60S ribosomal protein	1.45	0.39
P32895	Ribose-phosphate pyro	0.22	0.09
P39714	(R,R)-butanediol dehyd	0.25	0.10
P40327	26S protease regulator	0.34	0.13
P32610	V-type proton ATPase	0.62	0.21
P47154	CAAX prenyl protease	0.31	0.12
P46982	Alpha-1,2-mannosyltra	0.15	0.06
P53549	26S protease subunit R	0.33	0.12
Q06440	Coronin-like protein OS	0.22	0.09
P52918	Protein MSN5 OS=Sacc	0.10	0.04
Q08193	1,3-beta-glucanosyltra	0.20	0.08
P43621	Coatomer subunit delt	0.26	0.10
Q12176	Ribosome biogenesis p	0.13	0.05
Q00711	Succinate dehydrogena	0.14	0.06
P05318	60S acidic ribosomal pr	1.34	0.37
Q03835	Monothiol glutaredoxi	0.65	0.22
P46683	Ankyrin repeat-contain	0.52	0.18
P40693	Ribosome biogenesis p	0.29	0.11
P53903	Processing of GAS1 and	1.53	0.40
Q12389	ATP-dependent RNA he	0.13	0.05
P47047	ATP-dependent RNA he	0.08	0.03
Q05874	Protein N-methyltransf	0.61	0.21
P52553	Prefoldin subunit 6 OS=	1.01	0.30

P11633	Non-histone chromoso	1.25	0.35
P34077	Nucleoporin NIC96 OS=	0.16	0.06
P39926	Protein SSO2 OS=Sacch	0.32	0.12
Q12285	Ubiquitin-like protein M	0.49	0.17
P32597	Nuclear protein STH1/N	0.10	0.04
P17157	Cyclin-dependent prote	0.31	0.12
P39010	Palmitoyltransferase A	0.12	0.05
Q07623	Nucleolar protein 6 OS	0.45	0.16
Q08962	60S ribosome subunit b	0.99	0.30
P34227	Mitochondrial peroxire	0.38	0.14
Q06103	26S proteasome regula	0.34	0.13
Q06679	U3 small nucleolar RNA	0.11	0.05
P53849	Zinc finger protein GIS2	1.16	0.33
P38765	Uncharacterized isome	0.33	0.12
P43569	CCR4-associated factor	0.53	0.18
P39704	Protein ERP2 OS=Sacch	0.48	0.17
P39742	Translocation protein S	0.54	0.19
P53128	Methylenetetrahydrofo	0.23	0.09
Q05946	U3 small nucleolar RNA	0.17	0.07
P38787	2-dehydropantoate 2-r	0.24	0.09
P53337	ER-derived vesicles pro	0.31	0.12
P33317	Deoxyuridine 5~-tripho	0.84	0.26
P33201	Ribosome assembly fac	0.41	0.15
P39107	Mannan polymerase co	0.23	0.09
P38755	Oxysterol-binding prote	0.33	0.12
P32502	Translation initiation fa	0.39	0.14
P40557	ER-retained PMA1-sup	0.19	0.08
P32588	Nuclear and cytoplasm	0.20	0.08
P33327	NAD-specific glutamate	0.12	0.05
Q08822	Probable electron trans	0.14	0.06
P28007	H/ACA ribonucleoprote	0.54	0.19
P52593	Nucleoporin NUP188 O	0.08	0.03
P25847	DNA mismatch repair p	0.14	0.06
P40506	Phosphopantothenate-	0.25	0.10
P38197	UPF0001 protein YBL03	0.62	0.21
P38174	Methionine aminopept	0.22	0.09
P32843	Mitochondrial escape p	0.16	0.06
P08679	Citrate synthase, perox	0.20	0.08
P47096	3-hydroxyanthranilate	0.58	0.20
Q06287	Ribosomal RNA small s	0.40	0.15
P32485	Mitogen-activated prot	0.34	0.13
P53066	Ankyrin repeat-contain	0.59	0.20
P32623	Probable glycosidase C	0.21	0.08
P38217	Importin subunit beta-	0.10	0.04
P21801	Succinate dehydrogena	0.36	0.13
P23292	Casein kinase I homolo	0.16	0.06
Q04969	Signal peptidase compl	0.57	0.20
P39936	Eukaryotic initiation fa	0.10	0.04
P00431	Cytochrome c peroxida	0.26	0.10
P32860	NifU-like protein, mito	0.38	0.14
P40029	Peptide methionine su	0.55	0.19
P11491	Repressible alkaline ph	0.25	0.10

P38845	Cruciform DNA-recogn	0.20	0.08
P39692	Sulfite reductase [NAD	0.09	0.04
P19073	Cell division control pr	0.54	0.19
P28707	Co-chaperone protein	0.48	0.17
P53551	Histone H1 OS=Sacchar	0.40	0.15
P53295	Ribosome-interacting	0.26	0.10
P04037	Cytochrome c oxidase	0.72	0.24
P38784	Vacuolar ATPase assem	0.56	0.19
P32466	Low-affinity glucose tra	0.16	0.06
P53742	Nucleolar GTP-binding	0.19	0.08
P07285	Anthranilate phosphor	0.26	0.10
P35729	Nucleoporin NUP120 C	0.08	0.03
P38130	Probable mannosyltran	0.22	0.09
P49435	Adenine phosphoribos	0.58	0.20
Q06218	ATP-dependent RNA he	0.15	0.06
P52893	Probable alanine amin	0.24	0.09
Q06608	Pyridoxamine 5~-phos	0.52	0.18
P53276	U3 small nucleolar RN	0.12	0.05
Q04217	Probable ATP-depende	0.07	0.03
P32316	Acetyl-CoA hydrolase	0.27	0.10
P15367	Signal peptidase compl	0.65	0.22
P35180	Mitochondrial import	0.59	0.20
Q04493	Prefoldin subunit 5 OS	0.66	0.22
Q03178	Cell wall mannoprotei	0.31	0.12
P40056	Golgi to ER traffic prot	0.35	0.13
P10622	60S acidic ribosomal pr	0.54	0.19
P38930	Casein kinase II subuni	0.37	0.14
P39106	Alpha-1,3-mannosyltra	0.11	0.05
P35207	Antiviral helicase SKI2	0.07	0.03
P11353	Oxygen-dependent cop	0.28	0.11
P53905	U6 snRNA-associated S	1.05	0.31
P32340	Rotenone-insensitive	0.09	0.04
P11075	Protein transport prot	0.04	0.02
P40548	HSP70 co-chaperone S	0.67	0.22
Q12117	Protein MRH1 OS=Sacc	0.47	0.17
Q04338	t-SNARE VTI1 OS=Sacch	0.47	0.17
P53941	U3 small nucleolar ribo	0.33	0.12
P36059	ATP-dependent (S)-NA	0.28	0.11
P08067	Cytochrome b-c1 comp	0.49	0.17
P32911	Eukaryotic translation	1.11	0.32
P20433	DNA-directed RNA poly	0.45	0.16
P40008	Protein FMP52, mitoch	0.45	0.16
Q12018	Cell division control pr	0.11	0.05
Q03705	EKC/KEOPS complex su	0.57	0.20
P32787	Mitochondrial genome	0.36	0.13
Q07451	Endoplasmic reticulum	0.51	0.18
Q04781	E3 ubiquitin-protein lig	0.05	0.02
P25618	Protein CWH43 OS=Sac	0.09	0.04
P46989	Autophagy-related pro	0.36	0.13
Q05050	Eisosome protein 1 OS	0.11	0.05
P32499	Nucleoporin NUP2 OS=	0.13	0.05
P25043	Proteasome subunit be	0.39	0.14

Q04432	Glutathione-independe	0.44	0.16
P15274	AMP deaminase OS=Sa	0.11	0.05
P38276	UPF0303 protein YBR1	0.58	0.20
P12962	Cap-associated protein	0.29	0.11
P36149	Trafficking protein part	0.52	0.18
Q04792	Glutamate decarboxyla	0.15	0.06
P38773	2-deoxyglucose-6-phos	0.41	0.15
Q06053	tRNA-dihydrouridine(4	0.13	0.05
P38820	Adenylyltransferase an	0.10	0.04
P40312	Cytochrome b5 OS=Sac	0.42	0.15
P40043	Respiratory growth ind	0.28	0.11
P22936	DNA-(apurinic or apyri	0.12	0.05
P32477	Glutamate--cysteine lig	0.13	0.05
P36161	Nucleoporin NUP133 C	0.07	0.03
P20447	ATP-dependent RNA he	0.17	0.07
P37838	Nucleolar protein 4 OS	0.13	0.05
P52891	Nucleoporin NUP84 OS	0.12	0.05
Q07457	E3 ubiquitin-protein lig	0.12	0.05
P35178	Ribosomal RNA-proces	0.15	0.06
Q02486	ARS-binding factor 2, m	0.55	0.19
P43561	Iron transport multicop	0.14	0.06
P34216	EH domain-containing	0.07	0.03
P14743	Glycylpeptide N-tetrad	0.20	0.08
Q12160	Uncharacterized protei	0.82	0.26
P45978	Protein SCD6 OS=Sacch	0.27	0.10
P49334	Mitochondrial import r	0.75	0.24
P53721	Respiratory supercomp	0.45	0.16
Q3E841	Uncharacterized protei	1.37	0.37
P38230	Probable quinone oxid	0.29	0.11
P25296	Calcineurin subunit B C	0.61	0.21
P40553	Peroxiredoxin DOT5 OS	0.48	0.17
P25039	Elongation factor G, mi	0.12	0.05
Q01976	ADP-ribose pyrophospl	0.43	0.16
Q07648	D-tyrosyl-tRNA(Tyr) de	0.32	0.12
P0CX33	40S ribosomal protein	5.88	0.84
P39743	Reduced viability upon	0.20	0.08
P53044	Ubiquitin fusion degrac	0.27	0.10
P35189	Transcription initiation	0.19	0.08
P40580	Benzil reductase ((S)-be	0.39	0.14
P12904	5~-AMP-activated prot	0.29	0.11
P11632	Non-histone chromoso	0.54	0.19
Q08689	N-terminal acetyltrans	0.60	0.20
P53173	ER-derived vesicles pro	0.34	0.13
P32608	Retrograde regulation	0.15	0.06
P53844	Phosphatidylinositol tr	0.26	0.10
P38698	Exopolyphosphatase O	0.23	0.09
P34237	Protein CASP OS=Sacch	0.13	0.05
P32486	Beta-glucan synthesis-	0.13	0.05
P25574	ER membrane protein	0.11	0.05
P23643	Vacuolar protein sortin	0.04	0.02
P32463	Acyl carrier protein, mi	0.40	0.15
Q08965	Ribosome biogenesis p	0.07	0.03

P22133	Malate dehydrogenase	0.26	0.10
Q06178	Nicotinamide/nicotinic	0.23	0.09
P40348	Replication factor C sul	0.27	0.10
P38825	Protein TOM71 OS=Sac	0.14	0.06
P50623	SUMO-conjugating enz	0.68	0.23
Q08924	Regulator of Ty1 trans	0.09	0.04
P54003	Protein SUR7 OS=Sacch	0.15	0.06
P39007	Dolichyl-diphosphoolig	0.12	0.05
P43639	Casein kinase II subuni	0.16	0.06
P17891	Clathrin light chain OS=	0.19	0.08
P52871	Protein transport prot	0.62	0.21
P00546	Cyclin-dependent kina	0.32	0.12
P06785	Thymidylate synthase	0.31	0.12
P40582	Glutathione S-transfer	0.19	0.08
Q06506	Ribosomal RNA-proces	0.16	0.06
Q99383	Nuclear polyadenylate	0.17	0.07
P38811	Transcription-associat	0.02	0.01
P40515	Mitochondria fission 1	0.69	0.23
P40970	Serine palmitoyltransf	0.16	0.06
P32583	Suppressor protein SR	0.12	0.05
P46985	Probable alpha-1,6-ma	0.22	0.09
P07278	cAMP-dependent prot	0.22	0.09
Q05123	Actin-like protein ARP	0.19	0.08
P38789	Ribosome biogenesis p	0.10	0.04
P53909	Adenine deaminase OS	0.13	0.05
P53136	Ribosome biogenesis p	0.10	0.04
P04051	DNA-directed RNA poly	0.06	0.03
Q07896	Nucleolar complex-ass	0.06	0.03
P34221	Protein phosphatase 2	0.20	0.08
P38628	Phosphoacetylglucosa	0.16	0.06
Q02784	Monothiol glutaredoxi	0.32	0.12
P39003	High-affinity hexose tr	0.08	0.03
Q05926	Glutaredoxin-8 OS=Sac	0.44	0.16
Q12496	Uncharacterized protei	0.08	0.03
P36147	Presequence transloca	0.53	0.18
P32644	Putative ATP-depende	0.08	0.03
P47017	Sm-like protein LSm1	0.59	0.20
P25623	Suppressor of yeast pr	0.05	0.02
Q02795	Dolichyl-diphosphoolig	0.16	0.06
Q12513	Translation machinery-	0.32	0.12
P39929	Vacuolar-sorting prote	0.19	0.08
P19955	37S ribosomal protein	0.40	0.15
P38085	Valine/tyrosine/trypto	0.07	0.03
P38804	Restriction of telomere	0.47	0.17
Q12349	ATP synthase subunit	0.39	0.14
P25586	KRR1 small subunit pro	0.29	0.11
P35179	Protein transport prote	0.67	0.22
P53332	Phosphopantetheine a	0.15	0.06
P08964	Myosin-1 OS=Saccharo	0.04	0.02
Q07540	Frataxin homolog, mit	0.27	0.10
P38221	Phosphatidate cytidyly	0.20	0.08
P38353	Sec sixty-one protein h	0.09	0.04

P23255	Transcription initiation	0.06	0.03
P00044	Cytochrome c iso-1 OS	0.46	0.16
P34761	Protein WHI3 OS=Sacc	0.07	0.03
Q08687	Translation machinery-	0.25	0.10
P28273	5-oxoprolinase OS=Sac	0.07	0.03
P38836	Putative metallocarbox	0.21	0.08
Q08954	Smr domain-containing	0.42	0.15
P43577	Glucosamine 6-phosph	0.29	0.11
P40160	Serine/threonine-prote	0.10	0.04
P40513	Mitochondrial acidic pr	0.17	0.07
Q08179	Mitochondrial distribut	0.16	0.06
P53163	54S ribosomal protein	0.26	0.10
P39109	Metal resistance prote	0.06	0.03
Q06704	Golgin IMH1 OS=Sacch	0.05	0.02
P41895	Transcription initiation	0.06	0.03
Q12164	Pore membrane protei	0.16	0.06
P15731	Ubiquitin-conjugating e	0.32	0.12
P34223	UBX domain-containing	0.22	0.09
P08466	Mitochondrial nuclease	0.13	0.05
P33421	Succinate dehydrogena	0.24	0.09
P15496	Isopentenyl-diphospha	0.15	0.06
P40533	Protein TED1 OS=Sacch	0.19	0.08
P32628	UV excision repair prot	0.25	0.10
P30605	Myo-inositol transport	0.08	0.03
P53278	Uncharacterized protei	0.11	0.05
P61830	Histone H3 OS=Sacchar	0.36	0.13
P47165	Xanthine phosphoribos	0.22	0.09
P38985	Signal recognition part	0.33	0.12
P35732	RNA polymerase II deg	0.06	0.03
P07277	Mevalonate kinase OS=	0.10	0.04
P33202	Ubiquitin fusion degra	0.03	0.01
P00128	Cytochrome b-c1 comp	0.38	0.14
P48439	Dolichyl-diphosphoolig	0.13	0.05
Q3E772	Uncharacterized protei	0.56	0.19
P38341	MICOS complex subuni	0.45	0.16
P25358	Elongation of fatty aci	0.12	0.05
P53114	Mediator of RNA poly	0.08	0.03
P49017	2-methoxy-6-polypren	0.15	0.06
P17695	Glutaredoxin-2, mitoch	0.80	0.26
Q04562	Transmembrane 9 sup	0.06	0.03
P38112	ATP-dependent RNA he	0.06	0.03
P32621	Guanosine-diphosphat	0.09	0.04
P42949	Mitochondrial import i	0.33	0.12
Q3E747	Uncharacterized protei	0.60	0.20
P32794	ATPase family gene 2 p	0.06	0.03
Q12017	Phosducin-like protein	0.15	0.06
P32469	Diphthine methyl ester	0.15	0.06
P40010	Nuclear GTP-binding pr	0.09	0.04
P40545	1-(5-phosphoribosyl)-5	0.17	0.07
P0CT04	Protease B inhibitor 2	0.71	0.23
Q04223	Uncharacterized protei	0.14	0.06
P32626	Enolase-phosphatase E	0.21	0.08

Q07688	Phosphorelay interme	0.28	0.11
P25654	UPF0587 protein YCR0	0.25	0.10
P40529	ADP-ribosylation facto	0.15	0.06
P40018	Small nuclear ribonucl	0.23	0.09
P46964	Dolichyl-diphosphoolig	0.37	0.14
P47137	Uncharacterized oxido	0.16	0.06
Q02196	Adenylyl-sulfate kinase	0.22	0.09
P48362	Protein HGH1 OS=Sacc	0.11	0.05
P53073	ER membrane protein	0.25	0.10
P53877	Pre-rRNA-processing p	0.08	0.03
P06101	Hsp90 co-chaperone C	0.08	0.03
P43609	Chromatin structure-re	0.08	0.03
Q07657	Seventh homolog of se	0.08	0.03
P69771	Vacuolar protein-sorti	0.23	0.09
P20604	Serine/threonine-prote	0.14	0.06
P50108	Probable alpha-1,6-ma	0.11	0.05
P53064	RNA polymerase-assoc	0.07	0.03
P51402	60S ribosomal protein	0.58	0.20
P00175	Cytochrome b2, mitoc	0.07	0.03
P46151	Methylenetetrahydrof	0.07	0.03
Q99369	Family of serine hydrol	0.17	0.07
P36091	Mannan endo-1,6-alph	0.10	0.04
Q96VH5	MICOS complex subun	0.56	0.19
P40363	S-formylglutathione hy	0.15	0.06
Q03262	Phosphoribomutase O	0.07	0.03
Q07825	Putative Xaa-Pro amin	0.06	0.03
P23585	High-affinity glucose tr	0.08	0.03
P42942	Uncharacterized GTP-b	0.11	0.05
P23201	Protein SPA2 OS=Sacc	0.03	0.01
P53192	Golgi to ER traffic prot	0.19	0.08
Q08245	Protein ZEO1 OS=Sacc	0.45	0.16
P53250	Twinfilin-1 OS=Sacchar	0.14	0.06
P26754	Replication factor A pr	0.17	0.07
P34087	DNA-directed RNA pol	0.28	0.11
P38523	GrpE protein homolog,	0.20	0.08
Q06689	Cell membrane protei	0.07	0.03
P38962	Golgi apparatus memb	0.22	0.09
P53326	Uncharacterized prote	0.06	0.03
P38152	Tricarboxylate transpo	0.16	0.06
P08456	CDP-diacylglycerol--ser	0.16	0.06
P07274	Profilin OS=Saccharom	0.40	0.15
P39721	Protein AIM2 OS=Sacc	0.19	0.08
Q08746	Regulator of ribosome	0.23	0.09
P35184	Ribosome assembly pr	0.10	0.04
P38066	GTP cyclohydrolase-2	0.13	0.05
P32908	Structural maintenanc	0.03	0.01
P22135	Protein ATP12, mitoch	0.14	0.06
P34248	Probable intramembra	0.07	0.03
Q00618	Geranylgeranyl transfe	0.13	0.05
P18544	Acetylornithine amino	0.11	0.05
Q12408	Phosphatidylglycerol/p	0.28	0.11
P47124	Putative glycosyltransf	0.11	0.05

P40991	25S rRNA (cytosine(28	0.07	0.03
Q12123	Inactive diphosphatase	0.12	0.05
P32474	Protein disulfide-isome	0.08	0.03
P38244	Vacuolar membrane pr	0.04	0.02
P53946	Actin-related protein 5	0.06	0.03
Q03102	Uncharacterized memb	0.13	0.05
Q03941	Dephospho-CoA kinase	0.19	0.08
Q12040	Broad-specificity phosp	0.20	0.08
P40098	Uncharacterized mitoc	0.19	0.08
Q02776	Mitochondrial import i	0.09	0.04
P27351	AP-2 complex subunit	0.06	0.03
Q12233	ATP synthase subunit g	0.43	0.16
Q12512	Protein ZPS1 OS=Sacch	0.18	0.07
P48567	tRNA pseudouridine sy	0.11	0.05
Q04935	Cytochrome c oxidase	0.22	0.09
P29295	Casein kinase I homolo	0.09	0.04
P38314	Protein SDS24 OS=Sacc	0.09	0.04
P40096	Negative cofactor 2 co	0.35	0.13
P12611	Growth regulation prot	0.09	0.04
P47076	DNA-directed RNA poly	0.29	0.11
Q12402	Protein YOP1 OS=Sacch	0.26	0.10
P39960	GTPase-activating prot	0.02	0.01
Q05979	Kynureninase OS=Sacc	0.10	0.04
P52917	Vacuolar protein sortin	0.10	0.04
P32191	Glycerol-3-phosphate	0.07	0.03
Q92317	Negative cofactor 2 co	0.32	0.12
P25627	18S rRNA (guanine(157	0.16	0.06
Q05785	Epsin-2 OS=Saccharom	0.07	0.03
P25382	Ribosome assembly pr	0.09	0.04
P10507	Mitochondrial-processi	0.10	0.04
P04650	60S ribosomal protein	1.05	0.31
Q12028	AP-1 complex subunit	0.05	0.02
Q05583	Cytosolic iron-sulfur pr	0.13	0.05
P38875	GPI transamidase comp	0.07	0.03
Q06523	Uncharacterized protei	0.10	0.04
Q05788	Purine nucleoside phos	0.15	0.06
P38074	Protein arginine N-met	0.13	0.05
Q07897	Protein CMS1 OS=Sacc	0.15	0.06
P31787	Acyl-CoA-binding prote	0.58	0.20
P53172	Protein SDS23 OS=Sacc	0.08	0.03
Q02792	5~-3~ exoribonuclease	0.04	0.02
P16661	Chitobiosyldiphosphod	0.09	0.04
P25572	Putative uncharacteriz	0.41	0.15
P53297	PAB1-binding protein 1	0.06	0.03
P35176	Peptidyl-prolyl cis-tran	0.45	0.16
P32831	Negative growth regula	0.07	0.03
P39111	V-type proton ATPase	0.41	0.15
P36151	Uncharacterized protei	0.13	0.05
P0CX27	60S ribosomal protein	0.45	0.16
P33311	ATP-dependent perme	0.06	0.03
Q6Q547	H/ACA ribonucleoprote	0.98	0.30
P06839	DNA repair helicase RA	0.05	0.02

P40579	Uncharacterized oxido	0.19	0.08
P40471	NADPH-dependent 1-a	0.15	0.06
P36000	AP-1 complex subunit	0.06	0.03
P06633	Imidazoleglycerol-phos	0.22	0.09
O13297	mRNA-capping enzyme	0.08	0.03
P33333	Probable 1-acyl-sn-glyc	0.15	0.06
Q03774	tRNA (guanine-N(7)-)-n	0.10	0.04
P21375	Fumarate reductase 2	0.09	0.04
P25339	Pumilio homology dom	0.05	0.02
Q08979	Kelch repeat-containin	0.06	0.03
P38902	DNA-directed RNA poly	0.41	0.15
P32453	Protein ATP11, mitoch	0.14	0.06
P39540	Elongation of fatty acic	0.14	0.06
P48234	Ribosome biogenesis p	0.06	0.03
Q08818	Meiotic sister-chromat	0.06	0.03
P53953	SED5-binding protein 2	0.05	0.02
P32500	Nucleoporin NDC1 OS=	0.07	0.03
P47044	LOG family protein YJL	0.19	0.08
P25608	Uncharacterized protei	0.12	0.05
P13382	DNA polymerase alpha	0.03	0.01
P53169	YAP1-binding protein 2	0.07	0.03
P37297	Phosphatidylinositol 4-	0.02	0.01
P40491	ATP synthase assembly	0.29	0.11
P35197	ADP-ribosylation facto	0.13	0.05
P11914	Mitochondrial-processi	0.09	0.04
Q3E7B6	V-type proton ATPase	0.72	0.24
P38250	Increased sodium toler	0.05	0.02
P38719	ATP-dependent RNA he	0.10	0.04
P43610	Uncharacterized ATP-d	0.05	0.02
P40081	Putative magnesium-d	0.26	0.10
P38883	Pre-rRNA-processing p	0.06	0.03
P20435	DNA-directed RNA poly	0.30	0.11
P32342	Signal recognition part	0.29	0.11
P43555	Protein EMP47 OS=Sac	0.10	0.04
Q03834	DNA mismatch repair p	0.03	0.01
P25044	Tyrosine-protein phosp	0.13	0.05
Q12339	rRNA-processing prote	0.18	0.07
P52490	Ubiquitin-conjugating	0.31	0.12
Q02774	Secretory component p	0.22	0.09
Q07915	Ribosome biogenesis p	0.21	0.08
Q12114	Chitin biosynthesis pro	0.07	0.03
P52870	Protein transport prote	0.70	0.23
P41819	Dimethyladenosine tra	0.14	0.06
P07253	Cytochrome B pre-mRN	0.29	0.11
P53600	Coatomer subunit zeta	0.24	0.09
Q03880	V-type ATPase assemb	0.40	0.15
Q12387	N-terminal acetyltrans	0.05	0.02
Q99207	Nucleolar complex pro	0.05	0.02
P39993	ARF guanine-nucleotid	0.03	0.01
P32857	Membrane protein PTI	0.08	0.03
P39112	Exoribonuclease II, mit	0.04	0.02
P40046	Vacuolar transporter c	0.38	0.14

P47150	37S ribosomal protein	0.18	0.07
P00427	Cytochrome c oxidase	0.31	0.12
P22023	Killer toxin-resistance	0.03	0.01
P27514	Low-affinity phosphate	0.05	0.02
P53550	m7GpppN-mRNA hydr	0.04	0.02
P38081	Uncharacterized glycos	0.09	0.04
P49957	tRNA (carboxymethylu	0.16	0.06
P38145	Riboflavin synthase OS	0.20	0.08
P18899	Stress protein DDR48	0.11	0.05
P53107	Ran-specific GTPase-ac	0.10	0.04
P36036	RNA annealing protein	0.22	0.09
P39984	Histone acetyltransfer	0.11	0.05
P47068	Myosin tail region-inte	0.04	0.02
P07143	Cytochrome c1, heme	0.15	0.06
P43590	Uncharacterized peptid	0.08	0.03
P25037	Ubiquitin carboxyl-terr	0.05	0.02
P25441	DNA-directed RNA poly	0.11	0.05
Q03655	Probable 1,3-beta-gluc	0.09	0.04
Q12329	Heat shock protein 42	0.12	0.05
P40350	Dolichyl-phosphate bet	0.13	0.05
Q06144	Protein ORM2 OS=Sacc	0.21	0.08
P32447	Histone chaperone ASF	0.16	0.06
P53152	Ubiquitin-conjugating	0.35	0.13
P38922	Protein HRB1 OS=Sacch	0.09	0.04
Q12196	Serine/threonine-prote	0.09	0.04
P36080	Ribosomal RNA-proces	0.10	0.04
P14747	Serine/threonine-prote	0.07	0.03
P36148	Glycerol-3-phosphate	0.06	0.03
P38067	Succinate-semialdehyd	0.09	0.04
Q02046	Methylenetetrahydrof	0.14	0.06
P28789	Porphobilinogen deam	0.14	0.06
P34222	Peptidyl-tRNA hydrolas	0.23	0.09
Q02793	Antiviral protein SKI8	0.11	0.05
P53011	Nucleoporin SEH1 OS=	0.13	0.05
P38137	Peroxisomal-coenzyme	0.08	0.03
P32639	Pre-mRNA-splicing heli	0.02	0.01
Q05881	Uncharacterized protei	0.12	0.05
P54070	Mannosyltransferase K	0.09	0.04
P40541	Cohesin subunit SCC3	0.04	0.02
P14741	Translation initiation fa	0.15	0.06
P53188	rRNA-processing prote	0.38	0.14
P14922	General transcriptional	0.05	0.02
P32378	4-hydroxybenzoate pol	0.12	0.05
Q01217	Protein ARG5,6, mitoch	0.05	0.02
P40564	DnaJ-like protein 1 OS=	0.10	0.04
P24521	Phosphomevalonate ki	0.10	0.04
P38234	Protein RFS1 OS=Sacch	0.23	0.09
Q03148	Pyridoxal 5~-phosphat	0.16	0.06
P25555	Single-strand telomeri	0.10	0.04
P36154	Altered inheritance rat	0.29	0.11
P38793	tRNA (guanine(37)-N1)	0.09	0.04
P38797	Protein phosphatase 2	0.13	0.05

Q12008	Phosphoglycerate mut	0.14	0.06
P27882	Mitochondrial FAD-link	0.24	0.09
P42847	37S ribosomal protein	0.21	0.08
P36051	GPI ethanolamine phos	0.05	0.02
P36088	Free methionine-R-sulf	0.26	0.10
P39543	Protein SOP4 OS=Sacch	0.19	0.08
P38800	Membrane-anchored li	0.03	0.01
P53845	Protein transport prote	0.14	0.06
P40516	Protein-lysine N-methy	0.18	0.07
P36057	Signal recognition part	0.19	0.08
P40452	Cytochrome c oxidase	0.24	0.09
P53154	Glycerol uptake protei	0.08	0.03
P27692	Transcription elongatic	0.04	0.02
P20434	DNA-directed RNA poly	0.21	0.08
P40501	Vacuolar amino acid tr	0.09	0.04
Q03557	Glutamyl-tRNA(Gln) am	0.10	0.04
Q08444	20S-pre-rRNA D-site er	0.10	0.04
Q03713	Respiratory supercomp	0.29	0.11
Q03016	GLC7-interacting prote	0.03	0.01
P53075	Outer spore wall assem	0.07	0.03
Q06405	ATP synthase subunit f	0.51	0.18
Q04767	Golgi apparatus memb	0.28	0.11
P32899	U3 small nucleolar ribo	0.24	0.09
P32775	1,4-alpha-glucan-branc	0.06	0.03
Q08096	RNA 3~-terminal phosp	0.12	0.05
P32906	Endoplasmic reticulum	0.08	0.03
P25303	DnaJ-related protein S	0.12	0.05
P17536	Tropomyosin-1 OS=Sac	0.22	0.09
P48363	Prefoldin subunit 3 OS	0.22	0.09
P53552	THO complex subunit	0.03	0.01
P46682	AP-3 complex subunit	0.05	0.02
P35845	Oxysterol-binding prot	0.04	0.02
P53072	tRNA acetyltransferase	0.15	0.06
Q03104	Meiotic sister chromat	0.08	0.03
P40480	Protein HOS4 OS=Sacc	0.04	0.02
P43612	SIT4-associating protei	0.04	0.02
P32353	Delta(7)-sterol 5(6)-des	0.12	0.05
P42840	Uncharacterized memb	0.16	0.06
P25297	Inorganic phosphate tr	0.08	0.03
Q12089	ATPase expression pro	0.07	0.03
P40347	Low molecular weight	0.28	0.11
P12753	DNA repair protein RA	0.03	0.01
P12683	3-hydroxy-3-methylglu	0.04	0.02
Q08621	Putative uncharacteriz	0.39	0.14
Q03761	Transcription initiation	0.08	0.03
P32767	Importin beta-like prot	0.04	0.02
Q04213	ISWI one complex prot	0.09	0.04
Q12453	Cytoplasmic export prc	0.06	0.03
P35127	Ubiquitin carboxyl-terr	0.20	0.08
P53968	Transcriptional regulat	0.06	0.03
P38798	Nonsense-mediated m	0.04	0.02
Q03799	37S ribosomal protein	0.30	0.11

P38328	Actin-related protein 2	0.12	0.05
P53929	Uncharacterized protei	0.17	0.07
P48240	Exosome complex com	0.18	0.07
Q05567	Sphingosine-1-phospha	0.07	0.03
P28625	Protein YIM1 OS=Sacch	0.12	0.05
Q05931	Heat shock protein SSC	0.07	0.03
P46970	Nonsense-mediated m	0.04	0.02
P47818	Protein CCC1 OS=Sacch	0.15	0.06
P27929	37S ribosomal protein	0.09	0.04
P46957	DNA polymerase delta	0.09	0.04
Q12024	Ribosome biogenesis p	0.10	0.04
Q99216	Pre-rRNA-processing p	0.17	0.07
P36160	Ribosome biogenesis p	0.13	0.05
P27999	DNA-directed RNA poly	0.37	0.14
Q02206	Chromatin structure-re	0.07	0.03
P53206	Putative cysteine synth	0.12	0.05
P38888	ER degradation-enhanc	0.05	0.02

Filtered Pellet					Filtered Supernatant
protein access ID	protein description	emPAI	relative abundance		protein access ID
Q00955	Acetyl-CoA carboxylase	22.39	1.37		P00925
Q12019	Midasin OS=Saccharom	2.26	0.51		P32324
P33892	eIF-2-alpha kinase activ	3.75	0.68		P00549
Q05022	rRNA biogenesis protei	8.71	0.99		P10592
Q02455	Protein MLP1 OS=Sacch	6.32	0.86		P10591
P38811	Transcription-associate	2.00	0.48		P00359
P06105	Protein SCP160 OS=Sac	19.37	1.31		P19097
P10964	DNA-directed RNA poly	7.97	0.95		P00560
P35194	U3 small nucleolar RNA	2.60	0.56		P07149
P07259	Protein URA2 OS=Sacch	3.15	0.62		P00924
P08566	Pentafunctional AROM	5.57	0.82		P11484
P04050	DNA-directed RNA poly	3.94	0.69		P40150
P42945	U3 small nucleolar RNA	2.92	0.59		P06169
P07149	Fatty acid synthase sub	2.90	0.59		P15108
P38631	1,3-beta-glucan syntha	3.52	0.66		P00358
P16521	Elongation factor 3A O	18.23	1.28		P05030
P17255	V-type proton ATPase (	12.71	1.14		P16521
P0CS90	Heat shock protein SSC	25.50	1.42		P02994
P32324	Elongation factor 2 OS=	20.70	1.34		P05694
P19097	Fatty acid synthase sub	3.12	0.61		P02829
Q03434	Transposon Ty1-ML2 G	3.36	0.64		P0CS90
P33302	Pleiotropic ABC efflux t	4.36	0.73		P00360
Q12273	Transposon Ty1-OL Gag	3.36	0.64		Q00955
Q03640	Tricalbin-3 OS=Sacchar	3.32	0.64		P07259
Q12680	Glutamate synthase [N	2.08	0.49		P14540
Q12414	Transposon Ty1-PL Gag	3.36	0.64		P17255
P10592	Heat shock protein SSA	33.04	1.53		P16861
P22138	DNA-directed RNA poly	7.26	0.92		P00330
P23615	Transcription elongatic	3.82	0.68		P54115
P22137	Clathrin heavy chain O	2.90	0.59		P19882
P32657	Chromo domain-conta	3.56	0.66		P32589
P34241	Nucleolar pre-ribosoma	2.67	0.56		P22202
P10591	Heat shock protein SSA	32.66	1.53		P14126
P38144	ISWI chromatin-remod	6.77	0.89		P10081
P19524	Myosin-2 OS=Saccharo	2.78	0.58		P31539
P31539	Heat shock protein 104	11.69	1.10		P33892
P32558	FACT complex subunit	7.88	0.95		P25694
Q03280	E3 ubiquitin-protein lig	1.05	0.31		P39954
P22147	5~-3~ exoribonuclease	4.31	0.73		P16474
P47100	Transposon Ty1-JR2 Ga	2.87	0.59		P22137
P09440	C-1-tetrahydrofolate sy	8.61	0.98		P12709
P05030	Plasma membrane ATP	9.60	1.03		P09436
P39986	Manganese-transporti	4.31	0.73		Q03434
P15108	ATP-dependent molecu	13.72	1.17		P16140
P32597	Nuclear protein STH1/I	3.38	0.64		Q12414
P16474	78 kDa glucose-regulat	19.98	1.32		P60010
P19882	Heat shock protein 60,	24.69	1.41		P0C2I7
P19414	Aconitate hydratase, m	14.75	1.20		P19414
P39685	Nucleoporin POM152 (	3.04	0.61		Q12273
P02829	ATP-dependent molecu	12.64	1.13		P16862

P33416	Heat shock protein 78,	10.87	1.07	P47100
P47054	Nucleoporin NUP192 C	2.77	0.58	P00950
P47037	Structural maintenanc	3.82	0.68	P00942
P25694	Cell division control pr	12.68	1.14	P06105
P11484	Ribosome-associated	12.71	1.14	Q12680
P00549	Pyruvate kinase 1 OS=	39.07	1.60	P38011
Q03690	Clustered mitochondri	3.33	0.64	P0CX53
P53254	U3 small nucleolar RN	4.01	0.70	P37291
P08518	DNA-directed RNA poly	3.59	0.66	P46655
P21576	Vacuolar protein sortin	13.84	1.17	P06634
P05694	5-methyltetrahydropte	8.00	0.95	P38013
P40150	Ribosome-associated	11.77	1.11	P53978
P06786	DNA topoisomerase 2	3.09	0.61	P19358
P46367	Potassium-activated al	17.16	1.26	P38788
P30624	Long-chain-fatty-acid--	10.07	1.04	P32582
P53622	Coatomer subunit alph	3.30	0.63	P05737
P09624	Dihydrolipoyl dehydrog	19.92	1.32	P05750
Q06179	Protein FMP27, mitoch	1.14	0.33	P07245
P07245	C-1-tetrahydrofolate sy	5.62	0.82	P26637
P16861	ATP-dependent 6-phos	4.71	0.76	P40825
P32589	Heat shock protein hor	17.58	1.27	Q12213
P21954	Isocitrate dehydrogena	53.69	1.74	P30624
P36161	Nucleoporin NUP133 C	3.40	0.64	P33442
P07251	ATP synthase subunit a	17.13	1.26	P10659
P53914	RNA cytidine acetyltrar	4.47	0.74	P15019
P32908	Structural maintenanc	2.94	0.60	P07262
P07213	Mitochondrial import r	13.70	1.17	P23248
P00560	Phosphoglycerate kina	28.07	1.46	P29311
P32565	26S proteasome regula	6.30	0.86	P15705
P38737	Proteasome componer	1.29	0.36	P32454
P40064	Nucleoporin NUP157 C	2.13	0.50	P08566
Q12460	Nucleolar protein 56 O	18.61	1.29	P40024
P40989	1,3-beta-glucan syntha	1.43	0.39	P38972
Q08972	[NU+] prion formation	2.29	0.52	P38009
P00359	Glyceraldehyde-3-phos	127.20	2.11	P38088
P04051	DNA-directed RNA poly	2.27	0.51	P00815
P32454	Aminopeptidase 2, mit	3.62	0.66	P04802
P31688	Trehalose-phosphatase	4.41	0.73	P10664
P17967	Protein disulfide-isome	15.82	1.23	P17967
P06169	Pyruvate decarboxylas	14.68	1.20	P49626
Q12466	Tricalbin-1 OS=Sacchar	3.11	0.61	P52910
P32599	Fimbrin OS=Saccharom	7.73	0.94	P34760
P20967	2-oxoglutarate dehydr	3.59	0.66	P29453
P40053	Altered inheritance of	10.06	1.04	P40069
P00830	ATP synthase subunit b	12.20	1.12	P04807
P14126	60S ribosomal protein	33.64	1.54	P32327
P52593	Nucleoporin NUP188 C	1.46	0.39	P23254
P32568	Protein SNQ2 OS=Saccl	1.57	0.41	P34730
P05374	Phosphatidylethanolan	5.74	0.83	P0CX37
P38181	Nucleoporin NUP170 C	1.72	0.43	P05317
P38934	Nuclear segregation pr	14.85	1.20	P46367
P36775	Lon protease homolog,	3.25	0.63	P38427

P16603	NADPH--cytochrome P	5.71	0.83		P0CX55
P00925	Enolase 2 OS=Sacchar	23.81	1.39		P33416
P25655	General negative regul	0.95	0.29		P17076
P00927	Threonine dehydratase	12.18	1.12		P21576
Q04214	Transposon Ty1-MR1 G	1.24	0.35		P32565
P33334	Pre-mRNA-splicing fact	0.81	0.26		P04147
P32639	Pre-mRNA-splicing heli	0.92	0.28		P32074
P34077	Nucleoporin NIC96 OS=	3.81	0.68		P07244
P27692	Transcription elongati	2.41	0.53		P07806-2
Q99287	Protein SEY1 OS=Sacch	4.69	0.76		P11154
P60010	Actin OS=Saccharomyc	70.92	1.86		Q04214
P16140	V-type proton ATPase	9.70	1.03		P0C2H6
Q03104	Meiotic sister chromat	8.93	1.00		P53622
P38764	26S proteasome regula	3.32	0.64		Q03690
Q05050	Eisosome protein 1 OS=	4.59	0.75		P31688
P41810	Coatomer subunit beta	2.81	0.58		P53252
P16387	Pyruvate dehydrogena	92.43	1.97		P0CX43
P32368	Phosphoinositide phos	6.30	0.86		P03965
P02994	Elongation factor 1-alp	20.91	1.34		P41811
P07257	Cytochrome b-c1 comp	15.26	1.21		P05740
P25087	Sterol 24-C-methyltran	24.51	1.41		P31116
P53552	THO complex subunit 2	1.33	0.37		P02407
P53261	Pescadillo homolog OS	7.08	0.91		P38707
P04147	Polyadenylate-binding	6.76	0.89		P0CX39
P06168	Ketol-acid reductoisom	22.92	1.38		P46990
P32333	TATA-binding protein-a	1.10	0.32		P04456
P32191	Glycerol-3-phosphate	8.07	0.96		P26263
P49095	Glycine dehydrogenase	2.87	0.59		P41810
P06634	ATP-dependent RNA he	11.35	1.09		P26784
P38720	6-phosphogluconate d	14.03	1.18		P04801
P32563	V-type proton ATPase	3.39	0.64		P32861
P52910	Acetyl-coenzyme A syn	6.34	0.87		P38720
P40482	Protein transport prote	2.40	0.53		P26783
P47047	ATP-dependent RNA he	2.30	0.52		Q00055
P36016	Heat shock protein 70	4.26	0.72		P39015
P06208	2-isopropylmalate synt	8.58	0.98		P0CX35
P38427	Trehalose synthase cor	2.16	0.50		P14832
P25635	Periodic tryptophan pr	3.26	0.63		P38701
Q12499	Nucleolar protein 58 O	8.36	0.97		Q3E757
P32861	UTP--glucose-1-phosph	11.42	1.09		P26785
P37297	Phosphatidylinositol 4-	0.85	0.27		P0CX51
Q12754	Ribosomal RNA-proces	1.99	0.48		P05738
P39744	Nucleolar complex pro	7.47	0.93		P25443
P16547	Mitochondrial outer m	20.52	1.33		P32599
P54115	Magnesium-activated	11.11	1.08		P39730
P16862	ATP-dependent 6-phos	2.36	0.53		P41805
P40024	ABC transporter ATP-b	5.43	0.81		P05756
P00358	Glyceraldehyde-3-phos	49.57	1.70		P51401
P15424	ATP-dependent RNA he	6.19	0.86		P22515
P38250	Increased sodium toler	2.33	0.52		Q12363
P39522	Dihydroxy-acid dehydr	10.67	1.07		P39516
P32074	Coatomer subunit gam	2.21	0.51		P38968

Q12389	ATP-dependent RNA h	2.82	0.58	P00830
P34160	Nuclear cap-binding pr	2.93	0.59	Q12499
Q12464	RuvB-like protein 2 OS	13.06	1.15	P37012
P39985	DNA polymerase V OS=	2.37	0.53	P36008
P53312	Succinate--CoA ligase [	17.11	1.26	P05755
P48231	Tricalbin-2 OS=Sacchar	2.02	0.48	P40482
P10081	ATP-dependent RNA h	12.82	1.14	P11076
P89105	RNA polymerase-assoc	2.23	0.51	P15180
P40457	Protein MLP2 OS=Sacc	1.06	0.31	P0CX31
P07342	Acetolactate synthase	5.61	0.82	P07284
Q04728	Arginine biosynthesis b	11.72	1.10	Q05506
P04840	Mitochondrial outer m	33.43	1.54	P32497
P32898	Mitochondrial presequ	1.98	0.47	P0CX49
P37291	Serine hydroxymethylt	11.36	1.09	Q12230
P37292	Serine hydroxymethylt	11.68	1.10	Q03558
Q03532	ATP-dependent RNA h	9.17	1.01	P48589
Q08822	Probable electron tran	6.04	0.85	P38249
P39940	E3 ubiquitin-protein lig	2.61	0.56	P26321
P15705	Heat shock protein STI	5.35	0.80	P16467
Q12176	Ribosome biogenesis p	1.98	0.47	P19146
P49367	Homoaconitase, mitoc	3.77	0.68	P49090
P29453	60S ribosomal protein	88.51	1.95	P38934
P23248	40S ribosomal protein	67.65	1.84	P23301
P27472	Glycogen [starch] synth	3.88	0.69	Q08972
P32582	Cystathionine beta-syn	5.93	0.84	P16603
P33442	40S ribosomal protein	68.77	1.84	P47143
P16649	General transcriptional	3.76	0.68	P38708
P00890	Citrate synthase, mitoc	7.33	0.92	P0CX23
P43609	Chromatin structure-re	4.13	0.71	P06738
Q04660	Ribosome biogenesis p	2.26	0.51	P07213
P53115	Putative DNA helicase	1.22	0.35	P0CX82
Q04636	FACT complex subunit	6.52	0.88	P49089
P22202	Heat shock protein SSA	3.75	0.68	P07283
P36013	NAD-dependent malic	4.86	0.77	P54114
P54861	Dynamin-related prote	2.57	0.55	O13516
P18239	ADP,ATP carrier protei	33.12	1.53	P27472
P23254	Transketolase 1 OS=Sa	4.61	0.75	P00817
P41811	Coatomer subunit beta	2.27	0.51	P36105
Q06639	Chromatin structure-re	2.48	0.54	P00931
P53008	Mannosyl-oligosacchar	2.22	0.51	P50095
P00924	Enolase 1 OS=Saccharo	7.27	0.92	P54113
P40032	Prolyl 3,4-dihydroxylas	5.31	0.80	P04806
P33322	H/ACA ribonucleoprote	9.95	1.04	P32563
Q12220	U3 small nucleolar RN	2.15	0.50	P41940
P17076	60S ribosomal protein	63.17	1.81	P08524
Q03940	RuvB-like protein 1 OS	6.76	0.89	P0CX84
P38011	Guanine nucleotide-bi	28.16	1.46	P16120
P14906	Protein translocation p	3.76	0.68	P07280
P08964	Myosin-1 OS=Saccharo	0.77	0.25	P09624
P53075	Outer spore wall assen	5.18	0.79	P07251
Q08965	Ribosome biogenesis p	1.47	0.39	P38754
Q01852	Mitochondrial import i	10.16	1.05	P05739

P39954	Adenosylhomocysteina	9.69	1.03		P13188
P38249	Eukaryotic translation i	2.05	0.48		Q02326
P38687	Signal recognition part	3.81	0.68		P06103
Q02931	NET1-associated nucle	2.06	0.49		P06208
P38788	Ribosome-associated c	4.94	0.77		P54838
P40215	External NADH-ubiquir	5.54	0.82		P15303
P53920	Pro-apoptotic serine p	1.88	0.46		P38631
P07262	NADP-specific glutama	6.29	0.86		P46672
Q12363	Transcriptional modula	4.75	0.76		P32368
Q04439	Myosin-5 OS=Saccharo	1.54	0.40		P41277
Q04697	Glucose-signaling facto	7.61	0.94		P10964
P12695	Dihydrolipoyllysine-res	5.73	0.83		P09440
Q01217	Protein ARG5,6, mitoc	1.98	0.47		P29509
P12385	Eukaryotic peptide cha	8.07	0.96		Q07551
P07256	Cytochrome b-c1 comp	4.94	0.77		P35691
P43583	Proteasome activator	0.71	0.23		P38764
P36112	MICOS complex subuni	3.63	0.67		Q03195
Q12166	2-isopropylmalate synt	4.73	0.76		P40053
Q06679	U3 small nucleolar RN	2.60	0.56		Q12690
P29547	Elongation factor 1-gar	6.37	0.87		P32590
P32843	Mitochondrial escape	1.92	0.47		P0CX41
P32380	Spindle pole body com	1.65	0.42		P32905
P32891	D-lactate dehydrogena	2.90	0.59		P00958
P32660	Phospholipid-transport	0.79	0.25		Q04636
Q02785	ATP-dependent perme	0.93	0.29		P05759
P24783	ATP-dependent RNA h	7.00	0.90		P53221
P17505	Malate dehydrogenase	14.99	1.20		Q05022
P07275	Delta-1-pyrroline-5-car	5.19	0.79		Q01855
P32892	ATP-dependent RNA h	3.50	0.65		P07991
P40047	Aldehyde dehydrogena	4.23	0.72		P39522
P47108	Nucleolar pre-ribosom	1.38	0.38		P17709
Q04264	Sister chromatid cohes	1.30	0.36		P05743
P38688	Signal recognition part	3.08	0.61		P32527
P39730	Eukaryotic translation i	1.52	0.40		Q05050
P40825	Alanine--tRNA ligase, n	1.56	0.41		Q05911
Q12122	Homocitrate synthase,	6.52	0.88		P53852
P00360	Glyceraldehyde-3-phos	19.43	1.31		P50094
P02992	Elongation factor Tu, n	8.54	0.98		P37302
P40991	25S rRNA (cytosine(28	3.11	0.61		P38219
P22579	Transcriptional regulat	0.91	0.28		P00445
Q08773	ISWI chromatin-remod	1.22	0.35		P40106
P15646	rRNA 2~-O-methyltran	28.79	1.47		P05748
P27476	Nuclear localization se	9.26	1.01		P24783
Q07478	ATP-dependent RNA h	6.07	0.85		P06168
Q07878	Vacuolar protein sortin	0.39	0.14		P22147
P32590	Heat shock protein ho	3.29	0.63		P47079
P53131	Pre-mRNA-splicing fact	2.44	0.54		P21264
Q04373	Pumilio homology dom	3.23	0.63		P27476
P22023	Killer toxin-resistance	1.12	0.33		P29547
P32468	Cell division control pr	6.51	0.88		P0CX47
P32473	Pyruvate dehydrogena	7.28	0.92		P15624
Q07457	E3 ubiquitin-protein lig	2.80	0.58		P40531

P38129	Transcription initiation	2.03	0.48		P22203
P32916	Signal recognition part	3.17	0.62		Q03048
P53276	U3 small nucleolar RN	2.22	0.51		P32558
P23542	Aspartate aminotransf	6.66	0.88		P12945
P32457	Cell division control pr	6.10	0.85		P33322
P32492	Myosin-4 OS=Saccharo	0.90	0.28		P07702
P38968	Protein transport prot	0.97	0.29		P0C0W1
P15019	Transaldolase OS=Sacc	11.65	1.10		P07342
P33338	Protein SLA2 OS=Sacch	1.37	0.37		P02406
P25574	ER membrane protein	2.28	0.52		P39986
P04786	DNA topoisomerase 1	2.33	0.52		P48164
P09436	Isoleucine--tRNA ligase	1.32	0.37		P32449
P40495	Homoisocitrate dehydr	12.07	1.12		P13663
P25386	Intracellular protein tr	0.69	0.23		P38625
P37838	Nucleolar protein 4 OS	3.02	0.60		Q02753
P32340	Rotenone-insensitive	5.14	0.79		P39976
P40069	Importin subunit beta-	1.24	0.35		P12695
P39533	Homocitrate dehydrat	2.30	0.52		P04449
Q03921	Protein dopey OS=Sacc	0.70	0.23		Q12672
P38694	Putative aldehyde deh	2.47	0.54		P24000
P53049	Oligomycin resistance	0.81	0.26		P33302
Q03862	Probable metalloprote	3.21	0.62		Q12460
P10664	60S ribosomal protein	7.74	0.94		P38205
P33775	Dolichyl-phosphate-ma	2.21	0.51		P52489
P50095	Inosine-5~-monophosp	3.83	0.68		P54780
P00330	Alcohol dehydrogenase	13.14	1.15		P26786
P41338	Acetyl-CoA acetyltrans	6.50	0.88		P41338
P48570	Homocitrate synthase,	4.96	0.78		Q07478
P38295	Medium-chain fatty ac	9.80	1.03		P28319
P15303	Protein transport prot	2.17	0.50		P38697
P25847	DNA mismatch repair	1.58	0.41		P80210
P36008	Elongation factor 1-ga	6.55	0.88		Q03640
P38972	Phosphoribosylformylg	0.88	0.27		P31373
P49626	60S ribosomal protein	7.74	0.94		Q12019
Q06218	ATP-dependent RNA h	3.27	0.63		P13298
Q12265	Ribose-phosphate pyr	4.28	0.72		P32191
P32521	Actin cytoskeleton-reg	0.80	0.26		P39744
P15891	Actin-binding protein	3.87	0.69		P54839
P12684	3-hydroxy-3-methylglu	1.44	0.39		Q03862
P53125	Imitation switch two c	1.10	0.32		P54861
P07806-2	Isoform Cytoplasmic o	1.28	0.36		P36010
P31382	Dolichyl-phosphate-ma	2.28	0.52		P36013
P06103	Eukaryotic translation	2.60	0.56		Q08971
P40318	ERAD-associated E3 ub	1.24	0.35		P39517
P07267	Saccharopepsin OS=Sa	4.99	0.78		P14906
P43535	Protein GCN20 OS=Sac	1.87	0.46		P49367
P38626	NADH-cytochrome b5	62.97	1.81		P11986
P46655	Glutamate--tRNA ligas	2.40	0.53		P0CX45
P09938	Ribonucleoside-diphos	6.66	0.88		Q12166
P26321	60S ribosomal protein	13.11	1.15		P40991
Q04062	26S proteasome regul	7.65	0.94		P0CX29
P06738	Glycogen phosphoryla	1.61	0.42		P24784

P05750	40S ribosomal protein	39.96	1.61		P32528
P07278	cAMP-dependent prot	5.01	0.78		P32835
P05453	Eukaryotic peptide cha	3.11	0.61		P20967
P47912	Long-chain-fatty-acid--	2.16	0.50		P04050
P40016	26S proteasome regula	2.75	0.57		P38061
Q12018	Cell division control pr	1.59	0.41		P19524
P25491	Mitochondrial protein	8.86	0.99		P0C2H8
P29704	Squalene synthase OS=	6.30	0.86		P40032
P12683	3-hydroxy-3-methylglu	1.25	0.35		P47771
P47075	Vacuolar transporter c	2.48	0.54		P38791
P36006	Myosin-3 OS=Saccharo	0.94	0.29		P33401
P36060	NADH-cytochrome b5	16.95	1.25		P04840
P20447	ATP-dependent RNA h	3.58	0.66		Q99287
P0C2J3	Transposon Ty2-LR1 G	0.56	0.19		P07264
P32386	ATP-dependent bile ac	0.73	0.24		P53228
Q02776	Mitochondrial import i	6.14	0.85		Q03103
P29311	Protein BMH1 OS=Sac	18.21	1.28		P0C2H9
Q00402	Nuclear migration prot	0.37	0.14		P27616
P38009	Bifunctional purine bio	2.65	0.56		P32288
P28834	Isocitrate dehydrogen	7.64	0.94		P47120
P47117	Actin-related protein 3	5.63	0.82		P53090
Q05946	U3 small nucleolar RN	1.28	0.36		Q12122
P25039	Elongation factor G, mi	2.58	0.55		P43535
P17555	Adenylyl cyclase-assoc	3.35	0.64		O14455
P54783	D-arabinono-1,4-lacto	3.83	0.68		P36049
P53731	Actin-related protein 2	4.91	0.77		Q00764
P40010	Nuclear GTP-binding p	3.00	0.60		P38999
Q06440	Coronin-like protein O	3.47	0.65		P34160
Q02892	Nucleolar GTP-binding	2.76	0.58		P22146
Q02821	Importin subunit alpha	3.72	0.67		P38426
P32795	Mitochondrial inner m	1.66	0.42		P00890
Q03103	Endoplasmic oxidored	3.20	0.62		P09938
Q03195	Translation initiation f	3.20	0.62		P15424
P36049	rRNA-processing prote	4.01	0.70		P01123
P00431	Cytochrome c peroxid	7.14	0.91		P09733
P26637	Leucine--tRNA ligase, c	0.90	0.28		P25045
P35844	Oxysterol-binding prot	4.03	0.70		P39676
P21243	Proteasome subunit al	15.94	1.23		P14742
P21147	Acyl-CoA desaturase 1	4.00	0.70		P34077
P12709	Glucose-6-phosphate i	3.67	0.67		P38687
Q00764	Alpha,alpha-trehalose-	2.51	0.55		P53261
Q01939	26S protease regulator	6.15	0.85		P15625
P40341	Mitochondrial respirat	1.89	0.46		P18562
P38077	ATP synthase subunit g	6.76	0.89		P18759
P53252	Sphingolipid long chair	5.32	0.80		P09064
P39517	ATP-dependent RNA h	3.33	0.64		P31382
P25605	Acetolactate synthase	14.51	1.19		P29952
P08417	Fumarate hydratase, m	4.81	0.76		P07170
Q12213	60S ribosomal protein	16.92	1.25		P32457
P13382	DNA polymerase alpha	0.75	0.24		P38694
P05737	60S ribosomal protein	16.92	1.25		P06115
P07246	Alcohol dehydrogenase	7.01	0.90		Q02892

P38426	Trehalose synthase cor	0.96	0.29		P05453
P49687	Nucleoporin NUP145 C	0.91	0.28		P09734
P23641	Mitochondrial phospha	5.38	0.80		P25386
P40541	Cohesin subunit SCC3 (	1.10	0.32		P02557
P14540	Fructose-bisphosphate	4.88	0.77		P14120
P32419	Malate dehydrogenase	6.57	0.88		P32481
P40468	Cell morphogenesis pr	0.44	0.16		P32356
P38523	GrpE protein homolog,	16.75	1.25		Q08822
P43593	Ubiquitin carboxyl-terr	2.43	0.54		P27692
Q02486	ARS-binding factor 2, n	76.13	1.89		P38840
P0CX43	60S ribosomal protein	29.21	1.48		P38810
Q04947	Reticulon-like protein 1	8.71	0.99		P47912
P32379	Proteasome subunit al	12.63	1.13		P18239
P12945	N-terminal acetyltransf	1.47	0.39		P22336
P41921	Glutathione reductase	3.85	0.69		P32471
Q12230	Sphingolipid long chain	7.17	0.91		P39940
P25294	Protein SIS1 OS=Saccha	6.44	0.87		Q01560
Q03516	Uncharacterized protei	1.20	0.34		P32804
P0CX35	40S ribosomal protein	14.08	1.18		P05745
P53723	UPF0674 endoplasmic	4.44	0.74		P11745
P48015	Aminomethyltransfera	7.26	0.92		Q12068
Q01080	DNA-directed RNA poly	5.79	0.83		P41807
Q08179	Mitochondrial distribut	3.26	0.63		P32891
P21951	DNA polymerase epsilc	0.44	0.16		P38431-2
P22276	DNA-directed RNA poly	0.99	0.30		P40217
P22203	V-type proton ATPase s	16.12	1.23		P37303
P10614	Lanosterol 14-alpha de	3.03	0.61		P53131
Q06142	Importin subunit beta-	1.56	0.41		P38688
P32327	Pyruvate carboxylase 2	0.92	0.28		P23542
P01120	Ras-like protein 2 OS=S	5.65	0.82		Q02821
P23255	Transcription initiation	0.79	0.25		P53276
Q07451	Endoplasmic reticulum	25.07	1.42		P12385
P12753	DNA repair protein RAI	0.86	0.27		P04046
P35729	Nucleoporin NUP120 C	1.18	0.34		P25574
Q03834	DNA mismatch repair p	0.96	0.29		P00498
P0CX55	40S ribosomal protein	77.62	1.90		P38911
P38779	Proteasome-interactin	4.88	0.77		P31412
Q00055	Glycerol-3-phosphate c	3.10	0.61		P53075
P05755	40S ribosomal protein	42.66	1.64		P07560
P47079	T-complex protein 1 su	2.65	0.56		P38715
P0C2I8	Transposon Ty1-LR4 Ga	5.18	0.79		P38181
Q06078	U3 small nucleolar RNA	1.35	0.37		P53008
P53228	Transaldolase NQM1 C	5.63	0.82		Q06679
Q12267	Structural maintenance	0.84	0.26		Q12074
P40498	U3 small nucleolar RNA	1.46	0.39		P38115
P16622	Ferrochelatase, mitoch	4.39	0.73		P53691
P33767	Dolichyl-diphosphoolig	3.57	0.66		P0C2J3
P43603	LAS seventeen-binding	3.18	0.62		Q06218
Q12675	Phospholipid-transport	0.55	0.19		Q04373
P18759	Vesicular-fusion protei	1.74	0.44		P16387
P38328	Actin-related protein 2	4.75	0.76		P54885
P32499	Nucleoporin NUP2 OS=	1.80	0.45		Q02931

P38810	SED5-binding protein 3	1.15	0.33		P11075
P38891	Branched-chain-amino	4.01	0.70		P33775
Q04217	Probable ATP-depende	0.86	0.27		P33330
Q12252	Phosphate metabolism	1.12	0.33		P46680
P25045	Serine palmitoyltransfe	3.17	0.62		P39533
P26784	60S ribosomal protein	22.63	1.37		Q06706
P05626	ATP synthase subunit 4	8.59	0.98		P22768
P34730	Protein BMH2 OS=Sacc	10.23	1.05		P37292
Q04013	Citrate/oxoglutarate ca	5.81	0.83		P28274
P19358	S-adenosylmethionine	4.88	0.77		P30822
P53278	Uncharacterized protei	1.50	0.40		P28777
P01123	GTP-binding protein YF	19.08	1.30		P38129
Q00416	Helicase SEN1 OS=Sacc	0.48	0.17		P28241
P22146	1,3-beta-glucanosyltra	2.49	0.54		Q06639
P41805	60S ribosomal protein	26.26	1.44		P38737
Q12451	Oxysterol-binding prot	0.91	0.28		P02400
P25623	Suppressor of yeast pr	0.99	0.30		P12612
P38088	Glycine--tRNA ligase 1,	1.78	0.44		O14467
P32266	Dynamin-like GTPase N	1.24	0.35		P07263
P39960	GTPase-activating prot	0.44	0.16		P0C0T4
P40339	Replication factor C sul	5.99	0.84		P40215
P40970	Serine palmitoyltransfe	2.51	0.55		P42943
P09457	ATP synthase subunit 5	16.58	1.25		P38113
P28241	Isocitrate dehydrogena	3.13	0.62		P34167
O13516	40S ribosomal protein	33.78	1.54		P39935
P32602	Alpha-soluble NSF atta	5.30	0.80		P37838
P39007	Dolichyl-diphosphoolig	1.52	0.40		P24280
Q02354	U3 small nucleolar RNA	4.00	0.70		Q06142
P80210	Adenylosuccinate syntl	2.91	0.59		P43593
P43585	Vacuolar transporter cl	1.21	0.34		P11412
P49017	2-methoxy-6-polypreny	7.66	0.94		Q04067
Q02792	5~-3~ exoribonuclease	0.92	0.28		P07267
P07991	Ornithine aminotransfe	3.13	0.62		P32916
Q06103	26S proteasome regula	4.61	0.75		P32466
P28777	Chorismate synthase C	4.58	0.75		P32795
P26785	60S ribosomal protein	18.14	1.28		P49095
P25365	Putative guanine nucle	0.86	0.27		P10127
Q12746	Plasma membrane-ass	3.33	0.64		P40302
Q03558	NADPH dehydrogenase	4.94	0.77		P15891
Q12250	26S proteasome regula	3.29	0.63		P25294
P21827	Guanine nucleotide ex	2.43	0.54		P27809
P11914	Mitochondrial-process	3.87	0.69		P25655
Q04491	Protein transport prote	6.26	0.86		P33734
P39015	Suppressor protein STN	5.56	0.82		P43616
P0CX37	40S ribosomal protein	8.50	0.98		P07275
P53978	Elongation factor 3B O	0.99	0.30		P25632
Q08162	Exosome complex exor	1.02	0.31		Q05946
P38805	Ribosome production f	6.42	0.87		P32263
P32381	Actin-related protein 2	7.43	0.93		P32377
P04802	Aspartate--tRNA ligase	1.83	0.45		P47075
Q06010	A-factor-processing en	0.90	0.28		P15454
P39516	40S ribosomal protein	159.49	2.21		Q05905

P09733	Tubulin alpha-1 chain (	2.70	0.57		P38879
P49723	Ribonucleoside-diphos	7.24	0.92		P47077
P22135	Protein ATP12, mitoch	6.76	0.89		P39076
P32335	Protein MSS51, mitoch	4.78	0.76		Q03161
Q02206	Chromatin structure-re	1.66	0.42		Q07896
P53598	Succinate--CoA ligase [	8.70	0.99		Q05016
P40348	Replication factor C sul	4.20	0.72		Q04947
P40961	Prohibitin-1 OS=Saccha	7.12	0.91		P20449
Q08208	Nucleolar protein 12 O	4.09	0.71		P23638
P26783	40S ribosomal protein	15.49	1.22		Q12018
P00950	Phosphoglycerate mut	11.76	1.11		P0CX25
P38219	Obg-like ATPase 1 OS=	5.04	0.78		P38069
P36516	54S ribosomal protein	4.48	0.74		P00899
P33332	Exocyst complex comp	0.68	0.23		P04786
P38112	ATP-dependent RNA h	1.13	0.33		P24276
P50094	Inosine-5~-monophosp	2.20	0.51		P00927
P32598	Serine/threonine-prote	7.93	0.95		Q04409
P30771	ATP-dependent helicas	0.98	0.30		P05749
P02557	Tubulin beta chain OS=	4.23	0.72		P21304
Q12024	Ribosome biogenesis p	3.33	0.64		P53184
P22336	Replication factor A pr	1.39	0.38		P35719
Q06833	Uncharacterized PH do	1.25	0.35		P08518
P07560	Ras-related protein SE	15.02	1.20		P39077
P40531	Protein GVP36 OS=Sac	4.26	0.72		P22803
P38797	Protein phosphatase 2	5.42	0.81		P00812
P09950	5-aminolevulinate synt	2.83	0.58		P43585
P32527	Zuotin OS=Saccharomy	3.22	0.63		P05374
P53883	Nucleolar protein 13 O	3.67	0.67		Q01939
P38069	Alpha-1,2-mannosyltra	1.64	0.42		Q04869
P40302	Proteasome subunit al	9.66	1.03		P38912
Q07896	Nucleolar complex-ass	1.39	0.38		P53235
P33333	Probable 1-acyl-sn-gly	9.36	1.02		P21954
P11154	Pyruvate carboxylase 1	0.72	0.24		P49723
P38013	Peroxiredoxin type-2 C	22.21	1.37		P20459
P25582	27S pre-rRNA (guanosi	1.29	0.36		P07260
Q04305	U3 small nucleolar RN	2.39	0.53		P05744
P13587	Sodium transport ATPa	0.80	0.26		P38886
P21375	Fumarate reductase 2	2.04	0.48		P53912
P46971	Dolichyl-phosphate-ma	1.35	0.37		Q02642
P39006	Phosphatidylserine dec	1.49	0.40		P40525
P54114	Aldehyde dehydrogena	2.01	0.48		P39079
P14020	Dolichol-phosphate ma	14.95	1.20		Q07878
Q99207	Nucleolar complex pro	1.34	0.37		Q07527
P05317	60S acidic ribosomal pr	6.03	0.85		P21243
P28319	Cell wall protein CWP1	5.87	0.84		Q04178
P25349	Flavoprotein-like prote	8.96	1.00		P41911
P23638	Proteasome subunit al	6.09	0.85		Q05567
P38264	SRP-independent targe	65.17	1.82		P32843
P25632	Chromatin structure-re	2.10	0.49		P46673
P15790	Casein kinase II subuni	4.39	0.73		P36015
P0CX51	40S ribosomal protein	44.34	1.66		Q07457
P46673	Nucleoporin NUP85 OS	0.94	0.29		P20606

P21538	DNA-binding protein R	1.16	0.33		P37898
P19812	E3 ubiquitin-protein lig	0.40	0.15		P38225
Q08971	Protein PBDC1 homolo	23.33	1.39		P25491
P05739	60S ribosomal protein	12.11	1.12		Q04894
P53206	Putative cysteine synth	3.13	0.62		P17555
P48234	Ribosome biogenesis p	1.12	0.33		P39683
P53878	Uncharacterized oxido	2.35	0.53		P46982
P32366	V-type proton ATPase	3.09	0.61		P23615
P52891	Nucleoporin NUP84 OS	1.32	0.37		P32316
P36022	Dynein heavy chain, cy	0.20	0.08		P40016
Q01896	Sodium transport ATPa	0.80	0.26		P30605
P36148	Glycerol-3-phosphate	1.20	0.34		P35729
Q01163	37S ribosomal protein	2.66	0.56		Q04062
P47077	Nucleolar protein 9 OS	1.20	0.34		Q00711
P32497	Eukaryotic translation i	0.93	0.29		P22138
P36051	GPI ethanolamine phos	0.79	0.25		Q12159
P39958	Rab GDP-dissociation i	3.74	0.68		P36421
Q12480	Probable electron tran	4.20	0.72		P38882
P53941	U3 small nucleolar ribo	5.19	0.79		Q12449
Q08548	Lysophospholipid acylt	1.48	0.39		P33299
Q02725	Vacuolar transporter cl	1.08	0.32		P53337
P47154	CAAX prenyl protease	2.52	0.55		P39078
Q06106	Multiple RNA-binding	0.84	0.26		Q06010
P42940	Probable electron tran	6.04	0.85		P47169
P53852	Cysteine--tRNA ligase	1.24	0.35		P43609
Q02326	60S ribosomal protein	12.11	1.12		Q06833
Q06506	Ribosomal RNA-proces	1.95	0.47		Q04177
P37302	Aminopeptidase Y OS=	1.56	0.41		Q06151
P00942	Triosephosphate isome	5.83	0.83		P32266
Q05567	Sphingosine-1-phospha	2.14	0.50		P40970
P40368	Nucleoporin NUP82 OS	1.23	0.35		P12688
P53326	Uncharacterized protei	1.38	0.38		P32337
P32860	NifU-like protein, mito	8.42	0.97		P28273
P47068	Myosin tail region-inte	0.68	0.23		P23337
P0CX31	40S ribosomal protein	37.32	1.58		Q08745
P48837	Nucleoporin NUP57 OS	1.91	0.46		Q04336
Q12032	Altered inheritance of	52.06	1.72		Q12458
P34227	Mitochondrial peroxire	6.84	0.89		P27614
P32465	Low-affinity glucose tra	2.01	0.48		Q12176
P38689	Ribose-phosphate pyro	6.33	0.87		P32614
Q12154	ATPase GET3 OS=Sacch	9.69	1.03		Q12109
P32466	Low-affinity glucose tra	1.63	0.42		Q04175
P38230	Probable quinone oxid	4.20	0.72		P04076
Q12159	RNA annealing protein	15.69	1.22		P36114
P38789	Ribosome biogenesis p	2.57	0.55		P25375
Q02201	Oxysterol-binding prot	2.58	0.55		P40462
P15565	tRNA (guanine(26)-N(2	2.46	0.54		Q04225
P51601	GTP cyclohydrolase 1	13.65	1.17		P53981
P32500	Nucleoporin NDC1 OS=	1.43	0.39		P38555
P49090	Asparagine synthetase	1.76	0.44		P19881
P0CX45	60S ribosomal protein	8.25	0.97		P07246
P53040	Transcription initiation	2.99	0.60		P14843

P38111	Serine/threonine-prote	0.29	0.11		Q06631
P51996	GTP-binding protein YF	7.10	0.91		P52891
P46990	60S ribosomal protein	6.76	0.89		Q12117
P07280	40S ribosomal protein	32.81	1.53		Q03104
Q12377	26S proteasome regula	2.10	0.49		P38787
P46681	D-2-hydroxyglutarate--	2.29	0.52		Q01532
P32316	Acetyl-CoA hydrolase (	2.60	0.56		Q06506
Q08723	26S proteasome regula	3.92	0.69		P40054
P38989	Structural maintenance	0.64	0.21		Q12335
Q06685	Inositol hexakisphosph	0.72	0.24		P28272
P0CX82	60S ribosomal protein	9.78	1.03		P36046
P32319	Vacuolar protein sortin	0.41	0.15		Q03280
P05740	60S ribosomal protein	6.76	0.89		P39007
P0CX84	60S ribosomal protein	37.64	1.59		P47089
P50085	Prohibitin-2 OS=Saccha	4.91	0.77		P41056
P53327	Antiviral helicase SLH1	0.37	0.14		P09232
P80428	Actin-related protein 4	1.79	0.45		P49167
P32591	SWI/SNF complex subu	1.04	0.31		P14904
P39109	Metal resistance prote	0.47	0.17		P40498
P36101	tRNA threonylcarbamo	2.06	0.49		P16550
P14922	General transcriptional	0.70	0.23		P46951
P42943	T-complex protein 1 su	1.37	0.37		Q08647
P18963	Inhibitory regulator pro	0.27	0.10		Q08179
P53742	Nucleolar GTP-binding	1.54	0.40		P21524
P32476	Squalene monooxygen	2.89	0.59		P40510
P05759	Ubiquitin-40S ribosoma	31.44	1.51		P01120
P29468	Poly(A) polymerase OS	1.98	0.47		P08417
P38697	Inosine-5~-monophosp	1.70	0.43		Q12377
P38286	Very-long-chain 3-oxoa	2.78	0.58		P20448
P38882	U3 small nucleolar RNA	1.37	0.37		P32892
Q06632	Protein CFT1 OS=Sacch	0.59	0.20		P15873
P36048	Pre-mRNA-splicing fact	0.71	0.23		P40345
Q05931	Heat shock protein SSC	1.19	0.34		P39966
P38883	Pre-rRNA-processing p	1.25	0.35		P32621
Q12153	Ribosome biogenesis p	2.56	0.55		P50861
P33299	26S protease regulator	2.87	0.59		P38333
P11075	Protein transport prote	0.31	0.12		P38858
P53551	Histone H1 OS=Sacchai	3.55	0.66		Q12118
P05738	60S ribosomal protein	9.78	1.03		Q12149
Q05911	Adenylosuccinate lyase	1.81	0.45		P41921
P32899	U3 small nucleolar ribo	23.39	1.39		Q12466
P38712	ATP-dependent rRNA h	3.17	0.62		Q06252
Q12452	3-keto-steroid reducta	4.25	0.72		P15992
P53221	60S ribosomal protein	69.28	1.85		P47018
P13517	F-actin-capping protein	4.60	0.75		Q06440
P41895	Transcription initiation	1.11	0.32		P05319
Q04458	Fatty aldehyde dehydro	1.76	0.44		Q04080
P39101	Protein CAJ1 OS=Sacch	2.92	0.59		P32319
P29509	Thioredoxin reductase	2.92	0.59		P48234
P10127	Alcohol dehydrogenase	2.49	0.54		Q12447
P23180	Probable oxidoreducta	1.88	0.46		P10080
P10659	S-adenosylmethionine	3.28	0.63		P51996

Q07979	Chromatin structure-re	1.88	0.46		Q12265
P53250	Twinfilin-1 OS=Sacchar	4.18	0.71		P40341
Q04182	ATP-dependent perme	0.46	0.16		P35844
P53199	Sterol-4-alpha-carboxy	4.43	0.73		P28495
P33750	Protein SOF1 OS=Sacch	1.49	0.40		P25298
P05743	60S ribosomal protein	69.28	1.85		P41920
Q04693	Pre-mRNA-splicing fact	0.49	0.17		P39938
P36017	Vacuolar protein sortin	12.79	1.14		P32790
P47133	ER membrane protein	5.01	0.78		P43588
P32787	Mitochondrial genome	6.39	0.87		P02293
P02294	Histone H2B.2 OS=Sacc	49.67	1.70		P07257
P12687	54S ribosomal protein	3.59	0.66		P53326
P39968	Vacuolar protein 8 OS=	1.61	0.42		P36775
O14467	Multiprotein-bridging f	38.95	1.60		P23639
P02407	40S ribosomal protein	24.21	1.40		Q03102
P38555	GTP-binding protein YF	8.80	0.99		P20447
P32844	Exocyst complex comp	1.13	0.33		P49687
P25303	DnaJ-related protein S	2.84	0.58		P40581
P19262	Dihydrolipoyllysine-res	2.06	0.49		P00729
P01119	Ras-like protein 1 OS=S	3.47	0.65		P32898
P25298	mRNA 3~-end-processi	1.02	0.31		P32602
Q04177	U3 small nucleolar RN	1.19	0.34		P38624
Q04279	Eisosome protein SEG1	0.79	0.25		P38883
Q99297	Mitochondrial 2-oxodic	4.94	0.77		P35732
P39993	ARF guanine-nucleotid	0.53	0.18		Q05931
Q01560	Nucleolar protein 3 OS	2.13	0.50		P32379
P32803	Endosomal protein P24	6.32	0.86		P34216
P47127	Altered inheritance of	3.38	0.64		P32588
P38825	Protein TOM71 OS=Sac	1.50	0.40		P36148
P38138	Glucosidase 2 subunit	0.67	0.22		P35207
Q00711	Succinate dehydrogena	1.54	0.40		Q06106
P38137	Peroxisomal-coenzyme	2.47	0.54		P10622
P00447	Superoxide dismutase	9.56	1.02		Q04439
Q12029	Probable mitochondria	3.90	0.69		P25039
P22213	Protein SLY1 OS=Sacch	1.14	0.33		P47176
P32939	GTP-binding protein YF	8.12	0.96		Q12123
P53847	Protein transport prote	1.23	0.35		P38998
Q08647	Multisubstrate pseudo	1.22	0.35		P32598
P38130	Probable mannosyltrar	2.97	0.60		P11655
Q3E757	60S ribosomal protein	9.65	1.03		P17505
P39004	High-affinity hexose tra	1.84	0.45		P38137
P25342	Cell division control pr	3.04	0.61		Q06103
P46951	Cargo-transport protei	1.09	0.32		P14306
P03965	Carbamoyl-phosphate	0.64	0.21		Q04491
Q03655	Probable 1,3-beta-gluc	1.29	0.36		P32832
P07703	DNA-directed RNA poly	2.91	0.59		P40957
P32832	Chromatin structure-re	2.12	0.49		P33307
P23639	Proteasome subunit al	6.93	0.90		Q04792
P23301	Eukaryotic translation i	57.31	1.77		P41543
P38998	Saccharopine dehydrog	3.35	0.64		P31383
P34760	Peroxiredoxin TSA1 OS	7.69	0.94		P22217
Q12518	Epsin-1 OS=Saccharom	1.94	0.47		P39002

Q06631	Protein BFR2 OS=Sacch	1.52	0.40		P38112
P40483	Putative zinc metallopr	1.19	0.34		P29468
P45818	ATP-dependent RNA he	1.42	0.38		P07256
P47035	Nucleolar protein NET1	0.56	0.19		P13586
Q08245	Protein ZEO1 OS=Sacch	83.34	1.93		P53914
Q07657	Seventh homolog of se	1.12	0.33		P49166
P16451	Pyruvate dehydrogena	3.27	0.63		P32465
P35817	Bromodomain-contain	1.36	0.37		Q04924
P0CX53	60S ribosomal protein	7.08	0.91		P0CX27
Q99257	mRNA export factor M	1.49	0.40		P30771
P26786	40S ribosomal protein	15.61	1.22		Q04120
P46982	Alpha-1,2-mannosyltra	1.16	0.33		P25567
P31373	Cystathionine gamma-l	2.38	0.53		Q12189
P21965	Protein kinase MCK1 O	2.68	0.57		P54783
P46669	DNA-directed RNA poly	3.16	0.62		P33338
Q06505	Transcription factor SP	2.41	0.53		P40483
P15703	Glucan 1,3-beta-glucos	3.52	0.66		P32501
P51401	60S ribosomal protein	9.65	1.03		P38121
Q06287	Ribosomal RNA small s	7.71	0.94		P17883
P06780	GTP-binding protein RH	3.92	0.69		P40093
P25443	40S ribosomal protein	3.64	0.67		P47096
P30902	ATP synthase subunit d	12.49	1.13		P32591
P36139	Protein PET10 OS=Sacc	4.24	0.72		P38825
Q04080	GPI transamidase comp	1.34	0.37		P39958
P33399	La protein homolog OS	3.98	0.70		P53834
P22224	Exocyst complex comp	0.64	0.21		P89886
P53114	Mediator of RNA polyn	0.50	0.18		Q03532
P40217	Eukaryotic translation i	3.24	0.63		Q12250
P32784	Glycerol-3-phosphate (	1.16	0.33		P53633
P41807	V-type proton ATPase s	2.06	0.49		Q12464
P32804	Zinc-regulated transpo	1.75	0.44		P40413
P40008	Protein FMP52, mitoch	5.43	0.81		P38264
P20459	Eukaryotic translation i	4.02	0.70		P25343
P22515	Ubiquitin-activating en	0.71	0.23		P25087
P40066	Nucleoporin GLE2 OS=S	2.54	0.55		P23293
P40098	Uncharacterized mitoc	5.47	0.81		Q07451
Q06132	Suppressor of glycerol	0.66	0.22		Q08818
P25555	Single-strand telomeric	3.22	0.63		P07172
P32349	DNA-directed RNA poly	1.01	0.30		P33399
P17629	THO complex subunit H	1.01	0.30		P40055
P38071	Enoyl-[acyl-carrier prot	3.77	0.68		P49435
P17709	Glucokinase-1 OS=Sacc	1.76	0.44		P48836
Q06698	Putative ATP-depender	0.50	0.18		Q06408
P07253	Cytochrome B pre-mRN	24.92	1.41		P53920
P54113	Bifunctional purine bio	1.05	0.31		P34248
P25374	Cysteine desulfurase, r	1.81	0.45		P50107
P40055	U3 small nucleolar RNA	1.48	0.39		P15274
Q05506	Arginine--tRNA ligase, (	1.58	0.41		Q02725
P22082	Transcription regulator	0.34	0.13		P05626
P40496	37S ribosomal protein	5.34	0.80		P14065
P38701	40S ribosomal protein	38.76	1.60		P32366
P36105	60S ribosomal protein	27.97	1.46		Q02792

P14907	Nucleoporin NSP1 OS=	0.82	0.26		P00937
P43588	Ubiquitin carboxyl-terr	3.50	0.65		Q08686
Q07897	Protein CMS1 OS=Sacc	5.19	0.79		P05373
Q08199	Nucleotide exchange fa	1.91	0.46		P47047
P38205	Multisite-specific tRNA	0.94	0.29		P49954
Q12335	Protoplast secreted pro	6.44	0.87		Q99260
Q04781	E3 ubiquitin-protein lig	0.40	0.15		P32486
P13663	Aspartate-semialdehyd	3.09	0.61		P25373
P48589	40S ribosomal protein	14.11	1.18		P53303
P0CX41	60S ribosomal protein	86.94	1.94		Q04371
P04807	Hexokinase-2 OS=Sacch	2.69	0.57		P38199
P02309	Histone H4 OS=Sacchar	38.49	1.60		Q04013
P10507	Mitochondrial-processi	2.03	0.48		P15565
P40075	Vesicle-associated mem	4.69	0.76		P32178
Q03976	37S ribosomal protein	2.99	0.60		P23292
Q03529	Ceramide very long cha	2.14	0.50		P38875
P32902	37S ribosomal protein	2.23	0.51		P53847
P35691	Translationally-control	8.40	0.97		Q06205
P20484	Protein MAK11 OS=Sac	1.97	0.47		P39968
P24280	SEC14 cytosolic factor	2.82	0.58		P33315
P00427	Cytochrome c oxidase	13.54	1.16		P53295
P0CX23	60S ribosomal protein	14.60	1.19		Q08723
P27810	Alpha-1,2 mannosyltra	2.38	0.53		P41895
P13433	DNA-directed RNA poly	0.45	0.16		P47044
P32600	Serine/threonine-prote	0.26	0.10		P33298
P46677	Transcription initiation	0.66	0.22		P06780
P40012	Protoporphyrinogen ox	1.57	0.41		P40075
P09734	Tubulin alpha-3 chain	1.32	0.37		P38817
P41277	Glycerol-1-phosphate p	6.43	0.87		P0C0V8
Q06706	Elongator complex pro	0.40	0.15		Q12513
Q03124	Chromatin structure-re	1.37	0.37		Q05775
P32471	Elongation factor 1-bet	10.95	1.08		P40303
P20424	Signal recognition part	1.38	0.38		Q04432
P36018	GTP-binding protein YP	6.11	0.85		P15646
P53881	54S ribosomal protein	4.00	0.70		Q01976
P40212	60S ribosomal protein	6.99	0.90		P28834
P12688	Serine/threonine-prote	1.09	0.32		P51402
P21771	37S ribosomal protein	4.47	0.74		P40010
P32445	Single-stranded DNA-b	10.17	1.05		P38197
Q05892	MIOREX complex comp	3.42	0.65		Q12314
P40471	NADPH-dependent 1-a	5.38	0.80		Q06494
P46675	Protein STU2 OS=Sacch	0.75	0.24		P48362
P27809	Glycolipid 2-alpha-man	1.72	0.43		P53140
P31380	ATP-dependent helicas	0.61	0.21		P17423
P30656	Proteasome subunit be	2.77	0.58		P38822
P53064	RNA polymerase-assoc	1.36	0.37		P38323
P0CX39	40S ribosomal protein	4.23	0.72		P23724
P33298	26S protease regulator	1.96	0.47		P30656
P53073	ER membrane protein	4.74	0.76		Q08985
P30605	Myo-inositol transport	1.09	0.32		P47160
P11076	ADP-ribosylation factor	11.24	1.09		P47119
Q08096	RNA 3~-terminal phosp	2.21	0.51		P36136

P38234	Protein RFS1 OS=Sacch	6.60	0.88		Q99220
P53868	Alpha-1,2-mannosyltra	1.59	0.41		P32419
P23644	Mitochondrial import r	2.04	0.48		P38986
Q04225	Ribosome assembly pr	0.93	0.29		P16649
P23724	Proteasome subunit be	5.77	0.83		Q10740
P12612	T-complex protein 1 su	1.34	0.37		Q12178
P23292	Casein kinase I homolo	1.49	0.40		Q01662
P39935	Eukaryotic initiation fa	0.70	0.23		P25635
P33891	Protein transport prote	0.89	0.28		P43123
P35176	Peptidyl-prolyl cis-tran	10.00	1.04		P32458
Q01532-2	Isoform Cytoplasmic o	1.70	0.43		P06782
P38431	Eukaryotic translation i	2.45	0.54		P20051
Q06488	Chromatin structure-re	0.82	0.26		P40485
P32356	Neutral trehalase OS=S	1.04	0.31		P53953
P41940	Mannose-1-phosphate	1.90	0.46		Q07657
P38629	Replication factor C su	2.39	0.53		P25043
P89102	Exocyst complex comp	0.59	0.20		P40037
P04456	60S ribosomal protein	18.19	1.28		Q12374
Q12434	Rho GDP-dissociation i	8.31	0.97		P21965
P21801	Succinate dehydrogena	5.13	0.79		P0C0X0
P23337	Glycogen [starch] synt	1.02	0.31		P27810
Q12072	ISWI one complex prot	0.74	0.24		P17536
P53734	ATP-dependent RNA he	0.95	0.29		P45818
Q00245	GTP-binding protein RH	5.18	0.79		P25847
P14164	ARS-binding factor 1 O	0.78	0.25		P53064
P46956	Inorganic phosphate tr	2.84	0.58		P43621
P24276	Protein SSD1 OS=Sacch	0.40	0.15		P42838
P38754	60S ribosomal protein	20.33	1.33		Q12387
P0C2H6	60S ribosomal protein	13.82	1.17		P43556
P19158	Inhibitory regulator pr	0.17	0.07		Q08960
P22855	Alpha-mannosidase OS	0.51	0.18		P21734
P08678	Adenylate cyclase OS=	0.28	0.11		P28707
P10662	37S ribosomal protein	3.07	0.61		P35817
P53140	Protein RMD9, mitoch	1.00	0.30		Q08225
P38624	Proteasome subunit be	7.75	0.94		P32521
P08067	Cytochrome b-c1 comp	7.84	0.95		P38075
P02381	Ribosomal protein VAR	3.05	0.61		P38353
P28321	Monoglyceride lipase	2.73	0.57		P39729
P20448	ATP-dependent RNA he	0.91	0.28		Q06512
P48164	40S ribosomal protein	12.38	1.13		P15703
Q08954	Smr domain-containin	4.73	0.76		P32939
P38342	3-ketodihydrosphingos	2.63	0.56		O13563
P40303	Proteasome subunit al	5.07	0.78		P32468
P39013	Actin cytoskeleton-reg	2.59	0.56		P31384
P36057	Signal recognition part	4.65	0.75		P36017
P40957	Spindle assembly chec	0.71	0.23		P52918
P32288	Glutamine synthetase	2.82	0.58		P30657
P53877	Pre-rRNA-processing p	0.98	0.30		Q12154
P38333	Essential nuclear prote	1.16	0.33		Q03940
P32449	Phospho-2-dehydro-3-	1.89	0.46		Q12009
P33201	Ribosome assembly fa	3.72	0.67		P35997
P54781	Cytochrome P450 61 O	1.49	0.40		P38248

P29539	Telomere length regula	0.21	0.08		Q12040
P38988	Mitochondrial GTP/GD	4.44	0.74		P15700
P00815	Histidine biosynthesis t	0.71	0.23		P22696
P13586	Calcium-transporting A	0.64	0.21		P36047
P33310	ATP-dependent perme	0.75	0.24		P23641
P38143	Glutathione peroxidase	11.23	1.09		P25719
Q03798	Altered inheritance of r	3.96	0.70		P36112
Q08235	Ribosome biogenesis p	4.35	0.73		P25293
P31116	Homoserine dehydroge	2.83	0.58		P12904
P38353	Sec sixty-one protein h	1.88	0.46		P53173
P38199	Heterogeneous nuclea	2.09	0.49		P22141
P43636	Alpha-1,3/1,6-mannosy	1.43	0.39		P53278
P20433	DNA-directed RNA poly	4.26	0.72		P53081
P38251	Replication factor C sul	2.60	0.56		Q04347
P34248	Probable intramembra	0.87	0.27		P38795
Q05123	Actin-like protein ARP9	1.22	0.35		Q06685
P00128	Cytochrome b-c1 comp	16.40	1.24		P53145
P40086	Cytochrome c oxidase a	1.36	0.37		P53734
P38911	FK506-binding nuclear	2.05	0.48		Q02932
P05748	60S ribosomal protein	4.62	0.75		P25349
P40416	Iron-sulfur clusters trar	0.95	0.29		P21242
P28495	F-actin-capping protein	2.95	0.60		P38736
P53848	Folic acid synthesis pro	0.74	0.24		P48837
P48813	High-affinity glutamine	0.89	0.28		P25451
P05745	60S ribosomal protein	96.58	1.99		P17649
P40340	Tat-binding homolog 7	0.39	0.14		P40414
P41543	Dolichyl-diphosphoolig	1.39	0.38		Q05787
P34163	Sterol esterase TGL1 O	1.27	0.36		P36059
P36015	Synaptobrevin homolo	6.75	0.89		P53254
Q08818	Meiotic sister-chromat	0.91	0.28		P32496
P39076	T-complex protein 1 su	1.47	0.39		P02992
P0CX49	60S ribosomal protein	6.68	0.89		P46989
P53063	Decapping nuclease RA	1.57	0.41		P32473
Q00684	Tyrosine-protein phosp	1.13	0.33		P40319
P36010	Nucleoside diphosphat	14.04	1.18		P38845
P38625	GMP synthase [glutam	1.42	0.38		P39003
P40327	26S protease regulator	1.37	0.37		Q07505
P08456	CDP-diacylglycerol--ser	2.90	0.59		Q12402
P47150	37S ribosomal protein	2.83	0.58		P32628
P00044	Cytochrome c iso-1 OS=	19.26	1.31		Q04697
P39926	Protein SSO2 OS=Sacch	2.04	0.48		P54860
P15873	Proliferating cell nuclea	4.02	0.70		Q00402
P35178	Ribosomal RNA-proces	4.47	0.74		P40081
P38786	Ribonuclease P/MRP p	3.93	0.69		P52286
P38822	Protein BZZ1 OS=Sacch	0.81	0.26		P32626
P34111	Transcription factor tau	0.48	0.17		P38085
P53860	Phosphatidylinositol tra	2.55	0.55		P48363
P0C2H8	60S ribosomal protein	34.59	1.55		P53128
P35169	Serine/threonine-prote	0.18	0.07		P54837
P53903	Processing of GAS1 and	10.77	1.07		P38174
P08539	Guanine nucleotide-bir	1.38	0.38		P38777
P47039	Probable kynurenine--(	1.55	0.41		P20081

O14455	60S ribosomal protein	96.58	1.99		Q06567
P32874	Acetyl-CoA carboxylase	0.18	0.07		P38065
P05756	40S ribosomal protein	14.57	1.19		P38689
P40157	Vacuolar import and de	0.61	0.21		P32895
P11938	DNA-binding protein R	0.67	0.22		P39960
P25368	Ribosomal RNA-proces	2.39	0.53		P40362
P11655	Guanine nucleotide-ex	1.27	0.36		P25580
P35191	DnaJ homolog 1, mitoc	1.52	0.40		Q08193
P19146	ADP-ribosylation factor	8.52	0.98		P38891
P32905	40S ribosomal protein	2.81	0.58		Q99258
Q99260	GTP-binding protein YF	5.76	0.83		P33755
P17695	Glutaredoxin-2, mitoch	12.77	1.14		P04161
P43613	ER-localized J domain-	2.43	0.54		P16547
Q02932	Importin beta-like prot	0.48	0.17		Q06214
P25343	Reduced viability upon	4.47	0.74		P32803
P53617	Protein NRD1 OS=Sacc	1.25	0.35		P41812
P87108	Mitochondrial import i	78.65	1.90		Q99257
P38828	Protein LSM12 OS=Sac	6.21	0.86		P32380
P0C0W1	40S ribosomal protein	22.90	1.38		P32771
P36151	Uncharacterized protei	2.29	0.52		Q01476
P04037	Cytochrome c oxidase	10.29	1.05		P38351
Q03246	37S ribosomal protein	3.61	0.66		P25644
P32895	Ribose-phosphate pyro	1.21	0.34		P38628
P53946	Actin-related protein 5	0.71	0.23		P32523
P14832	Peptidyl-prolyl cis-tran	9.96	1.04		P33201
P28817	3-hydroxyisobutyryl-Co	1.30	0.36		Q04304
P00445	Superoxide dismutase	23.67	1.39		Q04781
P53081	NGG1-interacting facto	2.72	0.57		Q02046
P32835	GTP-binding nuclear pr	3.49	0.65		P38143
P36081	Uncharacterized protei	2.40	0.53		P53040
P41911	Glycerol-3-phosphate	1.34	0.37		P53973
P38781	Chromatin structure-re	0.52	0.18		Q12434
P36160	Ribosome biogenesis p	3.14	0.62		P40553
P52911	Glucan 1,3-beta-glucos	1.09	0.32		Q04493
P22803	Thioredoxin-2 OS=Sacc	16.45	1.24		P38234
P27929	37S ribosomal protein	1.30	0.36		P53839
P53691	Peptidyl-prolyl cis-tran	1.72	0.43		P43583
P0C2H9	60S ribosomal protein	34.59	1.55		Q07688
P24000	60S ribosomal protein	7.40	0.92		Q08951
Q05787	ERAD-associated E3 ub	0.64	0.21		Q07362
Q03761	Transcription initiation	0.85	0.27		P43619
P40185	Protein MMF1, mitoch	17.43	1.27		P32844
Q06704	Golgin IMH1 OS=Sacch	0.57	0.20		Q12389
P42949	Mitochondrial import i	12.07	1.12		P54781
P42838	Alkylphosphocholine re	1.20	0.34		P40029
P40350	Dolichyl-phosphate bet	2.82	0.58		P34221
P28000	DNA-directed RNA poly	8.97	1.00		Q03219
P18900	Hexaprenyl pyrophosp	1.44	0.39		P40327
P47008	Phosphatidylinositol tr	4.10	0.71		Q06488
P52893	Probable alanine amin	1.03	0.31		P34223
P39012	GPI transamidase com	1.11	0.32		P33317
P08679	Citrate synthase, pero	1.50	0.40		P40545

P40345	Phospholipid:diacylglyc	0.65	0.22		Q04458
P0CX47	40S ribosomal protein	9.49	1.02		Q12496
P25719	Peptidyl-prolyl cis-tran	5.50	0.81		Q03835
P36046	Mitochondrial interme	1.57	0.41		Q05515
P54780	60S ribosomal protein	3.64	0.67		Q03714
P53954	GDP-Man:Man(3)GlcN	1.10	0.32		P38074
Q04969	Signal peptidase compl	6.60	0.88		Q00245
P40035	Mitochondrial phospha	2.03	0.48		P38861
P29295	Casein kinase I homolo	1.09	0.32		P10614
P39676	Flavohemoprotein OS=	1.32	0.37		P40893
P20606	Small COPII coat GTPas	6.07	0.85		P40557
P38225	Very long-chain fatty a	0.73	0.24		P32492
Q06629	HDA1 complex subunit	0.84	0.26		Q03496
P47171	Histone transcription r	0.31	0.12		Q04660
P40078	Ribosome biogenesis p	3.85	0.69		P38698
P32458	Cell division control pr	1.20	0.34		P42846
P04449	60S ribosomal protein	7.29	0.92		P25369
P54837	Endoplasmic reticulum	4.71	0.76		P20436
P22696	Peptidyl-prolyl cis-tran	9.93	1.04		P36018
P49089	Asparagine synthetase	1.39	0.38		P40202
P23293	Serine/threonine-prote	0.89	0.28		P38261
Q12511	[Pyruvate dehydrogena	0.68	0.23		P40185
Q06409	DOCK-like protein YLR4	0.24	0.09		P33309
P89886	Translation machinery-	5.24	0.80		P38804
P40693	Ribosome biogenesis p	1.79	0.45		P53877
P32855	Exocyst complex comp	0.47	0.17		P32906
P02406	60S ribosomal protein	11.22	1.09		P25623
P53120	Uncharacterized memb	0.36	0.13		Q08023
P53235	Eukaryotic translation i	0.93	0.29		P32264
Q02457	Protein TBF1 OS=Sacch	1.11	0.32		P53200
P19454	Casein kinase II subuni	2.69	0.57		P53111
P38771	Ribosome-recycling fac	4.90	0.77		Q00416
P07283	Phosphomannomutase	3.25	0.63		P53334
P07244	Bifunctional purine bio	0.55	0.19		P46971
P00817	Inorganic pyrophospha	2.70	0.57		P33332
P48439	Dolichyl-diphosphoolig	1.58	0.41		Q05543
Q12374	Nuclear control of ATP	0.82	0.26		P53883
Q12136	Something about silen	0.60	0.20		P40509
O13297	mRNA-capping enzyme	0.99	0.30		P08679
P31384	Glucose-repressible alc	0.64	0.21		Q07834
P46985	Probable alpha-1,6-ma	1.42	0.38		P53313
P39107	Mannan polymerase co	1.27	0.36		P38789
P40533	Protein TED1 OS=Sacch	1.56	0.41		P10869
P0CX29	40S ribosomal protein	6.58	0.88		P13517
P38736	Golgi SNAP receptor co	3.35	0.64		P53731
P38256	Uncharacterized protei	4.46	0.74		P35197
P32906	Endoplasmic reticulum	0.96	0.29		P53600
P04801	Threonine--tRNA ligase	0.65	0.22		P40580
P38912	Eukaryotic translation i	7.40	0.92		Q12754
P53550	m7GpppN-mRNA hydr	0.61	0.21		P23642
Q04347	Bud site selection prot	1.02	0.31		P17629
P53136	Ribosome biogenesis p	1.26	0.35		Q12125

Q12386	Actin-like protein ARP8	0.68	0.23		P38217
P53549	26S protease subunit R	1.59	0.41		Q03750
P35723	Endoplasmic reticulum	3.92	0.69		P11353
P47006	DNA-directed RNA poly	4.73	0.76		P39993
P32481	Eukaryotic translation i	1.07	0.32		P39704
P43596	ISWI one complex prot	0.51	0.18		P32469
Q06205	FK506-binding protein	1.62	0.42		Q08208
P34167	Eukaryotic translation i	1.91	0.46		P38915
P35845	Oxysterol-binding prot	0.37	0.14		P38079
P14120	60S ribosomal protein	37.14	1.58		P39743
P38121	DNA polymerase alpha	0.71	0.23		Q12072
P12383	Transcription factor PD	0.41	0.15		P20604
P54839	Hydroxymethylglutaryl	1.34	0.37		P37262
P38221	Phosphatidate cytidyly	1.24	0.35		Q12285
P39526	AP-1 accessory protein	0.18	0.07		P40087
P25586	KRR1 small subunit prc	2.52	0.55		Q08977
P04806	Hexokinase-1 OS=Saccl	1.20	0.34		Q05788
P39002	Long-chain-fatty-acid--	0.94	0.29		P40047
P39742	Translocation protein S	7.59	0.93		P21375
Q05359	Protein ERP1 OS=Sacch	2.72	0.57		P38145
Q02204	54S ribosomal protein	3.01	0.60		P33310
Q05785	Epsin-2 OS=Saccharom	0.58	0.20		P14020
Q04958	Lysophospholipase NTE	0.29	0.11		P38630
P51998	54S ribosomal protein	2.75	0.57		P32610
P38707	Asparagine--tRNA ligas	0.97	0.29		P22213
P36141	Putative redox protein	9.63	1.03		P43577
P53292	37S ribosomal protein	1.91	0.46		P35723
P32480	Protein HIR2 OS=Sacch	0.54	0.19		P40533
P15180	Lysine--tRNA ligase, cyt	1.14	0.33		P19812
P53141	Myosin light chain 1 OS	11.84	1.11		Q06705
P38792	Exosome complex com	1.30	0.36		P34227
P40515	Mitochondria fission 1	7.08	0.91		Q06523
P40362	U3 small nucleolar RNA	0.64	0.21		P33891
P53889	Uncharacterized mitoc	4.05	0.70		P09457
P36521	54S ribosomal protein	2.16	0.50		P12383
P32904	54S ribosomal protein	2.93	0.59		P33311
Q04119	Endopolyphosphatase	0.72	0.24		Q04213
P43621	Coatomer subunit delta	1.02	0.31		P39985
Q12404	Protein disulfide-isome	2.18	0.50		P36135
P32331	Carrier protein YMC1, r	2.06	0.49		P19735
Q04924	Glucosidase 2 subunit I	0.69	0.23		Q02959
P32911	Eukaryotic translation i	12.59	1.13		Q12252
P40994	ADP-ribosylation factor	6.60	0.88		P38235
P20449	ATP-dependent RNA he	1.19	0.34		P32179
P21560	Protein CBP3, mitochor	1.61	0.42		P38314
P38902	DNA-directed RNA poly	20.35	1.33		P36091
P32608	Retrograde regulation	0.77	0.25		P11938
P09064	Eukaryotic translation i	1.81	0.45		P06197
P24784	ATP-dependent RNA he	1.00	0.30		P38828
Q06705	Phosphatidylinositol tr	1.44	0.39		Q07381
P36523	54S ribosomal protein	2.73	0.57		P39929
P53011	Nucleoporin SEH1 OS=S	1.59	0.41		P36009

P53629	Sterol O-acyltransferas	0.66	0.22	Q12522
P38341	MICOS complex subuni	18.74	1.30	P43610
P53044	Ubiquitin fusion degra	1.57	0.41	P32474
Q12125	Golgi to ER traffic prot	1.81	0.45	P50086
P25626	54S ribosomal protein	5.85	0.84	P37304
P32496	26S proteasome regula	2.75	0.57	P47045
P25375	Saccharolysin OS=Sacc	0.50	0.18	P00546
Q04599	54S ribosomal protein	2.34	0.52	P38773
P32332	Mitochondrial oxaloac	2.32	0.52	P51601
P23201	Protein SPA2 OS=Sacch	0.22	0.09	P14743
Q99316	Protein disulfide isome	2.62	0.56	Q12207
Q08960	S-adenosyl-L-methioni	0.51	0.18	P07347
P07260	Eukaryotic translation i	2.88	0.59	P39965
Q6Q560	Protein ISD11 OS=Sacc	60.81	1.79	P19454
P08466	Mitochondrial nucleas	2.09	0.49	P15496
Q06512	Nucleolar complex pro	1.10	0.32	P25605
P21825	Translocation protein S	2.82	0.58	Q12211
Q12449	Hsp90 co-chaperone A	1.91	0.46	Q12271
P38248	Cell wall protein ECM3	0.90	0.28	Q04170
Q12443	Reticulon-like protein	1.34	0.37	P32502
P15436	DNA polymerase delta	0.40	0.15	P21147
P21264	Phosphoribosylaminoi	0.82	0.26	P42938
P08524	Farnesyl pyrophosphat	1.24	0.35	P50101
P32915	Protein transport prot	1.43	0.39	P53900
P38719	ATP-dependent RNA h	1.67	0.43	P38616
P21242	Probable proteasome	1.83	0.45	P26754
P07263	Histidine--tRNA ligase,	1.03	0.31	Q12306
P38087	Carrier protein YMC2,	2.17	0.50	Q12008
P53299	Mitochondrial import i	15.54	1.22	P39936
P20434	DNA-directed RNA poly	3.43	0.65	P23180
P38886	26S proteasome regula	2.02	0.48	P50875
P33297	26S protease regulator	1.41	0.38	P32485
P0C0V8	40S ribosomal protein	26.15	1.43	P03874
Q08962	60S ribosome subunit	8.87	0.99	Q04344
P32561	Histone deacetylase RF	1.15	0.33	P39721
Q08227	Phosphatidylinositol 4,	1.60	0.41	Q08421
Q06143	Mitochondrial dicarbo	2.58	0.55	Q06625
Q02784	Monothiol glutaredoxi	7.99	0.95	P40506
P32897	Mitochondrial import i	3.95	0.69	Q06704
P39998	Enhancer of mRNA-de	0.71	0.23	P53549
Q02939	RNA polymerase II tran	0.76	0.25	P40459
P38885	Altered inheritance of	1.99	0.48	P12962
P0CX25	60S ribosomal protein	34.71	1.55	P38755
P40485	Phosphatidylinositol 4,	0.62	0.21	P40579
P37012	Phosphoglucomutase	0.81	0.26	Q01329
P47190	Dolichyl-phosphate-ma	0.63	0.21	Q12675
P10080	Single-stranded nuclei	3.77	0.68	P53946
P18496	Mitochondrial ATPase	1.78	0.44	Q04338
P13259	Choline-phosphate cyti	1.35	0.37	P32660
P43556	Rho-GTPase-activating	0.58	0.20	P13587
P00498	ATP phosphoribosyltra	2.18	0.50	P36076
Q07362	Protein PBP4 OS=Sacch	4.14	0.71	Q12276

P40518	Actin-related protein 2	10.65	1.07		P30902
Q03010	Transcriptional regulat	1.29	0.36		P25582
P32453	Protein ATP11, mitoch	1.77	0.44		P15731
P53295	Ribosome-interacting	0.98	0.30		P50278
P39077	T-complex protein 1 su	0.89	0.28		Q05359
P40018	Small nuclear ribonucle	4.31	0.73		Q06489
P25580	Protein PBN1 OS=Sacc	1.41	0.38		P47165
Q3E754	40S ribosomal protein	26.15	1.43		P38869
P36534	54S ribosomal protein	2.50	0.54		P53155
P25642	54S ribosomal protein	8.39	0.97		Q06623
Q06697	Cell division control pr	1.09	0.32		P46992
P07273	Transcription elongatio	1.91	0.46		Q06338
P39079	T-complex protein 1 su	0.87	0.27		Q12164
P33204	Actin-related protein 2	4.19	0.72		Q99321
Q06681	Membrane-anchored l	0.30	0.11		Q12038
Q06567	ABC1 family protein M	0.77	0.25		P25654
P53721	Respiratory supercomp	2.64	0.56		Q05584
Q05040	Factor arrest protein 8	0.89	0.28		Q12532
Q08023	Protein FMP25, mitoch	0.75	0.24		P24279
P43555	Protein EMP47 OS=Sac	1.11	0.32		P47122
P40364	Mitochondrial peculiar	2.16	0.50		P47039
Q12149	Exosome complex exor	0.48	0.17		P38230
P32387	54S ribosomal protein	4.40	0.73		P28007
P22353	54S ribosomal protein	3.00	0.60		P39925
Q3E705	rRNA-processing prote	2.35	0.53		Q06224
P38349	UBX domain-containin	1.12	0.33		Q03124
Q03714	U1 SNP1-associating p	0.48	0.17		P06786
P38428	Coupling of ubiquitin c	4.19	0.72		P40961
P38875	GPI transamidase com	0.85	0.27		P19073
Q06508	Lysophosphatidic acid	1.63	0.42		P15790
P19263	Mediator of RNA polyn	0.41	0.15		P32629
P11986	Inositol-3-phosphate s	0.88	0.27		P47117
P0CH08	Ubiquitin-60S ribosom	11.21	1.09		P53312
Q02753	60S ribosomal protein	4.95	0.77		Q08968
P53875	54S ribosomal protein	11.22	1.09		Q86ZR7
P12686	37S ribosomal protein	1.62	0.42		P47017
P47084	MIOREX complex comp	0.73	0.24		P40363
P33754	Translocation protein	4.62	0.75		P39715
Q12339	rRNA-processing prote	2.64	0.56		P32367
P38120	37S ribosomal protein	1.42	0.38		P17695
Q06554	Uncharacterized ATP-d	0.23	0.09		P13259
P47083	U3 small nucleolar RN	0.76	0.25		P18961
P32523	Pre-mRNA-processing	0.94	0.29		P38131
P38323	ATP-dependent clpX-li	1.07	0.32		P07278
P29496	Minichromosome mair	0.54	0.19		P38081
Q04935	Cytochrome c oxidase	2.95	0.60		Q08162
P40319	Elongation of fatty acic	1.04	0.31		P06839
P39525	3-oxoacyl-[acyl-carrier-	0.80	0.26		P39713
Q03337	Trafficking protein part	1.80	0.45		P39107
Q02969	Peroxisomal membran	1.31	0.36		P40161
P49334	Mitochondrial import	4.31	0.73		P32864
P35996	54S ribosomal protein	10.37	1.06		Q04958

P47116	Serine/threonine-prote	0.51	0.18		P25808
P38922	Protein HRB1 OS=Sacc	0.88	0.27		P53617
P07143	Cytochrome c1, heme	1.61	0.42		P09959
P38244	Vacuolar membrane pr	0.40	0.15		P40157
P33311	ATP-dependent perme	0.55	0.19		Q08641
P39729	Ribosome-interacting	1.81	0.45		P53144
P34222	Peptidyl-tRNA hydrola	2.46	0.54		P43596
Q04226	Transcription initiation	1.25	0.35		P53067
Q08204	Structural maintenanc	0.30	0.11		Q07716
P32790	Actin cytoskeleton-reg	0.32	0.12		Q12055
P15367	Signal peptidase compl	3.45	0.65		P39101
P34223	UBX domain-containin	1.02	0.31		Q04430
P05375	Phosphatidyl-N-methyl	3.99	0.70		P33324
Q03799	37S ribosomal protein	7.18	0.91		P08432
Q02950	37S ribosomal protein	1.60	0.41		P38260
Q05933	Actin-related protein 2	5.12	0.79		P36080
Q12450	Protein ERP4 OS=Sacc	3.00	0.60		P43569
P38339	RHO GTPase-activating	0.56	0.19		P36006
P43594	MICOS complex subuni	4.60	0.75		P40008
P26263	Pyruvate decarboxylas	0.58	0.20		P53093
P25618	Protein CWH43 OS=Sa	0.48	0.17		Q01477
Q06689	Cell membrane protei	0.79	0.25		Q08287
P23291	Casein kinase I homolo	0.99	0.30		P38765
Q03713	Respiratory supercomp	8.65	0.98		P53598
P38085	Valine/tyrosine/trypto	0.50	0.18		Q12284
P40509	Coatomer subunit epsi	1.29	0.36		P0CX33
P37303	Low specificity L-threo	0.92	0.28		Q99383
P38081	Uncharacterized glycos	0.77	0.25		P89105
P50110	Sorting assembly mach	1.39	0.38		P32568
P10834	Protein PET54 OS=Sacc	0.97	0.29		P32349
Q99190	Very-long-chain enoyl-	1.44	0.39		P43590
P39727	ER-derived vesicles pro	0.83	0.26		P36056
Q08920	Nuclear cap-binding pr	2.93	0.59		P02309
P33339	Transcription factor ta	0.32	0.12		P41832
P39743	Reduced viability upon	0.87	0.27		P00447
P33759	37S ribosomal protein	1.56	0.41		P12754
Q06156	Condensin complex su	0.28	0.11		P46683
P53969	Sorting assembly mach	0.99	0.30		P39714
P17442	Phosphate system posi	0.32	0.12		P40516
P32341	Vacuolar ATPase assen	2.02	0.48		P53959
P37267	Assembly factor CBP4	5.44	0.81		P32583
P00931	Tryptophan synthase	0.63	0.21		P20049
Q01802	Aspartate aminotransf	0.88	0.27		P32608
P27616	Phosphoribosylaminoi	1.26	0.35		Q12305
P31412	V-type proton ATPase	1.35	0.37		P40011
P0C0T4	40S ribosomal protein	9.15	1.01		P07285
Q03281	Inner nuclear membra	0.63	0.21		Q12462
Q12749	Structural maintenanc	0.29	0.11		P53265
P04911	Histone H2A.1 OS=Sac	9.23	1.01		P09032
Q02959	Histone deacetylase H	0.52	0.18		Q05785
P06839	DNA repair helicase RA	0.52	0.18		P46970
P53219	Abhydrolase domain-c	1.34	0.37		P32364

P38255	Transcriptional regulat	0.79	0.25		P40070
P36144	Ribosome biogenesis p	1.81	0.45		P32480
P38996	Nuclear polyadenylate	0.44	0.16		P53009
P25451	Proteasome subunit be	1.78	0.44		P30665
P50105	Transcription initiation	0.95	0.29		P32340
P25340	Delta(24(24(1)))-sterol	1.30	0.36		P38221
P38715	NADPH-dependent ald	1.74	0.44		Q3E772
Q12445	Nucleoporin POM34 O	1.28	0.36		P53315
P24279	DNA replication licensi	0.42	0.15		Q03178
P38756	tRNA threonylcarbamo	1.60	0.41		P38988
Q06511	Ribosomal RNA-proces	2.21	0.51		P42942
P53297	PAB1-binding protein 1	0.43	0.16		P36048
P40513	Mitochondrial acidic pr	1.54	0.40		P19658
P17883	Superkiller protein 3 O	0.22	0.09		P38288
Q12672	60S ribosomal protein	6.68	0.89		P40090
P53090	Aromatic/aminoadipat	0.80	0.26		P42940
P46992	Cell wall protein YJL17	0.92	0.28		P36036
P35180	Mitochondrial import r	2.98	0.60		P00431
P21306	ATP synthase subunit	27.78	1.46		P38254
P26754	Replication factor A pr	1.17	0.34		P38077
P41819	Dimethyladenosine tra	2.23	0.51		P36161
Q06214	WD repeat-containing	0.81	0.26		P32915
P42846	Protein KRI1 OS=Sacch	0.62	0.21		P38821
P38910	10 kDa heat shock prot	16.45	1.24		Q08245
P05319	60S acidic ribosomal pr	7.54	0.93		Q12028
P23585	High-affinity glucose tr	0.60	0.20		Q12386
P27882	Mitochondrial FAD-link	2.59	0.56		P01119
P40491	ATP synthase assembly	8.91	1.00		Q05933
P41896	Transcription initiation	1.24	0.35		P47069
P38146	GTP-binding protein YF	2.57	0.55		P06776
P53337	ER-derived vesicles pro	1.55	0.41		Q03677
P34162	Mediator of RNA polyn	2.40	0.53		P40467
Q08004	Bud site selection prot	3.49	0.65		Q05979
Q03048	Cofilin OS=Saccharomy	3.29	0.63		Q12153
P29469	DNA replication licensi	0.27	0.10		P38775
P53730	Dol-P-Man:Man(7)GlcN	0.82	0.26		P53628
Q06678	54S ribosomal protein	1.41	0.38		P32775
Q12063	Dehydrodolichyl dipho	1.16	0.33		P56628
P53829	Protein CAF40 OS=Sacc	1.21	0.34		Q04632
P38162	Mitochondrial interme	2.34	0.52		P36060
P32495	H/ACA ribonucleoprote	4.09	0.71		P38255
P38695	Probable glucose trans	0.76	0.25		P46681
Q07915	Ribosome biogenesis p	2.20	0.51		P53072
Q06493	LETM1 domain-contai	1.06	0.31		Q04728
P33314	Inhibitory regulator pr	0.25	0.10		P11491
P36528	54S ribosomal protein	1.40	0.38		P43555
P15624	Phenylalanine--tRNA li	0.87	0.27		Q08220
P32799	Cytochrome c oxidase	28.68	1.47		P38116
Q03028	Mitochondrial 2-oxodi	1.28	0.36		Q05166
Q96VH5	MICOS complex subuni	13.21	1.15		P38682
P46680	Actin-interacting prote	0.52	0.18		P38996
Q05543	Regulator of Ty1 transp	0.84	0.26		Q12044

P40079	U3 small nucleolar ribc	1.00	0.30		P25631
P48836	V-type proton ATPase s	5.25	0.80		Q06385
P38833	Uncharacterized protei	1.83	0.45		P38781
P46672	tRNA-aminoacylation c	0.95	0.29		P38063
P25617	Uncharacterized protei	2.06	0.49		P48015
Q12285	Ubiquitin-like protein M	1.68	0.43		P28000
P43586	60S ribosomal subunit	1.71	0.43		Q12510
P53236	Chromatin structure-re	0.36	0.13		P35179
Q05016	NADP-dependent 3-hy	2.62	0.56		P05375
P34216	EH domain-containing	0.21	0.08		P51862
P38065	AP-2 complex subunit a	0.33	0.12		P50108
Q08193	1,3-beta-glucanosyltra	0.72	0.24		P53066
P29478	Signal recognition part	1.86	0.46		Q03516
P41812	Ribonucleases P/MRP p	0.39	0.14		P39998
P28007	H/ACA ribonucleoprote	3.54	0.66		P22943
P38845	Cruciform DNA-recogn	0.59	0.20		P32569
P42934	Dolichyl-phosphate-ma	0.45	0.16		Q08581
P39925	Mitochondrial respirat	0.48	0.17		P39685
Q01454	DNA polymerase alpha	0.37	0.14		P32767
Q99383	Nuclear polyadenylate	0.88	0.27		P33767
Q04067	Eukaryotic translation i	1.50	0.40		Q03834
P39965	Probable proline--tRNA	0.53	0.18		Q12017
P38203	U6 snRNA-associated S	4.20	0.72		P53253
Q12517	mRNA-decapping enzy	1.43	0.39		P36154
P25372	Thioredoxin-3, mitoch	5.71	0.83		P45978
P38115	D-arabinose dehydrog	1.32	0.37		Q03653
P40159	Uncharacterized protei	1.54	0.40		P42941
P00425	Cytochrome c oxidase p	7.74	0.94		P52488
P02400	60S acidic ribosomal pr	4.38	0.73		P29496
P13856	Ras-related protein RSI	1.52	0.40		P38198
P20457	DNA primase large sub	0.69	0.23		P17891
P32569	Mediator of RNA polyn	0.52	0.18		P29469
P39704	Protein ERP2 OS=Sacch	2.20	0.51		P38604
Q02629	Nucleoporin NUP100/N	0.33	0.12		P40529
Q12387	N-terminal acetyltransf	0.42	0.15		P04819
P30822	Exportin-1 OS=Sacchar	0.35	0.13		Q05029
P32472	Peptidyl-prolyl cis-tran	8.38	0.97		P80428
P47045	Mitochondrial import i	0.68	0.23		Q12156
P48563	Protein MON2 OS=Sacc	0.22	0.09		Q12408
P40013	Protein BIM1 OS=Sacch	1.08	0.32		P32477
P13393	TATA-box-binding prot	2.36	0.53		P36000
Q12447	Polyamine N-acetyltrar	2.57	0.55		P53723
Q99220	Protein OS-9 homolog	0.58	0.20		P29704
P38878	Protein lunapark OS=Sa	1.76	0.44		Q03705
P32867	Protein SSO1 OS=Sacch	1.69	0.43		P54790
P39726	Glycine cleavage syster	3.45	0.65		P38166
P81449	ATP synthase subunit e	11.78	1.11		Q03629
P06704	Cell division control pr	3.45	0.65		P15732
P05744	60S ribosomal protein	13.58	1.16		P25569
Q05027	Transcription initiation	4.03	0.70		P38620
P22204	Cell cycle protein kinas	0.53	0.18		Q05934
P12904	5~-AMP-activated prot	1.16	0.33		P38836

P27697	Atypical kinase COQ8,	0.78	0.25		P25359
P40581	Peroxiredoxin HYR1 OS	3.45	0.65		P32867
P39996	Glutathione transferas	0.84	0.26		P37296
P53192	Golgi to ER traffic prote	2.36	0.53		Q02486
P40056	Golgi to ER traffic prote	1.84	0.45		P46675
Q06497	Peroxisomal adenine n	1.17	0.34		P22204
Q05775	Eukaryotic translation i	2.04	0.48		P21269
P38061	60S ribosomal protein	8.07	0.96		P41819
P38630	Replication factor C su	0.42	0.15		P53905
P40582	Glutathione S-transfera	1.40	0.38		P42842
P53879	GTP-binding protein RH	0.88	0.27		Q99369
P40467	Activator of stress gene	0.30	0.11		P25296
P40477	Nucleoporin NUP159 C	0.20	0.08		P47123
P41832	Protein BNI1 OS=Sacch	0.14	0.06		P46948
P36059	ATP-dependent (S)-NA	1.10	0.32		P11632
P41056	60S ribosomal protein	13.24	1.15		Q03957
Q12298	Uncharacterized ABC t	0.58	0.20		P35189
Q03880	V-type ATPase assemb	4.26	0.72		P38626
Q07716	Altered inheritance of	1.32	0.37		P36068
Q12164	Pore membrane protei	1.39	0.38		P12683
P43616	Cys-Gly metallodipepti	0.86	0.27		P48582
P32353	Delta(7)-sterol 5(6)-des	1.40	0.38		P52553
P25567	RNA-binding protein SF	0.63	0.21		P39727
P32774	Transcription initiation	9.82	1.03		P52917
P39990	13 kDa ribonucleoprote	4.40	0.73		Q02724
P53154	Glycerol uptake protei	0.54	0.19		P42935
P38351	RNA polymerase II-asso	0.89	0.28		P43611
P46959	tRNA (adenine(58)-N(1	1.11	0.32		P30619
O13563	26S proteasome regula	5.15	0.79		P06785
P50945	MICOS complex subuni	1.83	0.45		P38071
P53334	Probable family 17 gluc	0.79	0.25		P38627
P25644	DNA topoisomerase 2-	0.45	0.16		P38080
P38803	Pre-rRNA-processing p	0.86	0.27		P09880
Q08959	Phosphatidylglycerol p	1.13	0.33		P34237
P18544	Acetylornithine aminot	1.02	0.31		P21182
P39078	T-complex protein 1 su	0.63	0.21		Q12256
Q03973	High mobility group pr	1.78	0.44		Q07648
P39705	Nucleoporin NUP60 OS	0.75	0.24		P39932
P30619	Protein transport prote	0.48	0.17		P35845
P40540	ER membrane protein	3.29	0.63		P35180
P00546	Cyclin-dependent kinas	1.61	0.42		P06101
P61830	Histone H3 OS=Sacchar	5.19	0.79		Q08979
Q01855	40S ribosomal protein	9.29	1.01		P36165
Q12406	Actin-related protein 7	0.69	0.23		P40986
P42847	37S ribosomal protein	2.13	0.50		P43620
P20081	FK506-binding protein	5.67	0.82		P53960
P36527	54S ribosomal protein	5.51	0.81		P53552
P36517	54S ribosomal protein	0.89	0.28		P46678
P40553	Peroxiredoxin DOT5 OS	2.88	0.59		P43558
Q12743	DER1-like family memb	1.09	0.32		P33327
P08004	Chitin synthase 1 OS=S	0.24	0.09		P37298
P19955	37S ribosomal protein	4.40	0.73		P40210

P14693	Sorting assembly mach	0.86	0.27		P36016
Q03430	37S ribosomal protein	0.98	0.30		Q92317
P40564	DnaJ-like protein 1 OS=	0.79	0.25		P16451
P38084	Leu/Val/Ile amino-acid	0.51	0.18		P19263
P22217	Thioredoxin-1 OS=Sacc	10.60	1.06		P51534
P41057	40S ribosomal protein	51.95	1.72		P36120
Q07551	NADPH-dependent alp	1.21	0.34		P40165
P16661	Chitobiosyldiphosphod	0.88	0.27		P20434
Q02647	Dynein light chain 1, cy	8.13	0.96		P53730
P32583	Suppressor protein SR	0.78	0.25		P40471
Q12412	Protein PNS1 OS=Sacc	0.59	0.20		P53632
P19735	Pre-mRNA-splicing fact	0.37	0.14		Q03774
P33441	THO complex subunit	1.08	0.32		P41057
P11633	Non-histone chromoso	10.33	1.05		Q06287
P06102	General negative regul	0.42	0.15		P47050
Q02199	Nucleoporin NUP49/N	0.78	0.25		P15179
P39976	D-2-hydroxyglutarate--	0.53	0.18		P18480
Q12030	Transcription initiation	1.26	0.35		P40308
Q07623	Nucleolar protein 6 OS	2.05	0.48		Q12329
P32875	Lipoyl synthase, mitoc	0.65	0.22		P38816
P40548	HSP70 co-chaperone S	6.68	0.89		P09620
Q06090	54S ribosomal protein	4.55	0.74		P40517
P47124	Putative glycosyltransf	0.84	0.26		P35176
P32474	Protein disulfide-isom	0.61	0.21		P46682
P53305	Mitochondrial 37S ribo	3.44	0.65		P42945
P50087	MICOS subunit MIC26	1.39	0.38		P47154
P38079	Protein YRO2 OS=Sacc	0.83	0.26		P43612
P06787	Calmodulin OS=Saccha	3.25	0.63		P53043
Q99216	Pre-rRNA-processing p	1.17	0.34		P07277
P47130	Cop9 signalosome com	0.76	0.25		P54003
P40106	Glycerol-1-phosphate	2.24	0.51		P25040
Q08687	Translation machinery-	3.80	0.68		P16522
P35183	Protein AST1 OS=Sacch	0.97	0.29		P47137
P38164	SEH-associated protein	0.22	0.09		Q00618
P11632	Non-histone chromoso	19.14	1.30		P40541
P28625	Protein YIM1 OS=Sacc	0.97	0.29		P41734
Q02642	Nascent polypeptide-a	2.95	0.60		P40958
Q12114	Chitin biosynthesis pro	0.47	0.17		P23585
Q08745	40S ribosomal protein	5.15	0.79		P32769
P53845	Protein transport prot	0.70	0.23		P47019
P39103	Cytochrome c oxidase	16.53	1.24		P33331
P34247	U3 small nucleolar RN	2.54	0.55		P14741
P47076	DNA-directed RNA pol	4.77	0.76		P39979
Q03201	37S ribosomal protein	1.72	0.43		P48567
P20436	DNA-directed RNA pol	3.05	0.61		P47068
Q06169	Peroxisomal membran	0.61	0.21		Q02776
Q06224	Endoribonuclease YSH	0.38	0.14		P43560
P38122	3-methyl-2-oxobutano	0.96	0.29		P42937
P47818	Protein CCC1 OS=Sacc	0.99	0.30		Q07915
P53736	Uncharacterized prote	2.14	0.50		P39524
P23369	54S ribosomal protein	4.83	0.77		P40518
Q04213	ISWI one complex prot	0.66	0.22		Q00362

Q12099	ATP-dependent RNA h	0.68	0.23		P38286
P07284	Serine--tRNA ligase, cy	0.69	0.23		P17157
P32364	Kinesin-related protein	0.37	0.14		P26793
P31334	54S ribosomal protein	0.88	0.27		P32597
P38992	Sphingolipid C4-hydrox	1.52	0.40		Q06411
P47031	Mitochondrial outer m	0.41	0.15		P27801
P53600	Coatomer subunit zeta	1.95	0.47		Q03786
P32352	C-8 sterol isomerase O	1.12	0.33		P43579
Q12256	Polyamine transporter	0.38	0.14		P32794
P48526	Isoleucine--tRNA ligase	0.33	0.12		Q12108
P36036	RNA annealing protein	1.19	0.34		Q12012
P18562	Uracil phosphoribosylt	1.57	0.41		P21657
P53859	Exosome complex com	0.80	0.26		P46957
Q07541	Uncharacterized protei	2.95	0.60		P32381
P38314	Protein SDS24 OS=Sacc	0.64	0.21		P40050
P00958	Methionine--tRNA liga	0.47	0.17		P49955
P37293	Putative N-terminal ac	1.04	0.31		Q06168
P21304	Periodic tryptophan pr	0.45	0.16		P38250
Q06892	NADH kinase POS5, mi	0.66	0.22		P47042
P07170	Adenylate kinase OS=S	2.18	0.50		P47031
P53168	DASH complex subunit	1.34	0.37		P69771
P38985	Signal recognition part	4.42	0.73		Q08687
P38272	SWI5-dependent HO e	0.64	0.21		P25618
Q04231	DNA repair protein RA	2.92	0.59		P38281
P40040	Protein THO1 OS=Sacc	1.18	0.34		Q03533
P49167	60S ribosomal protein	7.12	0.91		Q02793
Q05948	Uncharacterized SVF1-	1.02	0.31		P36037
Q04228	UBX domain-containin	0.53	0.18		P33202
P38226	Uncharacterized acyltr	0.67	0.22		P36088
P00729	Carboxypeptidase Y OS	0.60	0.20		Q08746
P16467	Pyruvate decarboxylas	0.58	0.20		P47064
Q3E7A3	Uncharacterized protei	17.97	1.28		P33297
P00424	Cytochrome c oxidase	2.91	0.59		Q00539
P00410	Cytochrome c oxidase	2.14	0.50		P40043
Q04031	Ribosomal RNA-proces	1.31	0.36		Q06629
P38775	Putative uncharacteriz	0.45	0.16		P53177
P47017	Sm-like protein LSm1 O	2.98	0.60		P32911
P18962	Dipeptidyl aminopepti	0.29	0.11		P38888
P03874	Cytochrome B pre-mR	0.37	0.14		Q08235
Q12462	Peroxisomal membran	1.38	0.38		P38439
P14904	Vacuolar aminopeptida	0.51	0.18		P27351
P49166	60S ribosomal protein	14.47	1.19		Q03177
P48360	Probable NADPH:adren	0.65	0.22		P38295
Q04869	Uncharacterized protei	0.45	0.16		P39526
Q01159	mRNA-capping enzyme	0.86	0.27		P39926
P38816	Thioredoxin reductase	0.66	0.22		P40348
P47089	Translation machinery-	1.28	0.36		P20424
P36076	Coenzyme A biosynthe	0.54	0.19		P07703
P33296	Ubiquitin-conjugating	0.94	0.29		P40582
P38072	Protein SCO2, mitocho	1.22	0.35		Q05015
P69771	Vacuolar protein-sortin	4.07	0.71		Q08965
P32263	Pyrroline-5-carboxylat	1.16	0.33		Q12024

P38175	37S ribosomal protein	2.95	0.60		Q08444
P32588	Nuclear and cytoplasm	0.59	0.20		P40358
Q02795	Dolichyl-diphosphoolig	1.43	0.39		P06787
P32629	Mannan polymerase II	0.50	0.18		P40495
Q99247	Uncharacterized WD re	0.16	0.06		Q02785
P27999	DNA-directed RNA poly	3.83	0.68		P39106
P29366	Bud emergence protei	0.58	0.20		P53073
P36131	DASH complex subunit	1.28	0.36		P33204
P38819	Protein ERP5 OS=Sacch	1.15	0.33		P38089
P18851	Guanine nucleotide-bi	0.49	0.17		P40555
P38169	Kynurenine 3-monooxy	0.56	0.19		P33750
Q03941	Dephospho-CoA kinase	1.78	0.44		P18962
P34087	DNA-directed RNA poly	2.35	0.53		Q12220
P53724	54S ribosomal protein	4.48	0.74		P38276
Q08746	Regulator of ribosome	2.40	0.53		P53301
P38869	Protein SVP26 OS=Sacc	1.42	0.38		P33328
Q03063	Down-regulator of inva	0.61	0.21		P06100
P38132	DNA replication licensi	0.28	0.11		P40046
Q12117	Protein MRH1 OS=Sacc	0.90	0.28		Q07897
Q03648	Uncharacterized protei	0.57	0.20		P38793
P00045	Cytochrome c iso-2 OS	3.33	0.64		P53164
Q12428	Probable 2-methylcitra	0.63	0.21		P32802
P40090	MAU2 chromatid cohe	0.38	0.14		P35182
P50108	Probable alpha-1,6-ma	0.65	0.22		P39720
P40051	Intermediate cleaving	0.62	0.21		Q08282
O74700	Mitochondrial import i	4.87	0.77		P31380
P32621	Guanosine-diphosphat	0.51	0.18		P39682
Q12276	HMG2-induced ER-rem	0.23	0.09		Q12354
Q01662	Methionine aminopept	0.70	0.23		P36041
P04819	DNA ligase 1 OS=Sacch	0.32	0.12		P53893
Q12306	Ubiquitin-like protein	15.54	1.22		Q07953
P34237	Protein CASP OS=Sacch	0.36	0.13		P53125
P36009	Probable ATP-depende	0.40	0.15		P35169
P53220	Mitochondrial import i	1.82	0.45		Q06608
P38198	Protein STU1 OS=Sacch	0.11	0.05		P43603
P39952	Mitochondrial inner m	0.69	0.23		P22214
P09547	SWI/SNF chromatin-re	0.21	0.08		Q07825
P53973	Histone deacetylase H	0.34	0.13		P23291
Q05934	Vacuolar import and d	0.26	0.10		P53250
P38804	Restriction of telomere	3.69	0.67		P14747
P38879	Nascent polypeptide-a	3.49	0.65		P07273
P14843	Phospho-2-dehydro-3-	0.97	0.29		P40487
P39931	Protein SSP120 OS=Sac	1.80	0.45		Q12453
P25648	Mediator of RNA polyn	0.12	0.05		P36053
P38682	ADP-ribosylation facto	0.53	0.18		P32776
P32793	Protein YSC84 OS=Sacc	0.59	0.20		P05318
Q92317	Negative cofactor 2 co	1.32	0.37		P25037
Q12040	Broad-specificity phos	1.44	0.39		P07258
Q12305	Thiosulfate sulfurtrans	2.34	0.52		Q03016
P37298	Succinate dehydrogena	1.51	0.40		P12611
P47141	37S ribosomal protein	1.17	0.34		P53894
P06197	CDP-diacylglycerol--inc	1.11	0.32		P04911

Q04603	DNA polymerase epsil	1.88	0.46		P38930
P33324	CRAL-TRIO domain-co	0.68	0.23		P38932
P47069	Spindle pole body asse	0.27	0.10		Q06245
Q04338	t-SNARE VTI1 OS=Sacc	0.77	0.25		P53086
P29055	Transcription initiation	0.63	0.21		P19736
P45978	Protein SCD6 OS=Sacc	0.62	0.21		P28789
P38281	Actin patches distal pr	1.18	0.34		Q12511
P35196	Dehydrodolichyl dipho	1.04	0.31		P38328
P53632	Poly(A) RNA polymeras	0.43	0.16		P33421
P22133	Malate dehydrogenase	1.24	0.35		P41058
P23797	N-acetylglucosaminyl-	1.21	0.34		Q06147
P40202	Superoxide dismutase	1.33	0.37		Q02630
P53218	Ribonucleases P/MRP	2.58	0.55		P53152
P53898	Protein NSG2 OS=Sacc	0.99	0.30		P22579
P16120	Threonine synthase OS	0.51	0.18		Q04773
P32486	Beta-glucan synthesis-	0.34	0.13		P53848
Q03435	Non-histone protein 1	1.18	0.34		Q12502
P40014	Kinetochore protein SP	1.52	0.40		P19262
P36526	54S ribosomal protein	3.09	0.61		Q12133
P27614	Carboxypeptidase S OS	0.44	0.16		P53327
Q12284	FAD-linked sulfhydryl	1.31	0.36		Q04066
Q12035	rRNA-processing prote	1.08	0.32		Q05812
P36525	54S ribosomal protein	1.55	0.41		Q12242
P40096	Negative cofactor 2 co	5.03	0.78		Q01852
Q07807	mRNA-binding protein	0.34	0.13		Q99216
P40956	Protein GTS1 OS=Sacc	0.53	0.18		P53172
P32605	U1 small nuclear ribon	0.73	0.24		P53929
P40093	UPF0160 protein YER1	0.85	0.27		Q06493
P38620	Ribose-phosphate pyr	1.24	0.35		P48813
P53959	Conserved oligomeric	0.34	0.13		Q12204
P25043	Proteasome subunit b	1.68	0.43		P46995
P22517	Calcium/calmodulin-d	0.59	0.20		P33203
Q04651	ER-derived vesicles pr	0.58	0.20		P46674
P52286	Suppressor of kinetoch	1.84	0.45		P08456
P38969	Pentamidine resistanc	0.78	0.25		P22224
P53256	Exosome complex com	1.57	0.41		P36119
P53163	54S ribosomal protein	2.10	0.49		P53044
P40088	Plasma membrane iro	0.67	0.22		P35178
P15274	AMP deaminase OS=S	0.35	0.13		P50085
P43579	Ino eighty subunit 1 O	0.27	0.10		P38130
Q08553	Protein SYC1 OS=Sacch	2.03	0.48		P00572
P09959	Regulatory protein SW	0.37	0.14		P32259
Q06580	Myosin light chain 2 O	1.74	0.44		P32476
P53178	UDP-N-acetylglucosam	1.77	0.44		P40457
P38261	Exocyst complex comp	0.25	0.10		P47116
P32259	Mediator of RNA poly	0.24	0.09		Q06689
P35189	Transcription initiation	1.35	0.37		P20435
P53633	Prenylated Rab accept	3.20	0.62		P53865
Q3E824	Uncharacterized prote	5.74	0.83		P32913
P30657	Proteasome subunit b	1.61	0.42		Q12321
Q02630	Nucleoporin NUP116/	0.23	0.09		P89102
P22214	Protein transport prot	1.10	0.32		O13329

P38801	Exosome complex prot	1.44	0.39		Q06169
Q03362	Uncharacterized protei	1.51	0.40		P24482
P38827	Histone-lysine N-methy	0.16	0.06		P38962
P37304	Protein PAM1 OS=Sacc	0.29	0.11		P11325
P16370	DNA-directed RNA poly	0.93	0.29		Q06146
P32505	Nuclear polyadenylat	0.61	0.21		P32623
P38166	Protein transport prot	1.15	0.33		P53114
P38064	54S ribosomal protein	1.88	0.46		P32495
P36135	Probable secreted bet	0.87	0.27		Q02908
Q03957	CTD kinase subunit alp	0.36	0.13		P28321
Q12522	Eukaryotic translation i	0.70	0.23		P40469
P53201	SWR1-complex protein	0.67	0.22		P40460
P25808	ATP-dependent rRNA	0.40	0.15		P36106
P36090	Uncharacterized protei	0.37	0.14		P53296
P06773	Deoxycytidylate deami	0.68	0.23		P53323
P51402	60S ribosomal protein	8.80	0.99		P52893
P04076	Argininosuccinate lyas	0.57	0.20		P38238
Q03750	Transcription initiation	0.28	0.11		P46985
Q08873	Transgelin OS=Sacchar	1.27	0.36		P53091
P35725	Uncharacterized protei	2.40	0.53		Q08001
P25560	Protein RER1 OS=Sacch	2.50	0.54		Q07623
Q02260	Small nuclear ribonucl	3.17	0.62		P38138
P52870	Protein transport prot	7.34	0.92		P35725
Q08285	Exosome complex com	1.01	0.30		Q06504
P41058	40S ribosomal protein	24.98	1.41		P38779
Q06668	Methyltransferase OM	0.52	0.18		Q03305
Q03177	WD repeat-containing	0.28	0.11		P43639
P53313	Protein SDA1 OS=Sacch	0.31	0.12		P36149
Q08925	RNA-binding protein M	0.31	0.12		P20485
Q02772	Mitochondrial protein	3.28	0.63		Q99190
P06182	Cytochrome c heme ly	0.86	0.27		Q07844
P53215	tRNA(His) guanylyltran	1.31	0.36		P48231
P26570	Serine/threonine-prot	0.35	0.13		P35181
P04046	Amidophosphoribosylt	0.51	0.18		P32352
Q12118	Small glutamine-rich te	0.88	0.27		P32453
P06781	GTP-binding protein R	1.93	0.47		P40540
P22354	54S ribosomal protein	2.48	0.54		Q12455
Q12133	Signal peptidase compl	1.41	0.38		P47173
P41910	Repressor of RNA poly	0.52	0.18		P38993
Q03102	Uncharacterized mem	0.60	0.20		P00724
P47160	Epsin-3 OS=Saccharom	0.37	0.14		P25637
P23833	Protein SCO1, mitocho	1.02	0.31		P18899
P36421	Tyrosine--tRNA ligase,	0.70	0.23		P52490
P19658	Exocyst complex comp	0.39	0.14		Q03503
P40043	Respiratory growth ind	2.40	0.53		P32604
Q3E846	Cytochrome c oxidase	8.01	0.95		Q12412
Q04500	U3 small nucleolar RN	0.26	0.10		P53107
Q05779	Ubiquinone biosynthes	0.87	0.27		P23202
P53953	SED5-binding protein 2	0.27	0.10		Q12263
P32623	Probable glycosidase C	0.59	0.20		Q96VH5
Q12487	54S ribosomal protein	1.74	0.44		P34761
P41697	Bud site selection prot	0.24	0.09		Q12341

P06245	cAMP-dependent prot	0.70	0.23		Q05583
P28274	CTP synthase 1 OS=Sac	0.54	0.19		P00912
P38856	Clathrin coat assembly	0.30	0.11		Q12486
Q08287	60S ribosome subunit	0.28	0.11		Q06346
P40525	60S ribosomal protein	4.33	0.73		P14359
P13185	Serine/threonine prote	0.17	0.07		Q03262
P53076	Vacuolar import and de	0.24	0.09		P25382
P50947	Transcriptional regulat	0.65	0.22		P46956
P05749	60S ribosomal protein	1.77	0.44		Q08920
P11491	Repressible alkaline ph	0.45	0.16		P25659
P39932	Sugar transporter STL1	0.45	0.16		P39012
P40207	Uncharacterized protei	1.31	0.36		P47054
Q06217	Small nuclear ribonucle	5.06	0.78		P38167
P46995	Histone-lysine N-methy	0.39	0.14		P03875
P46671	Factor arrest protein 3	1.64	0.42		P38985
P36039	ER membrane protein	1.28	0.36		P28625
P53171	Genetic interactor of p	0.77	0.25		P32347
P23500	Mitochondrial RNA-spl	1.01	0.30		Q12452
P40367	GPI ethanolamine phos	0.28	0.11		P47025
P36163	Mitochondrial metallo	1.04	0.31		P07274
P53925	Uncharacterized vacuo	0.29	0.11		Q00684
P57744	Mitochondrial import i	5.33	0.80		Q12071
P43321	Small nuclear ribonucle	4.20	0.72		P53256
Q6Q547	H/ACA ribonucleoprote	29.37	1.48		P39931
Q07834	KH domain-containing	0.22	0.09		P38144
Q04472	Mitochondrial inner m	0.63	0.21		P25576
Q02555	Ribonuclease 3 OS=Sac	0.42	0.15		P32447
P35732	RNA polymerase II deg	0.25	0.10		Q96VH4
P35997	40S ribosomal protein	6.36	0.87		Q12234
P32573	Peroxisomal 2,4-dieno	1.11	0.32		Q12406
P34909	General negative regul	0.43	0.16		P29703
D6VTK4	Pheromone alpha fact	0.48	0.17		P53860
P38063	Ribose-phosphate pyr	1.19	0.34		P06102
P53045	Methylsterol monooxy	0.67	0.22		P52593
P32611	54S ribosomal protein	0.70	0.23		P40056
Q07830	GPI ethanolamine phos	0.18	0.07		P32500
P18961	Serine/threonine-prote	0.36	0.13		P39109
P40060	Ino eighty subunit 5 OS	2.66	0.56		Q03921
P53311	Mitochondrial pyruvat	2.13	0.50		P13382
P28005	Ribonuclease P/MRP p	1.58	0.41		P53079
Q08826	Sorting nexin-3 OS=Sac	2.45	0.54		P00410
P10849	Mitochondrial transcri	0.44	0.16		P40850
Q12402	Protein YOP1 OS=Sacch	2.18	0.50		P27882
P53184	Nicotinamidase OS=Sa	1.11	0.32		P38970
P40161	Histone chaperone RT	0.44	0.16		Q03769
P38930	Casein kinase II subuni	0.86	0.27		P38863
P40858	54S ribosomal protein	1.76	0.44		Q05874
P10962	Protein MAK16 OS=Sac	0.69	0.23		P53141
Q03778	Riboflavin kinase OS=S	1.14	0.33		P40347
P53072	tRNA acetyltransferase	1.00	0.30		Q04305
Q07648	D-tyrosyl-tRNA(Tyr) de	2.04	0.48		P06701
P40505	Transcriptional regulat	1.12	0.33		Q06001

P46989	Autophagy-related pro	0.85	0.27		P09950
P38817	ADP-ribosylation facto	0.34	0.13		P53759
P36520	54S ribosomal protein	0.68	0.23		Q12692
Q03429	Mitochondrial zinc mai	1.71	0.43		Q02455
Q08963	U2 small nuclear ribon	1.80	0.45		P53331
P53260	Glutamyl-tRNA(Gln) an	0.96	0.29		Q07951
P17558	37S ribosomal protein	0.92	0.28		P36090
P18852	Guanine nucleotide-bi	3.28	0.63		P20486
Q08237	RNA exonuclease 4 OS	1.04	0.31		P36051
P38961	25S rRNA (adenine(64	0.66	0.22		Q12180
P36147	Presequence transloca	0.89	0.28		P04037
P06701	Regulatory protein SIR	0.24	0.09		Q03088
P38993	Iron transport multico	0.38	0.14		Q12102
Q08058	Coenzyme Q-binding p	1.18	0.34		P34110
Q99325	Autophagy-related pro	0.88	0.27		Q07541
P22139	DNA-directed RNA pol	7.56	0.93		Q12277
P40155	Peroxisomal membran	0.83	0.26		P38274
P36080	Ribosomal RNA-proces	0.45	0.16		P40416
P40007	Nucleolar protein 16 O	1.01	0.30		P53333
P32585	Mediator of RNA poly	0.73	0.24		P53316
P33755	Nuclear protein localiz	0.53	0.18		Q05040
P53091	DNA replication licensi	0.18	0.07		Q05881
Q02773	Ribonuclease P protein	0.18	0.07		P53927
P42073	RNA end formation pro	0.37	0.14		P53137
P40529	ADP-ribosylation facto	0.54	0.19		Q3E747
P39081	Protein PCF11 OS=Sacc	0.22	0.09		P39013
Q03290	RNA polymerase II tran	0.63	0.21		P33759
P25651	Monopolin complex su	0.91	0.28		P08067
Q08223	Altered inheritance of	0.67	0.22		P47108
P0CX33	40S ribosomal protein	46.00	1.67		Q03010
Q06089	Uncharacterized mitoc	1.84	0.45		P32899
Q12028	AP-1 complex subunit	0.22	0.09		P33333
P26725	Probable mannosyltra	0.45	0.16		P47103
P40422	DNA-directed RNA pol	8.89	1.00		P34909
Q12692	Histone H2A.Z OS=Sacc	2.66	0.56		P11633
P32783	mRNA cap guanine-N7	0.59	0.20		P40477
Q00916	U1 small nuclear ribon	0.72	0.24		P38153
Q08742	Thiosulfate sulfurtrans	2.04	0.48		P36081
Q03525	Protein TMA23 OS=Sac	1.18	0.34		Q12181
P25348	54S ribosomal protein	1.37	0.37		P53741
P38755	Oxysterol-binding prot	0.46	0.16		P53898
Q04341	Mitochondrial interme	4.07	0.71		P53845
P38837	Protein NSG1 OS=Sacc	1.06	0.31		Q03784
Q12465	Bud site selection prot	0.15	0.06		P25340
P40015	Inositol phosphosphing	0.41	0.15		Q12158
P47019	Ribosome biogenesis p	1.63	0.42		P11914
Q07651	SUR7 family protein F	0.73	0.24		P53729
P52871	Protein transport prot	3.25	0.63		Q03771
Q06451	Polyamine transporter	0.41	0.15		Q12199
P43639	Casein kinase II subuni	0.78	0.25		P38856
P40033	37S ribosomal protein	3.34	0.64		P32657
P32317	Protein AFG1 OS=Sacc	0.38	0.14		P50106

Q12233	ATP synthase subunit g	3.17	0.62		P53207
Q06188	PWWP domain-contair	0.69	0.23		Q12114
P25382	Ribosome assembly pr	0.50	0.18		Q04779
P38616	Protein YGP1 OS=Sacch	0.46	0.16		Q03655
P38784	Vacuolar ATPase assen	0.95	0.29		P53236
P22936	DNA-(apurinic or apyri	0.57	0.20		Q12746
Q12331	FAS1 domain-containir	0.85	0.27		P47083
Q12102	Cleavage factor two pr	0.16	0.06		P32386
P36047	Protein phosphatase 1	0.62	0.21		P25332
Q12144	Pore and endoplasmic	1.05	0.31		P53940
P35207	Antiviral helicase SKI2 (	0.14	0.06		P38247
Q05166	Nucleoporin ASM4 OS=	0.38	0.14		Q03308
P32462	Delta(14)-sterol reduct	0.45	0.16		P47032
P40517	Ran-specific GTPase-ac	0.68	0.23		P39104
P38836	Putative metallocarbox	0.46	0.16		P36095
P36100	Transcription initiation	0.29	0.11		P53909
P32617	Chromatin-remodeling	2.52	0.55		P21825
P38884	Altered inheritance of r	0.47	0.17		P39726
P53905	U6 snRNA-associated S	3.17	0.62		Q04048
P53886	Anaphase-promoting c	0.13	0.05		P17898
P53330	Regulator of Ty1 transp	1.19	0.34		P25560
P53732	37S ribosomal protein	1.27	0.36		P47142
P38958	Protein PET100, mitoch	3.08	0.61		P53911
P38889	Transcription factor SK	0.31	0.12		P40578
Q12025	Uncharacterized protei	0.84	0.26		P38635
P48606	Tubulin-specific chaper	2.09	0.49		Q04767
P54838	Dihydroxyacetone kina	0.25	0.10		Q12463
Q03723	Dolichyl-diphosphoolig	0.63	0.21		P00128
P36104	COMPASS component	0.65	0.22		Q12246
P38276	UPF0303 protein YBR1	1.47	0.39		P22517
P38713	Oxysterol-binding prot	0.18	0.07		Q05123
P54860	E4 ubiquitin-protein lig	0.19	0.08		P22438
P04803	Tryptophan--tRNA ligas	0.55	0.19		P38710
Q12315	Nucleoporin GLE1 OS=	0.26	0.10		Q08773
P51862	RHO1 GDP-GTP exchan	0.13	0.05		Q07799
Q12207	Non-classical export pr	2.37	0.53		P25361
P53733	37S ribosomal protein	8.34	0.97		P23644
P47143	Adenosine kinase OS=S	0.67	0.22		P53100
P32529	DNA-directed RNA poly	2.74	0.57		P00175
Q06680	Condensin complex sul	0.17	0.07		P38910
P23642	Mannan polymerase I c	0.36	0.13		Q03148
Q03016	GLC7-interacting prote	0.14	0.06		P25365
Q08749	Mitochondrial import i	1.33	0.37		P22855
P38853	Kelch repeat-containin	0.15	0.06		P38218
P53301	Probable glycosidase C	0.43	0.16		Q03264
Q07350	Pre-mRNA-splicing fact	0.87	0.27		P36124
P39938	40S ribosomal protein	2.86	0.59		P38325
P53121	Putative flavin carrier p	0.17	0.07		P06633
P53844	Phosphatidylinositol tr	0.59	0.20		P20133
P38604	Lanosterol synthase OS	0.25	0.10		Q06263
P41834	Syntaxin UFE1 OS=Sacc	0.59	0.20		Q08202
P53155	Uncharacterized protei	0.54	0.19		P53297

P40557	ER-retained PMA1-sup	0.26	0.10		P25454
P11433	Cell division control pr	0.34	0.13		P33895
O13525	Ubiquinone biosynthes	0.84	0.26		Q12043
P32833	Origin recognition com	0.39	0.14		P35184
P39929	Vacuolar-sorting prote	0.68	0.23		P21827
P53927	Ribosome biogenesis p	1.09	0.32		P46964
P36056	37S ribosomal protein	0.30	0.11		P20095
P06244	cAMP-dependent prot	0.50	0.18		P47136
P46957	DNA polymerase delta	0.29	0.11		P27999
P53112	Peroxisomal membran	0.44	0.16		P34253
P32802	Transmembrane 9 sup	0.28	0.11		P32831
P38074	Protein arginine N-met	0.60	0.20		P38068
P40081	Putative magnesium-d	1.47	0.39		Q03768
P06115	Catalase T OS=Sacchar	0.34	0.13		Q06108
P37263	UPF0743 protein YCR0	2.63	0.56		P38623
Q07540	Frataxin homolog, mit	1.04	0.31		P05986
P19073	Cell division control pr	0.91	0.28		Q02948
P39524	Probable phospholipid	0.10	0.04		P47095
P40030	Ergosterol biosynthetic	2.88	0.59		P38712
P33330	Phosphoserine aminot	0.54	0.19		P38149
P38986	L-asparaginase 1 OS=S	0.40	0.15		P22035
P53874	Ubiquitin carboxyl-ter	0.24	0.09		P53192
P54000	RNA polymerase II tran	0.77	0.25		P25638
P28239	Inorganic pyrophospha	0.93	0.29		P39008
P38850	Regulator of Ty1 trans	0.16	0.06		P14164
Q03790	Nucleoporin NUP53 OS	0.43	0.16		P13186
P38915	Transcription factor SP	0.24	0.09		P25367
P17106	Centromere-binding pr	0.27	0.10		P43638
P54790	Origin recognition com	0.30	0.11		Q08924
P15992	Heat shock protein 26	1.19	0.34		Q02884
P06844	Protein SPT3 OS=Sacch	0.44	0.16		P39984
Q12001	Dolichyl pyrophosphat	0.25	0.10		P36040
P32388	54S ribosomal protein	2.18	0.50		P49334
P32857	Membrane protein PT	0.37	0.14		P12684
P20107	Zinc/cadmium resistan	0.34	0.13		P40472
Q12442	ADIPOR-like receptor I	0.67	0.22		P54007
P37370	Verprolin OS=Saccharo	0.26	0.10		P38798
P38717	Membrane-anchored li	0.18	0.07		Q02206
Q06630	Mitochondrial homolo	1.00	0.30		P53195
Q07534	Solute carrier family 25	0.73	0.24		P49775
P38174	Methionine aminopept	0.48	0.17		P38716
P53262	V0 assembly protein 1	0.60	0.20		P40051
P36531	54S ribosomal protein	1.54	0.40		P53859
P05986	cAMP-dependent prot	0.50	0.18		Q07807
P46964	Dolichyl-diphosphoolig	1.54	0.40		P43586
P53195	Conserved oligomeric	0.56	0.19		P38853
P35177	Transcriptional activat	0.13	0.05		Q04179
Q08968	UPF0061 protein FMP4	0.35	0.13		Q12034
P11412	Glucose-6-phosphate 1	0.28	0.11		P27466
P48353	Protein HLJ1 OS=Sacch	1.12	0.33		Q07938
Q04344	Hit family protein 1 OS	1.86	0.46		P16622
P36519	54S ribosomal protein	0.76	0.25		Q12000

Q12432	Chromatin modificatio	0.36	0.13		Q06451
P25296	Calcineurin subunit B C	1.59	0.41		P24521
P25573	Mitochondrial inner m	0.35	0.13		P48415
P25293	Nucleosome assembly	0.48	0.17		Q12160
P05318	60S acidic ribosomal pr	2.58	0.55		Q03761
P38325	Mitochondrial outer m	1.56	0.41		Q06339
P23285	Peptidyl-prolyl cis-tran	1.26	0.35		P35718
P53388	Dicarboxylic amino acid	0.41	0.15		P53258
Q12038	Lethal(2) giant larvae p	0.18	0.07		Q05031
Q12259	BTB/POZ domain-conta	0.29	0.11		Q99297
Q08760	Bud site selection prot	0.32	0.12		Q04399
P46676	Suppressor of mar1-1 p	0.17	0.07		P53246
P53157	Mitochondrial pyruvat	1.52	0.40		Q03920
P07236	Threonine--tRNA ligase	0.41	0.15		P38850
Q12283	Malonyl CoA-acyl carri	0.58	0.20		P53314
P48527	Tyrosine--tRNA ligase,	0.29	0.11		P46984
Q12359	Ammonia transport ou	1.16	0.33		P38256
P39718	Peroxisome assembly p	0.59	0.20		P31755
P38904	Protein SPP41 OS=Sacc	0.09	0.04		P36132
P33421	Succinate dehydrogena	0.89	0.28		P26755
P40474	Quinidine resistance pr	0.26	0.10		Q99207
P33328	Synaptobrevin homolo	3.17	0.62		Q08446
P19736	Pre-mRNA-splicing fact	0.35	0.13		P40169
P47822	Mediator of RNA polyn	3.21	0.62		P40339
P19956	54S ribosomal protein	2.37	0.53		P61830
P40452	Cytochrome c oxidase	1.34	0.37		P29366
Q08421	Enhancer of translatior	0.49	0.17		P37254
P53335	Protein PXR1 OS=Sacch	0.57	0.20		P47818
P32618	Uncharacterized protei	0.09	0.04		Q08962
Q03707	Inner nuclear membrai	0.22	0.09		P53165
Q08686	Thiosulfate sulfurtrans	0.73	0.24		Q99189
Q06385	Vacuolar protein sortin	0.61	0.21		Q06053
P53217	Uncharacterized meml	1.33	0.37		P42900
P40917	AP-1-like transcription	0.53	0.18		P43561
P40099	5-formyltetrahydrofola	1.16	0.33		Q04223
Q99181	Protein HSH49 OS=Sac	0.77	0.25		P53076
P36084	Splicing factor MUD2 C	0.26	0.10		P38758
P36091	Mannan endo-1,6-alph	0.33	0.12		Q08921
P53834	Hsp90 co-chaperone H	1.24	0.35		P22007
P50875	Transcription factor SP	0.23	0.09		Q99247
P06775	Histidine permease OS	0.24	0.09		P35194
Q06162	Central kinetochore su	1.84	0.45		Q08925
Q01976	ADP-ribose pyrophospl	0.71	0.23		Q02754
P28778	37S ribosomal protein	3.72	0.67		P53923
P38813	Protein BIG1 OS=Sacch	0.61	0.21		P38792
Q08986	S-adenosylmethionine	0.24	0.09		P40959
P21734	Ubiquitin-conjugating	0.79	0.25		P23594
P53743	Pre-rRNA-processing p	0.68	0.23		P38902
P38179	Dol-P-Man:Man(5)Glc	0.30	0.11		P25360
P53146	Protein transport prote	1.31	0.36		P47061
P26755	Replication factor A pr	0.94	0.29		P50946
P32792	UPF0744 protein YSC8	0.37	0.14		P40481

Q12514	General negative regul	0.33	0.12		P53388
P53253	Protein NNF2 OS=Saccl	0.14	0.06		Q04226
P53538	RNA polymerase II subu	0.80	0.26		P32783
P40312	Cytochrome b5 OS=Sac	3.03	0.61		P32784
P43561	Iron transport multicop	0.30	0.11		P40030
Q07824	Polyamine transporter	0.16	0.06		P31381
P32342	Signal recognition part	1.76	0.44		P40452
P38089	Protein phosphatase 2	0.37	0.14		Q12745
P38826	Origin recognition com	0.20	0.08		P53115
P37366	Cyclin CCL1 OS=Saccha	0.36	0.13		O13585
P33419	Spindle pole componen	0.38	0.14		P40006
Q12246	Sphingoid long chain b	0.31	0.12		P40548
P54791	Origin recognition com	0.36	0.13		P39005
P53174	Pheromone-regulated	0.67	0.22		P40564
P38262	SIR4-interacting protei	0.27	0.10		P33418
P47013	Dihydrosphingosine 1-	0.34	0.13		P53915
P26793	Flap endonuclease 1 O	0.38	0.14		P53849
Q04867	Putative methyltransfe	0.68	0.23		P53899
P32610	V-type proton ATPase	0.62	0.21		Q02774
Q04307	DNA-directed RNA poly	1.92	0.47		P39692
P38881	Nucleus-vacuole juncti	0.67	0.22		P53615
O13539	THO complex subunit	0.59	0.20		P28817
Q12510	DNA damage-binding	0.27	0.10		P38903
P35179	Protein transport prote	3.63	0.67		Q08826
P38116	ADP-ribosylation facto	0.58	0.20		Q08817
Q02159	Ubiquitin-conjugating	1.72	0.43		P47112
P53331	RNA exonuclease 1 OS	0.35	0.13		P22434
Q12078	Iron transporter SMF3	0.31	0.12		Q06078
P22141	Proteasome subunit be	0.87	0.27		Q06178
P25554	SAGA-associated facto	0.61	0.21		P35999
Q01519	Cytochrome c oxidase	5.33	0.80		Q06709
P0CX27	60S ribosomal protein	2.03	0.48		P40968
Q05812	Meiotic sister-chromat	0.19	0.08		P48240
P38334	Trafficking protein part	1.03	0.31		P53169
P38127	Mitochondrial carrier	0.56	0.19		P39742
P38208	Ribonucleases P/MRP	2.29	0.52		Q06839
P36120	ATP-dependent RNA he	0.25	0.10		Q12525
P35206	Mannosyl phosphorylir	0.51	0.18		P33412
P07347	N-terminal acetyltrans	0.66	0.22		P38995
P11978	Regulatory protein SIR	0.10	0.04		Q08954
P40165	NAD(P)H-hydrate epim	0.66	0.22		P05150
Q12375	Mitochondrial ornithin	0.56	0.19		P22354
Q03653	Protein EFR3 OS=Sacch	0.23	0.09		P32445
P43610	Uncharacterized ATP-d	0.16	0.06		P33313
P31383	Protein phosphatase P	0.22	0.09		P40084
Q3E7X8	Y~ element ATP-depen	0.14	0.06		P50113
P37299	Cytochrome b-c1 comp	4.01	0.70		P04650
P17536	Tropomyosin-1 OS=Sac	0.82	0.26		P33314
P40532	Nuclear membrane org	1.32	0.37		P49017
P38152	Tricarboxylate transpo	0.54	0.19		P43589
P53722	Mitochondrial inner m	0.67	0.22		Q06698
P40006	Increased recombinati	0.45	0.16		P34162

P32478	Cell wall mannoprotei	0.41	0.15		P22936
P39547	ULP1-interacting prote	0.67	0.22		P35177
P25371	Probable ATP-depende	0.13	0.05		Q04600
Q92316	Dolichyl-diphosphoolig	5.88	0.84		P53885
P46963	CTD kinase subunit ga	0.71	0.23		P38067
P38703	Sphingosine N-acyltran	0.47	0.17		Q12288
P54003	Protein SUR7 OS=Sacc	0.51	0.18		P53742
Q04409	Putative glucokinase-2	0.40	0.15		Q08732
P41800	Maintenance of mitoc	0.34	0.13		P40962
P20676	Nucleoporin NUP1 OS=	0.13	0.05		P53148
P50076	Dol-P-Glc:Glc(2)Man(9)	0.35	0.13		Q12311
Q06245	Exocyst complex comp	0.21	0.08		Q12443
Q12263	Serine/threonine-prot	0.16	0.06		Q12495
P53322	High-affinity nicotinic	0.26	0.10		Q06344
P14063	54S ribosomal protein	3.47	0.65		P06704
P35728	Protein MPE1 OS=Sacc	0.33	0.12		P38262
P32337	Importin subunit beta-	0.12	0.05		P25558
P19516	Cytochrome c oxidase	0.51	0.18		Q00578
P36068	SWI5-dependent HO e	0.94	0.29		P28003
Q06644	Probable dolichyl-phos	0.20	0.08		Q99385
Q01476	Ubiquitin carboxyl-ter	0.10	0.04		P48524
P25628	Sterol O-acyltransfera	0.22	0.09		P53206
Q04406	Early meiotic induction	0.93	0.29		Q03407
P46674	Nuclear mRNA export	0.10	0.04		P00425
P53930	Protein AF-9 homolog	0.72	0.24		P33753
Q12275	Uncharacterized protei	0.08	0.03		P18852
P09232	Cerevisin OS=Saccharo	0.22	0.09		Q05533
P25376	General amino acid pe	0.31	0.12		Q03790
Q12349	ATP synthase subunit	0.92	0.28		P25617
Q12082	Uncharacterized protei	2.90	0.59		Q06336
P31385	Transcriptional regulat	0.35	0.13		P32862
Q04048	Pre-mRNA-splicing fact	0.21	0.08		P40099
P28496	Sphingosine N-acyltran	0.33	0.12		P53949
Q12206	Transcriptional modul	0.44	0.16		P40515
P49954	Probable hydrolase NI	0.33	0.12		P35127
P46948	Exosome complex com	0.67	0.22		Q99288
Q06168	Chromatin structure-re	0.21	0.08		P14737
Q12341	Histone acetyltransfer	0.24	0.09		P53095
P40002	Transcriptional regulat	0.14	0.06		P25339
P38439	RNA polymerase-assoc	0.30	0.11		P41733
Q12211	tRNA pseudouridine sy	0.25	0.10		P39722
P28272	Dihydroorotate dehyd	0.50	0.18		Q02354
Q12277	Exosome complex com	0.38	0.14		Q04969
Q12160	Uncharacterized protei	1.44	0.39		P38747
Q12453	Cytoplasmic export pr	0.18	0.07		Q99312
P53336	Putative methyltransfe	0.44	0.16		Q12454
Q02608	37S ribosomal protein	1.77	0.44		P29295
P39984	Histone acetyltransfer	0.37	0.14		P32499
P22768	Argininosuccinate synt	0.49	0.17		P21951
P38861	60S ribosomal export	0.17	0.07		P54000
P38075	Pyridoxamine 5~-phos	0.68	0.23		P38244
P38888	ER degradation-enhan	0.17	0.07		Q06137

P13188	Glutamine--tRNA ligase	0.16	0.06		P48606
P41318	Target of rapamycin co	0.51	0.18		P08964
P36149	Trafficking protein part	1.84	0.45		P38349
P36000	AP-1 complex subunit	0.26	0.10		Q08873
P41814	tRNA (adenine(58)-N(1	0.30	0.11		P40433
Q01329	Pre-tRNA-processing p	0.17	0.07		Q03758
Q12020	Protein SRL2 OS=Sacch	0.37	0.14		P40492
P17423	Homoserine kinase OS	0.43	0.16		P23287
P38300	Inner membrane mito	0.56	0.19		Q07655
Q06001	Factor arrest protein 1	0.41	0.15		P31787
P38202	UPF0642 protein YBL0	3.44	0.65		P40851
P25299	mRNA 3~-end-processi	0.33	0.12		P39112
P19659	Mediator of RNA poly	0.17	0.07		P46959
P53628	Transcription regulator	0.25	0.10		Q03735
P47131	TMEM14 protein homo	1.28	0.36		Q04119
P32524	Pre-mRNA-splicing fact	0.53	0.18		P20107
P40438	VPS10 homolog 1 OS=	0.11	0.05		Q04748
P40356	Mediator of RNA poly	0.39	0.14		Q02648
P43638	MAP-homologous prot	0.10	0.04		P42936
P33417	Intrastrand cross-link r	0.32	0.12		Q07589
P48524	Ubiquitin ligase-bindin	0.14	0.06		Q12451
Q05636	Exosome complex com	0.72	0.24		P46669
P38744	Putative pterin-4-alpha	1.69	0.43		Q02890
P0C0X0	40S ribosomal protein	5.15	0.79		P38760
Q06213	Mediator of RNA poly	1.19	0.34		P39994
P38877	Chromosome transmis	0.84	0.26		P15801
P33309	Protein DOM34 OS=Sa	0.38	0.14		P12687
P00175	Cytochrome b2, mitoc	0.24	0.09		P39010
P38791	Deoxyhypusine syntha	0.55	0.19		Q12344
Q04183	Trafficking protein part	0.10	0.04		Q12483
P32463	Acyl carrier protein, mi	1.71	0.43		Q06624
P32451	Biotin synthase, mitoc	0.40	0.15		Q08961
P40462	Protein TMA108 OS=Sa	0.14	0.06		P39006
P10363	DNA primase small sub	0.34	0.13		Q08689
P43682	Protein transport prote	2.53	0.55		P42951
P38999	Saccharopine dehydro	0.33	0.12		P32522
P08425	Phenylalanine--tRNA li	0.29	0.11		P34087
P38242	UDP-N-acetylglucosam	0.41	0.15		P02381
Q9URQ5	High temperature letha	3.47	0.65		Q04311
P13298	Orotate phosphoribos	0.76	0.25		P25378
Q12180	Halotolerance protein	0.13	0.05		P32505
P81450	ATP synthase subunit J	14.35	1.19		P14736
P39543	Protein SOP4 OS=Sacc	1.03	0.31		Q06819
Q07914	Mitochondrial import i	1.19	0.34		P40856
Q08886	Guanine nucleotide-bi	0.15	0.06		Q12359
P21524	Ribonucleoside-diphos	0.21	0.08		P07807
Q08651	Probable oxidoreducta	0.45	0.16		Q12349
Q04493	Prefoldin subunit 5 OS	1.14	0.33		Q2V2Q1
Q08001	Membrane-anchored li	0.13	0.05		Q05021
P40351	Dolichyl pyrophosphat	0.32	0.12		P13185
P40156	Required for respirator	0.74	0.24		P53332
P03875	Putative COX1/OXI3 in	0.22	0.09		Q05778

P40308	Lipase 3 OS=Saccharon	0.29	0.11		Q08601
Q12074	Spermidine synthase O	0.52	0.18		P39677
O75012	37S ribosomal protein	2.58	0.55		P46969
P40499	Protein ICE2 OS=Sacch	0.28	0.11		P38237
Q03327	Mitochondrial fusion a	0.28	0.11		P32787
Q07349	MIOREX complex comp	0.21	0.08		P40318
P53309	Clathrin coat assembly	0.34	0.13		P43587
Q02888	Inner membrane assen	0.90	0.28		P32353
P39945	Protein AST2 OS=Sacch	0.47	0.17		P13574
P19807	Choline transport prot	0.25	0.10		P40470
P43560	Membrane-anchored li	0.28	0.11		P40018
P29029	Endochitinase OS=Sacc	0.27	0.10		P40562
Q03153	ATPase synthesis prote	0.22	0.09		P38146
P16892	Mitogen-activated prot	0.26	0.10		Q06144
P53378	Tubulin gamma chain (	0.31	0.12		Q12270
Q07825	Putative Xaa-Pro aminc	0.18	0.07		P38348
P27351	AP-2 complex subunit I	0.19	0.08		Q12309
Q05809	Cytochrome oxidase as	2.37	0.53		Q06505
P25367	[PIN+] prion protein RN	0.25	0.10		P53154
P53145	Large subunit GTPase 1	0.21	0.08		Q08281
Q01590	Integral membrane prc	0.28	0.11		P35183
P48236	Uncharacterized meml	0.31	0.12		P10363
P32378	4-hydroxybenzoate pol	0.41	0.15		P22134
Q08649	Histone acetyltransfera	0.31	0.12		
P40990	Protein MSS2, mitocho	0.40	0.15		
Q03705	EKC/KEOPS complex su	1.45	0.39		
P38068	Monothiol glutaredoxi	0.86	0.27		
P53009	Protein kinase-like prot	0.11	0.05		
P01097	ATPase inhibitor, mitoc	3.05	0.61		
Q04401	Succinate dehydrogena	1.43	0.39		
P38206	Oligosaccharide translc	0.15	0.06		
P14743	Glycylpeptide N-tetrad	0.30	0.11		
P53952	Uncharacterized protei	0.82	0.26		
P48237	Mitochondrial group I i	0.15	0.06		
Q06625	Glycogen debranching	0.08	0.03		
Q06405	ATP synthase subunit f	2.41	0.53		
P47140	Altered inheritance rat	0.29	0.11		
Q12165	ATP synthase subunit c	0.73	0.24		
Q3E6R5	Uncharacterized mitoc	1.07	0.32		
P39552	Multicopy suppressor c	0.68	0.23		
P47148	Uncharacterized protei	0.79	0.25		
P38787	2-dehydropantoate 2-r	0.24	0.09		
P07255	Cytochrome c oxidase :	6.06	0.85		
P40070	U6 snRNA-associated S	0.93	0.29		
Q03161	Glucose-6-phosphate 1	0.51	0.18		
P10663	37S ribosomal protein	1.77	0.44		
P33895	Kinetochore protein NU	0.19	0.08		
P53318	Ubiquinone biosynthes	0.30	0.11		
P39732	GLC7-interacting prote	0.18	0.07		
P06633	Imidazoleglycerol-phos	0.79	0.25		
P43611	Outer spore wall prote	0.17	0.07		
Q12239	Transmembrane protei	0.27	0.10		

Q03660	Trafficking protein part	0.12	0.05
P38086	DNA repair and recom	0.14	0.06
P17891	Clathrin light chain OS=	0.42	0.15
P39715	Shuttling pre-60S facto	0.48	0.17
P20084	54S ribosomal protein	3.25	0.63
Q03559	Uncharacterized protei	0.88	0.27
P40484	DBF2 kinase activator	0.14	0.06
P41813	Fork head protein hom	0.11	0.05
P50276	High-affinity methioni	0.25	0.10
P46962	CTD kinase subunit bet	0.28	0.11
P53320	Mitochondrial carrier	0.26	0.10
Q03088	Styryl dye vacuolar loc	0.17	0.07
Q3E790	Serine palmitoyltransf	3.18	0.62
Q12247	rRNA-processing prote	1.79	0.45
P36126	Phospholipase D1 OS=	0.08	0.03
P32913	Vacuolar protein sortin	0.25	0.10
Q04779	Transcriptional regulat	0.19	0.08
P40962	Zinc finger protein RTS	0.41	0.15
P47018	Maintenance of telom	0.19	0.08
P28791	Protein transport prot	0.38	0.14
Q08561	Ino eighty subunit 4 O	1.03	0.31
Q07508	Protein LUC7 OS=Sacc	0.36	0.13
P47149	Kinetochore-associate	0.48	0.17
Q05029	Protein BCH1 OS=Sacc	0.19	0.08
P30777	GPI mannosyltransfera	0.22	0.09
P53314	2~,3~-cyclic-nucleotide	0.41	0.15
P32901	Peptide transporter PT	0.15	0.06
P39723	Spindle pole compone	0.14	0.06
P40857	Very-long-chain (3R)-3	0.46	0.16
P50623	SUMO-conjugating enz	1.82	0.45
P21373	NAD(+) kinase OS=Sac	0.17	0.07
Q06344	Pre-rRNA-processing p	0.22	0.09
P12611	Growth regulation pro	0.29	0.11
P25373	Glutaredoxin-1 OS=Sac	1.11	0.32
P41920	Ran-specific GTPase-ac	0.84	0.26
P40478	Mitochondrial outer m	0.35	0.13
P47085	MEMO1 family protein	0.44	0.16
Q12425	Iron-sulfur assembly p	0.95	0.29
Q12080	Ribosome biogenesis p	0.20	0.08
P39542	Uncharacterized trans	0.23	0.09
Q04201	CUE domain-containin	3.17	0.62
P69852	DASH complex subunit	2.10	0.49
P00401	Cytochrome c oxidase	0.17	0.07
P38131	Probable mannosyltra	0.29	0.11
P38288	Protein TOS1 OS=Sacc	0.34	0.13
P32769	Elongation factor 1 alp	0.23	0.09
P41903	Peroxisomal acyl-coen	0.60	0.20
P17157	Cyclin-dependent prot	0.50	0.18
P31755	Initiation-specific alph	0.19	0.08
P13902	Protein INO4 OS=Sacc	1.24	0.35
P25358	Elongation of fatty aci	0.42	0.15
Q3E776	Uncharacterized protei	1.73	0.44

Q12109	Tryptophan--tRNA liga	0.33	0.12
P32566	Cell wall assembly regu	0.39	0.14
Q2V2P4	Uncharacterized protei	4.22	0.72
P25037	Ubiquitin carboxyl-ter	0.16	0.06
P53267	DASH complex subunit	0.44	0.16
P38210	Chromatin structure-re	1.02	0.31
Q04632	Conserved oligomeric	0.22	0.09
Q12004	RNA polymerase II tra	0.28	0.11
P36034	Protein COS9 OS=Sacc	0.33	0.12
Q12512	Protein ZPS1 OS=Sacch	0.40	0.15
P43554	SWI/SNF global transcr	0.14	0.06
Q01477	Ubiquitin carboxyl-ter	0.10	0.04
Q04002	Sister chromatid cohes	0.09	0.04
P53840	Topoisomerase 1-asso	0.07	0.03
Q06510	Lysophosphatidylcholi	0.24	0.09
P47135	Protein JSN1 OS=Sacch	0.08	0.03
P38041	Protein BOB1 OS=Sacc	0.14	0.06
Q08685	mRNA cleavage and po	0.21	0.08
P53983	Protein ASI3 OS=Sacch	0.20	0.08
P42900	Sigma-like sequence pr	0.21	0.08
P10622	60S acidic ribosomal pr	0.54	0.19
Q12745	Protein transport prot	0.19	0.08
Q12396	Protein EMP46 OS=Sac	0.20	0.08
P40567	U2 small nuclear ribon	1.95	0.47
P32644	Putative ATP-depende	0.12	0.05
P38187	Ubiquitin carboxyl-ter	0.12	0.05
P10961	Heat shock factor prot	0.11	0.05
Q12009	tRNA (guanine-N(7)-)-	0.32	0.12
P38080	Serine/threonine-prot	0.12	0.05
P32048	Lysine--tRNA ligase, mi	0.15	0.06
Q05530	Glutaredoxin-like prot	0.97	0.29
P25359	Exosome complex com	0.24	0.09
Q6Q595	Vesicle-associated me	0.60	0.20
P38970	Serine/threonine-prot	0.16	0.06
P49955	U2 snRNP component	0.14	0.06
Q06485	Autophagy-related pro	0.58	0.20
P25558	Bud site selection prot	0.08	0.03
P53159	Monopolar spindle pro	0.24	0.09
P39111	V-type proton ATPase	1.82	0.45
P53332	Phosphopantetheine a	0.31	0.12
P50874	Origin recognition com	0.29	0.11
Q08650	Diacylglycerol O-acyltr	0.22	0.09
P53938	N-glycosylation protei	0.25	0.10
Q03954	DASH complex subunit	0.64	0.21
Q01722	Glycolytic genes transc	0.18	0.07
P14772	Bile pigment transport	0.08	0.03
P34244	Probable serine/threo	0.09	0.04
Q03081	Transcriptional regulat	0.60	0.20
P56628	60S ribosomal protein	0.96	0.29
P36130	CCR4-associated factor	0.21	0.08
P37262	6-phosphogluconolact	0.31	0.12
P25441	DNA-directed RNA pol	0.35	0.13

P25270	rRNA methyltransferas	0.22	0.09
P23394	Pre-mRNA-splicing ATF	0.15	0.06
Q03579	Ceramide synthase sub	1.23	0.35
Q12486	Putative uncharacteriz	0.76	0.25
P39927	Protein PTI1 OS=Sacch	0.22	0.09
P53894	Serine/threonine-prote	0.18	0.07
P13574	Protein STE12 OS=Sacc	0.13	0.05
Q03330	Histone acetyltransfera	0.20	0.08
P46965	Signal peptidase compl	2.53	0.55
Q12367	Ribosomal lysine N-me	0.25	0.10
P14180	Chitin synthase 2 OS=S	0.14	0.06
P53224	Protein ORM1 OS=Sacc	0.45	0.16
P46949	Protein FYV8 OS=Sacch	0.11	0.05
Q03735	RNA-binding protein N	0.08	0.03
P36162	DASH complex subunit	0.85	0.27
P36064	COX assembly mitocho	1.01	0.30
P13186	Serine/threonine-prote	0.12	0.05
Q00539	Protein NAM8 OS=Sacc	0.09	0.04
Q00578	DNA repair helicase RA	0.16	0.06
P20486	Cyclin-dependent kinas	0.69	0.23
P43557	Protein FMP32, mitoch	0.48	0.17
P08525	Cytochrome b-c1 comp	1.32	0.37
P38247	Protein SLM4 OS=Saccl	0.66	0.22
P21657	Transcriptional activatc	0.09	0.04
Q07458	Transcriptional regulat	0.32	0.12
Q12155	Uncharacterized memb	1.07	0.32
Q05024	Protein TRI1 OS=Sacch	0.42	0.15
P32914	Transcription elongatic	2.33	0.52
Q08219	Outer spore wall prote	0.27	0.10
P53890	Bud neck protein 5 OS=	0.21	0.08
P53968	Transcriptional regulat	0.13	0.05
P48567	tRNA pseudouridine sy	0.23	0.09
P0C074	RDS3 complex subunit	1.52	0.40
Q02336	Transcriptional adapte	0.10	0.04
P40413	T-complex protein 1 su	0.25	0.10
Q08492	Bud site selection prot	0.47	0.17
P15442	eIF-2-alpha kinase GCN	0.08	0.03
P17898	Cholinephosphotransfe	0.23	0.09
Q12108	Restriction of telomere	0.16	0.06
Q05900	U1 small nuclear ribon	0.41	0.15
Q06839	PX domain-containing	0.08	0.03
P53266	Cytochrome oxidase as	0.23	0.09
Q06324	Mitochondrial MYO2 re	0.19	0.08
P22148	Protein MSN1 OS=Sacc	0.24	0.09
Q06144	Protein ORM2 OS=Sacc	0.46	0.16
Q00362	Protein phosphatase P	0.27	0.10
Q12329	Heat shock protein 42	0.39	0.14
P47042	Probable serine/threor	0.13	0.05
P36124	SET domain-containing	0.12	0.05
P42842	Essential for maintenar	0.15	0.06
Q02883	N-acyl-phosphatidyletl	0.09	0.04
P53853	Vacuolar protein sortin	0.36	0.13

Q12321	Mediator of RNA polyn	0.16	0.06
P38429	Transcriptional regulat	0.84	0.26
Q06170	Uncharacterized memb	0.40	0.15
P32830	Mitochondrial import i	1.08	0.32
P29056	Transcription factor IIIB	0.23	0.09
Q03768	Protein GIR2 OS=Sacch	0.35	0.13
P40046	Vacuolar transporter cl	0.90	0.28
P50861	6,7-dimethyl-8-ribityllu	0.65	0.22
P47088	GPI mannosyltransfera	0.22	0.09
P11747	Transcription initiation	0.63	0.21
Q08581	Kinetochore protein SL	0.10	0.04
Q06406	U6 snRNA-associated S	3.32	0.64
Q06624	DNA damage tolerance	0.27	0.10
P53912	Uncharacterized protei	0.41	0.15
P49018	GPI-anchor transamida	0.22	0.09
P80967	Mitochondrial import r	8.64	0.98
Q02774	Secretory component p	0.48	0.17
P38708	Putative proline--tRNA	0.13	0.05
P69850	DASH complex subunit	1.34	0.37
P06843	Protein SPT2 OS=Sacch	0.28	0.11
P40480	Protein HOS4 OS=Sacch	0.08	0.03
P39724	BolA-like protein 3 OS=	1.00	0.30
P53277	Pre-mRNA-splicing fact	0.76	0.25
P15454	Guanylate kinase OS=S	0.57	0.20
P42834	Mitochondrial DnaJ ho	0.76	0.25
P06782	Carbon catabolite-dere	0.14	0.06
Q00381	AP-2 complex subunit s	0.70	0.23
P36095	Vacuolar protein-sortin	0.43	0.16
P42840	Uncharacterized memb	0.33	0.12
P53062	Nucleus export protein	0.50	0.18
P06242	Serine/threonine-prote	0.30	0.11
P32570	Mediator of RNA polyn	0.95	0.29
P17121	GTPase-activating prot	0.14	0.06
P53741	UBP3-associated prote	0.18	0.07
P53438	Protein SOK2 OS=Sacch	0.18	0.07
P21957	Transcriptional repress	0.36	0.13
P27514	Low-affinity phosphate	0.10	0.04
P42844	Mitochondrial protein	0.59	0.20
P32367	Transcription factor tau	0.21	0.08
P38920	DNA mismatch repair p	0.11	0.05
P39001	Transcriptional regulat	0.11	0.05
P40160	Serine/threonine-prote	0.21	0.08
P53207	U1 small nuclear ribonu	0.14	0.06
Q3E772	Uncharacterized protei	1.42	0.38
P48412	Nonsense-mediated m	0.37	0.14
Q8TGJ3	Protein kish OS=Saccha	2.01	0.48
P04817	Arginine permease OS=	0.15	0.06
P35718	DNA-directed RNA poly	0.47	0.17
P40151	DNA-dependent ATPas	0.07	0.03
P36053	Transcription elongatio	0.76	0.25
Q3E798	Uncharacterized protei	0.59	0.20
P38274	Protein arginine N-met	0.10	0.04

Q05518	Protein PAL1 OS=Sacch	0.09	0.04
Q3E7A4	COX assembly mitocho	0.42	0.15
P18480	SWI/SNF chromatin-re	0.05	0.02
Q06538	Calcium permeable str	0.11	0.05
P43570	GTPase-activating prot	0.18	0.07
Q06107	Uncharacterized TLC d	0.29	0.11
P38783	Protein FYV4, mitochor	1.49	0.40
P51534	SWI5-dependent HO e	0.11	0.05
P53148	Spindle pole body com	0.14	0.06
Q07442	Bromodomain-contain	0.07	0.03
P25336	DNA mismatch repair p	0.08	0.03
P33331	Nuclear transport facto	0.90	0.28
Q02866	Protein MUK1 OS=Sacc	0.14	0.06
P53604	Protein MSO1 OS=Sacc	0.83	0.26
P38841	Uncharacterized protei	1.07	0.32
P12962	Cap-associated protein	0.29	0.11
P48415	COPII coat assembly pr	0.04	0.02
A5Z2X5	UPF0495 protein YPR0	0.77	0.25
P40089	U6 snRNA-associated S	1.42	0.38
Q04172	Sensitive to high expre	0.19	0.08
Q07953	Ribosome maturation	0.39	0.14
P32896	Protein PDC2 OS=Sacch	0.09	0.04
P39515	Mitochondrial import i	1.30	0.36
Q04430	Pantothenate kinase C	0.26	0.10
Q07800	Phosphatase PSR1 OS=	0.22	0.09
P29340	Ubiquitin-conjugating	0.24	0.09
P12868	E3 ubiquitin-protein lig	0.08	0.03
Q07872	Epsin-4 OS=Saccharom	0.64	0.21
P53173	ER-derived vesicles pro	0.34	0.13
P40210	Protein SIP5 OS=Sacch	0.09	0.04
P38304	Mediator of RNA polyn	0.45	0.16
O60200	Mitochondrial distribut	1.54	0.40
P37296	V-type proton ATPase	0.15	0.06
P38821	Aspartyl aminopeptida	0.30	0.11
P25385	Protein transport prote	0.41	0.15
P30665	DNA replication licensi	0.09	0.04
P38860	GTPase MTG2, mitocho	0.18	0.07
Q02724	Ubiquitin-like-specific	0.14	0.06
P40472	Probable secreted beta	0.21	0.08
P40460	Kinetochore protein N	0.12	0.05
P14681	Mitogen-activated prot	0.25	0.10
P39540	Elongation of fatty acic	0.29	0.11
Q03388	Vacuolar protein sortin	0.11	0.05
Q08045	Long chronological life	0.84	0.26
Q08689	N-terminal acetyltrans	0.60	0.20
P22438	Methionine--tRNA liga	0.15	0.06
P31109	Synaptobrevin homolo	1.02	0.31
Q3E833	EKC/KEOPS complex su	0.59	0.20
Q99252	Protein ECM3 OS=Sacc	0.15	0.06
P53093	Protein YIP4 OS=Sacch	0.20	0.08
Q12049	Protein THP3 OS=Sacch	0.19	0.08
P32785	Methionyl-tRNA formy	0.11	0.05

Q04598	54S ribosomal protein	1.15	0.33
Q08109	ERAD-associated E3 ub	0.25	0.10
Q04408	Uncharacterized protei	0.18	0.07
P53389	Protein HOL1 OS=Sacc	0.15	0.06
Q03020	Iron sulfur cluster asse	0.29	0.11
P36119	Uncharacterized protei	0.17	0.07
P22804	Protein transport prote	0.81	0.26
Q05471	Helicase SWR1 OS=Sac	0.06	0.03
Q12438	Monothiol glutaredoxi	0.44	0.16
P38167	Protein ECM21 OS=Sac	0.08	0.03
Q2V2P9	Uncharacterized protei	0.83	0.26
P04821	Cell division control pr	0.03	0.01
Q06053	tRNA-dihydrouridine(4	0.06	0.03
P38994	Probable phosphatidyli	0.11	0.05
P38228	Mitochondrial chapero	0.16	0.06
P32831	Negative growth regul	0.06	0.03
P09620	Pheromone-processing	0.12	0.05
P40071	Transmembrane 9 sup	0.12	0.05
P14908	Mitochondrial transcri	0.27	0.10
P53851	Protein TEX1 OS=Sacch	0.10	0.04
P32339	Heme-binding protein	0.29	0.11
P38921	Putative mitochondrial	0.35	0.13
P38170	Condensin complex su	0.12	0.05
Q12255	Vacuolar v-SNARE NYV	0.38	0.14
P47081	Cytochrome c oxidase	0.39	0.14
Q00873	Cytochrome c1 heme l	0.43	0.16
P40535	ATF/CREB activator 2	0.16	0.06
P35735	Protein SFK1 OS=Sacch	0.26	0.10
Q06108	Regulator of the glycer	0.08	0.03
P38768	Protein interacting wit	0.26	0.10
P53616	Probable secreted bet	0.24	0.09
Q03012	COMPASS component	0.25	0.10
P00127	Cytochrome b-c1 com	0.71	0.23
P53109	Probable metalloreduc	0.15	0.06
P40527	Probable phospholipid	0.07	0.03
P40959	Sorting nexin MVP1 OS	0.17	0.07
Q12186	Branchpoint-bridging	0.19	0.08
P47025	Mitochondrial division	0.12	0.05
P50896	Protein PSP1 OS=Sacch	0.10	0.04
P15731	Ubiquitin-conjugating	0.75	0.24
P53089	Uncharacterized protei	0.50	0.18
Q12046	Pre-mRNA-splicing fact	0.28	0.11
P38307	Degradation in the end	0.47	0.17
Q12674	Probable phospholipid	0.05	0.02
P00812	Arginase OS=Saccharo	0.30	0.11
Q06411	Pre-mRNA-splicing fact	0.06	0.03
P16522	Anaphase-promoting c	0.14	0.06
P23968	V-type proton ATPase	0.51	0.18
P40510	D-3-phosphoglycerate	0.20	0.08
P22289	Cytochrome b-c1 com	2.41	0.53
Q05021	Transcription initiation	0.15	0.06
Q07799	Uncharacterized protei	0.13	0.05

P36041	Protein EAP1 OS=Sacch	0.07	0.03
Q06337	Chromatin modificatio	0.09	0.04
P40494	Actin-regulating kinase	0.11	0.05
P40357	Protein transport prote	0.14	0.06
P52553	Prefoldin subunit 6 OS=	0.42	0.15
P38090	General amino acid per	0.15	0.06
P53865	Chaotic nuclear migrat	0.07	0.03
P25038	Translation initiation fa	0.06	0.03
P53298	Central kinetochore su	0.10	0.04
P36121	DNA-directed RNA poly	0.16	0.06
P15625	Phenylalanine--tRNA li	0.18	0.07
Q12224	Transcription factor RL	0.07	0.03
Q12257	IMPACT family membe	0.62	0.21
Q02863	Ubiquitin carboxyl-terr	0.18	0.07
P40561	RNA-binding protein S	0.18	0.07
P47158	Putative transferase C	0.18	0.07
P50106	DNA-directed RNA poly	0.38	0.14
P53972	25S rRNA (cytosine(22	0.18	0.07
P35210	Protein SPT23 OS=Sacc	0.04	0.02
P34232	mRNA transport regula	0.56	0.19
P53012	FIT family protein SCS3	0.11	0.05
Q08231	Nuclear mRNA export	0.19	0.08
P15179	Aspartate--tRNA ligase	0.13	0.05
Q04925	SVF1-like protein YDR2	0.22	0.09
P25619	30 kDa heat shock prot	0.29	0.11
P20604	Serine/threonine-prote	0.14	0.06
Q12324	Calcium channel YVC1	0.13	0.05
P53379	Aspartic proteinase MK	0.16	0.06
P53685	NAD-dependent protei	0.18	0.07
P00899	Anthranilate synthase	0.09	0.04
Q03661	Silent chromatin protei	0.03	0.01
P36165	Lipase 4 OS=Saccharon	0.10	0.04
P40050	MIOREX complex comp	0.06	0.03
P53193	J-type co-chaperone JA	0.53	0.18
P28627	Mitochondrial inner m	0.24	0.09
P38863	Spindle pole body com	0.10	0.04
Q12297	Transcription initiation	0.26	0.10
Q02981	ABC1 family protein YP	0.06	0.03
Q3E7B6	V-type proton ATPase	1.97	0.47
Q08422	AN1-type zinc finger pr	0.31	0.12
Q06623	HDA1 complex subunit	0.13	0.05
P35181	AP-1 complex subunit	0.66	0.22
Q04767	Golgi apparatus memb	0.64	0.21
P12887	Uracil-DNA glycosylase	0.12	0.05
P53198	Protein ERP6 OS=Sacch	0.20	0.08
Q12179	Uncharacterized protei	0.09	0.04
Q03631	Weak acid resistance p	0.04	0.02
P33308	Mediator of RNA polyn	0.71	0.23
P39722	Mitochondrial Rho GTP	0.06	0.03
P35999	Mitochondrial interme	0.11	0.05
P41815	Valine amino-acid perr	0.15	0.06
P53896	GPI mannosyltransfera	0.52	0.18

P43571	GPI inositol-deacylase	0.08	0.03
P07261	Glycolytic genes transc	0.11	0.05
Q03067	SAGA-associated facto	0.50	0.18
P11325	Leucine--tRNA ligase,	0.10	0.04
P87275	Altered inheritance of	0.34	0.13
Q05871	3,2-trans-enoyl-CoA is	0.34	0.13
P47155	Protein ILM1 OS=Sacch	0.48	0.17
P38153	AP-3 complex subunit	0.09	0.04
P33748	Zinc finger protein MS	0.06	0.03
Q99382	SRP-independent targe	0.57	0.20
P25569	Glucose-induced degra	0.06	0.03
Q03776	U1 small nuclear ribon	0.15	0.06
Q12124	Mediator of RNA poly	0.10	0.04
P33760	Peroxisomal ATPase PE	0.08	0.03
P54885	Gamma-glutamyl phos	0.10	0.04
P39979	D-amino-acid N-acetylt	0.65	0.22
P54070	Mannosyltransferase K	0.20	0.08
P28795	Peroxisomal biogenesi	0.10	0.04
P36037	Protein DOA1 OS=Sacc	0.06	0.03
P47050	Cullin-8 OS=Saccharom	0.05	0.02
P47136	Bud site selection prot	0.06	0.03
P38302	Pre-mRNA-splicing fact	0.79	0.25
Q05867	Uncharacterized protei	0.29	0.11
Q12446	Proline-rich protein LA	0.07	0.03
Q12345	Ino eighty subunit 3 O	0.18	0.07
Q06147	Sphingoid long chain b	0.06	0.03
P39677	Ribosome-releasing fa	0.11	0.05
P32910	DNA-directed RNA pol	0.14	0.06
P36146	Protein LAS1 OS=Sacch	0.17	0.07
P38298	Alkaline ceramidase YP	0.29	0.11
Q06252	Uncharacterized protei	0.52	0.18
P38336	RNases MRP/P 32.9 kD	0.33	0.12
Q08562	ATP-dependent helicas	0.05	0.02
P47096	3-hydroxyanthranilate	0.26	0.10
Q12287	Cytochrome c oxidase	0.72	0.24
P18410	Sporulation-specific pr	0.36	0.13
Q04748	Protein SOV1, mitocho	0.09	0.04
Q01448	Histone promoter cont	0.07	0.03
Q04772	Increased recombinati	0.22	0.09
Q02208	Topoisomerase 1-asso	0.12	0.05
P23202	Transcriptional regulat	0.26	0.10
P48240	Exosome complex com	0.18	0.07
Q06636	Glycosylphosphatidylin	0.20	0.08
P39005	Cell wall synthesis prot	0.17	0.07
Q12270	Rhomboid protein 2 O	0.37	0.14
P34218	Histone acetyltransfer	0.05	0.02
P36024	Phosphopantothenoyl	0.08	0.03
Q08970	Mitochondrial metal tr	0.09	0.04
P16550	Protein APA1 OS=Sacc	0.29	0.11
P01098	ATPase-stabilizing fact	0.58	0.20
P53739	Flippase kinase 1 OS=S	0.05	0.02
P53333	Pre-mRNA-splicing fact	0.07	0.03

P53981	Uncharacterized phos	0.19	0.08
P22136	ATPase expression pro	0.07	0.03
P80667	Peroxisomal membran	0.12	0.05
P18888	Transcription regulator	0.28	0.11
P54964	Oligoribonuclease, mit	0.16	0.06
P14306	Carboxypeptidase Y inh	0.21	0.08
P40454	Serine/threonine-prote	0.11	0.05
P39104	Phosphatidylinositol 4-	0.04	0.02
Q12181	NADPH-dependent difl	0.14	0.06
P34761	Protein WHI3 OS=Sacc	0.07	0.03
P40508	Uncharacterized protei	0.29	0.11
Q3E747	Uncharacterized protei	0.60	0.20
P07270	Phosphate system posi	0.15	0.06
P53212	Probable transcription	0.34	0.13
P46682	AP-3 complex subunit	0.05	0.02
Q12415	Transcription factor ta	0.10	0.04
P25361	Uncharacterized protei	0.85	0.27
P38812	Phosphatidylglyceroph	0.25	0.10
P18411	Protein FUN14 OS=Sac	0.24	0.09
P53296	Alcohol O-acetyltransf	0.08	0.03
Q08446	Protein SGT1 OS=Sacc	0.11	0.05
P04039	Cytochrome c oxidase	0.67	0.22
Q04675	tRNA-splicing endonuc	0.36	0.13
P25625	Protein PER1 OS=Sacc	0.12	0.05
Q12403	Protein ERP3 OS=Sacc	0.19	0.08
P21374	Pre-mRNA-splicing fact	0.18	0.07
P38698	Exopolyphosphatase O	0.23	0.09
P53139	Uncharacterized protei	0.34	0.13
P40204	Small nuclear ribonucl	0.72	0.24
P39731	Kinetochore-associate	0.15	0.06
P52917	Vacuolar protein sorti	0.22	0.09
P53086	Kinesin-like protein KI	0.05	0.02
P38297	Mitofusin FZO1 OS=Sa	0.05	0.02
P53843	Vacuolar protein sorti	0.31	0.12
Q04087	Monopolin complex su	0.13	0.05
Q3E756	UPF0768 protein YBL0	0.50	0.18
Q12493	Central kinetochore su	0.41	0.15
P41735	5-demethoxyubiquino	0.20	0.08
Q00723	Pre-mRNA-splicing fact	0.18	0.07
P28707	Co-chaperone protein	0.21	0.08
P25654	UPF0587 protein YCR0	0.25	0.10
P53137	CUE domain-containin	0.07	0.03
P36136	Sedoheptulose 1,7-bis	0.35	0.13
P40154	Ino eighty subunit 2 O	0.14	0.06
Q12328	Mitochondrial import i	0.24	0.09
P38823	E3 ubiquitin-protein lig	0.11	0.05
Q00246	GTP-binding protein R	0.16	0.06
P06100	General negative regul	0.23	0.09
Q3E762	Putative uncharacteriz	0.80	0.26
Q12251	Uncharacterized mitoc	0.14	0.06
Q12192	Repression factor of M	0.14	0.06
O13329	DNA replication fork-bl	0.15	0.06

P47029	Arrestin-related traffic	0.04	0.02
P53832	Cell wall integrity and s	0.09	0.04
Q07844	Ribosome biogenesis A	0.11	0.05
P38798	Nonsense-mediated m	0.04	0.02
P47093	U6 snRNA-associated S	0.45	0.16
P54999	Small nuclear ribonucle	0.61	0.21
Q12017	Phosducin-like protein	0.15	0.06
Q05949	Protein BUR2 OS=Sacc	0.11	0.05
Q08417	Sphingoid long-chain b	0.11	0.05
P40470	Regulator of rDNA tran	0.22	0.09
Q06707	SWR1-complex protein	0.36	0.13
P11746	Pheromone receptor tr	0.15	0.06
P11972	Protein SST2 OS=Sacch	0.06	0.03
P50101	Ubiquitin carboxyl-terr	0.03	0.01
P14065	Glycerol 2-dehydrogen	0.14	0.06
P31115	tRNA pseudouridine(3	0.10	0.04
P32363	Phosphatidylinositol N	0.10	0.04
P32776	RNA polymerase II tran	0.07	0.03
Q04659	Chromosome segregat	0.14	0.06
P40037	Protein HMF1 OS=Sacc	0.39	0.14
Q07622	Activator of C kinase p	0.07	0.03
P07274	Profilin OS=Saccharom	0.40	0.15
Q07381	Ribosome biogenesis p	0.05	0.02
P38177	Uncharacterized protei	0.09	0.04
Q06709	Cytoplasmic 60S subun	0.10	0.04
P47015	Altered inheritance of	0.12	0.05
Q12427	Protein STB3 OS=Sacch	0.09	0.04
P32607	Retrograde regulation	0.28	0.11
P40549	Alpha-1,3-mannosyltra	0.07	0.03
P54074	Protein ASI1 OS=Sacch	0.07	0.03
P39936	Eukaryotic initiation fa	0.05	0.02
P39008	Poly(A) ribonuclease P	0.10	0.04
Q03784	Trafficking protein part	0.21	0.08
Q03796	Polynucleotide 3~-pho	0.19	0.08
P46947	Pre-mRNA-splicing fact	0.17	0.07
Q03254	RNA polymerase II sub	0.06	0.03
P40358	DnaJ-like chaperone JE	0.06	0.03
Q12309	Pre-mRNA-splicing fact	0.06	0.03
Q03455	Probable zinc transpor	0.06	0.03
P40958	Mitotic spindle checkp	0.23	0.09
P49435	Adenine phosphoribos	0.25	0.10
P38165	Retrograde regulation	0.09	0.04
Q08230	Succinate dehydrogena	0.28	0.11
P38956	Transcription regulator	0.28	0.11
P53317	Nucleolar protein 19 O	0.23	0.09
Q12204	Probable phospholipas	0.06	0.03
P53188	rRNA-processing prote	0.38	0.14
P41733	GPI transamidase com	0.11	0.05
Q06417	Uncharacterized oxido	0.13	0.05
P34110	Vacuolar protein sortin	0.04	0.02
Q06346	Inositol phosphorylcer	0.20	0.08
Q03771	Assembly chaperone o	0.12	0.05

P50942	Polyphosphatidylinosit	0.04	0.02
Q99385	Vacuolar calcium ion tr	0.11	0.05
P39928	Osmosensing histidine	0.04	0.02
P49775	Bis(5~-adenosyl)-triph	0.22	0.09
P40091	Protein PEA2 OS=Sacch	0.10	0.04
Q12068	NADPH-dependent me	0.13	0.05
P38809	Uncharacterized protei	0.12	0.05
P25302	Regulatory protein SW	0.04	0.02
P36106	Transcription factor BY	0.07	0.03
Q08979	Kelch repeat-containin	0.06	0.03
Q3E835	MHF histone-fold com	0.55	0.19
P07390	COX3 mRNA-specific tr	0.09	0.04
Q3E793	BolA-like protein 1 OS=	0.45	0.16
P53900	Prefoldin subunit 4 OS	0.36	0.13
P39714	(R,R)-butanediol dehy	0.12	0.05
P53079	Conserved oligomeric	0.10	0.04
P38218	ADP-ribose 1~~-phosp	0.26	0.10
Q12052	Trimethylguanosine sy	0.14	0.06
P00420	Cytochrome c oxidase	0.17	0.07
P49704	Pre-mRNA-processing	0.09	0.04
P32329	Aspartic proteinase 3	0.08	0.03
Q3E834	Protein transport prot	0.63	0.21
P40354	Protein N-terminal ami	0.09	0.04
P17064	Purine-cytosine perme	0.08	0.03
P07807	Dihydrofolate reductas	0.21	0.08
P54857	Lipase 2 OS=Saccharon	0.13	0.05
P13712	Chromatin assembly fa	0.10	0.04
Q02771	Protein PET117, mitoch	1.12	0.33
Q99278	Mediator of RNA polyn	0.42	0.15
Q02100	CRE-binding bZIP prote	0.07	0.03
P38748	RING finger protein ET	0.07	0.03
P53066	Ankyrin repeat-contain	0.26	0.10
P49956	Chromosome transmis	0.06	0.03
Q2V2P3	Uncharacterized protei	0.71	0.23
P36533	54S ribosomal protein	0.77	0.25
P36110	Protein PRY2 OS=Sacch	0.15	0.06
Q12012	Uncharacterized protei	0.17	0.07
P25639	Uncharacterized memb	0.07	0.03
Q02793	Antiviral protein SKI8	0.11	0.05
P14359	Protein SNA3 OS=Sacch	0.36	0.13
P25515	V-type proton ATPase	0.32	0.12
Q08967	Flavin carrier protein 1	0.05	0.02
Q99189	mRNA transport regula	0.04	0.02
Q04461	Uncharacterized protei	0.09	0.04
P42944	Protein GZF3 OS=Sacch	0.08	0.03
Q12071	Vacuolar protein sortin	0.05	0.02
P16151	Protein ERD1 OS=Sacch	0.11	0.05
Q12458	Putative reductase 1 O	0.14	0.06
Q08278	Mediator of RNA polyn	0.20	0.08
P38793	tRNA (guanine(37)-N1)	0.09	0.04
P38932	Vacuolar protein sortin	0.07	0.03
P06104	Ubiquitin-conjugating	0.27	0.10

Q08215	Peroxisomal membran	0.11	0.05
P56508	Protein SNA2 OS=Sacch	0.65	0.22
Q08273	RING-box protein HRT1	0.38	0.14
P36066	Protein MRG3-like OS=	0.09	0.04
P32528	Urea amidolyase OS=S	0.02	0.01
Q99321	Diphosphoinositol poly	0.24	0.09
Q03219	Uncharacterized protei	0.16	0.06
P38191	Protein yippee-like MC	0.33	0.12
P40580	Benzil reductase ((S)-b	0.18	0.07
P39719	Flavin carrier protein 2	0.06	0.03
Q03667	Mitochondrial interme	0.32	0.12
P35688	Rho-GTPase-activating	0.04	0.02
P39720	Oleate-activated trans	0.04	0.02
Q02884	Elongator complex pro	0.10	0.04
Q04178	Hypoxanthine-guanine	0.20	0.08
Q05498	rRNA-processing prote	0.24	0.09
Q12184	Adrenodoxin homolog,	0.27	0.10
P39969	Protein BOI2 OS=Sacch	0.04	0.02
Q05776	Protein UPS1, mitocho	0.26	0.10
Q8TGU7	Uncharacterized protei	0.79	0.25
P38995	Copper-transporting A	0.04	0.02
P10862	Postreplication repair	0.09	0.04
P32351	Sugar utilization regula	0.13	0.05
P53735	Protein ZRG17 OS=Sac	0.07	0.03
P32604	Fructose-2,6-bisphosph	0.09	0.04
P38790	Hydroxyacyl-thioester	0.15	0.06
P43123	UDP-N-acetylglucosam	0.09	0.04
Q06350	Sporulation-specific ch	0.08	0.03
P39995	Chromatin modificatio	0.16	0.06
P38278	25S rRNA (adenine(21	0.13	0.05
Q03441	Sporulation protein R	0.10	0.04
P25638	TPR repeat-containing	0.44	0.16
P14905	Cytochrome B translati	0.11	0.05
P38291	Ribonucleases P/MRP	0.34	0.13
P57743	U6 snRNA-associated S	0.58	0.20
P40038	PHO85 cyclin-6 OS=Sac	0.10	0.04
Q04991	Protein FMP42 OS=Sac	0.09	0.04
P32909	Protein SMY2 OS=Sacc	0.06	0.03
P38714	Arginine--tRNA ligase,	0.07	0.03
P38962	Golgi apparatus memb	0.22	0.09
P40169	Uncharacterized plasm	0.15	0.06
P32893	Trafficking protein part	0.08	0.03
P33203	Pre-mRNA-processing	0.07	0.03
P53940	J domain-containing pr	0.08	0.03
P53507	Mitochondrial import	0.94	0.29
P32613	TRAPP-associated prot	0.31	0.12
Q03308	Vacuolar protein sortin	0.05	0.02
Q12496	Uncharacterized protei	0.04	0.02
P53942	Ribonuclease H2 subur	0.14	0.06
Q99177	Pre-mRNA-splicing fact	0.13	0.05
Q9ZZW7	Cytochrome b mRNA m	0.08	0.03
P32584	Protein-S-isoprenylcyst	0.18	0.07

Q3E785	Succinate dehydrogen	0.64	0.21
P0CX12	Protein COS2 OS=Sacc	0.11	0.05
Q12200	Niemann-Pick type C-r	0.04	0.02
Q04951	Probable family 17 glu	0.12	0.05
Q06563	Protein SYM1 OS=Sacc	0.23	0.09
P25656	Cell division control pr	0.11	0.05
P40986	Cell division control pr	0.09	0.04
Q03860	Golgi apparatus memb	0.34	0.13
P42841	Polyadenylation factor	0.09	0.04
Q12134	Protein HUA2 OS=Sacc	0.18	0.07
Q06819	Spliceosomal protein	0.32	0.12
P38702	Mitochondrial carrier	0.12	0.05
P32264	Glutamate 5-kinase OS	0.10	0.04
Q03769	Epsin-5 OS=Saccharom	0.10	0.04
P32791	Ferric/cupric reductase	0.06	0.03
Q04792	Glutamate decarboxyl	0.07	0.03
P25339	Pumilio homology dom	0.05	0.02
P32504	Centromere DNA-bindi	0.04	0.02
P33894	Dipeptidyl aminopepti	0.05	0.02
Q03433	Vacuolar protein sortin	0.16	0.06
P48510	Ubiquitin domain-cont	0.13	0.05
Q12330	Small nuclear ribonucl	0.56	0.19
P36145	Transcription initiation	0.13	0.05
P48582	Vacuolar-sorting prote	0.05	0.02
P40029	Peptide methionine su	0.24	0.09
P06838	DNA repair protein RA	0.21	0.08
P47026	GPI-anchored wall tran	0.09	0.04
Q12199	Type 2A phosphatase	0.12	0.05
P38876	Peptidyl-tRNA hydrola	0.25	0.10
P40449	Uncharacterized protei	0.19	0.08
Q05926	Glutaredoxin-8 OS=Sac	0.44	0.16
P25337	Pre-mRNA-splicing fact	0.28	0.11
P46998	Mitochondrial membr	0.26	0.10
Q08622	Genetic interactor of p	0.08	0.03
P34224	Uncharacterized protei	0.23	0.09
P25042	Repressor ROX1 OS=Sa	0.12	0.05
P40107	GDP-mannose transpo	0.13	0.05
Q04602	Vacuolar basic amino a	0.06	0.03
P81451	ATP synthase subunit	0.83	0.26
P32494	Chromatin-remodeling	0.06	0.03
P32773	Transcription initiation	0.16	0.06
Q06058	Seipin OS=Saccharomy	0.15	0.06
P04650	60S ribosomal protein	1.05	0.31
P22140	Choline/ethanolamine	0.11	0.05
P38857	Mitochondrial pyruvat	0.37	0.14
P39682	Pre-mRNA-processing	0.06	0.03
P40045	Topoisomerase I dama	0.38	0.14
Q12143	Kinetochore-associate	0.20	0.08
Q08747	Upstream activation fa	0.20	0.08
P53911	Chromatin modificatio	0.10	0.04
Q07505	Putative carboxymethy	0.16	0.06
P36154	Altered inheritance rat	0.29	0.11

Q12043	Lipase 5 OS=Saccharon	0.06	0.03
P53100	Putative 2-hydroxyacid	0.11	0.05
P38337	COMPASS component	0.33	0.12
Q03673	Altered inheritance of	0.23	0.09
P53259	Rhomboid protein 1, m	0.13	0.05
P24583	Protein kinase C-like 1	0.04	0.02
P53937	37S ribosomal protein	0.33	0.12
Q06407	Rho-type GTPase-activ	0.04	0.02
P49573	Copper transport prote	0.11	0.05
P21372	Pre-mRNA-processing	0.05	0.02
Q06005	Octanoyltransferase, m	0.13	0.05
Q05937	Zinc finger protein STP	0.13	0.05
Q02889	Protein MGR2 OS=Sacc	0.46	0.16
P06784	Serine/threonine-prote	0.08	0.03
P24482	DNA polymerase epsilc	0.06	0.03
P38312	ER-derived vesicles prc	0.32	0.12
Q08444	20S-pre-rRNA D-site er	0.09	0.04
P53849	Zinc finger protein GIS	0.29	0.11
Q06991	Protein PUN1 OS=Saccl	0.17	0.07
Q3E795	Uncharacterized protei	0.52	0.18
P38345	Succinate dehydrogena	0.35	0.13
Q12066	Nuclear rim protein 1 (	0.09	0.04
P38204	RNA polymerase I-spec	0.32	0.12
P40493	25S rRNA (uridine(2634	0.13	0.05
P53283	Polyamine transporter	0.07	0.03
P47032	Protein PRY1 OS=Sacch	0.16	0.06
P40466	Fork head protein hom	0.09	0.04
Q05521	Diacylglycerol pyropho	0.15	0.06
P32178	Chorismate mutase OS	0.17	0.07
P39713	Probable diacetyl redu	0.11	0.05
Q02196	Adenylyl-sulfate kinase	0.22	0.09
P38149	Probable di- and tripep	0.05	0.02
P40501	Vacuolar amino acid tr	0.09	0.04
P32345	Serine/threonine-prote	0.14	0.06
P54784	Origin recognition com	0.05	0.02
P07172	Histidinol-phosphate a	0.12	0.05
P05085	Arginine metabolism re	0.05	0.02
P07266	Mitochondrial RNA-spl	0.12	0.05
P40414	Tropomyosin-2 OS=Sac	0.28	0.11
P38151	PAB1-binding protein 2	0.11	0.05
P53166	ATP-dependent RNA he	0.08	0.03
Q02554	Cold sensitive U2 snRN	0.10	0.04
P00937	Multifunctional tryptop	0.09	0.04
P06785	Thymidylate synthase (	0.14	0.06
P33734	Imidazole glycerol phos	0.08	0.03
P38042	Anaphase-promoting c	0.06	0.03
Q12157	Anaphase-promoting c	0.27	0.10
P40005	Prefoldin subunit 2 OS=	0.43	0.16
P41821	Stretch-activated catio	0.08	0.03
P18414	ER lumen protein-retai	0.20	0.08
P43617	Uncharacterized mitoc	0.15	0.06
P32842	V-type proton ATPase	0.31	0.12

Q12488	DNA replication compl	0.21	0.08
Q07950	Sterol esterase 2 OS=S	0.08	0.03
P38705	Serine--tRNA ligase, mi	0.10	0.04
P53944	Mitochondrial N(5)-glu	0.14	0.06
P32564	Protein SCM4 OS=Sacc	0.26	0.10
P39009	DNA damage response	0.08	0.03
P50109	Protein PSP2 OS=Sacch	0.07	0.03
P38746	Obg-like ATPase homol	0.11	0.05
P40325	Proline-rich protein HU	0.23	0.09
P38903	Serine/threonine-prote	0.06	0.03
Q12408	Phosphatidylglycerol/p	0.27	0.10
P36027	Cell wall integrity sens	0.13	0.05
P52923	Apoptosis-inducing fac	0.12	0.05
P25627	18S rRNA (guanine(157	0.16	0.06
Q05905	Protein HRI1 OS=Sacch	0.19	0.08
Q12379	Anaphase-promoting c	0.27	0.10
Q12060	Transcriptional coactiv	0.09	0.04
Q06336	ADP-ribosylation facto	0.08	0.03
Q06325	Aspartic proteinase ya	0.08	0.03
Q12034	Protein SLF1 OS=Sacch	0.10	0.04
P40507	Protein AIR1 OS=Sacch	0.12	0.05
Q12417	Pre-mRNA-splicing fact	0.10	0.04
Q03375	Pre-mRNA-splicing fact	0.34	0.13
Q06178	Nicotinamide/nicotinic	0.11	0.05
P53540	Spindle pole body com	0.05	0.02
P34243	DNA polymerase alpha	0.06	0.03
P52867	Dolichyl-phosphate-m	0.06	0.03
P46972	Mitochondrial inner m	0.26	0.10
P38313	Central kinetochore su	0.13	0.05
P36012	Histone H3-like centro	0.19	0.08
Q02209	Uncharacterized protei	0.12	0.05
P32491	MAP kinase kinase MK	0.09	0.04
P39106	Alpha-1,3-mannosyltra	0.05	0.02
P32628	UV excision repair prot	0.12	0.05
Q12382	CTP-dependent diacylg	0.15	0.06
Q08748	Uncharacterized protei	0.03	0.01
Q04934	Protein IVY1 OS=Sacch	0.10	0.04
P53039	Protein transport prot	0.19	0.08
P25559	Sister chromatid cohes	0.11	0.05
P25338	Uncharacterized endo	0.26	0.10
P53010	PAB-dependent poly(A	0.04	0.02
P38806	Chromatin modificatio	0.15	0.06
Q07653	Protein HBT1 OS=Sacc	0.04	0.02
Q12697	Vacuolar cation-transp	0.03	0.01
P36114	Mitochondrial outer m	0.06	0.03
Q08951	AP-3 complex subunit	0.04	0.02
Q12000	Translation machinery-	0.13	0.05
P40492	Protein FYV10 OS=Sacc	0.08	0.03
P33313	Hsp70/Hsp90 co-chape	0.11	0.05
P53246	Late endosome and va	0.05	0.02
P14736	DNA repair protein RA	0.06	0.03
Q02825	tRNA-splicing endonuc	0.09	0.04

P43620	Sporulation protein RM	0.06	0.03
P38777	Family of serine hydrol	0.19	0.08
Q05031	Mannan endo-1,6-alph	0.10	0.04
Q07655	Protein WHI4 OS=Saccl	0.07	0.03
Q12091	Damage response prot	0.32	0.12
P53238	Peflin OS=Saccharomy	0.13	0.05
Q02896	Alkaline ceramidase YD	0.13	0.05
Q08144	T-SNARE affecting a lat	0.11	0.05
P20435	DNA-directed RNA poly	0.30	0.11
P38913	FAD synthase OS=Saccl	0.14	0.06
P53095	D-serine dehydratase (	0.10	0.04
P31244	DNA repair protein RAI	0.05	0.02
Q06408	Transaminated amino	0.07	0.03
P40851	Putative protease AXL1	0.03	0.01
Q06604	Protein BSP1 OS=Sacch	0.08	0.03
P53895	Protein ASI2 OS=Sacch	0.15	0.06
P27680	Ubiquinone biosynthes	0.14	0.06
Q03503	N-alpha-acetyltransfer	0.25	0.10
P40085	Endoplasmic reticulum	0.08	0.03
Q12158	Sister chromatid cohes	0.08	0.03
Q12175	MutS protein homolog	0.05	0.02
P47049	UBX domain-containin	0.11	0.05
P38172	MIOREX complex comp	0.17	0.07
P38873	Target of rapamycin co	0.03	0.01
P09798	Anaphase-promoting c	0.05	0.02
P32800	Peroxisomal biogenesi	0.16	0.06
P25334	Peptidyl-prolyl cis-tran	0.14	0.06
Q08964	Putative ISWI chromati	0.04	0.02
P53152	Ubiquitin-conjugating	0.35	0.13
P41930	Sulfite efflux pump SSU	0.09	0.04
Q05533	Inositol monophosphat	0.15	0.06
Q10740	Leukotriene A-4 hydrol	0.06	0.03
Q04174	GPI mannosyltransfera	0.08	0.03
P40214	Uncharacterized protei	0.13	0.05
Q3E7A7	Uncharacterized protei	0.48	0.17
O14464	54S ribosomal protein	0.53	0.18
P33749	Zinc finger protein MSI	0.07	0.03
P32501	Translation initiation fa	0.06	0.03
Q05942	Ribosome assembly pr	0.21	0.08
P25360	Inorganic phosphate tr	0.05	0.02
P20095	Pre-mRNA-splicing fact	0.05	0.02
P52490	Ubiquitin-conjugating	0.30	0.11
P10566	Mitochondrial RNA-spl	0.14	0.06
Q06146	Uncharacterized protei	0.14	0.06
P53127	E3 ubiquitin-protein lig	0.03	0.01
Q12476	Protein AIR2 OS=Sacch	0.12	0.05
Q07533	Cytokinesis protein 3 C	0.05	0.02
P32487	Lysine-specific permea	0.07	0.03
P38795	Glutamine-dependent	0.06	0.03
Q08213	RNA exonuclease NGL1	0.12	0.05
Q12274	Uncharacterized protei	0.27	0.10
Q08645	Folylpolyglutamate syn	0.08	0.03

Q03835	Monothiol glutaredoxi	0.18	0.07
Q3E7B2	Cytochrome c oxidase	0.59	0.20
P39706	COMPASS component	0.10	0.04
P07702	L-2-aminoadipate redu	0.03	0.01
P27801	Vacuolar membrane pr	0.04	0.02
P43589	Pre-mRNA-splicing fact	0.09	0.04
Q07798	Sporulation-specific pr	0.05	0.02
P13434	Transcriptional activat	0.33	0.12
P38227	Quinidine resistance pr	0.06	0.03
Q02948	Vacuolar protein sortin	0.08	0.03
P48743	RFX-like DNA-binding p	0.05	0.02
P32839	Mitochondrial chapero	0.10	0.04
P11709	Nuclear fusion protein	0.10	0.04
P53165	SAGA-associated facto	0.07	0.03
P47110	DNA polymerase delta	0.12	0.05
P14747	Serine/threonine-prote	0.07	0.03
P37020	Anion/proton exchang	0.05	0.02
Q12530	Ribonuclease MRP pro	0.22	0.09
P40522	Transcription factor VH	0.07	0.03
P32525	Protein ECM25 OS=Sac	0.07	0.03
Q12150	Protein CSF1 OS=Sacch	0.01	0.00
P38344	Cytoplasmic 60S subun	0.11	0.05

protein description	emPAI	relative abundance
Enolase 2 OS=Saccharc	44.30	1.66
Elongation factor 2 OS=	26.92	1.45
Pyruvate kinase 1 OS=S	42.67	1.64
Heat shock protein SSA	40.72	1.62
Heat shock protein SSA	43.11	1.64
Glyceraldehyde-3-phos	145.17	2.16
Fatty acid synthase sub	14.84	1.20
Phosphoglycerate kina	34.88	1.55
Fatty acid synthase sub	9.30	1.01
Enolase 1 OS=Saccharc	21.61	1.35
Ribosome-associated m	14.79	1.20
Ribosome-associated m	14.79	1.20
Pyruvate decarboxylase	18.72	1.29
ATP-dependent molecu	17.59	1.27
Glyceraldehyde-3-phos	64.68	1.82
Plasma membrane ATP	7.37	0.92
Elongation factor 3A O	16.73	1.25
Elongation factor 1-alp	18.95	1.30
5-methyltetrahydropte	15.46	1.22
ATP-dependent molecu	16.20	1.24
Heat shock protein SSC	27.33	1.45
Glyceraldehyde-3-phos	65.53	1.82
Acetyl-CoA carboxylase	10.20	1.05
Protein URA2 OS=Sacch	5.58	0.82
Fructose-bisphosphate	20.56	1.33
V-type proton ATPase c	14.44	1.19
ATP-dependent 6-phos	11.50	1.10
Alcohol dehydrogenase	11.46	1.10
Magnesium-activated a	19.29	1.31
Heat shock protein 60,	28.98	1.48
Heat shock protein hor	25.77	1.43
Heat shock protein SSA	9.70	1.03
60S ribosomal protein	33.64	1.54
ATP-dependent RNA he	24.95	1.41
Heat shock protein 104	13.57	1.16
eIF-2-alpha kinase activ	2.62	0.56
Cell division control pro	14.16	1.18
Adenosylhomocysteina	19.76	1.32
78 kDa glucose-regulat	19.98	1.32
Clathrin heavy chain OS	3.65	0.67
Glucose-6-phosphate is	9.08	1.00
Isoleucine--tRNA ligase	7.88	0.95
Transposon Ty1-ML2 G	2.61	0.56
V-type proton ATPase s	16.47	1.24
Transposon Ty1-PL Gag	2.69	0.57
Actin OS=Saccharomyc	31.72	1.51
Transposon Ty1-LR4 Ga	2.60	0.56
Aconitate hydratase, m	13.10	1.15
Transposon Ty1-OL Gag	2.61	0.56
ATP-dependent 6-phos	5.31	0.80

Transposon Ty1-JR2 Ga	2.44	0.54
Phosphoglycerate mut	20.24	1.33
Triosephosphate isome	12.73	1.14
Protein SCP160 OS=Sac	9.84	1.04
Glutamate synthase [N	3.06	0.61
Guanine nucleotide-bi	28.16	1.46
60S ribosomal protein	9.49	1.02
Serine hydroxymethylt	22.17	1.36
Glutamate--tRNA ligase	11.96	1.11
ATP-dependent RNA h	9.70	1.03
Peroxiredoxin type-2 C	28.56	1.47
Elongation factor 3B O	1.07	0.32
S-adenosylmethionine	16.81	1.25
Ribosome-associated c	7.90	0.95
Cystathionine beta-syn	13.77	1.17
60S ribosomal protein	20.24	1.33
40S ribosomal protein	33.33	1.54
C-1-tetrahydrofolate sy	8.57	0.98
Leucine--tRNA ligase, c	5.17	0.79
Alanine--tRNA ligase, n	7.50	0.93
60S ribosomal protein	20.24	1.33
Long-chain-fatty-acid--	11.48	1.10
40S ribosomal protein	68.77	1.84
S-adenosylmethionine	12.12	1.12
Transaldolase OS=Sacc	33.92	1.54
NADP-specific glutama	17.76	1.27
40S ribosomal protein	67.65	1.84
Protein BMH1 OS=Sacc	25.22	1.42
Heat shock protein STI	17.46	1.27
Aminopeptidase 2, mit	5.85	0.84
Pentafunctional AROM	4.02	0.70
ABC transporter ATP-b	7.47	0.93
Phosphoribosylformylg	3.99	0.70
Bifunctional purine bio	5.98	0.84
Glycine--tRNA ligase 1,	11.53	1.10
Histidine biosynthesis t	3.02	0.60
Aspartate--tRNA ligase	10.57	1.06
60S ribosomal protein	7.74	0.94
Protein disulfide-isome	14.52	1.19
60S ribosomal protein	7.74	0.94
Acetyl-coenzyme A syn	6.81	0.89
Peroxiredoxin TSA1 OS	19.62	1.31
60S ribosomal protein	74.79	1.88
Importin subunit beta-	2.70	0.57
Hexokinase-2 OS=Saccl	15.21	1.21
Pyruvate carboxylase 2	4.68	0.75
Transketolase 1 OS=Sa	6.72	0.89
Protein BMH2 OS=Sacc	19.55	1.31
40S ribosomal protein	6.99	0.90
60S acidic ribosomal pr	5.12	0.79
Potassium-activated al	12.04	1.12
Trehalose synthase cor	2.98	0.60

40S ribosomal protein	102.27	2.01
Heat shock protein 78,	12.16	1.12
60S ribosomal protein	53.33	1.74
Vacuolar protein sortin	12.16	1.12
26S proteasome regula	6.99	0.90
Polyadenylate-binding	8.67	0.99
Coatomer subunit gam	3.02	0.60
Bifunctional purine bio	3.89	0.69
Isoform Cytoplasmic of	4.61	0.75
Pyruvate carboxylase 1	3.74	0.68
Transposon Ty1-MR1 G	1.13	0.33
60S ribosomal protein	9.99	1.04
Coatomer subunit alph	3.30	0.63
Clustered mitochondria	3.77	0.68
Trehalose-phosphatase	4.67	0.75
Sphingolipid long chair	5.32	0.80
60S ribosomal protein	29.21	1.48
Carbamoyl-phosphate	4.97	0.78
Coatomer subunit beta	4.26	0.72
60S ribosomal protein	8.75	0.99
Homoserine dehydroge	12.01	1.11
40S ribosomal protein	17.80	1.27
Asparagine--tRNA ligas	7.22	0.91
40S ribosomal protein	3.25	0.63
60S ribosomal protein	8.75	0.99
60S ribosomal protein	18.19	1.28
Pyruvate decarboxylas	0.58	0.20
Coatomer subunit beta	2.65	0.56
60S ribosomal protein	28.18	1.47
Threonine--tRNA ligase	8.73	0.99
UTP--glucose-1-phosph	5.90	0.84
6-phosphogluconate d	16.90	1.25
40S ribosomal protein	15.49	1.22
Glycerol-3-phosphate	4.68	0.75
Suppressor protein STI	15.78	1.22
40S ribosomal protein	9.96	1.04
Peptidyl-prolyl cis-tran	17.65	1.27
40S ribosomal protein	19.35	1.31
60S ribosomal protein	7.40	0.92
60S ribosomal protein	18.14	1.28
40S ribosomal protein	59.80	1.78
60S ribosomal protein	15.61	1.22
40S ribosomal protein	3.64	0.67
Fimbrin OS=Saccharom	6.17	0.86
Eukaryotic translation i	2.68	0.57
60S ribosomal protein	17.88	1.28
40S ribosomal protein	14.57	1.19
60S ribosomal protein	19.31	1.31
Ubiquitin-activating en	5.13	0.79
Transcriptional modula	5.33	0.80
40S ribosomal protein	115.84	2.07
Protein transport prote	1.34	0.37

ATP synthase subunit	3.70	0.67
Nucleolar protein 58 O	5.19	0.79
Phosphoglucomutase	6.47	0.87
Elongation factor 1-ga	6.55	0.88
40S ribosomal protein	22.27	1.37
Protein transport prot	2.56	0.55
ADP-ribosylation facto	14.37	1.19
Lysine--tRNA ligase, cy	5.45	0.81
40S ribosomal protein	27.28	1.45
Serine--tRNA ligase, cy	10.68	1.07
Arginine--tRNA ligase,	12.17	1.12
Eukaryotic translation i	3.13	0.62
60S ribosomal protein	8.63	0.98
Sphingolipid long chai	5.38	0.80
NADPH dehydrogenas	10.13	1.05
40S ribosomal protein	14.11	1.18
Eukaryotic translation i	5.88	0.84
60S ribosomal protein	13.11	1.15
Pyruvate decarboxylas	0.58	0.20
ADP-ribosylation facto	13.93	1.17
Asparagine synthetase	5.60	0.82
Nuclear segregation pr	9.29	1.01
Eukaryotic translation i	32.91	1.53
[NU+] prion formation	2.79	0.58
NADPH--cytochrome P	6.13	0.85
Adenosine kinase OS=	7.93	0.95
Putative proline--tRNA	3.85	0.69
60S ribosomal protein	14.60	1.19
Glycogen phosphoryla	4.42	0.73
Mitochondrial import	14.72	1.20
60S ribosomal protein	9.78	1.03
Asparagine synthetase	5.62	0.82
Phosphomannomutase	23.94	1.40
Aldehyde dehydrogen	7.30	0.92
40S ribosomal protein	21.91	1.36
Glycogen [starch] synt	3.88	0.69
Inorganic pyrophosph	12.72	1.14
60S ribosomal protein	20.33	1.33
Tryptophan synthase	3.10	0.61
Inosine-5~-monophos	3.83	0.68
Bifunctional purine bio	2.92	0.59
Hexokinase-1 OS=Sacc	10.56	1.06
V-type proton ATPase	1.43	0.39
Mannose-1-phosphate	4.91	0.77
Farnesyl pyrophosphat	4.02	0.70
60S ribosomal protein	26.72	1.44
Threonine synthase OS	8.16	0.96
40S ribosomal protein	24.21	1.40
Dihydrolipoyl dehydro	10.39	1.06
ATP synthase subunit	6.48	0.87
60S ribosomal protein	14.71	1.20
60S ribosomal protein	9.37	1.02

Glutamine--tRNA ligas	5.82	0.83
60S ribosomal protein	12.11	1.12
Eukaryotic translation i	5.48	0.81
2-isopropylmalate synt	12.50	1.13
Dihydroxyacetone kina	5.60	0.82
Protein transport prot	2.35	0.53
1,3-beta-glucan syntha	1.62	0.42
tRNA-aminoacylation c	5.67	0.82
Phosphoinositide phos	7.90	0.95
Glycerol-1-phosphate	22.93	1.38
DNA-directed RNA pol	1.03	0.31
C-1-tetrahydrofolate s	5.74	0.83
Thioredoxin reductase	7.90	0.95
NADPH-dependent alp	29.93	1.49
Translationally-control	11.05	1.08
26S proteasome regula	2.64	0.56
Translation initiation f	4.53	0.74
Altered inheritance of	10.06	1.04
60S ribosomal protein	5.49	0.81
Heat shock protein ho	2.80	0.58
60S ribosomal protein	62.88	1.81
40S ribosomal protein	2.81	0.58
Methionine--tRNA liga	3.90	0.69
FACT complex subunit	7.10	0.91
Ubiquitin-40S ribosom	7.51	0.93
60S ribosomal protein	69.28	1.85
rRNA biogenesis prote	1.47	0.39
40S ribosomal protein	9.29	1.01
Ornithine aminotransf	7.39	0.92
Dihydroxy-acid dehydr	8.33	0.97
Glucokinase-1 OS=Sacc	6.62	0.88
60S ribosomal protein	69.28	1.85
Zuotin OS=Saccharomy	3.65	0.67
Eisosome protein 1 OS	4.59	0.75
Adenylosuccinate lyas	9.25	1.01
Cysteine--tRNA ligase	4.91	0.77
Inosine-5~-monophos	2.47	0.54
Aminopeptidase Y OS=	1.56	0.41
Obg-like ATPase 1 OS=	13.09	1.15
Superoxide dismutase	23.67	1.39
Glycerol-1-phosphate	11.39	1.09
60S ribosomal protein	3.64	0.67
ATP-dependent RNA h	7.00	0.90
Ketol-acid reductoiso	5.04	0.78
5~-3~ exoribonuclease	1.86	0.46
T-complex protein 1 su	4.77	0.76
Phosphoribosylaminoi	7.83	0.95
Nuclear localization se	11.68	1.10
Elongation factor 1-ga	3.47	0.65
40S ribosomal protein	12.61	1.13
Phenylalanine--tRNA li	5.55	0.82
Protein GVP36 OS=Sac	4.97	0.78

V-type proton ATPase	48.68	1.70
Cofilin OS=Saccharomy	6.69	0.89
FACT complex subunit	1.70	0.43
N-terminal acetyltrans	3.81	0.68
H/ACA ribonucleoprote	9.95	1.04
L-2-aminoadipate redu	2.91	0.59
40S ribosomal protein	22.90	1.38
Acetolactate synthase	5.61	0.82
60S ribosomal protein	8.25	0.97
Manganese-transporti	1.56	0.41
40S ribosomal protein	15.61	1.22
Phospho-2-dehydro-3-	3.62	0.66
Aspartate-semialdehy	8.32	0.97
GMP synthase [glutam	10.14	1.05
60S ribosomal protein	8.91	1.00
D-2-hydroxyglutarate--	4.03	0.70
Dihydrolipoyllysine-res	4.12	0.71
60S ribosomal protein	7.29	0.92
60S ribosomal protein	11.79	1.11
60S ribosomal protein	7.40	0.92
Pleiotropic ABC efflux t	1.16	0.33
Nucleolar protein 56 O	6.27	0.86
Multisite-specific tRNA	2.13	0.50
Pyruvate kinase 2 OS=	0.67	0.22
60S ribosomal protein	2.83	0.58
40S ribosomal protein	9.78	1.03
Acetyl-CoA acetyltrans	5.70	0.83
ATP-dependent RNA h	4.87	0.77
Cell wall protein CWP1	3.67	0.67
Inosine-5~-monophos	1.70	0.43
Adenylosuccinate synt	7.52	0.93
Tricalbin-3 OS=Sacchar	0.74	0.24
Cystathionine gamma-	2.38	0.53
Midasin OS=Saccharom	0.55	0.19
Orotate phosphoribos	16.12	1.23
Glycerol-3-phosphate	6.47	0.87
Nucleolar complex pro	6.12	0.85
Hydroxymethylglutaryl	2.59	0.56
Probable metalloprote	2.39	0.53
Dynamin-related prote	2.19	0.50
Nucleoside diphosphat	10.47	1.06
NAD-dependent malic	4.86	0.77
Protein PBDC1 homolo	30.75	1.50
ATP-dependent RNA h	3.33	0.64
Protein translocation p	4.06	0.70
Homoaconitase, mitoc	2.95	0.60
Inositol-3-phosphate s	3.12	0.61
60S ribosomal protein	9.98	1.04
2-isopropylmalate synt	4.73	0.76
25S rRNA (cytosine(28	2.36	0.53
40S ribosomal protein	6.58	0.88
ATP-dependent RNA h	1.00	0.30

Urea amidolyase OS=S	1.21	0.34
GTP-binding nuclear pr	6.88	0.90
2-oxoglutarate dehydr	2.17	0.50
DNA-directed RNA pol	0.89	0.28
60S ribosomal protein	5.62	0.82
Myosin-2 OS=Saccharo	0.73	0.24
60S ribosomal protein	23.90	1.40
Prolyl 3,4-dihydroxylas	4.55	0.74
Aldehyde dehydrogena	3.62	0.66
Deoxyhypusine synthas	9.95	1.04
Phosphoglucomutase 1	1.44	0.39
Mitochondrial outer m	7.62	0.94
Protein SEY1 OS=Sacch	5.00	0.78
3-isopropylmalate deh	4.16	0.71
Transaldolase NQM1 C	5.63	0.82
Endoplasmic oxidoredu	4.20	0.72
60S ribosomal protein	23.90	1.40
Phosphoribosylaminoi	14.11	1.18
Glutamine synthetase	3.77	0.68
Deoxyhypusine hydrox	6.95	0.90
Aromatic/aminoadipat	3.90	0.69
Homocitrate synthase,	3.22	0.63
Protein GCN20 OS=Sac	1.57	0.41
60S ribosomal protein	26.98	1.45
rRNA-processing prote	5.06	0.78
Alpha,alpha-trehalose-	3.15	0.62
Saccharopine dehydrog	5.83	0.83
Nuclear cap-binding pr	2.75	0.57
1,3-beta-glucanosyltra	1.36	0.37
Trehalose synthase cor	1.29	0.36
Citrate synthase, mito	2.76	0.58
Ribonucleoside-diphos	3.16	0.62
ATP-dependent RNA h	5.36	0.80
GTP-binding protein YF	12.46	1.13
Tubulin alpha-1 chain	1.55	0.41
Serine palmitoyltransfe	3.17	0.62
Flavohemoprotein OS=	6.36	0.87
Glutamine--fructose-6-	3.56	0.66
Nucleoporin NIC96 OS=	2.95	0.60
Signal recognition part	4.51	0.74
Pescadillo homolog OS	3.41	0.64
Phenylalanine--tRNA li	4.16	0.71
Uracil phosphoribosylt	10.59	1.06
Vesicular-fusion protei	1.45	0.39
Eukaryotic translation i	5.80	0.83
Dolichyl-phosphate-ma	1.95	0.47
Mannose-6-phosphate	3.31	0.63
Adenylate kinase OS=S	20.85	1.34
Cell division control pr	5.07	0.78
Putative aldehyde deh	2.04	0.48
Catalase T OS=Sacchar	1.97	0.47
Nucleolar GTP-binding	3.01	0.60

Eukaryotic peptide cha	2.02	0.48
Tubulin alpha-3 chain (	1.12	0.33
Intracellular protein tra	1.18	0.34
Tubulin beta chain OS=	2.30	0.52
60S ribosomal protein	6.56	0.88
Eukaryotic translation i	4.92	0.77
Neutral trehalase OS=S	2.00	0.48
Probable electron tran	5.15	0.79
Transcription elongatic	1.46	0.39
Aromatic amino acid ar	5.37	0.80
SED5-binding protein 3	1.35	0.37
Long-chain-fatty-acid--	2.16	0.50
ADP,ATP carrier protei	4.84	0.77
Replication factor A pr	2.81	0.58
Elongation factor 1-bet	4.23	0.72
E3 ubiquitin-protein lig	1.27	0.36
Nucleolar protein 3 OS	2.13	0.50
Zinc-regulated transpo	0.96	0.29
60S ribosomal protein	41.43	1.63
Ran GTPase-activating	4.69	0.76
NADPH-dependent me	5.28	0.80
V-type proton ATPase s	5.63	0.82
D-lactate dehydrogena	2.90	0.59
Isoform Short of Eukar	3.57	0.66
Eukaryotic translation i	5.09	0.78
Low specificity L-threo	4.73	0.76
Pre-mRNA-splicing fact	1.49	0.40
Signal recognition part	2.37	0.53
Aspartate aminotransf	5.92	0.84
Importin subunit alpha	4.10	0.71
U3 small nucleolar RN	1.86	0.46
Eukaryotic peptide cha	5.18	0.79
Amidophosphoribosylt	3.03	0.61
ER membrane protein	2.11	0.49
ATP phosphoribosyltra	9.09	1.00
FK506-binding nuclear	2.37	0.53
V-type proton ATPase s	3.95	0.69
Outer spore wall asser	5.63	0.82
Ras-related protein SE	6.25	0.86
NADPH-dependent ald	8.62	0.98
Nucleoporin NUP170 C	0.65	0.22
Mannosyl-oligosacchar	1.92	0.47
U3 small nucleolar RN	2.07	0.49
Spermidine synthase O	7.19	0.91
D-arabinose dehydroge	4.40	0.73
Peptidyl-prolyl cis-tran	3.24	0.63
Transposon Ty2-LR1 Ga	0.35	0.13
ATP-dependent RNA h	5.47	0.81
Pumilio homology dom	2.73	0.57
Pyruvate dehydrogena	4.55	0.74
Gamma-glutamyl phos	2.76	0.58
NET1-associated nucle	2.20	0.51

Protein transport prote	0.31	0.12
Dolichyl-phosphate-ma	1.14	0.33
Phosphoserine aminot	4.07	0.71
Actin-interacting prote	2.27	0.51
Homocitrate dehydrat	2.13	0.50
Elongator complex pro	1.30	0.36
Argininosuccinate synt	7.07	0.91
Serine hydroxymethylt	3.84	0.68
CTP synthase 1 OS=Sac	2.68	0.57
Exportin-1 OS=Sacchar	1.48	0.39
Chorismate synthase C	3.44	0.65
Transcription initiation	1.59	0.41
Isocitrate dehydrogen	1.90	0.46
Chromatin structure-re	1.76	0.44
Proteasome componer	0.79	0.25
60S acidic ribosomal p	4.38	0.73
T-complex protein 1 su	2.73	0.57
Multiprotein-bridging f	16.06	1.23
Histidine--tRNA ligase,	2.24	0.51
40S ribosomal protein	5.90	0.84
External NADH-ubiquir	2.59	0.56
T-complex protein 1 su	2.79	0.58
Alcohol dehydrogenase	0.64	0.21
Eukaryotic translation i	5.33	0.80
Eukaryotic initiation fa	0.85	0.27
Nucleolar protein 4 OS	2.56	0.55
SEC14 cytosolic factor	5.53	0.81
Importin subunit beta-	1.32	0.37
Ubiquitin carboxyl-terr	2.73	0.57
Glucose-6-phosphate 1	3.38	0.64
Eukaryotic translation i	4.37	0.73
Saccharopepsin OS=Sa	2.18	0.50
Signal recognition part	3.77	0.68
Low-affinity glucose tr	0.56	0.19
Mitochondrial inner m	1.82	0.45
Glycine dehydrogenase	0.93	0.29
Alcohol dehydrogenase	1.78	0.44
Proteasome subunit al	9.66	1.03
Actin-binding protein C	2.40	0.53
Protein SIS1 OS=Sacch	2.50	0.54
Glycolipid 2-alpha-mar	1.72	0.43
General negative regul	0.77	0.25
Imidazole glycerol pho	2.98	0.60
Cys-Gly metallodipepti	3.13	0.62
Delta-1-pyrroline-5-car	4.35	0.73
Chromatin structure-re	2.38	0.53
U3 small nucleolar RN	1.53	0.40
Pyrroline-5-carboxylat	2.99	0.60
Diphosphomevalonate	3.91	0.69
Vacuolar transporter c	2.68	0.57
Guanylate kinase OS=S	22.83	1.38
Protein HRI1 OS=Sacch	8.17	0.96

Nascent polypeptide-a	8.52	0.98
Nucleolar protein 9 OS	1.80	0.45
T-complex protein 1 su	1.91	0.46
Glucose-6-phosphate 1	8.09	0.96
Nucleolar complex-ass	0.86	0.27
NADP-dependent 3-hy	5.89	0.84
Reticulon-like protein	2.12	0.49
ATP-dependent RNA h	3.81	0.68
Proteasome subunit al	8.83	0.99
Cell division control pr	1.35	0.37
60S ribosomal protein	13.61	1.16
Alpha-1,2-mannosyltra	2.03	0.48
Anthranilate synthase	2.46	0.54
DNA topoisomerase 1	2.16	0.50
Protein SSD1 OS=Sacch	0.55	0.19
Threonine dehydratase	3.06	0.61
Putative glucokinase-2	2.51	0.55
60S ribosomal protein	1.77	0.44
Periodic tryptophan pr	1.09	0.32
Nicotinamidase OS=Sa	6.81	0.89
Uncharacterized protei	15.49	1.22
DNA-directed RNA poly	0.66	0.22
T-complex protein 1 su	1.81	0.45
Thioredoxin-2 OS=Sacc	6.71	0.89
Arginase OS=Saccharo	2.70	0.57
Vacuolar transporter c	1.32	0.37
Phosphatidylethanolan	0.92	0.28
26S protease regulator	2.46	0.54
Uncharacterized protei	3.94	0.69
Eukaryotic translation i	9.96	1.04
Eukaryotic translation i	1.51	0.40
Isocitrate dehydrogena	3.32	0.64
Ribonucleoside-diphos	5.52	0.81
Eukaryotic translation i	6.52	0.88
Eukaryotic translation i	5.93	0.84
60S ribosomal protein	8.94	1.00
26S proteasome regula	2.02	0.48
Uncharacterized protei	2.12	0.49
Nascent polypeptide-a	2.95	0.60
60S ribosomal protein	4.33	0.73
T-complex protein 1 su	2.00	0.48
Vacuolar protein sortin	0.35	0.13
tRNA (guanosine(18)-2	1.04	0.31
Proteasome subunit al	6.37	0.87
Hypoxanthine-guanine	15.09	1.21
Glycerol-3-phosphate	1.34	0.37
Sphingosine-1-phospha	1.72	0.43
Mitochondrial escape	2.22	0.51
Nucleoporin NUP85 OS	0.56	0.19
Synaptobrevin homolo	16.58	1.25
E3 ubiquitin-protein lig	2.38	0.53
Small COPII coat GTPas	4.69	0.76

Alanine/arginine amin	1.63	0.42
Very long-chain fatty a	1.21	0.34
Mitochondrial protein	2.87	0.59
NADP-dependent alco	4.80	0.76
Adenylyl cyclase-associ	1.67	0.43
Nicotinate phosphorib	3.65	0.67
Alpha-1,2-mannosyltra	1.01	0.30
Transcription elongati	0.70	0.23
Acetyl-CoA hydrolase	2.60	0.56
26S proteasome regula	2.47	0.54
Myo-inositol transport	0.45	0.16
Nucleoporin NUP120	1.10	0.32
26S proteasome regula	3.67	0.67
Succinate dehydrogena	2.32	0.52
DNA-directed RNA pol	0.86	0.27
RNA annealing protein	6.88	0.90
Tyrosine--tRNA ligase,	3.45	0.65
U3 small nucleolar RN	2.40	0.53
Hsp90 co-chaperone A	3.16	0.62
26S protease regulator	1.46	0.39
ER-derived vesicles pr	0.31	0.12
T-complex protein 1 su	1.08	0.32
A-factor-processing en	0.75	0.24
Sulfite reductase [NAD	0.51	0.18
Chromatin structure-re	1.63	0.42
Uncharacterized PH do	1.02	0.31
U3 small nucleolar RN	0.80	0.26
m7GpppX diphosphata	2.97	0.60
Dynamin-like GTPase	0.94	0.29
Serine palmitoyltransf	2.03	0.48
Serine/threonine-prot	1.23	0.35
Importin subunit beta-	0.72	0.24
5-oxoprolinase OS=Sac	1.23	0.35
Glycogen [starch] synt	0.90	0.28
40S ribosomal protein	5.15	0.79
Uncharacterized protei	1.11	0.32
Putative reductase 1 O	4.78	0.76
Carboxypeptidase S OS	1.23	0.35
Ribosome biogenesis p	0.84	0.26
Fumarate reductase 1	2.99	0.60
Tryptophan--tRNA liga	2.78	0.58
Importin beta SMX1 O	0.92	0.28
Argininosuccinate lyas	1.47	0.39
Mitochondrial outer m	0.58	0.20
Saccharolysin OS=Sacc	1.51	0.40
Protein TMA108 OS=Sa	1.10	0.32
Ribosome assembly pr	0.93	0.29
Uncharacterized phosp	5.47	0.81
GTP-binding protein Y	7.10	0.91
4-nitrophenylphosphat	4.05	0.70
Alcohol dehydrogenas	1.00	0.30
Phospho-2-dehydro-3-	2.48	0.54

Protein BFR2 OS=Sacch	1.16	0.33
Nucleoporin NUP84 OS	1.08	0.32
Protein MRH1 OS=Sacc	0.90	0.28
Meiotic sister chromat	2.03	0.48
2-dehydropantoate 2-r	1.97	0.47
Cysteine proteinase 1,	1.77	0.44
Ribosomal RNA-proces	1.95	0.47
D-3-phosphoglycerate	2.01	0.48
Protoplast secreted pro	3.76	0.68
Dihydroorotate dehydr	5.57	0.82
Mitochondrial interme	1.31	0.36
E3 ubiquitin-protein lig	0.37	0.14
Dolichyl-diphosphoolig	0.89	0.28
Translation machinery-	1.80	0.45
60S ribosomal protein	8.74	0.99
Cerevisin OS=Saccharo	0.72	0.24
60S ribosomal protein	7.12	0.91
Vacuolar aminopeptida	0.93	0.29
U3 small nucleolar RNA	1.19	0.34
Protein APA1 OS=Sacch	6.71	0.89
Cargo-transport protei	1.20	0.34
Multisubstrate pseudo	0.73	0.24
Mitochondrial distribut	1.96	0.47
Ribonucleoside-diphos	0.60	0.20
D-3-phosphoglycerate	2.01	0.48
Ras-like protein 2 OS=S	2.87	0.59
Fumarate hydratase, m	1.41	0.38
26S proteasome regula	1.12	0.33
ATP-dependent RNA he	0.81	0.26
ATP-dependent RNA he	1.06	0.31
Proliferating cell nucle	4.90	0.77
Phospholipid:diacylglyc	0.75	0.24
Protein phosphatase 2	2.99	0.60
Guanosine-diphosphat	0.93	0.29
6,7-dimethyl-8-ribityllu	6.41	0.87
Essential nuclear prote	1.16	0.33
6-phosphogluconolacto	4.35	0.73
Small glutamine-rich te	3.54	0.66
Exosome complex exor	0.66	0.22
Glutathione reductase	2.42	0.53
Tricalbin-1 OS=Sacchar	0.58	0.20
Uncharacterized protei	7.23	0.92
Heat shock protein 26	6.12	0.85
Maintenance of telome	0.56	0.19
Coronin-like protein OS	1.19	0.34
60S acidic ribosomal pr	4.56	0.75
GPI transamidase comp	1.34	0.37
Vacuolar protein sortin	0.61	0.21
Ribosome biogenesis p	1.24	0.35
Polyamine N-acetyltrar	14.71	1.20
Single-stranded nucleic	5.34	0.80
GTP-binding protein YP	4.54	0.74

Ribose-phosphate pyro	1.62	0.42
Mitochondrial respirat	1.48	0.39
Oxysterol-binding prot	1.35	0.37
F-actin-capping protei	1.91	0.46
mRNA 3~-end-processi	1.02	0.31
Ran-specific GTPase-ac	2.38	0.53
40S ribosomal protein	2.86	0.59
Actin cytoskeleton-regu	0.37	0.14
Ubiquitin carboxyl-term	3.50	0.65
Histone H2B.1 OS=Sacc	6.12	0.85
Cytochrome b-c1 comp	1.26	0.35
Uncharacterized protei	1.12	0.33
Lon protease homolog,	0.68	0.23
Proteasome subunit al	4.61	0.75
Uncharacterized memb	1.28	0.36
ATP-dependent RNA he	1.23	0.35
Nucleoporin NUP145 C	0.43	0.16
Peroxiredoxin HYR1 OS	3.45	0.65
Carboxypeptidase Y OS	0.60	0.20
Mitochondrial presequ	0.66	0.22
Alpha-soluble NSF atta	2.10	0.49
Proteasome subunit be	6.19	0.86
Pre-rRNA-processing p	1.13	0.33
RNA polymerase II deg	0.25	0.10
Heat shock protein SSC	1.34	0.37
Proteasome subunit al	4.12	0.71
EH domain-containing	0.46	0.16
Nuclear and cytoplasm	0.74	0.24
Glycerol-3-phosphate (	1.08	0.32
Antiviral helicase SKI2 (	0.79	0.25
Multiple RNA-binding c	0.52	0.18
60S acidic ribosomal pr	0.54	0.19
Myosin-5 OS=Saccharo	0.19	0.08
Elongation factor G, mi	2.39	0.53
Branched-chain-amino	2.44	0.54
Inactive diphosphatase	2.16	0.50
Saccharopine dehydrog	2.47	0.54
Serine/threonine-prote	3.69	0.67
Guanine nucleotide-ex	1.73	0.44
Malate dehydrogenase	4.56	0.75
Peroxisomal-coenzyme	2.47	0.54
26S proteasome regula	1.87	0.46
Carboxypeptidase Y inh	2.83	0.58
Protein transport prote	3.12	0.61
Chromatin structure-re	1.84	0.45
Spindle assembly checl	0.80	0.26
Importin alpha re-expo	0.91	0.28
Glutamate decarboxyla	1.71	0.43
Dolichyl-diphosphoolig	1.84	0.45
Protein phosphatase P	1.21	0.34
Thioredoxin-1 OS=Sacc	10.60	1.06
Long-chain-fatty-acid--	0.83	0.26

ATP-dependent RNA he	0.92	0.28
Poly(A) polymerase OS	1.57	0.41
Cytochrome b-c1 comp	0.93	0.29
Calcium-transporting A	0.64	0.21
RNA cytidine acetyltran	0.67	0.22
60S ribosomal protein	8.80	0.99
Low-affinity glucose tra	0.80	0.26
Glucosidase 2 subunit l	0.90	0.28
60S ribosomal protein	2.03	0.48
ATP-dependent helicas	0.53	0.18
Peroxiredoxin TSA2 OS	2.63	0.56
RNA-binding protein SF	0.80	0.26
Ribose-5-phosphate iso	2.77	0.58
D-arabinono-1,4-lacton	1.20	0.34
Protein SLA2 OS=Sacch	0.54	0.19
Putative zinc metallopr	1.07	0.32
Translation initiation fa	0.59	0.20
DNA polymerase alpha	0.71	0.23
Superkiller protein 3 O.	0.58	0.20
UPF0160 protein YER1!	1.66	0.42
3-hydroxyanthranilate	14.37	1.19
SWI/SNF complex subu	0.94	0.29
Protein TOM71 OS=Sac	1.06	0.31
Rab GDP-dissociation ii	2.60	0.56
Hsp90 co-chaperone H	4.03	0.70
Translation machinery-	3.97	0.70
ATP-dependent RNA he	2.19	0.50
26S proteasome regula	1.98	0.47
Prenylated Rab accepto	3.20	0.62
RuvB-like protein 2 OS=	1.49	0.40
T-complex protein 1 su	1.13	0.33
SRP-independent targe	6.28	0.86
Reduced viability upon	5.38	0.80
Sterol 24-C-methyltran	1.64	0.42
Serine/threonine-prote	1.14	0.33
Endoplasmic reticulum	1.77	0.44
Meiotic sister-chromat	1.28	0.36
Histidinol-phosphate a	2.70	0.57
La protein homolog OS	3.30	0.63
U3 small nucleolar RNA	1.30	0.36
Adenine phosphoribosy	1.47	0.39
V-type proton ATPase s	5.25	0.80
Transaminated amino a	1.06	0.31
Pro-apoptotic serine pr	0.53	0.18
Probable intramembra	0.87	0.27
Lactoylglutathione lyas	0.87	0.27
AMP deaminase OS=Sa	0.50	0.18
Vacuolar transporter cl	0.80	0.26
ATP synthase subunit 4	1.39	0.38
Glycerol 2-dehydrogen	2.33	0.52
V-type proton ATPase s	1.28	0.36
5~-3~ exoribonuclease	0.50	0.18

Multifunctional tryptop	1.62	0.42
Thiosulfate sulfurtrans	3.50	0.65
Delta-aminolevulinic ac	1.68	0.43
ATP-dependent RNA he	0.26	0.10
Probable hydrolase NIT	1.05	0.31
GTP-binding protein YF	1.15	0.33
Beta-glucan synthesis-a	0.34	0.13
Glutaredoxin-1 OS=Sac	12.59	1.13
Zinc finger protein ZPR	1.14	0.33
Protein-glutamate O-m	2.08	0.49
Heterogeneous nuclea	1.47	0.39
Citrate/oxoglutarate ca	1.28	0.36
tRNA (guanine(26)-N(2	1.40	0.38
Chorismate mutase OS	4.64	0.75
Casein kinase I homolo	1.14	0.33
GPI transamidase comp	1.12	0.33
Protein transport prote	0.90	0.28
FK506-binding protein	0.54	0.19
Vacuolar protein 8 OS=	1.25	0.35
Transketolase 2 OS=Sa	0.87	0.27
Ribosome-interacting (	2.50	0.54
26S proteasome regula	2.01	0.48
Transcription initiation	0.41	0.15
LOG family protein YJL(	4.65	0.75
26S protease regulator	1.43	0.39
GTP-binding protein RH	3.03	0.61
Vesicle-associated mer	1.84	0.45
ADP-ribosylation factor	0.93	0.29
40S ribosomal protein	15.94	1.23
Translation machinery-	2.98	0.60
Eukaryotic translation i	3.18	0.62
Proteasome subunit alp	3.37	0.64
Glutathione-independe	2.58	0.55
rRNA 2~-O-methyltrans	2.89	0.59
ADP-ribose pyrophospl	2.48	0.54
Isocitrate dehydrogena	1.31	0.36
60S ribosomal protein	14.47	1.19
Nuclear GTP-binding pr	0.77	0.25
UPF0001 protein YBL03	3.96	0.70
Protein arginine N-met	3.55	0.66
Putative pyridoxal redu	2.36	0.53
Protein HGH1 OS=Sacc	0.68	0.23
Protein RMD9, mitocho	0.88	0.27
Homoserine kinase OS=	1.32	0.37
Protein BZZ1 OS=Sacch	0.81	0.26
ATP-dependent clpX-lik	1.65	0.42
Proteasome subunit be	4.69	0.76
Proteasome subunit be	1.42	0.38
Homocysteine S-methy	1.77	0.44
Epsin-3 OS=Saccharom	0.69	0.23
Inosine triphosphate p	2.57	0.55
Sedoheptulose 1,7-bisp	3.51	0.65

Protein OS-9 homolog	0.47	0.17
Malate dehydrogenase	1.42	0.38
L-asparaginase 1 OS=Sa	1.19	0.34
General transcriptional	0.94	0.29
Leukotriene A-4 hydrol	0.95	0.29
Cytosine deaminase O	3.79	0.68
Methionine aminopept	1.35	0.37
Periodic tryptophan pr	0.65	0.22
UDP-N-acetylglucosam	1.20	0.34
Cell division control pr	1.68	0.43
Carbon catabolite-dere	0.58	0.20
Dihydroorotase OS=Sa	1.25	0.35
Phosphatidylinositol 4,	0.35	0.13
SED5-binding protein 2	0.46	0.16
Seventh homolog of se	0.57	0.20
Proteasome subunit be	2.73	0.57
Protein HMF1 OS=Sacc	6.34	0.87
Nuclear control of ATP	1.07	0.32
Protein kinase MCK1 O	1.38	0.38
40S ribosomal protein	5.15	0.79
Alpha-1,2 mannosyltra	2.06	0.49
Tropomyosin-1 OS=Sac	5.00	0.78
ATP-dependent RNA h	1.25	0.35
DNA mismatch repair	0.61	0.21
RNA polymerase-assoc	1.05	0.31
Coatomer subunit delt	0.86	0.27
Alkylphosphocholine r	0.81	0.26
N-terminal acetyltrans	0.58	0.20
Rho-GTPase-activating	0.33	0.12
S-adenosyl-L-methioni	0.44	0.16
Ubiquitin-conjugating	2.88	0.59
Co-chaperone protein	1.18	0.34
Bromodomain-contain	0.96	0.29
Probable dipeptidyl pe	0.69	0.23
Actin cytoskeleton-reg	0.27	0.10
Pyridoxamine 5~-phos	3.78	0.68
Sec sixty-one protein h	0.70	0.23
Ribosome-interacting	1.51	0.40
Nucleolar complex pro	0.95	0.29
Glucan 1,3-beta-glucos	1.61	0.42
GTP-binding protein Y	3.08	0.61
26S proteasome regula	3.75	0.68
Cell division control pr	0.83	0.26
Glucose-repressible alc	0.56	0.19
Vacuolar protein sortin	5.15	0.79
Protein MSN5 OS=Sacc	0.39	0.14
Proteasome subunit be	2.59	0.56
ATPase GET3 OS=Sacch	3.66	0.67
RuvB-like protein 1 OS	0.92	0.28
tRNA (guanine-N(7)-)-	0.52	0.18
40S ribosomal protein	6.36	0.87
Cell wall protein ECM3	0.54	0.19

Broad-specificity phosp	2.48	0.54
Uridylate kinase OS=Sa	10.27	1.05
Peptidyl-prolyl cis-tran	3.20	0.62
Protein phosphatase 1	1.63	0.42
Mitochondrial phospha	1.71	0.43
Peptidyl-prolyl cis-tran	3.07	0.61
MICOS complex subuni	0.71	0.23
Nucleosome assembly	1.42	0.38
5~-AMP-activated prot	1.79	0.45
ER-derived vesicles prc	0.34	0.13
Proteasome subunit be	2.48	0.54
Uncharacterized protei	0.43	0.16
NGG1-interacting factc	2.72	0.57
Bud site selection prot	1.37	0.37
Glutamine-dependent	0.68	0.23
Inositol hexakisphosph	0.39	0.14
Large subunit GTPase 1	0.79	0.25
ATP-dependent RNA h	0.49	0.17
Importin beta-like prot	0.37	0.14
Flavoprotein-like prote	2.45	0.54
Probable proteasome s	1.83	0.45
Golgi SNAP receptor cc	2.01	0.48
Nucleoporin NUP57 OS	0.64	0.21
Proteasome subunit be	1.78	0.44
4-aminobutyrate amin	1.42	0.38
Tropomyosin-2 OS=Sac	2.40	0.53
ERAD-associated E3 ub	0.56	0.19
ATP-dependent (S)-NA	0.64	0.21
U3 small nucleolar RN/	0.40	0.15
26S proteasome regula	1.80	0.45
Elongation factor Tu, n	0.99	0.30
Autophagy-related pro	1.92	0.47
Pyruvate dehydrogena	1.02	0.31
Elongation of fatty acic	0.27	0.10
Cruciform DNA-recogn	0.74	0.24
High-affinity hexose tr	0.45	0.16
Putative carboxymethy	0.83	0.26
Protein YOP1 OS=Sacch	0.59	0.20
UV excision repair prot	1.17	0.34
Glucose-signaling factc	1.27	0.36
E4 ubiquitin-protein lig	0.47	0.17
Nuclear migration prot	0.09	0.04
Putative magnesium-d	3.88	0.69
Suppressor of kinetoch	1.31	0.36
Enolase-phosphatase E	2.05	0.48
Valine/tyrosine/trypto	0.23	0.09
Prefoldin subunit 3 OS	1.23	0.35
Methylenetetrahydrof	0.98	0.30
Endoplasmic reticulum	2.88	0.59
Methionine aminopept	0.81	0.26
Family of serine hydrol	4.54	0.74
FK506-binding protein	3.56	0.66

ABC1 family protein M	0.53	0.18
AP-2 complex subunit	0.57	0.20
Ribose-phosphate pyr	1.89	0.46
Ribose-phosphate pyr	0.81	0.26
GTPase-activating prot	0.21	0.08
U3 small nucleolar RN	0.76	0.25
Protein PBN1 OS=Sacc	0.80	0.26
1,3-beta-glucanosyltra	0.31	0.12
Branched-chain-amino	0.71	0.23
3,4-dihydroxy-2-butan	4.15	0.71
Nuclear protein localiz	0.65	0.22
Phosphoribosylglycina	2.25	0.51
Mitochondrial outer m	0.37	0.14
WD repeat-containing	0.81	0.26
Endosomal protein P2	1.71	0.43
Ribonucleases P/MRP	0.39	0.14
mRNA export factor M	1.01	0.30
Spindle pole body com	0.34	0.13
S-(hydroxymethyl)glut	1.46	0.39
Ubiquitin carboxyl-terr	0.25	0.10
RNA polymerase II-ass	1.07	0.32
DNA topoisomerase 2-	0.45	0.16
Phosphoacetylglucosa	0.69	0.23
Pre-mRNA-processing	1.10	0.32
Ribosome assembly fa	1.82	0.45
UPF0659 protein YMR	4.41	0.73
E3 ubiquitin-protein lig	0.26	0.10
Methylenetetrahydrof	1.46	0.39
Glutathione peroxidas	3.49	0.65
Transcription initiation	1.26	0.35
Histone deacetylase H	0.42	0.15
Rho GDP-dissociation i	4.07	0.71
Peroxiredoxin DOT5 O	1.17	0.34
Prefoldin subunit 5 OS	3.57	0.66
Protein RFS1 OS=Sacch	2.38	0.53
Glyoxylate reductase 1	1.32	0.37
Proteasome activator	0.26	0.10
Phosphorelay interme	1.07	0.32
AP-3 complex subunit	0.55	0.19
Protein PBP4 OS=Sacc	2.22	0.51
Nicotinate-nucleotide	1.72	0.43
Exocyst complex comp	0.57	0.20
ATP-dependent RNA h	0.23	0.09
Cytochrome P450 61	0.70	0.23
Peptide methionine su	4.74	0.76
Protein phosphatase 2	0.72	0.24
Uncharacterized protei	0.82	0.26
26S protease regulator	1.16	0.33
Chromatin structure-re	0.32	0.12
UBX domain-containin	1.23	0.35
Deoxyuridine 5~-triph	3.57	0.66
1-(5-phosphoribosyl)-5	3.10	0.61

Fatty aldehyde dehydr	0.73	0.24
Uncharacterized protei	0.49	0.17
Monothiol glutaredoxi	1.28	0.36
Survival factor 1 OS=Sa	0.41	0.15
U1 SNP1-associating pr	0.41	0.15
Protein arginine N-met	0.80	0.26
GTP-binding protein RH	3.29	0.63
60S ribosomal export p	0.74	0.24
Lanosterol 14-alpha de	0.72	0.24
Regulation of enolase p	1.90	0.46
ER-retained PMA1-sup	0.41	0.15
Myosin-4 OS=Saccharo	0.15	0.06
tRNA (cytidine(32)-2~-(	0.26	0.10
Ribosome biogenesis p	0.36	0.13
Exopolyphosphatase O	1.55	0.41
Protein KRI1 OS=Sacch	0.62	0.21
LAS seventeen-binding	0.42	0.15
DNA-directed RNA poly	1.32	0.37
GTP-binding protein YP	3.16	0.62
Superoxide dismutase	1.76	0.44
Exocyst complex comp	0.25	0.10
Protein MMF1, mitoch	4.75	0.76
Protein DOM34 OS=Sa	1.11	0.32
Restriction of telomere	3.69	0.67
Pre-rRNA-processing p	0.70	0.23
Endoplasmic reticulum	0.82	0.26
Suppressor of yeast pr	0.48	0.17
Protein FMP25, mitoch	0.52	0.18
Glutamate 5-kinase OS	0.49	0.17
Protein-lysine N-methy	1.65	0.42
NADPH-dependent ald	1.08	0.32
Helicase SEN1 OS=Sacc	0.18	0.07
Probable family 17 gluc	0.59	0.20
Dolichyl-phosphate-ma	0.31	0.12
Exocyst complex comp	0.28	0.11
Regulator of Ty1 transp	1.03	0.31
Nucleolar protein 13 O	0.51	0.18
Coatomer subunit epsi	0.74	0.24
Citrate synthase, perox	0.73	0.24
KH domain-containing	0.28	0.11
Protein SDA1 OS=Sacch	0.39	0.14
Ribosome biogenesis p	1.07	0.32
Aspartokinase OS=Sacc	1.06	0.31
F-actin-capping protein	1.37	0.37
Actin-related protein 2	0.61	0.21
ADP-ribosylation factor	1.04	0.31
Coatomer subunit zeta	4.64	0.75
Benzil reductase ((S)-be	2.11	0.49
Ribosomal RNA-proces	0.23	0.09
Mannan polymerase I c	0.36	0.13
THO complex subunit H	0.38	0.14
Golgi to ER traffic prote	0.91	0.28

Importin subunit beta-	0.31	0.12
Transcription initiation	0.28	0.11
Oxygen-dependent cop	0.86	0.27
ARF guanine-nucleotid	0.22	0.09
Protein ERP2 OS=Sacch	1.17	0.34
Diphthine methyl ester	2.02	0.48
Nucleolar protein 12 O	1.26	0.35
Transcription factor SP	0.24	0.09
Protein YRO2 OS=Sacch	0.44	0.16
Reduced viability upon	0.71	0.23
ISWI one complex prot	0.42	0.15
Serine/threonine-prote	1.49	0.40
6-phosphogluconolact	0.97	0.29
Ubiquitin-like protein	1.68	0.43
DNA damage-inducible	0.81	0.26
UPF0662 protein YPL26	0.69	0.23
Purine nucleoside phos	1.29	0.36
Aldehyde dehydrogena	0.28	0.11
Fumarate reductase 2	0.53	0.18
Riboflavin synthase OS	1.43	0.39
ATP-dependent perme	0.36	0.13
Dolichol-phosphate ma	2.42	0.53
Replication factor C sul	0.49	0.17
V-type proton ATPase	1.62	0.42
Protein SLY1 OS=Sacch	0.66	0.22
Glucosamine 6-phosph	4.95	0.77
Endoplasmic reticulum	1.22	0.35
Protein TED1 OS=Sacch	1.35	0.37
E3 ubiquitin-protein lig	0.23	0.09
Phosphatidylinositol tr	0.49	0.17
Mitochondrial peroxire	1.59	0.41
Uncharacterized protei	0.33	0.12
Protein transport prote	0.50	0.18
ATP synthase subunit	2.42	0.53
Transcription factor PD	0.36	0.13
ATP-dependent perme	0.25	0.10
ISWI one complex prot	0.97	0.29
DNA polymerase V OS=	0.22	0.09
Probable secreted beta	0.46	0.16
Pre-mRNA-splicing fact	0.37	0.14
Histone deacetylase H	0.19	0.08
Phosphate metabolism	0.28	0.11
Uncharacterized protei	0.78	0.25
3~(2~),5~-bisphosphat	0.81	0.26
Protein SDS24 OS=Sacc	0.51	0.18
Mannan endo-1,6-alph	0.33	0.12
DNA-binding protein R	0.23	0.09
CDP-diacylglycerol--inc	0.75	0.24
Protein LSM12 OS=Sac	3.65	0.67
Ribosome biogenesis p	0.37	0.14
Vacuolar-sorting prote	0.19	0.08
Probable ATP-depende	0.40	0.15

Eukaryotic translation i	1.02	0.31
Uncharacterized ATP-d	0.21	0.08
Protein disulfide-isome	0.75	0.24
Probable 26S proteaso	1.48	0.39
Protein PAM1 OS=Sacc	0.36	0.13
Mitochondrial import i	0.54	0.19
Cyclin-dependent kinas	0.98	0.30
2-deoxyglucose-6-phos	0.99	0.30
GTP cyclohydrolase 1 C	2.83	0.58
Glycylpeptide N-tetrad	0.70	0.23
Non-classical export pr	1.07	0.32
N-terminal acetyltransf	1.33	0.37
Probable proline--tRNA	0.42	0.15
Casein kinase II subunit	0.61	0.21
Isopentenyl-diphospha	0.32	0.12
Acetolactate synthase	1.28	0.36
tRNA pseudouridine sy	0.57	0.20
Polyphosphatidylinosit	0.25	0.10
Uncharacterized protei	1.88	0.46
Translation initiation fa	0.94	0.29
Acyl-CoA desaturase 1	0.38	0.14
Probable ATP-depende	1.02	0.31
Ubiquitin carboxyl-terr	0.26	0.10
Prefoldin subunit 4 OS=	2.40	0.53
Protein YGP1 OS=Sacch	0.29	0.11
Replication factor A pro	0.36	0.13
Ubiquitin-like protein S	1.23	0.35
Phosphoglycerate muta	1.18	0.34
Eukaryotic initiation fac	0.15	0.06
Probable oxidoreducta	0.42	0.15
Transcription factor SP	0.52	0.18
Mitogen-activated prot	0.33	0.12
Cytochrome B pre-mRN	0.29	0.11
Hit family protein 1 OS	3.84	0.68
Protein AIM2 OS=Sacch	1.36	0.37
Enhancer of translation	0.49	0.17
Glycogen debranching	0.14	0.06
Phosphopantothenate-	0.96	0.29
Golgin IMH1 OS=Sacch	0.20	0.08
26S protease subunit R	0.77	0.25
Pantoate--beta-alanine	1.23	0.35
Cap-associated protein	0.29	0.11
Oxysterol-binding prot	0.94	0.29
Uncharacterized oxidor	0.98	0.30
Pre-tRNA-processing p	0.24	0.09
Phospholipid-transport	0.08	0.03
Actin-related protein 5	0.31	0.12
t-SNARE VTI1 OS=Sacch	0.77	0.25
Phospholipid-transport	0.08	0.03
Sodium transport ATPa	0.12	0.05
Coenzyme A biosynthe	0.54	0.19
HMG2-induced ER-rem	0.27	0.10

ATP synthase subunit c	1.03	0.31
27S pre-rRNA (guanosi	0.55	0.19
Ubiquitin-conjugating e	0.75	0.24
6-phosphogluconolacto	0.48	0.17
Protein ERP1 OS=Sacch	1.56	0.41
Methylthioribose-1-ph	0.87	0.27
Xanthine phosphoribos	1.20	0.34
Protein SVP26 OS=Sacc	0.70	0.23
Uncharacterized protei	0.38	0.14
HDA1 complex subunit	0.45	0.16
Cell wall protein YJL17	0.38	0.14
Protein BCP1 OS=Sacch	0.33	0.12
Pore membrane protei	0.34	0.13
Diphosphoinositol poly	1.36	0.37
Lethal(2) giant larvae p	0.13	0.05
UPF0587 protein YCR0	1.42	0.38
Hydroxyacylglutathion	1.82	0.45
Ribosome quality contr	0.22	0.09
DNA replication licensi	0.19	0.08
GPN-loop GTPase 1 OS	0.54	0.19
Probable kynurenine--	0.60	0.20
Probable quinone oxid	0.66	0.22
H/ACA ribonucleoprote	0.91	0.28
Mitochondrial respirat	0.40	0.15
Endoribonuclease YSH	0.17	0.07
Chromatin structure-re	0.43	0.16
DNA topoisomerase 2	0.06	0.03
Prohibitin-1 OS=Saccha	0.82	0.26
Cell division control pro	0.91	0.28
Casein kinase II subuni	0.37	0.14
Mannan polymerase II	0.63	0.21
Actin-related protein 3	0.33	0.12
Succinate--CoA ligase [	0.35	0.13
UPF0061 protein FMP4	0.35	0.13
Putative uncharacteriz	1.90	0.46
Sm-like protein LSm1 C	1.51	0.40
S-formylglutathione hy	0.99	0.30
Shuttling pre-60S facto	0.80	0.26
Transcription factor ta	0.47	0.17
Glutaredoxin-2, mitoch	2.21	0.51
Choline-phosphate cyti	0.94	0.29
Serine/threonine-prote	0.28	0.11
Probable mannosyltran	0.41	0.15
cAMP-dependent prote	0.82	0.26
Uncharacterized glycos	0.28	0.11
Exosome complex exon	0.23	0.09
DNA repair helicase RA	0.44	0.16
Probable diacetyl redu	0.50	0.18
Mannan polymerase co	0.67	0.22
Histone chaperone RTT	0.44	0.16
Rab proteins geranylge	0.32	0.12
Lysophospholipase NTE	0.13	0.05

ATP-dependent rRNA h	0.61	0.21
Protein NRD1 OS=Sacc	0.44	0.16
Regulatory protein SW	0.37	0.14
Vacuolar import and d	0.24	0.09
tRNA(Thr) (cytosine(32	0.30	0.11
HD domain-containing	1.08	0.32
ISWI one complex prot	0.37	0.14
Importin subunit beta-	0.23	0.09
Altered inheritance of	0.23	0.09
Adenylate kinase isoen	0.84	0.26
Protein CAJ1 OS=Sacch	0.52	0.18
Pantothenate kinase C	0.41	0.15
CRAL-TRIO domain-cor	0.68	0.23
Ornithine decarboxyla	0.09	0.04
Hsp70 nucleotide exch	1.37	0.37
Ribosomal RNA-proces	0.59	0.20
CCR4-associated factor	0.76	0.25
Myosin-3 OS=Saccharo	0.10	0.04
Protein FMP52, mitoch	1.53	0.40
Protein YIP4 OS=Sacch	0.43	0.16
Ubiquitin carboxyl-terr	0.20	0.08
60S ribosome subunit	0.39	0.14
Uncharacterized isome	0.33	0.12
Succinate--CoA ligase [	0.71	0.23
FAD-linked sulfhydryl c	1.31	0.36
40S ribosomal protein	5.86	0.84
Nuclear polyadenylate	0.48	0.17
RNA polymerase-assoc	0.16	0.06
Protein SNQ2 OS=Sacc	0.18	0.07
DNA-directed RNA poly	0.21	0.08
Uncharacterized peptic	0.46	0.16
37S ribosomal protein	0.30	0.11
Histone H4 OS=Saccha	2.41	0.53
Protein BNI1 OS=Sacch	0.07	0.03
Superoxide dismutase	1.07	0.32
Translation initiation f	0.39	0.14
Ankyrin repeat-contain	1.31	0.36
(R,R)-butanediol dehyc	0.75	0.24
Protein-lysine N-methy	0.63	0.21
Conserved oligomeric	0.16	0.06
Suppressor protein SR	0.58	0.20
Prephenate dehydroge	0.32	0.12
Retrograde regulation	0.33	0.12
Thiosulfate sulfurtrans	7.26	0.92
4-hydroxy-4-methyl-2-	1.49	0.40
Anthranilate phosphor	0.40	0.15
Peroxisomal membran	1.00	0.30
Uncharacterized protei	0.49	0.17
Translation initiation f	0.15	0.06
Epsin-2 OS=Saccharom	0.58	0.20
Nonsense-mediated m	0.22	0.09
Kinesin-related protein	0.14	0.06

U6 snRNA-associated S	1.41	0.38
Protein HIR2 OS=Sacch	0.21	0.08
Protein kinase-like prot	0.23	0.09
DNA replication licensi	0.20	0.08
Rotenone-insensitive N	0.28	0.11
Phosphatidate cytidyly	0.43	0.16
Uncharacterized protei	1.42	0.38
6-phosphogluconolacto	1.26	0.35
Cell wall mannoprotein	0.31	0.12
Mitochondrial GTP/GD	1.03	0.31
Uncharacterized GTP-b	0.36	0.13
Pre-mRNA-splicing fact	0.13	0.05
Exocyst complex comp	0.30	0.11
Protein TOS1 OS=Sacch	0.21	0.08
MAU2 chromatid cohe	0.21	0.08
Probable electron trans	0.92	0.28
RNA annealing protein	0.48	0.17
Cytochrome c peroxida	1.01	0.30
Probable tubulin--tyros	0.06	0.03
ATP synthase subunit g	0.51	0.18
Nucleoporin NUP133 O	0.24	0.09
Protein transport prote	0.43	0.16
Aspartyl aminopeptida	0.19	0.08
Protein ZEO1 OS=Sacch	3.39	0.64
AP-1 complex subunit g	0.35	0.13
Actin-like protein ARP8	0.15	0.06
Ras-like protein 1 OS=S	0.50	0.18
Actin-related protein 2	0.97	0.29
Spindle pole body asse	0.35	0.13
3~,5~-cyclic-nucleotide	0.17	0.07
1,2-dihydroxy-3-keto-5	1.43	0.39
Activator of stress gene	0.24	0.09
Kynureninase OS=Sacch	0.20	0.08
Ribosome biogenesis p	0.57	0.20
Putative uncharacterize	0.25	0.10
Transcription regulator	0.16	0.06
1,4-alpha-glucan-branc	0.42	0.15
60S ribosomal protein	1.75	0.44
Conserved oligomeric G	0.22	0.09
NADH-cytochrome b5 r	0.73	0.24
Transcriptional regulat	0.21	0.08
D-2-hydroxyglutarate--	0.27	0.10
tRNA acetyltransferase	0.74	0.24
Arginine biosynthesis b	0.63	0.21
Repressible alkaline ph	0.45	0.16
Protein EMP47 OS=Sac	0.45	0.16
Glutathione synthetase	0.52	0.18
ADP-ribosylation factor	2.14	0.50
Nucleoporin ASM4 OS=	0.38	0.14
ADP-ribosylation factor	0.67	0.22
Nuclear polyadenylated	0.23	0.09
Regulator of calcineurin	0.38	0.14

Ankyrin repeat-contain	0.76	0.25
Vacuolar protein sortin	0.43	0.16
Chromatin structure-re	0.26	0.10
Ribose-phosphate pyro	0.92	0.28
Aminomethyltransfera	0.70	0.23
DNA-directed RNA poly	0.78	0.25
DNA damage-binding p	0.27	0.10
Protein transport prote	0.67	0.22
Phosphatidyl-N-methyl	1.23	0.35
RHO1 GDP-GTP exchan	0.10	0.04
Probable alpha-1,6-ma	0.49	0.17
Ankyrin repeat-contain	1.52	0.40
Uncharacterized protei	0.09	0.04
Enhancer of mRNA-dec	0.36	0.13
12 kDa heat shock prot	3.90	0.69
Mediator of RNA polym	0.43	0.16
Kinetochore protein SL	0.28	0.11
Nucleoporin POM152 (	0.10	0.04
Importin beta-like prot	0.12	0.05
Dolichyl-diphosphoolig	0.46	0.16
DNA mismatch repair p	0.07	0.03
Phosducin-like protein	0.33	0.12
Protein NNF2 OS=Saccl	0.09	0.04
Altered inheritance rat	0.66	0.22
Protein SCD6 OS=Sacch	0.43	0.16
Protein EFR3 OS=Sacch	0.30	0.11
Phosphoserine phosph	0.72	0.24
Ubiquitin-activating en	0.39	0.14
Minichromosome mair	0.31	0.12
Protein STU1 OS=Sacch	0.06	0.03
Clathrin light chain OS=	0.70	0.23
DNA replication licensi	0.15	0.06
Lanosterol synthase OS	0.25	0.10
ADP-ribosylation facto	0.33	0.12
DNA ligase 1 OS=Sacch	0.32	0.12
Protein BCH1 OS=Saccl	0.19	0.08
Actin-related protein 4	0.29	0.11
Protein AIM7 OS=Sacch	1.26	0.35
Phosphatidylglycerol/p	0.62	0.21
Glutamate--cysteine lig	0.20	0.08
AP-1 complex subunit	0.26	0.10
UPF0674 endoplasmic	0.65	0.22
Squalene synthase OS=	0.31	0.12
EKC/KEOPS complex su	2.07	0.49
Origin recognition com	0.30	0.11
Protein transport prote	1.15	0.33
Uncharacterized protei	0.87	0.27
Ubiquitin-conjugating e	0.76	0.25
Glucose-induced degra	0.12	0.05
Ribose-phosphate pyro	0.71	0.23
Vacuolar import and de	0.15	0.06
Putative metallocarbox	0.33	0.12

Exosome complex com	0.24	0.09
Protein SSO1 OS=Sacch	0.53	0.18
V-type proton ATPase s	0.15	0.06
ARS-binding factor 2, m	2.68	0.57
Protein STU2 OS=Sacch	0.32	0.12
Cell cycle protein kinas	0.43	0.16
CCA tRNA nucleotidyltr	0.25	0.10
Dimethyladenosine tra	0.68	0.23
U6 snRNA-associated S	1.04	0.31
Essential for maintenan	0.32	0.12
Family of serine hydrol	0.36	0.13
Calcineurin subunit B C	1.59	0.41
Nuclear import protein	0.47	0.17
Exosome complex com	0.67	0.22
Non-histone chromoso	0.54	0.19
CTD kinase subunit alp	0.17	0.07
Transcription initiation	0.41	0.15
NADH-cytochrome b5 r	0.81	0.26
SWI5-dependent HO ex	0.18	0.07
3-hydroxy-3-methylglu	0.18	0.07
Vacuolar-sorting prote	0.16	0.06
Prefoldin subunit 6 OS=	1.84	0.45
ER-derived vesicles pro	0.35	0.13
Vacuolar protein sortin	0.34	0.13
Ubiquitin-like-specific p	0.22	0.09
Elongator complex pro	0.23	0.09
Outer spore wall prote	0.08	0.03
Protein transport prote	0.25	0.10
Thymidylate synthase (	0.31	0.12
Enoyl-[acyl-carrier prot	0.56	0.19
CTP synthase 2 OS=Sac	0.44	0.16
Serine/threonine-prote	0.08	0.03
tRNA ligase OS=Saccha	0.16	0.06
Protein CASP OS=Sacch	0.13	0.05
S-adenosylmethionine	0.35	0.13
Polyamine transporter	0.14	0.06
D-tyrosyl-tRNA(Tyr) de	0.74	0.24
Sugar transporter STL1	0.08	0.03
Oxysterol-binding prote	0.07	0.03
Mitochondrial import r	0.58	0.20
Hsp90 co-chaperone C	0.50	0.18
Kelch repeat-containin	0.37	0.14
Lipase 4 OS=Saccharom	0.10	0.04
Cell division control pro	0.18	0.07
Sporulation protein RM	0.06	0.03
Putative alanyl-tRNA ed	0.10	0.04
THO complex subunit 2	0.08	0.03
Transcription factor TF	0.23	0.09
Ubiquitin thioesterase	0.32	0.12
NAD-specific glutamate	0.12	0.05
Succinate dehydrogena	0.26	0.10
Protein SIP5 OS=Sacch	0.09	0.04

Heat shock protein 70	0.15	0.06
Negative cofactor 2 co	0.75	0.24
Pyruvate dehydrogena	0.11	0.05
Mediator of RNA poly	0.17	0.07
SWI5-dependent HO e	0.05	0.02
ATP-dependent RNA h	0.57	0.20
NAD(P)H-hydrate epim	0.66	0.22
DNA-directed RNA pol	0.45	0.16
Dol-P-Man:Man(7)Glc	0.46	0.16
NADPH-dependent 1-a	0.33	0.12
Poly(A) RNA polymera	0.15	0.06
tRNA (guanine-N(7)-)-	0.20	0.08
40S ribosomal protein	2.76	0.58
Ribosomal RNA small s	0.65	0.22
Cullin-8 OS=Saccharo	0.15	0.06
Aspartate--tRNA ligase	0.28	0.11
SWI/SNF chromatin-re	0.05	0.02
Lipase 3 OS=Saccharo	0.29	0.11
Heat shock protein 42	0.39	0.14
Thioredoxin reductase	0.29	0.11
Pheromone-processing	0.19	0.08
Ran-specific GTPase-ac	0.30	0.11
Peptidyl-prolyl cis-tran	0.74	0.24
AP-3 complex subunit	0.17	0.07
U3 small nucleolar RN	0.07	0.03
CAAX prenyl protease	0.31	0.12
SIT4-associating protei	0.13	0.05
Serine/threonine-prot	0.27	0.10
Mevalonate kinase OS	0.47	0.17
Protein SUR7 OS=Sacc	0.32	0.12
20S rRNA accumulatio	0.36	0.13
Anaphase-promoting c	0.14	0.06
Uncharacterized oxido	0.54	0.19
Geranylgeranyl transfe	0.61	0.21
Cohesin subunit SCC3	0.07	0.03
Isoamyl acetate-hydrol	0.19	0.08
Mitotic spindle checkp	0.87	0.27
High-affinity glucose tr	0.17	0.07
Elongation factor 1 alp	0.23	0.09
Ribosome biogenesis p	0.62	0.21
Nuclear transport fact	0.90	0.28
Translation initiation f	0.32	0.12
D-amino-acid N-acetyl	1.71	0.43
tRNA pseudouridine sy	0.11	0.05
Myosin tail region-inte	0.12	0.05
Mitochondrial import i	0.29	0.11
Membrane-anchored l	0.20	0.08
CDC25-like phosphata	1.24	0.35
Ribosome biogenesis p	0.47	0.17
Probable phospholipid	0.06	0.03
Actin-related protein 2	0.73	0.24
Protein phosphatase P	0.37	0.14

Very-long-chain 3-oxoa	0.27	0.10
Cyclin-dependent prot	0.50	0.18
Flap endonuclease 1 O	0.24	0.09
Nuclear protein STH1/	0.13	0.05
Pre-mRNA-splicing fact	0.12	0.05
Vacuolar membrane pr	0.19	0.08
Probable gluconokinas	0.52	0.18
Ino eighty subunit 1 OS	0.06	0.03
ATPase family gene 2 p	0.25	0.10
Restriction of telomere	0.16	0.06
Uncharacterized protei	0.38	0.14
Transcriptional activat	0.14	0.06
DNA polymerase delta	0.18	0.07
Actin-related protein 2	0.90	0.28
MIOREX complex comp	0.13	0.05
U2 snRNP component	0.14	0.06
Chromatin structure-re	0.10	0.04
Increased sodium toler	0.05	0.02
Probable serine/threor	0.21	0.08
Mitochondrial outer m	0.12	0.05
Vacuolar protein-sortir	0.50	0.18
Translation machinery-	2.07	0.49
Protein CWH43 OS=Sa	0.09	0.04
Actin patches distal pr	0.68	0.23
Serine/threonine-prote	0.07	0.03
Antiviral protein SKI8 C	0.11	0.05
Protein DOA1 OS=Sacc	0.19	0.08
Ubiquitin fusion degra	0.06	0.03
Free methionine-R-sulf	0.59	0.20
Regulator of ribosome	0.23	0.09
AP-3 complex subunit	0.53	0.18
26S protease regulator	0.48	0.17
Protein NAM8 OS=Sac	0.09	0.04
Respiratory growth ind	0.63	0.21
HDA1 complex subunit	0.28	0.11
tRNA wybutosine-synt	0.83	0.26
Eukaryotic translation i	1.11	0.32
ER degradation-enhan	0.11	0.05
Ribosome biogenesis p	0.32	0.12
RNA polymerase-assoc	0.30	0.11
AP-2 complex subunit	0.26	0.10
WD repeat-containing	0.10	0.04
Medium-chain fatty ac	0.20	0.08
AP-1 accessory protein	0.11	0.05
Protein SSO2 OS=Sacc	0.52	0.18
Replication factor C su	0.27	0.10
Signal recognition part	0.27	0.10
DNA-directed RNA pol	0.45	0.16
Glutathione S-transfer	0.69	0.23
Family of serine hydrol	0.21	0.08
Ribosome biogenesis p	0.15	0.06
Ribosome biogenesis p	0.20	0.08

20S-pre-rRNA D-site er	0.20	0.08
DnaJ-like chaperone JE	0.13	0.05
Calmodulin OS=Saccha	0.78	0.25
Homoisocitrate dehydr	0.26	0.10
ATP-dependent perme	0.06	0.03
Alpha-1,3-mannosyltra	0.17	0.07
ER membrane protein	0.55	0.19
Actin-related protein 2	1.03	0.31
Protein phosphatase 2	0.24	0.09
Probable 26S proteaso	0.46	0.16
Protein SOF1 OS=Sacch	0.18	0.07
Dipeptidyl aminopepti	0.16	0.06
U3 small nucleolar RN	0.09	0.04
UPF0303 protein YBR1	0.97	0.29
Probable glycosidase C	0.20	0.08
Synaptobrevin homolo	1.04	0.31
General negative regul	0.87	0.27
Vacuolar transporter c	0.90	0.28
Protein CMS1 OS=Sacc	0.15	0.06
tRNA (guanine(37)-N1)	0.18	0.07
NADH pyrophosphatas	0.11	0.05
Transmembrane 9 sup	0.13	0.05
Protein phosphatase 2	0.34	0.13
Oleate-activated trans	0.04	0.02
tRNA wybutosine-synt	0.13	0.05
ATP-dependent helicas	0.08	0.03
Pre-mRNA-processing	0.13	0.05
Acyl-protein thioestera	0.46	0.16
Protein EAP1 OS=Sacch	0.07	0.03
Ribosome assembly pr	0.08	0.03
Ribosome maturation	0.93	0.29
Imitation switch two c	0.07	0.03
Serine/threonine-prote	0.03	0.01
Pyridoxamine 5~-phos	0.51	0.18
LAS seventeen-binding	0.21	0.08
Protein transport prote	0.20	0.08
Putative Xaa-Pro amin	0.12	0.05
Casein kinase I homolo	0.46	0.16
Twinfilin-1 OS=Sacchar	0.13	0.05
Serine/threonine-prote	0.15	0.06
Transcription elongatic	0.14	0.06
2-(3-amino-3-carboxyp	0.21	0.08
Cytoplasmic export pro	0.18	0.07
Transcription elongatic	0.76	0.25
RNA polymerase II tran	0.14	0.06
60S acidic ribosomal p	0.53	0.18
Ubiquitin carboxyl-terr	0.22	0.09
Carbamoyl-phosphate	0.23	0.09
GLC7-interacting prote	0.11	0.05
Growth regulation prot	0.18	0.07
Serine/threonine-prote	0.18	0.07
Histone H2A.1 OS=Sacc	0.94	0.29

Casein kinase II subunit	0.36	0.13
Vacuolar protein sortin	0.23	0.09
Exocyst complex comp	0.10	0.04
Kinesin-like protein KIP	0.17	0.07
Pre-mRNA-splicing fact	0.35	0.13
Porphobilinogen deam	0.29	0.11
[Pyruvate dehydrogena	0.16	0.06
Actin-related protein 2	0.39	0.14
Succinate dehydrogena	0.53	0.18
40S ribosomal protein	6.06	0.85
Sphingoid long chain ba	0.06	0.03
Nucleoporin NUP116/N	0.04	0.02
Ubiquitin-conjugating e	1.44	0.39
Transcriptional regulat	0.08	0.03
Uncharacterized protei	0.79	0.25
Folic acid synthesis pro	0.16	0.06
Protein LDB19 OS=Sacc	0.11	0.05
Dihydrolipoyllysine-res	0.32	0.12
Signal peptidase compl	0.55	0.19
Antiviral helicase SLH1	0.04	0.02
Kynurenine formamida	0.36	0.13
Meiotic sister-chromat	0.06	0.03
UBA domain-containin	0.06	0.03
Mitochondrial import i	0.21	0.08
Pre-rRNA-processing p	0.17	0.07
Protein SDS23 OS=Sacc	0.18	0.07
Uncharacterized protei	0.36	0.13
LETM1 domain-contair	0.31	0.12
High-affinity glutamine	0.29	0.11
Probable phospholipas	0.06	0.03
Histone-lysine N-methy	0.12	0.05
Pre-mRNA-processing p	0.15	0.06
Nuclear mRNA export p	0.07	0.03
CDP-diacylglycerol--ser	0.16	0.06
Exocyst complex comp	0.05	0.02
Uncharacterized protei	0.08	0.03
Ubiquitin fusion degra	0.43	0.16
Ribosomal RNA-proces	0.33	0.12
Prohibitin-2 OS=Saccha	0.51	0.18
Probable mannosyltrar	0.22	0.09
Thymidylate kinase OS	0.46	0.16
Mediator of RNA polym	0.09	0.04
Squalene monooxygen	0.29	0.11
Protein MLP2 OS=Sacch	0.05	0.02
Serine/threonine-prote	0.17	0.07
Cell membrane protein	0.07	0.03
DNA-directed RNA poly	0.69	0.23
Chaotic nuclear migrat	0.07	0.03
Vacuolar protein sortin	0.16	0.06
Mediator of RNA polym	0.08	0.03
Exocyst complex comp	0.13	0.05
DNA replication fork-bl	0.15	0.06

Peroxisomal membran	0.17	0.07
DNA polymerase epsil	0.06	0.03
Golgi apparatus memb	0.83	0.26
Leucine--tRNA ligase,	0.15	0.06
Uncharacterized protei	0.14	0.06
Probable glycosidase	0.21	0.08
Mediator of RNA poly	0.04	0.02
H/ACA ribonucleoprot	0.72	0.24
Elongator complex pro	0.25	0.10
Monoglyceride lipase	0.30	0.11
DNA repair/transcripti	0.13	0.05
Kinetochore protein N	0.12	0.05
Transcription factor BY	0.07	0.03
Alcohol O-acetyltransf	0.08	0.03
EKC/KEOPS complex su	0.37	0.14
Probable alanine amin	0.15	0.06
tRNA (cytidine(32)/gua	0.31	0.12
Probable alpha-1,6-ma	0.22	0.09
DNA replication licensi	0.04	0.02
Membrane-anchored l	0.06	0.03
Nucleolar protein 6 OS	0.45	0.16
Glucosidase 2 subunit	0.09	0.04
Uncharacterized protei	0.63	0.21
N-terminal acetyltrans	0.22	0.09
Proteasome-interactin	0.25	0.10
Protein arginine N-met	0.22	0.09
Casein kinase II subuni	0.33	0.12
Trafficking protein part	0.52	0.18
Choline kinase OS=Sac	0.15	0.06
Very-long-chain enoyl-	0.29	0.11
Ribosome biogenesis A	0.11	0.05
Tricalbin-2 OS=Sacchar	0.11	0.05
AP-1 complex subunit	1.15	0.33
C-8 sterol isomerase O	0.46	0.16
Protein ATP11, mitoch	0.29	0.11
ER membrane protein	0.34	0.13
Spermine synthase OS	0.15	0.06
Uncharacterized protei	0.27	0.10
Iron transport multico	0.22	0.09
Invertase 2 OS=Saccha	0.08	0.03
Protein IMPACT homol	0.18	0.07
Stress protein DDR48	0.23	0.09
Ubiquitin-conjugating	1.22	0.35
N-alpha-acetyltransfer	0.97	0.29
Fructose-2,6-bisphosp	0.09	0.04
Protein PNS1 OS=Sacc	0.17	0.07
Ran-specific GTPase-ac	0.21	0.08
Transcriptional regulat	0.42	0.15
Serine/threonine-prote	0.12	0.05
MICOS complex subuni	0.56	0.19
Protein WHI3 OS=Sacc	0.14	0.06
Histone acetyltransfer	0.11	0.05

Cytosolic iron-sulfur pr	0.13	0.05
N-(5~-phosphoribosyl)a	0.47	0.17
Putative uncharacteriz	0.76	0.25
Inositol phosphorylcera	0.20	0.08
Protein SNA3 OS=Sacch	0.36	0.13
Phosphoribomutase OS	0.14	0.06
Ribosome assembly pr	0.18	0.07
Inorganic phosphate tr	0.31	0.12
Nuclear cap-binding pr	0.22	0.09
Silencing boundary-est	0.19	0.08
GPI transamidase comp	0.07	0.03
Nucleoporin NUP192 C	0.02	0.01
Protein ECM21 OS=Sac	0.08	0.03
Putative COX1/OXI3 int	0.05	0.02
Signal recognition part	0.33	0.12
Protein YIM1 OS=Sacch	0.25	0.10
Uroporphyrinogen dec	0.25	0.10
3-keto-steroid reducta	0.13	0.05
Mitochondrial division	0.06	0.03
Profilin OS=Saccharom	0.40	0.15
Tyrosine-protein phosp	0.35	0.13
Vacuolar protein sortin	0.10	0.04
Exosome complex com	0.46	0.16
Protein SSP120 OS=Sac	0.19	0.08
ISWI chromatin-remod	0.04	0.02
Nicotinamide mononu	0.17	0.07
Histone chaperone ASF	0.16	0.06
Putative nitroreductase	0.95	0.29
GRIP domain-containin	0.09	0.04
Actin-related protein 7	0.09	0.04
Protein farnesyltransfe	0.13	0.05
Phosphatidylinositol tr	0.26	0.10
General negative regul	0.05	0.02
Nucleoporin NUP188 C	0.05	0.02
Golgi to ER traffic prote	0.16	0.06
Nucleoporin NDC1 OS=	0.07	0.03
Metal resistance prote	0.06	0.03
Protein dopey OS=Sacc	0.08	0.03
DNA polymerase alpha	0.03	0.01
Conserved oligomeric (	0.10	0.04
Cytochrome c oxidase	0.18	0.07
Protein MKT1 OS=Sacc	0.10	0.04
Mitochondrial FAD-link	0.24	0.09
Serine/threonine-prote	0.16	0.06
Epsin-5 OS=Saccharom	0.10	0.04
Spindle pole body com	0.16	0.06
Protein N-methyltransf	0.37	0.14
Myosin light chain 1 OS	0.76	0.25
Low molecular weight	0.64	0.21
U3 small nucleolar RNA	0.08	0.03
Regulatory protein SIR	0.09	0.04
Factor arrest protein 1	0.19	0.08

5-aminolevulinate synt	0.17	0.07
tRNA-dihydrouridine(1	0.10	0.04
Histone H2A.Z OS=Sac	0.91	0.28
Protein MLP1 OS=Sacc	0.07	0.03
RNA exonuclease 1 OS	0.25	0.10
Proteasome chaperon	1.00	0.30
Uncharacterized protei	0.17	0.07
Cyclin-dependent kina	0.69	0.23
GPI ethanolamine pho	0.09	0.04
Halotolerance protein	0.08	0.03
Cytochrome c oxidase	0.31	0.12
Styryl dye vacuolar loc	0.11	0.05
Cleavage factor two pr	0.10	0.04
Vacuolar protein sortin	0.14	0.06
Uncharacterized protei	0.32	0.12
Exosome complex com	0.18	0.07
Protein arginine N-met	0.10	0.04
Iron-sulfur clusters tra	0.06	0.03
Pre-mRNA-splicing fact	0.07	0.03
Uncharacterized RNA-	0.11	0.05
Factor arrest protein 8	0.08	0.03
Uncharacterized protei	0.12	0.05
Ribosome biogenesis p	0.45	0.16
CUE domain-containin	0.07	0.03
Uncharacterized protei	0.60	0.20
Actin cytoskeleton-reg	0.12	0.05
37S ribosomal protein	0.14	0.06
Cytochrome b-c1 com	0.22	0.09
Nucleolar pre-ribosom	0.04	0.02
Transcriptional regulat	0.10	0.04
U3 small nucleolar rib	0.24	0.09
Probable 1-acyl-sn-gly	0.15	0.06
Peptidyl-prolyl cis-tran	0.11	0.05
General negative regul	0.07	0.03
Non-histone chromoso	1.25	0.35
Nucleoporin NUP159	0.06	0.03
AP-3 complex subunit	0.09	0.04
Uncharacterized protei	0.11	0.05
NADPH-dependent difl	0.14	0.06
UBP3-associated prote	0.18	0.07
Protein NSG2 OS=Sacc	0.15	0.06
Protein transport prote	0.14	0.06
Trafficking protein part	0.21	0.08
Delta(24(24(1)))-sterol	0.09	0.04
Sister chromatid cohes	0.08	0.03
Mitochondrial-process	0.19	0.08
Uncharacterized protei	0.10	0.04
Assembly chaperone o	0.24	0.09
Type 2A phosphatase	0.12	0.05
Clathrin coat assembly	0.07	0.03
Chromo domain-conta	0.09	0.04
DNA-directed RNA pol	0.38	0.14

U1 small nuclear ribon	0.07	0.03
Chitin biosynthesis pro	0.07	0.03
Transcriptional regulat	0.13	0.05
Probable 1,3-beta-gluc	0.09	0.04
Chromatin structure-re	0.14	0.06
Plasma membrane-ass	0.14	0.06
U3 small nucleolar RN/	0.15	0.06
ATP-dependent bile ac	0.03	0.01
Ribokinase OS=Sacchar	0.29	0.11
J domain-containing pr	0.08	0.03
Protein SLM4 OS=Saccl	0.29	0.11
Vacuolar protein sortin	0.05	0.02
Protein PRY1 OS=Sacch	0.16	0.06
Phosphatidylinositol 4-	0.04	0.02
Vacuolar protein-sortir	0.20	0.08
Adenine deaminase OS	0.13	0.05
Translocation protein S	0.56	0.19
Glycine cleavage syster	0.65	0.22
Pre-mRNA-splicing fact	0.15	0.06
Cholinephosphotransfe	0.11	0.05
Protein RER1 OS=Sacch	0.52	0.18
Vacuolar protein-sortir	0.22	0.09
Chromatin modificatio	0.21	0.08
Protein MGA2 OS=Sacc	0.04	0.02
Histidinol-phosphatase	0.27	0.10
Golgi apparatus memb	0.28	0.11
tRNA (guanine(10)-N2)	0.10	0.04
Cytochrome b-c1 comp	0.89	0.28
Sphingoid long chain b	0.07	0.03
Calcium/calmodulin-de	0.10	0.04
Actin-like protein ARP9	0.09	0.04
Methionine--tRNA ligas	0.15	0.06
Inositol monophosphat	0.33	0.12
ISWI chromatin-remod	0.11	0.05
Uncharacterized protei	0.13	0.05
Uncharacterized protei	0.36	0.13
Mitochondrial import r	0.25	0.10
Putative 2-hydroxyacid	0.11	0.05
Cytochrome b2, mitocl	0.07	0.03
10 kDa heat shock prot	0.50	0.18
Pyridoxal 5~-phosphat	0.34	0.13
Putative guanine nucle	0.13	0.05
Alpha-mannosidase OS	0.04	0.02
ADP-ribose 1~~-phospl	0.58	0.20
RNA exonuclease NGL2	0.17	0.07
SET domain-containing	0.06	0.03
Mitochondrial outer m	0.37	0.14
Imidazoleglycerol-phos	0.21	0.08
Geranylgeranyl transfe	0.13	0.05
Vacuolar protein sortin	0.13	0.05
Protein OPI10 OS=Sacc	0.19	0.08
PAB1-binding protein 1	0.06	0.03

DNA repair protein RAI	0.11	0.05
Kinetochore protein NU	0.09	0.04
Lipase 5 OS=Saccharon	0.06	0.03
Ribosome assembly pr	0.10	0.04
Guanine nucleotide ex	0.19	0.08
Dolichyl-diphosphoolig	0.36	0.13
Pre-mRNA-splicing fact	0.05	0.02
Bud site selection prot	0.06	0.03
DNA-directed RNA poly	0.37	0.14
Protein KTI12 OS=Saccl	0.14	0.06
Negative growth regula	0.06	0.03
Monothiol glutaredoxi	0.51	0.18
Protein GIR2 OS=Sacch	0.16	0.06
Regulator of the glycer	0.08	0.03
Serine/threonine-prote	0.23	0.09
cAMP-dependent prot	0.11	0.05
Vacuolar protein sortin	0.08	0.03
Methylthioribulose-1-p	0.40	0.15
ATP-dependent rRNA h	0.18	0.07
Probable di- and tripep	0.05	0.02
Myb-like DNA-binding	0.05	0.02
Golgi to ER traffic prote	0.19	0.08
TPR repeat-containing	0.44	0.16
Poly(A) ribonuclease P(	0.10	0.04
ARS-binding factor 1 O.	0.06	0.03
Serine/threonine-prote	0.04	0.02
[PIN+] prion protein RN	0.12	0.05
MAP-homologous prot	0.10	0.04
Regulator of Ty1 transp	0.18	0.07
Elongator complex pro	0.10	0.04
Histone acetyltransfera	0.23	0.09
Proteasome assembly (	0.35	0.13
Mitochondrial import r	0.74	0.24
3-hydroxy-3-methylglu	0.04	0.02
Probable secreted beta	0.10	0.04
Uncharacterized protei	0.12	0.05
Nonsense-mediated m	0.04	0.02
Chromatin structure-re	0.07	0.03
Conserved oligomeric (	0.16	0.06
Bis(5~-adenosyl)-triphc	0.49	0.17
Uncharacterized trans-	0.25	0.10
Intermediate cleaving p	0.08	0.03
Exosome complex com	0.16	0.06
mRNA-binding protein	0.10	0.04
60S ribosomal subunit	0.22	0.09
Kelch repeat-containin	0.04	0.02
Uridine nucleosidase O	0.13	0.05
Protein SLF1 OS=Sacch	0.10	0.04
Calcium/calmodulin-de	0.10	0.04
S-methyl-5~-thioadenc	0.13	0.05
Ferrochelatase, mitoch	0.11	0.05
Translation machinery-	0.13	0.05

Polyamine transporter	0.15	0.06
Phosphomevalonate ki	0.10	0.04
COPII coat assembly pr	0.02	0.01
Uncharacterized protei	0.35	0.13
Transcription initiation	0.08	0.03
Transcription factor tau	0.06	0.03
DNA-directed RNA poly	0.21	0.08
GTPase-activating prot	0.04	0.02
Mannan endo-1,6-alph	0.10	0.04
Mitochondrial 2-oxodic	0.32	0.12
Putative multicopper o	0.07	0.03
Late endosome and va	0.05	0.02
eRF1 methyltransferas	0.20	0.08
Regulator of Ty1 transp	0.08	0.03
2~,3~-cyclic-nucleotide	0.41	0.15
EKC/KEOPS complex su	0.41	0.15
Uncharacterized protei	0.66	0.22
Initiation-specific alpha	0.19	0.08
tRNA N6-adenosine thr	0.11	0.05
Replication factor A pro	0.39	0.14
Nucleolar complex pro	0.05	0.02
Protein SGT1 OS=Sacch	0.11	0.05
Uncharacterized plasm	0.15	0.06
Replication factor C sul	0.14	0.06
Histone H3 OS=Sacchar	0.36	0.13
Bud emergence protein	0.08	0.03
Aminodeoxychorismate	0.05	0.02
Protein CCC1 OS=Sacch	0.15	0.06
60S ribosome subunit b	0.58	0.20
SAGA-associated factor	0.07	0.03
mRNA transport regula	0.04	0.02
tRNA-dihydrouridine(4	0.06	0.03
Sigma-like sequence pr	0.14	0.06
Iron transport multicop	0.14	0.06
Uncharacterized protei	0.14	0.06
Vacuolar import and de	0.04	0.02
Putative oxidoreductas	0.08	0.03
Target of rapamycin co	0.05	0.02
Protein farnesyltransfe	0.21	0.08
Uncharacterized WD re	0.04	0.02
U3 small nucleolar RNA	0.02	0.01
RNA-binding protein M	0.15	0.06
Uncharacterized protei	0.23	0.09
Cytoplasmic tRNA 2-thi	0.09	0.04
Exosome complex com	0.13	0.05
Sorting nexin MVP1 OS	0.17	0.07
Serine/threonine-prote	0.25	0.10
DNA-directed RNA poly	0.41	0.15
Inorganic phosphate tr	0.05	0.02
Vacuolar protein sortin	0.10	0.04
Putative tyrosine-prote	0.19	0.08
Histidine protein meth	0.12	0.05

Dicarboxylic amino aci	0.07	0.03
Transcription initiation	0.12	0.05
mRNA cap guanine-N7	0.10	0.04
Glycerol-3-phosphate	0.06	0.03
Ergosterol biosynthetic	0.31	0.12
Nucleoside transporter	0.08	0.03
Cytochrome c oxidase	0.24	0.09
Protein transport prote	0.12	0.05
Putative DNA helicase	0.03	0.01
Dilute domain-containi	0.10	0.04
Increased recombinati	0.45	0.16
HSP70 co-chaperone S	0.29	0.11
Cell wall synthesis prot	0.17	0.07
DnaJ-like protein 1 OS=	0.10	0.04
Exportin-T OS=Sacchar	0.04	0.02
Nicotinamide riboside	0.18	0.07
Zinc finger protein GIS	0.66	0.22
CDC48-associated ubiq	0.16	0.06
Secretory component	0.48	0.17
Sulfite reductase [NAD	0.04	0.02
Carbonic anhydrase OS	0.20	0.08
3-hydroxyisobutyryl-Co	0.09	0.04
Serine/threonine-prote	0.06	0.03
Sorting nexin-3 OS=Sac	0.28	0.11
Leucine-rich repeat-co	0.11	0.05
Cell division cycle prote	0.07	0.03
3~,5~-cyclic-nucleotide	0.12	0.05
U3 small nucleolar RN	0.05	0.02
Nicotinamide/nicotinic	0.11	0.05
Mitochondrial interme	0.05	0.02
Cytoplasmic 60S subun	0.10	0.04
Pre-mRNA-processing	0.09	0.04
Exosome complex com	0.18	0.07
YAP1-binding protein 2	0.14	0.06
Translocation protein	0.24	0.09
PX domain-containing	0.04	0.02
Homocysteine S-methy	0.14	0.06
Ethanolamine-phospha	0.13	0.05
Copper-transporting A	0.04	0.02
Smr domain-containin	0.19	0.08
Ornithine carbamoyltr	0.13	0.05
54S ribosomal protein	0.23	0.09
Single-stranded DNA-b	0.83	0.26
Hsp70/Hsp90 co-chape	0.11	0.05
RNA polymerase II sub	0.19	0.08
L-aminoadipate-semial	0.16	0.06
60S ribosomal protein	1.05	0.31
Inhibitory regulator pr	0.04	0.02
2-methoxy-6-polypren	0.14	0.06
Pre-mRNA-splicing fact	0.09	0.04
Putative ATP-depende	0.03	0.01
Mediator of RNA polyn	0.23	0.09

DNA-(apurinic or apyri	0.12	0.05
Transcriptional activat	0.03	0.01
Translation machinery-	0.08	0.03
Signal transduction pr	0.12	0.05
Succinate-semialdehyd	0.09	0.04
Putative glutamine am	0.18	0.07
Nucleolar GTP-binding	0.18	0.07
Serine/threonine-prot	0.06	0.03
Zinc finger protein RTS	0.19	0.08
Spindle pole body com	0.05	0.02
NuA3 HAT complex co	0.06	0.03
Reticulon-like protein	0.11	0.05
Chromatin assembly fa	0.14	0.06
Pre-rRNA-processing p	0.07	0.03
Cell division control pr	0.28	0.11
SIR4-interacting protei	0.08	0.03
Bud site selection prot	0.03	0.01
DNA repair helicase RA	0.05	0.02
SWIRM domain-contai	0.11	0.05
Vacuolar calcium ion tr	0.23	0.09
Ubiquitin ligase-bindin	0.04	0.02
Putative cysteine synth	0.12	0.05
Serine/threonine-prot	0.06	0.03
Cytochrome c oxidase	0.31	0.12
tRNA (uracil(54)-C(5))-	0.07	0.03
Guanine nucleotide-bi	0.44	0.16
Inositol monophospha	0.15	0.06
Nucleoporin NUP53 OS	0.09	0.04
Uncharacterized protei	0.15	0.06
ADP-ribosylation facto	0.16	0.06
Glucose transport tran	0.04	0.02
5-formyltetrahydrofol	0.21	0.08
Tyrosine-protein phos	0.23	0.09
Mitochondria fission 1	0.30	0.11
Ubiquitin carboxyl-ter	0.19	0.08
Broad-range acid phos	0.13	0.05
DNA repair protein RA	0.03	0.01
D-serine dehydratase	0.10	0.04
Pumilio homology dom	0.05	0.02
GPI transamidase com	0.11	0.05
Mitochondrial Rho GT	0.06	0.03
U3 small nucleolar RN	0.09	0.04
Signal peptidase compl	0.25	0.10
OTU domain-containin	0.29	0.11
IMP-specific 5~-nucleo	0.10	0.04
Putative tyrosine-prote	0.20	0.08
Casein kinase I homolo	0.09	0.04
Nucleoporin NUP2 OS=	0.06	0.03
DNA polymerase epsilo	0.02	0.01
RNA polymerase II tra	0.15	0.06
Vacuolar membrane p	0.04	0.02
Putative 6-phosphofru	0.08	0.03

Tubulin-specific chaper	0.46	0.16
Myosin-1 OS=Saccharo	0.04	0.02
UBX domain-containin	0.10	0.04
Transgelin OS=Sacchar	0.23	0.09
6-phosphofructo-2-kin	0.05	0.02
Ubiquitin ligase-bindin	0.09	0.04
Protein FYV10 OS=Sacc	0.08	0.03
Serine/threonine-prote	0.08	0.03
Protein WHI4 OS=Sacch	0.07	0.03
Acyl-CoA-binding prote	0.58	0.20
Putative protease AXL1	0.03	0.01
Exoribonuclease II, mit	0.04	0.02
tRNA (adenine(58)-N(1	0.11	0.05
RNA-binding protein N	0.04	0.02
Endopolyphosphatase	0.13	0.05
Zinc/cadmium resistan	0.10	0.04
Protein SOV1, mitocho	0.05	0.02
tRNA (uracil-O(2)-)-me	0.07	0.03
Putative elongation fac	0.19	0.08
Uncharacterized protei	0.12	0.05
Oxysterol-binding prot	0.03	0.01
DNA-directed RNA poly	0.30	0.11
Peptide-N(4)-(N-acetyl	0.11	0.05
RNA-binding protein M	0.06	0.03
Putative 2-hydroxyacyl	0.08	0.03
DNA polymerase gamn	0.07	0.03
54S ribosomal protein	0.11	0.05
Palmitoyltransferase A	0.06	0.03
GTPase-activating prot	0.05	0.02
Vacuolar-sorting prote	0.19	0.08
DNA damage tolerance	0.13	0.05
Ribosomal lysine N-me	0.07	0.03
Phosphatidylserine dec	0.09	0.04
N-terminal acetyltrans	0.27	0.10
Phosphatidylinositol 4-	0.07	0.03
Pentatricopeptide repe	0.04	0.02
DNA-directed RNA poly	0.27	0.10
Ribosomal protein VAR	0.11	0.05
Protein VMS1 OS=Sacc	0.07	0.03
Rheb-like protein RHB1	0.22	0.09
Nuclear polyadenylate	0.08	0.03
DNA repair protein RAI	0.06	0.03
Spliceosomal protein D	0.32	0.12
SIT4-associating protei	0.04	0.02
Ammonia transport ou	0.36	0.13
Dihydrofolate reductas	0.21	0.08
ATP synthase subunit H	0.39	0.14
Antisense of depressin	0.44	0.16
Transcription initiation	0.07	0.03
Serine/threonine prote	0.04	0.02
Phosphopantetheine a	0.14	0.06
Proteasome chaperone	0.16	0.06

Metacaspase-1 OS=Sac	0.10	0.04
Ribosome-releasing fac	0.05	0.02
Ribulose-phosphate 3-	0.20	0.08
Ubiquitin carboxyl-terr	0.05	0.02
Mitochondrial genome	0.17	0.07
ERAD-associated E3 ub	0.03	0.01
Type 1 phosphatases r	0.29	0.11
Delta(7)-sterol 5(6)-de	0.12	0.05
Protein STE12 OS=Sacc	0.06	0.03
Regulator of rDNA tran	0.22	0.09
Small nuclear ribonucle	0.23	0.09
ATP-dependent DNA h	0.04	0.02
GTP-binding protein YI	0.24	0.09
Protein ORM2 OS=Sacc	0.21	0.08
Rhomboid protein 2 O	0.37	0.14
DNA mismatch repair p	0.09	0.04
Pre-mRNA-splicing fact	0.06	0.03
Transcription factor SP	0.11	0.05
Glycerol uptake protei	0.07	0.03
Restriction of telomere	0.03	0.01
Protein AST1 OS=Sacch	0.10	0.04
DNA primase small sub	0.10	0.04
DNA-3-methyladenine	0.15	0.06

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d: lower
u: higher

Gene name	UniProt ID	chromatin rank	non-chromatin rank	in chromatin
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ALG1	P16661	1	9	d
ALG5	P40350	1	13	d
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ARD1	P07347	1	97	d
ARF1	P11076	260	386	d
ARF2	P19146	259	383	d
CDC14	Q00684	9	1	u
CDC28	P00546	16	32	d
CDC33	P07260	79	260	d
CDC42	P19073	25	54	d
CDC48	P25694	69	369	d
CDC53	Q12018	1	11	d
CDC60	P26637	84	254	d
CET1	O13297	1	8	d
DED1	P06634	159	368	d
DIS3	Q08162	1	39	d
DPM1	P14020	86	287	d
DUG1	P43616	1	173	d
DYS1	P38791	1	235	d
EFB1	P32471	87	384	d
EMC4	P53073	1	25	d
ENP1	P38333	10	1	u
ERO1	Q03103	25	24	u
ERV1	P27882	1	24	d
ESS1	P22696	63	238	d
FPR1	P20081	249	364	d
FUN12	P39730	15	152	d
GAA1	P39012	8	1	u
GCD11	P32481	77	170	d
GCD7	P32502	1	39	d
GCN3	P14741	1	15	d
GDI1	P39958	1	58	d
GET1	P53192	1	19	d
GET2	P40056	1	35	d
GIS2	P53849	1	115	d
GLC7	P32598	69	91	d
GLN4	P13188	37	235	d
GRS1	P38088	83	351	d
HCR1	Q05775	39	62	d
HEM3	P28789	1	14	d
HSC82	P15108	211	424	d
HSP60	P19882	128	404	d
HSP82	P02829	207	406	d
HTS1	P07263	28	234	d
HYP2	P23301	174	469	d
KRS1	P15180	118	295	d
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MNL1	P38888	1	5 d
MNP1	P53163	27	26 u
MTR4	P47047	1	8 d
NAM7	P30771	1	24 d
NAT1	P12945	1	54 d
NHP2	P32495	115	177 d
NMD3	P38861	9	61 d
NMT1	P14743	1	20 d
NOG1	Q02892	15	56 d
NOG2	P53742	54	19 u
NOP1	P15646	175	247 d
NTF2	P33331	39	211 d
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PAM16	P42949	1	33 d
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PHO85	P17157	1	31 d
PRE1	P22141	1	87 d
PRE10	P21242	1	82 d
PRE5	P40302	104	279 d
PSE1	P32337	5	12 d
PUP2	P32379	19	155 d
RAD3	P06839	1	5 d
RAS2	P01120	16	222 d
RHO1	P06780	114	158 d
RNA1	P11745	37	85 d
RPB7	P34087	29	28 u
RPL10	P41805	231	412 d
RPL28	P02406	205	431 d
RPL30	P14120	201	415 d
RPL5	P26321	134	333 d
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RPN11	P43588	1	180 d
RPN2	P32565	6	123 d
RPN3	P40016	1	102 d
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RPN6	Q12377	34	46 d
RPN7	Q06103	1	34 d
RPN8	Q08723	29	64 d
RPN9	Q04062	1	239 d
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RPS31	P05759	146	174 d
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RPT4	P53549	1	33 d
RPT5	P33297	1	63 d
RPT6	Q01939	24	87 d

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SEC11	P15367	1	65	d
SEC13	Q04491	34	209	d
SEC21	P32074	21	148	d
SES1	P07284	113	366	d
SIT4	P20604	1	14	d
SKP1	P52286	144	88	u
SMT3	Q12306	51	269	d
SNU13	P39990	41	221	d
SRM1	P21827	20	1	u
SSS1	P35179	68	67	u
STE24	P47154	45	31	u
SUB2	Q07478	61	200	d
SUI2	P20459	15	200	d
SUI3	P09064	106	166	d
SUP45	P12385	108	309	d
THS1	P04801	111	358	d
TIF11	P38912	114	400	d
TIF35	Q04067	37	174	d
TIF5	P38431-2	1	114	d
TIF6	Q12522	1	42	d
TYS1	P36421	72	151	d
UBC1	P21734	1	79	d
UBC9	P50623	1	68	d
UBP6	P43593	1	94	d
UFD1	P53044	1	27	d
UTP22	P53254	12	14	d
VAS1	P07806-2	55	271	d
VPS74	Q06385	14	1	u
VTI1	Q04338	1	47	d
WBP1	P33767	62	61	u
WRS1	Q12109	11	77	d
YDJ1	P25491	87	87	d
YFH1	Q07540	1	27	d
YNL247W	P53852	12	164	d
YPK1	P12688	7	20	d
ZUO1	P32527	48	258	d
VMA9	Q3E7B6	1	72	d
YRB30	P53107	1	10	d
NIC96	P34077	11	16	d
PUF4	P25339	1	5	d
RPB4	P20433	74	45	u
CWH41	P53008	1	22	d
MNN2	P38069	1	75	d
PDI1	P17967	51	256	d
GIM5	Q04493	1	66	d
MPD2	Q99316	34	1	u
PRE9	P23638	19	276	d
PTP1	P25044	1	13	d

RPL11B	Q3E757	241	355	d
RPL39	P04650	101	105	d
YPR137C-B	P0C2I9	66	61	u
DOP1	Q03921	11	1	u
NDC1	P32500	15	7	u
POM34	Q12445	16	1	u
RET3	P53600	1	24	d
SFB3	P38810	1	15	d
UBP2	Q01476	1	18	d
DBP5	P20449	1	132	d
PRE2	P30656	17	110	d
SEC63	P14906	38	55	d
LTP1	P40347	1	28	d
VPS17	P32913	17	1	u
CAF20	P12962	1	29	d
CMP2	P14747	1	7	d
OST2	P46964	38	37	u
RPL37B	P51402	59	58	u
NMA111	P53920	1	41	d
RKR1	Q04781	1	5	d
APL6	P46682	1	5	d
ETT1	Q08421	36	22	u
PEP4	P07267	164	110	u
PHB1	P40961	83	112	d
RPL21B	Q12672	165	1	u
SHR3	Q02774	23	22	u
YPT7	P32939	1	198	d
RIO1	Q12196	1	9	d
RPL36B	O14455	288	466	d
UBC4	P15731	1	32	d
ABP1	P15891	25	92	d
AEP3	Q12089	1	7	d
APE1	P14904	29	64	d
APE2	P32454	31	207	d
APL4	Q12028	1	5	d
APL5	Q08951	1	14	d
ARX1	Q03862	8	66	d
ATG27	P46989	18	36	d
BET4	Q00618	1	13	d
BFR2	Q06631	18	26	d
BUD23	P25627	1	16	d
CAJ1	P39101	25	37	d
CBP6	P07253	1	29	d
CDC1	P40986	10	1	u
CDC11	P32458	23	1	u
CDC12	P32468	158	50	u
CEX1	Q12453	1	6	d
CHC1	P22137	37	206	d
CKB1	P43639	17	16	u
CKB2	P38930	1	37	d
CLU1	Q03690	44	198	d
COF1	Q03048	152	344	d

COR1	P07256	34	185	d
COX20	Q04935	1	22	d
CPR3	P25719	28	231	d
CPR6	P53691	1	159	d
CPS1	P27614	9	93	d
CRM1	P30822	5	21	d
CSE1	P33307	15	19	d
CTR9	P89105	5	26	d
CWH43	P25618	5	9	d
DAP2	P18962	1	17	d
DNF2	Q12675	1	5	d
DPH5	P32469	1	15	d
DTD1	Q07648	1	32	d
ECM14	P38836	1	21	d
ECM32	P32644	1	8	d
EDE1	P34216	1	7	d
ELP2	P42935	1	17	d
EMC1	P25574	1	11	d
EMC5	P40540	35	1	u
EMP24	P32803	23	119	d
EPS1	P40557	7	19	d
EUG1	P32474	1	8	d
FOB1	O13329	8	1	u
FPR3	P38911	37	104	d
FPR4	Q06205	25	71	d
GAB1	P41733	12	1	u
GCS1	P35197	1	13	d
GDA1	P32621	1	9	d
GET3	Q12154	14	194	d
GET4	Q12125	69	68	u
GIN4	Q12263	5	1	u
GUS1	P46655	116	317	d
HAT2	P39984	1	11	d
HCH1	P53834	32	121	d
HEF3	P53978	58	129	d
HER2	Q03557	1	10	d
HHF1	P02309	290	203	u
HOG1	P32485	1	34	d
HOS3	Q02959	7	1	u
HOS4	P40480	1	4	d
ILS1	P09436	104	338	d
IST2	P38250	10	5	u
KAP104	P38217	1	10	d
KAP122	P32767	1	4	d
KAP123	P40069	22	109	d
KRE5	P22023	1	3	d
KTR3	P38130	1	22	d
LSG1	P53145	23	22	u
MAS2	P11914	1	9	d
MEF1	P25039	1	12	d
MLP1	Q02455	1	24	d
MNS1	P32906	9	8	u

MPD1	Q12404	69	1	u
MRT4	P33201	42	41	u
MSN5	P52918	1	10	d
NAP1	P25293	23	48	d
NAT5	Q08689	1	60	d
NEW1	Q08972	12	170	d
NMD5	P46970	1	4	d
NNT1	Q05874	1	61	d
NUP192	P47054	4	1	u
NUP2	P32499	1	13	d
PBI2	P0CT04	72	71	u
PBP1	P53297	7	6	u
PEP1	P32319	1	17	d
PIM1	P36775	1	12	d
PIR1	Q03178	1	31	d
PLP2	Q12017	1	15	d
PMT1	P33775	37	43	d
PMT3	P47190	13	1	u
PMT4	P46971	7	1	u
PRB1	P09232	1	31	d
PRE4	P30657	18	62	d
PTC7	P38797	1	13	d
PUF6	Q04373	22	55	d
RAP1	P11938	6	1	u
RAT1	Q02792	5	4	u
RAX1	Q08760	11	1	u
RET2	P43621	18	26	d
RFA1	P22336	32	50	d
RLP24	Q07915	49	21	u
RPL12A	P0CX53	217	393	d
RPL14A	P36105	268	431	d
RPL14B	P38754	1	411	d
RPL16B	P26785	222	372	d
RPL17A	P05740	200	365	d
RPL17B	P46990	200	365	d
RPL18A	P0CX49	216	266	d
RPL19A	P0CX82	263	374	d
RPL1A	P0CX43	172	380	d
RPL22B	P56628	1	161	d
RPL23A	P0CX41	289	465	d
RPL24A	P04449	170	314	d
RPL24B	P24000	1	267	d
RPL25	P04456	235	423	d
RPL26B	P53221	283	461	d
RPL31A	P0C2H8	213	462	d
RPL33B	P41056	221	364	d
RPL36A	P05745	284	458	d
RPL38	P49167	198	263	d
RPL42A	P0CX27	106	45	u
RPL43A	P0CX25	214	137	u
RPL7A	P05737	262	430	d
RPL8A	P17076	271	454	d

RPL9A	P05738	227	357	d
RPL9B	P51401	1	332	d
RPN12	P32496	1	81	d
RPP2B	P02400	120	349	d
RPS11A	P0CX47	168	262	d
RPS12	P48589	238	427	d
RPS14A	P06367	282	471	d
RPS17A	P02407	232	439	d
RPS18A	P0CX55	277	448	d
RPS19A	P07280	212	460	d
RPS1A	P33442	269	459	d
RPS1B	P23248	275	452	d
RPS20	P38701	278	463	d
RPS21B	Q3E754	1	414	d
RPS22A	P0C0W1	281	446	d
RPS24A	P0CX31	240	407	d
RPS27A	P35997	192	337	d
RPS3	P05750	239	456	d
RPS30A	P0CX33	89	328	d
RPS7A	P26786	255	428	d
RPS7B	P48164	243	390	d
RPS9A	O13516	265	420	d
RPS9B	P05755	267	422	d
RRS1	Q08746	1	23	d
RSM7	P47150	1	18	d
RTG2	P32608	1	15	d
RVB1	Q03940	91	145	d
SBH1	P52870	1	70	d
SCJ1	P25303	13	12	u
SEC17	P32602	1	129	d
SEC24	P40482	11	58	d
SEC26	P41810	20	149	d
SEC31	P38968	4	61	d
SEC4	P07560	50	228	d
SEC5	P89102	5	1	u
SEC66	P33754	48	1	u
SEC7	P11075	1	4	d
SEH1	P53011	14	13	u
SFM1	Q12314	1	77	d
SGT2	Q12118	30	253	d
SHS1	Q07657	17	8	u
SNF4	P12904	1	29	d
SPA2	P23201	1	3	d
SPC3	Q12133	1	134	d
SPN1	Q06505	24	1	u
SPT6	P23615	4	40	d
SRO9	P25567	11	64	d
SRP102	P36057	1	19	d
SRP21	P32342	1	29	d
SSA2	P10592	248	447	d
SSD1	P24276	4	31	d
SSO2	P39926	16	32	d

SSQ1	Q05931	1	7	d
STM1	P39015	112	294	d
STT3	P39007	43	12	u
SWP1	Q02795	17	16	u
SXM1	Q04175	1	30	d
TAF6	P53040	19	1	u
TED1	P40533	1	19	d
TEF1	P02994	274	388	d
TEF4	P36008	139	293	d
TIF4631	P39935	6	49	d
TIF4632	P39936	1	10	d
TIM44	Q01852	1	47	d
TMA108	P40462	1	30	d
TMA22	P47089	1	86	d
TOM1	Q03280	1	8	d
TPA1	P40032	15	56	d
TRA1	P38811	2	2	d
TRX2	P22803	1	416	d
TUF1	P02992	65	116	d
TVP23	P38962	23	22	u
TWF1	P53250	1	14	d
UBA2	P52488	1	39	d
UFD4	P33202	1	3	d
UPF3	P48412	12	1	u
VAC8	P39968	1	25	d
VMA1	P17255	193	350	d
VPS1	P21576	150	94	u
VPS3	P23643	1	4	d
VPS4	P52917	1	10	d
VTC2	P43585	17	111	d
WHI3	P34761	1	7	d
YBR137W	P38276	1	58	d
YCK1	P23291	9	1	u
YER134C	P40081	1	26	d
YKE2	P52553	43	101	d
YMR31	P19955	1	40	d
YOL057W	Q08225	1	19	d
YPT31	P38555	48	291	d
YUH1	P35127	1	20	d
ASC1	P38011	202	434	d
GPI16	P38875	1	7	d
MCA1	Q08601	11	34	d
MNN1	P39106	6	11	d
MRPS8	Q03799	1	30	d
PGA3	Q12746	32	95	d
RPL35A	P0CX84	264	442	d
RPL37A	P49166	177	224	d
RPL4B	P49626	1	329	d
SDH3	P33421	1	24	d
SPC2	Q04969	1	57	d
TIM50	Q02776	10	9	u
USO1	P25386	1	29	d

YFR006W	P43590	1	8	d
YIF1	P53845	1	14	d
AAP1	P37898	11	41	d
ACC1	Q00955	77	353	d
ACS2	P52910	47	273	d
ACT1	P60010	258	453	d
AHA1	Q12449	14	105	d
ANP1	P32629	10	1	u
APE3	P37302	28	103	d
APL1	P27351	1	6	d
APL2	P36000	1	6	d
ARC1	P46672	1	182	d
ARL1	P38116	1	99	d
ARP2	P32381	25	173	d
ASF1	P32447	1	16	d
BCY1	P07278	36	22	u
BMH1	P29311	220	451	d
BMH2	P34730	194	417	d
BRE1	Q07457	1	12	d
CAF40	P53829	13	1	u
CAM1	P29547	66	213	d
CCT2	P39076	65	78	d
CCT3	P39077	39	167	d
CCT4	P39078	19	77	d
CCT5	P40413	1	36	d
CCT6	P39079	28	74	d
CCT7	P42943	9	74	d
CCT8	P47079	27	114	d
CDC37	P06101	1	8	d
CDC39	P25655	1	10	d
CHD1	P32657	10	1	u
CHS5	Q12114	1	7	d
CKA2	P19454	44	82	d
CLC1	P17891	1	19	d
CNB1	P25296	1	61	d
COP1	P53622	16	147	d
CPR1	P14832	219	375	d
CPR5	P35176	1	45	d
CSR1	Q06705	1	49	d
CYM1	P32898	1	18	d
DED81	P38707	59	306	d
DEF1	P35732	1	6	d
DHH1	P39517	40	77	d
DID2	P69771	24	23	u
DJP1	P40564	1	10	d
DNF1	P32660	6	1	u
DPS1	P04802	155	290	d
EFT1	P32324	244	440	d
EGD1	Q02642	33	225	d
EGD2	P38879	107	249	d
EMC2	P47133	74	126	d
ERP1	Q05359	47	113	d

ERP2	P39704	1	48	d
ERV25	P54837	110	189	d
ERV46	P39727	51	36	u
FES1	P38260	1	106	d
FRA1	Q07825	1	6	d
FRS1	P15624	16	269	d
FRS2	P15625	10	230	d
GBP2	P25555	1	10	d
GCD6	P32501	1	50	d
GCN1	P33892	24	130	d
GCN20	P43535	7	75	d
GCV3	P39726	1	65	d
GGA2	P38817	9	34	d
GIM3	P53900	1	142	d
GIP3	Q03016	1	3	d
GLR1	P41921	20	85	d
GPD1	Q00055	40	154	d
GPI17	Q04080	9	1	u
GRX1	P25373	1	182	d
GRX3	Q03835	1	65	d
GSF2	Q04697	52	106	d
GSP1	P32835	149	147	u
GTT1	P40582	1	19	d
GUP1	P53154	9	8	u
HEK2	P38199	1	41	d
HMT1	P38074	1	13	d
HOC1	P47124	12	11	u
HRB1	P38922	1	9	d
HRI1	Q05905	42	256	d
HRK1	Q08732	7	1	u
HRR25	P29295	1	9	d
HSP10	P38910	52	203	d
HSP104	P31539	106	376	d
HSP26	P15992	81	300	d
HSP78	P33416	12	96	d
IKI3	Q06706	1	24	d
IMH1	Q06704	1	5	d
IMP3	P32899	1	24	d
KAP95	Q06142	1	35	d
KAR2	P16474	78	324	d
KRE2	P27809	45	90	d
KTR1	P27810	68	85	d
KTR6	P54070	1	9	d
LAP2	Q10740	14	28	d
LAP3	Q01532	10	146	d
LHS1	P36016	6	69	d
LIA1	P47120	1	212	d
LSP1	Q12230	162	245	d
MAM33	P40513	1	17	d
MAP2	P38174	23	22	u
MAS1	P10507	1	10	d
MCD4	P36051	10	5	u

MCK1	P21965	40	55	d
MDH2	P22133	1	26	d
MDM20	Q12387	1	5	d
MDY2	Q12285	1	49	d
MES1	P00958	33	198	d
MET18	P40469	1	13	d
MGE1	P38523	1	20	d
MHR1	Q06630	20	1	u
MLC1	P53141	34	1	u
MNN10	P50108	12	11	u
MNN11	P46985	1	22	d
MNN5	P46982	16	15	u
MNN9	P39107	37	23	u
MRPL35	Q06678	13	1	u
MRPS18	P42847	1	21	d
MSS116	P15424	1	20	d
MYO2	P19524	12	14	d
NAM9	P27929	10	9	u
NAS6	P50086	1	44	d
NCE102	Q12207	29	108	d
NFU1	P32860	1	38	d
NGR1	P32831	1	7	d
NIP1	P32497	44	141	d
NMD2	P38798	5	4	u
NOP9	P47077	7	20	d
NPL3	Q01560	38	87	d
NUG1	P40010	19	9	u
NUP120	P35729	1	8	d
NUP133	P36161	8	7	u
NUP188	P52593	1	8	d
NUP57	P48837	29	1	u
NUP84	P52891	1	12	d
OPT1	P40897	6	1	u
OSM1	P21375	1	9	d
OST3	P48439	14	13	u
PAB1	P04147	154	354	d
PAM17	P36147	1	53	d
PAN5	P38787	13	24	d
PAT1	P25644	7	1	u
PDR17	P53844	1	26	d
PEX25	Q02969	24	1	u
PGA2	P53903	37	144	d
PHB2	P50085	73	99	d
PHO13	P19881	16	122	d
PHO8	P11491	1	25	d
PHO86	P46956	15	50	d
PHO88	P38264	171	399	d
PIL1	P53252	174	268	d
PMI40	P29952	49	153	d
PMT2	P31382	19	31	d
POM152	P39685	11	10	u
POM33	Q12164	17	16	u

PRC1	P00729	18	27	d
PRD1	P25375	1	68	d
PRE3	P38624	23	117	d
PRE6	P40303	19	93	d
PRE7	P23724	20	132	d
PRE8	P23639	1	199	d
PRT1	P06103	12	120	d
PSA1	P41940	81	236	d
PSD1	P39006	10	1	u
PTC2	P39966	1	59	d
PTC3	P34221	1	20	d
PTH2	P34222	1	23	d
PUP1	P25043	1	39	d
QCR2	P07257	43	274	d
RAD23	P32628	1	25	d
RBG1	P39729	27	41	d
RBG2	P53295	1	26	d
RFA2	P26754	1	17	d
RIO2	P40160	11	10	u
RIX1	P38883	1	6	d
RLI1	Q03195	52	250	d
RLP7	P40693	30	29	u
RPG1	P38249	75	165	d
RPL13A	Q12690	143	318	d
RPL13B	P40212	1	318	d
RPL15A	P05748	196	257	d
RPL16A	P26784	190	372	d
RPL20A	P0CX23	234	410	d
RPL21A	Q02753	165	343	d
RPL22A	P05749	96	163	d
RPL26A	P05743	276	461	d
RPL27A	P0C2H6	215	403	d
RPL2A	P0CX45	178	347	d
RPL3	P14126	242	389	d
RPL31B	P0C2H9	1	450	d
RPL32	P38061	163	264	d
RPL33A	P05744	224	367	d
RPL34B	P40525	138	160	d
RPL4A	P10664	186	329	d
RPL6A	Q02326	153	350	d
RPL6B	P05739	153	278	d
RPL7B	Q12213	262	430	d
RPL8B	P29453	280	454	d
RPN10	P38886	1	89	d
RPN13	O13563	1	212	d
RPP1A	P05318	54	128	d
RPP1B	P10622	55	54	u
RPP2A	P05319	55	356	d
RPS0A	P32905	119	160	d
RPS10A	Q08745	147	179	d
RPS15	Q01855	152	242	d
RPS16A	P0CX51	252	421	d

RPS2	P25443	156	345	d
RPS21A	P0C0V8	254	414	d
RPS23A	P0CX29	151	240	d
RPS25B	P0C0T4	197	259	d
RPS26A	P39938	95	161	d
RPS28B	P0C0X0	279	377	d
RPS29A	P41057	92	398	d
RPS29B	P41058	1	391	d
RPS4A	P0CX35	273	429	d
RPS6A	P0CX37	236	392	d
RPS8A	P0CX39	118	281	d
RSP5	P39940	12	29	d
RTF1	P53064	1	7	d
RTG3	P38165	10	1	u
RVB2	Q12464	33	32	u
SAR1	P20606	56	255	d
SBH2	P52871	63	62	u
SBP1	P10080	16	77	d
SCD6	P45978	1	27	d
SEC14	P24280	32	297	d
SEC18	P18759	7	57	d
SEC23	P15303	26	125	d
SEC27	P41811	6	169	d
SEC28	P40509	1	32	d
SEC53	P07283	187	408	d
SEC61	P32915	44	31	u
SEC72	P39742	1	54	d
SET2	P46995	7	1	u
SFB2	P53953	1	5	d
SFT2	P38166	1	115	d
SHP1	P34223	1	22	d
SIS1	P25294	67	160	d
SKI2	P35207	1	7	d
SLM1	P40485	14	1	u
SNF1	P06782	1	30	d
SNF7	P39929	20	19	u
SNL1	P40548	30	67	d
SNU114	P36048	1	13	d
SNX3	Q08826	29	1	u
SOP4	P39543	1	19	d
SRP1	Q02821	18	48	d
SRP14	P38985	1	33	d
SRP68	P38687	1	51	d
SRP72	P38688	15	38	d
SSA1	P10591	247	441	d
SSA4	P22202	1	202	d
SSB1	P11484	233	438	d
SSB2	P40150	233	438	d
SSC1	P0CS90	138	394	d
SSE1	P32589	203	457	d
SSE2	P32590	1	108	d
SSH1	P38353	31	9	u

SSM4	P40318	4	1	u
SSZ1	P38788	115	316	d
STE23	Q06010	1	38	d
STI1	P15705	16	278	d
STO1	P34160	1	27	d
SUI1	P32911	46	111	d
SUP35	P05453	21	64	d
SVP26	P38869	20	1	u
TAF12	Q03761	9	8	u
TAF14	P35189	1	19	d
TCP1	P12612	18	72	d
TFG1	P41895	1	6	d
TFS1	P14306	1	115	d
THO2	P53552	1	3	d
TIF1	P10081	245	444	d
TIF3	P34167	111	153	d
TIF34	P40217	1	198	d
TMA19	P35691	229	385	d
TMA20	P89886	27	187	d
TMA46	Q12000	28	1	u
TOM20	P35180	1	59	d
TOM22	P49334	1	75	d
TOM40	P23644	13	25	d
TOM70	P07213	1	72	d
TOM71	P38825	1	14	d
TPD3	P31383	8	40	d
TRM9	P49957	1	16	d
TRX1	P22217	116	344	d
TSA1	P34760	210	390	d
UBA1	P22515	19	210	d
UBA4	P38820	1	10	d
UBC13	P52490	1	31	d
UBP1	P25037	1	5	d
UBR1	P19812	1	11	d
UFD2	P54860	1	24	d
UTP8	P53276	1	12	d
VPS13	Q07878	1	7	d
VPS21	P36017	1	161	d
WTM1	Q12363	23	133	d
YAR1	P46683	1	52	d
YCK2	P23292	37	16	u
YDR341C	Q05506	85	350	d
YEF3	P16521	199	425	d
YET1	P35723	114	158	d
YET3	Q07451	1	51	d
YGR054W	P53235	23	70	d
YHI9	P38765	1	33	d
YHR020W	P38708	45	117	d
YMR027W	Q04371	1	69	d
YMR196W	Q04336	1	12	d
YPT1	P01123	137	304	d
YPT32	P51996	1	255	d

YPT52	P36018	1	137	d
YPT6	Q99260	1	47	d
YRA1	Q12159	169	321	d
YRA2	P36036	1	22	d
YRB1	P41920	51	201	d
ZPS1	Q12512	139	18	u
ABF1	P14164	20	1	u
CBF1	P17106	28	1	u
CRZ1	P53968	1	6	d
IXR1	P33417	8	1	u
REB1	P21538	18	1	u
RSC30	P38781	6	1	u
AAH1	P53909	1	13	d
AAT2	P23542	101	275	d
ABP140	Q08641	1	30	d
ACB1	P31787	1	58	d
ACH1	P32316	1	27	d
ACO1	P19414	109	348	d
ACO2	P39533	32	73	d
ACP1	P32463	1	40	d
ADE1	P27616	96	359	d
ADE12	P80210	64	243	d
ADE13	Q05911	98	323	d
ADE16	P54113	1	239	d
ADE17	P38009	35	319	d
ADE2	P21264	9	139	d
ADE3	P07245	68	304	d
ADE4	P04046	10	110	d
ADE5,7	P07244	19	256	d
ADE6	P38972	34	196	d
ADE8	P04161	1	116	d
ADH1	P00330	257	387	d
ADH3	P07246	79	144	d
ADH4	P10127	77	290	d
ADH6	Q04894	43	211	d
ADK1	P07170	133	370	d
ADO1	P47143	69	305	d
AFG2	P32794	1	6	d
AGE2	P40529	1	15	d
AHP1	P38013	226	435	d
AIM17	P23180	10	30	d
AIM2	P39721	1	19	d
AIM29	P36154	1	29	d
AIM45	Q12480	1	114	d
AIM9	P40053	8	80	d
AIP1	P46680	1	42	d
ALD2	P47771	1	41	d
ALD4	P46367	79	310	d
ALD5	P40047	1	52	d
ALD6	P54115	189	401	d
ALO1	P54783	9	117	d
ALT1	P52893	1	24	d

AMD1	P15274	1	11	d
APA1	P16550	1	231	d
APN1	P22936	1	12	d
APT1	P49435	1	58	d
ARA1	P38115	28	263	d
ARC15	P40518	33	223	d
ARC18	Q05933	59	266	d
ARC19	P33204	28	103	d
ARC35	P53731	62	81	d
ARC40	P38328	1	12	d
ARG1	P22768	82	303	d
ARG4	P04076	73	178	d
ARG5,6	Q01217	1	5	d
ARG7	Q04728	1	208	d
ARG8	P18544	1	11	d
ARI1	P53111	1	45	d
ARO1	P08566	16	226	d
ARO10	Q06408	8	93	d
ARO2	P28777	27	166	d
ARO3	P14843	13	118	d
ARO4	P32449	100	234	d
ARO7	P32178	18	148	d
ARO8	P53090	53	178	d
ARO9	P38840	19	107	d
ARP3	P47117	34	95	d
ARP5	P53946	1	6	d
ASN1	P49089	104	322	d
ASN2	P49090	114	342	d
ASP1	P38986	1	40	d
ATP1	P07251	103	315	d
ATP11	P32453	1	14	d
ATP12	P22135	1	14	d
ATP14	Q12349	1	39	d
ATP15	P21306	1	340	d
ATP2	P00830	157	277	d
ATP3	P38077	33	204	d
ATP4	P05626	99	132	d
ATP5	P09457	141	204	d
ATP7	P30902	129	193	d
AVT7	P40501	1	9	d
BAT1	P38891	90	193	d
BAT2	P47176	1	138	d
BBC1	P47068	1	4	d
BDH1	P39714	1	25	d
BEM2	P39960	1	2	d
BET3	P36149	1	52	d
BFR1	P38934	148	280	d
BMS1	Q08965	5	7	d
BNA1	P47096	27	58	d
BNA3	P47039	1	46	d
BNA5	Q05979	1	10	d
BRR2	P32639	1	2	d

BRX1	Q08235	16	52	d
CAB2	P40506	1	25	d
CAB4	P53332	1	15	d
CAF16	P43569	1	53	d
CAP1	P28495	1	85	d
CAP2	P13517	1	54	d
CAR1	P00812	1	214	d
CAR2	P07991	84	201	d
CBF5	P33322	42	83	d
CBR1	P38626	127	218	d
CCC1	P47818	1	15	d
CCR4	P31384	1	11	d
CCS1	P40202	1	97	d
CDC19	P00549	272	467	d
CDC21	P06785	1	31	d
CDC3	P32457	18	37	d
CDS1	P38221	10	20	d
CGI121	Q03705	1	57	d
CGR1	P53188	1	38	d
CIA1	Q05583	1	13	d
CIR2	Q08822	1	14	d
CIT1	P00890	44	104	d
CIT2	P08679	11	20	d
COA1	P40452	1	24	d
COQ2	P32378	1	12	d
COQ5	P49017	1	15	d
COX2	P00410	40	123	d
COX4	P04037	1	72	d
COX5A	P00424	1	73	d
COX5B	P00425	32	177	d
COX6	P00427	1	31	d
COY1	P34237	7	13	d
CPA2	P03965	48	302	d
CRN1	Q06440	15	22	d
CRP1	P38845	1	20	d
CTT1	P06115	1	24	d
CYB2	P00175	1	7	d
CYB5	P40312	1	42	d
CYC8	P14922	1	5	d
CYS3	P31373	93	201	d
CYS4	P32582	95	403	d
CYT1	P07143	1	15	d
DAK1	P54838	47	140	d
DBP10	Q12389	1	13	d
DBP2	P24783	48	272	d
DCP2	P53550	1	4	d
DCS1	Q06151	1	78	d
DCS2	Q12123	1	12	d
DDP1	Q99321	1	91	d
DDR48	P18899	1	11	d
DIM1	P41819	1	14	d
DIP2	Q12220	1	19	d

DLD1	P32891	1	66	d
DLD2	P46681	1	27	d
DLD3	P39976	30	146	d
DNM1	P54861	7	32	d
DOG2	P38773	1	41	d
DOT5	P40553	1	48	d
DPL1	Q05567	1	7	d
DRS1	P32892	7	18	d
DSS1	P39112	1	4	d
DUR1,2	P32528	1	102	d
DUS3	Q06053	1	13	d
DUT1	P33317	1	84	d
EBP2	P36049	34	61	d
ECM16	Q04217	1	7	d
ECM29	P38737	1	12	d
ECM33	P38248	12	24	d
EFM4	P40516	1	18	d
EFM5	P53200	1	92	d
EHT1	P38295	11	90	d
EIS1	Q05050	6	11	d
ELO3	P40319	28	43	d
EMG1	Q06287	19	40	d
EMI2	Q04409	1	96	d
EMP47	P43555	1	10	d
EMW1	P42842	1	26	d
ENO1	P00924	266	443	d
ENO2	P00925	287	468	d
ENP2	P48234	1	6	d
ERB1	Q04660	1	44	d
ERG1	P32476	20	67	d
ERG10	P41338	76	205	d
ERG11	P10614	9	48	d
ERG12	P07277	1	10	d
ERG13	P54839	68	210	d
ERG2	P32352	47	76	d
ERG20	P08524	60	248	d
ERG26	P53199	1	44	d
ERG27	Q12452	28	43	d
ERG3	P32353	1	12	d
ERG6	P25087	40	296	d
ERG8	P24521	1	10	d
ERG9	P29704	88	89	d
ETR1	P38071	1	57	d
FAA1	P30624	45	197	d
FAA4	P47912	1	53	d
FAS1	P07149	103	360	d
FAS2	P19097	145	413	d
FAT1	P38225	1	13	d
FBA1	P14540	230	449	d
FCY1	Q12178	1	169	d
FET3	P38993	23	30	d
FET5	P43561	1	14	d

FIS1	P40515	1	69	d
FKS1	P38631	40	115	d
FMC1	P40491	1	29	d
FMP10	P40098	1	19	d
FMP52	P40008	22	45	d
FOL2	P51601	1	127	d
FRD1	P32614	46	196	d
FSH1	P38777	1	68	d
FSH3	Q99369	1	17	d
FUM1	P08417	10	42	d
FUR1	P18562	1	251	d
GAD1	Q04792	1	15	d
GAR1	P28007	25	54	d
GAS1	P22146	73	88	d
GAS5	Q08193	10	20	d
GCV1	P48015	1	70	d
GCV2	P49095	5	64	d
GCY1	P14065	1	71	d
GDB1	Q06625	1	8	d
GDH1	P07262	184	409	d
GDH2	P33327	1	12	d
GEA2	P39993	1	3	d
GFA1	P14742	43	114	d
GLC3	P32775	1	6	d
GLK1	P17709	96	162	d
GLN1	P32288	94	220	d
GLT1	Q12680	16	197	d
GLY1	P37303	56	132	d
GNA1	P43577	1	29	d
GND1	P38720	218	373	d
GOR1	P53839	1	44	d
GPD2	P41911	62	129	d
GPH1	P06738	11	181	d
GPM1	P00950	245	405	d
GPM2	Q12008	1	14	d
GPP1	P41277	153	426	d
GPP2	P40106	94	285	d
GPX2	P38143	1	113	d
GRE2	Q12068	1	85	d
GRE3	P38715	30	134	d
GRX2	P17695	1	80	d
GRX5	Q02784	1	32	d
GSC2	P40989	1	61	d
GSH1	P32477	1	13	d
GSH2	Q08220	1	53	d
GSY2	P27472	14	80	d
GUA1	P38625	76	270	d
GUK1	P15454	59	307	d
GUT2	P32191	1	7	d
GVP36	P40531	48	163	d
HAM1	P47119	1	89	d
HAS1	Q03532	79	79	d

HBN1	Q96VH4	26	96	d
HEM1	P09950	9	37	d
HEM13	P11353	1	28	d
HEM15	P16622	54	89	d
HEM2	P05373	1	64	d
HFD1	Q04458	1	17	d
HGH1	P48362	1	11	d
HIS1	P00498	35	370	d
HIS3	P06633	1	22	d
HIS4	P00815	72	321	d
HIS5	P07172	13	93	d
HIS6	P40545	1	17	d
HIS7	P33734	1	128	d
HMF1	P40037	93	217	d
HMG1	P12683	1	4	d
HNT1	Q04344	1	312	d
HOM2	P13663	44	299	d
HOM3	P10869	1	27	d
HOM6	P31116	159	362	d
HPT1	Q04178	1	284	d
HRP1	Q99383	1	17	d
HSP31	Q04432	1	44	d
HSP42	Q12329	1	12	d
HXK1	P04806	132	341	d
HXK2	P04807	182	418	d
HYR1	P40581	29	112	d
IDH1	P28834	102	215	d
IDH2	P28241	118	193	d
IDP1	P21954	111	334	d
ILV2	P07342	57	135	d
ILV3	P39522	17	111	d
ILV5	P06168	180	363	d
ILV6	P25605	33	151	d
IMD3	P50095	79	283	d
IMD4	P50094	1	190	d
IMP4	P53941	1	33	d
INO1	P11986	74	219	d
IOC4	Q04213	1	9	d
IPI3	P53877	1	8	d
IPP1	P00817	140	419	d
IRC24	P40580	1	39	d
IRC5	P43610	1	5	d
ISW1	P38144	25	38	d
KEL3	Q08979	1	6	d
KES1	P35844	48	77	d
KGD1	P20967	10	111	d
KGD2	P19262	1	33	d
KRE6	P32486	1	13	d
KRR1	P25586	1	29	d
LAM4	P38800	1	3	d
LAT1	P12695	73	73	d
LCB2	P40970	1	16	d

LEU1	P07264	13	168	d
LEU4	P06208	42	265	d
LEU9	Q12166	1	127	d
LPD1	P09624	253	326	d
LSC1	P53598	1	244	d
LSC2	P53312	1	49	d
LSM1	P47017	1	59	d
LSM7	P53905	1	105	d
LYS1	P38998	77	139	d
LYS12	P40495	27	278	d
LYS2	P07702	1	180	d
LYS20	P48570	181	229	d
LYS21	Q12122	173	258	d
LYS4	P49367	1	133	d
LYS9	P38999	48	277	d
MAE1	P36013	15	46	d
MAK21	Q12176	5	13	d
MBF1	O14467	122	129	d
MCR1	P36060	33	100	d
MDH1	P17505	1	352	d
MDL2	P33311	1	6	d
MDN1	Q12019	2	38	d
MET10	P39692	1	9	d
MET13	P53128	1	23	d
MET14	Q02196	1	22	d
MET22	P32179	1	105	d
MET3	P08536	10	78	d
MET5	P47169	4	51	d
MET6	P05694	179	402	d
MIC12	P38341	1	45	d
MIR1	P23641	185	237	d
MIS1	P09440	100	136	d
MRI1	Q06489	1	37	d
MRP8	P35719	22	184	d
MSC1	Q03104	1	8	d
MSC6	Q08818	1	6	d
MSC7	P38694	1	30	d
MSH2	P25847	1	14	d
MSH6	Q03834	1	3	d
MTC1	P47018	32	43	d
MTD1	Q02046	1	14	d
MTR3	P48240	1	18	d
MVD1	P32377	12	150	d
MYO1	P08964	1	4	d
MYO5	Q04439	12	27	d
NAN1	Q02931	1	21	d
NAT10	P53914	5	13	d
NCL1	P38205	1	72	d
NCP1	P16603	14	156	d
NDE1	P40215	9	57	d
NDI1	P32340	1	9	d
NHP6B	P11633	51	121	d

NIF3	P53081	1	108	d
NIP7	Q08962	1	99	d
NIT3	P49954	17	78	d
NMA1	Q06178	1	23	d
NOB1	Q08444	1	10	d
NOC2	P39744	27	42	d
NOC3	Q07896	1	6	d
NOP13	P53883	12	36	d
NOP2	P40991	1	7	d
NOP56	Q12460	191	232	d
NOP58	Q12499	136	141	d
NOP7	P53261	32	50	d
NPC2	Q12408	1	28	d
NPT1	P39683	11	62	d
NQM1	P53228	1	46	d
NSA1	P53136	1	10	d
NSR1	P27476	25	227	d
NTH1	P32356	7	32	d
NUC1	P08466	1	13	d
NUT1	P53114	1	8	d
OLA1	P38219	131	325	d
OPI3	P05375	23	83	d
OXP1	P28273	1	7	d
OYE2	Q03558	105	336	d
PAA1	Q12447	121	288	d
PCM1	P38628	1	16	d
PDA1	P16387	195	292	d
PDB1	P32473	166	192	d
PDC1	P06169	218	424	d
PDC6	P26263	37	175	d
PDR16	P53860	13	42	d
PDX3	P38075	43	262	d
PET9	P18239	223	343	d
PFF1	P38244	1	4	d
PFK1	P16861	118	379	d
PFK2	P16862	80	331	d
PGI1	P12709	161	339	d
PGK1	P00560	285	455	d
PGM2	P37012	36	182	d
PMA1	P05030	183	298	d
PNC1	P53184	47	146	d
PNO1	Q99216	1	17	d
PNP1	Q05788	1	15	d
POB3	Q04636	9	57	d
POL1	P13382	1	3	d
POL30	P15873	19	241	d
POL31	P46957	1	9	d
POL5	P39985	14	23	d
POR1	P04840	251	432	d
PPX1	P38698	1	23	d
PRM15	Q03262	1	7	d
PRO2	P54885	34	168	d

PRO3	P32263	1	86	d
PRP43	P53131	32	63	d
PRS1	P32895	11	22	d
PRS3	P38689	32	145	d
PRS5	Q12265	1	30	d
PRX1	P34227	1	38	d
PST2	Q12335	26	261	d
PTM1	P32857	1	8	d
PUS1	Q12211	17	26	d
PUS4	P48567	1	11	d
PUS7	Q08647	1	28	d
PUT2	P07275	1	34	d
PWP1	P21304	1	45	d
PWP2	P25635	1	38	d
PYC1	P11154	1	234	d
PYC2	P32327	30	246	d
PYK2	P52489	1	41	d
QNS1	P38795	1	26	d
QRI1	P43123	10	55	d
RAD50	P12753	1	3	d
RCF1	Q03713	1	29	d
RCL1	Q08096	1	12	d
RDI1	Q12434	51	84	d
RDL1	Q12305	1	139	d
RET1	P22276	5	16	d
RFC2	P40348	1	27	d
RGI1	P40043	1	28	d
RHO3	Q00245	21	108	d
RIB1	P38066	1	13	d
RIB3	Q99258	1	85	d
RIB4	P50861	30	249	d
RIB5	P38145	1	20	d
RIP1	P08067	23	49	d
RKI1	Q12189	1	95	d
RNR1	P21524	6	39	d
RNR2	P09938	37	216	d
RNR4	P49723	80	320	d
RPA135	P22138	29	108	d
RPA190	P10964	47	116	d
RPB2	P08518	24	73	d
RPB5	P20434	1	21	d
RPB8	P20436	76	183	d
RPB9	P27999	1	37	d
RPC17	P47076	1	29	d
RPC19	P28000	1	131	d
RPC40	P07703	14	86	d
RPC53	P25441	1	11	d
RPO21	P04050	57	72	d
RPO31	P04051	1	6	d
RQC2	Q12532	1	22	d
RRB1	Q04225	1	39	d
RRP12	Q12754	1	32	d

RRP5	Q05022	23	145 d
RRP9	Q06506	1	16 d
RTC3	P38804	1	47 d
RTN1	Q04947	34	186 d
RTT10	Q08924	1	9 d
RVS161	P25343	1	206 d
RVS167	P39743	1	20 d
SAC1	P32368	71	158 d
SAC6	P32599	123	143 d
SAH1	P39954	208	382 d
SAM1	P10659	139	381 d
SAM2	P19358	137	433 d
SAM4	Q08985	1	67 d
SAP155	P43612	1	4 d
SCP160	P06105	54	371 d
SDH1	Q00711	8	14 d
SDH2	P21801	17	36 d
SDS23	P53172	1	8 d
SDS24	P38314	1	9 d
SER1	P33330	56	233 d
SER3	P40054	1	91 d
SER33	P40510	33	125 d
SEY1	Q99287	1	24 d
SHB17	P36136	17	171 d
SHM1	P37292	56	265 d
SHM2	P37291	228	436 d
SKI3	P17883	7	19 d
SKI8	Q02793	1	11 d
SLA1	P32790	1	19 d
SLA2	P33338	1	14 d
SMB1	P40018	1	23 d
SMC3	P47037	4	14 d
SNZ1	Q03148	1	16 d
SOD1	P00445	188	397 d
SOD2	P00447	45	140 d
SOL3	P38858	41	252 d
SPE3	Q12074	54	184 d
SPF1	P39986	20	88 d
SPT16	P32558	44	157 d
SQT1	P35184	1	10 d
SRV2	P17555	1	78 d
SSF1	P38789	1	10 d
STH1	P32597	7	10 d
STT4	P37297	1	2 d
SVF1	Q05515	1	84 d
SWH1	P35845	1	4 d
SYP1	P25623	1	5 d
TAF2	P23255	1	6 d
TAL1	P15019	261	445 d
TAN1	P53072	1	15 d
TCB1	Q12466	5	28 d
TCB2	P48231	5	15 d

TCB3	Q03640	10	28	d
TDH1	P00360	246	464	d
TDH2	P00358	286	470	d
TDH3	P00359	291	472	d
THR1	P17423	14	83	d
THR4	P16120	40	346	d
TKL1	P23254	141	327	d
TMA16	Q08687	1	25	d
TMA17	Q12513	1	32	d
TMN2	Q04562	1	6	d
TPI1	P00942	237	396	d
TPM1	P17536	1	22	d
TPM2	P40414	1	154	d
TPS1	Q00764	53	178	d
TPS2	P31688	1	151	d
TPS3	P38426	1	49	d
TRM1	P15565	9	34	d
TRM3	Q07527	1	9	d
TRM5	P38793	1	9	d
TRM8	Q12009	1	52	d
TRP2	P00899	10	94	d
TRP3	P00937	10	30	d
TRP4	P07285	1	26	d
TRP5	P00931	55	191	d
TRR1	P29509	73	301	d
TSL1	P38427	9	100	d
TSR1	Q07381	1	17	d
TUB1	P09733	61	112	d
TUB2	P02557	33	195	d
TUB3	P09734	61	93	d
TUM1	Q08686	1	124	d
TUP1	P16649	1	27	d
TVP18	Q04767	1	28	d
UGA1	P17649	10	70	d
UGA2	P38067	1	9	d
UGP1	P32861	67	268	d
URA1	P28272	51	72	d
URA2	P07259	66	282	d
URA4	P20051	1	79	d
URA5	P13298	47	289	d
URA6	P15700	51	84	d
URA7	P28274	25	55	d
URB1	P34241	3	12	d
URB2	P47108	1	11	d
UTP10	P42945	11	30	d
UTP13	Q05946	1	17	d
UTP20	P35194	4	16	d
UTP21	Q06078	10	20	d
UTP23	Q12339	1	18	d
UTP4	Q06679	1	11	d
UTR2	P32623	1	21	d
UTR4	P32626	1	21	d

VIP1	Q06685	9	39	d
VMA10	P48836	45	311	d
VMA13	P41807	125	166	d
VMA2	P16140	160	395	d
VMA22	P38784	1	56	d
VMA4	P22203	72	236	d
VMA5	P31412	72	247	d
VMA7	P39111	1	41	d
VMA8	P32610	1	62	d
VPH1	P32563	90	146	d
VTC1	P40046	1	38	d
VTC3	Q02725	23	155	d
VTC4	P47075	34	87	d
WHI2	P12611	1	9	d
XPT1	P47165	1	22	d
XRN1	P22147	12	131	d
YBL036C	P38197	1	62	d
YBP2	P53169	1	7	d
YBR056W	P38081	1	9	d
YBT1	P32386	6	11	d
YCF1	P39109	1	6	d
YCL042W	P25572	1	41	d
YCP4	P25349	20	172	d
YCR090C	P25654	1	25	d
YCR102C	P25608	1	12	d
YDL086W	Q07505	1	83	d
YDL124W	Q07551	155	335	d
YER156C	P40093	1	109	d
YGL242C	P53066	1	59	d
YGR169C-A	Q3E772	1	56	d
YGR210C	P42942	1	11	d
YGR266W	P53326	1	6	d
YHB1	P39676	106	286	d
YIM1	P28625	1	12	d
YIP3	P53633	102	238	d
YIR035C	P40579	1	19	d
YJL055W	P47044	1	19	d
YJL068C	P40363	1	15	d
YJL171C	P46992	13	39	d
YJR096W	P47137	1	16	d
YKL033W-A	Q86ZR7	21	136	d
YKL069W	P36088	1	26	d
YKL151C	P36059	1	28	d
YKR018C	P36114	1	34	d
YKR070W	P36151	1	13	d
YKT6	P36015	141	313	d
YLR179C	Q06252	25	372	d
YLR287C	Q05881	1	12	d
YLR363W-A	Q3E747	1	60	d
YME2	P32843	1	16	d
YML131W	Q03102	1	13	d
YMR090W	Q04304	1	46	d

YMR099C	Q03161	16	152	d
YMR130W	Q04223	1	14	d
YMR178W	Q03219	1	57	d
YMR226C	Q05016	19	240	d
YMR315W	Q04869	14	130	d
YNK1	P36010	174	378	d
YNL010W	P53981	20	162	d
YNL108C	P53929	1	17	d
YNL134C	P53912	13	99	d
YNL320W	P42840	1	16	d
YNR021W	P53723	23	35	d
YOL098C	Q12496	1	8	d
YOR203W	Q08621	1	39	d
YPD1	Q07688	1	28	d
YPL199C	Q08954	1	42	d
YPL225W	Q08971	1	400	d
YPL260W	Q08977	9	35	d
YPR063C	Q12160	82	82	d
YPR1	Q12458	1	176	d
YPR127W	Q06494	1	28	d
YPR148C	Q06523	1	10	d
YPR172W	Q06608	1	52	d
YSA1	Q01976	1	43	d
YTM1	Q12024	1	10	d
ZEO1	Q08245	1	45	d
ZPR1	P53303	1	40	d
ZRC1	P20107	11	34	d
ZRT1	P32804	76	76	d
ZTA1	P38230	15	29	d
ZWF1	P11412	65	188	d
ABF2	Q02486	256	55	u
ACF2	Q12168	7	1	u
ALE1	Q08548	15	1	u
ARP8	Q12386	6	1	u
ARP9	Q05123	20	19	u
ATO3	Q12359	37	1	u
ATP17	Q06405	52	51	u
ATP20	Q12233	44	43	u
AVT1	P47082	8	1	u
AYR1	P40471	16	15	u
BGL2	P15703	132	125	u
BUD2	P33314	9	1	u
BUR6	P40096	36	35	u
CAB5	Q03941	20	19	u
CAT2	P32796	7	1	u
CCP1	P00431	43	26	u
CDC10	P25342	48	47	u
CHO1	P08456	17	16	u
CHO2	P05374	27	15	u
CIS3	P47001	50	1	u
CMS1	Q07897	16	15	u
COQ1	P18900	21	1	u

COX1	P00401	9	1	u
CTP1	P38152	17	16	u
CYC1	P00044	107	46	u
DBP3	P20447	132	17	u
DBP8	P38719	11	10	u
DBP9	Q06218	24	15	u
DCW1	P36091	11	10	u
DIP5	P53388	8	1	u
ECM31	P38122	16	1	u
EDC3	P39998	9	1	u
ELO1	P39540	15	14	u
ELO2	P25358	13	12	u
ENB1	Q08299	8	1	u
ENT2	Q05785	8	7	u
ERG28	P40030	32	1	u
ERG4	P25340	19	1	u
ERV14	P53173	35	34	u
ERV29	P53337	32	31	u
ESF1	Q06344	8	1	u
FAL1	Q12099	12	1	u
FMP25	Q08023	8	1	u
FTR1	P40088	24	1	u
FUN30	P31380	5	1	u
GAS3	Q03655	19	9	u
GGC1	P38988	135	103	u
GPT2	P36148	13	6	u
GRX8	Q05926	45	44	u
GUD1	Q07729	10	1	u
HCA4	P20448	7	1	u
HHO1	P53551	95	40	u
HHT1	P61830	37	36	u
HMO1	Q03973	97	1	u
HNM1	P19807	9	1	u
HSP150	P32478	42	1	u
HTA1	P04911	204	158	u
HTB1	P02293	250	214	u
HTZ1	Q12692	167	153	u
HXT1	P32465	81	1	u
HXT2	P23585	28	8	u
HXT3	P32466	117	16	u
HXT6	P39003	95	8	u
HXT7	P39004	95	1	u
IDI1	P15496	33	15	u
IES4	Q08561	44	1	u
IFA38	P38286	64	44	u
ILV1	P00927	142	25	u
IMP2'	P32351	14	1	u
IRR1	P40541	5	4	u
ISW2	Q08773	9	1	u
ITC1	P53125	4	1	u
ITR1	P30605	17	8	u
KRI1	P42846	8	1	u

LAS17	Q12446	8	1	u
LHP1	P33399	56	55	u
LSB3	P43603	48	33	u
MAK16	P10962	15	1	u
MAK5	P38112	7	6	u
MCM4	P30665	6	1	u
MDH3	P32419	47	46	u
MET12	P46151	8	7	u
MGM101	P32787	37	36	u
MIC10	Q96VH5	57	56	u
MIC60	P36112	27	1	u
MIT1	P40002	8	1	u
MOT1	P32333	3	1	u
MRH1	Q12117	48	47	u
MXR1	P40029	56	55	u
NCB2	Q92317	33	32	u
NHP10	Q03435	23	1	u
NHP6A	P11632	124	54	u
NOP10	Q6Q547	176	98	u
NOP12	Q08208	21	20	u
NOP14	Q99207	23	5	u
NOP15	P53927	46	1	u
NOP4	P37838	21	13	u
NOP6	Q07623	46	45	u
NPL6	P32832	22	1	u
NRD1	P53617	9	1	u
ODC2	Q99297	16	1	u
OLE1	P21147	29	1	u
OSH7	P38755	34	33	u
PAN1	P32521	7	1	u
PAP1	P29468	26	1	u
PCS60	P38137	18	8	u
PDR5	P33302	37	32	u
PDS5	Q04264	4	1	u
PHO84	P25297	9	8	u
PHO91	P27514	6	5	u
PIC2	P40035	16	1	u
PIS1	P06197	22	1	u
PKR1	Q03880	41	40	u
PUB1	P32588	21	20	u
PXR1	P53335	83	1	u
QCR7	P00128	130	38	u
QCR9	P22289	85	1	u
QDR2	P40474	18	1	u
RAD9	P14737	4	1	u
RCF2	P53721	74	45	u
RDH54	P38086	5	1	u
RFS1	P38234	24	23	u
RIM1	P32445	157	139	u
RNQ1	P25367	13	1	u
ROK1	P45818	9	1	u
RPA34	P47006	20	1	u

RPA49	Q01080	12	1	u
RPB10	P22139	72	1	u
RPB11	P38902	42	41	u
RPC10	P40422	78	1	u
RPF2	P36160	14	13	u
RPO26	P20435	70	30	u
RRP1	P35178	34	15	u
RRP14	P36080	11	10	u
RRP15	Q06511	41	1	u
RSA4	P25382	10	9	u
RSC2	Q06488	16	1	u
RSC3	Q06639	39	1	u
RSC4	Q02206	8	7	u
RSC58	Q07979	10	1	u
RSC8	P43609	36	8	u
RSC9	Q03124	8	1	u
SAM3	Q08986	9	1	u
SAS10	Q12136	8	1	u
SFH1	Q06168	11	1	u
SGD1	Q06132	6	1	u
SHE10	P53075	8	7	u
SLC1	P33333	16	15	u
SMC1	P32908	4	3	u
SNQ2	P32568	16	12	u
SPB1	P25582	6	1	u
SPC110	P32380	25	1	u
SPC42	P36094	13	1	u
SPT5	P27692	14	4	u
SRP40	P32583	13	12	u
SUR7	P54003	33	15	u
TAT1	P38085	42	7	u
TCD2	P36101	11	1	u
TFC4	P33339	5	1	u
TGL1	P34163	17	1	u
TIM11	P81449	54	1	u
TNA1	P53322	9	1	u
TOP1	P04786	12	1	u
TOP2	P06786	31	1	u
TRM82	Q03774	11	10	u
TSC13	Q99190	30	1	u
TYW1	Q08960	6	1	u
UTP15	Q04305	10	1	u
VCX1	Q99385	12	1	u
VMA6	P32366	44	43	u
VPH2	P32341	21	1	u
YAP1801	P38856	8	1	u
YBL029C-A	Q3E756	51	1	u
YCR087C-A	P37263	31	1	u
YCS4	Q06156	5	1	u
YGR012W	P53206	13	12	u
YGR130C	P53278	24	11	u
YHM2	Q04013	132	125	u

YJR061W	P40355	5	1	u
YJU3	P28321	15	1	u
YKL100C	P34248	8	7	u
YKR011C	Q02209	13	1	u
YLR413W	Q06689	39	7	u
YLR455W	Q06188	15	1	u
YMC1	P32331	16	1	u
YNR034W-A	Q3E841	209	130	u
YOP1	Q12402	27	26	u
YOR1	P53049	4	1	u
YOR283W	Q12040	21	20	u
YRO2	P38079	14	1	u
YSW1	P38280	8	1	u

d: lower u: higher

Gene name	UniProt ID	nucleus rank	non-nucleus rank	in nucleus
AFG3	P39925	49	40	u
AKR1	P39010	1	6	d
ALA1	P40825	156	460	d
ALG1	P16661	89	1	u
ALG12	P53730	83	46	u
ALG3	P38179	31	1	u
ALG5	P40350	273	1	u
ALG6	Q12001	26	1	u
ALG8	P40351	33	1	u
ALG9	P53868	159	1	u
ARB1	P40024	445	459	d
ARD1	P07347	67	133	d
ARF1	P11076	614	544	u
ARF2	P19146	558	541	u
BCS1	P32839	11	1	u
BET2	P20133	1	13	d
BUD32	P53323	1	37	d
CCL1	P37366	37	1	u
CDC14	Q00684	114	35	u
CDC24	P11433	35	1	u
CDC28	P00546	161	98	u
CDC33	P07260	278	418	d
CDC42	P19073	92	91	u
CDC48	P25694	635	543	u
CDC53	Q12018	159	135	u
CDC60	P26637	91	381	d
CET1	O13297	100	1	u
CKS1	P20486	70	69	u
CMD1	P06787	312	78	u
CNS1	P33313	12	11	u
COQ8	P27697	79	1	u
CSL4	P53859	81	16	u
CYC3	P06182	87	1	u
CYT2	Q00873	44	1	u
DED1	P06634	615	495	u
DIE2	P50076	36	1	u
DIS3	Q08162	103	23	u
DPM1	P14020	664	224	u
DUG1	P43616	87	274	d
DYS1	P38791	56	498	d
EFB1	P32471	609	338	u
ELP3	Q02908	1	25	d
ELP4	Q02884	11	10	u
EMC4	P53073	409	55	u
ENP1	P38333	117	116	u
ERO1	Q03103	307	337	d
ERV1	P27882	252	24	u
ESA1	Q08649	32	1	u
ESS1	P22696	592	279	u
FAP7	Q12055	1	84	d

FPR1	P20081	457	300	u
FPR2	P32472	553	1	u
FUN12	P39730	153	242	d
GAA1	P39012	112	7	u
GCD11	P32481	108	370	d
GCD7	P32502	1	94	d
GCN3	P14741	1	32	d
GDI1	P39958	347	236	u
GET1	P53192	230	19	u
GET2	P40056	184	16	u
GIS2	P53849	30	66	d
GLC7	P32598	541	307	u
GLN4	P13188	17	410	d
GPI10	P30777	23	1	u
GPI11	Q06636	21	1	u
GPI12	P23797	122	1	u
GPI13	Q07830	19	1	u
GPI8	P49018	23	1	u
GRS1	P38088	178	519	d
HCR1	Q05775	203	278	d
HEM3	P28789	1	29	d
HLJ1	P48353	113	1	u
HRT1	Q08273	39	1	u
HSC82	P15108	649	570	u
HSF1	P10961	12	1	u
HSL7	P38274	11	10	u
HSP60	P19882	717	612	u
HSP82	P02829	634	563	u
HTS1	P07263	104	211	d
HYP2	P23301	758	617	u
ISM1	P48526	34	1	u
ISU1	Q03020	30	1	u
JAC1	P53193	54	1	u
KRS1	P15180	115	393	d
LST8	P41318	52	1	u
MAP1	Q01662	71	135	d
MDM38	Q08179	313	187	u
MEX67	Q99257	150	101	u
MMF1	P40185	685	361	u
MMS2	P53152	36	144	d
MNL1	P38888	18	11	u
MNP1	P53163	208	1	u
MOG1	P47123	1	47	d
MSR1	P38714	8	1	u
MTR2	P34232	57	1	u
MTR4	P47047	225	26	u
NAM2	P11325	11	15	d
NAM7	P30771	99	53	u
NAT1	P12945	148	315	d
NHP2	P32495	372	72	u
NMD3	P38861	18	74	d
NMT1	P14743	31	70	d

NOG1	Q02892	268	266	u
NOG2	P53742	154	18	u
NOP1	P15646	729	258	u
NTF2	P33331	91	90	u
NUS1	Q12063	117	1	u
ORM1	P53224	46	1	u
ORM2	Q06144	47	21	u
OST1	P41543	140	178	d
OXA1	P39952	70	1	u
PAC10	P48363	1	123	d
PAM16	P42949	626	1	u
PCP1	P53259	14	1	u
PDE1	P22434	1	12	d
PEX13	P80667	13	1	u
PFY1	P07274	41	40	u
PHO85	P17157	51	50	u
PKC1	P24583	5	1	u
PKH1	Q03407	1	6	d
PRE1	P22141	88	229	d
PRE10	P21242	183	177	u
PRE5	P40302	586	494	u
PSE1	P32337	13	72	d
PUP2	P32379	633	334	u
PUP3	P25451	178	172	u
RAD3	P06839	53	44	u
RAD6	P06104	28	1	u
RAS1	P01119	330	50	u
RAS2	P01120	456	256	u
RER1	P25560	243	52	u
RER2	P35196	105	1	u
RHO1	P06780	359	268	u
RNA1	P11745	1	358	d
RPB7	P34087	229	27	u
RPF1	P38805	491	1	u
RPL10	P41805	723	574	u
RPL28	P02406	612	472	u
RPL30	P14120	742	436	u
RPL5	P26321	641	537	u
RPN1	P38764	318	240	u
RPN11	P43588	332	296	u
RPN2	P32565	484	445	u
RPN3	P40016	267	228	u
RPN5	Q12250	316	189	u
RPN6	Q12377	208	112	u
RPN7	Q06103	403	180	u
RPN8	Q08723	359	191	u
RPN9	Q04062	532	306	u
RPP0	P05317	471	378	u
RPS13	P05756	659	548	u
RPS31	P05759	732	461	u
RPS5	P26783	668	557	u
RPT1	P33299	277	146	u

RPT2	P40327	138	116	u
RPT3	P33298	195	143	u
RPT4	P53549	159	77	u
RPT5	P33297	142	48	u
RPT6	Q01939	479	227	u
SBA1	P28707	22	118	d
SCL1	P21243	673	430	u
SCS2	P40075	406	178	u
SDS22	P36047	63	159	d
SEC11	P15367	329	1	u
SEC13	Q04491	482	273	u
SEC21	P32074	217	267	d
SEC62	P21825	273	56	u
SED5	Q01590	29	1	u
SES1	P07284	70	513	d
SGF73	P53165	8	7	u
SIT4	P20604	15	149	d
SKP1	P52286	184	131	u
SMP3	Q04174	9	1	u
SMT3	Q12306	669	123	u
SNU13	P39990	391	1	u
SRM1	P21827	236	19	u
SRO7	Q12038	19	13	u
SRP101	P32916	305	312	d
SSS1	P35179	342	67	u
STE14	P32584	19	1	u
STE24	P47154	245	31	u
SUB2	Q07478	474	367	u
SUI2	P20459	368	434	d
SUI3	P09064	181	409	d
SUP45	P12385	546	382	u
TFB3	Q03290	64	1	u
THS1	P04801	66	480	d
TIF11	P38912	524	499	u
TIF35	Q04067	151	342	d
TIF5	P38431-2	238	301	d
TIF6	Q12522	71	102	d
TIM13	P53299	669	1	u
TIM22	Q12328	25	1	u
TIM8	P57744	440	1	u
TRM7	P38238	1	31	d
TYS1	P36421	71	293	d
UBC1	P21734	80	257	d
UBC9	P50623	182	1	u
UBP10	P53874	25	1	u
UBP6	P43593	236	246	d
UFD1	P53044	157	43	u
UTP22	P53254	367	40	u
VAS1	P07806-2	129	353	d
VPS30	Q02948	9	8	u
VPS35	P34110	5	14	d
VPS74	Q06385	62	43	u

VTI1	Q04338	78	77	u
WBP1	P33767	337	46	u
WRS1	Q12109	34	250	d
YDJ1	P25491	568	256	u
YFH1	Q07540	105	1	u
YIP1	P53039	20	1	u
YME1	P32795	166	176	d
YNL247W	P53852	125	369	d
YPK1	P12688	110	123	d
YPK2	P18961	37	28	u
YTA12	P40341	188	148	u
ZUO1	P32527	309	304	u
VMA9	Q3E7B6	196	1	u
KSH1	Q8TGJ3	200	1	u
SNT2	P53127	4	1	u
SEC39	Q12745	20	12	u
VAR1	P02381	294	11	u
YUR1	P26725	46	1	u
CDC27	P38042	7	1	u
HDA1	P53973	35	42	d
TCM62	P38228	17	1	u
YRB30	P53107	1	21	d
MFT1	P33441	109	1	u
TIM9	O74700	416	1	u
RFA3	P26755	95	39	u
PEX22	P39718	60	1	u
CDC36	P06100	24	87	d
LIP2	Q06005	14	1	u
NIC96	P34077	352	262	u
PUF4	P25339	6	5	u
RPB4	P20433	383	1	u
APC1	P53886	14	1	u
RAD18	P10862	10	1	u
CWH41	P53008	218	185	u
CTK1	Q03957	37	17	u
GAL11	P19659	18	1	u
HRD3	Q05787	65	56	u
MNN2	P38069	164	193	d
NUP60	P39705	76	1	u
PDI1	P17967	672	547	u
TIM54	P47045	69	54	u
MSM1	P22438	16	15	u
VPS53	P47061	1	10	d
AST2	P39945	48	1	u
EFR3	Q03653	24	30	d
GGA1	Q06336	9	16	d
GIM5	Q04493	115	301	d
LYS5	P50113	1	16	d
MPD2	Q99316	255	1	u
MRPL13	Q02204	290	1	u
MRPL7	P36519	77	1	u
MUK1	Q02866	15	1	u

PMT5	P52867	7	1	u
PRE9	P23638	475	484	d
RPL11B	Q3E757	585	458	u
RPL39	P04650	106	105	u
YML039W	Q03434	322	237	u
YRB2	P40517	69	30	u
CDC23	P16522	15	14	u
CMK1	P27466	1	10	d
COA3	Q3E7B2	60	1	u
DDI1	P40087	1	81	d
DOP1	Q03921	71	8	u
EAP1	P36041	8	7	u
NDC1	P32500	144	7	u
NOT5	Q12514	34	1	u
NSP1	P14907	83	1	u
POM34	Q12445	129	1	u
RET3	P53600	194	354	d
SEC15	P22224	65	5	u
SFB3	P38810	116	135	d
UBP2	Q01476	11	25	d
UTP30	P36144	181	1	u
CNA1	P23287	1	8	d
DBP5	P20449	120	315	d
PRE2	P30656	269	142	u
SEC63	P14906	349	331	u
AXL1	P40851	4	3	u
BRO1	P48582	6	16	d
CSF1	Q12150	2	1	u
LTP1	P40347	1	64	d
MRP2	P10663	177	1	u
MRPL19	P53875	612	1	u
MRS6	P32864	1	32	d
PET309	P32522	1	4	d
PNG1	Q02890	1	11	d
RPD3	P32561	116	1	u
TFC3	P34111	49	1	u
UBC6	P33296	95	1	u
VPS17	P32913	26	16	u
YEH2	Q07950	9	1	u
YLH47	Q06493	107	31	u
CAF20	P12962	30	29	u
CMP2	P14747	8	15	d
OST2	P46964	154	36	u
RPL37B	P51402	567	546	u
INP53	Q12271	1	25	d
NMA111	P53920	187	53	u
RKR1	Q04781	41	26	u
SAP30	P38429	85	1	u
APL6	P46682	6	17	d
ETT1	Q08421	50	49	u
IFM1	P25038	7	1	u
INP54	Q08227	160	1	u

RML2	P32611	71	1	u
DRS2	P39524	11	6	u
RAM1	P22007	1	21	d
TFB2	Q02939	77	1	u
ZIM17	P42844	60	1	u
COS2	P0CX12	12	1	u
COX14	P39103	677	1	u
DOM34	P33309	39	111	d
EXO84	P38261	26	25	u
GIR2	Q03768	36	16	u
MLP2	P40457	107	5	u
MPE1	P35728	34	1	u
MRPL23	Q12487	174	1	u
MRPL24	P36525	155	1	u
NOT3	P06102	43	5	u
PEP4	P07267	423	206	u
PHB1	P40961	513	82	u
RKM5	Q12367	26	1	u
RPL21B	Q12672	502	521	d
SEC10	Q06245	22	10	u
SEC8	P32855	48	1	u
SEC9	P40357	15	1	u
SHR3	Q02774	49	48	u
YGR026W	P53217	134	1	u
YPT7	P32939	547	271	u
HIR3	P47171	32	1	u
MRPL15	P36523	265	1	u
MTQ2	Q03920	1	20	d
RPL36B	O14455	774	606	u
RRD1	P40454	12	1	u
TOM5	P80967	563	1	u
UBC4	P15731	76	75	u
UFE1	P41834	60	1	u
ABP1	P15891	356	222	u
ADA2	Q02336	11	1	u
AEP2	P22136	8	1	u
AFG1	P32317	39	1	u
AIM23	P47015	13	1	u
AKL1	P38080	13	8	u
ALG2	P43636	144	1	u
ALY2	P47029	5	1	u
AOS1	Q06624	28	13	u
APE1	P14904	52	93	d
APE2	P32454	341	412	d
APE4	P38821	31	19	u
APL4	Q12028	23	35	d
APL5	Q08951	5	55	d
APM3	P38153	10	9	u
APQ12	P40532	133	1	u
APS1	P35181	67	115	d
APS3	P47064	1	53	d
ARF3	P40994	500	1	u

ARP4	P80428	179	29	u
ARX1	Q03862	308	221	u
ASI1	P54074	8	1	u
ASI3	P53983	21	1	u
ASM4	Q05166	39	38	u
ATG27	P46989	86	185	d
BET4	Q00618	1	61	d
BFR2	Q06631	153	116	u
BLM10	P43583	72	26	u
BNI1	P41832	15	7	u
BOS1	P25385	42	1	u
BRE5	P53741	19	18	u
BRR6	P53062	51	1	u
BST1	P43571	9	1	u
BUD13	P46947	18	1	u
BUD20	Q08004	331	1	u
BUD23	P25627	17	1	u
BUD6	P41697	25	1	u
BUL1	P48524	15	4	u
BUL2	Q03758	1	9	d
CAJ1	P39101	282	52	u
CBK1	P53894	19	18	u
CBP3	P21560	161	1	u
CBP6	P07253	718	1	u
CBS2	P14905	12	1	u
CDC1	P40986	10	18	d
CDC11	P32458	121	164	d
CDC12	P32468	495	83	u
CDC31	P06704	329	28	u
CDC50	P25656	12	1	u
CDC73	Q06697	110	1	u
CEX1	Q12453	19	18	u
CHC1	P22137	280	304	d
CKB1	P43639	79	33	u
CKB2	P38930	87	36	u
CLU1	Q03690	319	312	u
COF1	Q03048	316	439	d
COG1	P53079	11	10	u
COG7	P53195	57	16	u
COG8	Q04632	23	22	u
COR1	P07256	420	93	u
COS9	P36034	34	1	u
COX20	Q04935	285	1	u
CPR2	P23285	127	1	u
CPR3	P25719	448	270	u
CPR4	P25334	15	1	u
CPR6	P53691	172	281	d
CPS1	P27614	45	123	d
CRM1	P30822	36	148	d
CSE1	P33307	1	91	d
CTR9	P89105	219	16	u
CUE1	P38428	377	1	u

CWH43	P25618	49	9	u
DAP2	P18962	30	16	u
DBF2	P22204	54	43	u
DBP1	P24784	101	100	u
DEP1	P31385	36	1	u
DER1	P38307	48	1	u
DIA4	P38705	11	1	u
DNF2	Q12675	56	8	u
DNF3	Q12674	6	1	u
DOA1	P36037	7	19	d
DPH1	P40487	1	21	d
DPH5	P32469	1	192	d
DTD1	Q07648	203	74	u
DUN1	P39009	9	1	u
EAF7	P53911	11	21	d
ECM1	P39715	49	80	d
ECM14	P38836	47	33	u
ECM32	P32644	13	1	u
EDE1	P34216	22	46	d
ELP2	P42935	1	23	d
EMC1	P25574	223	200	u
EMC5	P40540	316	34	u
EMP24	P32803	485	166	u
EMP46	Q12396	21	1	u
EMP65	P40085	9	1	u
ENT4	Q07872	65	1	u
ENT5	Q03769	11	10	u
ENV10	Q99382	58	1	u
ENV11	P53246	6	5	u
EPS1	P40557	27	41	d
ERD1	P16151	12	1	u
ERJ5	P43613	236	1	u
ERP4	Q12450	289	1	u
ERP5	P38819	116	1	u
ERP6	P53198	21	1	u
EUG1	P32474	62	75	d
EXO70	P19658	40	30	u
FCP1	Q03254	7	1	u
FLC1	Q08967	6	1	u
FMT1	P32785	12	1	u
FOB1	O13329	16	15	u
FPR3	P38911	204	219	d
FPR4	Q06205	162	54	u
FUB1	P25659	1	19	d
FUN19	P28003	1	11	d
FYV10	P40492	9	8	u
GAB1	P41733	12	11	u
GCD1	P09032	1	15	d
GCD2	P12754	1	39	d
GCS1	P35197	1	104	d
GDA1	P32621	52	93	d
GET3	Q12154	587	305	u

GET4	Q12125	181	91	u
GIM4	P40005	44	1	u
GIN4	Q12263	17	12	u
GIP4	P39732	19	1	u
GOS1	P38736	321	191	u
GPB1	Q08886	16	1	u
GPI14	P47088	23	1	u
GTB1	Q04924	70	90	d
GTF1	P53260	97	1	u
GUS1	P46655	234	522	d
GWT1	P47026	10	1	u
GYP5	Q12344	1	5	d
HAL5	P38970	17	16	u
HAT2	P39984	38	23	u
HCH1	P53834	125	329	d
HDA3	Q06623	14	45	d
HEF3	P53978	100	107	d
HHF1	P02309	745	223	u
HOG1	P32485	1	33	d
HOS3	Q02959	53	19	u
HOS4	P40480	9	1	u
HPM1	P40481	1	12	d
HRD1	Q08109	26	1	u
HSL1	P34244	10	1	u
ICP55	P40051	63	8	u
IKS1	P47042	14	21	d
ILS1	P09436	133	466	d
IMP1	P28627	25	1	u
IMP2	P46972	27	1	u
ISA2	Q12425	96	1	u
IST1	P53843	32	1	u
IST2	P38250	227	5	u
JEM1	P40358	7	13	d
KAP104	P38217	1	31	d
KAP114	P53067	1	23	d
KAP122	P32767	1	12	d
KAP123	P40069	125	244	d
KEX1	P09620	13	19	d
KIN1	P13185	18	4	u
KOG1	P38873	4	1	u
KRE5	P22023	113	1	u
KSS1	P14681	26	1	u
KTR3	P38130	286	22	u
LAA1	P39526	19	11	u
LCL2	Q08045	85	1	u
LIP5	P32875	66	1	u
LOA1	Q06508	163	1	u
LOS1	P33418	1	4	d
LRS4	Q04087	14	1	u
LSG1	P53145	22	79	d
MAK3	Q03503	26	97	d
MAS2	P11914	356	19	u

MBA1	P38300	57	1	u
MCX1	P38323	108	161	d
MDR1	P53258	1	4	d
MEC1	P38111	30	1	u
MEF1	P25039	251	221	u
MGR1	P25573	36	1	u
MGR2	Q02889	47	1	u
MGR3	Q04472	64	1	u
MKK2	P32491	10	1	u
MLP1	Q02455	485	7	u
MNS1	P32906	97	82	u
MNT3	P40549	8	1	u
MOB1	P40484	15	1	u
MON2	P48563	23	1	u
MPD1	Q12404	215	1	u
MRN1	Q08925	32	15	u
MRP10	O75012	251	1	u
MRP13	P12686	162	1	u
MRP17	P28778	346	1	u
MRP51	Q02950	160	1	u
MRPL1	Q04599	228	1	u
MRPL10	P36520	69	1	u
MRPL11	P36521	213	1	u
MRPL17	P36528	141	1	u
MRPL20	P22354	241	23	u
MRPL22	P53881	366	1	u
MRPL3	P36516	398	1	u
MRPL31	P14063	330	1	u
MRPL40	P36534	243	1	u
MRPL49	P40858	176	1	u
MRPL50	P53724	398	1	u
MRPL6	P32904	283	1	u
MRPS17	Q03246	340	1	u
MRPS28	P21771	397	1	u
MRPS35	P53292	190	1	u
MRPS5	P33759	156	14	u
MRT4	P33201	346	176	u
MSN5	P52918	1	39	d
MSS2	P40990	41	1	u
MSS51	P32335	412	1	u
MST1	P07236	42	1	u
MSY1	P48527	30	1	u
MTG2	P38860	19	1	u
MTR10	Q99189	5	4	u
MZM1	Q03429	171	1	u
NAP1	P25293	49	142	d
NAT2	P37293	105	1	u
NAT5	Q08689	61	27	u
NEW1	Q08972	224	251	d
NGG1	P32494	7	1	u
NMD5	P46970	1	22	d
NNT1	Q05874	1	37	d

NPA3	P47122	1	54	d
NUM1	Q00402	38	9	u
NUP116	Q02630	24	4	u
NUP145	P49687	92	43	u
NUP192	P47054	269	2	u
NUP2	P32499	180	6	u
NUP82	P40368	124	1	u
NVJ1	P38881	68	1	u
OCA1	P50946	1	19	d
OCA6	Q12454	1	20	d
OCT1	P35999	12	5	u
OM14	P38325	156	37	u
OMA1	P36163	105	1	u
OPI1	P21957	37	1	u
OTU1	P43558	1	32	d
PBN1	P25580	142	80	u
PBP1	P53297	44	6	u
PBY1	P38254	1	6	d
PCL6	P40038	11	1	u
PEA2	P40091	11	1	u
PEP1	P32319	42	61	d
PEP3	P27801	5	19	d
PEP5	P12868	9	1	u
PER1	P25625	13	1	u
PEX14	P53112	45	1	u
PEX15	Q08215	12	1	u
PEX17	P40155	84	1	u
PEX4	P29340	25	1	u
PEX6	P33760	9	1	u
PIM1	P36775	312	68	u
PIR1	Q03178	1	31	d
PLP2	Q12017	16	33	d
PMT1	P33775	217	114	u
PMT3	P47190	64	1	u
PMT4	P46971	136	31	u
PMT6	P42934	46	1	u
PMT7	Q06644	21	1	u
PNT1	P38969	79	1	u
POF1	P25576	1	17	d
POP5	P28005	158	1	u
PPZ1	P26570	36	1	u
PRB1	P09232	23	72	d
PRE4	P30657	161	235	d
PRK1	P40494	12	1	u
PRP19	P32523	95	110	d
PRP28	P23394	16	1	u
PTC7	P38797	444	1	u
PTH1	P38876	26	1	u
PUF6	Q04373	310	246	u
RAD4	P14736	7	6	u
RAP1	P11938	68	23	u
RAT1	Q02792	93	50	u

RAX1	Q08760	33	1	u
RBL2	P48606	207	46	u
RCK2	P38623	1	23	d
RCO1	Q04779	20	13	u
RET2	P43621	103	86	u
RFA1	P22336	140	253	d
RIA1	P53893	1	8	d
RKM1	Q08961	1	7	d
RLM1	Q12224	8	1	u
RLP24	Q07915	216	47	u
RMT2	Q03305	1	22	d
ROT2	P38138	68	9	u
RPL12A	P0CX53	511	493	u
RPL14A	P36105	725	587	u
RPL14B	P38754	701	550	u
RPL16B	P26785	688	575	u
RPL17A	P05740	504	482	u
RPL17B	P46990	504	482	u
RPL18A	P0CX49	502	478	u
RPL19A	P0CX82	589	496	u
RPL1A	P0CX43	730	613	u
RPL22B	P56628	97	169	d
RPL23A	P0CX41	771	630	u
RPL24A	P04449	521	454	u
RPL24B	P24000	524	458	u
RPL25	P04456	689	576	u
RPL26B	P53221	765	635	u
RPL31A	P0C2H8	740	598	u
RPL33B	P41056	644	481	u
RPL36A	P05745	774	623	u
RPL38	P49167	513	449	u
RPL40A	P0CH08	611	1	u
RPL42A	P0CX27	202	193	u
RPL43A	P0CX25	741	539	u
RPL7A	P05737	680	586	u
RPL8A	P17076	761	628	u
RPL9A	P05738	589	558	u
RPL9B	P51401	585	580	u
RPM2	Q02773	19	1	u
RPN12	P32496	267	174	u
RPP2B	P02400	389	343	u
RPS11A	P0CX47	581	532	u
RPS12	P48589	655	542	u
RPS17A	P02407	715	573	u
RPS18A	P0CX55	768	637	u
RPS19A	P07280	734	600	u
RPS1A	P33442	764	634	u
RPS1B	P23248	763	633	u
RPS20	P38701	746	581	u
RPS21B	Q3E754	722	1	u
RPS22A	P0C0W1	709	595	u
RPS24A	P0CX31	743	607	u

RPS27A	P35997	488	429	u
RPS3	P05750	749	618	u
RPS30A	P0CX33	752	413	u
RPS7A	P26786	670	496	u
RPS7B	P48164	630	558	u
RPS9A	O13516	739	591	u
RPS9B	P05755	750	593	u
RRF1	P38771	418	1	u
RRP43	P25359	25	24	u
RRS1	Q08746	234	23	u
RSM18	P40033	320	1	u
RSM22	P36056	31	30	u
RSM23	Q01163	259	1	u
RSM24	Q03976	288	1	u
RSM25	P40496	441	1	u
RSM26	P47141	118	1	u
RSM28	Q03430	99	1	u
RSM7	P47150	274	1	u
RTC6	O14464	54	1	u
RTG2	P32608	78	33	u
RTR1	P40084	1	19	d
RTS1	P38903	7	6	u
RTT101	P47050	6	15	d
RUD3	Q12234	1	9	d
RUP1	Q12242	1	6	d
RVB1	Q03940	504	92	u
SAM35	P14693	87	1	u
SAM50	P53969	100	1	u
SAS3	P34218	6	1	u
SBH1	P52870	523	1	u
SCC2	Q04002	10	1	u
SCJ1	P25303	275	1	u
SCY1	P53009	12	23	d
SDA1	P53313	32	39	d
SEC1	P30619	49	25	u
SEC12	P11655	128	168	d
SEC17	P32602	437	199	u
SEC20	P28791	39	1	u
SEC22	P22214	111	20	u
SEC24	P40482	234	232	u
SEC26	P41810	272	241	u
SEC3	P33332	69	28	u
SEC31	P38968	98	134	d
SEC4	P07560	666	425	u
SEC5	P89102	60	13	u
SEC6	P32844	114	57	u
SEC65	P29478	185	1	u
SEC66	P33754	404	1	u
SEC7	P11075	32	31	u
SEH1	P53011	159	1	u
SFM1	Q12314	1	299	d
SFT1	P43682	246	1	u

SGT2	Q12118	89	298	d
SGV1	P23293	90	114	d
SHS1	Q07657	113	57	u
SIL1	Q08199	190	1	u
SIN4	P32259	25	9	u
SKN7	P38889	32	1	u
SLF1	Q12034	11	10	u
SLH1	P53327	38	4	u
SLY1	P22213	115	66	u
SMC6	Q12749	30	1	u
SNF4	P12904	117	173	d
SPA2	P23201	23	1	u
SPC1	P46965	246	1	u
SPC105	P53148	15	5	u
SPC3	Q12133	142	55	u
SPN1	Q06505	235	11	u
SPO7	P18410	37	1	u
SPP1	Q03012	26	1	u
SPT14	P32363	11	1	u
SPT20	P50875	24	52	d
SPT3	P06844	45	1	u
SPT6	P23615	353	70	u
SPT7	P35177	14	3	u
SRO9	P25567	64	80	d
SRP102	P36057	405	1	u
SRP21	P32342	176	1	u
SRP54	P20424	139	27	u
SSA2	P10592	735	622	u
SSD1	P24276	41	55	d
SSO2	P39926	203	52	u
SSQ1	Q05931	120	134	d
STM1	P39015	451	559	d
STT3	P39007	153	89	u
SWC4	P53201	68	1	u
SWP1	Q02795	144	1	u
SXM1	Q04175	1	92	d
TAF10	Q12030	127	1	u
TAF6	P53040	288	126	u
TAH1	P25638	45	44	u
TED1	P40533	156	135	u
TEF1	P02994	705	578	u
TEF4	P36008	497	435	u
TFB4	Q12004	29	1	u
THP2	O13539	60	1	u
TIF4631	P39935	71	85	d
TIF4632	P39936	6	15	d
TIM12	P32830	109	1	u
TIM17	P39515	131	1	u
TIM21	P53220	182	1	u
TIM44	Q01852	598	21	u
TMA108	P40462	15	110	d
TMA22	P47089	129	174	d

TOM1	Q03280	106	37	u
TPA1	P40032	438	350	u
TPK1	P06244	51	1	u
TPK2	P06245	71	1	u
TPK3	P05986	51	11	u
TRA1	P38811	199	1	u
TRL1	P09880	1	16	d
TRS130	Q03660	13	1	u
TRX2	P22803	676	440	u
TSA2	Q04120	1	239	d
TUF1	P02992	559	99	u
TVP23	P38962	23	83	d
TWF1	P53250	376	13	u
UBA2	P52488	1	39	d
UBC5	P15732	1	76	d
UBC7	Q02159	172	1	u
UBP13	P38187	13	1	u
UBP15	P50101	4	26	d
UBP16	Q02863	19	1	u
UBP3	Q01477	11	20	d
UFD4	P33202	1	6	d
ULP1	Q02724	15	22	d
UPF3	P48412	38	1	u
URE2	P23202	27	42	d
USA1	Q03714	49	41	u
USE1	P53146	132	1	u
VAC8	P39968	161	125	u
VAN1	P23642	37	36	u
VID30	P53076	25	4	u
VMA1	P17255	636	545	u
VMS1	Q04311	1	7	d
VPS1	P21576	651	527	u
VPS16	Q03308	6	5	u
VPS4	P52917	23	34	d
VPS71	Q03433	17	1	u
VPS75	P53853	37	1	u
VTA1	Q06263	1	13	d
VTC2	P43585	122	132	d
WHI3	P34761	8	14	d
YBR137W	P38276	148	97	u
YCK1	P23291	100	46	u
YER134C	P40081	148	319	d
YGR201C	P42936	1	19	d
YIL108W	P40483	120	107	u
YKE2	P52553	43	178	d
YKL133C	P36066	10	1	u
YML6	P51998	267	1	u
YMR31	P19955	391	1	u
YOL057W	Q08225	1	69	d
YOS1	Q3E834	64	1	u
YOS9	Q99220	59	47	u
YPI1	P43587	1	29	d

YPS1	P32329	9	1	u
YPS7	Q06325	9	1	u
YPT31	P38555	567	448	u
YUH1	P35127	1	19	d
ASC1	P38011	727	609	u
DSK2	P48510	14	1	u
ENV9	Q08651	46	1	u
ERV41	Q04651	59	1	u
GPI16	P38875	86	112	d
IRC20	Q06554	24	1	u
MCA1	Q08601	1	10	d
MEF2	P39677	12	5	u
MNN1	P39106	6	17	d
MRPS8	Q03799	516	1	u
OST6	Q03723	64	1	u
PER33	Q12144	106	1	u
PGA3	Q12746	319	14	u
PHO81	P17442	33	1	u
PTR2	P32901	16	1	u
RBD2	Q12270	38	37	u
RPL35A	P0CX84	744	604	u
RPL37A	P49166	657	483	u
RPL4B	P49626	537	464	u
SAD1	P43589	10	9	u
SDH3	P33421	90	53	u
SDS3	P40505	113	1	u
SOL2	P37262	32	97	d
SPC2	Q04969	500	25	u
SWD2	P36104	66	1	u
TAF1	P46677	67	1	u
TIM50	Q02776	478	29	u
USO1	P25386	70	118	d
VPS45	P38932	8	23	d
WTM2	Q12206	45	1	u
YFR006W	P43590	1	46	d
YIF1	P53845	71	14	u
YIH1	P25637	1	18	d
AAP1	P37898	1	159	d
ACC1	Q00955	707	505	u
ACS2	P52910	487	442	u
ACT1	P60010	766	616	u
AHA1	Q12449	190	276	d
AIM10	P39965	54	42	u
ALG11	P53954	111	1	u
AME1	P38313	14	1	u
AMS1	P22855	52	4	u
ANP1	P32629	51	63	d
APC11	Q12157	28	1	u
APE3	P37302	156	154	u
APJ1	P53940	9	8	u
APL1	P27351	20	26	d
APL2	P36000	27	26	u

APL3	P38065	34	57	d
APS2	Q00381	71	1	u
ARC1	P46672	96	406	d
ARL1	P38116	59	203	d
ARP2	P32381	525	90	u
ASF1	P32447	1	16	d
ASI2	P53895	16	1	u
AST1	P35183	98	10	u
ATP23	P53722	68	1	u
BCH1	Q05029	20	19	u
BCP1	Q06338	1	33	d
BCY1	P07278	424	82	u
BET1	P22804	82	1	u
BMH1	P29311	690	602	u
BMH2	P34730	600	582	u
BRE1	Q07457	271	220	u
BUD4	P47136	7	6	u
BUR2	Q05949	12	1	u
CAF40	P53829	122	1	u
CAM1	P29547	489	294	u
CCT2	P39076	148	184	d
CCT3	P39077	90	175	d
CCT4	P39078	64	108	d
CCT5	P40413	26	113	d
CCT6	P39079	88	190	d
CCT7	P42943	138	251	d
CCT8	P47079	258	362	d
CDC16	P09798	6	1	u
CDC37	P06101	1	50	d
CDC39	P25655	96	77	u
CDC55	Q00362	28	37	d
CHD1	P32657	336	9	u
CHS5	Q12114	48	7	u
CIC1	P38779	417	25	u
CKA1	P15790	390	37	u
CKA2	P19454	262	61	u
CLC1	P17891	43	70	d
CMK2	P22517	60	10	u
CNB1	P25296	159	156	u
COG6	P53959	35	16	u
COP1	P53622	317	284	u
CPR1	P14832	594	571	u
CPR5	P35176	595	74	u
CPR7	P47103	1	11	d
CSM1	P25651	92	1	u
CSR1	Q06705	145	49	u
CTK2	P46962	29	1	u
CTK3	P46963	72	1	u
CUE4	Q04201	305	1	u
CYM1	P32898	197	66	u
DED81	P38707	98	451	d
DEF1	P35732	26	25	u

DFM1	Q12743	110	1	u
DHH1	P39517	319	287	u
DID2	P69771	371	50	u
DJP1	P40564	80	10	u
DMA1	P38823	12	1	u
DNF1	P32660	80	8	u
DPS1	P04802	183	510	d
DSL1	P53847	124	90	u
DUG2	P38149	6	5	u
EAF3	Q12432	37	1	u
ECM21	P38167	9	8	u
EFT1	P32324	704	605	u
EGD1	Q02642	285	262	u
EGD2	P38879	331	475	d
EMC2	P47133	424	1	u
EMC3	P36039	129	1	u
ENT3	P47160	38	69	d
EOS1	P53938	26	1	u
ERD2	P18414	21	1	u
ERP1	Q05359	264	154	u
ERP2	P39704	216	117	u
ERP3	Q12403	20	1	u
ERV25	P54837	407	257	u
ERV46	P39727	84	35	u
ETP1	P38748	8	1	u
FES1	P38260	1	137	d
FLC2	P39719	7	1	u
FPK1	P53739	6	1	u
FRA1	Q07825	19	12	u
FRS1	P15624	88	399	d
FRS2	P15625	19	336	d
FUS3	P16892	27	1	u
GBP2	P25555	309	1	u
GCD6	P32501	7	59	d
GCN1	P33892	348	238	u
GCN2	P15442	9	1	u
GCN20	P43535	186	155	u
GCN5	Q03330	21	1	u
GCV3	P39726	329	65	u
GGA2	P38817	35	93	d
GID7	P25569	7	12	d
GIM3	P53900	37	222	d
GIP3	Q03016	15	11	u
GLE1	Q12315	27	1	u
GLE2	P40066	247	1	u
GLO3	P38682	54	67	d
GLR1	P41921	355	224	u
GON7	P46984	1	41	d
GPA1	P08539	139	1	u
GPD1	Q00055	298	357	d
GPI17	Q04080	135	134	u
GRX1	P25373	112	531	d

GRX3	Q03835	19	128	d
GSF2	Q04697	530	127	u
GSP1	P32835	331	443	d
GTT1	P40582	141	69	u
GUP1	P53154	55	7	u
GZF3	P42944	9	1	u
HAT1	Q12341	25	11	u
HBS1	P32769	24	23	u
HDA2	Q06629	85	28	u
HEK2	P38199	207	147	u
HFI1	Q12060	10	1	u
HMT1	P38074	61	80	d
HOC1	P47124	85	1	u
HPA3	P39979	66	166	d
HPR1	P17629	102	38	u
HRB1	P38922	89	1	u
HRI1	Q05905	20	471	d
HRK1	Q08732	1	6	d
HRR25	P29295	110	9	u
HSP10	P38910	676	50	u
HSP104	P31539	620	538	u
HSP26	P15992	120	421	d
HSP78	P33416	608	527	u
HST1	P53685	19	1	u
ICE2	P40499	29	1	u
IKI3	Q06706	41	130	d
IMG1	P25626	466	1	u
IMG2	P25642	554	1	u
IMH1	Q06704	58	20	u
IMP3	P32899	712	24	u
INP52	P50942	5	1	u
JSN1	P47135	9	1	u
KAP120	Q02932	49	37	u
KAP95	Q06142	156	132	u
KAR2	P16474	700	585	u
KIN2	P13186	13	4	u
KIN28	P06242	31	1	u
KRE2	P27809	172	167	u
KTR1	P27810	232	196	u
KTR4	P38131	30	41	d
KTR6	P54070	21	1	u
LAP2	Q10740	7	95	d
LAP3	Q01532	170	171	d
LAS21	P40367	29	1	u
LDB19	Q12502	1	11	d
LEO1	P38439	31	30	u
LHS1	P36016	383	15	u
LIA1	P47120	1	444	d
LSP1	Q12230	515	392	u
MAM33	P40513	154	1	u
MAP2	P38174	49	81	d
MAS1	P10507	202	1	u

MCD4	P36051	80	9	u
MCK1	P21965	261	138	u
MDH2	P22133	125	1	u
MDJ1	P35191	153	1	u
MDJ2	P42834	77	1	u
MDM20	Q12387	43	58	d
MDY2	Q12285	168	164	u
MES1	P00958	48	321	d
MET18	P40469	1	13	d
MGE1	P38523	679	1	u
MHR1	Q06630	101	1	u
MIA40	P36046	157	131	u
MID2	P36027	14	1	u
MIP6	P38760	1	6	d
MKC7	P53379	17	1	u
MLC1	P53141	625	76	u
MMM1	P41800	35	1	u
MNN10	P50108	66	49	u
MNN11	P46985	143	22	u
MNN5	P46982	117	101	u
MNN9	P39107	128	67	u
MOT2	P34909	44	7	u
MPS2	P53159	25	1	u
MRP1	P10662	295	1	u
MRP20	P32387	391	1	u
MRP21	P38175	285	1	u
MRP4	P32902	219	1	u
MRP49	P32388	215	1	u
MRP7	P12687	339	11	u
MRPL16	P38064	187	1	u
MRPL25	P23369	414	1	u
MRPL27	P36526	297	1	u
MRPL28	P36527	449	1	u
MRPL32	P25348	138	1	u
MRPL33	P20084	312	1	u
MRPL35	Q06678	142	1	u
MRPL36	P36531	154	1	u
MRPL38	P35996	603	1	u
MRPL39	P36533	78	1	u
MRPL4	P36517	90	1	u
MRPL44	P19956	231	1	u
MRPL51	Q06090	399	1	u
MRPL8	P22353	289	1	u
MRPL9	P31334	89	1	u
MRPS12	P53732	128	1	u
MRPS16	Q02608	177	1	u
MRPS18	P42847	210	1	u
MRPS9	P38120	143	1	u
MSD1	P15179	14	28	d
MSF1	P08425	30	1	u
MSK1	P32048	16	1	u
MSO1	P53604	84	1	u

MSS116	P15424	480	390	u
MST28	P39552	69	1	u
MSW1	P04803	56	1	u
MTF2	P10849	45	1	u
MTQ1	P53944	15	1	u
MTW1	P39731	16	1	u
MVP1	P40959	18	17	u
MYO2	P19524	270	73	u
NAB2	P32505	62	8	u
NAM9	P27929	131	1	u
NAS2	P40555	1	46	d
NAS6	P50086	1	148	d
NAT3	Q06504	1	22	d
NCE102	Q12207	231	107	u
NCS2	P53923	1	9	d
NEO1	P40527	8	1	u
NFU1	P32860	556	1	u
NGR1	P32831	7	6	u
NIP1	P32497	94	274	d
NMD2	P38798	5	4	u
NOP53	Q12080	21	1	u
NOP9	P47077	121	174	d
NPL3	Q01560	210	202	u
NPL4	P33755	54	65	d
NTA1	P40354	10	1	u
NTO1	Q12311	1	6	d
NUG1	P40010	289	77	u
NUP1	P20676	14	1	u
NUP100	Q02629	34	1	u
NUP120	P35729	119	110	u
NUP133	P36161	325	24	u
NUP157	P40064	210	1	u
NUP159	P40477	21	6	u
NUP170	P38181	172	65	u
NUP188	P52593	147	5	u
NUP49	Q02199	79	1	u
NUP53	Q03790	44	9	u
NUP57	P48837	190	64	u
NUP84	P52891	133	108	u
NUP85	P46673	95	56	u
OCA2	P53949	1	23	d
OCH1	P31755	20	19	u
ORC2	P32833	40	1	u
OSM1	P21375	203	53	u
OST3	P48439	158	1	u
OST5	Q92316	468	1	u
PAB1	P04147	504	479	u
PAF1	P38351	90	107	d
PAM17	P36147	90	1	u
PAM18	Q07914	120	1	u
PAN5	P38787	25	188	d
PAT1	P25644	46	45	u

PDR17	P53844	60	1	u
PET123	P17558	93	1	u
PET494	P07390	10	1	u
PET54	P10834	98	1	u
PEX2	P32800	17	1	u
PEX25	Q02969	132	1	u
PEX3	P28795	11	1	u
PGA1	P53896	53	1	u
PGA2	P53903	607	1	u
PHB2	P50085	419	51	u
PHO13	P19881	1	330	d
PHO8	P11491	46	45	u
PHO86	P46956	275	31	u
PHO88	P38264	762	427	u
PIH1	P38768	27	1	u
PIL1	P53252	439	387	u
PMI40	P29952	1	285	d
PMT2	P31382	223	186	u
POM152	P39685	293	10	u
POM33	Q12164	140	34	u
PPH21	P23594	1	25	d
PPH3	P32345	15	1	u
PPT1	P53043	1	27	d
PRC1	P00729	61	60	u
PRD1	P25375	51	150	d
PRE3	P38624	538	424	u
PRE6	P40303	428	288	u
PRE7	P23724	462	358	u
PRE8	P23639	507	353	u
PRT1	P06103	253	395	d
PSA1	P41940	189	369	d
PSD1	P39006	150	9	u
PSR1	Q07800	23	1	u
PTC1	P35182	1	34	d
PTC2	P39966	1	265	d
PTC3	P34221	1	72	d
PTC4	P38089	38	24	u
PTC5	Q12511	69	16	u
PTH2	P34222	239	1	u
PTK2	P47116	52	17	u
PUP1	P25043	168	246	d
QCR2	P07257	667	126	u
RAD16	P31244	6	1	u
RAD23	P32628	13	117	d
RAM2	P29703	1	13	d
RBG1	P39729	181	150	u
RBG2	P53295	99	230	d
REF2	P42073	38	1	u
RFA2	P26754	118	36	u
RIO2	P40160	22	1	u
RIX1	P38883	126	113	u
RIX7	Q07844	12	11	u

RLI1	Q03195	307	348	d
RLP7	P40693	179	1	u
RMD9	P53140	101	88	u
RPG1	P38249	204	414	d
RPL13A	Q12690	1	396	d
RPL13B	P40212	508	1	u
RPL15A	P05748	404	303	u
RPL15B	P54780	343	254	u
RPL16A	P26784	708	610	u
RPL20A	P0CX23	660	549	u
RPL21A	Q02753	421	485	d
RPL22A	P05749	177	171	u
RPL26A	P05743	765	635	u
RPL27A	P0C2H6	650	501	u
RPL2A	P0CX45	549	500	u
RPL3	P14126	738	619	u
RPL31B	P0C2H9	740	598	u
RPL32	P38061	546	404	u
RPL33A	P05744	646	486	u
RPL34B	P40525	386	340	u
RPL4A	P10664	537	464	u
RPL6A	Q02326	627	525	u
RPL6B	P05739	627	492	u
RPL7B	Q12213	680	586	u
RPL8B	P29453	772	636	u
RPN10	P38886	201	192	u
RPN13	O13563	432	310	u
RPP1A	P05318	251	53	u
RPP1B	P10622	55	54	u
RPP2A	P05319	527	351	u
RPS0A	P32905	272	253	u
RPS10A	Q08745	432	380	u
RPS14B	P39516	776	638	u
RPS15	Q01855	579	490	u
RPS16A	P0CX51	751	629	u
RPS2	P25443	343	303	u
RPS21A	P0C0V8	722	560	u
RPS23A	P0CX29	499	437	u
RPS25B	P0C0T4	575	416	u
RPS26A	P39938	276	255	u
RPS28B	P0C0X0	432	380	u
RPS29A	P41057	755	248	u
RPS29B	P41058	719	420	u
RPS4A	P0CX35	654	499	u
RPS6A	P0CX37	557	445	u
RPS8A	P0CX39	380	282	u
RSM10	Q03201	172	1	u
RSM19	P53733	551	1	u
RSM27	P53305	328	1	u
RSP5	P39940	254	127	u
RTC1	Q08281	1	3	d
RTF1	P53064	137	105	u

RTG3	P38165	10	1	u
RVB2	Q12464	640	149	u
RXT2	P38255	80	21	u
SAC3	P46674	11	7	u
SAM37	P50110	140	1	u
SAR1	P20606	474	358	u
SBH2	P52871	312	1	u
SBP1	P10080	350	389	d
SCC4	P40090	39	21	u
SCD6	P45978	63	43	u
SEA4	P38164	23	1	u
SEC14	P24280	273	398	d
SEC16	P48415	5	2	u
SEC18	P18759	174	145	u
SEC23	P15303	214	217	d
SEC27	P41811	222	339	d
SEC28	P40509	130	74	u
SEC53	P07283	312	599	d
SEC61	P32915	144	43	u
SEC72	P39742	529	24	u
SED4	P25365	87	13	u
SET1	P38827	17	1	u
SET2	P46995	40	12	u
SET3	P36124	13	6	u
SFB2	P53953	28	46	d
SFH5	P47008	373	1	u
SFT2	P38166	116	115	u
SGF11	Q03067	51	1	u
SGF29	P25554	62	1	u
SHG1	P38337	34	1	u
SHP1	P34223	103	123	d
SIF2	P38262	28	8	u
SIN3	P22579	92	8	u
SIS1	P25294	493	230	u
SIS2	P36024	9	1	u
SKI2	P35207	15	79	d
SLK19	Q08581	11	28	d
SLM1	P40485	63	35	u
SLM4	P38247	67	29	u
SLN1	P39928	5	1	u
SLS1	P42900	22	14	u
SMC5	Q08204	31	1	u
SNA2	P56508	66	1	u
SNA3	P14359	37	36	u
SNF1	P06782	15	58	d
SNF7	P39929	69	19	u
SNF8	Q12483	1	19	d
SNL1	P40548	502	29	u
SNU114	P36048	72	13	u
SNX3	Q08826	238	28	u
SOL1	P50278	1	48	d
SOP4	P39543	104	1	u

SPT8	P38915	25	24	u
SRP1	Q02821	346	333	u
SRP14	P38985	393	33	u
SRP68	P38687	352	347	u
SRP72	P38688	296	219	u
SSA1	P10591	733	625	u
SSA4	P22202	348	495	d
SSB1	P11484	636	552	u
SSB2	P40150	623	552	u
SSC1	P0CS90	721	608	u
SSE1	P32589	686	603	u
SSE2	P32590	316	252	u
SSH1	P38353	187	70	u
SSL2	Q00578	17	5	u
SSM4	P40318	125	3	u
SSO1	P32867	169	53	u
SSU72	P53538	81	1	u
SSZ1	P38788	420	467	d
STE13	P33894	6	1	u
STE23	Q06010	91	75	u
STE7	P06784	9	1	u
STI1	P15705	442	569	d
STO1	P34160	283	247	u
SUI1	P32911	632	111	u
SUP35	P05453	299	192	u
SVP26	P38869	143	70	u
SWD1	P39706	11	1	u
SWM1	Q12379	28	1	u
SWS2	P53937	34	1	u
TAF12	Q03761	86	8	u
TAF14	P35189	136	41	u
TAF5	P38129	202	156	u
TAF9	Q05027	369	1	u
TCP1	P12612	135	246	d
TDA1	Q03533	1	7	d
TEX1	P53851	11	1	u
TFB1	P32776	8	14	d
TFG1	P41895	112	41	u
TFS1	P14306	22	254	d
THO1	P40040	119	1	u
THO2	P53552	134	8	u
THP1	Q08231	20	1	u
TIF1	P10081	639	601	u
TIF3	P34167	190	388	d
TIF34	P40217	311	377	d
TIM10	P87108	769	1	u
TIM18	Q08749	134	1	u
TIM23	P32897	362	1	u
TIP20	P33891	90	50	u
TLG2	Q08144	12	1	u
TMA19	P35691	555	514	u
TMA20	P89886	435	326	u

TMA46	Q12000	14	13	u
TMA64	Q04600	1	8	d
TOF2	Q02208	13	1	u
TOM20	P35180	287	58	u
TOM22	P49334	385	74	u
TOM40	P23644	203	25	u
TOM7	P53507	95	1	u
TOM70	P07213	648	551	u
TOM71	P38825	151	106	u
TOR1	P35169	19	3	u
TOR2	P32600	27	1	u
TPD3	P31383	23	121	d
TRX1	P22217	604	512	u
TSA1	P34760	534	583	d
TUB4	P53378	32	1	u
UBA1	P22515	72	379	d
UBC13	P52490	31	122	d
UBP1	P25037	17	22	d
UBP14	P38237	1	5	d
UBR1	P19812	41	23	u
UBX2	Q04228	54	1	u
UBX6	P47049	12	1	u
UBX7	P38349	113	10	u
UFD2	P54860	20	47	d
UTP5	Q04177	120	80	u
UTP8	P53276	218	179	u
VID22	Q05934	27	15	u
VMA3	P25515	33	1	u
VPS13	Q07878	40	35	u
VPS21	P36017	638	380	u
VPS24	P36095	44	20	u
VPS25	P47142	1	22	d
VPS54	Q12071	6	10	d
VRG4	P40107	14	1	u
VTH1	P40438	12	1	u
WHI4	Q07655	8	7	u
WTM1	Q12363	410	388	u
YAR1	P46683	1	131	d
YCH1	P42937	1	124	d
YCK2	P23292	150	114	u
YDR341C	Q05506	158	528	d
YEF3	P16521	691	566	u
YET1	P35723	359	122	u
YET3	Q07451	720	171	u
YGL082W	P53155	55	38	u
YGR054W	P53235	94	150	d
YHI9	P38765	1	33	d
YHR020W	P38708	14	318	d
YHR138C	P38841	108	1	u
YJR029W	P47100	277	225	u
YLR118C	Q12354	1	46	d
YMR027W	Q04371	1	198	d

YMR045C	Q04214	1	113	d
YMR196W	Q04336	1	111	d
YNG2	P38806	16	1	u
YNL040W	P53960	1	10	d
YOL103W-B	Q12273	322	237	u
YPL257W-B	Q12414	322	243	u
YPP1	P46951	110	120	d
YPT1	P01123	694	529	u
YPT10	P38146	250	24	u
YPT32	P51996	512	349	u
YPT52	P36018	477	276	u
YPT6	Q99260	461	115	u
YRA1	Q12159	671	443	u
YRA2	P36036	120	48	u
YRB1	P41920	85	220	d
ZPS1	Q12512	41	1	u
ABF1	P14164	79	6	u
ARG81	P05085	6	1	u
ASG1	P40467	31	24	u
BAS1	P22035	1	5	d
CBF1	P17106	28	1	u
CIN5	P40917	54	1	u
CRZ1	P53968	14	1	u
CST6	P40535	17	1	u
DAL81	P21657	10	14	d
FKH1	P40466	10	1	u
FKH2	P41813	12	1	u
GCR1	P07261	12	1	u
HAL9	Q12180	14	8	u
HAP3	P13434	34	1	u
INO4	P13902	125	1	u
IXR1	P33417	33	1	u
MCM1	P11746	16	1	u
MET31	Q03081	61	1	u
MSN1	P22148	25	1	u
MSN2	P33748	7	1	u
MSN4	P33749	8	1	u
OAF1	P39720	5	4	u
PDR1	P12383	42	36	u
PHO4	P07270	16	1	u
REB1	P21538	117	1	u
RFX1	P48743	6	1	u
RGT1	P32862	1	4	d
ROX1	P25042	13	1	u
RSC30	P38781	53	26	u
RTG1	P32607	29	1	u
SKO1	Q02100	8	1	u
SOK2	P53438	19	1	u
STB3	Q12427	10	1	u
STE12	P13574	14	6	u
SUM1	P46676	18	1	u
SWI4	P25302	5	1	u

TBF1	Q02457	112	1	u
UME6	P39001	12	1	u
WAR1	Q03631	5	1	u
AAH1	P53909	1	13	d
ABP140	Q08641	1	30	d
ABZ1	P37254	1	5	d
ACB1	P31787	1	58	d
ACL4	Q03771	13	24	d
ADD66	P36040	1	35	d
ADE1	P27616	127	542	d
ADE12	P80210	281	462	d
ADE13	Q05911	181	489	d
ADE16	P54113	106	261	d
ADE17	P38009	258	419	d
ADE2	P21264	83	465	d
ADE3	P07245	454	476	d
ADE4	P04046	52	268	d
ADE5,7	P07244	56	320	d
ADE6	P38972	89	327	d
ADE8	P04161	1	212	d
ADF1	Q2V2Q1	1	44	d
ADH5	P38113	1	64	d
ADH6	Q04894	1	364	d
ADI1	Q03677	1	143	d
ADK1	P07170	215	589	d
ADO1	P47143	68	468	d
AFG2	P32794	1	25	d
AIM2	P39721	1	136	d
AIM29	P36154	30	66	d
AIM7	Q12156	1	126	d
AIP1	P46680	53	213	d
ALD2	P47771	1	302	d
ALD3	P54114	200	455	d
AMD1	P15274	36	50	d
APA1	P16550	30	440	d
APT1	P49435	26	147	d
ARA1	P38115	133	344	d
ARG1	P22768	50	447	d
ARG3	P05150	1	13	d
ARG4	P04076	58	147	d
ARI1	P53111	1	108	d
ARO10	Q06408	8	106	d
ARO3	P14843	98	229	d
ARO4	P32449	188	302	d
ARO7	P32178	18	354	d
ARO8	P53090	81	321	d
ARO9	P38840	1	391	d
ASN1	P49089	140	404	d
ASN2	P49090	176	402	d
ASP1	P38986	41	119	d
BAT2	P47176	1	225	d
BDH1	P39714	13	75	d

BDH2	P39713	12	50	d
BDP1	P46678	1	23	d
BNA1	P47096	27	544	d
BNA5	Q05979	1	20	d
BNA6	P43619	1	167	d
BNA7	Q04066	1	36	d
BUD22	Q04347	103	137	d
CAB1	Q04430	27	41	d
CAB2	P40506	1	96	d
CAF16	P43569	1	76	d
CAR1	P00812	31	244	d
CAR2	P07991	301	457	d
CCA1	P21269	1	25	d
CCS1	P40202	134	170	d
CDC21	P06785	15	31	d
CDC40	P40968	1	9	d
CDC8	P00572	1	46	d
CGI121	Q03705	146	197	d
CIA1	Q05583	1	13	d
CKI1	P20485	1	15	d
CPA1	P07258	1	23	d
CPA2	P03965	65	372	d
CRP1	P38845	60	74	d
CTT1	P06115	35	188	d
CUZ1	P53899	1	16	d
CYS4	P32582	469	540	d
DAK1	P54838	26	402	d
DBP7	P36120	26	57	d
DBP9	Q06218	314	394	d
DCS1	Q06151	1	263	d
DCS2	Q12123	1	204	d
DDP1	Q99321	25	136	d
DDR48	P18899	1	23	d
DET1	Q99288	1	13	d
DLD3	P39976	54	329	d
DOG2	P38773	1	99	d
DSS1	P39112	1	4	d
DUR1,2	P32528	3	121	d
DUS1	P53759	1	10	d
DUT1	P33317	1	301	d
EBP2	P36049	367	375	d
ECT1	P33412	1	13	d
EFM4	P40516	1	63	d
EFM5	P53200	1	161	d
EMI2	Q04409	41	231	d
EMW1	P42842	16	32	d
ENO1	P00924	519	590	d
ENP2	P48234	113	124	d
ERG12	P07277	1	47	d
ERG13	P54839	135	235	d
ERG20	P08524	125	328	d
ERG8	P24521	1	10	d

FAS1	P07149	280	491	d
FAS2	P19097	300	553	d
FAT1	P38225	74	121	d
FBA1	P14540	417	588	d
FCY1	Q12178	1	314	d
FRD1	P32614	1	265	d
FSH1	P38777	20	349	d
FSH2	Q05015	1	21	d
FSH3	Q99369	1	36	d
FUN26	P31381	1	8	d
FUR1	P18562	157	511	d
GAD1	Q04792	8	166	d
GCY1	P14065	15	216	d
GDB1	Q06625	9	14	d
GDH1	P07262	483	572	d
GDH2	P33327	1	12	d
GFA1	P14742	1	300	d
GLC3	P32775	1	42	d
GLK1	P17709	176	438	d
GLN1	P32288	273	312	d
GLO1	P50107	1	87	d
GLO2	Q05584	1	176	d
GLT1	Q12680	206	269	d
GLY1	P37303	93	359	d
GMC1	Q04399	1	7	d
GNA1	P43577	1	371	d
GOR1	P53839	1	132	d
GPH1	P06738	161	346	d
GPM2	Q12008	1	118	d
GPP1	P41277	492	596	d
GPP2	P40106	220	515	d
GRE2	Q12068	14	385	d
GRE3	P38715	174	477	d
GSH1	P32477	1	20	d
GSH2	Q08220	1	52	d
GUA1	P38625	143	504	d
GUK1	P15454	58	594	d
HAM1	P47119	1	233	d
HBN1	Q96VH4	1	95	d
HEM12	P32347	1	25	d
HEM13	P11353	1	86	d
HEM2	P05373	1	164	d
HER1	Q12276	24	27	d
HGH1	P48362	1	68	d
HIS1	P00498	215	488	d
HIS2	P38635	1	27	d
HIS4	P00815	72	267	d
HIS5	P07172	13	244	d
HIS6	P40545	1	272	d
HIS7	P33734	9	264	d
HMF1	P40037	40	428	d
HNT1	Q04344	185	317	d

HNT2	P49775	23	49	d
HOM2	P13663	297	473	d
HOM3	P10869	1	106	d
HOM6	P31116	274	523	d
HPT1	Q04178	21	554	d
HSM3	P38348	1	9	d
HSP12	P22943	1	321	d
HSP31	Q04432	1	234	d
HTB1	P02293	1	421	d
HXK1	P04806	121	509	d
HXK2	P04807	262	555	d
HXT6	P39003	1	45	d
IAH1	P41734	1	19	d
IDI1	P15496	1	32	d
IMD4	P50094	216	228	d
INM1	P38710	1	33	d
INO1	P11986	89	273	d
IOC4	Q04213	67	97	d
IPP1	P00817	263	533	d
IRC24	P40580	19	200	d
IRC25	Q07951	1	100	d
IRC5	P43610	17	21	d
ISN1	Q99312	1	10	d
KAE1	P36132	1	11	d
KEL3	Q08979	7	37	d
KIP3	P53086	6	17	d
KTI12	P34253	1	14	d
LEU1	P07264	1	336	d
LRO1	P40345	66	75	d
LSB5	P25369	1	42	d
LSB6	P42951	1	7	d
LSM4	P40070	94	141	d
LYS2	P07702	4	260	d
LYS9	P38999	34	411	d
MAD1	P40957	72	80	d
MAD2	P40958	24	87	d
MAG1	P22134	1	15	d
MCM4	P30665	10	20	d
MDE1	P47095	1	40	d
MDG1	P53885	1	12	d
MET10	P39692	1	4	d
MET13	P53128	1	98	d
MET22	P32179	1	81	d
MET5	P47169	1	51	d
MET6	P05694	544	556	d
MEU1	Q07938	1	13	d
MGA2	P40578	1	4	d
MHT1	Q12525	1	14	d
MIP1	P15801	1	7	d
MKT1	P40850	1	10	d
MPH1	P40562	1	4	d
MPS3	P47069	28	35	d

MRI1	Q06489	1	87	d
MRP8	P35719	1	557	d
MRX1	P40050	7	13	d
MSC6	Q08818	92	128	d
MTC1	P47018	20	56	d
MTD1	Q02046	1	146	d
MVD1	P32377	1	322	d
MXR1	P40029	25	360	d
NAN1	Q02931	205	208	d
NCA2	Q12374	83	107	d
NCE103	P53615	1	20	d
NCL1	P38205	95	202	d
NGL2	Q03264	1	17	d
NIT3	P49954	34	105	d
NOB1	Q08444	10	20	d
NOP8	Q08287	29	39	d
NPC2	Q12408	28	62	d
NPT1	P39683	1	304	d
NPY1	P53164	1	11	d
NRK1	P53915	1	18	d
NTH1	P32356	105	190	d
OLA1	P38219	426	535	d
OPI10	Q08202	1	19	d
OSH7	P38755	47	94	d
OTU2	P38747	1	29	d
OXP1	P28273	1	123	d
OYE2	Q03558	420	503	d
PAA1	Q12447	250	550	d
PAM1	P37304	30	36	d
PAN6	P40459	1	123	d
PBA1	Q05778	1	16	d
PCM1	P38628	1	69	d
PDE2	P06776	1	17	d
PDX3	P38075	69	313	d
PFK1	P16861	407	518	d
PFK2	P16862	230	386	d
PFK26	P40433	1	5	d
PGI1	P12709	344	487	d
PGM1	P33401	1	144	d
PGM2	P37012	82	432	d
PNC1	P53184	112	442	d
PNP1	Q05788	1	129	d
POA1	P38218	27	58	d
POL30	P15873	368	368	d
PPM2	Q08282	1	13	d
PPX1	P38698	24	153	d
PRM15	Q03262	1	14	d
PRO1	P32264	11	49	d
PRO2	P54885	11	248	d
PRO3	P32263	117	265	d
PRP39	P39682	7	13	d
PRP40	P33203	8	15	d

PTA1	Q01329	18	24	d
PUB1	P32588	60	74	d
PUS1	Q12211	26	57	d
PWP1	P21304	46	109	d
PYC1	P11154	73	309	d
PYC2	P32327	93	357	d
PYK2	P52489	1	67	d
QNS1	P38795	7	68	d
QRI1	P43123	10	120	d
RAD51	P25454	1	11	d
RAD9	P14737	1	3	d
RBK1	P25332	1	29	d
RCN2	Q12044	1	38	d
RDL1	Q12305	228	453	d
REE1	P40893	1	183	d
RFC1	P38630	43	49	d
RHB1	P25378	1	22	d
RIB3	Q99258	1	335	d
RIB4	P50861	66	431	d
RIB5	P38145	1	143	d
RKI1	Q12189	1	249	d
RLF2	Q12495	1	14	d
RNR1	P21524	22	60	d
RPE1	P46969	1	20	d
RPO26	P20435	31	69	d
RQC2	Q12532	1	22	d
RRP14	P36080	46	59	d
RRP6	Q12149	49	66	d
RSC6	P25632	208	220	d
RTT10	Q08924	1	18	d
RTT103	Q05543	85	103	d
SAM1	P10659	315	526	d
SAM2	P19358	417	567	d
SAM4	Q08985	1	171	d
SAP155	P43612	1	13	d
SAP185	P40856	1	4	d
SDH1	Q00711	154	215	d
SDO1	Q07953	40	93	d
SDS23	P53172	1	18	d
SER1	P33330	55	332	d
SER2	P42941	1	72	d
SER3	P40054	1	191	d
SER33	P40510	21	191	d
SFA1	P32771	1	146	d
SHB17	P36136	36	297	d
SKI3	P17883	23	58	d
SLA1	P32790	33	37	d
SNZ1	Q03148	1	34	d
SOG2	Q08817	1	11	d
SOL3	P38858	1	341	d
SOL4	P53315	1	126	d
SPB4	P25808	41	61	d

SPC97	P38863	11	16	d
SPE1	P08432	1	9	d
SPE2	P21182	1	35	d
SPE3	Q12074	53	450	d
SPE4	Q12455	1	15	d
SPP382	Q06411	7	12	d
SQT1	P35184	1	10	d
SUC2	P00724	1	8	d
SVF1	Q05515	1	41	d
TAH11	P47112	1	7	d
TAL1	P15019	618	620	d
TCO89	Q08921	1	5	d
TDA10	P42938	1	102	d
TDA3	P38758	1	8	d
TFC1	P32367	22	47	d
TFC6	Q06339	1	6	d
THR1	P17423	44	132	d
THR4	P16120	52	470	d
TKL1	P23254	403	441	d
TKL2	P33315	1	87	d
TMA17	Q12513	1	264	d
TPI1	P00942	465	534	d
TPM1	P17536	83	373	d
TPM2	P40414	29	222	d
TPS1	Q00764	244	275	d
TPS3	P38426	97	129	d
TRM11	Q12463	1	10	d
TRM2	P33753	1	7	d
TRM3	Q07527	1	104	d
TRM44	Q02648	1	7	d
TRM5	P38793	10	18	d
TRM732	Q03496	1	26	d
TRM8	Q12009	33	52	d
TRM82	Q03774	1	20	d
TRP1	P00912	1	47	d
TRP2	P00899	10	227	d
TRP3	P00937	10	158	d
TRP4	P07285	1	40	d
TRP5	P00931	64	272	d
TRR1	P29509	282	467	d
TSL1	P38427	213	264	d
TSR1	Q07381	6	37	d
TSR4	P25040	1	36	d
TUM1	Q08686	74	296	d
TYR1	P20049	1	32	d
TYW3	P53177	1	83	d
UGA1	P17649	1	142	d
UGA2	P38067	1	9	d
URA1	P28272	51	400	d
URA2	P07259	303	401	d
URA4	P20051	1	125	d
URA5	P13298	77	562	d

URA6	P15700	1	506	d
URA7	P28274	55	242	d
URA8	P38627	1	44	d
URH1	Q04179	1	13	d
UTP13	Q05946	129	152	d
UTP18	P40362	65	76	d
UTP9	P38882	138	222	d
UTR4	P32626	1	195	d
VCX1	Q99385	12	23	d
VMA13	P41807	205	405	d
VMA5	P31412	136	324	d
VMA8	P32610	63	158	d
VTC4	P47075	241	242	d
XPT1	P47165	1	120	d
YBL036C	P38197	1	325	d
YBP2	P53169	1	14	d
YBR053C	P38235	1	78	d
YCR051W	P25631	1	76	d
YCR090C	P25654	26	142	d
YDL086W	Q07505	17	83	d
YDL124W	Q07551	122	614	d
YDL144C	Q07589	1	12	d
YDR248C	Q03786	1	52	d
YDR391C	Q04170	1	181	d
YEL020C	P39994	1	8	d
YER010C	P40011	1	149	d
YER156C	P40093	86	162	d
YGL101W	P53144	1	108	d
YGL242C	P53066	27	151	d
YGR111W	P53265	1	49	d
YGR210C	P42942	1	36	d
YGR250C	P53316	1	11	d
YHB1	P39676	133	429	d
YHR112C	P38716	1	25	d
YIP4	P53093	21	43	d
YIR035C	P40579	1	98	d
YJL055W	P47044	1	355	d
YJL068C	P40363	1	99	d
YJR096W	P47137	1	54	d
YJR142W	P47173	1	27	d
YKL033W-A	Q86ZR7	1	183	d
YKL069W	P36088	1	59	d
YKR018C	P36114	7	58	d
YKT6	P36015	503	565	d
YLL032C	Q07834	23	28	d
YLR126C	Q12288	1	18	d
YLR179C	Q06252	53	452	d
YLR256W-B/YLR256W-C	P0C2I7	1	236	d
YLR287C	Q05881	1	12	d
YLR345W	Q06137	1	8	d
YLR460C	P54007	1	12	d
YME2	P32843	191	210	d

YML079W	Q03629	1	87	d
YML131W	Q03102	61	128	d
YMR074C	Q04773	1	79	d
YMR090W	Q04304	1	345	d
YMR099C	Q03161	52	469	d
YMR130W	Q04223	1	14	d
YMR178W	Q03219	17	82	d
YMR226C	Q05016	255	415	d
YMR315W	Q04869	46	323	d
YNL010W	P53981	20	394	d
YNL108C	P53929	1	36	d
YNL134C	P53912	42	201	d
YNR029C	P53729	1	10	d
YOL098C	Q12496	5	49	d
YOR283W	Q12040	145	229	d
YOR289W	Q12012	18	38	d
YPD1	Q07688	1	107	d
YPL067C	Q02754	1	23	d
YPL260W	Q08977	1	69	d
YPR089W	O13585	1	10	d
YPR1	Q12458	15	363	d
YPR127W	Q06494	1	218	d
YPR148C	Q06523	1	33	d
YPR172W	Q06608	1	51	d
YSA1	Q01976	72	229	d
ZPR1	P53303	1	114	d
ZWF1	P11412	29	289	d
AAT1	Q01802	89	1	u
AAT2	P23542	501	417	u
ABD1	P32783	60	10	u
ABF2	Q02486	767	242	u
ACH1	P32316	253	236	u
ACK1	Q07622	8	1	u
ACO1	P19414	662	536	u
ACO2	P39533	225	202	u
ACP1	P32463	171	1	u
ADH1	P00330	642	516	u
ADH3	P07246	510	100	u
ADH4	P10127	242	172	u
ADP1	P25371	14	1	u
AGE2	P40529	55	33	u
AGP1	P25376	32	1	u
AGP2	P38090	16	1	u
AHP1	P38013	706	611	u
AI1	P03875	23	5	u
AIF1	P52923	13	1	u
AIM11	P87275	35	1	u
AIM14	P53109	16	1	u
AIM17	P23180	187	42	u
AIM18	P38884	48	1	u
AIM24	P47127	323	1	u
AIM25	P47140	30	1	u

AIM34	Q03673	24	1	u
AIM36	Q03798	363	1	u
AIM39	Q08223	68	1	u
AIM41	Q12032	756	1	u
AIM45	Q12480	378	1	u
AIM46	P38885	198	1	u
AIM6	Q07716	133	23	u
AIM9	P40053	596	502	u
AIR1	P40507	13	1	u
AIR2	Q12476	13	1	u
ALB1	P47019	163	62	u
ALD4	P46367	684	524	u
ALD5	P40047	380	28	u
ALD6	P54115	610	579	u
ALE1	Q08548	149	1	u
ALG13	P53178	177	1	u
ALG14	P38242	42	1	u
ALO1	P54783	354	120	u
ALT1	P52893	104	15	u
ANR2	P36090	38	17	u
ANT1	Q06497	118	1	u
APD1	P38281	119	68	u
APN1	P22936	58	12	u
ARC15	P40518	605	73	u
ARC18	Q05933	429	97	u
ARC19	P33204	377	103	u
ARC35	P53731	419	61	u
ARC40	P38328	410	39	u
ARE1	P25628	23	1	u
ARE2	P53629	67	1	u
ARG5,6	Q01217	197	1	u
ARG7	Q04728	621	63	u
ARG8	P18544	103	1	u
ARH1	P48360	66	1	u
ARO1	P08566	452	328	u
ARO2	P28777	400	292	u
ARP3	P47117	455	33	u
ARP5	P53946	72	31	u
ARP7	Q12406	70	9	u
ARP8	Q12386	69	15	u
ARP9	Q05123	123	9	u
ATF2	P53296	9	8	u
ATG33	Q06485	59	1	u
ATG40	Q99325	89	1	u
ATM1	P40416	96	6	u
ATO3	Q12359	117	36	u
ATP1	P07251	683	433	u
ATP10	P18496	178	1	u
ATP11	P32453	177	29	u
ATP12	P22135	504	1	u
ATP14	Q12349	93	39	u
ATP15	P21306	724	1	u

ATP16	Q12165	74	1	u
ATP17	Q06405	235	1	u
ATP18	P81450	656	1	u
ATP19	P81451	84	1	u
ATP2	P00830	629	308	u
ATP20	Q12233	305	1	u
ATP25	Q03153	23	1	u
ATP3	P38077	504	51	u
ATP4	P05626	561	139	u
ATP5	P09457	678	224	u
ATP7	P30902	631	103	u
AVT7	P40501	10	1	u
AYR1	P40471	443	33	u
BAP2	P38084	52	1	u
BAP3	P41815	16	1	u
BAT1	P38891	367	71	u
BBC1	P47068	69	12	u
BDF1	P35817	137	96	u
BDF2	Q07442	8	1	u
BEM1	P29366	59	8	u
BEM2	P39960	45	21	u
BET3	P36149	184	52	u
BFR1	P38934	663	490	u
BGL2	P15703	333	157	u
BI3	Q9ZZW7	9	1	u
BIG1	P38813	62	1	u
BIK1	P11709	11	1	u
BIM1	P40013	109	1	u
BIO2	P32451	41	1	u
BMS1	Q08965	148	15	u
BMT2	P38278	14	1	u
BMT5	P40493	14	1	u
BNA3	P47039	155	60	u
BNA4	P38169	57	1	u
BNI5	P53890	22	1	u
BOI1	P38041	15	1	u
BOI2	P39969	5	1	u
BOL1	Q3E793	46	1	u
BOL3	P39724	101	1	u
BPT1	P14772	9	1	u
BRF1	P29056	24	1	u
BRN1	P38170	13	1	u
BRR1	Q99177	14	1	u
BRR2	P32639	93	1	u
BRX1	Q08235	387	32	u
BSP1	Q06604	9	1	u
BUD2	P33314	26	4	u
BUD21	Q08492	48	1	u
BUD3	P25558	9	3	u
BUD31	P25337	29	1	u
BUR6	P40096	425	1	u
BYE1	P36106	8	7	u

BZZ1	P38822	82	81	u
CAB3	P36076	55	54	u
CAB4	P53332	32	14	u
CAB5	Q03941	178	1	u
CAF4	P36130	22	1	u
CAN1	P04817	16	1	u
CAP1	P28495	285	184	u
CAP2	P13517	402	137	u
CAT5	P41735	21	1	u
CBC2	Q08920	283	22	u
CBF2	P32504	5	1	u
CBF5	P33322	593	498	u
CBP2	P03874	38	29	u
CBP4	P37267	446	1	u
CBR1	P38626	760	81	u
CCC1	P47818	100	15	u
CCC2	P38995	5	4	u
CCM1	P48237	16	1	u
CCP1	P00431	514	101	u
CCR4	P31384	65	56	u
CDC10	P25342	293	1	u
CDC19	P00549	748	624	u
CDC25	P04821	4	1	u
CDC3	P32457	476	376	u
CDC9	P04819	33	32	u
CDS1	P38221	125	43	u
CEG1	Q01159	87	1	u
CEM1	P39525	81	1	u
CFT1	Q06632	60	1	u
CFT2	Q12102	17	10	u
CGR1	P53188	39	1	u
CHO1	P08456	280	16	u
CHO2	P05374	460	92	u
CHS1	P08004	25	1	u
CHS2	P14180	15	1	u
CIR1	P42940	472	92	u
CIR2	Q08822	472	380	u
CIT1	P00890	522	248	u
CIT2	P08679	151	73	u
CLF1	Q12309	7	6	u
CLP1	Q08685	22	1	u
CMC1	P36064	102	1	u
CMC2	Q3E7A4	43	1	u
CMR1	Q12510	28	27	u
CMS1	Q07897	434	15	u
CNM67	P53865	8	7	u
COA1	P40452	135	24	u
COA4	Q05809	231	1	u
COA6	Q3E846	545	1	u
COQ1	P18900	145	1	u
COQ10	Q08058	119	1	u
COQ11	Q05892	326	1	u

COQ2	P32378	42	1	u
COQ3	P27680	15	1	u
COQ4	O13525	85	1	u
COQ5	P49017	533	14	u
COQ6	P53318	31	1	u
COQ9	Q05779	88	1	u
COX1	P00401	18	1	u
COX11	P19516	52	1	u
COX12	Q01519	440	1	u
COX13	P32799	728	1	u
COX15	P40086	137	1	u
COX16	P47081	40	1	u
COX17	Q12287	73	1	u
COX2	P00410	211	18	u
COX3	P00420	18	1	u
COX4	P04037	601	31	u
COX5A	P00424	281	1	u
COX5B	P00425	537	31	u
COX6	P00427	645	1	u
COX8	P04039	68	1	u
COX9	P07255	473	1	u
COY1	P34237	37	13	u
CPD1	P53314	42	41	u
CPT1	P17898	24	11	u
CRH1	P53301	44	20	u
CRN1	Q06440	330	119	u
CSC1	Q06538	12	1	u
CSE2	P33308	72	1	u
CSE4	P36012	20	1	u
CSG2	P35206	52	1	u
CSM3	Q04659	15	1	u
CSN12	P47130	77	1	u
CST26	P38226	68	1	u
CTF18	P49956	7	1	u
CTF4	Q01454	38	1	u
CTF8	P38877	85	1	u
CTP1	P38152	55	1	u
CTR1	P49573	12	1	u
CTS1	P29029	28	1	u
CTS2	Q06350	9	1	u
CUE3	P53137	8	7	u
CUS1	Q02554	11	1	u
CWC2	Q12046	29	1	u
CWC21	Q03375	35	1	u
CWC22	P53333	8	7	u
CWP1	P28319	467	306	u
CYB2	P00175	25	7	u
CYB5	P40312	292	1	u
CYC1	P00044	696	1	u
CYC7	P00045	319	1	u
CYC8	P14922	71	1	u
CYK3	Q07533	6	1	u

CYR1	P08678	29	1	u
CYS3	P31373	232	220	u
CYT1	P07143	161	1	u
DAD2	P36162	86	1	u
DAD3	P69850	135	1	u
DAM1	P53267	45	1	u
DAP1	Q12091	33	1	u
DBP10	Q12389	273	23	u
DBP2	P24783	509	446	u
DBP3	P20447	338	123	u
DBP6	P53734	96	49	u
DBP8	P38719	167	1	u
DCC1	P25559	12	1	u
DCD1	P06773	69	1	u
DCP1	Q12517	144	1	u
DCP2	P53550	62	1	u
DCW1	P36091	34	33	u
DEG1	P31115	11	1	u
DFG5	Q05031	11	10	u
DFR1	P07807	22	21	u
DGA1	Q08650	23	1	u
DGK1	Q12382	16	1	u
DHR2	P36009	41	40	u
DIB1	Q06819	33	32	u
DIC1	Q06143	251	1	u
DIG1	Q03063	62	1	u
DIM1	P41819	219	68	u
DIP2	Q12220	212	9	u
DIP5	P53388	42	7	u
DLD1	P32891	280	259	u
DLD2	P46681	224	27	u
DNM1	P54861	250	207	u
DOT5	P40553	278	117	u
DPB2	P24482	7	6	u
DPB4	Q04603	187	1	u
DPL1	Q05567	211	167	u
DPP1	Q05521	16	1	u
DRS1	P32892	332	106	u
DSD1	P53095	11	10	u
DST1	P07273	190	14	u
DUO1	P53168	135	1	u
DUS3	Q06053	7	6	u
DYN1	P36022	21	1	u
DYN2	Q02647	548	1	u
EAF1	Q06337	10	1	u
EAF5	P39995	17	1	u
ECI1	Q05871	35	1	u
ECM16	Q04217	87	1	u
ECM25	P32525	8	1	u
ECM29	P38737	130	79	u
ECM3	Q99252	16	1	u
ECM31	P38122	97	1	u

ECM33	P38248	91	54	u
EDC3	P39998	72	36	u
EFG1	Q3E705	229	1	u
EHD3	P28817	131	9	u
EHT1	P38295	590	20	u
EIS1	Q05050	401	352	u
ELF1	P36053	77	76	u
ELO1	P39540	30	1	u
ELO2	P25358	43	1	u
ELO3	P40319	105	27	u
EMG1	Q06287	535	65	u
EMI1	Q04406	94	1	u
EMP47	P43555	112	45	u
EMP70	P32802	29	13	u
ENA1	P13587	81	12	u
ENA2	Q01896	81	1	u
END3	P39013	252	12	u
ENO2	P00925	714	626	u
ENT1	Q12518	193	1	u
ENT2	Q05785	59	58	u
EPT1	P22140	12	1	u
ERB1	Q04660	221	36	u
ERG1	P32476	279	29	u
ERG10	P41338	494	407	u
ERG11	P10614	292	72	u
ERG2	P32352	113	46	u
ERG24	P32462	46	1	u
ERG25	P53045	68	1	u
ERG26	P53199	394	1	u
ERG27	Q12452	382	13	u
ERG28	P40030	278	31	u
ERG3	P32353	141	12	u
ERG4	P25340	131	9	u
ERG5	P54781	150	70	u
ERG6	P25087	716	160	u
ERG7	P38604	26	25	u
ERG9	P29704	484	31	u
ERV14	P53173	35	34	u
ERV15	P38312	33	1	u
ERV2	Q12284	132	131	u
ERV29	P53337	155	31	u
ESC1	Q03661	4	1	u
ESF1	Q06344	23	7	u
ESF2	P53743	69	1	u
ETR1	P38071	350	56	u
EXG2	P52911	110	1	u
FAA1	P30624	597	517	u
FAA3	P39002	95	83	u
FAA4	P47912	213	204	u
FAD1	P38913	15	1	u
FAL1	Q12099	69	1	u
FAR10	Q06001	42	19	u

FAR3	P46671	164	1	u
FAR8	Q05040	90	8	u
FAU1	P40099	117	21	u
FBP26	P32604	10	9	u
FCF1	Q05498	25	1	u
FCF2	Q12035	109	1	u
FCY2	P17064	9	1	u
FET3	P38993	39	22	u
FET5	P43561	31	14	u
FIS1	P40515	511	30	u
FKS1	P38631	333	158	u
FLC3	P53121	18	1	u
FMC1	P40491	571	1	u
FMN1	Q03778	115	1	u
FMP10	P40098	447	1	u
FMP25	Q08023	76	52	u
FMP27	Q06179	115	1	u
FMP30	Q02883	10	1	u
FMP32	P43557	49	1	u
FMP33	P46998	27	1	u
FMP40	Q08968	36	35	u
FMP41	P53889	370	1	u
FMP42	Q04991	10	1	u
FMP45	Q07651	74	1	u
FMP46	P36141	584	1	u
FMP52	P40008	445	152	u
FOL1	P53848	75	16	u
FOL2	P51601	647	254	u
FRE1	P32791	7	1	u
FSF1	Q12029	358	1	u
FTR1	P40088	68	1	u
FUM1	P08417	413	141	u
FUN14	P18411	25	1	u
FUN30	P31380	62	8	u
FYV4	P38783	150	1	u
FYV7	Q12247	179	1	u
FYV8	P46949	12	1	u
FZO1	P38297	6	1	u
GAR1	P28007	334	91	u
GAS1	P22146	242	136	u
GAS3	Q03655	130	9	u
GAS5	Q08193	73	31	u
GCD10	P41814	31	1	u
GCD14	P46959	112	11	u
GCR2	Q01722	19	1	u
GCV1	P48015	518	70	u
GCV2	P49095	277	93	u
GEA2	P39993	54	22	u
GEF1	P37020	6	1	u
GEM1	P39722	7	6	u
GEP3	Q08622	9	1	u
GEP4	P38812	26	1	u

GEP7	P53171	78	1	u
GGC1	P38988	395	103	u
GND1	P38720	652	568	u
GNP1	P48813	90	29	u
GPD2	P41911	135	134	u
GPM1	P00950	622	586	u
GPT2	P36148	121	108	u
GPX2	P38143	613	295	u
GRX2	P17695	637	209	u
GRX5	Q02784	543	1	u
GRX6	Q12438	45	1	u
GRX7	P38068	87	51	u
GRX8	Q05926	45	1	u
GSC2	P40989	144	1	u
GSY1	P23337	103	90	u
GSY2	P27472	357	319	u
GTS1	P40956	54	1	u
GTT3	P39996	85	1	u
GUT2	P32191	546	432	u
GVP36	P40531	383	372	u
GYP8	P43570	19	1	u
HAS1	Q03532	576	207	u
HBT1	Q07653	5	1	u
HCA4	P20448	92	81	u
HCS1	P34243	7	1	u
HEH2	Q03281	64	1	u
HEM1	P09950	274	17	u
HEM14	P40012	157	1	u
HEM15	P16622	390	11	u
HEM25	Q07534	74	1	u
HFA1	P32874	19	1	u
HFD1	Q04458	176	73	u
HHO1	P53551	335	1	u
HHT1	P61830	434	36	u
HIP1	P06775	25	1	u
HIR2	P32480	55	21	u
HIS3	P06633	80	21	u
HMG1	P12683	126	18	u
HMG2	P12684	145	4	u
HMO1	Q03973	178	1	u
HMX1	P32339	30	1	u
HNM1	P19807	26	1	u
HOL1	P53389	16	1	u
HPC2	Q01448	8	1	u
HRP1	Q99383	89	48	u
HSH155	P49955	15	14	u
HSH49	Q99181	78	1	u
HSK3	P69852	208	1	u
HSP150	P32478	42	1	u
HSP30	P25619	30	1	u
HSP42	Q12329	40	39	u
HTA1	P04911	577	94	u

HTB2	P02294	754	1	u
HTD2	P38790	16	1	u
HTL1	Q9URQ5	330	1	u
HTZ1	Q12692	259	91	u
HUA1	P40325	24	1	u
HUA2	Q12134	19	1	u
HXT1	P32465	200	80	u
HXT2	P23585	61	17	u
HXT3	P32466	163	56	u
HXT5	P38695	77	1	u
HXT7	P39004	184	1	u
HYR1	P40581	329	293	u
IBA57	P47158	19	1	u
IDH1	P28834	531	131	u
IDH2	P28241	301	183	u
IDP1	P21954	757	286	u
IES1	P43579	28	6	u
IES2	P40154	15	1	u
IES3	Q12345	19	1	u
IES4	Q08561	104	1	u
IES5	P40060	259	1	u
IES6	P32617	245	1	u
IFA38	P38286	270	27	u
ILM1	P47155	49	1	u
ILV1	P00927	628	269	u
ILV2	P07342	453	403	u
ILV3	P39522	606	474	u
ILV5	P06168	710	374	u
ILV6	P25605	658	128	u
IMD2	P38697	170	165	u
IMD3	P50095	354	316	u
IML2	P47031	42	12	u
IMO32	P53219	135	1	u
IMP2'	P32351	14	1	u
IMP4	P53941	434	1	u
INA17	Q02888	91	1	u
INH1	P01097	294	1	u
INM2	Q05533	16	15	u
INO80	P53115	123	3	u
IOC2	Q12072	75	42	u
IOC3	P43596	52	37	u
IPI1	P38803	87	1	u
IPI3	P53877	99	70	u
IRA1	P18963	28	1	u
IRA2	P19158	18	1	u
IRC21	Q04772	23	1	u
IRC22	P40006	46	45	u
IRR1	P40541	111	7	u
ISC1	P40015	42	1	u
ISD11	Q6Q560	759	1	u
ISW1	P38144	505	4	u
ISW2	Q08773	123	11	u

ISY1	P21374	19	1	u
ITC1	P53125	111	7	u
ITR1	P30605	110	45	u
IVY1	Q04934	11	1	u
IZH2	Q12442	68	1	u
JIP5	Q06214	82	81	u
KEI1	Q06346	21	20	u
KEL1	P38853	16	4	u
KES1	P35844	369	135	u
KGD1	P20967	339	205	u
KGD2	P19262	205	32	u
KRE6	P32486	35	34	u
KRE9	P39005	18	17	u
KRI1	P42846	63	62	u
KRR1	P25586	245	1	u
LAC1	P28496	34	1	u
LAG1	P38703	48	1	u
LAM5	P43560	29	20	u
LAM6	Q08001	14	6	u
LAS1	P36146	18	1	u
LAS17	Q12446	8	1	u
LAT1	P12695	459	334	u
LCB1	P25045	305	277	u
LCB2	P40970	244	193	u
LCB3	P47013	35	1	u
LCB4	Q12246	32	7	u
LCB5	Q06147	7	6	u
LCP5	P40079	101	1	u
LDB7	P38210	103	1	u
LEA1	Q08963	180	1	u
LEM3	P42838	121	81	u
LEU4	P06208	560	530	u
LEU5	P38702	13	1	u
LEU9	Q12166	408	359	u
LHP1	P33399	364	284	u
LIP1	Q03579	124	1	u
LNP1	P38878	176	1	u
LOC1	P43586	171	22	u
LPD1	P09624	699	507	u
LRG1	P35688	5	1	u
LRP1	P38801	145	1	u
LSB3	P43603	306	21	u
LSC1	P53598	565	71	u
LSC2	P53312	682	35	u
LSM1	P47017	287	150	u
LSM12	P38828	481	304	u
LSM2	P38203	378	1	u
LSM3	P57743	59	1	u
LSM5	P40089	143	1	u
LSM6	Q06406	318	1	u
LSM7	P53905	305	104	u
LSM8	P47093	46	1	u

LUC7	Q07508	37	1	u
LYP1	P32487	8	1	u
LYS1	P38998	321	228	u
LYS12	P40495	626	26	u
LYS20	P48570	422	1	u
LYS21	Q12122	496	280	u
LYS4	P49367	350	262	u
MAE1	P36013	415	366	u
MAF1	P41910	53	1	u
MAK11	P20484	196	1	u
MAK16	P10962	70	1	u
MAK21	Q12176	197	84	u
MAK5	P38112	114	92	u
MBF1	O14467	747	561	u
MCD1	Q12158	9	8	u
MCM2	P29469	28	15	u
MCM3	P24279	43	19	u
MCM5	P29496	55	31	u
MCM6	P53091	19	4	u
MCM7	P38132	29	1	u
MCP2	Q06567	78	53	u
MCR1	P36060	681	73	u
MCT1	Q12283	59	1	u
MDH1	P17505	665	351	u
MDH3	P32419	498	142	u
MDL1	P33310	76	36	u
MDL2	P33311	56	25	u
MDM35	O60200	154	1	u
MDN1	Q12019	221	55	u
MDV1	P47025	13	6	u
MED1	Q12321	17	8	u
MED11	Q99278	43	1	u
MED2	Q12124	11	1	u
MED7	Q08278	21	1	u
MED8	P38304	46	1	u
MET14	Q02196	23	1	u
MET7	Q08645	9	1	u
MGM1	P32266	125	94	u
MGM101	P32787	490	17	u
MGS1	P40151	8	1	u
MHF1	Q3E835	56	1	u
MHP1	P43638	11	10	u
MIC10	Q96VH5	643	56	u
MIC12	P38341	693	1	u
MIC19	P43594	402	1	u
MIC26	P50087	140	1	u
MIC27	P50945	183	1	u
MIC60	P36112	342	71	u
MID1	P41821	9	1	u
MIR1	P23641	443	166	u
MIS1	P09440	562	408	u
MIT1	P40002	15	1	u

MIX14	Q04341	371	1	u
MIX17	Q03667	33	1	u
MIX23	P38162	228	1	u
MLC2	Q06580	174	1	u
MLH1	P38920	12	1	u
MMR1	Q06324	20	1	u
MMT2	Q08970	10	1	u
MOH1	P38191	34	1	u
MOT1	P32333	111	1	u
MPC1	P53157	153	1	u
MPC2	P38857	38	1	u
MPC3	P53311	210	1	u
MPM1	P40364	213	1	u
MPP10	P47083	77	15	u
MRD1	Q06106	85	52	u
MRH1	Q12117	91	90	u
MRH4	P53166	9	1	u
MRM1	P25270	23	1	u
MRS1	P07266	13	1	u
MRS3	P10566	15	1	u
MRS4	P23500	102	1	u
MRX12	P47084	74	1	u
MRX3	P38172	18	1	u
MRX9	Q07349	22	1	u
MSC1	Q03104	572	193	u
MSC2	Q03455	7	1	u
MSC3	Q05812	20	6	u
MSC7	P38694	240	194	u
MSH2	P25847	158	61	u
MSH3	P25336	9	1	u
MSH5	Q12175	6	1	u
MSH6	Q03834	97	7	u
MSI1	P13712	11	1	u
MSL1	P40567	194	1	u
MSL5	Q12186	20	1	u
MSS4	P38994	12	1	u
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MTR3	P48240	19	18	u
MUD1	P32605	74	1	u
MUD2	P36084	27	1	u
MUP1	P50276	26	1	u
MYO1	P08964	78	4	u
MYO3	P36006	95	10	u
MYO4	P32492	91	15	u
MYO5	Q04439	154	19	u
NAB3	P38996	45	23	u
NAB6	Q03735	9	4	u
NAM8	Q00539	10	9	u
NAT10	P53914	397	67	u
NCB2	Q92317	133	75	u
NCP1	P16603	458	422	u

NCR1	Q12200	5	1	u
NDC80	P40460	13	12	u
NDE1	P40215	450	235	u
NDI1	P32340	431	28	u
NET1	P47035	57	1	u
NFS1	P25374	181	1	u
NGL1	Q08213	13	1	u
NHP10	Q03435	119	1	u
NHP6A	P11632	695	54	u
NHP6B	P11633	602	125	u
NIF3	P53081	264	245	u
NIP7	Q08962	569	58	u
NKP1	Q12493	42	1	u
NKP2	Q06162	184	1	u
NMA1	Q06178	12	11	u
NNF1	P47149	49	1	u
NNF2	P53253	15	9	u
NOC2	P39744	526	421	u
NOC3	Q07896	140	86	u
NOC4	Q06512	111	95	u
NOP10	Q6Q547	731	1	u
NOP12	Q08208	372	126	u
NOP13	P53883	344	51	u
NOP14	Q99207	135	5	u
NOP15	P53927	110	45	u
NOP16	P40007	102	1	u
NOP19	P53317	24	1	u
NOP2	P40991	299	218	u
NOP4	P37838	291	232	u
NOP56	Q12460	692	426	u
NOP58	Q12499	552	383	u
NOP6	Q07623	204	45	u
NOP7	P53261	511	291	u
NPL6	P32832	209	178	u
NQM1	P53228	455	405	u
NRD1	P53617	126	44	u
NSA1	P53136	127	1	u
NSA2	P40078	355	1	u
NSG1	P38837	107	1	u
NSG2	P53898	100	15	u
NSL1	Q12143	21	1	u
NSR1	P27476	578	520	u
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NTE1	Q04958	30	13	u
NUC1	P08466	207	1	u
NUF2	P33895	20	9	u
NUR1	Q12066	10	1	u
NUT1	P53114	51	4	u
NUT2	Q06213	120	1	u
NYV1	Q12255	39	1	u
OAC1	P32332	226	1	u
ODC1	Q03028	129	1	u

ODC2	Q99297	420	32	u
OKP1	P53298	11	1	u
OLE1	P21147	366	38	u
OM45	P16547	703	37	u
OMS1	Q06668	53	1	u
OPI3	P05375	365	123	u
ORC1	P54784	6	1	u
ORC3	P54790	31	30	u
ORC4	P54791	37	1	u
ORC5	P50874	30	1	u
ORC6	P38826	21	1	u
ORT1	Q12375	57	1	u
OSH2	Q12451	92	3	u
OSH3	P38713	19	1	u
OSH6	Q02201	251	1	u
OSW7	P43611	18	8	u
PAL1	Q05518	10	1	u
PAN1	P32521	81	27	u
PAN2	P53010	5	1	u
PAP1	P29468	197	155	u
PAP2	P53632	44	15	u
PBP2	P38151	12	1	u
PBP4	Q07362	375	210	u
PCC1	Q3E833	60	1	u
PCF11	P39081	23	1	u
PCS60	P38137	240	228	u
PCT1	P13259	136	94	u
PDA1	P16387	773	350	u
PDB1	P32473	520	102	u
PDC1	P06169	661	577	u
PDC2	P32896	10	1	u
PDC5	P16467	59	58	u
PDC6	P26263	59	58	u
PDH1	Q12428	64	1	u
PDR12	Q02785	94	6	u
PDR15	Q04182	47	1	u
PDR16	P53860	248	26	u
PDR5	P33302	388	116	u
PDS5	Q04264	131	1	u
PDX1	P16451	314	11	u
PEF1	P53238	14	1	u
PET10	P36139	381	1	u
PET100	P38958	296	1	u
PET117	Q02771	113	1	u
PET191	Q02772	315	1	u
PET8	P38921	36	1	u
PET9	P18239	736	365	u
PEX11	Q12462	139	100	u
PEX30	Q06169	62	17	u
PFF1	P38244	41	4	u
PFS2	P42841	10	1	u
PGC1	Q08959	114	1	u

PGD1	P40356	40	1	u
PGK1	P00560	726	621	u
PHM7	Q12252	113	28	u
PHO23	P50947	66	1	u
PHO87	P25360	6	5	u
PHO91	P27514	11	1	u
PHS1	P40857	47	1	u
PIC2	P40035	202	1	u
PIK1	P39104	5	4	u
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PKR1	Q03880	383	1	u
PMA1	P05030	583	456	u
PMR1	P13586	65	64	u
PNO1	Q99216	118	17	u
PNS1	Q12412	60	17	u
POB3	Q04636	496	448	u
POL1	P13382	76	3	u
POL12	P38121	72	71	u
POL2	P21951	45	2	u
POL3	P15436	41	1	u
POL31	P46957	30	18	u
POL32	P47110	13	1	u
POL5	P39985	231	22	u
POP1	P41812	40	39	u
POP2	P39008	11	10	u
POP4	P38336	34	1	u
POP6	P53218	251	1	u
POP7	P38291	35	1	u
POP8	P38208	224	1	u
POR1	P04840	737	463	u
POR2	P40478	36	1	u
POS5	Q06892	67	1	u
PPA2	P28239	94	1	u
PPN1	Q04119	73	13	u
PRI1	P10363	35	10	u
PRI2	P20457	70	1	u
PRM8	P53174	68	1	u
PRP11	Q07350	88	1	u
PRP2	P20095	6	5	u
PRP21	P32524	54	1	u
PRP31	P49704	10	1	u
PRP38	Q00723	19	1	u
PRP42	Q03776	16	1	u
PRP43	P53131	237	149	u
PRP46	Q12417	11	1	u
PRP5	P21372	6	1	u
PRP6	P19735	38	37	u
PRP8	P33334	82	1	u
PRP9	P19736	36	35	u
PRS1	P32895	122	81	u
PRS2	P38620	125	71	u
PRS3	P38689	486	182	u

PRS4	P38063	120	92	u
PRS5	Q12265	384	158	u
PRX1	P34227	506	156	u
PRY1	P47032	17	16	u
PRY2	P36110	16	1	u
PSF1	Q12488	22	1	u
PSP1	P50896	11	1	u
PSP2	P50109	8	1	u
PST2	Q12335	493	311	u
PTI1	P39927	23	1	u
PTM1	P32857	38	1	u
PUF3	Q07807	35	10	u
PUN1	Q06991	18	1	u
PUS4	P48567	24	11	u
PUS7	Q08647	123	73	u
PUT2	P07275	434	341	u
PWP2	P25635	313	65	u
PXR1	P53335	58	1	u
QCR10	P37299	367	1	u
QCR6	P00127	72	1	u
QCR7	P00128	675	89	u
QCR8	P08525	133	1	u
QCR9	P22289	235	1	u
QDR2	P40474	27	1	u
QDR3	P38227	7	1	u
RAD10	P06838	22	1	u
RAD27	P26793	39	24	u
RAD33	Q04231	282	1	u
RAD50	P12753	87	1	u
RAI1	P53063	157	1	u
RAX2	Q12465	16	1	u
RCF1	Q03713	564	1	u
RCF2	P53721	257	1	u
RCL1	Q08096	217	1	u
RCM1	P53972	19	1	u
RDH54	P38086	15	1	u
RDI1	Q12434	550	332	u
RDL2	Q08742	203	1	u
REH1	Q06709	11	10	u
REI1	P38344	12	1	u
RET1	P22276	100	1	u
REX2	P54964	17	1	u
REX4	Q08237	105	1	u
RFC2	P40348	378	27	u
RFC3	P38629	233	1	u
RFC4	P40339	470	14	u
RFC5	P38251	253	1	u
RFM1	Q12192	15	1	u
RFS1	P38234	500	220	u
RFT1	P38206	16	1	u
RGA2	Q06407	5	1	u
RGC1	Q06108	9	8	u

RGD1	P38339	57	1	u
RGD2	P43556	59	33	u
RGI1	P40043	234	63	u
RGR1	P19263	42	17	u
RHO2	P06781	192	1	u
RHO3	Q00245	433	283	u
RHO4	Q00246	17	1	u
RHO5	P53879	89	1	u
RIF1	P29539	22	1	u
RIM1	P32445	599	83	u
RIM2	P38127	57	1	u
RIP1	P08067	539	22	u
RMD1	Q03441	11	1	u
RMD8	P43620	7	6	u
RMP1	Q12530	23	1	u
RNA14	P25298	103	102	u
RNA15	P25299	34	1	u
RNH201	P53942	15	1	u
RNH70	P53331	36	25	u
RNQ1	P25367	26	12	u
RNR2	P09938	501	276	u
RNR4	P49723	517	397	u
RNT1	Q02555	43	1	u
ROK1	P45818	143	125	u
ROM2	P51862	14	10	u
RPA12	P32529	266	1	u
RPA135	P22138	518	86	u
RPA14	P50106	39	38	u
RPA190	P10964	542	103	u
RPA34	P47006	408	1	u
RPA43	P46669	304	30	u
RPA49	Q01080	463	1	u
RPB10	P22139	528	1	u
RPB11	P38902	702	41	u
RPB2	P08518	339	66	u
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RPB9	P27999	354	37	u
RPC10	P40422	570	1	u
RPC11	Q04307	191	1	u
RPC17	P47076	411	1	u
RPC19	P28000	574	78	u
RPC25	P35718	48	21	u
RPC34	P32910	15	1	u
RPC37	P36121	17	1	u
RPC40	P07703	281	45	u
RPC53	P25441	36	1	u
RPC82	P32349	102	21	u
RPF2	P36160	302	1	u
RPO21	P04050	361	89	u
RPO31	P04051	222	1	u

RPO41	P13433	46	1	u
RPP1	P38786	360	1	u
RRB1	Q04225	94	93	u
RRG9	P40156	75	1	u
RRN10	P38204	33	1	u
RRP1	P35178	397	33	u
RRP12	Q12754	198	23	u
RRP15	Q06511	217	1	u
RRP17	Q04031	132	1	u
RRP3	P38712	305	18	u
RRP4	P38792	131	13	u
RRP40	Q08285	102	1	u
RRP42	Q12277	39	18	u
RRP45	Q05636	73	1	u
RRP46	P53256	157	46	u
RRP5	Q05022	566	147	u
RRP7	P25368	233	1	u
RRP8	P38961	67	1	u
RRP9	Q06506	194	186	u
RRT14	P40470	23	22	u
RRT8	Q08219	28	1	u
RSA3	Q05942	22	1	u
RSA4	P25382	51	18	u
RSB1	Q08417	12	1	u
RSC1	P53236	37	14	u
RSC2	Q06488	83	32	u
RSC3	Q06639	241	170	u
RSC4	Q02206	166	7	u
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RSC8	P43609	374	159	u
RSC9	Q03124	138	43	u
RSE1	Q04693	50	1	u
RSN1	Q03516	121	9	u
RSR1	P13856	153	1	u
RTC3	P38804	345	307	u
RTC5	Q12108	17	16	u
RTN1	Q04947	566	201	u
RTN2	Q12443	135	11	u
RTS2	P40962	42	19	u
RTT102	P53330	120	1	u
RTT106	P40161	45	44	u
RTT107	P38850	17	8	u
RVS161	P25343	397	392	u
RVS167	P39743	88	71	u
RXT3	Q07458	33	1	u
SAC1	P32368	484	467	u
SAC6	P32599	536	423	u
SAC7	P17121	15	1	u
SAH1	P39954	587	584	u
SAM3	Q08986	25	1	u
SAS10	Q12136	61	1	u
SCM4	P32564	27	1	u

SCO1	P23833	103	1	u
SCO2	P38072	123	1	u
SCP1	Q08873	128	23	u
SCP160	P06105	697	497	u
SCS22	Q6Q595	61	1	u
SCS3	P53012	12	1	u
SCS7	Q03529	211	1	u
SCT1	P32784	117	6	u
SCW10	Q04951	13	1	u
SCW4	P53334	80	59	u
SDH2	P21801	430	1	u
SDH4	P37298	152	26	u
SDH5	Q08230	29	1	u
SDH6	Q3E785	65	1	u
SDH7	Q04401	144	1	u
SDH8	P38345	36	1	u
SDS24	P38314	65	51	u
SEG1	Q04279	80	1	u
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SEN1	Q00416	49	18	u
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SEN54	Q02825	10	1	u
SEY1	Q99287	406	373	u
SFH1	Q06168	22	10	u
SFK1	P35735	27	1	u
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SGN1	P40561	19	1	u
SGT1	Q08446	12	11	u
SHE10	P53075	433	405	u
SHE2	P36068	95	18	u
SHE3	P38272	65	1	u
SHE4	P51534	12	5	u
SHE9	Q04172	20	1	u
SHM1	P37292	619	317	u
SHM2	P37291	616	592	u
SHY1	P53266	24	1	u
SIM1	P40472	22	10	u
SIP3	P38717	19	1	u
SIP5	P40210	10	9	u
SIR3	P06701	25	9	u
SIR4	P11978	11	1	u
SKI6	P46948	68	67	u
SKI8	Q02793	12	11	u
SLA2	P33338	138	54	u
SLC1	P33333	580	15	u
SMB1	P40018	385	23	u
SMC1	P32908	284	1	u
SMC2	P38989	65	1	u
SMC3	P47037	353	1	u
SMC4	Q12267	85	1	u
SMD1	Q02260	305	1	u
SMD2	Q06217	427	1	u

SMD3	P43321	378	1	u
SME1	Q12330	57	1	u
SMF3	Q12078	32	1	u
SMI1	P32566	40	1	u
SMX2	P40204	73	1	u
SMX3	P54999	62	1	u
SMY1	P32364	38	14	u
SMY2	P32909	7	1	u
SNC1	P31109	103	1	u
SNC2	P33328	305	104	u
SNF11	P38956	29	1	u
SNF12	P53628	26	16	u
SNF2	P22082	35	1	u
SNF5	P18480	6	5	u
SNF6	P18888	29	1	u
SNP1	Q00916	73	1	u
SNQ2	P32568	157	18	u
SNU71	P53207	15	7	u
SOD1	P00445	713	597	u
SOD2	P00447	582	107	u
SOF1	P33750	150	18	u
SOV1	Q04748	10	5	u
SPB1	P25582	130	55	u
SPC110	P32380	165	34	u
SPC19	Q03954	65	1	u
SPC25	P40014	153	1	u
SPC29	P33419	39	1	u
SPC34	P36131	129	1	u
SPC72	P39723	15	1	u
SPC98	P53540	6	1	u
SPF1	P39986	385	154	u
SPO14	P36126	9	1	u
SPO75	Q07798	6	1	u
SPP41	P38904	10	1	u
SPS19	P32573	112	1	u
SPT15	P13393	230	1	u
SPT16	P32558	540	165	u
SPT2	P06843	29	1	u
SPT23	P35210	5	1	u
SPT4	P32914	227	1	u
SPT5	P27692	235	146	u
SRB2	P34162	234	23	u
SRB4	P32569	53	43	u
SRB5	P32585	74	1	u
SRB6	P32570	96	1	u
SRB7	P47822	308	1	u
SRB8	P25648	13	1	u
SRC1	Q03707	23	1	u
SRL2	Q12020	38	1	u
SRP40	P32583	79	58	u
SRV2	P17555	321	163	u
SSF1	P38789	250	107	u

SSF2	Q12153	249	57	u
SSP120	P39931	180	19	u
SST2	P11972	7	1	u
SSU1	P41930	10	1	u
STE18	P18852	315	44	u
STE2	D6VTK4	49	1	u
STE4	P18851	50	1	u
STF1	P01098	59	1	u
STH1	P32597	323	13	u
STL1	P39932	46	8	u
STP3	Q05937	14	1	u
STT4	P37297	86	1	u
STU1	P38198	12	6	u
STU2	P46675	76	32	u
STV1	P37296	16	15	u
SUA7	P29055	64	1	u
SUB1	P54000	78	15	u
SUN4	P53616	25	1	u
SUR2	P38992	153	1	u
SUR7	P54003	52	32	u
SVL3	Q03088	18	11	u
SWC7	Q06707	37	1	u
SWH1	P35845	38	7	u
SWI1	P09547	22	1	u
SWI3	P32591	105	94	u
SWI6	P09959	38	37	u
SWP82	P43554	15	1	u
SWR1	Q05471	7	1	u
SYC1	Q08553	202	1	u
SYF1	Q04048	22	15	u
SYF2	P53277	77	1	u
SYM1	Q06563	24	1	u
SYP1	P25623	100	48	u
TAF11	Q04226	126	12	u
TAF13	P11747	64	1	u
TAF2	P23255	80	1	u
TAF3	Q12297	27	1	u
TAF4	P50105	96	1	u
TAF7	Q05021	16	7	u
TAF8	Q03750	29	28	u
TAH18	Q12181	15	14	u
TAN1	P53072	101	74	u
TAO3	P40468	45	1	u
TAT1	P38085	51	23	u
TAZ1	Q06510	25	1	u
TCA17	P32613	32	1	u
TCB1	Q12466	299	58	u
TCB2	P48231	201	11	u
TCB3	Q03640	318	74	u
TCD1	P38756	160	1	u
TCD2	P36101	205	1	u
TDA2	P40045	39	1	u

TDA5	Q06417	14	1	u
TDH1	P00360	698	632	u
TDH2	P00358	753	631	u
TDH3	P00359	775	639	u
TES1	P41903	61	1	u
TFA1	P36100	30	1	u
TFA2	P36145	14	1	u
TFC4	P33339	33	1	u
TFC7	Q12415	11	1	u
TFG2	P41896	125	1	u
TGL1	P34163	128	1	u
TGL2	P54857	14	1	u
TGL3	P40308	30	29	u
TGL4	P36165	11	10	u
TGL5	Q12043	7	6	u
TGS1	Q12052	15	1	u
THG1	P53215	132	1	u
THP3	Q12049	20	1	u
TIM11	P81449	624	1	u
TIP41	Q12199	13	12	u
TMA16	Q08687	351	197	u
TMA23	Q03525	119	1	u
TMC1	Q08422	32	1	u
TMN3	P40071	13	1	u
TNA1	P53322	27	1	u
TOA1	P32773	17	1	u
TOA2	P32774	591	1	u
TOF1	P53840	8	1	u
TOP1	P04786	227	204	u
TOP2	P06786	297	6	u
TOS1	P38288	35	21	u
TPO1	Q07824	17	1	u
TPO2	P53283	8	1	u
TPO3	Q06451	42	15	u
TPO4	Q12256	39	14	u
TPP1	Q03796	20	1	u
TPS2	P31688	392	356	u
TRI1	Q05024	43	1	u
TRM1	P15565	239	140	u
TRR2	P38816	67	29	u
TRS120	Q04183	11	1	u
TRS20	P38334	104	1	u
TRS23	Q03784	22	21	u
TRS31	Q03337	180	1	u
TRS65	P32893	9	1	u
TRX3	P25372	458	1	u
TSC10	P38342	256	1	u
TSC13	Q99190	145	29	u
TSC3	Q3E790	306	1	u
TUB1	P09733	263	153	u
TUB2	P02557	380	214	u
TUB3	P09734	133	112	u

TUP1	P16649	349	94	u
TVP15	Q03860	35	1	u
TVP18	Q04767	65	28	u
TY1A-LR4	P0C2I8	433	1	u
TY1B-MR1	Q04214	125	1	u
TY2B-LR1	P0C2J3	57	35	u
TYW1	Q08960	52	44	u
UAF30	Q08747	21	1	u
UGO1	Q03327	29	1	u
UGP1	P32861	617	416	u
UIP3	P39547	68	1	u
ULS1	Q08562	6	1	u
UME1	Q03010	130	10	u
UNG1	P12887	13	1	u
UPS1	Q05776	27	1	u
URB1	P34241	260	1	u
URB2	P47108	139	4	u
UTH1	P36135	88	46	u
UTP10	P42945	282	7	u
UTP11	P34247	247	1	u
UTP14	Q04500	27	1	u
UTP15	Q04305	233	8	u
UTP20	P35194	253	2	u
UTP21	Q06078	136	5	u
UTP23	Q12339	257	1	u
UTP25	P40498	147	119	u
UTP4	Q06679	253	197	u
UTP6	Q02354	366	9	u
UTP7	P40055	149	130	u
UTR1	P21373	18	1	u
UTR2	P32623	60	21	u
VBA4	Q04602	7	1	u
VHR1	P40522	8	1	u
VID27	P40157	62	24	u
VIP1	Q06685	73	39	u
VMA10	P48836	436	384	u
VMA11	P32842	32	1	u
VMA16	P23968	52	1	u
VMA2	P16140	588	564	u
VMA22	P38784	96	1	u
VMA4	P22203	674	627	u
VMA6	P32366	297	128	u
VMA7	P39111	182	1	u
VOA1	P53262	61	1	u
VPH1	P32563	324	143	u
VPH2	P32341	201	1	u
VPS72	Q03388	12	1	u
VRP1	P37370	27	1	u
VTC1	P40046	91	90	u
VTC3	Q02725	109	80	u
WHI2	P12611	30	18	u
WSC2	P53832	10	1	u

XRN1	P22147	385	179	u
YAF9	P53930	73	1	u
YAH1	Q12184	28	1	u
YAP1801	P38856	31	7	u
YAP1802	P53309	35	1	u
YBL028C	P38202	328	1	u
YBL029C-A	Q3E756	51	1	u
YBL059W	P34224	24	1	u
YBL086C	P38177	10	1	u
YBR056W	P38081	78	28	u
YBR096W	P38256	396	66	u
YBR126W-A	Q8TGU7	80	1	u
YBR230W-A	Q3E762	81	1	u
YBR255C-A	Q3E776	173	1	u
YBT1	P32386	74	3	u
YCF1	P39109	48	6	u
YCG1	Q06680	18	1	u
YCP4	P25349	573	226	u
YCR016W	P25617	205	15	u
YCR043C	P25361	86	36	u
YCR061W	P25639	8	1	u
YCR087C-A	P37263	256	1	u
YCS4	Q06156	29	1	u
YDC1	Q02896	14	1	u
YDL121C	Q07541	285	32	u
YDL157C	Q12082	280	1	u
YDL177C	Q12257	63	1	u
YDR056C	Q12025	85	1	u
YDR061W	Q12298	59	1	u
YDR115W	Q04598	116	1	u
YDR119W-A	Q2V2P9	84	1	u
YDR222W	Q04925	23	1	u
YDR262W	Q12331	86	1	u
YDR286C	Q05530	98	1	u
YDR381C-A	Q3E6R5	108	1	u
YDR476C	Q03362	152	1	u
YDR514C	Q04408	19	1	u
YEL043W	P32618	10	1	u
YEL077C	Q3E7X8	15	1	u
YFR045W	P43617	16	1	u
YGL010W	P25338	27	1	u
YGL108C	P53139	35	1	u
YGL140C	P53120	37	1	u
YGL185C	P53100	12	11	u
YGL204C	P53089	51	1	u
YGP1	P38616	47	29	u
YGR012W	P53206	301	12	u
YGR021W	P53212	35	1	u
YGR130C	P53278	151	43	u
YGR149W	P48236	32	1	u
YGR169C-A	Q3E772	143	142	u
YGR266W	P53326	139	112	u

YGR283C	P53336	45	1	u
YHC1	Q05900	42	1	u
YHL018W	P38744	169	1	u
YHM2	Q04013	464	128	u
YHR045W	P38775	46	25	u
YHR097C	P38809	13	1	u
YHR127W	P38833	183	1	u
YIL077C	P40508	30	1	u
YIL156W-B	Q2V2P4	379	1	u
YIL161W	P40449	20	1	u
YIM1	P28625	98	25	u
YIP3	P53633	307	279	u
YJL133C-A	Q3E7A3	687	1	u
YJL171C	P46992	93	38	u
YJL193W	P39542	24	1	u
YJR008W	P47085	45	1	u
YJR085C	P47131	129	1	u
YJR111C	P47148	80	1	u
YJU3	P28321	265	30	u
YKL018C-A	Q3E7A7	49	1	u
YKL023C-A	Q2V2P3	72	1	u
YKL063C	P35725	234	63	u
YKL077W	P36081	234	11	u
YKL091C	P33324	69	68	u
YKL100C	P34248	88	87	u
YKL151C	P36059	111	64	u
YKR011C	Q02209	13	1	u
YKR023W	P36119	18	8	u
YKR070W	P36151	224	1	u
YLF2	P38746	12	1	u
YLL007C	Q07799	14	13	u
YLR050C	Q12155	108	1	u
YLR099W-A	Q3E798	60	1	u
YLR108C	Q12259	30	1	u
YLR225C	Q05948	103	1	u
YLR257W	Q06146	15	14	u
YLR283W	Q05867	30	1	u
YLR326W	Q06170	41	1	u
YLR361C-A	Q3E795	53	1	u
YLR363W-A	Q3E747	61	60	u
YLR413W	Q06689	80	7	u
YLR419W	Q06698	51	3	u
YLR422W	Q06409	25	1	u
YLR455W	Q06188	70	1	u
YMC1	P32331	205	1	u
YMC2	P38087	214	1	u
YMR102C	Q03177	29	10	u
YMR111C	Q04461	10	1	u
YMR134W	P40207	132	1	u
YMR144W	P40214	14	1	u
YMR209C	Q03648	58	1	u
YMR295C	Q03559	89	1	u

YMR310C	Q04867	69	1	u
YNK1	P36010	653	508	u
YNL050C	P53952	83	1	u
YNL115C	P53925	30	1	u
YNL181W	P53878	229	1	u
YNL194C	P40169	16	15	u
YNL200C	P40165	67	66	u
YNL208W	P40159	154	1	u
YNL320W	P42840	34	1	u
YNR021W	P53723	395	65	u
YNR040W	P53736	211	1	u
YOL087C	Q99247	17	4	u
YOL107W	Q12239	28	1	u
YOP1	Q12402	215	59	u
YOR020W-A	Q3E824	460	1	u
YOR022C	Q12204	7	6	u
YOR093C	Q12275	9	1	u
YOR097C	Q12274	28	1	u
YOR1	P53049	82	1	u
YOR131C	Q12486	77	76	u
YOR296W	Q08748	4	1	u
YPC1	P38298	30	1	u
YPK9	Q12697	4	1	u
YPL109C	Q02981	7	1	u
YPL199C	Q08954	408	19	u
YPL216W	Q08964	5	1	u
YPL225W	Q08971	711	615	u
YPL245W	Q12179	10	1	u
YPR010C-A	A5Z2X5	78	1	u
YPR011C	Q12251	15	1	u
YPR063C	Q12160	145	35	u
YPR091C	Q06833	126	102	u
YPR097W	Q06839	9	4	u
YPR098C	Q06089	184	1	u
YPR114W	Q06107	30	1	u
YRO2	P38079	84	44	u
YSC83	P32792	38	1	u
YSC84	P32793	60	1	u
YSF3	P0C074	153	1	u
YSH1	Q06224	39	17	u
YSP2	Q06681	31	1	u
YTA7	P40340	40	1	u
YTM1	Q12024	319	20	u
YVC1	Q12324	14	1	u
ZEO1	Q08245	770	290	u
ZRC1	P20107	35	10	u
ZRG17	P53735	8	1	u
ZRT1	P32804	175	96	u
ZTA1	P38230	378	66	u

MLR

SUMMARY OUTPUT

Regression Statistics	
Multiple R	0.814525
R Square	0.663451
Adjusted R	0.36897
Standard E	1.874579
Observatio	16

ANOVA

	df	*SS*	*MS*	*F*	*ignificance F*
Regression	7	55.41883	7.916975	2.252951	0.138873
Residual	8	28.11238	3.514047		
Total	15	83.5312			

	Coefficients	*tandard Err*	*t Stat*	*P-value*	*Lower 95%*	*Upper 95%*	*ower 95.0%*	*pper 95.0%*
Intercept	12.94546	3.597418	3.598542	0.006997	4.6498	21.24112	4.6498	21.24112
X Variable	-40.0015	31.84803	-1.25601	0.24455	-113.443	33.44015	-113.443	33.44015
X Variable	-82.5034	60.00031	-1.37505	0.206392	-220.864	55.85754	-220.864	55.85754
X Variable	1.807268	12.26679	0.14733	0.886517	-26.48	30.09453	-26.48	30.09453
X Variable	-50.1723	37.09639	-1.35248	0.213205	-135.717	35.37215	-135.717	35.37215
X Variable	66.74995	29.79167	2.240558	0.055377	-1.94976	135.4497	-1.94976	135.4497
X Variable	-12.2094	13.27134	-0.91999	0.384481	-42.8132	18.39431	-42.8132	18.39431
X Variable	-25.2535	15.37279	-1.64274	0.139062	-60.7032	10.19623	-60.7032	10.19623

SR

Gene=((((-108.5782*((Hsf1-Rtg3)+(Gzf3*Mot2)))+(54531.1169*((Hsf1-Rtg3)*(Gzf3*Rlm1))))+(14.0344*(

		Gzf3	Hsf1	Rap1	Rlm1	Rtg3
	FUS1	0.033424	0.045323	0.222716	0.029384	0.037426
	HSP26	0.033424	0.045323	0.222716	0.029384	0.037426
	MNN1	0.033424	0	0.222716	0.029384	0.037426
	MSR1	0.033424	0.045323	0.222716	0	0
	VID24	0.033424	0.045323	0.222716	0	0.037426
	WSC4	0.033424	0.045323	0.222716	0.029384	0
	FMP48	0.033424	0.045323	0.222716	0.029384	0
	PCL1	0.033424	0	0.222716	0.029384	0
	GPD1	0	0.045323	0.222716	0.029384	0.037426
	HO	0	0.045323	0.222716	0.029384	0
	RPL24a	0	0.045323	0.222716	0.029384	0.037426
	RPL31a	0	0.045323	0.222716	0	0.037426
	RPS26b	0	0.045323	0.222716	0	0.037426
	SSA1	0	0.045323	0.222716	0	0.037426
	YCK1	0	0	0.222716	0	0
6	YPS6	0	0.045323	0	0.029384	0

(Skn7/3.4811)-(Mot2+Gzf3))))+(-1077.7952*((Skn7-Hsf1)*Rlm1)))+11.147548

Skn7	Mot2	Gene
0.117271	0	6.14385
0.117271	0	10.76684
0.117271	0.155336	6.78902
0.117271	0	6.10138
0	0	9.79227
0.117271	0	5.16977
0.117271	0	7.61195
0.117271	0.155336	4.55595
0	0	11.61025
0.117271	0	4.49923
0.117271	0	8.71049
0.117271	0	10.23539
0	0.155336	8.18411
0.117271	0	11.31334
0.117271	0.155336	9.51087
0	0	7.73191