SUPPLEMENTAL MATERIAL

METABOLIC HOMEOSTASIS IS MAINTAINED IN MYOCARDIAL HIBERNATION BY ADAPTIVE CHANGES IN THE TRANSCRIPTOME AND PROTEOME

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SUPPLEMENTAL MATERIAL AND METHODS

Hypoxyprobe™ staining. Hypoxyprobe™ (pimonidazole hydrochloride [1]) staining was performed according to the manufacturer's instruction (60 mg/kg body, Chemicon). Hypoxic cells activate pimonidazole hydrochloride and bind 2-nitroimidazole compounds. Oxygen competes for the addition of the first electron to Hypoxyprobe™, and it is believed that this competition accounts for the oxygen dependence of 2-nitroimidazole reductive activation and binding. The second part of the assay includes a primary antibody reagent that recognizes Hypoxyprobe™ adducts in hypoxic cells. To minimise non-specific background staining, a primary fluorescein (FITC)-conjugated mouse monoclonal antibody directed against pimonidazole protein adducts was used in combination with a secondary mouse anti-FITC Mab conjugated to horseradish peroxidase (HRP) as previously reported [2].

Real-time PCR (qPCR). For qPCR analysis, cDNA was generated from 5 mg of total RNA by using Verso cDNA kit (Thermo scientific) and the respective primers. Samples were normalized according to L19 mRNA levels by SYBR green qPCR. The primer sequences were as follows: for Kir6.2 F-TCTCCATCGAGGTCCAGGTG, R–CCCGACGATATTCTGCACAAT; for SUR2A F-TCTGCATCGGGTTCACACC, R-CCTGGGCCAAGAGGCTTT; for GLUT1 F-CTTTGGTCTCTCTCCGTGGC, R- AGCATGGAGTTCCGCCTG; for FOXO1 F-AATGATGGGCCCTAATTCGG, R- GCTGTGCATGTCCAGGGTG.

Difference in-gel electrophoresis (DIGE). Protein extracts were prepared from homogenized hearts using a standard lysis bufffer (9M urea, 1% DTT, 4% CHAPS, 0.8% Pharmalytes 3-10, protease and phosphatase inhibitors (Complete Mini, Roche). After centrifugation at 13,000 g for 10 min, the supernatant containing soluble proteins was harvested and the protein concentration was determined using a modification of the method described by Bradford. Solubilised samples were divided into aliquots and stored at –80°C. For DIGE, proteins were precipitated (ReadyPrep 2-D Clean-up kit, Biorad) and resuspended in DIGE buffer (30mM TrisCl pH 8.5, 8M urea, 4% w/v CHAPS). The fluorescence dye labelling reaction was carried out at a dye/protein ratio of 400 pmol/100μg. After incubation on ice for 30 min, the labelling reaction was stopped by scavenging non-bound dyes with 10mM lysine for 15 min. For two-dimensional gel electrophoresis (2-DE), extracts were loaded on nonlinear immobilized pH gradient 18-cm strips, 3-10 (GE healthcare). In addition to using a wide-range pH gradient, we separated cardiac proteins on a pH 4 to 7 gradient to increase spatial resolution for phosphoprotein staining. 100 μg per sample was applied to the IPG strip using an in-gel rehydration method. Samples were diluted in rehydration solution (8 M urea, 0.5% w/v CHAPS, 0.2% w/v DTT, and 0.2 % w/v Pharmalyte pH 3-10) and rehydrated overnight in a reswelling tray. Strips were focused at 0.05 mA/IPG strip for 35 kVh at 20°C (IPGphor, GE healthcare). Once IEF was completed the strips were equilibrated in 6M urea containing 30% v/v glycerol, 2% w/v SDS and 0.01% w/v Bromphenol blue, with addition of 1% w/v DTT for 15 min, followed by the same buffer without DTT, but with the addition of 4.8% w/v iodoacetamide for 15 min. SDS-PAGE was performed using 12% T (total acrylamide concentration), 2.6% C (degree of cross-linking) polyacrylamide gels without a stacking gel, using the Ettan DALT system (GE healthcare). The second dimension was terminated when the Bromphenol dye front had migrated off the lower end to the gels. After electrophoresis, fluorescence images were acquired using the Typhoon variable mode imager 9400 (GE healthcare). A pre-scan was performed to optimize the scanning parameters to exclude spot saturation. Differences in protein expression were analyzed using the Decyder software (version 6.5, GE healthcare).

Corrections for multiple testing were performed by the Benjamini-Hochberg equation, yielding False Discovery rates (FDR)[3]. Finally, gels were fixed overnight in methanol: acetic acid: water solution (4:1:5 v/v/v). Protein profiles were visualised by silver staining using the Plus one silver staining kit (GE healthcare) with slight modifications to ensure compatibility with subsequent mass spectrometry analysis [4]. For documentation, silver-stained gels were scanned in transmission scan mode using a calibrated scanner (GS-800, Biorad).

Principal Component Analysis (PCA). For proteomics, DIGE gels were analysed using the EDA module of the Decyder software (version 6.5, GE healthcare). Principal component analysis (PCA) was performed on all differentially expressed proteins after removal of missing values to give an initial overview of the groupings. PCA replaces a group of variables with a smaller number of new variables, called principal components (PC), which are linear combinations of the original variables. Projecting the observation on one of these axes generates a new variable designed to maximize the description of the variance in the data set. For pattern analysis, hierarchical clustering was performed on the Student's T-test<0.05 dataset.

LC-MS/MS. Gel pieces containing selected protein spots were treated overnight with modified trypsin (Promega) according to a published protocol modified for use with an Investigator ProGest (Genomic Solutions, Huntington, UK) robotic digestion system [5]. Following enzymatic degradation, peptides were separated by a Surveyor HPLC system on a reverse-phase column and applied online to a LCQ deca XP ion-trap mass spectrometer. Spectra were collected from the ion-trap mass analyzer using full ion scan mode over the mass-to-charge (m/z) range 300-2000. MS-MS scans were performed on each ion using dynamic exclusion. Spectra were searched against a mouse database (UniProt 15.13, 16214 entries) using the

SEQUEST algorithm incorporated in the Bioworks Browser 3.3.1 SP1 (Thermo Fisher Scientific). The following criteria were used: 1.5 AMU for the precusor ion, 1.0 AMU for fragment ions, one missed cleavage per peptide. Carbamidomethylation of cysteine as well as partial oxidation of methionine were assumed. Search results were imported into Scaffold (v2.06.00, Proteome Software). The following filter were applied: 99.0% protein probability, 95% peptide probability, a minimum of 2 peptides.

Immunoblotting. 50 μg of protein extracts were separated on 4-20% gradient gels (Novex, Invitrogen) and transferred to nitrocellulose membranes. Membranes were blocked in 5% PBS milk and probed with the following antibodies: lactate dehydrogenase (ab7639-1, 1:100, Abcam), glucose transporter 1 (GLUT-1, GT11-A, Alpha Diagnostics Intl.), IGFBP-2 (AF797, 0.1 μg/ml, R&D), peroxiredoxin 1 (LF-PA0001, 1:2000, Lab Frontier), peroxiredoxin 2 (LF-PA0007, 1:2000, Lab Frontier), SOD-1 (sc-11407, 1:100, Santa Cruz), and SOD-2 (06-984, 1:500, Upstate). After incubation with HRP-conjugated secondary antibodies and washing 3 times for 5 minutes each in 0.5% PBS tween, bands were detected on X-ray films using enhanced chemiluminescence (ECL, GE healthcare).

Phosphate-affinity gel electrophoresis (Phos-tag^{TM}). For phosphate-affinity gel electrophoresis, 50 μg of protein extracts were separated on 10% polyacrylamide gels containing 50 µM Phos-tag^{TM} (Wako Chemicals GmbH) and 50 µM $MnCl_2$ (Sigma). Gels were soaked in transfer buffer with 1mM EDTA for 10 min, then in transfer buffer for another 10 min prior to blotting onto a polyvinylidene fluoride (PVDF) membrane. Membranes were probed with antibodies to myosin light chain 2 (Abcam 89594) and cardiac troponin I (Cell Signaling Technology #4002).

Proton nuclear magnetic resonance spectroscopy (^{1}H-NMR). Frozen heart tissues were ground under liquid nitrogen using a mortar and pestle (n=5 and n=3 for for hibernating and control hearts, respectively). Water-soluble metabolites were extracted in 6% perchloric acid. Deproteinised extracts were transferred to ice cold centrifuge tubes and centrifuged at 3000 rpm for 10 minutes at 4°C. The supernatant was transferred to fresh cold centrifuge tubes and neutralised to pH 7 with 10M KOH. After neutralization, extracts were centrifuged, the supernatant was collected, freeze-dried and reconstituted in deuterium oxide (D_2O). Immediately before the NMR analysis[6], the pH was readjusted to 7 with PCA or KOH. 0.5ml of the extracts were placed in 5mm NMR tubes. ^{1}H-NMR was performed using a Bruker 600MHz spectrometer. The water resonance was suppressed by using gated irradiation centred on the water frequency. Sodium 3-trimethylsilyl-2,2,3,3-tetradeuteropropionate (TSP) was added to the samples for chemical shift calibration and quantification.

Network construction and pathway analysis. The previously published raw transcriptomics data [7] were first reanalyzed to correct for multiple testing[8]. This yielded a total of 166 induced and 195 repressed genes during hibernation at Baysian p<0.01 and a FDR<20%. The original 8 .cel files were uploaded into the Bioconductor R-package (www.bioconductor.org), 2 chips that did not pass QC were discarded, and the remaining 6 were normalized by the MAS5 module. Expression differences of the log2 normalized data were next statistically analyzed by a moderated t-test for micro-array data (Cyber-T) [9] and corrected for multiple testing by the Benjamini-Hochberg equation, yielding False Discovery rates (FDR) [3]. The network construction was based on the available normalized raw expression values of 1174 probes. Using a cutoff of ±2 fold change, we reduced this set to 397 differentially expressed probes. In cases where more than one probe mapped to the same gene, these probes were averaged, the average expression level was retained and so the dataset was reduced to 315 unique genes. The “mcxarray” program from MCL clustering package[10] was used to construct the network from expression data. Pairwise similarities in gene expression vectors were expressed through the Pearson correlation coefficient (PCC) and a threshold of PCC>0.7 was used to link correlated genes. The resulting network representation of the gene expression experiment included proteins as nodes, edges linked correlated proteins and visualisation was performed with the Cytoscape software[11]. Transcriptomics, proteomics and metabolomics data were analysed by the MetaCoreTM systems biology analysis suite version 5.1 (GeneGo Inc., St. Joseph, MI), using a filtering criterion of $p<0.05$ (www.genego.com).

Statistical analysis. Statistical analysis was performed using the analysis of variance and Student’s t-test. The Kruskal-Wallis test with the Dunn’s post test was used as a nonparametric test. Pairwise comparisons between metabolites were performed using the Bonferroni / Dunn test. Results were given as means±SE. A P value <0.05 was considered significant.

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SUPPLEMENTAL FIGURES

Supplemental Figure 1. PCA and heat map. (A) PCA for multivariate analysis of proteome dynamics in hibernating (red) compared to control (blue) hearts. The black ellipse represents the 95% significance level. Principal component 1 and 2 (PC1 and PC2) clearly separate the control and hibernating hearts based on their protein expression profiles. **(B)** Heat map. Hierarchical clustering was applied to rearrange the dataset. X- axis, spot maps; Y-axis, proteins. Red color denotes increase, green color denotes decrease. Black color indicates no change. More proteins are upregulated than downregulated during hibernation indicating a switch in gene and protein expression. Bar shows the log standard abundance value interval for the colors, +/- 0.3.

Supplemental Figure 2. Changes in the proteome of hibernating hearts. The user interface of the Decyder 2D software (version 6.5, GE healthcare) displays the experimental design view for “triose phosphate isomerase” (spot no 42, Table 1) and “creatine kinase” (B, spot no 27, Table 1). Note the consistency of the differential expression in the hibernating myocardium.

Supplemental Figure 3. Densitometry. Quantitative data for the phosphorylated bands of MLC-2 and TnI (highlighted with arrows in **Figures 4B and C**) as well as for SOD-2. *, denotes a significant difference, $p<0.05$ (n=4 per group)

Supplemental Figure 4. Pathway analysis. The combined map (thermometer 1 is proteomics, 2 is transcriptomics, the red color indicates an upregulation in the comparison hibernation vs control) revealed that protein changes were in the same pathway as transcriptomic changes and both datasets contributed the same number of focus molecules to the pathway analysis: Whereas proteomics identified 4 members of this pathway CCT6A (+1.25), HSPA5 (+2.18), TF (+1.32) and ALDOA (+1.52), transcriptomics identified 4 additional focus objects: EGLN3 (+6.91), BNIP (+3.2), SLC2A1 (+3.46) and VEGFA (+2.9).

Supplemental Table I: Peptides identified by LC-MS/MS

No.	Protein Name	Accession No.	Mw	Protein ide	Numbe	Numbe	Numbe	Sequence	Peptide sequence	Best Pepti	Best SEQ	Best SEQ	Best X!	Numbe	Numb	Numb	Numl	Calculated +	Start	Stop i
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	VEIIANDQGNR	95.00%	3.19	0.365	2	0	7	0	2	1,228.63	51	61
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	ITPSYVAFTPEGER	95.00%	2.63	0.567	3.92	0	4	0	2	1,566.78	62	75
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	NQLTSNPENTVFDAK	95.00%	3.82	0.599	4.4	0	4	0	2	1,677.81	83	97
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	TWNDPSVQQDIK	95.00%	3.68	0.473	3.89	0	3	0	2	1,430.69	103	114
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	ETAEAYLGK	95.00%	1.8	0.341	0	0	4	0	2	981.4894	156	164
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	VTHAVVTVPAYFNDAQR	95.00%	3.72	0.452	2.7	0	0	2	2	1,887.97	166	182
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	IINEPTAAAIAYGLDK	95.00%	4.32	0.672	4.24	0	2	0	2	1,659.90	199	214
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	VLEDSDLK	95.00%	2.04	0.228	0	0	1	0	2	918.4786	346	353
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	VLEDSDLKK	95.00%	1.91	0.348	1.24	0	2	0	2	1,046.57	346	354
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	KSDIDEIVLVGGSTR	95.00%	3	0.386	0	0	0	2	2	1,588.85	354	368
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	SDIDEIVLVGGSTR	95.00%	3.67	0.577	2.89	0	3	0	2	1,460.76	355	368
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	IQQLVK	95.00%	2.27	0.0929	0	0	1	0	2	728.4672	372	377
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	EFFNGKEPSR	95.00%	1.62	0.264	0	0	1	0	2	1,210.59	378	387
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	NTVVPTK	95.00%	1.66	0.304	0	0	1	0	2	758.4413	441	447
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	NTVVPTKK	95.00%	1.9	0.312	0	0	1	0	2	886.5363	441	448
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	SQIFSTASDNQPTVTIK	95.00%	2.65	0.532	1.51	0	1	0	2	1,836.93	449	465
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	VYEGERPLTK	95.00%	2.43	0.438	0	0	2	0	2	1,191.64	466	475
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	ITITNDQNR	95.00%	2.9	0.378	1.68	0	3	0	2	1,074.55	525	533
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	NELESYAYSLK	95.00%	3.46	0.409	1.14	0	2	0	2	1,316.64	564	574
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	ELEEIVQPIISK	95.00%	3.48	0.483	2.16	0	3	0	2	1,397.79	623	634
1	78 kDa glucose-regulated protein	GRP78_MOUSE	72406	100.00%	21	21	51	33.70%	LYGSGGPPPTGEEDTSEKDEL	95.00%	3.53	0.579	2.18	0	2	0	2	2,177.97	635	655
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	KGTDFQLNQLEGK	95.00%	3.62	0.3	4.05	0	0	2	2	1,477.77	122	134
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	AVSSFFSGSCVPCADPVAFPK	95.00%	2.83	0.568	4.57	0	2	0	2	2,230.03	168	188
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	CLKDGGGDVAFVK	95.00%	2.31	0.191	0	0	0	1	2	1,365.68	213	225
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	DGGGDVAFVK	95.00%	4.01	0.392	5.44	0	2	0	2	964.4742	216	225
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	DQYELLCLDNTR	95.00%	3.18	0.393	2.43	0	1	0	2	1,539.71	240	251
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	KPVDQYEDCYLAR	95.00%	2.83	0.253	0	0	0	2	2	1,656.77	252	264
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	SKDFQLFSSPLGK	95.00%	2.69	0.136	3.89	0	0	1	2	1,453.77	298	310
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	DFQLFSSPLGK	95.00%	3.31	0.495	4.15	0	2	0	2	1,238.64	300	310
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	DSAFGLLR	95.00%	2.75	0.219	2.74	0	2	0	2	878.4737	316	323
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	LYLGHNYVTAIR	95.00%	2.2	0.475	3.47	0	1	2	2	1,419.77	332	343
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	NQQEGVCPEGSIDNSPVK	95.00%	3.44	0.583	9.2	0	2	0	2	1,957.89	344	361
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	GYYAVAVVK	95.00%	3.43	0.525	4.57	0	1	0	2	969.5409	447	455
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	ASDTSITWNNLK	95.00%	2.86	0.416	4.7	0	2	0	2	1,349.67	456	467
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	CLVEKGDVAFVK	95.00%	2.81	0.366	5.15	0	0	1	2	1,364.72	543	554
2	Serotransferrin	TRFE_MOUSE	76706	100.00%	15	16	25	24.70%	NLKQEDFELLCPDGTR	95.00%	2.92	0.207	0	0	0	1	2	1,934.93	573	588
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	WCAVSEHENTK	95.00%	2.06	0.205	0	0	0	1	2	1,360.60	27	37
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	TSYPDCIK	95.00%	1.64	0.402	1.34	0	1	0	2	983.451	62	69
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	KGTDFQLNQLEGK	95.00%	2.42	0.361	0	0	1	1	2	1,477.77	122	134
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	KGTDFQLNQLEGKK	95.00%	2.9	0.419	1.7	0	0	1	2	1,605.86	122	135
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	GTDFQLNQLEGKK	95.00%	2.36	0.203	0	0	0	1	2	1,477.77	123	135
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	SAGWVIPIGLLFCK	95.00%	2.99	0.441	4.66	0	2	0	2	1,560.86	144	157
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	AVSSFFSGSCVPCADPVAFPK	95.00%	4.06	0.615	3.57	0	2	0	2	2,230.03	168	188
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	CLKDGGGDVAFVK	95.00%	4.21	0.426	2.72	0	2	2	2	1,365.68	213	225
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	DGGGDVAFVK	95.00%	4.08	0.412	2.41	1	3	0	2	964.4742	216	225
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	GDVAFVK	95.00%	2.01	0.326	1.7	0	2	0	1	735.4042	219	225
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	HTTIFEVLPEK	95.00%	3.78	0.493	4.92	0	2	0	2	1,313.71	226	236
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	HTTIFEVLPEKADR	95.00%	3.22	0.445	3.74	0	0	2	2	1,655.88	226	239
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	ADRDQYELLCLDNTR	95.00%	3.96	0.272	1.7	0	0	1	2	1,881.88	237	251
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	DQYELLCLDNTR	95.00%	4.85	0.481	3.82	0	1	0	2	1,539.71	240	251
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	KPVDQYEDCYLAR	95.00%	4.23	0.217	1.44	0	1	1	2	1,656.77	252	264
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	IPSHAVVAR	95.00%	1.93	0.438	0	0	1	2	2	949.5583	265	273
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	KNNGKEDLIWEILK	95.00%	2.3	0.236	0	0	0	1	2	1,699.94	274	287
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	NNGKEDLIWEILK	95.00%	3.05	0.164	0	0	1	2	2	1,571.84	275	287
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	VAQEHFGK	95.00%	1.47	0.246	1.54	0	1	0	2	915.4689	288	295
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	SKDFQLFSSPLGK	95.00%	3.79	0.512	6.89	0	2	0	2	1,453.77	298	310
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	DFQLFSSPLGK	95.00%	3.71	0.436	1.96	0	2	0	2	1,238.64	300	310
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	DLLFKDSAFGLLR	95.00%	3.24	0.336	2.6	0	1	2	2	1,494.83	311	323
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	DSAFGLLR	95.00%	2.58	0.221	2.7	0	2	0	2	878.4737	316	323
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	LYLGHNYVTAIR	95.00%	3.28	0.518	2.24	0	3	2	2	1,419.77	332	343
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	NQQEGVCPEGSIDNSPVK	95.00%	3.92	0.536	5.29	0	2	0	2	1,957.89	344	361
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	WCALSHLER	95.00%	2.91	0.39	2.24	0	2	0	2	1,171.57	362	370
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	TKCDEWSIISEGK	95.00%	3.96	0.285	0	0	0	2	2	1,552.73	371	383
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	IECESAETTEDCIEK	95.00%	4.19	0.57	3.08	0	2	0	2	1,813.75	384	398
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	GYYAVAVVK	95.00%	3.22	0.547	4.64	0	2	0	2	969.5409	447	455
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	ASDTSITWNNLK	95.00%	2.85	0.311	1.19	0	2	0	2	1,349.67	456	467
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	CAPNNKEEYNGYTGAFR	95.00%	2.55	0.265	2.12	0	0	1	2	1,990.87	526	542
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	CLVEKGDVAFVK	95.00%	3.56	0.384	1.89	0	0	2	2	1,364.72	543	554
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	HQTVLDNTEGKNPAEWAK	95.00%	4.28	0.618	1.62	0	0	2	2	2,038.00	555	572
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	NLKQEDFELLCPDGTR	95.00%	4.1	0.238	2.31	0	0	2	2	1,934.93	573	588
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	QEDFELLCPDGTR	95.00%	2.22	0.289	1.62	0	1	0	2	1,579.71	576	588
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	DFASCHLAQAPNHVVVSR	95.00%	4.84	0.594	3.51	0	0	2	2	2,007.98	593	610

3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	AVLTSQETLFGGSDCTGNFCLFK	95.00%	1.26	0.17	4.14	0	1	0	2	2,552.18	619	641
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	DLLFRDDTK	95.00%	2.23	0.171	0	0	1	0	2	1,122.58	646	654
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	LPEGTTPEK	95.00%	1.97	0.26	1.34	0	2	0	2	971.5052	659	667
3	Serotransferrin	TRFE_MOUSE	76706	100.00%	40	48	78	57.00%	LLEACTFHKH	95.00%	2.55	0.486	0	0	2	0	2	1,255.63	688	697
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	TVLPPDGPR	95.00%	1.46	0.281	3.25	0	1	0	2	951.5266	47	55
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	TSYPDCIK	95.00%	1.42	0.211	1.92	0	2	0	2	983.451	62	69
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	KGTDFQLNQLEGK	95.00%	2.65	0.388	3	0	2	2	2	1,477.77	122	134
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	KGTDFQLNQLEGKK	95.00%	2.97	0.394	1.03	0	0	2	2	1,605.86	122	135
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	DGGGDVAFVK	95.00%	4.1	0.441	6.12	2	3	0	2	964.4742	216	225
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	GDVAFVK	95.00%	2.37	0.283	2.66	2	1	0	1	735.4042	219	225
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	HTTIFEVLPEK	95.00%	3.12	0.553	4.8	0	3	0	2	1,313.71	226	236
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	ADRDQYELLCLDNTR	95.00%	2.64	0.324	0	0	0	2	2	1,881.88	237	251
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	DQYELLCLDNTR	95.00%	4.71	0.524	2.49	0	2	0	2	1,539.71	240	251
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	KPVDQYEDCYLAR	95.00%	4.06	0.534	1.47	0	1	3	2	1,656.77	252	264
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	IPSHAVVAR	95.00%	1.48	0.515	2.32	0	2	1	2	949.5583	265	273
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	VAQEHFGK	95.00%	1.61	0.39	1.72	0	3	0	2	915.4689	288	295
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	SKDFQLFSSPLGK	95.00%	3.91	0.541	2.28	0	2	2	2	1,453.77	298	310
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	DFQLFSSPLGK	95.00%	3.1	0.498	2.26	0	2	0	2	1,238.64	300	310
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	DSAFGLLR	95.00%	2.84	0.262	2.29	0	4	0	2	878.4737	316	323
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	LYLGHNYVTAIR	95.00%	3.01	0.551	3.74	0	1	4	2	1,419.77	332	343
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	NQQEGVCPEGSIDNSPVK	95.00%	4.59	0.504	4.96	0	3	0	2	1,957.89	344	361
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	TKCDEWSIISEGK	95.00%	3.4	0.543	2.33	0	2	2	2	1,552.73	371	383
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	IECESAETTEDCIEK	95.00%	3.82	0.503	4.01	0	4	0	2	1,813.75	384	398
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	GYYAVAVVK	95.00%	3.28	0.504	4.59	1	3	0	2	969.5409	447	455
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	ASDTSITWNNLK	95.00%	3.07	0.335	0	0	3	0	2	1,349.67	456	467
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	FDEFFSQGCAPGYEK	95.00%	3.58	0.652	5.43	0	2	0	2	1,781.75	498	512
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	CAPNNKEEYNGYTGAFR	95.00%	3.25	0.315	0	0	0	2	2	1,990.87	526	542
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	EEYNGYTGAFR	95.00%	2.4	0.491	2.08	0	2	0	2	1,306.57	532	542
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	CLVEKGDVAFVK	95.00%	3.03	0.388	3.4	0	0	1	2	1,364.72	543	554
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	HQTVLDNTEGK	95.00%	2.94	0.509	2.37	0	2	0	2	1,241.61	555	565
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	HQTVLDNTEGKNPAEWAK	95.00%	3.47	0.568	2.89	0	0	2	2	2,038.00	555	572
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	NPAEWAK	95.00%	1.53	0.335	1.57	0	1	0	2	815.4052	566	572
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	NLKQEDFELLCPDGTR	95.00%	2.18	0.297	0.854	0	0	1	2	1,934.93	573	588
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	QEDFELLCPDGTR	95.00%	3.26	0.396	1.77	0	3	0	2	1,579.71	576	588
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	DFASCHLAQAPNHVVVSR	95.00%	3.76	0.484	3.16	0	0	2	2	2,007.98	593	610
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	DLLFRDDTK	95.00%	2.48	0.335	1.64	0	3	0	2	1,122.58	646	654
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	LPEGTTPEK	95.00%	2.15	0.0879	2.74	0	1	0	2	971.5052	659	667
4	Serotransferrin	TRFE_MOUSE	76706	100.00%	34	43	90	45.90%	LLEACTFHK	95.00%	1.92	0.111	1.57	0	1	0	2	1,118.57	688	696
5	Aconitate hydratase, mitochondrial	ACON_MOUSE	85448	100.00%	6	6	8	7.95%	VAGILTVK	95.00%	1.59	0.245	0	0	1	0	2	800.5247	251	258
5	Aconitate hydratase, mitochondrial	ACON_MOUSE	85448	100.00%	6	6	8	7.95%	SQFTITPGSEQIR	95.00%	1.61	0.282	2.18	0	1	0	2	1,463.75	412	424
5	Aconitate hydratase, mitochondrial	ACON_MOUSE	85448	100.00%	6	6	8	7.95%	DGYAQILR	95.00%	2.36	0.222	2.89	0	3	0	2	935.4952	430	437
5	Aconitate hydratase, mitochondrial	ACON_MOUSE	85448	100.00%	6	6	8	7.95%	NTIVTSYNR	95.00%	2.37	0.41	1.31	0	1	0	2	1,067.55	466	474
5	Aconitate hydratase, mitochondrial	ACON_MOUSE	85448	100.00%	6	6	8	7.95%	VDVSPTSQR	95.00%	1.7	0.201	0.959	0	1	0	2	988.5064	556	564
5	Aconitate hydratase, mitochondrial	ACON_MOUSE	85448	100.00%	6	6	8	7.95%	NAVTQEFGPVPDTAR	95.00%	3.3	0.498	4.47	0	1	0	2	1,601.79	634	648
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	LPFSIR	95.00%	1.64	0.236	0	0	1	0	2	732.4409	35	40
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	NCDEFLVK	95.00%	1.91	0.0385	1.43	0	2	0	2	1,024.48	49	56
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	NIEVPFKPAR	95.00%	1.21	0.187	2.28	0	1	0	2	1,170.66	73	82
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	NQDLEFER	95.00%	2.49	0.141	2.47	0	2	0	2	1,050.49	142	149
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	DFESCLGAK	95.00%	2.49	0.18	0	0	1	0	2	1,026.46	388	396
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	GFQVAPDR	95.00%	1.78	0.253	1.44	0	2	0	2	889.4533	401	408
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	TSLSPGSGVVTYYLR	95.00%	3.87	0.531	5.03	0	2	0	2	1,599.84	469	483
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	IDFEKEPLGVNAQGR	95.00%	3.63	0.515	3.11	0	0	2	2	1,672.87	568	582
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	SWNALAAPSEK	95.00%	2.65	0.366	1.41	0	2	0	2	1,173.59	622	632
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	LYAWNPK	95.00%	1.58	0.202	0	0	2	0	2	891.4729	633	639
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	YQQAGLPLIVLAGK	95.00%	3.87	0.58	5.8	0	2	0	2	1,470.87	759	772
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	AVLAESYER	95.00%	3.16	0.469	3.96	0	2	0	2	1,037.53	794	802
6	Cytoplasmic aconitate hydratase	ACOC_MOUSE	98163	100.00%	13	13	22	14.80%	YTINIPEDLKPR	95.00%	2.11	0.539	2.74	0	0	1	2	1,458.80	835	846
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	IIQVAK	95.00%	1.68	-0.00165	1.46	0	1	0	2	671.4457	109	114
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	EFQEQLESAR	95.00%	3.05	0.0822	3.51	0	1	0	2	1,236.59	219	228
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	IIEEAPAPGINPEVR	95.00%	2.63	0.581	7.09	0	2	0	2	1,604.87	281	295
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	LGEAAVR	95.00%	2.45	0.114	2.41	0	2	0	2	715.4103	298	304
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	LVVWASDR	95.00%	2.57	0.519	3.05	0	2	0	2	945.5158	433	440
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	SNVDFLLR	95.00%	2.76	0.354	3.6	0	2	0	2	963.5264	461	468
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	DLLPSHSTIAK	95.00%	2.35	0.476	2.24	0	2	0	2	1,181.65	491	501
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	RLNISYTR	95.00%	2.12	0.282	0	0	2	2	2	1,022.57	540	547
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	LNISYTR	95.00%	2.29	0.137	1.92	0	2	0	2	866.4736	541	547
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	VLGDLSSEDGCTYLK	95.00%	4.57	0.603	8.04	0	1	0	2	1,656.78	581	595
7	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	MCCA_MOUSE	79327	100.00%	11	12	21	13.80%	VFFSEGAQANR	95.00%	3.69	0.507	4.68	0	2	0	2	1,225.60	693	703
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	GLQDVLR	95.00%	1.96	0.191	2.03	0	2	0	2	800.4632	29	35
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	QADLYISEGLHPR	95.00%	1.87	0.251	0	0	0	1	2	1,498.77	105	117
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	IITEGFEAAK	95.00%	2.84	0.34	3.02	0	2	0	2	1,078.58	118	127
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	ALQFLEQVK	95.00%	2.86	0.408	2.03	0	2	0	2	1,075.62	130	138
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	ETLIDVAR	95.00%	1.72	0.199	2.05	0	1	0	2	916.5105	146	153
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	SETDTSLIR	95.00%	1.95	0.242	1.28	0	1	0	2	1,021.52	200	208
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	TEVNSGFFYK	95.00%	2.79	0.47	3.09	0	1	0	2	1,191.57	242	251
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	GFVVINQK	95.00%	2.38	0.307	2.47	0	1	0	2	904.5257	288	295

8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	GIDPFSLDALAK	95.00%	2.79	0.476	3.54	0	2	0	2	1,246.67	296	307
8	T-complex protein 1 subunit zeta	TCPZ_MOUSE	57988	100.00%	10	10	14	19.20%	VLAQNSGFDLQETLVK	95.00%	4.29	0.633	8.33	0	1	0	2	1,761.94	450	465
9	Protein disulfide-isomerase	PDIA1_MOUSE	57128	100.00%	5	5	8	8.64%	NNFEGEITK	95.00%	2.53	0.0852	3.06	0	3	0	2	1,051.51	216	224
9	Protein disulfide-isomerase	PDIA1_MOUSE	57128	100.00%	5	5	8	8.64%	LLDFIK	95.00%	2.01	0	1.43	0	1	0	2	748.4611	227	232
9	Protein disulfide-isomerase	PDIA1_MOUSE	57128	100.00%	5	5	8	8.64%	YKPESDELTAEK	95.00%	2.48	0.189	4	0	0	1	2	1,409.68	329	340
9	Protein disulfide-isomerase	PDIA1_MOUSE	57128	100.00%	5	5	8	8.64%	QLAPIWDK	95.00%	1.77	0.439	2.64	0	1	0	2	970.5364	404	411
9	Protein disulfide-isomerase	PDIA1_MOUSE	57128	100.00%	5	5	8	8.64%	TVIDYNGER	95.00%	2.58	0.347	3	0	2	0	2	1,066.52	455	463
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	EIVHLQAGQCGNQIGAK	95.00%	3.9	0.347	9.15	0	0	1	2	1,822.92	3	19
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	INVYYNEATGGK	95.00%	3.43	0.39	7.41	0	3	0	2	1,328.65	47	58
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	FPGQLNADLR	95.00%	2.68	0.355	3.72	0	3	0	2	1,130.60	242	251
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	FPGQLNADLRK	95.00%	1.63	0.189	1.32	0	0	1	2	1,258.69	242	252
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	LAVNMVPFPR	95.00%	1.86	0.411	2.77	0	1	0	2	1,159.63	253	262
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	YLTVAAVFR	95.00%	2.49	0.514	4.29	0	1	0	2	1,039.59	310	318
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	NSSYFVEWIPNNVK	95.00%	3.12	0.558	3.57	0	1	0	2	1,696.83	337	350
10	Tubulin beta-2C chain	TBB2C_MOUSE	49813	100.00%	8	8	20	18.40%	TAVCDIPPR	95.00%	2.24	0.282	4.43	0	9	0	2	1,028.52	351	359
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	VYQVSR	95.00%	1.7	0.164	0	0	1	0	2	751.4102	53	58
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	TSGGAGGLGSLR	95.00%	2.65	0.474	2.89	0	2	0	2	1,032.54	59	70
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	TNEKVELQELNDR	95.00%	3.74	0.339	0	0	0	1	2	1,587.80	105	117
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	VELQELNDR	95.00%	3	0.295	1.15	0	2	0	2	1,115.57	109	117
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	FANYIEK	95.00%	1.73	0.244	0	0	1	0	2	884.4518	118	124
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	FLEQQNAALAAEVNR	95.00%	5.79	0.577	7.16	0	2	2	2	1,673.86	127	141
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	VAELYEEEMR	95.00%	3.38	0.366	3.42	0	2	0	2	1,268.58	150	159
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	QVEVLTNQR	95.00%	1.92	0.364	2.96	0	2	0	2	1,086.59	164	172
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	VDVERDNLIDDLQR	95.00%	3.27	0.356	0	0	0	2	2	1,699.86	175	188
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	DNLIDDLQR	95.00%	3.35	0.222	0	0	2	0	2	1,101.55	180	188
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	LQEEIQLR	95.00%	1.93	0.125	0	1	2	0	2	1,028.57	193	200
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	EEAENNLAAFR	95.00%	2.67	0.428	2.06	0	2	0	2	1,263.60	201	211
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	ADVDAATLAR	95.00%	4.02	0.412	2.54	2	2	0	2	1,002.52	212	221
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	IESLNEEIAFLK	95.00%	4.06	0.429	2.92	0	2	0	2	1,405.76	228	239
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	AQYETIAAK	95.00%	2.6	0.443	1.92	0	2	0	2	994.521	278	286
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	NISEAEEWYK	95.00%	1.94	0.289	1.13	0	1	0	2	1,268.58	287	296
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	VSDLTQAANK	95.00%	3.78	0.567	2.07	1	3	0	2	1,046.55	299	308
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	VSDLTQAANKNNDALR	95.00%	2.89	0.346	0	0	0	2	2	1,729.88	299	314
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	NNDALR	95.00%	2.05	0.0628	0	0	2	0	2	702.3535	309	314
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	HQIQSYTCEIDALK	95.00%	4.07	0.537	5.25	0	2	2	2	1,705.82	325	338
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	FASEANGYQDNIAR	95.00%	3.17	0.45	1.19	0	2	0	2	1,555.71	355	368
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	EYQDLLNVK	95.00%	2.36	0.414	1.37	0	2	0	2	1,121.58	386	394
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	KLLEGEESR	95.00%	1.68	0.325	0	0	1	2	2	1,060.56	406	414
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	LLEGEESR	95.00%	2.48	0.342	0	1	2	0	2	932.469	407	414
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	INLPIQTFSALNFR	95.00%	2.78	0.503	6.59	0	1	0	2	1,633.91	415	428
11	Desmin	DESM_MOUSE	53481	100.00%	26	33	58	50.70%	DGEVVSEATQQQHEVL	95.00%	2.8	0.571	1.3	0	2	0	2	1,768.84	454	469
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	TSGGAGGLGSLR	95.00%	2.82	0.473	2.4	0	5	0	2	1,032.54	59	70
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	TNEKVELQELNDR	95.00%	4.38	0.361	2.92	0	1	1	2	1,587.80	105	117
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	VELQELNDR	95.00%	3.1	0.297	0.959	0	4	0	2	1,115.57	109	117
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	FANYIEK	95.00%	2.67	0.277	1.28	1	5	0	2	884.4518	118	124
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	FLEQQNAALAAEVNR	95.00%	5.76	0.573	4.74	0	4	0	2	1,673.86	127	141
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	VAELYEEEMR	95.00%	3.24	0.465	0	0	2	0	2	1,284.58	150	159
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	RQVEVLTNQR	95.00%	3.05	0.401	1.6	0	3	1	2	1,242.69	163	172
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	QVEVLTNQR	95.00%	2.25	0.322	0.824	0	6	0	2	1,086.59	164	172
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	VDVERDNLIDDLQR	95.00%	3.42	0.325	0	0	0	1	2	1,699.86	175	188
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	DNLIDDLQR	95.00%	2.86	0.333	1.07	1	10	0	2	1,101.55	180	188
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	LQEEIQLR	95.00%	3.08	0.0716	0	0	1	0	2	1,028.57	193	200
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	EEAENNLAAFR	95.00%	2.51	0.433	3.11	0	6	0	2	1,263.60	201	211
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	ADVDAATLAR	95.00%	4.1	0.412	1.52	0	7	0	2	1,002.52	212	221
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	RIESLNEEIAFLKK	95.00%	3.4	0.305	0	0	0	2	2	1,689.95	227	240
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	IESLNEEIAFLK	95.00%	3.68	0.48	0	0	2	0	2	1,405.76	228	239
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	VHEEEIR	95.00%	2.34	0.252	1.21	0	3	0	2	911.4587	241	247
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	AQYETIAAK	95.00%	2.68	0.491	2	0	7	0	2	994.521	278	286
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	NISEAEEWYK	95.00%	3.52	0.426	1.77	0	2	0	2	1,268.58	287	296
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	VSDLTQAANK	95.00%	3.88	0.527	1.82	2	6	0	2	1,046.55	299	308
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	VSDLTQAANKNNDALR	95.00%	2.86	0.438	0.854	0	1	2	2	1,729.88	299	314
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	HQIQSYTCEIDALK	95.00%	3.85	0.651	2.85	0	4	2	2	1,705.82	325	338
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	FASEANGYQDNIAR	95.00%	2.54	0.542	1.92	0	2	0	2	1,555.71	355	368
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	EYQDLLNVK	95.00%	2.26	0.295	0	0	3	0	2	1,121.58	386	394
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	KLLEGEESR	95.00%	2.89	0.266	0.62	0	2	4	2	1,060.56	406	414
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	LLEGEESR	95.00%	2.8	0.263	1.16	0	1	0	2	932.469	407	414
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	INLPIQTFSALNFR	95.00%	2.74	0.54	3.55	0	1	0	2	1,633.91	415	428
12	Desmin	DESM_MOUSE	53481	100.00%	27	35	109	51.60%	DGEVVSEATQQQHEVL	95.00%	3.69	0.586	2.62	0	4	0	2	1,768.84	454	469
13	Fibrinogen gamma chain	FIBG_MOUSE	49375	100.00%	3	3	4	6.65%	DNCCILDER	95.00%	3.22	0.349	4.34	0	2	0	2	1,194.49	31	39
13	Fibrinogen gamma chain	FIBG_MOUSE	49375	100.00%	3	3	4	6.65%	TLEDILFR	95.00%	1.83	0.311	2.57	0	1	0	2	1,006.56	67	74
13	Fibrinogen gamma chain	FIBG_MOUSE	49375	100.00%	3	3	4	6.65%	YLQEIYNSNNQK	95.00%	4.12	0.421	4.46	0	1	0	2	1,513.73	134	145
14	Protein disulfide-isomerase A3	PDIA3_MOUSE	56662	100.00%	6	6	11	11.90%	LAPEYEAAATR	95.00%	2.21	0.428	2.96	0	2	0	2	1,191.60	63	73
14	Protein disulfide-isomerase A3	PDIA3_MOUSE	56662	100.00%	6	6	11	11.90%	YGVSGYPTLK	95.00%	2.7	0.509	4.55	0	2	0	2	1,084.57	95	104
14	Protein disulfide-isomerase A3	PDIA3_MOUSE	56662	100.00%	6	6	11	11.90%	QAGPASVPLR	95.00%	1.89	0.456	2.59	0	2	0	2	995.5639	131	140
14	Protein disulfide-isomerase A3	PDIA3_MOUSE	56662	100.00%	6	6	11	11.90%	LNFAVASR	95.00%	2.78	0.36	3.51	0	2	0	2	877.4895	297	304
14	Protein disulfide-isomerase A3	PDIA3_MOUSE	56662	100.00%	6	6	11	11.90%	SEPIPESNEGPVK	95.00%	2.05	0.297	2.57	0	2	0	2	1,382.68	367	379

14	Protein disulfide-isomerase A3	PDIA3_MOUSE	56662	100.00%	6	6	11	11.90%	DPNIVIAK	95.00%	2.79	0.154	3.09	0	1	0	2	869.5098	426	433
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	SILEDLR	95.00%	2.21	0	1.52	0	1	0	2	845.4734	190	196
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	TPCTVSCNIPVVSGK	95.00%	3.46	0.548	3.24	0	2	0	2	1,618.79	215	229
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	TENGGWTVIQNR	95.00%	3.44	0.361	2	0	2	0	2	1,374.68	264	275
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	QDGSVDFGR	95.00%	1.29	0.385	1.8	0	2	0	2	980.4439	276	284
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	GFGNIATNEDAK	95.00%	3.31	0.461	3.8	0	2	0	2	1,236.59	292	303
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	ISQLTR	95.00%	2.2	0.083	1.72	0	2	0	2	717.426	319	324
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	AHYGGFTVQNEASK	95.00%	2.17	0.276	1.18	0	0	2	2	1,508.71	344	357
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	YQVSVNK	95.00%	1.96	0.217	2.96	1	2	0	2	837.447	358	364
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	DNDGWVTTDPR	95.00%	1.95	0.211	5.16	0	1	0	2	1,275.56	401	411
15	Fibrinogen beta chain	FIBB_MOUSE	54736	100.00%	10	11	19	21.00%	IRPFFPQQ	95.00%	2.13	0.306	0	0	2	0	2	1,032.56	474	481
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	LDIDSAPITAR	95.00%	3.36	0.351	3.1	0	2	0	2	1,171.63	33	43
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	NTGIICTIGPASR	95.00%	4.54	0.579	2	0	2	0	2	1,359.71	44	56
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	EATESFASDPILYRPVAVALDTK	95.00%	2.82	0.591	1.82	0	0	3	2	2,493.29	93	115
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	PVAVALDTK	95.00%	2.67	0.611	2.48	0	1	0	1	913.536	107	115
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	TGLIKGSGTAEVELKK	95.00%	2.48	0.363	0	0	0	1	2	1,630.94	121	136
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GSGTAEVELKK	95.00%	2.25	0.327	0	0	1	0	2	1,118.61	126	136
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	CDENILWLDYK	95.00%	4.17	0.591	2.13	0	2	0	2	1,468.68	152	162
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	CDENILWLDYKNICK	95.00%	2.78	0.382	0	0	0	1	2	1,983.93	152	166
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	IYVDDGLISLQVK	95.00%	4.58	0.392	2.49	0	2	0	2	1,462.82	174	186
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	EKGADFLVTEVENGGSLGSK	95.00%	4.4	0.473	2.64	0	0	2	2	2,037.01	187	206
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	EKGADFLVTEVENGGSLGSKK	95.00%	3.27	0.305	0	0	0	1	2	2,165.11	187	207
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GADFLVTEVENGGSLGSK	95.00%	5.05	0.582	3.02	0	2	0	2	1,779.88	189	206
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GADFLVTEVENGGSLGSKK	95.00%	3.19	0.398	1.89	0	0	1	2	1,907.97	189	207
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	KGVNLPGAAVDLPAVSEKDIQDLK	95.00%	2.04	0.449	3.4	0	0	1	2	2,477.36	207	230
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GVNLPGAAVDLPAVSEK	95.00%	3.94	0.645	6.89	0	2	0	2	1,636.89	208	224
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GVNLPGAAVDLPAVSEKDIQDLK	95.00%	2.34	0.418	6.96	0	0	1	2	2,349.27	208	230
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GDLGIEIPAEK	95.00%	3.02	0.568	2.05	1	2	0	2	1,141.61	295	305
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GDLGIEIPAEKVFLAQK	95.00%	2.15	0.458	0	0	0	2	2	1,828.02	295	311
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GDYPLEAVR	95.00%	2.28	0.374	3.92	0	2	0	2	1,019.52	368	376
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	APIIAVTR	95.00%	2.66	0.436	3.01	2	1	0	2	840.5308	448	455
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	GIFPVLCK	95.00%	2.07	0.327	3.49	0	2	0	2	933.5233	468	475
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	DAVLNAWAEDVDLR	95.00%	3.81	0.632	5.08	0	2	0	2	1,586.78	476	489
16	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	23	25	40	37.70%	VNLAMDVGK	95.00%	2.23	0.366	0	0	1	0	2	962.4982	490	498
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	LDIDSAPITAR	95.00%	3.55	0.432	5.34	0	3	0	2	1,171.63	33	43
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	NTGIICTIGPASR	95.00%	3.78	0.601	1.68	0	4	0	2	1,359.71	44	56
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GSGTAEVELKK	95.00%	2.86	0.392	0	0	3	0	2	1,118.61	126	136
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	CDENILWLDYK	95.00%	4.29	0.566	2.62	0	4	0	2	1,468.68	152	162
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	VVEVGSK	95.00%	2.09	0.251	3.01	0	1	0	2	717.4147	167	173
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	EKGADFLVTEVENGGSLGSK	95.00%	3.07	0.334	0	0	0	1	2	2,037.01	187	206
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GADFLVTEVENGGSLGSK	95.00%	4.94	0.588	6.19	0	5	0	2	1,779.88	189	206
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GADFLVTEVENGGSLGSKK	95.00%	2.67	0.406	0	0	0	2	2	1,907.97	189	207
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	KGVNLPGAAVDLPAVSEK	95.00%	3.81	0.44	3.92	0	0	2	2	1,764.99	207	224
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GVNLPGAAVDLPAVSEK	95.00%	3.87	0.717	5.09	0	4	0	2	1,636.89	208	224
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GVNLPGAAVDLPAVSEKDIQDLK	95.00%	2.4	0.439	3.07	0	0	1	2	2,349.27	208	230
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	KAADVHEVR	95.00%	1.93	0.405	1.27	0	0	1	2	1,024.55	247	255
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	AADVHEVR	95.00%	1.69	0.437	1.8	0	2	0	2	896.459	248	255
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	IENHEGVR	95.00%	2.79	0.208	2.43	0	2	1	2	953.4805	271	278
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GDLGIEIPAEK	95.00%	3.28	0.484	1.66	0	4	0	2	1,141.61	295	305
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GDYPLEAVR	95.00%	2.55	0.375	2	0	4	0	2	1,019.52	368	376
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	APIIAVTR	95.00%	2.77	0.42	4.21	2	4	0	2	840.5308	448	455
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	GIFPVLCK	95.00%	2.4	0.366	3.44	0	3	0	2	933.5233	468	475
17	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	19	21	55	29.90%	VNLAMDVGK	95.00%	2.36	0.266	4.17	0	2	0	2	962.4982	490	498
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	LDIDSAPITAR	95.00%	2.88	0.425	3.51	0	2	0	2	1,171.63	33	43
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	NTGIICTIGPASR	95.00%	3.45	0.599	5.48	0	2	0	2	1,359.71	44	56
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	CDENILWLDYK	95.00%	2.58	0.541	4.74	0	1	0	2	1,468.68	152	162
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	GADFLVTEVENGGSLGSK	95.00%	3.85	0.437	4	0	2	0	2	1,779.88	189	206
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	GVNLPGAAVDLPAVSEK	95.00%	3.18	0.567	5.32	0	1	0	2	1,636.89	208	224
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	GDLGIEIPAEK	95.00%	2.97	0.51	0	0	1	0	2	1,141.61	295	305
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	GDYPLEAVR	95.00%	2.21	0.347	0	0	2	0	2	1,019.52	368	376
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	APIIAVTR	95.00%	2.05	0.34	3.06	0	2	0	2	840.5308	448	455
18	Pyruvate kinase isozymes M1/M2	KPYM_MOUSE	57828	100.00%	9	9	14	20.00%	GIFPVLCK	95.00%	1.69	0.341	0	0	1	0	2	933.5233	468	475
19	Cytosol aminopeptidase	AMPL_MOUSE	56125	100.00%	5	5	9	13.30%	DKDDDLPQFTSAGESFNK	95.00%	2.68	0.458	1.51	0	0	1	2	2,013.90	44	61
19	Cytosol aminopeptidase	AMPL_MOUSE	56125	100.00%	5	5	9	13.30%	GVLFASGQNLAR	95.00%	3.64	0.325	1.92	0	3	0	2	1,232.68	189	200
19	Cytosol aminopeptidase	AMPL_MOUSE	56125	100.00%	5	5	9	13.30%	TIQVDNTDAEGR	95.00%	1.87	0.231	0	0	1	0	2	1,318.62	357	368
19	Cytosol aminopeptidase	AMPL_MOUSE	56125	100.00%	5	5	9	13.30%	QVIDCQLADVNNLGK	95.00%	2.83	0.511	2.1	0	1	0	2	1,686.85	441	455
19	Cytosol aminopeptidase	AMPL_MOUSE	56125	100.00%	5	5	9	13.30%	SAGACTAAAFLR	95.00%	2.94	0.52	4.28	0	3	0	2	1,195.59	458	469
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	FYTDPVEAVK	95.00%	1.86	0.424	2.6	0	4	0	2	1,168.59	42	51
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	MISSYVGENAEFER	95.00%	1.63	0.203	0	0	1	0	2	1,631.74	111	124
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	AGGAGVPAFYTSTGYGTLVQEGGSPIK	95.00%	4.14	0.721	7.35	0	1	0	2	2,585.29	147	173
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	DGSVAIASKPR	95.00%	2.07	0.36	0	0	1	0	2	1,100.61	177	187
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	AGNVIFR	95.00%	2.34	0.166	2.77	0	3	0	2	776.4419	218	224
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	DEADADLINAGK	95.00%	3.49	0.383	2.96	0	3	0	2	1,231.58	357	368
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	CTLPLTGK	95.00%	2.55	0.38	4.35	0	3	0	2	889.482	456	463
19	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	SCOT1_MOUSE	55972	100.00%	8	8	18	18.70%	GVFDVDKK	95.00%	2.79	0.247	3.66	0	2	0	2	907.4891	474	481
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	GASIVEDK	95.00%	1.56	0.302	0	0	1	0	2	818.4261	77	84

20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	GASIVEDKLVEDLK	95.00%	2.79	0.338	2.39	0	1	0	2	1,515.83	77	90
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	LVEDLK	95.00%	1.85	0.108	0	0	1	0	2	716.4196	85	90
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	DDGSWEVIEGYR	95.00%	4.03	0.615	2.38	0	2	0	2	1,425.63	125	136
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	YSTDVSVDEVK	95.00%	2.48	0.468	1.89	1	2	0	2	1,241.59	152	162
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	CAVVDVPFGGAK	95.00%	3.07	0.493	2.64	0	3	0	2	1,219.61	172	183
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	PISQGGIHGR	95.00%	2.91	0.488	1.01	0	0	1	1	1,021.55	259	268
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	ELEDFK	95.00%	1.74	0.152	1.43	1	0	0	2	780.3781	347	352
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	LQHGSILGFPK	95.00%	2.26	0.218	1.51	0	0	1	2	1,196.68	353	363
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	IIAEGANGPTTPEADKIFLER	95.00%	2.36	0.38	0	0	1	1	2	2,242.17	400	420
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	NLNHVSYGR	95.00%	2.82	0.463	0	0	2	0	2	1,059.53	445	453
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	HGGTIPVVPTAEFQDR	95.00%	2.03	0.118	1.66	0	0	1	2	1,723.88	481	496
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	YNLGLDLR	95.00%	3.07	0.4	1.46	0	2	0	2	963.5265	528	535
20	Glutamate dehydrogenase 1, mitochondrial	DHE3_MOUSE	61320	100.00%	14	16	23	25.10%	TAAYVNAIEK	95.00%	2.75	0.393	1.12	0	2	0	2	1,079.57	536	545
21	Beta-enolase	ENOB_MOUSE	47008	100.00%	7	7	16	14.50%	TLGPALLEK	95.00%	2.46	0.4	3.05	0	3	0	2	941.5674	72	80
21	Beta-enolase	ENOB_MOUSE	47008	100.00%	7	7	16	14.50%	TAIQAAGYPDK	95.00%	3.27	0.511	2.96	0	2	0	2	1,134.58	229	239
21	Beta-enolase	ENOB_MOUSE	47008	100.00%	7	7	16	14.50%	YDLDFK	95.00%	2.29	0.238	2.3	0	1	0	2	800.3832	257	262
21	Beta-enolase	ENOB_MOUSE	47008	100.00%	7	7	16	14.50%	LGELYK	95.00%	1.6	0.134	1.64	0	3	0	2	722.409	276	281
21	Beta-enolase	ENOB_MOUSE	47008	100.00%	7	7	16	14.50%	ACNCLLLK	95.00%	2.62	0.407	2.77	0	2	0	2	991.507	336	343
21	Beta-enolase	ENOB_MOUSE	47008	100.00%	7	7	16	14.50%	VNQIGSVTESIQACK	95.00%	1.88	0.342	2.01	0	1	0	2	1,633.82	344	358
21	Beta-enolase	ENOB_MOUSE	47008	100.00%	7	7	16	14.50%	IEEALGDK	95.00%	1.98	0.257	2.52	0	4	0	2	874.4524	413	420
22	Adenosine kinase	ADK_MOUSE	40132	99.80%	2	2	3	3.88%	FGEILK	95.00%	1.8	0.276	0	0	1	0	2	706.4141	111	116
22	Adenosine kinase	ADK_MOUSE	40132	99.80%	2	2	3	3.88%	TVIFTQGR	95.00%	2.02	0.1	1.09	0	2	0	2	921.5159	277	284
23	Ornithine aminotransferase, mitochondrial	OAT_MOUSE	48338	99.80%	2	2	3	4.78%	IADEIQTGLAR	95.00%	0	0	5.26	0	2	0	1	1,186.64	261	271
23	Ornithine aminotransferase, mitochondrial	OAT_MOUSE	48338	99.80%	2	2	3	4.78%	LPSDVVTSVR	95.00%	2.8	0.295	3.44	0	1	0	2	1,072.60	363	372
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	LEEGPPVTTVLTR	95.00%	3.29	0.513	1.92	0	7	0	2	1,411.78	46	58
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	ADQLYK	95.00%	2.16	0.205	0	0	2	0	2	737.3835	78	83
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	AHGFTFTR	95.00%	1.94	0.39	2.8	0	2	0	2	936.4692	120	127
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	AILAELTGR	95.00%	3.32	0.383	2.6	0	6	0	2	943.5578	133	141
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	GAGIALACK	95.00%	0	0	2.35	0	1	0	1	860.4666	174	182
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	LPCIFICENNR	95.00%	2.73	0.429	1.41	0	2	0	2	1,435.68	216	226
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	AAASTDYYK	95.00%	2.36	0.435	1.92	0	2	0	2	989.458	236	244
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	GDFIPGLR	95.00%	1.82	0.394	1.36	1	2	0	2	874.4789	246	253
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	VDGMDILCVR	95.00%	3.65	0.413	2.66	0	2	0	2	1,193.57	254	263
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	EATKFAAAYCR	95.00%	1.7	0.29	0	0	0	1	2	1,287.62	264	274
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	FAAAYCR	95.00%	2.39	0.283	1.49	0	6	0	2	858.3932	268	274
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	TREEIQEVR	95.00%	2.86	0.252	0	0	2	1	2	1,159.61	303	311
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	EEIQEVR	95.00%	1.73	0.162	0	0	1	0	2	902.4584	305	311
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	EIDVEVR	95.00%	1.96	0.167	0	0	2	0	2	859.4526	337	343
24	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	ODPA_MOUSE	43215	100.00%	15	17	41	30.00%	GANQWIK	95.00%	2.7	0.0475	0	0	1	0	2	816.4369	379	385
25	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	99.80%	2	2	3	5.12%	QGLLGINIAEK	95.00%	1.9	0.401	2.03	0	1	0	2	1,155.67	96	106
25	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	99.80%	2	2	3	5.12%	SGSDWILNGSK	95.00%	2.77	0.392	0	0	2	0	2	1,163.57	191	201
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	LNYKPQEEYPDLSK	95.00%	3.13	0.456	0	0	1	1	2	1,723.85	12	25
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	VLTPDLYNKLR	95.00%	2.12	0.293	2.66	0	0	2	2	1,331.77	33	43
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	DLFDPIIQDR	95.00%	3.4	0.467	3.64	0	2	0	2	1,231.63	87	96
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	TDLNHENLKGGDDLDPNYVLSSR	95.00%	4.08	0.486	2.31	0	0	1	2	2,572.23	108	130
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	GGDDLDPNYVLSSR	95.00%	3.51	0.551	5.21	0	2	0	2	1,507.70	117	130
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	GYTLPPHCSR	95.00%	2.14	0.413	3.2	0	4	0	2	1,187.56	139	148
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	AVEKLSVEALNSLTGEFK	95.00%	3.41	0.417	1.66	0	0	1	2	1,935.04	153	170
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	LSVEALNSLTGEFK	95.00%	4.68	0.568	6.14	0	2	0	2	1,507.80	157	170
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	LSVEALNSLTGEFKGK	95.00%	3.59	0.428	1.28	0	2	2	2	1,692.92	157	172
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	YYPLK	95.00%	1.35	0.255	0	1	2	0	2	683.3769	173	177
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	DWPDAR	95.00%	1.44	0.159	0	1	0	0	2	759.3427	210	215
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	SFLVWVNEEDHLR	95.00%	3	0.417	1.29	0	1	2	2	1,643.82	224	236
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	RFCVGLQK	95.00%	2.35	0.413	0	0	0	2	2	1,007.55	252	259
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	FCVGLQK	95.00%	1.78	0.268	1.68	1	2	0	2	851.445	253	259
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	LANLSK	95.00%	1.72	0.151	0	0	1	0	2	645.3936	299	304
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	HPKFEEILTR	95.00%	1.96	0.201	0	0	0	1	2	1,269.70	305	314
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	FEEILTR	95.00%	2.7	0.243	0	0	2	0	2	907.489	308	314
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	RGTGGVDTAAVGAVFDISNADR	95.00%	3.51	0.423	4.12	0	0	1	2	2,149.06	320	341
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	GTGGVDTAAVGAVFDISNADR	95.00%	4.29	0.659	6.2	0	2	0	2	1,992.96	321	341
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	LGSSEVEQVQLVVDGVK	95.00%	4.66	0.437	3.34	0	2	0	2	1,785.96	342	358
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	LGSSEVEQVQLVVDGVKLMVEMEK	95.00%	2.17	0.166	0	0	0	1	2	2,678.36	342	365
26	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	22	27	44	50.90%	GQSIDDMIPAQK	95.00%	3.07	0.426	1.96	0	2	0	2	1,318.63	370	381
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	RIFSSEHDIFR	95.00%	2.87	0.358	1.26	0	0	1	2	1,406.72	51	61
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	IFSSEHDIFR	95.00%	2.98	0.414	1.64	0	2	0	2	1,250.62	52	61
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	FFQEEVIPHHTEWEK	95.00%	2.9	0.458	0	0	0	2	2	1,955.93	67	81
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	AGEVSREVWEK	95.00%	2.91	0.357	0	0	1	2	2	1,289.65	82	92
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	AGKQGLLGINIAEK	95.00%	2.44	0.378	1.21	0	0	1	2	1,411.83	93	106
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	QGLLGINIAEK	95.00%	3.03	0.451	2.8	0	1	0	2	1,155.67	96	106
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	CIGAIAMTEPGAGSDLQGVR	95.00%	4.57	0.549	7.48	0	2	0	2	2,002.97	166	185
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	RSGSDWILNGSK	95.00%	3.18	0.459	1.77	0	2	1	2	1,319.67	190	201
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	SGSDWILNGSK	95.00%	3.88	0.435	2.51	1	2	0	2	1,163.57	191	201
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	SPAHGISLFLVENGMK	95.00%	3.32	0.313	0	0	0	2	2	1,699.88	225	240
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	AQDTAELFFEDVR	95.00%	4.76	0.509	5.37	0	2	0	2	1,540.73	255	267
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	LPANALLGEENK	95.00%	3.97	0.472	5.29	0	1	0	2	1,268.69	268	279
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	GFYYLMQELPQER	95.00%	2.3	0.327	1.3	0	1	0	2	1,673.80	280	292

26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	THICVTR	95.00%	1.75	0.293	1.28	0	1	0	2	886.4569	339	345
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	AFVDSCLQLHETK	95.00%	3.85	0.604	2.34	0	2	1	2	1,547.75	346	358
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	AFVDSCLQLHETKR	95.00%	2.55	0.46	2.49	0	0	2	2	1,703.85	346	359
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	VQPIYGGTNEIMK	95.00%	2.06	0.401	1.96	0	1	0	2	1,449.74	407	419
26	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL_MOUSE	47891	100.00%	18	23	33	40.90%	VQPIYGGTNEIMKELIAR	95.00%	1.64	0.468	3.05	0	1	1	2	2,032.09	407	424
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	FKLNYKPQEEYPDLSK	95.00%	3.37	0.341	0	0	0	2	2	1,999.02	10	25
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	LNYKPQEEYPDLSK	95.00%	4.23	0.429	2	0	3	3	2	1,723.85	12	25
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	VLTPDLYNK	95.00%	2.09	0.411	1.42	1	8	0	2	1,062.58	33	41
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	DLFDPIIQDR	95.00%	3.29	0.457	2.41	1	8	0	2	1,231.63	87	96
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	HGGYKPTDK	95.00%	3	0.551	1.32	0	2	0	2	1,002.50	97	105
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	TDLNHENLK	95.00%	2.47	0.347	0	0	3	0	2	1,083.54	108	116
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	TDLNHENLKGGDDLDPNYVLSSR	95.00%	3.91	0.433	3.85	0	0	2	2	2,572.23	108	130
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	GGDDLDPNYVLSSR	95.00%	4.05	0.568	6.62	0	5	0	2	1,507.70	117	130
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	GYTLPPHCSR	95.00%	2.61	0.515	2.13	0	10	6	2	1,187.56	139	148
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	LSVEALNSLTGEFK	95.00%	4.59	0.577	7.21	2	8	0	2	1,507.80	157	170
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	LSVEALNSLTGEFKGK	95.00%	2.61	0.418	0	0	1	5	2	1,692.92	157	172
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	YYPLK	95.00%	1.85	0.194	1.02	3	3	0	2	683.3769	173	177
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	SFLVWVNEEDHLR	95.00%	2.4	0.484	0	0	2	5	2	1,643.82	224	236
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	RFCVGLQK	95.00%	2.83	0.396	0	0	0	2	2	1,007.55	252	259
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	FCVGLQK	95.00%	2.45	0.283	0	4	4	0	2	851.445	253	259
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	VLTCPSNLGTGLR	95.00%	0	0	2.8	0	1	0	1	1,387.74	280	292
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	LANLSK	95.00%	1.8	0.131	0	2	2	0	2	645.3936	299	304
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	HPKFEEILTR	95.00%	2.48	0.332	0	0	0	3	2	1,269.70	305	314
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	FEEILTR	95.00%	2.25	0.194	0	2	10	0	2	907.489	308	314
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	RGTGGVDTAAVGAVFDISNADR	95.00%	4.52	0.528	4.72	0	0	4	2	2,149.06	320	341
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	GTGGVDTAAVGAVFDISNADR	95.00%	4.96	0.667	5.18	0	5	0	2	1,992.96	321	341
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	LGSSEVEQVQLVVDGVK	95.00%	3.96	0.538	2.8	0	4	0	2	1,785.96	342	358
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	LGSSEVEQVQLVVDGVKLMVEMEK	95.00%	2.43	0.468	0	0	0	1	2	2,678.36	342	365
27	Creatine kinase M-type	KCRM_MOUSE	43028	100.00%	24	35	133	54.10%	GQSIDDMIPAQK	95.00%	2.49	0.482	2.33	0	6	0	2	1,318.63	370	381
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	KELSDIAHR	95.00%	2.8	0.312	1.21	0	0	2	2	1,068.58	14	22
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	ELSDIAHR	95.00%	1.98	0.335	1.42	0	3	0	2	940.4853	15	22
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	GILAADESTGSIAK	95.00%	4.88	0.623	5.28	2	7	0	2	1,332.70	29	42
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	GILAADESTGSIAKR	95.00%	2.9	0.463	0	0	4	0	2	1,488.80	29	43
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	RLQSIGTENTEENRR	95.00%	2.51	0.338	0	0	0	1	2	1,802.91	43	57
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	LQSIGTENTEENR	95.00%	2.68	0.456	0	0	1	0	2	1,490.71	44	56
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	QLLLTADDR	95.00%	2.49	0.501	2.35	0	3	0	2	1,044.57	61	69
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	ADDGRPFPQVIK	95.00%	3.29	0.387	1.66	0	1	3	2	1,342.71	88	99
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	GGVVGIKVDK	95.00%	2.13	0.413	2.21	0	3	1	2	971.5892	102	111
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	VDKGVVPLAGTNGETTTQGLDGLSER	95.00%	4.17	0.589	4.09	0	0	2	2	2,614.33	109	134
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	GVVPLAGTNGETTTQGLDGLSER	95.00%	5.73	0.721	6.96	0	6	0	2	2,272.14	112	134
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	DGADFAK	95.00%	1.89	0.351	0	2	4	0	2	723.3315	141	147
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	YASICQQNGIVPIVEPEILPDGDHDLK	95.00%	4.02	0.429	3.62	0	0	1	2	3,020.50	174	200
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	YASICQQNGIVPIVEPEILPDGDHDLKR	95.00%	5.04	0.626	3.06	0	0	1	2	3,176.61	174	201
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	CQYVTEK	95.00%	2.54	0.342	0	0	3	0	2	927.4246	202	208
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	VLAAVYK	95.00%	2.02	0.32	0	5	3	0	2	763.4718	209	215
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	ALQASALK	95.00%	2.19	0.207	0	1	6	0	2	801.4835	305	312
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	AAQEEYIK	95.00%	2.52	0.356	1.14	0	2	0	2	951.4788	323	330
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	AAQEEYIKR	95.00%	2.16	0.353	0	0	3	2	2	1,107.58	323	331
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	RALANSLACQGK	95.00%	1.56	0.344	0	0	0	1	2	1,288.68	331	342
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	ALANSLACQGK	95.00%	3.49	0.546	3.8	2	9	0	2	1,132.58	332	342
28	Fructose-bisphosphate aldolase A	ALDOA_MOUSE	39339	100.00%	22	30	85	52.50%	YTPSGQSGAAASESLFISNHAY	95.00%	4.26	0.654	3.74	0	1	0	2	2,258.04	343	364
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	SPPGQVTEAVK	95.00%	2.94	0.475	2.57	0	5	0	2	1,112.60	23	33
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	VAIDLGYR	95.00%	2.47	0.319	2.7	0	4	0	2	906.505	34	41
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	HIDCAQVYQNEK	95.00%	3.24	0.612	3.28	0	1	3	2	1,504.69	42	53
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	EVGVALQEK	95.00%	2.41	0.294	0	0	4	0	2	972.5367	54	62
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	QDLFIVSK	95.00%	1.69	0.162	1.72	0	1	0	2	949.536	71	78
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	LWCTFHDK	95.00%	2.73	0.449	0	0	1	0	2	1,106.51	79	86
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	TIGVSNFNPLQIER	95.00%	3.48	0.484	2.02	0	1	0	2	1,587.85	156	169
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	ILNKPGLK	95.00%	2.07	0.217	0	0	1	0	2	882.5779	170	177
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	LIEYCHSK	95.00%	1.94	0.247	0	0	1	0	2	1,049.51	196	203
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	PEDPSLLEDPR	95.00%	3.18	0.566	1.85	0	1	0	1	1,267.62	223	233
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	TTAQVLIR	95.00%	2.79	0.322	2.43	0	5	0	2	901.5472	244	251
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	NLVVIPK	95.00%	1.9	0.0407	1.8	1	0	0	2	782.5141	257	263
29	Aldose reductase	ALDR_MOUSE	35715	100.00%	13	14	30	38.60%	HKDYPFHAEV	95.00%	1.78	0.315	0	0	0	1	2	1,242.59	307	316
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	LVINGKPITIFQER	95.00%	3.74	0.502	2.36	0	2	2	2	1,627.95	65	78
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	IVSNASCTTNCLAPLAK	95.00%	3.71	0.603	4.66	0	2	0	2	1,819.90	144	160
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	DGRGAAQNIIPASTGAAK	95.00%	2.68	0.163	0	0	0	1	2	1,697.89	196	213
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	GAAQNIIPASTGAAK	95.00%	2.79	0.403	1.17	0	2	0	2	1,369.74	199	213
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	VIPELNGK	95.00%	1.98	0.215	2.85	1	0	0	2	869.5098	218	225
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	VPTPNVSVVDLTCR	95.00%	3.93	0.631	9.74	0	1	0	2	1,556.81	233	246
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	LISWYDNEYGYSNR	95.00%	4.31	0.481	2.29	0	2	0	2	1,779.80	308	321
30	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	8	9	15	29.10%	VVDLMAYMASKE	95.00%	2.73	0.514	3.72	0	2	0	2	1,356.65	322	333
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	VFVTGPLPAEGR	95.00%	3.69	0.532	3.38	0	2	0	2	1,242.68	9	20
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	KDLEQGVVGAHGLLCR	95.00%	4.75	0.521	4.07	0	0	1	2	1,751.92	43	58
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	DLEQGVVGAHGLLCR	95.00%	2.46	0.293	0	0	0	1	2	1,623.83	44	58
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	KLLDAAGANLR	95.00%	2.4	0.311	0	0	0	1	2	1,141.67	66	76

30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	LLDAAGANLR	95.00%	3.05	0.31	2.05	0	2	0	2	1,013.57	67	76
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	RLPEAIEEVK	95.00%	3.37	0.362	1.55	0	2	1	2	1,183.67	125	134
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	LPEAIEEVK	95.00%	3.13	0.35	1.24	0	2	0	2	1,027.57	126	134
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	LKPFGVQR	95.00%	1.98	0.125	2.32	0	0	1	2	944.5683	172	179
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	FLYTGR	95.00%	1.7	0.295	0	1	0	0	2	756.4045	180	185
30	Glyoxylate reductase/hydroxypyruvate reductase	GRHPR_MOUSE	35312	100.00%	10	12	18	23.50%	NCVILPHIGSATYK	95.00%	2.83	0.276	3.37	0	2	2	2	1,572.82	287	300
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	VGVNGFGR	95.00%	1.53	0.105	1.77	2	0	0	2	805.4321	4	11
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	AAICSGK	95.00%	1.18	0.492	0	0	2	0	2	706.3559	19	25
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	LVINGKPITIFQER	95.00%	2.55	0.458	0.921	0	0	4	2	1,627.95	65	78
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	PITIFQER	95.00%	2.24	0.261	2.49	0	4	0	1	1,003.56	71	78
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	IVSNASCTTNCLAPLAK	95.00%	3.76	0.609	2.85	0	2	0	2	1,819.90	144	160
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	GAAQNIIPASTGAAK	95.00%	3.11	0.426	4.16	2	3	0	2	1,369.74	199	213
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	LTGMAFRVPTPNVSVVDLTCR	95.00%	2.57	0.363	0.77	0	0	1	2	2,333.21	226	246
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	VPTPNVSVVDLTCR	95.00%	3.61	0.611	3.92	0	6	0	2	1,556.81	233	246
31	Glyceraldehyde-3-phosphate dehydrogenase	G3P_MOUSE	35792	100.00%	9	10	28	28.80%	LISWYDNEYGYSNR	95.00%	4.13	0.589	4.72	0	2	0	2	1,779.80	308	321
32	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	6	6	8	15.10%	LVIITAGAR	95.00%	3.36	0.35	4.92	0	2	0	2	913.5836	91	99
32	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	6	6	8	15.10%	LNLVQR	95.00%	1.69	0.00217	1.55	0	1	0	2	742.4576	107	112
32	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	6	6	8	15.10%	NVNIFK	95.00%	2.03	0.107	1.96	0	2	0	2	734.4201	113	118
32	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	6	6	8	15.10%	FIIPNIVK	95.00%	1.9	0	1.57	0	1	0	2	943.5982	119	126
32	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	6	6	8	15.10%	QVVDSAYEVIK	95.00%	2.27	0.476	2.96	0	1	0	2	1,250.66	233	243
32	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	6	6	8	15.10%	VTLTPEEEAR	95.00%	1.8	0.135	0	0	1	0	2	1,144.59	306	315
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	DQLIVNLLK	95.00%	2.76	0.311	0	0	2	0	2	1,055.65	6	14
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	DYCVTANSK	95.00%	2.97	0.546	2.26	0	2	0	2	1,057.46	82	90
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	LVIITAGAR	95.00%	2.75	0.378	0	0	2	0	2	913.5836	91	99
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	LNLVQR	95.00%	2.36	0.0923	0	0	3	0	2	742.4576	107	112
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	NVNIFK	95.00%	2.18	0.161	0	2	1	0	2	734.4201	113	118
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	ISGFPK	95.00%	1.34	0.245	0	1	0	0	2	648.3722	150	155
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	VIGSGCNLDSAR	95.00%	3.06	0.538	4.57	0	2	0	2	1,248.60	158	169
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	SLNPELGTDADK	95.00%	2.46	0.433	1.4	0	1	0	2	1,259.61	213	224
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	QVVDSAYEVIK	95.00%	2.57	0.507	2.16	0	3	0	2	1,250.66	233	243
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	VTLTPEEEAR	95.00%	1.78	0.366	1.96	1	1	0	2	1,144.59	306	315
33	L-lactate dehydrogenase A chain	LDHA_MOUSE	36481	100.00%	11	13	23	30.10%	SADTLWGIQK	95.00%	3.04	0.397	3.43	0	2	0	2	1,118.58	319	328
34	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1_MOUSE	36101	100.00%	4	4	11	10.10%	ELVECFQK	95.00%	2.22	0.362	0	0	4	0	2	1,052.51	87	94
34	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1_MOUSE	36101	100.00%	4	4	11	10.10%	AVVVSGAGK	95.00%	2.4	0.372	4.22	0	3	0	2	787.4678	103	111
34	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1_MOUSE	36101	100.00%	4	4	11	10.10%	SPVAVQGSK	95.00%	2.42	0.414	3.03	0	1	0	2	872.4842	267	275
34	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1_MOUSE	36101	100.00%	4	4	11	10.10%	INLIYSR	95.00%	2.59	0.225	1.92	0	3	0	2	878.51	276	282
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	KGIEESLK	95.00%	2.8	0.225	0	0	2	0	2	903.5153	68	75
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	KGIEESLKR	95.00%	2.5	0.198	1.2	0	0	2	2	1,059.62	68	76
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	GIEESLKR	95.00%	1.99	0.174	1.89	0	2	0	2	931.5214	69	76
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	AGDEFVEK	95.00%	3.36	0.291	4.24	1	5	0	2	894.421	88	95
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	LKNELFQR	95.00%	2.88	0.283	2.1	0	2	0	2	1,047.60	126	133
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	NELFQR	95.00%	2.53	0.043	2.07	0	2	0	2	806.4161	128	133
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	LVEVIK	95.00%	2.01	0.195	1.2	0	2	0	2	700.461	180	185
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	TFESLVDFCK	95.00%	3.34	0.522	3.85	1	4	0	2	1,245.58	193	202
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	DTPGFIVNR	95.00%	2.6	0.389	1.1	0	3	0	2	1,018.53	213	221
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	LLVPYLIEAVR	95.00%	2.86	0.371	4.1	0	4	0	2	1,285.79	222	232
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	KTGEGFYK	95.00%	2.47	0.103	3.36	0	0	1	2	929.4734	305	312
35	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	HCDH_MOUSE	34447	100.00%	12	14	32	22.00%	TGEGFYK	95.00%	1.78	0.327	2.4	0	1	0	2	801.3784	306	312
36	ATP synthase subunit gamma, mitochondrial	ATPG_MOUSE	32869	100.00%	5	5	8	15.10%	HLIIGVSSDR	95.00%	2.78	0.307	1.72	0	2	0	2	1,096.61	91	100
36	ATP synthase subunit gamma, mitochondrial	ATPG_MOUSE	32869	100.00%	5	5	8	15.10%	QMKNEVAALTAAGK	95.00%	1.68	0.185	0	0	0	1	2	1,431.76	113	126
36	ATP synthase subunit gamma, mitochondrial	ATPG_MOUSE	32869	100.00%	5	5	8	15.10%	NEVAALTAAGK	95.00%	2.98	0.305	3.14	0	2	0	2	1,044.57	116	126
36	ATP synthase subunit gamma, mitochondrial	ATPG_MOUSE	32869	100.00%	5	5	8	15.10%	EVMIVGVGEK	95.00%	2.69	0.391	2.38	0	2	0	2	1,060.57	127	136
36	ATP synthase subunit gamma, mitochondrial	ATPG_MOUSE	32869	100.00%	5	5	8	15.10%	THSDQFLVSFK	95.00%	3.19	0.597	0.854	0	1	0	2	1,308.66	144	154
37	Troponin I, cardiac muscle	TNNI3_MOUSE	24242	99.90%	2	2	5	9.48%	AYATEPHAK	95.00%	2.11	0.326	2.37	0	2	0	2	987.49	29	37
37	Troponin I, cardiac muscle	TNNI3_MOUSE	24242	99.90%	2	2	5	9.48%	NITEIADLTQK	95.00%	3.55	0.504	6.24	0	3	0	2	1,245.67	122	132
38	Apolipoprotein A-I	APOA1_MOUSE	30569	100.00%	6	6	8	19.70%	LGPLTR	95.00%	1.47	0.272	0	0	1	0	2	656.4097	87	92
38	Apolipoprotein A-I	APOA1_MOUSE	30569	100.00%	6	6	8	19.70%	VQPYLDEFQK	95.00%	2.05	0.359	3.89	0	1	0	2	1,266.64	120	129
38	Apolipoprotein A-I	APOA1_MOUSE	30569	100.00%	6	6	8	19.70%	EDVELYR	95.00%	2.06	0.237	1.8	0	2	0	2	923.4475	133	139
38	Apolipoprotein A-I	APOA1_MOUSE	30569	100.00%	6	6	8	19.70%	VAPLGAELQESAR	95.00%	2.8	0.591	6.49	0	1	0	2	1,340.72	142	154
38	Apolipoprotein A-I	APOA1_MOUSE	30569	100.00%	6	6	8	19.70%	LSPVAEEFR	95.00%	1.79	0.43	3.1	0	2	0	2	1,047.55	164	172
38	Apolipoprotein A-I	APOA1_MOUSE	30569	100.00%	6	6	8	19.70%	PALEDLR	95.00%	1.64	0.351	1.96	0	1	0	1	813.4472	230	236
39	Heat shock protein beta-1	HSPB1_MOUSE	22996	99.80%	2	2	4	9.09%	LFDQAFGVPR	95.00%	3.13	0.406	4.55	0	2	0	2	1,149.61	29	38
39	Heat shock protein beta-1	HSPB1_MOUSE	22996	99.80%	2	2	4	9.09%	EGVVEITGK	95.00%	2.3	0.446	2.92	0	2	0	2	931.5102	119	127
40	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	5	5	12	20.50%	FFVGGNWK	95.00%	2.12	0.368	1.68	0	2	0	2	954.4838	7	14
40	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	5	5	12	20.50%	IAVAAQNCYK	95.00%	2.93	0.403	2.28	0	3	0	2	1,137.57	60	69
40	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	5	5	12	20.50%	HVFGESDELIGQK	95.00%	3.22	0.227	2.55	0	0	1	2	1,458.72	101	113
40	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	5	5	12	20.50%	VVFEQTK	95.00%	1.75	0.406	2.44	0	2	0	2	850.4675	143	149
40	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	5	5	12	20.50%	IIYGGSVTGATCK	95.00%	4	0.613	5.24	0	4	0	2	1,326.67	207	219
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	KFFVGGNWK	95.00%	1.81	0.151	0	0	0	1	2	1,082.58	6	14
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	FFVGGNWK	95.00%	2.27	0.299	3.89	0	3	0	2	954.4838	7	14
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	IAVAAQNCYK	95.00%	3.15	0.463	2.66	1	12	0	2	1,137.57	60	69
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	VTNGAFTGEISPGMIK	95.00%	3.25	0.481	4.28	0	1	0	2	1,637.82	70	85
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	DLGATWVVLGHSER	95.00%	4.16	0.573	3.33	0	2	2	2	1,539.79	86	99
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	RHVFGESDELIGQK	95.00%	4.56	0.562	2.96	0	0	2	2	1,614.82	100	113
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	HVFGESDELIGQK	95.00%	4.43	0.54	6.39	0	1	2	2	1,458.72	101	113
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	LDEREAGITEK	95.00%	2.56	0.403	0	0	0	1	2	1,260.64	132	142

41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	EAGITEK	95.00%	1.51	0.152	0.678	0	1	0	2	747.389	136	142
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	VVFEQTK	95.00%	1.66	0.255	1.92	1	2	0	2	850.4675	143	149
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	VIADNVK	95.00%	1.7	0.293	0.959	1	1	0	2	758.4413	150	156
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	VIADNVKDWSK	95.00%	3.31	0.592	3.22	0	3	1	2	1,274.67	150	160
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	VVLAYEPVWAIGTGK	95.00%	2.86	0.502	5.06	0	1	0	2	1,602.89	161	175
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	TATPQQAQEVHEK	95.00%	2.67	0.405	0	0	2	3	2	1,466.72	176	188
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	SNVNDGVAQSTR	95.00%	3.92	0.55	4.8	0	1	0	2	1,247.60	195	206
41	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	16	23	47	58.20%	IIYGGSVTGATCK	95.00%	4.21	0.641	1.6	0	2	0	2	1,326.67	207	219
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	FFVGGNWK	95.00%	1.7	0.332	1.21	0	1	0	2	954.4838	7	14
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	IAVAAQNCYK	95.00%	3.11	0.433	1.96	2	5	0	2	1,137.57	60	69
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	VTNGAFTGEISPGMIK	95.00%	2.14	0.477	1.28	0	1	0	2	1,637.82	70	85
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	HVFGESDELIGQK	95.00%	3.51	0.545	4.16	0	3	2	2	1,458.72	101	113
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	LDEREAGITEK	95.00%	2.15	0.415	1.24	0	0	1	2	1,260.64	132	142
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	VVFEQTK	95.00%	2.13	0.22	0	1	2	0	2	850.4675	143	149
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	VIADNVK	95.00%	1.61	0.278	1.42	0	1	0	2	758.4413	150	156
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	VIADNVKDWSK	95.00%	3.14	0.486	1.66	0	2	1	2	1,274.67	150	160
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	VVLAYEPVWAIGTGK	95.00%	3.29	0.523	5.07	0	1	0	2	1,602.89	161	175
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	TATPQQAQEVHEK	95.00%	2.28	0.353	3.38	0	2	3	2	1,466.72	176	188
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	SNVNDGVAQSTR	95.00%	3.77	0.591	6.08	0	4	0	2	1,247.60	195	206
42	Triosephosphate isomerase	TPIS_MOUSE	26694	100.00%	12	17	35	51.80%	IIYGGSVTGATCK	95.00%	4.14	0.643	1.35	0	3	0	2	1,326.67	207	219
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	EAFTIMDQNR	95.00%	2.91	0.547	1.49	0	4	0	2	1,240.56	31	40
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	DGFIDK	95.00%	2.13	0.201	0	1	2	0	2	694.3414	41	46
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	DGFIDKNDLR	95.00%	2.81	0.358	0.854	0	2	3	2	1,192.60	41	50
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	DTFAALGR	95.00%	2.82	0.44	1	2	6	0	2	850.4424	51	58
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	NEEIDEMIK	95.00%	2.67	0.235	0	0	2	0	2	1,136.51	63	71
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	LKGADPEETILNAFK	95.00%	3.85	0.523	1.66	0	1	4	2	1,645.88	90	104
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	GADPEETILNAFK	95.00%	3.55	0.355	3.28	1	5	0	2	1,404.70	92	104
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	VFDPEGK	95.00%	1.97	0.403	0	0	14	0	2	791.3941	105	111
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	ADYVR	95.00%	1.84	0.259	1.13	0	2	0	2	623.3153	116	120
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	NLVHIITHGEEK	95.00%	2.3	0.366	0	0	0	2	2	1,389.75	154	165
43	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV_MOUSE	18847	100.00%	11	17	55	46.40%	NLVHIITHGEEKD	95.00%	2.85	0.432	1.8	0	1	3	2	1,504.78	154	166
44	Peroxiredoxin-2	PRDX2_MOUSE	21761	100.00%	6	7	15	24.70%	LSDYR	95.00%	1.62	0.145	0	0	1	0	2	653.3259	30	34
44	Peroxiredoxin-2	PRDX2_MOUSE	21761	100.00%	6	7	15	24.70%	SLSQNYGVLK	95.00%	2.45	0.276	2.52	1	4	0	2	1,108.60	110	119
44	Peroxiredoxin-2	PRDX2_MOUSE	21761	100.00%	6	7	15	24.70%	NDEGIAYR	95.00%	2.74	0.472	3.07	0	4	0	2	937.438	120	127
44	Peroxiredoxin-2	PRDX2_MOUSE	21761	100.00%	6	7	15	24.70%	GLFIIDAK	95.00%	2.62	0.225	2.77	0	2	0	2	876.5197	128	135
44	Peroxiredoxin-2	PRDX2_MOUSE	21761	100.00%	6	7	15	24.70%	QITVNDLPVGR	95.00%	2.56	0.311	2.59	0	1	0	2	1,211.68	140	150
44	Peroxiredoxin-2	PRDX2_MOUSE	21761	100.00%	6	7	15	24.70%	SVDEALR	95.00%	1.83	0.075	0.886	0	2	0	2	789.4107	151	157
45	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	3	3	5	24.70%	TVYHAEEIQCNGR	95.00%	1.88	0.322	1.85	0	1	0	2	1,576.72	16	28
45	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	3	3	5	24.70%	ALDSTTVAAHESEIYCK	95.00%	3.5	0.589	2.8	0	0	2	2	1,894.89	43	59
45	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	3	3	5	24.70%	NFGPTGIGFGGLTQQVEK	95.00%	3.56	0.582	1.96	0	2	0	2	1,849.95	175	192
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	TPAPSPQTSLPNPITYLTK	95.00%	4.84	0.704	7.66	0	3	0	2	2,026.09	17	35
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	AYDLVVDWPVTLVR	95.00%	3.51	0.529	3.04	0	2	0	2	1,645.90	36	49
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	TYYYHR	95.00%	1.56	0.172	1.34	0	1	0	2	902.416	61	66
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	RVPDITECK	95.00%	2.15	0.451	1.46	0	3	0	2	1,117.57	70	78
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	VPDITECK	95.00%	2.33	0.332	3.55	0	2	0	2	961.4666	71	78
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	ELEQFTK	95.00%	1.78	0.154	1.85	0	1	0	2	894.4574	128	134
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	AYQDRYLDLGAYYSAR	95.00%	3.21	0.536	1.62	0	0	1	2	1,924.92	138	153
45	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	NDUBA_MOUSE	21006	100.00%	8	8	17	40.30%	YLDLGAYYSAR	95.00%	3.12	0.585	3.7	0	4	0	2	1,291.63	143	153
46	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	6	9	13	39.20%	TVYHAEEIQCNGR	95.00%	3.4	0.434	0	0	2	2	2	1,576.72	16	28
46	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	6	9	13	39.20%	ALDSTTVAAHESEIYCK	95.00%	3.19	0.58	5.26	0	1	2	2	1,894.89	43	59
46	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	6	9	13	39.20%	FGESEKCPR	95.00%	1.84	0.294	0	0	0	1	2	1,109.51	114	122
46	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	6	9	13	39.20%	SLESTNVTDKDGELYCK	95.00%	2.49	0.267	1.44	0	0	1	2	1,958.90	153	169
46	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	6	9	13	39.20%	NFGPTGIGFGGLTQQVEK	95.00%	4.06	0.472	3.74	0	1	0	2	1,849.95	175	192
46	Cysteine and glycine-rich protein 3	CSRP3_MOUSE	20876	100.00%	6	9	13	39.20%	NFGPTGIGFGGLTQQVEKKE	95.00%	3.67	0.511	1.62	0	2	1	2	2,107.08	175	194
46	Glutathione S-transferase P 1	GSTP1_MOUSE	23592	100.00%	5	7	13	37.60%	FEDGDLTLYQSNAILR	95.00%	4.56	0.649	3.18	0	3	0	2	1,854.92	56	71
46	Glutathione S-transferase P 1	GSTP1_MOUSE	23592	100.00%	5	7	13	37.60%	SLGLYGK	95.00%	1.6	0.257	0	1	0	0	2	737.4199	76	82
46	Glutathione S-transferase P 1	GSTP1_MOUSE	23592	100.00%	5	7	13	37.60%	YVTLIYTNYENGKNDYVK	95.00%	3.13	0.555	1.96	0	2	1	2	2,197.08	104	121
46	Glutathione S-transferase P 1	GSTP1_MOUSE	23592	100.00%	5	7	13	37.60%	ALPGHLKPFETLLSQNQGGK	95.00%	3.8	0.456	3.49	0	1	3	2	2,135.16	122	141
46	Glutathione S-transferase P 1	GSTP1_MOUSE	23592	100.00%	5	7	13	37.60%	AFLSSPEHVNRPINGNGK	95.00%	1.98	0.294	0	0	0	2	2	1,937.00	192	209
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	RPFFPFHSPSR	95.00%	2.82	0.292	0	0	0	3	2	1,374.71	12	22
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	APSWIDTGLSEMR	95.00%	3.31	0.54	2.74	0	1	0	2	1,478.70	57	69
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	HFSPEELK	95.00%	2.36	0.388	0	1	5	0	2	986.4948	83	90
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	HFSPEELKVK	95.00%	3.12	0.236	2.74	0	0	1	2	1,213.66	83	92
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	VLGDVIEVHGK	95.00%	3.47	0.538	3.33	0	4	3	2	1,165.66	93	103
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	QDEHGFISR	95.00%	2.14	0.237	0.854	0	4	0	2	1,088.51	108	116
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	KQVSGPER	95.00%	1.7	0.147	0	0	1	0	2	900.4904	150	157
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	TIPITR	95.00%	1.45	0.153	0	1	0	0	2	700.4359	158	163
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	TIPITREEKPAVAAAPK	95.00%	1.62	0.271	0.921	0	0	1	2	1,792.03	158	174
47	Alpha-crystallin B chain	CRYAB_MOUSE	20051	100.00%	10	13	30	45.10%	EEKPAVAAAPK	95.00%	2.11	0.326	0	0	3	2	2	1,110.62	164	174
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	IGYPAPNFK	95.00%	1.56	0.206	0	1	1	0	2	1,006.54	8	16
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	DISLSEYK	95.00%	2.55	0.352	3.01	1	2	0	2	954.4785	28	35
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	DISLSEYKGK	95.00%	2.02	0.22	0	0	2	0	2	1,139.60	28	37
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	TIAQDYGVLK	95.00%	2.6	0.293	2.3	0	2	0	2	1,107.61	111	120
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	ADEGISFR	95.00%	2.78	0.425	4.21	0	2	0	2	894.4322	121	128
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	GLFIIDDK	95.00%	2.99	0.39	3.07	0	2	0	2	920.5096	129	136
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	GLFIIDDKGILR	95.00%	3.81	0.462	2.96	0	2	2	2	1,359.80	129	140

48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	QITINDLPVGR	95.00%	2.64	0.564	2.77	0	3	0	2	1,225.69	141	151
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	SVDEIIR	95.00%	2.13	0.138	2.44	2	1	0	2	831.4577	152	158
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	LVQAFQFTDK	95.00%	3.01	0.468	5.77	0	2	0	2	1,196.63	159	168
48	Peroxiredoxin-1	PRDX1_MOUSE	22160	100.00%	11	15	26	42.20%	SKEYFSK	95.00%	2.3	0.15	2.17	0	1	0	2	888.4467	191	197
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	AVILGPPGSGK	95.00%	2.17	0.395	0	0	2	0	2	995.5892	8	18
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	AVILGPPGSGKGTVCER	95.00%	1.76	0.247	1.11	0	0	2	2	1,697.90	8	24
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	GLLVPDHVITR	95.00%	2.41	0.337	0	0	1	2	2	1,219.72	61	71
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	SAQHWLLDGFPR	95.00%	2.72	0.366	2	0	1	2	2	1,426.72	81	92
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	YKDAAKPVIELYK	95.00%	3.01	0.521	1.85	0	0	2	2	1,537.86	174	186
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	DAAKPVIELYK	95.00%	2.28	0.318	0	0	0	2	2	1,246.70	176	186
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	GVLHQFSGTETNR	95.00%	2.59	0.463	1.96	0	1	2	2	1,445.71	189	201
49	Adenylate kinase isoenzyme 4, mitochondrial	KAD4_MOUSE	25044	100.00%	8	11	19	35.00%	IWPYVYTLFSNK	95.00%	3.25	0.581	4.64	0	2	0	2	1,530.80	202	213

Supplemental Table II. Overlap of significant protein and mRNA changes only

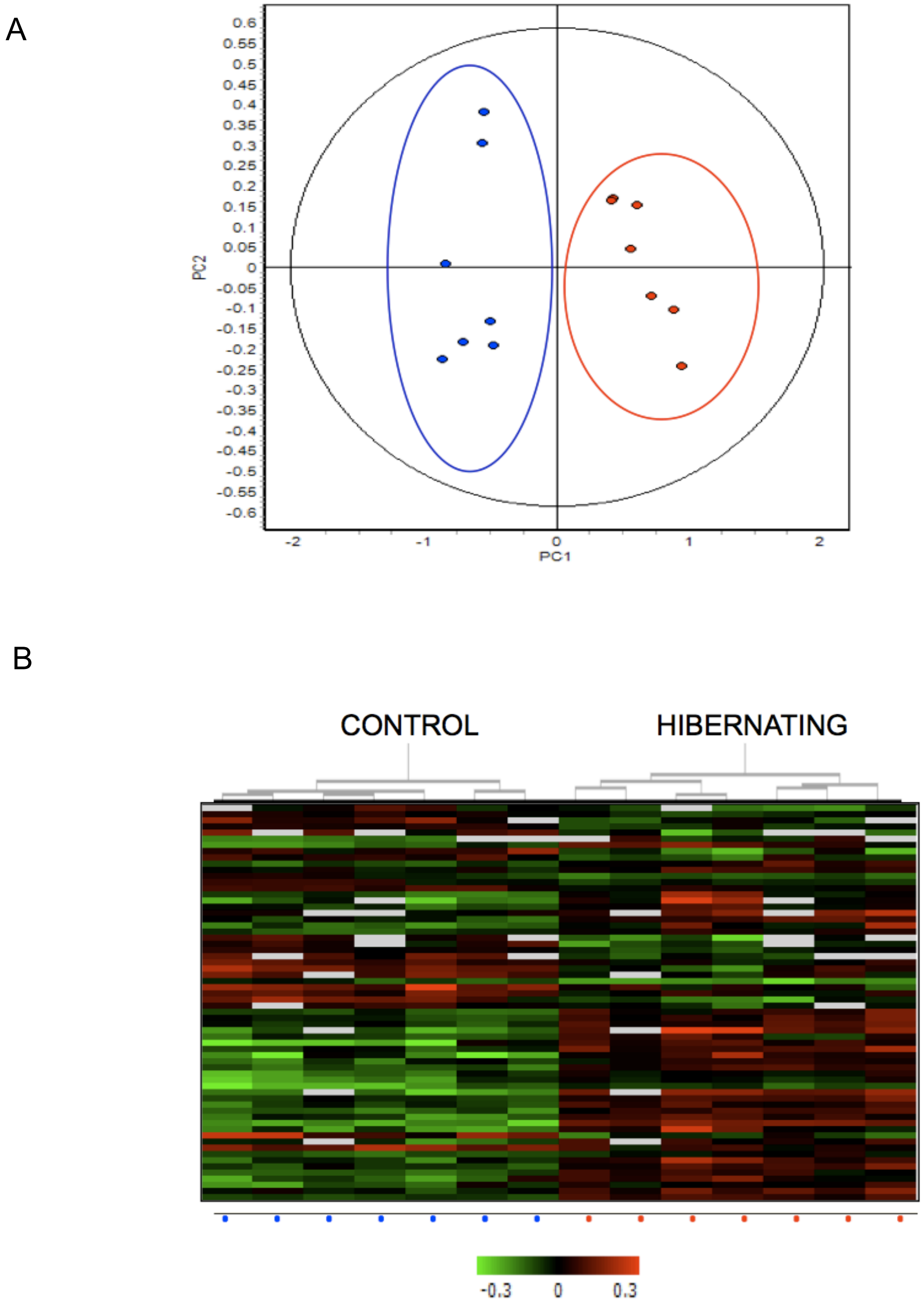
Protein identity	Gene Symbol	Gene Name	PROTEOMICS Fold change	PROTEOMICS P-value	TRANSCRIPTOMICS Fold change	TRANSCRIPTOMICS Bayes. p	TRANSCRIPTOMICS FDR
Adenylate kinase isoenzyme 4, mitochondrial	AK3L1	Adenylate kinase 3, alpha-like 1	1.21	0.004	2.65	0.0001	0.019
Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial	HADHSC	L-3_Hydroxyacyl-CoA dehydrogenase, short chain	-1.22	0.002	-1.70	0.0118	0.277
L-lactate dehydrogenase A	LDHA	Lactate dehydrogenase A	1.29	7.80E-05	1.84	0.0061	0.198
Methylcrotonoyl-CoA carboxylase alpha chain, mitochondrial	MCCC1	Methylcrotonyl-CoA carboxylase 1, alpha	-1.23	0.0001	-1.58	0.0215	0.354
Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	OXCT1	3-Oxoacid CoA transferase 1	-1.32	0.001	-1.59	0.0157	0.314
Protein disulfide-isomerase	P4HB	Prolyl 4-Hydroxylase, beta	1.32	0.001	1.53	0.0169	0.323
Pyruvate kinase, isozyme M2	PKM2	Pyruvate kinase, isozyme M2	1.54	7.30E-07	1.58	0.0102	0.258
Triosephosphate isomerase	TPI1	Triosephosphate isomerase 1	2.07	1.40E-08	1.80	0.0032	0.154
Serotransferrin	TRF	Transferrin	1.34	0.001	2.51	0.0338	0.421

Supplemental Table III: Pathway identification using Metacore^{TM}

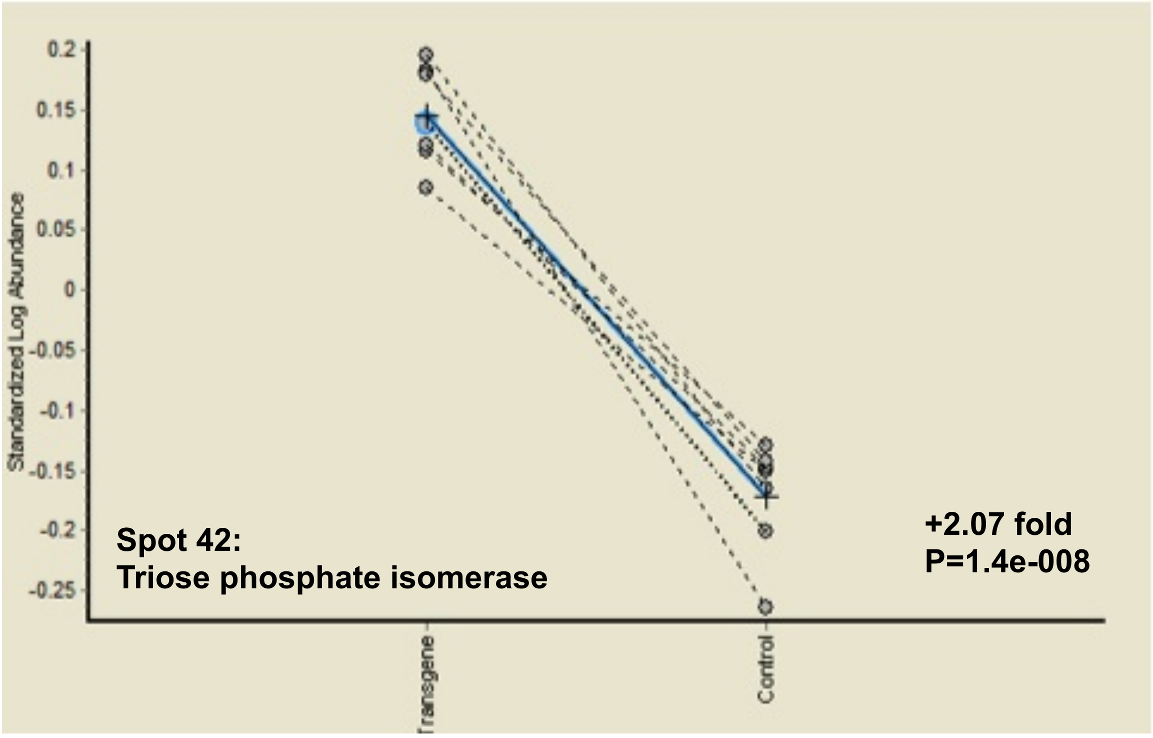
		COMBINED			TRANSCRIPTOMICS			PROTEOMICS			METABOLOMICS		
Map (objects)	Mapobjects	Rank	p-Value	Objects	Rank	p-Value	Objects	Rank	p-Value	Objects	Rank	p-Value	Objects
Transcription_Role of Akt in hypoxia induced HIF1 activation	29	1	1.4E-04	8	9	3.9E-02	4	7	1.1E-02	4			
Glycolysis and gluconeogenesis (short map)	36	2	6.8E-04	9	14	7.6E-02	4	8	2.4E-02	4	38	4.0E-01	1
Proline metabolism	14	3	7.2E-04	5	22	1.3E-01	2	1	6.6E-04	4			
Fructose metabolism	31	4	6.7E-03	8	3	1.1E-02	5	60	6.3E-01	1	16	1.6E-01	2
Cell adhesion_Endothelial cell contacts by non-junctional mechanisms	24	5	9.6E-03	5	1	3.6E-03	5						
Muscle contraction_Role of kappa-type opioid receptor in heart	16	6	1.1E-02	4	7	3.2E-02	3	33	4.0E-01	1			
Transport_Intracellular cholesterol transport in norm	47	7	1.5E-02	7	11	5.8E-02	5	35	4.4E-01	2			
Intracellular cholesterol transport in CF	47	8	1.5E-02	7	12	5.8E-02	5	34	4.4E-01	2			
Immune response _MIF - the neuroendocrine-macrophage connector	27	9	1.6E-02	5	6	3.1E-02	4	50	5.8E-01	1			
Urea cycle	27	10	1.6E-02	8	138	7.1E-01	1	3	8.6E-03	4	12	9.5E-02	3
Glycolysis and gluconeogenesis p. 1	19	11	2.0E-02	6	2	8.9E-03	4				11	7.4E-02	2
Transcription_P53 signaling pathway	32	12	3.2E-02	5	26	1.7E-01	3	26	2.6E-01	2			
Development_VEGF-family signaling	32	13	3.2E-02	5	4	1.3E-02	5						
Cell adhesion_Gap junctions	22	14	3.3E-02	4	44	2.6E-01	2	17	1.5E-01	2			
Leucine, isoleucine and valine metabolism	13	15	3.4E-02	6				2	6.5E-03	3	8	6.0E-02	3
Butanoate metabolism	24	16	4.3E-02	5	17	9.1E-02	3	18	1.7E-01	2	45	5.1E-01	1
Cell adhesion_Chemokines and adhesion	84	17	4.5E-02	9	8	3.3E-02	8	86	9.4E-01	1			
Glycolysis and gluconeogenesis p.3	15	18	4.9E-02	3				5	1.0E-02	3			
Glutathione metabolism	36	19	5.0E-02	6	5	2.1E-02	5				41	4.5E-01	1
Leucune, isoleucine and valine metabolism.p.2	28	20	7.0E-02	4	141	7.3E-01	1	4	9.8E-03	4			

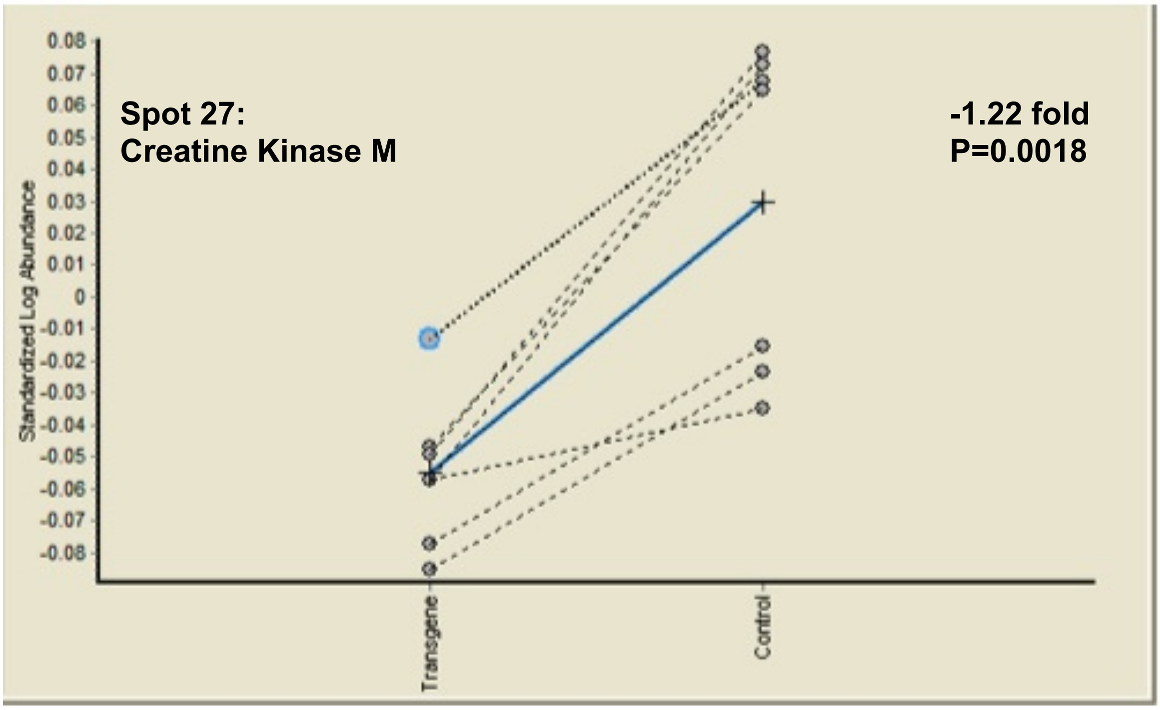
p-Value: Metacore statistics for pathway identification, Objects: genes/proteins/metabolites identified in map

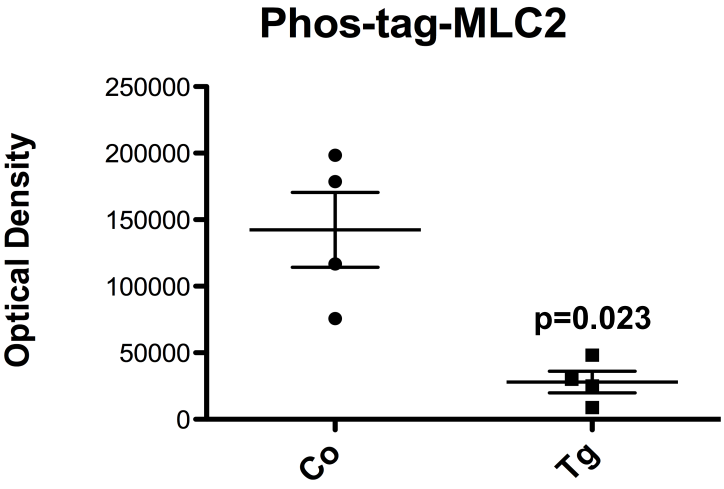
Supplemental Figure 1



Supplemental Figure 2



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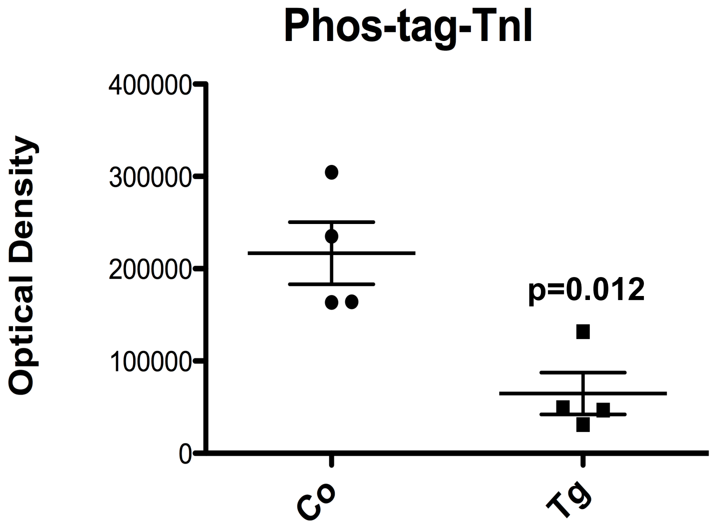
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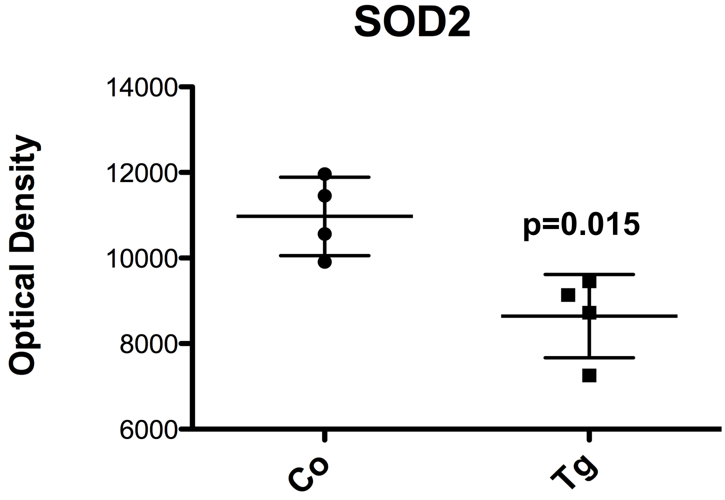
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Co
Tg

Supplemental Figure 4