



Libraries and Learning Services

University of Auckland Research Repository, ResearchSpace

Version

This is the Pre-print Manuscript version. This version is defined in the NISO recommended practice RP-8-2008 <http://www.niso.org/publications/rp/>

Suggested Reference

Freeman, O. J., Unwin, R. D., Dowsey, A. W., Begley, P., Ali, S., Hollywood, K. A., . . . Gardiner, N. J. (2016). Metabolic Dysfunction Is Restricted to the Sciatic Nerve in Experimental Diabetic Neuropathy. *Diabetes*, 65(1), 228- 238.
doi: [10.2337/db15-0835](https://doi.org/10.2337/db15-0835)

Copyright

Items in ResearchSpace are protected by copyright, with all rights reserved, unless otherwise indicated. Previously published items are made available in accordance with the copyright policy of the publisher.

For more information, see [General copyright](#), [Publisher copyright](#), [SHERPA/RoMEO](#).

Metabolic dysfunction is restricted to the sciatic nerve in experimental diabetic neuropathy

Oliver J. Freeman^{1,2}, Richard D. Unwin^{2,3}, Andrew W. Dowsey^{2,3}, Paul Begley^{2,3}, Sumia Ali¹, Katherine A. Hollywood^{2,3}, Nitin Rustogi^{2,3}, Rasmus S. Petersen¹, Warwick B. Dunn^{2,3†}, Garth J.S. Cooper^{2,3,4,5*} & Natalie J. Gardiner^{1*}

¹ Faculty of Life Sciences, University of Manchester, UK

² Centre for Advanced Discovery and Experimental Therapeutics (CADET), Central Manchester University Hospitals NHS Foundation Trust, Manchester Academic Health Sciences Centre, Manchester, UK

³ Centre for Endocrinology and Diabetes, Institute of Human Development, Faculty of Medical and Human Sciences, University of Manchester, UK

⁴ School of Biological Sciences, University of Auckland, New Zealand

⁵ Department of Pharmacology, Medical Sciences Division, University of Oxford, UK

† Present address: School of Biosciences, University of Birmingham, UK

*Joint corresponding authors: Natalie J. Gardiner and Garth J.S. Cooper

Email: natalie.gardiner@manchester.ac.uk; garth.cooper@manchester.ac.uk

Address: University of Manchester, AV Hill Building, Oxford Road, Manchester, M13 9PT, United Kingdom

Telephone: +44 161 275 5768; +44 161 701 0240

Word count: 4,490

Number of tables: 1, Number of figures: 6

Running title: Metabolic dysfunction in diabetic neuropathy

Abstract

High glucose levels in the peripheral nervous system (PNS) have been implicated in the pathogenesis of diabetic neuropathy (DN). However our understanding of the molecular mechanisms which cause the marked distal pathology is incomplete. Here we performed a comprehensive, system-wide analysis of the PNS of a rodent model of DN. We integrated proteomics and metabolomics from the sciatic nerve (SN), the lumbar 4/5 dorsal root ganglia (DRG) and the trigeminal ganglia (TG) of streptozotocin-diabetic and healthy control rats. Even though all tissues showed a dramatic increase in glucose and polyol pathway intermediates in diabetes, there was a striking upregulation of mitochondrial oxidative phosphorylation and perturbation of lipid metabolism in the distal SN that was not present in the corresponding cell bodies of the DRG or the cranial TG. This suggests that the most severe molecular consequences of diabetes in the nervous system present in the SN, the region most affected by neuropathy. Such spatial metabolic dysfunction suggests a failure of energy homeostasis and/or oxidative stress specifically in the distal axon/Schwann cell-rich SN. These data provide a detailed molecular description of the distinct compartmental effects of diabetes on the PNS which could underlie the distal-proximal distribution of pathology.

Introduction

Approximately 30-50% of patients with diabetes will develop diabetic neuropathy (DN), which typically presents with sensory symptoms in a distal ‘glove-and-stockings’ distribution (1; 2). DN is a poorly understood complication of diabetes and there are currently few treatments available (3). Raised glucose has long been thought to instigate pathology in DN, either through direct neurotoxicity, or from the activation of secondary pathways (4; 5). However, exactly how these pathways cause nerve conduction velocity deficits, neuropathic pain, distal axonopathy and numbness in the extremities continues to elude, and many clinical trials aimed at specific targets have failed due to lack of efficacy (3).

There is crossover between proposed pathogenic pathways in DN but how these interact is unclear. This question can be approached by implementing extensive ‘-omic’ technologies to measure many transcripts, proteins or metabolites in parallel. Gene microarrays were amongst the first of these technologies to be used and transcriptomic analyses have been performed on tissues such as the dorsal root ganglia (DRG) from streptozotocin (STZ)-diabetic rats compared to healthy controls (6), the sciatic nerve (SN) of *db/db* mice compared to those from *db/+* mice (7) and sural nerve biopsies from human patients whose neuropathy progressed over a year compared to those whose neuropathy did not (based on myelinated fibre density loss) (8). Common changes across these gene array studies highlight altered carbohydrate and lipid metabolism.

Since gene transcript levels do not always correlate with protein expression due to varying transcriptional/translational control, these studies have been expanded by the measurement of proteins through proteomics, using a cell culture-based method known as stable isotope labelling by amino acids in cell culture (SILAC). In neurons derived from the DRG of

diabetic rats (22 weeks post-STZ) compared to healthy controls and maintained in culture with high/normal glucose media respectively, there was significant downregulation of proteins related to oxidative phosphorylation and the tricarboxylic (TCA) cycle in diabetes/high glucose (9). In contrast, Schwann cells derived from the SN of neonatal rats and cultured in high glucose for 2, 6 or 16 days compared to normal glucose showed upregulation of oxidative phosphorylation and the TCA cycle at all time-points (10). Both findings strongly point to metabolic dysfunction and mitochondrial impairment occurring in DN.

These studies describe the effects of high glucose on a single cell type in culture, but do not replicate the multifaceted *in vivo* environment. The nervous system exists as a complex arrangement of cell types (encompassing neurons, glia, endothelial cells and more) and therefore primary single cell culture models are not able to address tissue-wide changes in diabetes and the distal-proximal presentation of DN. Tissue measurements address such limitations and targeted metabolomic analysis of the sural nerve, SN and DRG of *db/db* mice compared to *db/+* mice found that the metabolic intermediates of glycolysis and the TCA cycle are significantly downregulated in the sural nerve and SN, but not in the DRG in diabetes (11).

Targeted analyses are, however, based on *a priori* assumptions and therefore there is sufficient scope for a re-assessment of established theories and the generation of new targets by analysing proteins and metabolites in multiple nervous tissues alongside one another in an unbiased and holistic analysis. Since DN is a complex, multifactorial process with not all sites of the PNS affected equally, we combined proteomic and metabolomic analyses of three different regions of the PNS from control and diabetic rats (12 weeks post-STZ). The

integration of both technologies presented here provides novel insights into the distal-proximal pathogenesis of DN and these data enable generation of new therapeutic targets.

Research Design and Methods

All reagents were purchased from Sigma-Aldrich unless stated.

Animals

All animal experiments were carried out in accordance with the UK Animal (Scientific Procedures) Act 1986 and institutional ethical policies. Adult male Sprague-Dawley rats (initial weight 370 ± 19 g, mean \pm SD; Charles River) were randomly assigned to treatment groups and injected intraperitoneally with 55 mg/kg streptozotocin (in 0.9% sodium chloride; $n=16$) or an equivalent volume of saline ($n=14$) following an overnight fast. Hyperglycemia was confirmed 3 days post-STZ, and animals housed in groups of 2-3 under a 12 hour light-dark cycle with *ad libitum* access to food and water. After 12 weeks, nerve conduction velocity was measured in the sciatic nerve of terminally-anaesthetised rats (2% (v/v) isoflurane in oxygen) as previously described (12).

Cull and tissue collection

Terminally anaesthetised rats were culled by decapitation and blood glucose measured from core blood using a strip-operated reflectance photometer (12). SN, lumbar 4/5 DRG, trigeminal ganglia (TG) and plantar skin were dissected. All tissue collection was limited to a 90 minute time period each day to minimise circadian influences on metabolism and limit analyte degradation. Tissues destined for metabolomics were rapidly washed in ice-cold 0.9% NaCl in water. Tissues for proteomics were rapidly washed in ice-cold PBS followed by ice-cold 0.25 M sucrose. Tissue was snap frozen in liquid nitrogen to halt metabolic and proteolytic processes. The mass of each tissue was recorded and samples stored at -80°C. ~~and~~ Intraepidermal nerve fibre density was measured by quantification of PGP9.5-

immunoreactive nerve fibres in the glabrous surface of the hindpaw as previously described (12).

Metabolomics

Analysis of tissue metabolites was performed by lysing tissue in a mixture of choloroform, methanol and water to separate polar and non-polar metabolites, before analysis by gas- or liquid-chromatography mass spectrometry (GC-MS and LC-MS respectively). The weight of each sample was equalised and tissue lysed in 800 µL 50:50 MeOH:CHCl₃, containing isotopically labelled internal standards (0.016 mg/mL each of citric acid-*d*₄, ¹³C₆-D-fructose, L-tryptophan-*d*₅, L-alanine-*d*₇, stearic acid-*d*₃₅, benzoic acid-*d*₅, and leucine-*d*₁₀; Cambridge Isotopes) in a TissueLyser II (Qiagen). 400 µL H₂O was added and samples centrifuged at 2,400 x g for 15 min to cause separation of phases. After separation, tissue debris lay at the interface between the lower (non-polar, CHCl₃) phase and the polar (MeOH:H₂O) phase. Metabolites in the polar fraction were derivatised to methoxime/trimethylsilyl derivatives as described (13) and analysed by GC-MS (Agilent 7890A Gas Chromatograph and a LECO Pegasus HT time-of-flight MS). Metabolites in the non-polar fraction were resuspended in methanol and analysed by LC-MS (Accela UHPLC system coupled to an Orbitrap Velos MS). Instrumental analysis, data reduction and interpretation followed the protocol as previously described (14). Univariate statistical tests (mean ratio with confidence intervals, Mann-Whitney *P*-value, false discovery rate (FDR)-corrected *q*-value) were applied in R. All metabolites identified/quantified can be seen in Online Supplemental Table 1.

Proteomics sample fractionation and mass spectrometry

Proteomics was performed using 8-plex iTRAQ (isobaric tags for relative and absolute quantitation), a labelled method of analysis that allows simultaneous analysis of 8

independent tissue samples, as previously described (15) with the following modifications. Tissue was lysed in 1 M triethylammonium bicarbonate (TEAB) with 0.1% (w/v) sodium-dodecyl sulphate in the following volumes: SN 600 µL, DRG 150 µL, TG 250 µL in a TissueLyser II. 100 µg of protein was aliquoted and volumes equalised to 30 µL with 1 M TEAB before cysteine reduction, alkylation and digestion with 7.5 µg trypsin. Tryptic digests were dried in a SpeedVac Concentrator (Eppendorf), resuspended in 30 µL 1 M TEAB and labelled with iTRAQ reagent (iTRAQ 8-plex reagent-labeling kit; AB SCIEX). Labelled peptide samples were pooled within one 8-plex and dried in a SpeedVac Concentrator.

Peptides were fractionated off-line using high pH reverse phase chromatography on a 3 µm Extend-C18 column (4.6 x 100 mm; Agilent) at 45°C using a 30 minute gradient from 3% to 40% acetonitrile in 0.1% ammonium hydroxide at 0.75 mL/min, with 30 second fractions collected, dried in a SpeedVac Concentrator and stored at -20°C until analysis. For subsequent analysis by low pH reverse phase liquid chromatography-tandem mass spectrometry (LC-MS/MS) analysis, dried fractions were resuspended in 15 µL 3% (v/v) acetonitrile, 0.1% (v/v) trifluoroacetic acid, with 5 µL analysed by low-pH reverse phase chromatography as previously described (15).

Proteomic analysis

To identify proteins from their peptide spectra, raw data files were analysed using ProteinPilot v4.0 using default search settings against a rat-specific Uniprot database (15190 proteins; rel. 2011_04), which was concatenated with a reversed-sequence ‘decoy’ version of the same database to enable the False Discovery Rate (FDR) for identifications to be determined.

To identify differentially expressed proteins, protein-level quantification was performed on the ProteinPilot spectrum-level iTRAQ measurements by Bayesian mixed-effects modelling in R (16). For each protein identified, statistically significant FDR-controlled differential protein expression between diabetes and control animals was inferred using the measurements unique to that protein. We based our one-sided significance test on the posterior probability that the mean fold-change is at least 5% either above or below control expression (17). The reciprocal of this posterior probability represents the local FDR (lFDR) *i.e.* the probability that this specific test is a false discovery. In this study, we defined a ‘significant’ difference in protein expression using a global FDR threshold of 5% (17).

We framed the problem as a Generalised Linear Mixed Model (GLMM) with Poisson likelihood distribution and log-link. In the GLMM design, condition (diabetes/control) was treated as a fixed effect and subject as a random effect. Additional random effects were fitted for sample within each peptide, in order that technical peptide-level variation and biological protein-level variation were both captured. The sample normalization scaling factors represent the mass spectrometer’s exposure to each sample, and hence were included as a fixed offset within the model.

Finally, the set of measurements within each iTRAQ spectrum were assigned: (a) their own baseline fixed effect, to account for differences in the location of the MS/MS selection window across the chromatographic profile, as well as varying ionisation/fragmentation efficiencies across peptides and charge states; and (b) their own independent and identically distributed log-normal residual variance, to account for over-dispersion due to background contamination and incorrectly identified spectra. Residual variances were assigned inverse-Gamma priors, while random effects were assigned parameter-expanded Cauchy priors. The

model was then tested with different prior scale factors to establish that the priors were not informative to the outcome. For each protein, model inference was run initially with 8 chains of 20,000 samples each and 50% burn-in. Mixing was deemed successful if, for each significance test, the variance of the posterior probabilities for the 8 chains did not exceed 0.02 (tested using a Bayesian Generalised Linear Model with Binomial likelihood distribution, logit link, 200,000 samples and 50% burn-in). If this test failed, the model was continually re-run with double the number of samples (thinned to 10,000) until the test passed. All proteins identified/quantified can be seen in Online Supplemental Table 2.

The results of the Bayesian analysis were analysed with Ingenuity® Pathway Analysis (IPA®; Qiagen; www.qiagen.com/ingenuity). Protein lists were input into IPA® using Uniprot accession numbers, mean \log_2 ratios and global FDRs for each of the three tissues separately. Significant changes (global FDR <0.05) were compared to the user input dataset as the reference set. To assess solely the mitochondrial proteome, proteins localised to the mitochondria were extracted via upload of the SN dataset to ConsensusPathDB (Max-Planck Institute for Molecular Genetics; <http://cpdb.molgen.mpg.de/>). 197 proteins were reported as being present in any part of the mitochondria. All mitochondrial proteins were then divided into two groups based on whether they were annotated as involved in metabolism (127 proteins) or non-metabolic (70 proteins).

Results

Elevation of glucose and polyol intermediates throughout the peripheral nervous system in diabetes

Following 12 weeks of diabetes, rats displayed a phenotype of peripheral neuropathy (18), including decreased sensory and motor nerve conduction velocities in the SN and loss of intraepidermal nerve fibres in the hind paw (Table 1). To investigate the peripheral nervous system in diabetes, we first performed metabolomics on the distal SN, the corresponding lumbar 4/5 DRG and on the cranial TG of diabetic and control rats (Figure 1A). Analysis of polar metabolites by GC-MS identified and quantified 47 metabolites in the SN, 46 in the DRG, and 47 in the TG ($n=4$ per tissue). All tissues showed a similar extent of alteration with 18 metabolites (38.3%) in the SN, 16 (34.8%) in the DRG, and 19 (40.4%) in the TG significantly changed in diabetes (Figure 1B).

All tissues showed increases in glucose (SN: 4.8-fold, DRG: 14.6-fold, TG: 19.6-fold), sorbitol and fructose, and decreases in *myo*- and *scyllo*-inositol in diabetes (Figure 1C), characteristic of polyol pathway activation (19). Since free glucose should not normally accumulate, this indicates that impaired glucose utilisation is present in all three tissues in diabetes. All metabolites identified/quantified can be seen in Online Supplemental Table 1.

Dysregulation of lipid metabolism occurs in the sciatic nerve, is less severe in the DRG and not evident in the TG

Our GC-MS analysis also showed decreases in palmitic (16:0), stearic (18:0), and eicosanoic (20:0) fatty acids in the SN, but these were unchanged in the DRG or TG (Figure 1C). To explore lipid species more widely, we performed non-polar metabolomics by LC-MS. Initial analysis produced 9,166 putative metabolite features across the three tissues ($n=6$ per tissue).

We extracted features that showed potential changes ($q<0.1$) in any tissue and filtered these to 397 unique metabolite features (Online Supplemental Table 1). Of these, 257/397 (64.7%) in the SN (Figure 2A), 15/321 (4.7%) in the DRG (Figure 2B), and 1/365 (0.3%) in the TG (Figure 2C) were significantly altered in diabetes ($q<0.05$).

The most comprehensive lipid changes observed were in the triacylglycerols (TAGs). In the SN, 73 of 110 (66.4%) identified TAG species were significantly changed in diabetes (Figure 2E, inset). These exhibited a length-dependent phenomenon whereby relatively short-chain TAGs (<54:2) were reduced in diabetes, whilst longer chain species increased (Figure 2E). There was no change in any TAG species in either the DRG (Figure 2F) or TG (Figure 2G). Moreover, two abundant acylcarnitine species, palmitoylcarnitine (16:0) and linoleylcarnitine (18:2) showed increases in the SN (Figure 2H) but were unchanged in the DRG (Figure 2I) or TG (Figure 2J). Both families are functionally important in metabolism: TAGs for storage and acylcarnitines for fatty acid transport into the mitochondria for energy generation (Figure 2D). Beside alterations to metabolic lipids, we observed changes in major structural/membrane lipids, including phospholipids and sphingolipids/ceramides specifically in the SN (Online Supplemental Table 1). Interestingly, these lipid changes appear severe in the distal SN, moderate in the proximal DRG and not evident in the cranial TG, suggesting that lipid dysfunction presents distally in the PNS in diabetes.

Metabolic dysregulation in the sciatic nerve, but not in the dorsal root ganglia or trigeminal ganglia of diabetic rats

To investigate the putative underlying mechanism of this spatial grading of metabolic dysfunction, we analysed all three tissues by iTRAQ proteomics (control $n=4$, diabetic $n=6$ per tissue). We inferred differential protein expression between diabetic and control tissues

by Bayesian mixed effects modelling (see Methods). In the SN, 683 (28.9%) of the 2,356 proteins identified and quantified showed significant changes of expression in diabetes (Figure 3A and Online Supplemental Table 2). Ingenuity® Pathway Analysis highlighted coordinated dysregulation to oxidative phosphorylation, liver/retinoid X receptor (LXR/RXR) activation and glycolysis (Figure 3B). In contrast, only 85/1,649 (5.2%) proteins in the DRG (Figure 3C) and 60/1,734 (3.4%) proteins in the TG (Figure 3E) significantly changed. Pathway analysis showed changes in the ‘Acute Phase Response’ and LXR/RXR activation in both the DRG and TG (Figure 3D and Figure 3F), but overall protein expression in the DRG and TG was relatively unaffected (Online Supplemental Table 2), in spite of the higher levels of glucose.

Mitochondrial oxidative phosphorylation was particularly conspicuous between tissues with 32/37 (86%) identified proteins in the SN increased in diabetes whilst not one of the 29 oxidative phosphorylation proteins quantified in the DRG or TG was significantly altered (Figure 4). Dysregulation in the SN comprised increased expression in multiple subunits of complexes I, III, IV and V with no observed change in complex II. Since this upregulation could in principle be an artefact of increased mitochondrial numbers in the SN, we analysed the composition of the mitochondrial proteome. We found mitochondrial Rho GTPase 1 (Miro1), a protein mediating axonal transport of mitochondria (20), to be upregulated by diabetes in the SN (Online Supplemental Table 1), which might reflect aberrant mitochondrial transport and accumulation of mitochondria in axons. However, we found only 14/70 (20%) ‘non-metabolic’ mitochondrial proteins to be upregulated by diabetes compared to 86% of oxidative phosphorylation proteins. This disproportionate difference suggests

targeted effects on the proteins of oxidative phosphorylation rather than increased mitochondrial numbers.

In glycolysis, 8/13 (62%) proteins significantly increased in the SN, with the DRG (0/15) and TG (1/15) again unaffected (Figure 5B). Since we now have data on both the metabolites and proteins of glycolysis, we can integrate these to assess pathways in detail. We found that although multiple glycolytic proteins increased in the SN (Figure 5B), glycolytic intermediates glucose-6-phosphate, fructose 1,6-bisphosphate and glyceraldehyde-3-phosphate did not significantly change (Figure 5C). Whilst pathway analysis did not highlight the tricarboxylic acid (TCA) cycle, we found 6/13 (46%) TCA cycle enzymes were significantly increased in the SN, whereas none changed in either the DRG or TG (Figure 5E). Once again we saw a similar phenomenon whereby proteins of the TCA cycle showed increases in the SN (Figure 5E) without coincident increases in the metabolic intermediates citrate, succinate or malate (Figure 5F). Overall, we conclude that all tissues measured in the PNS of STZ-diabetic rats exhibit impaired glucose utilisation but that metabolic dysfunction is restricted to the SN.

Discussion

Our integrated metabolomic and proteomic analysis in experimental diabetic neuropathy has revealed coordinated dysregulation of sugar, lipid and mitochondrial metabolism in the distal axonal/glial compartment of the SN that is not present in the corresponding cell bodies of the lumbar 4/5 DRG or the cranial TG. Integrating both analyses allows construction of a comprehensive model of defective metabolism in the SN, where upregulation of protein components of glycolysis, the TCA cycle and oxidative phosphorylation occur alongside complex changes in lipid metabolism (Figure 6). Since diabetic neuropathy predominately presents with distal symptoms, these site-specific molecular changes may directly contribute to disease pathogenesis.

We measured accumulation of glucose, fructose and sorbitol in all tissues, supporting the view that the polyol pathway is prominently altered in DN (4). As the polyol pathway is usually a minor route for glucose metabolism, these alterations point to changes in the utilization of glucose in all tissues studied. Thus raised glucose levels cannot alone explain the pathogenesis of diabetic neuropathy. The differential impact of impaired glucose utilisation on the PNS implies that metabolic regulation differs throughout the nervous system, with some regions more susceptible to dysfunctional metabolism than others.

The synchrony of diabetes-induced dysregulation to glycolysis, the TCA cycle and oxidative phosphorylation in the SN indicates substantial bioenergetic dysfunction. We found that whilst protein components of glycolysis/TCA cycle increased, their metabolic intermediates showed no evidence of alteration. Since we did not perform flux experiments we cannot specifically comment upon pathway activity but we suggest that the discrepancy between protein and metabolite measures here indicates that upregulation of the enzymes of

glycolysis, the TCA cycle and oxidative phosphorylation may reflect a compensatory response to metabolite overload in the SN. Such changes might indicate reduced ATP production, since increased expression of respiratory chain components in cultured Schwann cells coincides with decreased respiration efficiency (10), and/or oxidative stress (21). Interestingly, glycolytic/TCA cycle intermediates decrease in the sural and sciatic nerves but not the DRG of *db/db* mice (11), supporting our interpretation that pathway activity may not be increased. However, since both studies rely upon steady-state measures, definitive pathway flux is currently unknown.

Even though the normalisation of all protein ratios was performed, the majority of our highlighted protein changes showed an upregulation in the SN in diabetes. In principle, spatial differences could result from differential metabolism or an artefact such as increased numbers of mitochondria in the SN. We observed evidence of altered mitochondrial transport through increased expression of Miro1 in the SN in diabetes (20), however, increases in ‘non-metabolic’ mitochondrial proteins were infrequent compared to the 86% of oxidative phosphorylation proteins. We believe this indicates mitochondria are dysfunctional in distal axons but do not change in number. To support this, analysis of human skin biopsies found no difference in mitochondrial numbers within intraepidermal nerve fibres between patients with and without DN, but that mitochondrial volume increased in DN (22).

The main question arising from this work is why does the SN show such a disrupted proteomic/metabolomic signature whilst the DRG and TG appear relatively-unaffected? We believe that there could be at least two, non-mutually-exclusive explanations for these observations. The first is due to a difference in composition of the tissues. Both the DRG and TG are largely neuronal, with smaller contributions from satellite glial cells. In the SN

however, there are a high proportion of Schwann cells which could be responsible for the disrupted tissue metabolism we have observed. This could be either a direct influence (the dysregulated proteins we have measured derive predominately from Schwann cells) and/or an indirect influence (metabolic dysfunction in Schwann cells impacts upon axonal health and protein expression).

Here, our data harmonises with elegant molecular studies of peripheral neuropathy. Schwann-cell specific mitochondrial dysfunction and/or metabolic stress in mice leads to symptoms of peripheral neuropathy with decreased conduction velocity, loss of both small unmyelinated fibres and degeneration of large myelinated fibres and thermal hypoalgesia (23; 24). This work demonstrates that Schwann cell metabolism plays a critical role in supporting neuronal function along long peripheral nerves, and its disruption can cause axonal degeneration/neuropathy. Since glucose is preferentially taken up into Schwann cells in peripheral nerve (25) and aldose reductase predominately localises to Schwann cells (26; 27), it is possible that high glucose levels principally instigate metabolic dysfunction in Schwann cells, which impacts upon neuronal health, resulting in neuropathy. This will require further investigation but represents an attractive target for future mechanistic and therapeutic studies in DN.

It is believed that glycolytic glia support neuronal oxidative metabolism through the transfer of lactate which can support neuronal function during metabolic stress in Schwann cells (24; 28). We did not observe any change in lactate levels in the SN, but this does not preclude alterations in the flux of lactate between neurons and glia. Lactate transfer is mediated by the monocarboxylate transporters (MCTs), of which MCT-1 is the main isoform expressed in peripheral nerve (29). We identified/quantified MCT-1 in both the SN and DRG but did not

observe significantly altered expression in either tissue (Online Supplemental Table 2). Changes in localisation of the MCTs in the PNS in diabetes could alter lactate transfer but there are few available data that address this point (5).

Besides impaired metabolic support from Schwann cells, another possibility is that metabolic stress in Schwann cells themselves could result in accumulation of toxic intermediates, such as acylcarnitines, which have been shown to be neurotoxic and coincident to the development of peripheral neuropathy (30). Our data support the presence of this phenomenon in diabetic neuropathy since we observed concomitant mitochondrial dysfunction and deficits in lipid utilization in the SN, including alterations to acylcarnitines, which were not present without metabolic stress in the DRG/TG.

Dysfunctional lipid metabolism has been linked to the pathogenesis of neuropathy previously (23; 24), but its mechanism is poorly understood. Our data add that there are profound changes to lipid intermediates in the SN but not the DRG or TG in STZ-diabetes. Total lipid content was ~20% higher in control SN than control DRG (data not shown). Theoretically this difference could make changes in the SN more detectable, but this relatively small difference is unlikely to solely explain the extensive difference between control and diabetic tissues we have observed. Importantly, these disease-associated lipid alterations occurred in the absence of protein changes to β -oxidation (Online Supplemental Table 2), highlighting that protein expression levels alone do not capture possible post-translational modification effects on protein activity.

The second hypothesis approaches the relationship between the cell bodies in the DRG and the axons in the SN. It is possible that the neuronal cell bodies in the DRG are more capable

of responding to metabolic insult through constant synthesizing and refolding of proteins than the axonal compartment, which would explain why we do not observe abundant alterations in the DRG proteome/metabolome. Perikaryal preservation is a key feature of diabetic neuropathy, as no neuronal loss was detected in the DRG after 12 months of hyperglycaemia in STZ-diabetes (31; 32). The DRG plays a crucial role in axonal support, evidenced by findings in STZ-diabetes, when direct support of DRG neurons through intrathecal administration of insulin (which did not reduce hyperglycemia) improved sciatic nerve conduction velocity and protected against distal axonal atrophy and intraepidermal nerve fibre loss (33; 34). Therefore even apparently small phenotypic changes in the DRG may impact on distal axon health and play a role in the pathogenesis of diabetic neuropathy.

Therefore, whilst our findings highlight that metabolic dysfunction is most evident in the sciatic nerve, this does not negate the role played by the DRG in the pathogenesis of the disease. We believe distal axon degeneration is most likely to result from a complex combination of both local axonal/Schwann cell dysfunction and failed axonal support from the cell body. In future work it will be important to study the fundamental mechanisms of metabolism within the PNS to allow dissection of the responses of Schwann cells, neurons and axons.

During our analysis we focused on mechanisms of dysfunction in carbohydrate/lipid metabolism since these signals were the most enriched and concordant in our datasets. However, these data contain many more dysregulated proteins and metabolites which could yield interesting targets for future study. For example, endoplasmic reticulum stress and eIF2 signaling, key stress pathways linked to the pathogenesis of peripheral neuropathy (30), appear prominently altered and LXR/RXR activation shows complex alteration that differs

between tissues. Data on all of these are provided as Online Supplemental Tables as a resource. Since similar changes in carbohydrate metabolism have been reported in the type 2 *db/db* mouse model of diabetes (11), we believe that these alterations may well be applicable to further models and patients with DN. Investigation of shorter and longer durations of diabetes would be beneficial to describe the dynamics of some of the key changes highlighted here and their relationship to disease progression. Likewise, the reversion of some of these key changes with insulin or experimental therapeutics would be of interest.

Whilst it remains unclear whether neuron-glial metabolic coupling is disrupted in diabetes, our measurements support the notion of a compartmentation of dysfunctional energy metabolism in peripheral neuropathy. The observation that metabolic regulation differs between the proximal cell bodies of the lumbar 4/5 DRG to the axonal/Schwann cell-rich SN may help explain the underlying molecular basis for the ‘glove-and-stocking’ distribution of peripheral neuropathies. These findings would not have been possible had we not integrated both protein and metabolite measures and the performance of both technologies in parallel has proven vital to help interpret pathway interactions. This comprehensive network view of dysfunctional metabolism identifies new therapeutic targets to rescue a healthy state of metabolism and treat the progression of diabetic neuropathy.

Acknowledgements

This research was funded by Medical Research Council grants MR/J500410/1 (O.J.F.) and MR/L011093/1 (A.W.D) and facilitated by the Manchester Biomedical Research Centre and the NIHR Greater Manchester Comprehensive Local Research Network. N.J.G was supported by a Juvenile Diabetes Research Foundation Career Development Award (2-2009-226).

O.J.F. designed the study, collected and analysed the data and wrote the manuscript. R.D.U. designed the study, analysed the data and wrote the manuscript. P.B performed the GC-MS analysis and analysed the data. K.A.H. and N.R. performed the UHPLC-MS analysis. S.A. and R.S.P assisted with the animal study and contributed to discussion. A.W.D developed and performed the Bayesian analyses. W.B.D designed the study and analysed the data. G.J.S.C. and N.J.G. designed and supervised the study and wrote the manuscript. G.J.S.C. and N.J.G. are guarantors of this work and, as such, had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis. All authors discussed the results and commented on the manuscript.

References

1. Callaghan BC, Cheng HT, Stables CL, Smith AL, Feldman EL: Diabetic neuropathy: clinical manifestations and current treatments. *Lancet Neurol* 2012;11:521-534
2. Said G: Diabetic neuropathy--a review. *Nat Clin Pract Neurol* 2007;3:331-340
3. Boulton AJ, Kempner P, Ametov A, Ziegler D: Whither pathogenetic treatments for diabetic polyneuropathy? *Diabetes Metab Res Rev* 2013;29:327-333
4. Tomlinson DR, Gardiner NJ: Glucose neurotoxicity. *Nat Rev Neurosci* 2008;9:36-45
5. Zenker J, Ziegler D, Chrast R: Novel pathogenic pathways in diabetic neuropathy. *Trends Neurosci* 2013;36:439-449
6. Price SA, Zeef LA, Wardleworth L, Hayes A, Tomlinson DR: Identification of changes in gene expression in dorsal root ganglia in diabetic neuropathy: correlation with functional deficits. *J Neuropathol Exp Neurol* 2006;65:722-732
7. Pande M, Hur J, Hong Y, Backus C, Hayes JM, Oh SS, Kretzler M, Feldman EL: Transcriptional profiling of diabetic neuropathy in the BKS db/db mouse: a model of type 2 diabetes. *Diabetes* 2011;60:1981-1989
8. Hur J, Sullivan KA, Pande M, Hong Y, Sima AA, Jagadish HV, Kretzler M, Feldman EL: The identification of gene expression profiles associated with progression of human diabetic neuropathy. *Brain* 2011;134:3222-3235
9. Akude E, Zhrebitskaya E, Chowdhury SK, Smith DR, Dobrowsky RT, Fernyhough P: Diminished superoxide generation is associated with respiratory chain dysfunction and changes in the mitochondrial proteome of sensory neurons from diabetic rats. *Diabetes* 2011;60:288-297
10. Zhang L, Yu C, Vasquez FE, Galeva N, Onyango I, Swerdlow RH, Dobrowsky RT: Hyperglycemia alters the schwann cell mitochondrial proteome and decreases coupled respiration in the absence of superoxide production. *J Proteome Res* 2010;9:458-471
11. Hinder LM, Vivekanandan-Giri A, McLean LL, Pennathur S, Feldman EL: Decreased glycolytic and tricarboxylic acid cycle intermediates coincide with peripheral nervous system oxidative stress in a murine model of type 2 diabetes. *J Endocrinol* 2013;216:1-11
12. Ali S, Driscoll HE, Newton VL, Gardiner NJ: Matrix metalloproteinase-2 is downregulated in sciatic nerve by streptozotocin induced diabetes and/or treatment with minocycline: Implications for nerve regeneration. *Exp Neurol* 2014;261:654-665
13. Begley P, Francis-McIntyre S, Dunn WB, Broadhurst DI, Halsall A, Tseng A, Knowles J, Goodacre R, Kell DB, HUSERMET Consortium: Development and performance of a gas chromatography-time-of-flight mass spectrometry analysis for large-scale nontargeted metabolomic studies of human serum. *Anal Chem* 2009;81:7038-7046
14. Dunn WB, Broadhurst D, Begley P, Zelena E, Francis-McIntyre S, Anderson N, Brown M, Knowles JD, Halsall A, Haselden JN, Nicholls AW, Wilson ID, Kell DB, Goodacre R, Consortium HSMH: Procedures for large-scale metabolic profiling of serum and plasma using gas chromatography and liquid chromatography coupled to mass spectrometry. *Nat Protoc* 2011;6:1060-1083
15. Unwin RD, Griffiths JR, Whetton AD: Simultaneous analysis of relative protein expression levels across multiple samples using iTRAQ isobaric tags with 2D nano LC-MS/MS. *Nat Protoc* 2010;5:1574-1582
16. Hadfield JD: MCMC Methods for Multi-Response Generalized Linear Mixed Models: The MCMCglmm R Package. *Journal of Statistical Software* 2010;33:1-22

17. Morris JS, Brown PJ, Herrick RC, Baggerly KA, Coombes KR: Bayesian analysis of mass spectrometry proteomic data using wavelet-based functional mixed models. *Biometrics* 2008;64:479-489
18. Biessels GJ, Bril V, Calcutt NA, Cameron NE, Cotter MA, Dobrowsky R, Feldman EL, Fernyhough P, Jakobsen J, Malik RA, Mizisin AP, Oates PJ, Obrosova IG, Pop-Busui R, Russell JW, Sima AA, Stevens MJ, Schmidt RE, Tesfaye S, Veves A, Vinik AI, Wright DE, Yagihashi S, Yorek MA, Ziegler D, Zochodne DW, Neurodiab TWGo: Phenotyping animal models of diabetic neuropathy: a consensus statement of the diabetic neuropathy study group of the EASD (Neurodiab). *J Peripher Nerv Syst* 2014;19:77-87
19. Finegold D, Lattimer SA, Nolle S, Bernstein M, Greene DA: Polyol pathway activity and myo-inositol metabolism. A suggested relationship in the pathogenesis of diabetic neuropathy. *Diabetes* 1983;32:988-992
20. Wang X, Schwarz TL: The mechanism of Ca²⁺-dependent regulation of kinesin-mediated mitochondrial motility. *Cell* 2009;136:163-174
21. Brownlee M: Biochemistry and molecular cell biology of diabetic complications. *Nature* 2001;414:813-820
22. Hamid HS, Mervak CM, Münch AE, Robell NJ, Hayes JM, Porzio MT, Singleton JR, Smith AG, Feldman EL, Lentz SI: Hyperglycemia- and neuropathy-induced changes in mitochondria within sensory nerves. *Ann Clin Transl Neurol* 2014;1:799-812
23. Viader A, Golden JP, Baloh RH, Schmidt RE, Hunter DA, Milbrandt J: Schwann cell mitochondrial metabolism supports long-term axonal survival and peripheral nerve function. *J Neurosci* 2011;31:10128-10140
24. Beirowski B, Babetto E, Golden JP, Chen YJ, Yang K, Gross RW, Patti GJ, Milbrandt J: Metabolic regulator LKB1 is crucial for Schwann cell-mediated axon maintenance. *Nat Neurosci* 2014;17:1351-1361
25. Véga C, Martiel JL, Drouhault D, Burckhart MF, Coles JA: Uptake of locally applied deoxyglucose, glucose and lactate by axons and Schwann cells of rat vagus nerve. *J Physiol* 2003;546:551-564
26. Jiang Y, Calcutt NA, Ramos KM, Rames KM, Mizisin AP: Novel sites of aldose reductase immunolocalization in normal and streptozotocin-diabetic rats. *J Peripher Nerv Syst* 2006;11:274-285
27. Ludvigson MA, Sorenson RL: Immunohistochemical localization of aldose reductase. I. Enzyme purification and antibody preparation--localization in peripheral nerve, artery, and testis. *Diabetes* 1980;29:438-449
28. Fünfschilling U, Supplie LM, Mahad D, Boretius S, Saab AS, Edgar J, Brinkmann BG, Kassmann CM, Tzvetanova ID, Möbius W, Diaz F, Meijer D, Suter U, Hamprecht B, Sereda MW, Moraes CT, Frahm J, Goebbel S, Nave KA: Glycolytic oligodendrocytes maintain myelin and long-term axonal integrity. *Nature* 2012;485:517-521
29. Morrison BM, Tsingalia A, Vidensky S, Lee Y, Jin L, Farah MH, Lengacher S, Magistretti PJ, Pellerin L, Rothstein JD: Deficiency in monocarboxylate transporter 1 (MCT1) in mice delays regeneration of peripheral nerves following sciatic nerve crush. *Exp Neurol* 2015;263:325-338
30. Viader A, Sasaki Y, Kim S, Strickland A, Workman CS, Yang K, Gross RW, Milbrandt J: Aberrant Schwann cell lipid metabolism linked to mitochondrial deficits leads to axon degeneration and neuropathy. *Neuron* 2013;77:886-898

31. Zochodne DW, Verge VM, Cheng C, Sun H, Johnston J: Does diabetes target ganglion neurones? Progressive sensory neurone involvement in long-term experimental diabetes. *Brain* 2001;124:2319-2334
32. Cheng C, Zochodne DW: Sensory neurons with activated caspase-3 survive long-term experimental diabetes. *Diabetes* 2003;52:2363-2371
33. Toth C, Brussee V, Zochodne DW: Remote neurotrophic support of epidermal nerve fibres in experimental diabetes. *Diabetologia* 2006;49:1081-1088
34. Brussee V, Cunningham FA, Zochodne DW: Direct insulin signaling of neurons reverses diabetic neuropathy. *Diabetes* 2004;53:1824-1830

Table 1—Phenotype of streptozotocin-diabetic rats after 12 weeks'

		Control	Diabetic	P-value
	n	14	16	
Blood glucose (mmol/L)		10.3 ± 2.4	40.4 ± 8.1	<0.0001
Body weight (g)		589 ± 46	350 ± 28	<0.0001
Motor nerve conduction velocity (m/s)		52.3 ± 15.6	34.1 ± 6.8	0.002
Sensory nerve conduction velocity (m/s)		48.0 ± 11.6	26.3 ± 9.7	0.0001
Intraepidermal nerve fibre density (fibres/mm)		12.4 ± 3.4	8.7 ± 1.7	0.003

Data presented as mean ± SD.

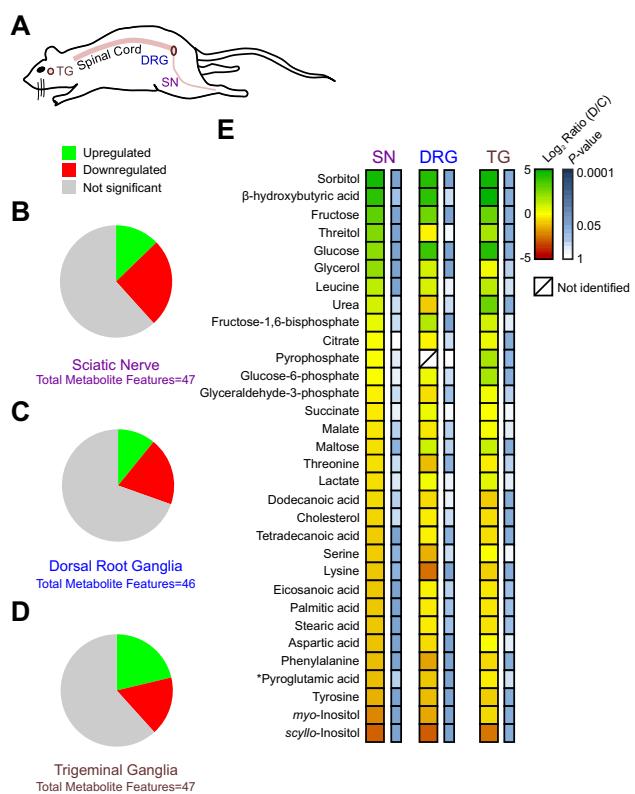


Figure 1–Impaired glucose utilization throughout the peripheral nervous system in diabetes. *A*: We analysed the sciatic nerve (SN), lumbar 4/5 dorsal root ganglia (DRG) and trigeminal ganglia (TG). *B-D*: Percentage of polar metabolite features in the SN (*B*), DRG (*C*) and TG (*D*) that were upregulated (green), downregulated (red) or not significantly changed in diabetes (grey; $n=4$). *E*: Selected polar metabolite features from the three tissues. Log₂ ratio (diabetes/control – D/C) and Mann-Whitney *P*-value is shown based on the key in the top right. *Pyroglutamic acid is a derivatisation product of glutamate/glutamine. All metabolites identified/quantified can be seen in Online Supplemental Table 1.

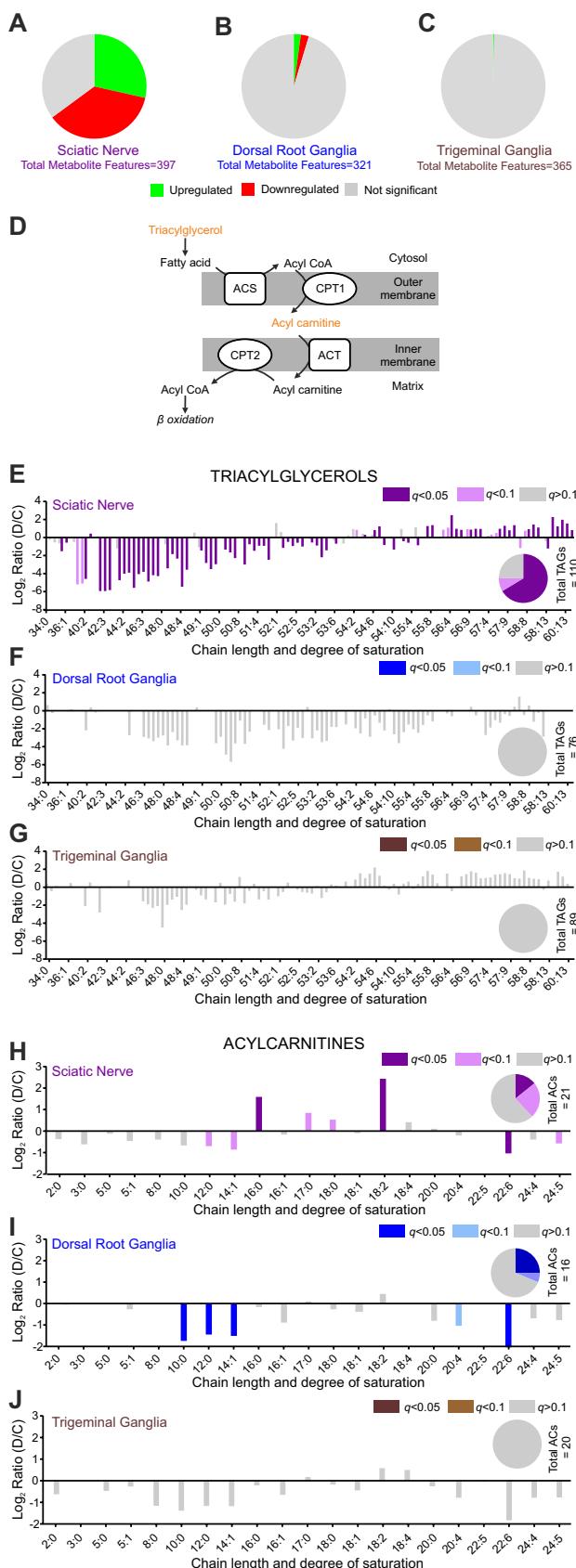


Figure 2– Dysregulation of lipid metabolism in the sciatic nerve in diabetes is less severe in the dorsal root ganglia and not evident in the trigeminal ganglia. *A-C:* Percentage of unique non-polar metabolite features in the sciatic nerve (SN; *A*), dorsal root ganglia (DRG; *B*) and trigeminal ganglia (TG; *C*) that were upregulated (green), downregulated (red) or not significantly changed in diabetes (*n*=6). *D:* Schematic of lipid incorporation into the mitochondria for catabolism via β oxidation. ACS, acyl CoA synthetase; ACT, acylcarnitine/carnitine translocase; CPT1/2, carnitine palmitoyltransferase I/II. *E-G:* All triacylglycerol species identified in SN (*E*), DRG (*F*) and TG (*G*) are denoted by number of carbons:degree of saturation and Log₂ ratio (diabetes/control – D/C) shown. Inset shows percentage of triacylglycerols that were significantly changed ($q < 0.05$; dark colour), approaching significant ($q < 0.1$; light colour) or not significantly changed ($q > 0.1$; grey). *H-J:* All acylcarnitine species identified in SN (*H*), DRG (*I*) and TG (*J*). Inset shows percentage of acylcarnitines that were significantly changed (dark colour), approaching significant (light colour) or not significantly changed (grey). All metabolites identified/quantified can be seen in Online Supplemental Table 1.

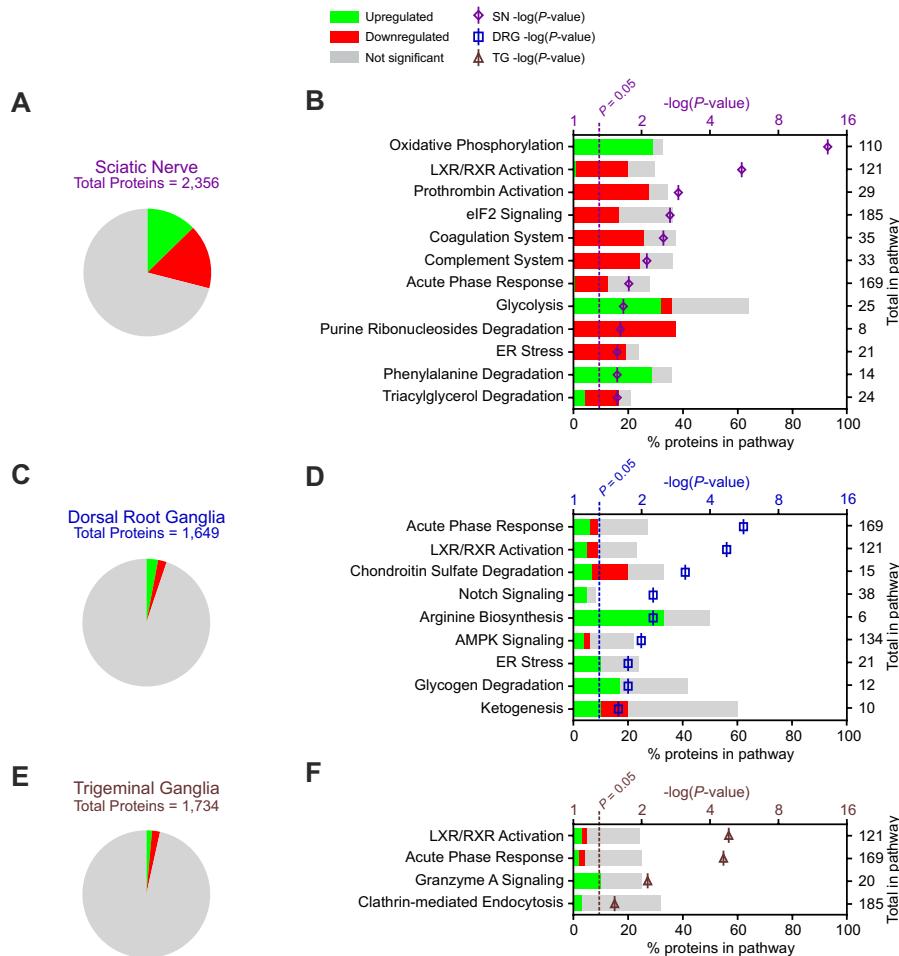


Figure 3—Proteomics reveals metabolic dysregulation in the sciatic nerve, but not in the dorsal root ganglia or trigeminal ganglia of diabetic rats. *A,C,E*: Percentage of proteins in SN (*A*), DRG (*C*) and TG (*E*) that were upregulated (green), downregulated (red) or not significantly changed in diabetes (grey; control $n=4$, diabetic $n=6$). *B,D,F*: Pathway analysis of SN (*B*), DRG (*D*) and TG (*F*). Plots show significantly altered pathways organised by their $-\log(P\text{-value})$ (top x axis), bars show percentage of proteins (bottom x axis). All proteins identified/quantified can be seen in Online Supplemental Table 2.

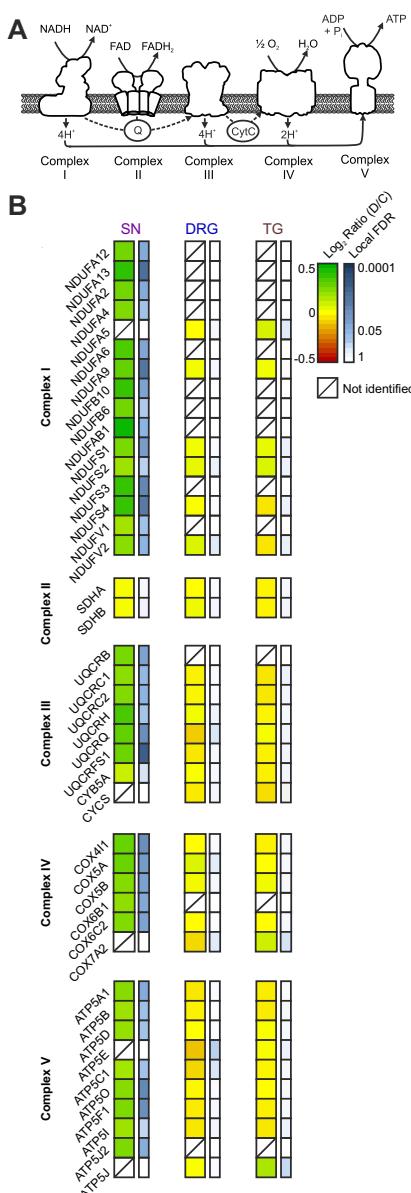


Figure 4—Dysregulated oxidative phosphorylation is restricted to the sciatic nerve. *A:* The oxidative phosphorylation electron transport chain. ADP, adenosine diphosphate; ATP, adenosine triphosphate; Q, Coenzyme Q/ubiquinol; CytC, Cytochrome C; FAD, oxidised flavin adenine dinucleotide; FADH₂, reduced flavin adenine dinucleotide; NAD⁺, oxidised nicotinamide adenine dinucleotide; NADH, reduced nicotinamide adenine dinucleotide; Pi, inorganic phosphate. *B:* All proteins identified/quantified from oxidative phosphorylation are shown. Each protein is identified by its gene symbol and the plot shows the posterior mean \log_2 ratio (diabetes/control – D/C) and local false discovery rate (FDR) in the sciatic nerve (SN), dorsal root ganglia (DRG) and trigeminal ganglia (TG).

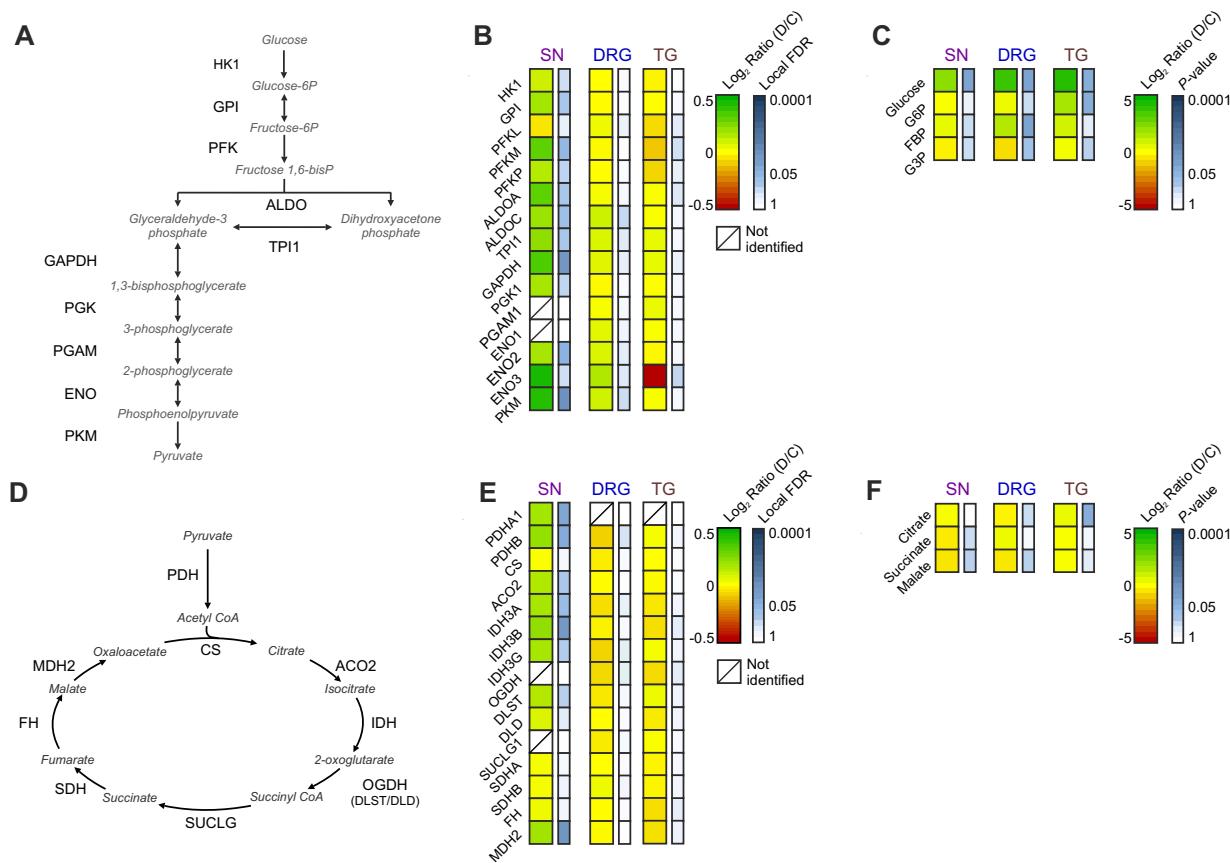


Figure 5—Glycolysis and the TCA cycle show upregulated protein expression in the sciatic nerve but no changes in metabolic intermediates. *A*: The glycolysis pathway is shown with proteins (non-italicised) annotated by their gene symbol and metabolites (*italicised*). *B*: Proteins identified/quantified from glycolysis. Each protein is identified by its gene symbol and the plot shows the posterior mean log₂ ratio (diabetes/control – D/C) and local false discovery rate (FDR) in the sciatic nerve (SN), dorsal root ganglia (DRG) and trigeminal ganglia (TG). *C*: Metabolites identified/quantified from glycolysis. Plot shows log₂ ratio and Mann-Whitney *P*-value in each tissue. *D*: The TCA cycle is shown. *E*: Proteins identified/quantified from the TCA cycle. *F*: Metabolites identified/quantified from the TCA cycle.

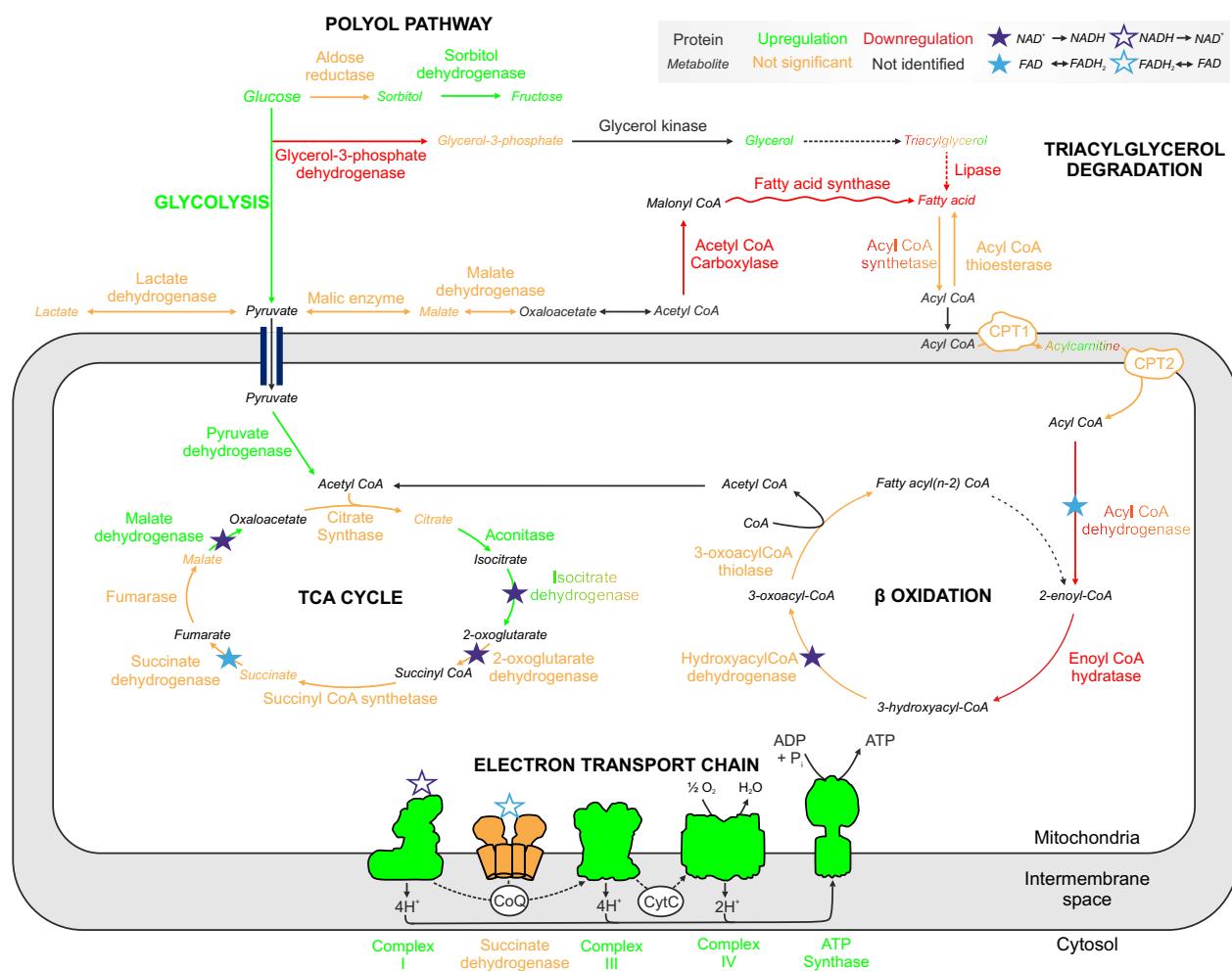


Figure 6—Schematic of protein and metabolite changes in the sciatic nerve in diabetes. Proteins (non-italicised) and metabolites (*italicised*) are highlighted with upregulation in green, downregulation in red, no significant change in orange and not identified in black. Where a protein/metabolite showed multiple isoforms/species altered in different directions, these are depicted in multiple colours. Stars denote the production (closed stars) or consumption (open stars) of electron donors NADH (purple) and FADH₂ (blue). ADP, adenosine diphosphate; ATP, adenosine triphosphate; CoA, coenzyme A; CoQ, Coenzyme Q/ubiquinol; CPT1/2, carnitine palmitoyltransferase 1/2; CytC, Cytochrome C; FAD, oxidised flavin adenine dinucleotide; FADH₂, reduced flavin adenine dinucleotide; NAD⁺, oxidised nicotinamide adenine dinucleotide; NADH, reduced nicotinamide adenine dinucleotide; O₂^{•-}, superoxide; Pi, inorganic phosphate.

Freeman et al. Supplemental Table 1

This document contains all metabolomic data from the study.

GC-MS Diabetic-Control

UHPLC-MS Diabetic-Control

Column headings are as follows for GC-MS:

Metabolite ID

SN Mean Log2 Ratio

SN l-95% CI

SN u-95% CI

SN P-value

DRG Mean Log2 Ratio

DRG l-95% CI

DRG u-95% CI

DRG P-value

TG Mean Log2 Ratio

TG l-95% CI

TG u-95% CI

TG P-value

Column headings are as follows for UHPLC:

mz

rt

Putative ID

SN Control

SN STZ

SN Mean Log2 Ratio

SN l-95% CI

SN u-95% CI

SN P-value

SN FDR

DRG Control

DRG STZ

DRG Mean Log2 Ratio

DRG I-95% CI

DRG u-95% CI

DRG P-value

DRG FDR

TG Control

TG STZ

TG Mean Log2 Ratio

TG I-95% CI

TG u-95% CI

TG P-value

TG FDR

Data in 2 sheets as follows:

Gas Chromatography-MS data from the sciatic nerve, dorsal root ganglia and trigeminal ganglia of streptozotocin-diabetic rats in comparison to healthy controls

Ultra-High Performance Liquid Chromatography-MS data from the sciatic nerve, dorsal root ganglia and trigeminal ganglia of streptozotocin-diabetic rats in comparison to healthy controls

S:

Metabolite identification

Sciatic nerve mean log2 ratio

Sciatic nerve lower 95% confidence interval

Sciatic nerve upper 95% confidence interval

Sciatic nerve Mann-Whitney P-value

Dorsal root ganglia mean log2 ratio

Dorsal root ganglia lower 95% confidence interval

Dorsal root ganglia upper 95% confidence interval

Dorsal root ganglia Mann-Whitney P-value

Trigeminal ganglia mean log2 ratio

Trigeminal ganglia lower 95% confidence interval

Trigeminal ganglia upper 95% confidence interval

Trigeminal ganglia Mann-Whitney P-value

C-MS:

Mass-to-Charge ratio

Retention time

Putative identification, categorised

Number of control rats (total n=6) in which this feature was identified in the sciatic nerve

Number of streptozotocin rats (total n=6) in which this feature was identified in the sciatic nerve

Sciatic nerve mean log2 ratio

Sciatic nerve lower 95% confidence interval

Sciatic nerve upper 95% confidence interval

Sciatic nerve Mann-Whitney P-value

Sciatic nerve false discovery rate

Number of control rats (total n=6) in which this feature was identified in the dorsal root ganglia

Number of streptozotocin rats (total n=6) in which this feature was identified in the dorsal root ganglia

Dorsal root ganglia mean log2 ratio
Dorsal root ganglia lower 95% confidence interval
Dorsal root ganglia upper 95% confidence interval
Dorsal root ganglia Mann-Whitney P-value
Dorsal root ganglia false discovery rate
Number of control rats (total n=6) in which this feature was identified in the trigeminal ganglia
Number of streptozotocin rats (total n=6) in which this feature was identified in the trigeminal ganglia
Trigeminal ganglia mean log2 ratio
Trigeminal ganglia lower 95% confidence interval
Trigeminal ganglia upper 95% confidence interval
Trigeminal ganglia Mann-Whitney P-value
Trigeminal ganglia false discovery rate

Metabolite ID	SN	Mean	L	SN I-95%	C	SN u-95%	t	SN p	-value
Lactate		-0.64386		-4.64386		1.063503		0.386476	
Alanine		-0.73697		-2.05889		1.117695		0.248213	
Beta-Hydroxybutyric acid		4.146492		0.941106		6.391802		0.083265	
Ethanolamine		0.678072		-0.18442		1.555816		0.148915	
Glycerol		2.160275		1.709291		2.541019		0.020921	
Leucine		1.327687		0.604071		2.107688		0.020921	
Glycine		-0.45403		-1.05889		0.201634		0.148915	
Serine		-0.97143		-1.78588		-0.1047		0.043308	
Phosphoric acid		-0.16812		-0.76121		0.641546		0.248213	
Urea		0.815575		-0.0145		1.608809		0.148915	
Benzoic acid		-0.12029		-0.25154		0.014355		0.083265	
Threonine		-0.59946		-1.64386		1.042644		0.248213	
Succinate		-0.39593		-2.18442		0.956057		0.563703	
Threitol and/or Erythritol		2.516015		1.726831		3.92505		0.020921	
Malate		-0.47393		-1.18442		0.344828		0.148915	
Aspartate		-1.152		-1.64386		-0.64386		0.020921	
2-Hydroxyglutaric acid		0.056584		-1.64386		1.344828		0.77283	
Creatinine		0.137504		-0.94342		1.981853		1	
N-Acetylglutamic acid		0.189034		-0.47393		1.195348		0.77283	
Glutamic acid		-1.152		-2.05889		-0.16812		0.083265	
Pyroglutamic acid		-1.2863		-2.05889		-0.25154		0.148915	
Dodecanoic acid		-0.73697		-1.59946		0.124328		0.148915	
Phenylalanine		-1.25154		-2.12029		0.097611		0.020921	
Pyroglutamic acid and/or glutamic acid		-0.13606		-0.68966		0.344828		0.288844	
Glycerol-2-phosphate		-0.37707		-1		0.411426		0.248213	
Pyrophosphate		0.124328		-2.05889		1.914565		0.4795	
Glycerol-3-phosphate		-0.35845		-1.25154		0.757023		0.248213	
Sorbitol		4.646163		3.678072		6.119771		0.020921	
Fructose		3.142413		2.403268		4.350497		0.020921	
Glyceraldehyde-3-phosphate		-0.26882		-0.78588		0.475085		0.248213	
Glucose		2.266037		1.372952		3.224966		0.020921	
Citrate		0.15056		-0.55639		1.157044		1	
Tetradecanoic acid		-0.94342		-1.39593		-0.57777		0.020921	
Lysine		-1.02915		-2.05889		-0.23447		0.043308	
<i>scyllo</i> -Inositol		-2.94342		-3.8365		-1.73697		0.020921	
<i>myo</i> -Inositol		-2.25154		-2.8365		-1.2863		0.020921	
Tyrosine		-1.47393		-2		-0.88897		0.020921	
Palmitic acid		-1.05889		-1.32193		-0.81097		0.020921	
Stearic acid		-1.05889		-1.32193		-0.81097		0.020921	
Glucose-6-phosphate		0.111031		-0.78588		0.978196		0.563703	
Tryptophan		-0.94342		-1.8365		-0.18442		0.083265	
Eicosanoic acid		-1.05889		-1.32193		-0.81097		0.020921	
Sucrose		0.731183				2.356144		1	
Maltose		-0.55639		-1.18442		-0.08927		0.043308	
Fructose-1,6-bisphosphate		0.443607		-0.57777		1.748461		0.248213	
Adenosine-5-monophosphate		-0.152		-1.88897		1.344828		0.563703	
Cholesterol		-0.78588		-1.39593		0.238787		0.248213	

DRG Mean	DRG I-95%	DRG u-95%	DRG p -value	TG Mean	L	TG I-95%	C	TG u-95%	c	TG p -value
0.238787	-1.64386	1.063503	0.563703	0.565597	-2.55639			0.4795		
-2.12029	-5.05889		0.083265	0.713696	-3.64386	3.343408		0.4795		
4.171527		5.975676	0.248213	5.072963				0.033895		
0.704872		5.289466	0.77283	0.411426	0.028569	0.782409		0.0771		
0.879706	0.400538	1.438293	0.020921	0.286881	-0.34008	1.111031		0.157299		
0.83996		3.24184	0.563703	1.378512	-2.8365	2.632268		0.288844		
-0.34008	-1.35845	1.744161	0.248213		-0.074	-0.81097	0.62293	0.723674		
-1.51457	-3.05889		0.248213	0.111031	-1.25154	2.070389		0.723674		
-0.32193	-0.68966	0.014355	0.083265	0.097611	-0.68966	0.910733		0.4795		
-1	-2.64386		0.386476	2.893362	0.887525			0.033895		
-0.49411	-1.73697		0.77283		-0.074	-0.32193	0.163499	0.372456		
-1.25154	-2.32193	-0.30401	0.043308	-0.34008	-1.12029	0.214125		0.157299		
0.367371	-1.39593	2.849999	0.77283	0.097611	-2.32193	1.895303		0.723674		
-0.16812	-2.94342		0.77283	1.718088	0.895303	2.759156		0.033895		
-0.41504	-1.05889	0.056584	0.148915	0.176323	-0.94342	1.769772		0.4795		
-0.64386	-1.05889	-0.20091	0.020921	0.163499	-1	0.863938		0.4795		
0.111031	-0.59946	0.956057	0.386476	-0.08927	-0.71312	0.516015		0.723674		
-0.2863	-1.94342	0.963474	0.77283	-0.13606	-0.8365	0.62293		0.4795		
-1.2863	-2.73697		0.386476	0.214125	-0.47393	1.176323		0.723674		
-0.8625	-4.64386	0.189034	0.248213	-0.05889	-1.47393	1.232661		1		
-1.02915	-1.55639	-0.62149	0.020921	-0.34008	-1.25154	0.823749		0.288844		
-0.68966		1.104337	0.563703	-0.97143	-3.32193	-0.08927		0.033895		
-1.68966	-3.32193	-0.91594	0.020921	-0.68966	-1.152	-0.32193		0.033895		
-0.21759	-0.64386	0.263034	0.386476	0.887525	-1.25154	3.460743		0.288844		
-0.16812	-0.76121	0.344828	0.77283	0.263034	-0.04394	0.604071		0.0771		
				1.722466	0.443607			0.049535		
-0.37707	-1.05889	0.097611	0.148915	0.097611	-0.66658	0.831877		0.4795		
4.256256	3.072106	5.035624	0.020921	4.778209	3.695994	7.263034		0.033895		
2.823749	1.773996	3.68818	0.020921	2.965323	2.31904	3.858976		0.033895		
-0.66658	-1.47393	-0.1047	0.083265	0.263034	-0.4344	0.925999		0.157299		
3.868884	2.555816	5.088311	0.020921	4.292045	3.408712	5.694323		0.033895		
-0.16812	-0.8625	0.298658	0.248213	0.411426	0.111031	0.773996		0.033895		
-0.21759	-0.37707	-0.04394	0.043308	-0.59946	-0.76121	-0.45403		0.033895		
-2.64386	-4.64386	-1.51457	0.020921	-0.8625	-1.51457	-0.34008		0.033895		
-3.05889	-3.32193	-2.73697	0.020921	-2.55639	-3.32193	-1.64386		0.033895		
-1.59946	-2.25154	-1.152	0.020921	-0.71312	-1.18442	-0.08927		0.033895		
-1.25154	-1.51457	-0.91594	0.020921	-0.91594	-1.51457	-0.13606		0.033895		
-0.37707	-0.8365	0.014355	0.083265	-0.49411	-1	0		0.0771		
-0.39593	-0.81097	-0.02915	0.083265	-0.51457	-1.05889	0.014355		0.0771		
0.356144	-0.57777	2.456806	0.248213	1.773996	1.028569	2.757023		0.033895		
-0.20091				-0.76121	-2.64386	0.275007		0.0771		
-0.23447	-0.51457	0.070389	0.148915	-0.45403	-1.05889	0.137504		0.0771		
-1	-2.64386		0.386476	-2.47393				0.288844		
0.9855	-0.39593	1.739848	0.148915	1.117695	-0.18442	1.996389		0.033895		
1.475085	0.765535	2.017922	0.020921	0.903038	-1.4344	3.526069		0.4795		
-0.0145	-2.18442	1.035624	0.723674	0.378512	-0.8625	1.744161		0.4795		
-0.32193	-1.32193	0.298658	0.248213	-0.62149	-1.12029	-0.16812		0.033895		

mz rt

566.3214 375.8161
520.3385 378.4922
550.3876 455.0785
544.3374 389.5309
580.4332 453.5058
576.4001 418.7375
570.3537 395.7063
674.4347 414.7727
502.3287 513.5795
580.2956 344.3451
506.3594 584.121
504.3048 378.1925

647.4651 995.1112
673.4802 995.8957
785.6042 744.0215
791.5603 567.2106
839.6504 819.548
837.635 770.0239
813.6353 804.5006
853.5651 962.7527
803.5611 528.8486
761.5217 538.2935
659.4233 357.5435
754.5699 572.2351
846.552 580.0334
764.5567 551.8723
899.7288 746.8955
872.5671 584.765
558.3542 402.8825
856.7115 764.5041
928.6298 676.8447
728.5197 514.7022
746.5683 536.1022
829.5751 534.2905
761.3945 548.2099
774.5991 567.6027
840.5704 606.8419
786.5992 559.3982
784.5823 534.7596
780.5524 502.2131
802.6306 605.7189

816.6463 627.7509
808.5828 530.1529
831.6655 652.4048
830.6618 653.1617
844.6778 675.5988
842.6615 636.6672
840.6448 603.8444
876.5852 652.1135
836.6146 560.9464
872.709 733.5355
852.5501 504.9917
868.679 722.9927
864.6462 595.0443
862.6299 564.0544
938.5325 529.1611
878.5681 495.7228
891.6637 647.9405
779.6611 653.3104
804.685 707.4154
478.3288 522.4009
564.4014 449.0944
848.6558 591.1109
548.4065 653.0036
846.6405 563.3425
674.5117 527.8578
726.5419 541.081
724.5276 530.1676
696.498 494.5724
722.5087 534.2933
812.5373 498.7441
814.5514 548.4312
803.6623 501.1003
780.587 635.1496
795.5975 565.0438
799.5424 554.1733
831.6931 532.0859
829.6773 567.5023
651.4734 502.5113
656.4235 425.4167
662.4752 491.3498
716.5228 519.5101
760.4899 490.9468
762.5057 491.4892
758.473 529.2574
846.5063 496.4053
786.5098 512.1703
820.5872 574.388

858.5066 489.7902
856.6752 662.1647
852.6436 654.112
886.7246 775.5323
880.675 707.9553
878.6599 660.3987
770.5097 524.5181
769.5884 575.388
634.4801 485.267
883.5586 610.2556
826.5706 584.3496
760.5112 510.0961
760.5155 547.3721
873.4781 498.9447
874.6519 838.7625
925.5103 507.0619
939.5823 384.897
898.6558 674.8813
765.5256 522.296
810.6546 562.6279
843.5909 580.7249
903.668 930.4666
849.6928 834.5807
571.3566 395.5193
621.2998 369.8685
642.3613 380.568
665.2677 367.2137
822.5115 592.7711
903.5928 930.5803
937.6779 852.8342
935.6625 801.2615
963.6932 867.1291
892.6249 580.6204
912.5987 704.9136
927.6355 835.1768
612.3247 391.258
626.3657 406.2438
682.3633 379.3445
696.379 379.3138
760.4115 549.0091
810.5259 538.8523
842.5881 582.8274
812.542 535.7942
866.5266 521.8436
836.5425 531.7937
860.6353 804.8823
874.6518 704.1785

866.5885 567.3681
888.671 874.2853
880.5117 485.005
918.6153 705.2608
694.5045 560.7003
774.564 470.2316
782.5326 470.6887
862.5195 566.568
796.5448 584.3852
676.455 464.2213
746.4571 534.7493

653.1423 508.5104
558.4852 491.732
644.5967 563.5627
692.4173 479.4602
618.485 809.9121
727.5141 501.4815
879.6548 981.7212
758.6471 528.3549
828.6279 558.1155
856.6593 592.6172
864.6537 785.3472
887.5632 509.6952
700.5716 498.9723
756.6331 558.4371
832.6598 603.2821
906.7024 867.8656
462.3419 351.2584
710.5237 508.1951
590.4536 685.0533
682.561 498.9335
739.6265 558.4253
626.3666 392.5178
482.4188 395.4073
416.2673 397.6259
386.2871 556.0152
701.5587 494.2684
799.6662 605.7516
827.6977 651.0702
790.7595 636.554
839.6968 634.972
703.5746 513.8561
729.5929 520.4912
809.6522 565.774
885.647 819.7948

801.682 642.6599
837.6816 602.1784
835.6663 625.3192
851.6985 834.6199
879.6755 870.3595
783.6396 558.7424
811.6683 594.0029
302.3051 320.4642
424.2206 368.9778
411.297 557.7337
465.3467 351.7982

330.0679 282.6432
316.2479 305.97
370.2945 337.8977
344.2794 329.6798
394.2944 337.8962
460.2828 385.3556
462.2976 386.2562
422.3243 356.775
424.3415 358.5639
450.354 362.2456
414.3577 370.9839
468.333 358.4351
448.3413 358.1214
472.3402 357.2501
618.3073 425.7458
430.3799 377.9289

423.2714 321.271
639.4755 409.2485
613.4419 411.2056
557.4146 481.2763
583.4328 487.5151
585.4478 501.937
542.4841 512.2676
675.5148 528.0009
731.5026 533.372
745.4472 535.5257
771.4505 551.9693
755.5759 575.0075
685.5364 611.1223
825.6727 611.9264
791.6344 617.0642
687.5523 646.6503

713.5676 654.0876
739.5833 656.073
715.5835 688.4914
741.599 693.1004
767.6146 705.4421
743.6149 733.9527
764.6749 744.7748
769.6306 744.9155
795.6451 755.2363
871.677 761.4977
909.7005 765.4246
745.6307 780.2241
766.6906 791.9471
771.6462 792.1547
873.6921 800.803
834.753 804.5006
792.7061 804.8023
797.6619 805.6087
899.7085 814.5289
915.6813 814.8243
949.7236 831.9067
886.7838 834.4811
920.7677 850.3817
925.7241 851.4848
912.7995 852.233
875.7083 852.2877
921.7011 853.1179
837.6928 854.3795
815.7121 856.4546
799.6773 861.5427
901.7237 865.8484
896.7687 866.229
938.8148 866.8376
947.7158 867.5763
825.693 877.8757
841.6667 877.9102
959.7861 879.3481
951.739 886.5428
889.7241 887.9806
888.7999 893.4633
846.7534 893.7525
913.6785 893.9344
661.5376 903.3773
927.739 903.6012
874.778 910.9059
840.712 919.2533
940.8304 929.1141

865.7242 935.5399
843.7413 938.7949
864.7999 943.6408
827.7087 943.6621
822.7536 943.9043
889.6789 944.603
953.7541 949.9097
924.7994 951.1391
930.7583 951.3562
891.7398 951.7587
853.7241 960.928
890.8156 960.928
831.7425 961.5648
915.6945 961.7181
862.7833 962.0389
894.8005 962.0444
813.7315 964.3142
874.7846 979.2138
916.831 979.5425
941.7099 980.7329
819.7419 991.6513
887.7863 991.9422
841.7243 992.3833
905.7552 998.2575
659.5237 999.9497
942.8463 1000.134
947.7439 1020.987
932.7744 1021.096
892.8312 1036.65
833.7581 1037.079
923.7267 1037.78
917.7096 1038.725
919.7708 1045.136
859.7737 1056.303
918.8468 1056.757
943.7252 1058.216
957.786 1058.808
933.7867 1098.227
904.8313 1168.679
946.8776 1169.28
932.862 1170.043
935.8023 1189.634
961.8177 1217.512
911.8027 1273.249

798.6419 556.6205

342.2635 317.9653
767.5396 545.941
905.68 1001.132
901.6459 865.8462
817.6092 750.3271

741.1946 534.54
725.1635 534.2915
838.1427 591.9708
891.2275 867.7132
580.2923 386.1644
853.2167 964.1982
751.128 507.8768

435.3119 711.1957
922.732 999.7683
754.2438 507.7178
647.5951 629.2842
213.146 297.3825
759.5718 529.3573
591.5341 1028.35
684.5301 560.5264
604.2933 376.3185
485.3586 448.194
396.31 343.7769
605.5494 570.4971
299.1613 332.3172
167.0701 320.2427
197.044 616.3268
181.0494 346.2316
454.8238 686.6308
856.212 918.3396
222.1804 350.4332
498.2027 371.8794
263.2364 1062.199
365.132 339.7252
557.9471 972.0942
765.034 526.1175
359.1666 523.9162
738.042 519.9767
770.0212 532.4018
736.0195 526.7684
249.021 344.8601
535.2086 318.622
462.2972 563.3703

446.1193 508.1084
257.19 375.8813
225.0935 318.9698
795.048 526.5268
214.9888 475.2127
463.2988 600.5343
297.2402 376.5379
689.6432 704.9442
857.8256 982.3291
356.3519 431.1123
293.1812 395.3873
417.3138 627.5791
878.1522 679.5263
325.1619 422.428
502.3287 513.5795
675.9178 392.5194
371.1005 535.0602
223.9628 652.2901
104.1067 401.4274
327.0814 331.1091
224.0923 343.0631
472.2467 363.6764
347.1342 345.3191
839.0203 405.5836
767.0493 542.6586
261.1095 288.688
487.293 398.8344
777.6947 861.6933
248.9767 474.2849
815.0472 517.9969
279.0989 318.0419
390.0741 533.3688
646.3385 448.9202
644.3214 431.578
657.3207 376.184
295.1935 408.9782
316.1491 404.8291
262.9159 473.5694
436.3541 417.0342

Putative ID**LYSOGLYCEROPHOSPHOLIPIDS**

LysoPC(18:1)
LysoPC(18:2)
LysoPC(20:0)
LysoPC(20:4)
LysoPC(22:0)
LysoPC(22:2)
LysoPC(22:5);LysoPC(20:2)
LysoPC(24:1)
LysoPC(dm16:0)
LysoPC(dm18:1)
LysoPC(dm18:1)
LysoPE(18:0)

GLYCEROPHOSPHOLIPIDS

PA(32:0)
PA(34:1)
PA(42:2)
PA(43:6)
PA(44:0)
PA(44:1);PS(38:0)
PA(44:2)
PA(44:4)
PA(44:6);PA(42:3)
PA(O-18:0/19:1);PA(O-20:0/17:1);PA(P-16:0/21:0);PA(P-18:0/19:0);PA(P-20:0/17:0)
PA(P-16:0/13:0)
PC(15:0/dm18:0);PE(18:0/dm18:0);PE(20:0/dm16:0)
PC(18:0/dm18:1);PC(18:1/dm18:0);PC(20:1/dm16:0);PC(P-18:0/18:1);PC(18:2/O-18:0)
PC(18:4/dm18:1);PC(20:5/dm16:0);PC(16:1/dm18:1);PC(18:2/dm16:0);PC(O-16:0/18:3);PC(O-16:0/18:3);PC(P-16:0/18:3)
PC(20:1/24:1);PC(20:2/24:0);PC(44:2)
PC(20:1/dm18:1);PC(20:2/dm18:0);PC(22:2/dm16:0)
PC(21:4);PC(O-16:0/3:1)
PC(24:0/dm18:1);PC(24:1/dm18:0)
PC(24:1/dm18:1)
PC(32:3);PE(35:3);PC(32:0);PC(30:0);PE(33:0);PE-NMe(32:0);PA(37:4)
PC(33:1);PE(36:1);PE-NMe2(34:1);PA(38:2);PC(O-14:0/O-16:0);PE-NMe(O-16:0/O-16:0)
PC(34:0);PE(37:0);PE-NMe(36:0)
PC(34:1);PE(37:1);PA(39:2);PE-NMe2(O-16:0/O-16:0)
PC(35:1);PE(38:1);PA(40:2);PC(O-12:0/O-20:0);PC(O-14:0/O-18:0);PC(O-16:0/O-16:0);PC(O-20:0/O-12:0)
PC(35:2);PE(38:2);PE-NMe2(36:2)
PC(36:2);PA(41:3)
PC(36:3);PC(34:0);PE(37:0);PE-NMe(36:0);PA(41:4)
PC(36:5);PC(34:2);PE(37:2);PE-NMe(36:2);PA(41:6)
PC(37:1);PE(40:1);PA(42:2);PC(O-16:0/O-18:0)

PC(38:1);PA(43:2)
PC(38:5);PC(36:2);PA(43:6)
PC(39:1);PE(42:1);PA(44:2);PC(O-18:0/O-18:0)
PC(39:1);PE(42:1);PA(44:2);PC(O-18:0/O-18:0)
PC(40:1)
PC(40:2)
PC(40:3);PC(38:0);PE(41:0);PE-NMe(40:0)
PC(40:4);PS(O-20:0/19:1);PS(P-18:0/21:0);PS(P-20:0/19:0)
PC(40:5);PC(38:2)
PC(42:1)
PC(42:11);PC(40:8);PC(38:5);PC(18:2/dm18:1);PC(18:3/dm18:0);PC(20:3/dm16:0);PC(O-16:0/20:4)
PC(42:3);PC(40:0);PE(43:0)
PC(42:5);PC(40:2)
PC(42:6);PC(40:3);PC(38:0);PE(41:0);PE-NMe(40:0)
PC(42:9)
PC(44:12);PC(42:9);PC(40:6);PE(43:6);PS(38:0);PC(20:3/dm18:1);PC(20:4/dm18:0);PC(22:4/dm16:0);PC(O-16:0/22
PC(44:6);PC(42:3);PC(40:0);PE(43:0)
PC(O-14:0/22:0);PC(O-16:0/20:0);PC(O-18:0/18:0);PC(O-20:0/16:0);PA(P-20:0/21:0)
PC(O-16:0/22:0);PC(O-18:0/20:0)
PC(O-16:2)
PC(O-18:0/3:1)
PC(O-20:0/22:6)
PC(O-3:1/O-18:1);PC(P-3:0/O-18:1)
PC(P-20:0/22:6)
PE(14:0/dm18:1);PE(14:1/dm18:0);PE(16:1/dm16:0)
PE(18:2/dm18:1);PE(18:3/dm18:0);PE(20:3/dm16:0);PE(O-16:0/20:4);PC(15:0/dm16:0);PE(16:0/dm18:0);PE(18:0/
PE(18:3/dm18:1);PE(18:4/dm18:0);PE(20:4/dm16:0);PE(16:0/dm18:1);PE(16:1/dm18:0);PE(18:1/dm16:0);PnE(34:
PE(18:4/dm16:0);PA(P-16:0/20:5)
PE(18:4/dm18:1);PE(20:5/dm16:0);PE(16:1/dm18:1);PE(18:2/dm16:0);PA(P-16:0/22:6);PC(O-14:0/15:0);PE(O-16:
PE(20:1/dm18:1);PE(20:2/dm18:0)
PE(20:1/dm18:1);PE(20:2/dm18:0)
PE(22:0/dm18:1);PE(22:1/dm18:0);PE(24:1/dm16:0)
PE(22:4/dm18:0);PE(20:0/dm18:1);PE(20:1/dm18:0);PE(22:1/dm16:0);PA(O-20:0/22:6)
PE(22:4/dm18:1);PE(22:5/dm18:0)
PE(22:5/dm18:1);PE(22:6/dm18:0);PE(P-18:0/22:6);PC(34:1);PE(37:1);PC(34:1);SQDG(31:0);PE(20:2/dm18:1);PE(21:
PE(24:0/dm18:1);PE(24:1/dm18:0)
PE(24:1/dm18:1)
PE(28:1)
PE(28:1);PC(O-10:0/O-12:0);PC(O-11:0/O-11:0);PC(O-16:0/O-6:0);PC(O-6:0/O-16:0)
PE(30:0);PC(27:0)
PE(34:2)
PE(38:7);PC(33:4);PE(36:4);PC(31:1);PE(34:1);PC(O-14:0/15:0);PE(O-16:0/16:0)
PE(38:7);PC(33:4);PE(36:4);PC(31:1);PE(34:1);PC(O-14:0/15:0);PE(O-16:0/16:0)
PE(38:9);PE(36:6);PS(O-16:0/16:1);PS(O-18:0/14:1);PS(P-16:0/16:0);PS(P-18:0/14:0);PS(P-20:0/12:0);PA(40:10);PE(41:
PE(40:6);PS(36:2)
PE(40:9);PA(42:10);PI(29:0)
PE(42:5);PC(39:5);PC(37:2);PE(40:2);PA(44:6)

PE(44:12);PS(P-18:0/22:6);PE(22:6/dm18:1)
PE(44:2)
PE(44:4);PC(39:1);PE(42:1);CerP(d18:1/26:1);PC(O-18:0/O-18:0)
PE(46:1);PC(O-20:0/O-20:0)
PE(46:4);PE(44:1)
PE(46:5);PE(44:2)
PE(O-16:1/22:6);PE(20:5/dm18:1);PE(22:6/dm16:0);PC(32:1);PE(35:1);PE-NMe(34:1);PE(18:2/dm18:1);PE(18:3/dm18:1);PE(O-18:1/20:4);PE(20:3/dm18:1);PE(20:4/dm18:0);PE(22:4/dm16:0);PE(O-16:0/22:5);PE(O-18:0/20:5);DG(41:0)
PE(P-16:0/13:0);PA(P-16:0/15:1)
PE(P-20:0/22:4)
PE(P-20:0/22:6);PC(36:1);PE(39:1);PC(36:2);PC(O-17:0/20:4)
PG(34:4)
PG(34:4)
PG(38:4)
PG(42:3)
PG(42:6)
PG(44:4);PA(44:1)
PG(44:5)
PG(O-16:0/17:1);PG(O-18:0/15:1);PG(P-16:0/17:0);PG(P-18:0/15:0);PG(P-20:0/13:0)
PG(O-20:0/18:0);PG(O-18:0/20:0);PG(O-16:0/22:0)
PG(O-20:0/19:1(9Z));PG(P-18:0/21:0);PG(P-20:0/19:0);PA(P-20:0/21:0)
PG(O-20:0/21:0)
PG(O-20:0/22:0)
PI(16:1)
PI(18:1)
PI(20:2)
PI(20:4)
PI(32:3)
PI(39:3);PI(37:0)
PI(41:0)
PI(41:1)
PI(43:1)
PI(O-18:0/20:3);PI(O-20:0/18:3);PI(P-16:0/22:2);PI(P-18:0/20:2);PI(P-20:0/18:2)
PI(P-18:0/22:6)
PI(P-20:0/22:4)
PS(21:0);LysoPC(20:4);PC(20:4);LysoPC(18:1);PC(O-16:1/2:0);PC(P-16:0/2:0);PC(18:1)
PS(22:0)
PS(25:0);PC(23:0);PE(26:0);PE-NMe2(24:0);PC(22:1)
PS(26:0);PC(24:0);PE(27:0)
PS(31:3);PE(32:3);PE(31:4)
PS(36:2);PG(38:7);PC(33:3);PE(36:3);PA(38:4);PC(31:0);PE(34:0);PE-NMe2(32:0);PC(31:0)
PS(38:0);PG(40:5);PE(38:1)
PS(38:4);PS(36:1);PC(33:2);PE(36:2);
PS(39:3);PC(20:4/dm18:1);PC(20:5/dm18:0);PC(22:5/dm16:0);PC(O-38:6);PC(36:4);PE(22:5/dm18:1);PE(22:6/dm18:0);
PS(40:6);PG(40:8);PS(36:0);PC(35:4);PE(38:4);PE-NMe2(36:4);PC(33:1);PE(36:1);PE-NMe2(34:1);PE(O-18:0/O-18:0)
PS(41:1);PG(41:3)
PS(42:1)

PS(42:5);PG(42:7);PE(40:3);PC(37:3);PC(35:0);PE(38:0);PE-NMe2(36:0)
PS(43:1)
PS(44:12);PS(42:9);PS(40:6);PE(42:10);PS(O-18:0/20:5);PS(P-16:0/22:4);PS(P-20:0/18:4);PS(P-18:0/20:4);PE(40:7)
PS(44:4);PC(40:1);PE(44:5);PS(O-20:0/20:0);PS(O-18:0/22:0);PE(42:2)
PS(O-16:0/14:0);PS(O-18:0/12:0);PG(P-16:0/14:1)
PS(O-16:0/20:2);PS(O-18:0/18:2);PS(P-16:0/20:1);PS(P-20:0/16:1);PS(P-18:0/18:1)
PS(O-18:0/17:2);PS(P-16:0/19:1);PS(P-18:0/17:1);PS(P-20:0/15:1);PC(14:1/dm18:1);PC(O-14:0/18:3)
PS(O-18:0/20:5);PS(P-16:0/22:4);PS(P-20:0/18:4);PS(P-18:0/20:4);PS(O-16:0/20:2);PS(O-18:0/18:2);PS(P-16:0/20:1)
PS(O-18:0/20:5);PS(P-16:0/22:4);PS(P-20:0/18:4);PS(P-18:0/20:4);PS(O-16:0/20:2);PS(O-18:0/18:2);PS(P-16:0/20:1)
PS(P-16:0/13:0)
PS(P-16:0/13:0)

SPHINGOLIPIDS AND CERAMIDES

Cer(d18:0/24:0)
Cer(d18:2/16:0)
Ceramide (d18:1/22:0)
CerP(d18:1/16:0)
CerP(d18:1/16:0)
Etn-1-P-Cer(d14:1/18:0)
Galabiosylceramide (d18:1/16:0);Lactosylceramide (d18:1/16:0);SM(d18:2/24:1);SM(d18:0/22:0);
GlcCer(d18:0/20:0)
GlcCer(d18:0/22:0)
GlcCer(d18:0/24:0)
GlcCer(d18:2/23:0);GalCer(d18:2/23:0)
Glc-GP(38:4)
Glucosylceramide (d18:1/16:0);Galactosylceramide (d18:1/16:0);GlcCer(d18:1/16:0)
Glucosylceramide (d18:1/20:0);Galactosylceramide (d18:1/20:0)
Glucosylceramide (d18:1/24:1);Galactosylceramide (d18:1/24:1)
Glucosylceramide (d18:1/26:1);Galactosylceramide (d18:1/26:1)
Glucosylsphingosine;Galactosylsphingosine
N-(2-hydroxydocosanoyl)-4,8-sphingadienine
N-(2-hydroxyhexadecanoyl)-4,8-sphingadienine
N-(2-hydroxynonadecanoyl)-phytosphingosine
N-(2-hydroxytricosanoyl)-phytosphingosine
N-(2-hydroxytridecanoyl)-4,8-sphingadienine
N-(2-hydroxyundecanoyl)-4,8-sphingadienine
N,N,N-trimethyl-sphingosine
Phytosphingosine;hydroxysphinganine
SM(d16:1/18:1);SM(d18:1/16:1);SM(d18:2/16:0)
SM(d17:1/24:1);SM(d18:2/23:0)
SM(d17:1/26:1);SM(d18:2/25:0);SM(d19:1/24:1)
SM(d18:0/22:0)
SM(d18:0/24:0)
SM(d18:1/16:0)
SM(d18:1/18:1)
SM(d18:1/22:0)
SM(d18:1/23:0)

SM(d18:1/23:0);CerP(d18:1/26:1)

SM(d18:1/24:0);SM(d18:0/24:1)

SM(d18:1/24:1)

SM(d18:1/25:0)

SM(d18:1/26:1)

SM(d18:2/22:1)

SM(d18:2/24:1);SM(d18:0/22:0)

Sphinganine

Sphingosine 1-phosphate

Sphingosine-1-phosphate (C19)

Sphingosyl-phosphocholine

ACYL CARNITINES

Acetylcarnitine

Decanoylcarnitine

Tetradecenoylcarnitine

Dodecanoylcarnitine

Tetradecanoylcarnitine

Arachidonoyl dopamine;Linoelaidyl carnitine;Linoleyl carnitine

Linoelaidyl carnitine;Linoleyl carnitine

Palmitoylcarnitine

Linoelaidyl carnitine;Linoleyl carnitine

Stearoylcarnitine

Heptadecanoyl carnitine

Linoelaidyl carnitine;Linoleyl carnitine

Eicosatetraenoyl carnitine;Vaccenyl carnitine;Elaidic carnitine;octadecenoyl carnitine

Cervonyl carnitine

Tetracosapentaenoyl carnitine

Stearoylcarnitine

ACYL GLYCERIDES

MG(18:2)

DAGe(30:1);DG(33:1)

DAGe(30:1)

DG(28:0)

DG(32:4);DG(30:1)

DG(32:3)

DG(30:0)

DG(35:2)

DG(42:8)

DG(40:10)

DG(39:6)

DG(41:4);DG(39:1)

TG(38:2)

TGe(48:3)

TG(42:0)

TG(38:1)

TG(40:2)
TG(42:3)
TG(42:4)
TG(42:2)
TG(46:6)
TG(44:4)
TG(44:2)
TG(46:5)
TG(46:3)
TG(54:10)
TG(57:12)
TG(44:3)
TG(44:1)
TG(46:4)
TG(52:6)
TG(49:2)
TG(46:2)
TG(48:5)
TG(56:10)
TG(54:7)
TG(60:13)
TG(53:4)
TG(56:8)
TG(58:11)
TG(55:5)
TG(54:8)
TG(58:13)
TG(51:6)
TG(49:3)
TG(48:4)
TG(56:9)
TG(54:6)
TG(57:6)
TG(60:14)
TG(50:5)
TG(48:2)
TGe(58:6)
TG(60:12)
TG(55:8)
TG(53:3)
TG(48:3)
TGe(52:5)
TG(36:0)
TG(58:10)
TG(52:4)
TG(51:5)
TG(57:5)

TG(53:6)
TG(51:3)
TG(51:1)
TG(49:4)
TG(48:1)
TGe(50:3)
TG(58:8)
TG(56:6)
TG(57:10)
TG(55:7)
TG(52:5)
TG(53:2)
TG(50:2)
TGe(52:4)
TG(51:2)
TGe(56:6);TGe(54:3)
TGe(50:4)
TG(52:3)
TG(55:3)
TGe(54:5)
TG(49:1)
TGe(52:0)
TG(51:4)
TG(54:4)
TG(36:1)
TG(57:4)
TG(56:5)
TG(57:9)
TG(53:1)
TG(50:1)
TGe(54:6);TG(51:0);TG(52:4);TG(50:1)
TGe(52:3)
TG(57:7)
TG(52:2)
TG(55:2)
TGe(54:4)
TG(60:9)
TG(58:7)
TG(54:2)
TG(57:2)
TG(56:2)
TG(56:3)
TG(60:8)
TG(56:4)

UBIQUINONES AND RELATED METABOLITES

3-Demethylubiquinone-9

Decylubiquinol
Ubiquinol 8
Ubiquinol-10
Ubiquinone-10;Ubisemiquinone
Ubiquinone-9

PORPHYRINS

131-hydroxy-magnesium-protoporphyrin IX 13-monomethyl ester
2-Acetyl-Protoporphyrin Ix
Coproporphyrin I Containing Co(III)
Heptacarboxylporphyrin III
Protoporphyrin;Protoporphyrin IX
Uroporphyrin III;Uroporphyrin I
Zinc protoporphyrin-9

OTHERS

(24R)-1alpha,24,25-trihydroxy-22-oxavitamin D3;(24S)-1alpha,24,25-trihydroxy-22-oxavitamin D3;(25R)-1alpha,25
1,2-didocosanoyl-sn-glycero-3-phosphocholine
10-Formyltetrahydrofolylpolyglutamate;Triglu-5-Formyl-Tetrahydrofolate
1-hexadecyl-tricosanoate
1-Nonanol
1-O-alpha-D-glucopyranosyl-(2-tetradecanoyloxy)-eicosan-1-ol;CE(18:3)
1-octadecyl-heptadecanoate
1-tetradecanyl-2-(8-[3]-ladderane-octanyl)-sn-glycerophosphoethanolamine
2-(8-[3]-ladderane-octanyl)-sn-glycero-3-phosphocholine
2alpha-(3-Hydroxypropyl)-1alpha,25-dihydroxy-19-norvitamin D3;MG(24:1);hexacosenoic acid
2-Arachidonoylglycerol;1-Arachidonoylglycerol;9-deoxy-9-methylene-16,16-dimethyl -PGE2;3alpha,7alpha,12alpha
2-octadecanoyl-1-hexadecyl-sn-glycerol;decyl hexacosanoate;dodecyl tetracosanoate;eicosanyl hexadecanoate;he
2-Polypropenylphenol;Tridecanoic acid;methyl lauric acid;dimethyl-undecanoic acid
3-(2-Hydroxyphenyl)propanoate;Tropate;Phenyllactate;Methoxyphenylacetic acid;Phenoxypropionic acid
3-(3,4-Dihydroxyphenyl)pyruvate;3,4,6-trihydroxy-cis-cinnamate
3-(4-Hydroxyphenyl)pyruvate;Caffeate;2-Hydroxy-3-(4-hydroxyphenyl)propanoate;trans-2,3-Dihydroxycinnamate;
3,5-Diiodo-4-hydroxyphenylpyruvate
3-Hydroxyisopentyl-CoA
3-Hydroxy-N6,N6,N6-trimethyl-L-lysine
3-Sulfodeoxycholic acid
4-Dodecylphenol;6-[3]-ladderane-1-hexanol
4-Hydroxy-3-polyprenylbenzoate
5-hydroxy-CTP
6-(Adenosine Tetraphosphate-Methyl)-7,8-Dihydropterin;3',5'-Cyclic diGMP
6-(alpha-D-Glucosaminyl)-1D-myo-inositol;Lactosamine
Adenophostin A
Adenophostin B
ADP-D-glycero-D-manno-heptose;ADP-L-glycero-D-manno-heptose
Allantoin
all-trans-Retinoyl-beta-glucuronide;13-cis-retinoyl-beta-D-glucuronide
Arachidonoyl dopamine

benzyladenine-7-N-glucoside;benzyladenine-9-N-glucoside
Deoxyestradiol
Descarboxy-nor-N(Omega)-Hydroxy-L-Arginine
Diadenosine triphosphate
Diethylthiophosphoric acid
dihydroxy-docosanoic acid
dimethyl-tridecanol
docosanyl icosanoate;eicosanyl docosanoate;hexacosanyl hexadecanoate;hexadecyl hexacosanoate;tetradecyl octatriacontanyl docosanoate;triacontanyl tetracosanoate;tetratriacontanyl icosanoate
Eicosanoyl-EA
Epsilon-(gamma-Glutamyl)-lysine
ergostatetraenol
Flavin adenine dinucleotide reduced;FADH2;FADH
Galactosylhydroxylysine
Gallopamil;N-(2R-methyl-3-hydroxy-ethyl)-16,16-dimethyl-5Z,8Z,11Z,14Z-docosatetraenoyl amine;N-(2-hydroxy-2Z,5Z,8Z,11Z,14Z-pentaenoyl)lysine
Gamma-Methyleneadenosine-5'-Diphosphate
Geranylbenzoquinone;Hexadecatetraenynoic acid
L-Serine O-sulfate
L-Valinol;Choline
N-Acetyl-aspartyl-glutamate;3-Methyluridine
N-Acetyl-L-tyrosine;N-benzyloxycarbonyl-L-serine-betalactone;2-Hydroxy-8-methylchromene-2-carboxylate;2-Hydroxy-8-methylchromene-2-carboxylate
N-arachidonoyl glutamic acid
N-Benzoyl-D-arginine
Nicotinamide 8-Bromo-Adenine Dinucleotide Phosphate
Nicotinic acid adenine dinucleotide phosphate;Guanosine diphosphate adenosine
Nomega,Nomega'-Dimethyl-L-arginine;Symmetric dimethylarginine;N,N-dimethylarginine;N3, N4-Dimethylarginine
N-palmitoyl tryptophan;4alpha-carboxy-5alpha-cholest-8,24-dien-3beta-ol;(22Z)-1alpha,25-dihydroxy-20-epivitamin D₃
O-(4-Hydroxy-3,5-diiodophenyl)-3,5-diiodo-L-tyrosine;thyroxine
Oxalosuccinate
P1,P2-Bis(5'-adenosyl) triphosphate;P1,P3-Bis(5'-adenosyl) triphosphate;Diadenosine triphosphate;5',5'-diadenosyl-5'-dihydroxy-2-methyl-4-oxopentyl triphosphate
p-Methoxystilbene;Hexyloxyphenol
S-(2-Hydroxyethyl)glutathione
S-(9-hydroxy-PGA1)-glutathione;S-(11-hydroxy-9-deoxy-delta12-PGD2)-glutathione
S-(PGA1)-glutathione;Gsh-prostaglandin A1;10,11-dihydro-12R-hydroxy-leukotriene C4;S-(9-hydroxy-PGA2)-glutathione
S-(PGA2)-glutathione;S-(PGJ2)-glutathione;S-(9-deoxy-delta9,12-PGD2)-glutathione
Tetradecyl Sulfate
Tetraethylengenetamine
Thiopyrophosphate
Tricosanoyl-EA

SN Control	SN STZ	SN Mean L	SN I-95% C	SN u-95% C	SN p -value	SN FDR	DRG Control
6	6	-0.64155	-0.93357	-0.35614	0.003948	0.008688	6
6	6	0.915936	0.713119	1.120294	0.003948	0.00025	6
5	5	0.713119	0.454032	0.971431	0.009023	0.089644	5
6	6	-0.18903	-0.33342	-0.04264	0.037373	0.059549	6
6	6	0.556393	0.321928	0.785875	0.003948	0.005262	6
2	6	0.888969	0.454032	1.395929	0.0455	0.050085	3
5	6	0.494109	0.268817	0.68966	0.00617	0.021012	6
4	6	2.473931	1.029146	3.321928	0.010515	0.098448	1
6	6	0.862496	0.556393	1.152003	0.003948	0.00695	6
6	6	-1.20789	-2.5008	-0.38957	0.016309	0.040885	0
6	6	-0.23879	-0.40054	-0.08406	0.010406	0.039404	6
6	6	0.340075	0.217591	0.473931	0.003948	0.003746	6
4	4	0.713119	0.37707	1.089267	0.020921	0.093927	1
5	5	0.761213	0.395929	1.120294	0.009023	0.097951	1
6	2	-2.91839	-3.19061	-2.59932	0.0455	0.003203	2
6	6	0.104697	0.0145	0.200913	0.016309	0.079231	6
6	2	-2.62994	-3.10936	-2.08746	0.0455	0.011057	3
6	6	-2.17632	-2.67807	-1.73552	0.003948	0.002501	1
6	3	-2.79701	-3.82985	-2.10434	0.020137	0.003943	3
5	4	-0.848	-1.24489	-0.41143	0.014306	0.04275	1
5	6	0.888969	0.666576	1.089267	0.00617	0.06111	6
6	6	0.217591	0.089267	0.358454	0.016309	0.03218	4
3	5	0.454032	0.136062	0.761213	0.025347	0.06177	5
6	6	0.168123	0.043943	0.286304	0.024975	0.05502	6
6	4	-0.52607	-0.85599	-0.21412	0.010515	0.032743	6
3	6	0.599462	0.395929	0.810966	0.020137	0.006366	3
6	6	-0.9855	-1.4489	-0.41143	0.006485	0.064097	6
6	6	-0.26303	-0.44361	-0.07039	0.024975	0.059726	6
6	6	0.643856	0.168123	1.184425	0.037373	0.058134	6
6	3	-1.4957	-2.1177	-0.87971	0.020137	0.022661	5
6	6	-0.23879	-0.44361	-0.04264	0.010406	0.077955	5
6	6	-0.37851	-0.51602	-0.23879	0.003948	0.006115	6
6	6	0.200913	0.074001	0.321928	0.016309	0.035091	6
5	6	0.514573	0.304006	0.713119	0.00617	0.104017	6
5	5	0.251539	0.089267	0.415037	0.009023	0.041726	5
6	6	0.713119	0.535332	0.888969	0.003948	0.000851	6
6	5	-0.31034	-0.65076	0	0.04461	0.148874	5
6	6	0.340075	0.184425	0.473931	0.003948	0.025311	6
6	6	0.415037	0.268817	0.556393	0.003948	0.015278	6
6	6	-0.926	-1.38405	-0.41143	0.003948	0.048218	4
6	6	0.434403	0.136062	0.736966	0.024975	0.053209	4

6	6	0.415037	0.268817	0.556393	0.003948	0.004088	6
6	6	-0.74846	-0.926	-0.58496	0.003948	0.00024	6
6	6	0.643856	0.251539	1	0.010406	0.053817	6
6	6	0.577767	0.168123	0.971431	0.024975	0.062865	6
6	6	0.304006	0.120294	0.494109	0.016309	0.034962	6
6	6	0.68966	0.434403	0.915936	0.003948	0.017685	6
6	6	1.058894	0.761213	1.358454	0.003948	0.00863	6
6	6	-0.53605	-0.91073	-0.17632	0.010406	0.043108	6
6	6	-0.44361	-0.64155	-0.26303	0.003948	0.0059	6
6	6	-0.54597	-0.87184	-0.18903	0.016309	0.060795	6
6	3	-1.19535	-1.66903	-0.7137	0.020137	0.016656	6
6	6	-1.50589	-2.28392	-0.70487	0.003948	0.050085	6
6	5	-0.35614	-0.60407	-0.11103	0.010587	0.050878	6
6	6	0.666576	0.494109	0.836501	0.003948	0.001063	6
4	6	1.120294	0.736966	1.473931	0.010515	0.093927	5
6	6	-0.07039	-0.50589	0.304006	0.262332	0.787146	6
2	6	1.152003	0.514573	1.736966	0.0455	0.046599	3
6	6	-1.32193	-2.49313	-0.65076	0.006485	0.010944	2
6	4	-1.68706	-2.62059	-1.04963	0.010515	0.004494	0
6	6	-0.21412	-0.36737	-0.07039	0.016309	0.04633	6
6	6	0.340075	0.089267	0.577767	0.006485	0.061068	6
6	6	-0.43296	-0.62293	-0.25096	0.003948	0.006467	6
5	6	0.862496	0.535332	1.120294	0.00617	0.027343	2
0	6						6
6	6	-0.51602	-0.85599	-0.18903	0.016309	0.039861	6
6	6	0.621488	0.358454	0.888969	0.003948	0.018311	6
6	6	-0.17632	-0.29866	-0.04264	0.024975	0.078805	5
6	6	1.736966	1.358454	2.184425	0.003948	0.001763	0
6	6	-0.22651	-0.37851	-0.07039	0.016309	0.04967	6
5	6	-0.93357	-1.30451	-0.59455	0.00617	0.06111	6
6	6	-0.21412	-0.38957	-0.04264	0.016309	0.065709	6
6	5	0.736966	0.217591	1.184425	0.02846	0.081945	6
5	5	-0.53605	-0.91839	-0.20163	0.009023	0.036084	6
6	6	-0.20163	-0.38957	-0.02857	0.024975	0.092291	6
6	6	-0.28688	-0.45418	-0.12433	0.006485	0.024951	6
6	3	0.494109	0.234465	0.761213	0.020137	0.034214	1
5	6	1	0.68966	1.286304	0.00617	0.006253	6
6	5	-1.15704	-1.94111	-0.37851	0.00617	0.064699	6
5	6	2.643856	1.556393	3.643856	0.00617	0.054289	0
5	6	-0.64155	-0.9486	-0.35614	0.010587	0.083913	4
6	6	0.494109	0.304006	0.68966	0.003948	0.004686	6
5	5	-1.03562	-1.74846	-0.51602	0.009023	0.089644	6
5	5	0.454032	0.152003	0.761213	0.009023	0.049523	5
4	6	0.785875	0.340075	1.217591	0.010515	0.039188	4
6	6	1.395929	0.514573	2.736966	0.010406	0.0373	3
6	6	0.888969	0.736966	1.029146	0.003948	0.003992	6
5	6	0.666576	0.454032	0.862496	0.00617	0.078117	5

Diabetes

5	6	1.184425	0.454032	1.736966	0.04461	0.079271	0
6	6	0.666576	0.304006	1.029146	0.010406	0.035348	6
6	6	0.666576	0.358454	0.943416	0.006485	0.026233	6
6	6	-0.96347	-1.50589	-0.52607	0.006485	0.007378	6
6	6	0.713119	0.340075	1.029146	0.003948	0.041607	6
4	4	1	0.395929	1.736966	0.020921	0.041204	3
6	6	-0.67807	-0.93357	-0.44361	0.003948	0.00209	6
6	6	-0.65992	-1.08406	-0.23879	0.010406	0.04349	6
6	6	-0.43296	-0.85599	-0.08406	0.037373	0.083725	6
6	6	-0.37851	-0.70487	-0.08406	0.024975	0.069411	6
6	6	-0.32193	-0.48543	-0.1635	0.010406	0.015417	6
5	4	-1.36737	-1.852	-0.73118	0.027486	0.058134	4
2	6	-0.90304	-1.8679	-0.32193	0.0455	0.041887	6
6	5	1.321928	0.888969	1.785875	0.00617	0.013853	0
6	2	0.535332	0.340075	0.736966	0.0455	0.091739	0
6	6	1.251539	0.577767	2	0.010406	0.033613	4
5	6	1.358454	1.152003	1.556393	0.00617	0.039302	6
5	6	1.434403	0.785875	2.058894	0.010587	0.032402	1
5	6	-0.60407	-0.99277	-0.27501	0.00617	0.097951	6
5	4	1.395929	0.810966	2	0.014306	0.038648	1
6	6	0.556393	0.340075	0.761213	0.003948	0.015664	6
6	6	0.395929	0.184425	0.621488	0.006485	0.02341	1
6	6	-1.4957	-1.95977	-1.12433	0.003948	0.00025	6
3	6	0.37707	0.120294	0.621488	0.020137	0.057116	6
6	6	0.713119	0.200913	1.286304	0.016309	0.057669	0
6	6	2.643856	2.120294	3.473931	0.003948	3.79E-05	6
6	4	0.888969	0.304006	1.599462	0.019016	0.05614	4
6	6	0.599462	0.321928	0.915936	0.003948	0.008952	5
5	6	0.454032	0.152003	0.785875	0.017622	0.046746	1
6	6	-1.08406	-1.48027	-0.774	0.003948	0.002927	1
6	6	-1.7866	-3.32912	-1.04264	0.003948	0.003569	0
6	6	0.473931	0.136062	0.836501	0.016309	0.047205	1
4	6	2.836501	2.473931	3.184425	0.010515	0.000999	4
6	6	-0.35614	-0.55582	-0.1635	0.024975	0.02175	6
6	4	-2.52857	-3.49953	-1.88362	0.010515	0.002136	1
6	5	-0.36737	-0.47508	-0.26303	0.00617	0.003395	6
3	6	2.473931	1.888969	2.943416	0.020137	0.093927	5
6	4	-0.61353	-0.926	-0.23879	0.033006	0.055985	6
6	6	-0.78241	-1.22651	-0.32193	0.010406	0.039861	6
6	5	0.168123	0.043943	0.304006	0.04461	0.070581	6
5	6	-0.61353	-0.9782	-0.27501	0.010587	0.023209	6
6	6	0.643856	0.395929	0.888969	0.003948	0.010529	6
6	6	-0.44361	-0.60407	-0.28688	0.003948	0.002742	6
6	6	-0.33342	-0.48543	-0.17632	0.003948	0.010529	6
6	6	-0.23879	-0.43296	-0.05658	0.024975	0.068113	6
6	2	-2.35614	-2.7866	-1.79077	0.0455	0.017607	1
6	6	-0.32193	-0.54597	-0.11103	0.010406	0.043178	6

6	6	0.943416	0.666576	1.251539	0.003948	0.001434	6
6	6	-2.85	-3.4957	-2.26003	0.003948	0.008825	5
6	6	-0.8953	-1.33914	-0.50589	0.003948	0.007996	6
6	6	-0.44361	-0.62293	-0.26303	0.003948	0.006428	6
4	6	-0.42223	-0.57531	-0.26303	0.010515	0.009727	6
6	6	1.599462	0.556393	2.395929	0.010406	0.095721	6
4	6	1.736966	0.415037	5.643856	0.033006	0.075161	5
5	6	-0.61353	-1	-0.27501	0.00617	0.096258	6
6	5	-0.53605	-0.91839	-0.15056	0.017622	0.056303	0
5	6	1.943416	1.358454	2.556393	0.00617	0.089644	2
6	6	-0.45418	-0.66903	-0.23879	0.006485	0.016266	6
6	6	-1.92979	-3.08236	-0.95606	0.010406	0.046599	6
6	6	-0.87971	-2.02857	-0.1635	0.037373	0.07347	6
5	6	1.184425	0.810966	1.514573	0.00617	0.017931	5
6	6	0.556393	0.104697	0.971431	0.016309	0.097933	6
5	5	-2.24793	-4.23802	-1.03562	0.009023	0.062779	5
6	6	-0.9782	-1.46467	-0.50589	0.006485	0.022704	6
6	6	-0.26303	-0.43296	-0.11103	0.003948	0.034229	1
6	6	0.666576	0.340075	1	0.003948	0.014972	6
2	6	1.888969	1.217591	2.943416	0.0455	0.075475	4
5	6	1.358454	0.943416	1.736966	0.00617	0.089644	6
6	2	-1.3505	-1.88362	-0.9486	0.0455	0.043336	1
6	6	0.971431	0.434403	1.556393	0.010406	0.032628	6
6	6	1.029146	0.217591	1.943416	0.024975	0.079384	6
6	6	0.621488	0.184425	1	0.024975	0.072962	6
6	6	-0.48543	-0.774	-0.21412	0.010406	0.021082	6
4	5	0.836501	0.454032	1.251539	0.014306	0.014689	0
6	6	0.268817	0.074001	0.454032	0.037373	0.050085	6
6	6	-1.02148	-1.38405	-0.68706	0.003948	0.002389	6
6	6	0.713119	0.37707	1.029146	0.006485	0.019045	5
6	6	1.089267	0.251539	2.184425	0.024975	0.075899	6
4	6	0.761213	0.304006	1.152003	0.019016	0.0511	4
6	6	2.836501	2.473931	3.184425	0.003948	0.002136	6
6	6	-0.40054	-1	0.043943	0.200185	0.210626	6
6	5	-0.18903	-0.33342	-0.04264	0.02846	0.065641	6
6	6	0.340075	0.089267	0.599462	0.024975	0.064434	6
6	6	0.68966	0.268817	1.120294	0.006485	0.039404	6
6	6	0.340075	0.089267	0.577767	0.010406	0.06125	6
6	6	0.321928	0.058894	0.599462	0.037373	0.080259	6
6	6	0.434403	0.089267	0.761213	0.006485	0.079378	5
6	6	0.621488	0.304006	0.971431	0.006485	0.012355	5
6	6	0.340075	0.152003	0.535332	0.010406	0.02484	6
6	6	0.514573	0.286304	0.736966	0.003948	0.009116	6
6	6	1.217591	0.943416	1.473931	0.003948	0.005385	6
6	5	-4.27277	-5.47962	-3.38267	0.00617	0.017728	1

Diabetes

6	6	0.621488	0.251539	1.029146	0.010406	0.026233	6
3	6	0.810966	0.454032	1.152003	0.020137	0.015573	1
6	6	-0.20163	-0.31034	-0.09761	0.010406	0.016136	6
6	6	-1.48543	-1.9486	-1.1177	0.003948	0.00023	1
6	6	0.810966	0.286304	1.514573	0.016309	0.034311	1
6	6	0.836501	0.577767	1.089267	0.003948	0.003882	6
6	6	0.514573	0.340075	0.68966	0.003948	0.002156	6
6	6	0.184425	0.043943	0.321928	0.010406	0.082739	5
5	6	0.535332	0.268817	0.810966	0.010587	0.013528	6
6	6	1	0.713119	1.286304	0.003948	0.004582	6
3	4	0.943416	0.358454	1.473931	0.033895	0.069376	5
6	5	-0.37851	-0.73985	-0.04264	0.04461	0.098815	2
6	6	-0.63227	-1.18903	-0.05658	0.037373	0.124095	6
6	6	-0.82375	-1.29278	-0.32193	0.006485	0.050521	6
6	6	-0.65992	-1.20789	-0.1375	0.010406	0.077526	6
6	6	-0.22651	-0.75702	0.321928	0.262332	0.514715	6
5	6	1.217591	0.943416	1.473931	0.00617	0.06111	6
6	6	0.713119	0.535332	0.888969	0.003948	0.003233	6
6	6	1.556393	0.862496	2.120294	0.003948	0.046175	6
6	6	2.395929	1.736966	2.943416	0.003948	0.025205	6
5	6	0.029146	-0.37851	0.454032	0.855132	0.933666	6
6	6	0.810966	0.304006	1.251539	0.010406	0.059179	6
5	6	2.643856	2.251539	3.058894	0.00617	0.06111	6
6	6	-0.1635	-0.57531	0.268817	0.262332	0.551818	6
6	6	-1	-1.5656	-0.44361	0.006485	0.036081	6
6	6	-0.53605	-0.8953	-0.1635	0.016309	0.055372	6
6	4	0.494109	0.120294	0.888969	0.019016	0.085487	6
6	5	0.217591	0.074001	0.358454	0.00617	0.098531	6
6	6	-0.1375	-0.23879	-0.04264	0.003948	0.067901	6
6	6	0.358454	0.120294	0.621488	0.024975	0.039696	6
6	5	-2.4489	-3.67129	-1.56071	0.00617	0.022669	5
6	3	-1.44361	-3.86295	-0.41143	0.038867	0.06177	0
6	5	-4.15218	err.	-2.76977	0.00617	0.028244	4
4	5	-0.33342	-0.60407	-0.07039	0.027486	0.075161	5
6	6	-0.50589	-0.85599	-0.17632	0.016309	0.042503	6
6	5	-0.78241	-1.0635	-0.4957	0.00617	0.007641	3
6	6	-0.65992	-0.9855	-0.34483	0.006485	0.014572	6
5	4	-0.20163	-0.34483	-0.07039	0.014306	0.085442	1
6	6	0.415037	0.286304	0.535332	0.003948	0.006564	6
6	4	-5.0009	-6.07403	-3.34483	0.010515	0.077167	2
5	6	0.37707	0.152003	0.599462	0.010587	0.026976	6
6	6	0.340075	0.234465	0.454032	0.003948	0.00209	6
6	4	-5.10978	-6.00787	-3.75916	0.010515	0.057566	1

6	5	-4.49442	-5.60318	-3.49697	0.00617	0.029708	4
6	2	-5.84875	-7.30797	-4.89724	0.0455	0.01452	2
6	3	-5.73471	-6.92125	-4.56071	0.020137	0.038174	2
6	5	-5.84172	-7.32706	-4.87971	0.00617	0.017685	5
6	6	-4.18428	-5.1469	-3.41819	0.003948	0.012859	5
6	3	-5.48896	-6.46156	-4.49953	0.020137	0.02797	5
6	4	-3.91169	-4.82528	-3.23113	0.010515	0.006332	1
6	6	-4.08066	-5.15421	-3.34199	0.003948	0.007451	6
6	6	-3.70487	-4.62176	-3.04963	0.003948	0.004582	6
5	6	-1.23879	-2.16672	-0.65076	0.00617	0.00858	2
6	6	-1.07039	-2.04963	-0.27501	0.024975	0.067473	1
6	5	-3.80323	-5.93475	-2.78241	0.00617	0.015627	6
6	2	-4.63169	-5.9241	-3.75702	0.0455	0.011798	1
6	6	-4.78031	-5.84122	-4.03474	0.003948	0.007956	6
6	6	-0.90304	-1.65076	-0.38957	0.010406	0.025205	5
6	3	-2.72465	-4.10434	-1.96347	0.020137	0.00209	3
6	2	-3.96901	err.	-2.29866	0.0455	0.010529	1
6	6	-3.47379	-4.43162	-2.80323	0.003948	0.004681	6
6	6	0.888969	0.304006	1.556393	0.016309	0.045086	6
6	6	1.152003	0.643856	1.836501	0.003948	0.006366	2
5	6	1.473931	0.621488	2.643856	0.00617	0.034388	0
6	6	-1.32769	-1.73552	-0.9782	0.003948	0.000678	5
6	5	0.836501	0.251539	1.556393	0.02846	0.052351	0
6	6	1.029146	0.454032	1.643856	0.016309	0.030648	6
6	6	-0.76553	-1.0635	-0.51602	0.003948	0.004536	4
6	6	-0.73985	-0.9782	-0.53605	0.003948	0.00376	6
6	6	-1.12433	-1.53107	-0.79909	0.003948	0.00209	1
6	6	-2.37573	-2.80529	-2.0036	0.003948	0.001063	5
6	4	-3.40327	-4.05658	-2.87578	0.010515	0.002899	0
6	6	-5.36036	-6.26266	-4.38059	0.003948	0.03218	6
6	6	0.785875	0.415037	1.251539	0.003948	0.011271	6
6	6	0.736966	0.268817	1.217591	0.003948	0.040963	4
6	6	0.888969	0.395929	1.473931	0.003948	0.023298	2
6	6	0.736966	0.234465	1.321928	0.003948	0.044603	0
6	6	-2.18903	-2.68482	-1.70929	0.003948	0.007094	6
5	5	-1.74416	-2.15056	-1.28688	0.009023	0.021547	6
6	2	-1.88753	-2.23573	-1.4489	0.0455	0.012907	1
6	6	1.888969	1.152003	3.058894	0.003948	0.007094	0
6	6	1.286304	0.643856	2.120294	0.003948	0.016563	5
6	6	-2.09424	-2.41143	-1.75702	0.003948	0.003883	5
6	6	-2.24489	-2.62994	-1.89142	0.003948	0.001684	6
6	6	-2.14731	-2.56803	-1.7866	0.003948	0.000537	5
4	5	-1.42223	-2.22033	-0.8953	0.014306	0.003994	0
6	6	1.358454	0.810966	1.888969	0.003948	0.02277	2
6	6	-0.848	-1.1375	-0.59455	0.003948	0.001295	1
6	6	-0.82375	-1.04264	-0.60407	0.003948	0.001502	6
6	6	0.415037	0.120294	0.68966	0.024975	0.056604	4

Diabetes

6	6	-0.58496	-0.75702	-0.42223	0.003948	0.001231	6
6	6	-1.37851	-1.848	-1.0072	0.003948	0.000363	1
6	6	-2.90497	-3.33485	-2.52857	0.003948	0.001415	6
6	6	-2.86196	-3.28983	-2.48543	0.003948	0.001415	6
6	6	-3.32625	-3.82273	-2.89142	0.003948	0.00232	6
6	4	-3.41007	-4.06953	-2.89142	0.010515	0.00225	5
6	6	0.836501	0.37707	1.321928	0.010406	0.023086	3
6	6	0.761213	0.251539	1.358454	0.024975	0.046376	0
6	6	1.286304	0.836501	1.836501	0.003948	0.002766	5
6	6	1.184425	0.761213	1.736966	0.003948	0.001854	6
6	6	-0.48543	-0.67807	-0.31034	0.003948	0.004666	6
6	6	-0.79909	-1.10434	-0.52607	0.003948	0.002011	6
6	6	-1.55582	-2.15381	-1.0635	0.003948	0.00302	5
6	6	-0.69599	-0.96347	-0.46467	0.003948	0.00225	5
6	6	-0.65992	-0.91073	-0.43296	0.003948	0.002328	3
6	3	-0.80735	-1.04963	-0.5656	0.020137	0.003645	1
6	6	-0.67807	-1.29278	-0.22651	0.006485	0.048051	1
6	6	-0.38957	-0.63227	-0.17632	0.003948	0.031457	6
6	6	-0.48543	-0.79077	-0.22651	0.003948	0.029713	6
6	6	-0.34483	-0.50589	-0.20163	0.003948	0.013914	5
6	6	-1.34483	-1.83592	-0.94111	0.003948	0.001063	1
6	6	-0.32193	-0.61353	-0.07039	0.010406	0.088337	1
6	6	-0.81558	-1.04963	-0.57531	0.003948	0.004088	3
6	6	0.217591	0.120294	0.321928	0.003948	0.01119	6
6	6	-0.47508	-0.83188	-0.17632	0.003948	0.042041	0
6	6	0.234465	0.043943	0.415037	0.037373	0.074869	4
6	6	0.888969	0.556393	1.217591	0.003948	0.007031	0
6	6	0.713119	0.304006	1.120294	0.010406	0.037504	6
6	6	-0.45418	-0.774	-0.1635	0.003948	0.034667	6
6	6	-1.244489	-2.36457	-0.50589	0.003948	0.026026	6
6	6	-0.42223	-0.76553	-0.1375	0.003948	0.054571	3
6	6	-0.73118	-1.26903	-0.27501	0.003948	0.030322	5
6	6	1.217591	0.836501	1.68966	0.003948	0.001434	3
6	6	-1.05658	-1.66903	-0.59455	0.003948	0.005542	6
6	6	-0.31034	-0.53605	-0.09761	0.010406	0.046376	6
6	6	-0.44361	-0.75702	-0.17632	0.003948	0.043291	3
5	6	1.152003	0.494109	1.943416	0.00617	0.032075	0
6	6	0.666576	0.136062	1.217591	0.016309	0.079836	6
6	6	0.761213	0.286304	1.184425	0.024975	0.06177	3
6	6	0.862496	0.340075	1.358454	0.010406	0.04967	1
6	6	0.785875	0.286304	1.251539	0.024975	0.057177	1
6	6	1	0.304006	1.68966	0.037373	0.072375	6
5	6	2.184425	1.358454	3.321928	0.00617	0.021012	0
6	6	2.395929	1.434403	3.836501	0.003948	0.024706	6
6	6	0.251539	0.089267	0.434403	0.016309	0.042606	5

6	6	-0.48543	-1.03562	0.089267	0.054664	0.208599	6
5	6	-0.76553	-1.11103	-0.47508	0.00617	0.058504	6
6	6	0.268817	0.058894	0.473931	0.010406	0.065342	1
4	6	0.643856	0.200913	1.217591	0.010515	0.071725	3
6	6	1.473931	0.473931	2.321928	0.006485	0.091483	6
6	6	-1.21412	-1.9855	-0.55582	0.010406	0.031066	6
6	6	-1.29278	-2.08746	-0.60407	0.010406	0.032369	6
6	6	0.785875	0.494109	1.058894	0.003948	0.008815	1
6	6	1.152003	0.454032	2.058894	0.003948	0.035011	0
4	5	-0.35614	-0.60407	-0.09761	0.014306	0.073277	6
6	4	-1.1635	-1.70929	-0.67807	0.010515	0.011351	1
6	6	-2.61589	-4.21335	-1.32193	0.006485	0.064434	6
6	6	0.434403	0.184425	0.666576	0.010406	0.028407	6
6	6	0.184425	0.152003	0.217591	0.003948	0.000104	6
6	6	-2.04963	-2.95047	-1.20163	0.006485	0.035091	6
6	6	0.454032	0.184425	0.68966	0.010406	0.04385	4
6	6	0.136062	0.043943	0.234465	0.016309	0.039861	6
6	6	0.494109	0.395929	0.599462	0.003948	0.000399	6
5	6	-0.94111	-2.03914	-0.18903	0.02846	0.070838	0
5	5	-1.10434	-1.51602	-0.54597	0.009023	0.067601	3
6	6	0.395929	-0.02857	0.761213	0.149541	0.190434	6
6	6	0.943416	0.184425	2	0.024975	0.07538	6
6	6	1.68966	1.251539	2.184425	0.003948	0.004088	6
6	6	0.152003	0.043943	0.251539	0.003948	0.049882	6
6	6	-1.07039	-1.9855	-0.42223	0.010406	0.026045	6
6	6	-0.8953	-1.65992	-0.26303	0.016309	0.051096	5
5	6	0.358454	0.074001	0.621488	0.02846	0.076348	2
6	6	-0.80735	-1.45943	-0.27501	0.016309	0.039668	6
6	6	0.577767	0.268817	0.888969	0.010406	0.023528	6
6	6	-1.62293	-2.01078	-1.28688	0.003948	0.000464	1
6	6	-0.36737	-0.61353	-0.12433	0.016309	0.050085	6
6	6	-0.63227	-1.22651	-0.1375	0.024975	0.065934	5
5	6	0.736966	0.268817	1.152003	0.02846	0.058984	1
6	6	-0.5656	-0.97085	-0.1635	0.016309	0.057586	3
5	6	1.286304	0.494109	2.643856	0.010587	0.031167	6
6	6	0.340075	0.184425	0.473931	0.003948	0.018044	6
6	5	-0.848	-1.1177	-0.58496	0.00617	0.004197	6
6	6	-0.46467	-0.62293	-0.31034	0.003948	0.002136	6
6	5	0.713119	0.358454	1.120294	0.00617	0.017187	6
6	6	-0.35614	-0.52607	-0.17632	0.003948	0.018875	6
6	5	-0.73118	-1.37295	-0.17632	0.017622	0.064097	0
6	6	-1.73985	-5.93946	-0.43296	0.016309	0.071572	0
6	6	-0.11103	-0.17632	-0.05658	0.010406	0.01779	6

Diabetes

6	6	-2.0635	-3.36036	-1.01436	0.010406	0.050193	6
6	6	-0.82375	-1.56071	-0.20163	0.024975	0.060795	0
6	6	-1.09085	-2.07039	-0.37851	0.016309	0.039696	2
6	6	-0.47508	-0.72247	-0.25096	0.003948	0.011369	6
6	6	-0.35614	-0.65076	-0.08406	0.037373	0.06177	6
6	6	-0.42223	-0.59455	-0.25096	0.003948	0.004582	1
6	6	-0.29866	-0.4957	-0.08406	0.010406	0.070073	6
6	6	-0.27501	-0.45418	-0.09761	0.016309	0.034311	6
6	6	-0.45418	-0.82375	-0.15056	0.006485	0.057817	1
6	6	-0.41143	-0.78241	-0.09761	0.037373	0.067166	6
6	6	-0.72247	-1.33342	-0.08406	0.037373	0.116231	6
6	6	-0.40054	-0.75702	-0.11103	0.037373	0.074404	6
6	6	0.666576	0.136062	1.152003	0.024975	0.091277	4
3	4	0.251539	0.168123	0.340075	0.033895	0.028787	0
6	6	0.862496	0.556393	1.152003	0.003948	0.00695	6
5	5	-0.79909	-1.29278	-0.31034	0.009023	0.04967	6
6	6	-1.29866	-2.14405	-0.58496	0.010406	0.033775	1
6	6	-0.26303	-0.4957	-0.04264	0.037373	0.087708	6
6	6	-0.29866	-0.46467	-0.1375	0.006485	0.020955	6
5	5	-0.8953	-1.64155	-0.21412	0.02828	0.079173	5
4	6	-0.50589	-0.83188	-0.21412	0.019016	0.028606	5
6	6	0.666576	0.136062	1.395929	0.010406	0.079267	5
6	6	-0.95606	-1.76977	-0.35614	0.010406	0.031746	6
6	6	-0.69599	-1.18269	-0.21412	0.016309	0.053943	5
6	6	-0.45418	-0.73118	-0.1635	0.010406	0.049523	6
6	5	-0.60407	-0.93357	-0.23879	0.017622	0.054807	6
6	6	-0.20163	-0.28688	-0.12433	0.003948	0.005218	6
6	6	-6.37643	-7.70002	-5.12391	0.003948	0.04586	1
6	6	-0.45418	-0.7137	-0.17632	0.016309	0.048788	6
6	6	0.915936	0.340075	1.836501	0.037373	0.041195	6
6	6	-1.07039	-2.1375	-0.35614	0.016309	0.039393	6
6	6	-1.52105	-2.79286	-0.52607	0.010406	0.061068	5
6	6	-0.41143	-0.76553	-0.08406	0.037373	0.07314	6
4	6	1.184425	0.761213	1.599462	0.010515	0.013123	6
5	6	-0.79909	-1.33342	-0.40054	0.00617	0.093927	6
6	6	0.074001	-0.22651	0.358454	0.748774	0.725396	6
6	6	-0.27501	-0.61353	0.0145	0.109315	0.176185	6
6	6	-0.41143	-0.79909	-0.07039	0.024975	0.079098	2
4	5	0.535332	0.251539	0.862496	0.014306	0.035715	6

DRG STZ	DRG Mean	DRG I-95%	DRG u-95%	DRG p-val	DRG FDR	TG Control	TG STZ
---------	----------	-----------	-----------	-----------	---------	------------	--------

6	-0.69599	-1.47508	-0.08406	0.037373	0.353672	6	6
6	0.736966	-0.11103	1.321928	0.054664	0.545614	6	6
6	0.304006	-0.47508	1.286304	0.583882	0.804572	4	6
6	-0.22651	-0.64155	0.152003	0.200185	0.684916	6	6
6	-0.01436	-0.73985	0.713119	1	0.979434	6	6
5	0.473931	-0.76553	1.643856	0.456057	0.724735	5	6
6	0.434403	-0.31034	1	0.200185	0.684916	6	4
2	0.358454					6	6
6	0.785875	0.556393	1.029146	0.003948	0.005728	5	6
0						6	5
6	-0.08406	-0.25096	0.089267	0.42334	0.71394	6	6
6	0.286304	-0.63227	1.434403	0.748774	0.792032	6	6
0						1	1
0						1	2
0						4	0
6	-0.08406	-0.28688	0.104697	0.336668	0.724735	6	6
0						4	0
0						5	2
0						5	1
0						2	0
6	0.666576	0.454032	0.888969	0.003948	0.023583	6	6
6	-0.23879	-1.32769	0.415037	0.135593	0.777548	6	5
3	0.251539	0.029146	0.454032	0.10105	0.450339	6	4
6	0.043943	-0.34483	0.37707	1	0.922939	6	6
6	0.043943	-0.41143	0.454032	0.87278	0.944256	3	2
3	0.120294	-0.34483	0.736966	0.512691	0.818179	3	4
6	0.268817	-0.75702	1.089267	0.87278	0.797704	5	6
6	-0.07039	-0.35614	0.200913	0.87278	0.81345	6	6
6	0.358454	-0.76553	1.120294	0.748774	0.745902	6	4
5	0.120294	-0.774	0.971431	0.916815	0.894348	3	3
6	-0.20163	-0.72247	0.304006	0.36131	0.738155	3	2
6	-0.21412	-0.37851	-0.05658	0.024975	0.257121	6	6
6	-0.04264	-0.90304	0.621488	0.748774	0.962996	6	6
6	0.268817	0.043943	0.514573	0.054664	0.386498	6	6
4	-0.1375	-0.47508	0.234465	0.327187	0.741537	6	4
6	0.37707	0.058894	0.666576	0.024975	0.381443	6	6
5	-0.26303	-0.37851	-0.15056	0.009023	0.067129	6	5
6	0.217591	-0.21412	0.599462	0.262332	0.705987	6	6
6	0.217591	-0.5656	0.836501	0.630954	0.795091	6	6
2	0.152003	-0.59455	0.971431	0.643429	0.843886	6	6
4	0.136062	-0.8953	0.971431	0.563703	0.886795	6	6

Diabetes

6	0.089267	-0.57531	0.888969	0.87278	0.912301	6	6
6	-0.67807	-1.42761	-0.07039	0.024975	0.369083	6	6
5	0.599462	-0.12433	1.358454	0.067889	0.529164	6	6
6	0.168123	-1.60407	1.434403	0.630954	0.912149	6	6
6	0.058894	-0.774	0.862496	0.630954	0.954783	6	6
6	0.340075	-0.59455	1.321928	0.42334	0.745065	6	6
6	0.415037	-0.42223	1	0.630954	0.703778	6	6
6	-0.58496	-1.03562	-0.15056	0.010406	0.266841	4	3
6	-0.62293	-1.21412	-0.1375	0.024975	0.296095	6	6
6	0.104697	-0.65992	0.785875	0.87278	0.89965	6	6
6	-0.29866	-1.25701	0.494109	0.630954	0.754326	6	6
5	0.286304	-0.61353	1.120294	0.583882	0.775485	6	6
6	-0.70487	-1.76977	-0.02857	0.054664	0.410527	6	6
6	0.089267	-0.48543	0.577767	0.748774	0.876623	6	6
6	0.577767	0.234465	1	0.00617	0.228388	3	5
6	-1.22651	-1.78241	-0.75702	0.003948	0.043339	6	6
6	0.810966	0.454032	1.152003	0.020137	0.096457	3	6
2	-0.21412	-0.50589	0.043943	0.121335	0.627365	6	4
0						3	6
6	0.168123	-0.38957	0.68966	0.87278	0.791811	6	6
6	-0.05658	-0.60407	0.514573	0.748774	0.929502	5	5
6	-0.04264	-0.22651	0.120294	0.748774	0.816823	5	6
4	0.234465	-0.848	1.029146	1	0.80104	5	6
6	0.888969	0.514573	1.251539	0.006485	0.076165	3	5
6	-0.37851	-0.87184	0.043943	0.109315	0.492624	6	6
6	0.535332	0.37707	0.713119	0.003948	0.00943	6	6
1	0.268817					6	6
6						1	6
6	0.104697	-0.09761	0.286304	0.336668	0.706635	6	6
6	0.089267	-0.97085	1.251539	0.748774	0.963771	6	6
5	0	-0.47508	0.494109	0.715001	0.998266	3	1
6	0.621488	-0.08406	1.152003	0.200185	0.541184	6	6
6	-0.42223	-1.14405	0.152003	0.200185	0.601474	5	6
6	-0.22651	-0.40054	-0.05658	0.037373	0.307086	6	6
6	-0.01436	-0.44361	0.358454	0.748774	0.973039	6	6
0						1	2
6	0.556393	0.217591	0.836501	0.016309	0.26369	6	6
6	-0.66903	-1.60881	0.234465	0.078169	0.580141	3	1
4						4	6
2	-0.07039	-0.31034	0.217591	0.354539	0.853589	3	1
6	0.473931	0.168123	0.785875	0.010406	0.157021	6	6
6	-0.29866	-1.05658	0.395929	0.336668	0.798497	6	5
3	0.736966	0.120294	1.434403	0.052632	0.402088	6	5
6	0.251539	-0.18903	0.68966	0.200825	0.684916	6	6
5	0.286304	-0.47508	1.029146	0.456057	0.738155	6	5
6	0.168123	-0.1375	0.454032	0.262332	0.70175	6	6
4	0.304006	0	0.556393	0.086411	0.585244	4	5

0						4	3
6	0.286304	-1.03562	1.358454	0.630954	0.816514	6	6
6	0.321928	-0.32193	0.888969	0.336668	0.704675	5	6
6	0.168123	-0.62293	0.836501	0.87278	0.835155	6	6
6	0.340075	-0.75702	1.184425	0.630954	0.76004	6	6
5	0.915936	0.120294	2.251539	0.025347	0.394176	4	6
5	-0.54597	-0.83996	-0.26303	0.00617	0.091866	6	6
6	-0.36737	-0.66903	-0.08406	0.024975	0.285568	6	6
6	-0.23879	-0.94111	0.340075	0.262332	0.745065	6	6
6	-0.36737	-0.73118	0.043943	0.078169	0.523307	5	4
6	-0.1635	-0.35614	0.0145	0.054664	0.496838	6	6
3	-0.61353	-1.60407	0.304006	0.0771	0.614961	5	4
6	-0.34483	-1.01436	0.200913	0.200185	0.678722	6	4
1						4	4
0						1	1
3	0.304006	-2.37016	1.68966	1	0.855488	6	5
6	0.535332	0.058894	0.943416	0.054664	0.489158	6	6
1	1.286304					1	0
6	-0.21412	-0.86394	0.358454	0.42334	0.813307	6	6
5	0.713119					6	4
6	0.104697	-0.09761	0.304006	0.262332	0.714887	6	5
1	-1.20789					2	4
6	-3.37573	-5.32769	err.	0.109315	0.703778	6	6
6	0.217591	-0.57531	0.761213	0.748774	0.787676	5	4
0						6	5
6	2.736966	2.120294	3.184425	0.003948	0.106368	6	6
1	0.304006					6	3
3	0.761213	0.217591	1.473931	0.052632	0.285568	6	6
0						1	2
0						2	2
0						0	0
0						0	2
6	1.943416	1.643856	2.251539	0.010515	0.024415	2	6
6	-0.36737	-0.926	0.152003	0.109315	0.607125	6	4
0						0	0
6	-0.08406	-0.25096	0.074001	0.336668	0.697021	6	4
6	2.321928	1.785875	2.736966	0.00617	0.181017	6	6
6	0.043943	-0.36737	0.395929	0.748774	0.912149	4	3
6	0.029146	-0.21412	0.251539	0.42334	0.932386	6	6
5	-0.29866	-0.64155	0.0145	0.04461	0.456975	6	4
6	-0.58496	-0.79909	-0.35614	0.003948	0.073434	4	4
6	-0.08406	-0.23879	0.074001	0.42334	0.719041	6	6
6	-0.67807	-1.5509	-0.01436	0.016309	0.413134	6	6
6	-0.20163	-0.70487	0.251539	0.336668	0.730585	5	5
6	-0.46467	-0.94111	-0.04264	0.037373	0.377482	6	6
0						1	0
6	-0.33342	-0.97085	0.217591	0.336668	0.687797	6	5

Diabetes

6	0.234465	-0.09761	0.556393	0.262332	0.607125	6	6	
3	-1.94486	-3.41143	err.	0.654721	0.728888	4	5	
6	-0.95606	-1.64155	-0.32193	0.016309	0.238515	4	4	
6	-0.34483	-1.16993	0.304006	0.336668	0.705987	4	2	
5	-0.25096	-0.54597	0.058894	0.067889	0.557638	6	6	
6	0.643856	-0.43296	1.358454	0.262332	0.662289	6	6	
6	0.454032	-1.17632	2.643856	0.583882	0.785701	5	6	
5	0.37707	-1.81558	1.434403	0.855132	0.856808	6	3	
0						6	6	
4	1.321928	0.089267		2	0.064078	0.522267	1	5
6	-0.35614	-0.7137	-0.01436	0.054664	0.394496	5	4	
6	-0.17632	-0.65992	0.340075	0.42334	0.758545	6	5	
6	0.321928	-0.18903	0.713119	0.109315	0.673119	6	6	
6	0.862496	0.358454	1.358454	0.010587	0.20696	3	5	
6	0.0145	-0.72247	0.736966	0.630954	0.980436	5	6	
5	0.761213	-0.20163	1.434403	0.117185	0.576157	4	2	
6	-0.47508	-1.07039	0.104697	0.109315	0.529891	6	6	
1	-1.76553					3	4	
6	0.785875	-0.08406	1.556393	0.109315	0.49592	6	6	
6	0.577767	-0.51602	1.321928	0.286422	0.702297	1	4	
6	0.666576	-0.57531	1.785875	0.109315	0.710691	6	6	
0						1	1	
6	0.200913	-0.94111	0.971431	0.87278	0.847878	6	6	
6	0.37707	-0.50589	0.943416	0.87278	0.724735	6	6	
6	0.152003	-0.36737	0.713119	0.521839	0.805431	6	6	
6	0.0145	-0.25096	0.268817	0.748774	0.967621	6	6	
0						0	1	
6	0.168123	-0.50589	0.736966	0.630954	0.818179	6	6	
5	-0.38957	-1.09761	0.340075	0.201243	0.6973	5	3	
6	0.286304	-0.66903	1	0.855132	0.765877	6	6	
6	0.37707	-0.58496	1	1	0.725968	6	6	
4	0.268817	-0.61353	0.971431	0.77283	0.76004	4	5	
6	2.395929	1.785875	2.943416	0.003948	0.104668	6	6	
6	-0.85599	-1.49057	-0.38957	0.003948	0.096457	5	5	
6	0.089267	-0.38957	0.556393	0.630954	0.857272	6	5	
6	0.043943	-0.1635	0.251539	0.521839	0.838462	6	6	
6	0.136062	-0.75702	0.810966	1	0.87462	6	6	
6	0.0145	-0.99277	0.785875	0.87278	0.985771	6	6	
6	0.043943	-1.07724	0.836501	0.87278	0.964967	6	6	
5	0.168123	-0.9855	1.152003	0.916815	0.875653	5	6	
6	0.029146	-1.02148	0.713119	0.583882	0.976616	6	6	
6	0.089267	-0.27501	0.395929	0.87278	0.827811	6	6	
6	0.136062	-0.23879	0.473931	0.42334	0.761837	6	6	
6	0.713119	0.184425	1.152003	0.024975	0.341333	6	6	
0						2	0	

6	0.494109	-0.81558	1.358454	0.42334	0.724735	6	6
4	2.321928					3	4
6	-0.01436	-0.1635	0.136062	0.87278	0.95851	6	6
0						2	3
0						3	3
6	0.321928	-0.18903	0.785875	0.262332	0.658058	6	6
6	0.200913	-0.21412	0.556393	0.42334	0.714887	6	6
3	-0.04264	-0.28688	0.168123	0.654721	0.875653	6	6
6	0.043943	-0.46467	0.494109	1	0.944256	6	4
6	0.494109	0.304006	0.713119	0.003948	0.033787	6	5
3	0.556393	-0.52607	1.321928	0.179712	0.705987	6	5
3	1.029146	-0.69599	err.	0.248213	0.724735	3	1
6	-1.70044	-2.72901	-1.05658	0.003948	0.012549	6	6
6	-1.46989	-2.31034	-0.8953	0.003948	0.018798	6	6
6	-1.40599	-2.28392	-0.81558	0.003948	0.027541	6	6
6	-1.17632	-2.04614	-0.57531	0.003948	0.069166	6	6
6	0.556393	0.37707	0.713119	0.003948	0.144966	6	6
6	0.268817	-0.05658	0.556393	0.109315	0.533311	6	6
6	-0.12433	-0.79909	0.395929	0.521839	0.845188	5	6
6	0.415037	-0.22651	0.943416	0.149541	0.658058	6	6
6	-0.9486	-1.67356	-0.41143	0.010406	0.098871	6	6
6	0.058894	-0.79909	0.68966	0.87278	0.940841	6	6
6	0.395929	-0.35614	0.971431	0.200185	0.721932	6	6
6	-1	-1.81147	-0.44361	0.010406	0.096457	6	6
6	-2	-2.7845	-1.40599	0.003948	0.027608	6	6
6	-0.73118	-1.43296	-0.09761	0.078169	0.358574	6	5
6	-0.22651	-0.88753	0.577767	0.521839	0.786409	6	5
6	-0.18903	-0.38957	0	0.078169	0.436512	6	5
6	0.029146	-0.11103	0.184425	0.42334	0.827811	5	4
6	0.089267	-0.01436	0.200913	0.109315	0.543016	6	6
5	-0.31034	-0.8953	0.599462	0.174525	0.742522	5	3
0						1	1
3	-0.28688	-0.91073	0.494109	0.723674	0.73438	4	1
4	-0.05658	-0.54597	0.395929	0.806496	0.908245	4	5
6	-0.37851	-0.87971	0.043943	0.109315	0.497796	6	6
1	-0.5656					6	5
6	-0.44361	-0.75702	-0.1635	0.010406	0.164925	6	4
4	1.251539					5	4
6	0.251539	-0.08406	0.556393	0.200185	0.607089	6	5
0						2	0
6	0.120294	-0.29866	0.473931	0.748774	0.792073	6	6
5	0.286304	-0.29866	0.836501	0.273322	0.714706	6	6
0						2	0

Diabetes

1	-2.08066				5	1
0					3	0
0					2	2
0					6	4
2	-2.88166		0.245278	0.693745	5	5
0					5	0
0					4	0
4	-3.27798	-5.06264 err.	0.055009	0.689457	6	6
6	-2.80116	-4.43229 err.	0.109315	0.703778	6	6
1	-2.51349				6	4
2	1.473931				5	4
4	-2.61589	-4.2211 err.	0.088082	0.702982	6	5
0					3	1
3	-2.97453	-4.75007 err.	0.121335	0.703778	6	4
6	-2.93168	-5.03122 err.	0.04461	0.706635	5	6
0					6	3
0					1	0
6	-3.73877	-5.4266 err.	0.016309	0.701328	6	6
6	-0.41143	-2.04264 err.	0.262332	0.886795	6	6
6	-1.24489	-3.21257 err.		1 0.835155	5	6
0					2	3
1	-3.25852				6	5
0					1	1
6	-0.12433	-1.58015 2.836501	0.630954	0.945187	6	6
2	-2.35614	-4.36947 err.	0.643429	0.741429	6	6
6	-2.10769	-3.89336 err.	0.200185	0.723868	6	6
0					1	1
1	-2.03562				5	5
0					0	0
6	-3.74201	-5.37539 err.	0.006485	0.697021	6	6
6	0.358454	-1.33914 err.	0.054664	0.876218	6	6
6	-0.43296	-2.68257 err.	0.200825	0.901338	6	6
6	-1.23266	-4.56621 err.		1 0.843886	3	6
0					0	0
6	-3.52982	-5.15137 err.	0.016309	0.684916	6	6
3	-2.26303	-3.39643 2.736966	0.121335	0.566346	6	5
0					0	0
2					2	4
6	-1.09761	-3.32193 err.	0.583882	0.751159	6	6
3	-3.38405	-6.01903 err.	0.025347	0.697281	6	6
2	-3.18269	-5.06867 err.	0.182422	0.702315	6	5
0					6	3
0					0	1
2	-1.11103 err.	err.	0.438578	0.724035	4	4
2	-3.19535				2	4
5	-1.45943	-3.37434 err.	0.201243	0.718007	6	6
6	-0.9486	-4.30961 err.	0.83117	0.817738	5	6

6	-1.7137	-3.53605	err.	0.336668	0.723483	6	6
0						1	1
3	-3.57652	-5.15299	err.	0.070701	0.702982	6	6
6	-3.50589	-4.97728	err.	0.006485	0.672278	6	5
3	-3.75489	-5.30961	err.	0.038867	0.700566	6	6
0						5	3
3	0.494109	-0.90304	1.599462	0.275234	0.724735	3	3
0						1	2
3	0.358454	-1.9486	1.68966	0.654721	0.829038	5	6
6	-0.41143	-2.24184	err.	0.630954	0.875653	6	6
6	-1.79077	-3.30159	err.	0.149541	0.684916	6	6
6	-2.09761	-4.06264	err.	0.149541	0.6973	6	6
5	-5.58856	-8.01061	err.	0.02828	0.724735	6	5
5	-2.7866	-4.88118	err.	0.0758	0.705458	6	5
2	-2.23879	-3.74846	err.	0.083265	0.724735	4	5
0						2	1
0						1	1
6	-1.60881	-3.43162	err.	0.262332	0.718591	6	6
6	-1.43829	-3.49953	err.	0.262332	0.719817	6	6
3	-1.61353	-4.52544	err.	0.654721	0.735328	5	4
0						2	1
0						0	1
0						3	3
6	-0.75702	-2.49057	err.	0.748774	0.80104	6	6
0						0	1
6	-1.76553	-5.07852	err.	0.286422	0.751159	5	6
0						0	2
6	-0.47508	-1.57046	0.810966	0.336668	0.734471	6	6
6	-2.95791	-4.91743	err.	0.054664	0.703778	6	6
6	-4.78712	-6.62293	err.	0.024975	0.724735	6	6
0						3	2
0						4	2
2	-0.27501	-2.22651	err.	0.563703	0.925072	3	5
6	-4.14568	-6.05463	err.	0.109315	0.724735	6	6
6	-2.28392	-4.45681	err.	0.109315	0.706635	6	6
2	-2.73552	-4.393	err.	0.083265	0.738155	4	4
3						2	6
6	-0.38957	-1.852	err.	0.42334	0.872279	6	6
3	-1.85599	-3.50589	err.	0.827259	0.76004	4	5
0						1	3
0						0	1
6	-0.20163	-1.62761	err.	0.630954	0.92279	5	6
0						0	0
6	-0.50589	-1.85599	2.251539	0.748774	0.789063	4	6
6	-0.20163	-0.87184	0.415037	0.715001	0.781987	3	6

Diabetes

6	-1.36177	-2.40599	-0.72247	0.006485	0.044921	6	6
6	-0.05658	-0.67807	0.535332	0.87278	0.958113	6	6
1	-2.08746					2	2
1	0.120294					5	5
6	0	-0.7137	0.556393		1 0.996445	6	6
6	-0.09761	-0.46467	0.304006	0.42334	0.827426	6	6
6	-0.09761	-0.4957	0.321928	0.521839	0.827811	6	6
2	0.556393					6	6
0						0	3
6	-0.08406	-0.35614	0.168123	0.630954	0.773248	5	5
0						0	0
5	-0.32193	-0.60407	-0.02857	0.04461	0.389131	6	6
6	0.200913	-0.31034	0.68966	0.42334	0.738155	4	4
6	-0.23879	-1.59455	3.643856	0.748774	0.901338	6	6
6	-0.27501	-0.70487	0.089267	0.200185	0.598791	6	4
2	0.666576	-0.27501	1.514573	0.164915	0.686328	3	0
6	-0.12433	-0.27501	0.029146	0.109315	0.551461	6	6
6	0.494109	-0.07039		1 0.109315	0.51966	6	6
0						0	3
5	0.074001	-0.76553	0.810966	0.881497	0.929089	1	2
6	0.915936	0.713119	1.089267	0.003948	0.019766	6	5
6	0.535332	-0.91839	1.68966	0.42334	0.724735	6	6
6	0.234465	-0.44361	0.736966	0.748774	0.751159	6	6
6	0	-0.25096	0.234465	0.87278	0.995511	6	6
6	0.029146	-0.58496	0.535332		1 0.962866	6	6
3	-0.15056	-0.73985	0.321928	0.296718	0.789856	6	6
3	0.104697	-0.52607	0.643856		1 0.845188	5	6
6	-0.11103	-0.26303	0.029146	0.109315	0.559792	6	6
6	0.217591	-0.55582	0.862496	0.521839	0.795065	6	6
0						1	0
6	0.058894	-0.22651	0.340075	0.521839	0.845188	6	6
6	-0.36737	-0.91073	0.058894	0.100348	0.542228	4	1
0						1	2
2	0.152003	-2.62293	1.514573		1 0.922939	6	6
6	0.666576	-0.1375	1.395929	0.149541	0.539493	5	6
6	0.058894	-0.22651	0.358454	0.630954	0.875653	6	5
6	-0.70487	-0.9486	-0.48543	0.003948	0.010058	6	3
5	-0.07039	-0.105658	0.514573	0.100348	0.930839	6	6
5	-0.29866	-0.74846	0.136062	0.100348	0.62359	4	6
6	-0.07039	-0.18903	0.058894	0.336668	0.6973	6	6
0						1	0
0						6	5
6	-0.18903	-0.50589	0.104697	0.200185	0.668631	6	6

4	-0.12433	-0.5656	0.340075	0.393769	0.809101	6	4
1						6	6
2	0.043943	-0.38957	0.599462	1	0.921039	6	5
6	-0.36737	-0.65992	-0.09761	0.016309	0.254948	6	6
6	-0.09761	-0.25096	0.058894	0.054664	0.636675	5	5
1	0.089267					5	5
6	0.029146	-0.07039	0.136062	0.748774	0.823716	6	6
6	-0.31034	-0.86394	0.184425	0.262332	0.670041	6	6
0						1	1
6	0.043943	-0.72247	0.68966	0.87278	0.959895	6	6
6	0.358454	0.168123	0.535332	0.010406	0.088265	6	5
6	-0.1635	-0.40054	0.074001	0.078169	0.635894	6	6
2	1 err.		2.736966	0.164915	0.766252	5	5
0						4	5
6	0.785875	0.556393	1.029146	0.003948	0.005728	5	6
3	-0.15056	-1.68257	0.713119	0.605577	0.900105	5	4
0						6	5
5	-0.4957	-1.09761	0	0.067889	0.421773	4	4
6	-0.15056	-0.25096	-0.05658	0.010406	0.220321	6	6
4	0.234465	-0.21412	0.68966	0.327187	0.6973	6	6
3	-0.87184	err.	0.304006	0.179712	0.683968	3	0
4	0.168123	-2.39232	1.286304	0.806496	0.914528	6	5
6	-0.1375	-0.36737	0.074001	0.200185	0.662915	6	6
4	-0.73118	-1.90689	0.168123	0.141645	0.545614	5	4
6	0.0145	-0.64155	0.535332	0.87278	0.980163	6	5
6	0.321928	-0.08406	0.68966	0.262332	0.562595	6	5
6	-0.26303	-0.68706	0.104697	0.149541	0.625229	6	6
0						4	1
6	-0.1375	-0.34483	0.074001	0.109315	0.645808	6	4
5	-0.50589	-1.02857	-0.02857	0.02846	0.394176	6	6
6	-0.22651	-0.82375	0.286304	0.42334	0.728392	6	6
5	0.089267	-0.51602	0.621488	0.754023	0.887936	6	5
6	-0.59455	-1.08406	-0.1375	0.037373	0.293264	6	4
6	-0.12433	-1.02857	0.862496	0.630954	0.901338	4	3
6	-0.83996	-1.38405	-0.38957	0.010406	0.181017	6	6
6	0.251539	0.120294	0.37707	0.016309	0.094589	6	6
6	-0.47508	-0.57531	-0.36737	0.003948	0.00455	6	4
2	0.321928	-5.83415	1.434403	1	0.847878	6	6
6	0.37707	-0.72247	1.120294	0.748774	0.741537	6	6

TG Mean L TG I-95% C TG u-95% C TG p-value TG FDR

	-0.85599	-2.27501	0.0145	0.109315	0.763195
0.454032	-0.46467	1.217591	0.336668	0.763195	
0.358454	-0.69599	2	0.522431	0.999906	
-0.55582	-1.29278	0.043943	0.109315	0.763195	
0.058894	-0.5656	0.68966	1	0.955004	
0.120294	-0.66903	0.810966	0.855132	0.909684	
0.184425	-0.31034	0.713119	0.669815	0.786415	
0.217591	-2.23266	2.943416	1	0.932007	
1.120294	0.358454	1.68966	0.00617	0.701423	
-0.44361	-1.09085	0.304006	0.273322	0.763195	
0.415037	-0.73118	1.089267	1	0.77755	
-0.12433	-0.85599	0.473931	0.748774	0.883743	

-1.35614

-0.76553

	-0.25096	-0.7137	0.234465	0.336668	0.763195
--	----------	---------	----------	----------	----------

	-0.73118	err.	1.68966	0.245278	0.818591
--	----------	------	---------	----------	----------

-1.55582

	1	0.736966	1.217591	0.003948	0.365914
0.888969	-0.5656	1.736966	0.100348	0.763195	
0.454032	-0.02857	0.971431	0.135593	0.763195	
0.217591	-0.01436	0.454032	0.054664	0.763195	
0.058894	-1.83592	1.395929	1	0.977411	
0.043943	err.	err.	0.723674	0.993463	
0.217591	-0.59455	1.434403	0.465209	0.855796	
-0.40054	-1.04963	0.104697	0.109315	0.763195	
0.621488	0.251539	1	0.019016	0.517455	
-0.42223	-4.04614	1.514573	0.512691	0.8352	
0.321928	-1.65535	1.286304	0.563703	0.851631	
-0.18903	-0.65076	0.251539	0.521839	0.779044	
-0.1375	-0.47508	0.152003	0.748774	0.776939	
0.556393	0.395929	0.713119	0.003948	0.029011	
-0.08406	-0.41143	0.200913	0.393769	0.851631	
0.286304	-0.07039	0.621488	0.078169	0.763195	
-0.43296	-0.91073	0.200913	0.144127	0.763195	
0.058894	-0.07039	0.200913	0.630954	0.792604	
0.152003	-0.20163	0.454032	0.336668	0.772799	
-0.37851	-1.40599	0.434403	0.630954	0.767957	
0.089267	-0.35614	0.434403	0.262332	0.880556	

0.089267	-0.1635	0.358454	0.262332	0.791465
-0.79909	-1.3505	-0.36737	0.003948	0.330369
0.152003	-0.69599	0.810966	0.521839	0.886947
0.217591	-0.63227	0.971431	0.42334	0.838564
0.136062	-0.35614	0.68966	0.630954	0.840856
0.184425	-0.23879	0.736966	0.262332	0.78519
0.643856	0.37707	0.888969	0.003948	0.433077
-0.4957	-1.0072	0.089267	0.0771	0.763195
-0.78241	-1.22033	-0.36737	0.003948	0.421603
0.268817	-0.32193	0.915936	0.200185	0.771149
-0.4957	-1.25096	0.043943	0.149541	0.763195
0.321928	-0.5656	2.120294	0.630954	0.820887
-0.61353	-0.95606	-0.26303	0.016309	0.496206
-0.27501	-0.76553	0.200913	0.42334	0.763195
0.915936	0.473931	1.321928	0.025347	0.999906
-1.59455	-2.82985	-0.50589	0.016309	0.64597
0.713119	0.152003	1.434403	0.038867	0.68918
0.621488	-0.17632	1.556393	0.135593	0.763195
-0.07039	-1.08406	1.556393	0.796253	0.9723
0.713119	-1.15056	1.556393	0.521839	0.767163
0.621488	0.043943	1.152003	0.016294	0.763195
-0.08406	-0.63227	0.494109	0.583882	0.917699
0.862496	-0.31034	1.736966	0.144127	0.763195
0.251539	-0.32193	0.666576	0.296718	0.767163
-0.57531	-1.10434	0.029146	0.078169	0.763195
0.535332	0.152003	0.971431	0.024975	0.554626
-0.31034	-0.82375	0.304006	0.336668	0.763195
0.434403				
0	-0.45418	0.473931	1	0.997402
-0.1375	-1	1.251539	0.630954	0.999906
1.556393				
0.136062	-1.23879	1.029146	0.87278	0.932137
-0.22651	-1.02148	0.599462	0.36131	0.833614
-0.31034	-0.57531	-0.05658	0.037373	0.62642
0.321928	-0.58496	0.943416	0.87278	0.784428
0.713119				
0.454032	0.136062	0.761213	0.010406	0.577621
-0.47508				
0.321928	-2.0321	err.	0.669815	0.903524
-0.78241				
0.535332	0.268817	0.810966	0.010406	0.296477
-0.926	-2.5509	1.599462	0.465209	0.999906
-0.25096	-1.32193	0.494109	0.715001	0.818591
0.358454	-0.15056	0.810966	0.037373	0.763195
0	-2.1635	1.089267	1	0.998908
0.454032	0.104697	0.736966	0.054664	0.715184
0.643856	0.286304	1.029146	0.014306	0.999906

0.888969	-1.04264	2.058894	0.288844	0.763195		
0.058894	-0.67807	0.915936	1	0.960983		
0.058894	-0.35614	0.535332	0.715001	0.931645		
0.785875	-0.02857	1.68966	0.037373	0.763195		
0.286304	-0.25096	0.943416	0.42334	0.763195		
-0.53605	-1.34483	0.434403	0.088082	0.763195		
0.089267	-0.57531	0.621488	0.87278	0.917766		
-0.74846	-1.73552	0.358454	0.200185	0.763195		
0.104697	-0.65992	1.029146	0.521839	0.922331		
-0.12433	-1.05658	0.494109	0.220671	0.897795		
-0.09761	-0.57531	0.304006	0.200185	0.874236		
0.494109	-0.50589	1.217591	0.220671	0.763195		
-0.08406	-0.21412	0.043943	0.088082	0.763195		
0.535332	-0.12433	1.395929	0.248213	0.763195		
0.621488						
0.340075	-1.03562	3.184425	0.465209	0.861115		
0.358454	-0.07039	0.785875	0.109315	0.999906		
-0.05658	-0.69599	0.599462	0.87278	0.999906		
0.074001	-0.37851	0.68966	0.393769	0.91589		
0.089267	-0.45418	0.556393	0.273322	0.896788		
0.577767	-1.87578	err.	0.643429	0.840856		
-0.73985	-3.23113	5.058894	0.748774	0.795243		
0.089267	-0.46467	0.68966	0.624206	0.900784		
-0.20163	-0.79909	0.454032	0.583882	0.810897		
3.058894	2.251539	3.836501	0.003948	0.421603		
0.340075	-1.09085	1.395929	0.796253	0.829694		
0.200913	0.043943	0.358454	0.016309	0.715184		
0.286304						
0.200913			1	0.970135		
3.184425	2.943416	3.473931	0.0455	0.123198		
0.473931	-0.21412	1.473931	0.135593	0.763195		
0.029146	-0.40054	0.535332	1	0.962227		
2.251539	1.286304	3.184425	0.003948	0.999906		
-0.11103	-1.22033	0.666576	0.4795	0.92251		
-0.1635	-0.51602	0.184425	0.200185	0.767862		
0.074001	-0.34483	0.434403	0.669815	0.895182		
-1.33342	-5.09466	0.089267	0.083265	0.763195		
0.029146	-0.54597	0.494109	0.630954	0.974171		
-0.55582	-1.45943	0.104697	0.109315	0.763195		
-0.95606	-1.66903	-0.33342	0.02828	0.554626		
-0.72247	-1.42223	-0.21412	0.010406	0.554626		
0.286304	-0.59455	1.286304	0.465209	0.809214		

-0.26303	-1.09761	0.535332	0.630954	0.802148
-0.76553	-1.5656	0.37707	0.141645	0.763195
-0.96347	-1.852	-0.12433	0.020921	0.763195
0.395929	-3.45812	2.395929	0.643429	0.875901
-0.1635	-0.58496	0.268817	0.630954	0.78519
0.415037	-1.79909	4.058894	0.42334	0.859691
0.136062	-1.43296	1.599462	0.715001	0.940999
-0.774	-1.43829	0.415037	0.3017	0.999906
-0.18903	-0.91839	0.358454	0.262332	0.816389
-0.05658				
-0.21412	-0.65992	0.200913	0.327187	0.763195
-0.37851	-0.848	0.074001	0.100348	0.763195
-1.02148	-2.04264	1.217591	0.521839	0.763195
0.286304	-0.20163	0.810966	0.10105	0.763195
-0.36737	-1.03562	0.434403	0.36131	0.767163
1.321928	0.136062	2	0.064078	0.763195
-1.36177	-2.73335	-0.1635	0.024975	0.763195
0.120294	-2.70487	1.888969	0.723674	0.961334
0.251539	0.0145	0.494109	0.037373	0.715184
-0.7137				
0.68966	0.234465	1.217591	0.016309	0.999906
-1.0072				
0.473931	-1.91073	err.	1	0.851631
0.494109	-0.44361	1.736966	0.200185	0.763195
0.268817	-0.42223	1.556393	0.630954	0.808592
-0.12433	-0.45418	0.184425	0.336668	0.783541
0.514573	-0.23879	1.888969	0.200185	0.763195
0	-0.36737	0.37707	0.881497	0.999963
0.666576	-0.09761	1.251539	0.149541	0.763195
0.514573	-0.42223	1.736966	0.200185	0.763195
-0.21412	-0.75702	0.494109	0.462433	0.803688
2.120294	1.434403	2.643856	0.003948	0.481211
-0.79077	-1.70929	-0.07039	0.02828	0.735303
-0.08406	-0.40054	0.184425	0.583882	0.819357
-0.18903	-0.79909	0.358454	0.521839	0.800469
0.074001	-0.74846	0.736966	0.748774	0.947873
0	-0.51602	0.434403	0.42334	0.996126
0.168123	-0.73118	0.888969	0.630954	0.876471
-0.18903	-0.94111	1.029146	0.715001	0.890653
0.251539	-0.08406	0.621488	0.054664	0.763195
-0.01436	-0.40054	0.321928	0.521839	0.974506
0.251539	-0.05658	0.514573	0.109315	0.763195
0.321928	-0.20163	0.915936	0.149541	0.763195

0.0145	-0.75702	1.251539	0.87278	0.998053
0.473931	-0.18903	1.058894	0.157299	0.763195
-0.17632	-0.40054	0.058894	0.109315	0.763195
-0.85599	-6.22362	err.	1	0.885512
1.029146	-1.17632	2.643856	0.12663	0.763195
0.234465	0.0145	0.454032	0.109315	0.763195
0.200913	0.074001	0.321928	0.010406	0.512827
-0.32193	-0.91073	0.535332	0.521839	0.776423
0.577767	0.043943	1.184425	0.055009	0.735303
0.200913	-0.22651	0.68966	0.144127	0.771888
0	-0.59455	0.713119	0.715001	0.998908

-0.51602				
-1.37851	-2.30451	-0.58496	0.006485	0.524901
-1.1635	-1.87971	-0.51602	0.016309	0.512827
-1.15704	-1.9782	-0.45418	0.016309	0.512827
-1	-2.02857	-0.27501	0.037373	0.554626
0.234465	-0.09761	0.577767	0.109315	0.999906
-0.09761	-0.54597	0.286304	0.630954	0.865468
-0.20163	-1.28096	0.599462	0.465209	0.858183
0.556393	-0.17632	1.152003	0.109315	0.763195
-0.80735	-1.51602	-0.17632	0.078169	0.632637
0.136062	-0.75702	0.836501	0.521839	0.903524
0.971431	-0.66903	2.251539	0.42334	0.999906
-0.774	-1.44489	-0.20163	0.054664	0.554626
-1.82375	-2.72247	-0.9855	0.003948	0.512827
-0.74846	-1.51096	0.120294	0.201243	0.763195
-0.1635	-0.78241	0.577767	0.583882	0.852165

-0.18903	-0.75702	0.234465	0.715001	0.78519
0.058894	-0.73985	0.810966	0.624206	0.956801
0.168123	-0.18903	0.473931	0.42334	0.767163
0.089267	-0.64155	0.621488	0.881497	0.913543
-0.64155				
-0.22651				
-0.07039	-0.37851	0.304006	0.624206	0.893883
-0.57531	-1.09761	0.029146	0.078169	0.763195
-0.29866	-0.79077	0.152003	0.144127	0.763195
-0.22651	-1.28688	0.621488	0.522431	0.849158
-0.28688	-1.09761	0.666576	0.462433	0.799948
0.395929	0.152003	0.666576	0.00617	0.512827
0.168123	-0.23879	0.514573	0.262332	0.782639
0.415037	-0.01436	0.915936	0.054664	0.763195

-1.97453					
-0.01436	-0.69599	0.556393	1	0.992821	
-2.68257	-4.4019	-1.1177	0.135593	0.683465	
-1.96347	-3.66789	-0.28688	0.02828	0.763195	
-2.17313	-4.12516	-0.46467	0.037373	0.763195	
-1.4489	-2.72465	0.074001	0.024975	0.763195	
0.268817	err.	5.643856	0.522431	0.930483	
0.836501	-0.26303	3.473931	0.141645	0.763195	
0.643856	err.	4.058894	0.715001	0.851726	
	0				
-1.78241	-4.40463	0.168123	0.088082	0.763195	
-0.41143	-4.02326	3.836501	0.465209	0.881933	
-1.23879	-3.1635	1.395929	0.438578	0.763195	
-1.82375	-3.2854	-0.08406	0.078169	0.763195	
1.473931	err.	err.	0.200185	0.763195	
1.152003	-3.09592	err.	0.36131	0.767163	
0.268817	err.	1.358454	0.563703	0.902064	
-0.43296	-2.81762	err.	0.855132	0.886947	
1.321928					
0.761213	-2.89336	3.184425	0.42334	0.787079	
0.268817	-2.82375	err.	0.521839	0.931665	
0.058894	-2.926	err.	1	0.988708	
0.621488					
-1.25096	-3.20789	err.	0.250592	0.763195	
-2.40599	-4.37226	-0.73118	0.024975	0.739374	
1.643856	-0.65992		0.054664	0.763195	
2.058894	-0.90304	err.	0.078169	0.763195	
1.321928	-1.58496	err.	0.196706	0.763195	
-1.48027	-2.82985	0.643856	0.149541	0.763195	
-1.26903	-2.28688	-0.15056	0.100348	0.763195	
1.058894	err.	err.	0.354539	0.767957	
1.286304	err.	err.	0.200185	0.767163	
-1.08406	-2.488	1.599462	0.521839	0.763195	
-0.94111	-2.29572	2.736966	0.855132	0.767163	
-0.774	-4.2502	err.	1	0.807939	
0.810966	-1.09761	2.943416	0.248213	0.763195	
	0	-2.1177	err.	1	0.999402
-0.32193	-1.84398	2.251539	1	0.882045	
1.286304	-0.87184	err.	0.201243	0.763195	

0.058894	-2.53854	3.836501	0.87278	0.986058
0.268817				
-1.67356	-3.46989	1.556393	0.149541	0.763195
-1.56071	-2.71149	0.836501	0.067889	0.763195
-1.83188	-3.54102	1.321928	0.078169	0.763195
-2.06005	-3.37434	err.	0.179712	0.763195
0.915936	-1.65076	err.	0.275234	0.767163
1.089267				
0.888969	-0.67807	2.473931	0.273322	0.763195
1.68966	err.	err.	0.149541	0.763195
-0.1635	-1.63691	1.836501	0.87278	0.934859
0.0145	-1.36737	2.251539	0.630954	0.996126
-0.63227	err.	err.	0.715001	0.876471
0.0145	-3.34199	5.643856	0.715001	0.998908
-0.28688	-1.57046	2.473931	1	0.893883
-0.43296				
-0.44361				
0.395929	-1.47508	3.321928	0.521839	0.852364
0.514573	-0.88753	2.473931	0.42334	0.78519
0.666576	-1.38957	5.643856	0.220671	0.783843
-0.79909				
-1.23879	-2.848	1.943416	0.12663	0.763195
0.888969	-1.02857	4.321928	0.200185	0.763195
0.971431	-1.26903	err.	0.201243	0.763195
1.321928	-0.90304	2.943416	0.262332	0.763195
-0.58496	-2.28392	err.	0.87278	0.837159
-1.81558	err.	err.	0.630954	0.772799
-0.87971			0.563703	0.807939
-0.61353	err.	err.	0.643429	0.851631
1.434403	err.	6.643856	0.296718	0.763195
-0.41143	err.	err.	1	0.913543
0.286304	-1.5656	4.643856	0.630954	0.902763
0	-3.12433	err.	0.77283	0.999727
1.599462	0.358454	2.943416	0.095581	0.707288
1.736966	-1.05658	err.	0.054664	0.763195
0.736966	-2.33056	4.643856	0.462433	0.78519
0.862496				
1.395929	-0.23879	3.473931	0.100348	0.763195
-0.32193	-1.94486	err.	1	0.914913
0.168123	-0.20163	0.556393	0.3017	0.767957

-1.0072	-1.848	-0.26303	0.037373	0.62642
0.029146	-0.47508	0.494109	0.748774	0.999906
0.074001	-1.26303	err.	1	0.970269
0.321928	-0.73985	1.643856	0.250592	0.817787
0.104697	-0.87184	1	1	0.932007

-0.41143	-0.79077	-0.02857	0.109315	0.763195
-0.4957	-0.93357	0	0.149541	0.763195
1.251539	-1.36177	2.251539	0.078169	0.763195

-0.1375	-0.87971	0.736966	0.464702	0.897799
---------	----------	----------	----------	----------

-0.59455	-1.3505	0.074001	0.149541	0.763195
----------	---------	----------	----------	----------

0.136062	-0.41143	0.810966	0.563703	0.861276
0.713119	-0.64155	2.643856	0.149541	0.763195
-0.37851	-0.7137	-0.08406	0.010515	0.707288

-0.31034	-0.70487	0.089267	0.149541	0.763195
0.251539	0.043943	0.454032	0.037373	0.664768

0.37707

-0.67807	-3.37573	0.556393	0.144127	0.763195
-0.31034	-1.36737	1.785875	0.87278	0.866711
0.200913	-0.50589	0.836501	0.42334	0.832924
-0.01436	-0.32193	0.286304	1	0.980376
-0.34483	-1.02857	0.268817	0.149541	0.763195
-0.40054	-0.93357	0.184425	0.262332	0.763195
-0.20163	-0.65076	0.286304	0.583882	0.780135
-0.35614	-1.02857	0.184425	0.149541	0.763195
0	-0.73118	0.761213	0.87278	0.998908

-0.50589	-1.5656	0.217591	0.336668	0.763195
----------	---------	----------	----------	----------

-0.04264

-0.09761

0.029146	-0.42223	0.599462	0.630954	0.97174
----------	----------	----------	----------	---------

-0.17632	-1.26303	1.68966	0.855132	0.919059
----------	----------	---------	----------	----------

0.120294	-0.64155	0.713119	1	0.893997
----------	----------	----------	---	----------

3.058894	err.	4.643856	0.070701	0.763195
----------	------	----------	----------	----------

-0.33342	-1.07724	0.268817	0.336668	0.763195
----------	----------	----------	----------	----------

0.888969	-0.73118	2.184425	0.200825	0.763195
----------	----------	----------	----------	----------

-0.22651	-0.926	0.321928	0.200185	0.786862
----------	--------	----------	----------	----------

-0.80735	-1.81558	0.514573	0.36131	0.763195
----------	----------	----------	---------	----------

0.0145	-0.15056	0.200913	0.630954	0.980376
--------	----------	----------	----------	----------

-0.35614	-0.774	0.058894	0.135593	0.763195
-0.55582	-1.07724	0	0.109315	0.763195
-0.17632	-0.58496	0.286304	0.273322	0.786415
0.321928	-1.5509	1.152003	0.336668	0.848376
0.029146	-1.03562	0.666576	0.916815	0.980376
0.234465	-0.60407	0.862496	0.754023	0.813247
0.104697	-0.32193	0.494109	1	0.852321
0.029146	-0.9782	0.915936	0.87278	0.98954
0.251539				
0.074001	-0.35614	0.599462	0.630954	0.905087
0.37707	-0.22651	0.971431	0.201243	0.763195
-0.29866	-0.86394	0.168123	0.149541	0.763195
0.217591	-1.05658	2.643856	0.347208	0.90782
0.736966	-0.21412	1.434403	0.086411	0.763195
1.120294	0.358454	1.68966	0.00617	0.701423
-0.5656	-1.01436	-0.01436	0.086411	0.763195
-0.45418	-0.96347	0.0145	0.100348	0.763195
-0.1375	-0.38957	0.089267	0.248213	0.763195
-0.01436	-0.37851	0.340075	0.87278	0.98577
0.340075	-0.83996	1.217591	0.748774	0.804239
0.268817	-0.78241	1.029146	0.201243	0.820887
-0.46467	-1.39506	0.217591	0.149541	0.763195
-0.45418	-0.88753	-0.04264	0.086411	0.739374
0	-0.87971	0.713119	0.715001	0.999322
-0.36737	-1.36737	0.666576	0.465209	0.78519
-0.67807	-1.70044	-0.04264	0.037373	0.763195
-2.02148				
0.089267	-0.78241	0.836501	0.669815	0.934859
-0.43296	-1.01436	0.120294	0.054664	0.763195
-0.42223	-1.1375	0.251539	0.200185	0.763195
-0.42223	-0.94111	0.089267	0.100348	0.763195
-0.58496	-1.18903	0.217591	0.286422	0.763195
-0.27501	-1.03562	0.915936	0.4795	0.818591
-0.58496	-1.31034	0.089267	0.149541	0.999906
-0.07039	-1.20789	0.943416	0.748774	0.966516
0.217591	-0.81558	2	0.393769	0.883743
1.736966	-0.57531	2.736966	0.024975	0.763195
0.120294	-0.58496	0.785875	0.521839	0.89524

Freeman et al. Supplemental Table 2

This document contains all proteomic da

SN Diabetic-Control
DRG Diabetic-Control
TG Diabetic-Control

Column headings are as follows:

Accession
Name
Peptides
Spectra
Mean Log₂ Ratio
l-95% CI
u-95% CI
IFDR
gFDR

ta in 3 sheets as follows:

Data from the sciatic nerve of streptozotocin-diabetic rats in comparison to healthy controls

Data from the dorsal root ganglia of streptozotocin-diabetic rats in comparison to healthy controls

Data from the trigeminal ganglia of streptozotocin-diabetic rats in comparison to healthy controls

UniProt accession number

Protein Name

Number of peptides for this protein

Number of spectra for this protein

The inferred mean \log_2 ratio for this comparison

The lower 95% credible interval

The upper 95% credible interval

Local false discovery rate for the one-sided Bayesian test on this protein (direction of the test is given by the sign of th

Global false discovery rate for the set of tests from the top of the spreadsheet to this entry. Where the FDR of this tes

e Mean Log₂ Ratio)

it is tied with others, the greatest gFDR of these entries should be taken

Accession	Name	Peptides	Spectra	Mean Log ₂ F	I-95% CI	u-95% CI	IFDR
sp P14046	Alpha-1-inh	13	30	-2.281154	-2.717715	-1.846525	0
tr Q5BKC4	C9 protein (C)	7	10	-0.793182	-1.013777	-0.563367	0
sp P01026	Complement C1q	50	100	-0.8821	-1.145616	-0.625892	1.25E-05
sp Q03626	Murinoglobin	18	33	-1.066785	-1.429025	-0.719474	1.25E-05
sp P12785	Fatty acid synthase	52	100	-0.638085	-0.846854	-0.432447	5E-05
tr Q68FY4	Group specific protein	26	50	-0.816746	-1.112522	-0.522832	7.5E-05
sp P31232	Transgelin (SMA)	12	45	-0.940675	-1.288807	-0.598326	8.75E-05
sp P08649	Complement C1s	5	6	-0.569335	-0.790179	-0.356773	0.000125
tr F1LR41	F Uncharacte	17	47	-0.711885	-0.988149	-0.421971	0.000175
sp P29826	Rano class I	2	3	-0.739445	-1.015277	-0.457204	0.000175
sp P62963	Profilin-1 O-type	11	31	-0.217966	-0.281104	-0.158066	0.0001875
sp P02770	Serum albumin	33	100	-0.521236	-0.726884	-0.313951	0.0002
tr B1WBS6	Glb1l protein	1	5	-0.467472	-0.616477	-0.306679	0.0002
tr D3Z8Y5	I Uncharacte	13	28	-0.764808	-1.085244	-0.442248	0.0002125
sp P20059	Hemopexin	21	49	-1.04607	-1.459215	-0.617238	0.000225
tr D3ZC54	I Uncharacte	2	5	-0.915909	-1.2834	-0.553127	0.000225
tr Q923Z2	Tropomyosin	3	7	-0.755547	-1.058266	-0.439409	0.0002375
sp Q63041	Alpha-1-macroglobulin	33	72	-0.867768	-1.251217	-0.499712	0.0002875
tr D3ZJ95	C Uncharacte	14	31	-0.740159	-1.046925	-0.42869	0.0002875
tr Q5I0M1	Apolipoprotein A-I	8	14	-0.561702	-0.788063	-0.339274	0.0003
tr D3ZXX2	I Uncharacte	54	100	-0.469293	-0.658713	-0.281143	0.000325
sp P16303	Carboxylester lipase	14	29	-1.575787	-2.27726	-0.871514	0.0003375
tr D4A7U1	Uncharacte	6	8	-0.360778	-0.488416	-0.230553	0.00035
sp P02680	Fibrinogen gamma chain	5	6	-0.717955	-1.034112	-0.419484	0.0004
tr D3ZZX3	I Uncharacte	32	59	-0.308126	-0.42422	-0.188592	0.000475
sp P36953	Afamin OS=	19	33	-0.641912	-0.947464	-0.344972	0.0005125
sp O35413	Sorbin and SH3 domain protein	2	3	-0.675928	-0.999833	-0.367296	0.0005375
sp Q63556	Serine protease inhibitor	7	11	-0.765822	-1.085544	-0.420049	0.0005875
sp P81155	Voltage-dependent K channel	5	13	0.3619773	0.2196575	0.5030236	0.000625
sp P24368	Peptidyl-prolyl-cis-trans isomerase	10	22	-0.413392	-0.592468	-0.240778	0.0006625
tr Q5RJR9	Serine (Or threonine) kinase	12	24	-0.462945	-0.668063	-0.253342	0.0006875
sp P20788	Cytochrome P450 2D6	7	15	0.2881161	0.1705463	0.407205	0.0007375
sp P06761	78 kDa glucosidase	23	42	-0.377969	-0.544216	-0.216542	0.0007625
sp Q9QXQ0	Alpha-actinin	22	43	-0.338512	-0.47875	-0.195392	0.0008
sp P18292	Prothrombin	10	16	-0.47749	-0.687364	-0.255174	0.000825
tr F1LQX0	F Uncharacte	8	16	-1.220326	-1.850752	-0.568682	0.0008625
sp P58775-	I Isoform 2 of	5	14	-0.762049	-1.123482	-0.410633	0.000875
sp Q62812	Myosin-9 O isoform	52	100	-0.31164	-0.441644	-0.186528	0.000975
tr D3ZFC6	I Uncharacte	19	38	-0.589273	-0.87174	-0.309539	0.0009875
sp Q5RJR8	Leucine-rich repeat kinase	3	6	-0.547505	-0.81128	-0.275534	0.0009875
sp Q66HDO	Endoplasmic reticulum protein	22	41	-0.268736	-0.375399	-0.162748	0.0010125
sp P18418	Calreticulin	16	34	-0.343447	-0.493158	-0.197034	0.0010375
tr D3ZUU6	RCG25681 (Uncharacterized)	8	15	-0.376953	-0.554605	-0.213772	0.0010375
sp P11598	Protein disulfide-isomerase	30	62	-0.299893	-0.431644	-0.174186	0.0011375
tr D4ADX5	Uncharacte	1	5	0.3228838	0.1753666	0.4741886	0.0013
sp Q9JI03	Collagen alpha-1(I) chain	3	4	0.5683491	0.2748914	0.8709956	0.0013875
sp Q8VHE9	All-trans-retinol binding protein	6	9	-0.939556	-1.439218	-0.469807	0.0014375
sp Q62736	Non-muscle myosin light chain	19	26	-0.382434	-0.559245	-0.212863	0.00145
sp P54690	Branched-chain aliphatic acyl carrier protein	5	6	0.4303075	0.2109388	0.657178	0.0017

tr D3ZYI8 C Uncharacte	6	13	-0.293786	-0.415673	-0.170421	0.0017
tr F1LZC5 F Uncharacte	3	7	0.4127086	0.2100579	0.6179222	0.0017625
tr Q6PDV8 RCG31311 C	4	8	-0.400005	-0.595939	-0.208881	0.0018
sp P52555 Endoplasmic	4	5	-0.401201	-0.621591	-0.198241	0.0018125
sp P07150 Annexin A1	22	52	-0.610721	-0.9359	-0.276287	0.00185
sp Q9Z1P2 Alpha-actini	21	38	-0.410186	-0.608706	-0.207608	0.0019
sp P01015 Angiotensin	6	11	-0.642059	-0.983974	-0.290353	0.00195
sp Q61RK9 Plasma glut	8	23	-0.540015	-0.812296	-0.254733	0.0019625
tr D3ZFF3 C Uncharacte	7	10	-0.44467	-0.677936	-0.224818	0.0022125
sp Q5BK63 NADH dehy	9	15	0.3027265	0.1573756	0.4511054	0.0022625
sp P02650 Apolipoprot	8	15	-0.608947	-0.953789	-0.282407	0.0023
sp Q63081 Protein disu	10	23	-0.329519	-0.478544	-0.174405	0.00245
tr F1LSF5 F Uncharacte	13	27	-1.247729	-1.998441	-0.512304	0.0024875
sp B0K020 CDGSH iron	4	8	0.4223658	0.2032897	0.6430963	0.0027125
tr F1LQL3 F Uncharacte	8	12	-0.257524	-0.377662	-0.133533	0.0027875
sp Q641Z6 EH domain-	8	17	-0.379535	-0.58534	-0.178079	0.002925
tr F1M4U5 Uncharacte	10	16	0.2866664	0.1512877	0.4188559	0.0029875
sp Q5XIF3 I NADH dehy	5	5	0.3944716	0.1857703	0.6066018	0.0029875
sp P38983 40S riboson	9	17	-0.303099	-0.451749	-0.15736	0.0032625
sp Q4AEF8 Coatomer s	12	18	-0.315908	-0.482656	-0.152207	0.0033125
sp P52944 PDZ and LIN	5	7	-0.413674	-0.637872	-0.181741	0.0035125
tr F1LZ56 F Uncharacte	8	14	-0.688428	-1.104296	-0.278273	0.00385
tr F1LST5 F Uncharacte	1	3	-0.348267	-0.521716	-0.166197	0.00395
tr F1LRK8 F Uncharacte	11	22	-0.187189	-0.268108	-0.107577	0.0040125
sp Q01177 Plasminoge	16	24	-0.448362	-0.711814	-0.186222	0.0041
tr F1M983 Uncharacte	7	9	-0.420552	-0.658673	-0.182441	0.0041125
sp P68035 Actin, alpha	2	3	-0.546673	-0.878649	-0.216982	0.004125
sp P34058 Heat shock	18	36	-0.186298	-0.26648	-0.10617	0.0041875
sp Q63798 Proteasome	5	6	-0.393394	-0.628389	-0.164562	0.0042125
sp P38659 Protein disu	11	13	-0.501837	-0.795257	-0.206302	0.0043125
tr Q7TQ11 Aa1018 OS=	5	7	-0.576029	-0.925986	-0.226073	0.004625
sp P52873 Pyruvate ca	16	20	-0.495619	-0.795874	-0.204685	0.0046375
sp Q9R1Z0 Voltage-dep	4	7	0.3583888	0.164359	0.554733	0.0046875
sp Q9Z2L0 Voltage-dep	9	19	0.4152614	0.170878	0.6524173	0.0047125
tr D3ZIA3 C Uncharacte	6	8	-0.280259	-0.43742	-0.132198	0.004775
tr F1MAG6 Uncharacte	15	32	-0.428821	-0.683284	-0.173873	0.0048
sp P47819 - Isoform 2 o	5	9	-0.354781	-0.531152	-0.173498	0.0048125
tr B2GV72 Carbonyl re	2	6	-0.422566	-0.667624	-0.17477	0.0048375
tr B2RZ44 E N-acetyltra	1	2	-0.350226	-0.55733	-0.150709	0.00495
sp Q64611 Cysteine sul	4	7	-0.673553	-1.112057	-0.244346	0.0049875
sp P27952 40S riboson	10	18	-0.27559	-0.422894	-0.132531	0.005025
tr Q5BJT9 C Creatine kir	8	11	0.3494003	0.1369522	0.5758505	0.0051625
sp P62630 Elongation f	15	55	-0.254568	-0.386337	-0.120467	0.0052125
sp O08619 Coagulation	5	11	-0.454166	-0.719968	-0.177676	0.0052125
tr B6DYQ7 Glutathione	9	28	0.2003953	0.1028421	0.2998646	0.00525
tr D3ZQN7 Uncharacte	34	56	0.409908	0.1664886	0.6539064	0.0052625
tr Q6AYJ9 C ADP-ribosyl	8	16	0.3459108	0.1460611	0.5402226	0.005325
sp Q62920 PDZ and LIN	4	7	-0.416292	-0.661633	-0.17341	0.0053625
sp P17077 60S riboson	1	4	-0.308046	-0.476165	-0.131523	0.0054
tr D3ZG43 NADH dehy	4	9	0.3947214	0.1691553	0.6305893	0.0054125

tr F1M614 Uncharacte	66	100	0.4981962	0.1876053	0.8135027	0.00545
sp Q8VI04 L-asparagin	9	19	-0.172555	-0.246116	-0.10163	0.0054875
sp Q6MG61 Chloride int	4	10	-0.275091	-0.419951	-0.132616	0.005725
sp P17425 Hydroxyme	11	17	-0.293184	-0.44909	-0.134314	0.00585
sp Q06647 ATP synthas	10	23	0.2350845	0.119628	0.3535386	0.0058625
sp P13941 Collagen alp	5	7	-0.449788	-0.720478	-0.161127	0.0061125
tr F1LZW6 Uncharacte	2	3	0.455345	0.1630685	0.7583066	0.0062125
tr D3ZV82 Uncharacte	2	4	-0.48822	-0.793686	-0.176238	0.0063875
tr B6DYQ4 Microsomal	2	3	-0.998079	-1.665963	-0.291563	0.0064375
sp P05545 Serine prote	13	30	-0.597873	-1.000537	-0.205486	0.006625
sp P12346 Serotransfe	2	11	-0.535964	-0.873499	-0.195587	0.0067875
tr F1LQD5 Uncharacte	2	3	-0.610309	-1.034449	-0.210506	0.006825
tr F1LM05 Uncharacte	10	28	-0.739447	-1.242795	-0.224707	0.006925
tr D3ZUM2 Sterile alph	4	5	0.5048986	0.1725296	0.8383848	0.0069625
sp P47875 Cysteine an	10	18	-0.238964	-0.359167	-0.112889	0.007
sp Q9WV78 Plasmalem	1	2	-0.438255	-0.713924	-0.158497	0.0072125
sp Q5XF0 Transgelin-	13	38	-0.393169	-0.630264	-0.145324	0.0073125
sp O35179 Endophilin-	8	13	0.2923426	0.120939	0.4667481	0.007375
sp P20595 Guanylate c	3	4	-0.464042	-0.742118	-0.169891	0.0075375
tr D3ZUM4 Beta-galact	5	9	-0.409139	-0.674201	-0.15876	0.007775
sp Q7TQ16 Cytochrome	4	8	0.3097907	0.1202044	0.4973349	0.0078375
tr D4AOY1 Uncharacte	14	20	-0.45349	-0.753381	-0.164059	0.0079375
sp P10888 Cytochrome	6	13	0.2985928	0.1225222	0.4728599	0.008025
sp P01048 T-kininogen	6	15	0.4361191	0.1620153	0.7199508	0.0080625
sp P14141 Carbonic an	16	74	-1.306517	-2.287319	-0.350127	0.008075
sp P19511 ATP synthas	5	10	0.2557681	0.1113123	0.4001561	0.008125
tr D4A0S8 Uncharacte	3	5	-0.253258	-0.396414	-0.113989	0.00815
sp Q6AYS7 Aminoacyla	9	19	-0.283851	-0.447164	-0.121958	0.0082875
sp P29314 40S riboson	11	17	-0.243116	-0.377195	-0.106931	0.008325
tr Q66HI5 Ferritin OS=	6	10	0.3084232	0.1223653	0.4950583	0.0083375
tr Q5XFV4 Fabp4 prote	10	36	-0.951369	-1.653075	-0.271367	0.00835
tr B5DF91 ELAV (Embr	4	5	-0.286937	-0.459916	-0.121141	0.0084375
sp P84100 60S riboson	4	4	-0.271798	-0.432538	-0.112882	0.0086625
tr Q6P9Y4 Solute carri	5	11	0.4504522	0.1521693	0.7495853	0.00885
sp Q9Z0W7 Chloride int	6	7	-0.232582	-0.360834	-0.104809	0.0089125
sp P11980 Pyruvate kin	4	13	0.4318806	0.1456952	0.729655	0.0092375
sp P50878 60S riboson	10	18	-0.235578	-0.372122	-0.105535	0.0092375
tr Q8K3R4 30 kDa adip	1	2	-0.549486	-0.944557	-0.149831	0.00925
sp P85972 Vinculin OS=	51	100	-0.256078	-0.403797	-0.112609	0.0093375
tr D3Z913 Uncharacte	20	28	0.2778033	0.1114751	0.4446014	0.0097
sp Q6AXV4 Sorting and	3	6	0.4128461	0.1274536	0.6891556	0.010075
sp P25093 Fumarylace	6	6	-0.564978	-0.96958	-0.169744	0.010275
sp O88644 Grifin OS=R	1	2	-1.250422	-2.210343	-0.278065	0.0103875
tr D3ZX87 Uncharacte	5	6	-0.255742	-0.41166	-0.107093	0.0109375
tr F1LN18 Uncharacte	9	11	-0.288473	-0.468067	-0.104503	0.0109625
sp Q01129 Decorin OS=	18	100	0.1817428	0.0885079	0.2712896	0.011025
sp P85973 Purine nucle	12	32	-0.358752	-0.595173	-0.122799	0.011025
sp P04636 Malate deh	16	59	0.1839511	0.0880399	0.2783689	0.0110375
sp Q5RKI0 WD repeat-	18	33	-0.155547	-0.22787	-0.08459	0.01105
tr Q4QQV0 Tubulin, bet	4	5	-0.325578	-0.538086	-0.107996	0.0111

sp P04041 Glutathione	6	10	-0.373205	-0.62682	-0.119714	0.011125
tr F1M6Q3 Uncharacte	5	10	0.6097628	0.1603541	1.0580384	0.011115
sp Q63355 Myosin-Ic C	35	59	-0.16486	-0.242578	-0.087392	0.0111875
sp Q1WIM3 Cell adhesic	7	16	0.3755462	0.1211352	0.6314692	0.0115125
sp P24090 Alpha-2-HS-	13	62	-0.404906	-0.690128	-0.130299	0.01155
sp P07340 Sodium/pot	8	19	0.5863758	0.156513	1.0254922	0.011775
sp P04797 Glyceraldehy	21	85	0.3522407	0.1200999	0.5940782	0.0118375
sp P61265 Syntaxin-1B	4	6	0.4454611	0.1287949	0.7588457	0.0121125
tr B7X6I3 B C38 protein	6	9	0.4960115	0.1417845	0.8810871	0.0122
sp Q5XIH7 Prohibitin-2	16	26	0.2868736	0.1009291	0.4676197	0.012775
tr F1M7I8 f Uncharacte	2	5	-0.743326	-1.294682	-0.156418	0.0128125
tr F1M957 Uncharacte	3	7	-0.380577	-0.65401	-0.114428	0.013125
tr D3ZUX5 Coiled-coil-l	2	3	0.3832402	0.1068014	0.6524531	0.01335
tr F1M2X2 Uncharacte	16	32	0.2590595	0.1009017	0.4223204	0.013375
tr D3Z7Y9 l Uncharacte	3	4	-0.776235	-1.332352	-0.177415	0.0134
sp P07151 Beta-2-micr	4	6	-0.401579	-0.678706	-0.115087	0.0135375
sp Q6IUR5 Neudesin O	3	5	-0.367258	-0.635623	-0.105958	0.0136
sp O35077 Glycerol-3-¶	14	26	-0.439028	-0.75574	-0.11547	0.01365
sp P62278 40S riboson	5	12	-0.207618	-0.325894	-0.085021	0.01365
sp Q68FX0 Isocitrate de	6	12	0.2139536	0.0885	0.3415856	0.013675
sp Q5MPA9 Serine/thre	4	5	0.40798	0.1194269	0.7093924	0.0137
sp Q66H86 Olfactomed	8	16	0.3080767	0.1055937	0.5217255	0.0137625
tr D3ZFH5 l Uncharacte	4	8	-0.301883	-0.509639	-0.096964	0.0137875
sp P60892 Ribose-pho	6	12	0.242174	0.0918442	0.3905369	0.0141
tr D3ZWG4 Uncharacte	10	45	0.5952229	0.1419476	1.0581068	0.0141375
sp Q8VBU2 Protein NDF	6	12	0.2007256	0.0884456	0.3242392	0.0141375
sp Q6B345 Protein S10	3	11	-0.221787	-0.355589	-0.085217	0.0142375
tr D3ZNA6 Microtubule	11	17	0.2383446	0.0924196	0.3799373	0.0143125
sp P11240 Cytochrome	8	20	0.2978941	0.0996273	0.4989676	0.0144625
sp O08730 Glycogenin-	3	7	0.3391415	0.103915	0.5766685	0.0144875
tr Q3MID6 Calumenin (1	2	-0.470425	-0.838751	-0.132041	0.014675
sp Q66HF1 NADH-ubiq	12	21	0.2595586	0.0911775	0.4277794	0.0152125
tr F1M853 Uncharacte	19	22	-0.344201	-0.59916	-0.097886	0.01545
sp P62853 40S riboson	4	6	-0.280933	-0.465252	-0.094623	0.01545
tr B1PLB1 E CD34 antigen	5	7	-0.403257	-0.695938	-0.101921	0.015575
tr D3ZW18 Uncharacte	7	12	0.2932223	0.0969631	0.486847	0.0156125
tr E9PSV0 E Uncharacte	5	6	-0.482809	-0.8555828	-0.108759	0.0157625
sp Q6PDV7 60S riboson	10	24	-0.273083	-0.455435	-0.094709	0.0157875
sp Q63560 Microtubule	15	27	0.2733757	0.0904175	0.4508226	0.0158125
tr O55158 D6.1A prote	2	4	0.3315145	0.095817	0.5609393	0.0158625
sp Q9WUW Complemer	4	6	-0.311279	-0.5173	-0.107515	0.015875
sp Q9EPB1 Dipeptidyl ¶	2	3	-0.417749	-0.737069	-0.099011	0.015925
tr B5DEN5 Eukaryotic t	6	10	-0.184647	-0.286738	-0.081516	0.015975
tr D3ZZ95 l 60S riboson	5	6	-0.235507	-0.373368	-0.091143	0.0160625
sp P00786 Pro-catheps	2	2	-0.380479	-0.68969	-0.102661	0.0162375
tr F1M7F7 Uncharacte	2	2	-0.822828	-1.462263	-0.157611	0.0164
tr F1M9K9 6-phosphog	12	34	-0.178548	-0.279243	-0.081254	0.0165
tr F1LQW3 Uncharacte	4	8	-0.250271	-0.417012	-0.087446	0.0165625
tr Q4KMA8 Erap1 prote	5	5	-0.397948	-0.688704	-0.109727	0.0166
sp P62832 60S riboson	6	15	-0.276377	-0.462243	-0.091116	0.0166375

sp P24054 SPARC-like	3	3	0.4080508	0.1041473	0.6958636	0.01675
sp POCOA9 Small VCP/tp	4	7	0.5880175	0.1098195	1.0602917	0.0172125
sp P97675 Ectonucleot	7	10	-0.274061	-0.470333	-0.086222	0.0174625
tr D3Z9L8 [Uncharacte	2	4	-0.243941	-0.404815	-0.088481	0.017875
sp Q66X93 Staphylococ	8	13	-0.212223	-0.340044	-0.077754	0.018225
sp Q4KLF8 Actin-relate	4	8	-0.23366	-0.383036	-0.082333	0.018325
tr F1LPY9 [Uncharacte	2	3	-0.233132	-0.37797	-0.084287	0.0184625
tr D3ZJP8 [Uncharacte	1	4	-0.595743	-1.078969	-0.095974	0.018575
sp P12075 Cytochrome	3	9	0.2430448	0.0801356	0.4023129	0.0189125
sp P06685 Sodium/pot	23	55	0.4189436	0.098142	0.7531403	0.0194625
sp P60881 Synaptosom	5	7	0.3245822	0.0944356	0.5568294	0.019525
tr B2RYS2 [RCG60159	3	5	0.2628931	0.0804664	0.4452329	0.019825
sp Q64428 Trifunctiona	26	44	0.1635769	0.078544	0.2546096	0.0198875
tr F1LPJ9 [Uncharacte	2	2	-0.500626	-0.915804	-0.099404	0.0199
tr D3ZFS9 [Uncharacte	4	7	-0.360402	-0.622952	-0.097328	0.0201875
tr D4ACL3 [Uncharacte	14	22	-0.287162	-0.495288	-0.081943	0.0204375
tr D3ZSE0 [40S riboson	3	7	-0.352543	-0.617441	-0.086508	0.0206875
sp P15304 Hormone-sen	7	13	-0.598901	-1.12114	-0.099015	0.0207375
sp Q9QZA6 CD151 anti-	9	18	0.5068764	0.0986892	0.9369116	0.02075
sp P62907 60S riboson	5	8	-0.250018	-0.427765	-0.081255	0.020775
tr D4A0T0 [RCG32945	4	5	0.3968051	0.0833553	0.7153523	0.020825
tr Q6AXM6 Intercellulai	1	3	-0.363928	-0.651338	-0.091378	0.0209625
sp P04785 Protein disu	20	36	-0.2498	-0.424419	-0.08092	0.0211125
sp P11951 Cytochrome	4	7	0.2442038	0.0820175	0.4146438	0.0211875
tr D3ZM87 Nebulin (Pro)	13	14	1.1404176	0.083704	2.1946625	0.0213
sp Q6QA69 1-acylglycer	2	3	-0.89187	-1.678605	-0.11771	0.0214375
sp Q9ESM2 Hyaluronan	5	6	0.5858362	0.0559581	1.1391758	0.021475
sp P00507 Aspartate a	18	44	0.1876507	0.0724513	0.3001064	0.02185
tr BOK031 [RCG30479,	6	8	-0.261047	-0.458227	-0.073475	0.021925
sp P05197 Elongation i	27	65	-0.208723	-0.34262	-0.074632	0.0219375
sp B4F795 Choline trar	9	16	0.3952947	0.0769362	0.7170265	0.0219625
tr Q9JKB7 [Guanine de	27	67	-0.296863	-0.511688	-0.073281	0.0220625
tr D3ZZR9 [FK506 bindi	6	10	-0.195818	-0.317397	-0.072661	0.022225
sp Q9JLA3 UDP-glucos	4	4	-0.344642	-0.615977	-0.076373	0.022325
tr Q4FZZ4 [Pyruvate de	12	24	0.1790748	0.0719009	0.284725	0.0229375
sp P21807 Peripherin C	26	100	0.423654	0.0788076	0.7711175	0.0231375
tr F1LQN3 [Uncharacte	14	25	0.2939648	0.0775409	0.5204003	0.0232125
tr Q9WVJ6 Tissue-type	7	9	-0.284301	-0.499934	-0.068861	0.0235625
tr Q5I0M7 Hnrpa1 pro	7	8	-0.234406	-0.401641	-0.069042	0.023775
tr Q5M860 Rho, GDP di	4	7	-0.333459	-0.597267	-0.076388	0.0240625
tr D3ZE37 [Uncharacte	2	3	-0.279459	-0.485772	-0.068385	0.02415
sp Q4V8H8 EH domain-	24	68	-0.27741	-0.47746	-0.065784	0.0242125
sp Q6AYD4 Endothelial	1	2	-0.693532	-1.342272	-0.073027	0.0243125
tr F1M8K0 Uncharacte	15	28	0.256966	0.0697879	0.4375842	0.02445
tr D3Z9Y9 [Uncharacte	3	4	-0.302004	-0.538069	-0.075098	0.024475
tr D3ZN79 Uncharacte	4	5	-0.293119	-0.517983	-0.070394	0.0246
tr Q6IRH6 [Slc25a3 pro	9	17	0.2743698	0.0644091	0.482599	0.0249875
sp P39069 Adenylate k	4	11	0.4624416	0.0710042	0.8514552	0.0250375
sp Q99PD6 Transformir	4	5	-0.397854	-0.716488	-0.07673	0.02505
tr F1LP22 [Uncharacte	2	3	0.3795024	0.0372029	0.8196304	0.0254375

tr D4A3L8 I RCG47053 (3	5	-0.43156	-0.813476	-0.062242	0.0255375
tr F1LSW7 I Uncharacte	3	6	-0.229283	-0.387699	-0.067644	0.025675
tr B5DEH4 I Uap1l1 prot	5	7	-0.284843	-0.504932	-0.070652	0.02575
tr B1H277 I Pgm2 prote	8	9	-0.273588	-0.478303	-0.066978	0.025825
tr D3ZC55 I Heat shock	21	49	0.2165527	0.0722372	0.3667053	0.025875
tr D4A3V2 I NADH dehy	3	6	0.3462561	0.0672533	0.6265532	0.026
sp O08628 I Procollagen	4	4	-0.290563	-0.501984	-0.074826	0.026075
sp P63245 I Guanine nu	6	10	-0.273681	-0.47717	-0.065382	0.0262375
tr D3ZJ82 I Uncharacte	6	14	0.4035155	0.0696923	0.7464525	0.0263375
tr B2RZC1 I Retinol binc	2	2	-1.097796	-2.255865	-0.037849	0.0273
tr B1WBMO I CD9 molecu	9	60	0.543621	0.0560508	1.0265629	0.0274875
tr D4A6F0 I Uncharacte	3	4	-0.315975	-0.585971	-0.059078	0.028275
sp O35142 I Coatomer s	6	10	-0.216533	-0.37735	-0.062892	0.0286
tr E9PTT4 E Uncharacte	5	7	0.2152626	0.0693817	0.365123	0.0287
tr D4A8P1 I Uncharacte	6	15	-0.230866	-0.397285	-0.068876	0.0287625
tr D3ZD09 I Uncharacte	4	6	0.2225675	0.0671942	0.3813482	0.0288125
sp P85969 I Beta-solubl	4	6	0.3712989	0.0474622	0.6882028	0.02885
sp Q924C3 I Ectonucleot	3	3	0.4136343	0.0598833	0.7550708	0.029
tr Q5RK10 I Neuroprote	4	9	-0.269149	-0.468325	-0.058475	0.0290125
sp P19643 I Amine oxid	13	27	0.4405908	0.0576874	0.8279664	0.0290875
tr E9PTV0 E Uncharacte	1	3	0.3085816	0.0637672	0.5635644	0.0291
sp P35053 I Glycan-1 (3	3	-0.276257	-0.497335	-0.068992	0.0291125
sp Q5U211 I Sorting nexi	4	8	-0.199419	-0.337	-0.066828	0.029175
sp Q68FS4 I Cytosol ami	13	27	-0.16819	-0.270395	-0.065476	0.0293625
sp Q6TEK3 I Vitamin K e	1	2	-0.331209	-0.607438	-0.063111	0.0294625
sp P09811 I Glycogen ph	4	5	-0.549107	-1.034485	-0.040095	0.0298375
tr F1LPP9 F Uncharacte	6	10	-0.218751	-0.384252	-0.061919	0.0298875
tr F1LXA0 F Uncharacte	1	3	0.2765701	0.0606681	0.4957173	0.0299375
sp P15999 I ATP synthas	26	53	0.2333675	0.0615672	0.4037186	0.0301375
tr Q6IMZ5 I Tropomodu	5	7	0.2726769	0.0601866	0.481611	0.0301625
tr D3ZS58 I NADH dehy	2	5	0.2728366	0.0562036	0.4826887	0.0302625
sp P61765 I Isoform 2 o	18	36	0.2487183	0.0621047	0.4338916	0.0303
tr F1LSD3 F Integrin bet	50	100	0.2815084	0.0589961	0.5064067	0.030325
sp Q91XU8 I Phosphatid	2	4	0.4657513	0.0329411	0.8827239	0.030575
tr F1LT35 F Uncharacte	5	8	-0.277229	-0.497699	-0.05425	0.030725
tr Q6MG98 I Histocompa	1	2	-1.313151	-2.710722	0.0302809	0.030725
sp P49432 I Pyruvate de	9	20	0.2121033	0.0608663	0.3686595	0.0309
tr F1LNN9 I Uncharacte	7	10	0.2108013	0.0590764	0.3584537	0.0311125
sp Q4FZY0 I EF-hand doi	5	11	-0.210493	-0.347308	-0.069051	0.031125
sp B0BN15 I Olfactomed	5	11	0.3383191	0.049984	0.6136485	0.0313
sp Q00981 I Ubiquitin c	12	46	0.2060632	0.0593224	0.348483	0.031825
sp P21396 I Amine oxid	10	17	0.26561	0.0599248	0.4771861	0.032
sp POC1Q3 I Lysophosph	1	2	0.3299876	0.0531723	0.6234644	0.032175
sp P14669 I Annexin A3	18	34	-0.247361	-0.439904	-0.060108	0.0323
sp Q9EST6 I Acidic leuci	3	5	-0.253879	-0.442652	-0.054691	0.0324375
tr Q5M7T5 I Serine (Or c	18	37	-0.342447	-0.632934	-0.047831	0.032475
sp P62632 I Elongation f	5	7	0.3731514	0.0541727	0.7056637	0.0326625
sp P61314 I 60S riboson	3	4	-0.256485	-0.455202	-0.057199	0.032725
tr D3ZHM9 I RCG53372 (1	2	-0.645951	-1.22511	-0.043574	0.0329125
tr D3ZW56 I Neurofascir	10	14	0.2394601	0.0523337	0.4191243	0.0333875

sp P13638 Sodium/pot	1	2	0.5945133	0.0305381	1.1761716	0.03395
sp Q9R0T3 Dnaj homol	1	2	-0.445784	-0.864915	-0.027333	0.0342
sp Q08420 Extracellula	4	12	0.2175654	0.0568717	0.3818144	0.03475
sp P13221 Aspartate a	17	46	0.1480257	0.0606276	0.23072	0.0348625
sp Q5U2R7 LDLR chape	2	3	-0.298696	-0.539045	-0.034286	0.0349125
sp Q64240 Protein AM	2	6	-0.36639	-0.697554	-0.048341	0.0351125
tr F1M0B2 Uncharacte	2	2	-0.637893	-1.325982	0.006413	0.035525
sp Q9HB97 Alpha-parvi	8	15	-0.183262	-0.314304	-0.057339	0.035775
sp Q9Z2Q1 Protein trar	10	14	-0.202533	-0.353014	-0.055692	0.03585
tr D3ZAF6 Uncharacte	2	5	0.2538816	0.0455945	0.4522972	0.0360625
tr F1MAA7 Uncharacte	40	77	0.2785602	0.0532391	0.5156343	0.0362375
sp P62890 60S riboson	4	5	-0.320422	-0.601572	-0.037462	0.0362375
tr D4A702 Uncharacte	4	5	-0.448014	-0.85361	-0.017204	0.0363
sp Q4KLZ6 Bifunctiona	2	4	-0.256622	-0.463539	-0.051837	0.0363875
tr D4A2A6 Uncharacte	23	37	0.9180442	-0.037115	1.8536547	0.0366
tr D3ZSD1 Uncharacte	17	24	0.2276394	0.0511838	0.3971844	0.0366375
tr B5DEY8 Sorting nexi	2	3	-0.246197	-0.437818	-0.048068	0.036975
tr D4A276 Mitochondr	1	3	0.3727736	0.0242232	0.7186758	0.037
sp Q5XI07 Lipoma-pre	5	7	-0.299905	-0.539743	-0.045947	0.037125
tr D3ZTM3 Uncharacte	6	9	0.1950918	0.0577623	0.3333601	0.03725
tr E9PTI3 Uncharacte	37	67	-0.456176	-0.884771	-0.023398	0.037275
sp P83732 60S riboson	1	2	-0.268859	-0.49088	-0.044003	0.0373375
sp P07722- Isoform S-N	10	21	0.4163307	0.0240258	0.8066762	0.037575
sp Q63377 Sodium/pot	9	20	0.2441377	0.0496334	0.4402119	0.037725
sp P13233 2',3'-cyclic-r	32	100	0.2621528	0.0470408	0.4776585	0.0381875
tr B2GV92 Ptges3 prot	1	4	-0.161359	-0.264091	-0.058182	0.0383875
sp P63055 Purkinje cel	2	7	0.2626887	0.0404156	0.4876501	0.0393125
sp Q66H98 Serum depr	13	21	-0.229737	-0.41614	-0.049705	0.0394625
sp P04639 Apolipoprot	19	38	0.3824669	0.0303715	0.7379279	0.03995
tr B2RZ09 Arginine-ric	1	3	-0.385841	-0.77508	0.008712	0.040225
tr B5DF65 Biliverdin re	5	13	-0.238265	-0.429215	-0.040335	0.0405875
sp Q9JHY2 Sideroflexin	8	15	0.296316	0.0361266	0.5573666	0.04095
sp Q63572 Dual specifi	2	6	0.4645031	0.0103268	0.9082825	0.041
tr D3ZF86 Uncharacte	2	9	0.298661	0.0406527	0.5574652	0.041225
tr F1LQS3 60S riboson	9	18	-0.215533	-0.378933	-0.046744	0.041275
sp O35331 Pyridoxal ki	4	5	-0.33457	-0.63401	-0.034443	0.0413375
tr O70188 Nuclear faci	2	3	-0.319786	-0.613717	-0.028061	0.041475
sp Q64119 Myosin ligh	8	17	-0.183739	-0.312126	-0.054738	0.041825
tr D4A6I2 Uncharacte	4	6	-0.319608	-0.610659	-0.036197	0.04205
tr F1M820 Uncharacte	17	28	-0.141442	-0.221039	-0.05845	0.0425125
tr F1LP60 Uncharacte	21	45	-0.140967	-0.223152	-0.059103	0.04285
sp P16391 RT1 class I	3	4	-0.290334	-0.556397	-0.027299	0.04335
sp P12839 Neurofilam	36	100	0.4214048	0.0100573	0.8327303	0.04345
tr D3ZZC1 RCG43947	4	6	-0.253588	-0.475076	-0.0482	0.0435
tr F1M200 Ubiquitin ca	2	3	0.4071122	0.0064436	0.8327413	0.0436625
sp Q05764 Beta-adduc	4	7	0.2093691	0.0456751	0.3763574	0.0438
tr D3ZPF0 Four and a l	2	3	-0.396382	-0.773799	-0.008945	0.0442
tr F1LRS7 Uncharacte	2	3	-0.390334	-0.750795	-0.003052	0.044275
sp Q63269 Inositol 1,4,	15	24	0.332375	0.0090268	0.6335772	0.0442875
tr F1M1V0 Uncharacte	20	47	0.2719872	0.0328141	0.5105969	0.0443375

sp O35112 CD166 anti-	5	6	0.2736738	0.0317512	0.5136366	0.04435
sp P07323 Gamma-enc	16	52	0.1782911	0.0492407	0.3025717	0.044775
tr O35370 Thrombom	1	3	-0.303579	-0.580504	-0.024263	0.0447875
tr F1LX07 F Uncharacte	3	4	0.4544203	-0.010017	0.9501721	0.044825
sp Q6AYC4 Macrophag	12	39	0.3888785	0.0032178	0.7556175	0.0449875
tr Q569A0 LOC681849	4	8	0.2214421	0.035313	0.4189931	0.0454125
tr D3ZNZ1 Uncharacte	2	4	0.2275995	0.0450299	0.4247079	0.0455375
tr D4AEH9 Amylo-1, 6-	17	21	0.4201988	0.0026187	0.8378831	0.0457625
tr D3ZZU0 Actin relate	5	7	-0.187375	-0.328384	-0.049945	0.0457625
tr D3ZC10 Uncharacte	4	6	0.2397464	0.0338237	0.4616773	0.04585
sp P85125 Polymerase	15	32	-0.147983	-0.24178	-0.053947	0.04625
sp P62703 40S riboson	10	21	-0.178357	-0.309557	-0.050147	0.0463375
tr Q4QR8 Asl protein	1	2	-0.272254	-0.5196	-0.029029	0.04635
sp Q9JIH7 Serine/thre	3	3	0.4796745	-0.023789	0.9697072	0.0469625
tr D3ZU77 Uncharacte	4	15	0.29583	0.0269911	0.573738	0.04735
tr Q5XI38 C Lymphocyte	12	26	-0.17989	-0.308452	-0.044275	0.0480375
sp P21531 60S riboson	9	20	-0.185875	-0.331248	-0.046906	0.0483125
sp Q9QX69 LanC-like pr	4	8	0.1600882	0.052622	0.2717751	0.048525
sp P32551 Cytochrome	10	23	0.2433148	0.0326111	0.4532842	0.0486375
tr D4ACN7 Uncharacte	7	7	-0.322238	-0.620432	-0.016351	0.048925
sp P19234 NADHdehy	4	9	0.2319267	0.0318416	0.4367302	0.049025
tr D3ZN61 Leucine-rich	4	6	0.2953021	0.0221173	0.5808406	0.049025
tr D3ZF13 I Acyl carrier	2	2	0.4820778	-0.056828	1.1025523	0.0494125
sp P41498 Low molecu	4	8	0.2489958	0.0281799	0.4646275	0.0496
tr D3ZY11 I Uncharacte	6	11	0.1822504	0.045289	0.3181968	0.04965
sp P31399 ATP synthas	7	12	0.3140156	0.0215341	0.6172926	0.0496875
tr F1LNFO F Uncharacte	37	60	0.2292033	0.0386082	0.4276281	0.0497125
tr Q6IMY8 Heterogene	11	19	-0.182401	-0.320957	-0.045317	0.0500375
sp P82471 Guanine nu	6	13	0.214434	0.0386381	0.3986044	0.0500875
sp P19939 Apolipoprot	2	3	-0.356721	-0.718908	0.0017145	0.050175
sp P05696 Protein kin	13	16	0.2205749	0.037595	0.407152	0.0502625
sp Q8VIJ5 I Bifunctiona	5	9	0.1826928	0.046874	0.3202942	0.050275
tr Q6P9V7 Proteasome	12	19	-0.213436	-0.391084	-0.037333	0.0504875
tr D3ZE88 I Uncharacte	10	19	0.4450126	-0.021088	0.9000522	0.0505375
tr D4A3B0 Uncharacte	31	55	-0.127746	-0.199101	-0.05615	0.05075
sp P97700 Mitochondr	4	8	0.2916599	0.0204402	0.5684544	0.050975
sp P37377 Alpha-synuc	8	14	0.2741083	0.0195423	0.5233477	0.051625
tr D3ZH41 Uncharacte	5	6	-0.248339	-0.457638	-0.032583	0.05165
tr D4A4D5 Uncharacte	5	11	-0.220873	-0.406806	-0.03512	0.05195
sp P31044 Phosphatid	9	24	0.1821057	0.0429218	0.3244822	0.05205
tr D3ZP91 I Uncharacte	2	2	-0.436683	-0.901927	0.0186517	0.052125
sp Q9EPF2 Cell surface	10	17	-0.158647	-0.273021	-0.048835	0.052325
tr D4ACR0 Uncharacte	9	13	-0.224959	-0.420537	-0.038119	0.052375
tr F1LRL9 F Uncharacte	56	100	0.264359	0.0237412	0.5047546	0.0524
tr F1LLW3 I Uncharacte	2	2	-0.423205	-0.858915	0.0285867	0.05255
tr D3ZS41 I Uncharacte	2	3	-0.346431	-0.685357	-0.005415	0.052675
tr F1LUD3 I Uncharacte	9	12	0.2128158	0.0342469	0.3875287	0.0527625
sp P08932 T-kininogen	5	8	0.3107695	0.0021882	0.6248517	0.052825
sp Q6P734 Plasma prot	11	18	-0.260275	-0.489743	-0.01865	0.0528375
sp P19527 Neurofilam	32	100	0.4585544	-0.030989	0.9354324	0.05315

tr D3ZFQ8	Cytochrome	3	4	0.2747655	0.0220831	0.5295821	0.0536625
tr D4ACG7	Uncharacte	12	25	0.3282128	-0.000303	0.6483763	0.05405
tr D3ZWX0	Uncharacte	18	28	-0.212518	-0.389393	-0.028881	0.0543
tr F1M7V6	Uncharacte	11	34	0.2695485	0.0228138	0.5255521	0.0544125
sp P18163	Long-chain-	13	20	-0.639303	-1.359076	0.0808117	0.0545125
tr Q642E2	RCG22700,	3	5	-0.199656	-0.358039	-0.035213	0.054675
sp Q8K4D8	Aldehyde de	1	2	-0.425178	-0.888062	0.0191431	0.0552125
tr D3ZKL0	I Uncharacte	4	4	0.3584891	-0.039367	0.7608752	0.0553875
tr D3ZR01	I Uncharacte	3	5	-0.360158	-0.713875	0.0211709	0.0557625
sp P19945	60S acidic ri	9	19	-0.208844	-0.385756	-0.031734	0.0558125
tr F1MAC0	Uncharacte	4	4	-0.34022	-0.675858	0.0154432	0.0561125
tr B2RZ72	E Actin relate	5	10	-0.157904	-0.268562	-0.046079	0.0565625
sp B0BNN3	Carbonic an	4	8	-0.374798	-0.767031	0.0123968	0.0565875
sp P62747	Rho-related	2	4	0.2098095	0.0295122	0.3924089	0.0566625
sp Q63198	Contactin-1	4	4	0.35287	-0.00374	0.7323911	0.0568625
tr D3ZU33	Uncharacte	5	9	-0.271267	-0.535281	-0.011867	0.0571125
tr D4A7U8	Similar to m	1	3	1.0878826	-0.209119	2.4085748	0.0571875
sp Q68FY0	Cytochrom	10	15	0.2280326	0.0192564	0.4261601	0.0572375
sp Q6V7V2	Rhotekin OS=	9	13	0.2504646	0.0166222	0.469536	0.0573125
sp Q5XIF6	Tubulin alph	4	13	0.4265843	-0.03586	0.8862212	0.057675
sp P02688	Myelin basic	16	100	0.4450807	-0.041485	0.9333464	0.0576875
sp Q7M0E3	Destrin OS=	13	24	-0.217365	-0.400956	-0.029137	0.0577
sp Q5XIP9	Transmemb	5	6	-0.294625	-0.563757	0.0020025	0.05805
sp P23457	3-alpha-hyd	5	8	-0.407898	-0.844305	0.0351557	0.0585
tr Q52KS1	I 6-phosphof	24	42	0.3152585	-0.003968	0.6357272	0.058775
sp P22062	Protein-L-is	9	25	0.1542393	0.046838	0.2645987	0.0588625
tr D3ZRF5	I RCG47744,	1	2	0.3480852	-0.008072	0.7081418	0.0589125
tr F1LM84	Uncharacte	29	68	0.246733	0.017282	0.4725272	0.058925
tr D4AAC4	Uncharacte	1	2	0.4184069	-0.03445	0.8937491	0.059225
sp P02091	Hemoglobir	3	29	-0.336808	-0.693743	0.0003745	0.0592375
sp P04466	Myosin regu	10	25	1.2649101	-0.337477	2.7634234	0.059275
sp P47728	Calretinin O	8	11	0.1947722	0.0305616	0.3640159	0.0594
sp P05982	NAD(P)H de	4	11	0.2364233	0.0220418	0.4501877	0.0597375
sp P02600	Myosin ligh	12	44	1.1978136	-0.268079	2.6410139	0.0598375
tr D4A4P4	Uncharacte	2	3	0.4409258	-0.034136	0.9506784	0.0599
tr D3ZZV4	I Uncharacte	17	26	0.2030366	0.0307325	0.3754617	0.0599375
tr F1LN42	F Uncharacte	17	19	-0.141571	-0.239226	-0.045528	0.060125
sp Q9ESN0	Protein Nib	2	11	-0.266741	-0.523526	-0.012378	0.0602625
sp P08461	Dihydrolipo	16	29	0.2214515	0.0222183	0.4139818	0.0603125
tr B5DEL9	E RCG62292,	8	16	-0.216153	-0.404229	-0.026941	0.0604625
sp P23565	Alpha-interi	18	28	0.2842058	0.0069124	0.5665159	0.0605
sp P22791	Hydroxyme	2	2	0.6709269	-0.135546	1.4518886	0.0607375
tr A1A5L1	Bleomycin h	3	4	-0.180979	-0.327335	-0.031478	0.0612625
tr Q6AXW2	RCG25684,	8	11	-0.267001	-0.532484	-0.008266	0.0616375
sp Q3KRE0	ATPase fam	2	3	-0.252513	-0.490652	-0.013033	0.0617375
tr D4A8H3	Similar to R	3	6	0.2646573	0.0081198	0.5311573	0.0618125
tr F1LSX1	F Uncharacte	2	2	0.2856063	-0.018791	0.5806456	0.0620375
sp P14604	Enoyl-CoA h	9	18	-0.152282	-0.266965	-0.042154	0.0628875
tr Q5PK6	Nit1 proteir	3	6	-0.238728	-0.454082	-0.016839	0.063075
tr D3ZSY4	I Eosinophil	3	4	-0.553045	-1.228049	0.0761362	0.0638875

sp Q794E4 Heterogene	3	7	-0.215673	-0.413661	-0.021238	0.064025
sp P59649 FXYD domai	2	3	0.3904419	-0.041865	0.8248988	0.0642125
sp P01835 Ig kappa ch	8	32	-0.517881	-1.106718	0.0737703	0.064275
sp O08557 N(G),N(G)-d	16	40	0.2232241	0.0178167	0.4249185	0.0649125
tr F1LYV8 F Uncharacte	2	3	-0.493451	-1.057416	0.0777551	0.0661
tr F1LRZ7 F Uncharacte	33	100	0.3902631	-0.035294	0.8294382	0.066375
tr F1LQ76 F Uncharacte	13	18	0.2928553	-0.007132	0.5977331	0.06645
sp P04762 Catalase OS	14	25	-0.239817	-0.474357	-0.011142	0.0672875
sp P62762 Visinin-like	8	17	0.2470013	-9.8E-05	0.4813365	0.06775
sp P01830 Thy-1 meml	4	10	0.3151529	-0.020851	0.6499687	0.068025
sp P63100- Isoform 2 o	5	8	0.1886933	0.0289711	0.3459199	0.068175
tr B4F7B7 F Dual specifi	7	23	0.3142746	-0.017828	0.6508099	0.068425
tr F1LM41 Uncharacte	7	18	-0.206053	-0.390859	-0.016467	0.068725
tr Q8R4I6 C Actinin alph	25	41	0.9936179	-0.258547	2.2689	0.068775
tr F1M5J5 I Uncharacte	6	11	1.3444315	-0.404384	3.0542999	0.0688125
tr F1LNF7 F Uncharacte	11	14	0.1766121	0.0298277	0.3226644	0.0688625
sp P62138 Serine/thre	1	3	-0.177777	-0.332523	-0.027709	0.0688875
tr D3ZD02 60S riboson	5	10	-0.228784	-0.444061	-0.006988	0.0697
sp Q4QQV8 Charged mu	4	6	0.2628491	0.0035977	0.5222056	0.070525
sp Q9JMI1 Acetoacetyl	3	3	-0.387998	-0.860319	0.0880516	0.0706
sp P68136 Actin, alpha	3	6	0.8655725	-0.216005	1.9675938	0.071025
tr D4ACL2 Similar to FI	1	2	-0.35002	-0.740081	0.0332977	0.071275
tr F1LQH0 Uncharacte	18	31	0.1577615	0.0360933	0.2840337	0.0714625
tr D3ZAA1 Uncharacte	1	2	-0.288206	-0.582992	0.0192537	0.071525
tr D3ZJH9 Malic enzym	5	7	-0.229404	-0.450619	-0.008451	0.071725
tr F1M7X5 Uncharacte	8	13	-0.168749	-0.305999	-0.030912	0.0718
sp Q9EQX9 Ubiquitin-cc	5	10	0.1761444	0.0336724	0.3215421	0.071925
sp P63259 Actin, cytop	8	81	-0.130432	-0.213393	-0.046599	0.0719625
sp Q9JHU0 Dihydropyri	16	36	0.2026813	0.0149891	0.3850691	0.0723375
tr D3ZCG2 Uncharacte	12	16	0.2315215	0.0056353	0.4516157	0.0725125
tr D3ZCR6 Periostin, o	18	31	-0.460748	-1.011647	0.0852862	0.0726375
sp Q2IBC5 Caveolin-2 C	2	5	-0.242794	-0.468777	-0.000857	0.0729875
tr F1MA59 Uncharacte	4	4	0.4028683	-0.055846	0.8673787	0.0731625
tr D4A656 Uncharacte	1	2	0.3490086	-0.072379	0.7881977	0.0732125
tr F1LRP1 F Uncharacte	4	6	0.7890121	-0.30605	1.9277318	0.0732375
sp P05942 Protein S10	7	18	0.2326336	0.0106266	0.4714832	0.0734
tr F1LUV9 F Uncharacte	8	11	0.2317194	0.0028274	0.4637501	0.07345
tr B5DEZ8 Plexin dom	2	2	0.3773021	-0.101803	0.8298142	0.073925
tr F1MAN8 Uncharacte	6	6	0.3218764	-0.072972	0.7187355	0.0741
sp P08934 Kininogen-1	5	8	-0.32942	-0.695873	0.0464994	0.07445
tr F1LQS6 F Uncharacte	1	3	-0.395868	-0.859432	0.0739871	0.0749625
sp P10719 ATP synthas	29	100	0.1885937	0.0163838	0.354291	0.0751875
tr D3ZCX0 RCG55799,	11	27	-0.138355	-0.237995	-0.04169	0.0754
tr D3ZG41 Uncharacte	2	2	-0.336421	-0.751642	0.0924718	0.0754875
tr Q7TNZ9 CKLF-like M	1	2	0.3982718	-0.07638	0.8640946	0.076075
tr C0KUC5 LIM and ser	3	4	-0.187903	-0.353735	-0.018258	0.0761625
sp Q91Y81 Septin-2 OS	13	25	-0.125686	-0.204709	-0.048724	0.076675
tr D4ADL1 Uncharacte	2	2	-0.49882	-1.161774	0.2041815	0.076725
sp P11730 Calcium/cal	4	5	0.2232428	0.0091553	0.4365605	0.076975
sp Q62910- Isoform 4 o	23	38	0.1719591	0.0281152	0.3189228	0.0776625

sp P62815 V-type prot	14	26	0.1665475	0.0279618	0.3056109	0.077875
tr D3ZUL3 Uncharacte	33	93	0.2185494	-0.001678	0.4313492	0.078325
tr Q5XIH1 Asporin OS-	13	24	0.3055364	-0.042697	0.6414802	0.07855
sp Q9EPH2 MARCKS-re	3	8	0.2297744	-0.007508	0.4575695	0.0789125
sp P09117 Fructose-bis	12	27	0.1974705	0.0111281	0.3813949	0.0790375
tr F1LZ50 Uncharacte	2	3	0.9191437	-0.312678	2.1791744	0.0794875
sp P12007 Isovaleryl-C	7	11	-0.184415	-0.347979	-0.017705	0.0795
sp P27867 Sorbitol deh	11	23	0.1367253	0.0406725	0.2312162	0.0798375
tr D3ZI32 Uncharacte	5	7	0.2123293	0.0031832	0.4178049	0.0799625
sp Q66H80 Coatomer s	8	10	-0.243181	-0.493481	0.0055372	0.0804
sp Q9Z0W5 Protein kin	7	8	0.20984	0.0041576	0.4074251	0.0805125
sp P11608 ATP synthas	2	4	0.2952881	-0.02599	0.6135332	0.081025
sp Q4KM35 Proteasome	2	2	-0.319635	-0.737178	0.0922985	0.0811
tr D4AAS8 Uncharacte	5	10	0.1913254	0.0157529	0.3713052	0.081475
tr D3ZIP8 RCG31867 (7	14	0.3494015	-0.064638	0.7536348	0.081725
tr D3ZSM1 Similar to pi	27	66	0.1665805	0.0236299	0.3081677	0.0817875
sp Q920P6 Adenosine c	3	3	-0.467264	-1.145749	0.185475	0.081975
tr D3Z8T2 Uncharacte	1	3	0.3080499	-0.051136	0.6630681	0.0822
tr B5DFC3 SEC23A (S.	5	7	-0.229631	-0.467771	0.0043677	0.0823375
tr Q5XIH3 NADHdehy	6	10	0.1842281	0.0193156	0.3542656	0.0827
sp P04177 Tyrosine 3-r	6	10	0.23048	-0.001636	0.4767232	0.08285
sp P62856 40S riboson	2	3	-0.209564	-0.416334	-0.00413	0.0835375
sp Q07969 Platelet glyc	10	19	-0.401818	-0.902727	0.0922785	0.0839125
sp Q5XIE1 UPF0670 pr	4	4	0.4665535	-0.127059	1.0639094	0.0841
tr D3ZVR9 Uncharacte	4	5	-0.231297	-0.475955	0.0034145	0.0841375
tr F1M2K6 Uncharacte	1	2	0.3953026	-0.087364	0.8694135	0.084425
tr B5DF74 Oxysterol-b	2	2	0.6343015	-0.230902	1.5316869	0.0852
sp P18445 60S riboson	3	3	-0.278832	-0.593597	0.0400739	0.0855
sp Q9EPJ0 Nuclear ubiq	2	3	-0.218742	-0.455331	0.0190012	0.0861
sp Q3B8Q2 Eukaryotic i	2	3	-0.367198	-0.866183	0.1304643	0.086275
sp Q6MG06 Guanine nucl	2	3	-0.415918	-0.956457	0.0913632	0.0863625
tr Q66HM2 Adaptor-rel	16	29	-0.118871	-0.192	-0.048098	0.08665
tr D3ZCF8 Uncharacte	5	9	0.3417643	-0.071408	0.7648068	0.0877375
sp P06866-I Isoform 2 o	11	18	-0.454523	-1.037334	0.1194255	0.088025
tr D3ZPF3 Capping pro	7	9	-0.17397	-0.336165	-0.010976	0.0881
sp P35434 ATP synthase	2	4	0.2080271	-0.011024	0.4136608	0.0884
sp Q68FR6 Elongation f	12	25	-0.141824	-0.248951	-0.0313	0.0884
sp P29975 Aquaporin-1	2	4	-0.440195	-1.051024	0.196846	0.0886875
tr D4A2C6 LSM4 homolog	1	2	-0.281516	-0.617359	0.0347736	0.0889
sp Q4QQW1 Putative ph	3	3	-0.278271	-0.58235	0.0469122	0.089
tr E9PSK7 Uncharacte	2	2	0.4349956	-0.168812	1.0524519	0.0890125
sp B2GUZ5 F-actin-capro	1	2	-0.214347	-0.427612	0.0056978	0.0891875
sp O88794 Pyridoxine-1	1	3	0.1971345	0.010264	0.3990265	0.090025
tr F1M396 Uncharacte	2	3	-0.368407	-0.908779	0.1422746	0.0912125
tr B2RZD6 Ndufa4 protein	2	4	0.2498345	-0.030583	0.5273195	0.0915125
sp Q71UF4 Histone-bin	2	2	-0.331655	-0.787551	0.1144149	0.0920125
sp Q6PST4 Atlastin-1 O	3	3	0.3784124	-0.103312	0.8645298	0.092125
sp P68370 Tubulin alphas	10	60	0.3226649	-0.07037	0.7082876	0.0921875
tr Q6PCU0 ATP synthase	10	18	0.1799477	0.0101567	0.3504682	0.0927875
sp Q9Z1H9 Protein kin	8	13	-0.158624	-0.301584	-0.025668	0.093175

tr D4A9P7 RCG40058 (1	2	0.3135396	-0.059989	0.661829	0.0933
sp Q2TA68 Dynamin-like	9	16	0.1541633	0.0278752	0.2833222	0.0936375
tr F1M1B3 Uncharacte	2	2	-0.350072	-0.793018	0.0762928	0.094525
sp P70470 Acyl-protein	2	2	-0.282394	-0.652074	0.0786205	0.094725
sp Q9JMB5 Proteasome	1	2	0.4087428	-0.186347	1.0724621	0.09515
sp P60868 40S ribosom	4	4	-0.222434	-0.49507	0.0466404	0.095225
sp P13832 Myosin regul	2	4	-0.250787	-0.566103	0.0626534	0.0952875
sp Q5M9I5 Cytochrome	1	2	0.3581619	-0.111382	0.8059399	0.0954875
sp Q921A4 Cytoglobin	3	4	-0.324586	-0.73403	0.0869216	0.0963625
tr D3ZNY5 Uncharacte	1	2	-0.254975	-0.575072	0.0601651	0.0966
tr D3ZJF2 Uncharacte	4	8	0.2814778	-0.042355	0.6119617	0.09665
sp POC548 Patatin-like	1	3	-0.204984	-0.415371	0.0138407	0.0966625
sp Q10758 Keratin, typ	1	2	0.3334748	-0.078935	0.7497381	0.0970375
tr F1LNF1 Uncharacte	7	13	-0.161986	-0.308407	-0.017581	0.0970875
tr Q6P736 Polypyrimid	2	6	-0.262592	-0.572938	0.0367686	0.0975625
tr F1LMB8 Uncharacte	2	2	0.3558546	-0.108105	0.8155565	0.097675
tr F1LQ81 Uncharacte	27	50	0.1803547	0.004121	0.3539327	0.0979
sp Q66HA6 ADP-ribosyl	2	3	0.1947908	-0.001545	0.3990646	0.0979
tr E9PSZ3 Uncharacte	4	13	0.218772	-0.01369	0.4693554	0.0987375
sp Q6AYG5 Enoyl-CoA thio	4	5	-0.282124	-0.624792	0.0781432	0.0989
sp P59215 Guanine nucleotid	8	14	0.2354721	-0.032663	0.4985238	0.09895
tr F1M4T3 Uncharacte	2	2	-0.32495	-0.787197	0.0789655	0.0993125
sp P63322 Ras-related GTPase	9	15	0.2095109	-0.014975	0.4335382	0.0997
sp Q9R0T4 Cadherin-1	7	10	0.2241218	-0.02653	0.4654125	0.1000625
sp Q5M936 Torsin-3A O	2	2	-0.283447	-0.621337	0.0700946	0.1000625
sp P62755 40S ribosomal protein S21	6	10	-0.167992	-0.330313	-0.015976	0.1004375
sp P85971 6-phosphogluconate dehydrogenase	4	7	-0.178199	-0.341898	-0.000883	0.1006625
tr D4AB41 Uncharacte	1	3	-0.317184	-0.705816	0.0797835	0.1008125
sp P04638 Apolipoprotein A-I	4	6	-0.326823	-0.74912	0.0832705	0.1013
tr Q5U2U8 Bcl2-associated protein X	7	10	0.1690324	0.0046564	0.327491	0.1021
tr D4A777 Uncharacte	2	4	-0.241064	-0.514107	0.0334932	0.1026
tr D3ZN64 Uncharacte	13	23	0.1910828	-0.00365	0.3849844	0.1028375
tr Q7TP58 Phosphoglycerate kinase	1	2	-0.367126	-0.858613	0.126081	0.1028625
sp Q6AYS8 Estradiol 17 beta-hydroxylase	8	9	0.2022464	-0.015431	0.4174129	0.1031875
sp P13264 Glutaminase	6	7	0.1968905	-0.013477	0.4026158	0.1031875
sp P48500 Triosephosphate isomerase	16	64	0.2233517	-0.034678	0.4718639	0.1034125
tr D4ABT8 Uncharacte	5	9	-0.247139	-0.537802	0.0429309	0.1043
tr Q7TP54 Ab2-162 OS	5	10	0.2030546	-0.016839	0.41397	0.10435
sp P05065 Fructose-bisphosphate aldolase	20	62	0.3170749	-0.089115	0.7204119	0.1047875
sp B2RZ78 Vacuolar protein	8	15	-0.127201	-0.218791	-0.036664	0.1049125
tr F1LMU0 Uncharacte	38	100	1.091932	-0.60117	2.7847982	0.105125
sp P47942 Dihydropyridine receptor 1B	23	66	0.1569013	0.0178069	0.3014259	0.105275
sp P11497-1 Isoform 2 of Annexin A5	6	6	-0.248033	-0.536023	0.0489461	0.1056125
tr Q6P9V1 Cd81 protein	5	17	0.3538278	-0.105202	0.8288441	0.1057125
sp P14668 Annexin A5	23	75	-0.123952	-0.214507	-0.036066	0.1058625
sp Q9Z1X1 Extended syntaxin	15	24	-0.139822	-0.255573	-0.027474	0.105875
tr Q6QI48 LRRGT0016	7	13	-0.216802	-0.457484	0.0285296	0.106075
sp Q6P6V0 Glucose-6-phosphate isomerase	21	46	0.179035	0.0019678	0.3634817	0.1062625
sp P12369 cAMP-dependent protein kinase regulatory subunit 1	2	2	-0.66296	-1.840122	0.4745382	0.1064625
sp P02688-1 Isoform 3 of Annexin A5	2	8	0.3828991	-0.148474	0.9097776	0.1066375

tr D4A929 Putative un	2	3	0.3044255	-0.076391	0.6898237	0.1073125
sp O09175 Aminopepti	5	7	-0.317917	-0.79081	0.132974	0.107525
sp Q9ER34 Aconitate h	27	47	0.1539843	0.0132987	0.2954842	0.1076125
sp P67779 Prohibitin C	9	13	0.1409262	0.0230385	0.2602499	0.1078
sp P13084 Nucleophos	3	4	-0.187268	-0.382392	0.009483	0.1080875
sp P19944 60S acidic ri	2	5	-0.246433	-0.568787	0.0705427	0.10815
tr F1LNH3 Uncharacte	23	51	0.2023601	-0.016512	0.4258296	0.1083625
tr F1M7Y0 Uncharacte	2	2	0.4924117	-0.277317	1.2704626	0.1086375
sp P48679 Prelamin-A/	7	17	-0.200297	-0.420684	0.0156977	0.10875
tr Q6AYI1 C DEAD (Asp-)	5	7	-0.18109	-0.372777	0.0047783	0.109025
sp Q6PCU2 V-type prot	7	14	0.1386795	0.0272845	0.2540676	0.1094875
sp P09812 Glycogen ph	25	51	0.7166827	-0.370307	1.7927693	0.109725
tr F1LZF4 F Uncharacte	21	38	0.2519704	-0.059178	0.5508166	0.109975
tr D4A6A3 Uncharacte	4	4	0.2756125	-0.063732	0.624994	0.1101125
tr F1M8F2 Uncharacte	7	13	0.2145489	-0.027311	0.462351	0.11045
sp P25886 60S riboson	3	7	-0.203252	-0.427922	0.0224524	0.1109875
tr D3ZJJ2 D Uncharacte	2	2	-0.388454	-0.974682	0.2117516	0.1110875
tr F1M3Q9 Uncharacte	2	2	-0.509569	-1.311818	0.2673308	0.111325
tr D4AE32 Uncharacte	2	6	-0.323207	-0.752196	0.1378311	0.1116125
tr F1LWW1 Uncharacte	2	4	-0.323911	-0.76927	0.1123685	0.111975
sp Q08290 Calponin-1'	2	2	-0.924697	-2.677508	0.7860933	0.1120375
tr F1LP72 F Uncharacte	6	9	-0.1225	-0.20877	-0.034289	0.1121875
tr F1LPV0 F Uncharacte	12	18	0.1784866	-0.009694	0.3580571	0.1124875
tr D3Z955 RCG40012,	8	11	0.2470292	-0.056142	0.5492204	0.11255
tr B6DYP8 Glutathione	9	21	-0.174352	-0.351033	0.0063481	0.11295
tr D4ADA2 Uncharacte	4	12	-0.276836	-0.636141	0.072526	0.113325
tr D3Z982 Uncharacte	3	7	-0.170246	-0.33816	0.0048616	0.1137625
tr F1M7S9 Uncharacte	70	91	0.6939369	-0.372217	1.7515136	0.1139625
sp Q64578 Sarcoplasm	26	53	0.923883	-0.529662	2.4255292	0.114
tr B1H216 Hemoglobir	13	100	-0.252788	-0.563228	0.0605603	0.11425
sp P06907 Myelin prot	15	100	0.5270774	-0.3232	1.3768845	0.11475
tr D3ZAP5 Uncharacte	5	7	0.1972616	-0.021672	0.4147468	0.1148125
sp P11762 Galectin-1 C	10	69	0.1437489	0.016659	0.2695178	0.1148875
sp P10760 Adenosylho	14	39	-0.153762	-0.300421	-0.00926	0.1150125
tr D3ZH18 Uncharacte	4	4	0.2820513	-0.084686	0.6275882	0.115225
sp P36972 Adenine ph	9	18	-0.150211	-0.287703	-0.012478	0.1153875
tr F1LRG1 F Uncharacte	5	6	-0.174022	-0.35552	0.0102269	0.11565
sp P50475 Alanyl-tRNA	22	29	0.1290089	0.0266674	0.2329347	0.117225
tr Q0R3X4 GIMAP4 OS	2	2	-0.509364	-1.406251	0.4226284	0.1175
sp Q920P0 L-xylulose r	3	3	-0.184428	-0.387121	0.0122723	0.118525
sp B1H267 Sorting nexi	3	5	-0.20862	-0.455692	0.037799	0.1188625
tr D3ZYD7 Uncharacte	4	4	-0.196852	-0.410444	0.0185064	0.1191
tr D3ZK56 Uncharacte	2	4	0.2125226	-0.034445	0.4627422	0.11915
tr F1LNY0 F Uncharacte	9	20	-0.165077	-0.328802	0.0057091	0.1194
sp P27139 Carbonic an	8	17	-0.195632	-0.415249	0.0273607	0.1205
sp P04692 Tropomyosi	8	19	0.8709296	-0.576541	2.2454089	0.1210375
sp P13471 40S riboson	3	6	-0.187204	-0.403499	0.019912	0.1213125
sp Q6PEC4 S-phase kin	9	20	0.1521799	0.0073569	0.3018561	0.12165
sp Q80W57 ATP-binding	2	2	0.4143224	-0.249062	1.0660485	0.1217125
sp Q642A6 von Willebr	8	16	0.1862265	-0.021419	0.3962892	0.121725

sp P63012 Ras-related	2	2	0.3149949	-0.131488	0.7870023	0.1222875
sp P52303 AP-1 compl	8	9	-0.137464	-0.257252	-0.021572	0.122325
sp Q9WU0E Advillin OS=	16	23	0.1770921	-0.015543	0.3683995	0.1223875
sp O35760 Isopentenyl	2	5	-0.210754	-0.454554	0.0459164	0.1232125
tr D3ZDU5 Profilin OS=	6	10	0.1652986	-0.003959	0.3368243	0.123425
sp P23593 Apolipoprot	3	4	-0.296622	-0.703168	0.1098846	0.123775
sp P18420 Proteasome	7	18	-0.138357	-0.260713	-0.018126	0.123825
tr F1M883 Uncharacte	7	14	-0.242553	-0.548526	0.069518	0.1239
sp P32038 Complemer	2	7	-0.198488	-0.433179	0.0358679	0.1242625
tr D3ZHC4 Heme bindi	5	7	0.1667269	-0.005029	0.3359071	0.124375
sp P12001 60S ribosom	4	5	-0.203272	-0.434009	0.0413234	0.124375
tr D3ZG61 RCG61079,	3	8	0.3314501	-0.139869	0.7780794	0.1245625
tr D3ZZ21 [NADHdehy	1	2	0.2728574	-0.11477	0.6575104	0.1247125
tr D4A6T3 [Uncharacte	3	4	0.242011	-0.060014	0.5437261	0.124875
tr D4ADB1 Uncharacte	7	7	0.7742514	-0.550731	2.139792	0.1263
tr D3ZZR3 [Uncharacte	1	2	-0.26666	-0.61126	0.098264	0.1263875
tr D3ZQ98 Uncharacte	5	9	0.1823706	-0.026986	0.3830181	0.1264
sp A2RRU1 Glycogen [s	3	4	0.2962361	-0.128558	0.7060793	0.127475
tr F1LT36 F Uncharacte	2	4	-0.241028	-0.54827	0.0702049	0.1275
sp Q1WIM2 Cell adhesic	2	4	0.2715202	-0.103953	0.6222868	0.1279125
sp Q6AYT7 Monoacylg	1	2	0.3846654	-0.193748	0.9661329	0.1279625
sp P60203 Myelin prot	10	19	0.3142321	-0.140598	0.7557417	0.1286125
tr D3ZQG6 Tripartite m	3	7	-0.293792	-0.602366	0.0912311	0.1291375
tr Q4QQS7 Uncharacte	4	4	-0.267273	-0.624566	0.1073923	0.13015
tr Q6PCT9 [Proteasome	3	4	-0.181226	-0.383123	0.0202262	0.1307
sp Q5FVQ9 Tubulin-spe	2	2	-0.298134	-0.721804	0.1307279	0.1309875
sp Q6AY30 Probable sa	8	15	0.2479062	-0.086146	0.5769896	0.1319125
sp Q32Q06 AP-1 compl	2	3	-0.318697	-0.790393	0.14346	0.1319375
sp Q63228 Glia matura	6	7	-0.170757	-0.355443	0.0174551	0.1322625
sp Q3B7U9 Peptidyl-pro	3	3	-0.211048	-0.484217	0.0642197	0.1333625
sp Q63083 Nucleobind	3	5	-0.220842	-0.510137	0.0535113	0.1335375
tr D3ZXY2 [PDZ domair	3	3	0.3802436	-0.243097	0.9939568	0.13355
sp P61751 ADP-ribosyl	3	4	-0.17251	-0.365779	0.0186694	0.13375
tr F1LSR9 F Uncharacte	2	2	-0.41048	-1.042438	0.2369098	0.1339125
tr Q566E4 [Heterogene	4	6	-0.23741	-0.554909	0.077581	0.134175
tr B2GV03 Phosphoryl	22	47	0.1689706	-0.016669	0.3560893	0.1342375
tr F1MAA0 Uncharacte	3	3	0.8047352	-0.664405	2.302826	0.1342625
tr Q5XIJ3 Q Isocitrate d	5	7	0.1766115	-0.026267	0.3825711	0.134275
tr Q5RK08 Glioblastom	3	3	0.1693148	-0.014577	0.3540264	0.1344
tr D3ZYF9 [Uncharacte	2	2	-0.357077	-0.998353	0.2592346	0.1344625
sp Q3ZAV8 Enhancer of	3	3	0.2948005	-0.127661	0.6934834	0.13455
sp Q6P9T8 Tubulin beta	2	13	0.2649138	-0.11194	0.6409472	0.134775
tr D4AC20 Cytidine de	2	5	0.2715273	-0.101295	0.6466559	0.135
sp P97846 Contactin-a	5	6	0.2655496	-0.097966	0.6474974	0.13515
tr D3ZSH6 [Uncharacte	7	11	-0.202013	-0.451015	0.0462857	0.13565
tr B5DESO RCG54604 C	2	2	-0.214372	-0.531245	0.0954702	0.1357375
sp B0BNA7 Eukaryotic t	1	2	-0.204135	-0.462064	0.050825	0.136425
tr D3ZT75 [Uncharacte	3	4	0.2592992	-0.110759	0.6171159	0.1378
tr F1M1E6 Uncharacte	8	14	0.1422959	0.0088799	0.287398	0.138425
sp P49242 40S ribosom	7	9	-0.171017	-0.368115	0.0199192	0.1386625

tr D4AE96 Importin 7 (4	6	-0.209732	-0.473365	0.0496438	0.1390125
tr D3ZR68 Uncharacte	2	2	0.4200402	-0.234837	1.1222606	0.1393875
sp P09739:- Isoform 2 o	6	14	0.8478975	-0.645263	2.3642595	0.139825
tr F1LM47 Uncharacte	14	20	0.1241798	0.0167708	0.2257276	0.1406875
sp P62271 40S riboson	6	9	-0.200919	-0.440556	0.0601276	0.141
tr D3ZBW0 Uncharacte	11	17	0.1383501	0.0094137	0.2727625	0.1411
sp Q63151 Long-chain-	2	4	0.2377451	-0.0834	0.5626663	0.142425
tr D3ZDL9 Uncharacte	1	2	0.1955399	-0.056218	0.445431	0.143225
sp P62912 60S riboson	3	5	-0.197946	-0.452703	0.0777878	0.1432875
tr D3ZKH2 Uncharacte	2	3	0.1984928	-0.038638	0.4659224	0.1437
tr B5DEN4 L-lactate de	22	65	0.2294567	-0.08592	0.5429169	0.143725
sp Q63425 Periaxin OS:	7	18	0.6907822	-0.545203	1.912137	0.1451875
sp P18645 UDP-glucos	2	2	-0.26518	-0.694901	0.1625747	0.1453625
tr B4F789 E Apolipoprot	1	2	0.9575467	-0.863942	2.7346664	0.1456875
tr Q6MGA6 Proteasome	2	2	-0.358296	-1.016613	0.2777947	0.146125
tr Q66H09 Tetratricope	3	5	0.2223365	-0.082218	0.527746	0.14635
sp Q62952 Dihydropyri	15	33	0.1629441	-0.024951	0.3422425	0.14655
sp Q5RKI1 Eukaryotic i	3	6	-0.140064	-0.280349	0.0002345	0.146775
sp Q5EB81 NADH-cytoc	2	4	0.2752047	-0.142662	0.6768062	0.14705
tr D4A7Q0 Uncharacte	1	2	-0.251543	-0.611073	0.1076462	0.1475125
sp Q8VII6 C Choline trar	9	16	0.196572	-0.060875	0.4532583	0.1478125
tr Q5D023 Dynclli2 pr	3	3	0.2189511	-0.127106	0.5864698	0.1478125
tr F1LQ82 F Uncharacte	5	10	-0.142274	-0.286938	0.0055966	0.1480875
sp P09650 Mast cell pr	15	62	-0.23054	-0.548933	0.0885682	0.1482625
tr D3ZHU9 Uncharacte	1	3	-0.208953	-0.498414	0.0653883	0.148725
sp Q5RKH0 Putative oxi	1	2	-0.235196	-0.573218	0.0890795	0.148925
tr F1LVL4 F Uncharacte	2	5	-0.283991	-0.725615	0.151986	0.149025
tr D3ZSL2 E RCG57402,	2	2	-0.23904	-0.58023	0.1340293	0.1495875
tr A0JN30 / Canopy 2 ho	4	4	-0.210784	-0.493571	0.0701779	0.1499
tr D4A9J5 I Uncharacte	3	3	-0.301028	-0.77185	0.16526	0.1499875
sp Q5PQNO Neurocalcin	2	3	0.1803763	-0.049916	0.3941044	0.150525
tr F1LW91 Uncharacte	6	7	-0.160588	-0.339642	0.0182333	0.150625
tr F1LPH5 F Uncharacte	2	3	0.3517329	-0.184949	0.9227474	0.1507375
sp P62804 Histone H4	13	52	-0.138694	-0.28313	-0.001677	0.1509375
tr F1M392 Uncharacte	7	8	0.1436761	0.0026451	0.2881789	0.1512375
tr F1M775 Uncharacte	4	7	-0.225057	-0.542411	0.0913688	0.1512625
tr E9PU73 Uncharacte	8	22	-0.151794	-0.318094	0.0151346	0.151375
sp Q62862 Dual specifi	1	3	-0.470469	-1.266613	0.3539675	0.1518875
sp Q01205 Dihydrolipo	9	18	0.1485836	-0.01243	0.3056354	0.1520625
tr F1LZF2 F Uncharacte	3	3	0.337173	-0.251594	0.95869	0.1521125
sp Q9EPH8 Polyadenyl	8	13	-0.128926	-0.248552	-0.012688	0.152275
sp P62268 40S riboson	2	3	-0.19347	-0.446969	0.0441705	0.152475
tr F1MAA5 Uncharacte	4	5	-0.226373	-0.543885	0.0894712	0.1529625
sp P20767 Ig lambda-2	5	12	-0.24882	-0.607913	0.1209559	0.153175
sp Q8R4C0 Calpain-5 O	1	2	0.3306904	-0.202876	0.8636169	0.153275
tr Q3KRE3 Guanine nu	2	8	-0.154133	-0.320052	0.0140817	0.1533875
sp P35559 Insulin-degr	1	2	-0.326043	-0.849509	0.1965951	0.1535125
tr F1LWG8 Uncharacte	4	7	1.0866228	-1.001618	3.3691071	0.1538375
sp Q75Q39 Mitochondr	2	2	0.2313113	-0.08913	0.5584046	0.1539125
tr D4A1J6 I Uncharacte	4	7	-0.189298	-0.43065	0.05203	0.1539875

sp Q4QRB4 Tubulin beta-1	7	17	0.2819048	-0.152023	0.7204056	0.1549625
tr D4A9U5 Uncharacte	1	2	0.3356405	-0.299689	0.9574127	0.1552625
tr D4A7I1 Uncharacte	2	3	0.2631856	-0.116319	0.6801229	0.1557
tr Q4KLK7 Nucleolar p	2	3	0.3187719	-0.207798	0.8358007	0.1557875
sp P15791 Calcium/cal	4	7	0.1747072	-0.035202	0.3835523	0.15615
tr D3ZE63 Uncharacte	1	9	-0.145052	-0.302256	0.0111425	0.1565375
sp P15800 Laminin sub	47	100	0.1606456	-0.022271	0.3491442	0.1570125
tr F1LU71 Uncharacte	6	13	0.1446837	-0.008037	0.2980404	0.1571875
sp P62329 Thymosin b	4	9	-0.150509	-0.313795	0.0198509	0.157475
tr F1LPT1 Uncharacte	4	5	-0.203905	-0.477436	0.0781483	0.1575125
tr D3Z8E0 Uncharacte	3	5	-0.222917	-0.541185	0.0904391	0.157975
tr F1M8B4 Uncharacte	2	2	-0.471147	-1.506664	0.5278465	0.1585
sp P62919 60S riboson	7	12	-0.140531	-0.292167	0.0048547	0.15895
sp Q64244 ADP-ribosyl	1	3	-0.26205	-0.672167	0.1464382	0.1590125
tr F1M780 Uncharacte	12	15	0.212474	-0.092861	0.5076398	0.1592125
tr Q6AY18 SAR1 gene l	3	4	-0.18645	-0.425366	0.0642277	0.1592375
tr B1WBQ5 Serine/thre	2	2	-0.247451	-0.661856	0.1583389	0.159575
tr F1M1B0 Uncharacte	2	2	0.2442709	-0.138096	0.639685	0.15965
tr F1LQ00 Uncharacte	2	2	0.2443872	-0.113826	0.6545501	0.15975
tr F1LNK0 Microtubule	2	2	0.3544911	-0.327399	1.056537	0.1598875
sp Q68FU1 Pleckstrin h	2	2	0.2386714	-0.177627	0.6205018	0.16015
tr Q7TP57 Ab2-131 OS	3	4	-0.191144	-0.441134	0.0692409	0.160475
sp P61980 Heterogene	12	28	-0.137073	-0.280035	0.0077947	0.1608875
tr Q642E5 Mevalonate	2	3	-0.203793	-0.478302	0.0721578	0.1616875
tr Q6UPE0 Choline deh	2	3	0.2212922	-0.091834	0.5487523	0.1618
tr D4A6X4 Acylphosph	2	2	0.2672967	-0.150959	0.7023151	0.162075
sp Q6P742 Proteolipid	1	3	-0.241519	-0.597581	0.1376176	0.1622625
tr F2Z3S2 Uncharacte	6	8	-0.15034	-0.318842	0.0225625	0.1628125
tr B2RYN1 Fructosamir	4	8	-0.140353	-0.289893	0.0027883	0.1630625
tr Q5XI39 Crystallin, z	1	2	-0.243435	-0.646151	0.185339	0.163125
sp Q64548 Reticulon-1	5	6	0.1914802	-0.059573	0.4830626	0.1632125
sp P50123 Glutamyl ar	1	2	0.2864541	-0.213126	0.7376825	0.1636125
tr Q7TQ85 Ac1164 OS=	4	6	0.1650312	-0.034231	0.3682468	0.1639375
tr D3Z9F8 Uncharacte	20	33	-0.120895	-0.229951	-0.011667	0.164125
tr D3ZGP9 Uncharacte	3	3	0.4739354	-0.409678	1.4514682	0.1641875
tr D3ZL10 Uncharacte	30	60	0.1352472	-0.003394	0.2754254	0.1650125
sp Q641Y2 NADHdehy	6	9	0.1884352	-0.054982	0.4401416	0.1651375
tr O89035 Mitochondr	4	6	-0.157728	-0.343879	0.0369338	0.165375
tr D3ZPD4 Uncharacte	1	2	-0.294874	-0.778472	0.1832584	0.1656
tr F1LRV9 Uncharacte	24	51	0.7748127	-0.795514	2.3428981	0.165625
tr B1WC26 N-acetylneu	6	9	-0.149647	-0.315884	0.0220314	0.1658125
tr D4A892 Uncharacte	12	33	-0.132864	-0.268774	0.0024119	0.166125
tr F1LSW0 Uncharacte	12	22	-0.181063	-0.418207	0.0681456	0.16665
sp P06765 Platelet fact	1	2	0.3012781	-0.213927	0.794476	0.166775
sp P40112 Proteasome	2	2	-0.214882	-0.548256	0.1107315	0.1674875
sp B3DMA2 Acyl-CoA de	2	3	-0.33308	-0.914351	0.2185425	0.16765
tr D3ZD10 Uncharacte	3	5	0.1844165	-0.068973	0.4389306	0.1676875
tr D3ZGP8 Uncharacte	12	24	0.1523105	-0.031849	0.328406	0.16875
sp P61212 ADP-ribosyl	3	5	-0.24186	-0.620753	0.1370114	0.169025
sp P62193 26S proteas	8	13	-0.128837	-0.253035	-0.004298	0.1700875

tr F1MA36 Uncharacte	5	8	0.2306421	-0.132393	0.5918792	0.1706375
tr Q6AZ35 Dync1i2 prc	2	4	-0.170151	-0.386753	0.0581239	0.171
tr D4A133 RCG52629 C	20	47	0.1286446	-0.000257	0.2597139	0.171575
tr D4ADU3 Uncharacte	2	4	-0.205076	-0.50118	0.0881998	0.17165
sp P24329 Thiosulfate	2	2	-0.197064	-0.483578	0.0862425	0.1721125
tr D4ADL4 Tax1 (Huma	2	6	0.1242719	0.0038863	0.2413293	0.172775
tr D4AC14 Uncharacte	1	2	-0.272443	-0.730038	0.163853	0.172875
sp P14841 Cystatin-C C	3	6	0.1823596	-0.061907	0.4372924	0.1731875
tr D3ZC07 Uncharacte	4	9	-0.203454	-0.499524	0.094881	0.1732625
sp P60669 Pleckstrin h	6	9	0.1673694	-0.048111	0.3840717	0.1733625
tr D3ZAS7 Uncharacte	2	3	-0.551929	-1.864273	0.6793492	0.173925
sp P23764 Glutathione	8	22	-0.301305	-0.819275	0.2202973	0.1739875
sp Q63610 Tropomyosi	3	5	-0.138665	-0.290064	0.0133675	0.1743
sp Q62651 Delta(3,5)-C	3	7	0.2394159	-0.151038	0.6074501	0.1746125
sp P85108 Tubulin bet	2	3	0.4886948	-0.423758	1.4344693	0.1748375
sp Q80Z29 Nicotinamic	4	4	-0.294763	-0.903697	0.2954017	0.1750625
sp P10499 Potassium v	2	2	0.3132015	-0.24351	1.0015611	0.1751625
sp P43138 DNA-(apurin	2	2	-0.289703	-0.829421	0.2721806	0.1752
tr D4ADD3 Similar to H	2	3	0.2479325	-0.140274	0.6526713	0.1754875
sp Q8CF97 Deubiquitin	1	2	-0.331268	-0.921146	0.2568067	0.176675
tr D4A8U7 Uncharacte	18	29	0.1078803	0.0220339	0.195331	0.17715
sp Q03344 ATPase inhib	3	5	0.1484611	-0.03323	0.3353007	0.1775
tr F1LT06 F Uncharacte	1	2	0.2938101	-0.228497	0.7942984	0.1775625
sp Q99PF5 Far upstream	5	9	-0.16271	-0.377153	0.0516616	0.1789875
tr D3ZSZ2 Uncharacte	2	2	-0.24861	-0.700352	0.2191535	0.1790625
sp Q63450 Calcium/cal	3	4	0.1738835	-0.089207	0.4507294	0.1795875
tr D3ZP00 Uncharacte	2	5	0.2205252	-0.132071	0.5658038	0.1797125
sp B0BN93 26S proteas	3	3	-0.168285	-0.396919	0.056825	0.180375
sp Q8CG45 Aflatoxin B1	6	8	-0.144906	-0.318108	0.0292351	0.181025
sp P32089 Tricarboxyl	10	18	0.2126986	-0.1262	0.5412861	0.1815125
tr B2RYR8 40S riboson	5	6	-0.162877	-0.376794	0.03648	0.1816625
sp P19633 Calsequestr	3	4	0.7220909	-0.866092	2.2486184	0.1824875
tr D4A1R8 RCG37481,	3	5	-0.253423	-0.689854	0.1908392	0.1830875
tr F1LR17 F Histone H2A	7	14	-0.145846	-0.322393	0.0272997	0.1838875
tr D4ADE5 RCG49977,	3	4	-0.150494	-0.338015	0.0360252	0.184025
sp B5DFC8 Eukaryotic t	4	6	-0.152756	-0.349745	0.0323075	0.1843
sp Q6P7B0 Tryptophan	22	33	0.1137215	0.0066827	0.2180286	0.1855375
tr F1M7H9 Uncharacte	2	4	-0.199392	-0.50874	0.105341	0.1860125
tr F1LUW5 Uncharacte	2	2	0.307973	-0.25361	0.8697661	0.1860375
sp P47860 6-phosphof	25	43	0.1461886	-0.033138	0.3299878	0.1866375
sp Q9R1J4 Myocilin OS	3	3	0.206445	-0.140238	0.5587897	0.186875
sp P20294 Ciliary neur	5	10	0.1247245	-0.00436	0.2510103	0.187675
sp P12749 60S riboson	5	6	-0.140895	-0.310326	0.0326577	0.1878125
tr E9PU13 Uncharacte	1	2	-0.312313	-0.880976	0.2516489	0.1881875
tr A1A5S1 PRP6 pre-m	5	5	-0.161056	-0.369645	0.0535121	0.1883125
tr D3ZGP5 RCG31562,	4	8	-0.13071	-0.27605	0.0101873	0.18915
tr F1MA17 Uncharacte	7	9	0.1462737	-0.030822	0.3251194	0.189475
sp P35745 Acylphosph	3	4	0.1376173	-0.046495	0.3165502	0.18965
sp O08815 STE20-like s	5	5	-0.195264	-0.528809	0.1313416	0.18975
sp Q9ESH6 Glutaredoxi	4	5	0.1484367	-0.072034	0.3527634	0.1897625

sp Q5PPN5 Tubulin poly	10	16	0.1726619	-0.076135	0.4283376	0.190275
sp B0BNE5 S-formylglu	2	4	0.2319245	-0.150736	0.6426198	0.1905875
sp P40307 Proteasome	3	4	-0.147611	-0.333841	0.0359455	0.190725
sp P02625 Parvalbumin	8	16	0.5362977	-0.567026	1.632246	0.1914
sp Q62771 Signal trans	2	2	-0.278195	-0.791239	0.2333153	0.191475
tr Q5M9I2 Mannosidas	2	2	-0.255513	-0.75229	0.2375086	0.1919125
sp P16617 Phosphogly	26	73	0.1725556	-0.07533	0.4182808	0.1933875
sp Q5U2X6 Coiled-coil c	2	5	-0.158629	-0.368164	0.0553169	0.1943125
tr D4A249 Similar to m	1	2	0.1895915	-0.1219	0.4901735	0.19455
tr D3ZCV0 RCG30552 C	5	7	0.5480171	-0.626534	1.7306557	0.194925
tr F1LRE2 F Uncharacte	2	2	-0.326414	-1.012758	0.4159622	0.19505
tr F1LP83 F Uncharacte	2	3	1.0591109	-1.683136	3.9960858	0.1951875
tr D3ZE72 I Methionine	1	2	-0.150327	-0.347959	0.051776	0.1958375
tr F1LM60 Uncharacte	4	4	-0.206639	-0.611894	0.1939424	0.1962125
tr D4ADE1 Uncharacte	5	6	0.1679596	-0.076907	0.3978889	0.1963
sp Q5BK18 Cytosolic Fe	2	2	-0.329901	-1.064764	0.3527598	0.1965
sp Q6AXM8 Serum para	4	4	0.2276782	-0.161708	0.6115753	0.1970375
tr F1LPT0 F Gap junctio	2	2	0.3072487	-0.287396	0.9099193	0.1970375
sp A0MZ67 Shootin-1 O	2	2	-0.268357	-0.761386	0.2384725	0.1978375
sp Q6RUV5 Ras-related	8	21	0.1428129	-0.031846	0.3286048	0.1984375
sp O89046 Coronin-1B	2	4	-0.104688	-0.188684	-0.020691	0.1988
sp Q5PPL3 Sterol-4-alp	1	2	0.211412	-0.142077	0.576307	0.2003
sp P62845 40S riboson	2	4	-0.18263	-0.466336	0.1077316	0.2013125
tr D4A962 Heterogene	2	5	-0.14637	-0.332374	0.0430677	0.201825
tr D3ZVS9 RCG54895,	4	4	0.2231952	-0.183899	0.6338359	0.201875
tr F1M3D3 Uncharacte	13	15	-0.151734	-0.355786	0.0444043	0.2019125
sp P41562 Isocitrate de	15	30	-0.122597	-0.257588	0.0105097	0.2022625
tr F1LU52 F Uncharacte	24	34	0.1412204	-0.03825	0.3263137	0.2023375
tr D3ZXH5 RCG32827,	3	3	-0.188817	-0.495359	0.1035288	0.2032
sp Q7TPB1 T-complex p	14	24	0.1047543	0.0111677	0.1953298	0.2033375
sp P61227 Ras-related	1	2	-0.213684	-0.570605	0.1583732	0.203825
sp P43278 Histone H1.	9	30	0.1237403	-0.014982	0.2607785	0.20405
tr D3ZKC6 Uncharacte	2	2	0.2006149	-0.239819	0.5955972	0.2044125
tr D3ZR87 Uncharacte	2	2	0.270919	-0.289837	0.8483679	0.2049125
sp P07483 Fatty acid-b	2	6	0.2914191	-0.275821	0.85409	0.2050625
tr F1M7T8 Uncharacte	7	9	0.6642223	-1.116603	2.4512075	0.2051
sp Q9JI85 Nucleobind	3	3	-0.244855	-0.717507	0.2162885	0.205825
tr Q5M9H7 Dnaj (Hsp40)	5	7	0.134151	-0.03003	0.2945602	0.206
tr F1M566 Uncharacte	10	23	0.1242227	-0.014523	0.2629091	0.20635
sp Q6AYN4 Phytanoyl-C	4	7	0.1378941	-0.032512	0.3102865	0.2064
tr Q6QI86 LRRG00122	1	2	-0.257803	-0.749001	0.2304662	0.2066375
sp Q6UPE1 Electron tra	4	6	0.1716503	-0.08389	0.4297933	0.2067125
tr F1LRE5 F Oxysterol-b	2	2	-0.27765	-0.872122	0.3047166	0.207475
tr E9PSU8 Uncharacte	4	6	-0.250087	-0.708279	0.2079726	0.2075375
tr Q6P9U0 Serine (Or c	5	9	0.1596397	-0.081546	0.4027652	0.2084
tr D3ZMX6 Uncharacte	1	2	-0.172596	-0.438131	0.085593	0.2089625
sp P29419 ATP synthas	2	3	0.1907577	-0.127892	0.5078064	0.2091125
sp Q9QXU8 Cytoplasmic	4	7	0.1334489	-0.022731	0.2934618	0.2092875
sp Q9R1T1 Barrier-to-a	4	10	0.120284	-0.00973	0.245746	0.20935
tr F1M789 Uncharacte	1	3	0.5021564	-0.948657	1.8773054	0.210325

tr F1M8A5 Uncharacte	2	2	-0.297943	-0.923657	0.3290077	0.2105625
tr Q56R20 Karyopherin	2	3	-0.178053	-0.469385	0.0946659	0.2106125
tr D3ZD31 Uncharacte	3	3	-0.222379	-0.698804	0.2388538	0.2108125
tr E9PTK8 E Uncharacte	4	5	-0.185751	-0.481943	0.1061037	0.2109625
tr F1M0U5 Uncharacte	2	2	0.2271279	-0.232004	0.6914982	0.2115375
tr F1MAL3 Uncharacte	13	19	0.115577	-0.001435	0.2327758	0.2117125
tr B0BNG3 Lman2 prot	2	3	-0.157775	-0.398511	0.0737922	0.21205
sp O70351 3-hydroxyac	6	17	-0.120993	-0.251711	0.0097249	0.2126625
tr E9PTJ6 E Glycylpeptid	1	2	-0.250311	-0.73101	0.2318884	0.212775
sp Q4KMC4 Glucosamin	3	4	-0.29327	-0.893262	0.3035866	0.214175
sp P01041 Cystatin-B C	3	6	-0.163008	-0.412407	0.0895611	0.2141875
tr D4A003 Uncharacte	7	9	0.1323483	-0.026462	0.2935287	0.2142
sp Q5RJR2 Twinfilin-1 C	2	2	-0.13686	-0.334376	0.0609048	0.2148625
sp Q6AXS3 Protein DEK	2	2	0.3078968	-0.307659	0.9483593	0.2160875
tr F2Z3S4 F Uncharacte	4	5	-0.195142	-0.534588	0.1683265	0.2164625
tr F1M9X1 Uncharacte	2	2	-0.502493	-1.480548	0.4358633	0.21695
tr B0BN81 Ribosomal p	8	11	-0.126055	-0.274324	0.0224412	0.2170375
tr F2Z3S8 F Uncharacte	6	16	1.0904492	-1.697504	3.8666349	0.217075
sp Q0ZCA7 C-type lectin	2	2	0.2407614	-0.231319	0.7722802	0.2173125
tr Q6QI88 LRRG00120	2	3	-0.172584	-0.451443	0.1221281	0.21735
tr D4A1A4 Uncharacte	2	2	-0.203679	-0.630891	0.2223173	0.217375
tr E9PT65 E Uncharacte	2	3	-0.218693	-0.631039	0.1922119	0.217525
tr Q9JJ10 C Neuronal C	2	2	-0.175168	-0.485209	0.1210063	0.219825
sp O35263 Platelet-act	3	4	0.1621806	-0.094528	0.4125575	0.2205625
sp P62161 Calmodulin	7	19	0.1060529	0.0048143	0.2079068	0.2206375
sp P23680 Serum amyl	1	3	-0.2458	-0.735328	0.2361493	0.220725
tr D4A311 NADH dehy	2	2	0.2260836	-0.25595	0.7305321	0.2213
sp P62744 AP-2 compl	2	3	-0.145586	-0.350667	0.0634449	0.222325
sp P50408 V-type prot	3	3	0.2128312	-0.176986	0.611083	0.2223875
tr D4AB58 Uncharacte	2	2	0.2120685	-0.210396	0.6621836	0.2224
sp Q6P7A2 Ubiquitin cc	3	4	0.1716511	-0.102127	0.4452205	0.2231625
tr B5DEL8 E NADH dehy	3	3	0.1688193	-0.096546	0.4511169	0.223275
tr D3ZL27 I Uncharacte	1	2	-0.35359	-1.141834	0.4448882	0.223725
sp Q6P7P5 Basic leucin	3	6	0.1453703	-0.069903	0.3580876	0.22445
tr D4A0E8 Protein argi	2	3	0.2296944	-0.208364	0.6734501	0.2248375
sp Q63347 26S proteas	6	7	0.1496988	-0.110639	0.4071181	0.22495
tr D4A0Q9 Uncharacte	2	2	0.3232036	-0.508172	1.2081735	0.2249875
tr D3Z9R8 RCG63555 C	1	2	0.1785938	-0.131549	0.4750604	0.2253875
sp A2RUW1 Toll-interac	2	3	0.1756568	-0.115971	0.4694164	0.2256375
sp P97629 Leucyl-cysti	2	3	-0.27139	-0.871536	0.2824617	0.2257875
tr F1LMW7 Uncharacte	1	5	-0.118562	-0.260153	0.0174799	0.2261625
sp Q5U318 Astrocytic p	7	20	0.1279769	-0.031702	0.2922583	0.2263125
sp Q6EV70 GDP-fucose	1	3	-0.15333	-0.390053	0.0839435	0.2266625
tr B2RYU2 RCG45615,	6	7	-0.144132	-0.350575	0.068414	0.226725
sp P50398 Rab GDP dis	20	44	0.1054817	0.0038539	0.2040777	0.2272
tr F1LU88 F Uncharacte	2	2	1.1321863	-2.366153	4.7860295	0.22765
tr D4A7C3 RCG50366 C	1	2	0.2544404	-0.259911	0.7757608	0.2284625
tr D3ZTC5 I Myotilin (Pr	2	2	0.9648242	-1.9514	3.9176001	0.229225
sp Q5U2Q7 Eukaryotic p	3	4	-0.170503	-0.457486	0.1259848	0.229575
sp P17046 Lysosome-a	1	2	-0.194649	-0.551601	0.1600449	0.230225

sp P34901 Syndecan-4	2	4	0.2115524	-0.307793	0.6892886	0.2308125
tr D3ZPA9 RCG32401,	1	2	-0.16819	-0.516839	0.1789201	0.2310375
tr D4A0M2 Uncharacte	3	3	0.2061834	-0.159234	0.6345111	0.231675
tr F1LQ14 Uncharacte	2	2	-0.193114	-0.643265	0.2073473	0.2325375
sp P09006 Serine prote	2	2	0.3898625	-0.698307	1.4368441	0.2331875
tr D3ZPI8 Complemer	1	2	-0.340292	-1.151473	0.4615769	0.2332
sp O08838 Amphiphysi	6	9	0.1747437	-0.127739	0.4821538	0.23375
tr D4A1B8 RCG55152,	4	6	0.1318138	-0.040891	0.3094172	0.233775
tr F1LZH4 Uncharacte	1	2	0.2086478	-0.198726	0.6169705	0.233925
sp P51886 Lumican OS	15	93	-0.132467	-0.321766	0.0476321	0.2348875
sp P27274 CD59 glycop	3	6	0.1807577	-0.136664	0.4950367	0.2355
sp Q5I0G4 Glycyl-tRNA	13	23	0.1212199	-0.027459	0.2683719	0.2357125
tr F1LSC3 Uncharacte	2	3	-0.197912	-0.570148	0.1901878	0.235775
sp P70500 CDP-diacylg	1	2	0.2012185	-0.176272	0.5800725	0.235925
tr D4ADE8 Uncharacte	12	24	-0.10641	-0.21089	-0.006741	0.236125
tr F1LM59 Uncharacte	6	6	-0.182157	-0.525548	0.1725515	0.236475
sp P97546 Neuroplasti	2	3	0.142959	-0.062701	0.3584143	0.2366375
sp Q99068 Alpha-2-ma	3	4	-0.167717	-0.45337	0.1239519	0.2369
tr E9PSR5 Uncharacte	2	3	-0.235323	-0.757843	0.2876182	0.23805
sp Q64640 Adenosine l	6	9	-0.118813	-0.259389	0.023183	0.2390125
tr Q6P3V8 Eukaryotic t	4	8	-0.131548	-0.312459	0.0443954	0.2403125
tr F1LY21 Uncharacte	7	19	0.1397915	-0.06478	0.3516149	0.2405875
sp O08949 Transcriptic	1	2	0.2553342	-0.301724	0.8006504	0.2406125
tr E9PU09 Uncharacte	19	26	0.110408	-0.007174	0.2319059	0.24085
tr D3ZJ13 Seryl-amino	5	8	0.1430325	-0.069009	0.3620752	0.24105
sp P62250 40S riboson	6	8	-0.150658	-0.394795	0.0921254	0.2412625
sp P06686 Sodium/pot	10	19	0.1239592	-0.034283	0.2869822	0.241525
tr D4A830 Uncharacte	3	3	0.1604754	-0.142	0.4785651	0.24195
sp Q5U204 Ragulator c	1	2	-0.279219	-1.050025	0.4511227	0.242425
tr Q4KLI4 Peptidyl-pro	2	4	0.1455194	-0.081186	0.3683763	0.2425125
tr Q56R17 Karyopherin	1	3	-0.180855	-0.516617	0.1438641	0.2432
sp Q9ESW0 DNA damag	9	12	0.1343368	-0.046595	0.3204489	0.2436625
sp Q2Q0I9 Fibronectin	2	3	-0.317859	-1.245496	0.606419	0.2440125
tr D3ZIF3 Uncharacte	1	2	-0.244031	-0.827307	0.3389872	0.2443375
sp Q8K4V4 Sorting nexi	4	8	-0.159453	-0.419561	0.0974669	0.244675
tr D3ZPP2 Similar to A	3	5	0.1266462	-0.049265	0.2940572	0.2447
sp P04550 Parathymos	2	6	-0.155598	-0.420872	0.1011131	0.24485
tr F1LZM7 Uncharacte	2	3	0.1838387	-0.175098	0.5474848	0.245275
tr Q06C60 BolA-like 1 (1	2	-0.173732	-0.485683	0.1444351	0.245775
tr F1LRE1 Uncharacte	6	11	-0.121711	-0.275826	0.0320571	0.246375
tr E9PTL9 Uncharacte	2	4	-0.198961	-0.586368	0.2010681	0.2465375
tr F1LS48 Uncharacte	9	19	-0.118463	-0.268712	0.0304964	0.247425
tr Q6IMX4 Phosphatidi	3	4	0.1550354	-0.113493	0.4141387	0.247575
tr Q3KRF2 High densit	11	17	-0.111885	-0.240312	0.0198151	0.2477
sp Q4KLL0 Transcriptic	4	5	-0.144266	-0.37053	0.0771172	0.2485375
tr D3ZZ38 Sorting nexi	6	7	-0.137749	-0.375748	0.1012988	0.2491125
sp A0JPJ7 Obg-like AT	7	9	0.1044005	0.0009804	0.2141926	0.24925
sp Q66H94 Peptidyl-pro	3	5	-0.146818	-0.382485	0.089246	0.250875
sp P37361 Metallothio	4	7	0.1473191	-0.105043	0.3989492	0.252775
sp P05369 Farnesyl pyr	6	10	-0.113933	-0.250943	0.0162347	0.2532

sp P10687	1-phosphat	5	10	0.1400296	-0.08132	0.3576298	0.2540875
sp P32851	Syntaxin-1A	2	2	0.3168968	-0.412565	1.0708745	0.2542375
tr D3ZE02	Uncharacte	1	2	0.2174147	-0.348482	0.7938259	0.25475
sp P04905	Glutathione	7	10	-0.130212	-0.324504	0.0614337	0.254775
sp P00564	Creatine kir	19	43	0.5861183	-1.037604	2.3038234	0.2551125
tr D3ZEL1	Uncharacte	1	2	-0.244172	-0.820792	0.3291107	0.256125
sp P09895	60S riboson	4	5	-0.137702	-0.344971	0.0650638	0.2561375
tr B2GV01	Metastasis-	4	5	-0.138929	-0.361287	0.0829694	0.2563375
sp Q99MCO	Protein pho	1	2	-0.317249	-1.149257	0.5728108	0.256775
sp Q63584	Transmemb	5	8	-0.114407	-0.25214	0.0250641	0.2572125
tr D3ZF34	Uncharacte	5	7	-0.140355	-0.372232	0.0863314	0.25765
tr D3ZHI9	Protein pho	1	2	-0.184558	-0.556177	0.184185	0.25785
sp P08699	Galectin-3 C	8	16	-0.12239	-0.293158	0.0472192	0.2580375
tr E9PTD4	Uncharacte	2	2	-0.168486	-0.489238	0.1660717	0.2584375
sp Q6AXM7	HBS1-like pi	4	7	0.1404475	-0.092618	0.3687617	0.25955
sp Q78P75	Dynein light	2	3	0.1441031	-0.134939	0.4064005	0.2596375
sp Q09073	ADP/ATP tr	5	13	0.1375132	-0.08298	0.3681442	0.2601125
sp Q66H39	ATP-binding	2	2	0.2036282	-0.283779	0.6874382	0.2605375
tr B6DYQ2	Glutathione	7	15	-0.161162	-0.464031	0.1338113	0.2606875
tr B2GV74	Kinesin light	2	2	0.1815955	-0.210377	0.5735186	0.261725
tr Q3KRC3	Signal recog	2	2	-0.183264	-0.589754	0.2197463	0.2619125
sp P38718	Brain protei	1	2	0.2758794	-0.615238	1.1421001	0.2638625
sp A0FKI7	Acyl-CoA-bi	2	3	0.1853764	-0.193872	0.5637825	0.2641625
tr D4A5J1	Similar to m	2	2	-0.163521	-0.481606	0.153962	0.2655375
tr D4A9H2	Dermatopo	3	8	-0.140317	-0.377741	0.0928466	0.2656875
tr D4A9I7	Uncharacte	2	2	0.1826704	-0.216118	0.6074704	0.2658125
tr Q3MHS8	Sin3-associat	2	2	-0.203968	-0.71431	0.2997842	0.2658625
sp Q66HRO	Solute carri	2	2	-0.215662	-0.754941	0.3316326	0.265925
tr D3ZM97	Olfactory re	1	3	-0.160325	-0.459585	0.1432671	0.2659875
tr E9PTB6	DNA-directe	2	5	-0.128161	-0.326159	0.0659791	0.26605
sp B0K025	Oligosaccha	1	2	-0.156116	-0.440323	0.1364698	0.266275
tr D3ZZW2	RCG25234 C	1	2	0.1375551	-0.084112	0.3699674	0.26645
tr D3ZL02	Uncharacte	3	3	0.1716064	-0.172315	0.5201105	0.2671125
sp P00697	Lysozyme C	3	6	0.1196431	-0.048702	0.2916755	0.267275
sp Q9Z1E1	Flotillin-1 O	12	18	0.1142648	-0.036784	0.264918	0.2678125
sp P47820	Angiotensin	5	8	-0.158579	-0.463391	0.1619757	0.2681625
sp O88767	Protein DJ-1	10	33	0.1060508	-0.016715	0.2293214	0.26845
sp P63047	Sulfotransf	2	3	0.1638889	-0.156742	0.4820918	0.26905
sp P25236	Selenoprote	2	2	-0.189261	-0.672621	0.2902397	0.269225
tr F1LMD9	Uncharacte	2	2	-0.195748	-0.682945	0.2978709	0.2695
sp P63219	Guanine nu	3	3	-0.139292	-0.378116	0.1057893	0.269675
sp Q62639	GTP-bindin	4	5	0.1305911	-0.072194	0.3346733	0.2703125
tr Q6IMX3	Acetyl-Coer	4	4	0.1638951	-0.201923	0.5318747	0.2704
tr F1LP91	F Uncharacte	2	3	0.2106856	-0.292179	0.7256647	0.2715125
tr F1M3H8	Uncharacte	2	2	-0.209839	-0.784345	0.3545097	0.2716625
tr D3ZZE3	RCG57700,	2	2	0.157519	-0.232431	0.5083034	0.271825
sp P60522	Gamma-am	1	2	0.242666	-0.396352	0.8652622	0.2722875
tr D3ZL50	Uncharacte	4	5	0.159523	-0.180463	0.4786621	0.2725875
sp Q80WE1	Fragile X me	2	3	0.173289	-0.200383	0.5586316	0.2738625
tr D3ZJS0	C Uncharacte	1	2	0.1040612	-0.013634	0.2216931	0.2739125

sp Q5U1X1 Oligoribonu	2	2	-0.293711	-1.062881	0.4426159	0.2741625
tr Q62669 Zero beta-1	5	11	-0.182881	-0.588749	0.2083301	0.2742625
tr F1M1S6 Uncharacte	1	2	-0.169768	-0.512131	0.1802786	0.274775
sp O35244 Peroxiredoxin	14	33	-0.117829	-0.287712	0.0512902	0.27495
sp O08618 Phosphoribosyl	4	6	-0.153093	-0.458822	0.1476738	0.2751375
tr F1LNYS Uncharacte	2	4	0.1342031	-0.08983	0.3569445	0.275225
sp P16290 Phosphogly	7	10	0.429139	-0.875935	1.7100292	0.275275
sp A1A5P0 Cdc42 effec	1	2	0.1950297	-0.279224	0.691543	0.2765
tr B2GUU6 Vitamin K epo	1	2	-0.139526	-0.39204	0.1092909	0.276825
sp Q6Q760 Sodium leak	1	2	0.1746803	-0.206025	0.5753561	0.2770875
tr F1LVE2 Uncharacte	2	2	-0.201879	-0.902029	0.5051759	0.2770875
sp P02466 Collagen alp	11	38	0.1454048	-0.125237	0.4132982	0.2773
tr D4ABY2 Uncharacte	2	2	0.3029506	-0.727674	1.2716007	0.2775625
sp P31211 Corticosteroid	6	10	-0.173173	-0.545635	0.2021418	0.2792375
tr F1M2F8 Uncharacte	3	3	0.1604069	-0.175291	0.4941253	0.2795625
sp Q5BJY6 Putative N-ter	1	2	0.3829972	-1.203455	1.8127944	0.28055
sp P11517 Hemoglobin	3	12	-0.166464	-0.526622	0.1910832	0.281175
tr D3ZJJ9 Uncharacte	3	3	-0.257699	-0.945823	0.3738991	0.2815625
sp Q68FT1 Ubiquinone	2	2	0.3584492	-0.890782	1.5882565	0.2823
tr F1MA55 Uncharacte	8	13	-0.122299	-0.310626	0.0680476	0.2826625
sp Q9QXU9 ProSAAS OS	3	3	0.1551468	-0.247625	0.5403008	0.284025
tr D4A7N1 Coiled-coil-I	1	2	0.2025556	-0.354898	0.7701241	0.2842
sp P81799 N-acetyl-D-t	2	2	-0.170499	-0.549438	0.1998556	0.28455
sp P09606 Glutamine s	7	8	-0.158639	-0.496284	0.1690648	0.2847625
sp P28064 Proteasome	2	3	-0.156811	-0.485764	0.1788053	0.284925
tr B5DFD8 SH3-binding	7	11	-0.112585	-0.273028	0.0453934	0.2852125
tr D3ZXH0 Uncharacte	2	2	-0.166531	-0.557942	0.2496002	0.28525
sp P42123 L-lactate de	18	54	0.096305	-0.001327	0.1943552	0.285475
tr Q68FX8 Peptidase (I	1	3	0.1402234	-0.120417	0.3945825	0.2863875
sp P05708 Hexokinase	24	47	0.1024853	-0.020071	0.2233628	0.286525
tr F1LVX2 Uncharacte	3	3	0.1551031	-0.179302	0.5045792	0.286575
tr F1M0Z4 Uncharacte	2	2	0.1604314	-0.205731	0.543649	0.2866875
sp POC089 Protein-tyro	1	2	0.179119	-0.229131	0.5730209	0.2867
sp P17475 Alpha-1-ant	18	100	0.1483122	-0.150973	0.4347708	0.287025
tr D4A115 Uncharacte	16	29	0.1322204	-0.101189	0.3705037	0.2883
tr D3ZAP9 Uncharacte	5	6	-0.127319	-0.345459	0.0907116	0.2886625
tr Q499Q4 Phosphoglu	22	36	0.2260764	-0.37596	0.8237614	0.2887
sp Q99J82 Integrin-link	7	15	-0.115581	-0.291041	0.0546881	0.28955
tr B1WC49 Api5 protein	2	2	-0.352337	-1.712846	1.055054	0.290025
tr F1LRI2 Uncharacte	12	23	-0.092316	-0.17543	-0.013234	0.2900375
tr D3ZJF9 Galactosida	2	2	0.1561759	-0.187149	0.4881514	0.290125
sp Q62638 Golgi appar	4	5	-0.114344	-0.279328	0.0554648	0.290475
sp Q4V7A0 WD repeat	3	5	-0.138249	-0.402196	0.1133044	0.2905875
tr E9PSV5 Phosphoser	9	10	-0.106112	-0.247422	0.0357208	0.2907625
tr F1M6T2 Uncharacte	2	2	0.2331004	-0.412337	0.919566	0.290925
sp P40615 H/ACA ribo	2	2	-0.277987	-1.173147	0.6198749	0.2911375
tr F1LQ02 Uncharacte	20	31	-0.104773	-0.240268	0.0343132	0.2913
tr D4A1Q9 Uncharacte	3	4	-0.140024	-0.413005	0.1318564	0.2913375
sp P83006 Platelet-act	2	2	-0.226504	-0.853756	0.3856853	0.2918875
sp Q6MGB5 Estradiol 17	2	2	-0.274711	-1.114607	0.5155802	0.2921875

tr Q80W83 Protein pho	2	2	-0.234211	-0.894131	0.4224844	0.2922125
sp Q5SGE0 Leucine-rich	4	6	-0.131827	-0.362999	0.097865	0.29225
sp Q04462 Valyl-tRNA :	4	4	-0.120439	-0.318307	0.0750667	0.292275
sp P50442 Glycine ami	2	2	0.4744713	-1.685491	2.4642009	0.2922875
sp P05370 Glucose-6-p	15	29	-0.089582	-0.162721	-0.015734	0.292325
tr Q5M885 LOC360919	2	2	-0.287936	-1.30813	0.7040445	0.2929375
tr D4A2Y2 Uncharacte	3	4	-0.124746	-0.329135	0.0892784	0.2930125
tr F1LRB7 Uncharacte	2	5	0.1208942	-0.063316	0.3166665	0.293375
sp P15429 Beta-enolas	12	29	0.4568689	-1.07015	1.9463986	0.2934625
tr F1LVF7 Uncharacte	1	3	0.2486394	-0.481157	0.9507929	0.2942875
tr F1LM93 Uncharacte	1	2	-0.154428	-0.481819	0.1639457	0.2952375
tr F1LMC6 Uncharacte	2	2	0.6156711	-1.917213	3.2592829	0.2960375
tr D4A301 Uncharacte	43	100	-0.118599	-0.312524	0.0766643	0.2963375
sp Q02293 Protein farn	2	2	0.1506527	-0.224116	0.4855086	0.2969875
tr F1M1J4 Uncharacte	2	2	0.2515684	-0.60665	1.1101663	0.297425
tr D3ZU08 RCG46917,	4	7	0.1157212	-0.064701	0.2927354	0.2974375
tr B0K034 Putative un	1	2	-0.173602	-0.584548	0.242896	0.2976
sp P32198 Carnitine O-	1	3	0.1366152	-0.122021	0.3957907	0.2979
sp Q9ERB4- Isoform V3	6	13	0.1233281	-0.092448	0.3385525	0.2984125
sp Q5FVM4 Non-POU do	3	4	-0.144858	-0.476053	0.1578467	0.298475
tr Q5U2R9 Similar to Se	2	2	-0.188074	-0.678242	0.252664	0.2985375
sp Q66HC5 Nuclear por	2	2	-0.182825	-0.659949	0.2850892	0.2986375
sp Q63768 Adapter mo	5	8	-0.110972	-0.271252	0.0449725	0.2988875
tr F1M403 Uncharacte	7	12	0.1088981	-0.041253	0.2580492	0.299125
sp Q62902 Protein ERG	3	3	-0.152898	-0.470792	0.1653148	0.299825
sp D4A1J4 3-hydroxybi	1	2	-0.149375	-0.467658	0.157817	0.300375
sp P07895 Superoxide	7	12	0.1055347	-0.035816	0.2472099	0.30055
sp O35264 Platelet-act	5	11	0.0940238	-0.002777	0.1914792	0.3007375
sp P04692- Isoform 5 o	2	6	0.1226538	-0.078577	0.3326873	0.3010375
sp P97829- Isoform 2 o	3	5	0.1161638	-0.06442	0.3060983	0.3011
tr F1LQL5 Uncharacte	3	4	-0.128529	-0.366018	0.1151378	0.30125
tr D4A0W9 Uncharacte	16	32	-0.092277	-0.18504	-0.001473	0.3027625
tr F1LQZ4 Uncharacte	1	2	-0.198049	-0.739791	0.3292295	0.3031375
sp P08081 Clathrin ligh	1	2	-0.124027	-0.34599	0.0916574	0.30365
tr Q6IRJ7 C Annexin A7	8	10	-0.100909	-0.223243	0.0202913	0.304725
sp Q32PX2 Aminoacyl t	1	2	-0.164057	-0.548578	0.214787	0.3051
sp P63329 Serine/thre	7	8	0.0991955	-0.013802	0.2148226	0.305375
sp P11884 Aldehyde de	16	42	-0.100549	-0.22868	0.0283392	0.3057625
sp Q00238 Intercellulai	2	3	-0.293323	-1.378148	0.777532	0.3060375
tr D4A8Q6 Uncharacte	3	4	-0.141395	-0.435863	0.1588256	0.30655
tr D4A9Z8 RCG63680 (3	5	0.1161065	-0.068834	0.3082311	0.3066375
tr D3ZWB1 LSM1 homc	2	2	-0.185129	-0.768317	0.3866995	0.30665
sp P22985 Xanthine de	1	2	-0.239303	-0.926238	0.4306071	0.30715
tr D3ZFP2 Uncharacte	2	2	-0.307072	-1.576328	0.8208274	0.3072625
tr D4A8M5 Uncharacte	3	3	-0.223955	-1.004646	0.5446762	0.3074375
tr D3ZZW8 Uncharacte	2	2	-0.207984	-0.859996	0.5301914	0.307475
sp Q9JM4 Pre-mRNA-1	2	2	-0.137855	-0.495415	0.2103568	0.307725
tr D4A030 Uncharacte	2	2	0.2620515	-0.677693	1.2532791	0.30855
tr D3ZE30 Uncharacte	2	2	0.1542291	-0.211465	0.5088952	0.3088
sp P25286 V-type prot	2	3	0.1861389	-0.300799	0.686804	0.3094125

tr F1LSK5	F	Uncharacte	2	4	-0.122387	-0.376042	0.1390661	0.3103
sp P52925	High mobili		3	3	-0.148567	-0.492687	0.1857602	0.3116125
tr D4A0H4	Cullin 2 (Pre		1	2	0.1606956	-0.272122	0.5890665	0.311675
tr D4A8R6	Uncharacte		11	23	0.1136202	-0.073076	0.3071177	0.3118
tr D3ZEU9	Uncharacte		1	2	0.1886596	-0.327746	0.709643	0.3123
tr D4A8P9	Uncharacte		5	11	0.1049176	-0.048563	0.250518	0.31235
sp Q9WU82	Catenin bet		11	21	0.0951492	-0.011448	0.202614	0.314675
tr F1M1H0	Uncharacte		3	3	-0.161153	-0.572502	0.246446	0.3149
sp Q6P7R8	Estradiol 17		5	7	0.1410141	-0.152432	0.4537532	0.3152875
sp Q66HD3	Nuclear aut		2	4	0.1405807	-0.142549	0.4321193	0.3160625
sp P11507	Sarcoplasm		7	12	0.1291506	-0.130718	0.389922	0.3161125
sp Q0ZHH6	Atlastin-3 O		3	6	-0.142051	-0.459066	0.1838233	0.3162
tr D4AA77	Uncharacte		3	5	-0.121886	-0.34673	0.0969516	0.31685
sp P51635	Alcohol deh		11	28	0.0883133	0.0070345	0.1671891	0.317175
tr O54857	Phosphatas		1	2	-0.19068	-0.863623	0.4611211	0.317225
sp P51673	Cellular reti		4	6	-0.129942	-0.396419	0.1341636	0.3173375
tr D4A3V5	Similar to KI		4	4	-0.154762	-0.516871	0.1940192	0.3177625
sp P11030	Acyl-CoA-bi		7	20	-0.092653	-0.193871	0.0057688	0.3179625
tr D4A8D5	Filamin, bet		58	100	0.1018774	-0.037718	0.244303	0.318
tr E9PTX9	E Uncharacte		5	9	0.1133585	-0.080108	0.3016538	0.3184625
tr F1LTN6	F Uncharacte		1	3	-0.187888	-0.73154	0.3458035	0.3201375
sp P50609	Fibromodul		12	26	-0.115595	-0.329768	0.0858648	0.320325
tr D3ZQ44	Uncharacte		3	3	0.181131	-0.332472	0.7024468	0.3203375
sp Q561R9	Beta-lactam		2	2	-0.164793	-0.654284	0.348276	0.3204375
sp P37285	Kinesin ligh		10	15	0.1033832	-0.051204	0.2585093	0.3206
sp P85834	Elongation 1		8	14	0.0919793	-0.002812	0.1860082	0.3206875
sp Q68FP1	Gelsolin OS		30	87	0.1021136	-0.043307	0.2466072	0.3209
sp P16409	Myosin ligh		6	7	0.5968494	-2.337017	3.7122131	0.3209625
sp Q62824	Exocyst con		3	4	-0.126123	-0.391242	0.1360684	0.3213625
sp Q920A6	Retinoid-inc		3	5	-0.158907	-0.570814	0.2720763	0.321475
tr Q6MGC4	H2-K region		2	4	-0.126805	-0.362901	0.0999572	0.3218125
tr F1LMA7	Uncharacte		2	3	0.1886706	-0.366957	0.7283131	0.322075
tr D3ZD04	Uncharacte		5	6	0.1119305	-0.078749	0.3102306	0.3229125
tr Q5U330	Guanylate c		2	3	-0.139937	-0.454238	0.1719106	0.3230375
sp Q07647	Solute carri		1	2	0.1569769	-0.250799	0.5647271	0.3230625
tr B2GV08	Adaptor-rel		3	3	-0.137501	-0.451703	0.1686564	0.3231375
tr Q66HM7	Sjogren syn		4	5	-0.113479	-0.326053	0.1184173	0.32315
sp P11980-	Isoform M2		3	8	-0.11347	-0.317353	0.0901314	0.3237625
sp O55004	Ribonucleas		3	3	0.1301013	-0.154766	0.4186753	0.3238125
tr F1LR89	F Uncharacte		4	6	-0.111474	-0.328137	0.1260133	0.3241125
tr B2RYP4	Sorting nexi		5	8	-0.102036	-0.245729	0.0348536	0.324125
tr F1M8W5	Uncharacte		2	5	0.158303	-0.248499	0.5661919	0.3244125
tr D4A0A1	Uncharacte		2	2	0.1626911	-0.293007	0.6370501	0.325425
sp D4A8G9	Zinc finger f		2	2	0.1558094	-0.307999	0.6016467	0.3255125
tr F1LRL8	F Uncharacte		3	5	-0.109773	-0.305656	0.0915099	0.3264125
sp P23514	Coatomer s		4	5	-0.115065	-0.31762	0.0862947	0.32645
tr D4A3E2	Uncharacte		4	4	-0.147799	-0.529727	0.2403845	0.32655
tr F1MA38	Uncharacte		13	27	0.1080605	-0.072921	0.2920026	0.3268375
tr D3ZZH8	Glutamine f		4	4	0.1351239	-0.171245	0.4333247	0.3272625
sp Q03114	Cyclin-depe		5	10	0.1031948	-0.043524	0.2580734	0.3277875

Diabetes

sp Q09426 2-hydroxyacid dehydrogenase	4	6	0.1501085	-0.239377	0.5223539	0.3280625
sp Q8R491 EH domain-containing protein	4	5	0.1437844	-0.209575	0.4964981	0.3283
sp Q641X3 Beta-hexosaminidase	1	2	-0.146125	-0.492176	0.2037977	0.3284375
tr F1LNN0 Uncharacterized protein	5	8	0.1074246	-0.069983	0.2826822	0.3292875
tr D3ZZQ9 Uncharacterized protein	7	12	0.0999809	-0.040588	0.2358358	0.3295125
sp P21708-2 Isoform 2 of protein	12	30	0.0964819	-0.032357	0.2231093	0.3296625
sp Q6AXT5 Ras-related GTP-binding protein	2	4	0.1323584	-0.158502	0.4456374	0.329875
sp Q6IMX7 Hsp70-binding protein	2	2	-0.138264	-0.483188	0.2130023	0.329875
tr F1LXV8 Uncharacterized protein	6	9	0.1070392	-0.069757	0.2812914	0.3305375
sp P62332 ADP-ribosyl cyclase	2	3	-0.134524	-0.46575	0.2251894	0.3309875
sp Q63570 26S proteasome-associated protein	3	4	0.1388898	-0.182262	0.4646736	0.331325
tr F2Z3Q9 Uncharacterized protein	8	12	0.1071636	-0.083034	0.2851062	0.3315375
tr D3ZXH6 Uncharacterized protein	4	5	-0.118299	-0.341519	0.1037606	0.331925
tr B1H271 Slc25a42 protein	1	2	-0.137582	-0.537181	0.2628813	0.3319625
tr D3ZH40 RCG51753 protein	2	2	0.2154845	-0.622191	1.058982	0.332575
tr F1M635 Uncharacterized protein	1	2	0.1938743	-0.39998	0.8044715	0.333275
sp P70627 Glutamate decarboxylase	2	3	0.1247535	-0.129915	0.3854342	0.3335625
tr F1M471 Uncharacterized protein	3	5	0.1207624	-0.119892	0.352249	0.333625
tr F1LNI9 Uncharacterized protein	1	2	-0.179967	-0.725895	0.3787003	0.333625
tr D4A9L2 RCG34610, protein	6	9	-0.111351	-0.326312	0.1066106	0.334325
tr D4A323 Uncharacterized protein	1	2	-0.146298	-0.527657	0.2281077	0.33455
tr D3ZQ23 Uncharacterized protein	6	7	0.1210381	-0.187439	0.4183887	0.335325
tr D3ZR44 Uncharacterized protein	2	2	-0.183988	-0.777122	0.3997367	0.3361375
sp Q6U6G5 Zinc finger protein	2	2	-0.150193	-0.606948	0.298556	0.336825
sp O08651 D-3-phosphoglycerate kinase	10	20	-0.119489	-0.373507	0.1274086	0.3370125
tr F1LUX2 Uncharacterized protein	1	2	0.6908173	-2.740512	4.2488874	0.3373
tr F1LN61 Uncharacterized protein	11	43	0.2294981	-0.575516	1.043066	0.3378
tr D3ZWX4 Uncharacterized protein	3	6	0.1145976	-0.106028	0.3287054	0.3379875
sp Q6AZ50 Ubiquitin-ligase complex subunit	2	2	0.1578169	-0.383146	0.6850641	0.3381875
tr F1LZG6 Uncharacterized protein	3	3	-0.139084	-0.517629	0.2402203	0.3383125
tr D3ZNL3 Uncharacterized protein	1	2	-0.192133	-0.808367	0.386487	0.33955
tr F1LS12 Uncharacterized protein	3	3	0.113429	-0.122896	0.3406556	0.339675
tr D4A4U0 Uncharacterized protein	3	4	-0.117623	-0.36053	0.1262973	0.3399625
tr F1M0Z1 Uncharacterized protein	2	3	-0.137874	-0.52298	0.2394994	0.341025
sp Q9R0I8 Phosphatidylinositol transfer protein	3	3	0.1443512	-0.279552	0.5588254	0.3415125
sp P19804 Nucleoside diphosphate kinase	4	7	-0.092362	-0.200636	0.0165393	0.341775
tr Q5U329 Slc4a1 protein	4	5	-0.124193	-0.373169	0.1184675	0.3422375
sp P20717 Protein-arginine methyltransferase	7	14	-0.098436	-0.251586	0.0573531	0.3425
sp P35738 2-oxoisovaleric acid dehydrogenase	2	2	-0.153161	-0.675581	0.3380793	0.3425
tr Q5M9F6 5,10-methylenetetrahydrofolate reductase	2	2	-0.174932	-0.737573	0.367176	0.34255
tr B4F772 Heat shock protein	16	20	0.1033576	-0.077541	0.2859368	0.3425625
tr F1M4K5 Uncharacterized protein	2	7	-0.112745	-0.357357	0.1507467	0.3427125
tr D4ADD7 Glutaredoxin-like protein	3	5	0.1452703	-0.233431	0.5427953	0.342725
sp P15650 Long-chain base oxidoreductase	11	19	0.0915077	-0.018298	0.2069863	0.3437625
tr Q6P792 Four and a one-domain protein	8	17	-0.162481	-0.653224	0.3302876	0.343925
tr D3ZQH5 Uncharacterized protein	2	2	0.153233	-0.35226	0.6569724	0.3439875
tr D4A1G4 Uncharacterized protein	5	15	0.1042647	-0.073244	0.2866921	0.3441375
sp Q641W2 UPF0160 protein	2	3	0.1212287	-0.148612	0.3938955	0.3441875
tr D3ZK51 Uncharacterized protein	2	2	-0.133143	-0.502938	0.266283	0.34535
sp Q4KLN7 ADP-ribosyl cyclase	2	2	-0.14795	-0.593589	0.291253	0.346025

tr D3ZN39 Ubiquitin cα	3	4	0.1430396	-0.246927	0.5297987	0.3470125
tr F1M8C9 Uncharacte	2	2	-0.18737	-1.187928	0.8334648	0.34765
tr D4A4U3 Similar to m	2	4	0.1361553	-0.219184	0.4998939	0.347775
tr F1LRX5 F Uncharacte	60	100	0.0863028	-0.00407	0.1739124	0.3478875
tr D4AD39 RAD23a hom	2	2	-0.142982	-0.598274	0.3198318	0.347925
sp Q5M7A4 Ubiquitin-lil	3	3	0.1293726	-0.205651	0.4660299	0.3480125
sp P07861 Neprilysin C	4	4	0.1199172	-0.143097	0.3947137	0.3485875
tr Q5U1W8 High-mobili	3	3	-0.14184	-0.616806	0.3275823	0.3488875
sp Q8K4G6 MACRO dom	2	2	0.2711807	-1.011304	1.5714193	0.348975
sp P84586 Heterogene	4	7	-0.116331	-0.356181	0.1271538	0.348975
tr D3ZRZ1 I Uncharacte	1	3	-0.105686	-0.299401	0.0871083	0.3490125
tr D3ZBS6 I Uncharacte	2	3	0.1257224	-0.176709	0.4346249	0.349025
sp P97571 Calpain-1 cat	9	15	0.093604	-0.030062	0.2177136	0.34915
tr D3ZFK1 I Growth arre	3	3	0.150938	-0.358635	0.6475187	0.349775
sp Q8CGS4 Charged mu	2	2	-0.115822	-0.411096	0.1770818	0.3498
tr D4A4J0 I Suppressor	3	6	-0.089442	-0.197389	0.020214	0.3502875
sp P81795 Eukaryotic t	5	10	-0.097733	-0.267538	0.0853987	0.3503875
tr D4ACJ1 I 40S riboson	2	2	-0.144143	-0.63878	0.4034472	0.3503875
tr Q5PQK2 Fusion, deri	4	4	-0.118401	-0.381203	0.1455186	0.35075
sp P08009 Glutathione	3	5	0.0947296	-0.047874	0.2315363	0.3509625
sp Q5XIE8 I Integral me	1	2	-0.133496	-0.476568	0.2241309	0.3510375
tr B0BMW0 RAB14, mem	3	8	0.1120948	-0.106533	0.3301228	0.351125
tr D3ZDK7 I Similar to R	4	7	0.1022745	-0.068403	0.273556	0.351275
sp O88370 Phosphatid	1	2	-0.117561	-0.371816	0.1454504	0.3515375
tr D4A351 I Uncharacte	2	2	-0.141456	-0.606493	0.3120318	0.3516375
tr D4A5L9 I Uncharacte	8	15	0.0986811	-0.068274	0.2584414	0.35175
sp Q64591 2,4-dienoyl-	2	3	-0.126973	-0.492734	0.2401296	0.351775
sp Q568Z6 IST1 homolo	1	2	0.1299348	-0.222805	0.4711561	0.3519625
sp P13668 Stathmin O'	12	29	0.0987879	-0.060785	0.256143	0.352275
sp Q6P756 Adaptein ear	2	4	-0.105807	-0.294702	0.0903124	0.3523125
sp Q64361 Latexin OS=	2	5	0.100202	-0.077382	0.2719901	0.3524375
tr F1LPK1 F Uncharacte	2	2	0.1874096	-0.550067	0.9681123	0.3525
tr Q5XIJ7 Q Calcium bin	1	3	0.1497133	-0.375569	0.6560471	0.3525625
tr F1LM42 I Uncharacte	8	9	0.1012967	-0.065475	0.2692031	0.3533625
sp Q794F9 4F2 cell-sur	6	8	0.1139287	-0.135849	0.3648434	0.353375
sp Q5BK81 Prostagland	1	2	0.118239	-0.183956	0.4204072	0.3537
sp Q9JL3 A 4-trimethyl-	12	21	-0.084703	-0.172041	0.0025645	0.3539625
sp Q6IN36 WAS/WASL	2	3	0.1307986	-0.216722	0.4684287	0.35455
sp P52631 Signal trans	6	10	0.0880668	-0.011246	0.1853808	0.354925
tr D3ZML0 Tripeptidyl	3	4	0.1015227	-0.07579	0.2749109	0.3552875
sp O70436 Mothers ag	2	3	-0.120988	-0.396146	0.1607857	0.3554375
tr D3ZHYS1 I Threonyl-tR	2	3	-0.12066	-0.442301	0.1962206	0.3555
tr D3ZPRO Chromosom	8	12	-0.098717	-0.260381	0.0608508	0.3558875
sp P28075 Proteasome	2	3	-0.111537	-0.342328	0.1140407	0.356375
tr D3ZQC6 Uncharacte	2	2	0.1554153	-0.315888	0.6624826	0.3564
tr D3ZRD9 Similar to ic	3	8	-0.111028	-0.349121	0.1280698	0.3566375
tr D3ZJ32 C RCG21039,	6	10	-0.092517	-0.217686	0.0372481	0.3567
sp P50904 Ras GTPase	2	2	0.2013464	-0.732099	1.1073347	0.357625
tr D3ZZC5 I TNFRSF1A-α	2	2	-0.285259	-1.815756	1.2640137	0.3576875
tr F2Z3T9 F Uncharacte	3	5	-0.11376	-0.346795	0.1165604	0.3577375

sp P42346 Serine/thre	2	2	0.1433408	-0.340772	0.6210478	0.3578875
tr F1LR42 F Uncharacte	1	2	-0.13876	-0.574122	0.2674533	0.358125
sp Q6AXQ0 SUMO-activ	2	2	-0.156754	-0.742621	0.4392485	0.3583625
tr D4A9D8 Oxysterol-b	4	7	-0.104891	-0.305614	0.0967776	0.3591375
sp Q68FS2 COP9 signal	6	8	0.1014254	-0.084336	0.2794591	0.3593125
tr Q5U1Z9 Metaxin 2 C	2	2	0.1830639	-0.561726	0.935817	0.3600875
sp P19139 Casein kina	3	3	0.1329311	-0.249639	0.5208444	0.3603625
sp Q9WTT7 Basic leucin	2	4	0.1311863	-0.238364	0.4961165	0.3606125
tr D3ZFG5 RCG41300 (14	100	0.1027988	-0.092338	0.2957971	0.3610875
sp B0BNA5 Coactosin-li	6	12	-0.086039	-0.182766	0.01292	0.36205
sp P50399 Rab GDP dis	22	37	-0.087154	-0.206984	0.0364973	0.3621625
tr D3ZLP4 Uncharacte	2	3	0.1101225	-0.147611	0.3583725	0.3629
sp Q5U2R3 FERM doma	2	2	0.1413533	-0.321422	0.6150179	0.363075
sp P62836 Ras-related	2	2	0.1378237	-0.253746	0.5485314	0.3642375
tr D4A8H8 Cytoplasmic	8	11	-0.091157	-0.216671	0.0315739	0.3643125
sp Q2PQA9 Kinesin-1 he	11	17	0.0914822	-0.067133	0.2418735	0.3644625
tr F1LUZ8 F Glyceraldehy	2	2	0.2096452	-0.797704	1.1359112	0.3644875
sp P61972 Nuclear tra	3	7	-0.093417	-0.23059	0.038563	0.3646625
sp Q9QZM5 Abl interact	3	3	-0.107152	-0.382566	0.1915003	0.365225
sp B2RYG6 Ubiquitin th	5	11	0.0938098	-0.035834	0.2316009	0.365675
tr F1LPB1 F Uncharacte	11	15	0.0867702	-0.030948	0.1992926	0.3657625
tr D4A111 Procollagen	9	18	0.104532	-0.105225	0.3095685	0.3658125
tr F1LXE1 F Uncharacte	8	8	0.1185639	-0.159216	0.4075854	0.3660125
tr B2RYX0 Un Naca protei	1	2	-0.107738	-0.375052	0.1579589	0.366325
tr F1MA64 Uncharacte	1	2	-0.166537	-0.8949	0.5760743	0.36695
tr D4A927 Uncharacte	4	4	-0.124136	-0.443917	0.1937107	0.367
tr B5DEIO B Pcyox1l pro	1	3	-0.109881	-0.353396	0.1278506	0.3670125
tr F1LPC9 F Uncharacte	3	5	-0.109799	-0.366191	0.1336385	0.367325
tr F1M668 Uncharacte	2	2	-0.210102	-1.170698	0.6551053	0.367575
sp P63255 Cysteine-ric	3	5	-0.120192	-0.444301	0.2089063	0.3678
sp O70437 Mothers ag	3	4	-0.13208	-0.520709	0.2493471	0.3678625
sp Q4V7F2 Cysteine-ric	1	2	0.1052639	-0.105132	0.3213192	0.3679875
tr F1LQP9 F Uncharacte	4	8	-0.099683	-0.278398	0.084725	0.36815
tr D4ADF5 RCG53732,	3	5	0.094627	-0.09487	0.2754856	0.3687625
tr Q7TP88 Ab1-219 OS	3	6	0.1042431	-0.109512	0.3206707	0.3695375
sp P51647 Retinal deh	8	12	-0.097803	-0.27488	0.0850694	0.3697
tr D4ACC2 Uncharacte	9	14	-0.096568	-0.275732	0.0843048	0.3698875
tr F1LNJ2 F Uncharacte	6	8	-0.096232	-0.269925	0.0842718	0.370575
sp P61983 14-3-3 prot	13	27	0.0835844	-0.006849	0.1735231	0.3707125
sp Q9JJ54 Heterogene	4	8	-0.096883	-0.264741	0.0737644	0.370925
sp P02563 Myosin-6 O	1	3	0.5253733	-3.149905	4.0167096	0.3729
sp Q63616 Vacuolar pr	2	2	0.1701451	-0.590131	0.9376524	0.3729375
tr D3ZN52 Uncharacte	2	2	0.1471318	-0.45308	0.7450108	0.3731
tr D3ZWC6 Syntrophin,	14	20	0.0899326	-0.043335	0.219208	0.373175
sp Q6AYK8 Eukaryotic t	2	2	-0.101466	-0.307776	0.1080955	0.3732125
sp Q9R080 G-protein-si	2	3	0.1375253	-0.30306	0.558739	0.373425
tr B1WBY1 Cul1 proteir	3	3	0.1323521	-0.301776	0.585891	0.37345
sp Q641Y0 Dolichyl-dip	9	17	-0.08641	-0.19308	0.0191612	0.3743375
tr F1LRT5 F Uncharacte	3	4	0.1133137	-0.166492	0.3974685	0.377125
tr D3ZU13 Uncharacte	7	10	-0.094086	-0.252025	0.0577259	0.3779875

tr D3ZRB2 RCG47968,	2	6	-0.100271	-0.298294	0.0954296	0.3780125
tr F1LRJ9 F Uncharacte	14	31	-0.096988	-0.28313	0.0847239	0.3784625
sp P55053 Fatty acid-b	4	8	0.0994362	-0.133192	0.3322122	0.379625
tr F1LQF8 F Uncharacte	6	14	0.0935007	-0.047097	0.2414233	0.3799625
tr D3ZNN0 Uncharacte	3	3	0.1358356	-0.313426	0.5821533	0.3800625
tr Q5U362 Annexin A4	18	44	0.0897682	-0.047632	0.2268144	0.380775
sp P22509 rRNA 2'-O-ri	3	3	-0.123594	-0.541454	0.3150649	0.380975
tr Q5PPH9 Acidic (Leuc	7	10	-0.101611	-0.312327	0.1074841	0.3816625
sp P02764 Alpha-1-acid	9	20	0.1256449	-0.267081	0.5329287	0.381675
sp P70566 Tropomodulin	10	18	0.0858174	-0.016786	0.1956903	0.3817625
tr D4A691 Uncharacte	1	2	-0.122993	-0.519087	0.2750036	0.38205
tr F1LSL1 F Uncharacte	4	6	-0.107529	-0.389226	0.1803741	0.3825625
sp Q32PX7 Far upstream	2	3	-0.126026	-0.546462	0.3155251	0.3833
tr F1M945 Uncharacte	2	2	0.1172661	-0.289125	0.5078816	0.3838375
sp A0JPQ4 Tripartite m	2	2	0.360549	-2.869479	3.2607334	0.3851625
tr D4A348 Uncharacte	2	2	-0.152247	-0.83222	0.5301098	0.38535
tr B2GVB1 S100 calcium	8	45	0.0887612	-0.044507	0.2255422	0.3855125
sp P69897 Tubulin beta	5	16	0.1216096	-0.238729	0.4738694	0.3856375
tr B2RYN9 RGD156223	3	5	0.1149139	-0.206812	0.4384231	0.38595
sp Q8K3X8 Heat shock	2	2	-0.134905	-0.635571	0.3640232	0.3864875
tr Q5BJZ3 C Nicotinamic	6	12	0.1094245	-0.193171	0.4129726	0.3867125
sp P62909 40S riboson	6	9	-0.088603	-0.219965	0.0429875	0.3871875
sp Q66HG6 Carbonic an	1	2	-0.162486	-0.833523	0.505351	0.387325
sp Q920G2 Na(+)/H(+) i	1	2	0.1319779	-0.314969	0.5944965	0.38795
sp Q6AYG3 Protein pru	8	11	0.0858848	-0.026988	0.2051791	0.3880375
sp Q5U2R0 Methionine	2	2	0.1495715	-0.71535	0.9446694	0.38805
tr F1LPG3 F Uncharacte	4	5	-0.121766	-0.524735	0.2656792	0.388175
tr D4A7D7 Hexose-6-ph	3	3	-0.124689	-0.522925	0.2861277	0.3892875
tr F1LQC0 F Uncharacte	3	3	0.1242245	-0.341742	0.5893582	0.3894875
sp P15865 Histone H1.	12	36	-0.103736	-0.358831	0.1447797	0.39
tr E9PTR4 E Uncharacte	2	3	-0.126946	-0.569956	0.3194428	0.3905375
tr D4A8B7 MMR_HSR1	1	21	-0.097154	-0.30304	0.1145589	0.3907625
tr F1LR64 F Uncharacte	3	3	0.1600457	-0.549758	0.8548439	0.3913125
tr F1LS55 F Uncharacte	5	6	0.091942	-0.075233	0.2567646	0.3915375
sp Q704E8 ATP-binding	1	2	0.1139086	-0.219033	0.4374391	0.391825
tr F1LNR0 F Uncharacte	6	7	0.1014042	-0.162847	0.3480842	0.392475
sp Q8K4M9 Oxysterol-b	1	2	0.1160709	-0.207465	0.4498238	0.3925875
tr Q6AYD5 G1 to S pha	4	4	-0.10979	-0.476349	0.2469357	0.3933875
sp D3Z8L7 Ras-related	2	5	-0.08698	-0.216757	0.0431452	0.394025
sp P41542 General ves	8	12	-0.085162	-0.192435	0.0262526	0.394375
sp P10824 Guanine nu	2	2	0.1236886	-0.381998	0.6503569	0.3945125
sp Q6Q0N1 Cytosolic nc	12	20	-0.083153	-0.191974	0.0223992	0.3946375
sp Q63716 Peroxiredox	14	36	-0.084086	-0.194036	0.0273865	0.3946625
tr D3ZJT2 E Uncharacte	1	4	-0.11791	-0.478712	0.2338447	0.394725
sp Q3B8Q0 Microtubule	3	5	0.1036122	-0.15611	0.3659736	0.3950375
tr D4AE00 Uncharacte	2	2	0.1244796	-0.310329	0.5801869	0.3956
tr B2GV15 Dihydrolipo	5	6	-0.099232	-0.324117	0.1203229	0.395675
sp P06238 Alpha-2-ma	14	30	-0.107127	-0.40231	0.1997965	0.3978625
tr D3ZH39 Ephrin rece	1	2	0.1211441	-0.371853	0.6154807	0.3979875
tr F1LNT6 F Uncharacte	4	7	0.1011631	-0.15408	0.3560546	0.3986125

sp P02564 Myosin-7 O	12	19	0.2817557	-1.460153	2.0182285	0.398925
sp Q6MG6C N(G),N(G)-d	14	40	0.0836596	-0.028485	0.1965258	0.3991125
tr Q68FS8 C RNA termin	6	10	0.0922994	-0.085912	0.2703803	0.3995375
tr F1LP76 F Uncharacte	2	3	-0.138125	-0.828238	0.5334607	0.3998125
sp Q8VH46 Actin filame	5	7	0.0937895	-0.11366	0.2925473	0.40005
sp B0BNF1 Septin-8 OS	6	9	-0.088509	-0.238966	0.0609211	0.4001
sp P97615 Thioredoxin	2	7	-0.107912	-0.394272	0.1803698	0.4008125
sp Q5XIT1 I Microtubule	6	12	0.0837378	-0.024678	0.1945325	0.40085
tr D3ZEL2 I Similar to al	2	2	-0.168956	-1.244348	0.8533442	0.4017625
sp Q924S5 Lon proteas	5	7	-0.10065	-0.363943	0.1470097	0.4019
sp P35465 Serine/thre	4	6	0.1004301	-0.1546	0.3566523	0.4021375
sp P32738 Choline O-a	3	8	0.0903417	-0.074316	0.2552003	0.4025625
tr D3ZUM0 Uncharacte	4	7	-0.114641	-0.498177	0.2709292	0.40265
tr B4F797 E RGD131134	2	3	0.116073	-0.279802	0.5047309	0.4039125
tr F1LR19 F Uncharacte	5	7	-0.107987	-0.471936	0.2230137	0.4039375
sp Q9ES53 Ubiquitin fu	3	5	0.0970399	-0.121368	0.3164602	0.4041125
tr D3ZPU7 Uncharacte	2	2	-0.116579	-0.534772	0.3049148	0.404275
sp Q5FVI6 V-type prot	6	10	0.0879143	-0.066291	0.2378233	0.4052
sp Q66HR2 Microtubule	5	6	-0.099655	-0.32932	0.1200381	0.4052125
tr D3ZD29 I RCG60860 C	2	3	-0.105549	-0.418987	0.2251799	0.405675
tr D3ZW1H Uncharacte	2	2	0.1003291	-0.6443	0.7286432	0.4059125
tr Q5XIA5 C Coenzyme A	1	2	0.1075915	-0.228708	0.4390169	0.406
tr B2RYQ2 Protein pho	5	8	-0.089369	-0.264263	0.0873684	0.4060375
sp P63041 Complexin-	4	4	0.1094692	-0.214228	0.4413488	0.406225
tr D3ZD06 I Uncharacte	2	2	0.1513175	-0.567849	0.8717549	0.4064375
sp Q6DGG0 Peptidyl-pro	8	14	-0.080785	-0.175922	0.0130611	0.4073
tr D3ZYI0 D Uncharacte	3	7	0.107104	-0.21684	0.4535142	0.4074875
tr Q05BA4 Myadm pro	2	2	-0.125306	-0.651758	0.4224083	0.4079375
sp O08678 Serine/thre	2	2	0.1204279	-0.491887	0.7277126	0.4081
tr Q68FT7 I Phenylalan	4	7	-0.085865	-0.221352	0.0518054	0.4082125
tr D3ZEX2 I Uncharacte	1	2	0.1218507	-0.361119	0.603462	0.4084625
tr F1M9V3 Enolase (Fr	1	2	0.1703996	-0.814677	1.1103069	0.4085
tr D3ZJN9 I Uncharacte	2	2	0.1312858	-0.506206	0.7445789	0.4088125
tr D4A080 I Uncharacte	5	6	-0.103882	-0.384619	0.1741179	0.4096375
tr D3ZPL1 I Uncharacte	1	2	-0.106797	-0.503579	0.3086579	0.4105
tr D3ZZ88 I Uncharacte	2	2	-0.141352	-0.997726	0.7646709	0.4109
tr D3ZI16 D COP9 (Cons	4	5	0.0905317	-0.1004	0.2727662	0.411475
sp B2GUZ1 Ubiquitin c	1	2	-0.107463	-0.474967	0.2542565	0.4134625
sp Q6AYP7 Cytosolic 5'	2	2	-0.129826	-0.818482	0.5829479	0.4134875
tr D3ZMY7 RCG57686 C	3	5	-0.094022	-0.347843	0.1633949	0.4135625
sp P11883 Aldehyde de	2	3	-0.115684	-0.731656	0.5039026	0.413875
sp Q02769 Squalene sy	2	4	0.1122942	-0.323759	0.5465468	0.4143
tr Q71SY3 C Translin OS	2	2	0.0948311	-0.215808	0.3801649	0.414675
sp P47727 Carbonyl re	10	21	0.0860624	-0.070433	0.2436821	0.41505
sp Q2KMM: Trafficking p	1	2	-0.115001	-0.559425	0.3371721	0.416275
tr D3ZUI1 E APAF1 inter	3	3	-0.097511	-0.51669	0.3417229	0.4166625
tr D4A857 I Uncharacte	2	2	-0.09899	-0.451611	0.2276333	0.417025
tr F1LQQ1 Malic enzym	7	12	-0.086456	-0.24693	0.0650007	0.41745
tr D4A6M1 Uncharacte	7	14	0.0877197	-0.078448	0.2581935	0.4179875
sp Q6XVN8 Microtubule	2	5	0.0845825	-0.069491	0.2436032	0.4181875

tr E9PU39	I Uncharacte	5	10	0.0932693	-0.126503	0.3310634	0.419125
sp P48508	Glutamate-	2	6	0.0937892	-0.130955	0.3259623	0.42
sp B5DF89	Cullin-3 OS=	7	16	0.0827111	-0.041599	0.2045906	0.420075
tr F1M1T3	I Uncharacte	2	5	0.0839102	-0.055896	0.2287964	0.4202375
tr Q498C9	I RCG33491,	1	2	-0.098472	-0.453562	0.2734861	0.4206875
sp P62749	Hippocalcin	2	3	0.0878002	-0.101263	0.2772704	0.420775
tr D4A994	I Similar to KI	3	5	-0.093281	-0.328865	0.1472192	0.4210625
tr F1LP57	F Uncharacte	2	2	0.112133	-0.379406	0.5839477	0.421125
tr F1LPV8	F Uncharacte	5	7	-0.083434	-0.266659	0.1098852	0.4211625
tr F1LPR6	F Uncharacte	2	4	0.2306185	-1.488611	1.9389234	0.4212375
tr D3ZRK9	I Uncharacte	10	14	-0.083583	-0.213679	0.0450615	0.42125
sp P18422	Proteasome	4	5	-0.090921	-0.291178	0.109191	0.4214125
tr F1LMW6	I Uncharacte	3	3	0.092304	-0.174724	0.3545575	0.4219625
sp Q6AYT0	Quinone ox	1	2	-0.146753	-0.962398	0.6427292	0.42205
tr F1LP82	F Uncharacte	4	8	0.088737	-0.091047	0.2676366	0.4229375
tr E9PU22	I Uncharacte	2	2	0.0971631	-0.274307	0.4658468	0.423175
tr D4A3N6	I Uncharacte	2	2	0.1037405	-0.360727	0.5505281	0.4233
tr D3ZXP3	I Histone H2A	3	4	-0.107687	-0.613987	0.4442705	0.4234875
tr F1M3D1	I Uncharacte	3	3	0.1413681	-0.625696	0.9273981	0.4235875
sp P86182	Coiled-coil c	2	2	-0.110882	-0.56875	0.3416677	0.425175
tr Q32KK0	I Arylsulfatas	2	5	-0.085891	-0.26623	0.0865073	0.4253875
sp B5DFC9	Nidogen-2 C	19	32	0.0833446	-0.058428	0.2302326	0.425475
sp Q9JLH7	CDK5 regulat	2	2	0.1312196	-0.634062	0.9542154	0.4255
tr B5DEP7	I RCG56468,	2	3	0.1025403	-0.237686	0.4501253	0.4257125
sp P32577	Tyrosine-pr	2	2	-0.134306	-0.933518	0.6569978	0.425725
tr B0BMS8	Myl9 protei	1	3	-0.150233	-1.157004	0.8806019	0.425825
tr E9PTV2	E Uncharacte	2	2	-0.108456	-0.714773	0.5095305	0.4258875
tr F1LPX3	F Uncharacte	1	2	0.090031	-0.132152	0.3207704	0.4262375
tr F1LNX5	F Uncharacte	2	3	-0.119793	-0.71791	0.5012557	0.42625
tr D3ZC84	I Ubiquitin c	5	11	-0.088999	-0.276569	0.0878942	0.4265
tr F1LMA1	I Uncharacte	13	19	0.081289	-0.041384	0.2076121	0.426575
tr D3ZME8	I Uncharacte	5	13	0.0902849	-0.128867	0.3122038	0.4270375
tr D3Z9Y8	I Uncharacte	2	3	0.0971536	-0.197367	0.3936939	0.42825
tr D4A781	I Uncharacte	9	13	-0.085162	-0.263613	0.093579	0.4283125
sp P15684	Aminopepti	6	9	-0.089296	-0.294041	0.10994	0.4284875
sp P63086	Mitogen-ac	7	9	0.0820111	-0.046181	0.2183892	0.428575
sp O35095	Neurochond	8	11	0.0835934	-0.104317	0.2561957	0.42875
tr F1LVF2	F Uncharacte	2	2	0.1115629	-0.527447	0.7453642	0.4287625
tr B0BMX3	S100 calcium	1	2	0.1065763	-0.331142	0.5333132	0.4289625
sp Q5XHZ0	Heat shock	5	9	0.0893835	-0.117962	0.2968827	0.4293375
sp Q62665	Galectin-8 C	1	2	-0.106185	-0.53252	0.3006275	0.42975
tr D3ZZR5	I Uncharacte	1	3	-0.098713	-0.507387	0.3377029	0.429825
tr F1LTN3	F Uncharacte	2	4	-0.125398	-0.684533	0.4281893	0.4306625
tr D3ZGS5	I Uncharacte	3	3	-0.113404	-0.656095	0.4235528	0.4308625
sp P47853	Biglycan OS	13	43	0.0889115	-0.143557	0.3163215	0.430925
tr D3ZC89	I Uncharacte	1	2	-0.105646	-0.52561	0.3132297	0.432275
tr F1LRV6	F GMP reduc	1	2	0.1048067	-0.399153	0.5987359	0.4335
tr B2GUZ3	Mthfd1l prc	2	2	0.0898447	-0.367984	0.4952212	0.43365
tr Q5RKJ4	C Farnesyltrai	2	4	0.0934735	-0.193289	0.3896152	0.4337125
sp B5DEH2	Erlin-2 OS=F	1	2	-0.094082	-0.380559	0.1857005	0.4342125

sp P70615 Lamin-B1 O	11	22	-0.086279	-0.283703	0.1186185	0.4345875
tr Q5I0E7 C Transmemb	2	2	-0.100052	-0.552269	0.3287978	0.4346625
sp Q63525 Nuclear mig	3	3	-0.090909	-0.327949	0.1359875	0.435275
sp Q63635 Syntaxin-6 C	1	2	-0.106627	-0.625553	0.4069357	0.435575
sp Q91XR8 Phospholipi	3	4	-0.092489	-0.526209	0.3611064	0.4364
tr B0BNB1 Commd1 pr	2	2	-0.109085	-0.676249	0.4693441	0.436475
sp P54311 Guanine nu	5	8	0.0864185	-0.133984	0.3002362	0.4370625
sp B0BN18 Prefoldin su	4	5	0.0820777	-0.066715	0.2281148	0.4376375
tr D3ZQM0 Splicing fact	2	2	-0.134596	-1.188379	0.8767369	0.4376375
tr D3ZNJ5 I Similar to in	1	2	-0.099112	-0.443901	0.2189163	0.438475
sp Q5HZ4 Methylthior	7	8	0.0811949	-0.065403	0.2311918	0.4385375
tr D4AAM0 Uncharacte	2	3	-0.089323	-0.360355	0.1891821	0.4385375
tr D3ZAW4 Abhydrolase	1	2	-0.089357	-0.38065	0.2007599	0.4396875
sp Q3T1J1 I Eukaryotic t	8	20	-0.08009	-0.21277	0.0533394	0.4398125
sp Q9Z2G8 Nucleosom	2	5	-0.08639	-0.284909	0.1175764	0.440025
tr Q7TSU1 Brefeldin A-	4	5	0.0911148	-0.201567	0.3926155	0.440775
sp P20651 Serine/thre	2	2	0.1122435	-0.351726	0.6101637	0.4408625
tr F1LNU7 I Uncharacte	2	2	0.1153583	-0.592262	0.7924351	0.4433625
sp P47196 RAC-alpha s	1	2	0.0897554	-0.213373	0.3936143	0.443425
tr Q9QX80 CArG-bindir	4	8	-0.090407	-0.401559	0.2070835	0.4436375
tr D3ZFX4 I Phosphoglu	4	5	0.0911036	-0.16595	0.3486829	0.4441625
sp Q9WVK7 Hydroxyacy	11	18	-0.079312	-0.213843	0.0561659	0.4444125
tr F1M4R4 Uncharacte	3	3	-0.09649	-0.513559	0.3396656	0.4444125
tr B5DFA2 I Pik3r4 prote	2	2	-0.119187	-1.027654	0.8217407	0.4448625
sp P05371 Clusterin O	8	17	0.0800431	-0.0725	0.2310224	0.4455875
tr D4A304 I RCG29222 C	1	2	0.099327	-0.382079	0.5538606	0.44625
tr B5DER3 I Hypertroph	3	4	-0.079147	-0.301705	0.1415178	0.4463625
tr D3ZK15 I Uncharacte	3	3	0.0991848	-0.379114	0.5855761	0.446375
tr F1M6G8 Peptidyl-pro	2	3	0.0896337	-0.179525	0.3753629	0.4465375
sp P62198 26S proteas	4	6	-0.083495	-0.269769	0.1014646	0.4467875
sp Q6AXS5 Plasminoge	2	3	-0.108577	-0.612278	0.3620562	0.44715
sp Q6AYT3 tRNA-splicir	6	10	-0.079088	-0.223692	0.0717268	0.4472875
tr D4ADF4 Uncharacte	2	2	0.0997243	-0.311347	0.5409958	0.447525
sp Q64057 Alpha-amin	9	17	-0.077272	-0.184118	0.0315073	0.447975
tr F1LNBO F Uncharacte	1	2	0.0897142	-0.221635	0.4116465	0.4483875
sp P68101 Eukaryotic t	4	5	-0.085647	-0.330929	0.1650368	0.449425
tr D3ZW08 Adenylosuc	3	4	0.088149	-0.157987	0.3387641	0.4496875
sp P46413 Glutathione	8	10	0.0784102	-0.082975	0.2348013	0.4517875
tr F1M9H8 Uncharacte	2	2	0.0969762	-0.784322	0.9188223	0.4519
sp P61023 Calcium-bin	2	2	0.0796514	-0.420993	0.5606114	0.4520625
sp P07687 Epoxide hyd	4	5	-0.082933	-0.33216	0.1753891	0.4522
tr Q7TP18 C Ac2-256 OS	2	3	-0.155993	-1.064097	0.6953628	0.4524
tr E9PSW5 Uncharacte	2	2	0.1318784	-0.830239	1.1392231	0.452475
sp P29147 D-beta-hyd	2	2	-0.103129	-0.770637	0.5643594	0.4526125
tr B2GV75 D2hgdh pro	3	3	-0.109335	-0.5999	0.361044	0.452775
sp Q5BJP3 Ubiquitin-fc	3	6	-0.084969	-0.316121	0.1304754	0.45295
tr Q45QN0 Guanine nu	7	11	0.0789097	-0.06084	0.225183	0.453075
sp P17220 Proteasome	3	6	-0.082457	-0.298151	0.1346583	0.4531
sp Q4V8E4 Coiled-coil c	3	4	-0.079175	-0.353295	0.2298221	0.4531625
sp Q7TT49 Serine/thre	2	2	-0.096485	-0.606397	0.4049697	0.45325

sp P04182 Ornithine ai	3	7	0.0861013	-0.192057	0.3471601	0.453525
tr D4A1D3 Uncharacte	2	2	0.1740746	-1.597109	1.9787152	0.4547375
tr D3ZGX7 Uncharacte	2	3	-0.083957	-0.377382	0.2102774	0.454775
tr F1LUM6 Uncharacte	3	4	-0.089339	-0.492178	0.3198749	0.4558125
tr Q6P685 Eukaryotic t	3	3	0.0907716	-0.316447	0.5075834	0.456925
tr D4A492 Uncharacte	3	7	0.0798913	-0.085502	0.2482052	0.457
tr F1LXL7 F Uncharacte	1	3	-0.088904	-0.485071	0.3023606	0.45735
sp Q6P9U8 Eukaryotic t	3	3	-0.085982	-0.379659	0.2047687	0.4575625
sp Q3T1I4 Protein PRR	2	3	-0.086879	-0.419337	0.2610475	0.457825
sp Q3KRD8 Eukaryotic t	1	2	-0.086175	-0.372773	0.2036194	0.4580875
sp Q499N5 Acyl-CoA sy	3	3	-0.082157	-0.305057	0.1431086	0.4589375
tr D3ZFF9 Uncharacte	1	2	0.1055401	-0.443684	0.6771941	0.4589625
tr D3ZS68 Uncharacte	6	12	-0.077576	-0.206905	0.0488119	0.459025
sp Q5PQN7 Protein LZIC	4	4	0.0862636	-0.225705	0.4015238	0.4592375
tr F2Z3S1 F Uncharacte	1	2	0.1021637	-0.827103	1.0617506	0.4595
tr D3ZGK8 Uncharacte	2	2	-0.093771	-0.669889	0.4797747	0.460825
tr D3ZX68 Uncharacte	2	3	0.0855629	-0.233141	0.4023739	0.46095
sp Q4KM62 Palmdelphi	2	3	-0.077697	-0.278124	0.1391393	0.4619875
tr D4A8I8 Polymerase	2	10	-0.075524	-0.219921	0.0700539	0.46225
tr D4AB17 Uncharacte	4	5	-0.083157	-0.395148	0.2327676	0.4626375
sp Q6AXX6 UPF0765 pr	3	7	0.0784335	-0.11737	0.276432	0.4627625
tr Q5XIN4 Myotubular	3	3	-0.082086	-0.395441	0.2206411	0.46285
tr D3ZUM6 Uncharacte	2	3	-0.082479	-0.323754	0.1621528	0.4633375
tr B2GUZ9 Fam49b prc	3	3	0.094841	-0.284493	0.4829457	0.4646875
sp P84817 Mitochondr	2	6	0.0792426	-0.129554	0.2924725	0.464825
sp Q562C6 Leucine zipr	1	2	0.1009906	-0.292384	0.5259608	0.46495
sp Q9Z269 Vesicle-assc	2	3	0.0784808	-0.135345	0.2938397	0.465175
sp Q923V4 F-box only p	2	2	-0.088898	-0.546932	0.3753589	0.4652
tr Q5M7T6 ATPase, H+	2	3	-0.078493	-0.265694	0.1133839	0.4658375
sp Q5U2N3 Membrane-	2	2	0.1113855	-0.756379	1.0270884	0.4658625
sp Q9Z339 Glutathione	4	8	-0.079808	-0.351552	0.1823053	0.466825
tr D3ZNQ6 Ubiquitin cæ	7	7	0.0775332	-0.18811	0.3375218	0.466975
tr D4AA81 Uncharacte	2	3	0.0920605	-0.678925	0.8555215	0.467875
tr Q7TQ75 Uncharacte	1	2	0.0788198	-0.115289	0.2749412	0.4683875
tr D4A640 Proteasome	3	5	-0.076233	-0.33077	0.1873024	0.46875
tr D3ZVT2 Uncharacte	2	2	0.1178057	-0.557453	0.8619112	0.468825
sp P12368 cAMP-depe	2	4	0.0786124	-0.22562	0.3790298	0.4691
tr F1LXS3 F Uncharacte	3	5	0.0783943	-0.167554	0.3244232	0.469125
tr Q6TXH8 LRRGT0002	1	5	-0.078512	-0.305846	0.1384756	0.46925
sp O88994 MOSC dom	2	4	-0.080687	-0.316878	0.1546643	0.4707125
sp O35964 Endophilin-	4	4	0.0780149	-0.235291	0.3731718	0.4709375
sp Q9QZ86 Nucleolar p	3	3	-0.080786	-0.4903	0.3297613	0.4715625
tr F1M7S4 Uncharacte	13	23	-0.07823	-0.308322	0.1623619	0.4721
sp Q6P686 Osteoclast-	7	10	0.0747211	-0.133455	0.2754556	0.4735375
tr D4AEC0 Histone H2A	2	9	0.0822292	-0.168643	0.3417646	0.4736875
sp P48199 C-reactive p	3	5	-0.082752	-0.451202	0.3049747	0.4737375
tr D3ZNL2 Thymopoiet	3	3	-0.082837	-0.506943	0.3395706	0.47385
tr D3ZUP5 RCG56448,	2	2	-0.074698	-0.441836	0.3203269	0.4741125
tr D3ZEA8 Uncharacte	2	2	0.0869179	-0.449749	0.6265655	0.4745
tr D3ZAE5 ATPase, Ca+	5	8	0.0752668	-0.102994	0.2569086	0.47465

sp P49744 Thrombosp	4	6	0.0799075	-0.299755	0.4403258	0.4753125
tr Q3B8R6 Alpha-2-gly	1	2	-0.080954	-0.667712	0.5307128	0.4754625
tr F1M0Y9 Uncharacte	1	2	0.0803568	-0.337128	0.5035188	0.4755
sp P20762 Ig gamma-2	4	7	-0.08806	-0.714522	0.4957743	0.4756625
tr D3ZWL6 Adenosylho	2	3	0.0805665	-0.244091	0.4047594	0.4757625
tr Q505I9 C Epsin 2 OS=	4	5	0.0731848	-0.134993	0.2790194	0.47585
sp Q00657 Chondroitin	13	16	0.0742423	-0.091803	0.2430387	0.4766625
tr F1LS57 F Uncharacte	3	3	0.0775169	-0.283922	0.4334769	0.477325
sp Q920Q0 Paralemmir	10	18	0.0787006	-0.215122	0.3650358	0.4773875
tr F1LMJ9 F Uncharacte	12	15	-0.07638	-0.237866	0.0736653	0.4777125
tr D3ZJ01 C Similar to R	2	2	0.0775361	-0.407443	0.5513053	0.478
tr Q5XI19 C Fermitin far	9	13	-0.07279	-0.16128	0.0138174	0.4783875
sp Q923S8 Pantothena	2	4	0.0811727	-0.196745	0.3675623	0.478625
tr F1LQJ7 F Uncharacte	8	9	-0.074076	-0.201765	0.0593258	0.47865
tr F1LQ84 F Uncharacte	6	11	-0.075087	-0.256402	0.1007964	0.478925
tr Q499P2 I Leukotriene	11	19	-0.073073	-0.216573	0.0717791	0.4789625
tr E2RUH2 Ribonucleas	16	32	-0.072219	-0.146734	0.0037707	0.47925
sp Q5FVC2 Rho guanine	3	3	-0.080565	-0.500511	0.3325754	0.4794625
tr D3ZRE3 I Uncharacte	2	2	-0.095725	-0.642356	0.404706	0.4803
tr B5DFH2 BPY2 intera	2	5	0.0731483	-0.275376	0.4143745	0.4806375
sp Q91V33 KH domain-	3	3	-0.077596	-0.348273	0.190285	0.481
tr D3ZD73 I RCG58047 C	2	4	-0.073605	-0.479665	0.3351113	0.4813
tr D3ZGN7 Uncharacte	2	2	0.0750928	-0.633267	0.7553952	0.481325
sp P63004 Platelet-act	8	16	0.0717315	-0.064958	0.2078887	0.4814375
sp P56558 UDP-N-acet	3	3	0.0706585	-0.206738	0.3367645	0.48165
tr F1M5R5 Uncharacte	3	3	0.0774187	-0.198642	0.355002	0.4819
sp Q3MQ06 Autophagy	1	3	-0.080594	-0.594788	0.4380525	0.482
tr Q66HL0 I 5' nucleotid	3	9	-0.075404	-0.292329	0.1290996	0.4825125
tr Q68G11 Casein kinase	2	3	0.1069158	-0.678629	1.0012321	0.4831125
tr E9PU28 I Inosine-5'-n	4	5	-0.07565	-0.334021	0.1869505	0.483675
sp Q66H59 N-acetylneur	2	3	-0.076186	-0.373385	0.2130132	0.4839875
tr B2RZB6 I LSM8 homc	1	2	-0.075372	-0.402373	0.2426184	0.48435
tr D3ZCF2 I Uncharacte	1	2	-0.064092	-0.781478	0.7320484	0.484525
sp Q5XII9 F Protein FAN	3	3	0.0739414	-0.170864	0.3183961	0.4847875
sp Q641X8 Eukaryotic t	5	5	-0.074808	-0.33306	0.1771609	0.4851
tr Q1KQ07 STAT6 OS=F	2	2	-0.077257	-0.326824	0.1545747	0.485425
sp P10959 Liver carbo>	13	36	0.0746831	-0.192945	0.3410031	0.48575
tr F1LVL2 F Uncharacte	2	4	0.0732719	-0.144127	0.2893987	0.4860625
tr D3ZC00 I Uncharacte	2	2	-0.078055	-0.637162	0.47116	0.48635
tr D3ZNM9 Uncharacte	4	8	0.0748836	-0.108761	0.257705	0.486925
tr Q5RKH2 Galactokina	2	3	-0.07436	-0.297281	0.1582474	0.4869625
sp Q5FVK6 Coiled-coil :	3	5	-0.071909	-0.333099	0.1910985	0.48745
tr F1LQ99 F Uncharacte	2	5	-0.072046	-0.523436	0.3907214	0.488225
tr B3SVE9 F Neuroprote	4	6	0.0850606	-0.204833	0.3893134	0.488375
tr F1LP08 F Uncharacte	2	2	0.0771829	-0.151192	0.3159726	0.4885
sp Q63537 Synapsin-2	3	4	0.0749792	-0.221083	0.3558196	0.4893
sp Q5XIF4 I Small ubiqu	1	2	-0.07326	-0.268044	0.1172152	0.48955
tr Q6P725 I Desmin OS=	11	17	-0.077772	-0.591795	0.4436821	0.4895625
tr D3Z964 I RCG61762,	5	5	-0.075216	-0.539711	0.3683572	0.48965
sp Q5EGY4 Synaptobre	4	6	0.0720772	-0.121119	0.2693963	0.4898875

sp P60901 Proteasome	5	7	-0.071474	-0.277682	0.128598	0.490225
sp P20759 Ig gamma-1	2	3	-0.059585	-0.717934	0.6387217	0.4902375
tr D3ZII8 Uncharacte	1	2	0.071456	-0.219705	0.3556495	0.4911625
tr O88565 RAB5A, mem	2	3	0.0734986	-0.214686	0.3622208	0.4924
sp P19357 Solute carri	2	2	-0.071422	-0.459607	0.3054197	0.4926125
sp Q63524 Transmemb	1	3	-0.071731	-0.34326	0.1997644	0.4928
tr Q66H18 Synaptophy	2	3	0.0814101	-0.429625	0.6172135	0.4929
sp Q99ML5 Prenylcyste	2	3	-0.071955	-0.447362	0.3041803	0.4936375
tr D4A9K3 D-tyrosyl-tR	2	2	-0.082424	-0.497214	0.313535	0.494025
tr Q1RP74 RCG53953,	6	11	0.0708846	-0.066607	0.2137967	0.4941
sp Q99P74 Ras-related	1	2	-0.077347	-0.697062	0.515761	0.4942
sp Q5QC9 BAG family	2	3	-0.076977	-0.381837	0.2095343	0.494475
tr D4AEI5 Uncharacte	2	3	0.0718466	-0.209064	0.3645834	0.4957875
sp P62959 Histidine tri	2	5	0.0721539	-0.040349	0.1877971	0.4961
sp Q6P0K8 Junction pla	4	7	-0.071803	-0.33301	0.1908794	0.496375
sp P97576 GrpE protei	2	3	0.0707396	-0.125914	0.2610143	0.496425
tr F1MA49 Uncharacte	2	2	-0.073765	-0.474812	0.3423971	0.496525
tr B1WC34 Protein kin	5	8	-0.070841	-0.199403	0.0605022	0.4968
tr Q6IMX8 Acyl-CoA th	6	8	0.0698537	-0.086975	0.2253007	0.496925
sp P06214 Delta-amin	2	2	-0.071349	-0.43455	0.2906467	0.4969375
tr Q4KM69 COP9 (Cons	3	5	0.0721889	-0.134037	0.2915789	0.498225
tr F1LUA1 Uncharacte	4	4	0.0763978	-0.114072	0.2826571	0.49825
sp Q9R1T5 Aspartoacyl	10	20	-0.069629	-0.218094	0.0767545	0.4983375
tr F1LRK0 Uncharacte	5	6	0.0710124	-0.151531	0.3038045	0.498625
tr D3ZWM5 Histone H2f	13	74	-0.070894	-0.248127	0.1143817	0.498775
tr B0BMY8 Histone H3	2	2	-0.067984	-0.544665	0.4329538	0.49965
tr D3ZDC1 Uncharacte	2	2	0.0700308	-0.548163	0.6484727	0.500675
tr F1LPH1 Uncharacte	6	6	-0.070837	-0.209874	0.0645731	0.5018
sp Q6DGG1 Abhydrolase	3	4	-0.070441	-0.221393	0.0762733	0.501925
tr D4ACM1 Uncharacte	2	2	-0.066541	-0.695666	0.5815545	0.5022625
tr F1LNG7 Uncharacte	2	3	0.0712466	-0.235676	0.3686871	0.5025375
tr D3ZRN3 Similar to cy	1	7	-0.067889	-0.364533	0.2314042	0.502575
tr Q6AY58 B-cell recep	2	5	0.0661221	-0.10396	0.2320271	0.5027
sp Q6P7S1 Acid cerami	8	12	0.070825	-0.119477	0.2673084	0.502825
tr D4A4J7 Uncharacte	2	2	-0.07405	-0.428413	0.2598486	0.5029625
tr B0K010 Thioredoxin	2	6	-0.070025	-0.349222	0.1986028	0.502975
tr F1LYU4 Uncharacte	1	2	-0.061706	-0.894956	0.8163758	0.5031
tr Q6XDA1 Erythroid sp	2	2	0.0544997	-0.612037	0.6854558	0.5035625
sp Q792I0 Protein lin-	3	3	0.0697435	-0.224435	0.3697255	0.5037625
sp Q5EB77 Ras-related	3	3	0.0706058	-0.171972	0.3180619	0.5039875
tr Q5IOF0 Developme	4	5	-0.070548	-0.333387	0.1934721	0.5040625
sp P63170 Dynein light	2	10	0.0700001	-0.059447	0.1932547	0.504125
sp Q4G061 Eukaryotic t	2	2	0.0673309	-0.238549	0.3574027	0.504125
tr Q6MG85 1-acylglycer	1	2	0.0664937	-0.401356	0.5409358	0.504225
tr D3ZJF4 Uncharacte	7	12	-0.070156	-0.24004	0.0914128	0.5049125
tr D4A8A0 Uncharacte	5	5	-0.068387	-0.317413	0.1819185	0.505
sp Q08163 Adenylyl cy	13	34	-0.070841	-0.1321	-0.007284	0.5053625
tr D3ZSA9 Similar to pl	2	2	0.0706032	-0.627095	0.7796993	0.5055375
tr D4ABT3 RCG25673,	2	2	0.0692008	-0.334235	0.4547461	0.5063125
tr D3ZMS6 DNA-directe	3	4	0.0637216	-0.291476	0.425087	0.506375

tr D3Z8Y0 Uncharacte	5	5	-0.066954	-0.377966	0.2329854	0.5067375
sp P97834 COP9 signal	4	4	-0.066943	-0.479634	0.3604005	0.5068875
sp O35274 Neurabin-2	2	2	-0.059545	-0.566447	0.4543971	0.5072375
sp Q6P6R2 Dihydrolipo	12	26	0.0700022	-0.039118	0.1813843	0.507475
sp B0BNM9 Glycolipid ti	2	2	-0.062527	-0.568982	0.4459206	0.507675
tr D3ZVI9 Parkinson d	1	3	-0.066898	-0.256992	0.1279856	0.5077375
sp Q9QYJ4 ATP-binding	3	4	-0.072144	-0.426998	0.2796141	0.5083875
sp Q9ES40 PRA1 family	2	3	0.0664572	-0.436394	0.5813057	0.508525
tr D3ZNZ9 Histone H2E	2	2	0.0663776	-0.452767	0.5774819	0.5085875
tr F1LWH6 Uncharacte	4	4	-0.069288	-0.314627	0.1704287	0.5087125
sp Q9WVH8 Fibulin-5 OS	7	18	0.0674471	-0.264189	0.399625	0.5090875
sp P40329 Arginyl-tRN	12	18	-0.0691	-0.189259	0.0500935	0.5093
sp Q9ES54 Nuclear pro	1	2	-0.065093	-0.201359	0.0810927	0.51065
tr Q99MI5 Spermidine	2	4	-0.0671	-0.322223	0.1808215	0.511175
sp P02454 Collagen alp	13	34	0.0697581	-0.189284	0.3368916	0.5113375
tr F1LV42 F Uncharacte	7	10	0.0671879	-0.179898	0.3064722	0.51165
tr D3ZVT5 I Uncharacte	6	8	0.0661039	-0.171309	0.3111642	0.511975
sp P18886 Carnitine O-	2	3	0.0687832	-0.174119	0.3157382	0.51205
tr B2RYJ7 B ARP1 actin-	2	8	-0.071118	-0.224406	0.0780707	0.51265
tr D3ZRE7 I SWAP comp	4	8	-0.06834	-0.21453	0.0788137	0.5131375
sp P16446 Phosphatid	6	9	-0.081659	-0.320395	0.1145968	0.513925
tr D4A8E3 I Uncharacte	2	3	0.061785	-0.266854	0.3896327	0.5139375
tr D3ZXF1 I Uncharacte	3	3	0.0670232	-0.181096	0.3140099	0.5149375
tr F1LPDO F Uncharacte	13	48	-0.067511	-0.240086	0.0957479	0.5152875
sp P08733 Myosin regi	2	3	0.0207342	-1.987001	2.0759097	0.5167125
sp P14882 Propionyl-C	4	5	-0.064106	-0.297513	0.1710006	0.516875
tr D4A978 I Uncharacte	3	4	0.058918	-0.258314	0.3842626	0.5172
tr F1LS02 F Uncharacte	2	3	-0.071587	-0.413217	0.2442483	0.51765
tr F1LZX9 F Uncharacte	2	3	-0.058011	-0.437759	0.3209031	0.5180875
sp P08426 Cationic try	1	5	0.0666185	-0.199663	0.3414591	0.518875
sp Q5XHY7 Signal trans	3	3	0.0586689	-0.431372	0.5345085	0.519225
sp Q5I0D5 Phospholysi	2	2	-0.05141	-1.091884	0.9348541	0.5192625
tr D4AC36 Uncharacte	2	3	-0.067738	-0.401351	0.2648001	0.5193
sp Q5FWT1 Protein FAN	1	2	0.0542607	-0.665908	0.7552641	0.5197
tr Q7TQN4 RELA OS=R&	2	2	-0.063249	-0.375672	0.2416335	0.520525
tr F1M971 Uncharacte	2	3	0.0610269	-0.402044	0.5115373	0.5206
tr D3ZX42 I G protein-c	2	2	0.0572741	-0.326123	0.430284	0.5209875
sp P16970 ATP-binding	2	2	-0.044689	-0.471546	0.4206968	0.5215
tr Q6PDW1 40S riboson	4	5	-0.065451	-0.300438	0.1702807	0.5215375
tr D3ZY46 I Engulfment	2	4	0.0676458	-0.140193	0.2844895	0.5216625
tr F1LQM9 Uncharacte	3	4	-0.061416	-0.373895	0.2602236	0.5216625
sp Q5XI72 I Eukaryotic t	6	13	0.0678783	-0.030207	0.1634779	0.522125
sp Q9Z1M9 Structural n	3	3	0.0632515	-0.203937	0.3318593	0.522275
tr B2RYJ3 B RGD156385	3	4	0.0611024	-0.29131	0.4075258	0.5223
tr Q68FT8 RCG33981,	2	3	-0.057294	-0.476548	0.3672677	0.5223375
tr F1M260 Uncharacte	2	3	0.0566888	-0.360382	0.4754655	0.5224625
sp P61589 Transformir	8	25	0.0676388	-0.034059	0.165413	0.5225
sp Q6NX65 Programme	2	2	0.0603644	-0.271163	0.3907255	0.5225125
sp Q63644 Rho-associa	2	2	0.0655698	-0.299007	0.4395907	0.522525
tr O08769 Cyclin depe	2	2	0.0571735	-0.331151	0.4125844	0.5235125

tr D3ZTJ0 C Uncharacte	2	2	-0.042209	-0.703672	0.6559038	0.52375
sp Q9QZ76 Myoglobin (6	14	-0.031506	-1.556129	1.4627013	0.52405
tr D4A3Q7 Uncharacte	13	22	-0.066592	-0.178443	0.0469186	0.524225
tr D3ZE32 I Uncharacte	11	36	0.0651486	-0.131008	0.266934	0.5248
tr D3ZRB0 I Uncharacte	1	2	0.0272309	-1.066747	1.10956	0.5252625
sp Q4V8C3 Echinoderm	2	5	0.0656747	-0.115574	0.2477951	0.5254
tr D3Z926 I Scavenger r	2	2	-0.060268	-0.373438	0.257578	0.5254375
tr D3ZBN0 RCG23067 (8	13	-0.063961	-0.281905	0.1507857	0.5256
sp Q5U2Q3 Ester hydro	3	4	-0.054584	-0.488294	0.3691584	0.526475
sp P54921 Alpha-solub	5	9	0.0655119	-0.125012	0.2616342	0.526975
sp Q32PZ3 Protein unc	3	5	-0.060699	-0.31219	0.1952521	0.5270375
sp P01256 Calcitonin g	1	2	0.0559817	-0.380674	0.4901698	0.5277625
tr D3ZGX8 Uncharacte	1	2	-0.054334	-0.547311	0.4376911	0.528175
tr F1LN59 F Uncharacte	4	6	0.0653446	-0.14159	0.2747805	0.52935
tr F1M790 Uncharacte	3	3	-0.034803	-0.485986	0.4681292	0.5305625
sp Q08851 Syntaxin-5 (1	2	0.0550937	-0.393514	0.5081988	0.5311
tr E9PT22 E Uncharacte	9	11	-0.061095	-0.273564	0.1561425	0.5313875
tr F1LQB5 I Microtubule	1	2	0.0565229	-0.254652	0.3557249	0.5315625
sp P09951 Synapsin-1 (2	3	-0.052003	-0.435315	0.3531901	0.5317625
tr B5DFI3 B Adaptor prc	2	3	-0.043126	-0.605998	0.5234554	0.5329875
tr D3ZLM5 NHL repeat	1	2	-0.0551	-0.610776	0.4808577	0.5330875
tr Q32KJ5 C Glucosamin	1	2	0.0492851	-0.430246	0.533121	0.53345
sp P85515 Alpha-centr	5	11	0.0633347	-0.099227	0.2237933	0.533775
tr F1M7F8 Uncharacte	3	4	-0.055644	-0.406868	0.2997195	0.5339375
tr D4ACG2 IlvB (Bacteri	6	12	-0.054095	-0.395687	0.3039577	0.534125
tr F1LSZ0 F Uncharacte	3	5	-0.064197	-0.206097	0.0848549	0.5345125
sp P56574 Isocitrate de	15	34	-0.057423	-0.369835	0.2623479	0.53495
tr F1LRB8 F S-adenosylr	4	4	-0.060973	-0.283198	0.1606274	0.535325
sp Q9Z254 PDZ domair	2	3	0.0603723	-0.250347	0.384325	0.5353875
sp P07153 Dolichyl-dip	12	21	-0.066587	-0.173672	0.0394521	0.536025
sp Q08603 Geranylgera	1	2	0.0551885	-0.275807	0.3835661	0.53605
tr B4F7A3 I Hspc159 pr	1	2	0.0180695	-1.080348	1.1074718	0.5361125
tr B6DYQ9 Glutathione	4	6	0.0634239	-0.216643	0.366528	0.536375
tr D3ZDS8 I Uncharacte	1	2	-0.009192	-1.410057	1.278744	0.5363875
sp P20650 Protein pho	3	4	-0.061446	-0.316419	0.2045871	0.536475
tr Q6GMM8 Solute carri	8	15	0.0648407	-0.096718	0.23382	0.536575
tr D4ABA5 RCG35999,	3	4	-0.059476	-0.418663	0.2922877	0.5367625
tr F1M7R8 Uncharacte	3	4	-0.061405	-0.269792	0.1451658	0.5373125
sp O08839 Myc box-de	4	5	0.0582121	-0.199035	0.3117152	0.5377125
tr D3ZZ63 I Uncharacte	4	4	0.058123	-0.360826	0.4981524	0.5378375
sp Q9EQP5 Prolargin O'	22	100	0.0634508	-0.095259	0.2245617	0.537875
sp O08697 ADP-ribosyl	1	2	-0.057746	-0.300669	0.1911015	0.5385
tr F1M7P5 Uncharacte	2	2	-0.052054	-0.438465	0.3443484	0.538925
tr F1LWZ5 Uncharacte	2	3	0.0595339	-0.177608	0.3030587	0.5398125
tr Q5M9F7 ARP10 actir	5	6	-0.057786	-0.264926	0.1547895	0.5402875
sp Q6AYQ4 Transmemb	2	4	-0.053073	-0.338652	0.2503789	0.5403875
sp Q64654 Lanosterol :	2	2	0.0389253	-0.804263	0.9309415	0.540575
sp Q63610- Isoform 2 o	2	3	0.0649341	-0.42431	0.5819472	0.5407
sp O08836 Immunoglo	2	2	0.0388865	-0.675291	0.7349593	0.5412125
tr F1MA65 Uncharacte	3	3	-0.057713	-0.303441	0.1821133	0.54165

sp Q64268 Heparin cof	5	7	-0.060366	-0.432974	0.2900043	0.5417375
tr D3ZDA1 Uncharacte	2	2	0.049921	-0.405888	0.4979673	0.54185
tr F1LTF8 F Uncharacte	33	67	0.0626089	-0.09114	0.2151775	0.5432
tr F1M8H6 Uncharacte	2	2	0.0949152	-0.517233	0.9083297	0.5436875
tr D3ZVQ9 Uncharacte	1	2	0.0583564	-0.198469	0.3125389	0.5437125
tr F1LWL1 Uncharacte	2	2	-0.052149	-0.48368	0.3696194	0.5438125
sp P97608 5-oxoprolin	2	2	0.0227891	-0.912946	0.9957214	0.5443
tr D4AEG7 Uncharacte	3	4	0.057498	-0.179395	0.2968056	0.544575
tr E9PTJ4 E Uncharacte	2	3	0.0465426	-0.442273	0.5277375	0.5449875
tr D3ZF26 I Uncharacte	2	2	-0.043941	-0.465021	0.3961707	0.5451
sp Q6BBI8 Ubiquitin-fc	2	5	0.0574535	-0.126572	0.2390453	0.54575
tr F1M5Z4 Uncharacte	8	13	-0.062433	-0.207066	0.0808569	0.5458625
sp O88339 Epsin-1 OS=	2	5	-0.052786	-0.366421	0.2623492	0.5459375
tr F1LMB9 Uncharacte	3	3	0.0500537	-0.402631	0.5341226	0.5465375
tr F1LW74 Uncharacte	12	18	0.0627103	-0.061848	0.188249	0.546975
sp Q8VHK7 Hepatoma-	4	5	-0.050786	-0.394467	0.3035463	0.547225
sp Q62894 Extracellula	11	16	-0.061383	-0.245926	0.1204768	0.5480125
sp Q8K1P9 Fatty acid d	1	2	0.0896341	-0.695422	1.0316747	0.5481375
sp A2VCX1 TIP41-like p	2	2	0.0368183	-0.66666	0.7552685	0.5484
tr Q3ZB97 Adaptor-rel	14	21	-0.063669	-0.159279	0.0363895	0.5488875
tr F1M7G3 Ubiquitin cæ	2	5	-0.056708	-0.249371	0.1471559	0.549275
sp Q6MG55 Abhydrolasi	3	6	0.0202205	-0.510145	0.5050119	0.549675
sp Q9JI92 S Syntenin-1	2	2	0.0465695	-0.426203	0.5353714	0.5503375
tr D3ZDQ6 Uncharacte	2	2	0.0523932	-0.273101	0.379777	0.550475
sp Q641Y8 ATP-dependen	9	13	-0.062545	-0.1806	0.0552839	0.5506625
tr D3ZI03 C Uncharacte	1	3	-0.046764	-0.400912	0.3160542	0.5508125
sp O35796 Complemer	6	14	0.0628669	-0.096383	0.2281903	0.551
sp Q08850 Syntaxin-4 C	2	2	0.047493	-0.314537	0.4095767	0.551275
sp Q9Z1Z9 PDZ and LIN	5	8	0.0276899	-0.674081	0.7532144	0.5513
tr Q6P503 ATPase, H+	2	3	-0.005863	-0.712182	0.7830977	0.5516125
tr B5DEX4 Uncharacte	2	2	-0.056653	-0.311607	0.2049808	0.5522
tr F1LRC0 F Uncharacte	2	2	0.0377562	-0.553554	0.645826	0.55225
sp Q5I0D7 Xaa-Pro dip	7	9	-0.059344	-0.242933	0.127453	0.552725
tr D4A2D3 Uncharacte	2	2	0.0400675	-0.70839	0.8620317	0.55315
tr F1M8Z9 Uncharacte	1	2	0.0532973	-0.233207	0.3361647	0.5537
tr D3ZW55 Inosine tripl	5	11	-0.06157	-0.179915	0.0636235	0.5548625
tr D3ZPM8 Uncharacte	1	2	-0.050331	-0.460037	0.3605676	0.555275
sp P08430 UDP-glucur	2	5	0.0238532	-0.540622	0.6000031	0.5579
sp A1L108 Actin-relate	3	6	0.0497025	-0.199662	0.2940998	0.5580375
sp Q9EQR2 Alkyldihydro	3	3	-0.042022	-0.473374	0.3742623	0.55825
sp P63029 Translation	7	14	0.0604116	-0.081905	0.203164	0.5587875
tr D4ADF9 Uncharacte	2	5	-0.044777	-0.378304	0.2944172	0.5592
sp Q5FWY5 AH receptor	3	5	-0.058497	-0.227272	0.1107126	0.5595
sp B1WC97 BTB/POZ dc	1	2	-0.041799	-0.496136	0.3780563	0.5595875
tr D4A3E8 Mitochondr	1	2	0.0414825	-0.323828	0.402518	0.5597875
sp O54924 Exocyst con	6	8	-0.05736	-0.217559	0.1069366	0.5598375
tr F1LMZ8 Uncharacte	4	7	0.0565434	-0.121576	0.2303551	0.560275
tr D3ZTR3 Uncharacte	2	7	0.0464927	-0.286505	0.3787898	0.560875
tr B0BMW7 O-sialoglycc	2	2	0.0143093	-0.921438	0.9645748	0.5610125
tr B2GV79 Pdxp protei	3	4	0.0570292	-0.131065	0.2499425	0.5614875

sp Q6AYH5 Dynactin su	16	27	0.0636533	-0.023408	0.1515994	0.561575
tr D3ZQ57 Plexin B2 O'	4	5	0.0532424	-0.288063	0.3929785	0.562275
tr D4AC12 Ankyrin rep	6	7	-0.044513	-0.407753	0.3161137	0.56245
tr D3ZCJ2 Uncharacte	1	3	0.0529392	-0.151193	0.2541495	0.5628625
tr F1LYK7 F Uncharacte	6	12	0.0614708	-0.055929	0.1798295	0.5630125
sp Q5XIN6 LETM1 and	4	5	0.0586489	-0.142952	0.2738205	0.5635875
tr F1LP21 F Uncharacte	1	2	0.0315485	-0.489411	0.5595762	0.5638875
tr D3ZSQ9 Uncharacte	5	6	-0.051351	-0.298657	0.1890536	0.5639125
tr F1LPS8 F Uncharacte	7	10	-0.061722	-0.207321	0.0714405	0.5640875
sp P35572 Insulin-like	1	4	0.0563404	-0.139922	0.2631754	0.564625
sp Q9ERH3 WD repeat-	4	4	0.0367536	-0.332284	0.3923818	0.5652875
tr F1M651 Uncharacte	4	6	0.0499796	-0.205558	0.3000988	0.5654625
sp P0C0A1 Vacuolar pr	3	5	-0.047988	-0.296985	0.1989273	0.565775
sp Q5M827 Pirin OS=Ra	2	2	0.0241517	-0.690511	0.7477949	0.5659375
sp Q99MI7 NEDD8-acti	3	5	0.0578468	-0.083822	0.1980825	0.5664125
sp Q99PD4 Actin-relate	5	6	0.0600258	-0.059846	0.1814718	0.5665
tr F1LM66 Uncharacte	3	4	-0.040924	-0.439045	0.3501023	0.5665875
tr Q3B8N7 RCG21437,	2	3	0.0522452	-0.155795	0.2593213	0.5685875
sp O08629 Transcriptic	2	5	-0.039024	-0.309607	0.2592925	0.5686625
tr Q0ZFS8 RCG61099,	2	4	0.0466155	-0.241251	0.3336047	0.5689625
tr F1LTS7 F Uncharacte	1	2	-0.029292	-0.456354	0.4074036	0.570075
tr D4AAK8 Uncharacte	1	2	-0.014639	-0.722911	0.6695202	0.5701625
tr B5DFK6 Adaptor-rel	6	10	0.0539583	-0.119515	0.230797	0.5705625
tr D3ZGY2 OTU domain	2	3	-0.047174	-0.335781	0.2422774	0.5707625
sp P04631 Protein S10	6	34	0.0513461	-0.173983	0.2855581	0.5721375
tr B1WC67 RCG29001	5	9	-0.04931	-0.292311	0.1997608	0.5728
sp Q63769 Sushi repea	4	9	-0.042354	-0.365517	0.2904082	0.5728125
tr D3ZBM3 Ferrochelat	2	3	-0.056251	-0.28541	0.1584133	0.5729625
tr D3ZJB1 Microfibrilla	2	4	-0.04856	-0.33182	0.2241164	0.572975
tr F1LYY0 F Uncharacte	2	3	-0.022323	-0.495751	0.4601309	0.5733875
tr F1LMA4 Uncharacte	1	2	-0.046157	-0.328753	0.2342246	0.574125
tr F1LRS2 F Uncharacte	3	3	-0.042398	-0.37593	0.3030243	0.574425
tr Q566E2 Dnajc7 prot	3	4	0.0501757	-0.157376	0.2617937	0.574475
tr F1M7X3 Uncharacte	4	9	-0.047571	-0.329255	0.2370614	0.57525
sp Q9EPX0 Heat shock	3	3	0.0385997	-0.281024	0.3380799	0.57545
sp Q6AYA6 Uncharacte	1	2	-0.02241	-0.615482	0.5529076	0.576375
tr D3ZZU3 Uncharacte	2	2	0.0442792	-0.274508	0.3687617	0.5768
tr D3ZC40 Uncharacte	3	3	-0.042909	-0.37805	0.2962953	0.577
tr D4ACH3 Uncharacte	2	6	-0.048746	-0.279531	0.175572	0.5770125
tr Q4KLJ0 High mobili	3	7	0.045789	-0.20053	0.2863723	0.5792
tr D4A7D8 Uncharacte	3	3	0.024063	-0.43623	0.5120768	0.5798125
tr D4A1P3 RCG61051,	2	4	-0.060057	-0.180885	0.0590454	0.58
sp O35795 Ectonucleos	7	13	-0.057418	-0.194962	0.0764121	0.58055
tr D3ZCD4 Uncharacte	2	2	-0.031543	-0.503154	0.4381097	0.5808625
sp O08700 Vacuolar pr	1	2	-0.031406	-0.46845	0.3974519	0.5809125
sp Q566C7 Diphosphoi	1	2	-0.048733	-0.250025	0.1592718	0.5812125
tr D4AD70 Uncharacte	2	2	0.0035418	-0.786386	0.7564646	0.581425
tr D3ZD19 Extracellula	3	4	-0.039702	-0.374804	0.2770627	0.581475
tr F1LRZ4 F Uncharacte	4	5	0.0443322	-0.22001	0.3040015	0.58165
tr D4A206 Uncharacte	2	3	0.0280272	-0.442143	0.5233275	0.5817875

sp Q5PPH0 Enolase-pho	4	9	-0.050859	-0.250252	0.1404523	0.5821
tr Q6QI16 LRRGT0019	3	5	0.0525792	-0.125013	0.2291359	0.5823875
tr D3ZYX5 Uncharacte	6	7	0.0444516	-0.204071	0.2817382	0.58265
tr D4A5T8 Periplakin (I	3	7	-0.053899	-0.215744	0.113869	0.582675
tr F1LM09 Ubiquitin cæ	2	3	0.0316535	-0.361928	0.4036874	0.5827
sp P61794 Lysophosph	1	2	0.0454222	-0.212974	0.3016945	0.58345
sp P30835 6-phosphof	5	9	-0.050363	-0.249548	0.1498139	0.5843
sp Q68FW9 COP9 signal	3	4	-0.041328	-0.33198	0.2455836	0.584325
tr Q5RKI5 Flightless I t	2	2	0.0233919	-0.505508	0.5700479	0.5845375
sp P28073 Proteasome	1	3	0.0525818	-0.119652	0.2301841	0.58455
tr Q6AYR1 RCG52996,	2	5	0.0502579	-0.166305	0.2695685	0.5846125
tr B1H248 Uncharacte	2	2	0.0166473	-0.582127	0.639016	0.5850125
tr F1M0G3 Uncharacte	2	2	0.0221621	-0.462451	0.4886162	0.5852
sp Q80ZG1 Synembryon	3	4	0.0401064	-0.30033	0.3966692	0.5852375
tr F1LU97 Uncharacte	2	3	0.0211103	-0.511495	0.5614164	0.58525
sp P14173 Aromatic-L-	2	2	0.0477834	-0.23558	0.356256	0.5854125
tr F1LSX8 Uncharacte	3	3	0.0382986	-0.249831	0.3386487	0.58545
tr D4A9A3 Uncharacte	3	6	0.0389292	-0.31256	0.4014763	0.5854875
tr D4AD82 Uncharacte	3	3	-0.0366629	-0.428153	0.3418332	0.5857375
tr D3Z9E1 Elastin micr	3	3	-0.006503	-0.7284	0.7098556	0.58595
tr E9PTI6 Uncharacte	4	4	-0.04579	-0.278741	0.1922611	0.5859625
sp Q66H15 Regulator o	2	2	-0.026258	-0.688967	0.6052491	0.586125
tr Q99PV2 Syntaxin bir	4	4	0.0417782	-0.27582	0.3597311	0.5863
sp P26342 Transformir	3	3	-0.041671	-0.305388	0.2266922	0.5866875
sp B2RZ37 Receptor ex	5	12	-0.054456	-0.205254	0.0973461	0.5878
tr F1MAB9 Uncharacte	3	4	-0.043741	-0.317704	0.2165761	0.5886625
tr D4A1H2 Similar to R	2	2	0.0330767	-0.370609	0.4076386	0.588725
tr Q5RJK5 Chromobox	1	2	-0.030417	-0.413437	0.3496616	0.5889125
tr D3ZBP4 Microtubule	4	4	0.0440778	-0.191979	0.2791808	0.5891375
sp Q80U96 Exportin-1 C	8	12	-0.054118	-0.207618	0.1027556	0.5893
tr D3ZYW2 Uncharacte	2	4	0.0438703	-0.195917	0.263652	0.5894375
sp P54313 Guanine nu	4	9	0.0574355	-0.061517	0.1734922	0.5902875
tr Q63910 Alpha globin	3	5	-0.007456	-0.618579	0.5741642	0.5903125
tr Q66H91 G protein-c	2	2	-0.008843	-0.627315	0.642934	0.590475
sp Q6MG49 Large prolin	2	2	0.0384766	-0.390783	0.5209646	0.590775
sp Q9ERU2 Zinc finger p	1	3	0.032897	-0.340605	0.3798059	0.5907875
tr D4A2X4 Uncharacte	3	5	-0.041133	-0.296096	0.2148629	0.590875
tr D3ZA69 Uncharacte	2	3	0.0402113	-0.239778	0.3063977	0.591175
tr D3ZJ08 Histone H3	1	2	-0.007917	-0.699055	0.6546478	0.591675
sp Q923W4 Hepatoma-	2	2	-0.020565	-0.562851	0.5541941	0.5922
tr F1LWF9 Uncharacte	21	37	0.0481559	-0.153626	0.2567509	0.59265
tr D4A2D7 Uncharacte	4	8	0.0478452	-0.156005	0.2627174	0.5931625
sp Q6AY63 ADP-sugar p	3	3	-0.030549	-0.46341	0.4009108	0.593175
tr D3ZSW9 Uncharacte	2	2	0.0247398	-0.391608	0.4391068	0.5931875
sp O88506 STE20/SPS1	6	11	-0.045056	-0.269309	0.1887486	0.5938125
tr D4A0J1 Uncharacte	5	14	0.0532188	-0.107309	0.2087421	0.59425
tr D3ZW98 Uncharacte	7	12	0.0593987	-0.042712	0.159204	0.594875
tr Q6IRI3 Protein kin	4	4	0.0373668	-0.262398	0.3276449	0.595
sp Q62881 Nucleolar p	2	3	0.0393491	-0.233491	0.3200169	0.5963625
tr Q4KLL7 Uncharacte	3	4	-0.007262	-0.471611	0.478029	0.5975625

tr F1M542 Uncharacte	1	2	-0.028448	-0.362667	0.3154573	0.5976
sp A0JPP1 Dr1-associa	2	3	-0.028756	-0.456385	0.4017399	0.5979625
sp P38062 Methionine	4	5	-0.04454	-0.274282	0.1795841	0.59875
tr B5DFG6 Car13 prote	1	3	0.0440823	-0.172965	0.2476169	0.5993125
tr D4AEK9 Uncharacte	3	4	-0.030638	-0.37758	0.3026132	0.599375
sp P39052 Dynamin-2	3	4	-0.035198	-0.312226	0.2562963	0.5996875
sp P50339 Chymase O'	10	24	-0.048199	-0.233924	0.1403563	0.60085
tr Q56R18 Karyopherin	2	4	-0.04189	-0.259153	0.1818752	0.600925
tr Q6AYS2 RCG24191 C	1	2	-0.037354	-0.312499	0.2407671	0.6013625
sp Q505J8 Phenylalanyl	2	2	0.0106175	-0.525185	0.5101187	0.6015875
tr D3ZZU1 Uncharacte	6	9	0.0504862	-0.10205	0.2052	0.603975
sp Q5XIU5 Proteasome	4	10	0.051015	-0.099166	0.2062631	0.604225
sp Q99N37 Rho GTPase	2	2	-0.0113	-0.567324	0.5289083	0.6044
tr F1LSP5 F Uncharacte	2	2	-0.016287	-0.472824	0.4270443	0.6050125
sp P11348 Dihydroptei	9	19	0.0615005	-0.009005	0.1293036	0.6052125
sp P35213 14-3-3 prot	5	5	0.0523486	-0.088761	0.187719	0.6061
sp Q5HZV9 Protein pho	8	14	-0.056885	-0.160168	0.0506267	0.6065625
tr D3ZUE2 Uncharacte	5	8	-0.044804	-0.252447	0.1591492	0.60685
sp P36365 Dimethylan	2	2	-0.001921	-0.625128	0.6371295	0.6069
sp P53987 Monocarbo	2	3	-0.042324	-0.261129	0.1819505	0.6080875
tr D3ZFY0 Selenophos	5	6	-0.049593	-0.2543	0.1389872	0.608775
tr Q498N3 Dctn4 prote	3	6	0.0356957	-0.231188	0.3047945	0.6087875
sp Q505J9 ATPase fam	1	2	0.0294611	-0.272252	0.3364245	0.6089625
sp P0C1X8 AP2-associa	9	13	0.0442267	-0.143944	0.2213595	0.6090625
sp Q497B0 Omega-ami	5	7	-0.038227	-0.301827	0.2208119	0.609075
sp P02651 Apolipoprot	19	32	0.0128717	-0.425272	0.4648378	0.6091125
tr D3ZWF5 RCG59696,	1	2	-0.035883	-0.288317	0.2158643	0.609275
sp Q63942 GTP-binding	3	4	0.0336382	-0.22297	0.2980017	0.6094625
sp Q27W01 RNA-bindin	2	2	0.016658	-0.387856	0.3942128	0.6095
sp P41499 Tyrosine-pr	5	6	0.0483521	-0.150866	0.2532161	0.610125
sp P70483 Striatin OS=	4	4	-0.04666	-0.241263	0.1478626	0.6105875
sp Q64303 Serine/thre	7	10	0.054335	-0.065477	0.1726974	0.611
tr D4A5X8 S-adenosyl	1	2	-0.04279	-0.25401	0.1654921	0.611325
sp P37397 Calponin-3	12	20	-0.046945	-0.205627	0.1198513	0.6113625
sp Q60587 Trifunctiona	13	27	0.0503215	-0.105401	0.1979292	0.6125625
tr D3ZD98 Uncharacte	4	6	0.0451246	-0.134616	0.2285069	0.612575
tr D3ZER6 Uncharacte	2	3	0.0255154	-0.298526	0.3416699	0.6126125
tr D4A870 Uncharacte	2	2	-0.000157	-0.528294	0.5350514	0.613
sp Q02589 [Protein AD	3	4	-0.030537	-0.348874	0.296206	0.6130375
sp Q66H71 Calcineurin	2	2	-0.016729	-0.494262	0.444015	0.6133
sp Q3KRD5 Mitochondr	3	5	0.0287699	-0.300869	0.3598985	0.613475
tr F1M164 Uncharacte	4	4	0.0094523	-0.494993	0.5373623	0.61395
tr D3ZWW7 Uncharacte	2	4	0.0271405	-0.268879	0.3136261	0.615
tr F1M095 Uncharacte	4	6	-0.041384	-0.242468	0.1631735	0.6158375
tr F1M6Z5 Uncharacte	5	7	-0.053559	-0.166025	0.0592274	0.6163
sp P70584 Short/branc	3	3	-0.029718	-0.427695	0.3633163	0.6164
sp Q99ND9 RWD domai	2	3	0.0385159	-0.197941	0.2730603	0.6165375
tr D3Z9J5 Uncharacte	2	2	-0.017333	-0.43947	0.3972844	0.6165875
tr Q6IN39 Hsd17b4 pr	8	11	-0.050832	-0.192418	0.0837353	0.6171625
sp Q03555- Isoform 2 o	2	2	-0.033148	-0.35504	0.2721713	0.6179375

tr D3ZMI4 Uncharacte	5	11	0.0420199	-0.157933	0.2444718	0.6191375
tr D3ZP47 Phosphohis	2	3	-0.022069	-0.435126	0.3888361	0.6201
tr D4A899 Uncharacte	3	3	-0.02249	-0.324997	0.2985223	0.6201375
sp O55156 CAP-Gly doi	1	2	-0.012128	-0.392311	0.3569899	0.62165
sp Q66HA8 Heat shock	16	28	0.0476367	-0.111625	0.2063768	0.6218125
sp Q5XII0 E Mammalian	2	3	-0.013676	-0.417515	0.3744775	0.6222875
sp Q8R424 STAM-bindin	3	3	-0.032337	-0.317452	0.2302377	0.6229125
sp Q5RK09 Eukaryotic t	2	3	-0.023156	-0.322779	0.2855239	0.623025
tr D4A4T0 STIP1 homo	4	5	0.0475525	-0.104515	0.1966463	0.623175
tr F1LTJ5 F: Uncharacte	14	35	0.0451263	-0.13063	0.2251082	0.6232625
sp O35889 Afadin OS=F	5	5	0.0291566	-0.241243	0.3135796	0.6233625
sp Q9JHW0 Proteasome	2	2	-0.017974	-0.367612	0.3495082	0.6243125
sp Q9QVC8 Peptidyl-pro	4	4	-0.040967	-0.271845	0.1740188	0.6243375
tr Q68FQ9 LanC lantibi	2	3	0.0175407	-0.345618	0.3947147	0.6244
tr D3ZFD0 Uncharacte	6	8	0.032062	-0.213275	0.2852203	0.624625
sp Q02356 AMP deami	3	3	-0.001227	-0.377373	0.4437105	0.62495
sp P26453 Basigin OS=	3	5	0.0400131	-0.167126	0.2443687	0.6249875
sp P17764 Acetyl-CoA	9	23	0.0425612	-0.149581	0.2343603	0.6254375
sp Q63413 Spliceosom	4	6	-0.042318	-0.22358	0.1402223	0.62585
sp Q498E0 Thioredoxin	3	6	0.0441031	-0.128659	0.21925	0.6282625
tr D3ZZA2 Uncharacte	7	9	0.038342	-0.161823	0.2378112	0.628725
tr A9CMB7 Aspartyl-tR	4	6	-0.023883	-0.27392	0.2549944	0.629725
sp Q9Z1N4 3'(2'),5'-bis	4	6	-0.035115	-0.252574	0.1835757	0.6305375
sp P69682 Adapton ear	3	4	0.0257453	-0.253443	0.2994677	0.6307125
tr F1LT49 F Uncharacte	6	8	0.0394115	-0.145864	0.2240393	0.631425
sp Q5HZA6 Prolyl endo	1	2	0.0281098	-0.243179	0.3100471	0.6322875
tr D3Z8X1 Uncharacte	2	3	-0.025024	-0.279266	0.2464029	0.63265
tr D3ZQ25 Fibulin 1 (Pr	6	9	0.0460883	-0.110916	0.2062496	0.633475
sp Q4KM74 Vesicle-traf	3	4	-0.034101	-0.265597	0.1935893	0.635475
tr D3ZJ46 E Tumor prot	4	4	-0.02805	-0.422059	0.3052212	0.636375
tr D4A739 Catenin (Ca	7	11	-0.028868	-0.291563	0.2327548	0.6369
tr F1M7U1 Uncharacte	5	6	0.038263	-0.148676	0.2359804	0.6371875
sp P00388 NADPH--cyt	7	12	-0.043707	-0.191858	0.1077231	0.6372
sp P84083 ADP-ribosyl	2	3	-0.036212	-0.24126	0.1667183	0.6372625
tr A9UMW1 Glutathione	8	19	0.0441079	-0.11911	0.2042371	0.6381875
tr F1LN70 F Uncharacte	1	2	0.0361446	-0.176251	0.2543323	0.6382375
sp P63331 Serine/thre	7	9	-0.051946	-0.156179	0.0551064	0.6383375
sp Q5U1Z2 Trafficking p	1	3	-0.039477	-0.221762	0.1401826	0.63945
tr D3ZIP3 Uncharacte	1	2	-0.017933	-0.341652	0.284929	0.639975
sp Q5XIT9 Methylcroto	3	4	0.0105114	-0.350449	0.3755813	0.6401625
sp Q4KMA2 UV excision	7	13	0.0517368	-0.049853	0.1508376	0.640375
tr D3ZM53 Uncharacte	9	17	-0.051086	-0.187224	0.075474	0.640575
sp Q9ER24 Ataxin-10 O	6	11	0.0434141	-0.107431	0.2010554	0.6407875
sp P43244 Matrin-3 OS	5	8	-0.034243	-0.234396	0.1674294	0.64125
tr D3ZBE5 NIMA (Neve	2	3	0.0387157	-0.140403	0.2126752	0.6417875
tr D3ZD97 DEAH (Asp-	4	6	-0.035409	-0.243539	0.165322	0.6429375
tr D3ZQM5 Uncharacte	51	100	-0.028698	-0.260256	0.2097966	0.6446625
tr O88321 Antiscreeto	2	2	0.0097616	-0.375777	0.3951805	0.6465375
sp Q08602 Geranylgera	3	3	0.0085505	-0.340808	0.355734	0.646625
tr D3ZKG1 RCG43751 (4	4	0.0264028	-0.243482	0.3033974	0.647175

sp Q6AYK6 Calcyclin-binding protein	2	2	0.0241165	-0.233276	0.2725332	0.64785
tr D4AEH3 Proteasome-associated protein	3	4	-0.019871	-0.384281	0.3251546	0.6478625
tr F1M9B2 Uncharacterized protein	4	6	0.0278185	-0.212543	0.2599668	0.6482375
sp P00762 Anionic trypsin inhibitor	1	2	-0.030234	-0.260203	0.1983125	0.6491125
sp Q5U2N0 CTP synthase	3	4	-0.014012	-0.355614	0.3144755	0.6501375
tr D4ACX1 Uncharacterized protein	2	3	-0.037777	-0.232666	0.1475873	0.6503375
sp B0BN85 Suppressor of Pseudomonas	4	5	-0.03237	-0.230109	0.1653261	0.6506625
tr B3Y9H3 S100 calcium-binding protein	4	11	0.0539817	-0.034372	0.1445697	0.6518
tr F1LW12 Uncharacterized protein	7	9	-0.030201	-0.239045	0.1789514	0.651875
sp Q68FX1 Mannose-6-phosphate isomerase	2	3	-0.019501	-0.279401	0.2463418	0.6520125
sp O35821 Myb-binding protein	4	5	-0.01427	-0.315617	0.2948156	0.652425
tr F1LYE8 Uncharacterized protein	10	19	-0.053793	-0.140062	0.0351047	0.6525125
sp Q80W92 Protein VAC14	1	2	-0.009215	-0.341022	0.3247653	0.6529625
tr D4ABR8 Lysyl-tRNA methyltransferase	4	7	-0.033097	-0.228368	0.1556345	0.653625
sp P61459 Pterin-4-alpha-monooxygenase	3	4	0.0332041	-0.20731	0.2775054	0.6549125
sp Q63135 Complemer	2	2	-0.005529	-0.388528	0.3973311	0.6550875
sp P63095 Guanine nucleotide-binding protein	6	10	0.0406922	-0.115055	0.2023481	0.6552375
tr F1M380 Uncharacterized protein	2	3	0.0008928	-0.360514	0.3816301	0.6552625
sp P17955 Nuclear pore protein	1	3	0.0050136	-0.395345	0.4269562	0.65535
sp P14659 Heat shock protein	17	36	0.0371606	-0.1427	0.2110178	0.6553625
sp O88453 Scaffold attachment protein	2	4	-0.019028	-0.296565	0.2457017	0.6560625
sp P19468 Glutamate-aminopeptidase	2	3	0.0197996	-0.242442	0.2698347	0.6579625
sp Q5PQT7 Pleckstrin homology domain-containing protein	3	3	0.0106394	-0.295243	0.3202267	0.658425
tr D3Z943 Uncharacterized protein	3	5	-0.031467	-0.24423	0.1787623	0.6585
tr D4A493 Uncharacterized protein	7	12	0.0388331	-0.112968	0.1967073	0.6611
tr D4A4L8 Similar to RPL36A	2	3	-0.022098	-0.262429	0.2293066	0.6612125
tr D3ZQL7 Similar to 21S rRNA processing protein	3	5	-0.023741	-0.279649	0.2302123	0.6617375
tr F1M6X5 Uncharacterized protein	2	4	0.0307482	-0.180152	0.2567131	0.6621125
tr D4A4L4 Uncharacterized protein	3	3	0.0107547	-0.320005	0.3556244	0.66275
tr D3ZVM5 Uncharacterized protein	4	4	0.0149838	-0.25056	0.2759191	0.6635125
tr F1LW44 Uncharacterized protein	3	4	-0.01541	-0.313205	0.2660704	0.663775
tr B4F7E8 Family with uncharacterized proteins	7	11	-0.046137	-0.163171	0.0737751	0.66405
tr D3ZEU2 Uncharacterized protein	3	4	0.0287188	-0.182019	0.2448967	0.6649875
sp Q6P4Z9 COP9 signal complex subunit	2	2	-0.01322	-0.33316	0.316664	0.6662375
tr D3ZGP4 RCG39700, putative	5	10	0.0304505	-0.173128	0.22979	0.6668125
tr Q4G079 Small inducible gene product	4	9	-0.028238	-0.250485	0.1958553	0.6668625
sp P50554 4-aminobutyrate aminotransferase	8	12	-0.019069	-0.264477	0.235477	0.6673875
sp P37805 Transgelin-2	4	5	0.032334	-0.149707	0.2204758	0.6676625
tr D3ZF54 Uncharacterized protein	3	5	-0.009459	-0.319185	0.3112439	0.668175
sp Q9QX79 Fetuin-B OS	14	49	-0.005513	-0.319849	0.3143525	0.6681875
tr Q8CHN5 Epididymal protein	2	4	-0.021585	-0.249402	0.2076439	0.671175
tr Q6IN22 Cathepsin B	4	5	0.0287484	-0.171631	0.2405751	0.671575
sp P54645 5'-AMP-activated protein kinase	2	3	0.0065007	-0.282879	0.292279	0.6742375
sp P42930 Heat shock protein	7	11	0.0409718	-0.096354	0.1817125	0.676275
sp Q5U2U2 Crk-like protein	4	4	-0.018345	-0.25146	0.220425	0.6763
sp Q562C9 1,2-dihydroxy-4-methyl-5-oxo-4,5-dihydrofuran-2-carboxylic acid	1	2	-0.009091	-0.304262	0.276462	0.67675
sp Q99PS8 Histidine-rich protein	14	36	0.0173188	-0.231771	0.2651107	0.6775875
sp P07632 Superoxide dismutase	7	37	-0.042869	-0.16979	0.0868106	0.6778625
sp P23928 Alpha-crystallin	10	28	-0.027303	-0.223505	0.1739405	0.6783
sp Q4V7C6 GMP synthase	4	10	-0.031613	-0.207179	0.143807	0.6784125

tr D3ZLN0 Uncharacte	2	3	-0.004486	-0.313263	0.2994297	0.67845
tr D3Z995 Uncharacte	2	3	-0.007436	-0.287813	0.2702457	0.6811375
sp A2RUV9 Adipocyte e	5	7	0.0201902	-0.207373	0.2544162	0.6813
sp P36876 Serine/thre	5	6	0.0371898	-0.128772	0.2134259	0.68155
tr D4A7R0 Uncharacte	2	2	0.0084781	-0.277149	0.2742137	0.6823625
tr BOBNJ4 Ethylmaloni	3	5	-0.017784	-0.260997	0.2130073	0.683625
sp P17256 Mevalonate	2	3	-0.011587	-0.277691	0.2577006	0.684025
tr F1M949 Uncharacte	7	10	0.0282924	-0.151963	0.2018519	0.6849875
tr F2Z3T7 Uncharacte	3	4	0.0018332	-0.293894	0.2891619	0.685175
tr Q5XIL4 Sorbin and	5	8	0.0353092	-0.124621	0.1964043	0.6853125
tr F1MAP9 Uncharacte	8	10	0.034637	-0.127477	0.2115522	0.685325
tr F1LM67 Uncharacte	3	3	0.0011657	-0.356072	0.3657675	0.685325
sp P21913 Succinate d	3	7	0.0205826	-0.193602	0.2358304	0.686225
sp O35094 Mitochondr	4	7	0.0033775	-0.286019	0.2922572	0.6871875
sp Q8CFN2 Cell division	1	5	-0.019004	-0.229842	0.2021902	0.687325
tr Q5U2S7 Proteasome	5	7	0.0277786	-0.15844	0.2208595	0.68825
sp P62828 GTP-binding	5	7	-0.036311	-0.177069	0.105818	0.6887
tr F1LR50 Uncharacte	1	4	0.0073839	-0.261898	0.2845131	0.6892
tr D3ZH7 Microtubule	2	3	-0.019919	-0.233446	0.1960686	0.6904
sp Q3B8Q1 Nucleolar R	3	6	-0.006347	-0.265616	0.2598808	0.6911875
sp O88637 Ethanolami	1	2	-0.001581	-0.27761	0.2899843	0.691275
tr D3ZD89 Uncharacte	4	6	0.0077362	-0.249213	0.270028	0.69175
sp P35467 Protein S10	2	3	0.011295	-0.233491	0.2513203	0.6919
tr Q5U3Z7 Serine hydr	4	6	0.0047641	-0.266717	0.276484	0.69205
sp P09495 Tropomyosi	4	12	-0.046898	-0.143676	0.0520009	0.6922875
sp Q63429 Polyubiquiti	7	28	0.0470041	-0.055946	0.1460049	0.6923625
tr F1LSQ6 Proteasome	9	19	-0.050497	-0.134589	0.0343322	0.692825
sp P08503 Medium-ch	2	2	0.0104451	-0.264493	0.2798582	0.6933625
sp P60123 RuvB-like 1	3	3	-0.014726	-0.241039	0.2111899	0.694
sp Q9JHL4-4 Isoform 4 o	7	9	-0.0162	-0.247996	0.2128917	0.69405
sp Q9JJ50 Hepatocyte	4	5	0.0198207	-0.22264	0.2649775	0.6941125
sp Q9Z270 Vesicle-assc	5	6	-0.017856	-0.226195	0.1950689	0.69435
sp Q62636 Ras-related	4	4	-0.011872	-0.313145	0.2569839	0.69615
sp P18614 Integrin alp	4	4	-0.010176	-0.279424	0.2520514	0.697
tr F1LPF5 Uncharacte	9	19	0.0347042	-0.117039	0.1789797	0.6976125
tr D3ZK62 Uncharacte	4	6	-0.022586	-0.213704	0.1746182	0.6976625
tr B2RYP5 Protein pho	4	6	-0.020242	-0.209771	0.1796772	0.6986875
sp P11915 Non-specifi	3	5	-0.008873	-0.251551	0.2434218	0.6993375
sp P97532 3-mercaptop	4	5	-0.034771	-0.173939	0.1018403	0.7027625
tr Q4QR73 Dnaj (Hsp40)	4	6	-0.018343	-0.225085	0.1748215	0.7035
sp Q4KM73 UMP-CMP k	6	11	0.0424665	-0.072032	0.1551538	0.7041125
sp P17988 Sulfotransfe	5	15	0.0187135	-0.190067	0.2271164	0.7044375
tr D3ZKG7 Inositol pol	1	2	-0.031275	-0.219714	0.154184	0.7051625
sp P61149 Heparin-bin	4	5	0.0233728	-0.161617	0.2092604	0.7060625
tr D3ZU44 Uncharacte	2	2	0.0270205	-0.144077	0.1960824	0.7077875
tr D4A746 GDP-mannose	2	3	-0.003885	-0.258126	0.241507	0.7079
sp P26376 Interferon-i	1	2	0.0003914	-0.265052	0.2677034	0.70955
tr Q499R7 Ppa1 protei	3	4	-0.01787	-0.236016	0.1887537	0.7109125
tr D3ZT90 Glutaryl-CoA	4	7	0.0205419	-0.168262	0.2123704	0.7112
sp Q62733 Lamina-assc	2	6	0.0309815	-0.114667	0.1801815	0.712

sp O35854 Branched-cl	4	6	-0.040056	-0.153965	0.0758348	0.712425
tr F1M1G5 Uncharacte	2	5	-0.029534	-0.193242	0.1253943	0.713625
tr Q5M949 Nipsnap ho	3	6	0.008735	-0.221745	0.2471846	0.713675
tr D4AEP0 Adenylosuc	6	10	0.0302908	-0.114395	0.1762564	0.7137625
tr Q4V8H5 Aspartyl am	10	16	-0.039365	-0.155582	0.0751421	0.7141875
tr D4A820 Cytochrom	12	18	0.0160887	-0.18242	0.2263162	0.715575
sp Q5FVQ4 Malectin OS	5	6	0.0042381	-0.249052	0.2555971	0.7156125
sp Q66HG4 Aldose 1-ep	2	3	0.006376	-0.237831	0.2359614	0.716025
tr Q5M9H2 Acyl-Coenz	9	17	0.0134263	-0.196438	0.2290396	0.717
sp Q9WV63 Kinesin-like	7	11	0.0219521	-0.159668	0.1994996	0.7175875
tr A1L1J8 A RAB5B, me	5	9	0.0297125	-0.115598	0.1768235	0.7181125
tr D3ZWS0 Similar to PI	7	10	0.0214609	-0.157455	0.1999311	0.7181375
sp P53042 Serine/thre	4	5	0.0155849	-0.193553	0.2375385	0.719025
sp P51583 Multifunctio	5	6	0.0247705	-0.13417	0.184374	0.7196875
sp Q6AY84 Secernin-1 (14	33	0.0053553	-0.230505	0.246617	0.72025
sp P55161 Nck-associat	5	7	0.0292254	-0.120315	0.1746374	0.7205125
tr Q5M963 Cytidine mc	3	8	-0.021602	-0.183945	0.1525043	0.72075
tr F1LQS4 F Uncharacte	45	86	0.0272322	-0.12977	0.184176	0.7208375
tr D3ZE45 Uncharacte	10	12	-0.034206	-0.163948	0.0995586	0.7212125
sp P37996 ADP-ribosyl	5	10	-0.024037	-0.188336	0.1369715	0.7213
sp P24155 Thimet oligo	8	14	-0.034598	-0.156979	0.0950318	0.7213625
tr D3ZBS2 Uncharacte	12	35	-0.00345	-0.24385	0.2414903	0.72155
sp Q6P747 Heterochro	13	23	0.0366272	-0.089159	0.1676462	0.722175
sp Q9JJ19 Na(+)/H(+) i	4	5	0.0207892	-0.151446	0.1954029	0.72245
sp Q4FZT9 26S proteas	11	15	-0.019	-0.202048	0.1712355	0.72255
sp Q9Z0V6 Thioredoxin	3	6	0.0253564	-0.137621	0.1957809	0.7228125
tr D4AB01 Histidine tri	4	9	-0.012052	-0.21401	0.1832162	0.7257875
sp Q5XI73 Rho GDP-di	11	33	0.0442288	-0.049039	0.1369159	0.727675
tr E9PU16 Uncharacte	5	9	-0.028897	-0.168933	0.1167356	0.729025
tr D4A137 Aldehyde de	3	6	-0.022632	-0.19169	0.1402309	0.7292375
tr Q5M964 Fumarate hy	10	13	0.0374355	-0.081056	0.1506202	0.7297
tr D4ABS5 Uncharacte	2	4	-0.003415	-0.241234	0.2270393	0.72985
sp O54975 Xaa-Pro am	8	14	0.0326487	-0.100528	0.1624272	0.7302625
tr D4ACB0 Synuclein, g	10	45	-0.033916	-0.161165	0.0924351	0.7305625
tr Q5PQZ9 NADHdehyd	2	3	-0.002927	-0.262234	0.2439266	0.7315875
sp B2RYW9 Fumarylace	2	3	0.0073696	-0.209316	0.2197487	0.73165
sp P68511 14-3-3 prot	6	10	0.0372341	-0.075225	0.1514803	0.7327125
sp Q4V8B0 Oxidation re	8	8	0.0182186	-0.155384	0.1923296	0.73275
sp P54319 Phospholipa	3	6	0.0227621	-0.136647	0.1825801	0.7330625
tr F1LRT9 F Uncharacte	3	5	-0.023307	-0.178151	0.135224	0.735025
tr F1M8L2 Uncharacte	5	10	-0.020456	-0.195951	0.1487311	0.7353
sp Q6PEC0 Bis(5'-nucle	3	5	0.0057922	-0.20214	0.2213516	0.7355875
sp P29266 3-hydroxyis	7	14	-0.034186	-0.152533	0.0855409	0.7355875
sp P09456 cAMP-depe	4	7	-0.007125	-0.215142	0.2037951	0.7369125
tr Q5U328 Nucleolin O	23	35	-0.031785	-0.165146	0.097758	0.737275
tr D3ZCA0 Proline synt	3	4	-0.017445	-0.189871	0.1509817	0.7376375
sp Q99JE6 1-phosphat	8	14	0.0167416	-0.153552	0.1899444	0.7394625
tr E9PTQ6 Uncharacte	3	3	-0.003924	-0.250879	0.2236298	0.7401875
sp Q6P7Q4 Lactoylgluta	8	21	0.0370788	-0.073315	0.1515389	0.7428125
sp P21775 3-ketoacyl-	7	11	0.0138199	-0.165886	0.1989533	0.7429625

tr B5DFN4 Prefoldin 5	6	10	-0.013856	-0.198771	0.1728637	0.7440375
sp O55096 Dipeptidyl peptidase-like 6	9	13	-0.029059	-0.159089	0.103752	0.744425
sp P62628 Dynein light chain 6	2	6	-0.023121	-0.170451	0.1305693	0.744475
tr F1M9V7 Uncharacte	10	16	0.0464956	-0.029195	0.1206281	0.744875
tr D3ZUB0 Reticulocalbin 3	3	4	0.0065566	-0.199925	0.2039743	0.744875
sp P38650 Cytoplasmic dynein 30	30	51	0.0364741	-0.072289	0.1460157	0.7464125
sp P63018 Heat shock protein 24	24	74	0.0467755	-0.02878	0.1219015	0.7465875
tr E9PTS1 Eukaryotic translation initiation factor 10	10	14	-0.032109	-0.149717	0.0817034	0.7475375
sp P46844 Biliverdin reductase A	10	18	0.0295775	-0.099715	0.1585139	0.7479375
sp P21670 Proteasome 26S subunit 3	3	7	-0.007718	-0.20079	0.1900983	0.7479875
sp Q63258 Integrin alpha 9	9	17	0.0149399	-0.15897	0.1921591	0.748625
sp Q9ES21 Phosphatidylinositol 7	7	11	0.0205013	-0.136006	0.1818996	0.748675
sp Q68FU3 Electron transfer protein 12	12	17	0.032292	-0.092635	0.1637281	0.75
tr F1MA29 Uncharacte	10	15	-0.003744	-0.211422	0.2027573	0.7504625
sp Q9WTV5 26S proteasome 5	5	8	0.0264716	-0.111184	0.1678613	0.75095
tr D3Z9Q9 Uncharacte	4	6	-0.00027	-0.206225	0.214414	0.751175
sp P13803 Electron transfer protein 10	10	16	0.0236523	-0.131289	0.1808921	0.7516375
tr Q6P6U2 Proteasome 12	12	20	0.0303919	-0.093982	0.1627195	0.752025
tr Q5U302 Catenin (Ca) 9	9	15	0.0287486	-0.094647	0.1550992	0.7533375
sp P23965 Enoyl-CoA c	9	16	0.0167871	-0.146754	0.1796584	0.7542125
sp P35704 Peroxiredoxin 6	6	13	0.0397625	-0.055265	0.1358611	0.7544375
tr F1M167 Uncharacte	2	3	0.0058614	-0.186555	0.2019215	0.7546375
sp Q5XIE6 3-hydroxyisobutyryl 3	3	6	-0.006541	-0.20105	0.1814975	0.759225
tr D4ADA8 Uncharacte	3	5	-0.001453	-0.207763	0.2067297	0.759275
sp P08082 Clathrin light chain 3	3	4	-0.034481	-0.159477	0.0773279	0.759275
tr E9PTA6 Eukaryotic translation initiation factor 5	5	7	-0.014523	-0.174511	0.1502326	0.7598125
sp O88761 26S proteasome 9	9	11	-0.004624	-0.204991	0.1966912	0.7602625
sp P62775 Myotrophin 2	2	6	-0.013418	-0.177326	0.1588779	0.761675
tr B0BNM1 Apoa1bp precursor 5	5	12	0.0214677	-0.126702	0.179025	0.7618375
tr F1LQI1 Uncharacte	7	11	0.0242155	-0.10895	0.1587578	0.7621625
sp B2GV06 Succinyl-CoA 6	6	7	0.0055499	-0.187871	0.2051105	0.762225
tr E9PTL2 Eukaryotic translation initiation factor 7	7	10	0.0352491	-0.067826	0.13711	0.7628875
tr F1LYY6 Uncharacte	7	13	0.0150873	-0.145499	0.1783671	0.7629375
tr F1LVS4 Uncharacte	7	8	-0.010632	-0.17842	0.1630661	0.76395
tr D3ZLA3 Copine III (F) 8	8	11	0.0252917	-0.102477	0.1520949	0.76515
tr Q3MIE4 Uncharacte	19	55	0.0418469	-0.04004	0.1272577	0.76995
tr Q6AZ73 Pleckstrin homology domain containing 2	2	7	-0.006675	-0.190913	0.1754394	0.7711875
tr Q5U2N2 Ubiquitin carboxy-terminal esterase L1 8	8	10	-0.006585	-0.186245	0.1721146	0.7713125
tr D3ZVQ0 Ubiquitin carboxy-terminal esterase L1 18	18	37	0.0327856	-0.076706	0.1377298	0.7718
sp Q02253 Methylmalonyl-CoA 15	15	32	0.0378233	-0.055076	0.1294616	0.7720375
tr D3ZFA6 Uncharacte	12	19	-0.015467	-0.170296	0.142198	0.773275
tr F1LR15 Uncharacte	7	10	-0.007297	-0.179412	0.1674413	0.7752125
tr F1LMH5 Uncharacte	3	4	0.0091411	-0.157772	0.1842607	0.776275
sp Q63028 Alpha-adducin 10	10	19	0.0371319	-0.056163	0.1288813	0.7770125
tr D3ZD23 ATP-binding cassette 5	5	7	-0.020468	-0.154758	0.1160864	0.7785375
tr D4A6A7 RCG36779 (1)	3	7	5.495E-06	-0.18429	0.1947694	0.7787
tr B0BNK1 RCG32615, putative 7	7	12	0.018216	-0.122838	0.1643232	0.7808625
sp P13676 Acylamino-acid 4	4	5	0.0027173	-0.181634	0.1857551	0.781575
sp P09527 Ras-related GTPase 8	8	13	0.0337337	-0.06463	0.1365169	0.7833875
sp Q920L2 Succinate dehydrogenase 11	11	14	0.0211845	-0.113118	0.1545849	0.7848125

tr F1M1Z5	Uncharacte	5	10	-0.031132	-0.131315	0.069443	0.7887625
tr D3ZWE4	Uncharacte	14	30	0.0206129	-0.110641	0.1509583	0.7895
sp Q62785	28 kDa heat	4	4	-0.010673	-0.170259	0.1419306	0.7897
sp P63036	Dnaj homol	4	7	0.0211688	-0.102823	0.1457814	0.7907
tr D3ZLC1	[Uncharacte	11	13	0.0027514	-0.17581	0.1873828	0.7911625
sp Q5XIG8	Serine-thre	4	6	0.0043174	-0.157547	0.1730435	0.7946125
sp Q01986	Dual specifi	11	18	0.0336204	-0.054736	0.1252295	0.7978375
tr Q5U344	Txnrd1 prot	13	22	0.0357363	-0.048893	0.1195456	0.79875
sp P61206	ADP-ribosyl	5	13	-0.022844	-0.137843	0.0948822	0.800425
sp P62260	14-3-3 prot	17	42	-0.037686	-0.120469	0.0449216	0.8007
sp Q6PEC1	Tubulin-spe	6	12	-0.027582	-0.128127	0.0772632	0.8016375
sp Q4KM49	Tyrosyl-tRN	14	24	0.0401236	-0.031321	0.1146315	0.8016625
tr F2W8B0	Catechol-O-	7	11	-0.023556	-0.142789	0.0928111	0.8019
sp P13086	Succinyl-Co	9	14	0.0103398	-0.141332	0.1590222	0.802275
sp Q9JLZ1	(Glutaredoxi	7	15	0.0107539	-0.138948	0.1554195	0.8040125
sp Q9QZA2	Programme	18	27	0.0473908	-0.006599	0.1016829	0.8045
tr E9PTY6	E Uncharacte	1	3	-0.006489	-0.164012	0.1502572	0.805125
tr F1M0R2	Uncharacte	15	29	0.0145337	-0.120844	0.154015	0.805925
sp Q07266	Drebrin OS=	6	9	0.0110915	-0.132864	0.1533401	0.807425
sp O88989	Malate deh	17	50	-0.026551	-0.135173	0.0783874	0.810075
sp P63039	60 kDa heat	29	66	0.0354654	-0.048118	0.1204167	0.811
tr Q5RKJ6	(Inositol poly	7	12	-0.009863	-0.15106	0.1298053	0.813575
tr Q6P9V6	Proteasome	3	7	0.0081398	-0.133309	0.1511225	0.813625
sp P10860	Glutamate c	18	32	-0.027131	-0.129994	0.0763582	0.8150375
tr Q8R3Z7	(EH-domain	13	22	-0.020397	-0.138719	0.0996471	0.81585
tr D4A996	[Uncharacte	15	19	-0.001309	-0.159511	0.1598704	0.818175
tr D3ZUY8	[Adaptor prc	9	12	-0.006056	-0.152787	0.1387937	0.8182875
sp Q6JE36	Protein NDF	8	26	-0.001882	-0.155843	0.1585467	0.8184375
tr D3ZVB7	Osteoglycin	18	83	0.0043812	-0.146871	0.1565134	0.8194875
sp Q9R063	Peroxiredox	12	30	0.0349942	-0.049047	0.1167496	0.81955
sp P50137	Transketola	31	70	-0.042722	-0.106803	0.0220028	0.82075
sp P10111	Peptidyl-prc	11	49	0.037117	-0.040833	0.1133224	0.8215
sp Q5RK30	Ribosome n	6	7	-0.011484	-0.144524	0.1198467	0.8225625
sp P07335	Creatine kir	20	80	-0.027656	-0.12495	0.0677139	0.8229625
sp P11232	Thioredoxin	8	22	-0.005624	-0.152118	0.1391782	0.82435
sp Q9Z1B2	Glutathione	9	15	-0.017418	-0.131385	0.1030263	0.8244375
tr F1LMY2	Uncharacte	10	15	-0.031706	-0.120217	0.0559439	0.8248125
sp Q05982	Nucleoside	4	8	0.001632	-0.149007	0.157807	0.8255375
sp A0JPM9	Eukaryotic t	5	7	-0.007884	-0.141304	0.1304078	0.827175
tr F1M978	Uncharacte	7	13	-0.033986	-0.11296	0.0441185	0.8274375
sp P31000	Vimentin O'	31	100	0.0052029	-0.143914	0.1483461	0.828575
sp P21263	Nestin OS=F	36	58	-0.004297	-0.149798	0.1425756	0.8290875
sp P62076	Mitochondr	2	4	0.0085015	-0.126213	0.1424455	0.8300625
sp P07943	Aldose redu	23	72	0.0145285	-0.111231	0.1382069	0.8304375
sp Q6AY12	NADH-cytoc	5	10	-0.002057	-0.153559	0.1438545	0.8311
tr Q6P2A5	Adenylate k	8	13	-0.01777	-0.133501	0.0996249	0.8313375
sp P84092	AP-2 compl	7	11	-0.02546	-0.117751	0.0738222	0.83145
sp Q07205	Eukaryotic t	7	12	0.0077924	-0.122046	0.1427698	0.8329
sp Q8VHF5	Citrate synt	12	27	0.0131662	-0.11271	0.1364664	0.8347375
tr F1M4A0	Uncharacte	8	14	-0.018293	-0.126773	0.0918545	0.8379875

sp O70196 Prolyl endo	9	18	-0.011293	-0.137806	0.113922	0.839375
tr F1M510 Uncharacte	10	21	0.0133519	-0.105537	0.1343239	0.8401
tr F1LSJ2 F: Uncharacte	4	10	-0.003692	-0.147154	0.1396645	0.841225
sp Q7M767 Ubiquitin-cc	1	2	0.0212268	-0.08171	0.1291104	0.8422875
tr D4AC23 RCG55994,	14	25	0.0341435	-0.04025	0.1113727	0.8428375
sp P85845 Fascin OS=F	12	27	0.0120846	-0.110052	0.1336266	0.8436625
tr Q5XI34 C Protein pho	14	28	0.0134569	-0.104905	0.1344818	0.84645
tr D4A4T2 I Uncharacte	5	6	-0.000632	-0.136862	0.141485	0.8484375
tr D4A8G5 Uncharacte	23	56	0.0279267	-0.0588	0.1130745	0.8490875
sp O35987 NSFL1 cofac	7	12	0.0007388	-0.13311	0.1360208	0.850125
sp P63102 14-3-3 prot	12	29	0.0307048	-0.048381	0.1120563	0.8507625
tr B2RZA9 I Ubiquitin ca	6	11	-0.01239	-0.128573	0.1015195	0.8542375
tr D3ZTB5 I Uncharacte	2	5	-0.003231	-0.132986	0.1319328	0.8548125
sp Q5M7U6 Actin-relate	7	10	0.0016297	-0.132721	0.1374952	0.8558
tr B2RZ27 E SH3 domair	6	14	-0.012841	-0.128253	0.0977319	0.856675
sp P82995 Heat shock	22	50	-0.003722	-0.136529	0.1289014	0.8567625
sp P56571 ES1 protein	5	9	0.012193	-0.104079	0.1256955	0.8597375
tr Q6AYD3 Proliferatio	7	10	-0.017854	-0.119897	0.0797325	0.8613375
tr F1M779 Uncharacte	53	100	-0.001736	-0.133192	0.1300031	0.8621125
sp P50503 Hsc70-inter	14	26	-0.020364	-0.115609	0.0746201	0.864325
tr Q32PX6 Ras homolo	3	5	-0.001779	-0.123522	0.1303149	0.8653625
sp P20070 NADH-cytoc	7	12	0.0082958	-0.102115	0.1244817	0.8720375
tr Q5XI77 C Annexin A1	13	29	0.0298779	-0.041295	0.1022927	0.8750375
sp Q9ESS6 Basal cell ac	9	18	-0.024095	-0.102746	0.0558096	0.87995
sp P97536 Cullin-assoc	16	30	-0.007656	-0.118166	0.1049068	0.8799625
tr D4ACB8 Chaperonin	15	22	0.021376	-0.06361	0.1040078	0.8818375
tr F1M953 Uncharacte	20	34	0.0340034	-0.02693	0.0965	0.8831875
tr D3ZN29 Uncharacte	22	50	-0.022453	-0.104627	0.0624122	0.883975
tr Q6PDW4 Proteasome	5	10	-3.97E-05	-0.122358	0.1181937	0.8840625
sp P62994 Growth fact	7	11	-0.010001	-0.112833	0.0937313	0.8866625
sp O35567 Bifunctiona	20	38	-0.02576	-0.101293	0.0500055	0.888375
tr Q6P7A4 Prosaposin	10	21	0.0017809	-0.115239	0.1180656	0.8886875
sp Q68FQ0 T-complex p	15	30	0.0284063	-0.043097	0.099254	0.8910875
tr F1LPR1 F Uncharacte	5	10	0.0049622	-0.101552	0.1143923	0.8926875
sp P49134 Integrin bet	11	23	-0.024034	-0.099001	0.0492671	0.89475
sp Q07009 Calpain-2 ca	15	33	0.0176928	-0.070309	0.1073471	0.8961375
tr D3ZUC9 Oxidative-st	7	16	0.0136227	-0.07525	0.1082611	0.8962
tr Q6IMZ3 Anxa6 prote	39	100	-0.03603	-0.091582	0.0212925	0.8995375
sp P25113 Phosphogly	6	21	-0.003684	-0.114219	0.1059526	0.9008625
sp O35814 Stress-induc	20	32	0.0245815	-0.04872	0.0976126	0.9055625
sp Q5I0D1 Glyoxalase i	17	37	0.0084638	-0.089944	0.1069602	0.9061125
tr Q5BJ93 C Enolase OS-	18	55	-0.009402	-0.101759	0.0875427	0.907475
tr F1LRF0 F Uncharacte	5	14	-0.003771	-0.107982	0.1008711	0.9075
sp Q6P502 T-complex p	22	48	0.0230046	-0.051181	0.0958568	0.909925
tr E9PTV3 E Uncharacte	67	100	0.0320877	-0.024565	0.0909132	0.9127875
tr Q2IBC6 C Caveolin OS	10	24	-0.007592	-0.099001	0.0792059	0.9256625
sp P28480 T-complex p	16	27	0.0147492	-0.063797	0.0891668	0.9272875
sp Q9EQS0 Transaldola	10	26	0.0027253	-0.08641	0.09705	0.9311125
sp Q07936 Annexin A2	27	100	-0.005787	-0.090217	0.0817437	0.9380625
tr Q5RKG9 Eukaryotic t	6	10	-0.00576	-0.089498	0.0755694	0.9411

sp Q5XIM9 T-complex β	22	42	-0.023478	-0.083977	0.0363464	0.9423
sp P26772 10 kDa heat	9	20	0.0083886	-0.066797	0.0844025	0.9521125
tr F2Z3Q8 Uncharacte	16	24	0.0033861	-0.073707	0.0810471	0.9559625
tr Q3MHS9 Chaperonin	16	28	-0.011693	-0.076275	0.055584	0.96135
sp Q5U300 Ubiquitin-lil	24	52	-0.008365	-0.078282	0.0636602	0.9619875
sp P46462 Transitional	37	98	0.0185731	-0.038685	0.0763744	0.9644125
tr F1LRV4 Uncharacte	24	46	0.0051284	-0.06557	0.0761574	0.964675

gFDR

0
0
4.167E-06
6.25E-06
1.5E-05
2.5E-05
3.393E-05
4.531E-05
5.972E-05
7.125E-05
8.182E-05
9.167E-05
0.0001
0.000108
0.0001158
0.0001227
0.0001294
0.0001382
0.0001461
0.0001538
0.0001619
0.0001699
0.0001777
0.000187
0.0001985
0.0002106
0.0002227
0.0002357
0.0002491
0.0002629
0.0002766
0.000291
0.0003053
0.0003199
0.0003343
0.000349
0.0003632
0.0003793
0.0003949
0.0004097
0.0004244
0.000439
0.0004529
0.0004685
0.0004869
0.0005065
0.0005263
0.0005456
0.0005917

0.0005691
0.0006147
0.0006375
0.0006597
0.0006817
0.0007039
0.0007261
0.0007478
0.0007731
0.0007983
0.0008233
 0.00085
0.0008764
0.0009056
 0.000935
0.0009656
0.0009962
0.0010259
0.0010588
0.0010915
0.0011261
0.0011644
0.0012031
0.0012416
0.0012802
 0.001318
0.0013549
0.0013917
0.0014279
0.0014644
0.0015039
0.0015426
0.0015809
0.0016187
0.0016563
0.0016932
0.0017295
0.0017652
0.0018014
0.0018372
0.0018726
0.0019088
0.0019447
0.0019798
0.0020146
0.0020488
0.0020829
0.0021168
0.0021503
0.0021832

0.0022159
0.0022483
0.0022824
0.002317
0.0023511
0.0023869
0.002423
0.00246
0.0024969
0.0025347
0.0025734
0.0026117
0.0026502
0.0026884
0.0027262
0.0027652
0.0028044
0.0028435
0.0028833
0.0029244
0.0029653
0.0030064
0.0030475
0.0030883
0.0031285
0.0031685
0.003208
0.003248
0.0032877
0.0033268
0.0033655
0.0034042
0.003444
0.0034847
0.0035252
0.0036092
0.0035675
0.0036504
0.0036916
0.0037348
0.0037801
0.0038262
0.0038724
0.0039218
0.0039707
0.0040193
0.0040673
0.0041147
0.0041616
0.0042081

0.0042543
0.0042999
0.0043452
0.0043921
0.0044386
0.0044859
0.004533
0.0045813
0.0046295
0.0046807
0.0047316
0.0047837
0.0048366
0.004889
0.0049409
0.004993
0.0050448
0.0050963
0.0051472
0.0051977
0.0052477
0.0052975
0.0053469
0.0053975
0.0054477
0.0054974
0.005547
0.0055965
0.0056463
0.0056957
0.0057456
0.0057979
0.005851
0.0059034
0.005956
0.0060082
0.0060606
0.0061126
0.0061642
0.0062155
0.0062664
0.006317
0.0063673
0.0064175
0.0064681
0.006519
0.00657
0.0066207
0.0066711
0.0067212

0.0067713
0.0068233
0.0068759
0.0069301
0.0069855
0.0070408
0.0070962
0.0071517
0.0072082
0.0072669
0.0073252
0.0073845
0.0074435
0.0075019
0.0075612
0.0076211
0.0076816
0.0077418
0.0078014
0.0078607
0.0079196
0.0079786
0.0080378
0.0080967
0.0081557
0.0082147
0.0082734
0.0083332
0.0083928
0.008452
0.0085107
0.0085694
0.0086282
0.008687
0.0087479
0.0088091
0.0088702
0.0089322
0.0089945
0.0090576
0.0091205
0.0091831
0.0092456
0.0093082
0.0093703
0.0094325
0.0094957
0.0095587
0.0096211
0.0096846

0.0097481
0.0098115
0.0098748
0.0099378
0.0100005
0.0100633
0.0101258
0.0101885
0.0102511
0.0103169
0.010383
0.0104515
0.0105208
0.0105899
0.0106588
0.0107273
0.0107954
0.0108636
0.0109313
0.0109988
0.0110658
0.0111324
0.0111988
0.0112653
0.0113317
0.011399
0.011466
0.0115327
0.0115996
0.0116661
0.0117325
0.0117986
0.0118643
0.0119304
0.0119966
0.0120623
0.0121282
0.0121943
0.0122601
0.012326
0.0123932
0.0124606
0.0125281
0.0125956
0.0126631
0.0127302
0.0127976
0.0128646
0.0129319
0.0130003

0.0130702
0.0131404
0.0132119
0.0132834
0.0133545
0.0134259
0.0134981
0.0135706
0.013643
0.0137155
0.0137882
0.0138604
0.0139323
0.014004
0.014076
0.0141476
0.0142199
0.0142917
0.0143635
0.0144353
0.0145066
0.0145778
0.0146492
0.0147206
0.0147931
0.0148657
0.0149406
0.0150156
0.0150917
0.015168
0.0152451
0.0153227
0.0154001
0.0154776
0.0155549
0.0156318
0.0157087
0.0157862
0.0158639
0.0159426
0.0160217
0.0161018
0.0161818
0.0162614
0.0163411
0.0164207
0.016501
0.016581
0.0166606
0.0167399

0.0168188
0.0168985
0.0169777
0.0170566
0.0171355
0.0172151
0.0172947
0.0173744
0.0174537
0.0175328
0.0176126
0.0176922
0.0177713
0.0178518
0.0179328
0.0180153
0.0180981
0.018181
0.0182637
0.0183468
0.0184297
0.0185122
0.0185953
0.0186784
0.0187612
0.0188437
0.0189258
0.0190083
0.0190905
0.0191725
0.0192543
0.0193358
0.0194173
0.0194986
0.0195799
0.0196615
0.0197443
0.0198267
0.0199095
0.0199922
0.0200746
0.020157
0.0202392
0.0203211
0.0204029
0.0204846
0.0205661
0.0206473
0.0207282
0.0208095

0.0208916
0.0209743
0.0210572
0.02114
0.0212226
0.0213052
0.0213887
0.0214722
0.0215563
0.02164
0.0217241
0.0218089
0.0218933
0.0219775
0.0220617
0.0221462
0.0222304
0.0223144
0.0223981
0.0224823
0.0225661
0.0226496
0.0227334
0.022818
0.0229028
0.0229874
0.0230717
0.0231557
0.02324
0.0233239
0.0234075
0.023491
0.0235749
0.0236587
0.0237422
0.0238254
0.0239086
0.0239918
0.0240747
0.0241576
0.0242402
0.024323
0.0244066
0.0244906
0.0245745
0.0246582
0.024742
0.0248273
0.0249127
0.0249995

0.0250862
0.025173
0.0252595
0.025347
0.0254368
0.0255268
0.0256165
0.0257077
0.0257995
0.0258915
0.0259834
0.0260755
0.0261678
0.0262598
0.0263515
0.0264429
0.026534
0.0266264
0.0267202
0.0268138
0.0269079
0.0270021
0.0270963
0.0271902
0.0272842
0.0273779
0.0274715
0.0275647
0.0276584
0.027752
0.0278455
0.0279394
0.0280332
0.0281268
0.02822
0.0283131
0.028406
0.0284995
0.0285929
0.0286867
0.0287811
0.0288756
0.0289702
0.0290646
0.0291597
0.0292547
0.0293503
0.0294456
0.029541
0.0296375

0.029734
0.0298309
0.029928
0.0300254
0.0301226
0.0302204
0.0303178
0.0304154
0.030513
0.030611
0.0307088
0.0308073
0.0309055
0.0310041
0.0311028
0.0312012
0.0312996
0.031398
0.0314964
0.031595
0.0316936
0.0317931
0.031893
0.0319928
0.0320923
0.032192
0.0322928
0.0323937
0.0324954
0.0325971
0.0326985
0.0328001
0.0329034
0.0330068
0.03311
0.0333163
0.0332133
0.0334194
0.0335225
0.0336255
0.033728
0.0338305
0.0339342
0.0340397
0.0341454
0.0342515
0.0343575
0.0344633
0.0345697
0.0346764

0.034783
0.0348898
0.0349979
0.0351059
0.0352143
0.0353224
0.0354302
0.0355381
0.0356471
0.0357561
0.0358648
0.0359732
0.0360819
0.0361902
0.036299
0.0364077
0.0365163
0.0366246
0.0367339
0.0368432
0.0369521
0.0370614
0.0371709
0.0372806
0.03739
0.0374997
0.0376093
0.0377188
0.0378288
0.0379399
0.0380513
0.0381628
0.038274
0.0383854
0.0384963
0.0386073
0.0387194
0.0388312
0.0389434
0.0390554
0.0391674
0.0392792
0.0393913
0.0395031
0.0396148
0.0397262
0.0398375
0.0399488
0.04006
0.0401711

0.040283
0.0403949
0.0405066
0.0406182
0.0407299
0.0408413
0.0409527
0.0410643
0.0411756
0.041287
0.0413988
0.0415106
0.0416225
0.0417342
0.0418461
0.0419586
0.0420708
0.042183
0.0422954
0.0424079
0.0425202
0.0426324
0.0427447
0.0428568
0.0429691
0.0430817
0.0431946
0.0433075
0.04342
0.0435326
0.0436457
0.0437585
0.043871
0.0439834
0.0440958
0.044208
0.0443204
0.0444348
0.0445493
0.0446651
0.044781
0.044897
0.0450126
0.0451283
0.0452454
0.0453629
0.0454804
0.0455982
0.0457156
0.0458327

0.0459504
0.0460677
0.0461847
0.0463027
0.0464206
0.0465387
0.0466565
0.0467741
0.0468919
0.0470094
0.0471267
0.0472438
0.0473608
0.0474778
0.0475965
0.0477149
0.0478331
0.0479525
0.0480716
0.0481909
 0.04831
0.0484297
0.0485498
 0.048671
0.0487927
0.0489145
0.0490373
0.0491597
0.0492823
0.0494061
0.0495298
0.0496532
0.0497765
0.0498997
0.0500229
0.0501459
0.0502685
0.0503908
0.0505129
0.0506347
0.0507563
0.0508779
0.0509995
0.0511209
0.0512427
0.0513643
0.0514865
0.0516103
0.0517347
0.0518591

0.0519836
0.0521083
0.0522332
0.052359
0.0524849
0.0526106
0.0527379
0.0528658
0.0529936
0.0531215
0.0532491
0.0533784
0.0535076
0.0536369
0.0537664
0.0538959
0.0540253
0.0541547
0.0542841
0.0544137
0.0545434
0.0546728
0.0548022
0.0549314
0.055061
0.0551905
0.0553197
0.0554494
0.0555791
0.0557086
0.0558385
0.0559682
0.0560976
0.056227
0.0563565
0.0564856
0.0566145
0.0567438
0.056873
0.0570018
0.0571306
0.0572592
0.0573882
0.0575171
0.0576459
0.0577744
0.0579027
0.0580311
0.0581593
0.0582872

0.0584162
0.0585451
0.0586743
0.0588033
0.0589324
0.0590617
0.0591912
0.0593207
0.0594502
0.0595794
0.0597088
0.0598386
0.0599687
0.0600985
0.0602283
0.0603577
0.0604872
0.0606165
0.0607456
0.0608745
0.0610034
0.0611324
0.0612617
0.0613916
0.0615213
0.061651
0.0617807
0.0619107
0.0620407
0.0621705
0.0623
0.0624298
0.0625596
0.0626893
0.0628188
0.0629489
0.0630789
0.0632089
0.0633389
0.0634685
0.0635981
0.0637277
0.0638576
0.0639874
0.0641178
0.064248
0.0643779
0.0645089
0.0646399
0.0647718

0.0649042
0.0650366
0.0651695
0.0653021
0.0654349
0.0655683
0.0657014
0.0658346
0.0659675
0.0661003
0.0662334
0.0663663
0.0664992
0.0666322
0.0667651
0.066898
0.0670307
0.0671631
0.0672955
0.067429
0.0675629
0.0676968
0.0678304
0.0679655
0.0681003
0.0682354
0.0683704
0.0685058
0.0686417
0.0687779
0.0689139
0.0690506
0.0691876
0.0693253
0.0694628
0.0696004
0.0697391
0.069878
0.0700166
0.0701556
0.0702945
0.0704341
0.0705735
0.070713
0.0708524
0.0709924
0.0711324
0.0712723
0.0714121
0.0715515

0.0716911
0.0718308
0.0719704
0.0721104
0.0722502
0.0723901
0.0725315
0.0726736
0.0728156
0.0729578
0.0730998
0.0732416
0.0733838
0.0735261
0.0736682
0.0738102
0.0739525
0.0740945
0.074237
0.0743799
0.074523
0.0746674
0.0748126
0.0749581
0.0751033
0.0752482
0.0753932
0.075538
0.0756834
0.0758286
0.075974
0.0761194
0.0762649
0.0764106
0.0765561
0.0767014
0.0768471
0.0769927
0.0771384
0.0772838
0.0774291
0.0775742
0.0777198
0.0778652
0.0780112
0.0781575
0.0783037
0.0784497
0.0785955
0.078742

0.0788885
0.0790347
0.0791808
0.0793267
0.079473
0.0796191
0.0797653
0.0799118
0.0800581
0.0802057
0.0803529
0.0804998
0.0806471
0.0807955
0.0809439
0.0810926
0.081241
0.0813891
0.0815372
0.0816849
0.0818324
0.0819798
0.0821293
0.0822793
0.082429
0.0825785
0.0827283
0.0828789
0.0830292
0.0831793
0.0833298
0.0834801
0.0836306
0.0837815
0.0839325
0.0840833
0.0842339
0.0843845
0.0845351
0.0846855
0.0848361
0.0849864
0.0851368
0.0852869
0.0854373
0.0855878
0.0857388
0.0858903
0.0860419
0.0861938

0.086346
0.0864982
0.0866507
0.0868038
0.0869572
0.0871103
0.0872637
0.0874168
0.0875698
0.0877234
0.0878773
0.0880311
0.0881847
0.0883381
0.0884914
0.0886448
0.088798
0.0889512
0.0891052
0.0892599
0.0894156
0.0895713
0.0897267
0.089882
0.0900372
0.0901923
0.0903474
0.0905025
0.0906579
0.090813
0.0909685
0.0911241
0.0912798
0.0914355
0.0915913
0.0917467
0.091902
0.0920574
0.092213
0.0923688
0.0925246
0.0926809
0.092837
0.092993
0.0931494
0.0933062
0.0934628
0.0936206
0.0937801
0.0939397

0.0940999
0.0942598
0.09442
0.0945799
0.0947398
0.0949003
0.0950606
0.0952208
0.0953811
0.0955414
0.0957019
0.0958623
0.0960226
0.0961829
0.096344
0.0965049
0.0966659
0.0968271
0.096988
0.0971497
0.0973112
0.0974744
0.0976375
0.0978016
0.0979655
0.0981293
0.0982928
0.098456
0.098619
0.0987817
0.0989443
0.0991068
0.0992695
0.0994322
0.099595
0.0997579
0.0999207
0.1000838
0.1002468
0.1004097
0.1005724
0.1007355
0.1008983
0.1010619
0.1012253
0.1013886
0.1015519
0.1017153
0.1018796
0.1020436

0.1022075
0.1023712
0.1025351
0.1026988
0.1028624
0.1030258
0.1031889
0.1033529
0.1035168
0.1038443
0.1036807
0.1040078
0.1041712
0.1043359
0.1045006
0.1046659
0.1048315
0.1049971
0.1051631
0.1053292
0.1054962
0.105663
0.1058299
0.1059967
0.1061633
0.1063298
0.1064961
0.1066623
0.106829
0.1069956
0.1071618
0.1073279
0.1074937
0.1076595
0.1078261
0.1079928
0.1081592
0.108326
0.108493
0.1086597
0.1088262
0.1089927
0.109159
0.1093252
0.1094912
0.1096571
0.1098228
0.1099883
0.1101539
0.1103196

0.1104849
0.11065
0.1108148
0.1109793
0.1111436
0.1113081
0.1114724
0.1116367
0.1118008
0.1119654
0.1121305
0.112296
0.1124615
0.1126273
0.1127932
0.1129588
0.1131243
0.1132897
0.1134553
0.1136206
0.1137857
0.1139506
0.1141154
0.1142802
0.1144453
0.1146105
0.1147757
0.1149407
0.1151057
0.1152704
0.115435
0.1156006
0.1157663
0.1159321
0.1160986
0.1162651
0.1164316
0.1165981
0.1167646
0.1169312
0.1170976
0.1172637
0.11743
0.1175961
0.117762
0.1179277
0.1180933
0.1182594
0.1184254
0.1185916

0.1187583
0.1189258
0.1190932
0.1192603
0.1194276
0.1195946
0.1197634
0.119932
0.1201007
0.1202698
0.1204386
0.1206072
0.1207761
0.120945
0.1211136
0.121282
0.1214506
0.1216189
0.1217871
0.1219553
0.1221247
0.122294
0.1224629
0.1226317
0.1228004
0.1229688
0.1231371
0.1233052
0.1234733
0.1236412
0.1238092
0.123977
0.1241453
0.1243135
0.1244813
0.124649
0.1248163
0.124984
0.1251513
0.1253187
0.1254857
0.1256527
0.1258203
0.1259877
0.1261556
0.1263232
0.1264906
0.126658
0.1268254
0.126993

0.1271606
0.1273281
0.1274954
0.1276631
0.1278308
0.1279983
0.1281657
0.1283328
0.1285002
0.1286676
0.1288351
0.1290025
0.1291699
0.1293371
0.1295045
0.1296723
0.1298399
0.1300074
0.1301745
0.130342
0.1305094
0.1306771
0.1308453
0.1310137
0.131182
0.1313503
0.1315187
0.1316869
0.1318551
0.1320231
0.1321918
0.1323603
0.1325289
0.132698
0.1328672
0.1330363
0.1332056
0.1333748
0.1335437
0.1337124
0.1338808
0.1340491
0.1342171
0.1343857
0.1345541
0.1347223
0.1348904
0.1350583
0.1352268
0.1353955

0.1355648
0.1357344
0.1359037
0.1360729
0.1362418
0.1364106
0.1365795
0.1367484
0.1370856
0.1369171
0.1372538
0.1374217
0.1375895
0.1377575
0.1379252
0.1380931
0.1382608
0.1384282
0.1385957
0.138763
0.1389301
0.1390971
0.1392639
0.1394307
0.1395972
0.1397636
0.1399298
0.1400958
0.1402618
0.1404276
0.1405933
0.1407587
0.1409239
0.1410895
0.1412548
0.1414201
0.1415854
0.1417509
0.1419164
0.1420819
0.1422473
0.1424125
0.1425777
0.1427431
0.1429082
0.1430732
0.1432381
0.1434034
0.1435685
0.1437333

0.1438981
0.1440627
0.1442273
0.1443922
0.1445571
0.1447222
0.1448873
0.1450524
0.1452176
0.1453832
0.1455487
0.1457145
0.1458801
0.1460464
0.1462126
0.1463785
0.1465443
0.1467099
0.1468757
0.1470416
0.1472073
0.1473727
0.1475381
0.1477035
0.1478691
0.1480345
0.1481996
0.1483647
0.1485298
0.1486948
0.1488596
0.1490242
0.1491887
0.1493535
0.1495185
0.1496834
0.1498483
0.1500134
0.1501783
0.1503432
0.1505092
0.1506751
0.1508409
0.1510064
0.1511717
0.151337
0.151502
0.1516674
0.1518347
0.1520023

0.1521697
0.1523372
0.1525054
0.1526735
0.1528414
0.1530096
0.1531777
0.1533461
0.1535142
0.1536822
0.1538501
0.1540182
0.1541865
0.154355
0.1545242
0.1546933
0.1548623
0.1550311
0.1551999
0.1553689
0.1555377
0.1557067
0.1558755
0.1560445
0.1562134
0.156382
0.1565504
0.1567195
0.1568884
0.1570574
0.1572266
0.1573957
0.157565
0.1577341
0.1579033
0.1580727
0.1582419
0.1584114
0.1585811
0.1587509
0.1589205
0.15909
0.1592592
0.1594282
0.1595973
0.1597664
0.1599354
0.1601057
0.1602759
0.1604463

0.1606166
0.1607868
0.1609571
0.1611274
0.1612975
0.1614675
0.1616377
0.1618078
0.1619782
0.1621485
0.1623187
0.1624889
0.162659
0.1628298
0.1630003
0.1631707
0.1633409
0.1635116
0.1636821
0.1638526
0.1640231
0.1641934
0.1643634
0.1645334
0.1647033
0.1648735
0.1650437
0.1652139
0.165384
0.1655539
0.1657238
0.1658934
0.166063
0.166233
0.1664034
0.1665737
0.1667443
0.166916
0.1670874
0.1672587
0.16743
0.1676013
0.1677726
0.167944
0.168116
0.168288
0.16846
0.1686321
0.1688043
0.1689764

0.1691489
0.1693218
0.1694945
0.1696671
0.1698397
0.1700122
0.1701846
0.1703568
0.1705288
0.1707007
0.1708723
0.1710438
0.1712154
0.1713868
0.1715587
0.1717304
0.171902
0.1720735
0.1722448
0.172417
0.1725891
0.172761
0.1729327
0.1731043
0.1732757
0.1734469
0.173618
0.173789
0.1739598
0.1741306
0.1743011
0.1744718
0.174643
0.1748141
0.174985
0.1751558
0.1753264
0.1754969
0.1756672
0.1758376
0.176008
0.1761782
0.1763488
0.1765193
0.1766895
0.1768605
0.1770321
0.1772035
0.1773747
0.1775461

0.1777174
0.1778886
0.17806
0.1782313
0.178403
0.1785744
0.1787461
0.1789179
0.1790894
0.1792613
0.179433
0.1796045
0.1797765
0.1799484
0.1801202
0.1802922
0.1804641
0.1806374
0.1808105
0.1809835
0.1811567
0.1813298
0.1815026
0.1816755
0.1818487
0.1820221
0.1821953
0.1823683
0.1825412
0.182714
0.1828869
0.1830596
0.1832322
0.1834049
0.1835776
0.1837508
0.1839239
0.1840982
0.1842723
0.1844463
0.1846202
0.184794
0.1849676
0.185141
0.1853144
0.1854876
0.1856607
0.1858336
0.1860063
0.1861788

0.1863513
0.1865243
0.1866971
0.1868704
0.1870442
0.1872178
0.1873914
0.1875649
0.1877384
0.1879118
0.1880856
0.1882591
0.1884324
0.1886057
0.1887789
0.1889527
0.1891264
0.1893005
0.1894746
0.1896487
0.1898227
0.1899965
0.1901703
0.1903449
0.1905193
0.1906935
0.1908677
0.1910416
0.1912158
0.1913897
0.191564
0.1917382
0.1919128
0.1920874
0.1922621
0.1924366
0.192611
0.1927852
0.1929593
0.1931341
0.1933089
0.1934838
0.1936588
0.1938345
0.19401
0.1941854
0.1943606
0.1945358
0.194711
0.1948861

0.1950613
0.1952365
0.1954114
0.1955863
0.1957609
0.1959354
0.1961102
0.1962852
0.19646
0.1966348
0.1968096
0.1969844
0.1971591
0.1973336
0.1975081
0.1976824
0.1978566
0.1980308
0.1982052
0.1983797
0.1985541
0.1987285
0.1989028
0.1990768
0.1992508
0.1994248
0.1995986
0.1997725
0.1999465
0.2001207
0.2002948
0.200469
0.200643
0.200817
0.200991
0.201165
0.2013389
0.2015129
0.2016868
0.2018608
0.2020346
0.2022086
0.2023827
0.2025568
0.2027307
0.202905
0.2030791
0.203253
0.2034268
0.2036005

0.2037743
0.2039478
0.2041216
0.204296
0.2044703
0.2046446
0.2048186
0.2049929
0.2051672
0.2053414
0.2055154
0.2056894
0.2058639
0.2060385
0.2062129
0.2063872
0.2065614
0.2067355
0.2069095
0.2070833
0.2072576
0.2074317
0.2076057
0.2077797
0.2079535
0.2081276
0.2083022
0.2084772
0.2086521
0.208827
0.2090018
0.2091764
0.2093509
0.2095253
0.2096996
0.2098736
0.2100475
0.2102215
0.2103954
0.2105692
0.2107429
0.2109164
0.2110897
0.2112628
0.2114362
0.2116094
0.2117826
0.2119557
0.212129
0.2123022

0.2124754
0.2126485
0.2128216
0.2129946
0.2131676
0.2133403
0.2135133
0.2136861
0.2138588
0.2140313
0.2142038
0.2143763
0.2145494
0.2147225
0.2148956
0.2150686
0.2152416
0.2154145
0.2155875
0.2157606
0.215934
0.2161071
0.2162806
0.2164542
0.2166283
0.2168024
0.2169764
0.2171506
0.2173247
0.2174991
0.2176735
0.2178477
0.2180218
0.2181959
0.2183702
0.2185444
0.2187186
0.218893
0.2190671
0.2192411
0.2194149
0.2195888
0.2197625
0.2199361
0.2201095
0.2202828
0.2204559
0.2206288
0.2208015
0.2209745

0.2211476
0.2213205
0.2214934
0.2216665
0.2218395
0.2220125
0.2221853
0.222358
0.222531
0.2227041
0.222877
0.2230501
0.2232233
0.2233969
0.2235711
0.2237453
0.2239195
0.2240936
0.2242676
0.2244421
0.2246165
0.2247909
0.2249653
0.2251395
0.2253137
0.2254879
0.2256621
0.2258364
0.2260105
0.2261848
0.2263589
0.2265328
0.2267066
0.2268803
0.2270539
0.2272273
0.2274006
0.227574
0.2277475
0.2279208
0.228094
0.2282673
0.2284406
0.2286143
0.228788
0.2289616
0.2291351
0.2293085
0.229482
0.2296555

0.2298289
0.2300021
0.2301759
0.2303498
0.2305235
0.2306971
0.231044
0.2312174
0.2313908
0.2315642
0.2317376
0.231911
0.2320842
0.2322576
0.232431
0.2326043
0.2327779
0.2329513
0.2331248
0.2332983
0.2334718
0.2336453
0.233819
0.2339927
0.2341662
0.2343396
0.2345129
0.2346862
0.2348593
0.2350324
0.2352056
0.2353787
0.2355518
0.235725
0.2358982
0.236072
0.2362457
0.2365947
0.2367694
0.236944
0.2371188
0.2372935
0.2374683
0.2376428
0.2378174
0.2379917
0.2381661
0.2383406
0.238515
0.2386895

0.2388639
0.2390384
0.2392129
0.2393873
0.2395617
0.2397362
0.2399106
0.2400849
0.2402591
0.2404334
0.2406079
0.2407823
0.2409566
0.2411309
0.2413052
0.2414794
0.2416534
0.2418283
0.2420031
0.2421779
0.242353
0.242528
0.2427031
0.242878
0.2430536
0.2432292
0.2434047
0.2435801
0.2437553
0.2439306
0.244106
0.2442814
0.2444567
0.2446322
0.2448076
0.2451587
0.2453343
0.2455098
0.2456851
0.2458614
0.2460378
0.2462141
0.2463905
0.246567
0.2467432
0.2469194
0.2470956
0.2472716
0.2474475
0.2476232

0.247799
0.2479747
0.2481504
0.2483259
0.2485013
0.2486768
0.2488526
0.2490283
0.2492038
0.2493792
0.2495545
0.2499047
0.2502545
0.2504292
0.2506036
0.250778
0.2509522
0.2511263
0.2513003
0.2514742
0.251648
0.2518217
0.2521686
0.252342
0.2525158
0.2526899
0.2528638
0.2530377
0.2532115
0.2533851
0.2535587
0.2537326
0.2539062
0.2540798
0.2542534
0.2544268
0.2546
0.2547732
0.2549465
0.2551199
0.2554665
0.2556399
0.2558131
0.2559861
0.2561592
0.2563324
0.2565058
0.256679
0.2570262
0.2572002

0.2573741
0.2575479
0.257722
0.2578962
0.2580703
0.2582443
0.2585927
0.2587668
0.2591148
0.2592888
0.2594637
0.2596386
0.2598135
0.2599884
0.2601633
0.2605132
0.2606882
0.2608632
0.2610381
0.2613881
0.2615633
0.2617384
0.2619135
0.2620883
0.2622631
0.2624376
0.2626121
0.2627865
0.2629607
0.2631351
0.2633095
0.2634839
0.2636584
0.2638327
0.2641816
0.264356
0.2645302
0.2647044
0.2648785
0.2650525
0.2652265
0.2654005
0.2655749
0.2659236
0.2660981
0.2662725
0.2666208
0.2667947
0.2671424
0.2673165

0.2678394
0.2681879
0.268362
0.2685368
0.2687114
0.2688861
0.2692353
0.2694098
0.2695843
0.2697586
0.2699328
0.2704554
0.2706293
0.2708032
0.270977
0.2711507
0.2713244
0.271498
0.2716717
0.2721937
0.2725422
0.2728911
0.2730657
0.2732403
0.2737635
0.2739381
0.2742872
0.2744619
0.2749866
0.275162
0.2753375
0.275513
0.2756883
0.2758635
0.276039
0.2762143
0.2763895
0.276565
0.2767407
0.2769162
0.2770917
0.2772672
0.2774425
0.2776179
0.2777934
0.2779693
0.2783221
0.2788526
0.2790292
0.279206

0.2793829
0.2795596
0.2797363
0.2799133
0.2802675
0.2804446
0.2806216
0.2809761
0.2811532
0.2813302
0.2815073
0.2816842
0.2818612
0.2820383
0.2822158
0.2823933
0.2827479
0.282925
0.2831019
0.2832786
0.2834556
0.2838106
0.2839882
0.2841656
0.2848755
0.2850534
0.2852313
0.2854093
0.2859428
0.2866527
0.2868301
0.2871846
0.2875393
0.287894
0.288249
0.2884263
0.2886038
0.2887811
0.2889586
0.2891359
0.2901999
0.2903777
0.291089
0.2918038
0.2919822
0.2921607
0.2925178
0.2926963
0.2928748
0.2930532

0.2932315
0.2939465
0.2943038
0.2944823
0.2948396
0.2951971
0.2953759
0.2959122
0.2960909
0.2962695
0.2966263
0.2968044
0.2969828
0.2976961
0.2978742
0.2980525
0.2982309
0.2987655
0.2991221
0.2998348
0.3000128
0.3001907
0.3003686
0.3005464
0.3007242
0.3009018
0.3010794
0.3017889
0.3023201
0.3024971
0.3026739
0.3028506
0.3039105
0.3040873
0.3044408
0.3046174
0.304971
0.305148
0.3062123
0.3065672
0.3067449
0.3069225
0.3074553
0.3081644
0.3088731
0.3090504
0.3095828
0.3101156
0.3104706
0.3110029

0.3113574
0.3120661
0.3122431
 0.31242
 0.31295
0.3136564
0.3138328
0.3140093
0.3141861
0.3147159
0.3152448
 0.315421
0.3157736
0.3163021
0.3170056
0.3173567
0.3177074
0.3178826
0.3180578
0.3182329
0.3184079
0.3187575
0.3191068
0.3192815
0.3194561
0.3198049
0.3206787
0.3212043
0.3220808
0.3224307
0.3227803
 0.322955
0.3231298
0.3233045
0.3238288
0.3240034
0.3245274
0.3247019
0.3250505
0.3264423
0.3269634
0.3273105
 0.327137
0.3283497
0.3285228
0.3286959
0.3290427
0.3295634
0.3316416
0.3318144

0.3321599
0.332678
0.3328505
0.3330231
0.3331955
0.3338851
0.3340575
0.3347464
0.3350907
0.3352626
0.3359496
0.3361212
0.3368071
0.3373212
0.3374925
0.3380059
0.338177
0.3385189
0.3390323
0.3393746
0.3397166
0.3400582
0.3419397
0.3421107
0.3422815
0.3424524
0.3431352
0.3439875
0.3441578
0.3443281
0.3444984
0.3450088
0.3455182
0.3461964
0.3465358
0.3485748
0.3492545
0.3494244
0.3497642
0.349934
0.3509519
0.3526441
0.3533195
0.3539939
0.3548361
0.3551728
0.3566865
0.3570224
0.3583644
0.3595359

0.3610417
0.3617115
0.3618788
0.3625476
0.3628819
0.3652169
0.3677111
0.3692007
0.3711768
0.371341
0.3721618
0.3723257
0.3726532
0.3729805
0.374288
0.3749403
0.3752663
0.3759175
0.3775423
0.3790008
0.3794869
0.3819084
0.3820695
0.3828749
0.3833577
0.3846451
0.3848058
0.3849665
0.385609
0.3857695
0.3864116
0.3868929
0.3873742
0.3884942
0.3888141
0.3891338
0.3894532
0.3900915
0.3907301
0.3908897
0.3918469
0.3920063
0.3924845
0.392644
0.393122
0.3934405
0.3935996
0.3947122
0.3959804
0.3975645

0.3985154
0.3993067
0.4005692
0.4013567
0.4019857
0.4024571
0.4051187
0.4069886
0.4079207
0.4090053
0.4097783
0.4125524
0.4134733
0.4145442
0.4156125
0.4159171
0.4181981
0.4198631
0.4209191
0.4228721
0.4234722
0.4291458
0.4316626
0.4366603
0.4368063
0.4375365
0.4388497
0.4395779
0.4398687
0.4427647
0.4442056
0.4447806
0.4463605
0.4476495
0.4485082
0.4496523
0.4499379
0.4529265
0.4550475
0.4581417
0.4591234
0.4602433
0.460383
0.4619201
0.4635938
0.4786403
0.480381
0.4846303
0.4915818
0.4936625

0.4945703
0.5056981
0.5095896
0.5166466
0.5173811
0.520427
0.5210328

Accession	Name	Peptides	Spectra	Mean Log ₂ F	I-95% CI	u-95% CI	IFDR	gFDR
sp P14046	Alpha-1-inh	6	21	-1.829666	-2.303982	-1.363989	0	0
sp P04639	Apolipoprot	19	79	1.0935994	0.7078843	1.4909045	3.75E-05	1.875E-05
sp P02651	Apolipoprot	13	28	0.6212528	0.3183673	0.9272876	0.0010875	0.000375
sp P01048	T-kininogen	4	15	0.9572221	0.441356	1.4611147	0.001425	0.0006375
sp P10959	Liver carbo>	13	45	0.5119437	0.2248347	0.8162295	0.00375	0.00126
sp P17475	Alpha-1-ant	22	100	0.4571214	0.1803036	0.744139	0.00565	0.0019917
sp P04276	Vitamin D-b	13	41	-0.400567	-0.655865	-0.156142	0.0070625	0.0027161
sp Q63416	Inter-alpha-	17	60	0.4608736	0.1546549	0.7671139	0.008225	0.0034047
sp Q6POK8	Junction pla	2	4	0.6413457	0.1966689	1.0792338	0.008425	0.0039625
sp P23680	Serum amyl	1	4	0.5977992	0.1598969	1.0460213	0.009575	0.0045238
sp Q6IFW6	Keratin, typ	4	8	-0.647781	-1.1185	-0.188774	0.010325	0.0050511
sp Q8VIJ5 !	Bifunctiona	9	14	0.2707431	0.1040743	0.4350431	0.010425	0.005499
sp Q5BK48	Tetratricope	1	2	0.4019861	0.1319213	0.6861588	0.011125	0.0059317
sp P31232	Transgelin C	10	36	-0.372658	-0.618675	-0.122332	0.011175	0.0063063
sp P20759	Ig gamma-1	3	9	0.5092703	0.1307857	0.8781815	0.0124625	0.0067167
sp P19132	Ferritin hea	5	5	0.4196795	0.0895587	0.7599041	0.0152625	0.0072508
sp P22791	Hydroxyme	14	42	0.2412572	0.0884355	0.3903463	0.0155625	0.0077397
sp P02793	Ferritin ligh	2	4	0.4240837	0.092068	0.7412051	0.018	0.0083097
sp P02650	Apolipoprot	14	42	-0.221046	-0.359026	-0.080935	0.018625	0.0088526
sp P29457	Serpin H1 O	15	45	-0.183489	-0.29201	-0.070793	0.0228625	0.0095531
sp Q6P7A9	Lysosomal a	3	13	0.2507064	0.0712094	0.4262449	0.0232	0.010203
sp B0BN15	Olfactomed	2	6	0.3337728	0.0749847	0.5970327	0.024075	0.0108335
sp Q64663	P2X purinoc	1	2	-0.511354	-0.959548	-0.073201	0.024275	0.0114179
sp P59649	FXYD doma	2	8	0.2305232	0.0709286	0.391258	0.0248125	0.011976
sp P29411	GTP:AMP pl	10	31	0.1514029	0.069646	0.2308748	0.0257	0.012525
sp P12785	Fatty acid s	43	100	-0.162461	-0.255896	-0.071027	0.0258125	0.0130361
sp Q05175	Brain acid s	4	11	0.2290408	0.0723463	0.3933049	0.0261	0.0135199
sp P20760	Ig gamma-2	10	39	0.7361038	0.0478226	1.4208765	0.0273375	0.0140134
sp P48199	C-reactive p	3	12	0.5326985	0.049493	1.0202385	0.0275375	0.0144797
sp P18445	60S riboson	7	18	-0.13897	-0.210961	-0.068347	0.0300625	0.0149992
sp Q1WIM3	Cell adhesic	10	35	0.2002995	0.0604837	0.3415325	0.0315875	0.0155343
sp P15651	Short-chain	6	10	-0.285946	-0.508325	-0.058561	0.0324375	0.0160625
sp P09895	60S riboson	16	57	-0.125114	-0.182426	-0.067492	0.0327375	0.0165678
sp Q6AYK6	Calcyclin-bi	7	14	-0.167134	-0.271739	-0.063089	0.032775	0.0170445
sp P02764	Alpha-1-acid	4	8	0.3958068	0.03422	0.7538101	0.033025	0.0175011
sp Q03626	Murinoglob	10	17	-0.389139	-0.734908	-0.043599	0.0334125	0.0179431
sp Q66HD0	Endoplasmic	27	100	-0.129532	-0.195219	-0.063521	0.036225	0.0184372
sp Q9QX79	Fetuin-B OS	11	58	0.3934744	0.0328623	0.7505556	0.0367125	0.0189181
sp Q8VIF7 !	Selenium-bi	11	25	0.1997132	0.051742	0.3482625	0.038175	0.0194119
sp Q5XIS7 !	Ubiquitin-a	1	2	-0.569331	-1.171082	0.0213094	0.0397625	0.0199206
sp P04182	Ornithine ai	7	23	0.2456269	0.0458217	0.4513139	0.04	0.0204104
sp P14669	Annexin A3	8	18	-0.265703	-0.487142	-0.037336	0.0414	0.0209101
sp P50442	Glycine ami	4	8	0.3799181	0.021084	0.7397815	0.0420125	0.0214009
sp O08984	Lamin-B rec	1	2	0.5775034	-0.043239	1.1799149	0.04705	0.0219838
sp Q5M7V8	Thyroid hor	3	5	-0.335588	-0.656868	-0.014553	0.049275	0.0225903

sp P97685 Neurofascir	4	8	0.3120471	0.0098755	0.628459	0.0512375	0.023213
sp P26051 CD44 antigen	3	5	-0.223558	-0.41111	-0.036984	0.0524625	0.0238354
sp P53534 Glycogen ph	27	100	0.1344837	0.0537532	0.2146928	0.0536	0.0244555
sp P02600 Myosin ligh	3	6	-1.194917	-2.798818	0.3861224	0.056475	0.0251089
sp P08932 T-kininogen	2	2	0.5112984	-0.066523	1.1061145	0.059	0.0257868
sp Q6AYC4 Macrophag	14	57	0.3896452	-0.03983	0.8072281	0.0632625	0.0265216
sp Q6FQ7 RNA polym	2	2	0.3587285	-0.033215	0.7609872	0.06885	0.0273356
sp P29266 3-hydroxyis	9	22	0.154214	0.0424031	0.2684553	0.0696625	0.0281342
sp Q9ESN0 Protein Nib	11	30	-0.15959	-0.286145	-0.034854	0.07225	0.0289512
sp P11167 Solute carri	4	19	-0.201318	-0.3874	-0.022345	0.073975	0.0297698
sp Q05820 Putative lys	3	12	0.27278	-0.012465	0.5633877	0.074775	0.0305734
sp B4F795 Choline trar	8	22	0.1890318	0.021276	0.3586554	0.074925	0.0313515
sp Q9ESB5 N-terminal	4	4	0.4457867	-0.107485	0.9934663	0.07665	0.0321325
sp Q6AYQ8 Fumarylace	1	3	-0.266285	-0.569858	0.0287331	0.076975	0.0328926
sp P18418 Calreticulin	22	100	-0.127496	-0.209355	-0.045453	0.0771375	0.03363
sp P49186 Mitogen-ac	1	3	0.4691822	-0.129728	1.0896963	0.078175	0.0343602
sp P07722 Myelin-assc	9	40	0.1633128	0.0288577	0.2995483	0.07905	0.035081
sp P07340 Sodium/pot	12	53	0.1401076	0.0375689	0.2405698	0.079975	0.0357937
sp P17425 Hydroxyme	15	39	-0.130324	-0.216723	-0.044774	0.0816625	0.0365104
sp O88884 A-kinase an	2	6	0.2303298	-0.008622	0.4683745	0.083475	0.0372329
sp P56536 Kinesin hea	1	2	0.3478551	-0.067455	0.7543285	0.0852375	0.0379602
sp Q812D3 Peptidyl-pro	2	3	0.414849	-0.115502	0.9316602	0.0852625	0.0386662
sp A2RRU1 Glycogen [s	8	19	0.1633954	0.0237209	0.3032865	0.085775	0.039359
sp P02770 Serum albu	27	100	-0.231194	-0.475446	0.0066481	0.086425	0.0400411
sp Q6MG6C N(G),N(G)-c	14	60	0.1016411	0.0559532	0.1487542	0.08655	0.0407055
sp Q8CHN6 Sphingosine	2	2	-0.405599	-0.949716	0.1374362	0.0865625	0.0413514
sp P36372 Antigen pep	1	2	0.3296833	-0.0758	0.7228817	0.0883	0.0420035
sp P42346 Serine/thre	2	2	-0.547853	-1.325054	0.2012034	0.089375	0.0426524
sp Q3KRE0 ATPase fam	2	2	-0.276765	-0.672893	0.089394	0.09025	0.0432956
sp Q9JJP9 Ubiquilin-1	5	14	0.341876	-0.068244	0.7607275	0.09035	0.043923
sp Q63797 Proteasome	8	24	-0.139574	-0.247888	-0.032479	0.0911	0.0445438
sp P30009 Myristoylat	4	15	-0.173899	-0.332429	-0.016381	0.0921	0.0451614
sp P09034 Argininosuc	4	9	0.2609093	-0.03458	0.5692734	0.0925125	0.0457684
sp P02696 Retinol-bind	2	4	-0.241309	-0.503555	0.026573	0.09365	0.0463745
sp P62630 Elongation f	13	73	-0.124632	-0.209004	-0.037332	0.0938875	0.0469684
sp P04462 Myosin-8 (F	1	2	-1.093555	-2.996845	0.7708127	0.0943125	0.0475529
sp Q63198 Contactin-1	5	13	0.1900051	0.0031457	0.3765545	0.0955	0.0481377
sp Q3B8Q2 Eukaryotic i	2	5	-0.229579	-0.473299	0.0249118	0.0959	0.0487131
sp P62282 40S riboson	13	45	-0.128913	-0.221127	-0.034681	0.0963375	0.0492801
sp Q6AXR4 Beta-hexos	2	2	-0.289989	-0.621591	0.049069	0.097975	0.0498529
sp P05544 Serine prote	11	30	-0.450107	-1.067899	0.1504108	0.0981125	0.0504141
sp P25286 V-type prot	6	10	-0.197028	-0.397864	0.0060372	0.0990625	0.0509733
sp P18422 Proteasome	4	10	-0.199145	-0.406192	0.0032206	0.10275	0.0515616
sp Q9QUR2 Dynactin su	4	6	0.2772518	-0.055916	0.6045191	0.10365	0.0521469
sp Q91XR8 Phospholipi	2	6	0.3165456	-0.081076	0.7161532	0.1046125	0.0527299
sp Q9QYU1 Peroxisoma	2	8	-0.218652	-0.511226	0.0506145	0.1062625	0.0533181
sp Q68FQ2 Junctional a	2	6	0.222831	-0.02387	0.482096	0.107525	0.0539073

sp P20761 Ig gamma-2	6	20	-0.485933	-1.173021	0.2246113	0.1078	0.0544868
sp Q6MG06 Guanine nu	4	9	-0.198726	-0.409168	0.0188606	0.109175	0.0550686
sp P51647 Retinal deh	8	20	-0.232424	-0.503462	0.0477506	0.1097	0.0556437
sp Q05764 Beta-adduc	9	24	0.1360389	0.0252241	0.244039	0.1098375	0.0562082
sp Q6VV72 Eukaryotic t	2	5	-0.165622	-0.324712	-0.002331	0.111475	0.056778
sp Q64240 Protein AM	3	11	0.237882	-0.041597	0.5305335	0.111525	0.0573366
sp P20280 60S riboson	7	39	-0.127518	-0.224618	-0.028239	0.11225	0.0578913
sp Q62764 DNA-bindin	1	3	-0.251551	-0.568632	0.0686342	0.11365	0.0584489
sp P40241 CD9 antiger	10	98	0.1399326	0.0187017	0.26171	0.1141125	0.059
sp Q5RKI1 Eukaryotic i	19	51	-0.112048	-0.184127	-0.0389	0.1142625	0.0595418
sp Q64122 Myosin regi	2	4	-0.40272	-0.946032	0.1671685	0.117025	0.0600999
sp P0C2X9 Delta-1-pyr	4	7	0.1967728	-0.027458	0.416968	0.11875	0.0606638
sp Q498E0 Thioredoxin	2	4	-0.200472	-0.42428	0.0224968	0.12115	0.0612399
sp P62747 Rho-related	2	5	0.1700563	-0.005427	0.3432581	0.1248125	0.0618396
sp Q71TY3 40S riboson	4	12	-0.146478	-0.291697	-0.007069	0.125625	0.0624357
sp Q99MZ8 LIM and SH:	8	13	-0.132646	-0.240617	-0.020461	0.1268875	0.0630325
sp O08730 Glycogenin-	5	8	0.1874478	-0.02615	0.3983013	0.126975	0.0636192
sp Q99MI7 NEDD8-acti	5	14	0.1663099	-0.015425	0.3363656	0.1312625	0.0642341
sp Q04931 FACT compl	2	2	-0.325886	-0.808282	0.1553216	0.13175	0.0648423
sp O08697 ADP-ribosyl	2	5	-0.220965	-0.510733	0.0613398	0.132375	0.0654453
sp Q9JJ22 Endoplasmic	2	2	0.2214801	-0.066373	0.5287536	0.1326375	0.0660399
sp P21807 Peripherin C	27	100	0.1385178	0.0109494	0.2650679	0.1331875	0.0666289
sp Q9WTT7 Basic leucin	2	2	-0.3226	-0.838472	0.1651689	0.133925	0.0672141
sp Q8VII6 Choline trar	7	30	0.1696084	-0.013084	0.3619073	0.1347	0.0677959
sp O08839 Myc box-de	8	15	-0.146817	-0.28812	-0.007966	0.1362375	0.0683809
sp P38659 Protein disu	19	46	-0.149087	-0.301017	0.0013884	0.1365875	0.0689589
sp P14604 Enoyl-CoA t	10	32	-0.112752	-0.189002	-0.033835	0.1367	0.0695282
sp P01257 Calcitonin C	1	4	-0.196582	-0.45842	0.0632893	0.13725	0.0700925
sp P13638 Sodium/pot	2	10	-0.169341	-0.353097	0.0210089	0.1379125	0.070653
sp P20762 Ig gamma-2	2	5	0.3779909	-0.188525	1.0136262	0.1383875	0.0712082
sp Q8VI04 L-asparagin	9	36	-0.131569	-0.250255	-0.012059	0.1396125	0.0717643
sp P20059 Hemopexin	19	73	-0.199716	-0.458805	0.0438366	0.1404125	0.0723179
sp Q6IFV4 Keratin, typ	5	9	-0.944695	-2.638223	0.777471	0.1405625	0.0728639
sp P01830 Thy-1 mem	3	12	0.1306354	0.0110943	0.247876	0.14135	0.0734074
sp O35550 Rab GTPase	2	4	0.3062216	-0.124455	0.7518752	0.142	0.0739475
sp P0COA9 Small VCP/p	4	9	0.1843193	-0.042343	0.4082965	0.1431875	0.0744885
sp P50339 Chymase O:	3	10	0.3056216	-0.167411	0.7807984	0.1445875	0.0750319
sp P63095 Guanine nu	9	23	0.1566223	-0.017239	0.3273396	0.1464125	0.075581
sp P47819 Glial fibrillai	3	7	-0.258501	-0.634026	0.1163337	0.147825	0.0761324
sp P05545 Serine prote	10	31	-0.286254	-0.718482	0.1535208	0.148175	0.0766782
sp Q920D2 Dihydrofolate	1	2	-0.232761	-0.583758	0.1097411	0.149975	0.0772293
sp P62076 Mitochondr	3	8	-0.137008	-0.266821	-0.001053	0.1509875	0.0777798
sp Q5U1Z0 Rab3 GTPas	3	4	0.2938621	-0.166822	0.7411266	0.1510875	0.0783228
sp Q6MG49 Large prolin	1	2	0.2603467	-0.112447	0.6350623	0.151275	0.0788592
sp Q4G009 Malignant T	2	4	-0.162357	-0.347744	0.0295679	0.1521625	0.0793943
sp Q5BJP3 Ubiquitin-fc	3	9	-0.146121	-0.296927	0.00269	0.1532375	0.0799293
sp Q9EPA0 Dystrophin-	17	47	0.1250011	0.0088053	0.2439699	0.1600125	0.0805055

sp P15684 Aminopeptidase N	2	5	-0.28152	-0.724852	0.1668224	0.160325	0.0810756
sp Q63425 Periaxin OS	30	100	0.1302093	-0.000165	0.2577055	0.1619125	0.0816489
sp P04646 60S ribosomal protein L13	7	18	-0.11519	-0.208581	-0.021796	0.162225	0.0822164
sp P16884 Neurofilament protein	26	100	0.1569606	-0.022618	0.3433948	0.1622375	0.082776
sp Q62868 Rho-associated protein kinase 2	2	2	0.337566	-0.234282	0.9689702	0.1640625	0.0833405
sp Q9Z0V6 Thioredoxin-like protein	5	20	-0.1242	-0.235492	-0.007959	0.1646125	0.0839009
sp A1A5P0 Cdc42 effector	2	2	0.3564138	-0.315729	1.0510821	0.1648125	0.0844551
sp Q62920 PDZ and LIN domain-containing protein 1	3	6	-0.178923	-0.408961	0.053606	0.16495	0.0850027
sp Q8R4A1 ERO1-like protein	4	10	-0.163965	-0.367928	0.0344179	0.1667875	0.0855553
sp P29418 ATP synthase subunit D	3	7	-0.119346	-0.223931	-0.013613	0.1688875	0.0861146
sp P56558 UDP-N-acetylglucosamine 4-epimerase	2	2	-0.367957	-1.086959	0.4055029	0.17205	0.0866875
sp Q64244 ADP-ribosyltransferase	1	3	-0.30388	-0.852999	0.2449586	0.1724375	0.0872554
sp P34058 Heat shock protein 70 kDa	26	100	-0.099365	-0.165512	-0.035643	0.1755125	0.087836
sp P07150 Annexin A1	12	38	-0.197099	-0.496666	0.0939444	0.1762	0.0884136
sp Q5M9G3 Caprin-1 OS	10	22	-0.1182	-0.224499	-0.010179	0.1764375	0.0889851
sp P62850 40S ribosomal protein S19	8	24	-0.111383	-0.203045	-0.019149	0.177775	0.089558
sp P11517 Hemoglobin subunit beta	3	24	0.3035635	-0.234488	0.8387367	0.178325	0.090127
sp Q66HR2 Microtubule-associated protein tau	4	11	-0.150244	-0.338016	0.0328864	0.179325	0.0906951
sp O54975 Xaa-Pro amino acid peptidase	10	19	0.1305809	-0.005156	0.2612221	0.1807375	0.091265
sp Q4VSI4 Ubiquitin carboxy-terminal hydrolase L1	4	8	0.1889368	-0.08199	0.450839	0.1813875	0.0918318
sp P62864 40S ribosomal protein S16	2	3	-0.594896	-1.825823	0.6348561	0.18195	0.0923951
sp Q62760 Mitochondrial membrane protein	2	3	0.1987344	-0.109488	0.4911028	0.18285	0.0929569
sp Q4V7E8 Leucine-rich repeat protein	2	4	0.259095	-0.249013	0.7808769	0.184975	0.0935249
sp Q9JMB5 Proteasome subunit beta type	4	5	0.2845271	-0.246781	0.7657769	0.1866	0.0940959
sp Q03344 ATPase inhibitor	3	7	0.1555316	-0.31529	0.4878983	0.1869125	0.0946619
sp P82808 Glucosaminidase	2	2	0.1859311	-0.138691	0.5098896	0.1869375	0.0952211
sp P47728 Calretinin O-linkage	9	18	0.1672455	-0.067021	0.3987823	0.188825	0.095785
sp P62738 Actin, aortic smooth muscle	7	18	-0.323327	-0.934738	0.2758175	0.190175	0.0963502
sp Q9Z0W7 Chloride intracellular channel 1	6	18	-0.114015	-0.215947	-0.009444	0.1938125	0.0969304
sp P02625 Parvalbumin	5	13	0.2369886	-0.174242	0.6353407	0.1938375	0.0975038
sp Q5XHY5 Threonyl-tRNA methyltransferase	8	23	-0.119671	-0.240329	0.0012215	0.194825	0.0980763
sp A1A5P9 Melanoma-associated antigen 1	1	3	0.3399893	-0.454987	1.1290025	0.1949625	0.0986428
sp P81795 Eukaryotic translation initiation factor 4B	11	17	-0.116366	-0.225136	-0.007086	0.198225	0.0992218
sp Q4G075 Leukocyte elastase inhibitor	4	7	-0.204534	-0.570619	0.0970254	0.1987375	0.099797
sp P01026 Complement component C1q	38	100	-0.183753	-0.465877	0.1003563	0.2015375	0.1003818
sp Q03346 Mitochondrial membrane protein	2	3	-0.211362	-0.568509	0.1327765	0.2016875	0.1009606
sp P62853 40S ribosomal protein S16	7	20	-0.114376	-0.228467	-0.003466	0.2026625	0.1015385
sp Q9QZA6 CD151 antigen	7	26	0.133633	-0.020674	0.3052247	0.2039625	0.1021172
sp Q0ZHH6 Atlastin-3 O-linkage	4	8	-0.158774	-0.377642	0.0586398	0.2041125	0.1026902
sp P20767 Ig lambda-2 chain	3	12	0.2818814	-0.269584	0.8210293	0.2055375	0.1032647
sp P12369 cAMP-dependent protein kinase regulatory subunit 1	4	9	-0.156071	-0.370115	0.0616575	0.2063	0.1038372
sp O55012 Phosphatidylethanolamine-binding protein	3	5	-0.137827	-0.312169	0.0314863	0.206475	0.1044042
sp Q63862 Myosin-11 (smooth muscle)	15	24	-0.272554	-0.792303	0.2644311	0.207925	0.104973
sp Q00566 Methyl-CpG-binding domain-containing protein	4	6	0.169568	-0.089917	0.430186	0.20935	0.1055434
sp P49088 Asparagine synthetase	6	10	-0.150603	-0.353004	0.0605908	0.209725	0.1061096
sp P16391 RT1 class I histocompatibility antigen	3	4	-0.25799	-0.852214	0.3457931	0.2105375	0.1066741
sp Q9Z1A5 NEDD8-activating enzyme substrate 1	1	3	1.3741835	-2.797456	5.3310554	0.2107	0.1072333

sp Q9Z1N4 3'(2'),5'-bis	6	8	-0.128478	-0.28349	0.0254179	0.212275	0.1077951
sp Q64632 Integrin bet	37	100	0.0998489	0.0211571	0.1774181	0.21245	0.1083517
sp P30427 Plectin OS=	50	100	0.0961193	0.0270893	0.1665005	0.2143375	0.1089125
sp Q64268 Heparin cof	1	3	0.2442926	-0.230722	0.7237044	0.2155125	0.1094736
sp Q6P6T4 Echinoderm	4	5	-0.154618	-0.378691	0.0784795	0.2160375	0.1100315
sp Q63622 Disks large l	3	4	0.3173299	-0.346919	1.0026025	0.2166	0.1105865
sp P31211 Corticoster	3	4	0.2530159	-0.381303	0.8554925	0.2172375	0.1111391
sp Q920G2 Na(+)/H(+) c	2	6	-0.174105	-0.443816	0.099185	0.217475	0.1116872
sp P24049 60S riboson	10	47	-0.108719	-0.216178	-0.00423	0.2174875	0.1122298
sp Q4KLP0 Probable 2-	3	3	0.1875697	-0.153328	0.5394444	0.2189	0.112774
sp P35427 60S riboson	10	42	-0.114219	-0.234904	0.0059761	0.2195	0.1133158
sp O35179 Endophilin-	8	20	0.1314813	-0.048551	0.2963126	0.221175	0.1138605
sp Q6AY72 UPF0449 pr	1	2	-0.264398	-0.88898	0.3171704	0.22255	0.1144067
sp Q561R9 Beta-lactam	2	4	-0.184594	-0.497215	0.130579	0.2235375	0.1149524
sp Q5XI31 GPI transam	3	3	-0.225495	-0.719017	0.2389018	0.2242125	0.115496
sp Q9QXQ0 Alpha-actin	20	53	-0.104695	-0.198763	-0.005739	0.225575	0.1160409
sp P09117 Fructose-bi	15	65	0.0998012	0.0146394	0.1831443	0.226325	0.1165842
sp Q4V7A0 WD repeat-	3	7	0.1528004	-0.075433	0.3808182	0.22635	0.1171222
sp Q9Z1P2 Alpha-actin	10	15	-0.141097	-0.343034	0.0653088	0.2264125	0.1176554
sp Q641Z6 EH domain-	4	5	-0.143308	-0.347766	0.0536454	0.2271375	0.1181868
sp Q63364 E3 ubiquitin	1	2	0.2976196	-0.478859	1.0875925	0.2287	0.1187207
sp P54921 Alpha-solub	7	21	-0.108765	-0.215215	-0.004359	0.2292	0.1192519
sp P21588 5'-nucleotid	2	2	0.3253827	-0.418673	1.1404199	0.2313375	0.1197882
sp Q6V7V2 Rhotekin O!	9	11	0.1365655	-0.038885	0.3235298	0.2326125	0.1203254
sp Q5S6T3 2-C-methyl-	1	4	-0.179972	-0.504273	0.1536174	0.2355	0.1208713
sp Q4KLL0 Transcriptic	2	6	-0.171077	-0.458813	0.1229134	0.235775	0.1214133
sp Q66HA8 Heat shock	22	68	-0.099463	-0.184766	-0.010056	0.23615	0.1219519
sp P26453 Basigin OS=	5	14	-0.110263	-0.225674	0.00847	0.2375625	0.1224922
sp Q5U312 Ankycorbin	2	3	0.2708711	-0.353364	0.8909215	0.2377875	0.1230284
sp P55051 Fatty acid-b	4	14	0.1487753	-0.089853	0.3837319	0.2383875	0.1235625
sp Q62667 Major vault	14	33	-0.121063	-0.278238	0.0346267	0.2416	0.1241065
sp Q5PQL7 Integral me	1	2	0.4805324	-1.022157	1.9685314	0.241625	0.1246455
sp P43278 Histone H1.	12	58	0.1140006	-0.022192	0.2472335	0.24285	0.1251853
sp Q9JI92 Syntenin-1	3	3	-0.168463	-0.462785	0.126936	0.2439625	0.1257252
sp Q5FVH2 Phospholip	3	4	-0.152529	-0.41528	0.1072959	0.245675	0.1262679
sp Q6P734 Plasma prot	2	9	-0.196205	-0.596133	0.1791197	0.245975	0.1268072
sp Q5MPA9 Serine/thre	4	5	0.1833008	-0.164521	0.519598	0.246175	0.1273424
sp P86182 Coiled-coil c	2	2	-0.327452	-1.259584	0.6009732	0.246375	0.1278738
sp P63055 Purkinje cel	5	23	0.1350821	-0.071072	0.3349656	0.247575	0.1284058
sp P70584 Short/branc	2	2	0.2651841	-0.354935	0.8795014	0.2484125	0.1289368
sp P63039 60 kDa heat	28	100	-0.093544	-0.166698	-0.020685	0.249575	0.1294683
sp O88339 Epsin-1 OS=	2	4	-0.195494	-0.614177	0.2282565	0.2499125	0.1299965
sp Q6P7S1 Acid cerami	10	32	0.1063888	-0.00434	0.2225696	0.2529875	0.1305336
sp Q6AYZ1 Tubulin alp1	1	2	0.1610045	-0.128689	0.4478001	0.2533875	0.1310678
sp Q5XIM4 ATP synthas	1	3	-0.149533	-0.402423	0.0977037	0.2555	0.1316064
sp Q5FVN1 Starch-bind	4	10	-0.135004	-0.343186	0.0611795	0.256425	0.1321445
sp P42930 Heat shock	12	53	-0.091845	-0.160914	-0.023587	0.2565875	0.1326785

sp Q6MG84 Epidermal g	3	5	-0.179882	-0.540994	0.1777243	0.2572375	0.1332108
sp P37397 Calponin-3	11	46	-0.105996	-0.222564	0.016651	0.2573375	0.133739
sp B0BNM9 Glycolipid ti	2	3	-0.157445	-0.43834	0.1300891	0.259075	0.1342701
sp Q5XI97 Alanyl-tRNA	1	2	-0.174381	-0.554151	0.2381148	0.261475	0.1348069
sp Q64591 2,4-dienoyl-	3	4	0.1834321	-0.199845	0.5655967	0.261875	0.1353408
sp A1L108 Actin-relate	5	5	-0.15325	-0.43123	0.1081598	0.2628	0.1358741
sp Q9QYU4 Mu-crystalli	2	3	-0.200049	-0.732727	0.3219783	0.2628125	0.136403
sp Q6YAT4 Epsilon-sarc	1	3	0.2170571	-0.257622	0.6873646	0.2628375	0.1369276
sp P56574 Isocitrate di	14	43	-0.098086	-0.195761	-0.001639	0.263575	0.1374509
sp Q63041 Alpha-1-ma	18	42	-0.134419	-0.350115	0.0833641	0.2640625	0.137972
sp Q5FVC7 Arf-GAP wit	2	2	0.1976548	-0.318484	0.704775	0.2644375	0.1384903
sp Q80Z30 Protein pho	2	2	-0.171143	-0.560719	0.2112621	0.2647875	0.1390058
sp P14141 Carbonic an	6	16	0.3418121	-0.589345	1.2573817	0.2652	0.1395188
sp B0BNE2 DNA-directe	2	2	0.1421032	-0.122833	0.3977803	0.2671375	0.1400354
sp Q923V8 15 kDa sele	2	8	-0.16567	-0.497498	0.1802981	0.26825	0.1405524
sp Q5XIK7 Katanin p60	2	2	0.2634059	-0.415653	0.9395772	0.2687125	0.1410671
sp P18645 UDP-glucos	2	3	-0.188911	-0.587508	0.2146443	0.2687625	0.1415779
sp Q923W4 Hepatoma-	2	5	0.1118995	-0.032955	0.2504641	0.2694625	0.1420874
sp Q80WE1 Fragile X me	5	9	0.1444749	-0.107085	0.3930269	0.270425	0.1425967
sp B2GV54 Neutral cho	5	12	0.1537461	-0.125544	0.4480002	0.270875	0.1431037
sp P58775 Tropomyosi	4	9	-0.223635	-0.755123	0.318398	0.2709625	0.1436071
sp P97675 Ectonucleot	2	4	-0.149978	-0.417221	0.1213724	0.271175	0.1441074
sp Q02293 Protein farr	1	2	-0.203045	-0.673704	0.2567986	0.2713125	0.1446042
sp P01835 Ig kappa ch	6	32	0.2379721	-0.348687	0.8225328	0.2738875	0.1451073
sp P11980 Pyruvate kin	25	100	0.0960428	0.0053552	0.1864136	0.2739625	0.1456067
sp Q4G064 Ubiquinone	2	2	-0.168243	-0.505533	0.1833788	0.274825	0.1461056
sp Q5XIN6 LETM1 and	11	25	-0.104334	-0.223438	0.0167528	0.2751375	0.1466019
sp P04785 Protein disu	26	99	-0.092645	-0.171593	-0.010994	0.277075	0.1471018
sp Q562C6 Leucine zipp	2	4	0.209393	-0.273833	0.7096166	0.277375	0.147599
sp Q63635 Syntaxin-6 C	1	2	0.1896491	-0.269313	0.6570549	0.2784375	0.1480965
sp Q62658 Peptidyl-pro	3	14	0.1110189	-0.037457	0.2616127	0.2790875	0.1485927
sp P52555 Endoplasmic	12	37	-0.095133	-0.179918	-0.009519	0.2793125	0.149086
sp P83732 60S ribosom	7	36	-0.10568	-0.233359	0.0272409	0.28105	0.1495821
sp Q9Z1K9 Disintegrin	3	4	-0.174853	-0.562745	0.2247956	0.28175	0.1500771
sp Q5M7A7 CB1 cannab	3	5	0.1463755	-0.129642	0.4210045	0.2860375	0.1505844
sp Q63396 Activated R	4	10	-0.117338	-0.291387	0.0568382	0.2871	0.1510919
sp Q9EPC6 Profilin-2 O	4	14	0.1335269	-0.110283	0.3751935	0.287725	0.151598
sp P51635 Alcohol deh	12	43	0.0944878	0.0018603	0.1861424	0.2887	0.1521039
sp Q9WUH4 Four and a l	5	8	-0.140892	-0.436374	0.1834004	0.2887	0.1526061
sp P05982 NAD(P)H de	6	15	0.1115076	-0.050232	0.266899	0.2903375	0.1531106
sp Q9Z1M9 Structural n	7	10	0.15043	-0.160434	0.441369	0.290525	0.1536121
sp Q58FK9 Kynurenine	4	4	0.2092006	-0.309042	0.7439492	0.290775	0.1541109
sp P62909 40S ribosom	19	76	-0.092987	-0.179684	-0.004544	0.291575	0.1546089
sp Q6AXS5 Plasminoge	13	23	-0.093777	-0.181272	-0.002548	0.292	0.1551049
sp Q99M63 WD40 repe	1	2	-0.14266	-0.411902	0.1209054	0.2936625	0.1556033
sp Q6IMF3 Keratin, typ	1	2	-0.169057	-0.604037	0.2850116	0.2945625	0.1561014
sp Q62825 Exocyst con	1	2	0.148412	-0.185597	0.496697	0.2954125	0.1565989

sp Q62651 Delta(3,5)-E	7	12	0.1263978	-0.096037	0.3626543	0.2956875	0.1570939
sp P42676 Neurolysin,	3	6	0.1554859	-0.179442	0.49691	0.2957125	0.1575855
sp P09650 Mast cell pr	9	27	0.1890368	-0.296002	0.6621091	0.2962625	0.1580755
sp P32089 Tricarboxyl-	9	35	-0.090439	-0.169768	-0.009863	0.297	0.1585647
sp Q62881 Nucleolar p	2	4	0.1437812	-0.136856	0.431543	0.2998125	0.1590603
sp Q9WUW Complemer	2	2	0.1863079	-0.331007	0.7203714	0.30045	0.1595546
sp O35331 Pyridoxal ki	3	6	-0.153118	-0.489925	0.1742415	0.3011	0.1600478
sp Q0VGK0 Gamma-am	2	6	0.1468129	-0.155577	0.4615973	0.3014625	0.1605388
sp Q66H12 Alpha-N-ac	2	8	0.1231495	-0.083195	0.3313839	0.302725	0.1610308
sp Q5M7A4 Ubiquitin-lil	1	3	-0.169846	-0.593088	0.2535824	0.3028125	0.1615197
sp Q4QQV3 Protein FAN	3	7	-0.118217	-0.321844	0.0836346	0.3029375	0.1620057
sp Q62696 Disks large l	2	3	0.1672721	-0.304964	0.6394468	0.3045625	0.1624939
sp B0BN3 Carbonic an	4	10	0.1734355	-0.250725	0.6117928	0.3048125	0.1629797
sp P62755 40S riboson	13	43	-0.09494	-0.200975	0.0084885	0.30535	0.1634639
sp P12711 Alcohol deh	4	6	0.1282538	-0.15976	0.3945921	0.305625	0.1639458
sp Q9R0J8 Legumain C	1	5	-0.130578	-0.376638	0.1231129	0.306225	0.1644265
sp P36953 Afamin OS=	10	22	-0.156469	-0.529187	0.1996936	0.306625	0.1649053
sp Q6PDV7 60S riboson	14	75	-0.096416	-0.207671	0.0131535	0.3069125	0.1653818
sp Q9Z0W5 Protein kin	10	30	0.0919835	0.0039473	0.1820504	0.30725	0.1658563
sp Q64361 Latexin OS=	3	8	0.0985152	-0.015704	0.2172612	0.3073	0.1663278
sp P63090 Pleiotrophir	5	12	-0.106929	-0.269739	0.0556624	0.3074625	0.1667966
sp Q5XI07 Lipoma-pre	2	5	-0.152408	-0.501255	0.1964939	0.310625	0.1672729
sp P04218 OX-2 memb	3	6	-0.124987	-0.351603	0.1049221	0.310675	0.1677462
sp Q6LED0 Histone H3.	2	14	-0.168307	-0.595951	0.2654407	0.310825	0.1682168
sp Q5PPL3 Sterol-4-alp	3	5	0.1656348	-0.201773	0.5674194	0.3121	0.1686886
sp Q924N5 Long-chain-	7	8	-0.1105	-0.274836	0.0580749	0.3121375	0.1691574
sp P32738 Choline O-a	3	3	0.1684349	-0.256568	0.6054414	0.3124	0.1696239
sp P83883 60S riboson	5	12	-0.089565	-0.174458	-0.002136	0.3126125	0.1700882
sp P97829 Leukocyte s	2	7	0.1195828	-0.093508	0.3362461	0.31315	0.1705512
sp Q924K2 FAS-associa	2	2	0.2313429	-0.553997	1.0292442	0.3132	0.1710113
sp P05426 60S riboson	12	44	-0.089763	-0.17531	-0.005812	0.313475	0.1714694
sp P40112 Proteasome	4	4	-0.161834	-0.567025	0.2377715	0.315325	0.1719305
sp Q3ZB98 Breast carci	12	43	0.1162782	-0.094287	0.3164422	0.3156125	0.1723895
sp Q6AYU3 DnaJ homol	3	4	-0.119151	-0.348506	0.1033042	0.3160625	0.1728471
sp Q9JID2 Guanine nu	1	2	0.1759851	-0.344133	0.7174641	0.3161625	0.1733021
sp Q99376 Transferrin	2	2	-0.285584	-1.381515	0.8500696	0.3177375	0.1737591
sp Q63615 Vacuolar pr	1	5	0.1478063	-0.213362	0.493418	0.317875	0.1742138
sp Q03348 Receptor-ty	2	2	-0.177395	-0.73634	0.3858071	0.3182625	0.1746667
sp Q10728 Protein pho	2	2	-0.188786	-0.727892	0.3506355	0.3190625	0.1751194
sp Q4KM65 Cleavage ar	2	3	-0.161721	-0.585373	0.2752688	0.3192375	0.1755698
sp Q63448 Peroxisoma	5	6	-0.129317	-0.388886	0.1227815	0.3199875	0.1760197
sp P53670 LIM domain	2	2	-0.208943	-0.822606	0.3410609	0.3209125	0.1764696
sp O09032 ELAV-like pi	1	3	0.1198673	-0.116494	0.3421433	0.32195	0.17692
sp Q05695 Neural cell :	10	25	0.1017015	-0.047482	0.2510368	0.322075	0.1773681
sp P62703 40S riboson	19	80	-0.096067	-0.21606	0.0244662	0.3222	0.1778137
sp P27274 CD59 glyco	3	11	0.1183647	-0.101187	0.3442639	0.3222625	0.1782568
sp O54924 Exocyst con	4	7	0.1101657	-0.062915	0.2945438	0.3224875	0.1786979

sp Q9WTV0 Prolactin re	4	5	-0.14322	-0.474702	0.1885566	0.3228875	0.1791375
sp P21396 Amine oxid	17	48	0.0906206	-0.001358	0.1848663	0.3246375	0.1795797
sp Q641X8 Eukaryotic t	4	6	-0.135252	-0.438728	0.1725544	0.32465	0.1800193
sp P62246 40S riboson	5	34	-0.097136	-0.224607	0.0300709	0.32495	0.1804572
sp P12839 Neurofilam	29	100	0.1068891	-0.061316	0.2760065	0.32515	0.180893
sp P62718 60S riboson	10	39	-0.091804	-0.196442	0.0116147	0.3262875	0.1813296
sp P62845 40S riboson	4	13	-0.101909	-0.244409	0.0375507	0.3266875	0.1817648
sp P31977 Ezrin OS=Rα	6	12	-0.099528	-0.235184	0.0313405	0.327025	0.1821984
sp P50878 60S riboson	18	80	-0.088907	-0.178825	-0.000935	0.3273	0.1826303
sp P19945 60S acidic ri	14	68	-0.092784	-0.201812	0.0172989	0.3304875	0.183069
sp Q8VIL3 ZW10 inter	4	11	-0.102977	-0.261652	0.0513153	0.33115	0.1835071
sp P24368 Peptidyl-pro	14	58	-0.089068	-0.185102	0.0007339	0.3315375	0.1839438
sp P63174 60S riboson	5	22	-0.094372	-0.210888	0.0198673	0.3321875	0.1843798
sp Q9JM53 Apoptosis-i	5	5	-0.116837	-0.344523	0.107465	0.332375	0.1848138
sp Q5FVI4 Cell cycle e	7	17	0.092708	-0.011951	0.1984714	0.33325	0.1852478
sp P28073 Proteasome	2	8	-0.103902	-0.275107	0.0609627	0.3338	0.1856809
sp Q9JID1 Programme	3	5	0.10088	-0.058828	0.2646804	0.333825	0.1861116
sp Q91XU1 Protein qua	5	8	0.1160986	-0.098219	0.3311338	0.3342	0.1865408
sp Q9JKB8 Pre-mRNA-s	2	2	-0.167839	-0.682495	0.4060681	0.3351	0.1869702
sp O08619 Coagulation	3	4	-0.147558	-0.522373	0.2065674	0.3360875	0.1873999
sp P23565 Alpha-inter	22	57	0.115947	-0.123672	0.3437624	0.3381375	0.1878331
sp Q5EB77 Ras-related	5	13	0.104546	-0.06312	0.2729062	0.339175	0.1882667
sp P47853 Biglycan OS	13	62	-0.154195	-0.588569	0.2790788	0.33935	0.1886984
sp P11598 Protein disu	25	100	-0.081364	-0.137723	-0.024003	0.3394375	0.1891278
sp P63245 Guanine nu	18	72	-0.09231	-0.206047	0.0222555	0.340075	0.1895567
sp Q9ERE6 Myosin pho	7	11	0.1080219	-0.077116	0.2928158	0.341075	0.1899859
sp Q99N37 Rho GTPase	3	3	0.1548392	-0.272942	0.5876932	0.3421125	0.1904156
sp Q62950 Dihydropyri	7	15	0.1050764	-0.063669	0.2795148	0.342275	0.1908434
sp B0BNG0 Tetrastricope	2	2	0.1555453	-0.394866	0.6851135	0.3425125	0.1912695
sp P46844 Biliverdin re	7	10	0.1039126	-0.071564	0.2794689	0.3426625	0.1916935
sp P06238 Alpha-2-ma	6	7	-0.159463	-0.639655	0.3278508	0.342725	0.1921154
sp P26772 10 kDa heat	11	48	-0.084517	-0.160847	-0.008908	0.3432125	0.1925363
sp Q9JHW5 Vesicle-assoc	2	4	-0.143402	-0.535317	0.2545969	0.343825	0.1929565
sp Q66X93 Staphylococ	21	51	-0.086259	-0.170855	-0.003969	0.34385	0.1933745
sp P49432 Pyruvate de	12	59	-0.087371	-0.176612	0.0065218	0.3440875	0.1937908
sp P41565 Isocitrate de	11	25	-0.085099	-0.158935	-0.011378	0.3441	0.1942049
sp P05696 Protein kin	19	36	0.0889393	-0.008797	0.1853753	0.3445375	0.1946179
sp P08011 Microsomal	2	2	-0.153456	-0.697286	0.375146	0.3445625	0.1950287
sp B2GV24 E3 UFM1-pr	4	7	-0.129984	-0.43723	0.1785452	0.3462375	0.1954419
sp P19527 Neurofilam	21	100	0.1039941	-0.075172	0.2839132	0.3466625	0.1958539
sp Q3T1I4 Protein PRR	2	2	0.1840846	-0.495043	0.8597653	0.3476375	0.1962664
sp Q6AYG3 Protein pru	6	13	0.1018929	-0.060137	0.2637557	0.3486375	0.1966793
sp Q5XI55 Peptide-N(4	1	3	0.2273386	-0.711746	1.1365777	0.34865	0.19709
sp P07895 Superoxide	7	23	-0.087123	-0.180234	0.0087012	0.349	0.1974995
sp P37377 Alpha-synuc	6	27	0.1109673	-0.110093	0.3401178	0.3493875	0.1979078
sp A0MZ67 Shootin-1 O	2	3	-0.152479	-0.709764	0.3900604	0.3508625	0.1983179
sp B5DF41 Syntaphilin	1	2	-0.377245	-2.454723	1.8715699	0.3509125	0.1987259

sp P13635 Ceruloplasn	22	69	0.0973511	-0.050324	0.2482046	0.3509625	0.1991318
sp Q4V8K2 Beta-cateni	3	4	-0.147703	-0.700019	0.4218024	0.35105	0.1995359
sp O35217 Multiple inc	2	4	0.1288473	-0.18573	0.4467884	0.351475	0.1999389
sp P62836 Ras-related	2	3	-0.133216	-0.477729	0.2169482	0.35165	0.2003402
sp Q6AXQ5 2',5'-phosph	2	4	-0.113994	-0.369744	0.1429983	0.3526375	0.2007421
sp Q1WIM1 Cell adhesic	11	49	0.0916603	-0.031371	0.2179899	0.3538125	0.2011449
sp P04177 Tyrosine 3-r	1	3	-0.128364	-0.482228	0.2019455	0.35385	0.2015457
sp P35952 Low-density	2	6	-0.115815	-0.373914	0.1516883	0.35605	0.2019502
sp P97576 GrpE protei	2	7	0.1189872	-0.165998	0.3975397	0.3564625	0.2023536
sp P07483 Fatty acid-b	1	2	-0.129285	-0.505619	0.2491641	0.3566125	0.2027553
sp Q6Q0N1 Cytosolic nc	10	26	-0.093729	-0.221542	0.0391254	0.3567375	0.2031553
sp Q9QXU8 Cytoplasmic	13	33	-0.086308	-0.181971	0.016489	0.357025	0.2035539
sp Q09073 ADP/ATP tr	9	39	-0.082054	-0.1484	-0.016009	0.357175	0.2039508
sp Q02769 Squalene sy	4	6	-0.11976	-0.449813	0.1827154	0.357875	0.2043476
sp P09006 Serine prote	5	13	-0.214545	-1.059462	0.6273361	0.3581	0.2047428
sp Q9EQT5 Tubulointer	3	5	-0.15233	-0.769136	0.4631089	0.3584375	0.2051369
sp P18265 Glycogen sy	3	3	-0.138975	-0.56978	0.2761927	0.35885	0.20553
sp Q6AXX6 UPF0765 pr	8	30	-0.088166	-0.187479	0.0145771	0.35915	0.2059219
sp Q5PQP1 RNA-bindin	1	3	-0.108539	-0.327166	0.1185474	0.3599875	0.2063139
sp Q9EPX0 Heat shock	2	6	0.1233843	-0.179754	0.4321647	0.36005	0.2067041
sp Q99J82 Integrin-link	10	23	-0.089096	-0.194412	0.0161208	0.360275	0.2070929
sp Q9JIL8 R DNA repair	4	4	0.1009627	-0.14598	0.3309487	0.3621375	0.2074844
sp Q66H20 Polypyrimid	2	2	-0.145435	-0.620908	0.3263731	0.362375	0.2078746
sp Q71UF4 Histone-bin	4	12	-0.091383	-0.215381	0.0301172	0.362475	0.208263
sp P21961 Mast cell ca	2	4	0.1288459	-0.244351	0.502988	0.3625	0.2086496
sp Q5FWY5 AH receptor	6	14	0.0912066	-0.032946	0.2115579	0.3635625	0.2090369
sp Q505J6 Mitochondr	3	9	0.0930802	-0.050803	0.2329926	0.3640625	0.2094235
sp Q62813 Limbic syste	1	2	-0.116963	-0.396856	0.1621026	0.3646125	0.2098095
sp P02454 Collagen alp	12	74	-0.18022	-0.853402	0.4903997	0.365275	0.2101953
sp Q63190 Emerin OS=	1	2	-0.136701	-0.529087	0.2555728	0.366175	0.2105814
sp P18395 Cold shock	13	29	-0.085575	-0.176007	0.0036169	0.366625	0.2109667
sp Q9WUL0 DNA topois	2	4	0.1233687	-0.179756	0.4367047	0.3667625	0.2113504
sp P80385 5'-AMP-acti	2	3	-0.134884	-0.52605	0.2403349	0.36755	0.2117342
sp Q6P7R8 Estradiol 17	8	21	-0.094063	-0.2463	0.0552822	0.3679375	0.212117
sp Q62714 Neutrophil	2	2	0.1415629	-0.429344	0.6709955	0.36885	0.2125002
sp O35821 Myb-bindin	6	10	-0.131387	-0.538384	0.2919243	0.3698	0.2128839
sp Q6QLM7 Kinesin hea	7	17	0.0908469	-0.043791	0.2264237	0.3706625	0.2132678
sp O08618 Phosphorib	4	8	0.1377911	-0.286237	0.5479361	0.3706625	0.2136498
sp Q08469 Orphan sod	2	2	-0.150594	-0.70029	0.4017149	0.370875	0.2140305
sp P17078 60S riboson	8	28	-0.086611	-0.185692	0.013263	0.3731	0.2144147
sp P19332 Microtubul	16	50	0.0843422	-0.01445	0.1799263	0.374275	0.2147999
sp P40190 Interleukin-	1	2	-0.132643	-0.645693	0.3623016	0.374925	0.2151849
sp Q53UA7 Serine/thre	1	2	-0.105936	-0.392106	0.1925769	0.3749875	0.2155681
sp Q9JHB5 Translin-ass	2	2	0.1580039	-0.463824	0.7709761	0.3750625	0.2159496
sp P29066 Beta-arresti	3	4	-0.112919	-0.386673	0.1633466	0.37575	0.216331
sp Q07803 Elongation f	4	6	-0.099083	-0.329412	0.1657559	0.3759125	0.216711
sp Q78P75 Dynein light	1	9	-0.102851	-0.311398	0.0976192	0.3764	0.2170903

sp Q9ES40 PRA1 family	4	12	0.0928412	-0.058767	0.239513	0.37655	0.2174682
sp P24268 Cathepsin D	18	89	0.0835741	-0.00669	0.1753965	0.3782375	0.2178482
sp P05371 Clusterin O-	6	19	0.093068	-0.050217	0.2369509	0.378575	0.2182273
sp Q5RK30 Ribosome n	3	5	0.1021338	-0.118393	0.3248268	0.379175	0.218606
sp Q5XI68 Protein Dr1	1	2	0.1234318	-0.225078	0.4746061	0.379675	0.2189841
sp Q5XIE6 3-hydroxyis	5	8	0.1004432	-0.125474	0.3228157	0.3802875	0.2193619
sp P13941 Collagen alp	7	16	-0.098707	-0.313819	0.1341244	0.380775	0.219739
sp P60892 Ribose-pho:	2	2	-0.108181	-0.395172	0.1788239	0.3815875	0.2201163
sp P62243 40S riboson	12	42	-0.082235	-0.165828	0.0051745	0.381725	0.2204921
sp Q6AY19 Uncharacte	2	2	0.1544432	-0.681922	0.9644731	0.3822375	0.2208674
sp P47196 RAC-alpha s	3	5	0.1002448	-0.110704	0.3107044	0.3822875	0.221241
sp Q9ES67 Rho guanin	2	3	-0.141293	-0.698125	0.4288045	0.3827125	0.2216139
sp P63326 40S riboson	8	27	-0.088852	-0.220858	0.0421088	0.3838875	0.2219878
sp Q9R080 G-protein-si	2	6	0.1919549	-0.787564	1.1650997	0.3839375	0.2223601
sp B2GV06 Succinyl-Co	12	28	0.0833132	-0.012032	0.17531	0.3843875	0.2227318
sp Q641Z8 Peflin OS=R	3	4	-0.135767	-0.668426	0.3987774	0.385425	0.2231041
sp P55260 Annexin A4	14	38	0.0847451	-0.024607	0.195464	0.3859125	0.2234758
sp Q9QZR6 Septin-9 OS	9	25	-0.082808	-0.171907	0.0053415	0.3875125	0.2238494
sp P23562 Band 3 anio	9	14	0.1564101	-0.50328	0.7933373	0.388875	0.2242245
sp P10499 Potassium v	2	4	0.1071528	-0.184243	0.4048071	0.38945	0.2245991
sp Q63151 Long-chain-	2	4	-0.106091	-0.385811	0.1810351	0.3897125	0.2249727
sp P80299 Epoxide hyc	1	2	0.2392054	-1.445317	1.9709658	0.390125	0.2253455
sp O88382 Membrane-	2	2	0.1225804	-0.330807	0.5802251	0.390375	0.2257172
sp P35435 ATP synthas	15	40	-0.078997	-0.138812	-0.015361	0.3904875	0.2260875
sp P81128 Glucocortic	4	4	-0.121068	-0.495552	0.2543167	0.390575	0.2264563
sp P0C219 Sarcolemm	2	5	0.1013236	-0.180772	0.3715853	0.3929125	0.2268287
sp Q5U2R0 Methionine	2	2	0.1375083	-0.320513	0.668671	0.3934125	0.2272005
sp P23593 Apolipoprot	2	11	-0.114505	-0.472899	0.2536893	0.3935125	0.2275709
sp Q7TQ16 Cytochrome	3	8	-0.100678	-0.338473	0.139172	0.393625	0.2279399
sp Q91ZN1 Coronin-1A	4	5	-0.108917	-0.412811	0.1922283	0.395375	0.2283112
sp O08815 STE20-like s	6	9	-0.088087	-0.245004	0.0692028	0.3955125	0.2286811
sp P21531 60S riboson	17	100	-0.08379	-0.195301	0.0264766	0.39585	0.2290501
sp P08289 Alkaline ph	11	14	-0.093581	-0.281058	0.1018917	0.3959625	0.2294178
sp Q5U2Y1 General tra	4	5	-0.124019	-0.577404	0.3243663	0.3969	0.2297859
sp Q8R1R5 CD99 antigen	1	4	0.1408891	-0.560719	0.8602673	0.3970625	0.2301527
sp O35274 Neurabin-2	2	5	0.0861643	-0.058902	0.2305179	0.3971375	0.2305181
sp P35465 Serine/thre	3	9	0.0960451	-0.099466	0.2928686	0.3974	0.2308825
sp Q6U6G5 Zinc finger C	4	6	-0.126057	-0.588111	0.3397486	0.3985	0.2312476
sp P83868 Prostagland	6	17	-0.08375	-0.197804	0.0329002	0.3986375	0.2316115
sp B3GN16 Septin-11 O	7	18	-0.085833	-0.202789	0.0318509	0.3987375	0.2319741
sp Q63100 Cytoplasmic	4	6	-0.099955	-0.359628	0.1552024	0.3992875	0.2323362
sp P06214 Delta-amino	3	7	0.1054085	-0.181914	0.4008803	0.3996125	0.2326975
sp P00564 Creatine kin	7	14	0.1932267	-0.836228	1.2021329	0.399625	0.2330572
sp Q62871 Cytoplasmic	9	14	-0.084874	-0.205682	0.0425061	0.4001375	0.2334166
sp D3ZZL9 GRIP and cc	3	3	-0.107216	-0.419177	0.1860476	0.4015625	0.2337774
sp O88664 Serine/thre	1	5	-0.10303	-0.368013	0.1669838	0.401875	0.2341373
sp Q64611 Cysteine sul	3	8	0.1022832	-0.167098	0.3662518	0.40195	0.2344959

sp O08590 Membrane	10	21	-0.090289	-0.269296	0.0990364	0.402275	0.2348537
sp O88794 Pyridoxine-1	3	3	0.1055612	-0.187902	0.4006938	0.4023375	0.23521
sp Q568Z6 IST1 homolog	2	2	-0.125255	-0.602527	0.349475	0.402725	0.2355657
sp Q6AYS7 Aminoacylase	12	39	-0.090811	-0.271784	0.0929637	0.402775	0.2359199
sp Q63617 Hypoxia up-regulated	28	84	-0.080818	-0.169506	0.007084	0.40295	0.236273
sp O08629 Transcriptic	5	7	0.0953911	-0.121621	0.3039503	0.4033625	0.2366256
sp Q8K581 Thioredoxin-like	1	2	-0.131353	-0.644068	0.361532	0.4034875	0.2369768
sp Q62717 Calcium-dependent	11	17	-0.083602	-0.206125	0.0431055	0.4037	0.2373271
sp Q8R511 Formin-binding	3	6	-0.110679	-0.466408	0.2505091	0.4061	0.2376809
sp Q4V8C2 Centromere	1	2	0.0961687	-0.16224	0.353143	0.4061625	0.2380334
sp Q9JJ19 Na(+) / H(+) exchanger	11	29	-0.081256	-0.185892	0.019033	0.406375	0.2383848
sp Q9EQV6 Tripeptidyl-peptidase I	1	6	-0.095428	-0.314469	0.1155749	0.4064125	0.2387349
sp P06761 78 kDa glucan-binding protein	26	100	-0.078559	-0.153814	-0.006948	0.4065125	0.2390837
sp Q498R3 DnaJ homolog	5	10	-0.096307	-0.349179	0.1615045	0.406775	0.2394316
sp P14659 Heat shock protein 70kDa	19	59	-0.092693	-0.299296	0.1205463	0.4077375	0.2397801
sp P19643 Amine oxidase	17	41	0.0828032	-0.022432	0.1917316	0.4078875	0.2401274
sp Q5RY4 Dehydrogenase	2	2	-0.112292	-0.498733	0.2647665	0.4079375	0.2404734
sp P16975 SPARC OS=I	7	16	-0.092122	-0.288011	0.1005835	0.4081125	0.2408183
sp B1H267 Sorting nexin 2	6	10	-0.09095	-0.265935	0.0898737	0.4083125	0.2411623
sp P23514 Coatomer subunit alpha	13	31	-0.081426	-0.187295	0.0249579	0.4089125	0.241506
sp Q5XIC0 Peroxisomal membrane protein	4	11	0.0851798	-0.047152	0.2177107	0.4092375	0.241849
sp P62856 40S ribosomal protein S21	2	6	-0.083435	-0.213987	0.0563076	0.4101875	0.2421926
sp O70513 Galectin-3-like	2	2	0.1593784	-0.76417	1.1162642	0.4104625	0.2425353
sp P97874 Cyclin-G-associated protein	3	3	-0.114291	-0.539117	0.315665	0.4117	0.2428791
sp P62271 40S ribosomal protein S21	9	53	-0.080874	-0.186407	0.0235048	0.4122875	0.2432227
sp Q5XIP9 Transmembrane protein	2	3	-0.139315	-0.935562	0.7096753	0.4124125	0.2435652
sp O89046 Coronin-1B	3	4	0.0966889	-0.10615	0.310669	0.4125125	0.2439065
sp Q5XI22 Acetyl-CoA acyltransferase	11	32	-0.080375	-0.177252	0.0143816	0.412525	0.2442465
sp Q6P7A2 Ubiquitin carboxy-terminal hydrolase L1	7	9	0.0890887	-0.092017	0.2738754	0.41295	0.2445859
sp P62832 60S ribosomal protein L13	12	57	-0.082286	-0.198752	0.0386137	0.4132875	0.2449247
sp O08678 Serine/threonine kinase	2	3	-0.117216	-0.651112	0.4048344	0.413525	0.2452626
sp Q5XIE1 UPF0670 pre-mRNA processing factor	8	20	-0.080167	-0.178246	0.0197945	0.4139375	0.2455999
sp O55096 Dipeptidyl peptidase-like	10	17	-0.081822	-0.185095	0.0288476	0.414775	0.2459376
sp P18614 Integrin alpha-5/beta-1	2	2	0.0982028	-0.316504	0.493512	0.4164625	0.2462773
sp P60123 RuvB-like 1	6	10	-0.088765	-0.269674	0.0899699	0.416925	0.2466166
sp A2RUV9 Adipocyte enhancer binding protein	2	3	0.1014615	-0.235269	0.4333978	0.41705	0.2469547
sp P27768 Troponin I, fast skeletal muscle	3	8	0.2282632	-1.338898	1.8631675	0.4184875	0.2472944
sp P20611 Lysosomal cathepsin D	1	2	-0.118027	-0.671614	0.454557	0.4187	0.2476331
sp Q3KRD5 Mitochondrial ribosomal protein	5	9	0.091124	-0.086481	0.2808586	0.418975	0.2479711
sp O08557 N(G),N(G)-diacetylmuramyl pentapeptide	17	66	0.0981446	-0.195287	0.3983941	0.4198375	0.2483094
sp Q5GFD9 Protein IMP	3	3	0.1084029	-0.29668	0.5043741	0.4199	0.2486465
sp P62425 60S ribosomal protein L13	14	57	-0.079027	-0.171218	0.0076423	0.4202375	0.248983
sp Q63184 Interferon- γ receptor subunit beta	2	2	-0.118926	-0.675038	0.4357915	0.4212	0.24932
sp Q63663 Interferon- β receptor subunit alpha	3	3	-0.137698	-0.87727	0.6369003	0.422725	0.2496587
sp P62275 40S ribosomal protein S21	4	15	-0.086334	-0.306087	0.1459967	0.4228375	0.2499962
sp P23358 60S ribosomal protein L13	9	35	-0.080491	-0.191891	0.0296614	0.424025	0.2503348
sp P11030 Acyl-CoA-bis(3-hydroxyacyl) ester	8	59	-0.083902	-0.237994	0.0686022	0.4243375	0.2506727

sp Q8R5M4	Optineurin	3	4	0.0849431	-0.21661	0.3537386	0.4247875	0.2510101
sp P02091	Hemoglobin	4	55	0.1194651	-0.448887	0.6896238	0.424825	0.2513463
sp Q8VHK2	Caskin-1 OS	5	7	-0.089126	-0.317366	0.1384436	0.425225	0.251682
sp P04937	Fibronectin	15	39	-0.09705	-0.411034	0.216141	0.42535	0.2520166
sp P62250	40S riboson	11	44	-0.077305	-0.161244	0.0108183	0.426425	0.252352
sp O35964	Endophilin-	2	4	0.1044468	-0.266046	0.4808768	0.4264625	0.2526862
sp Q64194	Lysosomal a	2	2	0.1223913	-0.430627	0.6804176	0.4269	0.2530199
sp Q62902	Protein ERG	6	10	-0.083877	-0.244455	0.0821158	0.4274	0.2533534
sp B0BNE5	S-formylglu	3	16	-0.081982	-0.217439	0.0493244	0.42745	0.2536856
sp Q5XIK2	Thioredoxin	5	11	-0.082128	-0.216097	0.0486677	0.4277125	0.2540171
sp P13596	Neural cell a	14	50	-0.077897	-0.164143	0.0072421	0.4280375	0.2543479
sp P17136	Small nucle	1	2	-0.132931	-1.103279	0.8092716	0.428675	0.2546787
sp Q80W92	Protein VAC	1	2	-0.122564	-0.880012	0.6074485	0.4291625	0.2550092
sp P26644	Beta-2-glyco	7	19	-0.085978	-0.284687	0.1110413	0.4293875	0.2553388
sp P02680	Fibrinogen g	4	7	-0.133679	-1.055739	0.792704	0.4299625	0.2556683
sp P63025	Vesicle-assoc	2	5	0.0943404	-0.17816	0.3576514	0.4308625	0.2559982
sp P08503	Medium-ch	8	11	0.0848367	-0.098246	0.270065	0.431325	0.2563278
sp P15429	Beta-enolas	3	8	0.1581899	-0.937705	1.2280454	0.43145	0.2566564
sp P54287	Voltage-dep	2	3	0.1200835	-0.689045	0.8791953	0.43145	0.2569837
sp P52631	Signal trans	6	13	0.0827156	-0.065897	0.2366741	0.432025	0.2573109
sp Q7TP36	Protein Shr	5	5	-0.087594	-0.287788	0.1097481	0.432025	0.2576368
sp Q6AXQ0	SUMO-activ	4	10	0.0943426	-0.177932	0.3636901	0.432125	0.2579618
sp P62193	26S proteas	10	28	-0.077656	-0.170642	0.0148238	0.4328125	0.2582868
sp P17046	Lysosome-a	2	3	0.1140846	-0.418724	0.6782407	0.4329875	0.2586109
sp Q6B345	Protein S10	4	10	-0.081358	-0.225591	0.0581775	0.4348125	0.2589372
sp P15178	Aspartyl-tRI	18	57	-0.081191	-0.222457	0.0597596	0.4353125	0.2592632
sp P16086	Spectrin alp	43	100	0.078096	-0.026663	0.182262	0.4365375	0.2595903
sp Q8CG45	Aflatoxin B1	5	16	-0.082985	-0.235828	0.0650919	0.436675	0.2599164
sp Q9Z0U4	Gamma-am	2	2	0.1136495	-0.48917	0.7259673	0.437175	0.2602422
sp P0C1X8	AP2-associa	6	8	0.095929	-0.176085	0.3905535	0.4372125	0.2605669
sp Q5PQM2	Kinesin ligh	2	3	0.1086798	-0.48782	0.7150902	0.437725	0.2608914
sp Q4KM74	Vesicle-traf	8	19	-0.078113	-0.177771	0.0220504	0.4388	0.2612167
sp P17988	Sulfotransfe	3	7	0.0955287	-0.249037	0.4399655	0.438825	0.2615408
sp P45479	Palmitoyl-p	5	19	0.0801858	-0.059051	0.21841	0.4388625	0.2618638
sp Q8R500	Mitofusin-2	4	4	0.0954923	-0.250723	0.4400451	0.439325	0.2621864
sp P63331	Serine/thre	1	2	0.0902599	-0.255519	0.4306997	0.4407125	0.2625104
sp P19468	Glutamate-	1	5	0.0876702	-0.166845	0.3425251	0.441625	0.2628349
sp P10252	CD48 antigen	5	20	0.0814484	-0.07956	0.2441103	0.442275	0.2631594
sp O88350	Putative hy	1	2	0.1066798	-0.364804	0.5823873	0.4422875	0.2634827
sp Q5XI78	2-oxoglutar	24	69	-0.074861	-0.148566	0.0002128	0.44325	0.2638066
sp Q63754	Beta-synucl	2	7	-0.08145	-0.26104	0.0905183	0.44395	0.2641306
sp Q5U316	Ras-related	2	5	0.0851895	-0.179465	0.3369233	0.4440625	0.2644537
sp Q6MG55	Abhydrolase	6	18	0.0814378	-0.087755	0.2470522	0.44445	0.2647762
sp Q9JLA3	UDP-glucos	20	34	-0.08014	-0.204999	0.0424582	0.44455	0.2650978
sp P00787	Cathepsin B	9	45	0.0762038	-0.031	0.1819897	0.44585	0.2654206
sp B0BNA7	Eukaryotic t	3	3	-0.085581	-0.358747	0.2061294	0.4466125	0.2657436
sp P40615	H/ACA ribo	2	3	-0.092637	-0.492654	0.3200217	0.446775	0.2660657

sp O55043 Rho guanin	1	3	-0.089379	-0.396512	0.2212009	0.4468125	0.2663867
sp Q64232 Trans-2,3-e	8	22	-0.077872	-0.196828	0.0465203	0.4478	0.2667084
sp Q63468 Phosphorib	2	2	0.1032356	-0.477826	0.7307241	0.4478625	0.267029
sp P10760 Adenosylho	14	71	-0.075988	-0.166221	0.0140222	0.4482875	0.2673493
sp P36201 Cysteine-ric	7	33	-0.075653	-0.166938	0.0207765	0.44865	0.267669
sp Q02356 AMP deami	1	2	-0.101608	-0.692287	0.5235539	0.449425	0.267989
sp P15943 Amyloid-like	1	2	-0.106339	-0.731639	0.545595	0.4505875	0.2683099
sp P69735 Rab3 GTPas	2	4	0.0904199	-0.260963	0.4270224	0.45075	0.26863
sp P37996 ADP-ribosyl	6	11	-0.083099	-0.326978	0.168118	0.4508	0.268949
sp Q6AY20 Cation-depe	5	12	-0.079093	-0.221297	0.0569846	0.4511	0.2692675
sp Q497B0 Omega-ami	1	3	0.0870308	-0.179843	0.358717	0.4513375	0.2695852
sp P02466 Collagen alp	11	76	-0.10635	-0.723918	0.5319788	0.4514125	0.269902
sp Q6PEB9 Coiled-coil c	3	4	0.0913096	-0.313335	0.5066742	0.451925	0.2702186
sp Q5XIU9 Membrane-	3	4	-0.08687	-0.377606	0.1975106	0.4519625	0.2705341
sp P09811 Glycogen ph	4	8	0.0839987	-0.187216	0.3523669	0.4526375	0.2708497
sp P61265 Syntaxin-1B	2	6	0.0812512	-0.09579	0.2556436	0.453475	0.2711657
sp P51111 Huntington	2	5	0.0832028	-0.23191	0.372762	0.45355	0.2714807
sp P07633 Propionyl-C	3	4	-0.094757	-0.631462	0.4659969	0.4554125	0.2717978
sp P63031 Brain protei	3	4	0.0836789	-0.166776	0.3352024	0.456225	0.2721152
sp P61314 60S riboson	8	25	-0.074431	-0.146027	-0.001293	0.4564875	0.272432
sp Q5EGY4 Synaptobre	4	9	0.0762577	-0.047013	0.1994907	0.45715	0.2727488
sp Q64578 Sarcoplasm	2	3	0.1536358	-2.089508	2.3750675	0.457375	0.273065
sp Q6AYA1 H/ACA ribo	3	4	-0.08434	-0.337763	0.1711077	0.4574	0.2733801
sp P08934 Kininogen-1	1	2	0.0845442	-0.40052	0.5450896	0.4576	0.2736945
sp Q6AYG5 Enoyl-CoA h	3	4	0.098509	-0.440149	0.647299	0.4578625	0.2740082
sp P62912 60S riboson	7	40	-0.075248	-0.194431	0.043676	0.4583625	0.2743217
sp Q6IRK9 Plasma glut	9	32	-0.076193	-0.189951	0.0327723	0.458825	0.274635
sp P70619 Glutathione	4	10	0.0806019	-0.147126	0.3024098	0.458925	0.2749473
sp Q4TU93 C-type man	2	3	0.0910444	-0.357079	0.5470746	0.45995	0.2752604
sp Q3T1K5 F-actin-cap	2	6	-0.079642	-0.518941	0.3898964	0.460225	0.2755728
sp P31044 Phosphatid	12	78	0.0786699	-0.09731	0.2592244	0.46085	0.2758852
sp P06866 Haptoglobin	10	26	0.1016196	-0.547779	0.7938595	0.4610125	0.2761969
sp Q6AYI5 Leucine-rich	5	9	0.0813107	-0.151652	0.314844	0.4610875	0.2765076
sp Q06486 Casein kina	4	4	-0.090546	-0.585872	0.3947038	0.4614625	0.276818
sp Q9Z2Z8 7-dehydroc	1	2	-0.159918	-2.77159	2.4063628	0.4615125	0.2771273
sp P61621 Protein trar	3	4	-0.091761	-0.453573	0.2553321	0.462075	0.2774366
sp Q6JAM9 Transmembr	2	6	-0.078115	-0.279624	0.1280549	0.462525	0.2777456
sp O88637 Ethanolami	2	3	0.08879	-0.427918	0.6116492	0.4628375	0.2783616
sp Q9QZ76 Myoglobin	3	6	-0.109801	-1.235572	1.0463177	0.4628375	0.2780541
sp P20070 NADH-cytoc	9	22	0.0745846	-0.014396	0.1653837	0.4634125	0.278669
sp Q4FZT0 Stomatin-li	4	6	0.0849394	-0.186787	0.3661339	0.46355	0.2789756
sp Q63678 Zinc-alpha-1	2	2	0.1017302	-0.915604	1.0832964	0.4637	0.2792814
sp Q5U2R7 LDLR chape	6	28	-0.074251	-0.164825	0.0181945	0.464175	0.279587
sp Q6PDU1 Serine/argin	3	4	0.0757269	-0.063604	0.2158711	0.46425	0.2798917
sp P12346 Serotransfe	28	100	-0.082161	-0.354923	0.1906149	0.4642625	0.2801955
sp Q62736 Non-muscle	12	22	-0.076298	-0.210542	0.0577605	0.4653375	0.2805
sp Q32PX2 Aminoacyl t	8	24	-0.078073	-0.223762	0.0664536	0.4656	0.2808039

sp Q63421 Calcium/cal	2	2	0.0924377	-0.510298	0.6918223	0.4656625	0.281107
sp Q63228 Glia matura	4	14	-0.07749	-0.22569	0.067743	0.4658125	0.2814093
sp P62749 Hippocalcin	3	8	0.0745837	-0.031762	0.1770612	0.465875	0.2817107
sp Q9QVC8 Peptidyl-pro	10	27	-0.073994	-0.178563	0.0364178	0.466725	0.2820125
sp P48500 Triosephosph	16	100	0.0758559	-0.07764	0.2272481	0.4679625	0.2823154
sp P06686 Sodium/pot	17	59	-0.074332	-0.172946	0.0211406	0.46805	0.2826174
sp B5DEN9 Vacuolar pr	1	2	0.0802899	-0.245991	0.3930456	0.4683125	0.2829188
sp Q9JL66 S-Electrogenic	3	6	0.0812573	-0.243535	0.4130536	0.4684	0.2832194
sp Q9WV25 Poly(U)-bind	3	3	-0.084339	-0.486193	0.3191797	0.468575	0.2835194
sp P19356 Porphobilin	2	3	0.0887804	-0.370496	0.5473724	0.4688375	0.2838187
sp P08010 Glutathione	10	32	0.0761013	-0.080714	0.2385293	0.4692125	0.2841178
sp Q9WB1 Ras-related	7	14	-0.074451	-0.177946	0.0256963	0.4693	0.284416
sp P19234 NADH dehy	5	14	0.0766714	-0.092303	0.2483617	0.4696625	0.2847138
sp Q62812 Myosin-9 O	37	100	-0.074877	-0.20253	0.0561821	0.47115	0.285013
sp P50123 Glutamyl ar	1	2	-0.109254	-1.48309	1.29397	0.4713125	0.2853116
sp Q5U2U2 Crk-like pro	2	3	-0.075127	-0.282206	0.129017	0.4715	0.2856095
sp Q6P7B0 Tryptophan	19	59	0.0732779	-0.038497	0.1848392	0.472	0.2859072
sp P01946 Hemoglobin	12	100	0.0903094	-0.549979	0.7163218	0.4723125	0.2862045
sp B1WBW4 Armadillo re	2	3	-0.08702	-0.606839	0.4205602	0.473	0.286502
sp P31399 ATP synthas	11	49	-0.072398	-0.132387	-0.013911	0.4734	0.2867991
sp O88941 Mannosyl-o	4	8	-0.077178	-0.293975	0.1397111	0.473425	0.2870954
sp Q68FX1 Mannose-6-	3	3	0.0837547	-0.290846	0.4728193	0.4736	0.2873909
sp Q0VGK4 Glyceropho	1	2	0.0996951	-0.723797	0.906481	0.474575	0.2876871
sp O35760 Isopentenyl	4	8	0.0779353	-0.152748	0.3055292	0.4745875	0.2879824
sp Q6P6Q2 Keratin, typ	2	6	-0.087409	-0.523482	0.3253907	0.4751875	0.2882776
sp Q6AYK1 RNA-bindin	3	6	0.0798935	-0.205698	0.3713378	0.4754875	0.2885725
sp P23928 Alpha-cryst	9	44	-0.078997	-0.384615	0.2270268	0.4756375	0.2888666
sp Q1WIM2 Cell adhesic	1	2	-0.078018	-0.432882	0.2828584	0.475725	0.2891599
sp P49242 40S riboson	14	61	-0.072666	-0.175118	0.030626	0.475825	0.2894525
sp P17764 Acetyl-CoA	14	54	-0.074245	-0.214299	0.0659266	0.4766125	0.2897454
sp P23711 Heme oxygen	4	9	-0.072191	-0.239167	0.1004224	0.4766375	0.2900374
sp Q794E4 Heterogene	3	8	0.0749177	-0.085838	0.2372411	0.4767875	0.2903288
sp P27139 Carbonic an	5	14	0.0843916	-0.361515	0.5562172	0.47825	0.2906215
sp Q6AY86 Vacuolar pr	2	4	-0.072287	-0.524225	0.4102934	0.4791	0.2909146
sp Q2TL32 E3 ubiquitin	6	7	0.0778355	-0.206755	0.3675346	0.479125	0.2912069
sp P17702 60S riboson	5	12	-0.072188	-0.179524	0.0396467	0.4796125	0.291499
sp Q7TPJ0 Translocon	2	5	0.076558	-0.191462	0.3595315	0.4799375	0.2917907
sp Q9R064 Golgi reasse	3	3	-0.078531	-0.334438	0.1799065	0.4801	0.2920817
sp P17077 60S riboson	11	33	-0.073637	-0.180857	0.0373565	0.4802	0.292372
sp Q5U2X6 Coiled-coil	6	18	-0.075037	-0.235272	0.0843524	0.4803	0.2926616
sp P53676 AP-3 compl	1	2	0.0784813	-0.377831	0.5440184	0.48055	0.2929506
sp P62268 40S riboson	7	31	-0.072527	-0.178736	0.0295514	0.480775	0.2932392
sp Q80X08 WASH comp	6	6	-0.075754	-0.380881	0.2362695	0.480875	0.2935269
sp O88761 26S proteas	11	26	0.0756518	-0.058708	0.2212429	0.4827	0.2938166
sp P07872 Peroxisoma	5	5	-0.075083	-0.263187	0.1034376	0.483175	0.2941062
sp Q9Z1Z3 Epsin-2 OS=	2	3	-0.082947	-0.581222	0.4089833	0.4832625	0.294395
sp Q6DGG1 Abhydrolas	1	3	0.0831157	-0.440133	0.6185959	0.48355	0.2946833

sp P08699 Galectin-3 C	3	10	-0.073491	-0.266259	0.1228056	0.48405	0.2949715
sp P16970 ATP-binding c	8	21	-0.071671	-0.170673	0.0258915	0.4840625	0.2952589
sp Q62703 Reticulocal	4	14	-0.073382	-0.221149	0.0801145	0.48415	0.2955455
sp P06399 Fibrinogen α	17	37	-0.078974	-0.563432	0.4035179	0.4842875	0.2958315
sp P47727 Carbonyl re	10	30	0.0743943	-0.117691	0.2717255	0.484475	0.2961169
sp P35171 Cytochrome	1	2	-0.073343	-0.35521	0.2229795	0.4847	0.2964018
sp P36365 Dimethylan	1	2	-0.082736	-0.706483	0.5293231	0.48515	0.2966865
sp Q91V33 KH domain-	9	22	-0.071528	-0.183459	0.0465153	0.4852875	0.2969705
sp Q9ROT4 Cadherin-1	6	16	0.0750113	-0.099609	0.2599685	0.4862125	0.2972551
sp P34064 Proteasome	7	14	-0.072029	-0.204097	0.0636799	0.48655	0.2975393
sp Q5U1X1 Oligoribonu	2	6	0.0722385	-0.173304	0.3229469	0.4871875	0.2978236
sp P61805 Dolichyl-dip	3	3	-0.071556	-0.303062	0.1684123	0.487225	0.2981072
sp P12001 60S ribosom	11	54	-0.071761	-0.155614	0.0133937	0.4872625	0.2983899
sp Q64566 Calcium-tra	1	2	0.0762837	-0.181893	0.3308196	0.487425	0.2986721
sp P62914 60S ribosom	4	12	-0.072201	-0.161925	0.0157422	0.489125	0.2989559
sp P09216 Protein kin	5	8	0.07698	-0.142134	0.3032398	0.490225	0.2992405
sp Q99JE6 1-phosphat	7	15	-0.074174	-0.255671	0.1050434	0.49025	0.2995243
sp Q641Y8 ATP-depend	14	32	-0.072184	-0.179558	0.0292653	0.4902625	0.2998073
sp Q5PQN0 Neurocalcir	3	7	0.0724364	-0.113334	0.2496612	0.490425	0.3000897
sp Q5HZV9 Protein pho	5	9	-0.073236	-0.258375	0.1073218	0.490875	0.3003719
sp P70541 Translation	1	4	-0.06955	-0.387951	0.2607009	0.4919625	0.3006549
sp P08009 Glutathione	6	17	0.0717459	-0.094857	0.2384007	0.492475	0.3009379
sp P60901 Proteasome	7	17	-0.073054	-0.224033	0.0713144	0.4927125	0.3012203
sp Q62780 Probable A1	2	2	-0.072129	-0.34286	0.2064476	0.493225	0.3015027
sp O08651 D-3-phosph	13	53	-0.071802	-0.267872	0.1193998	0.494125	0.3017855
sp P61149 Heparin-bin	5	15	0.0712401	-0.123777	0.2720836	0.494225	0.3020677
sp Q62930 Complement	7	15	-0.073598	-0.289935	0.1300305	0.4943125	0.3023492
sp Q923V4 F-box only p	3	5	0.0711393	-0.159218	0.2967504	0.4943875	0.3026299
sp P14480 Fibrinogen I	10	26	-0.072423	-0.589925	0.4406822	0.4948125	0.3029105
sp P85970 Actin-relate	9	21	-0.071266	-0.176356	0.0371261	0.495625	0.3031914
sp Q6IMX7 Hsp70-bind	2	3	-0.071724	-0.482421	0.3612989	0.49565	0.3034715
sp P49744 Thrombosp	2	3	0.074318	-0.288121	0.4371624	0.495875	0.3037512
sp P37361 Metallothio	3	7	0.0717534	-0.128302	0.2808004	0.4962625	0.3040306
sp Q4V8B7 Inactive hyc	3	3	-0.073102	-0.425598	0.2845105	0.4967625	0.3043099
sp Q921A4 Cytoglobin	2	5	-0.072388	-0.47101	0.3246564	0.4972	0.3045891
sp Q62638 Golgi appar	19	44	-0.07119	-0.18493	0.0453941	0.4974125	0.3048677
sp P62744 AP-2 compl	2	4	-0.070897	-0.432244	0.2769963	0.497425	0.3051456
sp Q8R491 EH domain-	8	19	0.0709683	-0.059643	0.201921	0.49755	0.3054228
sp Q6I7R3 Isochorismat	4	8	0.0706559	-0.13383	0.2822162	0.497875	0.3056997
sp P51146 Ras-related	3	6	-0.068816	-0.325847	0.190293	0.4979	0.3059759
sp P11275 Calcium/cal	2	3	-0.065194	-0.477468	0.3790707	0.498575	0.3062522
sp P53042 Serine/thre	5	10	-0.070498	-0.252793	0.1218897	0.499175	0.3065286
sp O35094 Mitochondr	5	14	-0.069929	-0.215016	0.0784766	0.4992	0.3068042
sp Q80W98 Small glutar	2	2	0.0707594	-0.603598	0.7166414	0.499675	0.3070798
sp P07323 Gamma-enc	15	83	0.0706736	-0.070153	0.2067662	0.5000875	0.3073551
sp D4ABP9 F-box only p	1	2	0.0697044	-0.362187	0.5001921	0.501625	0.3076318
sp Q9JII03 Collagen alp	4	14	-0.071134	-0.6279	0.4892655	0.501825	0.3079081

sp O88267 Acyl-coenzy	3	5	0.0695373	-0.133945	0.2780524	0.502175	0.308184
sp P04906 Glutathione	10	58	0.0699986	-0.066327	0.2057402	0.50265	0.3084599
sp Q711G3 Isoamyl ace	3	10	-0.069195	-0.236112	0.0942487	0.503375	0.3087359
sp Q29RW1 Myosin-4 O	21	48	0.0654831	-1.697381	1.8566173	0.50365	0.3090116
sp Q566C7 Diphosphoi	4	4	0.0728573	-0.154429	0.3104025	0.503925	0.3092869
sp Q8K3X8 Heat shock	3	8	-0.063301	-0.485286	0.3963392	0.5041625	0.3095618
sp P11240 Cytochrome	9	54	0.069959	-0.003484	0.1429597	0.5046125	0.3098365
sp P19139 Casein kina	3	8	0.0693269	-0.118598	0.2575736	0.5051375	0.3101112
sp Q66HC5 Nuclear por	2	2	-0.068515	-0.68545	0.563541	0.5051375	0.3103851
sp Q66H80 Coatomer s	8	16	-0.069033	-0.201007	0.065558	0.505525	0.3106588
sp P0C644 Inositol hex	2	2	-0.027289	-1.526015	1.2046315	0.5056125	0.3109318
sp Q64119 Myosin ligh	8	40	-0.069061	-0.214327	0.0710499	0.5068375	0.3112058
sp Q5PPJ9 Endophilin-	7	18	0.0701358	-0.054676	0.1966128	0.5071625	0.3114795
sp Q4FZX7 Signal recog	3	4	-0.066212	-0.351417	0.2285349	0.5075125	0.3117529
sp Q5PQL2 Cell differer	1	2	-0.069405	-0.517639	0.3619246	0.5076875	0.3120258
sp P70473 Alpha-meth	1	2	0.061544	-0.974845	1.1192541	0.508	0.3122984
sp Q925N3 PEX5-relate	2	2	-0.066873	-0.471049	0.3267637	0.5090125	0.3125716
sp P02688 Myelin basi	11	100	0.0649734	-0.318661	0.4582625	0.5092875	0.3128444
sp P54275 DNA misma	1	2	0.0620822	-0.470059	0.604357	0.5096	0.3131169
sp Q4FZY0 EF-hand doi	3	7	-0.062804	-0.412196	0.2810698	0.509625	0.3133887
sp P62902 60S riboson	6	23	-0.069103	-0.156695	0.0152669	0.510325	0.3136608
sp Q9JHL4 Drebrin-like	6	19	-0.068268	-0.198231	0.0590357	0.5116875	0.3139339
sp Q7TT49 Serine/thre	1	2	0.0657646	-0.472472	0.6011272	0.5119125	0.3142066
sp Q5U1Z2 Trafficking p	3	4	0.0670933	-0.258924	0.405005	0.51225	0.314479
sp P85972 Vinculin OS	41	100	-0.068955	-0.159999	0.0201958	0.5123875	0.3147509
sp Q9ERE4 Golgi phosph	4	6	-0.063697	-0.377181	0.253875	0.512425	0.315022
sp P97687 Ectonucleos	1	4	-0.064163	-0.401997	0.2712729	0.512475	0.3152925
sp Q7M0E3 Destrin OS=	12	50	-0.068817	-0.185853	0.0455295	0.51265	0.3155625
sp P30713 Glutathione	5	15	0.067884	-0.087787	0.2254152	0.513575	0.315833
sp P43138 DNA-(apurin	4	9	-0.068547	-0.272501	0.1425448	0.5141375	0.3161035
sp Q8K3P6 Calcium-bin	2	4	-0.066667	-0.35604	0.2165091	0.5156375	0.3163754
sp B2GUZ5 F-actin-cap†	2	5	-0.067872	-0.34304	0.2138636	0.5158875	0.3166468
sp Q68FW9 COP9 signal	5	5	0.0642654	-0.143938	0.269824	0.5172875	0.3169194
sp B5DFC9 Nidogen-2 C	18	79	0.06584	-0.147095	0.2899963	0.5179	0.3171921
sp P20650 Protein pho	3	8	0.0656313	-0.132112	0.2570143	0.5183125	0.3174647
sp P04916 Retinol-bind	1	3	0.0544666	-0.770988	0.859336	0.5184875	0.3177367
sp P85973 Purine nucle	9	26	-0.066838	-0.22518	0.0887722	0.5189	0.3180085
sp P11507 Sarcoplasm	14	36	-0.068726	-0.153	0.0141557	0.5195875	0.3182805
sp O55166 Vacuolar pr	2	2	-0.053914	-0.679442	0.6100262	0.520425	0.318553
sp P82995 Heat shock	22	100	-0.069031	-0.130773	-0.009603	0.52155	0.3188262
sp P63324 40S riboson	5	21	-0.065214	-0.202528	0.0803288	0.521775	0.319099
sp P41777 Nucleolar ai	3	6	-0.062691	-0.347066	0.2138104	0.5228	0.3193724
sp Q924C3 Ectonucleot	2	5	0.0640142	-0.219005	0.3522721	0.5229375	0.3196453
sp Q6IUR5 Neudesin O	2	3	0.0621952	-0.227545	0.3688728	0.523575	0.3199183
sp P21670 Proteasome	5	11	-0.067834	-0.300516	0.1529078	0.5249375	0.3201924
sp O08816 Neural Wisk	2	4	0.0591095	-0.23657	0.3360861	0.5250125	0.3204658
sp Q6XUX2 Dual serine,	2	2	0.0614212	-0.207274	0.3190375	0.5260375	0.3207399

sp Q5FWT1 Protein FAN	2	3	-0.061039	-0.312086	0.1831747	0.5260625	0.3210133
sp P80067 Dipeptidyl β	3	3	0.0585145	-0.371245	0.4732127	0.526275	0.3212863
sp Q99M64 Phosphatid	2	6	0.0707713	-0.383729	0.5611081	0.5263	0.3215585
sp P35745 Acylphosph	4	8	0.066089	-0.070996	0.2046769	0.5265625	0.3218304
sp P18886 Carnitine O-	3	4	0.0664985	-0.238928	0.3937437	0.5267375	0.3221018
sp O09175 Aminopepti	1	2	-0.04831	-0.842592	0.7702351	0.5269375	0.3223728
sp P0CC09 Histone H2/	4	15	-0.066517	-0.328813	0.1911367	0.5275	0.3226437
sp P27653 C-1-tetrahy	4	9	0.061598	-0.194867	0.3111063	0.528625	0.3229155
sp Q5U301 A-kinase an	2	4	0.0638231	-0.182899	0.3176838	0.5295375	0.3231877
sp P11497 Acetyl-CoA	4	8	-0.061848	-0.276308	0.1490113	0.5296125	0.3234593
sp O35889 Afadin OS=I	3	4	-0.051517	-0.353834	0.2707615	0.529875	0.3237306
sp P63074 Eukaryotic t	4	9	0.0621867	-0.156702	0.2756341	0.5300125	0.3240013
sp AOJPQ9 Chitinase dc	6	19	-0.065683	-0.197211	0.0658872	0.5301125	0.3242714
sp Q60587 Trifunctiona	17	65	-0.068297	-0.124012	-0.013468	0.530325	0.3245411
sp Q5M9F8 N-terminal	2	2	-0.034699	-0.959638	0.9109024	0.5310125	0.324811
sp Q9ESS6 Basal cell ac	8	13	-0.063806	-0.218763	0.0971261	0.531125	0.3250804
sp P49797 Regulator o	5	5	-0.057553	-0.375423	0.2692973	0.5312125	0.3253491
sp B2GUZ1 Ubiquitin cæ	2	5	-0.059836	-0.349568	0.2220453	0.5318875	0.325618
sp P14942 Glutathione	8	28	-0.064696	-0.221183	0.0919971	0.532675	0.3258873
sp Q01129 Decorin OS-	15	100	-0.057633	-0.388899	0.2965779	0.5326875	0.3261559
sp P09812 Glycogen pl	5	10	-0.051734	-0.600638	0.479967	0.5331875	0.3264244
sp Q66HG3 Beta-Ala-Hi	1	2	0.0580067	-0.273578	0.3818457	0.5333375	0.3266924
sp Q63524 Transmemb	4	19	-0.063879	-0.225799	0.0885764	0.5333875	0.3269598
sp Q5XI83 UPF0505 pr	3	4	0.0600199	-0.261059	0.3748199	0.5334375	0.3272266
sp P53987 Monocarbo	2	3	0.0622721	-0.147336	0.2753837	0.5336375	0.3274929
sp O35763 Moesin OS=	21	69	-0.066688	-0.159665	0.0274188	0.5338	0.3277588
sp Q63358 Myosin-IXb	4	5	-0.061793	-0.347021	0.2232446	0.5338	0.3280239
sp Q5FVQ8 NLR family i	2	3	-0.061105	-0.29126	0.1685346	0.5338	0.3282884
sp P46413 Glutathione	5	6	0.0630512	-0.168808	0.3083992	0.5338875	0.3285524
sp P35572 Insulin-like	1	2	0.0491878	-0.607269	0.7054486	0.534325	0.3288162
sp P97544 Lipid phosph	2	5	0.0562388	-0.262633	0.380461	0.535275	0.3290805
sp Q5FWT7 Ubiquitin-lil	4	11	0.0643125	-0.095483	0.2226546	0.535575	0.329608
sp P04466 Myosin regu	7	16	-0.001542	-1.488715	1.5113883	0.535575	0.3293446
sp Q5U2N3 Membrane-	1	2	-0.0494	-0.950452	0.8121197	0.536	0.3298712
sp Q63009 Protein argi	2	2	-0.024841	-1.190678	1.1354369	0.536575	0.3301345
sp Q5U2U7 mRNA cap ξ	1	2	-0.050209	-0.465695	0.3647966	0.536825	0.3303975
sp Q62799 Receptor ty	2	6	0.0556524	-0.287874	0.4018996	0.537425	0.3306606
sp Q80W57 ATP-bindin	1	2	-0.052683	-0.414806	0.3187313	0.537625	0.3309232
sp Q64649 Phosphoryl	1	2	-0.057096	-0.38314	0.272511	0.53835	0.3311861
sp P05964 Protein S10	9	70	0.0625826	-0.116021	0.2412582	0.53855	0.3314486
sp Q03555 Gephyrin O:	3	3	0.0728156	-0.138243	0.3240545	0.538725	0.3317106
sp P11762 Galectin-1 C	9	97	0.0626283	-0.088846	0.2178564	0.539875	0.3319735
sp Q63945 Protein SET	6	23	-0.064316	-0.175752	0.0504785	0.540075	0.3322359
sp Q5I0D1 Glyoxalase	14	48	0.0603617	-0.147636	0.2702252	0.5409125	0.3324987
sp P22062 Protein-L-is	9	31	0.0639763	-0.064378	0.1887434	0.5409375	0.3327609
sp Q91XU8 Phosphatid	4	9	-0.058795	-0.274526	0.1579539	0.5409875	0.3330225
sp P07943 Aldose redu	23	100	0.0587978	-0.176921	0.2880038	0.5417375	0.3332844

sp Q62632 Follistatin-r	4	10	-0.063821	-0.221954	0.0893176	0.5425375	0.3335466
sp P54290 Voltage-dep	2	2	0.067382	-0.266095	0.4427196	0.542825	0.3338085
sp Q8R424 STAM-bindin	1	2	0.0449519	-0.49938	0.5845504	0.54395	0.3340712
sp P62752 60S riboson	13	42	-0.064023	-0.186569	0.0593169	0.5442	0.3343335
sp P15650 Long-chain	12	36	-0.065696	-0.134754	0.0065882	0.5442	0.3345952
sp P70567 Tropomodu	4	7	0.0553494	-0.194291	0.3110195	0.5454	0.3348577
sp P63142 Potassium v	2	2	0.0489701	-0.393274	0.4805578	0.5454875	0.3351197
sp P10536 Ras-related	3	12	-0.063838	-0.17701	0.0526982	0.5458625	0.3353815
sp P27952 40S riboson	21	77	-0.064571	-0.172702	0.0434952	0.5460375	0.3356429
sp P97526 Neurofibror	1	2	0.0611267	-0.116356	0.2301019	0.54605	0.3359036
sp Q6AXS3 Protein DEK	2	2	-0.045092	-0.550826	0.4573824	0.5462	0.3361638
sp P21818 Stathmin-2	3	4	-0.057011	-0.302272	0.19254	0.5469625	0.3366837
sp P0C0A1 Vacuolar pr	1	2	0.0465165	-0.466499	0.5614184	0.5475125	0.3369436
sp P62074 Mitochondr	1	2	-0.042241	-0.583867	0.5128143	0.5479875	0.3372036
sp Q8R4C0 Calpain-5 O	3	4	0.052633	-0.25082	0.3605057	0.54815	0.337463
sp P37199 Nuclear por	2	2	-0.030116	-0.518835	0.4960614	0.5483125	0.3377221
sp Q9ESV1 Leucine zip	3	3	-0.044869	-0.543497	0.4619477	0.549175	0.3379815
sp P27615 Lysosome n	3	3	-0.05713	-0.309394	0.1920609	0.5493125	0.3382405
sp P11506 Plasma mer	3	3	-0.045863	-0.433481	0.3411849	0.549725	0.3384993
sp P05942 Protein S10	8	26	0.0627717	-0.078556	0.202305	0.549925	0.3387578
sp Q5HZY2 GTP-binding	3	8	-0.059764	-0.236312	0.1134379	0.5514125	0.3390175
sp P08033 Gap junctio	2	2	0.0361644	-0.590426	0.690006	0.5519375	0.3392771
sp Q924S1 1-acyl-sn-gly	2	2	-0.040737	-0.582017	0.5083836	0.552125	0.3395364
sp P17164 Tissue alpha	2	7	0.0457061	-0.364268	0.4674763	0.552875	0.3397959
sp P04797 Glyceraldehy	20	100	0.0623936	-0.06362	0.1886801	0.5531375	0.3400551
sp Q66H15 Regulator o	2	3	0.0439433	-0.482814	0.5793864	0.5534375	0.3403141
sp P22509 rRNA 2'-O-ri	2	3	-0.054936	-0.37281	0.2579735	0.553575	0.3405726
sp P84850 D-2-hydroxy	2	2	-0.03735	-0.620982	0.5208791	0.5540375	0.340831
sp P05369 Farnesyl pyr	12	32	-0.065061	-0.142393	0.0139369	0.5564	0.3410917
sp Q6UPR8 Endoplasmic	3	3	-0.053863	-0.319767	0.2147239	0.5564875	0.3413518
sp Q3ZU82 Golgin subf	4	6	-0.043818	-0.35658	0.2797727	0.556825	0.3416117
sp Q925S8 ATP-dependen	2	2	0.0118332	-0.739469	0.7195921	0.55695	0.3418712
sp Q63450 Calcium/cal	2	4	0.0378083	-0.359582	0.4060792	0.5578125	0.342131
sp O55165 Kinesin-like	3	5	-0.052475	-0.343286	0.2261414	0.55825	0.3423908
sp Q99NA5 Isocitrate de	11	44	-0.064268	-0.150508	0.0239872	0.5589375	0.3426508
sp Q8K4V4 Sorting nexi	1	2	-0.046646	-0.400084	0.3222816	0.558975	0.3429101
sp Q8CF97 Deubiquitin	2	3	-0.040621	-0.49443	0.4286543	0.559875	0.34317
sp Q9WTV5 26S proteas	3	17	0.0593357	-0.090771	0.2048215	0.5603375	0.3434298
sp Q64654 Lanosterol :	3	4	-0.045617	-0.367381	0.281902	0.5609	0.3436896
sp P48450 Lanosterol s	2	2	0.036463	-0.918827	1.0693757	0.5612625	0.3439492
sp P50430 Arylsulfatas	3	3	-0.048763	-0.297546	0.2239574	0.56235	0.3442095
sp Q9R1T1 Barrier-to-a	6	27	0.0611726	-0.064804	0.1792215	0.5626875	0.3444696
sp P30904 Macrophag	3	25	-0.054291	-0.250931	0.1475582	0.56285	0.3447293
sp P35815 Protein pho	2	2	-0.011682	-0.862832	0.907246	0.5631125	0.3449886
sp Q5PQJ7 Tubulin-spe	2	3	0.0343119	-0.437013	0.502635	0.5637875	0.3452482
sp P61515 60S riboson	3	4	-0.057292	-0.252639	0.1346065	0.563925	0.3455073
sp Q6P4Z9 COP9 signal	3	4	0.0388532	-0.352818	0.4305906	0.563975	0.3457658

sp P23764 Glutathione	5	20	-0.045979	-0.359271	0.278781	0.5645125	0.3460244
sp Q8K1P7 Transcriptic	5	6	0.0531776	-0.188908	0.3001254	0.564725	0.3462826
sp P0C0R5 Phosphoino	2	4	-0.016275	-0.986144	0.8581995	0.5648625	0.3465404
sp Q5HZA6 Prolyl endo	10	27	0.0615604	-0.053518	0.1788155	0.5649	0.3467976
sp Q63692 Hsp90 co-cl	6	20	0.0629799	-0.070709	0.2080533	0.5652	0.3470545
sp D4A4T9 Cysteine an	2	4	0.0482125	-0.212283	0.2988292	0.5654	0.3473111
sp P35559 Insulin-degr	1	2	-0.04567	-0.422068	0.3175591	0.565575	0.3475673
sp Q4QQV8 Charged mu	4	8	0.0532006	-0.174545	0.2780181	0.5659625	0.3478233
sp P43245 Multidrug r	3	5	0.0473424	-0.344443	0.4615819	0.566275	0.3483341
sp Q04462 Valyl-tRNA :	30	100	-0.063565	-0.154039	0.0266763	0.5665375	0.348589
sp Q63356 Myosin-le C	4	5	-0.035125	-0.409324	0.3499538	0.566825	0.3488437
sp Q9Z142 Transmemb	2	8	-0.046133	-0.358653	0.2622328	0.5669375	0.3490978
sp Q9EQP5 Prolargin O:	20	100	-0.052337	-0.289347	0.1715322	0.567125	0.3493517
sp Q6TEK3 Vitamin K e	1	2	-0.018986	-0.854825	0.7995096	0.5677	0.3496056
sp P04644 40S riboson	6	22	-0.062751	-0.156984	0.0313261	0.5679875	0.3498592
sp P20717 Protein-argi	8	13	-0.055817	-0.227686	0.1131614	0.5681875	0.3501125
sp Q5BK81 Prostagland	3	7	-0.051374	-0.283842	0.1786707	0.5684	0.3503654
sp P97846 Contactin-a	5	15	0.0520011	-0.206284	0.3199177	0.5695	0.350619
sp P62994 Growth fact	6	18	0.0607001	-0.051589	0.1711237	0.5699875	0.3508726
sp P60522 Gamma-am	3	8	-0.012361	-0.736799	0.7392106	0.570075	0.3511258
sp P61023 Calcium-bin	3	6	0.0471191	-0.229678	0.3192	0.5701	0.3513783
sp Q5RJR2 Twinfilin-1 (2	3	0.0423686	-0.434166	0.5300827	0.570625	0.3516309
sp Q4V8C3 Echinoderr	5	18	0.057231	-0.093191	0.2024206	0.57125	0.3518836
sp Q63060 Glycerol kin	4	5	0.0384578	-0.335497	0.3996569	0.5714	0.352136
sp P15800 Laminin suk	35	100	0.0425253	-0.284433	0.3712998	0.572025	0.3523884
sp Q9JMJ4 Pre-mRNA-1	3	4	0.0503443	-0.180031	0.2809161	0.5724375	0.3526408
sp Q9JHZ4 GRIP1-assoc	5	7	-0.048894	-0.290475	0.179143	0.5738	0.3528941
sp P47971 Neuronal pe	2	4	0.0360372	-0.333683	0.405446	0.574375	0.3531475
sp Q9WVH8 Fibulin-5 OS	10	36	0.0473886	-0.23076	0.313885	0.57445	0.3534004
sp Q9Z1B2 Glutathione	6	16	-0.05853	-0.185151	0.0682929	0.5746375	0.353653
sp Q5XIA9 Kelch doma	2	2	0.0017241	-0.932209	0.9872591	0.5747875	0.3539051
sp P05943 Protein S10	4	42	0.0554927	-0.113809	0.2226062	0.5750125	0.354157
sp Q5XIA8 Growth hor	2	4	-0.054924	-0.212949	0.1108047	0.5760375	0.3544094
sp Q62915 Peripheral p	4	7	0.0455103	-0.207687	0.3148558	0.576875	0.3549144
sp Q63584 Transmemb	6	28	-0.056213	-0.211426	0.0961678	0.577675	0.355167
sp Q8K4T4 Filamin-A-ir	4	6	0.0417652	-0.281867	0.3665385	0.577875	0.3554192
sp P05539 Collagen al β	4	9	-0.052283	-0.29252	0.2024503	0.5782125	0.3556712
sp P97839 Disks large-	2	3	0.0153543	-0.555484	0.6165448	0.5782375	0.3559227
sp Q8VBU2 Protein NDF	8	18	-0.056159	-0.210362	0.104497	0.578425	0.3561738
sp Q5XIM5 Protein CDV	6	8	-0.049939	-0.258425	0.1583425	0.578425	0.3564244
sp Q7TSA0 Mitochondr	2	7	-0.044514	-0.316841	0.2325686	0.5789125	0.3566749
sp P35738 2-oxoisoval	1	3	-0.057281	-0.19164	0.0786552	0.579075	0.3569251
sp P84060 Dystrobrevi	3	6	0.0469685	-0.20461	0.3012598	0.5798	0.3571755
sp P50408 V-type prot	4	9	-0.051469	-0.24438	0.1449568	0.5798375	0.3574254
sp Q5XIT9 I Methylcroto	2	3	0.0349608	-0.355712	0.4158928	0.5806875	0.3576757
sp P61751 ADP-ribosyl	5	11	0.0582459	-0.070802	0.191403	0.5812125	0.3581755
sp O08875 Serine/thre	2	2	0.007829	-0.698011	0.7684506	0.58155	0.3584251

sp Q5XIA1 Nicalin OS=	5	11	-0.049651	-0.252757	0.1521883	0.5817	0.3586743
sp Q4KLH4 Paraspeckle	4	7	0.0458938	-0.175729	0.2675105	0.5819625	0.3589232
sp P48675 Desmin OS=	2	3	-0.018954	-0.566946	0.5253219	0.58205	0.3591717
sp P51792 H(+)/Cl(-) e	3	3	-0.036938	-0.390003	0.3185777	0.5824875	0.3594201
sp O08836 Immunoglo	1	2	-0.003906	-0.613598	0.6253361	0.5827625	0.3596682
sp Q6AY09 Heterogene	4	12	-0.054486	-0.219643	0.1141792	0.583475	0.3599166
sp Q5PPN5 Tubulin poly	13	55	-0.060915	-0.159031	0.0329896	0.5836375	0.3601646
sp P18163 Long-chain-	3	4	-0.037675	-0.451276	0.3605907	0.5837	0.3604122
sp P47820 Angiotensin	1	2	0.0407152	-0.293773	0.3660631	0.5838125	0.3606593
sp Q9ES21 Phosphatid	7	20	-0.057912	-0.191483	0.0707983	0.5838375	0.3609059
sp Q6AXM8 Serum para	3	5	0.0388938	-0.385105	0.4990306	0.5840875	0.3611523
sp Q6P747 Heterochro	9	27	0.0611588	-0.030543	0.1510281	0.584175	0.3613982
sp O55148 Growth arr	2	3	-0.029848	-0.507706	0.4433152	0.5856625	0.3616451
sp P18292 Prothrombi	5	7	0.045349	-0.204197	0.2837084	0.5858625	0.3618918
sp Q9QYL8 Acyl-proteir	2	2	-0.009826	-0.705835	0.6823592	0.5860375	0.3623838
sp Q6AZ50 Ubiquitin-lil	2	3	-0.039516	-0.334461	0.2622636	0.586475	0.3626295
sp P97690 Structural n	2	3	-0.012727	-0.602657	0.6386767	0.58665	0.3628749
sp P13437 3-ketoacyl-	16	77	-0.056479	-0.187819	0.0741102	0.586825	0.3631199
sp P62762 Visinin-like	10	37	0.0598182	-0.045045	0.1664682	0.587	0.3633646
sp Q63347 26S proteas	14	39	0.0611949	-0.020147	0.1450547	0.5871875	0.3636089
sp P52944 PDZ and LIN	2	2	-0.035543	-0.411953	0.3438003	0.58745	0.363853
sp Q63016 Large neutr	2	5	0.0455941	-0.182355	0.2816861	0.5876125	0.3640968
sp P83888 Tubulin gan	1	3	0.0364818	-0.276547	0.3732964	0.587675	0.3643401
sp P40307 Proteasome	5	13	-0.060601	-0.154688	0.030621	0.587875	0.364583
sp Q66HG9 Mitochondr	1	2	-0.008325	-0.789851	0.7932629	0.5880375	0.3648257
sp Q4V8H8 EH domain-	19	69	-0.057927	-0.177948	0.0631966	0.5885375	0.3650683
sp P97849 Long-chain	8	30	0.0596292	-0.039893	0.1566184	0.589525	0.3655534
sp P47987 Plasmolipin	2	5	0.0407078	-0.259348	0.3424786	0.589775	0.3657958
sp Q8K1Q0 Glycylpeptid	8	15	-0.051756	-0.211391	0.1140254	0.5898375	0.3660377
sp Q63186 Translation	2	2	-0.013711	-0.585633	0.570681	0.5898625	0.3662792
sp P84100 60S riboson	9	46	-0.062307	-0.138492	0.0125934	0.589975	0.3665202
sp P97700 Mitochondr	12	27	-0.060486	-0.146817	0.0288416	0.5901375	0.3667609
sp P63312 Thymosin b	1	3	-0.050009	-0.270139	0.1701849	0.5902625	0.3670013
sp P11608 ATP synthas	2	3	-0.048069	-0.320641	0.2313819	0.5902875	0.3672411
sp P68101 Eukaryotic t	7	10	-0.045728	-0.256376	0.1573787	0.590675	0.3677197
sp Q505J9 ATPase fam	2	4	-0.034176	-0.319103	0.2631812	0.5908375	0.3679586
sp Q5XID7 Armadillo re	2	2	0.0095961	-0.684259	0.6913716	0.5911	0.3681973
sp Q9WU6E Pleckstrin h	4	10	0.0432492	-0.221528	0.3074307	0.5912875	0.3684356
sp Q91Z79 Liprin-alpha	3	5	0.0347407	-0.302032	0.3792367	0.591425	0.3686736
sp Q80Z29 Nicotinamic	2	3	-0.036383	-0.392716	0.3083621	0.5927875	0.3691503
sp P20651 Serine/thre	1	2	0.0135293	-0.481232	0.5244792	0.593275	0.3693888
sp P14740 Dipeptidyl p	2	2	-0.025348	-0.367308	0.3454988	0.5934875	0.3696269
sp P18484 AP-2 compl	24	60	-0.06214	-0.133449	0.0097075	0.5938375	0.3698649
sp Q9EST6 Acidic leuci	2	5	-0.046117	-0.278662	0.1861237	0.593925	0.3701025
sp B2GV38 Ubiquitin-lil	2	5	0.0393763	-0.226044	0.2999768	0.5945125	0.3703403
sp Q5I0M2 Nicotinate-	3	3	-0.040532	-0.34213	0.2611915	0.5945625	0.3705775
sp P70627 Glutamate c	5	8	-0.046344	-0.26245	0.170021	0.595025	0.3708148

sp Q6AYB5 Signal recog	2	3	-0.031702	-0.357442	0.2982357	0.5950375	0.3710516
sp P62907 60S ribosom	11	40	-0.060589	-0.152786	0.0317704	0.5957	0.3712885
sp A2RUW1 Toll-interac	6	13	0.0548733	-0.078186	0.1902484	0.5957125	0.371525
sp Q6P4Z6 Leucine carl	1	2	-0.024972	-0.503372	0.4279268	0.5960125	0.3717613
sp P85108 Tubulin bet	1	6	0.0447057	-0.180983	0.2707329	0.5963875	0.3719975
sp Q6NX65 Programme	1	2	0.0303848	-0.366332	0.4186399	0.5964125	0.3724685
sp P55053 Fatty acid-b	8	37	-0.043122	-0.29258	0.2008916	0.5964125	0.3722333
sp P61227 Ras-related	1	2	0.00058	-0.670691	0.6687064	0.5964625	0.3727033
sp Q63537 Synapsin-2	4	5	-0.039346	-0.291783	0.2115784	0.5971125	0.3729383
sp P85125 Polymerase	19	75	0.0533446	-0.093965	0.1962685	0.5973625	0.373173
sp O54783 Choline/eth	2	2	-0.011279	-0.584653	0.5912486	0.5976375	0.3734076
sp B0BNF1 Septin-8 OS	8	15	-0.054849	-0.192581	0.0807953	0.598325	0.3741093
sp P27791 cAMP-depe	2	3	-0.035594	-0.365315	0.2925234	0.5985625	0.3743429
sp P70623 Fatty acid-b	1	4	0.028987	-0.348083	0.3933672	0.5995625	0.374577
sp P11250 60S ribosom	3	5	-0.057243	-0.277324	0.133274	0.5996125	0.3748107
sp Q8K4F7 Scavenger r	5	7	-0.045919	-0.234292	0.1491982	0.5999625	0.3750442
sp Q6AY12 NADH-cytoc	7	15	0.0439658	-0.182765	0.2796038	0.6007875	0.3752782
sp P84586 Heterogene	10	19	-0.055113	-0.187539	0.0780629	0.6015125	0.3755124
sp Q02589 [Protein AD	3	4	-0.046094	-0.240645	0.1519525	0.601925	0.3757465
sp B0BNA5 Coactosin-li	8	18	-0.056665	-0.173481	0.0577368	0.6019625	0.3759802
sp P62890 60S riboson	5	16	-0.052656	-0.195796	0.0954369	0.6029625	0.3762144
sp Q62967 Diphosphor	2	4	0.0245162	-0.345752	0.3954465	0.603325	0.3764486
sp Q63531 Ribosomal p	2	5	-0.02658	-0.371117	0.3257826	0.603425	0.3766823
sp P04692 Tropomyosi	6	23	-0.030077	-0.36096	0.2999871	0.60395	0.3769161
sp Q4KLG2 GTPase IMA	2	6	-0.037902	-0.274647	0.2072034	0.604075	0.3771496
sp P63012 Ras-related	5	15	-0.052649	-0.190522	0.0883431	0.6044125	0.3773829
sp Q6DGG0 Peptidyl-pro	6	17	0.0520267	-0.086426	0.1901614	0.6052875	0.3776167
sp Q7TNY6 Golgi reside	3	6	-0.047304	-0.222248	0.1231217	0.6056875	0.3778504
sp P13668 Stathmin O:	11	45	0.0470966	-0.135745	0.2367507	0.605775	0.3783164
sp B1WBU8 UPF0639 pr	2	3	-0.002884	-0.626421	0.6266782	0.6067875	0.3785498
sp Q9ESR9 ATP-binding	3	7	-0.042281	-0.238802	0.1567119	0.609075	0.3790186
sp Q66H98 Serum depr	6	27	-0.045448	-0.243092	0.1514899	0.609175	0.3792529
sp P06687 Sodium/pot	14	43	0.053646	-0.07568	0.185076	0.6093875	0.379487
sp P69682 Adapton ear	2	4	0.0323277	-0.293837	0.3571839	0.610125	0.3797214
sp Q9Z1I6 Rho guanin	1	2	-0.017992	-0.514099	0.4451957	0.610225	0.3799554
sp Q4AEF8 Coatomer s	14	30	0.0544041	-0.063607	0.1693984	0.6104125	0.3801892
sp P62963 Profilin-1 O:	9	41	-0.058842	-0.14956	0.0314482	0.6108125	0.3806558
sp P06907 Myelin prot	8	100	0.0397752	-0.190814	0.2790483	0.6109875	0.3808887
sp O35568 EGF-contain	1	3	0.0077361	-0.46785	0.4469229	0.6109875	0.3811211
sp Q04631 Protein farr	3	5	-0.03155	-0.317144	0.2433584	0.61105	0.3813532
sp O08838 Amphiphysi	9	23	0.0530172	-0.070727	0.1848858	0.6111375	0.3815848
sp P54311 Guanine nu	6	21	0.0532852	-0.067979	0.1741804	0.611425	0.3820472
sp P04904 Glutathione	14	48	0.0527432	-0.079039	0.1880754	0.6115375	0.3822779
sp Q5NDF0 Uncharacte	3	4	-0.01321	-0.507835	0.4805162	0.611975	0.3825085
sp B2RYW9 Fumarylace	5	7	-0.042421	-0.260772	0.1674272	0.6120875	0.3827387
sp Q499N5 Acyl-CoA sy	5	14	-0.046801	-0.218241	0.1246949	0.612725	0.3829692
sp Q641X3 Beta-hexos	3	6	0.0371729	-0.203691	0.2747928	0.6129	0.3831993

sp P52632 Signal trans	2	3	-0.044335	-0.234303	0.146296	0.6133875	0.3834295
sp B0BN56 28S riboson	1	2	-0.012794	-0.517008	0.4735414	0.6139625	0.384347
sp Q4FZT6 Histone H2/	1	2	-0.024418	-0.426414	0.4061106	0.6141	0.3845757
sp P51871 Cytochrome	1	2	0.0438113	-0.154498	0.2541042	0.6141375	0.3848039
sp Q5I0D5 Phospholysi	4	7	0.0385303	-0.201424	0.2896231	0.6141625	0.3850316
sp Q5U2R3 FERM doma	3	7	0.0034607	-0.495913	0.5223032	0.614375	0.3852591
sp P31000 Vimentin O:	22	100	-0.055131	-0.170655	0.0562845	0.6144	0.3854862
sp Q4V8E4 Coiled-coil c	2	3	0.0129766	-0.441179	0.4744431	0.6145	0.385713
sp Q5U211 Sorting nexi	7	16	-0.055871	-0.164741	0.0561206	0.614575	0.3859394
sp Q9EQN5 DNA-bindin	6	8	0.0383063	-0.192285	0.2623169	0.6147625	0.3861655
sp P12007 Isovaleryl-C	7	13	-0.053381	-0.182194	0.071027	0.615475	0.3863918
sp P38656 Lupus La pr	9	16	-0.045028	-0.230619	0.1358971	0.615925	0.3866182
sp P39069 Adenylate k	9	34	0.0398759	-0.180905	0.2591317	0.616125	0.3868443
sp P13852 Major prion	2	2	-0.014608	-0.494974	0.4411887	0.6165875	0.3872957
sp Q9WV97 Mitochondr	2	3	-0.039159	-0.254035	0.1800817	0.6191875	0.3879762
sp Q9JHW0 Proteasome	4	13	-0.052196	-0.177421	0.0737215	0.6194	0.3882029
sp Q641Y2 NADHdehy	9	16	0.0476047	-0.103915	0.1954882	0.619625	0.3884293
sp Q9Z254 PDZ domair	3	6	0.032784	-0.224372	0.2773334	0.6202375	0.3886559
sp P11505 Plasma mer	5	10	-0.0473	-0.219696	0.1296294	0.620275	0.3888821
sp Q07266 Drebrin OS-	11	29	0.0564961	-0.040188	0.1586526	0.6205375	0.3891081
sp P25304 Agrin OS=R	6	7	0.0185353	-0.329573	0.3698894	0.6210625	0.3893342
sp Q4V8C7 Interferon-i	5	13	0.0355609	-0.19281	0.2651398	0.6214	0.3895601
sp P13233 2',3'-cyclic-ri	25	100	0.0538341	-0.060581	0.1703062	0.6217375	0.389786
sp P41498 Low molecu	6	13	0.0485247	-0.102263	0.1938726	0.6219625	0.3900116
sp Q08420 Extracellula	2	4	-0.00604	-0.469562	0.4644407	0.623275	0.3904638
sp P14841 Cystatin-C C	4	11	0.0405007	-0.163863	0.2523732	0.62335	0.3906895
sp Q0ZCA7 C-type lectii	4	13	0.0498047	-0.09234	0.1912215	0.623825	0.3911404
sp Q5FK6 Coiled-coil a	4	5	-0.033467	-0.30926	0.2436169	0.6246375	0.391366
sp Q68FR6 Elongation f	23	100	-0.051904	-0.177048	0.0739619	0.6246625	0.3915912
sp Q9WVS2 Probable O-	2	2	0.0021511	-0.46349	0.4845331	0.6252375	0.3920411
sp B2GUV7 Eukaryotic t	2	2	-0.027973	-0.31958	0.2701481	0.62705	0.3922673
sp Q5PPH0 Enolase-pho	5	18	-0.040059	-0.254386	0.1648623	0.6273375	0.3924934
sp P30835 6-phosphof	4	7	0.0356885	-0.181395	0.2556944	0.6275375	0.3927191
sp Q9Z339 Glutathione	3	4	0.0362423	-0.204442	0.2894659	0.6275625	0.3929445
sp Q62824 Exocyst con	4	5	0.0256784	-0.296916	0.3632177	0.6279	0.3933945
sp P0C0S7 Histone H2/	3	25	-0.04048	-0.239137	0.1565531	0.6279125	0.3936189
sp P43244 Matrin-3 OS	10	32	-0.042626	-0.225487	0.1361434	0.628075	0.3938431
sp Q64428 Trifunction	24	85	-0.061876	-0.120637	-0.001894	0.6281625	0.3940669
sp P84245 Histone H3.	4	24	0.0301056	-0.227419	0.2967846	0.6282625	0.3942904
sp P32577 Tyrosine-pr	3	4	-0.015999	-0.405668	0.3742974	0.628475	0.3945136
sp P85971 6-phosphog	3	8	0.0408023	-0.149226	0.2286868	0.6290625	0.3951818
sp P30349 Leukotriene	10	18	-0.050097	-0.185702	0.0795044	0.6293625	0.3954042
sp O35142 Coatomer s	15	34	-0.04969	-0.182986	0.0818945	0.63025	0.395627
sp Q5XIF6 Tubulin alp1	4	25	0.0493768	-0.101924	0.1985755	0.6304875	0.3958496
sp P70483 Striatin OS=	2	3	-0.008741	-0.400822	0.3679265	0.6305	0.3960718
sp P39052 Dynamin-2	4	7	0.0217986	-0.305662	0.3558214	0.6308625	0.396294
sp Q9Z1E1 Flotillin-1 O	17	38	0.0537527	-0.052814	0.1579025	0.631125	0.3965159

sp Q5BJT2 Ubiquitin-lil	2	4	0.0109494	-0.381224	0.3914866	0.6321875	0.397403
sp Q9JMI1 Acetoacetyl	2	3	0.006249	-0.387107	0.4166464	0.6322625	0.3976239
sp P28075 Proteasome	3	5	0.0351984	-0.178327	0.2552789	0.63245	0.3978446
sp Q68FR9 Elongation f	11	51	-0.055817	-0.146908	0.0395467	0.632575	0.398065
sp P24050 40S riboson	8	31	-0.059207	-0.130268	0.0087736	0.6328375	0.3982853
sp Q561S0 NADHdehy	8	17	-0.048597	-0.180724	0.0825606	0.6329375	0.3985052
sp P0C5W1 Microtubule	4	6	0.0312673	-0.210465	0.2680389	0.6335125	0.3989448
sp O35828 Coronin-7 (I)	4	8	0.0366519	-0.167087	0.2423275	0.633675	0.3991642
sp Q64559 Cytosolic ac	13	42	-0.057934	-0.137902	0.0180509	0.6336875	0.3993832
sp P97629 Leucyl-cysti	5	15	0.0249676	-0.258412	0.2996808	0.6337	0.3996017
sp Q6AY84 Secernin-1 (I)	14	44	0.027201	-0.238356	0.309074	0.6337375	0.3998199
sp Q99PF5 Far upstream	6	16	-0.050394	-0.172321	0.0693372	0.6342625	0.4000382
sp P63322 Ras-related	8	27	0.0570669	-0.027423	0.1408247	0.6347	0.4002565
sp P17955 Nuclear por	1	3	0.0158988	-0.314164	0.3555692	0.6351875	0.4004749
sp Q9QXU9 ProSAAS OS	2	4	-0.006926	-0.379621	0.3443655	0.6362125	0.4006937
sp Q9R1T5 Aspartoacyl	12	35	0.033134	-0.200027	0.2698015	0.6363375	0.4009123
sp Q9JIH7 Serine/thre	2	3	0.0088435	-0.39676	0.4204176	0.6367625	0.401349
sp Q00657 Chondroitin	4	10	-0.041143	-0.215751	0.129155	0.636975	0.401567
sp P62959 Histidine tri	4	11	-0.019728	-0.323539	0.2940359	0.63735	0.4017849
sp P62944 AP-2 compl	13	32	-0.057243	-0.1325	0.0179755	0.63805	0.4022204
sp P63041 Complexin-	4	14	0.0455042	-0.105273	0.1925445	0.63835	0.402438
sp Q5IOP2 Glycine clea	3	9	-0.03986	-0.222912	0.1471919	0.6388875	0.4026557
sp P84903 Stromal integr	2	5	-0.024671	-0.298753	0.236997	0.63985	0.4030916
sp Q8R478 WW domain	5	19	0.0413661	-0.142824	0.2239767	0.64055	0.4033096
sp P54690 Branched-cl	13	44	0.0504605	-0.072107	0.1725019	0.6405625	0.4035273
sp Q99MS0 SEC14-like p	2	3	-0.015901	-0.320157	0.2833289	0.6406875	0.4037446
sp Q02874 Core histon	8	44	-0.049564	-0.172507	0.0739696	0.6409375	0.4039619
sp Q6AYR6 Haloacid de	3	5	-0.020416	-0.296665	0.2679396	0.6409875	0.4041787
sp P09215 Protein kinet	2	2	-0.021192	-0.309829	0.2672737	0.641025	0.4043952
sp P12749 60S riboson	10	22	-0.055255	-0.144778	0.0359993	0.6416625	0.4046119
sp Q920A6 Retinoid-inc	7	16	-0.044334	-0.192184	0.109961	0.6422125	0.4050449
sp Q64303 Serine/thre	5	9	-0.030559	-0.266505	0.1997018	0.6426875	0.4052614
sp O08700 Vacuolar pr	2	4	-0.022937	-0.305465	0.2541311	0.64405	0.4054786
sp Q5XID1 Anamorsin	4	5	0.0008596	-0.385331	0.398315	0.6443625	0.4056958
sp Q4V8B0 Oxidation re	7	12	-0.043202	-0.194571	0.1059269	0.6452	0.4059133
sp O35112 CD166 antigen	7	20	-0.044879	-0.19109	0.0983932	0.64535	0.4061306
sp P29975 Aquaporin-	2	3	0.0098744	-0.397952	0.4185443	0.646	0.4063481
sp P29314 40S riboson	17	61	-0.053603	-0.152368	0.0432002	0.6464	0.4065655
sp P82471 Guanine nu	7	15	0.0398488	-0.127261	0.2012031	0.6467375	0.4067829
sp Q6PEC0 Bis(5'-nucle	5	8	-0.016974	-0.308828	0.2752711	0.646775	0.4069999
sp P21533 60S riboson	17	76	-0.054992	-0.143017	0.0317462	0.64755	0.4072172
sp Q924S5 Lon proteas	8	20	-0.045615	-0.180755	0.094943	0.647775	0.4074343
sp Q9Z2L9 Protein NDF	3	4	0.0142675	-0.326431	0.3503261	0.6482	0.4076514
sp Q9R1Z0 Voltage-dep	8	20	-0.048852	-0.170515	0.0726591	0.648275	0.4078681
sp P13084 Nucleophos	9	23	-0.052703	-0.156252	0.0522105	0.648775	0.408085
sp Q5XHY7 Signal trans	2	5	-0.011997	-0.335689	0.3209321	0.6488875	0.4083015
sp P62278 40S riboson	12	68	-0.04969	-0.164131	0.0670396	0.6490375	0.4085178

sp P04631 Protein S10	7	55	-0.032458	-0.24597	0.1862159	0.6492375	0.4087339
sp P26817 Beta-adrenergic receptor type 1	1	3	0.0045898	-0.338444	0.3416825	0.650125	0.4089504
sp Q62733 Lamina-associated protein	8	13	0.0455662	-0.085862	0.1770439	0.650375	0.4091667
sp P56571 ES1 protein	12	50	-0.05724	-0.128957	0.0149912	0.650825	0.4093831
sp Q5FVM6 Myotubularin-related protein	2	2	0.0178691	-0.298407	0.3267598	0.6519125	0.4096
sp Q811U3 ELKS/Rab6-interacting protein	3	4	-0.004393	-0.364814	0.3614523	0.6534375	0.4098179
sp P50554 4-aminobutyrate aminotransferase	15	41	-0.047771	-0.170004	0.073432	0.65585	0.4109075
sp P06685 Sodium/potassium ATPase alpha 1	21	100	0.0505224	-0.056179	0.1584508	0.656	0.4111253
sp Q6PST4 Atlastin-1 O-acyltransferase	11	20	-0.040352	-0.200423	0.1196994	0.6574125	0.4115618
sp Q6MG61 Chloride channel protein	3	6	0.0263995	-0.201848	0.2546464	0.6579375	0.4117802
sp P29410 Adenylate kinase	4	12	-0.032796	-0.22871	0.1552071	0.6591625	0.4119993
sp P38718 Brain protein	3	7	-0.02622	-0.255837	0.2036453	0.659175	0.412218
sp P51673 Cellular retinaldehyde-binding protein	2	7	-0.029227	-0.242488	0.1810005	0.65935	0.4124365
sp P85845 Fascin OS-binding protein	11	32	-0.035886	-0.212608	0.1458045	0.6594625	0.4126548
sp P16446 Phosphatidylethanolamine-binding protein	8	19	-0.039048	-0.20744	0.1231801	0.6602125	0.4128733
sp O35244 Peroxiredoxin 1	14	47	-0.043976	-0.183478	0.0927147	0.66055	0.4133094
sp P97532 3-mercaptopropionic acid reductase	5	8	0.0301841	-0.164193	0.2286538	0.661425	0.4135278
sp Q63965 Sideroflexin	3	7	-0.028616	-0.233256	0.1763531	0.6621125	0.4139642
sp P09456 cAMP-dependent protein kinase inhibitor	6	11	0.0305169	-0.16886	0.2312015	0.66285	0.4141828
sp P61959 Small ubiquitin-like modifier	1	4	0.0358406	-0.143151	0.2125781	0.6635625	0.4144015
sp Q5M9I5 Cytochrome P450 2D6	1	3	0.0266104	-0.24412	0.3044642	0.6638	0.4146201
sp Q704S8 Carnitine O-acyltransferase I	6	8	0.0292394	-0.171063	0.2313401	0.6648125	0.4148392
sp Q9JJ50 Hepatocyte nuclear factor 1 beta	4	10	-0.002588	-0.433027	0.4032849	0.6650625	0.4150581
sp B0BN18 Prefoldin subunit 1	4	9	-0.041788	-0.183091	0.0943762	0.6659	0.4152774
sp P09414 Nuclear factor I	1	3	0.0298185	-0.165615	0.230735	0.666075	0.4154964
sp Q91Y81 Septin-2 OS	13	46	-0.051228	-0.149804	0.0459091	0.6666625	0.4159341
sp Q642A6 von Willebrand factor-associated protein	11	44	0.0349166	-0.141913	0.2117071	0.66705	0.4163709
sp P35467 Protein S10	1	4	-0.029226	-0.236435	0.1750932	0.6674125	0.4165892
sp O88658 Kinesin-like protein 1	4	6	0.0105444	-0.27192	0.3076478	0.6678375	0.4170252
sp P38062 Methionine adenosyl transferase I	7	10	0.0423122	-0.091697	0.1733671	0.6684	0.4172432
sp P50398 Rab GDP dissociation inhibitor	19	80	0.0563568	-0.016039	0.1276994	0.66875	0.4176785
sp P97534 Peptidyl-prolyl isomerase	2	7	0.0399509	-0.102942	0.1856453	0.668875	0.4178958
sp Q5M7U6 Actin-related protein 2/3	6	15	-0.034971	-0.205434	0.1360014	0.669225	0.418113
sp P48508 Glutamate-amine ligase	3	8	-0.035137	-0.190404	0.1268396	0.66925	0.4183298
sp Q6MG08 ATP-binding cassette transporter A1	7	13	-0.029343	-0.213512	0.1560062	0.670325	0.4194116
sp P61972 Nuclear transport protein Ntf2	5	15	-0.028099	-0.228261	0.178954	0.6712	0.4196279
sp P24473 Glutathione S-transferase M1	6	8	-0.030784	-0.212327	0.1497074	0.67125	0.4198439
sp P32198 Carnitine O-acyltransferase II	6	15	0.0233141	-0.219773	0.274706	0.6719	0.4200601
sp Q5HZE4 Methylthioribose kinase	3	5	0.0146832	-0.244712	0.2764575	0.6719	0.4202759
sp P35571 Glycerol-3-phosphate acyltransferase	9	17	0.0290705	-0.162639	0.2240098	0.67215	0.4204915
sp P22734 Catechol O-methyltransferase	7	17	-0.031122	-0.216317	0.1599895	0.672325	0.420707
sp Q68FS2 COP9 signalosome complex subunit 2	7	19	-0.046477	-0.152684	0.0613325	0.6727625	0.4211374
sp Q8VHK7 Hepatoma-derived growth factor receptor	3	8	-0.044602	-0.15993	0.0708888	0.67285	0.4213522
sp P23965 3,2-trans-enoyl acyl carrier protein acyltransferase	9	34	-0.044473	-0.16998	0.0792121	0.67355	0.4219954
sp P35213 14-3-3 protein epsilon	4	7	-0.026023	-0.23794	0.1940412	0.6737125	0.4222095
sp Q5FVL2 Neighbor of TSPY protein	3	6	-0.011011	-0.277524	0.2647224	0.6740375	0.4224234
sp Q62835 Rab GTPase	2	5	0.0053009	-0.306701	0.3039993	0.6748125	0.4228513

sp P08649 Complemer	9	14	-0.025372	-0.232316	0.1774956	0.675325	0.4232787
sp P24329 Thiosulfate	11	26	0.04869	-0.048573	0.1425197	0.6758125	0.4234924
sp P19944 60S acidic ri	2	11	0.0170399	-0.232748	0.2751857	0.6761375	0.4237059
sp P97615 Thioredoxin	2	5	-0.023361	-0.242117	0.197856	0.676575	0.4239195
sp Q5U2Q3 Ester hydro	4	5	0.0157002	-0.238782	0.2759203	0.6765875	0.4241327
sp P42123 L-lactate de	20	100	0.0442959	-0.074902	0.1703209	0.676625	0.4243456
sp P55161 Nck-associat	6	9	0.0227056	-0.186589	0.229327	0.6779875	0.4245593
sp B0BN85 Suppressor	5	11	0.0325646	-0.134638	0.2099736	0.6782125	0.4247728
sp Q9ES53 Ubiquitin fu	3	6	-0.010309	-0.281692	0.2625362	0.6792625	0.426049
sp O08837 Cell division	5	6	-0.014281	-0.268979	0.2425006	0.68	0.4262615
sp Q63798 Proteasome	6	9	-0.02712	-0.225392	0.1676664	0.6804625	0.426686
sp Q9Z2Q1 Protein tra	17	41	-0.051444	-0.135341	0.0303546	0.6813125	0.4268985
sp Q63569 26S proteas	13	44	-0.05041	-0.135862	0.0379349	0.681625	0.427111
sp P41499 Tyrosine-pr	7	8	-0.016186	-0.267708	0.2348216	0.6823875	0.427959
sp Q27W01 RNA-bindin	2	6	0.0371085	-0.107921	0.1767747	0.6825125	0.4281704
sp P12368 cAMP-depe	7	12	0.0355483	-0.121336	0.1921368	0.683425	0.4283822
sp Q63258 Integrin alp	15	35	0.053148	-0.024552	0.1294594	0.6837375	0.428594
sp P54319 Phospholip	6	11	0.0350608	-0.119177	0.1842193	0.6840375	0.4288056
sp P24090 Alpha-2-HS	14	82	0.0099838	-0.257773	0.2781764	0.68525	0.4292296
sp P47875 Cysteine an	13	37	-0.045893	-0.156148	0.0617565	0.685425	0.4294414
sp Q9ESH6 Glutaredoxi	4	13	-0.026203	-0.216809	0.1641408	0.6857625	0.429653
sp Q00438 Polypyrimid	4	7	-0.033288	-0.193678	0.129226	0.6862875	0.4298648
sp P34067 Proteasome	4	17	-0.041439	-0.16696	0.0812451	0.6875	0.4304994
sp P04764 Alpha-enol-	18	91	0.053723	-0.02015	0.1254327	0.68785	0.4307111
sp Q8R431 Monoglycer	12	41	-0.031791	-0.195827	0.1348502	0.6895	0.431556
sp Q62645 Glutamate	2	6	0.0326576	-0.125499	0.1895223	0.6899625	0.4317676
sp P04897 Guanine nu	7	30	0.0400547	-0.08181	0.1688979	0.69	0.4319789
sp P04256 Heterogene	8	30	-0.0501	-0.133136	0.03393	0.6909625	0.4324015
sp O88989 Malate deh	21	80	0.0509089	-0.033842	0.1334882	0.6910375	0.4326126
sp Q8CH84 ELAV-like pi	2	5	-0.016827	-0.2451	0.2069975	0.6911875	0.4328235
sp P51886 Lumican OS	13	100	-0.014275	-0.259723	0.2130243	0.6924625	0.4332454
sp O35095 Neurochond	16	33	-0.047466	-0.140251	0.0462145	0.6924625	0.4334563
sp Q5U2V8 Transmemb	3	4	0.0120165	-0.238253	0.2670051	0.692575	0.433667
sp P08460 Nidogen-1 (7	40	0.0069928	-0.258098	0.2739261	0.6931625	0.4338778
sp Q5FVI6 V-type prot	9	19	-0.043372	-0.147662	0.0638834	0.6934375	0.4340885
sp Q923S8 Pantothena	2	4	0.0266769	-0.205781	0.2906929	0.69395	0.4342992
sp P62332 ADP-ribosyl	2	8	0.0145515	-0.227512	0.2585964	0.6941375	0.4345098
sp P01041 Cystatin-B C	4	10	-0.029742	-0.196689	0.1378633	0.6952625	0.434721
sp P39032 60S ribosom	5	18	-0.048454	-0.144146	0.0495298	0.6952875	0.4349318
sp Q63413 Spliceosom	15	26	-0.049617	-0.136486	0.034444	0.6955625	0.4351425
sp P35565 Calnexin OS	22	85	-0.050937	-0.132247	0.031273	0.6956	0.4353528
sp P97521 Mitochondr	3	5	0.0189261	-0.187654	0.2279718	0.696675	0.4357741
sp Q794F9 4F2 cell-sur	8	24	0.0421886	-0.075447	0.1617739	0.6967	0.4359844
sp P21263 Nestin OS=F	40	98	-0.014814	-0.247488	0.2147174	0.6975875	0.436195
sp Q5U2Z3 Nucleosom	8	20	0.0350747	-0.108313	0.1752958	0.6979125	0.4366157
sp Q4QQT4 Serine/thre	5	18	0.0386905	-0.088713	0.1653147	0.698125	0.4368257
sp Q4V7D2 Protein rog	2	2	-0.014662	-0.246482	0.2270832	0.69875	0.4372457

sp P14882 Propionyl-C	6	18	-0.036549	-0.170413	0.0967876	0.699425	0.437665
sp P11348 Dihydroptero	7	24	-0.046216	-0.148936	0.0521366	0.6995125	0.4378745
sp P97834 COP9 signal	5	8	-0.026614	-0.202247	0.1485418	0.6996125	0.4380837
sp Q66HF9 Leucine-rich	1	2	-0.000778	-0.335392	0.3442653	0.7002	0.4382931
sp Q63081 Protein disu	14	58	-0.052795	-0.126253	0.0211666	0.7003875	0.4385022
sp P07151 Beta-2-micr	3	8	0.0262854	-0.149905	0.1974612	0.7006	0.4389199
sp Q5XII0 E Mammiliar	10	30	-0.030525	-0.191589	0.1283687	0.7006	0.4387112
sp P54645 5'-AMP-acti	6	7	0.0167791	-0.189695	0.2312225	0.7015375	0.439129
sp Q68FT9 Selenocyste	3	5	-0.008394	-0.251431	0.2351265	0.7018125	0.439338
sp Q99JD4 CLIP-associ	9	16	-0.034284	-0.16997	0.1031079	0.7018625	0.4395467
sp Q6P686 Osteoclast-	9	29	0.0443738	-0.055483	0.1496841	0.7022875	0.4401716
sp Q9EPB1 Dipeptidyl p	3	9	0.0062647	-0.249873	0.2613104	0.7036125	0.4405884
sp P13221 Aspartate a	20	81	0.0365797	-0.096447	0.1696607	0.7048	0.4414204
sp P02564 Myosin-7 O	2	3	0.0009668	-0.26623	0.2938336	0.7058625	0.442252
sp Q7TP47 Heterogene	14	41	-0.043988	-0.147523	0.0610757	0.7066125	0.4426668
sp Q5RKH0 Putative oxi	2	5	0.0107232	-0.214981	0.2399595	0.7085	0.4430823
sp P10688 1-phosphat	5	11	0.0192739	-0.17331	0.2061083	0.708975	0.4437063
sp Q5U318 Astrocytic p	10	41	0.0137358	-0.205847	0.2314932	0.7090625	0.4439138
sp Q00981 Ubiquitin ca	17	100	0.0375822	-0.090405	0.1663115	0.709075	0.4441209
sp P07335 Creatine kir	19	100	-0.041789	-0.154201	0.0717942	0.709425	0.444328
sp Q99ML5 Prenylcyste	6	18	-0.036644	-0.161844	0.0884888	0.7101875	0.4449486
sp Q4V7C7 Actin-relate	15	50	-0.052815	-0.121865	0.0161484	0.7104875	0.4451552
sp Q9EQR2 Alkyldihydru	4	8	-0.00391	-0.240967	0.2505224	0.7105125	0.4453616
sp Q62991 Sec1 family	7	11	-0.018613	-0.209745	0.1720692	0.7107375	0.4455678
sp Q62625 Microtubul	2	9	0.0196275	-0.172194	0.2152548	0.7114875	0.4459798
sp P21775 3-ketoacyl-	10	33	-0.018762	-0.215801	0.1823609	0.7127375	0.4461866
sp Q9QX69 LanC-like pr	8	14	0.039544	-0.07461	0.1586834	0.7128875	0.4463932
sp Q91Y78 Ubiquitin ca	3	8	0.0202563	-0.171772	0.210979	0.7134875	0.4468061
sp Q5XIE0 Acidic leuci	2	5	-0.001603	-0.287264	0.3103601	0.7136375	0.4472181
sp P41123 60S riboson	8	32	-0.043147	-0.149939	0.0588772	0.7137125	0.4474238
sp P48679 Prelamin-A/	28	100	-0.038291	-0.156635	0.0855732	0.713825	0.4476292
sp P52590 Nuclear por	4	5	0.0113618	-0.219811	0.2233096	0.713925	0.4478343
sp P86252 Transcriptic	9	56	-0.052363	-0.117277	0.0140026	0.715175	0.4480401
sp P85969 Beta-solubl	7	14	-0.019327	-0.20424	0.1647319	0.7152	0.4482456
sp Q9JLZ1 Glutaredoxi	12	33	-0.042951	-0.141134	0.0559562	0.715575	0.4486561
sp P97697 Inositol moi	8	22	-0.039579	-0.149033	0.0745248	0.715925	0.4488612
sp Q6P9T8 Tubulin bet	2	19	-0.025215	-0.191692	0.1447837	0.716575	0.4490665
sp P62260 14-3-3 prot	16	63	-0.055142	-0.109071	0.0014595	0.7168125	0.4492717
sp Q5BJS0 Putative AT	4	5	0.009862	-0.21307	0.2446898	0.7175375	0.4496816
sp Q6JE36 Protein NDF	14	61	-0.026808	-0.193718	0.1326407	0.71835	0.4500915
sp Q62818 Translation	3	9	0.0090723	-0.206616	0.2309203	0.71855	0.4502965
sp Q9EPF2 Cell surface	9	26	0.0340963	-0.100099	0.1744273	0.7192625	0.4505016
sp Q05096 Myosin-Ib C	11	24	0.0318578	-0.101646	0.1748266	0.720075	0.4509122
sp Q6AXM7 HBS1-like pi	3	7	-0.016021	-0.208472	0.1722853	0.7206375	0.4513223
sp A1L1J9 Lipase matu	2	5	-0.020836	-0.303489	0.2275161	0.7208625	0.4515271
sp B5DEH2 Erlin-2 OS=I	8	14	0.0301256	-0.109861	0.166753	0.72135	0.451732
sp Q4QQW Putative ph	7	20	0.02361	-0.144928	0.1904105	0.7226625	0.4523466

sp O35952 Hydroxyacy	5	10	-0.03032	-0.168107	0.1090207	0.7238	0.4529619
sp P62329 Thymosin b	2	9	-0.020164	-0.201293	0.1561628	0.7242375	0.4531667
sp Q63768 Adapter mo	6	16	-0.030203	-0.168444	0.1078646	0.7242875	0.4535756
sp P84817 Mitochondr	4	7	0.0103015	-0.213096	0.2337157	0.72455	0.4541871
sp P16036 Phosphate	12	39	-0.04904	-0.127936	0.0290923	0.72465	0.4545935
sp P29419 ATP synthas	5	23	-0.041405	-0.138963	0.0566234	0.72475	0.4547963
sp Q5XI81 Fragile X me	9	22	-0.032184	-0.158538	0.0962953	0.7261625	0.4554051
sp O35795 Ectonucleos	7	15	-0.009454	-0.232163	0.2080445	0.726475	0.455608
sp Q63270 Cytoplasmic	9	13	-0.012246	-0.211275	0.1906744	0.7267875	0.4558108
sp P15865 Histone H1.	15	100	0.0186228	-0.163367	0.2048547	0.727025	0.4560135
sp P27867 Sorbitol deh	4	13	0.0357594	-0.088227	0.1554444	0.728575	0.4572288
sp P13676 Acylamino-	4	10	-0.000158	-0.2338	0.2341698	0.7288625	0.4576323
sp P20294 Ciliary neur	6	13	0.0058487	-0.222753	0.2421544	0.7293625	0.457834
sp Q4KLF8 Actin-relate	2	8	-0.001778	-0.272272	0.240795	0.729375	0.4580355
sp Q63610 Tropomyosi	8	36	0.0303895	-0.108037	0.170777	0.7303625	0.4588396
sp P41350 Caveolin-1 (9	32	0.0218798	-0.147676	0.1885657	0.7304125	0.4592407
sp Q3SWU3 Heterogene	5	16	-0.026733	-0.172961	0.1162299	0.7319375	0.4604416
sp Q68FT1 Ubiquinone	3	5	-0.010865	-0.207928	0.1949306	0.73215	0.4608405
sp P30839 Fatty aldehy	6	21	0.0318688	-0.096089	0.1636366	0.7342875	0.4622356
sp Q9WV63 Kinesin-like	2	7	-0.013199	-0.204218	0.1797687	0.734775	0.4624345
sp P63036 DnaJ homol	7	18	-0.03633	-0.15143	0.0811227	0.735	0.4630299
sp Q9Z270 Vesicle-assc	8	30	-0.051372	-0.11484	0.0118447	0.7359	0.463624
sp O35783 Calumenin (6	18	-0.031534	-0.168063	0.0992779	0.737025	0.4642177
sp Q63525 Nuclear mig	8	16	0.0303362	-0.111603	0.1797707	0.7373625	0.4646131
sp Q9JI85 Nucleobind	5	8	0.0031486	-0.208129	0.2199642	0.7381625	0.465402
sp Q9WVR7 Protein pho	5	13	0.0020229	-0.215993	0.231554	0.7381875	0.4655988
sp P62919 60S riboson	17	76	-0.045864	-0.131997	0.03612	0.7382	0.4657953
sp P13697 NADP-depe	8	22	-0.038994	-0.141143	0.0619886	0.73825	0.4661876
sp P04041 Glutathione	6	21	0.0165401	-0.160355	0.1932668	0.7388875	0.4663838
sp P08644 GTPase KRα	5	8	-0.015791	-0.198679	0.1696362	0.7393375	0.4667759
sp Q66HG5 Transmemb	4	9	0.0139535	-0.165833	0.1921383	0.740325	0.4669723
sp Q3B8Q0 Microtubul	6	16	-0.027014	-0.167545	0.1135893	0.7412125	0.4673651
sp P84092 AP-2 compl	10	25	0.0436993	-0.042089	0.1301511	0.741625	0.4677577
sp P62138 Serine/thre	3	4	-0.001929	-0.241049	0.2313614	0.7418875	0.4679537
sp P61078 Ubiquitin-cc	2	9	-0.036532	-0.144317	0.0714967	0.742125	0.4681497
sp O35796 Complemer	6	19	-0.02961	-0.16233	0.104425	0.74245	0.4685412
sp Q62745 CD81 antigen	4	21	0.0019374	-0.221404	0.2290551	0.742825	0.4687368
sp O35303 Dynamin-1-	21	56	-0.04377	-0.127461	0.0436421	0.742975	0.4689323
sp P51583 Multifunctio	5	6	-8.25E-05	-0.219398	0.2246716	0.7442125	0.4695193
sp P14562 Lysosome-a	2	5	0.0100594	-0.183464	0.1979144	0.74425	0.4699096
sp Q5PQN7 Protein LZIC	3	10	-0.011394	-0.19786	0.1704442	0.7443125	0.4701043
sp P67874 Casein kina	3	12	0.0164054	-0.152129	0.1960495	0.7454125	0.470883
sp P27605 Hypoxanthi	9	31	0.0264575	-0.116585	0.1658489	0.74765	0.4716624
sp P11232 Thioredoxin	10	66	0.0096932	-0.175971	0.2037746	0.7486125	0.4720521
sp P49911 Acidic leuci	5	15	-0.016093	-0.178152	0.1461644	0.7492875	0.4722473
sp Q9Z1H9 Protein kina	6	17	0.0248359	-0.115957	0.1645705	0.749375	0.4724423
sp Q01177 Plasminoge	10	25	0.0133677	-0.164632	0.1917047	0.7503625	0.4728325

sp Q9WVK7 Hydroxyacylglucuronidase	11	38	-0.048794	-0.11658	0.0175184	0.750775	0.4730277
sp P70500 CDP-diacylglycerol acyltransferase	3	8	-0.008872	-0.19437	0.1918389	0.751075	0.4734175
sp P70645 Bleomycin hydrolase	2	9	0.0105883	-0.172247	0.1999017	0.7512	0.4736121
sp Q6IRE4 Tumor susceptibility gene 141 protein	5	14	0.0175796	-0.140134	0.1768416	0.7522	0.474196
sp P60881 Synaptosomal-associated protein 25 kDa	4	9	0.0172003	-0.149471	0.1734994	0.7529125	0.474973
sp P50503 Hsc70-interacting protein	14	65	-0.043428	-0.127265	0.0397364	0.7529125	0.4747791
sp Q75WE7 von Willebrand factor-associated protein	10	23	0.0299777	-0.092861	0.1518244	0.753125	0.4753604
sp P24155 Thimet oligopeptidyl proteinase	11	16	-0.024105	-0.164698	0.1100653	0.75325	0.4755537
sp P62775 Myotrophin	2	13	-0.01612	-0.186805	0.1545541	0.754025	0.4757474
sp Q5FVJ0 Protein RUFY1	22	66	0.0320746	-0.085353	0.1543157	0.7547375	0.4763276
sp Q80U96 Exportin-1 C-terminal domain	10	21	-0.026367	-0.160083	0.1000171	0.7583125	0.4774921
sp Q9QXJ0 Tubulin--tyrosine kinase	2	8	-0.007643	-0.189327	0.1766199	0.7585125	0.4776861
sp P05197 Elongation factor 1-alpha	29	100	-0.051844	-0.107492	0.0053069	0.7586875	0.4778801
sp Q62698 Cytoplasmic dynein 1	8	11	0.0205663	-0.125668	0.1693254	0.759475	0.4788475
sp Q5XF0 Transgelin-2	12	45	-0.033859	-0.145628	0.0770972	0.7597375	0.4794256
sp Q05140 Clathrin coat protein	5	13	-0.005842	-0.189405	0.18681	0.7601625	0.4798103
sp P62898 Cytochrome c oxidase subunit 6A1	10	55	-0.040107	-0.135061	0.0517142	0.760475	0.4800026
sp P52303 AP-1 complex	9	16	-0.024537	-0.154261	0.1063573	0.7605375	0.4801946
sp P17074 40S ribosomal protein S16	13	57	-0.042775	-0.126699	0.0389458	0.7617375	0.4809623
sp Q6AXV4 Sorting and assembly protein for membrane proteins	7	20	-0.022418	-0.165869	0.1208008	0.7618125	0.4811539
sp Q6URK4 Heterogeneous nuclear ribonucleoprotein K	11	31	-0.038652	-0.133438	0.0572639	0.76215	0.4819182
sp Q641Y0 Dolichyl-diphosphate acetyltransferase	13	45	-0.03745	-0.137415	0.0606212	0.7625	0.482109
sp Q68FP1 Gelsolin OS-kinase	28	100	0.0331124	-0.076761	0.1438217	0.7631	0.4826804
sp Q6PCU2 V-type proton ATPase subunit C	8	24	0.0414061	-0.040098	0.1275898	0.763775	0.483061
sp Q9WTP0 Band 4.1-like protein	7	18	-0.021702	-0.161476	0.1197167	0.7638125	0.483251
sp Q03114 Cyclin-dependent kinase 5	5	10	0.0012067	-0.200234	0.2019695	0.76405	0.483441
sp Q9R063 Peroxiredoxin 6	12	63	0.045626	-0.028706	0.1187445	0.7644375	0.483631
sp P25886 60S ribosomal protein L13	6	37	-0.027179	-0.155609	0.0975563	0.764525	0.4838208
sp Q64640 Adenosine deaminase	6	21	-0.03455	-0.134629	0.065433	0.7648625	0.4840106
sp P21913 Succinate dehydrogenase	8	21	0.0358661	-0.061205	0.1322145	0.76535	0.4845789
sp P40329 Arginyl-tRNA transferase	32	96	-0.03239	-0.14218	0.0777214	0.766475	0.4849576
sp Q5XIU5 Proteasome ATPase subunit	3	10	0.0099747	-0.159396	0.1879284	0.7698	0.486098
sp P50399 Rab GDP dissociation inhibitor	20	70	-0.048502	-0.109382	0.012467	0.7702375	0.4864782
sp Q5M7W Microtubule-associated protein tau	34	100	0.0206089	-0.117453	0.1687176	0.770575	0.4866682
sp Q66H76 Paxillin OS-kinase	2	4	-0.002165	-0.195164	0.1879342	0.7706	0.486858
sp Q80Z70 Protein serine/threonine phosphatase	6	10	0.0014827	-0.198444	0.1955559	0.7707	0.4870476
sp Q64380 Sarcosine dehydrogenase	3	7	-0.003798	-0.184961	0.1836637	0.7709	0.4876151
sp P04550 Parathyroid hormone receptor	2	13	0.0257398	-0.098995	0.1504496	0.7717375	0.4881819
sp Q62636 Ras-related GTP-binding protein	6	10	-0.02811	-0.150947	0.0932623	0.771875	0.4885588
sp Q08877 Dynamin-3	11	26	0.0204141	-0.122502	0.1646548	0.772	0.488747
sp P10111 Peptidyl-prolyl isomerase	13	95	0.0378024	-0.055568	0.1308387	0.772025	0.488935
sp Q7M767 Ubiquitin-conjugating enzyme E2B	6	18	-0.015497	-0.170764	0.1403326	0.77215	0.4891228
sp Q9JHY2 Sideroflexin	9	21	0.0360746	-0.056894	0.1323074	0.772675	0.4896852
sp Q32Q06 AP-1 complex	5	9	0.0161437	-0.131652	0.1649372	0.7730875	0.4904331
sp Q642G4 Peroxisomal membrane protein	4	8	0.0090016	-0.161263	0.1758769	0.7742125	0.4909928
sp P69897 Tubulin beta-1 chain	4	36	0.031334	-0.079621	0.1396252	0.774375	0.4919228
sp P0C5H9 Mesencephalic trigeminal nucleus-specific protein	7	14	-0.019579	-0.153994	0.1163033	0.774375	0.4921082

sp Q5QD51 A-kinase an	28	69	0.020917	-0.118765	0.1605864	0.774575	0.492663
sp O55171 Acyl-coenzy	6	16	0.0152655	-0.131817	0.1644696	0.7753875	0.4930328
sp P00388 NADPH--cyt	11	21	0.0220538	-0.109393	0.1503559	0.775575	0.4934019
sp Q6AYT7 Monoacylgly	11	43	-0.033375	-0.13629	0.0739806	0.7756875	0.4935861
sp P47198 60S ribosom	2	9	0.0181152	-0.127467	0.1633814	0.776	0.4937703
sp Q5FVI3 Leucine-rich	3	3	0.0006164	-0.210452	0.2118543	0.776075	0.4939544
sp Q5I0D7 Xaa-Pro dipeptid	8	15	-0.02032	-0.154164	0.1132172	0.7763875	0.4943219
sp O35263 Platelet-act	3	7	0.0094313	-0.155271	0.1779675	0.776975	0.4950554
sp P60203 Myelin prot	10	46	0.018441	-0.125614	0.1672275	0.7776875	0.4952388
sp O35814 Stress-induc	26	78	-0.044449	-0.117264	0.0282758	0.7786375	0.4959714
sp Q4V7F2 Cysteine-rich	6	16	-0.010721	-0.176139	0.1562403	0.7792625	0.4963376
sp Q32PX7 Far upstream	3	5	0.0049681	-0.168657	0.1820807	0.779525	0.4967032
sp P62628 Dynein light	5	20	-0.022538	-0.147357	0.1067886	0.779525	0.4965205
sp Q63544 Gamma-synt	10	68	0.0234521	-0.10323	0.1516109	0.7795875	0.4968857
sp Q4KMA2 UV excision	11	27	0.0381699	-0.046456	0.1237351	0.779725	0.4970681
sp Q6AYT3 UPF0027 pr	10	35	-0.03738	-0.128495	0.0521217	0.781	0.4981596
sp Q9Z1X1 Extended s	28	81	-0.041777	-0.115892	0.0369249	0.7818375	0.4990665
sp P07687 Epoxide hydrol	5	9	-0.024285	-0.144519	0.0964247	0.7820625	0.4992476
sp P62198 26S proteas	7	23	-0.02367	-0.146733	0.0986753	0.7820875	0.4994284
sp P20069 Mitochondr	4	13	-0.014304	-0.161273	0.1315487	0.78355	0.5001519
sp Q99MZ4 Gamma-glu	6	14	-0.007291	-0.172847	0.1575166	0.7835625	0.5003325
sp P69060 N-acylneur	5	16	-0.031752	-0.135536	0.0701834	0.7841875	0.5005133
sp P33124 Long-chain-	11	33	-0.007519	-0.18495	0.1671179	0.7847875	0.5008748
sp Q7TQ94 Nitrilase ho	1	4	-0.002539	-0.179972	0.1756731	0.7856625	0.5012364
sp P60825 Cold-inducil	3	12	0.0023345	-0.177064	0.1783878	0.785975	0.5015976
sp P27321 Calpastatin	9	15	-0.023333	-0.144422	0.0969396	0.7864	0.5017782
sp Q62785 28 kDa heat	5	10	-0.016851	-0.154515	0.1302176	0.7864625	0.5019587
sp Q5RK09 Eukaryotic t	2	8	0.0014093	-0.176072	0.1845116	0.7873	0.5021394
sp Q99N27 Sorting nexi	7	11	-0.013581	-0.157602	0.1322842	0.787375	0.5023199
sp P45592 Cofilin-1 OS	20	91	-0.011001	-0.170052	0.1445937	0.7874375	0.5025002
sp P20788 Cytochrome	10	50	-0.042698	-0.114075	0.0325696	0.7875	0.5026804
sp Q9JJW3 Up-regulate	2	6	0.0235707	-0.099461	0.1452816	0.78785	0.5030404
sp O35854 Branched-cl	6	9	-0.00846	-0.165082	0.156931	0.7878625	0.5032201
sp Q3B7U9 Peptidyl-pro	5	14	0.0209207	-0.107332	0.1556974	0.787975	0.5033997
sp Q9ER24 Ataxin-10 O	14	27	-0.030474	-0.132294	0.0670927	0.7890625	0.5039383
sp P04905 Glutathione	11	32	-0.008442	-0.173095	0.1575654	0.789475	0.5044761
sp Q99068 Alpha-2-ma	8	13	0.0032098	-0.167532	0.1714411	0.7894875	0.504655
sp P62859 40S ribosom	3	14	0.009935	-0.143365	0.1670456	0.7897	0.5048338
sp P60868 40S ribosom	4	18	-0.029271	-0.13784	0.0778202	0.7901625	0.5050127
sp Q00715 Histone H2f	12	95	-0.018361	-0.15486	0.1176288	0.790575	0.5051917
sp P45953 Very long-cl	12	30	-0.031946	-0.128683	0.0625717	0.7907875	0.5053705
sp Q9QUL6 Vesicle-fusi	30	100	0.0328543	-0.065571	0.1291846	0.7917875	0.5057281
sp Q05962 ADP/ATP tr	8	54	-0.043202	-0.116862	0.0286244	0.7918	0.5059069
sp P00406 Cytochrome	4	27	0.0304234	-0.071962	0.1342042	0.7919875	0.5060856
sp O35509 Ras-related	2	7	0.0101944	-0.135382	0.1690147	0.7921375	0.5064424
sp O88767 Protein DJ-1	13	50	0.0145655	-0.12797	0.1614286	0.7922	0.5066206
sp P61107 Ras-related	5	15	0.0197209	-0.107696	0.1542722	0.792475	0.5067987

sp Q63362 NADH dehy	3	5	-0.001416	-0.176355	0.1729993	0.7925	0.5069766
sp Q9JLT0 I Myosin-10 (36	79	-0.036865	-0.125362	0.0503255	0.792925	0.5073321
sp P02401 60S acidic ri	6	27	-0.014424	-0.154011	0.1284366	0.794025	0.5076879
sp P70615 Lamin-B1 O	15	47	0.0085589	-0.151288	0.1705508	0.7943375	0.5078659
sp Q71UE8 NEDD8 OS=	4	17	-0.01643	-0.149207	0.1208407	0.7946375	0.5080438
sp Q6AY30 Probable sa	12	42	-0.040959	-0.117925	0.0340811	0.7947625	0.508399
sp P63029 Translation:	9	36	0.0219823	-0.104043	0.1446153	0.7955375	0.5085768
sp P61980 Heterogene	20	81	-0.043786	-0.113833	0.0230762	0.796525	0.5089324
sp Q01205 Dihydrolipo	10	41	-0.042377	-0.11166	0.0271001	0.7971625	0.5092882
sp Q9EQZ1 TSC22 dom:	2	6	-0.006072	-0.163255	0.1514058	0.797175	0.5096434
sp Q9Z1A6 Vigilin OS=R	14	37	0.0290968	-0.073765	0.1304284	0.7977375	0.5101751
sp Q6P7P5 Basic leucin	4	11	-0.000337	-0.176636	0.1685866	0.798625	0.510706
sp P09495 Tropomyosi	7	17	0.0199943	-0.104805	0.1533931	0.7986625	0.5108829
sp Q9Z2S9 Flotillin-2 O	11	26	-0.00512	-0.170624	0.1653317	0.7991875	0.5115892
sp P61354 60S riboson	9	30	-0.039318	-0.113396	0.0387962	0.799325	0.5119413
sp P63100 Calcineurin	5	13	-0.019417	-0.144513	0.103818	0.8000125	0.5128197
sp O35987 NSFL1 cofac	9	28	-0.02437	-0.138566	0.0899961	0.800275	0.5131699
sp P63159 High mobili	13	49	-0.022276	-0.14462	0.0971536	0.8005625	0.513345
sp O89049 Thioredoxin	8	23	-0.011779	-0.158782	0.1305642	0.800675	0.5135198
sp P25235 Dolichyl-dip	14	42	-0.018778	-0.149066	0.1112633	0.8010625	0.5138694
sp O88453 Scaffold att	8	14	-0.009464	-0.154251	0.1364341	0.8010625	0.5140438
sp P61212 ADP-ribosyl	5	11	-0.002667	-0.161361	0.1616647	0.801575	0.5143925
sp P19511 ATP synthas	8	24	-0.038601	-0.115396	0.0370763	0.8017125	0.5145668
sp P25113 Phosphogly	13	66	0.0169537	-0.117551	0.1511737	0.802625	0.5150896
sp P07632 Superoxide	10	72	-0.022387	-0.13953	0.0954866	0.802725	0.5154373
sp Q6UPE1 Electron tra	4	18	-0.029025	-0.12875	0.0715085	0.80325	0.5159581
sp P85834 Elongation f	13	34	-0.038575	-0.116124	0.0400277	0.8033875	0.5161314
sp P21708 Mitogen-ac	13	57	0.0326709	-0.062059	0.1258419	0.80355	0.5163047
sp P12075 Cytochrome	5	21	0.0274553	-0.075794	0.1311909	0.803775	0.5164778
sp Q793F9 Vacuolar pr	4	10	0.0051089	-0.148544	0.1691778	0.80385	0.5166509
sp Q5RKI0 WD repeat-	17	35	-0.025897	-0.133316	0.0824957	0.80525	0.5171697
sp Q9ES54 Nuclear pro	5	11	-0.002064	-0.166717	0.1641568	0.805375	0.5175157
sp Q6PEC4 S-phase kin	11	66	0.0432576	-0.022506	0.1081398	0.805925	0.5178612
sp Q8CFN2 Cell division	8	26	0.037404	-0.044163	0.1183458	0.8060125	0.5180339
sp Q9QZA2 Programme	13	21	0.029522	-0.067845	0.1266401	0.8067	0.5185517
sp Q6BBI8 Ubiquitin-fc	2	7	-0.001316	-0.168071	0.1677966	0.8067625	0.5187239
sp P60669 Pleckstrin h	10	19	0.0103723	-0.132222	0.1566966	0.8069375	0.5188961
sp Q9ESW0 DNA damag	13	33	-0.035366	-0.117434	0.0457563	0.8069875	0.5190681
sp Q9EPH8 Polyadenyl	19	62	-0.035363	-0.119755	0.0501465	0.8087875	0.5201001
sp Q5XHZ0 Heat shock	9	17	-0.02208	-0.137195	0.0910894	0.8088625	0.5202718
sp P62804 Histone H4	12	100	0.0052575	-0.150969	0.1651999	0.8091875	0.5206147
sp P62982 Ubiquitin-4f	7	47	0.0262555	-0.078962	0.1350925	0.80935	0.5209572
sp Q63570 26S proteas	8	20	-0.011809	-0.150763	0.1280171	0.8103625	0.5218121
sp P62997 Transforme	5	13	-0.015629	-0.146492	0.1092521	0.8107375	0.5219828
sp O70196 Prolyl endo	14	34	-0.014653	-0.144798	0.1197559	0.8113875	0.5223243
sp Q9QY17 Protein kin	7	16	-0.001198	-0.168453	0.1671917	0.8119	0.5230061
sp P62632 Elongation f	14	74	-0.032381	-0.120933	0.0609253	0.81195	0.5231762

sp P19804 Nucleoside	5	28	-0.021033	-0.138376	0.0977248	0.8121875	0.5233462
sp B5DF89 Cullin-3 OS-	11	21	-0.018025	-0.136755	0.101332	0.8125	0.5235162
sp Q63560 Microtubule	18	58	0.0195902	-0.100669	0.1415651	0.8127125	0.5238558
sp P13803 Electron tra	14	28	-0.030728	-0.123574	0.0667861	0.8128375	0.5240254
sp Q6RJR6 Reticulon-3	8	22	-0.004346	-0.156629	0.1508801	0.8131125	0.5243642
sp P63255 Cysteine-ric	4	16	0.0227174	-0.087542	0.1368802	0.81475	0.5258848
sp P63004 Platelet-act	11	25	-0.037457	-0.111626	0.0369129	0.8148625	0.5260532
sp Q75Q39 Mitochondr	10	28	-0.010612	-0.152313	0.1312194	0.814875	0.5263894
sp Q07205 Eukaryotic t	7	17	0.0195155	-0.094286	0.1350511	0.81565	0.5270604
sp P62083 40S ribosom	14	57	-0.028727	-0.128029	0.0686785	0.8167625	0.5278976
sp Q9Z1W6 Protein LYR	3	10	0.001235	-0.15277	0.1588202	0.8170125	0.5282319
sp Q5BK32 FAS-associa	3	7	-0.014437	-0.152029	0.1407171	0.8172	0.5287322
sp Q07439 Heat shock	11	16	-0.014943	-0.14044	0.1141433	0.8172875	0.529065
sp P04642 L-lactate de	19	100	-0.036937	-0.117399	0.0394448	0.81795	0.5295636
sp P62161 Calmodulin	6	66	0.0214735	-0.092144	0.1350802	0.8188375	0.5305581
sp P08082 Clathrin ligh	7	25	-0.034375	-0.119275	0.0463016	0.819325	0.5310539
sp Q9WVCC Septin-7 OS	10	42	-0.040189	-0.109063	0.0274103	0.8200875	0.5317144
sp Q6PEC1 Tubulin-spe	8	15	0.0211283	-0.087461	0.1322031	0.8210625	0.5318796
sp Q68A21 Transcriptic	14	42	-0.039197	-0.111681	0.0314772	0.8216125	0.53221
sp P15146 Microtubulk	37	83	-0.019259	-0.131448	0.0989471	0.8223	0.5327051
sp P00173 Cytochrome	3	16	0.0096119	-0.127975	0.1510572	0.82235	0.5330346
sp Q4QRB4 Tubulin bet	11	84	-0.019346	-0.134257	0.0993081	0.8234125	0.5336936
sp P07153 Dolichyl-dip	21	61	-0.03097	-0.119754	0.0612741	0.8239625	0.5340227
sp Q920J4 Thioredoxin	8	24	0.0194055	-0.095808	0.1369715	0.824575	0.5346795
sp Q5XIM9 T-complex p	24	100	-0.047473	-0.097683	0.0021813	0.82525	0.5348437
sp P18421 Proteasome	7	22	0.0296705	-0.057196	0.1179081	0.826375	0.5353368
sp O88902 Tyrosine-pr	4	10	-0.009885	-0.13989	0.1192921	0.8267125	0.5356651
sp Q5XI73 Rho GDP-di	10	53	0.0189697	-0.092506	0.1366236	0.8273875	0.5358295
sp P38652 Phosphoglu	10	17	0.0007457	-0.15501	0.1592848	0.8280375	0.535994
sp Q07936 Annexin A2	24	100	0.0252767	-0.072151	0.128188	0.8285125	0.536323
sp P70566 Tropomodu	14	31	-0.023363	-0.126056	0.0760599	0.829225	0.5366519
sp Q4KM73 UMP-CMP k	5	11	0.0028504	-0.146607	0.1478499	0.8292875	0.5369803
sp Q6P6S9 Ectonucleos	1	4	0.0119938	-0.119635	0.1401769	0.8297125	0.5371445
sp P05065 Fructose-bi	21	100	0.0211516	-0.089401	0.1269422	0.83075	0.5384543
sp Q9JIL3 II Interleukin	6	11	0.0032381	-0.141861	0.1426667	0.830775	0.5386174
sp Q05982 Nucleoside	5	18	0.0052937	-0.135893	0.1522511	0.83095	0.5387805
sp P63170 Dynein light	2	16	-0.014679	-0.140288	0.1076302	0.831025	0.5389434
sp Q6PCT3 Tumor prot	6	10	-0.008751	-0.140212	0.1226223	0.8311375	0.5392687
sp O55156 CAP-Gly doi	18	41	0.0282815	-0.061386	0.1174317	0.8337	0.5413761
sp B0BN93 26S proteas	7	14	-0.008357	-0.140857	0.1209647	0.8338125	0.5415377
sp P18420 Proteasome	6	28	-0.023554	-0.124515	0.0745714	0.83385	0.5416991
sp Q9EPH2 MARCKS-re	4	21	0.0106674	-0.113456	0.1375099	0.8364875	0.5437914
sp Q64548 Reticulon-1	11	31	-0.034946	-0.10745	0.0381142	0.8374375	0.5445929
sp P37805 Transgelin-3	6	13	-0.009481	-0.136239	0.1177163	0.8375625	0.544753
sp Q5FVM4 Non-POU do	7	22	-0.020779	-0.126322	0.0844791	0.8384125	0.5452333
sp Q64057 Alpha-amin	8	16	-0.005353	-0.137379	0.126724	0.839725	0.5463508
sp O35077 Glycerol-3-p	12	34	0.0140932	-0.102249	0.1343571	0.8400375	0.5466697

sp P63018 Heat shock	25	100	-0.026771	-0.120062	0.064177	0.8400875	0.5468289
sp Q68FQ0 T-complex p	26	86	-0.045671	-0.097412	0.0057826	0.84085	0.5473062
sp P41562 Isocitrate de	13	43	-0.027601	-0.118524	0.0625082	0.8412	0.5477829
sp Q6P7Q4 Lactoylgluta	6	31	-0.003212	-0.144081	0.1366154	0.841825	0.548259
sp P15205 Microtubule	36	100	0.0249105	-0.071888	0.1201322	0.8421125	0.5485758
sp Q5BK63 NADHdehyd	11	41	0.0237719	-0.069864	0.1199125	0.84285	0.5490508
sp P97571 Calpain-1 cat	14	29	0.0101141	-0.114271	0.1320018	0.84335	0.5498407
sp Q68FU3 Electron tra	12	40	-0.021706	-0.124152	0.0822835	0.844075	0.5501561
sp AOJPM9 Eukaryotic t	6	13	0.0166666	-0.093973	0.129848	0.8448875	0.5503142
sp P81155 Voltage-dep	9	28	0.0323355	-0.045845	0.1116485	0.8450875	0.5504721
sp P48004 Proteasome	6	18	-0.021688	-0.121742	0.0821297	0.84545	0.5512601
sp Q2PQA9 Kinesin-1 he	12	31	-0.011378	-0.132793	0.1070709	0.84595	0.5515747
sp Q62847 Gamma-aduc	10	24	0.0068667	-0.123836	0.1363156	0.846325	0.5520459
sp P26284 Pyruvate de	16	70	-0.038137	-0.103423	0.0257244	0.84655	0.5523595
sp Q63028 Alpha-addu	16	40	0.0250247	-0.067058	0.1202707	0.846925	0.5525163
sp Q505J8 Phenylalanyl	12	27	-0.017278	-0.122027	0.08767	0.847125	0.5528295
sp Q9Z2G8 Nucleosom	5	20	0.0042929	-0.124005	0.1362917	0.8475	0.5531424
sp P13086 Succinyl-Co	13	45	-0.041008	-0.102285	0.0175622	0.8477125	0.5537667
sp Q6P9U8 Eukaryotic t	6	24	-0.001862	-0.141843	0.1370463	0.8485875	0.5543898
sp O88994 MOSC dom	6	13	0.0022218	-0.134051	0.1349855	0.8486375	0.5545453
sp Q6AYK8 Eukaryotic t	7	19	0.0046765	-0.123566	0.1389091	0.8486625	0.5547007
sp O35824 DnaJ homol	9	13	-0.002499	-0.137944	0.1284318	0.8487	0.5548559
sp Q6AXT5 Ras-related	5	16	-0.013658	-0.124875	0.0968789	0.8500625	0.5559412
sp Q99PD4 Actin-relate	6	11	-0.008797	-0.130482	0.1074176	0.8504375	0.5564052
sp P70580 Membrane-	4	20	-0.004687	-0.13543	0.1244356	0.85145	0.5571768
sp P62483 Voltage-gat	6	13	0.0023785	-0.130423	0.1348862	0.8526125	0.5582548
sp Q68FS4 Cytosol ami	14	30	-0.014967	-0.126116	0.0933761	0.8537	0.5588693
sp Q4V8F9 Hydroxystei	10	22	0.0041186	-0.124772	0.135677	0.8538625	0.5590229
sp P97546 Neuroplasti	4	8	-0.008385	-0.133033	0.1087563	0.8551	0.5597905
sp P61203 COP9 signal	10	26	0.0181589	-0.079547	0.119739	0.8552375	0.5599438
sp P11915 Non-specific	12	42	-0.008087	-0.134804	0.1124936	0.8557875	0.5604035
sp Q5RJR8 Leucine-rich	13	40	-0.027022	-0.110432	0.0611043	0.85655	0.5608625
sp Q5XI72 Eukaryotic t	9	44	0.0234005	-0.070949	0.1141419	0.856875	0.5614734
sp Q499N6 UBX domain	4	9	-0.001911	-0.132686	0.1276106	0.85705	0.5616259
sp P17220 Proteasome	5	16	0.0080746	-0.108326	0.1252763	0.8600625	0.5631533
sp P68511 14-3-3 prot	13	46	-0.032417	-0.105693	0.0400376	0.861375	0.5642194
sp Q8VHF5 Citrate synt	18	86	-0.031897	-0.103681	0.0442878	0.8633125	0.565887
sp Q02253 Methylmalic	20	64	0.0263518	-0.060852	0.108995	0.86435	0.5660387
sp Q62951 Dihydropyri	7	20	-0.011306	-0.121813	0.098493	0.864975	0.5672484
sp Q6TUG0 DnaJ homol	6	17	0.001514	-0.123275	0.130358	0.8661625	0.568152
sp Q9JK11 Reticulon-4	30	100	0.0321804	-0.0392	0.1041795	0.86665	0.568453
sp Q9HB97 Alpha-parvi	5	15	-0.002605	-0.127951	0.1212829	0.8668875	0.5687536
sp Q5EB81 NADH-cyto	10	20	0.0045393	-0.118307	0.1265132	0.867975	0.569504
sp P63329 Serine/thre	6	14	0.0116063	-0.095694	0.1183303	0.868	0.5696539
sp Q62826 Heterogene	17	40	-0.024171	-0.109464	0.0608239	0.8683625	0.5701031
sp P16638 ATP-citrate	33	100	0.0007544	-0.132067	0.1290132	0.868575	0.570402
sp B2RZ78 Vacuolar pr	7	17	-0.024437	-0.105501	0.06164	0.8691	0.5707008

sp P62828 GTP-binding	9	27	-0.018851	-0.115134	0.0794653	0.8701125	0.571149
sp P38983 40S ribosom	9	51	-0.002085	-0.126081	0.1278333	0.8705	0.5712985
sp P36876 Serine/thre	7	20	-0.025128	-0.104511	0.0568304	0.87215	0.5730848
sp P21571 ATP synthas	7	28	0.009261	-0.101049	0.1232845	0.8723	0.5733816
sp P63047 Sulfotransf	3	12	0.0189181	-0.07282	0.1125116	0.8723125	0.5735298
sp Q4V7C6 GMP synthet	7	20	-0.007867	-0.121152	0.1045546	0.8724875	0.573678
sp O88563 Canalicular	5	12	-0.01391	-0.119032	0.0893465	0.873025	0.5739741
sp P63086 Mitogen-ac	7	17	0.011984	-0.092207	0.118828	0.87425	0.5750092
sp P11442 Clathrin hea	37	100	-0.032337	-0.103413	0.0367508	0.874275	0.5751568
sp P52873 Pyruvate ca	18	50	-0.026148	-0.106795	0.0523197	0.8749	0.5758932
sp P11884 Aldehyde de	18	85	0.0173697	-0.078018	0.1137286	0.8750875	0.5760403
sp Q63083 Nucleobind	10	26	-0.015733	-0.112799	0.08207	0.8751375	0.5761873
sp Q1JU68 Eukaryotic t	18	47	-0.021041	-0.107871	0.0692219	0.8755875	0.5766278
sp Q66HF1 NADH-ubiqu	20	65	0.0249109	-0.056085	0.1084653	0.8769875	0.5775077
sp Q5RJQ4 NAD-depen	5	21	-0.00106	-0.125541	0.1234805	0.87825	0.578823
sp Q62940 E3 ubiquitin	16	48	0.0269333	-0.047976	0.1003853	0.878275	0.5789688
sp B5DFC8 Eukaryotic t	9	21	-0.008105	-0.118026	0.10198	0.879425	0.5796972
sp B2RZ37 Receptor ex	5	16	-0.013522	-0.117848	0.0849459	0.8799375	0.5799883
sp Q9WTT6 Guanine de	21	66	0.0084025	-0.099418	0.1191528	0.880125	0.5805696
sp Q63507 60S ribosom	7	25	-0.004463	-0.122544	0.112821	0.8809625	0.5810046
sp P15999 ATP synthas	24	100	-0.042462	-0.091576	0.0080563	0.8818125	0.5818735
sp Q63598 Plastin-3 OS	13	32	0.0216322	-0.061544	0.1035293	0.8833625	0.5824524
sp P84083 ADP-ribosyl	4	12	-0.004852	-0.116422	0.1063643	0.8834375	0.5827418
sp P41542 General ves	15	31	-0.015462	-0.10815	0.0752581	0.8849125	0.5837544
sp Q5XI32 F-actin-cap	9	23	-0.018612	-0.107071	0.0698229	0.8849625	0.5840428
sp P13383 Nucleolin O	20	76	0.0273035	-0.047507	0.1023463	0.88525	0.5844745
sp P16617 Phosphogly	27	90	-0.007589	-0.118393	0.0987232	0.885575	0.584762
sp P09606 Glutamine s	12	18	0.0097198	-0.096761	0.1110433	0.8857625	0.5849056
sp Q9Z269 Vesicle-assoc	7	26	-0.012026	-0.113757	0.0872201	0.886425	0.5853365
sp P25809 Creatine kir	10	34	-0.012824	-0.112953	0.0847307	0.8879625	0.5859113
sp Q9WU82 Catenin bet	15	45	0.020778	-0.065623	0.1036521	0.8887375	0.5866294
sp Q63355 Myosin-Ic C	23	49	0.0096905	-0.093501	0.1128952	0.8891875	0.5869163
sp P11730 Calcium/cal	6	25	0.0093567	-0.095172	0.1102303	0.889675	0.5872031
sp P36972 Adenine ph	7	23	-0.000808	-0.117334	0.1139026	0.889825	0.5876325
sp Q68FX0 Isocitrate d	7	35	-0.023372	-0.102446	0.0560932	0.889875	0.5877754
sp Q9EPJ0 Nuclear ubi	3	8	-0.003559	-0.112743	0.109702	0.891475	0.588917
sp Q2TA68 Dynamin-lik	18	42	0.0231978	-0.054761	0.1000613	0.8942875	0.5911928
sp P52296 Importin su	15	28	0.0127484	-0.08116	0.1051324	0.8943	0.5913345
sp Q5SGE0 Leucine-rich	22	43	-0.016826	-0.103958	0.0673372	0.895225	0.592183
sp P48721 Stress-70 pr	23	85	-0.031302	-0.096544	0.0326543	0.8954625	0.5926063
sp Q6AYN4 Phytanoyl-C	9	27	-0.002996	-0.114127	0.1072234	0.8956625	0.592888
sp P62815 V-type prot	13	36	0.0260975	-0.042489	0.0977738	0.89575	0.5930287
sp P35704 Peroxiredox	8	36	0.0047018	-0.10183	0.1145007	0.8960625	0.5934504
sp Q64537 Calpain sma	9	16	0.0144674	-0.075594	0.1045664	0.896175	0.593731
sp O35264 Platelet-act	6	18	0.0031604	-0.107318	0.1131071	0.896975	0.5944314
sp Q9JLJ3 4-trimethyl	13	26	0.0084021	-0.087801	0.1090083	0.8979625	0.5952701
sp P32551 Cytochrome	12	48	-0.020009	-0.101269	0.0652948	0.8981875	0.5954098

sp P04762 Catalase OS	20	45	0.0014446	-0.113475	0.1117625	0.8987875	0.5959675
sp Q09167 Serine/arginine-rich	5	8	0.0002518	-0.110485	0.1084747	0.90045	0.5974973
sp A0JPJ7 C-Obg-like AT	13	36	0.0056517	-0.098837	0.109585	0.9014625	0.5980524
sp Q9JHU0 Dihydropyridine-binding protein	20	62	0.0135837	-0.077815	0.1046138	0.90225	0.5983299
sp O35567 Bifunctional protein	19	67	-0.011637	-0.107306	0.082637	0.9023	0.5986072
sp Q4FZT9 26S proteasome-associated protein	13	37	0.0175841	-0.063404	0.1004156	0.9030375	0.5991612
sp P13471 40S ribosomal protein S16	7	24	0.0019976	-0.101088	0.1069486	0.9031125	0.5994378
sp Q5I0G4 Glycyl-tRNA ligase	15	31	0.0020258	-0.106621	0.1100806	0.904075	0.5999906
sp O88506 STE20/SPS1 kinase	8	18	-0.005228	-0.104581	0.0968272	0.9043125	0.6008172
sp P54313 Guanine nucleotide-exchange factor	5	22	0.0068734	-0.091742	0.1052153	0.9044375	0.601092
sp Q4KM49 Tyrosyl-tRNA ligase	23	73	-0.038007	-0.08817	0.0125077	0.904775	0.6015035
sp P49134 Integrin beta-1	10	32	0.0107213	-0.08033	0.1014293	0.904925	0.6017775
sp Q9EQX9 Ubiquitin-conjugating enzyme E2C	7	24	0.0126561	-0.076985	0.1031559	0.9055125	0.6023247
sp P15791 Calcium/calmodulin-binding protein	6	22	-0.012859	-0.101512	0.074877	0.9061375	0.6031435
sp Q5FVQ4 Malectin OS	8	17	0.0041834	-0.097711	0.1028892	0.907225	0.6039601
sp Q6RUV5 Ras-related GTPase	8	32	0.0262536	-0.040551	0.0933447	0.907925	0.6049102
sp P08081 Clathrin light chain	5	15	-0.015493	-0.098623	0.0673921	0.9081	0.605451
sp P67779 Prohibitin C	11	41	0.0163164	-0.065827	0.1022625	0.9087875	0.6059907
sp Q4G061 Eukaryotic translation initiation factor 4B	13	28	0.0009629	-0.106607	0.1063028	0.9088	0.6061254
sp B2RYG6 Ubiquitin thioesterase-like protein	10	28	0.0031009	-0.099755	0.1055761	0.9095875	0.6066643
sp P97852 Peroxisomal membrane protein	13	31	0.0045965	-0.093495	0.104039	0.9098625	0.6070678
sp O70351 3-hydroxyacyl-CoA thioesterase	7	28	0.007031	-0.090954	0.1008027	0.910075	0.6072022
sp P47942 Dihydropyridine-binding protein	22	100	-0.007219	-0.102154	0.0910079	0.9102625	0.6073365
sp B0K020 CDGSH iron-sulfur protein	5	19	0.0054927	-0.096941	0.1038883	0.910975	0.6080072
sp Q5XIF3 NADH dehydrogenase 1	7	21	0.0108613	-0.075953	0.1031557	0.9114875	0.6085428
sp Q63269 Inositol 1,4,5-trisphosphate receptor	27	62	0.0071857	-0.089495	0.1031778	0.91275	0.6094789
sp Q6NYB7 Ras-related GTPase	5	11	0.0120688	-0.074119	0.0997266	0.9137625	0.6100128
sp P59215 Guanine nucleotide-exchange factor	9	22	0.002578	-0.09959	0.102024	0.914575	0.6106798
sp P37285 Kinesin light chain	16	43	0.0154103	-0.066434	0.0985814	0.91485	0.6112121
sp P08461 Dihydrolipoyl acetyltransferase	17	75	-0.017166	-0.098508	0.061249	0.9162	0.6133279
sp Q9EQS0 Transaldolase	22	81	0.0218662	-0.0473	0.0957393	0.9180875	0.6141182
sp P50475 Alanyl-tRNA ligase	27	81	0.0038048	-0.093141	0.100992	0.9187625	0.6149074
sp Q9Z2L0 Voltage-dependent anion channel	15	68	0.0230267	-0.049253	0.0913039	0.919425	0.6153016
sp P35434 ATP synthase subunit F	3	12	-0.001555	-0.102228	0.101091	0.919475	0.6154329
sp Q01986 Dual specificity phosphatase	8	25	-0.00516	-0.099981	0.0871118	0.9204375	0.6159581
sp Q6AYS8 Estradiol 17-beta-glucuronidase	12	32	0.0060387	-0.084315	0.0986355	0.9217375	0.6168759
sp P63102 14-3-3 protein	11	66	0.0221562	-0.046644	0.0921522	0.9243625	0.6190954
sp Q63377 Sodium/potassium ATPase alpha-1 subunit	8	33	-0.016791	-0.092257	0.0571882	0.9270625	0.6209164
sp P21575 Dynamin-1	16	46	0.0194199	-0.050893	0.0892038	0.92725	0.6211759
sp P13264 Glutaminase	14	34	-0.001723	-0.099366	0.0923933	0.9275375	0.6215645
sp Q07009 Calpain-2 catalytic subunit	18	75	0.0037106	-0.089661	0.0988414	0.9275875	0.6216939
sp Q5XIT1 Microtubule-associated protein tau	5	19	0.00621	-0.082688	0.0911754	0.928425	0.6224692
sp Q64560 Tripeptidyl-peptidase I	19	45	0.0126619	-0.066349	0.0921099	0.9311125	0.624144
sp P14408 Fumarate hydratase	11	28	-0.00453	-0.094856	0.0845311	0.9322125	0.6246595
sp P85968 6-phosphogluconate dehydrogenase	13	43	-0.011671	-0.09184	0.0702315	0.9324125	0.6247884
sp P10860 Glutamate decarboxylase	24	100	-0.035934	-0.082347	0.0119644	0.933075	0.6249174
sp Q9JJ54 Heterogeneous nuclear ribonucleoprotein K	10	38	-9.07E-05	-0.093703	0.0965965	0.9353375	0.6274843

sp P61765 Syntaxin-binding protein 1	17	53	0.0119944	-0.065297	0.0900078	0.9359625	0.6279951
sp P05765 40S ribosomal protein S19	3	15	-0.002231	-0.09072	0.0872018	0.937175	0.6290143
sp Q9QWN8 Spectrin beta chain	15	36	0.0178033	-0.049803	0.0864033	0.9390625	0.6305391
sp Q7TPB1 T-complex protein 1 subunit beta	25	90	-0.027857	-0.081205	0.0255794	0.9407375	0.6321841
sp Q6P799 Seryl-tRNA transferase	15	56	0.0026539	-0.082818	0.0909925	0.940875	0.6324362
sp Q66HA6 ADP-ribosyl cyclase 1	10	44	-0.006	-0.088214	0.0776304	0.9420375	0.6338178
sp P28023 Dynactin subunit DHC1	27	69	-0.019222	-0.082679	0.0459551	0.9425875	0.6341936
sp P62870 Transcriptic	8	26	0.0098403	-0.064575	0.0859805	0.9462875	0.6364462
sp P05370 Glucose-6-phosphate isomerase	20	46	0.0070779	-0.071133	0.0872448	0.946925	0.6376915
sp Q62910 Synaptosomal-associated protein 25 kDa	20	44	0.0042548	-0.074907	0.0859393	0.9471625	0.6378157
sp P61589 Transformin	11	38	0.0223807	-0.034998	0.0832449	0.94805	0.6389305
sp Q3T1J1 Eukaryotic translation initiation factor 4E	8	46	-0.009373	-0.085834	0.0678867	0.948375	0.639301
sp Q920L2 Succinate dehydrogenase complex, subunit L2	15	33	-0.001263	-0.087341	0.0839322	0.9484	0.6394244
sp Q5XIG8 Serine-threonine kinase	9	28	0.0036367	-0.076992	0.0835615	0.94855	0.6397941
sp P05708 Hexokinase	26	100	0.0009098	-0.084872	0.0862607	0.9486125	0.6399172
sp P29315 Ribonuclease	12	35	0.0107425	-0.063516	0.0821274	0.9494	0.6406548
sp Q9QYF3 Myosin-Va	19	37	-0.004321	-0.083386	0.0762682	0.950025	0.6417567
sp Q06647 ATP synthase	10	36	-0.01352	-0.081652	0.0539408	0.950775	0.642732
sp P10888 Cytochrome c oxidase	9	25	-0.004114	-0.083213	0.0737315	0.9541875	0.6455228
sp Q63716 Peroxiredoxin 1	15	80	0.0097862	-0.060967	0.0806772	0.9563625	0.6481696
sp Q68FY0 Cytochrome c oxidase	12	53	-0.023521	-0.078084	0.030645	0.9570125	0.6488862
sp Q6P6R2 Dihydrolipoamide acetyltransferase	14	50	-0.002641	-0.08343	0.0764295	0.9575375	0.6497199
sp A7VJC2 Heterogeneous nuclear ribonucleoprotein C	13	57	0.0055898	-0.069049	0.0807459	0.95865	0.6501956
sp P28480 T-complex protein 1 subunit beta	28	80	-0.020911	-0.077644	0.0333935	0.9610375	0.6526822
sp Q5XIH7 Prohibitin-2	18	61	-0.016727	-0.074791	0.0418679	0.9649125	0.6557365
sp P05712 Ras-related GTPase	8	27	-0.0058	-0.077223	0.0630604	0.9663125	0.6570227
sp Q08163 Adenylyl cyclase	17	57	-0.022382	-0.074311	0.0299637	0.966975	0.6584179
sp P00507 Aspartate aminotransferase	23	95	-0.015068	-0.072029	0.0452828	0.9702	0.6611876
sp P47860 6-phosphofructokinase	26	100	-0.003193	-0.072012	0.0691555	0.9704375	0.6616469
sp Q62952 Dihydropyridine receptor 1D	17	76	0.0041035	-0.066976	0.0728872	0.9705625	0.6618763
sp Q3KR86 Mitochondrial ribosomal protein L13	28	78	-0.003461	-0.07382	0.0662139	0.9713	0.6629054
sp P10960 Sulfated glycoprotein 2	11	60	0.0052544	-0.06527	0.0735092	0.9720125	0.6634759
sp P48037 Annexin A6	30	100	0.0220582	-0.024772	0.0687846	0.97735	0.6694486
sp P97536 Cullin-associating factor 1	22	71	0.0064073	-0.055931	0.0674868	0.9783375	0.6706724
sp P61983 14-3-3 protein epsilon	9	53	-0.017273	-0.069146	0.0332107	0.978775	0.6719996
sp P09527 Ras-related GTPase	12	41	0.0070848	-0.053469	0.0679579	0.979325	0.6732079
sp P46462 Transitional endoplasmic reticulum membrane protein	28	100	0.0206373	-0.027136	0.0666145	0.9795375	0.6737548
sp P10719 ATP synthase	19	100	-0.025102	-0.067335	0.0166905	0.9799375	0.6747353
sp P11951 Cytochrome c oxidase	6	25	-0.003882	-0.066342	0.0596526	0.9804375	0.6758191
sp O88600 Heat shock protein 70 kDa	33	83	-0.016039	-0.066869	0.0351379	0.9810375	0.676682
sp Q5U300 Ubiquitin-ligase complex subunit R3	30	100	0.0013837	-0.060992	0.062806	0.98125	0.6771122
sp P34926 Microtubule-associated protein tau	39	100	-0.003734	-0.066314	0.0579515	0.981425	0.6775415
sp P04636 Malate dehydrogenase	18	100	-0.009202	-0.064835	0.0459032	0.98185	0.6782906
sp P85515 Alpha-centromere protein	14	42	-0.005185	-0.066792	0.0544286	0.9820125	0.6783974
sp Q6P502 T-complex protein 1 subunit alpha	28	92	-0.016712	-0.064353	0.0304935	0.984175	0.6815795
sp P38650 Cytoplasmic dynein 1	46	100	-0.018012	-0.065074	0.0283088	0.9848	0.6829443
sp P68255 14-3-3 protein epsilon	12	33	-0.005392	-0.062362	0.0514583	0.9865375	0.6844063

sp P14668 Annexin A5	24	100	0.0126425	-0.033509	0.0594488	0.989325	0.6884351
sp Q6P6V0 Glucose-6- β	18	67	-0.00281	-0.057822	0.0551746	0.9898125	0.6890487
sp Q9ER34 Aconitate h	30	100	-0.00436	-0.054026	0.0475859	0.991775	0.6922931
sp P50137 Transketola	28	100	-0.004547	-0.054962	0.0472899	0.992325	0.6931966
sp P47858 6-phosphof	18	65	-0.008681	-0.055001	0.0382405	0.99255	0.6936969
sp Q6AYH5 Dynactin su	17	63	-0.009605	-0.056605	0.0376631	0.993025	0.6949911

Accession	Name	Peptides	Spectra	Mean Log ₂ F	I-95% CI	u-95% CI	IFDR	gFDR
sp P14046	Alpha-1-inh	6	12	-1.858501	-2.516495	-1.210852	0.0001125	0.0001125
sp P08932	T-kininogen	3	5	0.816442	0.4434611	1.2028821	0.0003125	0.0002125
sp Q6P7A9	Lysosomal α	5	11	0.395494	0.2291513	0.5612608	0.0004375	0.0002875
sp P04639	Apolipoprot	19	40	0.6681859	0.3490578	0.9831805	0.0009	0.0004406
sp P22791	Hydroxyme	8	10	0.3204246	0.1603425	0.4785332	0.0019625	0.000745
sp P17475	Alpha-1-ant	19	50	0.4842831	0.2350939	0.7422014	0.002075	0.0009667
sp Q9QX79	Fetuin-B OS	9	18	0.3679312	0.1799857	0.558146	0.0023875	0.0011696
sp P01048	T-kininogen	3	8	0.8630611	0.3653278	1.368615	0.0026125	0.00135
sp P04276	Vitamin D-b	17	22	-0.367573	-0.566721	-0.169997	0.004025	0.0016472
sp Q80WL1	Gliomedin C	3	3	-0.453352	-0.826281	-0.107127	0.0117	0.0026525
sp Q9ESB5	N-terminal	3	4	0.7931817	0.2369261	1.3771669	0.01205	0.0035068
sp P20759	Ig gamma-1	2	5	0.3097443	0.0974196	0.5357222	0.014625	0.0044333
sp P39032	60S riboson	3	8	0.2677986	0.0926407	0.4499649	0.015525	0.0052865
sp Q63416	Inter-alpha-	10	19	0.2695997	0.0887707	0.446548	0.0165	0.0060875
sp P02651	Apolipoprot	10	16	0.3394625	0.0840482	0.5900039	0.02015	0.007025
sp P19939	Apolipoprot	2	4	-0.381163	-0.688157	-0.074161	0.024625	0.008125
sp Q03626	Murinoglob	8	13	-0.485643	-0.90293	-0.057735	0.0276375	0.0092728
sp Q9Z217 !	Synaptic ve	1	2	-0.344502	-0.642125	-0.050179	0.0287125	0.0103528
sp P10959	Liver carbo	9	14	0.3609927	0.0477958	0.679224	0.0296125	0.0113664
sp P83953	Importin su	1	2	-0.688511	-1.313314	-0.017481	0.0322875	0.0124125
sp P00787	Cathepsin B	5	9	0.208405	0.0627324	0.3564388	0.0330875	0.013397
sp P02764	Alpha-1-acid	5	8	0.3157604	0.0506587	0.5810325	0.0332875	0.0143011
sp P50442	Glycine ami	1	2	0.7343147	0.0175289	1.4406061	0.033425	0.0151326
sp P20760	Ig gamma-2	11	24	0.5745579	-0.00175	1.1302206	0.0379	0.0160813
sp P11167	Solute carri	3	6	-0.225425	-0.405293	-0.051728	0.0386875	0.0169855
sp Q6AYU3	DnaJ homol	2	5	0.3410639	0.025202	0.6597062	0.04085	0.0179034
sp Q63041	Alpha-1-ma	18	29	-0.29475	-0.562625	-0.045234	0.041825	0.0187894
sp Q63945	Protein SET	3	6	0.3796278	0.0149608	0.7507103	0.04345	0.0196701
sp P14882	Propionyl-C	5	6	-0.219414	-0.397183	-0.04193	0.04815	0.0206522
sp P02625	Parvalbumin	4	6	-0.410032	-0.838192	-0.000915	0.0488125	0.0215908
sp Q921A4	Cytoglobin	1	2	0.5162774	-0.049718	1.0643511	0.05295	0.0226024
sp Q6P5P3	Tetratricope	1	3	0.4161388	-0.022843	0.8563517	0.053375	0.0235641
sp O88370	Phosphatid	1	5	-0.295105	-0.581685	-0.026237	0.0539375	0.0244845
sp P21818	Stathmin-2	1	2	-0.284376	-0.566294	-0.016663	0.0544375	0.0253654
sp P85845	Fascin OS=F	7	12	-0.208963	-0.387334	-0.034174	0.056125	0.0262443
sp P00762	Anionic try	1	2	-0.436827	-0.901537	0.0345817	0.0569625	0.0270976
sp Q499N6	UBX domai	1	2	0.3871182	-0.0158	0.7966929	0.058175	0.0279375
sp P24090	Alpha-2-HS-	12	45	-0.345725	-0.71541	0.0045617	0.05955	0.0287694
sp P15865	Histone H1.	15	46	0.3450369	-0.013423	0.7073244	0.0617	0.0296138
sp Q75WE7	von Willebr	3	3	-0.344223	-0.682577	0.0131979	0.062925	0.0304466
sp P14141	Carbonic an	1	2	-1.062518	-2.342217	0.279319	0.0641375	0.0312683
sp P17078	60S riboson	5	6	0.1974384	0.0227404	0.3783252	0.0673625	0.0321277
sp P20762	Ig gamma-2	4	5	0.4676666	-0.085254	1.0133731	0.0679125	0.0329599
sp Q6P7S1	Acid cerami	6	7	0.2354789	0.0069258	0.4621365	0.07165	0.0338392
sp Q6P734	Plasma prot	1	2	-0.409786	-0.950552	0.1295661	0.0780875	0.0348225

sp Q63618 Espin OS=R	2	2	-0.379648	-0.842907	0.0873513	0.083025	0.0358704
sp P20059 Hemopexin	16	30	-0.21528	-0.43219	-0.000933	0.0839375	0.0368931
sp Q9WUL0 DNA topoisomerase I	2	2	0.34456	-0.0837	0.7725299	0.0873625	0.0379445
sp Q69BT7 Trafficking protein	1	3	-0.243682	-0.50802	0.0222123	0.08865	0.0389793
sp P51146 Ras-related GTPase	1	2	0.3006167	-0.046778	0.6599169	0.090175	0.0400033
sp Q6AYC4 Macrophagelike receptor	11	18	0.3890062	-0.097627	0.8875687	0.0914625	0.0410123
sp P84245 Histone H3-like protein	2	2	0.3121291	-0.110445	0.7374298	0.0917875	0.0419887
sp B5DFC9 Nidogen-2 C-terminal domain	17	26	0.1505424	0.0221775	0.2746351	0.093	0.0429512
sp Q5XIU9 Membrane protein	2	2	0.4189814	-0.121008	0.9941784	0.09305	0.0438789
sp Q5RKI8 ATP-binding cassette	2	4	0.2387986	-0.027541	0.4967378	0.0939625	0.0447895
sp Q925B3 Transient receptor potential channel	3	3	-0.262467	-0.565916	0.0386621	0.0968625	0.0457194
sp Q64548 Reticulon-1	7	11	0.1389622	0.0355317	0.2478908	0.0969875	0.0466189
sp Q63625 PHD and RII domains	2	2	0.5009879	-0.196011	1.1911157	0.0973875	0.0474942
sp Q9QZ76 Myoglobin-like protein	5	9	-1.117661	-2.807736	0.5781407	0.101475	0.0484091
sp P02696 Retinol-binding protein	2	2	-0.350413	-0.810098	0.1022763	0.10185	0.0492998
sp Q62784 Type I inositol transporter	1	2	-0.468841	-1.114168	0.1907132	0.102525	0.0501723
sp P49186 Mitogen-activated protein kinase	2	2	0.3159628	-0.074828	0.7205118	0.10295	0.0510236
sp P24268 Cathepsin D	16	34	0.1309001	0.0323361	0.2299227	0.1045875	0.0518738
sp P06765 Platelet factor 4	3	4	0.4379077	-0.171001	1.0525424	0.1048375	0.0527014
sp P22734 Catechol O-methyltransferase	3	6	0.2142907	-0.028076	0.4477212	0.1053125	0.0535108
sp Q05140 Clathrin coat protein	3	3	-0.248044	-0.527274	0.0467542	0.1067375	0.0543172
sp P29411 GTP:AMP phosphotransferase	6	9	0.1571055	0.0082479	0.2979888	0.1105625	0.0551567
sp O35820 Deoxyribonucleic acid binding protein	2	2	-0.34838	-0.818196	0.1126641	0.1107125	0.0559737
sp P84100 60S ribosomal protein L13	5	10	0.1717008	-0.002844	0.3387293	0.1112125	0.0567743
sp Q6AXQ8 Meiosis-specific protein	2	2	0.3473077	-0.225731	0.8749138	0.1129	0.0575761
sp P52632 Signal transduction protein	1	3	-0.317811	-0.809341	0.1757298	0.1131	0.0583581
sp P08649 Complement component C3	4	4	-0.201482	-0.435996	0.0289569	0.113725	0.0591271
sp Q923J6 Dynein heavy chain	3	3	-0.257834	-0.596982	0.0696201	0.11475	0.059889
sp P19944 60S acidic ribosomal protein L14	2	4	0.3055435	-0.112551	0.7111912	0.116525	0.0606544
sp P69736 Endothelial nitric oxide synthase	4	5	-0.202377	-0.424444	0.0312028	0.1183375	0.0614235
sp Q62930 Complement component C1q	4	6	-0.18968	-0.397982	0.016428	0.118775	0.0621781
sp P48199 C-reactive protein	3	6	0.2638457	-0.077658	0.5987425	0.120925	0.0629411
sp Q29RW1 Myosin-4 O-linkage beta-N-acetylgalactosaminidase	26	36	-0.891175	-2.338797	0.593472	0.1219625	0.0636978
sp Q499S9 Rhomboid family protein	3	3	0.2371979	-0.060187	0.5069896	0.1230625	0.0644492
sp P17764 Acetyl-CoA acyltransferase	10	17	-0.161979	-0.324742	0.0071152	0.1234	0.0651861
sp P22199 Mineralocorticoid receptor	2	2	0.4288339	-0.228608	1.0900572	0.1241375	0.0659139
sp O54922 Exocyst complex component	2	2	-0.389576	-0.973669	0.183455	0.1254125	0.0666395
sp Q5XIC0 Peroxisomal membrane protein	2	2	0.4328682	-0.274863	1.2012077	0.1275125	0.0673729
sp Q66HC5 Nuclear pore protein	2	2	-0.345667	-0.878599	0.224149	0.1301375	0.0681201
sp P23680 Serum amyloid A	2	4	0.3070631	-0.120539	0.7508271	0.13125	0.0688628
sp B0BN85 Suppressor of P-element insertion	2	3	0.3270922	-0.181793	0.8674118	0.1339	0.069619
sp Q9JMD2 Scm-like wingless protein	2	2	-0.190219	-0.451406	0.0544997	0.1360625	0.0703828
sp P07150 Annexin A1	14	21	-0.193237	-0.423468	0.046377	0.1364125	0.0711331
sp Q9WUH4 Four and a half finger protein	2	4	-0.303356	-0.757894	0.1294334	0.136425	0.0718667
sp Q63679 Lysine-specific demethylase	1	2	0.4310004	-0.255226	1.1215065	0.136775	0.0725879
sp P07308 Acyl-CoA dehydrogenase	1	2	-0.297211	-0.712559	0.1430613	0.1369	0.0732946
sp P12785 Fatty acid synthase	44	71	-0.120903	-0.219449	-0.020756	0.1382625	0.0740008

sp Q3T1G7 Conserved c	2	2	0.2953093	-0.138754	0.7386364	0.1408	0.0747191
sp Q91V33 KH domain-	8	9	-0.165192	-0.344245	0.0177078	0.1415375	0.0754299
sp Q63132 Proto-onco	2	2	-0.359704	-1.012675	0.2958333	0.1417375	0.0761279
sp Q6MG64 Protein G7c	1	2	0.2698507	-0.194337	0.7244226	0.14395	0.0768344
sp P53042 Serine/thre	2	3	-0.297528	-0.765792	0.1421111	0.1453875	0.0775411
sp Q80WE1 Fragile X me	2	4	0.2708105	-0.133037	0.6790555	0.1471125	0.078251
sp Q9WTVO Prolactin re	2	3	-0.209398	-0.499103	0.0702637	0.1491875	0.0789676
sp P55051 Fatty acid-b	3	6	0.2677651	-0.135443	0.6705393	0.1500625	0.0796785
sp Q9R1K2 Teneurin-2	2	2	0.2849628	-0.184097	0.7580479	0.1504125	0.0803788
sp P34067 Proteasome	1	3	0.2310769	-0.082866	0.5435313	0.1506375	0.0810676
sp P00564 Creatine kir	10	14	-0.678361	-1.927465	0.5545816	0.1523625	0.0817598
sp Q99ND9 RWD domai	2	2	0.5029366	-0.402817	1.4103785	0.152425	0.0824393
sp Q8VD52 Pyridoxal ph	1	2	0.2054681	-0.060854	0.4863318	0.1532875	0.083114
sp Q09429 ATP-binding	3	3	-0.70887	-2.123235	0.5757568	0.1555625	0.0837975
sp P18445 60S riboson	6	8	0.1441667	-0.002238	0.2961553	0.155675	0.0844693
sp P25286 V-type prot	6	9	-0.177939	-0.400829	0.0349421	0.1573875	0.0851444
sp Q8VIF7 Selenium-bi	8	10	0.1457039	-0.007728	0.2994884	0.1595625	0.0858272
sp Q5XIM5 Protein CD\	2	2	0.3505392	-0.288661	0.9894527	0.1606125	0.086507
sp P08753 Guanine nu	1	2	-0.282197	-0.749392	0.1850809	0.1611	0.0871791
sp Q63016 Large neutr	3	6	0.1731879	-0.039948	0.3883573	0.1627875	0.0878541
sp Q4QQW Putative ph	3	6	0.1944789	-0.059206	0.4537656	0.163075	0.0885198
sp Q68FT1 Ubiquinone	2	2	-0.285977	-0.869331	0.2858056	0.1647625	0.0891886
sp Q64663 P2X purinoc	2	3	0.2007199	-0.107562	0.503465	0.1666125	0.0898618
sp Q9ERB4 Versican co	2	2	0.4710253	-0.398914	1.3719913	0.1683625	0.0905386
sp P04550 Parathymos	1	3	0.2036789	-0.08283	0.4951149	0.1685875	0.0912057
sp Q63198 Contactin-1	6	10	-0.138988	-0.284598	0.005948	0.169275	0.0918673
sp O89107 Deoxyribon	2	2	0.3723245	-0.268407	1.0505949	0.169775	0.092522
sp Q9WVR7 Protein pho	2	4	0.2053197	-0.090771	0.5069883	0.1704625	0.0931715
sp O88563 Canicular	4	5	0.2091297	-0.115971	0.5245926	0.1722875	0.0938253
sp Q63448 Peroxisoma	2	5	0.2115654	-0.090272	0.5311011	0.1728375	0.094473
sp B5DFC8 Eukaryotic t	4	5	0.1908706	-0.073238	0.4480299	0.174	0.0951195
sp Q4QQR9 Protein MEI	1	2	-0.270514	-0.722785	0.1874678	0.176	0.0957718
sp Q9EPA0 Dystrophin-	10	17	0.1395681	-0.013858	0.2905851	0.1766875	0.0964191
sp P47728 Calretinin O	8	15	0.1867706	-0.083726	0.4414684	0.176725	0.0970564
sp Q99068 Alpha-2-ma	2	2	-0.226318	-0.581234	0.1187477	0.178725	0.0976995
sp P19132 Ferritin hea	3	4	0.2050198	-0.100101	0.5050469	0.178825	0.0983333
sp Q5XI07 Lipoma-pre	1	3	0.2721577	-0.164099	0.7260853	0.1795625	0.098963
sp Q05096 Myosin-Ib C	5	6	0.2504351	-0.141775	0.6664608	0.1797875	0.0995847
sp Q4G009 Malignant T	2	2	-0.205811	-0.516868	0.1144787	0.1821	0.1002146
sp Q09167 Serine/argin	1	3	0.2068928	-0.11397	0.5278039	0.182375	0.100837
sp Q91ZN1 Coronin-1A	3	3	-0.187542	-0.462837	0.0849843	0.1832625	0.1014568
sp P53534 Glycogen ph	28	54	0.1131579	0.0123213	0.2169338	0.183975	0.1020726
sp Q62935 von Willebr	3	3	-0.287563	-0.78687	0.2206828	0.184025	0.1026796
sp Q3KRC6 Leucine-rich	2	2	0.280376	-0.206856	0.7926572	0.1858375	0.1032911
sp P05369 Farnesyl py	6	9	-0.142493	-0.310719	0.0326765	0.1863	0.103897
sp P0C6C0 A-kinase an	2	3	0.1821747	-0.115816	0.4941475	0.18645	0.1044952
sp P50617 Dendrin OS	4	5	0.2210325	-0.12442	0.5709907	0.1894625	0.1051065

sp P0C2X9 Delta-1-pyr	2	2	-0.226617	-0.59573	0.1550926	0.1894625	0.105709
sp Q9JJP9 Ubiquilin-1	4	9	0.2558507	-0.176083	0.7469526	0.1905625	0.1063108
sp O88775 Embigin OS-	2	2	-0.247875	-0.700392	0.2037142	0.1911875	0.1069085
sp P01244 Somatotrop	1	3	-0.353855	-1.0885	0.2884093	0.1914875	0.1075
sp Q01812 Glutamate i	2	2	-0.196408	-0.541306	0.1693124	0.1931875	0.1080951
sp P09215 Protein kin*	2	2	-0.26677	-0.741216	0.2282159	0.193825	0.1086863
sp P02650 Apolipoprot	12	23	-0.135045	-0.293622	0.0247755	0.1949	0.1092768
sp Q06000 Lipoprotein	1	2	0.2439397	-0.194842	0.7011277	0.1950625	0.1098604
sp O54975 Xaa-Pro am	3	3	0.3478622	-0.353397	1.073814	0.1951	0.1104363
sp P52590 Nuclear por	2	2	0.2506441	-0.17817	0.6908134	0.195175	0.111005
sp P97878 Exocyst con	2	2	-0.194763	-0.523704	0.1297818	0.19535	0.1115673
sp Q62720 Zinc transpo	1	2	0.230482	-0.182473	0.6569005	0.1955875	0.1121238
sp Q62976 Calcium-act	1	2	-0.161891	-0.385151	0.0642009	0.197125	0.112683
sp P01835 Ig kappa ch	7	19	0.2840337	-0.24844	0.8290218	0.1978625	0.1132397
sp P04182 Ornithine ai	6	9	0.1362902	-0.023352	0.2979843	0.1989375	0.1137962
sp P15429 Beta-enolas	2	3	-0.9653	-3.20846	1.2200488	0.201325	0.1143609
sp P06302 Prothymosin	1	4	-0.189214	-0.494036	0.1310823	0.2013375	0.1149184
sp P29457 Serpin H1 O	13	20	-0.122341	-0.260514	0.0050312	0.2014	0.1154693
sp Q6AYK6 Calcyclin-bii	3	3	-0.233667	-0.67113	0.2456786	0.202075	0.1160174
sp Q64578 Sarcoplasm	5	5	-0.26243	-0.755642	0.2135751	0.2023	0.1165601
sp P35859 Insulin-like	2	2	-0.367845	-1.121036	0.3804863	0.20235	0.1170963
sp Q9JKB8 Pre-mRNA-s	1	2	-0.204525	-0.568292	0.1542935	0.2035375	0.1176332
sp P62332 ADP-ribosyl	1	2	-0.303713	-0.915552	0.3151685	0.203675	0.1181643
sp Q6AYG5 Enoyl-CoA f	1	2	0.2020361	-0.175648	0.5666609	0.2037375	0.1186893
sp P04937 Fibronectin	11	19	-0.176119	-0.44964	0.0965356	0.2041125	0.1192101
sp Q562C6 Leucine zipper	2	2	0.22381	-0.195627	0.6261141	0.2042375	0.1197255
sp P05544 Serine prote	6	10	-0.469065	-1.562102	0.5566112	0.205775	0.1202438
sp P61354 60S ribosom	7	11	0.1243045	-0.012422	0.2668909	0.2063375	0.1207594
sp O88778 Protein bas	3	4	0.2200103	-0.144799	0.6030804	0.2064375	0.1212693
sp P48675 Desmin OS-	6	6	-0.322725	-0.963136	0.3495265	0.20815	0.1217834
sp P08721 Osteopontin	1	2	-0.301555	-0.936099	0.3220932	0.208875	0.1222957
sp Q9EQX9 Ubiquitin-cc	3	5	-0.160024	-0.39341	0.0694574	0.2088875	0.1228021
sp P02600 Myosin ligh	6	16	-0.769065	-2.590008	1.0787251	0.2098625	0.1233083
sp P63255 Cysteine-ric	4	6	0.2018493	-0.146519	0.5440632	0.21005	0.1238097
sp Q2TL32 E3 ubiquitir	9	9	-0.151516	-0.355017	0.0677849	0.2113	0.1243125
sp A0JPQ9 Chitinase de	2	4	0.1899433	-0.119767	0.4985198	0.212125	0.1248143
sp P29066 Beta-arrestin	2	2	-0.286428	-0.913947	0.3582981	0.2125125	0.1253126
sp Q6URK4 Heterogene	8	14	0.1195022	-0.010899	0.2482355	0.214	0.1258136
sp P05964 Protein S10	8	34	0.1226497	-0.017538	0.2621046	0.21415	0.1263099
sp P13852 Major prion	3	4	-0.152428	-0.36656	0.0660018	0.2142125	0.126801
sp Q62769 Protein unc	3	3	0.2121616	-0.163089	0.5914144	0.2144875	0.1272881
sp P08683 Cytochrome	2	2	0.2039549	-0.149051	0.6113023	0.216225	0.1277795
sp O09175 Aminopeptid	2	2	-0.244425	-0.782577	0.2817171	0.2178625	0.1282745
sp P37361 Metallothio	4	6	-0.212448	-0.642924	0.211083	0.2179625	0.1287645
sp O08618 Phosphorib	3	3	-0.18774	-0.500812	0.1231086	0.2185875	0.1292527
sp Q62829 Serine/thre	1	2	0.1496356	-0.061698	0.3709497	0.219575	0.1297409
sp Q4G074 KIF1-bindin	4	4	-0.249451	-0.820179	0.3217473	0.2208375	0.1302307

sp B2GV06 Succinyl-CoA ligase (ADP-ribosyl transferase)	4	4	0.2551405	-0.303289	0.788723	0.2210375	0.1307163
sp Q810U0 Coiled-coil coiled-coil forming protein	2	2	-0.224637	-0.67349	0.2462308	0.2219625	0.1312017
sp P29975 Aquaporin-1	2	4	-0.176916	-0.475619	0.1225449	0.2230875	0.1316878
sp Q63474 Epithelial diaphragm protein	3	3	0.1511227	-0.067061	0.3709838	0.2242375	0.1321749
sp P10252 CD48 antigen	3	5	0.1500287	-0.067054	0.3697022	0.2258	0.1326651
sp Q6AY61 Serine protease inhibitor, clade A (alpha-1 antitrypsin)	1	4	-0.391219	-1.296306	0.5201294	0.2269625	0.1331563
sp Q3ZAV8 Enhancer of zeste homolog 2	2	3	0.1950882	-0.173497	0.553946	0.227075	0.1336429
sp P11661 NADH-ubiquinone oxidoreductase, subunit 2	2	2	0.2141168	-0.187901	0.6187737	0.2278375	0.1341284
sp P55108 Bone morphogenic protein 2	2	2	-0.274045	-0.881221	0.3129868	0.2289875	0.1346149
sp P63159 High mobility group protein HMG-1	10	14	0.1542548	-0.064582	0.3946795	0.231425	0.1351088
sp P23928 Alpha-crystallin	6	15	-0.124088	-0.284117	0.0291686	0.2315375	0.1355983
sp Q3LUD4 Leucine zipper protein	2	3	0.3189746	-0.455381	1.1268518	0.232	0.1360852
sp Q04631 Protein farnesyltransferase	3	4	0.2714596	-0.300237	0.8317883	0.23205	0.1365674
sp Q5XIU5 Proteasome ATPase subunit	2	3	0.1801536	-0.128906	0.4907892	0.2326125	0.1370476
sp Q5EIC4 Enhanced aminopeptidase	3	3	0.1964566	-0.177232	0.5857777	0.232875	0.1375244
sp Q9WTR8 PH domain containing protein	2	2	0.1996302	-0.193704	0.5916863	0.2329	0.1379965
sp P04692 Tropomyosin binding protein	8	16	-0.309522	-0.991789	0.4013161	0.2335125	0.1384671
sp Q9Z1Z1 Eukaryotic translation initiation factor 3 subunit D	2	2	0.2162148	-0.257543	0.7072934	0.2335625	0.1389332
sp P59649 FXYD domain containing sodium/potassium channel	2	5	-0.146156	-0.365701	0.0685642	0.2344875	0.1393993
sp O35800 Hypoxia-inducible factor 1 subunit alpha	1	2	0.2394673	-0.259124	0.7529637	0.2353375	0.139865
sp P21571 ATP synthase, mitochondrial	4	6	0.1672767	-0.123073	0.4510599	0.23575	0.1403283
sp P47727 Carbonyl reductase	7	12	0.1452929	-0.080563	0.3740672	0.237	0.140793
sp Q62806 Zinc finger protein	2	2	0.275573	-0.359469	0.9374246	0.2375	0.1412557
sp P07825 Synaptophylin	2	2	0.2098452	-0.257452	0.6829046	0.2390125	0.1417213
sp Q9EQR2 Alkyldihydroxyacetone phosphate acyltransferase	2	4	0.2102463	-0.244271	0.6631195	0.23945	0.1421844
sp Q8CGU4 Arf-GAP with PDZ-binding motif	2	2	0.1875974	-0.176213	0.5347416	0.239475	0.1426433
sp Q63803 Guanine nucleotide exchange factor	3	4	0.2185942	-0.218309	0.6593771	0.2408375	0.1431043
sp Q4QQS3 Protein OSC	3	3	-0.221107	-0.697592	0.3257852	0.2408625	0.1435612
sp Q00715 Histone H2B	11	59	0.1277983	-0.042281	0.300105	0.2413625	0.144016
sp Q5XI69 Probable ATP-dependent helicase	2	2	-0.257859	-0.879114	0.3461137	0.2415625	0.1444677
sp P07895 Superoxide dismutase	6	7	-0.122296	-0.274728	0.0342583	0.2418875	0.1449166
sp Q9QYJ6 cAMP and calcium sensor	3	3	-0.185542	-0.538087	0.1688001	0.2420625	0.1453622
sp Q6V7V2 Rhotekin O-glycosidase	3	3	0.2633699	-0.314006	0.8484326	0.24245	0.1458055
sp P48450 Lanosterol cyclase	2	2	-0.217565	-0.670831	0.2353141	0.2438125	0.146251
sp P12749 60S ribosomal protein L13	4	9	0.1192225	-0.023747	0.2656108	0.2442125	0.1466943
sp P62912 60S ribosomal protein L14	5	17	0.1208834	-0.027404	0.274742	0.2447125	0.1471358
sp P61959 Small ubiquitin-like modifier	1	2	0.1618276	-0.121363	0.4447646	0.2473	0.147585
sp Q64604 Receptor-type tyrosine kinase	3	3	0.2526092	-0.334911	0.8519788	0.248075	0.1480336
sp P20236 Gamma-amino butyrate receptor	2	3	0.2395907	-0.25466	0.7645926	0.2483375	0.1484794
sp Q5FVM7 DnaJ homolog	3	3	-0.18706	-0.580133	0.2350458	0.2484125	0.1489216
sp O54921 Exocyst complex component	2	2	0.2013362	-0.202684	0.6019604	0.2491	0.1493629
sp Q920F3 KH domain-containing protein	2	2	-0.227426	-0.789796	0.3143302	0.2492875	0.1498012
sp Q9WTL3 Semaphorin-like protein	2	2	-0.280785	-0.968924	0.4308019	0.2496375	0.1502371
sp Q8VHU4 Elongator complex component	1	2	0.2035844	-0.250168	0.6268365	0.24965	0.1506693
sp Q03114 Cyclin-dependent kinase inhibitor	3	4	0.240507	-0.256976	0.7657955	0.250175	0.1511001
sp O35179 Endophilin-2	6	9	0.14781	-0.093571	0.375918	0.2507375	0.1515296
sp P50339 Chymase O-linker	2	3	-0.198872	-0.657215	0.2833019	0.2507375	0.1519554

sp Q68FW7	Threonyl-tRNA methyltransferase	2	2	0.2722921	-0.317476	0.9212199	0.2510875	0.152379
sp Q02253	Methylmalonyl-CoA epoxidase	17	27	0.1006788	0.0083774	0.1915611	0.25145	0.1528006
sp P18266	Glycogen synthase kinase 3 beta	2	3	-0.289421	-1.136209	0.5983819	0.2523875	0.1532226
sp Q62745	CD81 antigen	3	7	-0.12253	-0.289258	0.0442814	0.253675	0.1536464
sp P15127	Insulin receptor	3	3	0.2392884	-0.359513	0.8588982	0.25425	0.1540691
sp P50609	Fibromodulin	7	16	-0.279041	-0.957544	0.3997423	0.254425	0.154489
sp Q9WTT2	Caseinolytic protease S1	2	2	0.2407746	-0.299422	0.8170977	0.2548375	0.1549071
sp Q4V8C2	Centromere protein C	2	2	-0.19343	-0.597468	0.2082918	0.2551	0.1553229
sp Q5FVQ4	Malectin OS=Homo sapiens	3	4	0.1642551	-0.150155	0.4817376	0.2556	0.1557372
sp Q6MG06	Guanine nucleotide exchange factor	2	4	-0.185641	-0.567328	0.2291804	0.2556875	0.1561486
sp Q9JII03	Collagen alpha-1(I) chain	2	2	-0.236197	-0.780151	0.3136427	0.256225	0.1565587
sp Q6P7P5	Basic leucin zipper transcription factor 3	3	3	0.1642498	-0.148545	0.4708702	0.2562875	0.1569658
sp Q9EQN5	DNA-bindin	4	6	-0.161336	-0.453342	0.1352342	0.2571125	0.1573729
sp P20761	Ig gamma-2 chain	4	7	-0.29807	-1.054309	0.4717423	0.2576875	0.157779
sp P07687	Epoxide hydrolase	4	6	0.1568707	-0.113468	0.4302899	0.2579625	0.158183
sp Q6P7A2	Ubiquitin carboxy-terminal hydrolase L1	2	2	-0.329576	-1.31811	0.700601	0.2587625	0.1585869
sp P04466	Myosin regulatory light chain	10	17	-0.57907	-2.235444	1.0951592	0.259	0.1589886
sp P16970	ATP-binding cassette subfamily A member 1	3	3	0.1833781	-0.222281	0.5781402	0.25905	0.1593872
sp P0C089	Protein-tyrosine phosphatase type I	1	2	-0.158767	-0.450059	0.1473988	0.2595125	0.1597845
sp Q3T1I9	RNA polymerase II subunit H	2	2	-0.168341	-0.600104	0.2907211	0.2596	0.1601791
sp Q9QYM2	Poly(ADP-ribose) polymerase 1	2	2	-0.281961	-1.079587	0.4819835	0.25985	0.1605715
sp P04644	40S ribosomal protein S21	3	7	-0.131249	-0.325671	0.0689982	0.2612875	0.1609664
sp P81799	N-acetyl-D-glucosaminidase	2	2	-0.255065	-0.87254	0.3637881	0.261475	0.161359
sp Q64361	Latrexin OS=Homo sapiens	5	12	0.1366868	-0.076892	0.3697361	0.2623375	0.1617519
sp O88941	Mannosyl-oligosaccharide glucosidase	3	3	0.1853066	-0.245699	0.5870126	0.2625625	0.1621427
sp Q64303	Serine/threonine-specific protein phosphatase 2A	4	4	-0.126726	-0.344061	0.1298779	0.2636875	0.1625347
sp Q68FS2	COP9 signal recognition particle subunit 3B	2	2	-0.193607	-0.625302	0.2483334	0.26495	0.1629287
sp Q8K3P7	Histidine triad nucleic acid binding protein	3	3	-0.271715	-0.924625	0.4124555	0.2652625	0.1633207
sp B0BNM9	Glycolipid transfer protein	3	7	-0.160295	-0.463593	0.1420328	0.265625	0.1637112
sp P46101	Dipeptidyl aminopeptidase 4	2	2	-0.179973	-0.564631	0.1943849	0.266375	0.1641016
sp Q6AXM8	Serum parathyroid hormone/PTH1 receptor	2	3	-0.244375	-0.889497	0.3337117	0.2671875	0.164492
sp P11505	Plasma membrane protein PMP22	3	3	-0.142005	-0.378925	0.1039122	0.2675125	0.1648808
sp Q9JHY8	DNA ligase III	2	2	0.3982696	-0.811492	1.5274196	0.2677375	0.1652675
sp Q9Z1C8	Rap guanine nucleotide exchange factor	2	2	0.169382	-0.189263	0.5295786	0.2697	0.1656586
sp Q498T2	Friend of PTF1 transcription factor	2	2	-0.210365	-0.722655	0.3019056	0.2698	0.1660472
sp P23811	Secretin receptor	1	2	-0.185071	-0.614388	0.2393476	0.27025	0.1664346
sp P08009	Glutathione S-transferase M1	6	10	0.1241052	-0.061112	0.2995323	0.2705625	0.1668202
sp Q9EPC6	Profilin-2 OS=Homo sapiens	5	7	-0.129933	-0.330661	0.0691445	0.270575	0.1672031
sp Q5PQQ8	Integrin beta-1	1	3	0.1857037	-0.214118	0.5915846	0.2717625	0.1675875
sp Q5U2Z3	Nucleosome assembly protein 1	3	3	0.314305	-0.611811	1.2591636	0.2720875	0.1679703
sp P07151	Beta-2-microglobulin	2	3	-0.148135	-0.408819	0.1287207	0.2727875	0.1683528
sp P05545	Serine protease inhibitor 1A	5	11	-0.233821	-0.822613	0.3551224	0.274725	0.1687396
sp P49797	Regulator of mTOR complex 1	2	2	0.2007778	-0.268667	0.6550882	0.2750875	0.169125
sp P01026	Complement component C1q	40	70	-0.151288	-0.447377	0.1301984	0.2756	0.1695093
sp P14604	Enoyl-CoA hydratase	11	18	-0.100182	-0.204192	0.0006594	0.2758	0.1698917
sp P28064	Proteasome activator subunit 1	1	2	-0.166317	-0.524532	0.2023204	0.2763875	0.1702734
sp P50116	Protein S10	3	7	-0.266255	-1.062443	0.5424757	0.2765375	0.1706529

sp Q9R1J4 Myocilin OS	1	2	0.2164644	-0.298541	0.7322386	0.2770625	0.1710316
sp Q6MG48 Protein PRR	2	2	0.2161496	-0.313986	0.7391501	0.278475	0.1714126
sp P02770 Serum albu	36	100	-0.16123	-0.493373	0.1707631	0.2788375	0.1717922
sp Q9R1T1 Barrier-to-a	5	9	0.1244414	-0.068975	0.3176158	0.279025	0.1721698
sp P18886 Carnitine O-	2	2	-0.261853	-1.077529	0.4708472	0.281575	0.1725536
sp Q64244 ADP-ribosyl	2	4	-0.18128	-0.612729	0.2422147	0.2818625	0.1729358
sp Q5XIG0 ADP-ribose	2	2	-0.211641	-0.788395	0.424974	0.2819625	0.1733157
sp Q5XIG4 OCIA domai	3	4	0.1550589	-0.141882	0.4727031	0.2833875	0.1736979
sp Q62760 Mitochondr	2	2	0.1530698	-0.148686	0.4571216	0.2833875	0.1740775
sp P62193 26S proteas	6	9	0.1329533	-0.08194	0.3552954	0.28415	0.174457
sp Q7TQ94 Nitrilase ho	1	2	-0.163871	-0.499488	0.176691	0.2842	0.1748341
sp Q05175 Brain acid s	7	14	0.1127156	-0.035737	0.2690242	0.2845625	0.1752099
sp Q9Z1N3 Myosin-IYa	4	4	-0.131471	-0.358301	0.1056129	0.286525	0.1755898
sp Q924R9 Nucleosom	2	2	-0.385852	-1.935203	1.2139996	0.2867375	0.1759679
sp O08653 Telomerase	5	6	-0.118878	-0.298529	0.0640338	0.286825	0.1763437
sp P18297 Sepiapterin	2	4	-0.174428	-0.568575	0.2304642	0.286825	0.1767169
sp Q63228 Glia matura	4	6	-0.130967	-0.356638	0.1050606	0.287025	0.1770883
sp P54319 Phospholip	3	3	0.1831368	-0.237988	0.6073692	0.2871875	0.1774578
sp P38656 Lupus La pr	2	2	0.1870923	-0.291644	0.6408859	0.2875375	0.177826
sp Q5PQS0 Pleckstrin h	2	2	0.5153008	-0.483019	2.1299234	0.288875	0.1781961
sp P17425 Hydroxyme	5	5	-0.141201	-0.410489	0.1358757	0.288925	0.178564
sp P17077 60S riboson	4	4	0.1591979	-0.232819	0.5414049	0.2890875	0.17893
sp Q9ESH6 Glutaredoxi	3	6	0.1836264	-0.252088	0.6304414	0.2893875	0.1792945
sp Q6Q0N3 5'-nucleotid	4	4	-0.168394	-0.523369	0.1770099	0.289525	0.1796571
sp Q6AZ50 Ubiquitin-lil	1	2	0.1904957	-0.281313	0.6700299	0.2901125	0.1800193
sp Q6IMZ0 Nuclear faci	2	2	-0.183729	-0.656454	0.3138329	0.290125	0.1803791
sp Q4QQT4 Serine/thre	3	4	0.1560867	-0.162849	0.4812911	0.29055	0.1807379
sp Q64611 Cysteine sul	1	3	-0.137987	-0.391454	0.1183264	0.2907625	0.1810952
sp P70550 Ras-related	2	2	-0.218307	-0.782939	0.3492405	0.291775	0.1814534
sp Q5FVQ8 NLR family I	3	3	-0.19338	-0.664504	0.30023	0.2922125	0.1818106
sp Q99JD2 Tektin-1 OS	2	2	-0.216938	-0.864335	0.422547	0.2931875	0.1821688
sp Q641X2 RNA polymer	2	2	0.2706762	-0.666599	1.1868333	0.29345	0.1825254
sp Q66HF8 Aldehyde de	5	8	0.101078	-0.014276	0.219276	0.293575	0.1828802
sp P62856 40S riboson	2	5	0.1144302	-0.058667	0.2846346	0.2938625	0.1832337
sp P18292 Prothrombi	3	3	-0.2032	-0.748304	0.3755962	0.2939375	0.1835851
sp P97696 Cytohesin-3	2	2	-0.267713	-1.042332	0.5331691	0.29435	0.1839356
sp Q924T8 Cysteinyl leu	1	6	-0.123262	-0.334427	0.0881436	0.2946625	0.1842849
sp P97532 3-mercaptop	5	7	0.116948	-0.060633	0.2998266	0.295875	0.1846358
sp Q9QUZ8 Glucocortic	2	2	-0.16462	-0.60926	0.3822991	0.2969375	0.1849879
sp Q62969 Prostacyclir	2	2	0.18598	-0.289947	0.640469	0.2971375	0.1853384
sp P54921 Alpha-solub	5	8	-0.121446	-0.319577	0.0795869	0.2974	0.1856875
sp Q9Z0G8 WAS/WASL	2	2	-0.239896	-1.021113	0.5053854	0.2974375	0.1860345
sp Q08406 Ciliary neur	2	2	-0.260714	-1.279669	0.860745	0.2975	0.1863796
sp P37377 Alpha-synuc	4	11	0.1478817	-0.160023	0.467021	0.297675	0.1867231
sp P27768 Troponin I,	3	7	-0.594282	-2.706043	1.499688	0.2983875	0.1870667
sp P47858 6-phosphof	13	26	-0.106066	-0.253607	0.0286468	0.2993375	0.1874111
sp Q9Z2Q1 Protein trar	5	8	-0.123919	-0.340641	0.0882979	0.2997	0.1877545

sp Q62847 Gamma-adc	8	10	0.1133742	-0.056149	0.2800979	0.30015	0.1880971
sp P11497 Acetyl-CoA	3	6	-0.128995	-0.358853	0.0925241	0.3004	0.1884385
sp P83883 60S riboson	6	8	0.1236225	-0.076852	0.3357812	0.3012625	0.1887804
sp P97607 Protein jagg	2	2	0.2134526	-0.374759	0.8017378	0.30225	0.1891232
sp Q5XI31 GPI transam	3	3	0.1817322	-0.332306	0.7036218	0.302775	0.1894655
sp Q3KRE0 ATPase fam	2	2	0.1763621	-0.233267	0.6034409	0.3028	0.1898059
sp P67874 Casein kina	2	4	0.185355	-0.345285	0.7345833	0.30295	0.1901446
sp P05371 Clusterin O	4	7	0.1328656	-0.102565	0.3833331	0.3032125	0.1904821
sp Q62799 Receptor ty	1	2	0.1417884	-0.225349	0.5066813	0.303775	0.1908193
sp Q5PQQ6 IQ domain-	1	2	0.2417662	-0.507534	1.0632251	0.304	0.1911552
sp Q5FVH2 Phospholipa	2	3	0.1843837	-0.287151	0.6510979	0.3042875	0.1914899
sp O35264 Platelet-act	2	6	-0.129752	-0.367036	0.1022874	0.3043625	0.1918228
sp P62634 Cellular nuc	1	2	-0.223849	-0.892694	0.4356105	0.3044	0.1921539
sp Q5FVQ9 Tubulin-spe	2	3	0.1864935	-0.295414	0.6563604	0.3052125	0.1924855
sp P10824 Guanine nu	1	2	0.1412455	-0.136673	0.420278	0.3056375	0.1928163
sp Q6AY56 Tubulin alpI	2	2	0.1887407	-0.372833	0.7439098	0.3063375	0.1931473
sp P97633 Casein kina	2	3	0.1774926	-0.268949	0.6300184	0.3068375	0.1934778
sp Q66HD0 Endoplasmic	24	48	-0.090191	-0.178365	0.0018069	0.3083375	0.1938107
sp Q63190 Emerin OS=	2	2	-0.296957	-1.338367	0.7022509	0.3103125	0.1941474
sp Q4FZX7 Signal recoξ	2	3	-0.142112	-0.444127	0.1511349	0.3103625	0.1944823
sp P60892 Ribose-pho	2	2	0.1503525	-0.252525	0.5622238	0.3108375	0.1948167
sp Q4TU93 C-type man	2	3	-0.138225	-0.42774	0.1627981	0.3109875	0.1951496
sp Q6MG55 Abhydrolasi	5	8	-0.116151	-0.299663	0.0767646	0.3116	0.1954823
sp Q63100 Cytoplasmic	3	4	-0.126686	-0.37646	0.1206474	0.311775	0.1958136
sp Q6IG03 Keratin, typ	5	5	0.1346161	-0.179308	0.4320353	0.31185	0.1961433
sp Q9EPF2 Cell surface	5	6	-0.113934	-0.325936	0.1014666	0.3120125	0.1964715
sp Q9ES53 Ubiquitin fu	2	2	0.1705563	-0.272378	0.6182309	0.313075	0.1968009
sp P09739 Troponin T,	2	2	-0.292213	-1.330838	0.7072924	0.3132625	0.1971289
sp Q6TUG0 DnaJ homol	3	6	0.1382873	-0.163137	0.4352437	0.3154125	0.1974612
sp P05539 Collagen alp	2	2	0.1610493	-0.261639	0.5860148	0.3160625	0.1977934
sp Q5RK23 Abhydrolasi	2	2	-0.227953	-0.968359	0.4703338	0.3167125	0.1981256
sp P09812 Glycogen ph	4	5	-0.206092	-0.829757	0.4282687	0.3169625	0.1984566
sp Q3ZB98 Breast carci	16	34	0.1174474	-0.094623	0.3317444	0.3189875	0.1987914
sp B1H224 PWWP dom	2	2	0.3061029	-0.940165	1.5486823	0.3193875	0.1991255
sp Q4V8C7 Interferon-i	2	2	0.1906591	-0.351994	0.7617048	0.3194125	0.1997882
sp Q9WV48 SH3 and mu	3	3	-0.147832	-0.516163	0.2110307	0.3194125	0.1994578
sp P23764 Glutathione	5	10	-0.161816	-0.582941	0.2622426	0.3194625	0.200117
sp P54100 Proto-onco	3	3	-0.162019	-0.639514	0.3652694	0.3197	0.2004446
sp Q8K4F7 Scavenger r	2	3	-0.152776	-0.523493	0.227368	0.319775	0.2007707
sp P29147 D-beta-hyd	4	4	0.1680592	-0.28526	0.6055936	0.3201	0.2010958
sp B0BNA7 Eukaryotic t	1	2	0.1396768	-0.173421	0.4503843	0.32185	0.2014239
sp Q8K4K7 Actin-bindir	2	2	-0.163999	-0.613003	0.3154064	0.3236625	0.2017552
sp Q6AYA6 Uncharacte	2	3	-0.153987	-0.549365	0.2413957	0.323775	0.202085
sp P17136 Small nucle	2	2	0.168326	-0.287824	0.6243969	0.324225	0.2024142
sp Q63180 Disintegrin	1	2	-0.119987	-0.374022	0.1320882	0.324525	0.2027425
sp Q9JHW1 Carboxypept	3	3	0.1543396	-0.285156	0.5728279	0.32475	0.2030696
sp Q6QBQ4 Phospholipi	2	2	0.1716227	-0.383639	0.7305315	0.3247875	0.203395

sp P62738 Actin, aortic	8	18	-0.222361	-0.942354	0.5022017	0.324875	0.203719
sp P56574 Isocitrate dehydrogenase (NADP+)	11	20	-0.130159	-0.41271	0.1582052	0.325025	0.2040416
sp Q6LED0 Histone H3.3	2	3	0.1657586	-0.240283	0.6004541	0.325075	0.2043626
sp D4A4T9 Cysteine arylamidase-like	3	3	-0.145737	-0.498042	0.1878626	0.325525	0.2046832
sp P62278 40S ribosomal protein S19	10	22	0.0945626	-0.020796	0.2069844	0.32575	0.2050026
sp Q63610 Tropomyosin-binding protein 1	5	12	-0.093418	-0.20353	0.0173113	0.3273	0.2053244
sp P50279 Syntaxin-2 (alpha 1B) binding protein	1	2	0.1245346	-0.132185	0.3744097	0.3274	0.2056448
sp Q08602 Geranylgeranyltransferase I	2	3	-0.158029	-0.579383	0.255966	0.327675	0.2059643
sp P31044 Phosphatidylethanolamine N-methyltransferase	10	24	0.1216234	-0.121537	0.3694989	0.3282375	0.2062836
sp P97546 Neuroplastin	3	5	-0.099825	-0.236781	0.041326	0.32875	0.2066025
sp P47853 Biglycan OS	12	31	-0.18137	-0.730406	0.3732034	0.3291875	0.2069209
sp Q9JJM9 Septin-5 OS	2	4	-0.142564	-0.488091	0.2157434	0.329875	0.2072394
sp Q6AYN4 Phytanoyl-CoA thioesterase	5	9	-0.112741	-0.329003	0.1041371	0.3308125	0.2075587
sp Q03346 Mitochondrial membrane protein	1	2	0.2300821	-0.578866	1.054192	0.3310625	0.207877
sp Q62902 Protein ERG	2	2	-0.167246	-0.6688	0.2998629	0.3310875	0.2081938
sp P56558 UDP-N-acetylglucosaminidase	2	3	-0.137168	-0.460961	0.2061147	0.3314875	0.2085099
sp P21263 Nestin OS=Human	17	22	-0.095404	-0.215441	0.0270837	0.33215	0.2088261
sp Q62824 Exocyst complex component 6	3	3	-0.139446	-0.476877	0.1940395	0.3327875	0.2091423
sp O88453 Scaffold attachment region kinase 1	5	9	0.1240497	-0.120957	0.3650392	0.3332125	0.209458
sp P26644 Beta-2-glycoprotein I	7	13	-0.096078	-0.226832	0.0355252	0.335825	0.2097788
sp Q64240 Protein AM	3	4	0.1203903	-0.144182	0.381065	0.3359375	0.2100982
sp Q4FZU8 Protein FANCI	2	2	0.1399608	-0.206609	0.5013911	0.3365125	0.2104174
sp Q9QUR2 Dynactin subunit alpha	2	2	-0.189511	-0.769548	0.2759763	0.3371125	0.2107365
sp P43138 DNA-(apurinic/added base)	3	4	0.1485816	-0.234829	0.5253504	0.337375	0.2110547
sp Q3B8Q2 Eukaryotic initiation factor 4E	3	3	0.1297121	-0.143072	0.4107153	0.3378375	0.2113725
sp Q63151 Long-chain base oxidase	2	2	-0.209114	-1.015713	0.559823	0.33925	0.2116922
sp Q5FVL2 Neighbor of RPLP0	2	3	0.1425953	-0.25543	0.5494383	0.3392875	0.2120103
sp Q9WUD1 Transient receptor potential cation channel subfamily V member 1	2	3	0.164421	-0.333096	0.6460279	0.3403625	0.2123296
sp P36407 E3 ubiquitin-protein ligase	2	2	-0.155229	-0.607451	0.2986716	0.3411875	0.2126494
sp Q5I0H4 Transmembrane protein	2	2	-0.139056	-0.526981	0.2585916	0.3414875	0.2129683
sp Q9WTY8 Zinc finger protein 14	1	3	0.1124869	-0.102431	0.3348964	0.3415875	0.2132859
sp Q6IRK9 Plasma glutathione reductase	7	13	-0.108481	-0.307105	0.0819004	0.3417625	0.2136023
sp Q4V7E8 Leucine-rich repeat kinase 2	2	3	-0.164745	-0.659251	0.3389218	0.3422375	0.2139184
sp Q91XU8 Phosphatidylethanolamine N-methyltransferase	2	6	0.1389708	-0.221452	0.4894374	0.342525	0.2142336
sp A1A5Q4 UPF0704 protein	2	2	-0.18207	-0.91938	0.5911679	0.3429125	0.2145482
sp P54311 Guanine nucleotide exchange factor	4	8	0.103232	-0.072259	0.2809043	0.3450625	0.2148665
sp Q4KM74 Vesicle-trafficking protein	5	8	-0.101434	-0.269074	0.0659596	0.3454625	0.2151843
sp Q6JAM9 Transmembrane protein	2	3	0.1247629	-0.157446	0.4128235	0.3458125	0.2155013
sp P41123 60S ribosomal protein L13	9	23	0.0930751	-0.023253	0.2121215	0.346025	0.2158174
sp P02401 60S acidic ribosomal protein L13	6	16	0.0952539	-0.03104	0.2256078	0.34635	0.2161327
sp P19139 Casein kinase 1 epsilon	2	5	-0.14606	-0.539897	0.2386328	0.3464625	0.2164467
sp P20272 Cannabinoid receptor 1	2	2	0.1539762	-0.313146	0.6178703	0.34665	0.2167597
sp P18484 AP-2 complex	15	26	-0.09223	-0.206241	0.0217887	0.3468125	0.2170716
sp P43278 Histone H1.2	8	23	0.115089	-0.134371	0.358251	0.3468875	0.2173821
sp P23514 Coatomer small subunit	2	2	0.1777393	-0.397426	0.7587004	0.3472625	0.2176921
sp Q5XI22 Acetyl-CoA acetyltransferase	6	9	-0.10632	-0.340859	0.1357146	0.34735	0.2180008
sp Q8R511 Formin-binding protein 1	3	5	-0.105843	-0.288055	0.07791	0.3477375	0.218309

sp Q5BJT7 Coiled-coil c	2	2	-0.237603	-1.275975	0.8487922	0.3480375	0.2186164
sp D4A615 Tonsoku-lik	3	3	-0.156622	-0.630603	0.3303327	0.3481375	0.2189226
sp P35171 Cytochrome	2	4	0.1027218	-0.17326	0.3509867	0.3485125	0.2192282
sp P07896 Peroxisoma	2	2	0.1756558	-0.448253	0.806193	0.3493875	0.2195345
sp Q8CF97 Deubiquitin	2	2	-0.140457	-0.53334	0.2630894	0.349925	0.2198406
sp Q641Z6 EH domain-	2	2	-0.176483	-0.792722	0.4043973	0.3499375	0.2201453
sp Q5PQM2 Kinesin light	2	2	0.1586827	-0.323026	0.6391435	0.3502	0.2204491
sp Q6IMF3 Keratin, typ	3	3	-0.375983	-1.829283	0.40158	0.3504875	0.2207522
sp P70619 Glutathione	2	5	-0.106432	-0.304906	0.0900804	0.3505125	0.221054
sp Q6TEK4 Vitamin K e	3	3	-0.134653	-0.496953	0.2435028	0.3509875	0.2213555
sp P21139 Alpha-manr	2	2	-0.155147	-0.650126	0.3111991	0.351425	0.2216566
sp Q6B345 Protein S10	2	3	-0.145957	-0.656158	0.3344641	0.3514625	0.2219564
sp Q80Z30 Protein pho	1	2	-0.154705	-0.68383	0.3666875	0.352075	0.2222562
sp B2GUZ5 F-actin-cap	3	7	0.1140381	-0.127666	0.3448722	0.352375	0.2225553
sp Q6P7R8 Estradiol 17	6	12	-0.109001	-0.314461	0.0862163	0.353175	0.2228549
sp P56720 Sterol regul	2	3	0.1081177	-0.108797	0.3146686	0.35325	0.2231533
sp Q3KR56 GRAM dom	1	2	0.1258463	-0.264604	0.5096116	0.3533375	0.2234505
sp P54690 Branched-cl	8	13	0.1024691	-0.067168	0.2816247	0.3539625	0.2237478
sp P40615 H/ACA ribo	3	3	0.1570378	-0.481689	0.7591558	0.354925	0.2240459
sp O35787 Kinesin-like	2	2	0.1032175	-0.214273	0.3854751	0.355175	0.2243433
sp P63329 Serine/thre	7	9	-0.092206	-0.213339	0.0264849	0.35535	0.2246396
sp Q5MYW· Zinc finger	2	7	0.1309354	-0.209812	0.4741347	0.355525	0.2249351
sp P97603 Neogenin (F	1	2	-0.14098	-0.650457	0.3764542	0.355925	0.2252301
sp Q4V897 Coiled-coil c	2	2	0.1868385	-0.520436	0.9015332	0.3575875	0.2255276
sp Q80U96 Exportin-1 C	4	8	0.1032939	-0.070841	0.2746626	0.3576	0.2258237
sp Q63524 Transmemb	4	5	0.1137762	-0.128989	0.358115	0.3585375	0.2261206
sp P97690 Structural n	2	2	-0.146744	-0.628603	0.3404713	0.3585875	0.2264163
sp D3ZTE0 Coagulation	1	3	0.232704	-0.963336	1.4935916	0.3586875	0.2267109
sp O88900 Growth fact	2	2	0.1641951	-0.478246	0.7651394	0.3588625	0.2270045
sp Q924U5 Dual specifi	2	2	-0.156253	-0.673024	0.3666975	0.3597875	0.2272989
sp Q6AY30 Probable sa	9	19	0.089641	-0.026816	0.2018864	0.3607625	0.2275942
sp P20611 Lysosomal a	2	2	0.1253248	-0.209082	0.4607318	0.361925	0.2278908
sp Q5EGY4 Synaptobre	2	3	0.12528	-0.346663	0.5638297	0.3623125	0.2281868
sp P27139 Carbonic an	9	18	-0.118302	-0.435181	0.2195638	0.3627625	0.2284826
sp B0BN15 Olfactomed	2	2	-0.10711	-0.842084	0.8540539	0.3627875	0.2287771
sp Q7M6Z5 Kinesin-like	5	6	0.1163597	-0.208368	0.4428164	0.36455	0.2290742
sp Q9Z339 Glutathione	1	2	0.1519304	-0.360431	0.6610131	0.364825	0.2293706
sp Q99MZ4 Gamma-glu	2	3	0.1558229	-0.373787	0.7249521	0.3650125	0.2296661
sp P45479 Palmitoyl-p	3	3	-0.157778	-0.651199	0.3309884	0.3655375	0.2299615
sp Q99JE6 1-phosphat	3	3	0.1346228	-0.288947	0.5354117	0.3660125	0.2302566
sp P63324 40S riboson	5	8	0.1064641	-0.108367	0.3211735	0.3662375	0.230551
sp Q66HE5 NUAK famil	2	2	0.1194971	-0.181876	0.4279775	0.3666375	0.2308449
sp Q5RK09 Eukaryotic t	3	3	0.1383485	-0.300134	0.5944654	0.36785	0.2311402
sp Q64654 Lanosterol :	2	3	0.1208789	-0.187734	0.4209383	0.3680125	0.2314345
sp Q9WTP0 Band 4.1-lik	3	4	-0.106841	-0.313319	0.0979448	0.36855	0.2317288
sp Q1HG60 ATP-depend	2	2	-0.151624	-0.747292	0.4532818	0.3693625	0.2320235
sp P18437 Non-histone	2	3	0.1236999	-0.425874	0.6219466	0.3700625	0.2323184

sp Q62868 Rho-associa	2	3	0.1367648	-0.296917	0.5640543	0.3703875	0.2326128
sp P09605 Creatine kir	1	2	-0.559745	-4.490083	3.310267	0.3716875	0.2329087
sp P05712 Ras-related	5	7	-0.09456	-0.243284	0.0542833	0.3724875	0.2332051
sp Q5PPL3 Sterol-4-alp	1	3	0.1261853	-0.22358	0.4887629	0.373025	0.2335013
sp Q9JKC9 Synergin ga	2	2	0.1964209	-0.810638	1.2414078	0.3738625	0.233798
sp P81128 Glucocortic	4	5	-0.134576	-0.59267	0.3228595	0.374625	0.2340951
sp Q63347 26S proteas	8	12	0.0954629	-0.06187	0.2506225	0.37465	0.2343911
sp O88677 Protein BTG	1	4	0.1041809	-0.090201	0.3127812	0.3748	0.234686
sp Q9R0T3 DnaJ homol	2	2	-0.269642	-1.688868	1.0222203	0.375025	0.2349802
sp P61107 Ras-related	6	10	-0.095075	-0.256958	0.0740798	0.375325	0.2352738
sp O35987 NSFL1 cofac	9	13	0.0945475	-0.055318	0.2504421	0.3754125	0.2355664
sp Q9QZM6 Sodium/pot	2	2	0.176966	-0.523636	0.9084455	0.3765125	0.2358601
sp P01946 Hemoglobir	14	100	-0.139993	-0.605847	0.3415541	0.376525	0.2361525
sp Q9WUW Complemer	3	4	-0.114803	-0.503942	0.3200286	0.3769875	0.2364447
sp P62775 Myotrophin	2	5	0.1263718	-0.283072	0.5250183	0.37725	0.2367362
sp Q9QZA6 CD151 anti ξ	5	13	0.0913001	-0.05406	0.2268071	0.37765	0.2370274
sp P15800 Laminin su κ	43	71	0.0952658	-0.083637	0.2714743	0.3781375	0.2373183
sp P63086 Mitogen-ac	7	13	-0.093496	-0.250225	0.0743515	0.37815	0.2376081
sp Q6IRE4 Tumor susc	3	3	-0.134583	-0.564965	0.2847993	0.3781875	0.2378967
sp Q00438 Polypyrimid	3	5	-0.105928	-0.348805	0.1392458	0.3782375	0.2381843
sp Q9QY17 Protein kin α	3	3	0.1335174	-0.30067	0.5601269	0.3787375	0.2384718
sp Q5XIK2 Thioredoxin	4	7	-0.099804	-0.292463	0.0895993	0.379075	0.2387587
sp P32089 Tricarboxyl	10	20	-0.081897	-0.157649	-0.009685	0.3792625	0.2390449
sp Q27W01 RNA-bindin	3	3	-0.135979	-0.6663	0.3874141	0.3793375	0.23933
sp P63331 Serine/thre	6	7	-0.111126	-0.390517	0.1644942	0.3800375	0.2396154
sp Q3MHT4 Speckle tar ξ	2	2	0.1338554	-0.3018	0.5717152	0.3803625	0.2399003
sp Q62651 Delta(3,5)-D	2	2	-0.114645	-0.450527	0.243759	0.3820375	0.2401875
sp Q00657 Chondroitin	9	11	0.1160069	-0.200769	0.4397896	0.3820875	0.2404736
sp Q5I0C3 Methylcroto	1	2	0.1325913	-0.293312	0.5580418	0.3823625	0.2407591
sp B5DFA1 TBC1 doma	3	3	-0.137474	-0.690498	0.4263241	0.3826875	0.2410441
sp Q920G2 Na(+)/H(+) c	2	2	0.128441	-0.364189	0.6281343	0.3835375	0.2413296
sp P53563 Bcl-2-like pr	1	2	0.1280859	-0.295862	0.5594254	0.3838	0.2416146
sp Q62844 Tyrosine-pr	2	4	0.1178796	-0.239496	0.4787532	0.38435	0.2418995
sp Q66HG5 Transmemb	2	2	0.1225235	-0.295817	0.5363231	0.3853875	0.2421853
sp P85108 Tubulin bet	1	3	-0.125106	-0.608543	0.3770872	0.38635	0.2424719
sp Q0ZHH6 Atlastin-3 O	5	9	-0.096476	-0.279229	0.0908572	0.3866625	0.242758
sp P62997 Transforme	2	2	-0.150963	-0.748016	0.4395438	0.3869375	0.2430435
sp B2RYN7 Spastin OS=	2	2	-0.139206	-0.641433	0.3471514	0.3876375	0.2433292
sp POC644 Inositol hex	2	2	0.1285772	-0.277232	0.5530727	0.38785	0.2436143
sp Q6KC51 Actin-bindir	2	2	0.1304406	-0.366841	0.6286039	0.3882	0.2438989
sp P42346 Serine/thre	3	3	-0.111549	-0.390614	0.1682707	0.388475	0.244183
sp P84082 ADP-ribosyl	1	2	0.2987559	-1.852372	2.4356262	0.3886125	0.2444662
sp Q9QYP2 Cadherin EC	2	5	0.1059548	-0.159254	0.3719391	0.3892625	0.2447495
sp P62282 40S riboson	9	14	0.086122	-0.032928	0.2090096	0.3897125	0.2450326
sp Q9JKU6 Spermatid p	4	4	-0.121728	-0.48587	0.2140508	0.390075	0.2453154
sp Q9ESS6 Basal cell ac	7	9	-0.093583	-0.263513	0.0780608	0.3903125	0.2455975
sp P20294 Ciliary neur	4	4	0.1057558	-0.156081	0.3702434	0.390325	0.2458785

sp P70623 Fatty acid-b	1	3	0.1258534	-0.438717	0.6732118	0.3918	0.2461613
sp Q66HA4 Tax1-bindin	2	2	-0.16529	-0.889329	0.5505749	0.39215	0.2464437
sp P55053 Fatty acid-b	7	15	0.0996652	-0.133475	0.3391128	0.394	0.2467285
sp P10960 Sulfated gly	10	24	0.08617	-0.027288	0.2055769	0.394275	0.2470128
sp P24329 Thiosulfate	4	4	-0.097215	-0.31741	0.1312183	0.3945625	0.2472966
sp Q3MHC2 Integrator c	2	2	-0.122521	-0.546868	0.3032511	0.394675	0.2475794
sp Q63604 BDNF/NT-3	3	3	-0.106633	-0.397538	0.1935009	0.3948125	0.2478615
sp Q5U2X6 Coiled-coil c	6	8	-0.097651	-0.309642	0.1170248	0.3957625	0.2481443
sp P97629 Leucyl-cysti	4	5	0.1065073	-0.166363	0.3861543	0.39585	0.2484262
sp Q08290 Calponin-1	3	4	0.2714308	-1.146506	1.7844736	0.3963125	0.2487079
sp Q6P6T4 Echinoderm	3	3	0.1215552	-0.31448	0.5529317	0.3964	0.2489886
sp O88656 Actin-relate	2	2	-0.134459	-0.630547	0.3316872	0.3967	0.2492689
sp Q71LX6 Xin actin-bii	4	4	0.1051462	-0.153895	0.3720392	0.397425	0.2495495
sp Q9Z1P2 Alpha-actin	11	12	-0.150521	-0.863402	0.548125	0.3979125	0.24983
sp Q99MC0 Protein pho	3	4	-0.14238	-0.802914	0.5200479	0.3981125	0.2501098
sp Q63357 Myosin-Id C	4	9	-0.148006	-0.802951	0.5616384	0.39825	0.2503887
sp P21807 Peripherin C	31	100	0.0853398	-0.037476	0.205587	0.398375	0.2506669
sp P63047 Sulfotransfe	1	2	0.1021852	-0.205377	0.3977536	0.3984625	0.2509442
sp P0C5W1 Microtubule	4	4	-0.097176	-0.331812	0.1450774	0.398875	0.2512212
sp O88618 Formimidoyl	2	3	0.0958538	-0.129155	0.3246621	0.3989375	0.2514973
sp Q62780 Probable A1	2	2	-0.099215	-0.339926	0.1362482	0.3994375	0.2517733
sp Q32KJ2 Arylsulfatas	3	3	-0.121968	-0.600036	0.3686115	0.39995	0.2520493
sp Q63210 Guanine nu	1	2	0.0973785	-0.181396	0.3848979	0.4007	0.2523256
sp Q5FVI4 Cell cycle e>	4	12	0.0850506	-0.02532	0.1956872	0.401	0.2526014
sp P51647 Retinal deh	3	3	-0.11836	-0.533421	0.2983992	0.401325	0.2528768
sp Q68FS4 Cytosol ami	13	21	-0.091489	-0.297822	0.1177257	0.4020375	0.2531525
sp Q62736 Non-muscle	10	16	-0.099094	-0.408073	0.2140988	0.4024375	0.253428
sp Q6MG08 ATP-binding	3	4	-0.100529	-0.368603	0.1854073	0.4024625	0.2537024
sp Q6PCT3 Tumor prot	3	5	-0.111045	-0.469334	0.2373785	0.4026	0.2539761
sp O70351 3-hydroxyac	6	10	-0.085424	-0.210856	0.0426722	0.4030125	0.2542496
sp P70567 Tropomodu	3	4	-0.112119	-0.4837	0.2661335	0.4034125	0.2545228
sp P84060 Dystrobrevi	3	4	0.1312971	-0.317929	0.6089603	0.4042375	0.2547965
sp P15651 Short-chain	3	5	-0.095402	-0.297459	0.1027517	0.404725	0.2550701
sp Q5EB59 Mediator of	2	3	-0.11231	-0.458002	0.2178616	0.4061375	0.2553453
sp P13676 Acylamino-	3	4	-0.090102	-0.281017	0.1012117	0.406225	0.2556196
sp Q6AXV7 Ig-like V-typ	2	2	-0.123998	-0.64634	0.4082101	0.4065	0.2558934
sp P13941 Collagen alp	2	3	0.1201757	-0.303465	0.5336794	0.40695	0.2561671
sp P24368 Peptidyl-pro	8	15	-0.085462	-0.243314	0.0743586	0.4072375	0.2564403
sp Q6MGA5 Bromodom	2	4	-0.110667	-0.449868	0.2250065	0.408875	0.2567154
sp Q5U2R3 FERM doma	1	2	0.1828807	-0.86354	1.2772014	0.4095875	0.2569909
sp P62850 40S riboson	5	8	0.099479	-0.259782	0.4506436	0.409925	0.2572659
sp B2GV54 Neutral cho	1	2	0.1157369	-0.272329	0.4925405	0.4102	0.2575405
sp Q6AY86 Vacuolar pr	3	3	0.1291037	-0.485965	0.7520537	0.4102375	0.2578141
sp P02634 Protein S10	3	4	0.1001876	-0.154047	0.3817898	0.4106625	0.2580876
sp P13697 NADP-depe	7	8	-0.097033	-0.363	0.1700115	0.4107	0.2583601
sp Q64122 Myosin regi	1	2	-0.164351	-1.106762	0.7825889	0.41105	0.2586323
sp P41498 Low molecu	5	9	0.0959218	-0.12013	0.3210756	0.4112	0.2589037

sp Q63060 Glycerol kinase	2	4	-0.100616	-0.379389	0.1842385	0.4113125	0.2591744
sp P62250 40S ribosomal protein S20	7	11	0.0845334	-0.063434	0.2312364	0.41145	0.2594444
sp P08010 Glutathione S-transferase	5	7	0.0882096	-0.083565	0.2567645	0.4115875	0.2597137
sp P24054 SPARC-like protein	2	2	-0.123378	-0.777037	0.5553555	0.411725	0.2599823
sp P09650 Mast cell protease 1	8	18	0.1171386	-0.329206	0.5540311	0.4120125	0.2602504
sp Q7TNJ2 ATP-binding cassette, subfamily A (P-type), member 2	2	4	0.0989154	-0.176106	0.3690252	0.4121875	0.2605179
sp P36970 Phospholipid transfer protein	2	2	0.1410941	-0.548467	0.8126895	0.413225	0.2607863
sp Q99ML5 Prenylcysteine O-acyltransferase	4	6	0.1016664	-0.175231	0.3916411	0.4137625	0.2610547
sp B3DMA2 Acyl-CoA dehydrogenase	2	2	-0.120736	-0.625361	0.3603639	0.4137875	0.2613222
sp Q6Q760 Sodium leak channel	3	3	-0.107402	-0.56463	0.3296551	0.4140125	0.2615891
sp Q5XIM9 T-complex protein 1 subunit alpha	20	49	0.0782931	0.0047269	0.1521902	0.4140625	0.2618552
sp P21775 3-ketoacyl-CoA thioesterase	7	9	-0.093351	-0.389349	0.2112216	0.4140875	0.2621204
sp Q64268 Heparin cofactor II	1	2	0.1154672	-0.317839	0.5489982	0.41535	0.2623869
sp Q5HZY0 UBX domain-containing protein 1	2	2	0.1097525	-0.297015	0.5101146	0.4155125	0.2626527
sp Q6MG49 Large prolin-rich protein	3	3	0.1159043	-0.432729	0.6836599	0.4159	0.2629183
sp Q62673 Serine/threonine-protein kinase	3	3	-0.112336	-0.521671	0.2877571	0.4160375	0.2631832
sp O54874 Serine/threonine-protein kinase	3	3	0.1075599	-0.377525	0.5683349	0.4163875	0.2634478
sp Q68FR6 Elongation factor 1-alpha	28	73	0.0817798	-0.03732	0.1976982	0.417025	0.2637126
sp B3GNI6 Septin-11	3	5	-0.09371	-0.354318	0.1713071	0.4182125	0.2639785
sp Q9ZON7 Potassium voltage-gated channel subfamily M member 1	2	2	-0.129621	-1.438886	1.4492027	0.41825	0.2642436
sp P68101 Eukaryotic translation initiation factor 4E	5	7	0.0892331	-0.115127	0.2997612	0.4190375	0.2645091
sp O08629 Transcriptic	4	6	0.0984537	-0.165755	0.3680534	0.4191	0.2647738
sp O35783 Calumenin	3	4	-0.115969	-0.683184	0.4704747	0.4193375	0.2650381
sp P07722 Myelin-associated glycoprotein	6	12	0.0880255	-0.157698	0.3096785	0.4199125	0.2653023
sp P85968 6-phosphogluconate dehydrogenase	11	19	0.0873626	-0.070651	0.2493103	0.4203875	0.2655665
sp B2GUV7 Eukaryotic translation initiation factor 4B	2	2	-0.114141	-0.640459	0.4090051	0.420475	0.26583
sp Q63258 Integrin alfa-5/beta-1	9	13	0.0837535	-0.074471	0.2317965	0.4207125	0.266093
sp Q4KLF8 Actin-related protein 2/3 complex subunit 2A	4	6	-0.088079	-0.297457	0.1271052	0.4207125	0.266355
sp P04462 Myosin-8 (Fibronectin type III domain containing)	2	3	-0.256917	-2.22159	1.6418445	0.421475	0.2666175
sp P17220 Proteasome activator complex subunit 1	5	8	-0.088296	-0.281337	0.1063834	0.4215875	0.2668793
sp Q6AYK8 Eukaryotic translation initiation factor 4B	3	3	0.1189381	-0.360641	0.5949887	0.4217	0.2671403
sp Q62703 Reticulocalbin	2	3	0.1217546	-0.351613	0.6279688	0.42215	0.2674013
sp P70627 Glutamate transporter	5	8	-0.095653	-0.360475	0.1703555	0.42245	0.2676619
sp Q7TNY6 Golgi residence protein	2	2	-0.108952	-0.574392	0.3372988	0.4225	0.2679217
sp Q9JIL9 Nibrin OS-FERM domain-containing protein	2	2	0.1498126	-0.529174	0.8564718	0.4226625	0.2681809
sp P58200 Vesicle transport protein	2	2	-0.106972	-0.498531	0.2913215	0.422875	0.2684396
sp Q62667 Major vault protein	8	11	-0.088898	-0.288692	0.1053957	0.4234125	0.2686983
sp Q920A6 Retinoid-inducible protein	2	2	-0.114541	-0.626146	0.404215	0.4243125	0.2689576
sp P48768 Sodium/calciumpotin ATPase	3	3	-0.146029	-0.916297	0.5530387	0.424425	0.2692163
sp Q6AXX6 UPF0765 protein	3	3	-0.112762	-0.681101	0.4819506	0.425825	0.2694765
sp P22509 rRNA 2'-O-ribose methyltransferase	4	5	-0.088713	-0.321434	0.1378831	0.4263375	0.2697366
sp P11608 ATP synthase	2	4	0.0979055	-0.196539	0.3963746	0.42655	0.2699962
sp P05065 Fructose-bisphosphate aldolase	21	49	-0.078861	-0.174423	0.0111038	0.426925	0.2702556
sp Q62658 Peptidyl-prolyl cis-trans isomerase	3	9	0.0886617	-0.088547	0.2699556	0.4272125	0.2705146
sp Q6P9T8 Tubulin beta-1 chain	2	7	-0.094094	-0.366715	0.1813263	0.427825	0.2707738
sp P14669 Annexin A3	3	4	-0.096431	-0.444751	0.2588792	0.428725	0.2710336
sp Q9WVCC Septin-7 OS	10	20	-0.078294	-0.170746	0.0148566	0.42905	0.271293

sp P00388 NADPH--cyt	6	10	-0.084012	-0.243302	0.0745378	0.4293125	0.2715521
sp Q5XHY7 Signal trans	1	2	0.1019805	-0.239771	0.4631036	0.429375	0.2718104
sp Q4V7A0 WD repeat-	1	2	0.1204909	-0.571147	0.8442147	0.4296875	0.2720684
sp Q63796 Mitogen-ac	2	2	0.126102	-0.548278	0.7994328	0.4297125	0.2723255
sp Q9Z0V6 Thioredoxin	2	2	-0.11223	-0.616522	0.4009329	0.4307875	0.2725836
sp P21670 Proteasome	3	4	0.0886355	-0.116432	0.2939446	0.430875	0.272841
sp Q9JIX3 F Bis(5'-aden	2	2	-0.087463	-0.6158	0.5283437	0.4310125	0.2730978
sp Q08877 Dynamin-3	4	12	-0.090701	-0.331519	0.1303094	0.43135	0.2733543
sp Q8VIJ5 Bifunctiona	6	7	0.0894902	-0.120864	0.3060283	0.431575	0.2736103
sp P54313 Guanine nu	4	5	-0.090617	-0.313538	0.1342295	0.4317875	0.2738658
sp O88204 Low-density	2	2	-0.117659	-0.732535	0.5026037	0.4318875	0.2741207
sp Q69FB3 Junctophilin	2	2	0.1009737	-0.213808	0.4495717	0.432075	0.274375
sp P70566 Tropomodu	7	7	0.0908319	-0.154121	0.3320912	0.43245	0.2746292
sp P47819 Glial fibrilla	28	58	0.1597067	-0.920259	1.2642468	0.4326125	0.2748828
sp Q62785 28 kDa heat	5	5	0.0944784	-0.189679	0.3832912	0.432625	0.2751356
sp Q9Z2F5 C-terminal-l	2	2	-0.11739	-0.648994	0.3891407	0.4331375	0.2753884
sp Q6P799 Seryl-tRNA	6	9	0.0889524	-0.130269	0.3148595	0.4334	0.2756408
sp P17702 60S riboson	4	7	0.079437	-0.028395	0.1928902	0.4338875	0.2758932
sp B0BNN3 Carbonic an	5	8	-0.106284	-0.575107	0.3831059	0.4353	0.276147
sp Q6AYM2 Tektin-2 OS	2	2	-0.088707	-0.345956	0.1767781	0.4355625	0.2764004
sp Q8K585 High mobili	4	5	0.0832029	-0.081419	0.2530989	0.435575	0.2766531
sp Q641X8 Eukaryotic t	4	4	0.1096032	-0.426466	0.6607045	0.4371125	0.2769074
sp Q9EPX0 Heat shock	4	4	-0.095229	-0.415729	0.2193339	0.437475	0.2771615
sp Q9R1T5 Aspartoacyl	9	11	-0.090262	-0.296658	0.1099682	0.4375625	0.2774148
sp Q68FQ2 Junctional a	2	2	-0.129793	-0.736336	0.4020195	0.4379375	0.277668
sp P09811 Glycogen pl	2	4	-0.103114	-0.50299	0.3114184	0.4387875	0.2779218
sp Q6RFZ7 Pleckstrin h	2	2	-0.094215	-0.528708	0.3413022	0.4390375	0.2781751
sp P84586 Heterogene	8	11	-0.080557	-0.22181	0.0655598	0.43925	0.278428
sp Q4VSI4 Ubiquitin cæ	3	4	-0.090201	-0.39824	0.2480477	0.4400875	0.2786813
sp P0C0A9 Small VCP/β	3	8	0.0832631	-0.122318	0.2830422	0.440225	0.2789342
sp P23593 Apolipoprot	3	6	0.1055649	-0.359144	0.5729042	0.4403375	0.2791863
sp A2VD12 Pre-B-cell le	2	2	-0.108631	-0.664432	0.4650583	0.4405875	0.2794381
sp Q6RJR6 Reticulon-3	4	6	0.086599	-0.15171	0.3186317	0.44095	0.2796897
sp Q3SWU3 Heterogene	1	2	0.0960605	-0.236579	0.4341918	0.44105	0.2799407
sp Q5U2U2 Crk-like pro	2	4	-0.094525	-0.463399	0.2823589	0.441525	0.2801916
sp P49088 Asparagine	2	3	-0.08444	-0.385702	0.2344974	0.4418	0.2804421
sp Q6AXS3 Protein DEK	1	2	0.1153415	-0.626482	0.8458019	0.442025	0.2806923
sp P07340 Sodium/pot	12	33	-0.078336	-0.186098	0.0217712	0.442175	0.2809418
sp P62982 Ubiquitin-4l	8	36	0.0764453	-0.022075	0.1758997	0.4425125	0.2811912
sp Q5RJQ4 NAD-depen	5	9	-0.100564	-0.534053	0.3497121	0.4428	0.2814402
sp P63174 60S riboson	4	6	0.0902227	-0.128762	0.3242139	0.44325	0.2816891
sp Q8R4C0 Calpain-5 O	2	2	-0.110929	-0.839377	0.6212248	0.4435125	0.2819377
sp Q5M9G3 Caprin-1 OS	6	7	0.0813033	-0.081424	0.2363169	0.444425	0.2821869
sp P24049 60S riboson	7	10	0.0833173	-0.079798	0.2509536	0.4450875	0.2824364
sp Q5U1Z0 Rab3 GTPas	3	4	0.0859992	-0.150677	0.3294558	0.4452125	0.2826853
sp P20070 NADH-cyto	7	14	0.0801458	-0.061711	0.2216554	0.4457125	0.2829342
sp P16975 SPARC OS=f	5	7	-0.088274	-0.354371	0.1778766	0.4459375	0.2831827

sp P85970 Actin-relate	6	9	-0.092595	-0.412589	0.222092	0.4460625	0.2834306
sp A1L1K3 Anaphase-p	2	2	-0.095525	-0.599323	0.4151121	0.4462125	0.283678
sp Q62881 Nucleolar p	2	3	-0.094187	-0.44918	0.2759125	0.4464875	0.283925
sp Q6AXS5 Plasminoge	5	7	0.085575	-0.138754	0.3058633	0.4475375	0.2841729
sp Q64060 Probable A1	2	4	0.0828685	-0.180428	0.3267726	0.4477625	0.2844204
sp Q9Z340 Partitioning	1	2	0.1010744	-0.395291	0.5883386	0.4478125	0.2846672
sp Q3KRE8 Tubulin bet	1	2	0.1105909	-0.524847	0.750977	0.44845	0.2849143
sp P28840 Neuroendo	1	2	-0.125187	-0.972573	0.728017	0.4486125	0.2851608
sp P20069 Mitochondr	2	2	0.1059179	-0.448776	0.6765282	0.448725	0.2854067
sp Q9Z2K3 Zinc finger	1	2	-0.132741	-1.412113	1.1127909	0.4489875	0.2856524
sp P70628 Interphotor	2	2	0.1713884	-0.431078	0.9535228	0.4491	0.2858974
sp P49816 Tuberin OS-	3	5	0.0992683	-0.232226	0.4696475	0.4493	0.286142
sp Q9QXQ0 Alpha-actin	20	27	-0.080089	-0.272624	0.1095196	0.4494875	0.2863862
sp Q4L208 Sodium/hyc	2	3	-0.092407	-0.464492	0.2543402	0.44975	0.28663
sp Q7TT49 Serine/thre	2	2	-0.100161	-0.602147	0.4412653	0.449775	0.2868732
sp Q8VII6 C Choline trar	9	19	0.0764118	-0.061753	0.2116125	0.450275	0.2871163
sp Q9WUB5 Nuclear rec	3	3	-0.092702	-0.60145	0.426306	0.450275	0.2873587
sp Q64680 Cytochrome	2	2	0.0929997	-0.384881	0.583816	0.450375	0.2876006
sp P13471 40S riboson	4	9	0.0793638	-0.075518	0.2341487	0.4504375	0.2878419
sp P36201 Cysteine-ric	4	10	-0.088458	-0.423032	0.2431332	0.451175	0.2880835
sp Q0ZCA7 C-type lectii	3	5	0.0796861	-0.224881	0.3664473	0.4524125	0.2883262
sp Q4QQV8 Charged mu	2	3	-0.094956	-0.578463	0.3671461	0.452475	0.2885683
sp P50475 Alanyl-tRNA	20	30	-0.076891	-0.187942	0.0376361	0.452575	0.2888098
sp O08838 Amphiphysi	7	11	0.0852098	-0.165415	0.3288201	0.4528875	0.2890511
sp Q01986 Dual specifi	2	4	0.1038911	-0.39149	0.6095955	0.452925	0.2892918
sp Q62950 Dihydropyri	2	7	-0.080617	-0.243809	0.076332	0.4542625	0.2895337
sp P34064 Proteasome	2	3	0.0912265	-0.298329	0.4985278	0.4545	0.2897752
sp Q9EPB1 Dipeptidyl p	2	7	-0.079312	-0.241551	0.0914418	0.4545625	0.2900161
sp Q505J8 Phenylalanyl	5	5	0.0871842	-0.199282	0.3676669	0.45505	0.290257
sp Q460M5 Leucine-rich	2	6	-0.080866	-0.252448	0.0926688	0.45565	0.2904981
sp P04631 Protein S10	4	19	0.0960722	-0.281527	0.4931749	0.4557625	0.2907387
sp P62853 40S riboson	3	5	0.0854587	-0.17696	0.3573285	0.4564625	0.2909796
sp Q62839 Golgin subf	2	2	-0.0762	-0.521099	0.4415389	0.4568	0.2912202
sp Q9Z1W6 Protein LYR	2	6	0.1023372	-0.409636	0.6224683	0.4569875	0.2914605
sp P62828 GTP-binding	6	13	-0.085832	-0.407335	0.2404552	0.457175	0.2917003
sp Q04931 FACT compl	4	4	0.0813472	-0.184341	0.345142	0.4576	0.29194
sp P06907 Myelin prot	10	100	-0.077415	-0.221468	0.0667121	0.4577125	0.2921793
sp Q6U6G5 Zinc finger	1	2	0.0930515	-0.456391	0.6241843	0.45835	0.2924187
sp Q812D1 PC4 and SFF	2	2	0.0941932	-0.442127	0.6474256	0.4586	0.2926578
sp O55096 Dipeptidyl p	7	9	-0.075266	-0.25407	0.1164049	0.458625	0.2928963
sp P63100 Calcineurin	5	5	0.0823154	-0.169843	0.3390652	0.4587	0.2931341
sp O54963 RE1-silencir	3	5	0.0774875	-0.053764	0.2164291	0.45905	0.2933718
sp Q63362 NADHdehy	2	3	0.0817254	-0.284648	0.4352159	0.4592	0.2936091
sp Q63754 Beta-synucl	1	2	0.1491207	-1.183664	1.5286566	0.4609	0.2938481
sp P60203 Myelin prot	11	53	0.10137	-0.542573	0.7623269	0.4613125	0.294087
sp Q794F9 4F2 cell-sur	4	7	-0.078967	-0.250968	0.0972616	0.461425	0.2943253
sp Q5PQQ1 tRNA modif	2	2	0.093184	-0.442264	0.5959645	0.461475	0.2945631

sp Q2PQA9 Kinesin-1 he	10	13	0.0769404	-0.058544	0.209505	0.4617625	0.2948006
sp Q4FZZ1 PX domain-	2	3	0.0837855	-0.219827	0.377999	0.462025	0.2950378
sp P02454 Collagen alp	11	26	-0.086468	-0.466322	0.2714467	0.4636625	0.2952766
sp P06238 Alpha-2-ma	2	2	0.0965004	-0.429955	0.6374854	0.464025	0.2955153
sp P05696 Protein kinet	5	7	0.0754126	-0.072062	0.2242393	0.4640375	0.2957534
sp Q68FQ0 T-complex p	17	26	0.0741038	-0.009436	0.157195	0.464525	0.2959914
sp Q10743 Disintegrin :	2	2	0.0791555	-0.284686	0.4250811	0.4646625	0.296229
sp Q32Q06 AP-1 compl	2	2	-0.092969	-0.663239	0.4551192	0.46515	0.2964665
sp Q63484 RAC-gamma	2	2	0.1145203	-1.017517	1.236957	0.4652625	0.2967036
sp Q63569 26S proteas	7	9	0.0788068	-0.111857	0.276336	0.465575	0.2969405
sp Q80ZG5 Pre-mRNA-s	3	3	-0.091273	-0.645386	0.4303993	0.466975	0.2971786
sp Q2M2R8 Peroxisoma	2	2	0.0901876	-0.520246	0.7175909	0.467825	0.2974173
sp Q9WVH8 Fibulin-5 OS	8	12	0.0788904	-0.073399	0.2359101	0.4679875	0.2976555
sp Q9JIP0 Transient re	2	2	-0.087745	-0.596161	0.4367433	0.468125	0.2978933
sp Q64649 Phosphoryl:	4	5	0.0803979	-0.208556	0.3720335	0.468275	0.2981306
sp Q66HA6 ADP-ribosyl	8	22	0.073318	-0.015691	0.1643691	0.46855	0.2983676
sp Q6RFY2 Phosphatas	1	3	0.088854	-0.443618	0.610709	0.46925	0.2986049
sp O35952 Hydroxyacy	4	6	-0.077724	-0.261061	0.1036435	0.4693	0.2988417
sp P38983 40S riboson	9	21	0.0749484	-0.031588	0.1823675	0.4695875	0.2990782
sp Q62807 Synaptotagi	2	2	0.0783489	-0.329344	0.4522822	0.4699125	0.2993144
sp P13635 Ceruloplasn	19	36	0.0753747	-0.053639	0.2070461	0.4701875	0.2995504
sp O35094 Mitochondr	4	6	0.0831743	-0.230904	0.3908881	0.47065	0.2997864
sp P20767 Ig lambda-2	3	8	0.0844747	-0.245511	0.4222525	0.4706625	0.3000218
sp Q6AY84 Secernin-1 (10	20	0.0774582	-0.117297	0.2777825	0.4707625	0.3002567
sp Q4FZY0 EF-hand do	4	5	0.0761731	-0.121517	0.280426	0.4713875	0.3004917
sp P06687 Sodium/pot	11	21	-0.076353	-0.214613	0.0549343	0.471425	0.3007262
sp P23562 Band 3 anio	7	15	0.0931792	-0.442536	0.6567181	0.471625	0.3009603
sp Q4V8K2 Beta-cateni	2	2	-0.084765	-0.53873	0.3527054	0.4717875	0.301194
sp P02680 Fibrinogen	2	2	-0.092195	-0.681126	0.5082435	0.4725	0.301428
sp P09456 cAMP-depe	3	3	-0.087212	-0.549493	0.3676648	0.4725875	0.3016615
sp Q793F9 Vacuolar pr	5	6	0.0809497	-0.298355	0.4519961	0.4732125	0.3018953
sp Q5EB77 Ras-related	2	2	0.0830425	-0.358791	0.5207303	0.4733125	0.3021285
sp P05943 Protein S10	5	19	0.0778017	-0.114187	0.2702271	0.47345	0.3023613
sp Q8VHK7 Hepatoma-	4	7	0.0784478	-0.150085	0.3020693	0.47365	0.3025937
sp P35465 Serine/thre	2	2	-0.083277	-0.498687	0.3549592	0.4741	0.3028261
sp P63039 60 kDa heat	28	54	-0.071882	-0.127751	-0.014723	0.474125	0.3030579
sp P52555 Endoplasmic	5	6	-0.078283	-0.307601	0.1508462	0.4745375	0.3032896
sp P85969 Beta-solubl	3	6	0.0751448	-0.074286	0.2298697	0.47505	0.3035214
sp P08461 Dihydrolipo	13	25	-0.073855	-0.185234	0.0352878	0.4752	0.3037528
sp Q4V7C6 GMP synthet	4	6	-0.076642	-0.329437	0.1733797	0.4760375	0.3039846
sp Q63356 Myosin-Ie C	3	3	0.0804359	-0.339787	0.5157083	0.476275	0.3042162
sp Q5XIE1 UPF0670 pr	5	7	-0.073831	-0.31429	0.1878532	0.476425	0.3044474
sp P40241 CD9 antigen	9	44	0.0756397	-0.091806	0.2496793	0.47685	0.3046785
sp P84092 AP-2 compl	6	8	-0.074645	-0.226959	0.0750427	0.4776	0.30491
sp Q6P4Z6 Leucine car	2	3	-0.078646	-0.353184	0.1749481	0.477775	0.3051411
sp P62747 Rho-related	3	4	0.0766471	-0.143566	0.3001972	0.4779	0.3053717
sp Q4KM73 UMP-CMP k	4	6	-0.074871	-0.310152	0.1580953	0.477975	0.3056019

sp Q5RKH0 Putative oxi	2	3	-0.073785	-0.467463	0.3388033	0.4780375	0.3058315
sp P20717 Protein-argi	5	8	0.0807865	-0.318855	0.4750777	0.47835	0.3060609
sp P60522 Gamma-am	2	3	0.0775394	-0.34353	0.4833743	0.478525	0.3062899
sp P58775 Tropomyosi	7	12	-0.097363	-1.250494	1.0813481	0.4787125	0.3065186
sp Q2V057 Probable pr	1	2	0.0793461	-0.315069	0.4666891	0.4787625	0.3067467
sp Q64232 Trans-2,3-e	4	7	0.0753121	-0.094892	0.2417362	0.4788375	0.3069744
sp Q9QY78 Inhibitor of	4	5	-0.075597	-0.319184	0.1662976	0.478875	0.3072014
sp Q5RKH1 Serine/thre	4	4	-0.077394	-0.376686	0.2307244	0.47975	0.3074291
sp O35763 Moesin OS-	16	25	-0.071348	-0.143939	0.0029372	0.4803625	0.3076569
sp O55035 Peptidyl-pro	2	2	0.0842083	-0.402162	0.6078893	0.4803875	0.3078842
sp Q63624 Splicing fact	2	2	-0.129559	-0.817686	0.4479366	0.4804625	0.308111
sp Q9QXU9 ProSAAS OS	3	4	0.0812561	-0.422001	0.5813669	0.480475	0.3083372
sp Q4G075 Leukocyte ε	3	3	-0.113391	-1.238113	0.9278007	0.480875	0.3085633
sp Q8R4T5 General rec	2	2	0.0910417	-0.325553	0.5366303	0.4809625	0.308789
sp Q99PF5 Far upstream	7	8	0.0748483	-0.094879	0.2439616	0.4810875	0.3090142
sp Q62645 Glutamate	1	6	-0.075702	-0.250025	0.1001498	0.4812125	0.309239
sp P11883 Aldehyde de	2	2	0.0824944	-0.705945	0.8372604	0.481525	0.3094636
sp Q62714 Neutrophil	1	3	-0.075484	-0.30023	0.137756	0.4818	0.309688
sp Q03410 Synaptonem	2	3	-0.07735	-0.514041	0.3509263	0.4819625	0.309912
sp P09606 Glutamine s	7	10	-0.073897	-0.320679	0.177683	0.4819875	0.3101355
sp Q923V4 F-box only p	2	3	0.07533	-0.200972	0.3430381	0.48225	0.3103587
sp Q4V7C7 Actin-relate	13	27	-0.07246	-0.180538	0.0349386	0.482275	0.3105814
sp P51792 H(+)/Cl(-) e	2	2	0.0855107	-0.349071	0.5293904	0.483075	0.3108046
sp P04905 Glutathione	6	9	0.0750846	-0.129532	0.2778204	0.4833125	0.3110275
sp B1H228 Coiled-coil c	2	2	-0.083504	-0.587996	0.4091675	0.4834	0.3112499
sp P41562 Isocitrate de	9	20	-0.072419	-0.228411	0.0874347	0.4836	0.311472
sp O35923 Breast canc	4	4	-0.081205	-0.789776	0.6446701	0.483725	0.3116937
sp Q99MI7 NEDD8-acti	2	4	0.072786	-0.171324	0.3190673	0.48375	0.3119148
sp O35162 Heat shock	2	2	0.0793579	-0.628825	0.7983311	0.483875	0.3121356
sp Q64632 Integrin bet	39	56	0.0723263	-0.034865	0.1797766	0.4842375	0.3123562
sp P70580 Membrane-	2	5	0.0747302	-0.123239	0.2802949	0.4844	0.3125765
sp Q6AYG3 Protein pru	2	4	0.0763009	-0.267672	0.405708	0.4844375	0.3127963
sp O35821 Myb-bindin	3	4	-0.075984	-0.352175	0.1990012	0.4847625	0.3130159
sp Q711G3 Isoamyl ace	2	2	-0.077754	-0.512002	0.3542647	0.4850375	0.3132353
sp O08697 ADP-ribosyl	3	4	-0.075265	-0.410287	0.2565377	0.4862375	0.3134557
sp A1L108 Actin-relate	2	2	0.0758187	-0.337889	0.4708093	0.486625	0.3138958
sp Q5U2Y0 WD repeat	1	3	-0.097296	-1.369745	1.1748043	0.486625	0.313676
sp Q9JKL7 ! Splicing reg	2	2	-0.073577	-0.584281	0.4308972	0.4868	0.3141152
sp P26772 10 kDa heat	10	24	-0.069857	-0.165875	0.0264944	0.48705	0.3143344
sp P11030 Acyl-CoA-bi	8	27	0.0758511	-0.249053	0.4072232	0.4873125	0.3145533
sp P53812 Phosphatid	2	2	-0.067772	-0.51801	0.3920467	0.48805	0.3147727
sp D3ZAP3 Uncharacte	1	2	0.0767528	-0.346682	0.4919669	0.4882875	0.3149917
sp P11884 Aldehyde de	16	41	0.0716894	-0.058027	0.1961158	0.4887625	0.3152109
sp Q5RJR2 Twinfilin-1 (2	3	0.0752304	-0.564876	0.6956503	0.489225	0.31543
sp O35263 Platelet-act	3	6	0.0744771	-0.117677	0.2711559	0.4892875	0.3156487
sp P42930 Heat shock	12	28	-0.072241	-0.175792	0.0313775	0.4893125	0.3158669
sp Q4V8H8 EH domain-	14	21	-0.073889	-0.285373	0.1361707	0.489575	0.3160848

sp P00406 Cytochrome	3	8	0.0736709	-0.067465	0.2130998	0.48965	0.3163023
sp Q5I0D5 Phospholysi	1	3	-0.07691	-0.837701	0.7057478	0.49015	0.3165199
sp P60669 Pleckstrin h	8	12	0.0735524	-0.099183	0.2433426	0.4904875	0.3167374
sp P47196 RAC-alpha s	1	2	-0.074019	-0.492038	0.3600048	0.490625	0.3169545
sp Q9QZ86 Nucleolar p	2	2	-0.073997	-0.320497	0.182311	0.49095	0.3171714
sp Q9HB97 Alpha-parvi	5	6	-0.073075	-0.287017	0.1436233	0.4909875	0.3173879
sp P97846 Contactin-a	4	10	0.0709731	-0.163219	0.2970296	0.4919	0.3176049
sp O35509 Ras-related	10	19	-0.07198	-0.175056	0.0285189	0.492175	0.3178218
sp Q63692 Hsp90 co-cl	4	9	-0.06995	-0.260151	0.1270255	0.4929125	0.318039
sp Q8K4T4 Filamin-A-ir	3	4	0.0712833	-0.513369	0.677485	0.4932125	0.3182561
sp Q63345 Myelin-olig	2	4	0.08448	-0.847892	1.0760991	0.4936875	0.3184732
sp O08730 Glycogenin-	3	6	0.0726501	-0.17627	0.3239992	0.49445	0.3186907
sp D3ZXK7 E3 ubiquitin	2	3	0.0749705	-0.292135	0.4455206	0.4945625	0.3189079
sp Q63486 Ras-related	2	3	0.072589	-0.368741	0.5105461	0.494725	0.3191247
sp Q9JLS3 Serine/thre	2	2	0.0772787	-0.564877	0.7400047	0.4949625	0.3193412
sp O35889 Afadin OS=I	5	5	-0.071169	-0.272696	0.1248719	0.4950125	0.3195573
sp Q505J6 Mitochondr	2	4	0.0726201	-0.077735	0.223461	0.495075	0.3197729
sp Q62774 Myosin-Ia (I	3	3	0.0932956	-0.954302	1.1487603	0.495225	0.3199882
sp Q6P742 Proteolipid	1	3	0.0887446	-0.536986	0.7832801	0.495275	0.320203
sp O35824 Dnaj homol	7	10	-0.070494	-0.195865	0.0639485	0.49645	0.3204187
sp O54861 Sortilin OS=	5	5	0.0790375	-0.195281	0.3826796	0.498675	0.3206366
sp Q9R283 Short transi	2	2	0.069585	-0.708953	0.8538498	0.498675	0.320854
sp P47863 Aquaporin-	2	3	-0.071178	-1.210223	1.0504703	0.498775	0.321071
sp Q62611 Interleukin-	3	3	0.0712088	-0.291233	0.4280543	0.4987875	0.3212875
sp Q4KLL9 Kinesin-like	2	2	-0.089825	-2.535286	2.3026117	0.4993	0.321504
sp Q3ZU82 Golgin subf	6	7	0.0707103	-0.148435	0.2862518	0.49955	0.3217204
sp Q9EQZ1 TSC22 dom:	1	4	-0.055195	-0.364694	0.2800148	0.4998625	0.3219366
sp Q4FZT0 Stomatin-li	4	5	0.0696583	-0.16557	0.3089848	0.4998875	0.3221523
sp P36972 Adenine ph	4	6	0.0717025	-0.155376	0.3013989	0.5	0.3223676
sp B5DF41 Syntaphilin	2	2	0.07016	-0.597111	0.7789928	0.5000875	0.3225825
sp O35346 Focal adhes	3	4	0.0688001	-0.353525	0.4788568	0.50025	0.322797
sp Q9JMC1 Phosphatid	2	2	-0.063598	-0.446539	0.3491354	0.5009	0.3230119
sp Q5XHY1 Leucine-rich	2	2	-0.068862	-0.490148	0.3436397	0.5014625	0.3232269
sp P57097 Tyrosine-pr	2	2	0.0709124	-1.0255	1.2283024	0.50175	0.3234417
sp Q920R4 G-protein c	4	4	-0.06889	-0.516799	0.3775501	0.50185	0.3236561
sp Q08326 Guanine nu	1	2	0.0710579	-0.386201	0.5498211	0.5019125	0.3238701
sp Q99J82 Integrin-link	5	5	-0.06714	-0.369548	0.2344452	0.502	0.3240837
sp B1WBU8 UPF0639 pr	3	4	0.0681168	-0.186497	0.3119845	0.50205	0.3242969
sp P02091 Hemoglobir	3	32	-0.070876	-0.52849	0.3890469	0.502175	0.3245096
sp O35112 CD166 anti-	3	3	-0.067401	-0.434536	0.3152557	0.50265	0.3247225
sp Q9EPJ0 Nuclear ubi	2	4	0.0708933	-0.120288	0.2672675	0.5032	0.3249354
sp Q792I0 Protein lin-	5	7	0.0768292	-0.133092	0.3008683	0.503575	0.3251484
sp Q99JD4 CLIP-associ	8	10	-0.068084	-0.265674	0.1323345	0.5038375	0.3253611
sp Q9JLH7 CDK5 regulat	3	3	-0.062875	-0.456487	0.3463283	0.504525	0.3255741
sp P69735 Rab3 GTPas	2	3	0.0741379	-0.223642	0.3810158	0.5048125	0.325787
sp Q9Z142 Transmemb	2	4	0.0697332	-0.211969	0.362928	0.5054	0.3260001
sp P10536 Ras-related	3	3	-0.070399	-0.367309	0.2111018	0.505475	0.3262127

sp P0C0A2 Vacuolar pr	2	2	-0.066751	-0.755749	0.6335908	0.5064125	0.326426
sp Q7M0E3 Destrin OS=	10	17	-0.067962	-0.29816	0.168894	0.506425	0.3266387
sp P15390 Sodium cha	3	3	-0.064324	-0.510044	0.3793858	0.5068125	0.3268514
sp Q8R4A1 ERO1-like p	2	2	-0.063353	-0.570312	0.4348624	0.5071625	0.3270641
sp P62483 Voltage-gat	4	6	-0.071629	-0.260948	0.1012234	0.507275	0.3272763
sp Q5XI32 F-actin-cap†	6	10	-0.067052	-0.261118	0.1280442	0.508425	0.3274895
sp Q63413 Spliceosom	8	13	0.0691831	-0.032402	0.1667146	0.5088125	0.3277025
sp Q32PX2 Aminoacyl t	5	5	-0.068189	-0.287251	0.1494039	0.5088375	0.3279151
sp Q5HZV9 Protein pho	3	4	-0.065637	-0.370471	0.2523084	0.509	0.3281274
sp P26770 Adenylate c	2	2	-0.073265	-0.502506	0.3617381	0.50915	0.3283394
sp P0C7L8 Protein pho	3	3	0.0610819	-1.097027	1.2029284	0.50925	0.328551
sp Q9JJ50 † Hepatocyte	3	6	0.0686101	-0.321857	0.466395	0.5094	0.3287623
sp P13803 Electron tra	10	15	-0.06815	-0.20753	0.078518	0.5096375	0.3289733
sp Q62920 PDZ and LIN	2	2	-0.065546	-0.566579	0.4368457	0.5098625	0.3291841
sp P30835 6-phosphof	3	3	-0.070403	-0.353612	0.2012327	0.509975	0.3293946
sp P63095 Guanine nu	6	10	-0.068056	-0.247169	0.1125594	0.510625	0.3296053
sp Q99M63 WD40 repe	4	7	0.0655064	-0.17854	0.2946411	0.51065	0.3298156
sp Q71UE8 NEDD8 OS=	4	8	0.0680936	-0.183372	0.3222382	0.510675	0.3300254
sp Q5BJS7 Copine-9 O†	2	4	0.0649624	-0.361979	0.4684362	0.511075	0.3302352
sp P62907 60S riboson	7	14	0.0692044	-0.053885	0.1922159	0.51145	0.330445
sp P62898 Cytochrome	6	14	-0.061373	-0.488006	0.3587932	0.5115875	0.3306544
sp Q99N27 Sorting nexi	6	8	-0.068835	-0.292017	0.1429755	0.5115875	0.3308633
sp P62893 60S riboson	1	2	0.0561131	-0.984573	1.1250028	0.511725	0.3310719
sp P22756 Glutamate i	2	2	0.0476624	-0.753359	0.8221062	0.5118125	0.3312801
sp P31232 Transgelin C	16	45	-0.055818	-1.130976	1.0009119	0.51255	0.3314887
sp Q9QZR8 PDZ domair	2	2	-0.067148	-0.655176	0.4947267	0.5128	0.3316971
sp Q566C7 Diphosphoi	2	3	0.0664181	-0.246159	0.389974	0.512875	0.3319051
sp Q5U2Y1 General tra	1	4	-0.063602	-0.647081	0.5222995	0.5139625	0.3321139
sp P21396 Amine oxid	5	7	0.0685211	-0.153375	0.2839321	0.51435	0.3323227
sp A0JPP8 Coiled-coil c	2	2	-0.062668	-0.458185	0.3394505	0.5147125	0.3325314
sp Q4QR80 28S riboson	1	2	0.0617776	-0.302714	0.4048873	0.5148	0.3327397
sp P0COR5 Phosphoino	3	3	-0.064193	-0.491813	0.3432127	0.51485	0.3329475
sp Q4G055 RNA-bindin	2	2	0.0537574	-0.842665	0.9752665	0.5160875	0.3331564
sp P35467 Protein S10	1	2	-0.054756	-0.76691	0.6926629	0.5165375	0.3333652
sp Q5U2Q3 Ester hydro	2	4	0.0639087	-0.33408	0.4714574	0.516575	0.3335737
sp B2RZ78 Vacuolar pr	6	13	0.0699456	-0.093675	0.2454045	0.517025	0.3337821
sp Q6I7R3 Isochorismat	1	4	-0.062395	-0.414564	0.2775268	0.5171375	0.3339903
sp Q62835 Rab GTPase	2	3	-0.062666	-0.400093	0.2777848	0.517625	0.3341985
sp P13638 Sodium/pot	2	9	-0.060459	-0.422829	0.3064959	0.5181375	0.3344068
sp Q9Z1M9 Structural n	6	6	0.0660308	-0.179687	0.3042799	0.518875	0.3346154
sp Q9R0I8 Phosphatid	2	3	-0.058743	-0.359604	0.2567991	0.5193125	0.3348241
sp P13668 Stathmin O†	12	26	-0.064058	-0.298642	0.1701535	0.5200125	0.3350332
sp Q3KRD5 Mitochondr	5	7	-0.066311	-0.30961	0.1827957	0.5200375	0.3352417
sp O54772 SWI/SNF-re	1	3	0.0634783	-0.268218	0.3983789	0.5200625	0.3354499
sp Q5XI78 2-oxoglutar	19	34	-0.067947	-0.187459	0.0509836	0.520175	0.3356576
sp P11506 Plasma mer	2	2	0.0594216	-0.549035	0.7029418	0.520225	0.335865
sp Q66H10 F-box only p	2	2	-0.068434	-0.596979	0.4387528	0.5205375	0.3360723

sp P06686 Sodium/pot	16	21	-0.062982	-0.339811	0.2106549	0.5206375	0.3362792
sp P63055 Purkinje cel	3	12	0.0647695	-0.205375	0.3415354	0.52095	0.336486
sp P70645 Bleomycin t	3	3	0.0596407	-0.40253	0.5296026	0.5211625	0.3366926
sp Q62871 Cytoplasmic	6	12	0.0677318	-0.056498	0.1893093	0.521425	0.336899
sp P11517 Hemoglobir	3	17	-0.057211	-0.525788	0.4124912	0.5215	0.337105
sp Q6IMX7 Hsp70-bind	5	6	0.061673	-0.27143	0.4095625	0.52185	0.337311
sp P08289 Alkaline pho	5	8	-0.060762	-0.401209	0.2698455	0.52215	0.3375168
sp P61972 Nuclear tra	3	5	0.065019	-0.101283	0.2356813	0.5225625	0.3377226
sp P32577 Tyrosine-pr	2	2	-0.058998	-0.441449	0.3358495	0.5228875	0.3379284
sp P97834 COP9 signal	3	3	-0.059981	-0.402344	0.2720419	0.5241375	0.338135
sp P63029 Translation:	7	16	0.0679694	-0.090487	0.2297693	0.5252875	0.3383425
sp P20595 Guanylate c	2	2	0.0481296	-0.697582	0.787257	0.52585	0.3385502
sp P15146 Microtubul	9	10	0.0661486	-0.116629	0.2508284	0.5259	0.3387574
sp Q6F6B3 Protein TAN	2	2	-0.059597	-0.476957	0.3334585	0.5273625	0.3389658
sp P09626 Potassium-t	2	2	0.056162	-0.302285	0.4003044	0.5281375	0.3391746
sp Q66H86 Olfactomed	3	5	0.0594511	-0.290334	0.4160663	0.52855	0.3393834
sp Q9QUH6 Ras GTPase	2	9	-0.061564	-0.298102	0.1874069	0.5286375	0.3395919
sp Q6AYE2 Endophilin-	2	2	0.0453231	-0.87636	0.963281	0.5286625	0.3397998
sp Q5XIS1 Protein pho	2	2	0.0672582	-0.216822	0.3665234	0.528775	0.3400075
sp P62138 Serine/thre	3	4	0.064209	-0.138138	0.2686208	0.529275	0.3402153
sp Q5U300 Ubiquitin-lil	27	46	0.0663433	-0.074482	0.2041036	0.5294125	0.3404227
sp P27653 C-1-tetrahy	7	11	-0.063804	-0.234097	0.1086382	0.529625	0.34063
sp Q80VJ4 Putative gly	2	2	-0.062872	-0.412712	0.2628061	0.5299875	0.3408371
sp Q9Z2X3 26S proteas	2	2	0.0559229	-0.42593	0.5198543	0.5300875	0.341044
sp P35446 Spondin-1 C	2	4	-0.065591	-0.224946	0.0879478	0.5302625	0.3412505
sp Q63862 Myosin-11 (18	28	-0.04083	-0.912687	0.8134597	0.5302875	0.3414567
sp P83732 60S riboson	6	10	0.0658777	-0.079634	0.2108005	0.5305375	0.3416626
sp P13596 Neural cell :	17	25	0.0649494	-0.056774	0.1856423	0.531475	0.3418692
sp P05370 Glucose-6- β	11	19	-0.059932	-0.329048	0.2018093	0.5315375	0.3420754
sp Q63584 Transmemb	4	9	0.0673017	-0.047829	0.1851748	0.5322625	0.3422819
sp A4L9P8 Protein KIA/	2	2	-0.048794	-0.530511	0.4438363	0.5327	0.3424884
sp P18421 Proteasome	7	8	-0.060127	-0.240117	0.1207884	0.532825	0.3426946
sp Q4V8C3 Echinoderm	3	8	-0.060171	-0.302554	0.1797446	0.53345	0.342901
sp Q6AXM7 HBS1-like pi	5	6	0.0582342	-0.258984	0.3728016	0.53405	0.3431077
sp Q811U3 ELKS/Rab6-	2	2	-0.047239	-0.479229	0.4004118	0.5340625	0.3433139
sp P46844 Biliverdin re	6	6	-0.060965	-0.27811	0.1565877	0.5341125	0.3435197
sp Q6BBI8 Ubiquitin-fc	2	3	-0.059239	-0.305727	0.1882248	0.5341625	0.3437252
sp P12346 Serotransfe	35	100	-0.059933	-0.340603	0.2198252	0.5341875	0.3439302
sp Q6AXQ0 SUMO-activ	2	3	-0.052618	-0.500497	0.4038629	0.5342875	0.3441349
sp Q5U211 Sorting nexi	2	3	0.0580533	-0.295474	0.4176177	0.5344625	0.3443393
sp Q62639 GTP-binding	3	4	0.0580703	-0.223849	0.3369809	0.534475	0.3445433
sp P02466 Collagen al β	7	16	-0.055175	-0.456689	0.3245301	0.534975	0.3447474
sp Q5U2N3 Membrane-	2	2	-0.061747	-0.251157	0.1325986	0.5353875	0.3449515
sp Q63644 Rho-associa	3	3	-0.059901	-0.400996	0.2899208	0.535675	0.3451555
sp Q5XI55 Peptide-N(4	2	2	-0.057093	-0.352778	0.2465214	0.5358	0.3453592
sp Q68FX0 Isocitrate d	7	14	-0.064973	-0.212032	0.0777366	0.5364375	0.3455631
sp Q4QR75 Exosome cc	2	2	-0.038719	-0.558138	0.5100091	0.5364625	0.3457666

sp O08700 Vacuolar pr	3	3	-0.049722	-0.52172	0.4218358	0.5368625	0.3459701
sp P30009 Myristoylat	8	16	-0.060436	-0.262451	0.1501922	0.5372	0.3461736
sp Q62698 Cytoplasmic	4	4	-0.047394	-0.43386	0.3675396	0.5372	0.3463766
sp Q66HA8 Heat shock	18	26	-0.065444	-0.16887	0.0438511	0.5387	0.3465807
sp Q9ES21 Phosphatid	5	6	-0.061693	-0.262283	0.1366904	0.5389625	0.3467848
sp Q9ESW0 DNA damag	10	13	0.0641543	-0.090944	0.2157209	0.53935	0.3469887
sp P70579 Metabotrop	2	2	-0.056438	-0.460005	0.3219999	0.5393875	0.3471923
sp P08082 Clathrin ligh	7	14	-0.065089	-0.171699	0.0420507	0.5397375	0.3473959
sp Q5S6T3 2-C-methyl-	1	2	-0.044904	-0.562672	0.4772036	0.5400625	0.3475993
sp O35567 Bifunctiona	12	20	-0.06506	-0.181792	0.0518659	0.5401375	0.3478024
sp P0C0S7 Histone H2/	2	5	0.0583395	-0.165577	0.2798063	0.5406875	0.3480057
sp Q10758 Keratin, typ	2	2	-0.04157	-0.641869	0.5885844	0.54115	0.348209
sp Q9JLA3 UDP-glucos	6	6	0.0530706	-0.275972	0.3748492	0.5412125	0.3484119
sp P04646 60S riboson	5	9	0.0638795	-0.066764	0.2015219	0.5413625	0.3486146
sp P50408 V-type prot	2	2	-0.041623	-0.547028	0.5067934	0.541525	0.348817
sp Q68FR9 Elongation	4	11	0.065487	-0.058936	0.1919133	0.541625	0.3490191
sp P18163 Long-chain-	2	2	0.0513023	-0.344697	0.4469673	0.5416875	0.3492209
sp P21708 Mitogen-ac	14	26	0.0633368	-0.103347	0.2334771	0.541925	0.3494225
sp P52591 Nuclear env	2	2	-0.049999	-0.401983	0.3117482	0.541925	0.3496236
sp Q9ES54 Nuclear pro	2	2	-0.036599	-0.75867	0.7118687	0.5424625	0.3498249
sp Q80ZF0 Collagen al β	3	4	-0.052565	-0.598059	0.4653864	0.5431875	0.3500265
sp P23785 Granulins O	2	3	-0.050792	-0.587973	0.4809175	0.543375	0.3502279
sp P16303 Carboxylest	6	8	-0.029584	-0.654467	0.6364628	0.5433875	0.3504289
sp P62749 Hippocalcin	2	4	0.0569695	-0.199078	0.3226959	0.5435375	0.3506297
sp Q9ESR9 ATP-binding	2	2	-0.048981	-0.524457	0.425513	0.5447125	0.3508312
sp P41350 Caveolin-1 (9	17	-0.056741	-0.316411	0.2100931	0.5450875	0.3510327
sp Q5FWY5 AH receptor	1	2	0.0471569	-0.363599	0.4660255	0.5455	0.3512342
sp Q08834 Alpha-1,6-n	2	2	0.0438475	-0.490181	0.5604578	0.5457	0.3514356
sp P26817 Beta-adren	4	4	-0.047691	-0.669157	0.5652868	0.546025	0.3516368
sp O70173 Phosphatid	2	2	0.0232548	-0.90471	0.9937444	0.54645	0.351838
sp Q4QR83 Stimulated	3	3	0.0475679	-0.448413	0.5192358	0.5464625	0.3520389
sp P62914 60S riboson	4	5	-0.060354	-0.225845	0.1094153	0.546575	0.3522394
sp P05714 Ras-related	1	2	-0.049334	-0.39127	0.2949888	0.5474625	0.3524405
sp Q6Q0N1 Cytosolic nc	4	7	0.0632936	-0.070333	0.1994134	0.5475125	0.3526412
sp Q78ZR5 Homeodom	2	2	0.0492729	-0.34108	0.4362408	0.5478625	0.3528418
sp Q641Y8 ATP-depend	8	13	-0.063123	-0.232696	0.0970238	0.5480875	0.3530423
sp O88902 Tyrosine-pr	3	3	0.0363995	-0.773079	0.8414012	0.5487625	0.353243
sp Q5I0H9 Protein disu	2	2	0.0496402	-0.403242	0.5185859	0.5488125	0.3534434
sp Q6AY20 Cation-depe	4	8	0.0603949	-0.106922	0.2244397	0.548925	0.3536435
sp Q63525 Nuclear mi \circ	6	7	0.060675	-0.104785	0.2229347	0.548925	0.3538432
sp Q62665 Galectin-8 C	1	2	-0.045681	-0.443275	0.3447061	0.54955	0.3540431
sp Q02874 Core histon	8	18	0.0605224	-0.103606	0.2239944	0.5496625	0.3542427
sp O88267 Acyl-coenzy	3	4	-0.056651	-0.37487	0.2566423	0.5501125	0.3544423
sp Q9JJ54 Heterogene	6	10	0.0643292	-0.116173	0.2649425	0.5505125	0.354642
sp Q8CG45 Aflatoxin B1	5	7	-0.057624	-0.283469	0.1655086	0.550625	0.3548414
sp P62859 40S riboson	3	7	0.0569474	-0.15768	0.2837058	0.5515375	0.3550413
sp Q80W92 Protein VAC	2	2	0.0258458	-0.878236	0.9691726	0.5515625	0.3552408

sp P07633 Propionyl-C	2	2	-0.030981	-0.81473	0.760032	0.551825	0.3554402
sp P41777 Nucleolar a	2	2	0.0579049	-0.161904	0.2852705	0.552075	0.3556394
sp P62744 AP-2 compl	2	3	-0.037944	-0.5226	0.4366737	0.5524375	0.3558386
sp O88506 STE20/SPS1	8	13	0.0611123	-0.085399	0.2039245	0.552575	0.3560375
sp Q704S8 Carnitine O-	6	6	0.0559059	-0.168125	0.2734979	0.5527	0.3562361
sp Q71UF4 Histone-bin	3	4	-0.0523	-0.308091	0.2017616	0.5533	0.356435
sp Q4KMA0 5-azacytidir	2	3	0.0538244	-0.183637	0.2993168	0.5542625	0.3568334
sp P14408 Fumarate h	10	19	-0.062502	-0.181827	0.0620672	0.5547625	0.3570325
sp Q704E8 ATP-binding	2	4	-0.046645	-0.388655	0.2979462	0.554775	0.3572312
sp Q62838 Muscle, ske	2	2	-0.024087	-0.734354	0.7219688	0.555	0.3574298
sp Q3T1J8 UPF0549 pr	2	2	-0.031916	-0.70307	0.6210602	0.55565	0.3576286
sp Q99M64 Phosphatid	2	2	0.048062	-0.331449	0.4371341	0.55645	0.3578278
sp Q62910 Synaptojani	17	25	0.0627228	-0.07788	0.2112493	0.55655	0.3580268
sp P83868 Prostagland	4	8	0.0619094	-0.069304	0.1986764	0.556825	0.3582256
sp Q6DGG0 Peptidyl-pro	5	8	0.0568767	-0.135556	0.2587535	0.5576375	0.3584248
sp Q3T1J1 Eukaryotic t	6	10	0.061452	-0.119459	0.2445191	0.55765	0.3586236
sp Q9R1T9 Potassium v	3	3	0.0406944	-0.4255	0.5013408	0.55785	0.3588222
sp B0K025 Oligosaccha	1	2	0.025674	-0.705068	0.7739525	0.557875	0.3590205
sp Q60587 Trifunctiona	14	28	-0.064085	-0.162137	0.0305763	0.558575	0.3592191
sp P09414 Nuclear fac	1	2	0.049431	-0.254125	0.3543564	0.558625	0.3594173
sp P14659 Heat shock-	16	24	-0.06068	-0.222619	0.0983408	0.5587	0.3596152
sp Q66HG3 Beta-Ala-Hi	1	2	0.0421242	-0.328744	0.3984667	0.5587875	0.3598128
sp P62628 Dynein light	3	5	-0.046371	-0.350949	0.2524008	0.5590125	0.3600102
sp P32198 Carnitine O-	3	6	0.0506064	-0.231997	0.3358177	0.5597125	0.3602079
sp Q64380 Sarcosine d	2	3	-0.041112	-0.423071	0.3576129	0.5597125	0.3604052
sp Q05764 Beta-adduc	5	7	0.0545151	-0.167903	0.2756979	0.5597375	0.3606022
sp POCB49 YLP motif-co	2	2	-0.019832	-0.838757	0.7939173	0.5602625	0.3607993
sp P41413 Proprotein	2	2	-0.0292	-0.664171	0.5974632	0.5603625	0.3609961
sp P04906 Glutathione	7	25	0.0601383	-0.089278	0.2126254	0.560875	0.361193
sp Q66H80 Coatomer s	3	5	0.0574954	-0.1422	0.2597647	0.561025	0.3613897
sp P85973 Purine nucle	6	8	0.0475023	-0.282801	0.3665081	0.561225	0.3615862
sp O88420 Sodium cha	5	5	-0.047634	-0.336004	0.255215	0.5616625	0.3617828
sp P47860 6-phosphof	17	31	-0.059246	-0.203343	0.0877079	0.5622125	0.3619795
sp P97521 Mitochondr	2	2	-0.047817	-0.555592	0.4210479	0.5631625	0.3621767
sp P51886 Lumican OS	16	61	-0.047956	-0.349161	0.2527914	0.5632625	0.3623736
sp Q5PQN2 Bifunctiona	2	2	0.0304489	-0.358481	0.3910755	0.5633	0.3625702
sp P62804 Histone H4	11	61	0.0587435	-0.089386	0.2065661	0.5634875	0.3627666
sp P26051 CD44 antige	1	2	0.0468437	-0.330228	0.4169369	0.5637	0.3629629
sp Q9Z1B2 Glutathione	2	5	-0.05573	-0.236405	0.1222153	0.5638125	0.3631588
sp Q5SGE0 Leucine-rich	6	9	0.0577889	-0.093798	0.2099472	0.5638625	0.3633544
sp P56571 ES1 protein	11	21	-0.061377	-0.164799	0.0457551	0.5639	0.3635497
sp Q63755 PR domain :	2	2	-0.009614	-0.708009	0.716313	0.5652125	0.3637459
sp Q5XI63 Kinesin-like	4	4	-0.018747	-0.449422	0.4443448	0.56535	0.3639418
sp Q5M7A7 CB1 cannab	2	2	-0.016287	-0.724352	0.6764734	0.565425	0.3641374
sp Q63537 Synapsin-2	1	3	0.0387036	-0.366411	0.4451859	0.56555	0.3643328
sp P63245 Guanine nu	10	19	0.0603772	-0.059885	0.1853081	0.5656625	0.3645279
sp P35559 Insulin-degr	2	3	-0.043585	-0.327956	0.2463423	0.565775	0.3647227

sp Q5M9F8 N-terminal	3	3	-0.043747	-0.583076	0.4496981	0.5667125	0.364918
sp Q6AYT3 UPF0027 pr	9	14	0.059546	-0.066092	0.1848471	0.5669875	0.3651133
sp Q9QXU8 Cytoplasmic	5	5	-0.049972	-0.315718	0.2143981	0.5670875	0.3653082
sp P63012 Ras-related	2	2	-0.048812	-0.489173	0.3740353	0.5671375	0.3655028
sp Q62951 Dihydropyri	6	8	-0.049477	-0.298733	0.1968789	0.5675	0.3656974
sp P0C588 Metal trans	3	3	0.0346117	-0.383247	0.4540707	0.5675375	0.3658917
sp Q8VHZ8 Down syndr	2	2	0.0288374	-0.495813	0.5434642	0.567675	0.3660857
sp P62963 Profilin-1 O:	9	18	-0.061341	-0.171717	0.0535307	0.5681875	0.3662799
sp Q4L1J4 Membrane-	1	2	0.0372076	-0.386833	0.4498426	0.5682875	0.3664737
sp O70143 SHC-transfc	2	2	0.0029052	-0.875583	0.8808456	0.5684125	0.3666674
sp A7VJC2 Heterogene	11	20	0.0625285	-0.04955	0.175571	0.5689	0.3668611
sp Q63797 Proteasome	5	7	0.0579604	-0.09193	0.2164057	0.568925	0.3670544
sp P36953 Afamin OS=	9	16	-0.047152	-0.339811	0.2548149	0.5690875	0.3672476
sp Q10728 Protein pho	2	2	-0.039542	-0.376137	0.31415	0.5695125	0.3674408
sp Q6AYQ3 Phenylalanyl	2	2	0.0395646	-0.392571	0.466985	0.569525	0.3676336
sp Q4V8F9 Hydroxystei	2	2	-0.031223	-0.581651	0.4978885	0.569625	0.3678261
sp Q09426 2-hydroxyac	3	3	-0.034773	-0.368998	0.317542	0.5701125	0.3680188
sp O35274 Neurabin-2	2	2	-0.052649	-0.296809	0.1922498	0.57015	0.3682111
sp P70541 Translation	1	2	0.0377569	-0.362174	0.4146305	0.570325	0.3684032
sp P50411 Protein pho	1	2	0.0447605	-0.276429	0.3602679	0.5703625	0.368595
sp O89046 Coronin-1B	3	3	0.046592	-0.233996	0.326473	0.57045	0.3687866
sp Q9JHZ4 GRIP1-assoc	4	5	-0.053425	-0.248248	0.1368499	0.570475	0.3689777
sp Q8K4G9 Podocin OS	2	2	-0.038871	-0.58949	0.4953708	0.5708	0.3691688
sp Q8CJ99 Sodium cha	2	2	-0.031134	-0.528108	0.4728907	0.5709875	0.3693598
sp P18596 Sarcoplasm	1	3	-0.044583	-0.315975	0.2392043	0.5711375	0.3695505
sp P36876 Serine/thre	3	3	0.0171808	-0.711745	0.7527508	0.5715875	0.3697413
sp P58365 Cadherin-2:	3	5	0.0512827	-0.16573	0.2738235	0.57165	0.3699318
sp P27321 Calpastatin	5	5	-0.05243	-0.295368	0.1823108	0.572475	0.3701227
sp Q9Z2G8 Nucleosom	5	5	-0.032292	-0.412971	0.3740716	0.5726375	0.3703133
sp Q8K3X0 Protein CAS	2	2	-0.047973	-0.773065	0.5742712	0.57265	0.3705037
sp Q63505 General trai	4	5	-0.051655	-0.373255	0.2517324	0.5726625	0.3706937
sp O55171 Acyl-coenzy	4	7	0.0432558	-0.242034	0.3173209	0.5728	0.3708835
sp P04897 Guanine nu	7	12	0.0569046	-0.086822	0.2015292	0.57325	0.3710733
sp Q5M7V8 Thyroid hor	5	5	0.0474143	-0.220417	0.3300773	0.574175	0.3712636
sp P47198 60S riboson	4	10	0.0585219	-0.079643	0.1937357	0.5743	0.3714538
sp P38444 Activin rece	2	4	0.0394593	-0.336778	0.4332175	0.5743625	0.3716436
sp A2RRU3 U3 small nu	2	2	-0.015419	-0.475243	0.482363	0.574675	0.3718333
sp P19527 Neurofilam	25	100	-0.064567	-0.133344	0.0032471	0.574925	0.3720229
sp P97576 GrpE protei	5	7	-0.046096	-0.314271	0.2154032	0.57505	0.3722123
sp O35550 Rab GTPase	2	2	-0.033243	-0.522312	0.4238942	0.5753375	0.3724016
sp Q63531 Ribosomal p	2	3	-0.024736	-0.723721	0.6633767	0.5754375	0.3725907
sp Q8VHK0 Acyl-coenzy	2	3	0.045051	-0.215806	0.3205581	0.575675	0.3727796
sp Q9EQV9 Carboxypep	1	2	-0.034163	-0.511303	0.4279488	0.5759625	0.3729684
sp P37397 Calponin-3	8	16	0.0568116	-0.108281	0.2342027	0.575975	0.3731569
sp Q6AXU3 Interferon-s	2	2	0.039873	-0.338989	0.3949019	0.5765	0.3733456
sp B0BNF1 Septin-8 OS	3	5	0.051129	-0.147572	0.2560266	0.5766875	0.373534
sp Q9WTZ3 Membrane-	2	4	0.0524086	-0.138589	0.2550825	0.5768375	0.3737223

sp O35413 Sorbin and	5	6	-0.016308	-0.651109	0.6140626	0.5770875	0.3739104
sp P41542 General ves	11	15	0.0535708	-0.154578	0.2719404	0.57715	0.3740982
sp P08033 Gap junctio	1	3	0.0366467	-0.392812	0.4550911	0.5773	0.3742858
sp Q6DGG1 Abhydrolas	2	2	0.0228211	-0.48774	0.5251294	0.577675	0.3744735
sp Q5HZA6 Prolyl endo	7	11	-0.053112	-0.225133	0.1215373	0.577925	0.374661
sp Q6PECO Bis(5'-nucle	3	3	0.0277154	-0.429146	0.4647081	0.5780375	0.3748483
sp Q5XHZ0 Heat shock	5	6	0.0539857	-0.125503	0.2260048	0.578675	0.3750358
sp Q8CG09 Multidrug r	2	2	0.0218859	-0.688425	0.782924	0.5789875	0.3752232
sp O35828 Coronin-7 (I	3	3	0.0394319	-0.273404	0.3581341	0.57905	0.3754104
sp P61265 Syntaxin-1B	4	6	0.0511959	-0.147821	0.2442969	0.5791125	0.3755973
sp O70593 Small glutar	2	5	-0.044358	-0.303326	0.2118646	0.5792	0.3757839
sp P63090 Pleiotrophin	3	4	0.0557062	-0.106539	0.2255509	0.5793375	0.3759703
sp Q9R0T4 Cadherin-1	6	7	-0.054783	-0.216588	0.1003007	0.5797625	0.3761568
sp Q3B7D1 Ubiquitin-cc	1	2	0.0083789	-0.752113	0.7488054	0.580175	0.3763432
sp Q62764 DNA-bindin	2	4	-0.036586	-0.388247	0.3113939	0.5802125	0.3765294
sp Q9JJ79 [I] Cytoplasmic	3	3	-0.037309	-0.391467	0.3168804	0.5804375	0.3767155
sp Q99J86 Attractin OS	2	2	-0.027521	-0.636882	0.5654077	0.580675	0.3769014
sp Q63544 Gamma-syn	10	35	0.0513546	-0.161767	0.2677807	0.58125	0.3770875
sp O35831 Cyclin-depe	2	2	0.015076	-0.533757	0.5635322	0.5816125	0.3772736
sp P50123 Glutamyl ar	2	2	0.0106035	-0.670387	0.6706293	0.5816375	0.3774594
sp P62815 V-type prot	8	16	-0.058374	-0.175417	0.0604235	0.58205	0.3776452
sp Q9QWNt Spectrin bet	14	28	0.0610352	-0.036351	0.1582043	0.582075	0.3778307
sp Q7TP36 Protein Shr	2	2	0.0209434	-0.480396	0.5362067	0.58255	0.3780163
sp P07335 Creatine kir	20	50	-0.054063	-0.215836	0.1102323	0.5825875	0.3782016
sp O55081 Retinoblast	2	2	0.0239867	-0.470912	0.5280224	0.5830125	0.378387
sp Q63663 Interferon-i	3	4	-0.033575	-0.439931	0.3646691	0.5834625	0.3785724
sp P50554 4-aminobut	9	16	0.0524449	-0.133648	0.2360641	0.58475	0.3787586
sp P29315 Ribonucleas	10	18	0.0600399	-0.0448	0.1700996	0.584825	0.3789446
sp Q3B7L1 Pleckstrin h	1	2	-0.05104	-0.216403	0.1251603	0.58485	0.3791303
sp Q5U312 Ankycorbin	4	4	0.0363475	-0.313793	0.3736384	0.5850875	0.3793158
sp Q5M827 Pirin OS=Ra	3	3	0.0313588	-0.38616	0.4487055	0.5854	0.3795013
sp B2RYT9 Translation	1	2	-0.041726	-0.352575	0.2582797	0.585875	0.3796869
sp Q62688 Inactive ph	1	3	-0.039092	-0.345668	0.2638898	0.5863875	0.3798726
sp P11348 Dihydroptei	8	13	-0.054154	-0.212883	0.0988184	0.58675	0.3802436
sp Q6TRW4 Sister chron	2	3	0.0388115	-0.255975	0.3311639	0.5868375	0.3804287
sp Q6UPE1 Electron tra	3	3	0.0437606	-0.248869	0.3259074	0.587175	0.3806138
sp Q2Q0I9 Fibronectin	3	3	0.0201497	-0.474359	0.5093317	0.587975	0.3807993
sp Q5FVK6 Coiled-coil :	2	2	0.0282303	-0.493693	0.6031789	0.5880125	0.3809845
sp P07483 Fatty acid-b	4	7	-0.051469	-0.228503	0.1218107	0.588525	0.3811698
sp Q4QQV3 Protein FAN	3	3	0.0360032	-0.321711	0.3879333	0.5886375	0.3813548
sp Q6DTM3 Jouberin OS	2	2	0.0101118	-0.580791	0.594492	0.5890375	0.3815399
sp Q68FP5 Snurportin-	2	3	0.0214411	-0.396182	0.4326417	0.589825	0.3817254
sp O88763 Phosphatid	2	2	0.019517	-0.707885	0.8022987	0.5900375	0.3819107
sp Q5BJS0 Putative AT	4	4	-0.042814	-0.290721	0.2075646	0.5908625	0.3820965
sp P23711 Heme oxygen	2	4	-0.041853	-0.28568	0.2160066	0.59145	0.3822824
sp O88658 Kinesin-like	5	5	-0.047674	-0.271852	0.1639456	0.5918375	0.3824683
sp Q63046 Runt-related	1	2	-0.043859	-0.297527	0.2052264	0.59185	0.382654

sp Q32PX7 Far upstream binding protein 1	3	3	-0.027873	-0.409999	0.3718656	0.59225	0.3828396
sp Q8VIL3 ZW10 interactor	3	3	0.0271213	-0.321708	0.3762245	0.592525	0.3830252
sp Q6MG61 Chloride intracellular channel 1	3	4	0.037684	-0.24245	0.3281717	0.592675	0.3832105
sp B0BN18 Prefoldin subunit 1	2	2	-0.03793	-0.360779	0.2590865	0.592925	0.3833958
sp Q75Q39 Mitochondrial ribosomal protein L12	6	12	0.0490384	-0.143371	0.2477414	0.5933	0.3835811
sp P09527 Ras-related GTPase	7	12	-0.050863	-0.231703	0.1254937	0.5933875	0.3839507
sp P27274 CD59 glycoprotein	5	12	-0.03648	-0.348483	0.2668185	0.5935375	0.3841352
sp Q9Z1H9 Protein kinase C theta	6	15	-0.046976	-0.272053	0.1686631	0.593725	0.3843195
sp Q924S5 Lon protease homolog	5	7	-0.042386	-0.27424	0.1919799	0.593725	0.3845035
sp P51583 Multifunctional protein	4	4	-0.029123	-0.393413	0.3646458	0.594075	0.3846875
sp P62836 Ras-related GTPase	3	3	0.0437096	-0.296954	0.3747379	0.594175	0.3848713
sp P19234 NADH dehydrogenase (ubiquinone) oxidoreductase subunit 3	3	3	0.0201337	-0.462271	0.5173814	0.594475	0.385055
sp Q9JIH7 Serine/threonine-protein kinase	4	4	-0.038287	-0.293953	0.2329689	0.59515	0.3854226
sp Q9ES40 PRA1 family protein	1	3	-0.031825	-0.323321	0.2854926	0.595675	0.3856064
sp Q63270 Cytoplasmic dynein intermediate chain	5	5	-0.040144	-0.34956	0.2505537	0.5958	0.38579
sp P21531 60S ribosomal protein L16	16	30	0.0594812	-0.034477	0.1531373	0.5959125	0.3859733
sp P68255 14-3-3 protein epsilon	10	15	-0.048753	-0.24605	0.1548031	0.596	0.3861564
sp P63004 Platelet-activating factor acetylhydrolase	7	12	0.051495	-0.113829	0.2273473	0.596025	0.3863393
sp Q7TPJ0 Translocon of membrane proteins, Sec61 complex subunit 2	2	4	0.0391417	-0.225939	0.3090561	0.5965625	0.3865222
sp Q9Z2X5 Homer protein	1	3	0.0232428	-0.504788	0.5205593	0.5966875	0.386705
sp P20650 Protein phosphatase 1	2	3	0.0251143	-0.368335	0.4109111	0.597275	0.3870701
sp Q9JI92 Syntenin-1	2	2	-0.010876	-0.626779	0.6127936	0.597325	0.3872525
sp Q6P6Q2 Keratin, type I cytoskeletal-associated protein	4	5	0.0428722	-0.200316	0.2873919	0.5975	0.3876165
sp P63057 Noelin-3 OS	2	2	0.0070629	-0.549159	0.5503759	0.597925	0.3877984
sp Q9ERC1 Myosin-XVI	3	3	-0.02132	-0.530775	0.4912346	0.5983	0.3879804
sp Q5PPJ9 Endophilin-2	3	4	-0.031633	-0.346771	0.2903405	0.59845	0.3881621
sp Q498E0 Thioredoxin-like protein	2	3	0.0147533	-0.457436	0.4816454	0.5997625	0.3883447
sp P02564 Myosin-7 O	4	5	0.010883	-0.486732	0.5192263	0.60055	0.38871
sp P62994 Growth factor receptor-binding protein 2	3	5	0.041171	-0.202167	0.2918104	0.6024375	0.3892597
sp Q9Z1N4 3'('2'),5'-bis(3-oxo-2-methylpropyl)-1,2,4,5-tetrahydropyran	3	3	-0.033578	-0.326219	0.2607628	0.6033125	0.3896262
sp P70584 Short-branched-chain acyl-CoA thioesterase	5	5	0.0357127	-0.233849	0.3135172	0.603575	0.3898095
sp Q8R431 Monoglyceride lipase	6	13	-0.053371	-0.208626	0.0934518	0.6036625	0.3899926
sp Q3MJK5 Cyclin-dependent kinase inhibitor 1C	3	3	-0.02352	-0.486121	0.4219281	0.6036625	0.3901754
sp O88664 Serine/threonine-protein kinase	1	2	0.0060362	-0.444644	0.4323773	0.60435	0.3903584
sp Q6AYS6 Sorting nexin 6	2	2	-0.003733	-0.527158	0.5253278	0.604525	0.3905413
sp Q68FW9 COP9 signal recognition particle subunit 7	4	4	-0.01522	-0.431446	0.4056084	0.6052	0.3907245
sp Q9JHL4 Drebrin-like protein	3	4	-0.009244	-0.515736	0.5101513	0.60545	0.3910902
sp Q66HF1 NADH-ubiquinone oxidoreductase subunit 14	14	21	0.0532084	-0.075734	0.1779247	0.6055	0.3912727
sp Q5HZY2 GTP-binding protein	2	3	-0.022262	-0.386068	0.3449071	0.6056375	0.391455
sp P04041 Glutathione S-transferase	3	6	-0.028787	-0.33705	0.2898873	0.606075	0.3918191
sp P13264 Glutaminase	10	13	0.047405	-0.128039	0.2319502	0.6062	0.392001
sp Q63617 Hypoxia up-regulated protein	12	17	-0.050153	-0.212258	0.1102803	0.607	0.392365
sp Q7TSA0 Mitochondrial ribosomal protein L2	2	4	-0.023959	-0.416802	0.3504725	0.6071	0.3925467
sp Q9JHW0 Proteasome activator complex subunit 3	3	3	0.0365916	-0.224219	0.3007314	0.60755	0.3927285
sp P24473 Glutathione S-transferase	3	3	0.0295121	-0.28965	0.3455508	0.60765	0.39291
sp P37996 ADP-ribosyl cyclase	2	5	0.0196764	-0.359746	0.4045333	0.60805	0.3930915
sp Q561S0 NADH dehydrogenase (ubiquinone) oxidoreductase subunit 5	5	6	0.0454231	-0.143385	0.2325036	0.6083125	0.393273

sp P23606 Protein-glut	2	2	-0.028377	-0.418665	0.3699049	0.6084625	0.3934543
sp Q4FZT9 26S proteas	6	9	-0.04069	-0.244169	0.1773926	0.6089875	0.3938166
sp O88553 Zinc finger p	2	2	-0.021261	-0.422694	0.4052131	0.6091875	0.3939975
sp P19332 Microtubule	9	17	0.0570578	-0.04824	0.167533	0.610225	0.3945403
sp O08839 Myc box-de	5	5	-0.034573	-0.335675	0.2547602	0.610525	0.3947212
sp P05765 40S ribosom	4	8	0.0501971	-0.099886	0.1938931	0.6107125	0.3949019
sp P39052 Dynamin-2	5	5	0.0368886	-0.20746	0.2877004	0.6108875	0.3950825
sp Q8VBU2 Protein NDF	4	7	-0.021059	-0.368193	0.3384048	0.611025	0.3952629
sp P18395 Cold shock d	4	4	0.0421653	-0.161437	0.2540618	0.611075	0.395443
sp P02688 Myelin basic p	16	100	-0.038831	-0.283947	0.2019781	0.6114	0.3956232
sp Q63189 Bone marrow	2	3	0.0096964	-0.468537	0.5059387	0.611775	0.3958033
sp P11762 Galectin-1 C	11	34	0.0559046	-0.047475	0.158444	0.6117875	0.3959831
sp O08678 Serine/thre	1	2	-0.013339	-0.431965	0.4081495	0.612125	0.3961629
sp P69682 Adapton ear	1	2	-0.025382	-0.362763	0.3145052	0.61215	0.3963425
sp P62076 Mitochondri	2	4	-0.017632	-0.417291	0.3556349	0.612425	0.3965219
sp Q4AEF8 Coatomer s	5	9	0.0428412	-0.164267	0.2436161	0.61275	0.3967014
sp Q9ZOU4 Gamma-am	1	4	-0.035909	-0.291993	0.2230025	0.6130375	0.3968808
sp P50753 Troponin T,	1	2	-0.036969	-0.296802	0.213734	0.613075	0.3970599
sp P97557 Potassium v	2	2	-0.018244	-0.45085	0.4101698	0.6130875	0.3972387
sp Q9QZ81 Protein arg	3	5	0.0298948	-0.271813	0.334102	0.613375	0.3974175
sp Q5FWT1 Protein FAN	1	3	-0.022551	-0.369303	0.3231953	0.613675	0.3975962
sp O88277 Protocadhe	7	47	-0.049362	-0.189799	0.0946386	0.6137625	0.3977747
sp P70615 Lamin-B1 O	11	15	0.0495483	-0.102504	0.2044693	0.6139875	0.3979531
sp P09034 Argininosuc	2	3	0.0339727	-0.22324	0.2940722	0.6149875	0.3983106
sp P11915 Non-specific	8	13	-0.016961	-0.531597	0.479858	0.61515	0.3984891
sp Q3B7U9 Peptidyl-pro	2	2	-0.005144	-0.471218	0.4483837	0.61555	0.3988455
sp Q794E4 Heterogene	2	2	0.0004202	-0.515604	0.5097644	0.6155625	0.3990235
sp P16638 ATP-citrate	37	65	-0.055302	-0.163129	0.0499421	0.6156125	0.3992011
sp P48004 Proteasome	7	9	0.0505303	-0.084368	0.1901736	0.6157875	0.3995559
sp Q9ESM2 Hyaluronan	3	4	-0.005705	-0.76911	0.7233032	0.6160375	0.3999097
sp P0CC10 Leucine-rich	2	2	-0.006193	-0.467901	0.4678365	0.6160375	0.4000863
sp P33124 Long-chain-	4	4	-0.027042	-0.326085	0.2716111	0.61625	0.4002628
sp P13084 Nucleophos	7	9	0.0491085	-0.091649	0.1869712	0.6164875	0.4004391
sp Q5PQN1 Probable E3	2	2	-0.007087	-0.511237	0.4815789	0.616525	0.4006153
sp Q5XIF3 I NADHdehy	5	7	-0.040575	-0.233782	0.1658604	0.6167625	0.4007913
sp Q6PEC1 Tubulin-spe	9	11	0.0533654	-0.07601	0.1914574	0.61685	0.4009671
sp Q62671 E3 ubiquitin	3	3	-0.003714	-0.51325	0.516166	0.616875	0.4011426
sp Q6AY97 Coiled-coil c	3	3	0.0269677	-0.371177	0.4471397	0.6174875	0.4014934
sp Q5U2R7 LDLR chape	2	2	0.017544	-0.416642	0.4663687	0.6174875	0.4016685
sp P29994 Inositol 1,4,	4	4	-0.019312	-0.353569	0.3177475	0.6176875	0.4018436
sp Q66H76 Paxillin OS=	2	2	0.004725	-0.487226	0.5127679	0.61785	0.4020185
sp P19643 Amine oxid	13	26	-0.059939	-0.144565	0.0209428	0.6181125	0.4021933
sp P30349 Leukotriene	4	5	0.0204165	-0.308426	0.3530998	0.618575	0.4023683
sp P10760 Adenosylho	11	24	-0.045665	-0.220798	0.1307368	0.619025	0.4025433
sp Q64119 Myosin ligh	8	20	-0.038891	-0.25825	0.1815245	0.6193	0.4028928
sp P84817 Mitochondr	2	2	0.002332	-0.507681	0.4932246	0.6193875	0.4030673
sp Q6P730 Disabled ho	2	4	0.0385223	-0.197119	0.2804471	0.620425	0.4039388

sp B0BNE5 S-formylglu	3	5	-0.015683	-0.431056	0.4024596	0.620425	0.4037649
sp P97609 Protein hair	2	2	-0.006826	-0.453424	0.437327	0.6205375	0.4041125
sp B2RYJ4 L-aminoacid	3	3	0.0066665	-0.479684	0.512467	0.62065	0.404286
sp O70196 Prolyl endo	3	6	0.0224806	-0.29584	0.3633812	0.620875	0.4044594
sp Q6AXM5 Choline/eth	1	3	-0.01356	-0.407806	0.3690602	0.6211125	0.4046327
sp P50904 Ras GTPase	4	4	-0.033986	-0.326839	0.2405633	0.621675	0.4051518
sp Q7TSP2 Kinesin-like	4	4	0.0232136	-0.386053	0.4545779	0.621825	0.405497
sp P25030 Keratin, typ	2	2	-0.021596	-0.393387	0.3527774	0.6218375	0.4056693
sp Q5XII0 E Mammiliar	6	13	-0.05112	-0.183214	0.0833991	0.6221375	0.4058415
sp P85971 6-phosphog	3	3	0.0350981	-0.217448	0.2957854	0.6223125	0.4061853
sp Q9EST6 Acidic leucii	4	4	-0.028925	-0.346054	0.2597902	0.6229	0.4067003
sp P62243 40S riboson	8	17	0.0541717	-0.058103	0.1702614	0.6232125	0.4072133
sp Q9Z270 Vesicle-assc	5	8	0.0455829	-0.115709	0.2127296	0.6233625	0.4073841
sp P48679 Prelamin-A/	37	100	0.0435099	-0.143095	0.2306059	0.6233875	0.4075546
sp Q8R5I7 Myocardin	2	2	0.0382083	-0.214809	0.2936209	0.6235375	0.4077249
sp P38062 Methionine	1	2	-0.030793	-0.275801	0.2297094	0.6236125	0.407895
sp Q66H44 Transmemb	1	4	-0.036074	-0.399786	0.2930992	0.6241875	0.4082351
sp P05982 NAD(P)H de	3	5	0.0177719	-0.337107	0.3553819	0.624625	0.4084052
sp P86410 Ral GTPase-	3	5	0.0259084	-0.272106	0.3323654	0.6250875	0.4085754
sp Q9QYV8 DNA polym	2	3	-0.015721	-0.388525	0.3474199	0.6252125	0.4089152
sp B5DEH2 Erlin-2 OS=F	3	4	0.0351004	-0.202918	0.2731645	0.6256	0.4090851
sp Q924N5 Long-chain-	3	3	0.0185529	-0.2836	0.2911741	0.62615	0.4094246
sp P25886 60S riboson	5	14	0.0493181	-0.112689	0.2208798	0.6262125	0.4095941
sp O70277 Tripartite m	3	4	0.0297543	-0.23831	0.3139045	0.6262125	0.4097633
sp Q05695 Neural cell :	5	8	-0.036974	-0.240527	0.1665371	0.626925	0.4099328
sp Q9JHY2 Sideroflexin	7	11	0.0440976	-0.121972	0.2043268	0.627075	0.4102713
sp Q9JIR4 F Regulating	2	2	0.0084387	-0.432174	0.4604546	0.6272	0.4104402
sp O88994 MOSC dom:	2	3	-0.02356	-0.365097	0.3215872	0.6275125	0.4106092
sp P45953 Very long-cl	6	8	0.0340962	-0.213022	0.2726245	0.6276625	0.410778
sp P51650 Succinate-s	3	3	0.0137726	-0.375638	0.4022591	0.62785	0.4109466
sp P12847 Myosin-3 O	5	8	-0.019245	-0.388473	0.3562942	0.6284875	0.4111155
sp P12711 Alcohol deh	2	3	-0.027861	-0.278239	0.2390443	0.62855	0.4112842
sp Q5M7U6 Actin-relate	6	9	-0.040103	-0.226408	0.1516716	0.6286	0.4114527
sp P31399 ATP synthas	10	23	-0.051036	-0.188586	0.0841588	0.6288	0.411621
sp P38652 Phosphoglu	10	13	0.0344008	-0.195187	0.240786	0.6291	0.4117893
sp P07632 Superoxide	10	38	-0.043388	-0.212044	0.1313684	0.6295	0.4121257
sp Q5I0G4 Glycyl-tRNA	13	19	-0.048145	-0.181918	0.0904983	0.6295	0.4122935
sp Q63358 Myosin-IXb	5	6	-0.03139	-0.301418	0.2293488	0.62985	0.4124614
sp P14841 Cystatin-C C	3	6	0.032732	-0.210584	0.2776688	0.6299875	0.4127965
sp Q9JK71 Membrane-	4	4	0.0415077	-0.177021	0.2683456	0.6299875	0.4129637
sp Q9EPH2 MARCKS-re	4	12	0.0308393	-0.232107	0.300084	0.630175	0.4131307
sp P04797 Glyceraldehy	22	78	0.0452095	-0.11313	0.2116703	0.6304875	0.4132978
sp Q9JIL8 R DNA repair	1	2	-0.002438	-0.34433	0.3700311	0.6308125	0.4134649
sp P15791 Calcium/cal	1	2	0.0325402	-0.205853	0.2685318	0.630875	0.4136317
sp Q7TPB1 T-complex p	17	24	0.0520283	-0.066584	0.1692651	0.631475	0.4137988
sp O35077 Glycerol-3-p	7	15	-0.039163	-0.231204	0.1561809	0.6316125	0.4139657
sp Q01129 Decorin OS-	16	48	-0.038334	-0.241772	0.1647328	0.6317625	0.4141325

sp P21533 60S ribosomal large subunit	10	19	0.0554377	-0.044208	0.1584065	0.63195	0.4142991
sp Q5U318 Astrocytic programme	7	19	-0.024789	-0.301811	0.2576845	0.6340125	0.4147993
sp Q9ZQA2 Programme	12	19	-0.05047	-0.169264	0.0739912	0.6343375	0.4151338
sp Q63186 Translation	4	4	-0.03104	-0.269177	0.2101754	0.6346125	0.4154678
sp POC5H9 Mesencephalic	4	4	-0.006393	-0.380801	0.3731498	0.6347125	0.4156345
sp Q62812 Myosin-9 O	50	87	-0.045945	-0.193666	0.1097822	0.6348625	0.4158011
sp Q9Z0Y8 Voltage-dependent	2	2	-0.006933	-0.545623	0.5094053	0.6348625	0.4159675
sp Q497B3 Keratinocyte	1	2	0.0171295	-0.33136	0.3706838	0.63545	0.416134
sp Q4KMA2 UV excision repair protein	9	16	0.052752	-0.056596	0.161328	0.6357375	0.4167981
sp Q9Z0W7 Chloride channel	3	7	0.0342062	-0.202342	0.2755029	0.6358	0.4169637
sp P62161 Calmodulin	9	32	0.0495901	-0.079436	0.1792311	0.6370625	0.4174605
sp Q56R16 Importin subunit	2	2	-0.017486	-0.383064	0.339858	0.637425	0.4176262
sp P60901 Proteasome	5	7	-0.041171	-0.225655	0.1387361	0.637875	0.4177921
sp P62755 40S ribosomal small subunit	13	23	0.0556089	-0.030261	0.1436181	0.6381	0.4179579
sp Q4G061 Eukaryotic translation factor	4	8	-0.037204	-0.237613	0.1631786	0.6382375	0.4181235
sp Q62968 Sodium channel	3	3	-0.010956	-0.314568	0.3280295	0.6388	0.4182893
sp P15650 Long-chain base transporter	9	13	-0.052831	-0.154136	0.0529039	0.6391875	0.4184551
sp P70483 Striatin OS=	3	5	0.018449	-0.289727	0.3249124	0.640025	0.418787
sp O35244 Peroxiredoxin	8	15	-0.033764	-0.248819	0.1870348	0.64045	0.4189531
sp Q6AYA1 H/ACA ribonucleoprotein	3	3	-0.028239	-0.28044	0.2337447	0.6404625	0.4191189
sp Q9ER24 Ataxin-10 OS=	3	4	0.0154911	-0.304493	0.3232855	0.640575	0.4192845
sp P39069 Adenylate kinase	6	13	-0.029324	-0.266345	0.2072041	0.6409125	0.4194501
sp P21575 Dynamin-1	14	25	-0.048693	-0.176545	0.0780924	0.64155	0.4197815
sp P52631 Signal transduction	7	9	-0.030922	-0.231343	0.1828141	0.6416	0.4199469
sp Q0VGK2 Tetraspanin	1	3	0.0126645	-0.321004	0.3499277	0.641825	0.4201122
sp P28073 Proteasome	3	10	0.0430534	-0.114588	0.2012436	0.6420375	0.4204424
sp Q9QVC8 Peptidyl-prolyl isomerase	8	14	-0.042204	-0.204542	0.1269918	0.64205	0.4206072
sp P69897 Tubulin beta-tubulin	4	12	-0.002341	-0.416431	0.4025649	0.6423875	0.4207719
sp Q4V7F2 Cysteine-rich protein	3	6	-0.027754	-0.253289	0.2066188	0.6437	0.4209374
sp Q9WTT6 Guanine deaminase	11	24	-0.030393	-0.244364	0.178488	0.6439	0.4211028
sp P08934 Kininogen-1	2	5	0.0261559	-0.229655	0.2873871	0.6442125	0.4212682
sp Q78P75 Dynein light chain	1	3	-0.001223	-0.381066	0.3737614	0.64455	0.4214336
sp O88794 Pyridoxine-binding protein	2	3	0.027228	-0.219337	0.2644649	0.6448375	0.421764
sp O88637 Ethanolamine kinase	1	3	-0.022286	-0.281543	0.253265	0.6449125	0.4219289
sp P06866 Haptoglobin	8	13	-0.007397	-0.367757	0.3441087	0.6449375	0.4220936
sp P97534 Peptidyl-prolyl isomerase	2	5	0.0285795	-0.225463	0.2819068	0.6457125	0.4229151
sp Q7TP98 Interleukin-8 receptor	3	5	-0.026475	-0.262047	0.2123482	0.646	0.4232428
sp Q64057 Alpha-amino acid oxidase	4	5	0.0029379	-0.401686	0.4061388	0.6467125	0.4237341
sp P07943 Aldose reductase	20	47	0.0283371	-0.209144	0.2705887	0.6473	0.4240613
sp Q6AXT5 Ras-related GTPase	2	3	0.0317948	-0.223618	0.2996959	0.6477875	0.4243884
sp O88761 26S proteasome	6	7	-0.03297	-0.250669	0.1722439	0.6478875	0.4245516
sp P41499 Tyrosine-protein kinase	6	9	0.0316895	-0.177455	0.236217	0.64795	0.4247147
sp P52873 Pyruvate carboxylase	11	13	0.0446119	-0.090605	0.1871096	0.6482	0.4248777
sp Q2LAP6 Testin OS=R	1	2	0.0064792	-0.337544	0.3618569	0.650175	0.4253687
sp O35303 Dynamin-1	14	21	-0.045272	-0.183258	0.0927409	0.6504125	0.4255323
sp B2RYW9 Fumarylacetoacetate	2	4	-0.020381	-0.296014	0.2531371	0.6510125	0.4256962
sp Q63716 Peroxiredoxin	10	25	0.0307925	-0.194998	0.2525445	0.6514	0.4258601

sp Q91Z79 Liprin-alpha	5	5	0.0255526	-0.206399	0.2572275	0.651425	0.4260238
sp P45592 Cofilin-1 OS	13	30	0.037812	-0.141739	0.2209194	0.651875	0.4263509
sp Q64640 Adenosine I	6	11	-0.032928	-0.237691	0.173412	0.6523	0.4265145
sp P35745 Acylphosph	2	3	0.0073114	-0.380135	0.3991003	0.6524625	0.426678
sp P24155 Thimet oligo	6	7	-0.029421	-0.239557	0.1871422	0.6529	0.4271674
sp Q64537 Calpain sma	2	3	-0.017578	-0.399204	0.346773	0.6530875	0.4273304
sp Q62640 Glutamate i	2	2	0.0095894	-0.335075	0.3560155	0.6540625	0.4278193
sp Q62632 Follistatin-r	3	3	0.0025947	-0.382375	0.3905795	0.6547625	0.4279826
sp Q4KLH5 Arf-GAP doi	2	3	0.0253362	-0.227687	0.2833216	0.6550125	0.4283087
sp Q8VI04 L-asparagin	10	19	-0.039382	-0.200853	0.1326654	0.65685	0.4286355
sp P27881 Hexokinase	4	4	0.0213008	-0.234617	0.2862954	0.6569	0.4289625
sp Q63425 Periaxin OS:	48	100	0.0338734	-0.161861	0.2272571	0.657075	0.4291258
sp Q5FVI6 V-type prot	5	6	0.0320401	-0.206623	0.2847239	0.6571125	0.4294517
sp P85125 Polymerase	15	26	-0.033234	-0.233084	0.1658817	0.6571125	0.4292889
sp Q9EQP5 Prolargin O!	21	57	-0.004685	-0.350998	0.349621	0.658	0.4297777
sp P97685 Neurofascir	4	4	0.0125827	-0.311226	0.3418301	0.658275	0.4299407
sp P25235 Dolichyl-dip	6	11	0.0422637	-0.099996	0.1835871	0.6590375	0.4302668
sp Q4KLH4 Paraspeckle	2	2	0.0087049	-0.334188	0.3641401	0.65905	0.4304296
sp Q5XIF6 Tubulin alpI	4	10	-0.032168	-0.225238	0.1630482	0.6605125	0.4310821
sp Q63377 Sodium/pot	6	10	-0.035033	-0.216565	0.1473013	0.6610625	0.4314078
sp P62268 40S riboson	8	14	0.0498609	-0.058477	0.1598808	0.6617125	0.4317337
sp P60123 RuvB-like 1	4	8	0.0314752	-0.166012	0.2274134	0.662075	0.4318966
sp Q5I0D7 Xaa-Pro dip	4	5	0.0069797	-0.316291	0.313053	0.6634375	0.4325483
sp P12007 Isovaleryl-C	7	9	-0.039886	-0.186275	0.108656	0.6638875	0.4327113
sp O35142 Coatomer s	4	4	-0.015535	-0.315393	0.2971658	0.664675	0.4328747
sp A2RUW1 Toll-interac	5	7	0.026854	-0.187746	0.2410685	0.6648625	0.4330379
sp Q66HB6 Cancer-assc	3	3	0.0089685	-0.308971	0.3108908	0.6656	0.4333644
sp Q8VHK2 Caskin-1 OS	4	5	0.0193949	-0.223844	0.2721388	0.665625	0.4335275
sp Q5MPA9 Serine/thre	3	4	0.0093088	-0.2875	0.3158805	0.665825	0.4338533
sp Q9Z1I6 Rho guanin	2	2	0.0012575	-0.343479	0.3446897	0.6664625	0.4340163
sp Q63028 Alpha-addu	14	24	0.0495022	-0.050097	0.1500708	0.666475	0.4341791
sp Q9JLZ1 Glutaredoxi	12	21	0.0351435	-0.154612	0.2216858	0.6672875	0.4343422
sp P38659 Protein disu	12	20	-0.04451	-0.16183	0.0779038	0.668225	0.4345058
sp P35571 Glycerol-3-p	5	6	-0.015407	-0.291185	0.2585911	0.668325	0.4346692
sp P23565 Alpha-interi	18	39	-0.017188	-0.270632	0.2510779	0.668425	0.4349954
sp P52303 AP-1 compl	2	3	-0.011838	-0.316831	0.2794623	0.66845	0.4351582
sp P30713 Glutathione	2	4	0.0056756	-0.298476	0.3172765	0.6685125	0.4353208
sp Q9WTY2 GTP-binding	2	4	-0.01856	-0.256455	0.2284864	0.66855	0.4354832
sp O08590 Membrane	5	7	-0.021157	-0.27992	0.2412167	0.6686375	0.4356455
sp Q6VV72 Eukaryotic t	5	6	-0.018768	-0.25778	0.2267665	0.6689625	0.4358077
sp Q5PQX1 Torsin-1A-ir	4	4	0.0130966	-0.256388	0.2729293	0.6691	0.4359698
sp P35704 Peroxiredox	7	16	-0.043957	-0.169797	0.0864324	0.66915	0.4361318
sp P08503 Medium-ch	5	6	0.0116196	-0.304871	0.357434	0.6695375	0.4362937
sp P30904 Macrophag	2	10	-0.038175	-0.19993	0.118477	0.669975	0.4367789
sp Q5TKR9 Histone ace	2	2	0.0108695	-0.394507	0.4215874	0.6704875	0.4369406
sp Q6AYH5 Dynactin su	10	19	0.0500659	-0.040855	0.14398	0.6705125	0.4371021
sp Q0VGK0 Gamma-am	3	4	0.0242012	-0.209732	0.2652625	0.6712125	0.4372639

sp P10354 Chromogranin A	2	3	-0.00924	-0.31101	0.2850522	0.6713125	0.4374255
sp Q920F5 Malonyl-CoA acyltransferase	5	5	0.0135903	-0.253528	0.2702665	0.6717625	0.4380706
sp Q3B8Q0 Microtubule-associated protein tau	6	8	0.0243032	-0.185223	0.2362086	0.67285	0.4383934
sp P29419 ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	5	10	-0.041295	-0.181382	0.0958061	0.6733375	0.4385548
sp Q6AXV4 Sorting and assembly of membrane proteins, alpha polypeptide	4	5	0.0232166	-0.205557	0.2582106	0.674175	0.4387167
sp Q6UE39 Polypeptidyl-prolyl isomerase-like protein kinase	2	2	0.0054349	-0.345133	0.3440336	0.67425	0.4388783
sp Q8R478 WW domain-containing protein 1	6	10	0.0257235	-0.18737	0.2286928	0.67455	0.43904
sp P08460 Nidogen-1 (laminin receptor)	5	9	0.0323292	-0.146412	0.2175982	0.674825	0.4393628
sp P62890 60S ribosomal protein L13	4	10	0.0363318	-0.113294	0.1791772	0.6757625	0.4398469
sp P04636 Malate dehydrogenase, mitochondrial	17	53	-0.059131	-0.108665	-0.006857	0.6759	0.4401691
sp O88764 Death-associated protein kinase	3	4	-0.021112	-0.26105	0.2111379	0.676425	0.4404909
sp Q9WV63 Kinesin-like protein 1	5	6	0.0128058	-0.25327	0.2665077	0.6772	0.4408131
sp Q641Y2 NADH dehydrogenase (ubiquinone) 1 flavoprotein	6	12	0.0291762	-0.155336	0.2094774	0.678425	0.4412966
sp P50878 60S ribosomal protein L10	15	25	0.0444951	-0.072068	0.1631613	0.679075	0.4417799
sp P62329 Thymosin beta 10	4	11	0.0185511	-0.220333	0.2577953	0.6791	0.4419407
sp Q07205 Eukaryotic translation initiation factor 4B	5	8	0.0240557	-0.185474	0.2388278	0.6792875	0.4421014
sp P81795 Eukaryotic translation initiation factor 4E	8	13	-0.038963	-0.175705	0.1011922	0.679825	0.4424225
sp A4L9P7 Sister chromatid cohesion protein SMC3	3	3	0.031501	-0.1652	0.2265944	0.6799375	0.4425829
sp Q7TP47 Heterogeneous nuclear ribonucleoprotein D	9	10	0.0095734	-0.255869	0.2756709	0.6807625	0.4430645
sp Q6PDU1 Serine/arginine-rich splicing factor 1	4	5	0.0149654	-0.228173	0.2592862	0.6809	0.4432248
sp P11654 Nuclear pore complex protein	2	2	0.0147434	-0.310181	0.3732951	0.68145	0.4438646
sp Q7M767 Ubiquitin-conjugating enzyme E2C	2	3	-0.024442	-0.244066	0.1822058	0.6815875	0.4440243
sp Q6AYS7 Aminoacyl-tRNA ligase, mitochondrial	14	21	-0.034135	-0.188203	0.1199523	0.6817375	0.4441838
sp P11730 Calcium/calmodulin-dependent protein kinase II	5	7	-0.024728	-0.224876	0.1743389	0.68235	0.4446619
sp P82995 Heat shock protein 27	23	63	-0.038139	-0.18318	0.1108023	0.6828375	0.4448213
sp P27605 Hypoxanthine-guanine phosphoribosyltransferase	4	9	0.0288628	-0.152936	0.2109106	0.682925	0.4449806
sp P31977 Ezrin OS=Ras-binding domain-containing protein	6	6	-0.004987	-0.283502	0.2799303	0.6833375	0.4451399
sp P29418 ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide	3	4	0.0173231	-0.233615	0.2488381	0.683475	0.4452991
sp Q6FY0 Cytochrome c oxidase subunit IV	10	21	-0.048383	-0.155233	0.0526646	0.6848625	0.4456183
sp Q07439 Heat shock protein 23	7	13	0.0285985	-0.151116	0.2086582	0.6855125	0.4464151
sp Q5PPN5 Tubulin polymerization-promoting protein	10	20	0.0288083	-0.16272	0.21744	0.6859625	0.4470498
sp Q6QLM7 Kinesin heavy chain	9	12	-0.025879	-0.223395	0.1656134	0.6861375	0.4472082
sp P55161 Nck-associated protein	2	3	-0.017506	-0.259481	0.2195552	0.6862	0.4473665
sp P52296 Importin subunit alpha 2	10	13	0.0396337	-0.092545	0.1672523	0.6862875	0.4476825
sp P62198 26S proteasome non-ATPase regulatory subunit 1	4	6	0.0097083	-0.252766	0.2729687	0.68665	0.447998
sp Q5PPH0 Enolase-phosphatase	4	5	0.0156081	-0.213788	0.2527337	0.68725	0.448471
sp P62752 60S ribosomal protein L10	7	10	0.0288046	-0.165803	0.2370668	0.6879	0.4486287
sp Q9WU6E Pleckstrin homology domain-containing protein	5	6	-0.019994	-0.228403	0.1942054	0.6887625	0.4487868
sp Q9Z244 GMP reductase	3	5	0.0087491	-0.258166	0.2724208	0.6889375	0.4491025
sp P63312 Thymosin beta 10	1	2	0.0232128	-0.184127	0.2344929	0.689525	0.4494179
sp P08081 Clathrin light chain	8	13	-0.038533	-0.170359	0.0923569	0.6895625	0.4495755
sp Q7TP65 Ankyrin repeat domain-containing protein 1	4	6	0.031358	-0.133606	0.1952437	0.6898625	0.4497331
sp Q9Z2S9 Flotillin-2 O-linked N-acetylgalactosaminyl transferase	8	9	-0.015215	-0.236161	0.2171878	0.6900125	0.4498905
sp Q5U1W5 U11/U12 small nucleolar RNA-associated protein	1	2	0.0104066	-0.253053	0.2588154	0.69025	0.4500479
sp P97924 Kalirin OS=F1	4	5	-0.025718	-0.208944	0.1622266	0.690275	0.4502051
sp P62944 AP-2 complex	7	7	-0.014383	-0.249725	0.2172015	0.690475	0.4505192
sp P60868 40S ribosomal protein S2	6	10	0.0390958	-0.09687	0.1798246	0.690675	0.450676

sp O08651 D-3-phosph	13	27	0.0250298	-0.171923	0.2288682	0.6912875	0.4508331
sp Q68A21 Transcriptic	8	15	0.0357737	-0.108541	0.1757635	0.691375	0.45099
sp P08541 UDP-glucur	2	2	0.0032016	-0.282049	0.3216183	0.6914875	0.4511468
sp Q1WIM3 Cell adhesic	9	23	0.0275009	-0.156257	0.211574	0.69165	0.4513034
sp P16446 Phosphatid	7	13	-0.03017	-0.20284	0.1360669	0.6924375	0.4516172
sp O54898 Voltage-dep	2	3	-0.027006	-0.22674	0.1645139	0.6930375	0.4522432
sp Q5XI81 Fragile X me	4	4	-0.020779	-0.241556	0.2033809	0.6930875	0.4523994
sp Q9QYV0 Disintegrin	1	3	-0.037085	-0.171996	0.1013335	0.6931	0.4525554
sp P36506 Dual specifi	2	3	0.0206496	-0.236716	0.2826866	0.6931125	0.4527112
sp Q63312 Pleckstrin h	7	8	-0.02017	-0.230205	0.1874554	0.6931625	0.4528668
sp P34058 Heat shock	17	43	-0.03132	-0.197081	0.1360544	0.69375	0.4530227
sp P12001 60S riboson	8	28	0.0378686	-0.094291	0.1753415	0.6940375	0.4531785
sp P26453 Basigin OS=	3	4	0.0135602	-0.281841	0.2931214	0.6941375	0.4534895
sp P31422 Metabotrop	4	4	0.0181133	-0.198273	0.2299805	0.6958875	0.4538019
sp P50398 Rab GDP dis	13	24	0.0362586	-0.104839	0.1758074	0.6970375	0.4545826
sp Q68FP1 Gelsolin OS	19	45	-0.039421	-0.165327	0.0905086	0.6972	0.4547385
sp P40307 Proteasome	3	4	-0.025103	-0.218323	0.1650118	0.6980375	0.4555162
sp P62870 Transcriptic	6	13	0.0327766	-0.121316	0.1858267	0.6982	0.4556715
sp Q5XIN6 LETM1 and	8	10	-0.016603	-0.219131	0.1914425	0.69935	0.4561373
sp Q64560 Tripeptidyl-	8	8	0.0203086	-0.178446	0.2174928	0.699475	0.4564476
sp P61149 Heparin-bin	4	8	-0.027013	-0.203833	0.1491095	0.70045	0.456758
sp Q05982 Nucleoside	3	4	0.0121303	-0.220437	0.2532783	0.701675	0.4573799
sp Q62940 E3 ubiquitir	10	15	-0.031359	-0.183163	0.1194897	0.703375	0.4580018
sp P47942 Dihydropyri	17	50	-0.04141	-0.152579	0.0742484	0.7039625	0.4586229
sp B4F795 Choline trar	6	8	0.020434	-0.177386	0.2255038	0.70455	0.4590878
sp Q6P686 Osteoclast-	6	13	0.0083422	-0.244879	0.2869086	0.7050125	0.4592429
sp Q99PD4 Actin-relate	3	4	-0.021807	-0.214814	0.16309	0.70605	0.459863
sp Q6P7B0 Tryptophan	13	20	0.0337249	-0.115705	0.1820062	0.7061375	0.4601724
sp Q63598 Plastin-3 OS	10	18	0.0316349	-0.112459	0.1802698	0.706475	0.4606354
sp P62630 Elongation i	13	41	-0.044929	-0.142294	0.0545313	0.7068875	0.4607897
sp P10688 1-phosphat	3	4	-0.009495	-0.246363	0.2258914	0.707075	0.4609439
sp P63170 Dynein light	2	7	0.0392302	-0.085189	0.1631594	0.7074625	0.4612521
sp Q9R1Z0 Voltage-dep	5	9	-0.008877	-0.246378	0.2304062	0.7083125	0.4618679
sp Q9Z1X1 Extended s	19	30	-0.039953	-0.156654	0.0798514	0.708825	0.4621755
sp Q499N5 Acyl-CoA sy	3	4	-0.004661	-0.25966	0.2509256	0.7098375	0.4627902
sp B0BNA5 Coactosin-li	7	15	0.0395683	-0.084429	0.1617897	0.7099625	0.4629437
sp Q6PST4 Atlastin-1 O	3	4	0.0004284	-0.256379	0.2644653	0.710275	0.4634036
sp P13233 2',3'-cyclic-1	33	100	-0.006361	-0.248867	0.2408066	0.71095	0.463557
sp P62083 40S riboson	8	21	0.037104	-0.090184	0.1650582	0.7111625	0.4637103
sp P48037 Annexin A6	39	93	-0.051872	-0.123061	0.020745	0.711425	0.4638636
sp Q6NYB7 Ras-related	6	8	0.0284988	-0.129076	0.1796964	0.7118875	0.4641699
sp Q6P9U8 Eukaryotic t	5	10	0.0195868	-0.16831	0.2057996	0.71305	0.4647823
sp Q99MZ8 LIM and SH	5	7	-0.019895	-0.201388	0.1642412	0.7131375	0.4649353
sp POC1X8 AP2-associa	3	5	0.0137174	-0.204739	0.2315234	0.7131875	0.4650882
sp P14480 Fibrinogen I	10	12	-0.009945	-0.242261	0.2277493	0.7133	0.4652409
sp P05426 60S riboson	7	13	0.0374047	-0.089604	0.1699462	0.7133625	0.4653935
sp P85515 Alpha-centr	8	12	0.0359762	-0.091327	0.1656611	0.71395	0.4655463

sp Q9R063 Peroxiredoxin-1	11	25	-0.018433	-0.213248	0.1736334	0.7148	0.4660046
sp P13383 Nucleolin O	26	42	0.0516109	-0.016149	0.1206336	0.7154	0.4663103
sp P82471 Guanine nucleotide-binding protein G(I)	5	9	0.0228369	-0.14768	0.1904592	0.7159125	0.4669199
sp P59215 Guanine nucleotide-binding protein G(II)	7	10	-0.029124	-0.188341	0.1296463	0.7160625	0.467224
sp Q91XU1 Protein quaternary 1	5	6	-0.010761	-0.235241	0.2055917	0.716375	0.4673761
sp P11250 60S ribosomal protein L10	3	6	-0.005965	-0.247697	0.2325423	0.716375	0.4675279
sp P63036 DnaJ homologous protein 1	4	6	-0.024685	-0.182404	0.1379841	0.7165375	0.4678311
sp Q642A6 von Willebrand factor A domain-containing protein	8	19	0.033064	-0.107369	0.1663487	0.7167375	0.4679826
sp Q6AYT7 Monoacylglyceride lipase	7	14	-0.031438	-0.174666	0.1079051	0.7167875	0.468134
sp P63041 Complexin-1	6	14	0.0255074	-0.142219	0.1964962	0.7175625	0.4682856
sp P04764 Alpha-enolase	15	39	0.0112666	-0.203285	0.2424549	0.7187	0.4688921
sp P37805 Transgelin-1	7	10	-0.02293	-0.1919	0.1464021	0.7187125	0.4690435
sp Q01205 Dihydrolipoyl acetyltransferase-like protein	11	21	0.0380233	-0.07685	0.1584018	0.719375	0.4694974
sp P13437 3-ketoacyl-CoA thioesterase	11	19	-0.028966	-0.1746	0.1188204	0.7199875	0.4699511
sp P35427 60S ribosomal protein L10	7	15	0.0350063	-0.088509	0.1601007	0.7204875	0.4704039
sp AOJPJ7 C-type lectin domain-containing protein 7	8	11	0.0262797	-0.132075	0.1864281	0.720725	0.4705547
sp P14942 Glutathione S-transferase	8	13	-0.020211	-0.198635	0.162789	0.72095	0.4707054
sp Q9QYF3 Myosin-Va	14	17	-0.02635	-0.178503	0.1256135	0.72105	0.470856
sp P97571 Calpain-1 catalytic subunit	8	10	0.0215083	-0.15284	0.1997565	0.7216	0.4711571
sp P09495 Tropomyosin	8	22	0.0446594	-0.045675	0.1382617	0.72175	0.4713076
sp Q7TQ16 Cytochrome c oxidase subunit IV	4	6	0.0222868	-0.143519	0.1869945	0.7232	0.4717601
sp P30839 Fatty aldehyde binding protein	7	7	0.0103175	-0.201487	0.2311694	0.723275	0.4722115
sp AOJPM9 Eukaryotic translation initiation factor 4B	3	6	0.0037753	-0.23578	0.2368679	0.7232875	0.4723617
sp Q9QYL8 Acyl-protein thioesterase-like protein 8	4	4	0.0069297	-0.223462	0.2466168	0.7234	0.4725118
sp P62959 Histidine triad nucleic acid binding protein	4	7	0.0108051	-0.20355	0.2359073	0.72535	0.4734117
sp P01256 Calcitonin gene-related peptide receptor	1	4	-0.005232	-0.235786	0.2276734	0.7255	0.4738613
sp P01041 Cystatin-B	5	9	-0.008172	-0.231735	0.2173033	0.7257375	0.4740109
sp Q4KLM4 Ectoderm-nitric oxide synthase	2	3	-0.020645	-0.197252	0.1564864	0.725875	0.4741605
sp P05197 Elongation factor 1-alpha	32	65	0.0454011	-0.04695	0.135829	0.726075	0.4744593
sp P35213 14-3-3 protein epsilon	4	7	0.0239675	-0.1436	0.190106	0.7264625	0.4746086
sp P49242 40S ribosomal protein S21	13	28	0.0450312	-0.040358	0.1313811	0.72715	0.4752054
sp O88767 Protein DJ-1	14	41	0.0110884	-0.197653	0.221208	0.7271875	0.4753543
sp Q9JMJ4 Pre-mRNA-processing factor 14	4	5	0.0128768	-0.187685	0.2273359	0.72755	0.4755033
sp P00173 Cytochrome P450 2D6	4	9	-0.029469	-0.178131	0.1137431	0.7282625	0.4758014
sp P29266 3-hydroxyisobutyrate dehydrogenase	7	11	0.0312644	-0.098667	0.1580946	0.729875	0.4765463
sp O89049 Thioredoxin-like protein	8	11	0.0237133	-0.127958	0.1773763	0.7306375	0.4769933
sp O08557 N(G),N(G)-dihydropyrimidyl ribonucleotidyl transferase	13	23	0.0055813	-0.219846	0.2300169	0.730825	0.4771423
sp Q6P7Q4 Lactoylglutathione acetyltransferase	7	15	-0.0306	-0.167664	0.1032777	0.7330875	0.4778889
sp Q4KM49 Tyrosyl-tRNA transferase	18	31	0.0377352	-0.078411	0.1571335	0.7336	0.4783366
sp P06399 Fibrinogen-like protein 1	13	19	-0.009716	-0.208288	0.2021584	0.7346375	0.4786353
sp Q5XIP9 Transmembrane protein 147	5	5	-0.007268	-0.207919	0.1936489	0.7349	0.4789339
sp Q9EPH8 Polyadenylate-binding protein 1	16	23	0.0383624	-0.068013	0.1511274	0.735475	0.4790833
sp Q6MG6C N(G),N(G)-dihydropyrimidyl ribonucleotidyl transferase	14	35	0.0398761	-0.067092	0.1425434	0.7359125	0.4793819
sp Q5XF0 Transgelin-2	8	17	-0.032175	-0.15619	0.096717	0.73665	0.4798299
sp O35854 Branched-chain alpha-ketoacid dehydrogenase kinase	2	3	-0.007073	-0.216322	0.2061182	0.7367625	0.479979
sp P97874 Cyclin-G-associated protein	5	6	0.0023609	-0.222409	0.2258748	0.73715	0.480277
sp B5DF89 Cullin-3 OS-domain containing protein	4	7	-0.009208	-0.206186	0.189308	0.7374125	0.4805748

sp Q920J4 Thioredoxin	6	16	0.0276073	-0.113798	0.1670678	0.7382875	0.4808727
sp Q8CH84 ELAV-like pi	5	9	0.0191411	-0.144242	0.182004	0.7383375	0.4810216
sp P97700 Mitochondr	10	18	0.027961	-0.109219	0.1677928	0.738725	0.4814674
sp Q9WVK7 Hydroxyacy	11	21	-0.043208	-0.130667	0.0414705	0.7398	0.4822089
sp Q6PCU2 V-type prot	9	16	-0.024114	-0.172632	0.129285	0.7399625	0.4823572
sp P62632 Elongation i	14	29	0.0417915	-0.058864	0.1386863	0.7400625	0.4825053
sp P20280 60S riboson	7	14	0.0240404	-0.125576	0.1795512	0.7409125	0.4832445
sp P50137 Transketola	26	49	0.0166936	-0.16293	0.1930587	0.7426875	0.4841305
sp P23965 3,2-trans-er	6	11	0.0215482	-0.132775	0.1795052	0.7430125	0.4845732
sp P61078 Ubiquitin-cc	1	2	0.0155926	-0.165127	0.194564	0.7435375	0.4848682
sp P23978 Sodium- an	1	2	-0.00175	-0.22606	0.2289145	0.743575	0.4850154
sp P11232 Thioredoxin	7	27	0.0160181	-0.163071	0.1920606	0.7448875	0.4856045
sp Q63560 Microtubule	17	27	-0.034699	-0.15054	0.0792091	0.7465	0.4870742
sp O88600 Heat shock	23	33	0.0304763	-0.101645	0.1757574	0.747375	0.4873676
sp P11507 Sarcoplasm	10	15	-0.021577	-0.176852	0.135952	0.7489625	0.4881025
sp P32551 Cytochrome	14	25	-0.04394	-0.124602	0.0366969	0.749	0.4882491
sp Q00981 Ubiquitin ca	20	78	0.0033215	-0.209857	0.211079	0.749775	0.4894183
sp Q63081 Protein disu	11	19	-0.033998	-0.142053	0.0763539	0.7500375	0.4895641
sp Q6P747 Heterochro	14	24	0.034622	-0.074059	0.1455082	0.7502375	0.4897098
sp P62832 60S riboson	9	17	0.0322075	-0.085907	0.1478854	0.750575	0.4902915
sp Q9ESN0 Protein Nib	5	6	-0.002589	-0.206191	0.1989028	0.7508875	0.4905818
sp Q9JIL3 II Interleukin	3	3	-0.005381	-0.24347	0.2261764	0.7515	0.4911614
sp Q6XVN8 Microtubule	5	8	0.0242022	-0.118084	0.1696885	0.75325	0.4915963
sp Q9JJ19 I Na(+)/H(+) c	7	8	0.0078338	-0.178269	0.2016219	0.7535625	0.4917416
sp P50399 Rab GDP dis	17	32	-0.025365	-0.166324	0.1240674	0.7537875	0.4921767
sp Q63638 Striated mu	4	4	-0.000555	-0.222142	0.2138056	0.7540125	0.4923216
sp P01830 Thy-1 meml	4	6	0.0140474	-0.155995	0.1836957	0.7546375	0.493045
sp Q6PEC4 S-phase kin	12	23	0.0229932	-0.126159	0.1748111	0.75495	0.4936216
sp P62845 40S riboson	3	5	0.0109324	-0.182908	0.1986594	0.75575	0.4941966
sp Q9ERE6 Myosin pho	5	6	-0.009786	-0.195458	0.1676311	0.7569625	0.4947714
sp Q4V8B0 Oxidation re	8	8	-0.011024	-0.203628	0.177812	0.75735	0.4952024
sp P84083 ADP-ribosyl	3	8	0.025172	-0.107314	0.1577867	0.7578	0.4957756
sp P27867 Sorbitol de	6	9	0.0112805	-0.162129	0.1853638	0.7578625	0.4959187
sp Q99NA5 Isocitrate de	11	19	-0.042761	-0.126545	0.0406837	0.760075	0.4967773
sp Q66H98 Serum depr	6	8	0.0025725	-0.192836	0.1955492	0.760525	0.497207
sp P18422 Proteasome	3	5	0.0025688	-0.197244	0.1999369	0.761175	0.4976361
sp P55260 Annexin A4	11	19	0.0249848	-0.109984	0.1653663	0.7613375	0.497779
sp Q01177 Plasminoge	6	9	0.0153989	-0.144389	0.1722129	0.761925	0.4982075
sp P20788 Cytochrome	9	14	-0.02175	-0.16061	0.1196671	0.7621375	0.4983503
sp P97849 Long-chain	7	11	-0.017534	-0.173343	0.1331789	0.76215	0.4984929
sp P69060 N-acylneur	1	3	0.0177387	-0.138423	0.1874407	0.763875	0.4997739
sp Q9JHU0 Dihydropyri	17	34	0.036157	-0.068204	0.1414484	0.76465	0.5000582
sp P41565 Isocitrate de	8	10	0.0209368	-0.121608	0.1580951	0.7648125	0.5002004
sp Q5RJR8 Leucine-rich	10	17	0.0292542	-0.087987	0.1485549	0.7648875	0.5006261
sp P61980 Heterogene	15	30	0.0398007	-0.047655	0.1274862	0.7651125	0.5009093
sp Q2TA68 Dynamin-lik	7	12	0.0051028	-0.177298	0.1886413	0.76885	0.5026065
sp P49432 Pyruvate de	11	18	0.0209953	-0.114274	0.1569421	0.769575	0.5031732

sp Q64559 Cytosolic ac	8	12	0.0020849	-0.19731	0.1975397	0.7707625	0.5037393
sp Q9QX69 LanC-like pr	9	14	0.020326	-0.121339	0.1619979	0.7708375	0.5038808
sp P86252 Transcriptic	8	19	0.0237359	-0.110675	0.1551128	0.77115	0.5043046
sp P63326 40S ribosom	5	9	-0.016184	-0.164124	0.1280821	0.772475	0.5047289
sp P50503 Hsc70-inter	12	21	-0.027614	-0.146213	0.0969738	0.7729875	0.5052937
sp Q62717 Calcium-dej	10	13	0.0242397	-0.100845	0.1482941	0.774925	0.5069833
sp P62260 14-3-3 prot	14	29	-0.035821	-0.13251	0.0605018	0.775275	0.5071237
sp B2RYG6 Ubiquitin th	6	9	0.003791	-0.177572	0.183719	0.7755125	0.5075443
sp B0K020 CDGSH iron	5	9	-0.025172	-0.148591	0.0954773	0.775725	0.5076843
sp P28480 T-complex p	15	28	0.0363696	-0.056182	0.1271831	0.77625	0.5082437
sp P21913 Succinate d	6	11	-0.018155	-0.16408	0.1264059	0.777325	0.5089423
sp Q6AYS8 Estradiol 17	7	9	0.0078801	-0.15731	0.172988	0.777375	0.509221
sp Q9JLJ3 / α 4-trimethyl	10	18	-0.028494	-0.138262	0.0817378	0.778	0.5094997
sp Q91Y81 Septin-2 OS	8	12	-0.025341	-0.143128	0.0952968	0.77825	0.5097782
sp P60881 Synaptosomal	4	9	0.002599	-0.175533	0.1823847	0.7783125	0.5099172
sp Q6P6R2 Dihydrolipo	11	23	-0.040745	-0.121869	0.0384514	0.778325	0.5100562
sp Q62638 Golgi appar	11	17	0.0199291	-0.116471	0.1553821	0.7785125	0.510195
sp P42123 L-lactate de	17	51	-0.008599	-0.176227	0.1609076	0.780025	0.5115811
sp P10111 Peptidyl-pro	11	35	0.0009574	-0.185572	0.19994	0.7806625	0.5122716
sp Q5RKI0 WD repeat-	14	20	-0.030661	-0.136119	0.0730338	0.7810625	0.5125471
sp Q5XHY8 Uncharacte	1	2	0.0121109	-0.153464	0.1703004	0.7810875	0.5128223
sp O08562 Sodium cha	1	2	-0.007618	-0.185997	0.1657519	0.7812	0.5129597
sp P04256 Heterogene	5	9	0.015437	-0.134899	0.1663355	0.781375	0.5133713
sp P06685 Sodium/pot	22	63	-0.031984	-0.137056	0.0740871	0.78215	0.5139189
sp Q9Z272 ARF GTPase	5	6	-0.003107	-0.192487	0.1791525	0.782225	0.5141924
sp P61203 COP9 signal	9	13	-0.002902	-0.186235	0.173622	0.7842	0.5154216
sp Q9WVB1 Ras-related	8	12	-0.032416	-0.132863	0.0647635	0.785225	0.5161031
sp Q5XIH7 Prohibitin-2	15	23	0.0303837	-0.073982	0.1357683	0.786275	0.516376
sp P18418 Calreticulin	22	53	-0.033226	-0.131106	0.0683198	0.7864125	0.5166487
sp Q9Z1E1 Flotillin-1 O	7	12	0.0066939	-0.156221	0.1690928	0.788025	0.5181442
sp Q9EQS0 Transaldola	17	38	0.0127015	-0.134717	0.1693783	0.7912375	0.5199049
sp A2RRU1 Glycogen [s	6	7	-0.001344	-0.17161	0.1729451	0.79195	0.5204464
sp P07323 Gamma-en	12	29	-0.014827	-0.162929	0.1303797	0.7938	0.5209879
sp Q63355 Myosin-Ic C	12	17	-0.0057	-0.169748	0.1583914	0.79405	0.5213943
sp Q5M9I5 Cytochrome	2	8	-0.016	-0.154614	0.118172	0.7943	0.5219348
sp Q9Z1A6 Vigilin OS=R	14	19	-0.022706	-0.142141	0.0936481	0.794875	0.5226087
sp Q9Z0W5 Protein kin	8	10	0.0008974	-0.175722	0.1693025	0.7949875	0.5227432
sp O55156 CAP-Gly doi	14	19	-0.010698	-0.160747	0.1376132	0.795425	0.5231465
sp P12075 Cytochrome	5	13	0.0278823	-0.081127	0.1314987	0.79585	0.5235492
sp Q07266 Drebrin OS=	7	13	-0.014733	-0.151139	0.1214599	0.7965875	0.5246194
sp Q9QXY2 SRC kinase :	1	2	-0.011869	-0.158688	0.1397092	0.7967125	0.524886
sp P62718 60S ribosom	6	14	0.0138368	-0.130358	0.1561111	0.7967375	0.5251522
sp Q07936 Annexin A2	26	82	-0.025092	-0.139251	0.091302	0.7967375	0.5250192
sp P51635 Alcohol deh	12	25	0.013605	-0.13152	0.162173	0.7978875	0.5259494
sp P85972 Vinculin OS:	42	72	-0.010256	-0.163489	0.1402831	0.798525	0.52648
sp P63102 14-3-3 prot	11	33	0.0219336	-0.100017	0.1466736	0.799575	0.5271425
sp P97852 Peroxisoma	10	13	0.0143705	-0.131721	0.1571054	0.80005	0.5279351

sp P37285 Kinesin light chain 1	12	19	0.0161217	-0.118975	0.1527164	0.8000625	0.5280669
sp P47752 Sphingosine kinase 1	1	5	0.0038411	-0.158343	0.1714062	0.8005	0.5281987
sp P04762 Catalase OS	10	12	0.0135361	-0.125915	0.1541867	0.8011	0.5284625
sp O54924 Exocyst complex component 1	1	3	0.0042377	-0.164573	0.1719065	0.8016375	0.5287263
sp P40329 Arginyl-tRNA transferase	17	24	0.0266019	-0.077585	0.1315788	0.8019125	0.52899
sp Q9JLT0 Myosin-10 (Myo10)	30	41	-0.020764	-0.143482	0.1042484	0.8022375	0.5296474
sp P47875 Cysteine arylamidase-like protein	9	17	0.0061723	-0.154369	0.1606606	0.8032875	0.5301723
sp P12839 Neurofilament protein	31	100	-0.037086	-0.12046	0.0452755	0.8034	0.5303036
sp P25113 Phosphoglycerate kinase	11	28	-0.00334	-0.164727	0.1646019	0.8035875	0.5305658
sp P04904 Glutathione S-transferase	6	11	-0.021132	-0.140493	0.0991854	0.8050625	0.531221
sp Q06647 ATP synthase, mitochondrial	9	17	-0.005419	-0.168965	0.1467903	0.8056875	0.5313523
sp P35435 ATP synthase, mitochondrial	8	15	-0.019575	-0.142135	0.1015983	0.805775	0.5314835
sp Q08163 Adenylyl cyclase	12	21	0.0198288	-0.098752	0.1485995	0.8060875	0.5316148
sp Q8CFN2 Cell division cycle 10 homolog	8	11	-0.019177	-0.143244	0.1029332	0.80635	0.5318772
sp P09117 Fructose-bisphosphate aldolase	11	24	0.0116879	-0.138077	0.158685	0.8071	0.5322706
sp P08699 Galectin-3 C-terminal domain	3	4	0.003343	-0.15665	0.1658857	0.8080875	0.5333166
sp Q62733 Lamina-associated polypeptide-like	10	15	-0.008156	-0.172602	0.1448175	0.8084875	0.5339685
sp Q00566 Methyl-CpG binding domain protein 1	5	7	-0.00967	-0.149151	0.1301695	0.8087	0.5342286
sp O88989 Malate dehydrogenase	13	32	-0.008847	-0.154753	0.1436891	0.810125	0.5347492
sp P10860 Glutamate decarboxylase	18	42	-0.004058	-0.163838	0.1663137	0.811625	0.535271
sp P63322 Ras-related GTPase	6	9	-0.007976	-0.149315	0.139318	0.8118	0.5354014
sp P67779 Prohibitin C-terminal domain	12	21	0.0291899	-0.068084	0.123865	0.81215	0.5357922
sp P23358 60S ribosomal protein L13	8	17	-0.025631	-0.128549	0.0759618	0.81255	0.5365715
sp P06761 78 kDa glucosidase	31	63	-0.034117	-0.117102	0.0525267	0.8138875	0.5377352
sp P16617 Phosphoglycerate kinase	22	44	0.0067486	-0.14215	0.1591077	0.81605	0.5392839
sp Q5FVJ0 Protein RUFY1	21	37	0.0060154	-0.146052	0.1572369	0.8161875	0.5394126
sp Q5XHY5 Threonyl-tRNA methyltransferase	6	8	0.0020541	-0.151585	0.1567752	0.81765	0.540184
sp P48500 Triosephosphate isomerase	12	31	0.0099057	-0.129407	0.1474433	0.8185125	0.5408269
sp P62909 40S ribosomal protein S16	16	32	0.0376299	-0.034185	0.1130509	0.8200625	0.541469
sp Q5XIT1 Microtubule-associated protein tau	7	16	0.0045283	-0.140498	0.1504135	0.8210125	0.5421113
sp P31000 Vimentin O-linked beta-N-acetylglucosaminidase	31	100	-0.033398	-0.118487	0.0512178	0.8212375	0.5422397
sp Q03344 ATPase inhibitor protein	5	8	0.0143314	-0.113325	0.1392389	0.821725	0.5424964
sp Q4QRB4 Tubulin beta-4 chain	12	64	-0.02328	-0.130095	0.0858904	0.822825	0.5437763
sp P10888 Cytochrome c oxidase subunit I	9	21	-0.027443	-0.128953	0.0678635	0.82305	0.5442862
sp P62246 40S ribosomal protein S8	8	12	-0.006695	-0.145543	0.1370098	0.8266125	0.5464467
sp Q1WIM1 Cell adhesion molecule	10	24	-0.007234	-0.158015	0.1324426	0.8268625	0.5467005
sp Q6P502 T-complex protein 1 subunit alpha	22	40	0.0413364	-0.022125	0.1047114	0.8274625	0.5475863
sp Q09073 ADP/ATP translocase	7	13	-0.01922	-0.130247	0.0915073	0.827675	0.5477127
sp Q6RUV5 Ras-related GTPase	7	23	0.0193386	-0.093915	0.1362078	0.828525	0.5480918
sp P11240 Cytochrome c oxidase subunit II	6	11	0.0025305	-0.145611	0.1550859	0.829425	0.5487232
sp P19511 ATP synthase, mitochondrial	7	15	-0.030273	-0.117842	0.0579566	0.8295	0.5488493
sp Q63570 26S proteasome non-ATPase regulatory subunit 1	4	6	0.0011562	-0.151183	0.1515963	0.8297125	0.5492273
sp Q66X93 Staphylococcal nuclease	16	26	0.0247445	-0.072527	0.1232151	0.8297625	0.5494787
sp P34926 Microtubule-associated protein tau	50	100	-0.016378	-0.135728	0.1061018	0.8299	0.5497298
sp Q9Z2L0 Voltage-dependent proton channel	10	12	-0.005044	-0.146909	0.1371349	0.83065	0.5501063
sp P18420 Proteasome subunit large	7	15	-0.014733	-0.13179	0.1036534	0.8313125	0.550858
sp P11951 Cytochrome c oxidase subunit III	7	16	-0.005417	-0.147104	0.1396022	0.8320125	0.5518566

sp Q5I0D1 Glyoxalase I	14	27	0.0152361	-0.109441	0.1348969	0.83205	0.5521054
sp P62902 60S ribosomal large subunit	7	11	0.0033732	-0.142805	0.158689	0.83275	0.5523542
sp P10719 ATP synthase, mitochondrial	25	59	-0.037634	-0.107835	0.0355348	0.8336125	0.5529761
sp Q5XI72 Eukaryotic translation initiation factor 4B	10	20	0.0040655	-0.136184	0.1474525	0.8364375	0.5542197
sp Q1JU68 Eukaryotic translation initiation factor 4A	18	31	0.0199089	-0.087082	0.1241109	0.83705	0.5547168
sp P17074 40S ribosomal small subunit	9	15	-0.016408	-0.132747	0.0985742	0.83705	0.554841
sp Q920L2 Succinate dehydrogenase complex, subunit 2	13	25	-0.016048	-0.130694	0.0988461	0.8372875	0.555213
sp Q63083 Nucleobindin	7	10	0.0019324	-0.141483	0.1393937	0.8374125	0.5553369
sp P11980 Pyruvate kinase	32	93	0.0139598	-0.108898	0.1316611	0.8388625	0.5562043
sp Q5M7W1 Microtubule-associated protein tau	35	67	0.0212498	-0.081126	0.1296936	0.838975	0.5563279
sp O35095 Neurochondrin	12	21	-0.014796	-0.130008	0.1028889	0.8401	0.5569458
sp P13221 Aspartate aminotransferase	17	33	0.024448	-0.073954	0.1222563	0.8417625	0.5583028
sp Q9QUL6 Vesicle-fusion-associated membrane protein	36	67	-0.031518	-0.11591	0.0470322	0.8426625	0.559041
sp P35434 ATP synthase, mitochondrial	3	8	0.0113663	-0.110152	0.1310911	0.843575	0.5594099
sp P61589 Transforming growth factor beta receptor type I	9	20	0.023361	-0.070989	0.1187608	0.843625	0.5596556
sp P81155 Voltage-dependent potassium channel subunit alpha	7	13	-0.004183	-0.13958	0.1360122	0.8444875	0.5601469
sp P04785 Protein disulfide-isomerase	22	37	-0.038972	-0.101647	0.0219703	0.8464	0.5617398
sp Q8R491 EH domain-containing protein 1	4	13	0.0062741	-0.125397	0.1366286	0.8474	0.5625939
sp P16884 Neurofilament protein	26	100	-0.037573	-0.104888	0.0288166	0.847725	0.5628377
sp P85834 Elongation factor 1-alpha	10	16	0.0205674	-0.075577	0.1219656	0.8499125	0.5644183
sp P19804 Nucleoside diphosphate kinase	4	7	-0.011817	-0.133403	0.1026261	0.850025	0.5646609
sp P97697 Inositol monophosphate phosphatase	6	9	-0.004464	-0.13417	0.1247254	0.8502375	0.5649033
sp P09895 60S ribosomal protein L13	14	21	-0.018307	-0.121489	0.0826075	0.8504625	0.5651454
sp Q64428 Trifunctional protein	22	35	0.0281581	-0.057406	0.1096081	0.850475	0.5652664
sp Q68FU3 Electron transfer flavoprotein	8	12	-0.010231	-0.125427	0.1087707	0.8506625	0.5656288
sp Q9WU82 Catenin beta 1	12	19	0.0172178	-0.087126	0.1187968	0.850725	0.5657494
sp P13086 Succinyl-CoA ligase	13	24	0.0109474	-0.105748	0.1319569	0.8527625	0.5665955
sp P62762 Visinin-like protein	11	19	-0.007433	-0.12627	0.1138852	0.8551875	0.5681627
sp P61314 60S ribosomal protein L10	6	10	-0.005557	-0.131052	0.1177813	0.8555125	0.5682833
sp Q5FVM4 Non-POU domain containing octamer binding protein	7	12	-0.011746	-0.12258	0.1000459	0.8564125	0.5686451
sp P61765 Syntaxin-binding protein 1	20	32	-0.008791	-0.129067	0.1194895	0.8581125	0.5699695
sp Q05962 ADP/ATP translocase	7	20	-0.011818	-0.129898	0.0992551	0.858175	0.5700896
sp Q6JE36 Protein NDF	9	32	0.0211538	-0.072632	0.1147885	0.8585625	0.5703299
sp Q5EB81 NADH-cytidine nucleotide exchange protein	6	14	-0.00044	-0.132911	0.1381803	0.8600125	0.57117
sp P14668 Annexin A5	22	64	-0.008544	-0.131178	0.1159115	0.8603375	0.57129
sp Q5XI73 Rho GDP-dissociation inhibitor	11	22	0.0153867	-0.093147	0.1194991	0.8609	0.5718893
sp Q6P6V0 Glucose-6-phosphate isomerase	22	36	-0.005582	-0.13063	0.1195569	0.8617625	0.5722487
sp Q5RKI1 Eukaryotic translation initiation factor 4E	11	25	-0.022689	-0.110871	0.0692489	0.8619125	0.5723685
sp P22062 Protein-L-isozyme	8	16	-0.013053	-0.121531	0.0994799	0.864225	0.5735657
sp P15999 ATP synthase, mitochondrial	34	98	-0.033262	-0.103327	0.0374617	0.865675	0.5741651
sp P62271 40S ribosomal protein S16	8	25	0.0129114	-0.092075	0.1137992	0.87075	0.5790339
sp P97536 Cullin-associa	20	31	-0.011811	-0.11736	0.0947505	0.87175	0.579741
sp P49134 Integrin beta 1	9	21	-0.003466	-0.124301	0.1170504	0.873725	0.5808011
sp Q9JK11 Reticulon-4	24	44	0.0199201	-0.067937	0.1106996	0.8749625	0.5817415
sp P05942 Protein S10	8	16	-0.014724	-0.113813	0.0853711	0.8755	0.5824453
sp P15178 Aspartyl-tRNA synthetase	17	30	0.0144589	-0.084325	0.113807	0.8776	0.5836152
sp P62425 60S ribosomal protein L10	16	30	-0.016584	-0.108958	0.0766468	0.8797625	0.5847862

sp P15205 Microtubule-associated protein 1A OS=Homo sapiens	53	100	-0.009175	-0.115366	0.0998386	0.8810375	0.5859534
sp Q9QZR6 Septin-9 OS=Homo sapiens	12	17	0.0030107	-0.110962	0.1184767	0.8813	0.586419
sp P61983 14-3-3 protein epsilon OS=Homo sapiens	10	15	-0.004133	-0.124286	0.1124563	0.88165	0.5868835
sp Q641Y0 Dolichyl-diphosphate acetyltransferase OS=Homo sapiens	9	21	0.0100808	-0.093325	0.1118626	0.8826	0.587926
sp Q63269 Inositol 1,4,5-trisphosphate receptor OS=Homo sapiens	27	37	0.0010205	-0.115997	0.1227341	0.8864375	0.590804
sp P25809 Creatine kinase OS=Homo sapiens	7	15	0.0106103	-0.088999	0.1105804	0.8876375	0.5911489
sp Q5BK63 NADH dehydrogenase 1 OS=Homo sapiens	9	18	0.0069073	-0.10303	0.1155956	0.88785	0.5914937
sp P19945 60S acidic ribosomal P0 protein OS=Homo sapiens	12	26	0.0102243	-0.093756	0.1139987	0.88865	0.5918383
sp Q5QD51 A-kinase anchor protein 1 OS=Homo sapiens	21	31	-0.006214	-0.11	0.1020954	0.889575	0.5925272
sp Q3KR86 Mitochondrial ribosomal protein L13 OS=Homo sapiens	18	30	-0.01628	-0.107071	0.078517	0.8907125	0.5938998
sp Q9Z269 Vesicle-associated membrane protein-associated protein OS=Homo sapiens	9	12	-0.001409	-0.118642	0.1117354	0.89125	0.5943559
sp P43244 Matrin-3 OS=Homo sapiens	11	15	0.0057466	-0.097271	0.1109508	0.8917875	0.5948114
sp P28023 Dynactin subunit DHC1 OS=Homo sapiens	21	29	0.0064653	-0.09739	0.1126513	0.892275	0.5954932
sp P24050 40S ribosomal protein S1 OS=Homo sapiens	8	17	0.0257899	-0.047554	0.0963401	0.894	0.5965142
sp Q62952 Dihydropyrimidyl nucleoside triphosphate dehydrogenase OS=Homo sapiens	14	29	0.0121301	-0.077564	0.1110612	0.8962875	0.5980968
sp Q04462 Valyl-tRNA : tRNA ligase OS=Homo sapiens	18	26	-0.016419	-0.102237	0.0713704	0.89685	0.5989989
sp B2RZ37 Receptor expressed in breast cancer OS=Homo sapiens	5	12	-0.006538	-0.114278	0.0981746	0.897075	0.5995608
sp Q6PDV7 60S ribosomal protein L13 OS=Homo sapiens	12	24	-0.00777	-0.108905	0.0922586	0.8981375	0.6001218
sp P63018 Heat shock protein 70 OS=Homo sapiens	28	81	0.0083443	-0.088516	0.1099841	0.9024875	0.603037
sp P11598 Protein disulfide-isomerase OS=Homo sapiens	29	77	-0.015584	-0.10162	0.0720885	0.90795	0.6069249
sp P27952 40S ribosomal protein S12 OS=Homo sapiens	15	36	0.0107065	-0.079937	0.1016684	0.9109375	0.6088063
sp Q62826 Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens	15	25	-0.010237	-0.098221	0.0804852	0.9137375	0.6109
sp Q07009 Calpain-2 catalytic subunit OS=Homo sapiens	13	32	0.0101287	-0.075489	0.0966904	0.920575	0.6142026
sp P68511 14-3-3 protein epsilon OS=Homo sapiens	7	15	-0.000932	-0.102089	0.1009918	0.920625	0.6143126
sp P07153 Dolichyl-diphosphate acetyltransferase OS=Homo sapiens	22	35	-0.007785	-0.096515	0.0849821	0.9241625	0.6173795
sp P35565 Calnexin OS=Homo sapiens	15	31	0.0084164	-0.075272	0.0912867	0.9333375	0.6244176
sp P16036 Phosphate carrier OS=Homo sapiens	11	22	-0.00062	-0.094128	0.0924668	0.936225	0.6264532
sp P62703 40S ribosomal protein S12 OS=Homo sapiens	14	28	0.0108715	-0.065446	0.0864028	0.9422	0.6315502
sp P29314 40S ribosomal protein S12 OS=Homo sapiens	14	29	0.0071654	-0.071436	0.0857006	0.94485	0.6340731
sp P62919 60S ribosomal protein L13 OS=Homo sapiens	16	36	0.0145206	-0.053205	0.0855613	0.944975	0.6341777
sp Q63507 60S ribosomal protein L13 OS=Homo sapiens	8	17	-0.003105	-0.087171	0.0841174	0.9451375	0.6342824
sp P26284 Pyruvate dehydrogenase OS=Homo sapiens	19	34	0.0073022	-0.069342	0.0869431	0.948575	0.6370957
sp P30427 Plectin OS=Homo sapiens	73	100	0.0292226	-0.018448	0.0794813	0.9533625	0.6403082
sp Q8VHF5 Citrate synthase OS=Homo sapiens	17	37	0.0033342	-0.075374	0.0805558	0.9572	0.6435973
sp P04642 L-lactate dehydrogenase OS=Homo sapiens	16	38	0.0113834	-0.057119	0.0802006	0.95915	0.6452326
sp P46462 Transitional endoplasmic reticulum protein OS=Homo sapiens	42	91	-0.002541	-0.07998	0.075445	0.9623	0.6474735
sp Q9ER34 Aconitase homolog OS=Homo sapiens	29	47	-0.009025	-0.075278	0.05717	0.96375	0.648489
sp P48721 Stress-70 protein OS=Homo sapiens	25	51	0.0056742	-0.061997	0.0754958	0.9668125	0.6509199
sp P16086 Spectrin alpha OS=Homo sapiens	62	100	0.0249128	-0.021055	0.0725918	0.9697875	0.6534335
sp O35814 Stress-inducible protein OS=Homo sapiens	27	39	-0.002647	-0.073483	0.067464	0.9709375	0.6552298
sp P05708 Hexokinase OS=Homo sapiens	25	52	-0.015882	-0.07043	0.0375201	0.9792375	0.6627022
sp P11442 Clathrin heavy chain OS=Homo sapiens	56	100	0.0190909	-0.027889	0.0677362	0.9802375	0.6630918
sp P00507 Aspartate aminotransferase OS=Homo sapiens	20	51	0.0085485	-0.045924	0.0627002	0.986875	0.6682323
sp P38650 Cytoplasmic dynein OS=Homo sapiens	70	100	-0.000971	-0.054479	0.0518659	0.992875	0.6731175