

Supplemental Material Belonging to:

Proteome-wide protein concentrations in the human heart

Thin Thin Aye^{1,2,5}, Arjen Scholten^{1,2,5}, Nadia Taouatas^{1,2}, Andras Varro⁴, Toon A.B. Van Veen³, Marc A. Vos³, and Albert J. R. Heck^{1,2,6}

¹ Biomolecular Mass Spectrometry and Proteomics Group, Bijvoet Center for Biomolecular Research and Utrecht Institute for Pharmaceutical Sciences, Utrecht University, Padualaan 8, 3584 CH Utrecht, The Netherlands

² Netherlands Proteomics Centre, The Netherlands

³ Department of Medical Physiology, University Medical Centre Utrecht, Yalelaan 50, 3584 CM Utrecht, The Netherlands

⁴ Department of Pharmacology & Pharmacotherapy, Faculty of Medicine, University of Szeged, Hungary

⁵ These authors contributed equally to this work

⁶ To whom correspondence should be addressed: E-mail: a.scholten@uu.nl and a.j.r.heck@uu.nl. Telephone: (+31) 30 253 6793, Fax: (+31) 30 253 6919

SUPPLEMENTAL METHODS

Proteolysis and mass spectrometry analysis

Method A (Trypsin in-gel digestion): The LV protein extract (50 μ g) was loaded onto two different SDS-PAGE gradient gels (4-15% and 10-20%, BioRad). Both gel lanes were cut into 70 pieces using Mickle gel slicer prior to in-gel digestion. Gel pieces were subsequently treated with DTT (6.5mM in 50mM ammonium bicarbonate, pH 8.5) and iodoacetamide (54mM in 50mM ammonium bicarbonate, pH 8.5) for respective reduction and alkylation of cysteine residues. The alkylated proteins were digested with trypsin (Roche Diagnostics, Almere, The Netherlands) for 16hr at 37°C. After digestion, the supernatants were collected and the remaining gel pieces were extracted with acetonitrile.

The MS analysis was performed using a nano LC–LTQ-FTICR (Thermo, San Jose, CA). An Agilent 1200 series LC system was equipped with a 20mm Aqua C18 (Phenomenex, Torrance, CA) trapping column (packed in-house; inner diameter, 100 μ m; resin, 5 μ m) and a 400mm ReproSil-Pur C18-AQ (Dr. Maisch, GmbH, Ammerbuch, Germany) analytical column (packed in-house; inner diameter, 50 μ m; resin, 3 μ m). Trapping was performed at 5 μ L/min for 10 min in solvent A (0.1 M acetic acid in water), and elution was achieved with a gradient of 10–35% B (0.1 M acetic acid in 80/20 acetonitrile/water) in 45 min in a total analysis time of 60 min. The flow rate was passively split to 100nL/min when performing the elution analysis. Nanospray was achieved using a distally coated fused-silica emitter (New Objective, Cambridge, MA) (outer diameter, 360 μ m; inner diameter, 20 μ m; tip inner diameter, 10 μ m) biased to 1.7 kV. The LTQ-FTICR mass spectrometer was operated in data-dependent mode, automatically switching between MS and MS/MS. Full-scan MS spectra (150–1500 m/z) was acquired to a target value of 100,000. The two most intense peaks above a threshold of 500 were selected for collision induced dissociation in the linear ion trap at normalized collision energy of 35% after accumulation to a target value of 10,000.

Method B (Lys-C/Trypsin In-solution digestion): 50 μ L (200 μ g protein amount) was diluted to 200 μ L total volume with 96mg of urea to get final urea concentration of 8M. Subsequently, digestion with 4 μ g Lys-C (Roche Diagnostics, Almere, The Netherlands) for 4hr at 37°C, was followed by reduction with 2 μ M Dithiothreitol for 15min at 65 °C and alkylation with 4 μ M iodoacetamide in the dark for 30 minutes at room temperature. Further digestion was performed in 2M urea with 4 μ g trypsin (Roche Diagnostics, Almere, The Netherlands) for 16hr at 37°C. The resulting peptide mixture was separated using strong

cation exchange (SCX) as described previously [1]. Briefly, prior to SCX fractionation, the trypsin digested samples were desalted using a small plug of C18 material (3M Empore C₁₈ extraction disk) packed into a GELoader tip (Eppendorf) onto which ~10µL of Aqua C₁₈ (5µm, 200 Å) material was packed. The eluted desalted peptide mixture was dried *in vacuo* and subsequently reconstituted in 10% formic acid. SCX was performed using two in-line coupled Zorbax BioSCX-Series II columns (Agilent Technologies, Amstelveen, The Netherlands; 0.8mm inner diameter x 50mm L, 3.5µm), a FAMOS autosampler (LC-packing, Amsterdam, The Netherlands) and a Shimadzu LC-9A binary pump and a SPD-6A UV-detector (Shimadzu, Tokyo, Japan). After injection, the first 5 minutes were ran isocratic at 100 % solvent A (20 % acetonitrile, 0.05 % formic acid, pH 3.0), followed by a linear gradient of 1 % min⁻¹ solvent B (500mM KCl in 20 % acetonitrile and 0.05 % formic acid, pH 3.0). A total of 50 SCX fractions (1 min each, i.e. 50µl elution volume) were manually collected and dried in a vacuum centrifuge.

The 50 dried SCX fractions were diluted in 20µl of 10% formic acid, and 10µl of these were subjected to nano LC–LTQ-Orbitrap (Thermo, San Jose, CA). The LC set up was the same as described above in method A. The LTQ-Orbitrap mass spectrometer was operated in data-dependent mode, automatically switching between MS and MS/MS. Full-scan MS spectra (350–1500 *m/z*) were acquired with a resolution of 60,000 at 350 *m/z* after accumulation to a target value of 500,000. The two most intense peaks above a threshold of 500 were selected for collision induced dissociation in the linear ion trap at normalized collision energy of 35% after accumulation to a target value of 10,000.

Method C (Lys-C/chymotrypsin In-solution digestion): 100 µg of protein material was taken up in 8M urea and reduced and alkylated as described above in method B samples. Primary digestion was performed using 2µg Lys-C similarly as above, followed by digestion with 2µg chymotrypsin (Roche Diagnostics, Almere, The Netherlands) in 2M urea for 16hr at 37 °C prior to SCX fractionation. A refined SCX-method was performed as reported previously [2] using an Agilent 1100 HPLC system (Agilent Technologies) with two C18 Opti-Lynx (Optimized Technologies, Oregon OR) guard columns and a polysulfoethyl A SCX column (PolyLC, Columbia, MD; 2.1mm inner diameter x 200mm, 5µm, 200-Å). The digested tissue lysate was dissolved in 0.05% formic acid (FA), and loaded onto the guard column at 100µl/min and subsequently eluted onto the SCX column with 80% acetonitrile (ACN) and 0.05% formic acid. Separation of different peptide populations was performed using a nonlinear 65 min gradient: from 0 to 10 min, 100% solvent A (5mM KH₂PO₄, 30%

acetonitrile, pH 2.7); from 10 to 15 min, up to 26% solvent B (5mM KH₂PO₄, 30% acetonitrile, 350mM KCl, pH 2.7); from 15 to 40 min, to 35% solvent B; and from 40 to 45 min, to 60% solvent B. At 49 min, the concentration of solvent B was 100%. The column was subsequently washed for 6 min with high salt concentration and finally equilibrated with 100% solvent A for 9 min. The flow rate applied during the SCX gradient was 200 μ L/min. A total of 50 fractions were collected and dried in a vacuum centrifuge.

The analysis was performed using a nano LC–Orbitrap-ETD (Thermo, San Jose, CA). An Agilent 1200 series LC system was connected to an Orbi-trap Mass Spectrometer with an ETD source at the back. LC set up as well as elution gradient is same as described in method A and B with 90 min analysis time. The LTQ-Orbitrap-ETD mass spectrometer was operated in data-dependent mode, automatically switching between MS and MS/MS. Full-scan MS spectra (350–1500 m/z) were acquired with a resolution of 60,000 at 350 m/z after accumulation to a target value of 500,000. Parent ions were isolated for a more accurate measurement by performing a single ion monitoring scan and fragmented by CAD and ETcaD in data-dependent mode. Ions were fragmented using CAD with normalized collision energy of 35 and 30 ms activation time. ETD fragmentation was performed with supplemental activation; fluoranthene was used as reagent anion, and ion/ion reaction in the ion trap was taking place for 100 ms.

Method D (Lys-N In-solution digestion): 200 μ g of lysate was reduced and alkylated as described above in method C, followed by Lys-N digestion (from *Grifola Frondosa*, Seikagaku Corp. (Tokyo, Japan). Lys-N was added at a ratio of 1:85 (w/w) and the sample was incubated overnight at 37 °C. The digest was dried in *vacuo* and re-suspended in 0.05% formic acid (FA), followed by a refined SCX fractionation as mentioned in method C.

The analysis was performed using a nano-LC–LTQ-ETD setup (Thermo, San Jose, CA). An Agilent 1200 series LC system was connected to an LTQ-XL-Linerar Ion Trap with an ETD source at the back. LC set up as well as elution gradient is same as described in methods A, B and C. The LTQ-ETD mass spectrometer was operated in data-dependent mode, automatically switching between MS and MS/MS. Full-scan MS spectra (350–1500 m/z) was acquired with an automatic gain control value of 100,000. Parent ions were isolated for a more accurate measurement by performing a single ion monitoring scan and fragmented by CID and ETcaD. Ions were fragmented using CAD with normalized collision energy of 35% and 30 ms activation time. ETcaD fragmentation was performed with supplemental

activation; fluoranthene was used as reagent anion, and ion/ion reaction in the ion trap was taking place for 100 ms.

SUPPLEMENTAL RESULTS AND DISCUSSION

Redundancy Reduction and Combination of Data

127,091 out of 130,019 (98%) spectra matched to two-unique peptides-per-protein category “high quality data”. These spectra identified 36,124 peptides (95%) belonging to 2,049 unique proteins (57%). Typically, the problem with the two-peptides-per-protein demand is that in a single dataset a large part of proteins is identified with a single unique peptide sequence (43% of total spectra), even when all individual spectra are within the threshold of below 1% FDR. This may be due to relative low expression of proteins with abundance levels close to the mass spectrometer’s dynamic range limitation. To partly overcome this issue, we applied the different proteases, to generate a larger variety of peptides and hence increase the potential to identify more than one unique peptide sequence per protein. For instance, β -adrenergic receptor kinase 1, which was observed at 1310th position of total 3,584 proteins identified, has minimum 2 unique peptides in which one unique peptide was from trypsin in-solution digestion whereas another unique peptide was in the chymotrypsin CID experiment (Supplemental Table 1). Due to computation limitations, not all data could be combined for a single Mascot search. Therefore the data of the single peptide sequence identifications from the seven analyses (I-VII) were combined and investigated for overlapping protein identifications. In this way an additional 262 proteins could be included in the high quality protein dataset achieving a gain of 11% and resulting in a final high quality protein dataset with 2,306 proteins (Supplemental Table 2).

Complementary Quantitative Information Contributed by different proteases

Supplemental figure 2A shows the contribution of the different proteases in terms of relative spectral coverage in the form of heat map. Since trypsin yielded by far most spectra, direct comparison of F_{abb} values between the four methods is not feasible. Therefore, the spectral counts (n) of every protein i in method A, B, C and D were normalized to the total spectral counts (N) of method A-I, through the following calculation:

$$n_{\text{normalized, methodX}} = (N_{\text{total, methodX}} / N_{\text{total, methodA-I}}) * n_{\text{protein } i}$$

With these normalized spectral counts ($n_{\text{normalized, methodX}}$) a relative spectral coverage for each protein in each dataset (method A, B, C and D) was calculated by dividing the normalized spectral count by the sum of all normalized spectral counts over each dataset for each protein. As seen in supplemental figure 2, all red areas show protein identifications where a particular method yielded a high relative spectral coverage and thus a higher abundance in one

particular method. It shows that each dataset yielded a significant amount of extra information to the total dataset. The clustering analysis also shows that the two trypsin datasets are more alike than the LysN and LysC/Chymotrypsin datasets, as expected. The individual contribution is demonstrated further in supplemental figures 2B-E where the relative spectral coverage contribution is plotted for proteins where a particular method delivered >50% of relative spectral coverage for around 40 proteins each. These data indicate that when performing quantitation by means of spectral counting, a multiple protease setup is crucial to quantify more confidently.

Abundant GTPase signaling nodes of the human LV

The small GTPase proteins are a class of signaling proteins that are also heavily involved in the functioning of the ventricle by acting as GDP-GTP-regulated molecular switches. The small GTPases can be classified in five main families: Ras, Rho, Rab, Arf and Ran [3]. They are activated by proteins referred to as GEFs (Guanine Exchange Factors), which promote the exchange of GDP for GTP. GAPs (GTPase Activating Proteins), promote the intrinsic GTPase activity whereby GTP is converted to GDP and the GTPase becomes inactivated. For Rab and Rho, an additional level of regulation is induced by GDIs (Guanine Dissociation Inhibitors) which sequester the GTPases in the cytoplasm, away from their functional environment at the membrane. Most functional studies on GTPases in the heart have focused on Ras, RhoA and Rac1 [4]. All three cause hypertrophic gene expression when expressed as constitutively active mutants in cardiac myocytes. Also in animal models several other cardiac pathologies are linked to over activity of one of these small GTPases. Currently, not much additional functional information on any other GTPases is available in the cardiac context, while our overview clearly identifies the presence of many more specific GTPases. In total, we identified 109 GTPase signaling related proteins, of which 69 proteins were classified in a concentration dependent manner to the above-mentioned 5 main families of small GTPases (Supplemental figure 5). They are classified in 5 different functional subcategories: GTPases, GAPs, GEFs, GDIs and other reported interactors. In agreement with current literature, also in our data, the Ran GTPase is most abundant [5]. Also the above-mentioned RhoA and Rac1 were found, however Rac1 was only observed with one unique peptide sequence. For the Ras family, RRAS2 (also called TC21) was found most abundant, closely followed by RRAS2. The Arf family is represented by SAR1A, Arf1, ARL3 and SAR1B in the higher abundance region. Interestingly, SAR1A dependent COPII-coated vesicles have recently been assigned to regulate trafficking of several crucial cardiac

receptors (β 1-adrenergic and angiotensin type II receptor) [6]. SAR1B mutations are linked to cardiac and muscle abnormalities [7]. The Rho family is represented by its most common members, RhoA, Cdc42 and Rac1. Overall the GTPases of all families are widely distributed in terms of their abundance in the LV proteome. In contrast, several of the GTPase associated signaling proteins have different distributions. For instance the GDIs seem relatively high abundant, whereas the GEFs observed are overall of lower abundance. The GAPs have a wide distribution, although the RhoGAPs (and also the RhoGEFs) seem relatively more abundant than the ones connected to the other classes.

Data Availability

The scaffold data of the four described methods can be downloaded at ProteomeCommons.org.

Method A (2 datasets) : Title: Heart Analysis_Method A-I (Trypsin in-gel digestion)

9xKYUeM9tO1nVi81gjned4wshvhpzjaIAB6EONrSHnGINw/i7mQzr+FKFsM5pZiVvDiTcl
71MkOGfPgKbjappYgb6IwAAAAAAAAABww==

Title: Heart Analysis_Method A-II_Trypsin_IG

J8psmAXlDt3skfNsF/MAGtZCo8CbCV81t0tpx4s9+JOjCDWYELJgLoxu5iTWFao+uS5Y5
ZdZCch30paQHr4kKU4ccGYAAAAAAAAABYA==

Method B (1 dataset): Title: Heart Analysis_Method B_Trypsin_IS

fm++LOF9+r1a2g6P5epvBpw34tah1CfWd/FQYGinWETuRIQfAFsWNs7r9+Hhg2NPIDTO
AVEFdA5BkW8OFkzqAP+bHIMAAAAAAAAABuQ==

Method C (2 datasets): Title: Heart Analysis_Method C-I_chymo_CID

bPMs2/ADsznaQ6VzwbkzKPl6lHpHKM44H91HjQjbbP/lp8znVOIGLIKBeYnclMloPSaSK
YTGS2pAC9FXdIygEbBfKsAAAAAAAAABvg==

Title: Heart Analysis_Method C-II_chymo_ETD

2EdTNjySmwndwS+viD58ZxXvd5e4NbMj+9RXiEGWj3YmdAm7VEgsZaIzryqqQqBhU+
gdnoBB7UJklImZNtbxDtCKC6UAAAAAAAAABxQ==

Method D (2 datasets): Title: Heart Analysis_D-I_LysN_CID

+G2zLL8YsCARn+T1+B4DAZmUDZarmLHr5KusWFWIIEA76YAQChl2LZjq4RW6N+sp
3z3b35WH8ptwOUUPrPekjuj/UeUAAAAAAAAABqw==

Title: Heart Analysis_Method D-II_LysN_ETD

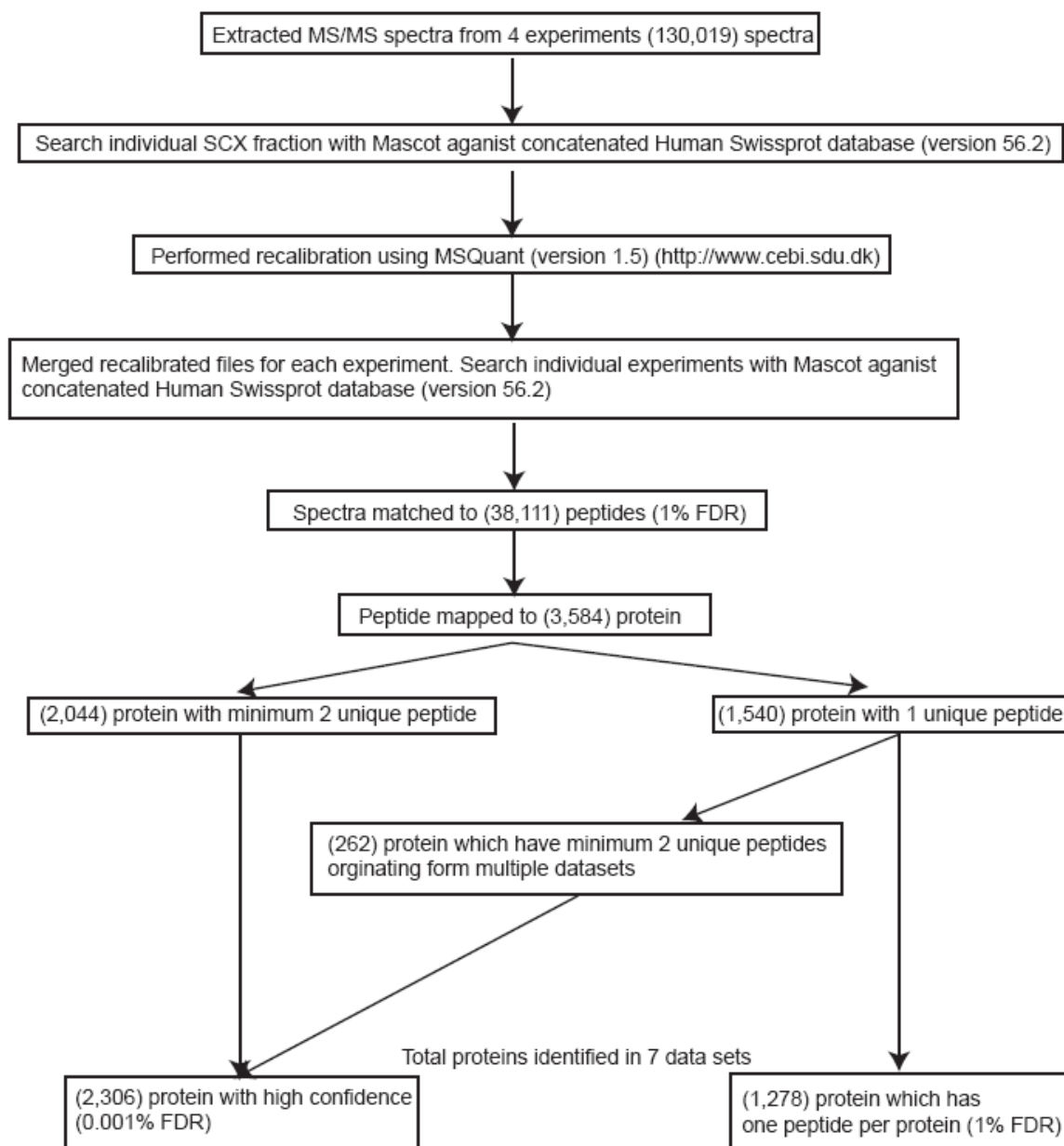
k0slf+5JsW4JAQIRzTiUQMf5PmgWCVjlZjo8jMSxy3PtTyVJYjpcQXdtvsZ/68aGuF2Fwh
DXjUg45Cijac1VLwI6PigAAAAAAAAABvg==

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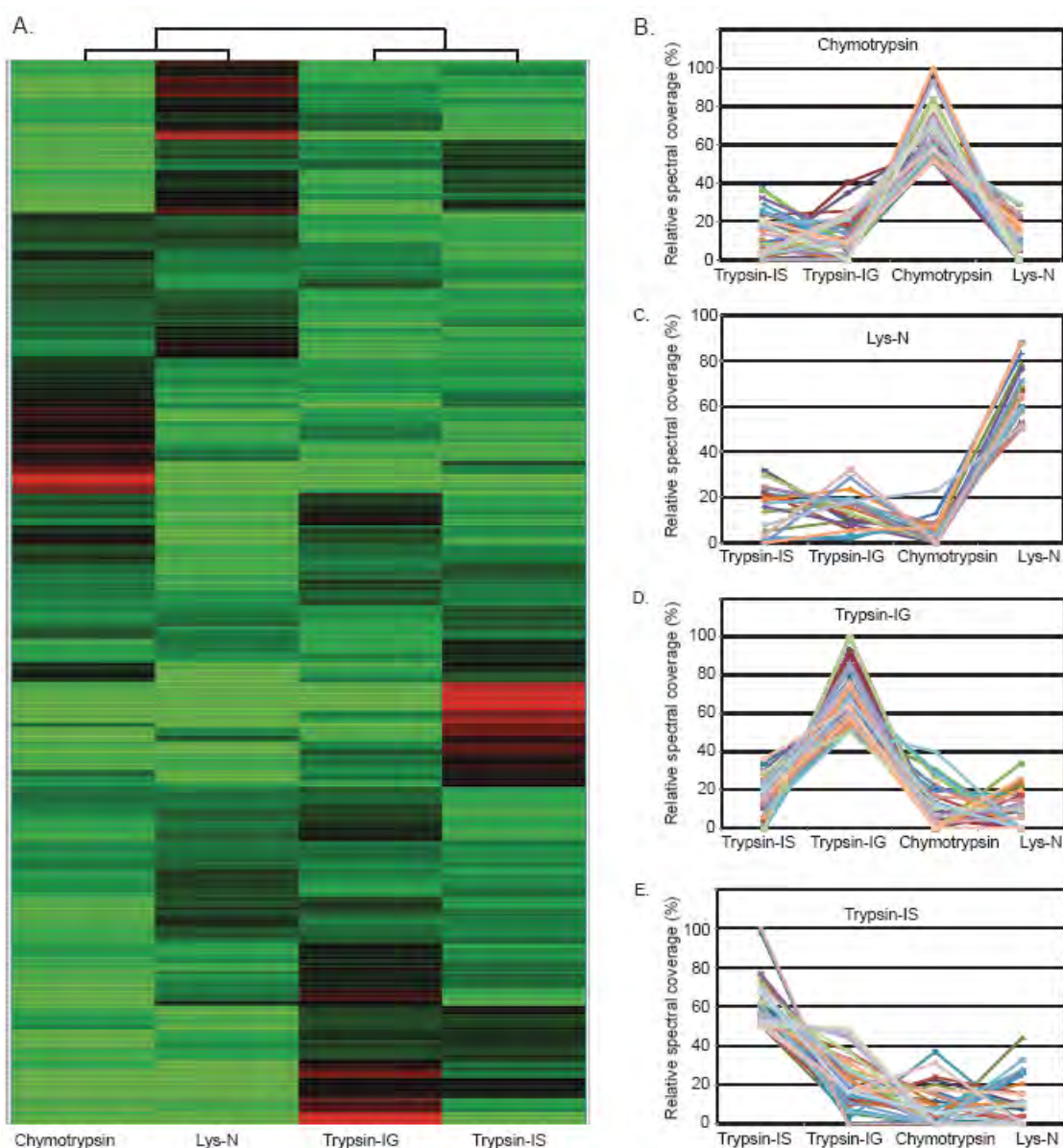
SUPPLEMENTAL FIGURES

Supplemental figure 1. Flow chart demonstrating the data analysis pipeline used for the 4 methods. The subsequent division into “High Quality data” and single-peptide match data is also depicted.



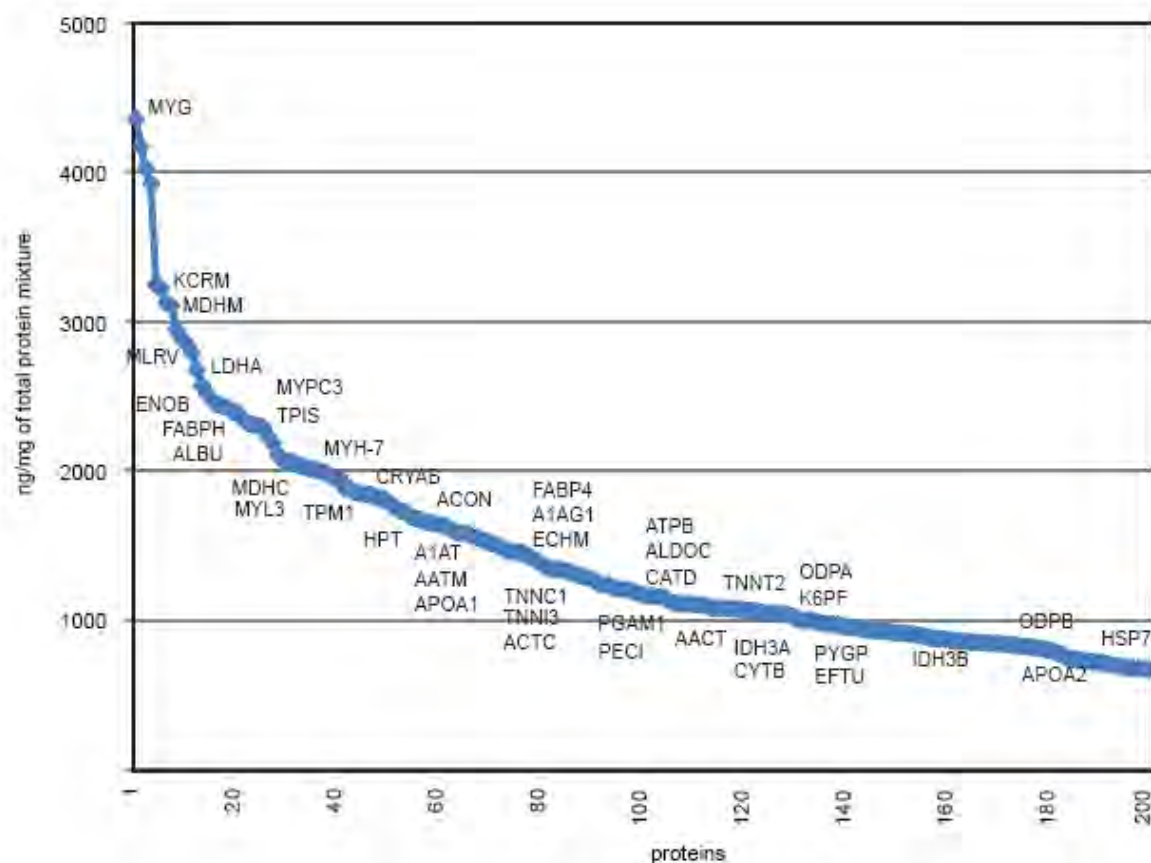
Supplemental figure 2. Specific Spectral Contribution of individual proteases increases the accuracy of absolute protein abundance

(A) Hierarchical clustering analysis was carried out for the overall top 500 proteins (based on the overall F_{abb} calculated by the normalized spectral counts). Only proteins with a minimum of 2 unique peptides and at least 5 spectra were considered. The heat map was generated with a gradient color spectrum going from red (high relative spectral contribution) to green (low relative spectral contribution). All red areas show protein identifications where a particular method yielded a high relative spectral coverage and thus a higher abundance in that particular method. Proteins which were identified with at least 50% relative spectral coverage by a single analysis method were selected: (B) Trypsin in-gel (41 proteins) (C) Trypsin-in solution (41 proteins), (D) LysC/chymotrypsin (39 proteins) and (E) Lys-N (20 proteins).



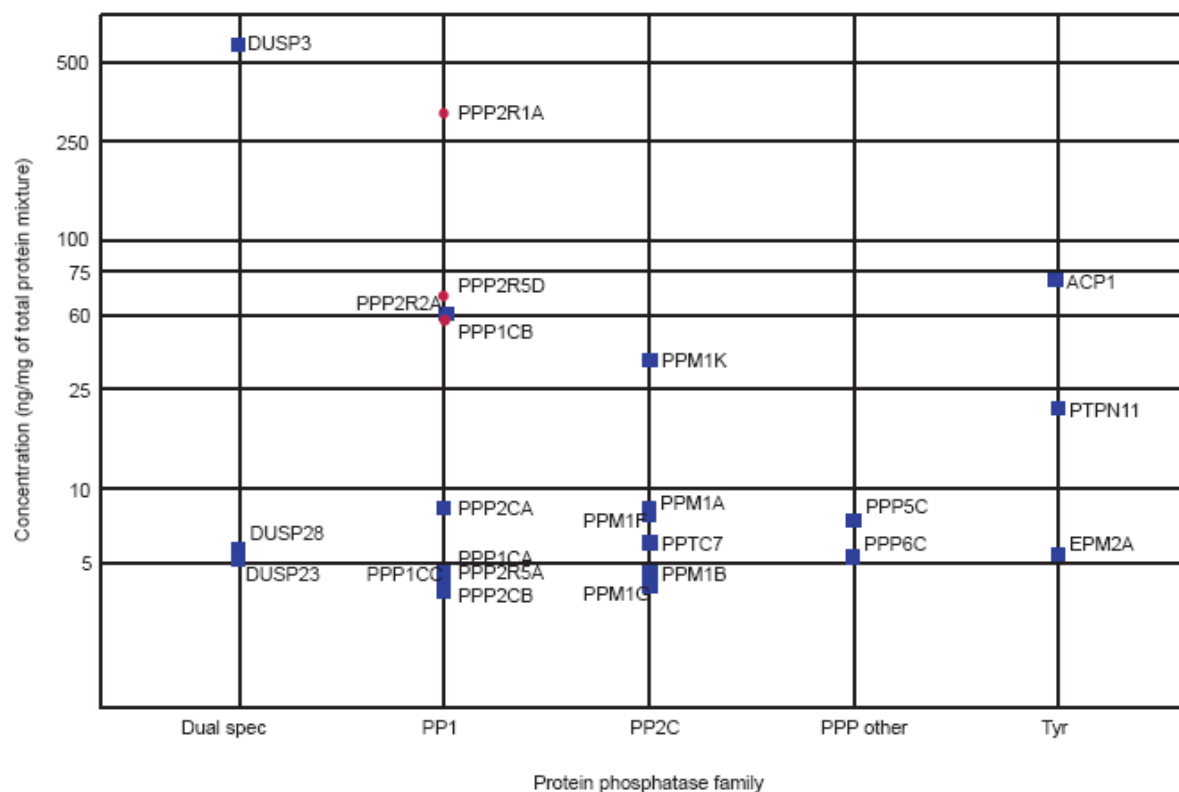
Supplemental figure 3. Known cardiovascular disease biomarkers identified in human left ventricle

The absolute concentration (ng/mg of total protein concentration) of top 200 proteins is depicted. A detailed list of currently identified biomarkers used for various diagnostics in CVD is mentioned. For acronyms, refer to supplemental table 2. Abbreviations are gene names from Uniprot/Swissprot (www.expasy.org).

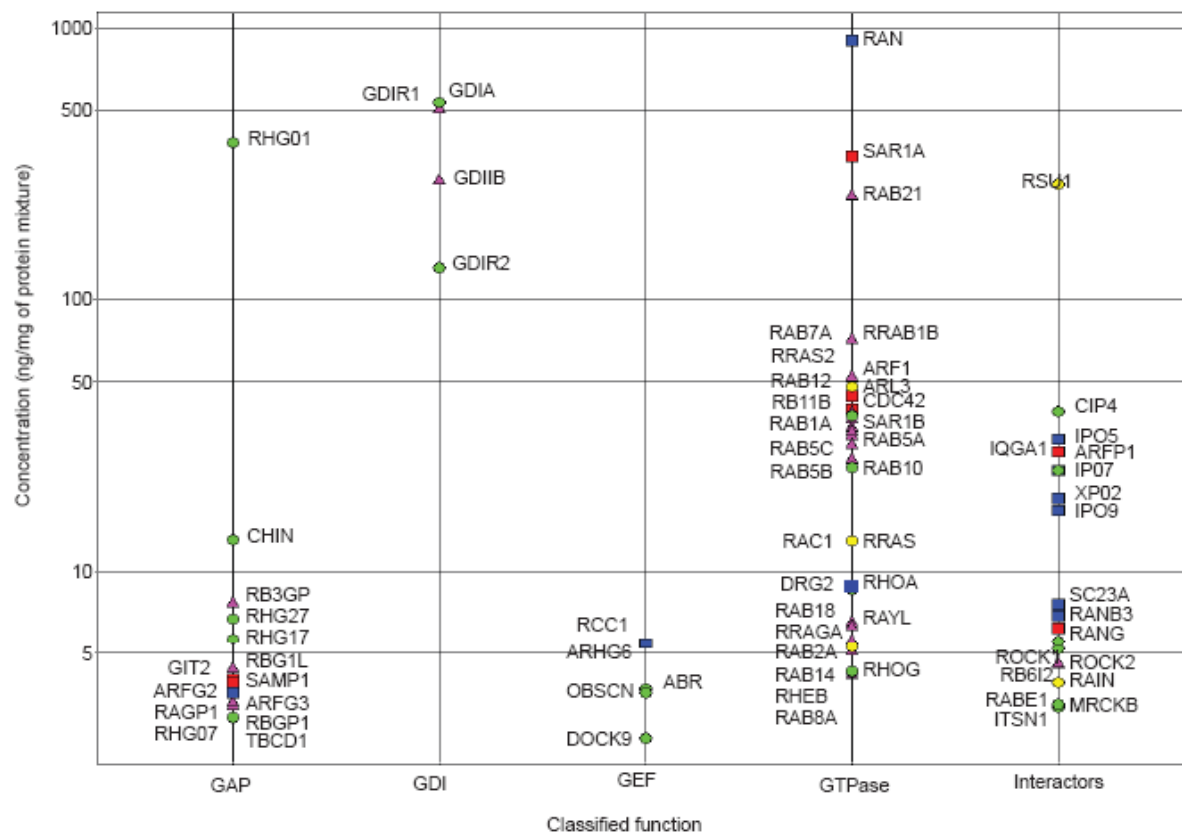


Supplemental Figure 4. Phosphatases observed in human left ventricle

Absolute concentrations of the 19 “high quality” phosphatases (blue squares) and 4 regulatory subunits (red circles) observed in the human left ventricle is sorted by phosphatase family. For acronyms and their meaning refer to supplemental table 6.



Supplemental Figure 5. Absolute concentrations of the 69 “high quality” GTPase signaling proteins observed in the human left ventricle is sorted by five main classes (Ras=yellow circle, Rho=green circle, ARF=red square, Ran=blue square, Rab=pink triangle). For acronyms and their meaning refer to supplemental table 8.



SUPPLEMENTAL TABLES

Supplemental Table 1. List of proteins identified from four different methods which are shown in Figure 1. The table includes protein accession number, Uniprot code number, gene name, molecular weight, protein name, number of unique peptides and number of spectral counts as well as their respective molecular function and biological processes.

Supplemental Table 2. List of proteins which have met ≥ 2 unique peptide per protein criteria. The table includes protein accession number, Uniprot code number, gene name, molecular weight, protein name, number of unique peptides and number of spectral counts as well as their respective molecular function and biological processes.

Supplemental Table 3. List of top 200 proteins ranked by their spectral count index F_{abb} .

Supplemental Table 4. List of 2,306 proteins with their respective protein concentrations (ng/mg of total protein) estimated based on APEX.

Supplemental Table 5. List of proteins present in both plasma and LV ranked by their abundance in each. Proteins in the Top200 of plasma and present in our LV proteome (A), as well as proteins in the Top200 of LV and also present in plasma (B) are highlighted. All other overlapping LV and plasma proteins are also listed (C).

Supplemental Table 6. List of signaling proteins observed in our data set. Protein kinases (Supplemental Table 5A) and protein phosphatases (Supplemental Table 5B) are listed with their respective kinase/phosphatase family, Uniprot code number, gene name, molecular weight, protein name and concentrations (ng/mg).

Supplemental Table 7. List of phosphorylated proteins observed in our data set. The table describes protein accession number, Uniprot code number, gene name, protein name, and their respective phosphorylation sites and substrates.

Supplemental Table 8. List of small GTPase proteins which are observed in our data set. The table includes GTPase protein accession number, Uniprot code number, gene name,

molecular weight, protein name, concentration (ng/mg) as well as their respective molecular function and biological processes.

Supplemental Table 9. List of uncharacterized proteins which are observed in our data set.

# Protein	# UniProt	Gene names	Protein Description	MW (kDa)	Unique peptides							# of total peptides	Spectral counts							# of total spectral	Molecular Function	Biological process	Pathway	Final Quality	
					I	II	III	IV	V	VI	VII		I	II	III	IV	V	VI	VII						
MYG_HUMAN	P02144	MB	Myoglobin OS=Homo sapiens GN=MB PE=1 SV=2	17166.4	23	19	24	11	12	16	22	127	503	282	453	90	240	305	481	2354	Other transfer/carrier	Transport:Bi	0	High Quality	
ENO1_HUMAN	P06733	ENO1 (ENO1)	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	47152.2	19	4	18	8	15	7	6	77	77	6	88	13	43	13	11	251	Lysase	Glycolysis	Glycolysis	0	High Quality
HBB_HUMAN	P64871	HBB	Hemoglobin subunit beta OS=Homo sapiens GN=HBB	15990	14	14	18	20	7	2	9	93	335	164	338	141	239	106	33	1356	Other transfer/carrier	Transport:Bi	0	High Quality	
HBA_HUMAN	P64905	HBA1; HBA2	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA	15239.6	9	9	13	12	15	5	6	69	161	115	323	192	188	48	95	1122	Other transfer/carrier	Transport:Bi	0	High Quality	
KRBM_HUMAN	P04732	KRBM (KRM)	Creatine kinase M-type OS=Homo sapiens GN=KRM	43083.6	31	18	48	20	23	17	21	178	521	267	684	445	656	84	193	2850	Other kinase	Muscle cont	0	High Quality	
MDHM_HUMAN	P40926	MDH2	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2	35513.7	22	12	28	12	9	11	10	104	229	57	483	99	131	24	30	3053	Dehydrogenase	Tricarboxyl	0	High Quality	
PARK7_HUMAN	Q94997	PARK7	Protein DL1-1 OS=Homo sapiens GN=PARK7 PE=1 SV=1	19873.1	13	9	15	8	7	4	6	60	104	38	65	22	55	13	18	315	Other RNA-binding protein	mRNA trans	0	High Quality	
MLV1_HUMAN	P10916	MYL2	Myosin regulatory light chain 2, ventricular/cardiac	18771.8	15	15	17	13	15	8	9	92	173	156	154	87	114	42	67	793	Other actin family cyto	Muscle cont	0	High Quality	
KAD1_HUMAN	P00568	AK1	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1	21617.1	20	18	20	4	7	9	8	86	164	72	148	34	30	26	24	498	Nucleotide kinase	Nucleoside, De novo	0	High Quality	
AATC_HUMAN	P17174	GOT1	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1	46230.1	21	14	31	16	22	8	10	122	210	38	164	74	105	16	21	628	Transaminase	Amino acid	Asparagin	0	High Quality
G3P_HUMAN	P04406	GAPDH (GAP)	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH	36035.3	24	11	23	14	23	11	14	120	263	58	504	212	307	100	59	1503	Molecular function un	Biological pr	0	High Quality	
LDHA_HUMAN	P00338	LDHA (PIC19)	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA	36671.2	17	2	16	8	6	9	6	64	71	2	42	17	29	14	14	419	Dehydrogenase	Glycolysis	0	High Quality	
HSP70_HUMAN	P11142	HSPA8 (HSC7)	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8	70881.8	23	13	27	14	7	4	7	96	132	59	105	28	70	14	94	412	Hsp 70 family chaperon	Protein foldi	Parkinson	0	High Quality
KCR5_HUMAN	P17540	CKMT2	Creatine kinase, sarcoplasmic mitochondrial OS=Homo sapiens GN=CKMT2	47487.6	20	8	36	10	13	11	10	108	370	66	686	117	196	70	114	1619	Other kinase	Muscle cont	0	High Quality	
ENOB_HUMAN	P13929	ENO3	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=1	46970.2	25	10	29	11	9	9	9	105	154	30	241	31	46	21	40	563	Lysase	Glycolysis	Glycolysis	0	High Quality
DECR_HUMAN	P16698	DECR1 (DECR)	2,4-dienyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1	36050.9	19	5	19	12	14	10	7	86	159	18	110	49	140	35	23	534	Dehydrogenase/Reduct	Fatty acid be	0	High Quality	
FABP_HUMAN	P05413	FABP3 (FABP)	Fatty acid-binding protein, heart OS=Homo sapiens GN=FABP3	14840.5	16	17	23	9	14	6	2	87	205	142	270	64	306	7	2	996	Other transfer/carrier	Lipid and fat	0	High Quality	
EEF1A2_HUMAN	O05639	EEF1A2 (EEF1)	Elongation factor 1, alpha 2 OS=Homo sapiens GN=EEF1A2	50452.6	18	3	22	10	14	9	4	80	145	10	290	52	88	36	28	649	Translation elongation	Translatio	0	High Quality	
MYPC3_HUMAN	P14896	MYBPC3	Myosin-binding protein C, cardiac-type OS=Homo sapiens GN=MYBPC3	140588.8	43	16	56	24	13	11	178	201	38	171	51	104	30	31	626	Molecular function un	Muscle cont	0	High Quality		
ALBU_HUMAN	P02768	ALB (GIG20)	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=1	69348.9	48	20	93	23	35	31	30	280	713	201	1129	197	299	160	170	2869	Other transfer/carrier	Transport ph	0	High Quality	
CYC_HUMAN	P99999	CYCS (CYC)	Cytochrome c OS=Homo sapiens GN=CYC PE=1 SV=1	11731.4	10	14	14	2	3	10	3	63	82	113	106	2	10	86	94	493	Mitochondrial carrier	Oxidative pr	Apoptosis	0	High Quality
THEM2_HUMAN	O09P13	ACOT13	Thioesterase superfamily member 2 OS=Homo sapiens GN=THEM2	14942.6	4	6	5	1	4	3	3	26	12	37	7	19	5	12	10	58	Esterase	Acy-CoA me	0	High Quality	
S10A6_HUMAN	P06703	S100A6 (CAC)	Protein S100-A6 OS=Homo sapiens GN=S100A6	10162.4	3	3	2	2	2	2	2	14	13	17	2	8	0	0	0	58	Growth factor/calmod	Signal trans	0	High Quality	
ACBP_HUMAN	P07108	DBI	Acy-CoA-binding protein OS=Homo sapiens GN=ACBP	10026.8	7	11	7	3	5	5	4	42	35	62	33	6	12	15	23	86	Other receptor/Other t	Lipid and fat	0	High Quality	
TPIS_HUMAN	P06174	TPPI (TPPI)	Triosephosphate isomerase OS=Homo sapiens GN=TPIS	26651.1	20	14	30	10	7	7	6	97	112	51	228	51	65	14	18	529	Isoomerase	Glycolysis/O	0	High Quality	
PIPA_HUMAN	P62937	PIPA (CYPA)	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PIPA	17994.9	10	7	6	6	5	7	47	73	18	28	68	132	16	26	361	Other isomerase	Protein foldi	0	High Quality		
PRDX3_HUMAN	P03048	PRDX3 (AOP1)	Thioredoxin-dependent peroxidoreductase, mitochondrial	27674.7	8	6	12	9	1	3	4	46	35	13	74	39	34	5	5	205	Peroxidase	Antioxidatio	0	High Quality	
MYH7_HUMAN	P12883	MYH7 (MYH)	Myosin 7 OS=Homo sapiens GN=MYH7 PE=1 SV=1	22308.5	212	127	190	20	36	80	78	743	2907	1034	1238	92	259	270	354	6154	Actin binding motor pr	Wnt signa	0	High Quality	
MDH1_HUMAN	P04925	MDH1 (MDH)	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1	36408.9	23	9	27	15	23	11	9	117	206	27	325	137	248	34	39	1016	Dehydrogenase	Tricarboxyl	TCA cycle	0	High Quality
ANXA6_HUMAN	P08133	ANXA6 (ANXA)	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=1	75859.5	41	5	42	8	14	10	12	132	161	10	150	18	50	25	432	Transfer/carrier protei	Biological pr	0	High Quality		
MYL3_HUMAN	P08050	MYL3	Myosin light chain 3 OS=Homo sapiens GN=MYL3	21914.5	15	10	19	8	8	6	8	74	137	69	157	55	86	44	52	600	Actin binding cytoskele	Muscle cont	0	High Quality	
PGAM2_HUMAN	P15259	PGAM2 (PGA)	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2	28748.9	9	9	26	5	6	4	5	75	98	39	212	21	18	13	31	432	Mutase	Glycolysis	Glycolysis	0	High Quality
ES1_HUMAN	P03042	C21orf33 (HE)	ES1 protein homolog, mitochondrial OS=Homo sapiens GN=ES1	28151.6	11	3	14	9	12	8	5	62	58	13	81	23	47	13	14	249	Molecular function un	Biological pr	0	High Quality	
LDHB_HUMAN	P07195	LDHB	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB	36620.6	23	8	30	13	14	12	11	113	341	59	299	132	163	73	105	1172	Dehydrogenase	Glycolysis	0	High Quality	
CRIP2_HUMAN	P52943	CRIP2 (CRP2)	Cysteine-rich protein 2 OS=Homo sapiens GN=CRIP2	22474.5	6	3	5	3	3	7	5	32	41	19	36	14	11	23	21	165	Actin binding cytoskele	Muscle deve	0	High Quality	
ACADM_HUMAN	P11310	ACADM	Medium-chain specific acyl-CoA dehydrogenase	46571.7	17	6	22	14	18	7	6	89	97	10	184	92	96	12	13	604	Dehydrogenase	Acy-CoA me	0	High Quality	
KCRB_HUMAN	P12277	CKB (CKB)	Creatine kinase B-type OS=Homo sapiens GN=KCRB	42627.1	17	6	20	12	12	7	6	78	158	42	228	68	76	21	16	609	Other kinase	Muscle cont	0	High Quality	
PEBP1_HUMAN	P30086	PEBP1 (PBP)	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1	21038.9	14	11	16	9	8	6	6	70	79	57	89	64	48	16	22	375	Transfer/carrier protei	Other signa	FGF signa	0	High Quality
GSTO1_HUMAN	P78417	GSTO1 (GST)	Glutathione transferase omega-1 OS=Homo sapiens GN=GSTO1	27549.2	12	1	6	5	3	6	3	38	24	1	7	20	11	5	6	74	Other transferase	Detoxificati	0	High Quality	
ALDOA_HUMAN	P04075	ALDOA (ALDA)	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA	39402.6	27	23	39	15	16	13	13	146	260	115	380	153	146	84	1169	Aldolase	Glycolysis	Fructose	0	High Quality	
TYB10_HUMAN	P63313	TMSB10 (PTM)	Thymosin beta-10 OS=Homo sapiens GN=TYB10	5008	1	1	1	1	1	1	1	6	1	1	1	2	3	8	16	16	Molecular function un	Biological pr	0	Matchup	
SCOT_HUMAN	P55809	OXC1T	Succinyl-CoA:3-oxoacid-coenzyme A transferase	56140.8	20	9	16	10	9	7	10	81	108	44	145	34	25	12	31	399	Other transferase	Carbohydrat	0	High Quality	
THIL_HUMAN	P24752	ACAT1 (ACA)	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=THIL	45181.8	21	14	39	19	19	10	9	131	251	89	390	107	101	37	33	1008	Acetyltransferase	Protein aceti	0	High Quality	
CSRFP3_HUMAN	P50461	CSRFP3 (CLP)	Cysteine and glycine-rich protein 3 OS=Homo sapiens GN=CSRFP3	20950.5	10	4	13	7	8	10	10	62	71	18	95	46	55	39	62	386	Actin binding cytoskele	Muscle deve	0	High Quality	
SOD2_HUMAN	P00441	SOD1	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD2	15917.3	6	5	12	5	7	4	7	46	42	22	87	19	31	9	19	229	Other oxidoreductase	Immunity an	0	High Quality	
FABP5_HUMAN	O01469	FABP5	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5	15146.4	8	7	16	5	6	5	8	55	30	26	107	9	26	7	14	219	Other transfer/carrier	Lipid and fat	0	High Quality	
CRYAB_HUMAN	P02511	CRYAB (CRYA)	Alpha-crystallin B chain OS=Homo sapiens GN=CRYAB	20141.4	21	21	17	7	6	4	5	81	90	94	55	16	15	19	33	322	Structural protein	Muscle cont	Angiogen	0	High Quality
TPM1_HUMAN	P09493	TPM1 (C15orf)	Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1	31632.9	29	42	23	5	7	16	20	142	103	181	123	9	50	56	90	612	Actin binding motor pr	Muscle cont	0	High Quality	
PGM1_HUMAN	P63871	PGM1	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1	63293	29	5	23	12	11	12	9	101	96	7	88	29	64	29	41	354	Mutase	Monosaccha	0	High Quality	
PRDX6_HUMAN	P30041	PRDX6 (AOP2)	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=1	25018.1	11	4	14	3	6	6	4	48	23	7	70	5	19	11							

Gene	Accession	Protein	Function	EC	GO	KEGG	UniProt	RefSeq	Ensembl	NCBI	EMBL	GenBank	TrEMBL	SwissProt	InterPro	Protein	Category	Quality						
HSPB1_HUMAN	P04792	HSPB1 (HSP27)	Heat shock protein beta-1 OS=Homo sapiens GN=	22764.6	18	9	12	5	4	1	2	51	115	62	98	5	9	2	3	294	Other chaperones	Protein fold	p38 MAPK	High Quality
KPF6_HUMAN	P08237	KPF6 (PFKFB)	6-phosphofruktokinase, muscle type OS=Homo sa	85165.5	34	5	46	12	13	9	7	126	296	13	196	29	29	34	4	637	Carbohydrate kinase	Glycolysis	Glycolysis	High Quality
PYGB_HUMAN	P11216	PYGB	Phosphoglycolate phosphatase, brain form OS=Homo sa	96680.3	32	2	37	15	10	15	10	126	194	7	99	50	60	24	49	437	Phosphorylase	Glycolysis	Heterotrimer	High Quality
HINT2_HUMAN	O98638	HINT2	Histidine triad nucleotide-binding protein 2 OS=	17143.7	3	5	4	1	1	1	1	15	14	8	8	0	4	1	2	37	Nucleotide phosphatase	Biological proc		High Quality
1433Z_HUMAN	P63104	YWHAZ	14-3-3 protein zeta/delta OS=Homo sapiens GN=	27272.9	12	3	12	2	4	8	10	51	55	15	26	4	8	12	14	134	Other chaperones	Signal transd	EGF rece	High Quality
ARHL1_HUMAN	O8NDY3	ADPRHL1 (AR)	Protein ADP-ribosylarginine hydrolase-like prot	40087.8	8	3	9	1	3	4	5	33	19	6	34	3	9	14	12	97	Hydrolase	Biological proc		High Quality
HINT1_HUMAN	P49773	HINT1 (HINT)	Histidine triad nucleotide-binding protein 1 OS=	13784.1	4	2	9	2	3	2	1	23	11	3	38	3	3	5	2	65	Nucleotide phosphatase	Biological proc		High Quality
EFTU_HUMAN	P49411	TUFM	Elongation factor Tu, mitochondrial OS=Homo sapi	49524.3	22	9	26	10	16	4	5	92	104	20	142	22	55	8	33	384	Translation elongation	Protein bios		High Quality
HSPB7_HUMAN	O9UB9Y	HSPB7 (CVH5)	Heat shock protein beta-7 OS=Homo sapiens GN=	18592.7	7	7	9	1	1	1	1	26	25	28	44	0	5	2	4	108	Other chaperones	Protein fold		High Quality
ESTD_HUMAN	P10768	ESD	S-formylglutathione hydrolase OS=Homo sapiens	31445.6	7	6	10	3	2	4	3	29	12	21	4	2	5	4	4	48	Esterase	Biological proc		High Quality
EHD2_HUMAN	Q9UNZ4	EHD2 (PAST2)	EH domain-containing protein 2 OS=Homo sapien	61145.2	20	6	16	3	6	1	3	55	61	8	59	9	14	5	160	Other G-protein modu	Endercytosol		High Quality	
DEST_HUMAN	P60981	DSTN (ACTDP)	Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	18488.2	5	2	13	3	5	3	5	33	12	3	34	0	22	10	5	86	Non-motor actin bindi	Cell structur	Cytoskele	High Quality
TBA1B_HUMAN	P68363	TUBA1B	Tubulin alpha-1B chain OS=Homo sapiens GN=TU	50133.7	17	5	2	12	13	8	8	65	131	9	9	36	33	17	21	25	Molecular function un	Biological proc		High Quality
ADHX_HUMAN	P11766	ADH5 (ADHX)	Alcohol dehydrogenase class-3 OS=Homo sapien	39705.8	7	3	14	2	2	6	5	41	19	3	26	14	7	9	9	87	Dehydrogenase/Reduct	Other carbo		High Quality
1433T_HUMAN	P27348	YWHAQ	14-3-3 protein theta OS=Homo sapiens GN=YWH	27747.4	8	2	4	2	3	2	2	24	12	5	5	3	6	4	6	41	Other chaperones	Signal transd	EGF rece	High Quality
MTCRA_HUMAN	P56277	MTCP1 (C6.18)	Protein b6 MTCP1 OS=Homo sapiens GN=MTCP1	7728.7	1	2	1	1	1	1	1	5	1	1	3	1	0	0	1	6	Other miscellaneous fu	Other signal		High Quality
TBB2C_HUMAN	P68371	TUBB2C	Tubulin beta-2C chain OS=Homo sapiens GN=TU	49812.7	25	10	32	17	2	6	7	99	192	47	216	62	19	8	11	555	Tubulin	Intracellular	Huntingtin	High Quality
CRYM_HUMAN	Q14894	CRYM (THBP)	Mu-crystallin homolog OS=Homo sapiens GN=CR	33757.1	10	6	9	5	8	5	5	48	46	11	47	18	34	12	14	182	Other lyase	Vision		High Quality
ADH1B_HUMAN	P00325	ADH1B (ADH4)	Alcohol dehydrogenase 1B OS=Homo sapiens GN=	39836.3	8	10	6	2	6	5	5	37	19	26	16	14	6	8	9	89	Dehydrogenase/Reduct	Other carbo		High Quality
S10AB_HUMAN	P31949	S100A11 (ML)	Protein S100-A11 OS=Homo sapiens GN=S100A11	11723.1	5	2	5	1	2	1	1	16	12	7	9	1	4	0	1	34	Signaling molecule/Calc	DNA replicat		High Quality
ODO1_HUMAN	O02218	OGDH	2-oxoglutarate dehydrogenase E1 component, m	115918.7	38	5	44	6	7	6	9	115	145	7	101	25	12	12	327	Dehydrogenase	Tricarboxylic	TCA cycle	High Quality	
AL9A1_HUMAN	P49189	ALDH9A1 (AL)	4-trimethylaminobutyraldehyde dehydrogenase	53784	11	6	14	3	5	6	2	47	38	10	73	6	10	7	3	147	Dehydrogenase	Other metabol		High Quality
DHE3_HUMAN	P00367	GLUD1 (GLU)	Glutamate dehydrogenase 1, mitochondrial OS=	61381.7	19	7	17	3	8	2	2	56	43	13	48	6	32	0	3	145	Dehydrogenase	Amino acid	Glutamin	High Quality
TRFE_HUMAN	O02787	TF (PRO1400)	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV	77032.2	26	3	33	6	5	19	21	113	91	3	185	22	33	36	38	398	Transfer/carrier protein	Transport/mT		High Quality
GELS_HUMAN	P06376	GSN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	85679.8	20	8	18	8	11	4	8	77	85	21	99	17	27	6	13	268	Non-motor actin bindi	Cell structur	FAS signa	High Quality
GRHRP_HUMAN	O9UB07	GRHRP (GLXR)	Glyoxylate reductase/hydroxypruvate reductase	35651.1	8	1	11	3	4	3	2	32	21	1	27	6	8	5	3	71	Reductase	Amino acid		High Quality
HSDL2_HUMAN	O6VY16	HSDL2	Hydroxysteroid dehydrogenase-like protein 2 OS=	45378.6	27	10	17	2	5	4	2	70	117	33	151	7	13	6	7	334	Dehydrogenase/Reduct	Other metabol		High Quality
ANXA5_HUMAN	P08758	ANXA5 (ANXA)	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 S	35920.6	19	2	16	2	4	5	3	51	64	3	57	11	21	6	9	171	Transfer/carrier protein	Lipid, fatty a		High Quality
RAN_HUMAN	P62826	RAN (ARA24)	GTP-binding nuclear protein Ran OS=Homo sapi	24405.4	4	6	3	6	3	2	2	25	4	3	7	8	7	2	2	33	Small GTPase	RNA localiza		High Quality
KAD4_HUMAN	P27144	AK31 (AK3)	Adenylate kinase isoenzyme 4, mitochondrial OS	25250.5	6	2	6	1	2	2	2	21	13	4	12	5	11	6	4	55	Nucleotide kinase	Purine meta	De novo	High Quality
PDIA3_HUMAN	P31001	PDIA3 (ERP57)	Protein disulfide-isomerase A3 OS=Homo sapien	56766.2	20	12	23	2	2	4	2	65	48	23	44	4	5	5	2	131	Other isomerase	Purine meta		High Quality
IDH3B_HUMAN	O43837	IDH3B	Isocitrate dehydrogenase [NAD] subunit beta, m	42165.3	13	14	5	4	2	2	2	40	37	85	7	13	2	2	3	147	Dehydrogenase	Tricarboxylic		High Quality
TGM2_HUMAN	P21980	IGM2	Protein-glutamine gamma-glutamyltransferase 2	77311.1	27	7	16	9	4	8	8	80	157	33	73	22	33	7	29	354	Acyltransferase/Other	Protein fold		High Quality
KAD2_HUMAN	P54819	AK2 (ADK2)	Adenylate kinase isoenzyme 2, mitochondrial OS	24641.8	5	7	1	2	1	1	1	24	19	9	21	1	4	1	0	55	Nucleotide kinase	Purine meta	De novo	High Quality
CALR_HUMAN	P27797	CALR (CRIC)	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV	48124.9	8	6	14	2	5	8	6	49	25	8	39	6	17	11	11	117	Other select calcium bi	Protein fold		High Quality
PIPF_HUMAN	P30405	PCPI (CYP3)	Peptidyl-prolyl cis-trans isomerase, mitochondr	22022.4	5	6	4	5	4	3	3	27	13	21	23	25	5	4	8	81	Other isomerase	Protein fold		High Quality
PIMT_HUMAN	P22061	PIMT	Protein-L-isospartate-(D-aspartate)-O-methyltr	24632.9	9	6	9	2	2	4	2	34	25	13	38	9	6	8	8	108	Methyltransferase	Protein fold		High Quality
ECHB_HUMAN	P55084	HADHB (MST)	Trifunctional enzyme subunit beta, mitochondr	51278	29	10	17	6	6	6	4	78	97	14	84	12	23	8	9	247	Acetyltransferase	Protein fold		High Quality
PDLI5_HUMAN	O69HC4	PDLI5 (ENH)	PDZ and LIM domain protein 5 OS=Homo sapien	63953	12	9	16	3	4	1	6	51	51	20	98	6	12	1	8	196	Actin binding cytoskele	Muscle deve		High Quality
QCRC1_HUMAN	P31930	UQCRC1	Cytochrome b-c1 complex subunit 1, mitochon	52627.9	14	3	17	5	6	2	2	49	33	3	61	17	17	2	2	135	Reductase/Metallopro	Proteolysis/E		High Quality
GDPL1_HUMAN	O8N335	GDPL1 (KIAA)	Glycerol-3-phosphate dehydrogenase 1-like prot	38401.3	13	18	5	6	8	5	5	55	30	17	23	25	9	2	6	164	Dehydrogenase	Phospholipid		High Quality
ATOX1_HUMAN	O00244	ATOX1 (HAH)	Copper transport protein ATOX1 OS=Homo sapie	7383.7	2	5	1	2	1	1	1	11	2	2	24	0	2	2	4	34	Molecular function un	Biological proc		High Quality
HEBP2_HUMAN	O9Y524	HEBP2 (Co6r)	Heme-binding protein 2 OS=Homo sapiens GN=H	22857.7	8	6	8	1	2	1	2	27	11	9	16	2	1	4	3	46	Other miscellaneous fu	Protein bios		High Quality
CASQ2_HUMAN	O14958	CASQ2	Calsequestrin-2 OS=Homo sapiens GN=CASQ2 PE	46419.8	12	6	12	3	5	9	7	54	60	10	33	9	22	17	16	167	Select calcium binding	Calcium meta		High Quality
FKBP3_HUMAN	O00688	FKBP3 (FKBP)	FK506-binding protein 3 OS=Homo sapiens GN=F	25159.4	9	10	4	1	3	2	2	29	14	16	7	0	1	7	2	47	Other chaperones/Other	Protein fold		High Quality
GRP75_HUMAN	P38646	HSPA9 (GRP7)	Stress-70 protein, mitochondrial OS=Homo sapi	73663.3	32	20	31	5	10	9	9	116	128	109	232	11	29	20	20	549	Hsp 70 family chaperon	Protein fold	Parkinson	High Quality
LGUL_HUMAN	O04760	GLO1	Lactoylglutathione lyase OS=Homo sapiens GN=C	20760.8	7	5	8	2	3	2	2	27	20	7	21	2	0	4	6	60	Other lyase	Other carbo		High Quality
ALAT1_HUMAN	P24298	GPT (AAT1)	L-Alanine aminotransferase 1 OS=Homo sapiens G	54619.1	10	2	11	3	1	1	1	29	26	3	25	9	3	1	2	69	Glyoxylate transferase	Other polys		High Quality
CALM_HUMAN	P62158	CALM1 (CALM)	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 S	16820	5	1	3	1	2	2	2	14	12	1	9	1	12	0	6	41	Calmodulin related pro	Calcium meta	T cell acti	High Quality
SMXP_HUMAN	O9UHP9	SMXP (SRMX)	Small muscular protein OS=Homo sapiens GN=SN	9295.7	4	3	3	1	2	1	1	15	7	6	19	3	1	3	2	41	Molecular function un	Biological proc		High Quality
EZR_HUMAN	P15311	EZR (VLZ)	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	69396.6	17	14	22	1	2	6	8	70	48	51	46	2	2	10	11	170	Molecular function un	Biological proc		High Quality
K1C9_HUMAN	P35527	KRT9	Keratin, type I cytoskeletal 9 OS=Homo sapien	62113	31	21	18	22	20	1	1	114	853	261	55	176	193	1	1	1540	Intermediate filament	Cell structur		High Quality
THIO_HUMAN	P10599	TXN (TRDX)	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=	11719.3	3	2	1	1	1	3	1	13	6	3	2	3	8	5	2	29	Other oxidoreductase	Electron trans	Hypoxia r	High Quality
PHPT4_HUMAN	O9NRX4	PHPT1 (PHPT)	14 kDa phosphohistidine phosphatase OS=Homo	13814.6	4	6	10	1</																

ABHD4_HUMAN	Q9NUJ1	ABHD10	Abhydrolase domain-containing protein 10, mito	33915.3	8	4	5	5	1	1	24	15	4	20	16	1	1	57	Molecular function	Biological pr	0	High Quality		
TPM2_HUMAN	P07951	TPM2 (TMSB)	Tropomyosin beta chain OS=Homo sapiens GN=1	32833.7	10	16	7	2	2	4	7	48	18	34	10	2	4	5	9	82	Actin binding mot	Muscle cont	0	High Quality
PSME1_HUMAN	Q06323	PSME1 (IFI5)	Proteasome activator complex subunit 1 OS=Hori	28705.8	12	1	5	1	1	2	2	24	25	2	15	9	13	2	2	80	Other miscellaneous fu	Proteolysis	0	High Quality
TX1B3_HUMAN	Q14907	TAX1BP3 (TIP)	Tax1-binding protein 3 OS=Homo sapiens GN-TA	13716.6	2	1	1	1	1	1	7	3	1	1	4	2	1	0	12	Molecular function	Biological pr	0	High Quality	
PGS2_HUMAN	P07585	DCN (SLR1B)	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1	39730.2	7	3	3	2	3	5	4	24	18	5	3	5	5	1	41	Receptor:Extracellular	Cell adhesio	0	High Quality	
MCCB_HUMAN	Q9HCC0	MCCC2 (MCC)	Methylcrotonyl-CoA carboxylase beta chain, mi	61316.7	14	3	15	3	6	6	50	43	5	28	10	21	8	11	126	Other ligase	Amino acid m	0	High Quality	
SRCH_HUMAN	P23327	HRC (HCF)	Sarcoplasmic reticulum histidine-rich calcium-bi	80220.4	17	7	3	5	1	3	4	44	86	32	18	12	4	3	15	Other select calcium bi	Calcium ion	0	High Quality	
AK1A1_HUMAN	P14550	AKR1A1 (ALD)	Alcohol dehydrogenase [NADP+]-OS=Homo sapie	36555.6	8	1	9	2	3	2	2	27	12	11	6	7	4	4	45	Reductase	Other metal	0	High Quality	
DBL0H_HUMAN	Q9NR28	DIABLO (SMA)	Diablo homolog, mitochondrial OS=Homo sapie	27112.7	7	6	1	3	2	1	20	17	11	4	4	11	3	1	47	Molecular function	Biological pr	0	High Quality	
GYS1_HUMAN	P13807	GYS1 (GYS)	Glycogen [starch] synthase, muscle OS=Homo sap	83769.1	21	1	11	4	5	3	48	73	3	18	8	13	5	9	129	Synthase:Glycosyltra	Glycogen me	Heterotri	High Quality	
ACOT1_HUMAN	Q626X2	ACOT1 (CTE)	Acyl-coenzyme A thioesterase 1 OS=Homo sapie	46260.2	1	5	1	4	4	2	5	22	10	24	1	9	10	4	8	66	Molecular function	Biological pr	0	High Quality
CAH2_HUMAN	P00918	CA2	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2	29228.6	8	1	9	1	1	2	2	24	9	1	14	1	1	2	3	31	Dehydratase	Other carbo	0	High Quality
TPP3_HUMAN	Q9B9W30	TPP3 (CGI-3)	Tubulin polymerization-promoting protein family	18967.9	6	6	2	1	1	1	2	18	10	11	3	0	2	2	4	32	Serine protease	Proteolysis	0	High Quality
PTMA_HUMAN	P06454	PTMA (TMSA)	Prothymosin alpha OS=Homo sapiens GN=PTMA	12184.2	2	1	1	1	2	2	9	3	1	2	1	10	9	2	26	Miscellaneous functio	Nucleoside,	0	High Quality	
IC1_HUMAN	P05155	SERPINC1 (C)	Plasma protease C1 inhibitor OS=Homo sapiens C	55137.5	9	2	2	5	1	1	19	29	6	2	7	1	0	9	45	Serine protease inhibi	Proteolysis	0	High Quality	
NAMPT_HUMAN	P43490	NAMPT (PBC1)	Nicotinamide phosphoribosyltransferase OS=Hor	55504.3	13	2	9	5	4	4	41	35	2	26	7	10	5	6	91	Other cytokine	Ligand-medi	0	High Quality	
EHD4_HUMAN	Q9H223	EHD4 (HCA10)	EH domain-containing protein 4 OS=Homo sapie	61159.6	22	4	12	4	6	4	55	38	5	25	7	9	5	4	93	Other G-protein modu	Endocytosis	0	High Quality	
MYH9_HUMAN	P35759	MYH9	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	226519.5	73	27	40	5	6	11	14	176	283	60	78	9	18	14	21	483	Actin binding motor pr	Muscle devel	Inflamma	High Quality
ODPX_HUMAN	Q00330	PDXH (PDX1)	Pyruvate dehydrogenase protein X component, n	54105.8	6	6	9	2	2	4	3	32	31	18	42	3	10	6	5	115	Molecular function	Carbonylhydr	0	High Quality
PYGM_HUMAN	P11217	PYGM	Glycogen phosphorylase, muscle form OS=Homo	97076.8	42	1	22	3	6	5	7	86	176	8	50	5	18	10	8	275	Phosphorylase	Glycogen me	Heterotri	High Quality
MACD1_HUMAN	Q9BQ69	MACROD1 (L)	MACRO domain-containing protein 1 OS=Homo s	35488.4	4	2	4	1	2	1	3	17	11	4	16	2	4	3	4	44	Other select calcium bi	Cell cycle co	0	High Quality
IPYR2_HUMAN	Q9H2U2	PPA2 (HSPC1)	Inorganic pyrophosphatase 2, mitochondrial OS=	37903.4	10	3	2	3	5	1	24	19	7	5	7	5	1	4	34	Pyrophosphatase	Polyphospho	0	High Quality	
CO3_HUMAN	P01024	C3 (CPAMD1)	Complement C3 OS=Homo sapiens GN=C3 PE=1-3	187131.1	55	5	32	9	13	5	10	129	146	7	71	28	50	8	20	330	Complement compone	Complement	0	High Quality
PF4A_HUMAN	Q9N9P4	PF4D (PF4A)	Prefoldin subunit 4 OS=Homo sapiens GN=PF4D	15296.6	4	3	1	1	1	1	11	6	5	5	5	2	1	1	20	Molecular function	Biological pr	0	High Quality	
K6PP_HUMAN	Q01813	PKPF (PKF)	6-phosphofructokinase type C OS=Homo sapiens	85579.4	26	3	27	2	2	3	6	67	116	5	55	4	5	7	199	Carbohydrate kinase	Glycolysis	Glycolysis	High Quality	
IF4A2_HUMAN	Q14240	IF4A2 (DDX2)	Eukaryotic initiation factor 4A-II OS=Homo sapie	46385.6	15	3	3	1	4	3	34	37	3	6	1	4	3	7	61	RNA helicase:Translati	Protein bios	0	High Quality	
IPYR_HUMAN	Q15181	PPA1 (IOPPP)	Inorganic pyrophosphatase OS=Homo sapiens G	32642.6	9	1	3	2	1	5	3	24	11	1	4	4	3	7	4	34	Pyrophosphatase	Polyphospho	0	High Quality
MYOM2_HUMAN	P54296	MYOM2	Myomesin-2 OS=Homo sapiens GN=MYOM2 PE=2	164776.4	35	11	36	9	13	7	117	102	21	104	29	35	8	7	306	Actin binding cytoskele	Proteoglycan	0	High Quality	
TCB2_HUMAN	P78371	CCT2 (990B.1)	T-complex protein 1 subunit beta OS=Homo sapie	57471.9	16	2	16	2	1	2	3	42	29	2	27	7	2	4	4	75	Chaperonin	Protein foldi	0	High Quality
BCAT2_HUMAN	Q15382	BCAT2 (BCAT)	Branched-chain-amino-acid aminotransferase, m	44270.2	8	6	2	3	2	2	4	25	16	9	5	7	3	5	45	Transporter:Membran	Intracellular	0	High Quality	
SBP1_HUMAN	Q13228	SELENBP1 (S)	Selenium-binding protein 1 OS=Homo sapiens G	52374	17	2	20	2	3	1	45	41	2	39	3	0	4	1	90	Other defense and inm	Immunity ar	0	High Quality	
PGM5_HUMAN	Q15124	PGM5 (PGMR)	Phosphoglucomutase-like protein 5 OS=Homo sa	62209.1	20	2	3	5	2	2	32	37	3	13	29	2	2	9	84	Mutase	Monosacha	0	High Quality	
PTRF_HUMAN	Q6NZ12	PTRF (FKS13)	Polymerase 1 and transcription release factor OS=H	43458.5	11	5	6	1	2	1	5	31	36	21	20	1	3	5	9	95	Other transcription fac	mRNA trans	General t	High Quality
LIS1_HUMAN	P43034	PAFAH1B1 (L)	Platelet-activating factor acetylhydrolase IB subu	46619.4	10	8	2	3	3	5	31	14	20	2	2	3	4	5	48	Esterase	Neurogenes	0	High Quality	
TEBP_HUMAN	Q15185	PTGES3 (P23)	Prostaglandin E synthase 3 OS=Homo sapiens G	18679.9	2	3	1	1	1	3	10	2	6	2	2	2	0	4	16	Molecular function	Biological pr	0	High Quality	
QCR2_HUMAN	P22695	UOCCR2	Cytochrome b-c1 complex subunit 2, mitochondr	48425.4	14	1	10	3	4	3	4	39	52	1	18	11	13	5	6	106	Reductase:Metallopro	Proteolysis:E	0	High Quality
CALU_HUMAN	Q43852	CALU	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=	37089.6	4	3	2	1	2	3	4	19	4	8	2	4	20	3	4	5	Select calcium binding	Calcium memo	0	High Quality
VIME_HUMAN	P08670	VIM	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	53634.6	10	13	10	1	1	3	3	41	24	38	27	1	2	6	6	104	Intermediate filament	Extracellu	0	High Quality
ACDSB_HUMAN	P54954	ACADSB	Short/branched chain specific acyl-CoA dehydro	47469.1	10	14	2	1	2	3	32	16	36	2	1	3	6	3	61	Dehydrogenase	Acyl-CoA me	0	High Quality	
CN159_HUMAN	Q7Z3D6	C14orf159 (U)	UFP0317 protein C14orf159, mitochondrial OS=H	66418.8	13	4	18	1	4	5	49	29	6	59	1	4	8	7	114	Molecular function	Biological pr	0	High Quality	
RD23A_HUMAN	P54725	RAD23A	UV excision repair protein RAD23 homolog A OS=	39591.1	3	2	1	4	2	1	13	5	4	2	10	11	0	2	34	Damaged DNA-binding	DNA repair	0	High Quality	
SKP1_HUMAN	P63208	SKP1 (EMC1)	S-phase kinase-associated protein 1 OS=Homo sa	18640.3	1	1	2	1	1	2	8	3	1	13	0	2	1	2	22	Ubiquitin-protein ligan	Proteolysis:C	0	High Quality	
APOH_HUMAN	P02749	APOH (B2G1)	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APC	38280.5	1	1	7	3	3	3	21	3	2	13	7	8	4	4	21	Apolipoprotein	Blood clottri	0	High Quality	
KAP2_HUMAN	P13861	PKR2A (PK)	CAMP-dependent protein kinase type II-alpha res	45500.8	14	6	10	1	1	1	33	25	7	20	3	3	0	2	60	Kinase modulator	Protein phos	GABA-B	High Quality	
SVIM_HUMAN	Q9NSE4	IARS2	Isoleucyl-tRNA synthetase, mitochondrial OS=Hor	113776.1	23	1	9	2	1	3	2	41	56	1	16	9	6	4	3	95	Aminoacyl-tRNA synth	Amino acid	0	High Quality
DHSA_HUMAN	P13140	SDHA (SDH)	Succinate dehydrogenase [ubiquinone] flavoprot	72673.7	12	1	19	4	3	2	2	43	19	1	53	8	7	6	101	Dehydrogenase	Carbohydrat	0	High Quality	
FIBG_HUMAN	P02679	FGG (PRO206)	Fibrinogen gamma chain OS=Homo sapiens GN=F	51495.3	9	9	9	2	4	2	27	21	42	8	11	2	1	2	85	Other signaling molecu	Blood clottri	Blood coa	High Quality	
AMP_L_HUMAN	P28838	LAP3 (LAPFP)	Cytosolic aminopeptidase OS=Homo sapiens GN=L	56149.7	16	7	14	2	3	2	44	34	11	32	12	11	2	0	102	G-protein coupled rec	G-protein m	Inflamma	High Quality	
ODBA_HUMAN	P12694	BCKDHA	2-oxoisovalerate dehydrogenase subunit alpha,	50454	10	2	6	1	1	1	20	20	3	10	2	0	1	0	36	Dehydrogenase	Amino acid	0	High Quality	
TIM10_HUMAN	P62072	TIMM10 (TIM)	Mitochondrial import inner membrane transloc	10314.9	1	1	1	1	1	1	4	1	1	1	1	0	0	1	4	Mitochondrial carrier	Mitochondr	0	Matchup	
RS17_HUMAN	P08708	RPS17	40S ribosomal protein S17 OS=Homo sapiens GN	15532.2	2	2	1	1	1	1	9	2	2	2	9	7	1	2	23	Ribosomal protein	Protein bios	0	High Quality	
ACOT9_HUMAN	Q9Y305	ACOT9 (CGI-)	Acyl-coenzyme A thioesterase 9 OS=Homo sapie	46337.2	13	1	12	1	3	1	31	39	1	22	2	10	1	1	75	Esterase	Fatty acid m	0	High Quality	
RHG01_HUMAN	Q07960	ARHGAP1 (C)	Rho GTPase-activating protein 1 OS=Homo sapie	50419.9	12	3	1	3	2	1	22	21	5	2	4	2	1	3	35	Other G-protein modu	Cell motility	PDGF sign	High Quality	
TCPE_HUMAN	P48643	CCT5 (CCTE)	T-complex protein 1 subunit epsilon OS=Homo s	59654.3	15	5	9	1	3	1	35	21	6	25	1	4	1	1	49	Chaperonin	Protein foldi	0	High Quality	
TCGP_HUMAN	P49368	CCT3 (CCTG)	T-complex protein 1 subunit gamma OS=Homo s	60517.4	14	2	10	1	1	1	30	19	2	16	3	1	1	1	53	Chaperonin	Protein foldi	0	High Quality	
GLNA_HUMAN	P15104	GLUL (GLNS)	Glutamine synthetase OS=Homo sapiens GN=GLL	42046.9	1	1	1	1	1	1	5													

PABP4_HUMAN	Q13310	PABPC4 (APP)	Polyadenylate-binding protein 4 OS=Homo sapiens	70765.8	5	4	1	1	1	11	6	4	0	2	1	0	13	Other RNA-binding protein	mRNA poly	0	High Quality		
LDHD_HUMAN	Q96W12	LDHD	Probable D-lactate dehydrogenase, mitochondrial	54851	6	3	15	1	1	27	12	6	61	1	1	0	82	Dehydrogenase	Other carbon	0	High Quality		
SDPR_HUMAN	O85810	SDPR	Serum deprivation-response protein OS=Homo sapiens	47154.9	3	3	5	1	1	1	3	17	4	5	1	3	3	Other transcription factor	mRNA trans	General	High Quality		
PARVA_HUMAN	Q9NV07	PARGA (MXRA)	Alpha-parvin OS=Homo sapiens GN=PARVA PE=1	42226.7	8	1	2	1	2	15	11	2	2	0	2	3	1	21	Actin and actin related	Cell motility	Integrin s	High Quality	
NIBA_HUMAN	Q9Z870	FAM129A	Protein Niba OS=Homo sapiens GN=FAM129A P=1	103116.4	10	1	14	3	4	3	39	22	1	30	8	17	7	93	Molecular function unc	Oncogenesis	0	High Quality	
COO5_HUMAN	Q5YK3	COO5	Ubiquitinome biosynthesis methyltransferase COO	37123.1	11	4	2	1	1	19	23	5	3	1	1	0	33	Methyltransferase	Other carbon	0	High Quality		
HNRNP4_HUMAN	Q14103	HNRNP4 (AU)	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens	38416.5	4	1	6	2	2	1	16	9	1	9	6	10	1	36	Molecular function unc	Biological pr	0	High Quality	
FERM2_HUMAN	Q96AC1	FERM2 (KIN)	Fermitin family homolog 2 OS=Homo sapiens GN=FERM2	77845.9	18	1	7	2	3	2	34	44	1	17	5	7	1	2	77	Other lyase	Porphyrim	Heme bio	High Quality
RSU1_HUMAN	Q15404	RSU1 (RSP1)	Ras suppressor protein 1 OS=Homo sapiens GN=RSU1	31524.2	8	6	1	1	1	18	18	8	2	2	2	2	3	33	Growth factor:Kinase n	Intracellular	0	High Quality	
COO3_HUMAN	Q9NZ46	COO3 (CUG2)	Hexaprenyldihydroxybenzoate methyltransferase	40980.1	5	2	1	2	2	1	13	8	5	1	2	2	1	19	Methyltransferase	Coenzyme m	0	High Quality	
AZMG_HUMAN	P01023	A2M (CPAMA)	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M	163258.8	11	21	7	9	1	2	51	32	65	13	25	2	1	138	Other cytokine:Serine	Proteolysis i	Blood coa	High Quality	
AASS_HUMAN	Q9UDR5	AASS	Alpha-aminoacidic semialdehyde synthase, mito	102117.4	21	1	12	2	1	37	37	1	17	0	3	1	0	59	Dehydrogenase:Reduc	Amino acid c	0	High Quality	
TC2P_HUMAN	P40227	CCT16A (CCT6)	T-complex protein 1 subunit zeta OS=Homo sapiens	58007.3	11	2	12	1	2	31	22	2	28	5	3	4	0	6	Chapererin	Protein fold	0	High Quality	
TCPH_HUMAN	Q99832	CCT7 (CCTH)	T-complex protein 1 subunit eta OS=Homo sapiens	59349.8	10	10	3	1	3	28	14	17	5	1	2	3	0	42	Chapererin	Protein fold	0	High Quality	
GCST_HUMAN	P48728	AMT (GCST)	Aminomethyltransferase, mitochondrial OS=Homo sapiens	43927.6	3	2	1	1	1	8	4	2	2	2	1	0	4	0	Dehydrogenase	Amino acid c	0	High Quality	
TRAP1_HUMAN	Q12931	TRAP1 (HSP7)	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens	80094.9	16	1	5	1	1	2	27	34	1	6	2	2	1	3	49	Hsp 90 family chaper	Protein fold	0	High Quality
LASP1_HUMAN	Q14847	LASP1 (MSP7)	LIM and SH3 domain protein 1 OS=Homo sapiens	29698.8	2	4	1	1	1	9	2	7	1	2	4	0	0	16	Non-motor actin bindi	Muscle cont	0	High Quality	
MARE3_HUMAN	Q9UPY8	MAPRE3	Microtubule-associated protein RP/EB family member 3	31964.8	2	3	1	1	1	7	3	3	5	0	0	1	0	12	Non-motor microtubul	Cell cycle/Ce	0	High Quality	
ROA2_HUMAN	P22626	HNRNP2B1	Heterogeneous nuclear ribonucleoprotein A2/B	37412.3	5	2	3	1	1	14	7	9	3	2	2	1	3	27	Molecular function unc	Biological pr	0	High Quality	
PURA1_HUMAN	Q8N142	ADSSL1 (ADSS)	Adenylosuccinate synthetase isozyme 1 OS=Homo sapiens	50190.8	15	3	12	1	2	34	26	5	33	0	2	2	3	71	Synthetase:Other ligas	Nucleoside, Wnt signa	High Quality		
FA9_HUMAN	P00740	F9	Coagulation factor IX OS=Homo sapiens GN=F9 P=1	51759.6	5	2	1	3	3	14	6	8	1	0	5	6	0	26	Oxidoreductase:Serine	Proteolysis i	Blood coa	High Quality	
LRC20_HUMAN	Q8TCA0	LRRC20 (UNO)	Leucine-rich repeat-containing protein 20 OS=Homo sapiens	20491.7	4	1	1	1	1	7	10	1	3	0	0	1	0	15	Molecular function unc	Biological pr	0	High Quality	
PAZ24_HUMAN	Q9UQ80	PAZ24 (EBP1)	Proliferation-associated protein 24 OS=Homo sapiens	43768.7	9	2	7	2	1	3	24	17	2	16	2	0	2	4	43	Other transcription fac	Protein bios	0	High Quality
CFAB_HUMAN	P00751	CFB (BF) (BFD)	Complement factor B OS=Homo sapiens GN=CFB	85515.2	16	9	3	3	3	37	41	22	4	4	3	3	0	77	Serine protease:Compl	Proteolysis c	0	High Quality	
MSRB3_HUMAN	Q8XL7	MSRB3 (UNO)	Methionine-R-sulfoxide reductase B3 OS=Homo sapiens	11992.3	1	3	1	1	1	7	1	5	4	1	0	1	0	12	Reductase	Protein mod	0	High Quality	
FKBP4_HUMAN	Q02790	FKBP4	FK506-binding protein 4 OS=Homo sapiens GN=FKBP4	51787.9	3	1	11	1	1	18	4	1	26	2	0	1	1	35	Other chaperones:Oth	Protein fold	0	High Quality	
HNRNP_K_HUMAN	P61978	HNRNP_K (HNR)	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens	50960.5	5	10	6	1	2	25	8	15	10	5	7	0	1	48	Ribonucleoprotein	mRNA trans	0	High Quality	
ATPF1_HUMAN	Q5TC12	ATPAF1 (ATP)	ATP synthase mitochondrial F1 complex assembly	36418.9	11	2	5	1	2	22	25	4	8	5	5	0	1	48	Chaperone	Protein cont	0	High Quality	
HIBCH_HUMAN	Q6NVN1	HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	43466.9	9	2	6	1	3	24	19	5	13	0	1	4	5	47	Synthetase:Dehydroge	Carbohydrat	0	High Quality	
RAB21_HUMAN	Q9UL25	RAB21 (KIAA)	Ras-related protein Rab-21 OS=Homo sapiens GN=RAB21	24329.9	2	6	1	1	1	10	3	9	0	1	1	0	0	14	Small GTPase	Intracellular	0	High Quality	
DCMC_HUMAN	Q95822	MLYCD	Malonyl-CoA decarboxylase, mitochondrial OS=Homo sapiens	54986.4	12	1	7	1	1	2	26	20	3	10	1	2	3	41	Molecular function unc	Biological pr	0	High Quality	
NDUAA_HUMAN	Q95299	NDUFA10	NADH dehydrogenase [ubiquinone] 1 alpha subunit	43077.3	3	6	1	1	2	2	15	7	8	2	2	2	2	23	Oxidoreductase	Oxidative ph	0	High Quality	
NDUS1_HUMAN	P28331	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit	79450.5	19	1	12	1	2	4	40	52	2	26	1	1	4	4	90	Reductase	Electron tra	0	High Quality
PURA_HUMAN	Q00577	PURA (PUR1)	Transcriptional activator protein Pur-alpha OS=Homo sapiens	34893.1	2	4	1	1	1	9	3	7	1	3	1	0	0	15	Other transcription fac	General MR	0	High Quality	
TKT_HUMAN	P29401	TKT	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=1	67861.4	7	2	3	1	1	15	8	2	6	0	1	1	1	19	Transketolase	Penrose-pho	0	High Quality	
STRAP_HUMAN	Q9Y3F4	STRAP (MAV)	Serine-threonine kinase receptor-associated prot	38421.4	4	2	1	1	1	9	6	3	1	0	1	1	0	12	Other miscellaneous fu	Receptor pr	0	High Quality	
DESM_HUMAN	P17661	DES	Desmin OS=Homo sapiens GN=DES PE=1 SV=3	53518.6	7	5	17	1	1	32	11	10	26	0	1	2	1	51	Intermediate filament	Extracellu	0	High Quality	
GDE_HUMAN	P35573	AGL (GDE)	Glycogen debranching enzyme OS=Homo sapiens	174749.6	18	4	27	3	2	63	36	5	55	5	6	4	6	117	Glycosyltransferase:GN	Glycogen me	0	High Quality	
ACTZ_HUMAN	P61163	ACTR1A (CTR)	Alpha-actinin OS=Homo sapiens GN=ACTR1A	42597.2	7	3	1	2	1	15	11	9	2	4	0	2	0	28	Actin and actin related	Exocytosis:E	Cytoskele	High Quality	
PDIA4_HUMAN	P13667	PDIA4 (ERP7)	Protein disulfide-isomerase A4 OS=Homo sapiens	72916.2	20	4	4	2	2	35	33	13	10	3	3	2	1	65	Other isomerase	Protein disu	0	High Quality	
IFAH_HUMAN	Q15056	IFAH (KIAA)	Eukaryotic translation initiation factor 4H OS=Homo sapiens	27368	5	3	2	1	2	13	9	11	3	2	0	0	4	29	Translation initiation f	Protein bios	0	High Quality	
MAOM_HUMAN	P23368	ME2	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens	65428.2	11	8	1	1	1	22	16	15	7	7	1	0	0	46	Dehydrogenase:Acyltra	Tricarboxyl	Pyruvate	High Quality	
TXND4_HUMAN	Q98S26	ERP44	Thioredoxin domain-containing protein 4 OS=Homo sapiens	46954.3	3	2	4	1	1	12	4	2	7	2	1	0	2	18	Other isomerase	Protein bios	0	High Quality	
GDCH_HUMAN	Q92947	GDCH	Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens	48110.5	8	1	10	1	1	24	21	3	31	2	5	1	2	65	Dehydrogenase	Acyl-CoA me	0	High Quality	
PSD7_HUMAN	P51665	PSMD7 (MOV)	26S proteasome non-ATPase regulatory subunit 7	37007.5	7	2	2	1	1	12	11	4	0	2	1	0	0	18	Other miscellaneous fu	Proteolysis i	Cell cycle	High Quality	
BW2_HUMAN	Q9Y6E2	BZW2 (HSPC)	Basic leucine zipper and W2 domain-containing	48146	10	1	1	1	1	17	18	1	2	2	2	1	2	28	Nuclease:Translation i	Protein bios	0	High Quality	
U1A1_HUMAN	Q13564	NAE1 (APPBP)	NEDD8-activating enzyme E1 regulatory subunit 1	60230.3	8	3	2	2	2	18	11	3	4	4	2	0	0	25	Basic helix-loop-helix t	Nucleoside,	0	High Quality	
CNS3_HUMAN	Q9UN52	COP3 (CNS3)	COP9 signalosome complex subunit 3 OS=Homo sapiens	47856.3	3	1	3	1	1	2	12	6	4	4	2	1	2	20	Other enzyme activat	Protein bios	0	High Quality	
NIP51_HUMAN	Q9BPW8	NIPSNAP1	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIP51	33292.9	4	1	1	1	1	6	6	4	0	2	0	1	0	9	Membrane traffic prot	General yesi	0	High Quality	
CATZ_HUMAN	Q9UBR2	CTSZ	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1	33850.2	3	3	2	1	1	10	5	12	4	3	2	0	0	26	Cysteine protease	Proteolysis	0	High Quality	
EEF1A3_HUMAN	Q5VTE0	EEF1A3	(Putative elongation factor 1-alpha-like) 3	50167.4	3	3	2	1	2	4	10	20	11	1	4	4	0	52	Translation elongation	Translatio	0	High Quality	
PSB1_HUMAN	P20618	PSMB1 (PSC5)	Proteasome subunit beta type-1 OS=Homo sapiens	26472.5	5	4	1	2	1	13	5	9	9	10	2	0	2	35	Other proteases	Proteolysis	Parkinson	High Quality	
SMYD1_HUMAN	Q8N812	SMYD1	SET and MYND domain-containing protein 1 OS=Homo sapiens	56598.7	13	7	1	1	1	23	22	32	0	4	1	3	0	62	Transcription cofactor	mRNA trans	0	High Quality	
TXNR2_HUMAN	Q9NWN7	TXNR2 (KIA)	Thioredoxin reductase 2, mitochondrial OS=Homo sapiens	56487.8	7	1	9	2	1	20	10	1	13	0	8	0	2	34	Reductase	Electron tra	0	High Quality	
MK01_HUMAN	P28482	MAPK1 (ERK2)	Mitogen-activated protein kinase 1 OS=Homo sapiens	41373.9	2	1	2	1	1	8	2	1	1	3	2	0	0	10	Non-receptor serine/th	Protein pho	Angiotens	High Quality	
ATPD_HUMAN	P30049	ATP5D	ATP synthase subunit delta, mitochondrial OS=Homo sapiens	17471.9	4	5	3	2	2	16	20	22	25	16	14	0	0	97	Hydrogen transporter:	Nucleoside,	0	High Quality	
LRPRC_HUMAN	P42704	LRPPRC (LRP)	Leucine-rich PPR motif-containing protein, mitoch	157894.2	15	13	1	5	4	38	23	22	0	1	5	6	0	57	Serine/threonine prote	Protein pho	0	High Quality	
RS2_HUMAN	P15880	RPS2 (RPS4)	40S ribosomal protein S2 OS=Homo sapiens GN=RS2	31307.2	5	1	1	1	1	8	7	2	1	0	0	1	0	11	Ribosomal protein	Protein bios	0	High Quality	
MIF_HUMAN	P14174	MIF (GLIP)	Macrophage migration inhibitory factor OS=Homo sapiens	12458.5	3	1	3																

CX6B1_HUMAN	P14854	COX6B1 (COX)	Cytochrome c oxidase subunit VIb isoform 1 OS=	10174.3	3	3	5	2	2	15	8	7	15	12	24	0	0	66	Oxidase	Oxidative ph	0	High Quality	
SSB_HUMAN	Q04837	SSBP1	Single-stranded DNA-binding protein, mitochon	17241.7	5	4	2	1	1	12	10	8	6	0	4	0	0	28	Single-stranded DNA-b	DNA replicat	0	High Quality	
DBPA_HUMAN	P19698	CSDA (DBPA)	DNA-binding protein A OS=Homo sapiens GN=C	40071.4	2	1	1	1	1	7	3	2	1	3	0	2	1	12	Other transcription fac	mRNA trans	0	High Quality	
DP13A_HUMAN	Q9UK61	APPL1 (APPL)	DCC-interacting protein 13-alpha OS=Homo sa	79647.1	8	1	9	2	2	24	13	1	13	6	3	1	1	38	Molecular function un	Biological pr	0	High Quality	
UBIQ_HUMAN	P62988	RPS27A (UBA)	Ubiquitin OS=Homo sapiens GN=RPS27A PE=1 SV	8547.2	8	9	1	2	1	20	76	56	1	0	5	0	0	138	Ribosomal protein	Proteolysis	0	High Quality	
LAC_HUMAN	P01842	IGLC1 (IGLC2)	Ig lambda chain C regions OS=Homo sapiens GN	11218.4	4	3	5	3	2	17	15	4	21	4	4	0	0	48	Molecular function un	Biological pr	0	High Quality	
BLVRB_HUMAN	P30043	BLVRB (FLR)	Flavin reductase OS=Homo sapiens GN=BLVRB PE	22100.7	6	2	8	3	3	22	13	3	21	7	5	0	0	49	Reductase	Biological pr	0	High Quality	
GDIR2_HUMAN	P52566	ARHGDB16 (GDI)	RHO GDP-dissociation inhibitor 2 OS=Homo sapie	22970.4	8	2	4	2	1	17	14	3	10	0	0	1	2	30	Other signaling molecu	Intracellular	0	High Quality	
D3D2_HUMAN	P42126	DCI	3,2-trans-enoyl-CoA isomerase, mitochondrial OS	32798.5	7	3	6	1	2	19	43	12	19	2	4	0	0	80	Synthetase:Dehydroge	Carbohydrat	0	High Quality	
EEA1_HUMAN	Q15705	EEA1 (ZFV2)	Early endosome antigen 1 OS=Homo sapiens GN	162450	22	3	7	1	1	34	36	3	15	1	0	1	0	56	Membrane traffic regu	Endocytosis	0	High Quality	
KNG1_HUMAN	P01042	KNG1 (BDK)	Kinasein 1 OS=Homo sapiens GN=KNG1 PE=1 SV	71939.6	2	1	9	1	1	12	10	1	1	1	0	1	0	13	Cysteine protease inh	Blood clotting	0	High Quality	
FBLN1_HUMAN	P23142	FBLN1 (P231)	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=3	77240.8	6	6	1	2	1	16	7	10	1	0	4	1	0	23	Signaling molecule/Ce	Cell commur	0	High Quality	
CALD1_HUMAN	Q05682	CALD1 (CAD)	Caldesmon OS=Homo sapiens GN=CALD1 PE=1 SV	93232.8	8	13	2	1	4	5	33	13	19	2	0	2	4	5	95	Non-motor actin bindi	Mitosis/cell	0	High Quality
S10AA_HUMAN	P06903	S100A10 (AN)	Protein S100-A10 OS=Homo sapiens GN=S100A10	11185.5	5	1	3	3	2	14	13	1	7	0	0	5	6	32	Calmodulin related pr	Developmen	0	High Quality	
BHD2_HUMAN	Q9BU71	BHD2 (DHR5)	3-hydroxybutyrate dehydrogenase type 2 OS=Ho	26705.9	2	1	1	1	1	6	2	1	1	2	1	0	1	7	Dehydrogenase:Reduct	Other metab	0	High Quality	
SNX3_HUMAN	Q06049	SNX3	Sorting nexin-3 OS=Homo sapiens GN=SNX3 PE=1	18745	6	2	3	1	1	12	10	2	8	0	0	0	1	21	Molecular function un	Biological pr	0	High Quality	
CI005_HUMAN	Q9UQ88	TIGAR	Uncharacterized protein C120F5 OS=Homo sapie	30045.1	2	1	1	1	1	5	2	2	2	0	0	1	0	7	Other synthase/synth	Vitamin bios	0	Cobalam	
APM2_HUMAN	Q15847	APM2 (C10ar)	Adipose most abundant gene transcript 2 protei	7836.7	1	1	3	1	1	6	1	1	7	0	0	0	1	10	Molecular function un	Biological pr	0	High Quality	
ACSL1_HUMAN	P31241	ACSL1 (FACL1)	Long-chain-fatty-acyl-CoA ligase 1 OS=Homo sap	77927.1	20	2	4	1	1	28	33	3	7	0	4	1	0	48	Other ligase	Fatty acid m	0	High Quality	
ACY2_HUMAN	P14621	ACY2 (ACYF)	Acylphosphatase 2 OS=Homo sapiens GN=ACY2F	11121.4	8	5	1	1	1	16	17	12	1	0	0	1	1	32	Other phosphatase	Miscellaneous	0	High Quality	
VPS35_HUMAN	Q060K1	VPS35 (MEM3)	Vacuolar protein sorting-associated protein 35 O	91692	10	4	2	2	1	19	24	6	5	0	7	3	0	45	Other membrane traffi	Other intrac	0	High Quality	
IMA3_HUMAN	Q00055	KPNAB3	Importin subunit alpha-3 OS=Homo sapiens GN=	57868.9	4	1	1	2	1	9	5	2	1	0	2	1	0	11	Transfer/carrier protei	Nuclear tran	0	High Quality	
CYB5_HUMAN	P00167	CYB5A (CYB5)	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1	15312.3	3	2	1	1	1	6	4	5	0	0	0	1	0	10	Oxidase	Steroid met	0	High Quality	
CYTA_HUMAN	P01040	CSTA (STF1)	Cystatin A OS=Homo sapiens GN=CSTA PE=1 SV=	10988.6	1	1	1	3	7	12	6	1	14	65	0	0	0	86	Cysteine protease inh	Proteolysis	0	High Quality	
PP1L1_HUMAN	Q9Y3C6	PP1L1 (CYPL1)	Peptidyl-prolyl cis-trans isomerase-like 1 OS=Hor	18219.3	5	1	2	1	1	9	9	1	2	1	0	0	0	13	Other isomerase	Protein fold	0	High Quality	
DSC1_HUMAN	Q08554	DSC1 (CDHF1)	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1	100028.2	2	2	2	3	2	12	2	3	2	9	3	0	1	20	Cadherin/Other cell j	Cell adhesio	0	High Quality	
MCEE_HUMAN	Q069E7	MCEE	Methylmalonyl-CoA epimerase, mitochondrial OS	18730.8	1	1	4	1	3	10	2	1	5	0	0	1	3	12	DNA glycosylase	Biological pr	0	Methylma	
CLH1_HUMAN	Q00610	CLTC (CLH1)	Clathrin heavy chain 1 OS=Homo sapiens GN=CL	191600.9	4	1	7	1	1	14	11	1	10	0	1	1	24	Vesicle coat protein	Ligand-medi	0	Heterotri		
ELOB_HUMAN	Q15370	TCEB2	Transcription elongation factor B polypeptide 2	13115.2	1	3	5	2	2	13	1	3	12	7	3	0	0	26	Transcription cofactor	mRNA trans	0	High Quality	
NDUUV2_HUMAN	P19404	NDUUF2	NADH dehydrogenase [ubiquinone] flavoprotein	27373.8	5	6	4	1	2	18	11	8	9	3	4	0	0	35	Dehydrogenase:Reduct	Oxidative ph	0	Parkinson	
FHIT_HUMAN	P49789	FHIT	Bis(5'-adenosyl)-triphosphatase OS=Homo sapie	16839.6	2	2	2	1	1	5	6	9	0	0	0	1	0	16	Nucleotide phosphat	Biological pr	0	High Quality	
RO60_HUMAN	P10155	TROVE2 (RO6)	60 kDa SS-A/Ro ribonucleoprotein OS=Homo sap	60654.1	6	4	4	1	1	12	7	8	0	2	0	1	18	Other RNA-binding pr	Other nucle	0	High Quality		
CALL5_HUMAN	Q9NZT1	CALML5 (CLS)	Calmodulin-like protein 5 OS=Homo sapiens GN=	15902.9	3	4	2	4	7	20	17	25	3	8	18	0	0	71	Calmodulin related pr	Calcium met	0	High Quality	
THM_HUMAN	P25325	MPST (TST2)	3-mercaptopyruvate sulfurtransferase OS=Homo	33160.8	8	5	4	1	1	18	15	6	7	1	0	0	0	29	Transfer/carrier protei	Sulfur metab	0	High Quality	
DCTN1_HUMAN	Q14203	DCTN1	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1	141679.6	18	8	4	2	1	34	41	11	8	2	1	0	1	64	Non-motor microtubul	General vers	0	Huntingc	
HMG81_HUMAN	P09429	HMG81 (HM)	High mobility group protein B1 OS=Homo sapien	24876.7	12	9	7	6	3	34	23	26	0	0	14	11	74	Molecular function un	Biological pr	0	High Quality		
DYHC1_HUMAN	Q14204	DYHC1 (HD)	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sa	532387.6	51	15	22	5	4	100	128	36	6	7	2	1	212	Microtubule binding m	General vers	0	Huntingc		
MK03_HUMAN	P27361	MAPK3 (ERK)	Mitogen-activated protein kinase 3 OS=Homo sap	43119.4	1	2	2	1	1	6	1	3	5	0	0	1	0	10	Non-receptor serine/th	Protein bios	0	Angiotens	
LAMA2_HUMAN	P24043	LAMA2 (LKM)	Laminin subunit alpha-2 OS=Homo sapiens GN=L	342752.6	22	6	27	1	3	65	68	7	55	1	5	3	7	146	Extracellular matrix li	Extracellular	0	Integrin s	
VATA_HUMAN	P38606	ATP6V1A (AT)	Vacuolar ATP synthase catalytic subunit A OS=H	68287.4	6	3	3	1	1	11	8	1	1	1	0	1	14	Other ion channel/Hyd	Other nucle	0	High Quality		
PSMD2_HUMAN	Q13200	PSMD2 (TRAF)	26S proteasome non-ATPase regulatory subunit	100184.2	18	1	2	1	1	25	35	1	2	2	1	2	2	45	Other enzyme regulato	Proteolysis/s	0	Ubiquitin	
TAGL_HUMAN	Q01995	TAGLN (SM2)	Transglutinin OS=Homo sapiens GN=TAGLN PE=1 SV	22592.9	13	3	8	1	2	27	49	15	36	0	0	1	3	104	Non-motor actin bindi	Muscle cont	0	High Quality	
K22E_HUMAN	P35908	KRT2 (KRT2)	Keratin, type II cytoskeletal 2 epidermal OS=Hom	65848.4	36	32	14	3	1	85	90	292	18	0	11	0	0	1011	Intermediate filament	Ectoderm de	0	High Quality	
KAT_HUMAN	Q08NFU3	KAT	Putative thiosulfate sulfurtransferase KAT OS=Ho	12512.7	2	4	1	1	1	8	3	5	3	0	4	0	0	15	Miscellaneous functio	Mitosis	0	High Quality	
DYL2_HUMAN	Q069J2	DYNNL2 (DLC2)	Dynein light chain 2, cytoplasmic OS=Homo sapie	10332.1	2	3	1	4	2	11	4	17	0	0	6	3	0	33	Cytoskeletal protein	Intracellular	0	High Quality	
INP4B_HUMAN	Q15327	INP4B	Type II inositol-3,4-bisphosphate 4-phosphatase	14070.4	4	6	2	1	1	14	6	12	3	2	0	0	0	24	Molecular function un	Biological pr	0	High Quality	
GLRX1_HUMAN	P35754	GLRX (GRX)	Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1	11757.8	3	2	5	2	1	13	11	12	14	3	2	0	0	42	Other oxidoreductase	Sulfur redox	0	High Quality	
AT1F1_HUMAN	Q09U12	ATP1F1 (ATP)	ATPase inhibitor, mitochondrial OS=Homo sapie	12230.8	1	6	3	1	1	3	3	11	3	1	4	0	0	22	Other miscellaneous fu	Oxidative ph	0	High Quality	
CAND2_HUMAN	Q07155	CAND2 (KIAA)	Cullin-associated NEDD8-dissociated protein 2 O	122667.6	4	2	3	1	1	11	6	2	6	1	0	0	1	16	Transcription factor	mRNA trans	0	High Quality	
ACO31_HUMAN	Q05TJ3	C1orf31	Uncharacterized protein C1orf31 OS=Homo sapie	14098.5	2	2	1	1	1	5	3	2	6	0	0	0	2	7	Molecular function un	Biological pr	0	High Quality	
SPB3_HUMAN	P29508	SERPINB3 (SC)	Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1	44547.9	5	5	1	8	1	14	6	1	16	0	0	0	0	23	Serine protease inhibi	Proteolysis	0	High Quality	
COX5A_HUMAN	P20674	COX5A	Cytochrome c oxidase subunit 5A, mitochondrial	16756.6	3	2	3	3	1	12	4	4	13	8	4	0	0	33	Oxidase	Oxidative ph	0	High Quality	
SRB52_HUMAN	Q04875	SORBS2 (ARG)	Sorbin and SH3 domain-containing protein 2 OS	124092.1	8	5	2	1	1	17	15	13	5	0	2	1	0	36	Cytoskeletal protein	Biological pr	0	High Quality	
AN32A_HUMAN	P39687	ANP32A (C15)	Acidic leucine-rich nuclear phosphoprotein 32 fa	28568.1	5	5	5	2	1	17	6	6	6	2	2	0	0	22	Phosphatase inhibitor	Biological pr	0	High Quality	
PEA15_HUMAN	Q15121	PEA15	Astrocytic phosphoprotein PEA-15 OS=Homo sap	15023.2	1	4	2	1	1	8	2	6	2	0	0	2	1	14	Molecular function un	Biological pr	0	High Quality	
EF1D_HUMAN	P29692	EEF1D (EF1D)	Elongation factor 1-delta OS=Homo sapiens GN=	31103.9	6	5	4	1	1	17	11	7	7	0	0	1	2	28	Translation elongatio	Protein bios	0	High Quality	
FLNB_HUMAN	Q07569	FLNB (FLN1)	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=1	278171.9	30	3	15	1	1	50	62	5	26	0	1	0	1	95	Non-motor actin bindi	Cell structur	0	Integrin s	
DDAH1_HUMAN	Q09476	DDAH1 (DDA)	(N(G),N(G)-dimethylarginine dimethylaminohydr	31103.7	1	2	3	1	1	7	2	3	5	0	0	2	12	Other hydrolase	Angiogenesis	0	High Quality		
GLSK_HUMAN	Q09425	GLS (GLS1)	Glutaminase kidney isoform, mitochondrial OS=H	73444.2	4</																		

