SUPPLEMENTAL TABLE A. All priority 1 proteins measured in the nucleus accumbens shell of P, NP and W rats

Protein_ID	Annotation	Best_Sequence	ID_Confidence	q_NC_NE	q_NC_PC	q_NC_WC	q_PC_PE	q_PC_WC	q_WC_WE	p_NC_NE	p_NC_PC	p_NC_WC	p_PC_PE	p_PC_WC	p_WC_WE	FC_NC_NE	FC_NC_PC	FC_NC_WC	FC_PC_PE	FC_PC_WC	FC_WC_WE	mean_NC	mean_NE	mean_PC	mean_PE	mean_WC	mean_WE	%CV_Sample	mean_log2_NC	mean_log2_NE	mean_log2_PC	mean_log2_PE	mean_log2_WC	mean_log2_WE	se_log2_NC	se_log2_NE	se_log2_PC	se_log2_PE	se_log2_WC	se_log2_WE	Number_Sequences	Number_Peptides	ClusterRank
IPI00231611.7	Isoform_Mitochondrial_of_Fumarate_hydratase,_mitochondrial_precursor	AAAEVNQEYGLDPK	99.99997477	0.27061826	0.997658493	1.03172E-05	0.560474035	2.93E-07	0.353175547	0.1517431	0.254660824	1.18E-08	0.196252909	3.35E-10	0.056899675	-1.058569021	1.047388784	-1.302941848	-1.054031715	-1.364686677	1.081424119	10583.85929	9998.270375	11085.4155	10517.15555	8123.048087	8784.460122	8.765403015	13.3696	13.2875	13.4364	13.3605	12.9878	13.1007	0.03991	0.03991	0.04207	0.03991	0.03991	0.04207	5	6	127
IPI00215349.3	WD_repeat_protein_1	YAPSGFYIASGDISGK	99.99991238	0.000843899	0.997658493	0.99643308	0.001882086	0.977979004	0.000165737	1.04E-06	0.18576579	0.926325672	4.30E-06	0.15830224	1.89E-07	1.190876637	-1.044458714	1.002938071	1.181212736	1.047527408	1.215042631	16331.63994	19448.96844	15636.46291	18469.98913	16379.62346	19901.94078	7.068887129	13.9954	14.2474	13.9326	14.1729	13.9996	14.2806	0.03221	0.03221	0.03395	0.03221	0.03221	0.03395	6	6	99
IPI00213015.1	Dynactin_2	ENLATVEGNFASIDAR	100	0.22381884	0.997658493	0.639633748	0.000237451	0.244428157	0.03637813	0.113572074	0.344379001	0.018808076	2.71E-07	0.001676079	0.000208446	1.045408286	-1.027419638	1.069205026	1.182236513	1.09852224	1.119724562	16261.6762	17000.09104	15827.68676	18712.06921	17387.06593	19468.72478	6.1755608	13.9892	14.0533	13.9502	14.1917	14.0857	14.2489	0.02815	0.02815	0.02967	0.02815	0.02815	0.02967	10	11	92
IPI00475835.2	D-3-phosphoglycerate_dehydrogenase	AGTGVDNVDLEAATR	99.99999751	0.459335412	0.997658493	0.005974944	0.903404554	0.010961334	0.343015874	0.331246451	0.957804431	2.04855E-05	0.773947913	3.75817E-05	0.041325383	-1.028928636	-1.001589502	-1.145955141	1.008662346	-1.144136534	-1.064495083	11367.43412	11047.83531	11349.39423	11447.70661	9919.615269	9318.6107	6.508736872	13.4726	13.4315	13.4703	13.4828	13.2761	13.1859	0.02966	0.02966	0.03127	0.02966	0.02966	0.03127	4	5	127
IPI00358537.2	PREDICTED:_similar_to_heat_shock_protein_12A	ELSDQAGSDFENSDVR	99.77766	0.140003788	0.997658493	0.99643308	0.020224353	0.977979004	0.000770944	0.058313422	0.066442397	0.403411398	9.77195E-05	0.296373244	2.18E-06	1.051901164	-1.05163115	-1.022261685	1.120028005	1.028729889	1.153764691	15110.21941	15894.45739	14368.36425	16092.97034	14781.16576	17053.98715	5.849192274	13.8832	13.9562	13.8106	13.9741	13.8515	14.0578	0.02666	0.02666	0.0281	0.02666	0.02666	0.0281	2	2	30
26006161	mKIAA0417_protein_[Mus_musculus]	EIQTIMQFGDTEIK	99.984118	0.135794857	0.997658493	0.99643308	0.020224353	0.977979004	0.000770944	0.054780908	0.069601756	0.404530036	0.000115568	0.305583269	2.64E-06	1.053448502	-1.05173596	-1.022520385	1.120241046	1.028572119	1.154340047	15099.34434	15906.38167	14356.59226	16082.84393	14766.79052	17045.89767	5.93074783	13.8822	13.9573	13.8094	13.9732	13.8501	14.0571	0.02703	0.02703	0.0285	0.02703	0.02703	0.0285	2	2	30
IPI00358441.1	PREDICTED:_similar_to_NADH_dehydrogenase_(ubiquinone)_1_alpha_subcomplex,_9	IHISDVMATDLPLGEDLGVQPTPELK	99.99995184	0.000843899	0.997658493	0.99643308	0.199585822	0.988483763	0.384065202	1.93E-06	0.304181541	0.32130081	0.011449237	0.949901737	0.07385132	1.195128944	-1.036091507	-1.033859072	1.093703826	1.002159322	1.06431183	6634.750188	7929.381988	6403.633411	7003.678364	6417.460916	6830.17957	7.446111799	12.6958	12.953	12.6447	12.7739	12.6478	12.7377	0.03392	0.03392	0.03576	0.03392	0.03392	0.03576	4	4	52
IPI00231641.4	Phosphoglucomutase-1	INQDPQVMLAPLISIALK	99.99991206	0.016478465	0.997658493	0.99643308	0.043836361	0.977979004	0.013033525	0.001676095	0.182040103	0.850333181	0.000300592	0.130316061	5.95818E-05	1.214429268	-1.084854672	1.011176326	1.262786448	1.096979362	1.301031267	8049.00659	9774.949177	7419.433031	9369.15948	8138.964913	10589.04784	13.1618368	12.9746	13.2549	12.8571	13.1937	12.9906	13.3703	0.05979	0.05979	0.06302	0.05979	0.05979	0.06302	4	4	99
IPI00205493.1	Isoform_Syn1_of_Alpha-synuclein	EQVTNVGGAVVTGVTAVAQK	100	0.008921586	0.997658493	0.99643308	0.590307582	0.977979004	0.641885332	0.000515926	0.655859879	0.20016962	0.221955651	0.093012151	0.297101211	-1.178296161	-1.020611705	1.059171876	1.057881302	1.081003215	1.049109822	22829.79856	19375.26345	22368.74067	23663.4725	24180.68057	25368.18948	9.931169607	14.4786	14.2419	14.4492	14.5304	14.5616	14.6307	0.0452	0.0452	0.04764	0.0452	0.0452	0.04764	11	20	18
IPI00765886.1	PREDICTED:_similar_to_malic_enzyme_3,_NADP(+)-dependent,_mitochondrial_isoform_1	SLIYTPDYDSFSLDTYTWPK	99.9999939	0.005112477	0.997658493	0.99643308	0.271569898	0.977979004	0.89121073	0.000164616	0.112179451	0.443784732	0.026176192	0.391160128	0.704820371	1.223615513	-1.085973697	-1.039083467	1.12393129	1.045126529	-1.019632989	8084.451314	9892.260038	7444.426452	8367.023826	7780.367576	7630.556937	11.14342681	12.9809	13.2721	12.8619	13.0305	12.9256	12.8976	0.05068	0.05068	0.05342	0.05068	0.05068	0.05342	4	5	37
IPI00230925.4	Thymosin_beta-4	KTETQEKNPLPSKETIEQEK	99.99906043	0.015074205	0.997658493	0.99643308	0.450498174	0.977979004	0.45490106	0.001386846	0.61805024	0.437462617	0.102786782	0.21212905	0.138809809	-1.214035717	-1.03002593	1.045943131	1.102901082	1.077348547	1.092708818	23748.39511	19561.52918	23056.11385	25428.61291	24839.47075	27142.30872	12.88887978	14.5355	14.2557	14.4929	14.6342	14.6003	14.7283	0.05856	0.05856	0.06173	0.05856	0.05856	0.06173	11	15	18
IPI00211336.1	PREDICTED:_similar_to_SH3_domain_binding_glutamic_acid-rich_protein-like_3	VYSTSVTGSR	99.99997351	0.057159746	0.997658493	0.836075007	0.225498692	0.806688502	0.647257068	0.014571139	0.640084261	0.065930486	0.014679361	0.025573364	0.304025891	-1.098312163	-1.018090977	1.072183963	1.10101521	1.091580819	1.040366336	13011.50469	11846.81835	12780.29663	14071.30098	13950.72666	14513.86638	8.310940358	13.6675	13.5322	13.6416	13.7805	13.7681	13.8251	0.03785	0.03785	0.0399	0.03785	0.03785	0.0399	2	3	8
IPI00231651.6	Brain_acid_soluble_protein_1	AEGAGTEEEGTQKESEPQAAADATEVK	99.99999667	0.11883265	0.997658493	0.731411129	0.23197177	0.897927856	0.562676245	0.041964902	0.941159405	0.038451328	0.016989029	0.036943318	0.225713556	-1.134287857	-1.004615134	1.136936825	1.165445586	1.142183941	1.079083216	9657.49013	8514.143978	9613.124273	11203.57325	10979.95617	11848.28641	13.5732274	13.2374	13.0556	13.2308	13.4517	13.4226	13.5324	0.06164	0.06164	0.06498	0.06164	0.06164	0.06498	7	11	18
IPI00210941.1	Tropomyosin	IQVLQQQADDAEER	99.99999976	0.120487706	0.997658493	0.846402451	0.908565709	0.977979004	0.426869209	0.042962474	0.457229147	0.097708548	0.800576184	0.376276198	0.109074685	-1.06241269	1.022707864	1.050438043	1.007640444	1.027114468	1.050088582	15046.0528	14162.15463	15387.71651	15505.28549	15804.94626	16596.59361	6.531508726	13.8771	13.7898	13.9095	13.9205	13.9481	14.0186	0.02977	0.02977	0.03138	0.02977	0.02977	0.03138	19	26	32
905379	GABA_transaminase	NLLLAEVINIIK	99.99999946	0.126343985	0.997658493	0.685064733	0.454617724	0.977979004	0.590127084	0.047115808	0.62014812	0.0332474	0.107164676	0.109091606	0.252978018	1.089142511	-1.021744532	-1.096193306	-1.073288372	-1.072864373	-1.051135047	10377.75333	11302.85231	10156.89637	9463.343344	9467.083284	9006.53376	9.410248777	13.3412	13.4644	13.3102	13.2081	13.2087	13.1368	0.04284	0.04284	0.04515	0.04284	0.04284	0.04515	11	13	20
IPI00198966.3	50_kDa_protein	TLLTGLLDLQAQYPQFVSR	99.99999961	0.079555274	0.997658493	0.639633748	0.502800017	0.977979004	0.730183609	0.023366521	0.683563043	0.02772483	0.139744473	0.078559618	0.453965581	1.114377758	-1.019713068	-1.110688148	-1.074033854	-1.089216352	-1.036584972	11486.23239	12800.00191	11264.18083	10487.7335	10341.54583	9976.553893	10.39303169	13.4876	13.6439	13.4595	13.3564	13.3362	13.2843	0.04729	0.04729	0.04985	0.04729	0.04729	0.04985	14	17	20
48427970	GABT_MOUSE_4-aminobutyrate_aminotransferase,_mitochondrial_precursor_((S)-3-amino-2-methylpropionate_t	NLLLAEVINIIK	99.99999946	0.121895949	0.997658493	0.639633748	0.367357043	0.977979004	0.670153176	0.043882542	0.724047858	0.02777838	0.064357219	0.070210802	0.332514202	1.097089797	-1.016495877	-1.106902175	-1.091013889	-1.088939169	-1.046118195	10807.70575	11857.02371	10632.31637	9745.353823	9763.921319	9333.478153	10.05690172	13.3998	13.5335	13.3762	13.2505	13.2532	13.1882	0.04577	0.04577	0.04824	0.04577	0.04577	0.04824	11	13	20
IPI00365944.4	Myosin_light_polypeptide_6	VLDFEHFLPMLQTVAK	99.99999668	0.079206356	0.997658493	0.846402451	0.733834025	0.988483763	0.587595758	0.023173517	0.077456041	0.079210941	0.417298961	0.953463564	0.248469063	-1.055236627	1.043444086	1.042000503	-1.019491007	-1.001385396	1.027938789	15682.14547	14861.25962	16363.44195	16050.5996	16340.80346	16797.34573	5.141738192	13.9368	13.8593	13.9982	13.9703	13.9962	14.0359	0.02344	0.02344	0.02471	0.02344	0.02344	0.02471	5	6	79
IPI00231150.4	Glutathione_S-transferase_alpha_(Fragment)	ADVYLVQVLYHVEELDPSALANFPLLK	99.99995329	0.021225334	0.997658493	0.99643308	0.984163624	0.977979004	0.260206946	0.003007933	0.523342979	0.836495444	0.969996041	0.402298769	0.023645525	1.284371809	-1.054505973	1.01681483	1.003126622	1.072237312	-1.212352979	6146.735229	7894.693444	5829.018882	5847.244021	6250.091539	5155.339779	18.12292185	12.5856	12.9467	12.509	12.5135	12.6097	12.3319	0.08201	0.08201	0.08645	0.08201	0.08201	0.08645	2	2	4
IPI00231733.6	Guanine_nucleotide-binding_protein_G(i),_alpha-1_subunit	LLLLGAGESGK	99.9999872	0.004964405	0.997658493	0.99643308	0.003796321	0.977979004	0.03637813	0.000025239	0.366679158	0.909560599	0.000013016	0.427607492	0.000300995	1.219390765	-1.040946446	-1.004908035	1.236489896	1.035862397	1.186175387	15839.64758	19314.71998	15216.58261	18815.15065	15762.28573	18696.83537	9.613085282	13.9513	14.2374	13.8934	14.1996	13.9442	14.1905	0.04376	0.04376	0.04612	0.04376	0.04376	0.04612	5	5	19
IPI00209824.2	Calmodulin-dependent_protein_kinase_II_beta_M_isoform	AGAYDFPSPEWDTVTPEAK	99.99999981	0.00800401	0.997658493	0.874148118	0.629348071	0.988483763	0.865028531	0.000408442	0.111352689	0.121881223	0.258594542	0.92939803	0.662364704	1.208958872	-1.087176991	-1.082193307	1.060717137	1.00460517	1.022922001	16191.94566	19575.39636	14893.56912	15797.86399	14962.15654	15305.1191	11.26715147	13.983	14.2568	13.8624	13.9474	13.869	13.9017	0.05124	0.05124	0.05401	0.05124	0.05124	0.05401	11	13	52
IPI00363569.3	PREDICTED:_similar_to_Ran-specific_GTPase-activating_protein	TLEEDEEELFK	99.99998692	0.005112477	0.997658493	0.99643308	0.57026792	0.977979004	0.893774223	0.000164594	0.295298831	0.474928002	0.204443772	0.722754476	0.713997922	-1.107930174	1.027785099	1.018325118	-1.033875178	-1.009289746	1.009598286	14787.23127	13346.71771	15198.09596	14700.12655	15058.20902	15202.74201	5.646413531	13.8521	13.7042	13.8916	13.8435	13.8783	13.892	0.02574	0.02574	0.02713	0.02574	0.02574	0.02713	6	6	80
IPI00193445.1	Creatine_kinase,_ubiquitous_mitochondrial_precursor	SEVELVQLVIDGVNYLIDCER	100	0.008921586	0.997658493	0.869092652	0.792374134	0.870828243	0.31993257	0.000581178	0.528320582	0.118551469	0.522116069	0.033837898	0.037294997	1.089411146	1.015357354	-1.037782123	1.015591813	-1.053719711	1.052650338	11046.52615	12034.20871	11216.17157	11391.05202	10644.35964	11204.78877	5.228582143	13.4313	13.5549	13.4533	13.4756	13.3778	13.4518	0.02384	0.02384	0.02513	0.02384	0.02384	0.02513	16	21	88
IPI00555166.1	Creatine_kinase,_mitochondrial_1,_ubiquitous	GTGGVDTAATGSVFDISNLDR	100	0.008820518	0.997658493	0.932336177	0.855934899	0.867565465	0.353175547	0.000473788	0.45529538	0.139544458	0.660401791	0.031334305	0.057227868	1.08653958	1.017343517	-1.033946112	1.010151893	-1.051878374	1.045454935	11216.5894	12187.26834	11411.12451	11526.96903	10848.33075	11341.44092	4.977964694	13.4533	13.5731	13.4782	13.4927	13.4052	13.4693	0.0227	0.0227	0.02392	0.0227	0.0227	0.02392	18	23	88
225775	1313192A_calmodulin_dependent_protein_kinase_II	AGAYDFPSPEWDTVTPEAK	99.99999981	0.008921586	0.997658493	0.99643308	0.668421481	0.977979004	0.801751113	0.000520852	0.139039502	0.453051918	0.304010568	0.446808008	0.534195313	1.34373659	-1.131171105	-1.06222629	1.088897274	1.064905958	-1.052677865	18808.77467	25274.03874	16627.70078	18105.85806	17706.93763	16820.85111	17.99802352	14.1991	14.6254	14.0213	14.1442	14.112	14.038	0.08146	0.08146	0.08586	0.08146	0.08146	0.08586	10	12	9
IPI00231247.8	Dual_specificity_mitogen-activated_protein_kinase_kinase_1	LCDFGVSGQLIDSMANSFVGTR	99.99987704	0.00800401	0.997658493	0.99643308	0.954046054	0.996058404	0.421432785	0.000370371	0.686173682	0.672226998	0.898438798	0.9937817	0.100469152	1.170146403	1.017370406	1.017708136	-1.005450844	1.000331964	-1.073450639	8995.94883	10526.57717	9152.212111	9102.595281	9155.250318	8528.804201	9.244087634	13.1351	13.3617	13.1599	13.1521	13.1604	13.0581	0.04208	0.04208	0.04436	0.04208	0.04208	0.04436	4	4	26
50489	pro-alpha-2(I)_collagen_[Mus_musculus]	IPGGK	98.6922	0.042852312	0.997658493	0.639633748	0.384902361	0.977979004	0.426572047	0.009197079	0.132717114	0.018817	0.069942258	0.408703119	0.105723475	-1.254210804	1.140394364	1.225088908	-1.172517352	1.074267768	-1.15211949	16871.31221	13451.73567	19239.94935	16409.09562	20668.85746	17939.85575	18.88477508	14.0423	13.7155	14.2318	14.0022	14.3352	14.1309	0.0854	0.0854	0.09002	0.0854	0.0854	0.09002	2	2	36
IPI00214262.1	NSFL1_cofactor_p47	ASSSILINEAEPTTNIQIR	99.99999934	0.004964405	0.997658493	0.99643308	0.471474337	0.977979004	0.863903236	5.18166E-05	0.646850084	0.520498947	0.118542119	0.866536284	0.658541095	-1.257275564	1.024872506	1.034142532	-1.088300802	1.009045053	-1.023980052	10595.94458	8427.70263	10859.49227	9978.392235	10957.71695	10701.10392	11.64263635	13.3712	13.0409	13.4067	13.2846	13.4197	13.3855	0.05294	0.05294	0.0558	0.05294	0.05294	0.0558	5	5	27
IPI00199076.2	cGMP-dependent_3',5'-cyclic_phosphodiesterase	NLFTHLDDVSVLLQEIITEAR	99.99943431	0.004964405	0.997658493	0.99643308	0.519827808	0.977979004	0.421432785	3.09886E-05	0.773818175	0.651808317	0.156314658	0.879081712	0.099675407	1.209641407	-1.012453392	-1.019106615	1.063562394	-1.006571387	1.074459874	4711.015246	5698.639111	4653.068759	4948.828948	4622.691266	4966.896277	9.344626215	12.2018	12.4764	12.184	12.2729	12.1745	12.2781	0.04254	0.04254	0.04484	0.04254	0.04254	0.04484	3	3	22
IPI00324302.3	Acetyl-CoA_acetyltransferase,_mitochondrial_precursor	EVYMGNVIQGGEGQAPTR	100	0.859558688	0.997658493	0.005974944	0.454617724	0.773591433	0.260206946	0.778023407	0.033447684	1.77987E-05	0.108588691	0.019255201	0.023483378	1.00666822	-1.054052998	-1.117230796	1.040125567	-1.059937971	1.057859249	15683.124	15787.70253	14878.87614	15475.89948	14037.49705	14849.69609	5.248146486	13.9369	13.9465	13.861	13.9177	13.777	13.8581	0.02393	0.02393	0.02522	0.02393	0.02393	0.02522	6	7	59
IPI00212523.1	Protein_DJ-1	GPGTSFEFALAIVEALSGK	100	0.047374348	0.997658493	0.639633748	0.360181899	0.977979004	0.403264892	0.011261559	0.12626904	0.021857312	0.058864013	0.458500602	0.08526172	-1.13243934	1.078482674	1.118367513	-1.098471732	1.036982364	-1.08904428	15574.15334	13752.74842	16796.45454	15290.74809	17417.62713	15993.49764	10.61198138	13.9269	13.7474	14.0359	13.9004	14.0883	13.9652	0.04828	0.04828	0.05089	0.04828	0.04828	0.05089	13	21	70
IPI00324020.5	glutamine_synthetase_1	IQLMYIWVDGTGEGLR	100	0.009985522	0.997658493	0.959908311	0.792374134	0.977979004	0.838529975	0.00078743	0.749340303	0.163548419	0.517092795	0.296609636	0.608533182	1.185431913	-1.015865726	-1.06973346	1.032482226	-1.053026431	1.025574018	17022.93224	20179.52714	16757.06918	17301.37609	15913.24651	16320.21216	10.69625562	14.0552	14.3006	14.0325	14.0786	13.9579	13.9944	0.04866	0.04866	0.05129	0.04866	0.04866	0.05129	12	15	83
IPI00187747.1	Ras-related_protein_Rap-1A_precursor	INVNEIFYDLVR	99.99999448	0.001789678	0.997658493	0.99643308	0.560474035	0.977979004	0.898992978	6.14E-06	0.773291121	0.828254424	0.194119555	0.617927712	0.72887016	1.25015005	-1.013285153	1.009719025	1.061787568	1.023133297	1.016010027	8660.607063	10827.05836	8547.058086	9075.160015	8744.779723	8884.783885	9.943668198	13.0803	13.4024	13.0612	13.1477	13.0942	13.1171	0.04525	0.04525	0.0477	0.04525	0.04525	0.0477	3	3	52
IPI00192337.1	Calcium/calmodulin-dependent_protein_kinase_type_II_alpha_chain	ITQYLDAGGIPR	100	0.005176531	0.997658493	0.99643308	0.630797204	0.977979004	0.948770577	0.000183397	0.236246966	0.504468538	0.265295281	0.588733091	0.849014128	1.326701004	-1.090226208	-1.048293566	1.084568734	1.040000858	-1.013888734	15299.54772	20297.92531	14033.36996	15220.15429	14594.7168	14394.79136	15.78736082	13.9012	14.309	13.7766	13.8937	13.8332	13.8133	0.07158	0.07158	0.07545	0.07158	0.07158	0.07545	18	23	9
6680067	glucose_phosphate_isomerase_1_[Mus_musculus]	ILLANFLAQTEALMK	100	0.042852312	0.997658493	0.99643308	0.758226296	0.977979004	0.343015874	0.009207125	0.329704607	0.834909355	0.446270335	0.43889092	0.043940104	1.154287831	-1.055080758	-1.011171464	-1.042708739	1.043424182	-1.119094116	11751.59293	13564.72071	11138.09805	10681.88809	11621.76085	10384.97181	11.90180955	13.5206	13.7276	13.4432	13.3829	13.5045	13.3422	0.05411	0.05411	0.05703	0.05411	0.05411	0.05703	8	11	14
56541238	Fumarate_hydratase_1_[Rattus_norvegicus]	AAAEVNQEYGLDPK	99.99997477	0.314674317	0.997658493	0.006622587	0.797906375	0.000639864	0.280710986	0.194199007	0.327313546	3.02747E-05	0.553840915	1.46E-06	0.028231505	-1.048171359	1.037009677	-1.177635318	-1.022140626	-1.22121922	1.086486777	10558.2241	10072.99428	10948.98056	10711.81429	8965.614349	9741.021437	8.011376305	13.3661	13.2982	13.4185	13.3869	13.1302	13.2499	0.03649	0.03649	0.03846	0.03649	0.03649	0.03846	5	5	127
IPI00382226.1	Ab2-162	NLNQALLDLHALGSAR	99.99998443	0.126343985	0.997658493	0.846402451	0.727515376	0.977979004	0.602776182	0.046407642	0.55870481	0.094540515	0.392109668	0.29000223	0.261905782	-1.06857098	1.019849912	1.056916862	-1.029239411	1.036345495	1.038604678	12516.60945	11713.40949	12765.06305	12402.4235	13229.01559	13739.71747	7.277989661	13.6116	13.5159	13.6399	13.5983	13.6914	13.7461	0.03316	0.03316	0.03495	0.03316	0.03316	0.03495	3	4	96
IPI00371769.1	Phosphoglycerate_kinase_2	LGDVYVNDAFGTAHR	100	0.015074205	0.997658493	0.99643308	0.90918008	0.977979004	0.384065202	0.001398035	0.955915271	0.72212486	0.804520299	0.771091577	0.073175376	-1.10509542	-1.001690714	-1.010639966	1.007594128	-1.008934147	1.057190745	20487.75024	18539.34953	20453.16978	20608.49376	20272.05625	21431.43025	6.626132297	14.3225	14.1783	14.32	14.331	14.3072	14.3874	0.0302	0.0302	0.03183	0.0302	0.0302	0.03183	5	10	68
IPI00362791.3	PREDICTED:_similar_to_ubiquilin_2	NPAMMQEMMR	99.99992819	0.274843203	0.997658493	0.795267491	0.412110301	0.977979004	0.480223035	0.155482726	0.015939971	0.056793407	0.077241245	0.554131809	0.153649414	-1.05654489	1.102624702	1.077181371	-1.073234254	-1.023620285	1.05841033	15850.87401	15002.55612	17477.56523	16284.94913	17074.2662	18071.57971	8.54875718	13.9523	13.8729	14.0932	13.9913	14.0595	14.1414	0.03893	0.03893	0.04104	0.03893	0.03893	0.04104	2	2	125
435585	non-muscle_myosin_light_chain_3	VLDFEHFLPMLQTVAK	99.99999668	0.38476358	0.997658493	0.728765365	0.919964679	0.992757535	0.453249617	0.256362477	0.045226245	0.037479362	0.824274267	0.979142574	0.133643887	-1.026061297	1.048394127	1.04902864	-1.005153309	1.000605224	1.035716281	12346.30312	12032.71496	12943.79167	12877.4303	12951.62557	13414.20946	5.015829297	13.5918	13.5547	13.66	13.6526	13.6608	13.7115	0.02287	0.02287	0.02411	0.02287	0.02287	0.02411	4	5	79
IPI00211864.1	Beta-synuclein	TKEGVVQGVASVAEK	100	0.022798879	0.997658493	0.99643308	0.454617724	0.977979004	0.72233375	0.003551071	0.871033787	0.341698618	0.108510128	0.277629659	0.437527872	-1.134806016	-1.006963925	1.040529099	1.071931662	1.047775266	1.033840638	19706.38962	17365.42576	19570.10487	20977.81503	20505.07183	21198.97655	9.277658822	14.2664	14.0839	14.2564	14.3566	14.3237	14.3717	0.04224	0.04224	0.04452	0.04224	0.04224	0.04452	13	22	8
IPI00191354.2	33_kDa_protein	TIDDLEDKLK	99.99993858	0.26742745	0.997658493	0.685064733	0.792374134	0.977979004	0.624688993	0.148231215	0.501077311	0.032198038	0.517527958	0.148998982	0.28565631	-1.037302611	1.017522334	1.056461735	1.016846313	1.038268842	1.02804467	14726.90482	14197.30816	14984.95456	15237.39579	15558.41141	15994.74193	5.584351087	13.8462	13.7933	13.8712	13.8953	13.9254	13.9653	0.02546	0.02546	0.02683	0.02546	0.02546	0.02683	13	18	32
IPI00210978.1	Complexin-1	MLGGDEEKDPDAAKKEEER	99.9976353	0.015074205	0.997658493	0.99643308	0.706612353	0.977979004	0.516390929	0.001379548	0.619037856	0.980766308	0.357061268	0.602651383	0.188261379	-1.207914952	-1.029133083	1.001354537	1.054795466	1.030527081	1.079546669	7074.042132	5856.407458	6873.787508	7250.439898	7083.624182	7647.102888	12.54369202	12.7883	12.5158	12.7469	12.8239	12.7903	12.9007	0.057	0.057	0.06009	0.057	0.057	0.06009	6	7	8
IPI00188304.2	Lactoylglutathione_lyase	GLAFVQDPDGYWIEILNPNK	99.99999999	0.016275878	0.997658493	0.959908311	0.892326425	0.977979004	0.385912453	0.001633239	0.981727332	0.164223242	0.754653206	0.182775849	0.075418319	-1.131614023	1.000880028	1.053892247	-1.012080464	1.052965608	-1.071803561	15430.86384	13636.15467	15444.44343	15260.09441	16262.46777	15172.99285	8.333220127	13.9135	13.7351	13.9148	13.8975	13.9893	13.8892	0.03795	0.03795	0.04001	0.03795	0.03795	0.04001	5	6	57
IPI00364311.1	Glucose_phosphate_isomerase	ILLANFLAQTEALMK	100	0.024155562	0.997658493	0.99643308	0.918768065	0.977979004	0.494461272	0.00411308	0.235038935	0.753179089	0.820066124	0.375591797	0.172920171	1.159664208	-1.06279652	-1.015720054	1.011656707	1.046347875	-1.072564186	11018.5734	12777.8452	10367.52867	10488.37992	10848.0416	10114.1188	11.06681626	13.4276	13.6414	13.3398	13.3565	13.4051	13.3041	0.05034	0.05034	0.05306	0.05034	0.05034	0.05306	20	28	14
IPI00189759.1	NADH_dehydrogenase_1_alpha_subcomplex_10-like_protein	LLQYSDALEHLLSTGQGVVLER	99.99998258	0.059090409	0.997658493	0.795267491	0.733834025	0.977979004	0.931974488	0.015532336	0.7864592	0.054267401	0.416439964	0.106130834	0.81173482	1.132730453	-1.014033745	-1.103062599	-1.042812656	-1.087796737	-1.012327236	13591.62617	15395.64888	13403.52453	12853.24306	12321.7179	12171.67479	11.17293174	13.7304	13.9102	13.7103	13.6498	13.5889	13.5712	0.05082	0.05082	0.05356	0.05082	0.05082	0.05356	2	2	20
IPI00230866.6	Guanine_nucleotide-binding_protein_alpha-12_subunit	ILLLGAGESGK	99.28372	0.004964405	0.998795589	0.99643308	0.943668993	0.977979004	0.421432785	9.94843E-05	0.995156738	0.665366285	0.878960262	0.678181694	0.102855253	1.232425218	-1.00031068	-1.021796715	-1.0078244	-1.021479362	1.088238535	14020.11873	17278.74788	14015.76432	13906.95078	13721.04503	14931.76993	11.11825437	13.7752	14.0767	13.7748	13.7635	13.7441	13.8661	0.05057	0.05057	0.0533	0.05057	0.05057	0.0533	2	2	93
IPI00422053.1	Galpha13	ILLLGAGESGK	99.28372	0.004964405	0.998795589	0.99643308	0.943668993	0.977979004	0.421432785	9.94843E-05	0.995156738	0.665366285	0.878960262	0.678181694	0.102855253	1.232425218	-1.00031068	-1.021796715	-1.0078244	-1.021479362	1.088238535	14020.11873	17278.74788	14015.76432	13906.95078	13721.04503	14931.76993	11.11825437	13.7752	14.0767	13.7748	13.7635	13.7441	13.8661	0.05057	0.05057	0.0533	0.05057	0.05057	0.0533	2	2	93
IPI00196751.2	Heat_shock_70_kDa_protein_1A/1B	VEIIANDQGNR	99.99999994	0.024155562	0.997658493	0.86359048	0.23197177	0.92052399	0.088176923	0.00416856	0.282906578	0.110161674	0.016993726	0.621403059	0.001310057	-1.10665138	1.038409496	1.056485817	-1.089439014	1.0174077	-1.12527448	19910.59557	17991.75055	20675.35151	18977.97971	21035.26182	18693.44964	7.57087499	14.2812	14.135	14.3356	14.212	14.3605	14.1902	0.03449	0.03449	0.03636	0.03449	0.03449	0.03636	6	8	53
IPI00209163.1	PREDICTED:_similar_to_histone_2,_H2be	LLLPGELAK	99.969293	0.008921586	0.997658493	0.99643308	0.974820419	0.92052399	0.287857444	0.000556612	0.270185713	0.355678091	0.943138671	0.048379502	0.030266154	1.171762697	1.050574171	-1.040971374	1.003177756	-1.093617639	1.103632187	16096.20816	18860.93628	16910.26054	16963.99723	15462.68087	17065.11231	9.656971039	13.9744	14.2031	14.0456	14.0502	13.9165	14.0588	0.04395	0.04395	0.04633	0.04395	0.04395	0.04633	3	4	25
IPI00421549.3	NADH_dehydrogenase_(Ubiquinone)_1_alpha_subcomplex_10	SIYSDFVFLEAMYNQGFIR	99.99999846	0.021329062	0.997658493	0.932336177	0.911527876	0.977979004	0.993109576	0.003104709	0.809173157	0.138160419	0.81126463	0.093526227	0.964616622	1.147801771	1.011143915	-1.069209133	1.011018662	-1.081124309	-1.002037276	9801.293807	11249.94239	9910.518593	10019.71925	9166.863156	9148.225696	9.961659109	13.2588	13.4576	13.2747	13.2906	13.1622	13.1593	0.04533	0.04533	0.04779	0.04533	0.04533	0.04779	3	3	83
IPI00197986.1	MIPP65	VSTQPTTGTQEASAELRPAAAPESGAR	98.6355	0.562373851	0.997658493	0.542581856	0.903743337	0.977979004	0.592840196	0.431903118	0.378835478	0.01054159	0.787031341	0.09603236	0.256106965	-1.039902678	1.046076896	1.14005377	-1.013877501	1.089837444	1.060007442	10298.45253	9903.28494	10772.97325	10625.51762	11740.78962	12445.32437	11.07926183	13.3301	13.2737	13.3951	13.3752	13.5192	13.6033	0.05039	0.05039	0.05312	0.05039	0.05039	0.05312	2	2	112
IPI00365775.3	PREDICTED:_similar_to_malic_enzyme_3,_NADP(+)-dependent,_mitochondrial	SLIYTPDYDSFSLDTYTWPK	99.9999939	0.005449046	0.997658493	0.99643308	0.430171333	0.977979004	0.994839219	0.000211734	0.462484629	0.589887259	0.093900257	0.832669105	0.984606587	1.25976685	-1.045065552	-1.031934298	1.106954294	1.012724893	-1.00115512	7131.437617	8983.948704	6823.914161	7553.761082	6910.747737	6902.774201	13.01477995	12.8	13.1331	12.7364	12.883	12.7546	12.753	0.05913	0.05913	0.06233	0.05913	0.05913	0.06233	3	3	37
IPI00389830.1	48_kDa_protein	NIFSFYLNRDPTGQPGGELMLGGTDSR	99.99995408	0.190389371	0.997658493	0.456464817	0.973913878	0.867565465	0.917773279	0.089979693	0.622839022	0.007334346	0.939353498	0.030686436	0.777766096	-1.054672632	1.015785318	1.08979126	1.002422955	1.072855888	-1.00902085	10498.97907	9954.727898	10664.70879	10690.5489	11441.69562	11339.40455	6.897554236	13.358	13.2812	13.3806	13.384	13.482	13.4691	0.03143	0.03143	0.03313	0.03143	0.03143	0.03313	5	5	32
109966	A35244_hexokinase_(EC_2.7.1.1),_tumor_-_mouse	SANLVAATLGAILNR	100	0.009763259	0.997658493	0.99643308	0.430171333	0.977979004	0.959191605	0.000658323	0.20751482	0.945875647	0.092935105	0.185197222	0.86625445	1.176432315	-1.060546202	1.003062729	1.082021238	1.063794368	1.007825844	10190.76833	11988.74918	9608.981028	10397.12155	10221.9799	10301.97552	10.04934219	13.315	13.5494	13.2302	13.3439	13.3194	13.3306	0.04573	0.04573	0.04821	0.04573	0.04573	0.04821	19	21	47
IPI00470301.1	Chaperonin_subunit_5	IADGYEQAAR	99.99990244	0.018644305	0.997658493	0.99643308	0.855934899	0.977979004	0.426572047	0.002383548	0.597968935	0.198394828	0.666971766	0.464169995	0.106114908	-1.116195404	1.018937493	1.045855318	1.015419693	1.026417543	-1.059868922	8668.77137	7766.356448	8832.936166	8969.137332	9066.280635	8554.152731	7.706897712	13.0816	12.923	13.1087	13.1308	13.1463	13.0624	0.03511	0.03511	0.03701	0.03511	0.03511	0.03701	4	4	114
IPI00202543.1	Hexokinase-1	SANLVAATLGAILNR	100	0.008921586	0.997658493	0.99643308	0.467884871	0.977979004	0.909020933	0.000569799	0.256441748	0.808868906	0.113000653	0.172239733	0.753188773	1.180877711	-1.054839236	1.011070843	1.077889686	1.066517195	-1.01481615	9929.55457	11725.58967	9413.334495	10146.53616	10039.48311	9892.908292	10.15234141	13.2775	13.5174	13.2005	13.3087	13.2934	13.2722	0.0462	0.0462	0.0487	0.0462	0.0462	0.0487	21	24	47
IPI00365545.1	Dihydrolipoamide_dehydrogenase	NQVTATTADGSTQVIGTK	99.99999999	0.018644305	0.997658493	0.99643308	0.626617454	0.977979004	0.358348992	0.002328148	0.504634502	0.231008381	0.252106011	0.613776163	0.058564464	-1.118180907	1.024371577	1.043182803	-1.042379019	1.018363675	-1.071770512	17668.66857	15801.26118	18099.28187	17363.43647	18431.6512	17197.38599	7.811926511	14.1089	13.9478	14.1436	14.0838	14.1699	14.0699	0.03559	0.03559	0.03751	0.03559	0.03559	0.03751	14	18	57
IPI00362291.1	16_kDa_protein	LNDFASAVR	99.99999127	0.009985522	0.998795589	0.99643308	0.706612353	0.977979004	0.486515155	0.000771373	0.995396224	0.408309543	0.361020259	0.424150271	0.163523993	-1.23266914	1.000348798	1.050015009	-1.05699589	1.049648894	-1.088727877	22005.44928	17851.87003	22013.12472	20826.1214	23106.05201	21222.98189	13.14743641	14.4256	14.1238	14.4261	14.3461	14.496	14.3733	0.05972	0.05972	0.06296	0.05972	0.05972	0.06296	7	9	27
12847763	unnamed_protein_product_[Mus_musculus]	ISGLIYEETR	99.99999958	0.004964405	0.997658493	0.99643308	0.88196112	0.977979004	0.673644494	0.000100596	0.68917708	0.852565104	0.727743918	0.561743137	0.361166557	1.310094302	1.026849405	-1.012047357	-1.023324521	-1.039220226	1.062566766	12113.63698	15870.00677	12438.88092	12155.3629	11969.4369	12718.32585	14.411006	13.5643	13.954	13.6026	13.5693	13.5471	13.6346	0.06541	0.06541	0.06895	0.06541	0.06541	0.06895	8	9	23
IPI00231260.4	Peroxiredoxin-6	VVDSLQLTASNPVATPVDWK	100	0.032730769	0.997658493	0.885264043	0.454617724	0.977979004	0.393067374	0.00658356	0.239881391	0.124442831	0.108315977	0.741917801	0.081504683	-1.070619291	1.029880038	1.038358628	-1.04129291	1.008232599	-1.044975463	16758.93222	15653.4936	17259.68976	16575.24948	17401.78186	16652.81385	5.393715278	14.0326	13.9342	14.0751	14.0167	14.0869	14.0235	0.02459	0.02459	0.02592	0.02459	0.02459	0.02592	9	14	128
IPI00196509.2	Isoform_AMPH2-1_of_Myc_box-dependent-interacting_protein_1	VFEEMNVDLQEELPSLWNSR	99.99999957	0.011647769	0.997658493	0.99643308	0.920774602	0.977979004	0.900010096	0.000958445	0.89960584	0.382694396	0.827118671	0.329820954	0.734300895	-1.088630094	-1.003163719	1.02158015	-1.005483996	1.024812142	-1.008538345	13706.54902	12590.63946	13663.32211	13588.80118	14002.3384	13883.79378	5.426690244	13.7426	13.6201	13.738	13.7301	13.7734	13.7611	0.02474	0.02474	0.02608	0.02474	0.02474	0.02608	16	19	100
20141789	PRDX5_MOUSE_Peroxiredoxin-5,_mitochondrial_precursor_(Prx-V)_(Peroxisomal_antioxidant_enzyme)_(PLP)_(	ALNVEPDGTGLTCSLAPNILSQL	99.99999482	0.005112477	0.997658493	0.99643308	0.599018937	0.977979004	0.66199794	0.000175285	0.492538828	0.742770162	0.227284899	0.712870696	0.31550323	-1.156806906	1.02591565	1.011959007	-1.046268145	-1.013791707	-1.038231534	21129.06613	18264.98963	21676.6396	20718.05369	21381.74878	20594.39352	8.069843567	14.3669	14.1568	14.4039	14.3386	14.3841	14.33	0.03676	0.03676	0.03874	0.03676	0.03676	0.03874	6	9	113
IPI00197711.1	L-lactate_dehydrogenase_A_chain	GYTSWAIGLSVADLAESIMK	99.99999977	0.021329062	0.997658493	0.99643308	0.727515376	0.977979004	0.697837817	0.003120137	0.152291658	0.601203087	0.394009475	0.351094078	0.397986188	1.145465825	-1.067572416	-1.02330534	1.039442619	1.043258912	-1.039103239	11707.79749	13410.88191	10966.74785	11399.3051	11441.15743	11010.60703	9.819271482	13.5152	13.7111	13.4208	13.4767	13.4819	13.4266	0.04469	0.04469	0.04711	0.04469	0.04469	0.04711	13	16	48
IPI00204447.3	Vesicle_associated_membrane_protein_2B	LQQTQAQVDEVVDIMR	100	0.101319119	0.997658493	0.99643308	0.507087091	0.977979004	0.353175547	0.033464258	0.045193825	0.7635395	0.145461554	0.084648157	0.054967036	1.099969076	-1.096333087	-1.013278649	1.068474748	1.081966039	-1.091972044	14195.10636	15614.17803	12947.8044	13834.40204	14009.08464	12829.16053	9.776800498	13.7931	13.9306	13.6604	13.756	13.7741	13.6471	0.0445	0.0445	0.0469	0.0445	0.0445	0.0469	6	7	48
IPI00230868.4	guanine_nucleotide_binding_protein,_alpha_q_polypeptide	VRVPTTGIIEYPFDLQSVIFR	99.99986629	0.017295034	0.997658493	0.99643308	0.64602549	0.92052399	0.214048911	0.001838215	0.319378875	0.29426723	0.282774586	0.046796198	0.015166894	1.147769833	1.044310777	-1.045477193	-1.047919303	-1.091803099	1.114393596	7392.747919	8485.173041	7720.32632	7367.290879	7071.170917	7880.067587	9.406766703	12.8519	13.0507	12.9144	12.8469	12.7877	12.944	0.04282	0.04282	0.04514	0.04282	0.04282	0.04514	2	2	25
IPI00454264.1	LRRGT00046	LKTQPTDEEMLFIYSHFK	99.99998104	0.044155864	0.997658493	0.99643308	0.876899711	0.988483763	0.836004321	0.00958813	0.272624341	0.227406801	0.712301738	0.936439839	0.589502476	-1.109687604	1.045064794	1.048399244	1.014849547	1.003190663	1.02181807	21705.23464	19559.7703	22683.37658	23020.21445	22755.75159	23252.23818	8.668432543	14.4058	14.2556	14.4693	14.4906	14.4739	14.5051	0.03947	0.03947	0.04161	0.03947	0.03947	0.04161	3	7	21
IPI00208215.1	PRx_III	HLSVNDLPVGR	99.99999692	0.076373123	0.997658493	0.99643308	0.88970951	0.977979004	0.302595389	0.021560193	0.223397387	0.880133354	0.748869321	0.17356648	0.034236507	1.098364338	-1.051407251	1.006018582	1.013178634	1.057735232	-1.092493827	12458.21602	13683.66019	11849.08703	12005.24181	12533.19681	11472.09851	8.871349312	13.6048	13.7402	13.5325	13.5514	13.6135	13.4858	0.04039	0.04039	0.04258	0.04039	0.04039	0.04258	3	4	126
IPI00215463.1	Calmodulin-like_3	KMKDTDSEEEIREAFR	99.99922428	0.015933658	0.997658493	0.99643308	0.706612353	0.977979004	0.849367056	0.001566051	0.96649628	0.568206913	0.360422588	0.607468816	0.631040794	-1.366696714	1.00406674	1.055227391	-1.092782212	1.050953437	1.047552305	23891.18675	17480.97182	23988.34598	21951.62559	25210.63465	26409.45844	21.15971992	14.5442	14.0935	14.55	14.422	14.6217	14.6888	0.09548	0.09548	0.1006	0.09548	0.09548	0.1006	5	8	76
IPI00324381.5	Syntaxin-1A	FMDEFFEQVEEIR	99.99999934	0.023226989	0.997658493	0.99643308	0.649849423	0.977979004	0.300507042	0.003721005	0.79999781	0.384604574	0.285191061	0.551901449	0.03356849	1.231465202	1.018092726	1.061938022	-1.079002547	1.043066113	-1.166162872	10601.59047	13055.48975	10793.40214	10003.12943	11258.23201	9654.082017	15.41559133	13.372	13.6724	13.3979	13.2882	13.4587	13.2369	0.06992	0.06992	0.0737	0.06992	0.06992	0.0737	2	2	12
IPI00357924.1	Isocitrate_dehydrogenase_[NAD]_subunit_beta,_mitochondrial_precursor	NIANPTAMLLSASNMLR	99.99998649	0.091194258	0.997658493	0.99643308	0.792374134	0.988483763	0.666788291	0.029182163	0.287645463	0.256177206	0.512218183	0.965720937	0.329202905	1.094270734	-1.045327615	-1.047191963	1.027605171	-1.001783505	-1.041480962	14010.8162	15331.62613	13403.27759	13773.27736	13379.41534	12846.52895	8.998992033	13.7743	13.9042	13.7103	13.7496	13.7077	13.6491	0.04097	0.04097	0.04319	0.04097	0.04097	0.04319	6	6	28
IPI00193173.4	Brain-specific_polypeptide_PEP-19	KVQEEFDIDMDAPETER	100	0.005112477	0.997658493	0.99643308	0.855934899	0.977979004	0.924766593	0.000147932	0.434587859	0.986462587	0.671052961	0.425026639	0.792839772	-1.346089225	-1.060476575	1.001238167	-1.032361884	1.061789622	1.019879083	24349.80208	18089.29277	22961.18808	22241.41403	24379.95121	24864.60229	16.33640769	14.5716	14.1428	14.4869	14.441	14.5734	14.6018	0.07404	0.07404	0.07804	0.07404	0.07404	0.07804	4	5	143
38051985	Prdx3_protein_[Rattus_norvegicus]	YLVLFFYPLDFTFVCPTEIVAFSDK	99.99959997	0.127795487	0.997658493	0.99643308	0.608678208	0.977979004	0.178834944	0.049066248	0.63008725	0.734290906	0.238601858	0.417872751	0.011205994	1.098481932	-1.023471245	1.016032901	-1.058751797	1.039880457	-1.134217195	9040.788988	9931.143355	8833.456764	8343.274403	9185.739059	8098.747841	10.45074279	13.1422	13.2777	13.1088	13.0264	13.1652	12.9835	0.04755	0.04755	0.05012	0.04755	0.04755	0.05012	3	3	10
415898	heat_shock_rotein_70_[Rattus_rattus]	QTQTFTTYSDNQPGVLIQVYEGER	99.9999953	0.045301902	0.997658493	0.86359048	0.269624476	0.977979004	0.119761122	0.010046384	0.364999271	0.115474384	0.024959523	0.522244983	0.002977102	-1.095465383	1.032558941	1.056146861	-1.084313336	1.022844139	-1.115461373	22119.55292	20191.92324	22839.74214	21063.78422	23361.49639	20943.34861	7.641579844	14.433	14.3015	14.4793	14.3625	14.5118	14.3542	0.03481	0.03481	0.03669	0.03481	0.03481	0.03669	4	6	53
IPI00369397.5	PREDICTED:_similar_to_Histone_H2A.x	VTIAQGGVLPNIQAVLLPK	99.99999981	0.004964405	0.997658493	0.99643308	0.908280262	0.977979004	0.88013542	5.44077E-05	0.514926056	0.894165751	0.795815568	0.601435118	0.681979217	1.314279519	1.04275361	1.008342947	-1.016746018	-1.034125952	1.026660279	9660.230013	12696.24246	10073.23972	9907.331365	9740.824799	10000.5179	13.9639541	13.2378	13.6321	13.2982	13.2743	13.2498	13.2878	0.0634	0.0634	0.06683	0.0634	0.0634	0.06683	6	7	23
IPI00212258.1	PREDICTED:_similar_to_14_kDa_phosphohistidine_phosphatase	AKYPDYEVTWADDGY	99.99996903	0.004964405	0.997658493	0.99643308	0.989435424	0.977979004	0.837394717	0.000102125	0.876590423	0.985937349	0.97812759	0.890127789	0.603361039	-1.209694037	1.007279846	1.000801544	1.001281252	-1.006473113	-1.024594944	9302.354712	7689.840925	9370.074419	9382.079843	9309.810962	9086.333112	10.14173896	13.1834	12.9087	13.1938	13.1957	13.1845	13.1495	0.04615	0.04615	0.04865	0.04615	0.04615	0.04865	2	3	118
IPI00231340.8	11_kDa_protein	ISGLIYEETR	99.99999958	0.005098407	0.997658493	0.99643308	0.796416454	0.977979004	0.774104485	0.000135876	0.624390327	0.937558188	0.533886593	0.571678452	0.504658093	1.284433428	1.031216853	-1.004793006	-1.039856191	-1.036159482	1.042818677	12627.87468	16219.66437	13022.0772	12522.95972	12567.63792	13105.76755	13.64520598	13.6243	13.9855	13.6687	13.6123	13.6174	13.6779	0.06197	0.06197	0.06532	0.06197	0.06197	0.06532	9	10	23
IPI00208115.4	Synaptic_vesicle_glycoprotein_2A	MADGAPLAGVR	99.99959365	0.021329062	0.997658493	0.99643308	0.283004764	0.977979004	0.766408058	0.003109718	0.148654203	0.752368273	0.031696534	0.252428132	0.495756527	1.27538112	-1.12539831	-1.025190095	1.194710767	1.097745985	1.056835857	7928.838428	10112.29083	7045.361947	8417.169773	7734.017787	8173.587316	17.67371098	12.9529	13.3038	12.7825	13.0391	12.917	12.9968	0.08001	0.08001	0.08434	0.08001	0.08001	0.08434	2	2	122
IPI00207370.1	Neurabin-2	ERPGEQSEVAQLIQQTLEQER	99.99995946	0.045275136	0.997658493	0.99643308	0.750164383	0.977979004	0.985763927	0.009986401	0.071209279	0.533205551	0.440667992	0.223773749	0.945206782	-1.101091155	1.070517543	1.02284667	-1.029164919	-1.046606079	1.002558308	7771.776381	7058.249759	8319.822954	8084.052223	7949.335593	7969.672442	8.065297679	12.924	12.7851	13.0223	12.9809	12.9566	12.9603	0.03674	0.03674	0.03872	0.03674	0.03674	0.03872	2	2	113
IPI00230937.4	Phosphatidylethanolamine-binding_protein_1	GNDISSGTVLSEYVGSGPPK	100	0.011211969	0.997658493	0.99643308	0.341387261	0.977979004	0.45250857	0.000909771	0.442982439	0.522628217	0.049146866	0.884030204	0.129308345	-1.196501075	1.041323974	1.033359501	-1.111284444	-1.007707359	-1.084080906	24865.83879	20782.12824	25893.39406	23300.4198	25695.35077	23702.42905	11.43718271	14.6019	14.3431	14.6603	14.5081	14.6492	14.5327	0.05201	0.05201	0.05482	0.05201	0.05201	0.05482	14	25	69
IPI00204831.1	Mitochondrial_import_inner_membrane_translocase_subunit_Tim8_A	AEACFVNCVER	99.9959369	0.023226989	0.998795589	0.99643308	0.940752994	0.977979004	0.931989435	0.003703583	0.987889792	0.319039222	0.868864101	0.324589111	0.81754998	-1.103498299	-1.000507844	1.033135264	1.005538597	1.033659935	1.007748599	15491.12808	14038.19842	15483.265	15569.02056	16004.4307	16128.4426	7.254680218	13.9192	13.7771	13.9184	13.9264	13.9662	13.9773	0.03305	0.03305	0.03484	0.03305	0.03305	0.03484	4	4	96
16905129	neuronal_calcium-binding_protein_2_[Mus_musculus]	ETANQIQSLLSSVESAVEAIEEQTSQIR	99.99999675	0.994610183	0.997658493	0.99643308	0.342215144	0.977979004	0.071235349	0.992336788	0.856993556	0.51044165	0.052798908	0.644628885	0.000930588	1.000326996	-1.006323146	-1.022704683	-1.071411959	-1.016278606	-1.129999042	6032.254158	6034.226681	5994.351004	5594.814349	5898.334346	5219.769334	7.586027242	12.5585	12.559	12.5494	12.4499	12.5261	12.3498	0.03456	0.03456	0.03643	0.03456	0.03456	0.03643	3	5	24
IPI00212226.1	Isoform_Delta_1_of_Calcium/calmodulin-dependent_protein_kinase_type_II_delta_chain	AGAYDFPSPEWDTVTPEAK	99.99999981	0.009770659	0.997658493	0.99643308	0.733834025	0.977979004	0.837394717	0.000669988	0.548822495	0.913999095	0.418868906	0.620697378	0.599438633	1.351422223	-1.052949997	-1.009071985	1.072154078	1.04348353	-1.046217814	37689.53384	50934.47362	35794.2295	38376.92911	37350.68894	35700.68147	18.77052033	15.2019	15.6364	15.1274	15.228	15.1888	15.1237	0.08489	0.08489	0.08949	0.08489	0.08489	0.08949	5	6	9
IPI00196730.1	Isoform_A_of_Calcium/calmodulin-dependent_protein_kinase_type_II_gamma_chain	AGAYDFPSPEWDTVTPEAK	99.99999981	0.009811376	0.997658493	0.99643308	0.737520205	0.977979004	0.888891758	0.000715626	0.603937455	0.787960525	0.43155468	0.796821409	0.70197052	1.342917784	-1.044929078	-1.022405103	1.069027672	1.022030383	-1.032931031	23381.93484	31400.01611	22376.57591	23921.17886	22869.54043	22140.43314	18.48164949	14.5131	14.9385	14.4497	14.546	14.4811	14.4344	0.08361	0.08361	0.08813	0.08361	0.08361	0.08813	5	7	9
IPI00231069.4	Acyl-CoA-binding_protein	LKTQPTDEEMLFIYSHFK	99.99998104	0.037855522	0.997658493	0.99643308	0.89755911	0.977979004	0.883541706	0.007873949	0.437090496	0.284254215	0.762155907	0.788252665	0.694716221	-1.126300805	1.03522635	1.04765505	1.013540319	1.012005781	1.01759896	21263.80342	18879.32898	22012.8496	22310.91061	22277.13104	22669.18539	9.643456884	14.3761	14.2045	14.4261	14.4455	14.4433	14.4684	0.04389	0.04389	0.04627	0.04389	0.04389	0.04627	6	12	21
IPI00193259.2	Tyrosine_3-monooxygenase	FDPYTLAIDVLDSPHTIQR	99.938857	0.4244201	0.997658493	0.959908311	0.341387261	0.977979004	0.421432785	0.297336596	0.299610286	0.153692533	0.048742869	0.719264884	0.100334318	1.059133393	-1.060505105	-1.082213795	-1.119810016	-1.020470142	-1.098344285	6264.917091	6635.382899	5907.484144	5275.434278	5788.982843	5270.645028	12.24866115	12.6131	12.696	12.5283	12.3651	12.4991	12.3638	0.05567	0.05567	0.05868	0.05567	0.05567	0.05868	3	3	135
IPI00373045.1	Eukaryotic_translation_initiation_factor_4B	SPPYTAFLGNLPYDVTEDSIKDFFR	99.99999126	0.02581863	0.997658493	0.99643308	0.938351951	0.977979004	0.849367056	0.004691614	0.670933299	0.434863811	0.864356197	0.238174954	0.637753321	-1.133270474	-1.018761124	1.03388253	1.007496097	1.053279328	1.020816452	7928.491221	6996.115582	7782.483091	7840.821338	8197.12856	8367.763694	9.488847681	12.9528	12.7723	12.926	12.9368	13.0009	13.0306	0.04319	0.04319	0.04553	0.04319	0.04319	0.04553	3	3	96
IPI00231783.4	L-lactate_dehydrogenase_B_chain	IVADKDYSVTANSK	99.99999999	0.242832763	0.997658493	0.99643308	0.788902735	0.977979004	0.251205819	0.125962364	0.190650932	0.843428565	0.49615351	0.262516703	0.020096466	1.04510162	-1.039398113	-1.005646394	-1.020174387	1.033562215	-1.072392171	13046.35356	13634.76525	12551.83494	12303.61701	12973.10232	12097.34897	6.349084927	13.6714	13.735	13.6156	13.5868	13.6632	13.5624	0.02894	0.02894	0.0305	0.02894	0.02894	0.0305	24	30	17
IPI00400646.6	Protein_phosphatase_inhibitor_2	KLHYNEGLNIK	99.969142	0.126343985	0.997658493	0.99643308	0.722873392	0.977979004	0.417502686	0.047194625	0.806680171	0.672905962	0.384981715	0.867799586	0.093043456	1.093129431	-1.011130897	-1.01877173	-1.040218162	-1.007556719	-1.080044541	16694.66356	18249.42808	16510.88262	15872.51908	16387.05028	15172.56896	9.818468761	14.0271	14.1556	14.0111	13.9542	14.0003	13.8892	0.04469	0.04469	0.0471	0.04469	0.04469	0.0471	2	2	14
29747871	Citrate_synthase_like_[Mus_musculus]	GLVYETSVLDPDEGIR	99.99999967	0.027146056	0.997658493	0.99643308	0.797906375	0.977979004	0.579003633	0.004994874	0.433187725	0.960243222	0.547476217	0.46195319	0.240713102	1.147208288	-1.03874044	-1.002348763	-1.029565657	1.036306402	-1.058769434	13202.89719	15146.47308	12710.48732	12345.48496	13171.95938	12440.81946	10.50177378	13.6886	13.8867	13.6337	13.5917	13.6852	13.6028	0.04778	0.04778	0.05036	0.04778	0.04778	0.05036	6	8	14
IPI00190943.2	Isoform_1_of_Glial_fibrillary_acidic_protein,_astrocyte	HLQEYQDLLNVK	99.99999088	0.091373951	0.997658493	0.99643308	0.275217474	0.977979004	0.673644494	0.029448519	0.084986883	0.313148786	0.028622617	0.447970308	0.360321719	-1.096068005	1.076704128	1.042606928	-1.099385177	-1.032703792	1.039607588	15544.74781	14182.28408	16737.09414	15224.0493	16207.06176	16848.98439	9.179471381	13.9241	13.7918	14.0308	13.8941	13.9843	14.0404	0.04179	0.04179	0.04405	0.04179	0.04179	0.04405	14	17	56
IPI00230956.1	Isoform_GLAST-1A_of_Excitatory_amino_acid_transporter_1	IVQVTAADAFLDLIR	100	0.00800401	0.997658493	0.99643308	0.676746044	0.977979004	0.453723009	0.000420782	0.48372633	0.727528884	0.311782861	0.717025163	0.134302011	1.24321836	-1.042755511	-1.020443324	1.062501041	1.02186519	1.09448212	7764.501281	9652.970547	7446.137855	7911.529224	7608.94907	8327.858712	12.97207201	12.9227	13.2368	12.8623	12.9497	12.8935	13.0237	0.05893	0.05893	0.06212	0.05893	0.05893	0.06212	5	8	52
IPI00231955.5	Calmodulin	EAFSLFDKDGDGTITTK	99.99999996	0.018472664	0.997658493	0.99643308	0.333651543	0.977979004	0.697837817	0.002237831	0.740804332	0.36958339	0.041058499	0.585758991	0.397553221	-1.279381781	1.026521857	1.071803037	-1.179277245	1.044111267	-1.06944908	31772.64818	24834.376	32615.31781	27657.03989	34054.02081	31842.58275	17.25748826	14.9555	14.6001	14.9933	14.7554	15.0555	14.9587	0.07816	0.07816	0.08238	0.07816	0.07816	0.08238	15	26	36
230824	Chain_,_Calmodulin	EAFSLFDKDGDGTITTK	99.99999996	0.0199371	0.997658493	0.99643308	0.336582112	0.977979004	0.684782715	0.002597519	0.730168805	0.347544697	0.04684636	0.567170947	0.370956579	-1.311539095	1.03100543	1.084636879	-1.196370421	1.05201859	-1.082712762	38393.85412	29273.89223	39584.27206	33086.96985	41643.3901	38462.08482	19.34203368	15.2286	14.8373	15.2726	15.014	15.3458	15.2311	0.08743	0.08743	0.09216	0.08743	0.08743	0.09216	14	23	36
119348	ENOG_MOUSE_Gamma-enolase_(2-phospho-D-glycerate_hydro-lyase)_(Neural_enolase)_(Neuron-specific_enol	FTANVGIQIVGDDLTVTNPK	100	0.005098407	0.997658493	0.99643308	0.502800017	0.977979004	0.883541706	0.000139483	0.705813657	0.423188027	0.141358633	0.249213353	0.694212246	-1.160545299	1.014219665	-1.029660181	-1.05712785	-1.044301605	-1.014814822	23604.08085	20338.7846	23939.72298	22646.00538	22924.14651	22589.48727	8.109413738	14.5267	14.3119	14.5471	14.467	14.4846	14.4634	0.03694	0.03694	0.03893	0.03694	0.03694	0.03893	25	46	34
IPI00555185.1	RAB10,_member_RAS_oncogene_family	LQIWDTAGQER	99.99960398	0.022654948	0.997658493	0.99643308	0.908280262	0.977979004	0.648595629	0.003416645	0.67401046	0.970357432	0.798248596	0.700558726	0.305395885	1.211156325	-1.02751014	-1.002334195	-1.016618795	1.025117316	-1.068659617	13722.58461	16620.19514	13355.1817	13136.86287	13690.62802	12811.02776	14.03037482	13.7443	14.0206	13.7051	13.6813	13.7409	13.6451	0.0637	0.0637	0.06714	0.0637	0.0637	0.06714	3	3	14
37700232	nucleoside-diphosphate_kinase_1_[Mus_musculus]	VMLGETNPADSKPGTIR	100	0.1613318	0.997658493	0.99643308	0.719614739	0.977979004	0.260206946	0.07135475	0.657765594	0.918014909	0.381601416	0.587239967	0.022343614	-1.079985242	1.019319094	-1.004333014	1.038624185	-1.023735818	1.106418029	30798.82723	28517.82231	31393.83266	32606.39385	30665.95123	33929.36131	9.367286438	14.9106	14.7996	14.9382	14.9929	14.9044	15.0502	0.04264	0.04264	0.04495	0.04264	0.04264	0.04495	8	11	41
IPI00194404.5	Nucleoside_diphosphate_kinase_A	VMLGETNPADSKPGTIR	100	0.033255198	0.997658493	0.99643308	0.868162741	0.977979004	0.448976523	0.006765057	0.844857766	0.774051572	0.694530193	0.63497576	0.122325756	-1.113666575	1.00774103	-1.011074309	1.015604743	-1.018901066	1.063522283	26214.85469	23539.23094	26417.78468	26830.0274	25927.72307	27574.71123	8.549404254	14.6781	14.5228	14.6892	14.7116	14.6622	14.7511	0.03893	0.03893	0.04104	0.03893	0.03893	0.04104	13	18	5
IPI00231925.7	Guanine_nucleotide-binding_protein_G(i),_alpha-2_subunit	LLLLGAGESGK	99.9999872	0.004964405	0.997658493	0.99643308	0.225498692	0.977979004	0.260206946	0.000088736	0.849608744	0.763661131	0.01494374	0.629881792	0.022639642	1.235943893	-1.009805136	1.015177601	1.137571209	1.025131555	1.127826548	13292.89514	16429.27257	13163.82208	14974.78499	13494.6494	15219.62384	11.17853764	13.6984	14.004	13.6843	13.8702	13.7201	13.8936	0.05084	0.05084	0.05359	0.05084	0.05084	0.05359	5	5	19
IPI00231633.4	Ras-related_protein_Rab-1B	LQIWDTAGQER	99.99960398	0.024156887	0.997658493	0.99643308	0.524394136	0.977979004	0.559541198	0.004224004	0.354653852	0.895165947	0.160015125	0.292774475	0.221898052	1.135797583	-1.041672857	1.00565023	1.064295494	1.047558548	-1.055533808	14541.75738	16516.49288	13960.00412	14857.56948	14623.92165	13854.52701	9.536052401	13.8279	14.0116	13.769	13.8589	13.836	13.7581	0.04341	0.04341	0.04575	0.04341	0.04341	0.04575	3	3	67
15986733	AF408432_1_GTP-binding_protein_RAB4_[Mus_musculus]	LQIWDTAGQER	99.99960398	0.149131355	0.997658493	0.99643308	0.143798088	0.977979004	0.146792151	0.064595181	0.808754206	0.379514678	0.004437198	0.538336521	0.00664537	1.118762119	1.014966115	1.0540932	-1.199209907	1.038550139	-1.18846384	17242.03487	19289.73546	17500.08115	14593.00914	18174.71171	15292.60807	13.34927751	14.0736	14.2355	14.0951	13.833	14.1496	13.9005	0.06063	0.06063	0.06391	0.06063	0.06063	0.06391	2	2	102
IPI00388687.3	PREDICTED:_similar_to_solute_carrier_family_25_(mitochondrial_carrier,_Aralar),_member_12	NIFLQYASTEVDGEHYMTPEDFVQR	99.99994504	0.009811376	0.997658493	0.99643308	0.614611321	0.977979004	0.670153176	0.000709497	0.86770303	0.5795476	0.242332464	0.708984422	0.339199344	1.265782952	1.011322936	1.037174075	-1.0827922	1.025561706	-1.067030491	3886.567281	4919.550604	3930.574632	3630.035968	4031.046825	3777.817841	14.71723368	11.9243	12.2643	11.9405	11.8258	11.9769	11.8833	0.06678	0.06678	0.0704	0.06678	0.06678	0.0704	2	3	54
IPI00331865.3	Isoform_2_of_Drebrin-like_protein	VAGTGEGGLEELVEELNSGK	99.99999978	0.183443568	0.997658493	0.99643308	0.175566192	0.977979004	0.37527005	0.085327465	0.888746116	0.69440283	0.007910386	0.808221583	0.065618649	-1.062854765	-1.005032239	-1.013825381	1.103670843	-1.008749114	1.069459976	10023.71415	9430.934949	9973.524984	11007.48872	9887.022299	10573.77463	7.783098655	13.2911	13.2032	13.2839	13.4262	13.2713	13.3682	0.03545	0.03545	0.03737	0.03545	0.03545	0.03737	6	6	40
IPI00189358.2	Transcriptional_activator_protein_Pur-beta	GGGGPGGEQETQELASK	99.9999643	0.086069493	0.997658493	0.99643308	0.367357043	0.977979004	0.69561724	0.026558586	0.845823458	0.953428277	0.064566901	0.8016175	0.387378749	-1.067174998	1.005734529	-1.001672732	1.056808028	-1.007416854	1.025834357	9144.645458	8569.021457	9197.085695	9719.553998	9129.374459	9365.225975	6.374774509	13.1587	13.0649	13.167	13.2467	13.1563	13.1931	0.02905	0.02905	0.03063	0.02905	0.02905	0.03063	9	10	40
IPI00188688.1	Histone_H2a	VTIAQGGVLPNIQAVLLPK	99.99999981	0.004964405	0.997658493	0.99643308	0.797906375	0.977979004	0.994839219	6.86656E-05	0.605214508	0.694088809	0.544629004	0.893034542	0.984235159	1.364714964	1.039137453	1.028824003	-1.046044791	-1.010024505	1.001466707	10892.24139	14864.80482	11318.53598	10820.31676	11206.19938	11222.63559	16.17005518	13.411	13.8596	13.4664	13.4015	13.452	13.4541	0.0733	0.0733	0.07726	0.0733	0.0733	0.07726	5	6	3
IPI00200624.1	PREDICTED:_similar_to_H2A_histone_family,_member_J	VTIAQGGVLPNIQAVLLPK	99.99999981	0.004964405	0.997658493	0.99643308	0.797906375	0.977979004	0.994839219	6.86656E-05	0.605214508	0.694088809	0.544629004	0.893034542	0.984235159	1.364714964	1.039137453	1.028824003	-1.046044791	-1.010024505	1.001466707	10892.24139	14864.80482	11318.53598	10820.31676	11206.19938	11222.63559	16.17005518	13.411	13.8596	13.4664	13.4015	13.452	13.4541	0.0733	0.0733	0.07726	0.0733	0.0733	0.07726	5	6	3
IPI00559107.2	PREDICTED:_similar_to_Histone_H2A_type_1	VTIAQGGVLPNIQAVLLPK	99.99999981	0.004964405	0.997658493	0.99643308	0.797906375	0.977979004	0.994839219	6.86656E-05	0.605214508	0.694088809	0.544629004	0.893034542	0.984235159	1.364714964	1.039137453	1.028824003	-1.046044791	-1.010024505	1.001466707	10892.24139	14864.80482	11318.53598	10820.31676	11206.19938	11222.63559	16.17005518	13.411	13.8596	13.4664	13.4015	13.452	13.4541	0.0733	0.0733	0.07726	0.0733	0.0733	0.07726	5	6	3
IPI00767428.1	PREDICTED:_similar_to_H3_histone,_family_2_isoform_2	FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK	99.9967638	0.004964405	0.997658493	0.99643308	0.62797337	0.977979004	0.994153085	8.04003E-05	0.310938669	0.516365847	0.255322206	0.700163561	0.972679266	1.377704846	1.081875021	1.050129729	-1.09249231	-1.030229877	-1.002650223	9585.369121	13205.80949	10370.17142	9492.214562	10065.88107	10039.27476	16.85674487	13.2266	13.6889	13.3402	13.2125	13.2972	13.2934	0.07637	0.07637	0.0805	0.07637	0.07637	0.0805	4	4	3
IPI00195160.1	Sulfated_glycoprotein_1_precursor	EVVDSYLPVILDMIK	99.99999875	0.05841529	0.997658493	0.913310826	0.541686564	0.977979004	0.579003633	0.015149563	0.647100279	0.130472975	0.174381756	0.305423974	0.24152723	-1.150304762	1.026722725	1.089427864	-1.082062647	1.0610731	-1.070204158	18901.57873	16431.80081	19406.68041	17934.89541	20591.90654	19241.10122	12.5134121	14.2062	14.0042	14.2443	14.1305	14.3298	14.2319	0.05687	0.05687	0.05994	0.05687	0.05687	0.05994	5	5	70
26337455	unnamed_protein_product_[Mus_musculus]	KGFNEGLWEIENNPGVK	99.99989761	0.005112477	0.997658493	0.99643308	0.86551567	0.977979004	0.976526859	0.000155259	0.743734195	0.785315823	0.685076795	0.554314937	0.907332956	-1.350680931	1.02519005	-1.020378268	-1.031352024	-1.046081647	1.00889359	61987.42962	45893.46619	63548.89605	61617.07598	60749.46082	61289.74162	16.58706289	15.9197	15.486	15.9556	15.911	15.8906	15.9034	0.07516	0.07516	0.07923	0.07516	0.07516	0.07923	2	2	29
IPI00208306.1	Translationally-controlled_tumor_protein	DLISHDELFSDIYK	100	0.024155562	0.997658493	0.99643308	0.733834025	0.988483763	0.849367056	0.004009806	0.689636533	0.613753242	0.4070582	0.92653308	0.628131329	-1.081207732	1.010755486	1.013253438	1.022516822	1.002471372	1.013064715	13667.84767	12641.27813	13814.85201	14125.91856	13848.99364	14029.9268	5.802818153	13.7385	13.6259	13.7539	13.7861	13.7575	13.7762	0.02645	0.02645	0.02788	0.02645	0.02645	0.02788	3	6	121
IPI00197411.1	PREDICTED:_similar_to_Transcriptional_activator_protein_Pur-alpha	DYLGDFIEHYAQLGPSQPPDLAQAQDEPR	99.99994648	0.335603949	0.997658493	0.99643308	0.091880843	0.988483763	0.168229846	0.211718149	0.736566346	0.658407783	0.00189012	0.92500096	0.009805397	-1.034024899	-1.009237325	-1.011836144	1.093087093	-1.002575033	1.075617836	17330.78622	16760.51151	17172.16139	18770.66797	17128.05609	18423.23748	5.92223602	14.081	14.0328	14.0678	14.1962	14.0641	14.1692	0.02699	0.02699	0.02846	0.02699	0.02699	0.02846	8	8	40
IPI00231963.4	D-dopachrome_decarboxylase	PFVELETNLPASR	99.99999811	0.163109754	0.997658493	0.99643308	0.416332803	0.977979004	0.902279665	0.072327525	0.564035622	0.380302993	0.08375237	0.780061521	0.73970827	-1.050871425	1.016265984	1.024224736	1.050221003	1.007831367	1.009326179	22396.52285	21312.33045	22760.82433	23903.89576	22939.0727	23153.00659	6.054196445	14.451	14.3794	14.4743	14.545	14.4855	14.4989	0.0276	0.0276	0.02909	0.0276	0.0276	0.02909	7	7	43
IPI00365705.6	PREDICTED:_similar_to_Potassium-transporting_ATPase_alpha_chain_1	VIMVTGDHPITAK	100	0.017888166	0.997658493	0.99643308	0.733834025	0.977979004	0.907672112	0.001962587	0.894791394	0.700449523	0.416987421	0.612613157	0.751033839	1.446727724	-1.01558257	1.044783849	-1.099876241	1.061064267	1.037809261	11706.13841	16935.59498	11526.52552	10479.83863	12230.38435	12692.80614	25.73481845	13.515	14.0478	13.4927	13.3553	13.5782	13.6317	0.1155	0.1155	0.1218	0.1155	0.1155	0.1218	4	7	74
IPI00231475.6	Histone_H3.3	FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK	99.9904234	0.007569333	0.997658493	0.99643308	0.630797204	0.977979004	0.883541706	0.000320075	0.445658011	0.581931676	0.264665687	0.819566917	0.69173191	1.356853784	1.064498229	1.044833793	-1.096044709	-1.018820636	-1.032959582	11918.85883	16172.14871	12687.60412	11575.80892	12453.22648	12055.87004	17.84053363	13.541	13.9812	13.6311	13.4988	13.6042	13.5574	0.08076	0.08076	0.08512	0.08076	0.08076	0.08512	4	4	3
21362640	LGUL_MOUSE_Lactoylglutathione_lyase_(Methylglyoxalase)_(Aldoketomutase)_(Glyoxalase_I)_(Glx_I)_(Ketone-al	VLGLTLLQK	99.99925493	0.07564012	0.997658493	0.99643308	0.333651543	0.977979004	0.892168205	0.021054746	0.735713618	0.207671134	0.043018629	0.119898694	0.707193573	-1.082604133	-1.011698626	1.043481196	1.073682041	1.055688492	1.013029177	10374.66577	9583.064994	10254.69987	11010.28709	10825.76865	10966.8195	7.469803764	13.3408	13.2263	13.324	13.4266	13.4022	13.4209	0.03403	0.03403	0.03587	0.03403	0.03403	0.03587	4	5	8
IPI00764762.1	PREDICTED:_similar_to_histone_2a	VTIAQGGVLPNIQAVLLPK	99.99999981	0.005989378	0.997658493	0.99643308	0.805073754	0.977979004	0.883229884	0.000239575	0.70942437	0.597538976	0.567692007	0.887346355	0.690433418	1.428149222	1.035378831	1.049146857	-1.054816529	1.013297574	-1.037862187	15348.50722	21919.95863	15891.51946	15065.67163	16102.83811	15515.39145	20.4034076	13.9058	14.42	13.956	13.879	13.975	13.9214	0.09214	0.09214	0.09712	0.09214	0.09214	0.09712	4	5	3
IPI00213663.1	Isoform_Glt1_of_Excitatory_amino_acid_transporter_2	NDEVSSLDAFLDLIR	100	0.027999298	0.997658493	0.99643308	0.733834025	0.977979004	0.962983009	0.005215869	0.715172716	0.933894767	0.408024094	0.655986775	0.878240504	1.213301314	-1.025306183	1.005540909	-1.058459322	1.030987311	-1.010541454	10624.79596	12891.0789	10362.55914	9790.228995	10683.66699	10572.22041	14.90596363	13.3751	13.6541	13.3391	13.2571	13.3831	13.368	0.06763	0.06763	0.07129	0.06763	0.06763	0.07129	10	13	54
294543	dynein_heavy_chain	FGNPLLVQDVESYDPVLNPVLNR	99.99988218	0.00800401	0.997658493	0.99643308	0.412110301	0.977979004	0.70028075	0.000364421	0.608857659	0.269270723	0.077112219	0.11527887	0.405268208	1.20667766	-1.026396249	1.056545145	1.095562548	1.084433974	-1.043377668	3518.579898	4245.791757	3428.091149	3755.688275	3717.538509	3562.983865	11.04783034	11.7808	12.0518	11.7432	11.8749	11.8601	11.7989	0.05025	0.05025	0.05297	0.05025	0.05025	0.05297	5	5	95
IPI00327630.1	Dynein_heavy_chain,_cytosolic	FGNPLLVQDVESYDPVLNPVLNR	99.99988218	0.00800401	0.997658493	0.99643308	0.412110301	0.977979004	0.70028075	0.000364421	0.608857659	0.269270723	0.077112219	0.11527887	0.405268208	1.20667766	-1.026396249	1.056545145	1.095562548	1.084433974	-1.043377668	3518.579898	4245.791757	3428.091149	3755.688275	3717.538509	3562.983865	11.04783034	11.7808	12.0518	11.7432	11.8749	11.8601	11.7989	0.05025	0.05025	0.05297	0.05025	0.05025	0.05297	5	5	95
57012721	CISY_MOUSE_Citrate_synthase,_mitochondrial_precursor	GLVYETSVLDPDEGIR	99.99999967	0.129634737	0.997658493	0.99643308	0.691591891	0.977979004	0.28876815	0.050076047	0.482130491	0.830240122	0.329689829	0.363018474	0.030722885	1.113710088	-1.039823487	1.011635701	-1.055775061	1.051922562	-1.130337061	15883.8952	17690.05432	15275.56878	14468.5827	16068.71545	14215.86181	12.04850921	13.9553	14.1107	13.8989	13.8206	13.972	13.7952	0.05477	0.05477	0.05773	0.05477	0.05477	0.05773	10	12	10
IPI00189416.2	PREDICTED:_similar_to_tumor_protein,_translationally-controlled_1	VKPFMTGAAEKIK	99.9925129	0.009811376	0.997658493	0.99643308	0.855934899	0.977979004	0.977970118	0.000710584	0.949191355	0.835993122	0.669530586	0.890394143	0.91314467	-1.16897838	1.002857345	1.009065027	1.019310928	1.006189995	1.004896051	15862.39468	13569.45086	15907.71902	16214.91183	16006.18771	16084.55483	9.7212415	13.9533	13.7281	13.9574	13.985	13.9663	13.9734	0.04425	0.04425	0.04664	0.04425	0.04425	0.04664	2	3	118
IPI00326412.3	Gamma-enolase	CITGDQLGALYQDFVR	100	0.00800401	0.997658493	0.99643308	0.623815123	0.977979004	0.917773279	0.000420353	0.612182816	0.547817682	0.249526049	0.276877521	0.776471333	-1.152987152	1.019990877	-1.023115448	-1.046229941	-1.043568423	-1.01113744	24329.38154	21101.17314	24815.7472	23719.20953	23779.70304	23517.77524	8.461421522	14.5704	14.365	14.599	14.5338	14.5374	14.5215	0.03853	0.03853	0.04062	0.03853	0.03853	0.04062	29	58	34
IPI00464512.1	Similar_to_Murine_homolog_of_human_ftp-3	STGEAFVQFASQEIAEK	100	0.009811376	0.997658493	0.99643308	0.121228319	0.977979004	0.440189179	0.000723463	0.508737601	0.722865591	0.00351086	0.31601345	0.117025451	-1.12341541	1.022383346	-1.011612551	-1.107107883	-1.034255825	-1.054456217	23716.50898	21111.07677	24247.3638	21901.53659	23444.26129	22233.50853	7.250075985	14.5336	14.3657	14.5655	14.4187	14.5169	14.4404	0.03303	0.03303	0.03482	0.03303	0.03303	0.03482	5	5	71
IPI00188924.3	Ubiquinol-cytochrome-c_reductase_complex_core_protein_2,_mitochondrial_precursor	AVAQGNLSSADVQAAK	99.99999999	0.091194258	0.997658493	0.99643308	0.727515376	0.977979004	0.96842601	0.029166167	0.358219695	0.271626826	0.390871636	0.877807647	0.889781069	1.089546252	-1.037081088	-1.043394047	-1.034569913	-1.006087238	-1.005484953	13029.56797	14196.31695	12563.69258	12143.87971	12487.67712	12419.55644	8.564268231	13.6695	13.7932	13.617	13.5679	13.6082	13.6003	0.039	0.039	0.04111	0.039	0.039	0.04111	9	9	111
IPI00196794.2	Ras-related_protein_Rab-14	LQIWDTAGQER	99.99960398	0.07564012	0.997658493	0.99643308	0.726452056	0.977979004	0.348219477	0.021092788	0.437045423	0.577211769	0.38900807	0.189565046	0.052850495	1.14461947	-1.04675826	1.032371434	-1.051990772	1.080643326	-1.122550571	15760.40396	18039.66523	15056.39322	14312.28639	16270.59085	14494.30544	12.74988231	13.944	14.1389	13.8781	13.805	13.99	13.8232	0.05793	0.05793	0.06107	0.05793	0.05793	0.06107	2	2	10
IPI00368293.4	Histone_H2A_type_1	VTIAQGGVLPNIQAVLLPK	99.99999981	0.005232712	0.997658493	0.99643308	0.792374134	0.977979004	0.994153085	0.000197348	0.554679286	0.801013042	0.515883804	0.729212886	0.974422101	1.302281361	1.041098753	1.016841978	-1.045307159	-1.023855009	1.002184643	11486.70588	14958.92297	11958.79517	11440.46041	11680.16473	11705.68172	14.82264459	13.4877	13.8687	13.5458	13.4819	13.5118	13.5149	0.06726	0.06726	0.07089	0.06726	0.06726	0.07089	5	6	23
IPI00566481.2	PREDICTED:_similar_to_histone_2,_H2ac	VTIAQGGVLPNIQAVLLPK	99.99999981	0.005232712	0.997658493	0.99643308	0.792374134	0.977979004	0.994153085	0.000197348	0.554679286	0.801013042	0.515883804	0.729212886	0.974422101	1.302281361	1.041098753	1.016841978	-1.045307159	-1.023855009	1.002184643	11486.70588	14958.92297	11958.79517	11440.46041	11680.16473	11705.68172	14.82264459	13.4877	13.8687	13.5458	13.4819	13.5118	13.5149	0.06726	0.06726	0.07089	0.06726	0.06726	0.07089	5	6	23
IPI00325762.1	Ras-related_protein_Rab-3A	MSESLDTADPAVTGAK	99.9999999	0.018395497	0.997658493	0.99643308	0.842694959	0.977979004	0.421432785	0.002102343	0.808962567	0.368976413	0.638459354	0.265716784	0.101407957	1.209870749	-1.014800253	1.054779484	-1.028987227	1.070390487	-1.106081557	12644.21224	15297.86253	12459.80399	12108.80336	13336.85567	12057.7507	13.21595448	13.6262	13.901	13.605	13.5638	13.7031	13.5577	0.06003	0.06003	0.06328	0.06003	0.06003	0.06328	11	12	12
IPI00210532.1	Transgelin-3	TTDIFQTVDLWEGK	99.99999947	0.05841529	0.997658493	0.99643308	0.930552243	0.977979004	0.910343272	0.015288116	0.835748734	0.227839113	0.845936094	0.331907077	0.75636521	-1.086844457	1.007133175	1.041348436	1.006683289	1.033972926	1.010695814	15817.20914	14553.33285	15930.03606	16036.50109	16471.226	16647.39916	7.434162521	13.9492	13.8291	13.9595	13.9691	14.0077	14.023	0.03387	0.03387	0.0357	0.03387	0.03387	0.0357	11	13	96
631898	S39345_unc-18_protein_homolog,_67K_-_rat	VLVVDQLSMR	99.99999984	0.017784128	0.997658493	0.99643308	0.868162741	0.977979004	0.673446244	0.001910523	0.648698658	0.839406302	0.692012468	0.514419759	0.353270659	1.202355182	-1.026884846	1.011543422	1.023330379	1.038738612	-1.055725954	12953.36329	15574.54347	12614.23161	12908.52641	13102.88943	12411.26012	12.65097391	13.661	13.9269	13.6228	13.656	13.6776	13.5994	0.05749	0.05749	0.0606	0.05749	0.05749	0.0606	21	29	48
IPI00231563.1	Isoform_3_of_Tropomyosin_1_alpha_chain	IQLVEEELDR	99.99989008	0.422851169	0.997658493	0.99643308	0.544217174	0.977979004	0.393067374	0.295754189	0.622101696	0.259439979	0.177312243	0.541940002	0.081758014	-1.031367114	1.015007702	1.033902312	1.041942978	1.018615237	1.05477209	14253.45386	13819.96155	14467.36545	15074.16984	14736.67889	15543.83759	6.545596081	13.799	13.7545	13.8205	13.8798	13.8471	13.9241	0.02983	0.02983	0.03144	0.02983	0.02983	0.03144	12	16	101
IPI00369419.3	PREDICTED:_similar_to_Cofilin-2	KEDLVFIFWAPESAPLK	100	0.131902815	0.997658493	0.99643308	0.199585822	0.994226451	0.643748362	0.052007396	0.550005701	0.527046322	0.011633002	0.985592241	0.299434953	-1.058083951	-1.017704554	-1.018243336	1.079274603	-1.000529409	1.031043453	15704.42156	14842.32092	15431.21871	16654.52245	15423.05361	15901.83844	6.35462167	13.9389	13.8574	13.9136	14.0236	13.9128	13.9569	0.02896	0.02896	0.03053	0.02896	0.02896	0.03053	8	14	40
IPI00382300.3	Ac2-048	LQIWDTAGQER	99.99960398	0.009985522	0.997658493	0.99643308	0.940752994	0.977979004	0.621993365	0.000776729	0.740567583	0.501692641	0.870690129	0.746013272	0.283628974	1.208179527	1.018278	1.036481271	1.008941154	1.017876524	-1.060724277	16385.00685	19796.02983	16684.492	16833.6706	16982.75271	16010.52514	11.88443068	14.0001	14.2729	14.0262	14.0391	14.0518	13.9667	0.05403	0.05403	0.05695	0.05403	0.05403	0.05695	4	4	26
IPI00364439.3	PREDICTED:_similar_to_Peptidyl-prolyl_cis-trans_isomerase_A	HTGPGILSMANAGPNTNGSQFFICTAK	99.99999538	0.088290774	0.997658493	0.99643308	0.473411924	0.977979004	0.485775688	0.027849433	0.881970021	0.636093767	0.120071821	0.542894085	0.161668334	-1.094500895	1.006135883	-1.019174882	1.066940784	-1.02542842	1.059932049	37398.61027	34169.55657	37628.08378	40146.9372	36694.9882	38894.19402	8.940830256	15.1907	15.0604	15.1995	15.293	15.1633	15.2473	0.04071	0.04071	0.04291	0.04071	0.04071	0.04291	5	8	40
47605479	CMC1_MOUSE_Calcium-binding_mitochondrial_carrier_protein_Aralar1_(Mitochondrial_aspartate_glutamate_carr	YGQVTPLEIDILYQLADLYNASGR	99.99999373	0.005065768	0.997658493	0.99643308	0.966345081	0.977979004	0.827199838	0.00011	0.91765039	0.561799031	0.92136262	0.644265575	0.575731087	1.225433245	1.005198227	1.028767992	1.004962511	1.023447878	1.028502968	5147.677287	6308.134879	5174.436081	5200.114275	5295.765626	5446.710662	10.89307003	12.3297	12.623	12.3372	12.3443	12.3706	12.4112	0.04955	0.04955	0.05223	0.04955	0.04955	0.05223	6	8	50
IPI00231880.6	Histone_H2A.Z	VGATAAVYSAAILEYLTAEVLELAGNASK	99.99999436	0.005098407	0.997658493	0.99643308	0.855934899	0.988483763	0.95987527	0.000132766	0.564256095	0.519393632	0.669916023	0.959406653	0.868824244	1.38232748	1.04786633	1.052193695	-1.035147786	1.004129692	1.013463676	7453.041025	10302.54342	7809.790743	7544.614259	7842.042776	7947.625502	17.67336835	12.8636	13.3307	12.9311	12.8812	12.937	12.9563	0.08001	0.08001	0.08434	0.08001	0.08001	0.08434	3	4	3
IPI00191730.1	Syntaxin-1B2	AIEQSIEQEEGLNR	100	0.055289859	0.997658493	0.99643308	0.554634429	0.977979004	0.453249617	0.014027827	0.927844142	0.301243663	0.185149688	0.273258774	0.13343547	1.105125719	-1.003682592	1.041907792	-1.055742745	1.045744713	-1.063518867	12716.02274	14052.80378	12669.36663	12000.42974	13248.92317	12457.62871	8.808652212	13.6344	13.7786	13.6291	13.5508	13.6936	13.6047	0.04011	0.04011	0.04228	0.04011	0.04011	0.04228	11	12	64
IPI00327144.6	Cofilin-1	EILVGDVGQTVDDPYTTFVK	100	0.029768056	0.997658493	0.99643308	0.630797204	0.977979004	0.569356066	0.005681446	0.945649599	0.800313206	0.263853528	0.858666425	0.233388179	-1.083071106	-1.001948452	-1.007056687	1.032618268	-1.005098301	1.034855672	18932.20149	17480.10947	18895.38473	19511.71946	18799.53903	19454.80959	6.190565936	14.2086	14.0934	14.2057	14.2521	14.1984	14.2478	0.02822	0.02822	0.02974	0.02822	0.02822	0.02974	19	33	124
IPI00326305.3	Sodium/potassium-transporting_ATPase_alpha-1_chain_precursor	GVGIISEGNETVEDIAAR	100	0.021225334	0.997658493	0.99643308	0.686643596	0.977979004	0.66199794	0.0030068	0.873341493	0.704143543	0.324822076	0.833368614	0.319741266	1.214533505	1.01032883	1.024124698	-1.065834602	1.013654829	1.06655901	11619.65093	14112.45537	11739.66833	11014.53106	11899.97149	12692.02182	14.02845067	13.5043	13.7847	13.5191	13.4271	13.5387	13.6316	0.06369	0.06369	0.06713	0.06369	0.06369	0.06713	24	32	77
IPI00188956.1	Thy-1_membrane_glycoprotein_precursor	VISLTACLVNQNLR	99.99999957	0.009811376	0.997658493	0.99643308	0.817753948	0.977979004	0.538840577	0.000740058	0.562174275	0.813391661	0.593035882	0.419195642	0.20999387	1.178255994	-1.027791177	1.010910339	1.025591424	1.039004727	1.061457978	15898.99403	18733.08501	15469.08982	15864.96585	16072.45744	17060.23818	10.25385164	13.9566	14.1933	13.9171	13.9536	13.9723	14.0584	0.04666	0.04666	0.04918	0.04666	0.04666	0.04918	7	8	50
IPI00324633.2	Glutamate_dehydrogenase_1,_mitochondrial_precursor	GFIGPGIDVPAPDMSTGER	99.99999994	0.009811376	0.997658493	0.99643308	0.831101159	0.977979004	0.924766593	0.00073838	0.86187588	0.717170843	0.606941304	0.598811075	0.796711283	1.083025195	1.004002116	-1.008130868	1.01189345	-1.012165525	1.005932288	13147.05273	14238.58934	13199.66876	13356.65836	13041.01793	13118.38101	4.974704105	13.6825	13.7975	13.6882	13.7053	13.6708	13.6793	0.02268	0.02268	0.02391	0.02268	0.02268	0.02391	22	25	62
IPI00191728.1	Calreticulin_precursor	HEQNIDCGGGYVK	99.99999831	0.113901111	0.997658493	0.846402451	0.83893122	0.92052399	0.708668856	0.0395725	0.773646207	0.075695995	0.628791136	0.045099891	0.41851394	-1.064649921	-1.008852482	1.055250315	1.014935561	1.0645919	-1.025171646	9425.431122	8853.08019	9342.724814	9482.263653	9946.189159	9701.974492	6.642144139	13.2023	13.112	13.1896	13.211	13.2799	13.2441	0.03027	0.03027	0.03191	0.03027	0.03027	0.03191	8	12	114
IPI00326433.10	10_kDa_heat_shock_protein,_mitochondrial	VLQATVVAVGSGGK	99.99999996	0.016275878	0.997658493	0.99643308	0.733834025	0.977979004	0.98752724	0.001636888	0.844501528	0.560285424	0.421620808	0.71034478	0.949154753	-1.137142339	1.007863914	1.022931531	-1.032712057	1.014950051	-1.002549519	17556.76939	15439.37711	17694.83431	17134.33497	17959.37299	17913.70165	8.664857763	14.0997	13.9143	14.111	14.0646	14.1324	14.1288	0.03946	0.03946	0.04159	0.03946	0.03946	0.04159	12	18	57
IPI00231650.6	Histone_H1.2	ASGPPVSELITK	99.958383	0.016770492	0.997658493	0.99643308	0.453191645	0.977979004	0.167542381	0.001727075	0.664307329	0.553819743	0.105140462	0.314106725	0.00957385	1.187146777	1.023552402	-1.031419425	1.091945411	-1.05571183	1.154299582	19503.36184	23153.35315	19962.71286	21798.19269	18909.24427	21826.93274	11.64746642	14.2514	14.4989	14.285	14.4119	14.2068	14.4138	0.05296	0.05296	0.05582	0.05296	0.05296	0.05582	2	2	25
IPI00204899.1	Septin-7	STLINSLFLTDLYSPEYPGPSHR	99.9999852	0.024155562	0.997658493	0.99643308	0.788902735	0.977979004	0.697837817	0.004165554	0.604771599	0.374888752	0.496464703	0.727416958	0.396284986	1.097211502	-1.016695142	-1.02808775	1.022015734	-1.01120553	1.027570499	9865.570127	10824.61702	9703.567685	9917.198846	9596.038979	9860.606559	6.928663403	13.2682	13.402	13.2443	13.2757	13.2282	13.2675	0.03157	0.03157	0.03328	0.03157	0.03157	0.03328	7	7	126
IPI00231451.4	Sodium/potassium-transporting_ATPase_alpha-3_chain	GVGIISEGNETVEDIAAR	100	0.021225334	0.997658493	0.99643308	0.783271466	0.977979004	0.666788291	0.002975011	0.92914193	0.907941528	0.474544591	0.840349253	0.326920895	1.22589234	-1.006016904	1.007621843	-1.049547504	1.013684607	1.068697248	11782.28525	14443.81324	11711.81637	11158.91975	11872.08797	12687.66775	14.68961884	13.5243	13.8182	13.5157	13.4459	13.5353	13.6311	0.06666	0.06666	0.07027	0.06666	0.06666	0.07027	47	66	77
IPI00208245.1	Protein_kinase_C_and_casein_kinase_substrate_in_neurons_protein_1	ALYDYDGQEQDELSFK	100	0.02581863	0.997658493	0.99643308	0.686643596	0.977979004	0.967192189	0.004653077	0.968965093	0.860494978	0.322860465	0.833711304	0.884914606	-1.07891714	-1.001032004	1.004545952	1.026683611	1.005582648	1.00384509	23476.46422	21759.28377	23452.26138	24078.0524	23583.1871	23673.86657	5.747104313	14.5189	14.4093	14.5174	14.5554	14.5255	14.531	0.0262	0.0262	0.02761	0.0262	0.0262	0.02761	20	26	121
IPI00206043.3	PREDICTED:_similar_to_protein_(peptidyl-prolyl_cis/trans_isomerase)_NIMA-interacting_1	GQMQKPFEDASFALR	99.99969906	0.703566371	0.997658493	0.99643308	0.091880843	0.977979004	0.119761122	0.5893876	0.539255286	0.783157117	0.001517937	0.379011962	0.003399124	-1.016342711	-1.019133586	1.008291398	1.108138081	1.027583628	1.098719739	17798.78556	17512.58249	17464.62466	19353.21566	17946.36237	19718.02258	6.681829736	14.1195	14.0961	14.0921	14.2403	14.1314	14.2672	0.03045	0.03045	0.0321	0.03045	0.03045	0.0321	2	2	30
31543349	N-ethylmaleimide_sensitive_fusion_protein_[Mus_musculus]	VLDDGELLVQQTK	100	0.073490061	0.997658493	0.99643308	0.367357043	0.977979004	0.883229884	0.020083399	0.168855786	0.25184803	0.063252636	0.790182786	0.689640815	1.076701476	-1.045159339	-1.036348109	1.061924515	1.008502192	-1.012793389	13819.07517	14879.01864	13221.97932	14040.74398	13334.39513	13165.95791	6.897840113	13.7544	13.861	13.6907	13.7773	13.7029	13.6845	0.03143	0.03143	0.03313	0.03143	0.03143	0.03313	25	28	28
46577034	RB39B_MOUSE_Ras-related_protein_Rab-39B	LQIWDTAGQER	99.99960398	0.140204014	0.997658493	0.99643308	0.691591891	0.977979004	0.285873291	0.058805569	0.854002023	0.780229352	0.334438854	0.648916544	0.029077398	1.092477801	-1.008735852	1.012922354	-1.046888478	1.021771093	-1.111342279	19052.18477	20814.08891	18887.18909	18041.26178	19298.38385	17364.93267	10.26329857	14.2177	14.3453	14.2051	14.139	14.2362	14.0839	0.0467	0.0467	0.04923	0.0467	0.0467	0.04923	2	2	10
IPI00212731.1	Cathepsin_D_precursor	NIFSFYLNRDPTGQPGGELMLGGTDSR	99.99995408	0.384647147	0.997658493	0.685064733	0.849985868	0.977979004	0.809289183	0.254089067	0.637150273	0.033666038	0.650277361	0.105146949	0.549391742	-1.038903513	1.016263615	1.074877099	1.015626091	1.057675472	1.02070081	12752.16996	12274.64322	12959.56635	13162.07371	13707.01546	13990.76178	7.410344381	13.6385	13.5834	13.6617	13.6841	13.7426	13.7722	0.03376	0.03376	0.03559	0.03376	0.03376	0.03559	4	4	32
IPI00190397.1	Complexin-2	AALEQPCEGSLTRPK	100	0.082059774	0.997658493	0.99643308	0.666252843	0.977979004	0.802908043	0.024946171	0.879785731	0.321517841	0.298597146	0.265261923	0.536305774	-1.12391329	-1.007931049	1.051939038	1.056089455	1.060282018	1.032886935	12170.71268	10828.87157	12074.94569	12752.22282	12802.84779	13223.89421	11.34865502	13.5711	13.4026	13.5597	13.6385	13.6442	13.6909	0.05161	0.05161	0.0544	0.05161	0.05161	0.0544	4	6	8
IPI00192246.1	Cytochrome_c_oxidase_polypeptide_Va,_mitochondrial_precursor	WVTYFNKPDIDAWELR	100	0.015839877	0.997658493	0.99643308	0.950644423	0.977979004	0.763172892	0.001538731	0.814651386	0.601559147	0.890889631	0.458440116	0.490175046	-1.178712175	-1.011975063	1.026171031	-1.006988776	1.038459494	-1.035733827	20913.44966	17742.62631	20665.97333	20522.54585	21460.77621	20720.3585	11.02891081	14.3521	14.1149	14.335	14.3249	14.3894	14.3388	0.05016	0.05016	0.05288	0.05016	0.05016	0.05288	11	19	57
IPI00190348.1	PREDICTED:_similar_to_H2B_histone_family,_member_T	KESYSVYVYK	99.9991991	0.015074205	0.997658493	0.99643308	0.89755911	0.977979004	0.300507042	0.001422854	0.374513623	0.629203924	0.761853119	0.177033315	0.033217011	1.140519624	1.036557691	-1.01913115	1.012286227	-1.056388232	1.09164745	14780.29615	16857.21781	15320.62965	15508.86238	14502.84014	15831.98845	8.740627168	13.8514	14.0411	13.9032	13.9208	13.824	13.9506	0.0398	0.0398	0.04195	0.0398	0.0398	0.04195	6	7	25
IPI00215523.1	Branched-chain-amino-acid_aminotransferase,_cytosolic	HITMDDLSTALEENRVK	99.99993828	0.753613797	0.997658493	0.99643308	0.149698425	0.977979004	0.071235349	0.654567412	0.498120445	0.855429026	0.00540791	0.616381922	0.000852777	1.019161529	1.030003992	1.00775257	-1.134059778	-1.022080244	-1.165794202	10883.71441	11092.26302	11210.2693	9885.077942	10968.09117	9408.25675	9.451981834	13.4099	13.4373	13.4525	13.271	13.421	13.1997	0.04303	0.04303	0.04535	0.04303	0.04303	0.04535	3	3	24
IPI00207891.2	31_kDa_protein	LTLSALVDGK	99.99987635	0.010258389	0.997658493	0.99643308	0.966345081	0.977979004	0.849394654	0.000820671	0.654836167	0.686110145	0.920462925	0.401864364	0.63874478	1.261810845	-1.030700315	1.026958976	1.006770445	1.05848694	1.032266447	12148.52784	15329.14417	11786.67326	11866.47428	12476.03971	12878.59718	14.71519951	13.5685	13.904	13.5249	13.5346	13.6069	13.6527	0.06677	0.06677	0.07039	0.06677	0.06677	0.07039	3	3	74
IPI00362072.2	Actin-like_protein_2	DLMVGDEASELR	99.99994995	0.02581863	0.997658493	0.99643308	0.626575268	0.977979004	0.985692829	0.004687406	0.263619319	0.969251909	0.251346193	0.248213736	0.941465847	1.152880284	-1.057486807	1.00186637	1.059051895	1.059460469	-1.003656015	10317.10327	11894.38495	9756.247739	10332.37265	10336.3588	10298.70658	10.79594109	13.3328	13.538	13.2521	13.3349	13.3354	13.3302	0.04911	0.04911	0.05177	0.04911	0.04911	0.05177	3	3	47
IPI00362341.2	PREDICTED:_similar_to_RAN_binding_protein_1	TLEEDEEELFK	99.99998692	0.018472664	0.997658493	0.99643308	0.343544627	0.977979004	0.962983009	0.002142656	0.398643076	0.846480289	0.053789273	0.302948599	0.875708468	-1.132675597	1.03429078	-1.007531246	-1.08131201	-1.042080279	1.006246568	13584.52162	11993.30298	14050.34546	12993.79396	13482.97799	13567.20032	8.638372794	13.7297	13.5499	13.7783	13.6655	13.7189	13.7278	0.03934	0.03934	0.04146	0.03934	0.03934	0.04146	2	2	80
IPI00202027.3	Ratsg1	STGEAFVQFASQEIAEK	100	0.028579115	0.997658493	0.99643308	0.467884871	0.977979004	0.993109576	0.005356543	0.251087791	0.918963333	0.114965997	0.293532332	0.959086585	-1.087537963	1.035025193	1.002955869	-1.048698651	-1.03197481	-1.001530123	14945.72791	13742.71833	15469.20491	14750.85802	14989.90553	14967.00417	6.462223314	13.8674	13.7464	13.9171	13.8485	13.8717	13.8695	0.02945	0.02945	0.03104	0.02945	0.02945	0.03104	7	8	80
IPI00367377.3	36_kDa_protein	IFVGGIKEDTEEYNLR	99.9966258	0.022756225	0.997658493	0.846402451	0.416332803	0.757639751	0.8224463	0.003492146	0.320086785	0.093440328	0.082783246	0.010173318	0.56410805	-1.101398044	1.033083943	-1.055408726	-1.059027574	-1.090325808	1.018998503	26033.49604	23636.77345	26894.78673	25395.73793	24666.74323	25135.37442	7.065375788	14.6681	14.5287	14.715	14.6323	14.5903	14.6174	0.03219	0.03219	0.03393	0.03219	0.03219	0.03393	4	4	103
IPI00205745.3	Isoform_Mitochondrial_of_Peroxiredoxin-5,_mitochondrial_precursor	ETDLLLDDSLVSLFGNR	99.99999999	0.008921586	0.997658493	0.99643308	0.792374134	0.977979004	0.849367056	0.000502544	0.720401896	0.790366814	0.511830606	0.537998045	0.636158612	-1.140311804	1.013165376	-1.009497422	-1.024297368	-1.022787836	-1.017446003	18539.03132	16257.86146	18783.10465	18337.55044	18364.61482	18049.71937	7.922616188	14.1783	13.9888	14.1971	14.1625	14.1646	14.1397	0.03609	0.03609	0.03804	0.03609	0.03609	0.03804	14	19	34
IPI00190557.2	Prohibitin-2	IYLTADNLVLNLQDESFTR	99.9999053	0.024155562	0.997658493	0.99643308	0.269624476	0.977979004	0.69561724	0.004112201	0.299364717	0.632999352	0.024959508	0.563927894	0.388080659	1.199359495	-1.067386479	-1.029512404	1.154461871	1.036788361	1.0556411	7668.805988	9197.655279	7184.657237	8294.412835	7448.969003	7863.437828	13.60197615	12.9048	13.1671	12.8107	13.0179	12.8628	12.9409	0.06177	0.06177	0.06511	0.06177	0.06177	0.06511	2	2	35
IPI00205693.1	Sodium/potassium-transporting_ATPase_alpha-2_chain_precursor	GVGIISEGNETVEDIAAR	100	0.014413657	0.997658493	0.99643308	0.876899711	0.977979004	0.426869209	0.001284294	0.911683687	0.882493274	0.713545822	0.798936423	0.108207426	1.227474212	-1.006917658	1.008982458	-1.023092852	1.015962253	1.106380596	11232.09347	13787.10507	11154.92749	10903.14283	11332.98527	12538.595	13.52296444	13.4553	13.751	13.4454	13.4125	13.4682	13.6141	0.06142	0.06142	0.06474	0.06142	0.06142	0.06474	33	41	77
IPI00464724.1	Protein_phosphatase_3,_catalytic_subunit,_gamma_isoform	YENNVMNIR	99.99994551	0.101319119	0.997658493	0.99643308	0.705475595	0.977979004	0.366287193	0.033418513	0.88487738	0.799429605	0.346690864	0.695133668	0.062106695	1.157399557	-1.010050939	1.017232311	-1.067448514	1.027456451	-1.140019586	12066.57166	13965.84468	11946.49813	11191.63873	12274.50657	10766.92604	15.04332946	13.5587	13.7696	13.5443	13.4501	13.5834	13.3943	0.06825	0.06825	0.07194	0.06825	0.06825	0.07194	5	6	10
IPI00480805.1	Ubiquinol_cytochrome_c_reductase_core_protein_2	AVAQGNLSSADVQAAK	99.99999999	0.126343985	0.997658493	0.970109364	0.788902735	0.977979004	0.924766593	0.045930204	0.276772018	0.174209295	0.49414169	0.809902212	0.796710362	1.072321075	-1.03931068	-1.048163207	-1.024449891	-1.008517691	1.009124701	13914.7695	14921.1006	13388.46003	13068.92621	13275.38442	13396.51833	7.646056782	13.7643	13.8651	13.7087	13.6739	13.6965	13.7096	0.03483	0.03483	0.03672	0.03483	0.03483	0.03672	10	10	111
IPI00200145.1	60S_acidic_ribosomal_protein_P1	AAGVNVEPFWPGLFAK	99.9999897	0.00800401	0.997658493	0.99643308	0.733834025	0.977979004	0.674046005	0.000376047	0.217727285	0.983969102	0.41039703	0.210672738	0.362829335	-1.15274666	-1.049066451	1.000754722	1.032373036	1.049858205	-1.035873383	19543.03799	16953.45444	18628.98004	19232.05669	19557.78756	18880.48083	8.370110545	14.2544	14.0493	14.1853	14.2312	14.2555	14.2046	0.03812	0.03812	0.04018	0.03812	0.03812	0.04018	2	2	116
IPI00776522.1	31_kDa_protein	NLYADTVLSGGTTMYPGIADR	99.99997102	0.139230592	0.997658493	0.836075007	0.343544627	0.977979004	0.119761122	0.057760805	0.868491153	0.065433927	0.05356104	0.101839914	0.003672354	-1.081284041	1.006908902	1.078744611	-1.085164506	1.071342808	-1.13416374	19300.75361	17849.846	19434.10062	17908.89816	20820.58394	18357.6526	9.023966715	14.2364	14.1236	14.2463	14.1284	14.3457	14.1641	0.04109	0.04109	0.04331	0.04109	0.04109	0.04331	4	6	105
IPI00551702.2	Dihydrolipoyllysine-residue_succinyltransferase_component_of_2-_oxoglutarate_dehydrogenase_complex,_mitoch	NVETMNYADIER	100	0.018395497	0.997658493	0.99643308	0.541686564	0.977979004	0.683461668	0.002099697	0.876878814	0.570783654	0.174577999	0.691080754	0.36945985	-1.131033279	1.006101609	1.021933386	-1.055252364	1.015735764	-1.036005901	14453.15882	12778.72109	14541.34634	13779.9704	14770.16552	14256.83533	8.518970935	13.8191	13.6415	13.8279	13.7503	13.8504	13.7994	0.0388	0.0388	0.04089	0.0388	0.0388	0.04089	9	10	57
IPI00231139.6	transketolase	NMAEQIIQEIYSQVQSK	99.99999998	0.023226989	0.997658493	0.99643308	0.797906375	0.983201098	0.811601962	0.003746354	0.528063685	0.445620058	0.547613464	0.910584535	0.555274274	1.144556757	-1.029454777	-1.03477748	1.028047592	-1.00517041	1.027503716	8975.116508	10272.53025	8718.320329	8962.848224	8673.47491	8912.027702	9.970684586	13.1317	13.3265	13.0898	13.1297	13.0824	13.1215	0.04538	0.04538	0.04783	0.04538	0.04538	0.04783	8	9	126
IPI00207964.2	Isoform_4_of_Tropomyosin_1_alpha_chain	SLQEQADAAEER	99.99999928	0.28341012	0.997658493	0.99643308	0.706612353	0.977979004	0.496640976	0.164215921	0.464568872	0.301775634	0.353462759	0.78181038	0.174566916	-1.041597589	1.022106082	1.030585718	1.028175193	1.008296239	1.041695965	13513.79381	12974.10243	13812.53084	14201.70156	13927.1229	14507.82772	6.46571084	13.7221	13.6633	13.7537	13.7938	13.7656	13.8245	0.02947	0.02947	0.03106	0.02947	0.02947	0.03106	12	15	101
IPI00197888.2	Isoform_1_of_Tropomyosin_1_alpha_chain	IQLVEEELDR	99.99989008	0.512834081	0.997658493	0.99643308	0.608678208	0.977979004	0.38112535	0.386237325	0.460675564	0.27791204	0.238410076	0.747233536	0.070449263	-1.025898525	1.022595829	1.032605179	1.036506014	1.009788177	1.05709504	14074.51153	13719.20438	14392.53679	14917.95094	14533.41349	15363.19931	6.550010956	13.7808	13.7439	13.813	13.8648	13.8271	13.9072	0.02985	0.02985	0.03147	0.02985	0.02985	0.03147	10	13	101
IPI00207335.1	Platelet-activating_factor_acetylhydrolase_IB_subunit_beta	DKEPDVLFVGDSMVQLMQQYEIWR	99.99999908	0.908474472	0.997658493	0.99643308	0.341387261	0.977979004	0.15504909	0.843898424	0.22254994	0.546271444	0.048336786	0.073643096	0.008328351	-1.005917806	1.038541449	-1.018272988	-1.063897033	-1.057518704	-1.087662162	11002.92072	10938.19063	11426.98923	10740.69095	10805.47246	9934.585237	6.674376512	13.4256	13.4171	13.4802	13.3908	13.3995	13.2782	0.03042	0.03042	0.03206	0.03042	0.03042	0.03206	5	5	134
IPI00231505.4	Guanine_nucleotide-binding_protein_G(o)_subunit_alpha_1	AMDTLGVEYGDKER	100	0.106631451	0.997658493	0.99643308	0.423679834	0.980938512	0.916967389	0.036071896	0.938087438	0.960901677	0.087841504	0.900221286	0.774444457	1.110412825	1.003910453	-1.002400317	-1.090883511	-1.006320156	-1.014508444	15765.26575	17505.95329	15826.91508	14508.34569	15727.51473	15502.59618	10.91528759	13.9445	14.0956	13.9501	13.8246	13.941	13.9202	0.04965	0.04965	0.05234	0.04965	0.04965	0.05234	14	21	111
IPI00369349.3	PREDICTED:_similar_to_ATPase,_H+_transporting,_V1_subunit_E-like_2_isoform_2	HMMAFIEQEANEKAEEIDAK	99.9994454	0.049803297	0.997658493	0.99643308	0.198010279	0.977979004	0.405470553	0.012066627	0.170105795	0.332606692	0.010840992	0.662310085	0.08665485	-1.146868958	1.078200173	1.052870516	-1.153768603	-1.024057714	-1.099129202	14745.51	12857.18817	15898.61143	13779.72272	15525.11271	14124.9206	11.82051068	13.848	13.6503	13.9566	13.7503	13.9223	13.786	0.05374	0.05374	0.05665	0.05374	0.05374	0.05665	4	4	69
IPI00211616.1	4F2_cell-surface_antigen_heavy_chain	YLVVLNFQDVGLSAR	99.99999993	0.214570897	0.997658493	0.99643308	0.727515376	0.977979004	0.710536491	0.107162836	0.203167278	0.27583725	0.393632658	0.829146142	0.422261686	-1.075385017	1.060458503	1.050034386	1.039956564	-1.009927406	1.037529656	11673.28734	10854.98417	12379.03681	12873.66059	12257.3531	12717.36735	9.937343691	13.5109	13.4061	13.5956	13.6521	13.5814	13.6345	0.04522	0.04522	0.04767	0.04522	0.04522	0.04767	5	6	21
IPI00325189.4	Nucleoside_diphosphate_kinase_B	VMLGETNPADSKPGTIR	100	0.05841529	0.997658493	0.99643308	0.83893122	0.977979004	0.670153176	0.015196552	0.428419347	0.753545067	0.627407951	0.625544197	0.344498801	-1.086307349	1.02740653	1.01046148	1.016678296	-1.016769615	1.03284539	24548.69503	22598.29601	25221.48957	25642.14103	24805.51072	25620.25738	7.382875375	14.5834	14.4639	14.6224	14.6462	14.5984	14.645	0.03364	0.03364	0.03546	0.03364	0.03364	0.03546	10	16	118
IPI00188732.2	21_kDa_protein	AGGAFDPYTLVR	99.99985096	0.029768056	0.997658493	0.99643308	0.792374134	0.977979004	0.752607186	0.005647432	0.79305797	0.552103508	0.519929213	0.401300508	0.475061112	1.250073054	-1.021163489	1.047352347	-1.052799523	1.069517977	-1.058806174	5606.019102	7007.933418	5489.835039	5214.511327	5871.477265	5545.37498	17.41518392	12.4528	12.7748	12.4225	12.3483	12.5195	12.4371	0.07886	0.07886	0.08312	0.07886	0.07886	0.08312	2	2	54
IPI00214192.1	SH3-containing_GRB2-like_protein_1	TIEYLQPNPASR	99.99997424	0.259972433	0.997658493	0.99643308	0.091880843	0.977979004	0.998755577	0.141127892	0.309230876	0.754632258	0.001800703	0.188443727	0.998755577	-1.0421182	-1.029554772	1.008711804	1.097822135	1.038524051	1.000044452	13028.52035	12501.96028	12654.51892	13892.41098	13142.02226	13142.60645	6.179122813	13.6694	13.6099	13.6274	13.762	13.6819	13.682	0.02816	0.02816	0.02969	0.02816	0.02816	0.02969	4	5	91
IPI00208551.3	PREDICTED:_similar_to_chromosome_3_open_reading_frame_10	RIEYIEAR	99.9955853	0.023303514	0.997658493	0.99643308	0.794117156	0.977979004	0.687585021	0.00380846	0.675780346	0.904177397	0.530055228	0.763210916	0.377189497	-1.1467237	-1.019719791	-1.005481849	1.029785047	1.014160318	1.042221253	10505.15374	9161.015626	10302.00044	10608.846	10447.88004	10889.00262	10.13070618	13.3588	13.1613	13.3306	13.373	13.3509	13.4106	0.0461	0.0461	0.04859	0.0461	0.0461	0.04859	3	3	68
IPI00470288.3	Creatine_kinase_B-type	TFLVWINEEDHLR	100	0.140565361	0.997658493	0.99643308	0.903404554	0.977979004	0.670153176	0.059117775	0.72130135	0.374244838	0.781571285	0.609641663	0.336919675	1.081830308	-1.015133516	-1.037208414	-1.011740417	-1.021745807	-1.041424683	18427.52355	19935.45347	18152.80773	17942.1593	17766.46169	17059.76628	9.133515006	14.1696	14.283	14.1479	14.1311	14.1169	14.0583	0.04158	0.04158	0.04383	0.04158	0.04158	0.04383	26	43	55
IPI00230837.5	tyrosine_3-monooxygenase/tryptophan_5-monooxygenase_activation_protein,_beta_polypeptide	TAFDEAIAELDTLNEESYK	99.99999999	0.312831382	0.997658493	0.99643308	0.90918008	0.996058404	0.260206946	0.191186801	0.933419669	0.924888079	0.804497008	0.993440071	0.023473678	1.046880306	-1.002988213	-1.003282764	-1.008882164	-1.000293674	-1.086509142	14284.71513	14954.38694	14242.15654	14116.76909	14237.97521	13104.3308	7.74719599	13.8022	13.8683	13.7979	13.7851	13.7975	13.6778	0.03529	0.03529	0.0372	0.03529	0.03529	0.0372	17	32	134
IPI00782342.1	44_kDa_protein	DATNVGDEGGFAPNILENK	100	0.005098407	0.997658493	0.846402451	0.117623759	0.977979004	0.147881653	0.000127461	0.612432191	0.078201131	0.003226252	0.220891621	0.007127887	-1.164203378	-1.019413855	-1.068195961	-1.123569086	-1.047853092	-1.111473314	21158.70061	18174.40234	20755.75145	18473.05316	19807.883	17821.28526	8.224493901	14.369	14.1496	14.3412	14.1731	14.2738	14.1213	0.03746	0.03746	0.03948	0.03746	0.03746	0.03948	10	15	107
IPI00187731.4	Isoform_2_of_Tropomyosin_beta_chain	IQLVEEELDR	99.99989008	0.562373851	0.997658493	0.929766668	0.83893122	0.977979004	0.47991263	0.431527969	0.257029078	0.1340254	0.628222423	0.738568523	0.152475099	-1.023511926	1.035119764	1.045633777	1.014779568	1.010157291	1.044706782	13793.11871	13476.26575	14277.52978	14488.54551	14422.55081	15067.33664	6.56220281	13.7517	13.7181	13.8015	13.8226	13.816	13.8791	0.02991	0.02991	0.03152	0.02991	0.02991	0.03152	8	11	79
IPI00189519.1	19_kDa_protein	STELLIR	99.981907	0.009271791	0.997658493	0.99643308	0.715782389	0.977979004	0.979161445	0.000614587	0.454646542	0.653453221	0.370993137	0.754925626	0.922916778	1.278003556	1.053439485	1.030840563	-1.064349276	-1.021922811	1.006741946	11893.80773	15200.32858	12529.40669	11771.89384	12260.61945	12343.27988	15.12606576	13.5379	13.8918	13.613	13.5231	13.5817	13.5914	0.06862	0.06862	0.07233	0.06862	0.06862	0.07233	3	3	23
IPI00387771.5	Peptidyl-prolyl_cis-trans_isomerase_A	VKEGMSIVEAMER	100	0.253547667	0.997658493	0.99643308	0.557987386	0.977979004	0.343015874	0.13592685	0.374842985	0.680101962	0.190773603	0.199769129	0.046065282	-1.052322074	1.031450745	-1.01405992	1.046925093	-1.04595286	1.073259005	26564.46089	25243.66023	27399.93298	28685.67739	26196.14518	28115.24872	7.539871417	14.6972	14.6236	14.7419	14.808	14.6771	14.7791	0.03435	0.03435	0.03621	0.03435	0.03435	0.03621	20	36	104
IPI00555213.1	Phosphoprotein_enriched_in_astrocytes_15	ISEEDELDTK	99.99969984	0.126343985	0.997658493	0.846402451	0.656666972	0.977979004	0.893304386	0.04725495	0.33623231	0.093145338	0.291184897	0.490644958	0.710559832	-1.084361449	1.040543108	1.070544675	-1.044630546	1.028832603	-1.01539594	14067.72471	12973.28001	14638.07399	14012.68042	15060.12778	14831.7786	8.929307698	13.7801	13.6633	13.8374	13.7744	13.8784	13.8564	0.04066	0.04066	0.04286	0.04066	0.04066	0.04286	3	4	84
IPI00188313.1	Creatine_kinase,_sarcomeric_mitochondrial_precursor	LGYILTCPSNLGTGLR	100	0.022654948	0.997658493	0.99643308	0.733834025	0.977979004	0.979042717	0.003417661	0.915150146	0.520271631	0.424712601	0.464362208	0.920859607	1.184485888	1.006088662	-1.036367941	-1.04667499	-1.042678035	1.005676357	13186.22199	15618.89386	13266.50844	12674.90727	12723.49468	12795.71778	12.38679836	13.6867	13.931	13.6955	13.6297	13.6352	13.6434	0.0563	0.0563	0.05934	0.0563	0.0563	0.05934	2	2	111
IPI00777730.1	39_kDa_protein	VNQIGSVTESLQACK	100	0.004964405	0.997658493	0.066410512	0.908280262	0.977979004	0.927911986	4.23243E-05	0.051274452	0.000379489	0.796428871	0.094231178	0.80174547	-1.123369171	-1.054770186	-1.103934436	-1.006954009	-1.046611338	-1.006767732	33368.63682	29704.07029	31635.93099	31417.45373	30227.00963	30023.81647	5.821592064	15.0262	14.8584	14.9493	14.9393	14.8836	14.8738	0.02654	0.02654	0.02797	0.02654	0.02654	0.02797	8	15	58
IPI00561435.2	50_kDa_protein	FTATAGIQVVGDDLTVTNPK	100	0.004964405	0.997658493	0.205619659	0.63922298	0.977979004	0.836004321	4.46098E-05	0.099678223	0.001409963	0.279004859	0.114139654	0.58776072	-1.129588204	-1.048217734	-1.096618684	-1.031209306	-1.046174519	-1.01544146	29174.62549	25827.66479	27832.60056	26990.25347	26604.16599	26199.60582	6.119754802	14.8324	14.6566	14.7645	14.7202	14.6994	14.6773	0.02789	0.02789	0.0294	0.02789	0.02789	0.0294	13	22	58
202225	alpha-tubulin	TIQFVDWCPTGFK	100	0.046230241	0.997658493	0.99643308	0.919905782	0.977979004	0.503151385	0.010725416	0.839869776	0.798220291	0.822132939	0.652301159	0.181134499	1.220431475	-1.01582617	1.019527476	1.017623895	1.035662692	-1.110495928	19584.47835	23901.51379	19279.35992	19619.13734	19966.91379	17980.1774	16.94860787	14.2574	14.5448	14.2348	14.26	14.2853	14.1341	0.07678	0.07678	0.08093	0.07678	0.07678	0.08093	28	55	4
IPI00192628.7	Vesicle-associated_membrane_protein_1	VNVDKVLER	99.9941298	0.703271862	0.997658493	0.86359048	0.279701276	0.977979004	0.448976523	0.586741594	0.005322771	0.110277377	0.030231403	0.190085562	0.123313898	1.030235554	-1.176759794	-1.092511489	1.132763457	1.077114343	-1.091599955	8825.755924	9092.607544	7500.048835	8495.781244	8078.410174	7400.522635	12.22278146	13.1075	13.1505	12.8727	13.0525	12.9799	12.8534	0.05556	0.05556	0.05856	0.05556	0.05556	0.05856	3	3	129
6093900	RAB3B_RAT_Ras-related_protein_Rab-3B	TYSWDNAQVILVGNK	99.99999907	0.054262451	0.997658493	0.99643308	0.81234446	0.977979004	0.271960735	0.013602909	0.61668712	0.270471437	0.576532468	0.118416123	0.027040667	1.193930467	-1.036552002	1.080352665	-1.040878197	1.119841718	-1.17609964	16937.81718	20222.57597	16340.5378	15698.7992	18298.81593	15558.89935	15.60960946	14.048	14.3037	13.9962	13.9384	14.1595	13.9255	0.07079	0.07079	0.07462	0.07079	0.07079	0.07462	4	4	12
IPI00287309.1	Glycoprotein_m6a	QFGIVTIGEEK	99.997252	0.005098407	0.997658493	0.639633748	0.333651543	0.92052399	0.893774223	0.000126238	0.873071533	0.023277491	0.043859246	0.039245047	0.713056083	1.17159458	1.006324259	1.093467229	1.084494664	1.086595319	1.014625909	15235.41151	17849.72555	15331.7642	16627.21646	16659.42321	16903.08242	8.561959116	13.8951	14.1236	13.9042	14.0213	14.0241	14.045	0.03899	0.03899	0.0411	0.03899	0.03899	0.0411	4	4	106
IPI00372700.1	PREDICTED:_similar_to_aminopeptidase_puromycin_sensitive	NAATEDLWESLESASGKPIAAVMNTWTK	99.99980057	0.137871433	0.997658493	0.99643308	0.88970951	0.977979004	0.195033964	0.05656668	0.692283341	0.425027797	0.745637433	0.243144155	0.013596654	1.097294899	-1.01965809	1.039024961	1.016081059	1.059450207	-1.133109465	9221.308987	10118.49531	9043.530453	9188.959999	9581.170208	8455.643967	10.67667054	13.1708	13.3047	13.1427	13.1657	13.226	13.0457	0.04857	0.04857	0.0512	0.04857	0.04857	0.0512	2	2	126
IPI00464815.10	Alpha-enolase	VNQIGSVTESLQACK	100	0.005112477	0.997658493	0.307157315	0.925859	0.977979004	0.837394717	0.000174025	0.201715733	0.003041077	0.835918411	0.088982425	0.603583178	-1.102072163	-1.032435138	-1.077568648	-1.0051519	-1.043715588	1.012980654	22431.56052	20353.98523	21726.84723	21615.4864	20816.82737	21087.04341	5.376689972	14.4532	14.313	14.4072	14.3998	14.3455	14.3641	0.02451	0.02451	0.02584	0.02451	0.02451	0.02584	36	68	58
IPI00358461.1	PREDICTED:_similar_to_heme_binding_protein_1	IPNQFGQSPPTPSDQSVK	99.99997969	0.118068559	0.997658493	0.86359048	0.507654338	0.977979004	0.359553375	0.041425197	0.168785132	0.111528305	0.147829685	0.857741081	0.059994049	-1.081951188	1.055492246	1.062876321	-1.058501432	1.006995859	-1.077249545	18527.77476	17124.40909	19555.9226	18475.10263	19692.73307	18280.56755	8.437734886	14.1774	14.0638	14.2553	14.1733	14.2654	14.158	0.03843	0.03843	0.0405	0.03843	0.03843	0.0405	3	3	110
IPI00210635.1	N-ethylmaleimide_sensitive_factor	VLDDGELLVQQTK	100	0.062048852	0.997658493	0.99643308	0.333651543	0.977979004	0.993109576	0.016380897	0.183234962	0.229067785	0.039928505	0.87019946	0.958832223	1.079113809	-1.043449697	-1.03806059	1.068707512	1.005191515	-1.001636886	13917.94561	15019.04731	13338.39634	14254.84437	13407.64282	13385.73191	6.87092987	13.7647	13.8745	13.7033	13.7992	13.7108	13.7084	0.03131	0.03131	0.033	0.03131	0.03131	0.033	26	29	28
IPI00205372.3	Isoform_1_of_Syntaxin-binding_protein_1	VLVVDQLSMR	99.99999984	0.016770492	0.997658493	0.99643308	0.797906375	0.977979004	0.700610506	0.001751302	0.622947325	0.688046557	0.551379503	0.378835013	0.406754442	1.201243585	-1.02863974	1.022688557	1.034822378	1.051978091	-1.048907121	13088.00553	15721.88268	12723.6048	13166.67097	13384.95349	12760.85673	12.47293119	13.676	13.9405	13.6352	13.6846	13.7083	13.6394	0.05668	0.05668	0.05975	0.05668	0.05668	0.05975	23	32	48
395937	0_beta-2_globin_[Rattus_norvegicus]	FGDLSSVSAIMGNPQVK	100	0.766051406	0.997658493	0.795267491	0.788902735	0.977979004	0.520988984	0.6697478	0.582747195	0.054086796	0.492983853	0.17802018	0.19413455	-1.024295165	1.032297402	1.116604034	1.040497922	1.081668938	1.078568844	12781.8105	12478.63988	13194.62976	13728.98485	14272.22116	15393.57309	12.56320661	13.6418	13.6072	13.6877	13.7449	13.8009	13.91	0.05709	0.05709	0.06018	0.05709	0.05709	0.06018	8	11	112
IPI00200053.3	PREDICTED:_similar_to_ATP_synthase_D_chain,_mitochondrial	TIDWVSFVEIMPQNQK	99.99999968	0.131877733	0.997658493	0.99643308	0.903404554	0.977979004	0.343015874	0.051846789	0.955993647	0.710754476	0.781492558	0.759702532	0.043057139	-1.101132815	-1.002761556	-1.018214506	1.013963554	-1.015410394	1.10865357	9979.853007	9063.260009	9952.36898	10091.33942	9801.326679	10866.27582	10.85632565	13.2848	13.1458	13.2808	13.3008	13.2588	13.4076	0.04938	0.04938	0.05206	0.04938	0.04938	0.05206	2	3	72
IPI00358127.2	PREDICTED:_similar_to_ARP3_actin-related_protein_3_homolog_B	DITYFIQQLLR	99.99999765	0.331386212	0.997658493	0.99643308	0.869438709	0.977979004	0.370871244	0.207542451	0.738167259	0.60494607	0.696544611	0.86526861	0.064425633	1.086178502	-1.022616975	-1.034286953	-1.026440733	-1.011411876	-1.133978832	8160.225708	8863.461736	7979.747948	7774.192594	7889.711539	6957.547455	14.5599476	12.9944	13.1137	12.9621	12.9245	12.9458	12.7644	0.06608	0.06608	0.06965	0.06608	0.06608	0.06965	2	2	89
IPI00191897.4	PREDICTED:_similar_to_Nucleoside_diphosphate_kinase_B	NIIHGSDSVESAEK	99.99999878	0.02581863	0.997658493	0.99643308	0.342215144	0.977979004	0.673644494	0.004672769	0.339204997	0.591857224	0.051903364	0.662108227	0.356806135	-1.152109846	1.048612178	1.026176064	-1.102860854	-1.021863806	-1.046813969	25719.88089	22324.15683	26970.18033	24454.74444	26393.12614	25212.81424	10.74078975	14.6506	14.4463	14.7191	14.5778	14.6879	14.6219	0.04886	0.04886	0.0515	0.04886	0.04886	0.0515	4	5	69
IPI00205396.1	NORBIN	IFDAVGFTFPNR	100	0.01347102	0.997658493	0.99643308	0.557987386	0.977979004	0.579003633	0.001154659	0.63037215	0.616070731	0.189681493	0.334040755	0.241264209	1.151933797	-1.020659235	1.020958423	1.057743538	1.042050643	1.05134892	11606.51746	13369.93974	11371.58913	12028.22492	11849.77176	12458.24475	9.213515694	13.5026	13.7067	13.4731	13.5541	13.5326	13.6048	0.04195	0.04195	0.04421	0.04195	0.04195	0.04421	7	7	50
IPI00371187.2	Ras-related_protein_Rab-35	LQIWDTAGQER	99.99960398	0.077552552	0.997658493	0.99643308	0.842694959	0.988483763	0.580472536	0.022157872	0.84370214	0.891527694	0.638522009	0.94861194	0.243466767	1.173013419	-1.013870981	-1.009316404	-1.033397264	1.004512537	-1.085476617	24103.62531	28273.87593	23773.85857	23005.53658	23881.13898	22000.60195	15.21802774	14.557	14.7872	14.5371	14.4897	14.5436	14.4253	0.06903	0.06903	0.07276	0.06903	0.06903	0.07276	2	2	14
IPI00362927.1	Tubulin,_alpha_4	SIQFVDWCPTGFK	99.99999999	0.049553692	0.997658493	0.99643308	0.841678007	0.977979004	0.581679511	0.011949519	0.750786348	0.912735204	0.631979944	0.671521597	0.244637783	1.240436816	-1.027503062	1.009149795	1.041789367	1.036904504	-1.105168662	21874.05084	27133.37797	21288.55052	22178.18557	22074.19391	19973.59739	18.65350739	14.4169	14.7278	14.3778	14.4369	14.4301	14.2858	0.08437	0.08437	0.08894	0.08437	0.08437	0.08894	31	62	4
IPI00566219.2	26_kDa_protein	YALYDATYETK	99.99999992	0.136000901	0.997658493	0.99643308	0.243871572	0.977979004	0.971144876	0.055488368	0.493159965	0.784026723	0.020355776	0.342339761	0.896782925	-1.079436999	-1.028054673	1.010807933	1.100687907	1.03916582	1.005239836	27142.01222	25144.6006	26401.33149	29059.6263	27435.36128	27579.11808	8.741831401	14.7282	14.618	14.6883	14.8267	14.7437	14.7513	0.03981	0.03981	0.04196	0.03981	0.03981	0.04196	6	7	91
IPI00231146.4	Histidine_triad_nucleotide-binding_protein_1	CLAFHDISPQAPTHFLVIPK	99.99999518	0.045665559	0.997658493	0.99643308	0.792374134	0.977979004	0.985470885	0.010437842	0.78373595	0.318685741	0.51580833	0.48452107	0.935915778	-1.075150429	1.007758801	1.027834551	-1.018499356	1.019921185	-1.002266061	15229.94651	14165.40988	15348.11264	15069.33956	15653.86523	15618.47282	6.103064437	13.8946	13.7901	13.9058	13.8793	13.9342	13.931	0.02782	0.02782	0.02932	0.02782	0.02782	0.02932	3	4	100
33468975	zinc_finger_protein_of_the_cerebellum_5_[Mus_musculus]	LGLAAAAAAAAELYGR	98.2684	0.014413657	0.997658493	0.99643308	0.797906375	0.977979004	0.486515155	0.001262538	0.80203907	0.245022764	0.555875525	0.168511112	0.164025109	-1.26659714	1.018104245	-1.084899065	-1.043112595	-1.104540344	1.105731946	44919.63316	35464.81495	45732.86922	43842.6968	41404.4353	45782.20681	15.58997126	15.4551	15.1141	15.4809	15.42	15.3375	15.4825	0.0707	0.0707	0.07452	0.0707	0.0707	0.07452	2	2	145
31981588	ATPase,_H+_transporting,_lysosomal,_V1_subunit_H_[Mus_musculus]	LGESVQDLSSFDEYSSELK	99.99999691	0.057159746	0.997658493	0.99643308	0.984163624	0.977979004	0.426572047	0.014632895	0.764541232	0.600696561	0.964314939	0.419543419	0.10710818	1.131115585	-1.015204556	1.026021578	1.002255584	1.041621781	-1.085647001	9811.085523	11097.47174	9664.146469	9685.944762	10066.38545	9272.245434	10.94016528	13.2602	13.4379	13.2384	13.2417	13.2973	13.1787	0.04976	0.04976	0.05245	0.04976	0.04976	0.05245	4	4	33
IPI00189795.1	Tubulin_alpha-1_chain	LIGQIVSSITASLR	100	0.044880751	0.997658493	0.99643308	0.903404554	0.977979004	0.551321188	0.009796827	0.89491697	0.766261149	0.778967906	0.673610327	0.217378068	1.234248967	-1.010760432	1.023730716	1.023009924	1.034746501	-1.105930333	21750.11582	26845.05798	21518.56674	22013.70732	22266.26164	20133.512	17.68569459	14.4087	14.7124	14.3933	14.4261	14.4426	14.2973	0.08007	0.08007	0.0844	0.08007	0.08007	0.0844	34	72	4
IPI00204843.1	Guanine_nucleotide-binding_protein_G(o)_subunit_alpha_2	AMDTLGVEYGDKER	100	0.149131355	0.997658493	0.99643308	0.423679834	0.977979004	0.91254317	0.064485249	0.9851165	0.870882774	0.089640632	0.889012039	0.761272145	1.104556886	-1.001014391	-1.008636366	-1.098065403	-1.007614251	-1.016656498	17145.81714	18938.53039	17128.4422	15598.74498	16999.00749	16720.50248	11.81292151	14.0656	14.209	14.0641	13.9291	14.0532	14.0293	0.05371	0.05371	0.05661	0.05371	0.05371	0.05661	13	19	111
IPI00213685.1	GTP-binding_protein_Rab-3D	YADDSFTPAFVSTVGIDFK	99.99999956	0.045665559	0.997658493	0.99643308	0.784582613	0.977979004	0.348219477	0.01037407	0.781727084	0.29300559	0.477922894	0.195121771	0.051474023	1.199122727	-1.01972844	1.075224616	-1.051419857	1.09643712	-1.150079697	16017.37791	19206.80187	15707.49357	14939.31608	17222.27901	14974.857	15.35628294	13.9674	14.2293	13.9392	13.8668	14.072	13.8703	0.06965	0.06965	0.07342	0.06965	0.06965	0.07342	5	5	12
IPI00207725.3	PREDICTED:_similar_to_purine-nucleoside_phosphorylase	LTQPQAFDYNEIPNFPQSTVQGHAGR	99.99991326	0.01347102	0.997658493	0.85147197	0.797906375	0.92052399	0.983012577	0.001133334	0.674173113	0.100230415	0.554699686	0.045250064	0.928114524	1.148546338	-1.017611231	1.069569609	1.024854073	1.088406047	-1.003750162	7467.357807	8576.606467	7338.124402	7520.506678	7986.858973	7957.018864	9.004589575	12.8664	13.0662	12.8412	12.8766	12.9634	12.958	0.041	0.041	0.04322	0.041	0.041	0.04322	2	2	106
IPI00195372.1	Elongation_factor_1-alpha_1	IGGIGTVPVGR	99.99988808	0.024299689	0.997658493	0.99643308	0.733834025	0.977979004	0.983012577	0.004276745	0.395413465	0.963518332	0.40429256	0.37139075	0.930818584	1.145883533	-1.040938171	1.00209668	1.040153642	1.043120685	-1.004092843	16180.6139	18541.09902	15544.26031	16168.41897	16214.53946	16148.44641	10.21673964	13.982	14.1784	13.9241	13.9809	13.985	13.9791	0.04649	0.04649	0.049	0.04649	0.04649	0.049	8	8	47
IPI00198620.1	ATP_synthase_delta_chain,_mitochondrial_precursor	AQSELSGAADEAAR	99.99999998	0.020340485	0.997658493	0.99643308	0.682953528	0.977979004	0.70028075	0.002712419	0.898457429	0.635374256	0.320012511	0.556087397	0.401904856	-1.213086991	-1.008114082	1.029689633	-1.065318398	1.038044619	-1.054704222	29644.75041	24437.44813	29406.14654	27603.15282	30524.89217	28941.66111	13.78052917	14.8555	14.5768	14.8438	14.7525	14.8977	14.8209	0.06257	0.06257	0.06596	0.06257	0.06257	0.06596	5	7	27
IPI00231407.4	drebrin_1	KSESEVEEAAAIIAQRPDNPR	99.99986453	0.006107202	0.997658493	0.970109364	0.788902735	0.977979004	0.924766593	0.000251268	0.517203345	0.175174034	0.487771384	0.495914016	0.790199176	-1.145982384	-1.023495813	-1.048799658	-1.025200299	-1.024722959	-1.009569535	12816.15449	11183.55279	12521.9413	12214.14129	12219.83091	12104.00125	7.762736033	13.6457	13.4491	13.6122	13.5763	13.5769	13.5632	0.03536	0.03536	0.03727	0.03536	0.03536	0.03727	6	6	39
IPI00339167.4	Tubulin_alpha-2_chain	SIQFVDWCPTGFK	99.99999999	0.047752907	0.997658493	0.99643308	0.888968762	0.977979004	0.568233426	0.011460698	0.852544601	0.823109842	0.741975163	0.68678402	0.229241599	1.239799675	-1.015862147	1.018594824	1.028278773	1.034751925	-1.107936168	21806.17227	27035.28529	21465.68049	22072.7036	22211.6542	20047.77427	18.49136872	14.4124	14.7226	14.3897	14.43	14.439	14.2912	0.08365	0.08365	0.08818	0.08365	0.08365	0.08818	34	71	4
IPI00201797.1	Protein_kinase_C_gamma_type	TFCGTPDYIAPEIIAYQPYGK	99.99998592	0.008921586	0.997658493	0.99643308	0.832680567	0.977979004	0.880480913	0.000580166	0.865491512	0.847356401	0.609586351	0.721403415	0.684259453	1.169353873	-1.00749282	1.008291366	1.022785909	1.015846312	1.018094956	10435.75411	12203.08948	10358.14241	10594.1621	10522.28077	10712.68097	9.565922304	13.3492	13.575	13.3385	13.371	13.3612	13.387	0.04354	0.04354	0.0459	0.04354	0.04354	0.0459	3	3	50
IPI00213318.4	Dynamin-3	ALLQMVQQFAVDFEK	99.99999999	0.022756225	0.997658493	0.99643308	0.207517756	0.977979004	0.811601962	0.003505225	0.452419932	0.977541587	0.012332484	0.468941564	0.554540615	1.13753458	-1.033308382	-1.001192292	1.118753338	1.032077845	1.026077693	8468.967668	9633.743576	8195.973062	9169.272221	8458.882213	8679.470346	9.44032407	13.048	13.2339	13.0007	13.1626	13.0463	13.0834	0.04297	0.04297	0.0453	0.04297	0.04297	0.0453	7	7	15
IPI00358083.1	Protein_phosphatase_1_regulatory_subunit_7	AIENIDTLTNLESLFLGK	100	0.018395497	0.997658493	0.99643308	0.23197177	0.977979004	0.248149304	0.002076778	0.571039833	0.835845383	0.016138001	0.443118596	0.019568345	-1.067810347	1.011926409	-1.004223947	-1.053072449	-1.016200733	-1.051372894	19812.1564	18554.00302	20048.44429	19038.04844	19728.8229	18764.81979	4.528142597	14.2741	14.1794	14.2912	14.2166	14.268	14.1957	0.02065	0.02065	0.02176	0.02065	0.02065	0.02176	6	6	71
51708092	PREDICTED:_similar_to_phosphoglycerate_kinase_1_[Mus_musculus]	LGDVYVNDAFGTAHR	100	0.091033233	0.997658493	0.99643308	0.86551567	0.977979004	0.47716202	0.028922559	0.62619844	0.91559497	0.685835065	0.555316506	0.151055862	-1.090906454	1.019686451	-1.004132787	1.016316243	-1.023900598	1.059693243	16012.03556	14677.73474	16327.2557	16593.65518	15946.13358	16898.01001	8.675501872	13.9669	13.8413	13.995	14.0183	13.9609	14.0446	0.03951	0.03951	0.04164	0.03951	0.03951	0.04164	30	53	5
IPI00198327.2	Voltage-dependent_anion-selective_channel_protein_2	YQLDPTASISAK	99.99993831	0.018644305	0.997658493	0.99643308	0.930552243	0.977979004	0.885563065	0.002407779	0.547944923	0.975516542	0.848500949	0.52833471	0.698329731	1.282897352	-1.049712421	1.002410747	1.015520172	1.052243012	1.031757481	12231.6143	15691.90561	11652.34788	11833.19433	12261.10163	12650.48332	17.59303914	13.5783	13.9377	13.5083	13.5306	13.5818	13.6269	0.07965	0.07965	0.08396	0.07965	0.07965	0.08396	3	3	74
IPI00201407.1	Serine/threonine-protein_phosphatase_2B_catalytic_subunit_beta_isoform	LFEVGGSPANTR	100	0.135882909	0.997658493	0.99643308	0.792374134	0.977979004	0.454572839	0.055284932	0.492827602	0.91225289	0.520803869	0.562469504	0.135592584	1.107396353	-1.037611146	-1.005778065	-1.035162208	1.031650204	-1.084407596	11976.21463	13262.4164	11542.10291	11150.04279	11907.41282	10980.56936	11.67354002	13.5479	13.6951	13.4946	13.4448	13.5396	13.4227	0.05308	0.05308	0.05595	0.05308	0.05308	0.05595	9	11	17
IPI00762998.1	PREDICTED:_neural_cell_adhesion_molecule_L1	AFGAPVPSVQWLDEEGTTVLQDER	99.99999985	0.07324906	0.997658493	0.99643308	0.498231465	0.977979004	0.799607172	0.019923744	0.418826618	0.233406041	0.137435006	0.721369099	0.528544506	-1.091763621	1.031078441	1.04505711	-1.058294818	1.013557329	-1.024114666	9901.69306	9069.447701	10209.42224	9647.049265	10347.83473	10104.1759	8.187360822	13.2735	13.1468	13.3176	13.2359	13.337	13.3027	0.03729	0.03729	0.03931	0.03729	0.03729	0.03931	6	6	84
IPI00372826.3	Hypothetical_protein	AFGYYGPLR	99.99943824	0.088290774	0.997658493	0.99643308	0.993116531	0.977979004	0.568233426	0.027630043	0.613929559	0.940580219	0.986918901	0.665632984	0.229140474	-1.092311568	1.020524347	1.002922638	-1.000659697	-1.017550415	1.049918458	17539.75186	16057.46233	17899.74381	17887.94319	17591.01421	18469.13052	8.72887611	14.0983	13.971	14.1277	14.1267	14.1026	14.1728	0.03975	0.03975	0.0419	0.03975	0.03975	0.0419	3	3	5
IPI00231368.4	Thioredoxin	EAFQEALAAAGDK	99.99969831	0.045665559	0.997658493	0.99643308	0.733834025	0.977979004	0.872410761	0.010433949	0.677029856	0.368246293	0.42066864	0.644178487	0.673999628	-1.127628919	1.019642588	1.041879377	-1.038413277	1.021808416	-1.019840352	22742.64018	20168.54994	23189.36449	22331.53698	23695.08779	23234.11476	10.13290355	14.4731	14.2998	14.5012	14.4468	14.5323	14.504	0.04611	0.04611	0.0486	0.04611	0.04611	0.0486	4	4	57
IPI00364780.2	Vacuolar_ATPase_subunit_H	GAVDAAVPTNIIAAK	99.9980816	0.043420553	0.997658493	0.99643308	0.998662363	0.977979004	0.503151385	0.009378839	0.818956014	0.608111188	0.998662363	0.467340428	0.179761149	1.157341019	-1.012882352	1.028333325	-1.000093734	1.041580677	-1.078595689	10531.36974	12188.38619	10397.42642	10396.45192	10829.75846	10040.60981	12.1543095	13.3624	13.5732	13.3439	13.3438	13.4027	13.2936	0.05525	0.05525	0.05824	0.05525	0.05525	0.05824	3	3	33
IPI00209150.1	Ras-related_protein_Rab-3C	LGEQLGFEFFETSAK	99.99995078	0.054504449	0.998795589	0.99643308	0.842694959	0.977979004	0.271928686	0.013766267	0.989678276	0.193615581	0.634285274	0.201086677	0.026726705	1.155719812	-1.000758324	1.077616424	-1.028297774	1.078433607	-1.142213277	12727.15847	14709.02919	12717.51447	12367.54061	13714.995	12007.38537	12.74304937	13.6356	13.8444	13.6345	13.5943	13.7435	13.5516	0.0579	0.0579	0.06103	0.0579	0.0579	0.06103	6	6	12
IPI00565738.1	Phosphoglycerate_kinase_1	LGDVYVNDAFGTAHR	100	0.079206356	0.997658493	0.99643308	0.903404554	0.977979004	0.562676245	0.023109655	0.596745986	0.973455705	0.781361495	0.574570405	0.224715203	-1.091749375	1.020722098	-1.001254591	1.010806595	-1.022002687	1.048476999	16247.22402	14881.8258	16583.9006	16763.1161	16226.86594	17013.49571	8.399962563	13.9879	13.8613	14.0175	14.033	13.9861	14.0544	0.03825	0.03825	0.04032	0.03825	0.03825	0.04032	31	55	5
31980942	inositol_(myo)-1(or_4)-monophosphatase_1_[Mus_musculus]	SLLVTELGSSR	99.99967345	0.00800401	0.997658493	0.99643308	0.813181576	0.983712483	0.915790782	0.00039606	0.678563619	0.592494639	0.583632034	0.914869719	0.76717102	-1.126342151	-1.013540878	-1.017060575	-1.017958474	-1.003472674	1.009651472	18925.63967	16802.74476	18672.79365	18343.37464	18608.17353	18787.7698	7.032486913	14.2081	14.0364	14.1887	14.163	14.1836	14.1975	0.03204	0.03204	0.03378	0.03204	0.03204	0.03378	4	4	116
203476	creatine_kinase-B	TFLVWINEEDHLR	100	0.138396984	0.997658493	0.99643308	0.928678435	0.977979004	0.786403956	0.057098642	0.823797738	0.352790593	0.839525305	0.49401639	0.516779742	1.07455119	-1.008532709	-1.03525471	-1.007756752	-1.026495918	-1.025093064	17297.10561	18586.62541	17150.76314	17018.7529	16708.06754	16299.07383	8.277257515	14.0782	14.182	14.066	14.0548	14.0283	13.9925	0.0377	0.0377	0.03974	0.0377	0.0377	0.03974	26	38	55
IPI00193983.2	Clathrin_heavy_chain	TSIDAYDNFDNISLAQR	100	0.030758203	0.997658493	0.99643308	0.849985868	0.977979004	0.666788291	0.005975879	0.546359243	0.743350452	0.650835612	0.357905311	0.327630221	1.224881186	-1.045131342	1.023565121	1.03364851	1.069759988	-1.074484007	10607.18651	12992.54319	10149.14211	10490.64561	10857.14614	10104.52094	15.92181333	13.3728	13.6654	13.3091	13.3568	13.4064	13.3027	0.07218	0.07218	0.07609	0.07218	0.07218	0.07609	53	65	48
IPI00188804.1	60S_acidic_ribosomal_protein_P2	YVASYLLAALGGNSNPSAK	99.99999994	0.131487826	0.997658493	0.894475657	0.257388081	0.988483763	0.167542381	0.051457112	0.118230569	0.126759979	0.022591011	0.938089277	0.009440758	-1.077881145	1.063321163	1.060118382	-1.095091303	-1.003021155	-1.109811145	15520.41515	14399.00421	16503.1859	15070.14607	16453.4774	14825.47501	8.426905143	13.9219	13.8137	14.0105	13.8794	14.0061	13.8558	0.03838	0.03838	0.04045	0.03838	0.03838	0.04045	5	6	53
IPI00392583.3	Dynein_light_chain_2A,_cytoplasmic	EIDPQNDLTFLR	99.9915366	0.181938962	0.997658493	0.846402451	0.792374134	0.977979004	0.670153176	0.084211748	0.184794631	0.081525883	0.513412645	0.701802496	0.340960534	-1.078160561	1.060803454	1.078893538	-1.029322828	1.017053191	-1.043113862	20029.587	18577.55489	21247.45508	20642.16834	21609.79199	20716.61855	9.580699336	14.2898	14.1813	14.375	14.3333	14.3994	14.3385	0.04361	0.04361	0.04597	0.04361	0.04361	0.04597	3	3	110
IPI00213598.1	WAS_protein_family,_member_1	YAEDIFGELFNEAHSFSFR	99.99962745	0.045046287	0.997658493	0.991204521	0.691591891	0.806688502	0.460425361	0.009884442	0.321225039	0.188045658	0.334469904	0.025503538	0.141021711	1.188122715	-1.068467309	1.08964733	1.066540171	1.16425255	-1.103892818	6422.15634	7630.309829	6010.625019	6410.573037	6997.885507	6339.279858	14.46676601	12.6488	12.8975	12.5533	12.6462	12.7727	12.6301	0.06566	0.06566	0.06921	0.06566	0.06566	0.06921	2	2	95
31560539	peroxiredoxin_2_[Mus_musculus]	KEGGLGPLNIPLLADVTK	99.99999978	0.203675302	0.997658493	0.99643308	0.908280262	0.977979004	0.39372157	0.099626319	0.80996401	0.975958152	0.797979077	0.832761378	0.082344054	-1.094710065	1.013492791	1.001635728	1.014368736	-1.0118377	1.103216677	23838.27496	21775.87996	24159.91981	24507.06733	23877.26788	26341.80012	12.11270314	14.541	14.4104	14.5603	14.5809	14.5434	14.6851	0.05506	0.05506	0.05804	0.05506	0.05506	0.05804	7	9	72
IPI00196795.1	Ras-related_protein_Rab-15	LLLIGDSGVGK	99.9978783	0.093066444	0.997658493	0.99643308	0.86551567	0.994226451	0.647039646	0.03031307	0.840902939	0.823890945	0.683837431	0.987328611	0.301705343	1.164261715	-1.014256881	-1.015393265	-1.029152594	-1.001120411	-1.075941719	24315.85436	28310.0183	23974.05906	23294.95082	23947.22834	22256.99395	15.3611899	14.5696	14.789	14.5492	14.5077	14.5476	14.442	0.06967	0.06967	0.07344	0.06967	0.06967	0.07344	2	2	14
IPI00389420.6	Splicing_factor,_arginine/serine-rich_2	DAEDAMDAMDGAVLDGR	100	0.084214263	0.997658493	0.99643308	0.855934899	0.988902496	0.34532203	0.025793626	0.420960693	0.385295392	0.663956149	0.967429184	0.047393815	-1.096809942	-1.034124215	-1.03588085	1.018239085	-1.001698669	1.087638507	11934.13002	10880.7639	11540.32546	11750.81043	11520.75551	12530.41733	9.021207102	13.5428	13.4095	13.4944	13.5205	13.4919	13.6131	0.04107	0.04107	0.04329	0.04107	0.04107	0.04329	2	2	68
IPI00201561.2	Peroxiredoxin-2	KEGGLGPLNIPLLADVTK	99.99999978	0.23149517	0.997658493	0.99643308	0.733834025	0.988483763	0.386695018	0.117996395	0.913294055	0.948987381	0.418599954	0.962818458	0.07758681	-1.08033528	1.005479603	1.00313005	1.041561473	-1.002342227	1.094089869	20545.33399	19017.55351	20657.91426	21516.48762	20609.64192	22548.80043	10.90213148	14.3265	14.215	14.3344	14.3932	14.331	14.4608	0.04959	0.04959	0.05227	0.04959	0.04959	0.05227	12	14	41
IPI00231426.5	Phosphoglycerate_kinase_1	LGDVYVNDAFGTAHR	100	0.079647274	0.997658493	0.99643308	0.930552243	0.977979004	0.589134502	0.023575593	0.610954932	0.978945412	0.846506083	0.593136257	0.2507713	-1.094589259	1.020582972	-1.00102802	1.007774615	-1.021632152	1.047319872	16446.41132	15025.18975	16784.92734	16915.42369	16429.52144	17206.96428	8.680258808	14.0055	13.8751	14.0349	14.0461	14.004	14.0707	0.03953	0.03953	0.04166	0.03953	0.03953	0.04166	30	53	5
IPI00369093.1	Ubiquinol-cytochrome_c_reductase_complex_11_kDa_protein,_mitochondrial_precursor	SQTEEDCTEELFDFLHAR	99.99999985	0.018472664	0.997658493	0.99643308	0.990640456	0.988483763	0.916967389	0.002209965	0.947530778	0.982969408	0.980488554	0.931002874	0.772587899	-1.22664347	1.00431913	-1.001361606	-1.001602931	-1.005686617	1.019114005	26681.91411	21751.97176	26797.15676	26754.27151	26645.63325	27154.93801	14.25666445	14.7036	14.4089	14.7098	14.7075	14.7016	14.7289	0.06471	0.06471	0.06822	0.06471	0.06471	0.06822	2	5	118
38014843	Cd81_protein_[Rattus_norvegicus]	QFYDQALQQAVMDDDANNAK	99.99988218	0.00800401	0.997658493	0.99643308	0.972747387	0.977979004	0.847855771	0.000398727	0.388215371	0.546541969	0.934642416	0.781033091	0.621114914	1.212018873	1.046458111	1.03130927	-1.004309687	-1.014688941	1.026289446	13848.88827	16785.11395	14492.28146	14430.09228	14282.48685	14657.96552	11.39498551	13.7575	14.0349	13.823	13.8168	13.802	13.8394	0.05182	0.05182	0.05462	0.05182	0.05182	0.05462	2	2	131
IPI00211846.5	PREDICTED:_similar_to_Protein_KIAA1045	LAEAPSCSVSISHVGPIADSSPAGSSSQSQEK	99.9985534	0.047383211	0.997658493	0.99643308	0.879103848	0.977979004	0.353175547	0.011317818	0.721107226	0.389624178	0.72036581	0.62936501	0.056350265	1.111661799	-1.014975117	-1.035588639	1.015017032	-1.020309387	1.084189497	8997.667104	10002.3628	8864.913979	8998.038677	8688.45675	9419.933557	9.031634994	13.1353	13.2881	13.1139	13.1354	13.0849	13.2015	0.04112	0.04112	0.04334	0.04112	0.04112	0.04334	2	2	16
IPI00201467.1	Synaptotagmin-2	HWSDMLANPR	99.99999552	0.015074205	0.997658493	0.99643308	0.797906375	0.977979004	0.825130502	0.001433202	0.780325559	0.544519907	0.552332124	0.38609769	0.567689786	1.114435465	-1.009309778	1.019819371	1.019968653	1.029313664	-1.019192316	18171.43016	20250.88622	18003.8186	18363.3306	18531.57648	18182.61009	7.203444243	14.1494	14.3057	14.136	14.1645	14.1777	14.1503	0.03282	0.03282	0.0346	0.03282	0.03282	0.0346	3	3	67
IPI00213013.1	Stress-induced-phosphoprotein_1	LAYINPDLALEEK	99.99983461	0.095220193	0.997658493	0.99643308	0.88196112	0.977979004	0.931989435	0.0311234	0.645356325	0.31224753	0.725826183	0.598161012	0.818411457	-1.042566189	1.008988405	1.019384548	-1.006838777	1.01030353	1.004470481	17212.42868	16509.67474	17367.14095	17249.17767	17546.08382	17624.52326	4.208941283	14.0712	14.011	14.0841	14.0742	14.0989	14.1053	0.01919	0.01919	0.02023	0.01919	0.01919	0.02023	10	11	100

SUPPLEMENTAL TABLE A. All priority 1 proteins measured in the nucleus accumbens shell of P, NP and W rats

IPI00464645.1	Pyruvate_dehydrogenase_(Lipoamide)_beta	IMEGPAFNFLDAPAVR	100	0.008921586	0.997658493	0.99643308	0.733834025	0.977979004	0.673446244	0.000538774	0.957546231	0.78152536	0.423140986	0.828401272	0.352584104	-1.181626681	-1.002489134	-1.012690636	-1.038235791	-1.010176172	-1.044558858	23352.49999	19763.01007	23294.51682	22436.63436	23059.85577	22076.16697	10.14120585	14.5113	14.2705	14.5077	14.4536	14.4931	14.4302	0.04615	0.04615	0.04864	0.04615	0.04615	0.04864	12	16	34
IPI00231502.3	Isoform_2_of_AP-2_complex_subunit_beta-1	LASQANIAQVLAELK	99.9999997	0.091974668	0.997658493	0.99643308	0.269624476	0.977979004	0.45250857	0.029747236	0.179867089	0.653867023	0.024520601	0.361566255	0.130322468	1.061016287	-1.037708364	-1.012023737	1.065096656	1.025379471	1.042740696	11904.56782	12630.92973	11471.96864	12218.75544	11763.12114	12265.88512	5.931090008	13.5392	13.6247	13.4858	13.5768	13.522	13.5824	0.02704	0.02704	0.0285	0.02704	0.02704	0.0285	20	21	78
IPI00372934.3	PREDICTED:_similar_to_MAGUK_p55_subfamily_member_2	AALESGVSTK	99.981948	0.126828827	0.997658493	0.99643308	0.792374134	0.977979004	0.697837817	0.048162148	0.756282546	0.583131996	0.51796898	0.822451727	0.396379752	-1.108104253	1.016393572	1.028410466	-1.034505057	1.011823071	1.045576355	6899.905511	6226.765659	7013.019608	6779.106161	7095.935039	7419.341896	11.37930555	12.7524	12.6043	12.7758	12.7269	12.7928	12.8571	0.05175	0.05175	0.05455	0.05175	0.05175	0.05455	2	2	96
IPI00201417.3	PREDICTED:_similar_to_peptidylprolyl_isomerase_D	VFFDVDIGGER	99.99996884	0.072332557	0.997658493	0.99643308	0.788902735	0.977979004	0.569356066	0.019426458	0.453179829	0.845929354	0.492879927	0.34858573	0.23429033	-1.082555901	1.025865618	-1.00644299	-1.023608647	-1.03247526	1.041496419	12563.41932	11605.33078	12888.37992	12591.12059	12482.99153	13000.99098	7.363617468	13.6169	13.5025	13.6538	13.6201	13.6077	13.6663	0.03355	0.03355	0.03536	0.03355	0.03355	0.03536	2	2	5
IPI00361708.3	36_kDa_protein	NASCTTNCLAPLAK	99.99907029	0.190287877	0.997658493	0.99643308	0.88970951	0.977979004	0.448976523	0.089380934	0.318650543	0.913544438	0.79438961	0.37190014	0.123534425	-1.172478618	1.099761061	1.010079142	-1.030794062	-1.088787022	1.159337021	13092.36401	11166.39894	14398.47213	13968.3305	13224.32381	15331.44817	20.7737245	13.6764	13.4469	13.8136	13.7699	13.6909	13.9042	0.09377	0.09377	0.09885	0.09377	0.09377	0.09885	7	8	98
IPI00231721.4	Protein-L-isoaspartate_(D-aspartate)_O-methyltransferase_1	ELVDDSITNVK	99.99999233	0.07822723	0.997658493	0.99643308	0.832680567	0.977979004	0.520988984	0.022529442	0.981815017	0.803518469	0.609997992	0.791058433	0.196170182	-1.075710016	1.000730615	-1.007791804	1.01649907	-1.008528112	1.042636931	15645.46127	14544.31124	15656.89207	15915.21623	15524.49743	16186.41435	6.948609971	13.9335	13.8282	13.9345	13.9581	13.9223	13.9825	0.03166	0.03166	0.03338	0.03166	0.03166	0.03338	8	10	124
IPI00734686.2	cytochrome_c_oxidase_subunit_II	MLISSEDVLHSWAVPSLGLK	99.99999566	0.021936122	0.997658493	0.99643308	0.974820419	0.977979004	0.802908043	0.003259081	0.624073856	0.716173232	0.944740247	0.399864316	0.536801378	1.307620515	-1.045024345	1.032294413	1.006240946	1.078772793	1.057113618	9206.019729	12037.98026	8809.383024	8864.36191	9503.322731	10046.09187	19.62661613	13.1684	13.5553	13.1048	13.1138	13.2142	13.2943	0.0887	0.0887	0.09349	0.0887	0.0887	0.09349	3	5	74
IPI00231631.11	Beta-enolase	AAVPSGASTGIYEALELR	99.99999833	0.008921586	0.997658493	0.959908311	0.923529101	0.977979004	0.901207579	0.000502708	0.667609496	0.156231181	0.832759384	0.337312978	0.736427876	-1.108651256	-1.012407406	-1.040791312	-1.006077833	-1.028036051	-1.009708564	28332.16806	25555.52787	27984.94746	27815.88714	27221.7569	26960.01388	6.22006346	14.7902	14.6413	14.7724	14.7636	14.7325	14.7185	0.02835	0.02835	0.02988	0.02835	0.02835	0.02988	11	18	58
IPI00194324.1	Pyruvate_dehydrogenase_E1_component_subunit_beta,_mitochondrial_precursor	IMEGPAFNFLDAPAVR	100	0.008921586	0.997658493	0.99643308	0.77206551	0.977979004	0.670153176	0.000554148	0.922002825	0.750043198	0.460592224	0.831891845	0.344483209	-1.179475351	-1.0045442	-1.014468985	-1.034850423	-1.009879889	-1.044944359	23120.71812	19602.54456	23016.12824	22241.01931	22790.95612	21810.6887	10.05471454	14.4969	14.2588	14.4904	14.4409	14.4762	14.4127	0.04576	0.04576	0.04823	0.04576	0.04576	0.04823	11	15	34
9790051	phosphofructokinase,_platelet_[Mus_musculus]	AIGVLTSGGDAQGMNAAVR	99.998578	0.022756225	0.997658493	0.99643308	0.903404554	0.977979004	0.512969092	0.003510961	0.95693981	0.324871602	0.783091367	0.365382728	0.185841374	1.147497754	1.002510637	1.045724372	1.012871248	1.043105513	-1.063923285	7758.128542	8902.435075	7777.606388	7877.713887	8112.864099	7625.422068	10.08422247	12.9215	13.12	12.9251	12.9436	12.986	12.8966	0.04589	0.04589	0.04837	0.04589	0.04589	0.04837	3	5	33
IPI00204322.2	98_kDa_protein	VYSPHVLNLTLVDLPGMTK	99.99999999	0.014433657	0.997658493	0.99643308	0.218704741	0.977979004	0.449461272	0.001284875	0.849873825	0.994099043	0.013497207	0.844239109	0.172491811	1.066639144	-1.00371045	1.000140838	1.051054461	1.00385181	1.0272976	15168.29971	16179.10222	15112.22655	15883.77314	15170.43598	15584.55248	4.239307331	13.8888	13.9818	13.8834	13.9553	13.889	13.9278	0.01933	0.01933	0.02038	0.01933	0.01933	0.02038	33	36	78
IPI00191766.1	Isoform_1_of_Neural_cell_adhesion_molecule_L1_precursor	AFGAPVPSVQWLDEEGTTVLQDER	99.99999985	0.086135686	0.997658493	0.99643308	0.805073754	0.977979004	0.948495187	0.026677453	0.618791051	0.248495971	0.567485018	0.5279509	0.846263123	-1.068834399	1.015122224	1.034647915	-1.017403455	1.019234818	-1.005859796	10387.5539	9718.581205	10544.63681	10364.26284	10747.46099	10684.84995	6.532824005	13.3426	13.2465	13.3642	13.3393	13.3917	13.3833	0.02977	0.02977	0.03138	0.02977	0.02977	0.03138	5	5	100
IPI00204394.1	Calicin	YIYISGGTTEQISGLK	99.87857	0.113901111	0.997658493	0.99643308	0.718361311	0.977979004	0.939686077	0.039523571	0.64229465	0.460286784	0.374112315	0.798318134	0.831219455	-1.194327387	1.041190549	1.064551839	1.080531182	1.022437094	1.018678873	17865.36479	14958.51555	18601.24898	20099.22954	19018.60695	19373.8531	18.97038882	14.1249	13.8687	14.1831	14.2949	14.2151	14.2418	0.08578	0.08578	0.09042	0.08578	0.08578	0.09042	2	2	21
IPI00390362.1	NADH_dehydrogenase_[ubiquinone]_flavoprotein_3,_mitochondrial_precursor	TESVFKEPTLVPESSDTTTYK	99.99996347	0.030758203	0.997658493	0.99643308	0.255767282	0.977979004	0.482325939	0.005913168	0.48648617	0.865882513	0.02192291	0.390409839	0.155373223	-1.189424871	1.044477859	-1.010309616	-1.157991847	-1.055246025	-1.093641312	20445.13563	17189.09376	21354.49149	18440.96878	20236.50503	18503.7862	13.57469082	14.3195	14.0692	14.3823	14.1706	14.3047	14.1755	0.06165	0.06165	0.06498	0.06165	0.06165	0.06498	2	2	7
IPI00400615.1	ATPase,_H+_transporting,_V1_subunit_E_isoform_1	IQMSNLMNQAR	99.99999995	0.045477159	0.997658493	0.99643308	0.430171333	0.992757535	0.444862176	0.010186884	0.473549558	0.444952358	0.093470957	0.978389868	0.120494098	-1.079661344	1.021549013	1.022370435	-1.051753526	1.000804095	-1.047720492	16070.12732	14884.41482	16416.4227	15608.6215	16429.62305	15681.30354	6.433775197	13.9721	13.8615	14.0029	13.9301	14.004	13.9368	0.02932	0.02932	0.03091	0.02932	0.02932	0.03091	11	13	128
IPI00207146.1	Zero_beta-1_globin	FGDLSSVSAIMGNPQVK	100	0.908474472	0.997658493	0.639633748	0.813638662	0.977979004	0.673446244	0.851327128	0.451561736	0.02697695	0.586446312	0.151122711	0.352622824	-1.010215642	1.042947687	1.130686941	1.03081185	1.084126227	1.053371772	12733.48616	12604.72084	13280.35994	13689.55241	14397.58652	15166.01123	12.10972144	13.6363	13.6217	13.697	13.7408	13.8135	13.8886	0.05505	0.05505	0.05802	0.05505	0.05505	0.05802	7	10	112
IPI00191790.1	Neuronal_calcium_binding_protein_NECAB2	ETANQIQSLLSSVESAVEAIEEQTSQIR	99.99999675	0.360449564	0.997658493	0.99643308	0.117623759	0.977979004	0.071235349	0.231638458	0.960392332	0.504335143	0.00287457	0.484374481	0.000771676	-1.046851168	1.001941427	-1.025762122	-1.12931819	-1.027753565	-1.148973441	10180.83575	9725.198825	10200.6011	9032.530597	9925.143001	8638.270171	8.474441227	13.3136	13.2475	13.3164	13.1409	13.2769	13.0765	0.03859	0.03859	0.04068	0.03859	0.03859	0.04068	3	5	24
IPI00763106.1	PREDICTED:_similar_to_Fascin_(Singed-like_protein)_isoform_1	SSYDVFQLEFNDGAYNIK	99.99999998	0.1968362	0.997658493	0.99643308	0.279701276	0.977979004	0.119761122	0.095381199	0.786466224	0.326080858	0.031006884	0.221547569	0.00358409	-1.071149486	1.011385174	-1.040932986	-1.096559336	-1.052784189	-1.135247916	25959.51079	24235.18952	26255.06434	23943.13146	24938.69552	21967.62061	9.066885901	14.664	14.5648	14.6803	14.5473	14.6061	14.4231	0.04128	0.04128	0.04351	0.04128	0.04128	0.04351	4	4	24
IPI00191114.1	PREDICTED:_similar_to_Rho-related_GTP-binding_protein_RhoC_precursor	LVIVGDGACGK	99.9999999	0.076373123	0.997658493	0.99643308	0.557987386	0.977979004	0.480223035	0.021591223	0.818028911	0.22166894	0.189499136	0.335208639	0.153671371	1.087500051	1.008448332	1.044772829	-1.049554539	1.036020187	-1.054083394	12158.41452	13222.27641	12261.13284	11682.22554	12702.78114	12051.02102	7.930280141	13.5697	13.6907	13.5818	13.512	13.6329	13.5569	0.03612	0.03612	0.03808	0.03612	0.03612	0.03808	4	4	65
IPI00197362.2	PREDICTED:_similar_to_calmodulin_1	EAFSLFDKDGDGTITTK	99.99999996	0.05841529	0.997658493	0.99643308	0.271569898	0.977979004	0.54925	0.01524335	0.652588185	0.365976032	0.026567349	0.665438324	0.215933715	-1.229114386	1.038981797	1.077853481	-1.21263023	1.037413249	-1.111596382	32123.64094	26135.59918	33375.87818	27523.54126	34624.57821	31148.51648	18.53805403	14.9713	14.6737	15.0265	14.7484	15.0795	14.9269	0.08386	0.08386	0.0884	0.08386	0.08386	0.0884	9	16	61
IPI00327662.3	Spectrin_beta_chain,_brain_2	LAQAASLYQFQADANDMEAWLVDALR	99.99998868	0.047029537	0.997658493	0.99643308	0.169558539	0.977979004	0.440189179	0.011072097	0.375211035	0.461220748	0.007363685	0.864189573	0.116992122	1.087805902	-1.029790821	-1.023997541	1.095868746	1.005657513	1.05370912	9485.374026	10318.24585	9210.971623	10094.01592	9263.082815	9760.594841	7.152249711	13.2115	13.3329	13.1691	13.3012	13.1773	13.2528	0.03259	0.03259	0.03435	0.03259	0.03259	0.03435	14	15	15
IPI00231920.3	profilin_2	YVWAATAGGVFQSITPAEIDVIIGK	99.99999996	0.020340485	0.997658493	0.99643308	0.792374134	0.977979004	0.924766593	0.002690856	0.458965357	0.804972729	0.51576321	0.327891304	0.796739694	-1.127602247	-1.029636814	1.00950072	1.025945795	1.039419104	-1.010185888	14978.01944	13283.06989	14546.89581	14924.32658	15120.32141	14967.86047	8.535099885	13.8706	13.6973	13.8284	13.8654	13.8842	13.8696	0.03887	0.03887	0.04097	0.03887	0.03887	0.04097	7	8	116
IPI00206977.1	Citrate_synthase	GLVYETSVLDPDEGIR	99.99999967	0.24560781	0.997658493	0.99643308	0.699730801	0.977979004	0.351794446	0.127716061	0.358999286	0.783477047	0.341866213	0.237774742	0.053874807	1.063583088	-1.038592116	1.011060868	-1.04002928	1.050079847	-1.08405466	15744.01092	16745.06376	15158.99329	14575.54473	15918.15335	14683.90289	8.922696844	13.9425	14.0314	13.8879	13.8313	13.9584	13.8419	0.04063	0.04063	0.04282	0.04063	0.04063	0.04282	12	12	64
IPI00203630.1	Isoform_1_of_Growth_factor_receptor-bound_protein_2	RGDFIHVMDNSDPNWWK	99.9984528	0.144334023	0.997658493	0.99643308	0.450498174	0.988483763	0.832460662	0.062187345	0.342712185	0.352461873	0.100587856	0.964789556	0.582530385	-1.073245539	1.037160367	1.035408879	-1.065770641	-1.00169159	1.021300629	11123.29898	10364.16977	11536.64484	10824.69755	11517.16252	11762.48533	8.307213013	13.4413	13.3393	13.4939	13.402	13.4915	13.5219	0.03783	0.03783	0.03988	0.03783	0.03783	0.03988	3	3	56
IPI00199465.1	Glutaminase_kidney_isoform,_mitochondrial_precursor	SVINLLFAAYTGDVSALRR	99.9985026	0.052500436	0.997658493	0.99643308	0.272822502	0.977979004	0.993109576	0.012952468	0.54391762	0.419964598	0.028061743	0.857591468	0.963016408	1.183202946	-1.041879074	-1.054573251	1.163863106	-1.012183926	1.003133822	4621.387906	5468.039786	4435.627918	5162.463685	4382.235091	4395.968234	14.69418897	12.1741	12.4168	12.1149	12.3338	12.0975	12.102	0.06668	0.06668	0.07029	0.06668	0.06668	0.07029	3	4	37
IPI00210351.1	Adenylate_kinase_isoenzyme_1	IIFVVGGPGSGK	99.99999983	0.054262451	0.997658493	0.99643308	0.977277605	0.977979004	0.837394717	0.013643131	0.578982591	0.751121943	0.951589165	0.805081747	0.604838241	-1.1043379	1.022549152	1.012470459	1.002439184	-1.009954555	1.02100863	14293.06989	12942.65994	14615.36649	14651.01606	14471.31104	14775.33345	8.707946282	13.803	13.6598	13.8352	13.8387	13.8209	13.8509	0.03965	0.03965	0.0418	0.03965	0.03965	0.0418	12	16	118
IPI00371036.1	Mitochondrial_fission_1_protein	GLLQTEPQNNQAK	99.99988564	0.202114931	0.997658493	0.99643308	0.507654338	0.977979004	0.502382198	0.098632086	0.07873546	0.196415795	0.147235102	0.605537406	0.177986836	-1.064697354	1.071099572	1.04999379	-1.057969754	-1.020100863	-1.053689505	9520.273692	8941.765149	10197.16107	9638.424001	9996.228255	9486.882242	8.350342341	13.2168	13.1263	13.3159	13.2346	13.2872	13.2117	0.03803	0.03803	0.04009	0.03803	0.03803	0.04009	3	3	110
IPI00194974.2	Hnrpk_protein	IITITGTQDQIQNAQYLLQNSVK	100	0.072859085	0.997658493	0.99643308	0.117623759	0.977979004	0.348219477	0.019733123	0.283846295	0.586222978	0.003035433	0.584818896	0.049736025	-1.057679387	1.026273647	1.01284946	-1.077320782	-1.013253882	-1.049290919	11419.50918	10796.75876	11719.54134	10878.41387	11566.24371	11022.91414	5.215854659	13.4792	13.3983	13.5166	13.4092	13.4976	13.4282	0.02378	0.02378	0.02507	0.02378	0.02378	0.02507	13	15	71
IPI00199077.1	Calcium/calmodulin-dependent_3',5'-cyclic_nucleotide_phosphodiesterase_1B	IVEPTFSVLTDVAEK	99.9999997	0.995178317	0.997658493	0.222448964	0.626617454	0.977979004	0.977970118	0.994040971	0.14687049	0.001779592	0.252795384	0.088868086	0.911586526	-1.000233061	-1.048103468	-1.107713366	-1.037582281	-1.056874059	-1.003566066	10914.45875	10911.91561	10413.53176	10036.3431	9853.143498	9818.131395	6.95185018	13.414	13.4136	13.3462	13.2929	13.2664	13.2612	0.03168	0.03168	0.03339	0.03168	0.03168	0.03339	7	7	28
IPI00779178.1	Protein	LFEVGGSPANTR	100	0.240762232	0.997658493	0.99643308	0.733834025	0.977979004	0.418312577	0.124095733	0.443687795	0.924760242	0.422890101	0.499835911	0.095778861	1.085421889	-1.042462553	-1.004988874	-1.04448232	1.037287656	-1.095707042	13661.64955	14828.65346	13105.17055	12547.04872	13593.83164	12406.44726	11.76635371	13.7378	13.8561	13.6778	13.6151	13.7307	13.5988	0.0535	0.0535	0.05639	0.0535	0.0535	0.05639	13	15	17
IPI00471526.3	Similar_to_14-3-3_protein_sigma	DSTLIMQLLR	99.9984048	0.839607981	0.997658493	0.99643308	0.257388081	0.977979004	0.03637813	0.755167407	0.684068589	0.804977899	0.022650151	0.867506804	0.0003326	-1.016356877	1.021997568	1.012927208	-1.133050713	-1.008954602	-1.226719247	41359.67923	40694.05166	42269.49158	37305.91323	41894.34439	34151.53425	11.61177508	15.3359	15.3125	15.3673	15.1871	15.3545	15.0597	0.0528	0.0528	0.05565	0.0528	0.0528	0.05565	3	6	24
IPI00199600.1	PREDICTED:_similar_to_vacuolar_H+_ATPase_G1	EAAALGSHGSCSSEVEKETQEK	99.99996865	0.018274321	0.997658493	0.99643308	0.437197748	0.983201098	0.359553375	0.002025839	0.833191776	0.922159632	0.096433332	0.908020562	0.059846608	-1.238007675	1.014388399	1.006470996	-1.121048686	-1.007866498	-1.138654466	12687.73154	10248.50798	12870.28768	11480.57871	12769.8338	11214.8454	14.76856201	13.6311	13.3231	13.6518	13.4869	13.6405	13.4531	0.06701	0.06701	0.07064	0.06701	0.06701	0.07064	2	2	81
IPI00204316.1	ATP_synthase_coupling_factor_6,_mitochondrial_precursor	RLASGGPVDTGPEYQQEVDRELFK	99.9999881	0.075722809	0.997658493	0.99643308	0.666252843	0.977979004	0.570211715	0.021202387	0.873939411	0.334776791	0.298210539	0.273369288	0.235904733	-1.112594237	-1.007381925	1.044681341	-1.049666061	1.052393101	-1.056873999	21466.04205	19293.68437	21308.74251	20300.4968	22425.1736	21218.39842	10.06496524	14.3898	14.2358	14.3792	14.3092	14.4528	14.373	0.0458	0.0458	0.04828	0.0458	0.0458	0.04828	7	10	117
IPI00367525.3	PREDICTED:_similar_to_Gamma-soluble_NSF_attachment_protein	AVQLYQQTANVFENEER	100	0.052500436	0.997658493	0.99643308	0.667740008	0.977979004	0.849367056	0.013020108	0.636444921	0.766997384	0.302000132	0.447503766	0.630309856	-1.0668427	-1.012366636	1.007522426	1.027315057	1.019982089	1.012593965	14441.10014	13536.29747	14264.69386	14654.33479	14549.73224	14732.97106	5.630501667	13.8179	13.7245	13.8002	13.839	13.8287	13.8468	0.02567	0.02567	0.02706	0.02567	0.02567	0.02706	8	9	121
IPI00231697.4	Stathmin	ASGQAFELILSPR	99.9999015	0.24587381	0.997658493	0.99643308	0.210777717	0.977979004	0.924766593	0.128223418	0.456871944	0.401583184	0.012767107	0.121838058	0.793840647	-1.048119371	-1.023691591	1.026046581	1.083904454	1.050355257	1.008238851	13136.4734	12533.37527	12832.45219	13909.15208	13478.63361	13589.68207	6.806361037	13.6813	13.6135	13.6475	13.7637	13.7184	13.7302	0.03102	0.03102	0.03269	0.03102	0.03102	0.03269	5	6	91
IPI00188119.1	Isoform_Long_of_Potassium-transporting_ATPase_alpha_chain_2	VIMVTGDHPITAK	100	0.045844003	0.997658493	0.99643308	0.780681315	0.977979004	0.849367056	0.010531022	0.983580796	0.698128109	0.470193204	0.69059075	0.63109896	1.272445043	-1.001930704	1.0360415	-1.070211167	1.03804179	1.046085436	15631.86443	19890.6884	15601.74208	14578.19032	16195.26028	16941.62591	20.51161127	13.9322	14.2798	13.9294	13.8315	13.9833	14.0483	0.09262	0.09262	0.09763	0.09262	0.09262	0.09763	4	7	77
IPI00231954.5	6-phosphofructokinase_type_C	EIGWGDVGGWTGQGGSILGTK	99.99995566	0.032488675	0.997658493	0.99643308	0.706612353	0.977979004	0.69561724	0.006460605	0.58844275	0.686788003	0.361223845	0.352001136	0.385659071	1.128428571	-1.024102261	1.017413342	1.041115929	1.041935304	-1.039010974	9535.442511	10760.06577	9311.025374	9693.857205	9701.486431	9337.231923	9.541749049	13.2191	13.3934	13.1847	13.2429	13.244	13.1888	0.04343	0.04343	0.04578	0.04343	0.04343	0.04578	6	8	67
IPI00231643.4	Superoxide_dismutase	HVGDLGNVAAGKDGVANVSIEDR	99.99999991	0.032488675	0.997658493	0.99643308	0.486148755	0.977979004	0.503151385	0.006449314	0.552762376	0.693509343	0.126745277	0.330046362	0.179524525	-1.169032636	1.034352072	-1.022043274	-1.09168858	-1.057152578	-1.07994238	22000.23176	18819.17671	22755.9853	20844.75895	21525.73411	19932.29871	12.34938142	14.4252	14.1999	14.474	14.3474	14.3938	14.2828	0.05613	0.05613	0.05916	0.05613	0.05613	0.05916	10	21	60
IPI00778867.1	28_kDa_protein	MTDQEAIQDLWQWR	99.99992508	0.122629636	0.997658493	0.99643308	0.813181576	0.977979004	0.386337182	0.044286817	0.881545436	0.555655652	0.582833663	0.470444473	0.076378746	-1.210338816	1.014349834	-1.056467795	-1.053995944	-1.071627932	1.187718972	13992.44898	11560.77025	14193.2383	13466.12232	13244.558	15730.8128	20.93221902	13.7724	13.4969	13.7929	13.717	13.6931	13.9413	0.09448	0.09448	0.09959	0.09448	0.09448	0.09959	3	3	11
IPI00454288.1	LRRGT00199	HLIIGVSSDR	99.99998898	0.112419204	0.997658493	0.99643308	0.903404554	0.977979004	0.847855771	0.038800685	0.432050785	0.245255142	0.775917266	0.72622661	0.620827169	1.064977835	-1.024452909	-1.035515621	1.00876784	-1.010798654	1.015299002	15537.68469	16547.28981	15516.81202	15299.7922	15004.78059	15234.33875	6.647514604	13.9235	14.0143	13.8886	13.9012	13.8731	13.895	0.03029	0.03029	0.03193	0.03029	0.03029	0.03193	6	7	126
IPI00358226.2	14_kDa_protein	AQVAQPGGDTIFGK	99.99999918	0.326142987	0.997658493	0.821454277	0.908280262	0.977979004	0.973339629	0.203140489	0.411111263	0.062899928	0.795473609	0.311827443	0.899922012	-1.027265568	1.017926665	1.040465434	1.005602453	1.02214184	1.002713539	16362.98351	15928.67903	16656.31724	16749.63347	17025.11874	17071.31707	4.669445608	13.9981	13.9593	14.0238	14.0318	14.0554	14.0593	0.02129	0.02129	0.02244	0.02129	0.02129	0.02244	6	7	100
IPI00366087.1	PREDICTED:_similar_to_Dihydropyrimidinase-related_protein_4	TIDAHGLMVLPGGVDVHTR	99.99999947	0.891046753	0.997658493	0.307157315	0.572971917	0.829890438	0.344866854	0.819763013	0.481553601	0.003510369	0.208827472	0.02750494	0.046901892	1.006866045	-1.022000525	-1.095694636	1.039839238	-1.072107703	1.064482948	15851.68194	15960.5197	15510.44345	16128.36769	14467.24373	15400.13426	6.688735811	13.9523	13.9622	13.921	13.9773	13.8205	13.9107	0.03048	0.03048	0.03213	0.03048	0.03048	0.03213	9	9	59
IPI00207217.1	Enoyl-CoA_hydratase,_mitochondrial_precursor	IFPVETLVEEAIQCAEK	99.99990602	0.126343985	0.997658493	0.981106763	0.341556205	0.977979004	0.673644494	0.047360945	0.498029718	0.178281115	0.049574444	0.521282718	0.361843328	1.06365484	1.021528196	1.042327433	-1.064767845	1.020360904	-1.02913187	15286.39006	16259.44277	15615.47845	14665.61799	15933.42371	15482.39265	6.801365596	13.9	13.989	13.9307	13.8402	13.9598	13.9183	0.03099	0.03099	0.03267	0.03099	0.03099	0.03267	3	3	65
IPI00208348.1	Pyridoxal_kinase	MGPDTVVITSSDLPSPK	100	0.034281415	0.997658493	0.959908311	0.560474035	0.92052399	0.766408058	0.007052177	0.543885607	0.163504935	0.195567086	0.052243648	0.495351879	-1.125806821	1.026868363	-1.061517713	-1.058549509	-1.090038957	-1.030246877	16004.8253	14216.31581	16434.84877	15525.81965	15077.30404	14634.65153	9.466074561	13.9662	13.7953	14.0045	13.9224	13.8801	13.8371	0.04309	0.04309	0.04542	0.04309	0.04309	0.04542	16	23	130
IPI00231736.8	Fructose-bisphosphate_aldolase_C	TPSALAILENANVLAR	100	0.135559745	0.997658493	0.998666993	0.83893122	0.977979004	0.590127084	0.054113703	0.16208348	0.998666993	0.627493572	0.161609439	0.254260469	-1.074559935	1.054614408	-1.000061265	-1.018471115	-1.054679018	1.04417065	18266.98345	16999.50171	19264.62393	18915.23838	18265.8644	19072.6795	8.173809093	14.157	14.0532	14.2337	14.2073	14.1569	14.2192	0.03723	0.03723	0.03924	0.03723	0.03723	0.03924	26	36	90
21703836	hexokinase_domain_containing_1_[Mus_musculus]	FLSQIESDR	99.9985859	0.18233324	0.997658493	0.99643308	0.505620061	0.977979004	0.916967389	0.084602623	0.114574084	0.771052947	0.144075769	0.192558356	0.770676624	1.079172069	-1.074072317	-1.012757674	1.068265015	1.060542265	-1.013131878	13602.24737	14679.16544	12664.18206	13528.70263	13430.90032	13256.81347	9.713266412	13.7316	13.8415	13.6285	13.7237	13.7133	13.6944	0.04421	0.04421	0.0466	0.04421	0.04421	0.0466	3	4	1
IPI00206222.3	29_kDa_protein	AAELIANSLATAGDGLIELR	99.99999938	0.018644305	0.997658493	0.99643308	0.555941486	0.977979004	0.801751113	0.00234779	0.850894829	0.77867566	0.187113995	0.644664186	0.534022881	-1.143596972	1.008173341	-1.011918719	-1.059291422	-1.020189476	-1.027342728	13561.53236	11858.6641	13672.37539	12907.09535	13401.80008	13045.11116	9.398626022	13.7272	13.5337	13.739	13.6559	13.7101	13.6712	0.04278	0.04278	0.0451	0.04278	0.04278	0.0451	2	2	34
IPI00361686.5	Complement_component_1,_q_subcomponent_binding_protein	AEEQEPELTSTPNFVVEVTK	99.99999951	0.045590773	0.997658493	0.99643308	0.325364867	0.977979004	0.673644494	0.010264437	0.481254137	0.318245681	0.037928247	0.096967261	0.359543955	-1.129525901	1.033886579	-1.047156454	-1.105236306	-1.082641004	-1.044383	11796.17214	10443.47202	12195.90405	11034.65746	11264.95672	10786.23141	10.25107413	13.526	13.3503	13.5741	13.4298	13.4596	13.3969	0.04665	0.04665	0.04917	0.04665	0.04665	0.04917	5	10	60
IPI00206170.6	Synaptotagmin-1	HWSDMLANPR	99.99999552	0.080741141	0.997658493	0.99643308	0.492037154	0.977979004	0.894800678	0.02426848	0.61299736	0.325342109	0.130460137	0.649160857	0.719832994	1.064883853	1.014264254	1.027264482	-1.043695732	1.012817398	-1.010088222	13255.86969	14115.96159	13444.95478	12882.06358	13617.28412	13481.28195	6.063283809	13.6943	13.785	13.7148	13.6531	13.7332	13.7187	0.02764	0.02764	0.02913	0.02764	0.02764	0.02913	12	14	65
IPI00202549.1	Isoform_R-type_of_Pyruvate_kinase_isozymes_R/L	GDLGIEIPAEK	99.99988987	0.257850777	0.997658493	0.846402451	0.233298216	0.977979004	0.112902208	0.139386763	0.222923919	0.08598769	0.017597351	0.640350108	0.001806435	1.086950178	-1.027930088	-1.102094133	1.150194917	-1.027181683	1.20648123	27256.72164	29626.69844	25404.0053	29219.55777	24731.75459	29838.39769	12.46815558	14.7343	14.8546	14.6328	14.8346	14.5941	14.8649	0.05666	0.05666	0.05973	0.05666	0.05666	0.05973	3	3	123
IPI00212603.1	Pyridoxine-5'-phosphate_oxidase	ELDSNPFASLVFYWEPLNR	99.99995583	0.626526601	0.997658493	0.99643308	0.519459064	0.977979004	0.38112535	0.503369372	0.248980248	0.53948428	0.154947218	0.083081624	0.068063131	-1.039259009	1.070845122	-1.035926362	1.088425359	-1.109316692	1.115604406	12048.70437	11593.55297	12902.2963	14043.18648	11630.85023	12975.42777	12.82995628	13.5566	13.501	13.6553	13.7776	13.5057	13.6635	0.05829	0.05829	0.06145	0.05829	0.05829	0.06145	2	2	104
IPI00363828.3	ARP3_actin-related_protein_3_homolog	DITYFIQQLLR	99.99999765	0.583189779	0.997658493	0.99643308	0.842694959	0.977979004	0.485775688	0.455221279	0.545388017	0.291162171	0.637207634	0.669482004	0.161689555	1.035741923	-1.029619682	-1.051036257	-1.023010419	-1.020800472	-1.070448876	10273.06894	10640.24818	9977.537457	9753.114211	9774.228882	9130.962815	10.46567998	13.3266	13.3772	13.2845	13.2516	13.2548	13.1566	0.04762	0.04762	0.05019	0.04762	0.04762	0.05019	3	3	55
IPI00389636.3	Serine/threonine-protein_phosphatase_2A_65_kDa_regulatory_subunit_A_beta_isoform	LNIISNLDCVNEVIGIR	99.99987198	0.121352217	0.997658493	0.99643308	0.423679834	0.977979004	0.759583735	0.043409422	0.399392558	0.246906562	0.088770815	0.772854012	0.485265495	1.158406016	-1.063967224	-1.086735108	1.134923434	-1.021399046	1.052629569	7156.411374	8290.029985	6726.157733	7633.67403	6585.23988	6931.818215	15.98277187	12.805	13.0172	12.7156	12.8982	12.685	12.759	0.07246	0.07246	0.07638	0.07246	0.07246	0.07638	2	2	37
IPI00212014.2	Transitional_endoplasmic_reticulum_ATPase	IVSQLLTLMDGLK	99.99999995	0.292065533	0.997658493	0.99643308	0.541686564	0.977979004	0.8224463	0.171901428	0.606660316	0.27972099	0.174839205	0.587941511	0.564903116	-1.036934937	1.014031853	1.029013671	1.037697946	1.014774504	1.015704962	15052.05924	14515.91485	15263.26753	15838.66137	15488.77473	15732.02536	5.859745678	13.8777	13.8253	13.8978	13.9512	13.9189	13.9414	0.02671	0.02671	0.02816	0.02671	0.02671	0.02816	18	20	43
1041087	synapsin_II	QTAASAGLVDAPAPSAASR	100	0.073874881	0.997658493	0.86359048	0.162018264	0.757639751	0.894800678	0.020431681	0.35183975	0.114773919	0.006519429	0.015585732	0.717122001	-1.05969476	1.023676748	-1.039653928	-1.073158566	-1.064269552	-1.009115249	19546.54397	18445.44741	20009.34255	18645.28057	18801.01006	18631.18257	5.425221199	14.2546	14.171	14.2884	14.1865	14.1985	14.1854	0.02473	0.02473	0.02607	0.02473	0.02473	0.02607	4	5	85
54038641	Transgelin_2_[Rattus_norvegicus]	TTDIFQTVDLWEGK	99.99999947	0.081915892	0.997658493	0.99643308	0.706612353	0.977979004	0.176288606	0.024808813	0.783211118	0.363852764	0.349460895	0.541181237	0.010678053	-1.127453346	1.014856451	1.048693621	-1.051633383	1.033341829	-1.151688539	13463.70628	11941.69704	13663.72918	12992.86367	14119.30289	12259.6539	11.64451326	13.7168	13.5437	13.7381	13.6654	13.7854	13.5816	0.05295	0.05295	0.05581	0.05295	0.05295	0.05581	2	2	105
IPI00394488.2	Similar_to_NipSnap2_protein	SYQLRPGTMIEWGNYWAR	99.9982302	0.079848781	0.997658493	0.99643308	0.162018264	0.977979004	0.119761122	0.023817751	0.325316269	0.498374966	0.006665894	0.743219146	0.002897579	1.206277738	-1.08564364	-1.056454685	1.263507604	1.027629159	1.29524356	19552.30206	23585.5067	18009.87114	22755.60914	18507.46874	23971.67969	18.15779704	14.2551	14.5256	14.1365	14.4739	14.1758	14.549	0.08217	0.08217	0.08661	0.08217	0.08217	0.08661	2	2	99
34855391	PREDICTED:_similar_to_biliverdin_reductase_B_(flavin_reductase_(NADPH))_[Rattus_norvegicus]	HDLGHFMLR	99.99975015	0.103480936	0.997658493	0.99643308	0.560474035	0.977979004	0.683461668	0.03443789	0.259458004	0.730152601	0.197523454	0.425864304	0.369082799	-1.13311179	1.069718389	1.020152856	-1.080216602	-1.048586379	-1.055019568	9921.124104	8755.644583	10612.80889	9824.704481	10121.06309	9593.246796	12.91877923	13.2763	13.096	13.3735	13.2622	13.3051	13.2278	0.05869	0.05869	0.06187	0.05869	0.05869	0.06187	2	2	71
IPI00196661.1	14-3-3_protein_theta	TAFDEAIAELDTLNEDSYK	100	0.252744602	0.997658493	0.99643308	0.740830571	0.977979004	0.187778298	0.134604554	0.681727932	0.365601689	0.43433838	0.636097506	0.012661622	1.053314901	1.014586305	1.031684521	-1.028050781	1.016852402	-1.09491762	15699.19779	16536.19896	15928.19108	15493.58395	16196.61935	14792.54608	7.65310049	13.9384	14.0133	13.9593	13.9194	13.9834	13.8526	0.03486	0.03486	0.03675	0.03486	0.03486	0.03675	17	26	33
IPI00198717.7	Malate_dehydrogenase,_cytoplasmic	VIVVGNPANTNCLTASK	99.99999997	0.092932042	0.997658493	0.99643308	0.88970951	0.977979004	0.343015874	0.030163086	0.799060652	0.284696572	0.74800342	0.42949386	0.044959521	-1.055773939	-1.006421567	-1.026670656	-1.008112712	-1.020119887	1.05274303	21060.4051	19947.83573	20926.0272	20757.62655	20513.30188	21595.23557	5.448754694	14.3622	14.2839	14.353	14.3414	14.3243	14.3984	0.02484	0.02484	0.02618	0.02484	0.02484	0.02618	18	21	133
IPI00569808.2	PREDICTED:_similar_to_neuron_navigator_3	DGDILGK	99.9931936	0.045301902	0.997658493	0.99643308	0.279701276	0.977979004	0.386337182	0.010095852	0.765657499	0.5903435	0.03053112	0.820834084	0.07638438	-1.304090836	1.031083684	1.055341656	-1.255064289	1.023526676	-1.202874154	15917.67952	12205.95918	16412.45964	13076.9872	16798.59026	13965.37634	22.51254651	13.9583	13.5753	14.0025	13.6747	14.0361	13.7696	0.1014	0.1014	0.1069	0.1014	0.1014	0.1069	2	3	2
IPI00190776.1	Isoform_V0_of_Versican_core_protein_precursor_(Fragment)	VSVPTHPDDVGDASLTMVK	99.908795	0.955265633	0.997658493	0.846402451	0.733834025	0.977979004	0.485775688	0.931247526	0.050920332	0.097640078	0.401468309	0.722854432	0.159886491	-1.003217831	1.079051957	1.064502	-1.032731208	-1.013668323	1.055786875	11911.58716	11873.38063	12853.22143	12445.85361	12679.90835	13387.28081	8.300534264	13.5401	13.5354	13.6498	13.6034	13.6303	13.7086	0.0378	0.0378	0.03985	0.0378	0.0378	0.03985	2	2	79
45829444	Rad23b_protein_[Mus_musculus]	SNLFEDATSALVTGQSYENMVTEIMSMGYER	99.99954059	0.143984005	0.997658493	0.99643308	0.243871572	0.977979004	0.826498686	0.061828876	0.174350601	0.620617645	0.020078779	0.376221791	0.570520236	-1.107825691	1.078865482	1.027074657	-1.141347932	-1.05042557	-1.031968391	7433.063771	6709.596855	8019.27593	7026.144882	7634.311422	7397.815175	12.03957921	12.8597	12.712	12.9693	12.7785	12.8983	12.8529	0.05473	0.05473	0.05769	0.05473	0.05473	0.05769	2	3	51
IPI00189690.1	Ras-related_protein_Rab-8B	LQIWDTAGQER	99.99960398	0.076937917	0.997658493	0.99643308	0.930552243	0.977979004	0.544653269	0.021894333	0.921498588	0.669458647	0.844013773	0.607415988	0.213504081	1.12805644	-1.005201129	1.022132622	-1.010413208	1.027448865	-1.068201989	26123.99737	29469.34346	25988.82613	25720.98813	26702.18992	24997.32279	11.43878567	14.6731	14.8469	14.6656	14.6507	14.7047	14.6095	0.05202	0.05202	0.05483	0.05202	0.05202	0.05483	3	3	33
54035288	Enolase_3,_beta_[Rattus_norvegicus]	VNQIGSVTESIQACK	100	0.01347102	0.997658493	0.86359048	0.962127414	0.977979004	0.985931583	0.001142198	0.679665052	0.113891892	0.907148705	0.255464969	0.94649932	-1.096756889	-1.011508017	-1.04407	-1.00323482	-1.032191522	1.001859889	23521.44795	21446.36444	23253.84233	23178.86287	22528.61201	22570.51274	6.00254726	14.5217	14.3884	14.5052	14.5005	14.4595	14.4622	0.02736	0.02736	0.02884	0.02736	0.02736	0.02884	13	22	58
IPI00207355.3	Heat_shock-related_70_kDa_protein_2	IINEPTAAAIAYGLDK	100	0.185794486	0.997658493	0.959908311	0.930552243	0.977979004	0.271928686	0.086845651	0.632349547	0.153124822	0.849727134	0.35674532	0.026570477	-1.067244441	1.018608778	1.055549526	1.00732163	1.036265884	-1.091388811	24730.98863	23172.75002	25191.2021	25375.64276	26104.78332	23918.86655	8.35269139	14.594	14.5001	14.6206	14.6312	14.672	14.5459	0.03804	0.03804	0.0401	0.03804	0.03804	0.0401	11	21	114
IPI00189362.2	17_kDa_protein	EAFSLFDKDGDGTITTK	99.99999996	0.118667356	0.997658493	0.99643308	0.46981881	0.977979004	0.426572047	0.041770909	0.709459807	0.275048663	0.116840017	0.487616412	0.107252401	-1.211287114	1.035976725	1.106608635	-1.16236091	1.068179051	-1.167228118	38293.73672	31614.08743	39671.41996	34130.03624	42376.17972	36304.9682	20.75204082	15.2248	14.9483	15.2758	15.0588	15.371	15.1479	0.09368	0.09368	0.09875	0.09368	0.09368	0.09875	6	9	61
IPI00331955.5	Guanine_nucleotide-binding_protein_G(z)_subunit_alpha	IAAPDYIPTVEDILR	99.9984304	0.079206356	0.997658493	0.99643308	0.848375486	0.977979004	0.406234571	0.022915019	0.880414566	0.405090216	0.644765369	0.508467922	0.088634682	1.141112615	-1.008784446	-1.04839872	-1.027190856	-1.039269314	1.105590662	7021.93198	8012.815166	6960.785335	6776.525801	6697.768558	7404.990376	12.64073239	12.7777	12.9681	12.765	12.7263	12.7095	12.8543	0.05744	0.05744	0.06055	0.05744	0.05744	0.06055	2	2	93
IPI00196107.1	ATP_synthase_B_chain,_mitochondrial_precursor	HVIQSISAQQEK	99.99997638	0.034281415	0.997658493	0.99643308	0.901157331	0.977979004	0.894800678	0.007051335	0.641253521	0.758140052	0.767271099	0.444796084	0.719202205	1.201600668	-1.032024112	1.020470627	1.020210172	1.053150293	1.024610031	9557.864762	11484.73669	9261.28048	9448.452551	9753.520249	9993.554681	14.71661154	13.2225	13.4874	13.177	13.2059	13.2517	13.2868	0.06678	0.06678	0.07039	0.06678	0.06678	0.07039	6	6	50
IPI00339148.2	60_kDa_heat_shock_protein,_mitochondrial_precursor	ILQSSSEVGYDAMLGDFVNMVEK	100	0.029532584	0.997658493	0.99643308	0.719177452	0.977979004	0.959191605	0.005569002	0.702768573	0.916929648	0.378625796	0.629213053	0.865348501	-1.111523285	1.014514038	-1.003838522	-1.03391153	-1.018408273	1.006420311	17914.7711	16117.31518	18174.78677	17578.66727	17846.26781	17960.84639	8.187268678	14.1289	13.9763	14.1497	14.1015	14.1233	14.1326	0.03729	0.03729	0.03931	0.03729	0.03729	0.03931	37	50	80
1580888	2116232A_2-oxoglutarate_carrier_protein	LGIYTVLFER	99.99990846	0.018644305	0.997658493	0.99643308	0.691591891	0.977979004	0.70956869	0.002392047	0.759263251	0.965643749	0.335125671	0.791337576	0.420867889	1.16363343	1.015136196	1.002056387	1.048584923	-1.013052967	1.040358131	9458.038876	11005.69022	9601.197605	10067.67105	9477.488267	9859.981983	10.64329794	13.2073	13.426	13.229	13.2974	13.2103	13.2674	0.04842	0.04842	0.05104	0.04842	0.04842	0.05104	3	3	131
IPI00202616.1	PREDICTED:_similar_to_NADH_dehydrogenase_(ubiquinone)_Fe-S_protein_3	SLADLTAVDVPTR	99.99979836	0.269895028	0.997658493	0.99643308	0.572971917	0.988483763	0.485775688	0.150832764	0.853148087	0.79554322	0.2072059	0.94645843	0.160584773	1.06290185	-1.008028248	-1.010956354	-1.056434324	-1.002904786	-1.063095551	10292.75977	10940.19341	10210.78506	9665.328761	10181.21082	9576.948013	9.37572321	13.3293	13.4174	13.3178	13.2386	13.3136	13.2254	0.04268	0.04268	0.04499	0.04268	0.04268	0.04499	2	2	17
IPI00209908.1	Cytochrome_c_oxidase_subunit_2	VVLPMELPIR	99.998661	0.058395471	0.997658493	0.99643308	0.896013588	0.977979004	0.673446244	0.015015978	0.689465185	0.933385747	0.758795507	0.630722119	0.35182107	1.356243649	-1.051280987	1.010226542	-1.039165683	1.062031955	1.12403799	10511.71768	14256.45033	9998.961086	9622.104779	10619.21619	11936.40243	27.59195524	13.3597	13.7993	13.2876	13.2321	13.3744	13.5431	0.1236	0.1236	0.1303	0.1236	0.1236	0.1303	2	2	75
IPI00211800.2	Isoform_6_of_Gephyrin	DLVQDPSLLGGTISAYK	99.99997456	0.446302616	0.997658493	0.99643308	0.279701276	0.977979004	0.673644494	0.317257403	0.961567487	0.494793627	0.030982232	0.537449761	0.359859909	-1.033551819	-1.001627044	-1.022723579	1.077296828	-1.021062265	1.031503239	11088.48181	10728.52043	11070.46967	11926.18186	10842.11027	11183.67185	7.31730644	13.4368	13.3892	13.4344	13.5418	13.4044	13.4491	0.03334	0.03334	0.03514	0.03334	0.03334	0.03514	6	7	40
IPI00388191.2	34_kDa_protein	AAVPSGASTGIYEALELR	99.99999833	0.020560165	0.997658493	0.453836823	0.505620061	0.977979004	0.214644651	0.00281968	0.172774607	0.006224048	0.144462875	0.169457878	0.015454415	-1.118185239	-1.051896848	-1.106930541	1.05572786	-1.052318526	1.095980845	24897.58192	22266.06205	23669.2238	24988.259	22492.45187	24651.2964	7.978575718	14.6037	14.4426	14.5307	14.609	14.4572	14.5894	0.03634	0.03634	0.03831	0.03634	0.03634	0.03831	6	10	45
IPI00231767.4	Triosephosphate_isomerase	VTNGAFTGEISPGMIK	100	0.015074205	0.997658493	0.737211716	0.975456216	0.977979004	0.463761691	0.001447124	0.596888284	0.039751202	0.948700846	0.134343456	0.143103608	-1.118789486	-1.01840814	-1.072908578	-1.002218483	-1.053515321	1.052285084	25044.59333	22385.43858	24591.90216	24537.46622	23342.70957	24563.18509	7.470634789	14.6122	14.4503	14.5859	14.5827	14.5107	14.5842	0.03404	0.03404	0.03588	0.03404	0.03404	0.03588	22	33	45
IPI00189995.1	Calretinin	HFDADGNGYIEGK	99.9999998	0.111177592	0.997658493	0.99643308	0.082790115	0.977979004	0.264457644	0.038245092	0.282280228	0.699715015	0.00084654	0.481506783	0.025085697	-1.133854286	1.068171642	1.023178558	-1.239900419	-1.043978834	-1.150294225	15035.06496	13260.13858	16060.03003	12952.67732	15383.55608	13373.58369	13.26866836	13.876	13.6948	13.9712	13.661	13.9091	13.7071	0.06027	0.06027	0.06353	0.06027	0.06027	0.06353	16	18	7
IPI00361239.4	49_kDa_protein	SIQFVDWCPTGFK	99.99999999	0.037855522	0.997658493	0.99643308	0.686643596	0.977979004	0.855911166	0.007871677	0.641226796	0.887628395	0.326449984	0.546534415	0.648536118	1.328157699	-1.050680353	1.014684611	1.11014001	1.066109185	-1.049543057	23542.82266	31268.58117	22407.217	24875.1481	23888.53985	22760.8955	23.26134593	14.523	14.9324	14.4517	14.6024	14.544	14.4743	0.1047	0.1047	0.1104	0.1047	0.1047	0.1104	6	10	9
IPI00201410.1	Isoform_1_of_Serine/threonine-protein_phosphatase_2B_catalytic_subunit_alpha_isoform	LFEVGGSPANTR	100	0.378350913	0.997658493	0.99643308	0.706612353	0.977979004	0.418312577	0.2486306	0.32145999	0.799425657	0.348072467	0.455190199	0.096570446	1.054239955	-1.047658868	-1.011629018	-1.045025473	1.035615675	-1.081892427	13634.16862	14373.68532	13013.93902	12453.2266	13477.43924	12457.28217	10.1488398	13.7349	13.8111	13.6678	13.6042	13.7183	13.6047	0.04618	0.04618	0.04868	0.04618	0.04618	0.04868	18	21	17
IPI00206666.2	Isoform_1_of_Neurofascin_precursor	LTVSWLKDDEPLYIGNR	99.99999266	0.201425078	0.997658493	0.970109364	0.908280262	0.977979004	0.147881653	0.098065238	0.844093831	0.172341831	0.796015203	0.128531325	0.007436335	-1.070657453	1.008263665	-1.057684134	-1.0108781	-1.066424481	1.122987717	14411.66469	13460.57475	14530.75785	14374.39179	13625.67918	15301.47035	9.081059179	13.8149	13.7165	13.8268	13.8112	13.734	13.9014	0.04134	0.04134	0.04358	0.04134	0.04134	0.04358	6	8	97
IPI00198880.4	16_kDa_protein	LQIWDTAGQER	99.99960398	0.213661392	0.997658493	0.959908311	0.573080061	0.977979004	0.146792151	0.106464419	0.86276017	0.167846825	0.209585365	0.240368143	0.006423219	1.082189756	1.008618479	1.069562864	-1.064769258	1.060423626	-1.150614853	22804.11167	24678.37065	23000.64842	21601.53315	24390.431	21197.73697	10.78244105	14.477	14.591	14.4894	14.3988	14.574	14.3716	0.04905	0.04905	0.0517	0.04905	0.04905	0.0517	2	2	12
6755929	ubiquitin_carboxy-terminal_hydrolase_L1_[Mus_musculus]	PSPACALLLLFPLTAQHENFR	99.99999757	0.020467082	0.997658493	0.99643308	0.998662363	0.977979004	0.80914378	0.002760132	0.764529595	0.536647575	0.997985552	0.762101671	0.547372224	-1.137315373	-1.012745014	-1.025790671	-1.000106705	-1.012881483	1.025800853	21152.31692	18598.46215	20886.12299	20883.89457	20620.50037	21152.52688	9.173046769	14.3685	14.1829	14.3503	14.3501	14.3318	14.3685	0.04176	0.04176	0.04402	0.04176	0.04176	0.04402	21	36	116
26353870	unnamed_protein_product_[Mus_musculus]	SEIIPMFSNLASDEQDSVR	99.99999428	0.221969591	0.997658493	0.932336177	0.984163624	0.977979004	0.520988984	0.112380033	0.851309237	0.139584045	0.970532752	0.105244818	0.195757474	1.042238002	1.00497048	-1.039182196	-1.000977416	-1.04434743	1.035095781	10747.41927	11201.36879	10800.83911	10790.29251	10342.18958	10705.15679	5.732961615	13.3917	13.4514	13.3989	13.3974	13.3363	13.386	0.02613	0.02613	0.02755	0.02613	0.02613	0.02755	12	13	88
6755923	ubiquitin-activating_enzyme_E1,_Chr_Y_1_[Mus_musculus]	QNRYDGQVAVFGSDLQEK	99.9986612	0.536851033	0.997658493	0.639633748	0.607567384	0.977979004	0.343015874	0.409847417	0.166931337	0.026673385	0.235388963	0.41684518	0.046258141	1.033642858	-1.059031075	-1.095095596	1.050346072	-1.034054262	1.08713236	12838.47699	13270.40005	12122.85201	12733.18998	11723.61302	12745.11909	8.922832148	13.6482	13.6959	13.5654	13.6363	13.5171	13.6377	0.04063	0.04063	0.04282	0.04063	0.04063	0.04282	3	3	123
IPI00204644.1	Isoform_SNAP-25b_of_Synaptosomal-associated_protein_25	ENEMDENLEQVSGIIGNLR	100	0.474076133	0.997658493	0.99643308	0.336582112	0.977979004	0.248149304	0.349145993	0.15044826	0.950602993	0.045887587	0.134551433	0.019442359	1.02095	-1.0334543	1.001367033	1.04719817	1.034867066	1.055883109	17492.49506	17858.96284	16926.23957	17725.12709	17516.40789	18495.27921	4.910149534	14.0944	14.1244	14.047	14.1135	14.0964	14.1749	0.02239	0.02239	0.0236	0.02239	0.02239	0.0236	11	17	78
112350	D30411_synapsin_IIb_-_rat	TNTGSAMLEQIAMSDR	100	0.339730285	0.997658493	0.959908311	0.243871572	0.757639751	0.494461272	0.21470954	0.264627932	0.152737954	0.01990978	0.014106568	0.170774683	-1.024493143	1.022571256	-1.028351392	-1.048692372	-1.051562574	-1.027872365	23276.87627	22720.38268	23802.26461	22697.08949	22635.13859	22021.35144	4.309795424	14.5066	14.4717	14.5388	14.4702	14.4663	14.4266	0.01965	0.01965	0.02072	0.01965	0.01965	0.02072	20	28	85
IPI00231408.1	Isoform_IIb_of_Synapsin-2	TNTGSAMLEQIAMSDR	100	0.343795616	0.997658493	0.959908311	0.243213193	0.757639751	0.493400874	0.218457557	0.264250965	0.156245483	0.019457055	0.014516263	0.169166014	-1.02433543	1.022632833	-1.02815712	-1.048981748	-1.051427229	-1.028034809	23283.14998	22730.00553	23810.11363	22698.31071	22645.51743	22027.96757	4.317979983	14.507	14.4723	14.5393	14.4703	14.4669	14.427	0.01969	0.01969	0.02076	0.01969	0.01969	0.02076	20	28	85
IPI00365423.1	Protein_phosphatase_2_(Formerly_2A),_regulatory_subunit_A_(PR_65),_alpha_isoform	SEIIPMFSNLASDEQDSVR	99.99999428	0.1968362	0.997658493	0.959908311	0.973913878	0.977979004	0.535693726	0.095354015	0.863022422	0.167197531	0.939409501	0.130386986	0.206802996	1.044279323	1.004553886	-1.036376335	1.002003559	-1.041095875	1.034066614	10726.29642	11201.24956	10775.14274	10796.73138	10349.80832	10702.39124	5.707983434	13.3889	13.4514	13.3954	13.3983	13.3373	13.3856	0.02602	0.02602	0.02743	0.02602	0.02602	0.02743	12	13	88
IPI00191733.1	Glutamate_decarboxylase_2	MVISNPAATHQDIDFLIEEIER	99.99990524	0.03271951	0.997658493	0.99643308	0.808701932	0.977979004	0.847855771	0.006543902	0.716935532	0.574343127	0.573023083	0.364572177	0.619185041	1.150044129	-1.018652298	1.028283466	1.029171731	1.047463316	-1.025671839	8404.456675	9665.496055	8250.564682	8491.247935	8642.163838	8425.856601	11.06724255	13.0369	13.2386	13.0103	13.0518	13.0772	13.0406	0.05034	0.05034	0.05306	0.05034	0.05034	0.05306	7	9	67
462569	MAP1A_RAT_Microtubule-associated_protein_1A_(MAP_1A)_[Contains:_MAP1_light_chain_LC2]	DTDLQQTQATEPR	99.9999998	0.032052758	0.997658493	0.99643308	0.733834025	0.977979004	0.849367056	0.006300656	0.728150367	0.683093576	0.426118471	0.457195634	0.632172685	-1.096328982	1.011664984	-1.013349341	-1.026977717	-1.025170045	-1.016107925	13119.00025	11966.29887	13272.03318	12923.38963	12946.17732	12740.9471	7.232172548	13.6794	13.5467	13.6961	13.6577	13.6602	13.6372	0.03295	0.03295	0.03473	0.03295	0.03295	0.03473	37	44	39
IPI00200257.1	T-cadherin	INENTGSVSVTR	99.9999571	0.832692474	0.997658493	0.860437254	0.860955313	0.977979004	0.613231168	0.743714922	0.369306361	0.103095834	0.675972915	0.481299693	0.274295422	-1.01440634	1.041322053	1.074875194	1.018970949	1.032221675	1.050640147	12528.39276	12350.46773	13046.09167	13293.58841	13466.4586	14148.40204	9.753935431	13.6129	13.5923	13.6713	13.6984	13.7171	13.7884	0.04439	0.04439	0.0468	0.04439	0.04439	0.0468	2	3	32
IPI00372709.3	immunoglobulin_superfamily,_member_8	VASGDLQVQR	99.9977251	0.88886412	0.997658493	0.99643308	0.090063224	0.977979004	0.421432785	0.816739146	0.936263555	0.687286837	0.001338082	0.755044786	0.099427712	-1.011136418	1.003933141	1.019433837	-1.180149396	1.015439968	-1.085408288	15131.72735	14965.07007	15191.24257	12872.30466	15425.79487	14212.02683	10.66223092	13.8853	13.8693	13.891	13.652	13.9131	13.7948	0.04851	0.04851	0.05113	0.04851	0.04851	0.05113	2	2	102
IPI00201699.3	Transforming_protein_RhoA_precursor	LVIVGDGACGK	99.9999999	0.140003788	0.997658493	0.99643308	0.416332803	0.977979004	0.45250857	0.05840158	0.560451052	0.218375278	0.080834505	0.533560159	0.130307738	1.069344332	1.021074373	1.044108712	-1.065425134	1.022558924	-1.056238099	10785.20171	11533.09432	11012.49307	10336.24299	11260.92307	10661.34907	7.75821487	13.3968	13.4935	13.4269	13.3354	13.459	13.3801	0.03534	0.03534	0.03725	0.03534	0.03534	0.03725	5	5	65
51769129	PREDICTED:_similar_to_heterogeneous_nuclear_ribonucleoprotein_A3_isoform_1_[Mus_musculus]	SSGSPYGGGYGSGGGSGGYGSR	99.99975346	0.073490061	0.997658493	0.737211716	0.505620061	0.661166637	0.673446244	0.020157274	0.442850786	0.040441328	0.144401305	0.006800571	0.350111224	-1.060517938	1.019665687	-1.05286851	-1.03802583	-1.073573893	1.024029501	14682.10666	13844.27941	14970.84037	14422.41603	13944.86255	14279.95064	5.485302369	13.8418	13.757	13.8699	13.816	13.7674	13.8017	0.02501	0.02501	0.02636	0.02501	0.02501	0.02636	6	6	103
IPI00204375.2	Ubiquitin_carboxyl-terminal_hydrolase_isozyme_L1	NEAIQAAHDSVAQEGQCR	99.99999804	0.018472664	0.997658493	0.99643308	0.903404554	0.977979004	0.892168205	0.00220382	0.854822514	0.621563553	0.778923459	0.765771155	0.707616839	-1.144284368	-1.007936028	-1.020996018	-1.012204432	-1.012957162	1.016344008	20386.50771	17815.9453	20225.99366	19982.1232	19967.27446	20293.61974	9.376609643	14.3153	14.1209	14.3039	14.2864	14.2853	14.3087	0.04268	0.04268	0.04499	0.04268	0.04268	0.04499	22	39	116
IPI00369350.2	S-phase_kinase-associated_protein_1A	VDQGTLFELILAANYLDIK	99.99999998	0.016770492	0.997658493	0.99643308	0.842694959	0.977979004	0.996576476	0.001763298	0.857420362	0.314782332	0.636295459	0.423100843	0.991543295	-1.114781521	-1.006131252	-1.034013111	-1.016234249	-1.027711949	1.000360622	13631.00582	12227.51325	13547.93998	13331.51288	13182.62378	13187.37772	7.378207695	13.7346	13.5778	13.7258	13.7026	13.6863	13.6869	0.03362	0.03362	0.03543	0.03362	0.03362	0.03543	4	4	39
IPI00206712.2	Inositol_monophosphatase	SLLVTELGSSR	99.99967345	0.282660512	0.997658493	0.99643308	0.342215144	0.977979004	0.930900473	0.162166374	0.754651739	0.877698583	0.050522689	0.644094628	0.808553553	-1.041213034	-1.009235662	1.004414357	1.060330872	1.013690788	1.007151717	16131.25108	15492.74793	15983.63165	16947.93808	16202.46017	16318.33558	6.375226765	13.9776	13.9193	13.9643	14.0488	13.9839	13.9942	0.02906	0.02906	0.03063	0.02906	0.02906	0.03063	4	4	91
IPI00325609.3	Neurofilament_triplet_M_protein	VQSLQDEVAFLR	99.99999886	0.191571685	0.997658493	0.99643308	0.121228319	0.977979004	0.995931319	0.091954409	0.162229807	0.345143391	0.003602213	0.625883501	0.987963869	-1.059056292	1.049884068	1.032352189	-1.110382372	-1.016982459	1.000520613	13969.93476	13190.9275	14666.81193	13208.79393	14421.89272	14429.40094	7.483436294	13.77	13.6873	13.8403	13.6892	13.816	13.8167	0.03409	0.03409	0.03594	0.03409	0.03409	0.03594	22	26	56
12846963	unnamed_protein_product_[Mus_musculus]	LRVDPVNFK	99.99961663	0.344051204	0.997658493	0.99643308	0.495500246	0.977979004	0.384065202	0.219013766	0.529200265	0.99038116	0.131944637	0.536865442	0.074618382	-1.085005712	-1.04360127	-1.000794663	1.108616863	1.042772617	1.130398363	23042.7544	21237.44985	22080.03676	24478.30108	23024.05772	26026.80931	14.74186986	14.492	14.3743	14.4305	14.5792	14.4909	14.6677	0.06689	0.06689	0.07051	0.06689	0.06689	0.07051	3	5	30
IPI00189278.4	Isoform_Beta-II_of_Protein_kinase_C_beta_type	LTDFNFLMVLGK	99.99999181	0.021329062	0.997658493	0.99643308	0.259982111	0.977979004	0.673644494	0.003058371	0.957837577	0.579452024	0.023175548	0.553804343	0.359379037	1.098996733	-1.001659494	1.017087057	1.075760571	1.018774906	1.029284017	14047.32287	15437.96194	14024.05005	15086.52008	14287.35027	14705.74127	6.801108121	13.778	13.9142	13.7756	13.881	13.8025	13.8441	0.03099	0.03099	0.03267	0.03099	0.03099	0.03267	5	6	78
IPI00196530.1	AP-2_complex_subunit_mu-1	IPTPLNTSGVQVICMK	99.99983965	0.135346768	0.997658493	0.99643308	0.726452056	0.977979004	0.670153176	0.053829343	0.253761626	0.989542948	0.389378302	0.248592286	0.337622772	1.119509821	-1.070197376	1.00075384	1.05235251	1.071004133	-1.058544498	15948.24602	17854.21805	14902.15392	15682.31909	15960.26844	15077.56027	12.84725467	13.9611	14.124	13.8632	13.9369	13.9622	13.8801	0.05837	0.05837	0.06153	0.05837	0.05837	0.06153	5	5	48
IPI00201737.1	Isoform_2_of_Septin-5	MESPIPILPLPTPDSETEK	99.99999808	0.932837436	0.997658493	0.86359048	0.733834025	0.977979004	0.534993302	0.895354392	0.934296053	0.109663404	0.400709773	0.101529013	0.205437428	-1.004502325	-1.002896804	1.056873322	1.030027845	1.059934877	1.045791146	12408.26207	12352.64643	12372.42159	12743.93875	13113.96116	13714.46447	7.610573559	13.599	13.5925	13.5948	13.6375	13.6788	13.7434	0.03467	0.03467	0.03655	0.03467	0.03467	0.03655	9	9	32
117104	COX5B_MOUSE_Cytochrome_c_oxidase_polypeptide_Vb,_mitochondrial_precursor	ASGGGVPTDEEQATGLER	99.99998558	0.017888166	0.997658493	0.99643308	0.87575432	0.977979004	0.248149304	0.001947248	0.754713083	0.467739283	0.706771069	0.692307762	0.018618322	-1.179593419	-1.016465135	-1.037715743	-1.019863007	-1.020906382	-1.134637896	38500.59551	32638.85557	37876.94648	37139.24929	37101.29268	32698.79565	11.35280884	15.2326	14.9943	15.209	15.1807	15.1792	14.9969	0.05163	0.05163	0.05442	0.05163	0.05163	0.05442	2	2	107
IPI00210036.1	Isoform_IIa_of_Synapsin-2	TNTGSAMLEQIAMSDR	100	0.25485023	0.997658493	0.869092652	0.279701276	0.626346674	0.666788291	0.137473496	0.186318731	0.118949527	0.029494877	0.005726598	0.32549123	-1.026462438	1.024108787	-1.027828797	-1.040622576	-1.052608502	-1.01781388	22531.14699	21950.28882	23074.34561	22173.59697	21921.1089	21537.44347	3.872953999	14.4596	14.422	14.494	14.4366	14.42	14.3946	0.01766	0.01766	0.01862	0.01766	0.01766	0.01862	21	29	85
IPI00568014.2	Protein	LLTETEDWLYEEGEDQAK	100	0.023226989	0.997658493	0.99643308	0.975456216	0.977979004	0.947691562	0.003769409	0.976657175	0.868451738	0.947638312	0.848951752	0.843716259	-1.064952886	1.000626889	-1.00345917	-1.001407595	-1.004088227	1.004232105	10445.98802	9808.873384	10452.5365	10437.84424	10409.97814	10454.03426	4.641602421	13.3507	13.2599	13.3516	13.3495	13.3457	13.3518	0.02116	0.02116	0.02231	0.02116	0.02116	0.02231	8	8	124
IPI00192274.3	31_kDa_protein	IFVGGIKEDTEEYNLR	99.9966258	0.126607778	0.997658493	0.99643308	0.04606193	0.92052399	0.725898654	0.047749219	0.281509394	0.322173317	0.000368495	0.044311014	0.445516811	-1.084759693	1.0458861	-1.040922994	-1.170107673	-1.088686891	-1.032200865	15166.04786	13981.02083	15861.95864	13555.98207	14569.807	14115.28336	8.990811288	13.8886	13.7712	13.9533	13.7266	13.8307	13.785	0.04094	0.04094	0.04315	0.04094	0.04094	0.04315	2	2	60
IPI00778225.1	Ubiquilin_1	NPAMMQEMMR	99.99992819	0.896465088	0.997658493	0.577998545	0.423679834	0.977979004	0.900010096	0.828846007	0.001953066	0.014532535	0.090296161	0.426394433	0.734408239	1.005709523	1.091807966	1.068497023	-1.047561207	-1.021816572	1.009224992	8336.031043	8383.625805	9101.345099	8688.127278	8907.024356	8989.191584	5.864289638	13.0251	13.0334	13.1519	13.0848	13.1207	13.134	0.02673	0.02673	0.02818	0.02673	0.02673	0.02818	3	4	125
IPI00231261.6	Mitochondrial_2-oxoglutarate/malate_carrier_protein	LGIYTVLFER	99.99990846	0.018472664	0.997658493	0.99643308	0.788902735	0.977979004	0.670153176	0.002236662	0.884399393	0.599006322	0.486288161	0.713736033	0.335556792	1.16699098	1.007234173	1.025730337	1.035199315	1.018363321	1.049119843	8339.698453	9732.352867	8400.029271	8695.70455	8554.281708	8974.466682	10.76811537	13.0258	13.2486	13.0362	13.0861	13.0624	13.1316	0.04898	0.04898	0.05163	0.04898	0.04898	0.05163	3	3	50
IPI00199273.1	Hsc70-interacting_protein	AIDLFTDAIK	99.9389	0.018472664	0.997658493	0.99643308	0.525414564	0.988483763	0.837394717	0.00223671	0.526246281	0.475169575	0.16274583	0.950733853	0.591749922	-1.15386437	-1.029600889	-1.032527546	-1.066879649	-1.002842515	-1.02497911	16409.48906	14221.33267	15937.71842	14938.6282	15892.54362	15505.23661	9.975301394	14.0022	13.7958	13.9602	13.8668	13.9561	13.9205	0.0454	0.0454	0.04785	0.0454	0.0454	0.04785	2	2	117
IPI00421711.1	Similar_to_CG6105-PA	NLADKAPSMVAAAVTYSKPR	99.99936689	0.067757834	0.997658493	0.99643308	0.903743337	0.977979004	0.837394717	0.018042943	0.826599672	0.786372168	0.872508695	0.598569912	0.856973304	1.209884846	-1.030562334	-1.017326206	-1.022077453	1.013010702	1.043374595	11556.78056	13982.37367	11214.05293	10971.82303	11359.95563	11852.6891	17.57942807	13.4965	13.7713	13.453	13.4215	13.4717	13.5329	0.07959	0.07959	0.0839	0.07959	0.07959	0.0839	4	5	50
IPI00194042.3	Cytochrome_c_oxidase_polypeptide_VIa-liver,_mitochondrial_precursor	ALTYFVALPGVGVSMLNVFLK	99.99999992	0.024156887	0.997658493	0.99643308	0.792374134	0.977979004	0.89995049	0.004213361	0.594041911	0.38868018	0.523923955	0.757939163	0.731274055	-1.128068179	-1.022428523	-1.035613944	1.026893056	-1.012896179	-1.0143831	10626.22558	9419.843389	10393.12318	10672.62602	10260.79809	10115.30859	9.019795531	13.3753	13.2015	13.3433	13.3816	13.3249	13.3043	0.04107	0.04107	0.04329	0.04107	0.04107	0.04329	4	5	119
IPI00569089.1	Adenylate_kinase_1	IIFVVGGPGSGK	99.99999983	0.077614763	0.997658493	0.99643308	0.984163624	0.977979004	0.883229884	0.022264349	0.497229748	0.780097503	0.967654491	0.683129853	0.690213094	-1.085070844	1.024636678	1.009771891	1.001451611	-1.014720936	1.014370616	13690.73499	12617.36509	14028.09222	14048.39246	13824.51936	14023.18621	7.759746968	13.7409	13.6231	13.776	13.7781	13.7549	13.7755	0.03535	0.03535	0.03726	0.03535	0.03535	0.03726	15	19	118
IPI00196508.1	Amphiphysin	LVDGSLLTDLTYLGQFPDIK	100	0.130445536	0.997658493	0.99643308	0.792374134	0.977979004	0.883541706	0.050538728	0.673452677	0.451216942	0.523338468	0.753985023	0.693232282	-1.053921012	1.011489016	1.020115107	1.017470409	1.008528112	-1.010749418	14532.9161	13789.37884	14699.88501	14956.69802	14825.24727	14667.57933	5.871475637	13.827	13.7513	13.8435	13.8685	13.8558	13.8403	0.02676	0.02676	0.02821	0.02676	0.02676	0.02821	13	17	121
IPI00421909.3	Atlastin-like_protein	ILIPWLLSPESLDIK	99.989884	0.018546689	0.997658493	0.99643308	0.792374134	0.980938512	0.898992978	0.002267995	0.508126388	0.581954159	0.509169427	0.899321943	0.729468588	1.161994986	1.032526178	1.02623975	1.032444613	-1.006125691	-1.016841629	5671.128929	6589.823379	5855.589077	6045.571396	5819.937935	5723.54244	10.48302993	12.4694	12.686	12.5156	12.5617	12.5068	12.4827	0.0477	0.0477	0.05028	0.0477	0.0477	0.05028	2	2	26
IPI00201307.1	PREDICTED:_similar_to_ubiquinol-cytochrome_c_reductase_binding_protein	DDTMHETEDVKEAIR	99.99994928	0.018644305	0.997658493	0.99643308	0.736310101	0.977979004	0.836004321	0.00237547	0.722675371	0.323229194	0.430005099	0.541955655	0.58862173	-1.110783339	-1.012126999	-1.033336885	-1.02723438	-1.020955755	-1.01855489	20402.59849	18367.75704	20158.14073	19623.70199	19744.38228	19384.70128	7.362472105	14.3165	14.1649	14.2991	14.2603	14.2692	14.2426	0.03354	0.03354	0.03536	0.03354	0.03354	0.03536	8	9	39
IPI00212796.2	GTP-binding_nuclear_protein_Ran	SNYNFEKPFLWLAR	99.99986994	0.329926837	0.997658493	0.99643308	0.467884871	0.977979004	0.343015874	0.206251405	0.426535942	0.711619595	0.113472795	0.250052522	0.04256075	1.123252209	-1.077636117	1.034330497	1.162065697	1.114631901	-1.214059994	14871.7334	16704.7074	13800.32941	16036.88911	15382.2874	12670.12131	20.51649544	13.8603	14.028	13.7524	13.9691	13.909	13.6291	0.09264	0.09264	0.09765	0.09264	0.09264	0.09765	2	2	108
31560543	S-phase_kinase-associated_protein_1A_[Mus_musculus]	VDQGTLFELILAANYLDIK	99.99999998	0.023098199	0.997658493	0.99643308	0.813638662	0.977979004	0.994839219	0.003642916	0.941486925	0.387204175	0.586749709	0.360517003	0.976708743	-1.105041551	1.002488439	-1.029013377	-1.018601361	-1.031574014	1.000989817	13530.66742	12244.48747	13564.37655	13316.63021	13149.55171	13162.17047	7.343683691	13.7239	13.5798	13.7275	13.7009	13.6827	13.6841	0.03346	0.03346	0.03527	0.03346	0.03346	0.03527	4	4	39
IPI00230972.1	Isoform_Tau-E_of_Microtubule-associated_protein_tau	IGSLDNITHVPGGGNK	99.99976325	0.434397384	0.997658493	0.846402451	0.49686816	0.977979004	0.28876815	0.217700422	0.751800242	0.081769918	0.134012624	0.164609766	0.03102195	1.036271749	1.009371058	1.051986649	-1.04566889	1.042219945	-1.067199972	13251.20367	12787.38305	13375.38147	12791.22062	13940.08934	13062.30295	6.391419011	13.6938	13.6424	13.7073	13.6429	13.767	13.6731	0.02913	0.02913	0.0307	0.02913	0.02913	0.0307	10	13	73
IPI00231810.1	Isoform_2_of_Alpha-adducin	SLVQGELVTASK	99.99998363	0.265492465	0.997658493	0.99643308	0.797906375	0.977979004	0.496640976	0.146172081	0.402172496	0.894740857	0.539910421	0.47765669	0.175385213	1.034164679	-1.019957761	-1.003032222	-1.014540365	1.016874372	-1.032663896	12496.99954	12923.95552	12252.46772	12076.86569	12459.22042	12065.12639	5.095184006	13.6093	13.6578	13.5808	13.56	13.6049	13.5586	0.02323	0.02323	0.02449	0.02323	0.02323	0.02449	8	8	128
IPI00327244.1	Isoform_1_of_Alpha-adducin	SLVQGELVTASK	99.99998363	0.265492465	0.997658493	0.99643308	0.797906375	0.977979004	0.496640976	0.146172081	0.402172496	0.894740857	0.539910421	0.47765669	0.175385213	1.034164679	-1.019957761	-1.003032222	-1.014540365	1.016874372	-1.032663896	12496.99954	12923.95552	12252.46772	12076.86569	12459.22042	12065.12639	5.095184006	13.6093	13.6578	13.5808	13.56	13.6049	13.5586	0.02323	0.02323	0.02449	0.02323	0.02323	0.02449	8	8	128
IPI00214665.2	ATP-citrate_synthase	SFDELGEIIQSVYEDLVAK	99.99999996	0.021657858	0.997658493	0.99643308	0.972747387	0.977979004	0.967255906	0.003192987	0.911242893	0.693412901	0.933946439	0.785294009	0.886559127	1.335976939	1.010839446	1.03783546	-1.008047951	1.026706531	-1.013893737	8247.335186	11018.24962	8336.731726	8270.173769	8409.376906	8442.084796	21.17942786	13.0097	13.4276	13.0253	13.0137	13.0633	13.0434	0.09557	0.09557	0.1007	0.09557	0.09557	0.1007	2	2	3
IPI00230848.6	Myotrophin	GPDGLTALEATDNQAIK	99.99999999	0.354123355	0.997658493	0.99643308	0.733834025	0.977979004	0.69561724	0.226638947	0.334392412	0.900311381	0.421118284	0.398215153	0.386885308	-1.04437733	1.0361636	1.004477229	1.03000699	-1.031545136	1.032327155	13583.35856	13006.17906	14074.58172	14496.91755	13644.17437	14085.25171	7.94780021	13.7296	13.6669	13.7808	13.8235	13.736	13.7819	0.0362	0.0362	0.03816	0.0362	0.0362	0.03816	7	8	104
IPI00215384.1	Nucleolin-related_protein_NRP	TLVLSNLSYSATEETLQEVFEK	99.9938169	0.267573173	0.997658493	0.99643308	0.866963199	0.977979004	0.849367056	0.148902929	0.257500819	0.944332823	0.688616484	0.230546019	0.63289892	-1.063386418	1.050578024	-1.002947488	1.017518679	-1.05367459	-1.020923105	9879.046254	9290.175316	10378.70889	10560.53016	9850.013455	9648.144315	9.400343563	13.2702	13.1815	13.3413	13.3664	13.2659	13.236	0.04279	0.04279	0.04511	0.04279	0.04279	0.04511	2	2	119
IPI00198498.2	Cortactin_isoform_C	YGVQADRVDK	99.978293	0.173697467	0.997658493	0.99643308	0.423679834	0.977979004	0.686505831	0.078610511	0.703011166	0.228401853	0.087104543	0.122548906	0.375701612	-1.087927609	-1.018673514	1.058923669	-1.087798308	1.078697495	-1.044064062	7941.231337	7299.411552	7795.658987	7166.456254	8409.157822	8054.254644	10.53251126	12.9551	12.8336	12.9285	12.807	13.0377	12.9755	0.04792	0.04792	0.05051	0.04792	0.04792	0.05051	2	2	73
66857	KIRTPR_pyruvate_kinase_(EC_2.7.1.40),_erythrocyte_splice_form_R_-_rat	GDLGIEIPAEK	99.99988987	0.31421831	0.997658493	0.846402451	0.17923342	0.977979004	0.119761122	0.193558479	0.232180979	0.097426764	0.008808042	0.666099415	0.00322966	1.103713566	-1.097515448	-1.134796181	1.233085338	-1.033968299	1.268316335	20837.64005	22998.786	18986.19293	23411.59613	18362.45168	23289.39742	16.87059672	14.3469	14.4893	14.2127	14.5149	14.1645	14.5074	0.07643	0.07643	0.08056	0.07643	0.07643	0.08056	2	2	123
25742751	collapsin_response_mediator_protein_1_[Rattus_norvegicus]	IVFEDGNISVSK	99.99999981	0.072859085	0.997658493	0.99643308	0.706612353	0.977979004	0.849367056	0.019734404	0.894336333	0.551667932	0.359884589	0.654789635	0.635487129	1.0807146	-1.004434439	-1.019520841	1.031096498	-1.015019797	1.015932511	18079.22364	19538.48093	17999.05946	18559.12487	17733.05941	18015.59157	7.224395272	14.142	14.254	14.1357	14.1798	14.1142	14.137	0.03292	0.03292	0.0347	0.03292	0.03292	0.0347	17	21	62
IPI00210495.1	RAD23b_homolog	QIIQQNPSLLPALLQQIGR	99.99974319	0.173697467	0.997658493	0.99643308	0.271569898	0.977979004	0.670153176	0.078564274	0.211144058	0.500086205	0.026474554	0.547780412	0.333678871	-1.086697644	1.062122408	1.031966437	-1.114869194	-1.029221853	-1.047548816	7871.359162	7243.375564	8360.346949	7498.948748	8122.97847	7754.272017	10.38870502	12.9424	12.8224	13.0293	12.8725	12.9878	12.9208	0.04727	0.04727	0.04983	0.04727	0.04727	0.04983	3	4	51
IPI00362915.3	PREDICTED:_similar_to_carbonyl_reductase_3	TVEEGAETPVYLALLPPDATEPHGQLVR	99.99984592	0.020304085	0.997658493	0.846402451	0.765226641	0.977979004	0.792689469	0.002719813	0.741418003	0.095102323	0.452139627	0.191645442	0.521816153	-1.137791647	-1.014073383	-1.072193516	-1.032428025	-1.057313578	-1.027540863	25326.94265	22259.73684	24975.45352	24190.98756	23621.61519	22988.49228	9.187948347	14.6284	14.4421	14.6082	14.5622	14.5278	14.4886	0.04183	0.04183	0.04409	0.04183	0.04183	0.04409	3	4	130
IPI00568311.1	46_kDa_protein	QTVAVGVIK	99.85613	0.08732837	0.997658493	0.99643308	0.819846373	0.977979004	0.998192766	0.027146648	0.43511265	0.888520971	0.595111192	0.51890814	0.996466613	1.202683974	-1.067795612	-1.01150001	1.045503238	1.055655562	1.000371169	29905.75653	35967.17412	28007.00453	29281.41393	29565.75011	29576.724	18.30130262	14.8681	15.1344	14.7735	14.8377	14.8516	14.8522	0.08281	0.08281	0.08729	0.08281	0.08281	0.08729	2	2	47
IPI00324893.4	14-3-3_protein_zeta/delta	TAFDEAIAELDTLSEESYK	100	0.155279398	0.997658493	0.99643308	0.719177452	0.977979004	0.931989435	0.068264256	0.618128318	0.37373941	0.378937778	0.711571669	0.817462911	1.064226929	-1.017375076	-1.030449924	1.030952677	-1.01285155	-1.007999912	14350.62261	15272.31902	14105.53781	14542.14196	13926.55992	13816.03288	7.486036193	13.8088	13.8986	13.784	13.828	13.7656	13.7541	0.03411	0.03411	0.03595	0.03411	0.03411	0.03595	24	52	55
IPI00231639.6	Glutathione_S-transferase_Mu_1	PMILGYWNVR	99.99985355	0.020560165	0.997658493	0.99643308	0.886734314	0.977979004	0.633473404	0.002814309	0.403785167	0.860096769	0.737762949	0.5062382	0.29248372	1.084935559	1.022733013	1.004614561	1.009029654	-1.018035227	1.028806585	11410.68991	12379.86324	11670.08927	11775.46614	11463.34524	11793.56506	5.816977341	13.4781	13.5957	13.5105	13.5235	13.4847	13.5257	0.02652	0.02652	0.02795	0.02652	0.02652	0.02795	9	9	131
IPI00199693.2	Microtubule-associated_protein_1A	DTDLQQTQATEPR	99.9999998	0.027260756	0.997658493	0.99643308	0.786739785	0.977979004	0.898224099	0.005047134	0.886311827	0.640270143	0.482833445	0.550312842	0.725765072	-1.102455526	1.004928907	-1.015780682	-1.024483363	-1.02078737	-1.012141842	13273.79378	12040.20795	13339.21907	13020.43504	13067.57848	12910.81738	7.458403661	13.6963	13.5556	13.7034	13.6685	13.6737	13.6563	0.03398	0.03398	0.03582	0.03398	0.03398	0.03582	36	43	39
IPI00339162.1	PREDICTED:_similar_to_triosephosphate_isomerase	VTNGAFTGEISPGMIK	100	0.020735096	0.997658493	0.639633748	0.813181576	0.977979004	0.384065202	0.002867368	0.463041031	0.02653534	0.583621474	0.144112836	0.073350708	-1.104260381	-1.024361016	-1.07503057	1.018118276	-1.049464548	1.061304694	22715.06898	20570.39208	22174.86671	22576.63707	21129.69585	22425.04539	7.094461624	14.4714	14.3283	14.4366	14.4625	14.367	14.4528	0.03233	0.03233	0.03407	0.03233	0.03233	0.03407	20	33	45
IPI00358757.3	PREDICTED:_similar_to_Histidine_triad_nucleotide-binding_protein_2	DVAPQAPVHFLVIPR	99.989138	0.101319119	0.997658493	0.99643308	0.830715275	0.977979004	0.925779845	0.033336702	0.398988035	0.861958077	0.605710109	0.499307527	0.798815752	-1.112386326	1.043488324	1.008550201	-1.026338455	-1.034641928	1.012906496	10218.45527	9186.066954	10662.83876	10389.2032	10305.82571	10438.8372	10.92684218	13.3189	13.1652	13.3803	13.3428	13.3312	13.3497	0.0497	0.0497	0.05239	0.0497	0.0497	0.05239	2	4	113
IPI00203502.1	Nuclear_transport_factor_2	NINDAWVCTNDMFR	99.99999952	0.457933182	0.997658493	0.99643308	0.23197177	0.977979004	0.410471294	0.329711891	0.049428569	0.501834091	0.01702431	0.18172385	0.09006913	-1.037943923	1.081378679	1.025929542	-1.100619386	-1.054047705	-1.069473562	14396.78701	13870.48028	15568.37171	14145.1064	14770.08264	13810.61034	8.477802624	13.8135	13.7597	13.9263	13.788	13.8504	13.7535	0.03861	0.03861	0.0407	0.03861	0.03861	0.0407	2	2	71
IPI00207252.1	Asparaginase-like_sperm_autoantigen	GNLAYATSTGGIVNK	99.99934533	0.156418331	0.997658493	0.99643308	0.149698425	0.977979004	0.974941498	0.065855881	0.259361841	0.355038454	0.005765261	0.817397948	0.90474571	-1.083648687	1.051366292	1.04070359	-1.13484672	-1.010245667	-1.005296142	14713.42778	13577.67324	15469.20201	13631.09374	15312.31712	15231.64815	9.581898927	13.8448	13.7289	13.9171	13.7346	13.9024	13.8948	0.04361	0.04361	0.04597	0.04361	0.04361	0.04597	5	5	56
IPI00326606.4	Isoform_2_of_Protein_NDRG2	SCFQPLFQFGDMQEIIQNFVR	99.99999997	0.659286841	0.997658493	0.846402451	0.090063224	0.977979004	0.348219477	0.537978062	0.021993338	0.0925184	0.001258717	0.49127748	0.052805222	-1.018947611	1.076213827	1.053256704	-1.11940253	-1.021795904	-1.063582403	10016.73355	9830.469629	10780.14273	9694.89384	10550.19176	9919.486947	6.776614472	13.2901	13.263	13.3961	13.243	13.365	13.276	0.03089	0.03089	0.03256	0.03089	0.03089	0.03256	7	8	71
IPI00190559.3	Ubiquitin-conjugating_enzyme_E2_N	SNEAQAIETAR	99.99999995	0.104062945	0.997658493	0.99643308	0.765696444	0.977979004	0.827199386	0.03496515	0.58756376	0.424701461	0.454546945	0.189675387	0.574865196	-1.065035463	-1.016449239	1.023688663	1.02278138	1.040527562	-1.01701771	12682.2647	11907.83325	12477.0271	12761.271	12982.69059	12765.45183	6.513277869	13.6305	13.5396	13.607	13.6395	13.6643	13.64	0.02968	0.02968	0.03129	0.02968	0.02968	0.03129	6	8	121
IPI00209976.1	ATPase_inhibitor,_mitochondrial_precursor	GSDSSESMDSGAGSIR	99.99999967	0.040213211	0.997658493	0.99643308	0.855934899	0.977979004	0.917773279	0.00854818	0.512639099	0.814264208	0.668495606	0.378052432	0.778271741	-1.13907966	-1.032794916	1.011312781	-1.021303201	1.044478699	-1.013950219	7444.927305	6535.914536	7208.524353	7058.162894	7529.150135	7425.561917	10.68323776	12.862	12.6742	12.8155	12.7851	12.8783	12.8583	0.0486	0.0486	0.05123	0.0486	0.0486	0.05123	4	5	117
IPI00369480.3	PREDICTED:_similar_to_OTU_domain,_ubiquitin_aldehyde_binding_1	AFGFSHLEALLDDSKELQR	99.99999776	0.103480936	0.997658493	0.99643308	0.090063224	0.977979004	0.713885578	0.03465133	0.400657867	0.570654354	0.001228901	0.166594315	0.428331347	1.143637409	-1.055341176	1.03593998	1.242766012	1.093270116	1.052052376	16311.94404	18654.94941	15456.55985	19208.88724	16898.19498	17777.78617	13.90076571	13.9936	14.1873	13.9159	14.2295	14.0446	14.1178	0.06311	0.06311	0.06653	0.06311	0.06311	0.06653	2	2	15
IPI00206188.1	CD166_antigen_precursor	EIDPGTQLYTMTSSLEYK	99.99932542	0.324679034	0.997658493	0.932336177	0.788902735	0.977979004	0.45250857	0.20111547	0.332791938	0.136507937	0.494111454	0.623129894	0.12692553	1.036871241	-1.028485658	-1.043197951	-1.019982083	-1.014304811	1.045574252	10318.53445	10698.99162	10032.7451	9836.197385	9891.252597	10342.03903	6.259142335	13.333	13.3852	13.2924	13.2639	13.2719	13.3362	0.02853	0.02853	0.03007	0.02853	0.02853	0.03007	3	3	16
IPI00231849.1	Cytochrome_c,_somatic	ADLIAYLK	99.99974255	0.283070069	0.997658493	0.99643308	0.149698425	0.977979004	0.562676245	0.16304836	0.122518328	0.373226412	0.004890978	0.489771355	0.224714238	1.061289267	-1.070156759	-1.0384821	1.135388868	1.030500919	1.054504246	14350.84174	15230.3943	13410.03701	15225.60674	13819.05546	14572.25266	9.421330487	13.8088	13.8947	13.711	13.8942	13.7544	13.8309	0.04289	0.04289	0.04521	0.04289	0.04289	0.04521	5	5	15
IPI00371946.3	PREDICTED:_similar_to_Myristoylated_alanine-rich_C-kinase_substrate	EAEAAEPEQPEQPEQPAAEEPR	99.99999926	0.126828827	0.997658493	0.99643308	0.175566192	0.977979004	0.348219477	0.048412375	0.334523774	0.698212523	0.00822653	0.554691091	0.051412912	-1.253178376	1.118222589	1.044493722	-1.370547257	-1.070588138	-1.257006796	11397.74458	9095.069621	12745.21545	9299.362267	11904.87266	9470.810101	25.36066273	13.4765	13.1509	13.6377	13.1829	13.5393	13.2093	0.1139	0.1139	0.1201	0.1139	0.1139	0.1201	2	2	136
IPI00767087.1	PREDICTED:_similar_to_Myristoylated_alanine-rich_C-kinase_substrate_(MARCKS)_(Protein_kinase_C_substrat	EAEAAEPEQPEQPEQPAAEEPR	99.99999926	0.126828827	0.997658493	0.99643308	0.175566192	0.977979004	0.348219477	0.048412375	0.334523774	0.698212523	0.00822653	0.554691091	0.051412912	-1.253178376	1.118222589	1.044493722	-1.370547257	-1.070588138	-1.257006796	11397.74458	9095.069621	12745.21545	9299.362267	11904.87266	9470.810101	25.36066273	13.4765	13.1509	13.6377	13.1829	13.5393	13.2093	0.1139	0.1139	0.1201	0.1139	0.1139	0.1201	2	2	136
1718091	VATE_MOUSE_Vacuolar_ATP_synthase_subunit_E_(V-ATPase_E_subunit)_(Vacuolar_proton_pump_E_subuni	IQMSNLMNQAR	99.99999995	0.088290774	0.997658493	0.99643308	0.691591891	0.977979004	0.485775688	0.027791258	0.714016774	0.490881268	0.335009624	0.760186784	0.16005651	-1.059492864	1.009711346	1.017870385	-1.025851429	1.008080565	-1.038090045	15417.43745	14551.71495	15567.16153	15174.86947	15692.95299	15117.14044	5.713106086	13.9123	13.8289	13.9262	13.8894	13.9378	13.8839	0.02604	0.02604	0.02745	0.02604	0.02604	0.02745	9	11	128
IPI00561065.2	Dihydropyrimidinase-related_protein_1	IVFEDGNISVSK	99.99999981	0.079848781	0.997658493	0.99643308	0.722873392	0.977979004	0.869447467	0.023734025	0.870044382	0.535840786	0.384903505	0.66016343	0.666742	1.079214601	-1.005542454	-1.020602972	1.029897021	-1.014977505	1.014665937	19161.81382	20679.70927	19056.19753	19625.91922	18774.99317	19050.34604	7.326460613	14.2259	14.3359	14.218	14.2605	14.1965	14.2175	0.03338	0.03338	0.03519	0.03338	0.03338	0.03519	16	20	62
IPI00231929.6	pyruvate_kinase,_muscle	FGVEQDVDMVFASFIR	100	0.625825611	0.997658493	0.639633748	0.83893122	0.977979004	0.146792151	0.502090947	0.290052027	0.026974929	0.62895872	0.248683441	0.006878261	1.015073345	-1.02414079	-1.05167496	1.011114989	-1.026885141	1.066102347	19905.4384	20205.47994	19436.23239	19652.26591	18927.36745	20178.51085	4.952414845	14.2809	14.3025	14.2465	14.2624	14.2082	14.3005	0.02258	0.02258	0.0238	0.02258	0.02258	0.0238	42	55	16
IPI00209082.1	Alpha-actinin-1	VGWEQLLTTIAR	99.99999998	0.39443367	0.997658493	0.991231607	0.797906375	0.977979004	0.849367056	0.264157864	0.281517405	0.189183632	0.553787442	0.837033099	0.62422958	1.042950445	-1.042531838	-1.050813571	1.023072906	-1.007943866	-1.019041196	10752.43028	11214.25194	10313.76682	10551.73539	10232.48116	10041.28332	8.344886369	13.3924	13.453	13.3323	13.3652	13.3209	13.2937	0.03801	0.03801	0.04006	0.03801	0.03801	0.04006	16	17	28
IPI00395311.1	Isoform_1_of_Neuronal_cell_adhesion_molecule_precursor	ISWLTNGVPVEIALDDPSR	99.99999988	0.748535567	0.997658493	0.577998545	0.336582112	0.977979004	0.994839219	0.648445668	0.19914935	0.012639583	0.046929163	0.230312746	0.984573203	1.014242928	1.042068028	1.082924952	1.066613415	1.039207541	1.000615792	11981.89015	12152.54735	12485.94464	13317.67604	12975.48782	12983.47801	6.904140752	13.5486	13.569	13.608	13.7011	13.6635	13.6644	0.03146	0.03146	0.03316	0.03146	0.03146	0.03316	4	5	43
IPI00210815.1	Rho-related_GTP-binding_protein_RhoB_precursor	QVELALWDTAGQEDYDR	99.99999952	0.04655723	0.997658493	0.639633748	0.430312025	0.977979004	0.286328928	0.010854486	0.173612123	0.027198471	0.094422753	0.40888468	0.029450976	1.098233539	1.05155063	1.083938509	-1.064038093	1.030800114	-1.085002946	11869.4491	13035.42709	12481.32668	11730.15023	12865.75296	11857.80464	7.942289852	13.535	13.6702	13.6075	13.5179	13.6512	13.5335	0.03618	0.03618	0.03813	0.03618	0.03618	0.03813	2	3	65
6678413	triosephosphate_isomerase_1_[Mus_musculus]	VTNGAFTGEISPGMIK	100	0.026047968	0.997658493	0.639633748	0.706612353	0.977979004	0.343015874	0.004763057	0.365339873	0.026805481	0.354296926	0.197660308	0.042740085	-1.109592597	-1.033635585	-1.083671314	1.034437605	-1.048407514	1.078151596	23981.76238	21613.12399	23201.37071	24000.37034	22130.10724	23859.61044	7.896562758	14.5497	14.3996	14.5019	14.5508	14.4337	14.5423	0.03597	0.03597	0.03792	0.03597	0.03597	0.03792	17	24	45
IPI00369311.3	40_kDa_protein	LAQSNGWGVMVSHR	99.99999063	0.022798879	0.997658493	0.846402451	0.888263512	0.977979004	0.91254317	0.003569653	0.447128615	0.098666343	0.7400504	0.387964785	0.760706448	-1.128216711	-1.031590938	-1.068708995	1.01363561	-1.035981372	1.012508358	29278.916	25951.50003	28382.29276	28769.30265	27396.52808	27739.21367	8.854107288	14.8376	14.6635	14.7927	14.8122	14.7417	14.7596	0.04032	0.04032	0.0425	0.04032	0.04032	0.0425	3	8	58
13637776	ENOA_MOUSE_Alpha-enolase_(2-phospho-D-glycerate_hydro-lyase)_(Non-neural_enolase)_(NNE)_(Enolase_1)	VNQIGSVTESLQAAK	100	0.024155562	0.997658493	0.525813238	0.566591115	0.977979004	0.421432785	0.004134882	0.18465425	0.009614881	0.200735138	0.208814694	0.103070418	-1.095835239	-1.043032421	-1.085471962	1.041447984	-1.040688612	1.053377946	23178.46573	21151.41484	22222.19105	23143.25607	21353.35277	22493.14126	6.828860284	14.5005	14.3685	14.4397	14.4983	14.3822	14.4572	0.03112	0.03112	0.0328	0.03112	0.03112	0.0328	26	48	45
IPI00231194.4	NG,NG-dimethylarginine_dimethylaminohydrolase_1	SFCSMAGPNLIAIGSSESAQK	100	0.143982956	0.997658493	0.99643308	0.635195397	0.977979004	0.983012577	0.061542429	0.916723816	0.50986639	0.269322848	0.590922128	0.932457645	-1.072022886	-1.003936661	-1.022446973	1.042634879	-1.020429887	-1.003189647	15973.74903	14900.56718	15911.11258	16589.48073	15592.55818	15542.98155	8.151848844	13.9634	13.8631	13.9577	14.018	13.9286	13.924	0.03713	0.03713	0.03914	0.03713	0.03713	0.03914	7	10	119
IPI00421876.2	Ubiquilin-1	NPAMMQEMMR	99.99992819	0.908474472	0.997658493	0.639633748	0.536459109	0.977979004	0.985692829	0.84573809	0.00903568	0.027371399	0.168601434	0.61725216	0.942938049	-1.006151916	1.091340815	1.073801545	-1.046019069	-1.016333809	-1.002320484	6887.737117	6845.623417	7516.868638	7186.167879	7396.06276	7378.940047	7.022279205	12.7498	12.741	12.8759	12.811	12.8525	12.8492	0.032	0.032	0.03373	0.032	0.032	0.03373	2	3	125
IPI00679201.2	Mitochondrial_import_inner_membrane_translocase_subunit_Tim9	FQEYHIQQNEALAAK	99.99951563	0.173761429	0.997658493	0.99643308	0.966345081	0.977979004	0.562676245	0.079134053	0.984536967	0.901450467	0.916634237	0.888736221	0.225091141	-1.08749587	1.00093755	-1.005845069	-1.005074243	-1.006788099	1.06085573	10203.81864	9382.857374	10213.38524	10161.82169	10144.52321	10761.87557	10.50163823	13.3168	13.1958	13.3182	13.3109	13.3084	13.3936	0.04778	0.04778	0.05036	0.04778	0.04778	0.05036	2	2	68
IPI00326596.2	Stathmin-2	DLSLEEIQK	99.998439	0.023403989	0.997658493	0.99643308	0.884024126	0.977979004	0.485775688	0.003851628	0.187937967	0.898816367	0.730996346	0.23179958	0.158302823	-1.118593835	-1.052087838	-1.004744358	-1.013241323	1.047119926	-1.055984495	15511.98117	13867.39376	14743.99818	14551.31946	15538.73428	14620.22819	8.296948925	13.9211	13.7594	13.8478	13.8289	13.9143	13.8357	0.03779	0.03779	0.03983	0.03779	0.03779	0.03983	2	2	117
IPI00363265.2	Stress-70_protein,_mitochondrial_precursor	VQQTVQDLFGR	99.99999982	0.080099163	0.997658493	0.99643308	0.768669536	0.977979004	0.764419202	0.023983978	0.872458826	0.631001208	0.457687804	0.758589405	0.492722777	-1.073180725	-1.005046756	-1.014782793	1.023622361	-1.009687149	1.021791495	15886.21055	14802.92198	15806.43931	16179.82471	15654.78904	15995.93029	6.799069136	13.9555	13.8536	13.9482	13.9819	13.9343	13.9654	0.03098	0.03098	0.03266	0.03098	0.03098	0.03266	13	15	124
IPI00421955.1	Dopamine-and_cAMP-regulated_phosphoprotein_DARPP-32	IAESHLQTISNLSENQASEEEDELGELR	99.99999532	0.024155562	0.997658493	0.959908311	0.367357043	0.977979004	0.673446244	0.004129844	0.624082179	0.162194458	0.063539998	0.379140539	0.34837714	-1.273104959	-1.041600593	-1.120856508	-1.169688953	-1.076090505	-1.081374394	22733.47651	17856.71821	21825.52185	18659.25278	20282.23625	18755.97977	18.13984442	14.4725	14.1242	14.4137	14.1876	14.3079	14.1951	0.08209	0.08209	0.08653	0.08209	0.08209	0.08653	7	9	86
IPI00212969.2	32_kDa_protein	LFIGGLSFETTEESLR	99.99999999	0.469115163	0.997658493	0.99643308	0.486148755	0.773591433	0.708668856	0.343124234	0.057363091	0.632687135	0.127277477	0.019450299	0.418722055	-1.021330752	1.04503717	-1.010662879	-1.035748602	-1.056180275	1.01864658	13457.65534	13176.5888	14063.75005	13578.34327	13315.67194	13563.96368	4.935930177	13.7161	13.6857	13.7797	13.729	13.7008	13.7275	0.02251	0.02251	0.02372	0.02251	0.02251	0.02372	16	19	103
IPI00213559.1	Isoform_RTN1-B_of_Reticulon-1	GARPAQQDGEPAWGSGAGAGVVSSR	99.99999076	0.418903536	0.997658493	0.577998545	0.560474035	0.757639751	0.119761122	0.290480929	0.861396138	0.014436407	0.197927402	0.010946948	0.003786598	1.033003584	-1.005496235	1.079994653	-1.041580305	1.085930558	-1.099332756	11842.38508	12233.22622	11777.65233	11307.48371	12789.71256	11634.06848	6.806623656	13.5317	13.5785	13.5238	13.465	13.6427	13.5061	0.03102	0.03102	0.0327	0.03102	0.03102	0.0327	6	8	73
54855	triosephosphate_isomerase_[Mus_musculus]	VVLAYEPVWAIGTGK	100	0.047345444	0.997658493	0.639633748	0.525414564	0.977979004	0.260548875	0.011200579	0.255084821	0.01802162	0.162765053	0.225518107	0.024148536	-1.087580136	-1.0384611	-1.081084149	1.047529479	-1.041044434	1.079145569	22304.21655	20508.11292	21478.14323	22498.9882	20631.34149	22264.22074	7.14667734	14.445	14.3239	14.3906	14.4576	14.3326	14.4424	0.03256	0.03256	0.03432	0.03256	0.03256	0.03432	14	20	45
IPI00193918.1	Cytochrome_c_oxidase_polypeptide_Vb,_mitochondrial_precursor	ASGGGVPTDEEQATGLER	99.99998558	0.025075146	0.997658493	0.99643308	0.632794061	0.977979004	0.533584354	0.004441883	0.840900582	0.554121457	0.266858296	0.707097762	0.204286581	-1.173702906	-1.011223343	-1.032581895	-1.064058575	-1.021121498	-1.073708773	20381.87436	17365.44594	20155.66047	18942.24712	19738.74854	18383.70797	12.08838439	14.315	14.0839	14.2989	14.2093	14.2687	14.1661	0.05493	0.05493	0.0579	0.05493	0.05493	0.0579	5	6	107
IPI00471577.1	Ubiquinol-cytochrome_c_reductase_core_protein_1	NALISHLDGTTPVCEDIGR	99.99999998	0.265492465	0.997658493	0.959908311	0.507654338	0.977979004	0.7054999	0.146551841	0.588391521	0.166217919	0.147548523	0.414743545	0.414430798	1.060077977	-1.02239384	-1.057157523	1.061614214	-1.034002242	1.03402557	12863.57039	13636.38768	12581.81523	13357.03389	12168.07345	12582.09909	8.86889136	13.651	13.7352	13.6191	13.7053	13.5708	13.6191	0.04038	0.04038	0.04257	0.04038	0.04038	0.04257	15	20	59
IPI00197553.1	Isoform_B23.1_of_Nucleophosmin	MSVQPTVSLGGFEITPPVVLR	99.99999997	0.175419295	0.997658493	0.99643308	0.855934899	0.977979004	0.421432785	0.080191678	0.964096532	0.554069482	0.671041425	0.595328793	0.102593664	-1.109788789	-1.002716513	-1.035377325	1.025949666	-1.032572329	1.104799154	13316.57532	11999.19791	13280.49868	13625.12319	12861.56747	14209.44886	13.10945345	13.7009	13.5507	13.697	13.734	13.6508	13.7946	0.05955	0.05955	0.06277	0.05955	0.05955	0.06277	5	5	72
IPI00213457.1	ATPase,_H+_transporting,_V1_subunit_C,_isoform_1	VGTLDVLVGLSDELAKLDAFVEGVVK	99.99999545	0.13567018	0.997658493	0.99643308	0.919964679	0.977979004	0.755856757	0.054423124	0.985017702	0.843915369	0.825339741	0.862754569	0.481156815	1.069236973	-1.000659711	-1.00675411	-1.007782166	-1.006090382	-1.025109225	6570.584723	7025.512117	6566.252894	6515.547821	6526.503994	6366.642533	7.617825789	12.6818	12.7784	12.6809	12.6697	12.6721	12.6363	0.0347	0.0347	0.03658	0.0347	0.0347	0.03658	4	4	55
IPI00328017.4	Microtubule_associated_protein_2	TTATSGESAQAPSAFK	100	0.377770752	0.997658493	0.846402451	0.868162741	0.977979004	0.948770577	0.247817613	0.436774659	0.096210866	0.694360783	0.390842451	0.847937767	-1.043479649	1.02975387	1.06363588	1.014892654	1.032903018	-1.00723573	12981.43785	12440.52805	13367.68586	13566.76619	13807.52307	13708.33328	8.156036642	13.6642	13.6028	13.7065	13.7278	13.7532	13.7428	0.03715	0.03715	0.03916	0.03715	0.03715	0.03916	47	58	43
IPI00203773.3	ribosomal_protein,_mitochondrial,_L12	IQQLVQDIASLTLLEISDLNELLK	99.99977082	0.141733437	0.997658493	0.99643308	0.576914427	0.983201098	0.248149304	0.06041894	0.339706193	0.388092241	0.213623171	0.907757773	0.019242282	-1.091069768	1.045979445	1.040313276	-1.060497906	-1.005446598	-1.119305213	3066.89896	2810.910036	3207.913271	3024.912404	3190.535706	2850.460866	10.17966109	11.5826	11.4568	11.6474	11.5627	11.6396	11.477	0.04632	0.04632	0.04883	0.04632	0.04632	0.04883	2	3	71
IPI00370384.3	PREDICTED:_similar_to_Alpha-centractin	TLFSNIVLSGGSTLFK	99.99989169	0.287569668	0.997658493	0.959908311	0.984163624	0.977979004	0.40581774	0.16842046	0.458214041	0.151516021	0.971781238	0.506193373	0.087656632	1.050310003	-1.027351019	-1.052484033	-1.001284192	-1.024463901	1.06486448	10841.80999	11387.26148	10553.17003	10539.63511	10301.16339	10969.34299	7.870234614	13.4043	13.4751	13.3654	13.3635	13.3305	13.4212	0.03585	0.03585	0.03779	0.03585	0.03585	0.03779	2	2	16
IPI00364842.2	Charged_multivesicular_body_protein_5	IDQIEDLQDQLEDMMEDANEIQEALGR	99.99998862	0.126343985	0.997658493	0.99643308	0.423679834	0.977979004	0.96842601	0.046336314	0.415110825	0.524421149	0.090178977	0.844031393	0.889845157	-1.109515545	1.043911118	1.033169226	-1.094525636	-1.01039703	1.007307366	8953.31134	8069.568181	9346.461252	8539.280344	9250.28575	9317.880973	11.4223072	13.1282	12.9783	13.1902	13.0599	13.1753	13.1858	0.05194	0.05194	0.05475	0.05194	0.05194	0.05475	2	2	56
IPI00208205.1	Heat_shock_cognate_71_kDa_protein	SQIHDIVLVGGSTR	100	0.195605735	0.997658493	0.99643308	0.813181576	0.977979004	0.536288365	0.094337851	0.831741659	0.265786233	0.580702329	0.382166204	0.207773435	-1.058140419	1.007302312	1.038011232	1.019119355	1.0304863	-1.04442031	21655.30667	20465.43755	21813.44047	22230.49937	22478.45155	21522.41902	7.425815847	14.4024	14.3209	14.4129	14.4403	14.4563	14.3936	0.03383	0.03383	0.03566	0.03383	0.03383	0.03566	37	70	114
202221	alpha-tubulin	IHFPLATYAPVISAEK	99.9990356	0.088290774	0.997658493	0.99643308	0.488320952	0.992757535	0.983012577	0.027785811	0.613185905	0.583525309	0.128916731	0.977470308	0.92917305	1.285013171	-1.059590895	-1.063018403	1.19195768	-1.003234747	1.010216923	17736.34934	22791.44252	16738.86538	19952.01914	16684.89397	16855.36224	25.15453758	14.1144	14.4762	14.0309	14.2842	14.0263	14.0409	0.113	0.113	0.1191	0.113	0.113	0.1191	2	2	37
IPI00382376.1	Isoform_1_of_Heterogeneous_nuclear_ribonucleoprotein_A3	SSGSPYGGGYGSGGGSGGYGSR	99.99975346	0.076373123	0.997658493	0.577998545	0.706612353	0.600855383	0.520988984	0.021646325	0.630341611	0.014496595	0.361785525	0.004806843	0.197489431	-1.061343621	1.012584245	-1.065663637	-1.024052357	-1.079074209	1.034297828	14456.95904	13621.37459	14638.88895	14295.05908	13566.15591	14031.44559	5.626700889	13.8195	13.7336	13.8375	13.8032	13.7277	13.7764	0.02565	0.02565	0.02704	0.02565	0.02565	0.02704	5	5	103
IPI00213463.1	Alpha-actinin-4	VGWEQLLTTIAR	99.99999998	0.292178655	0.997658493	0.959908311	0.59819944	0.988483763	0.916967389	0.172868497	0.186831502	0.162024192	0.226290302	0.965889848	0.773508188	1.059336882	-1.058995315	-1.06094709	1.053872005	-1.001843044	1.012473819	11321.91826	11993.72559	10691.18825	11267.14399	10671.52016	10804.63477	9.346688788	13.4668	13.55	13.3841	13.4598	13.3815	13.3994	0.04255	0.04255	0.04485	0.04255	0.04255	0.04485	7	8	28
IPI00231997.5	NADH_dehydrogenase_[ubiquinone]_1_alpha_subcomplex_subunit_5	KLENLLQGGEVEEVILQAEK	99.99994948	0.902134763	0.997658493	0.99643308	0.117623759	0.988483763	0.343015874	0.836150049	0.596110818	0.536886406	0.00316039	0.943043911	0.043332303	-1.010284874	-1.027338247	-1.031075172	1.169487576	-1.003637483	1.110428662	6947.047198	6876.325061	6762.181025	7908.286696	6737.672855	7481.70505	11.04092827	12.7622	12.7474	12.7233	12.9491	12.718	12.8692	0.05022	0.05022	0.05293	0.05022	0.05022	0.05293	2	5	38
IPI00557167.2	PREDICTED:_similar_to_Ubiquitin-conjugating_enzyme_E2_L3	TDQVIQSLIALVNDPQPEHPLR	99.99763	0.116752327	0.997658493	0.99643308	0.225498692	0.977979004	0.287857444	0.040696525	0.804628055	0.489556327	0.014947342	0.66986558	0.03021253	-1.110809084	1.012871479	1.035459077	-1.138245284	1.022300556	-1.121448505	11934.46426	10743.9383	12088.07847	10619.92406	12357.64934	11019.36405	11.2306629	13.5428	13.3912	13.5613	13.3745	13.5931	13.4278	0.05108	0.05108	0.05384	0.05108	0.05108	0.05384	3	3	82
IPI00366069.1	Similar_to_phospholysine_phosphohistidine_inorganic_pyrophosphate_phosphata	SALQAIGVEAHQAIMIGDDIVDGVGGAQQCGMR	99.9952972	0.28341012	0.997658493	0.970109364	0.855934899	0.977979004	0.841589364	0.164141051	0.396093635	0.174590488	0.662126946	0.630407742	0.611715241	-1.054534616	1.033632844	1.053155418	1.017135127	1.018887339	-1.01993939	6914.705041	6557.115274	7147.266235	7269.73555	7282.259076	7139.893945	8.428618105	12.7555	12.6788	12.8032	12.8277	12.8302	12.8017	0.03839	0.03839	0.04046	0.03839	0.03839	0.04046	2	2	43
IPI00362347.2	PREDICTED:_similar_to_glyceraldehyde-3-phosphate_dehydrogenase	LISWYDNEYGYSNR	100	0.221160806	0.997658493	0.99643308	0.838783791	0.977979004	0.443669775	0.111530585	0.807381707	0.675172373	0.617501625	0.515196371	0.119157025	-1.150061832	1.021982506	-1.037069091	-1.045589427	-1.059866469	1.150957308	23151.54133	20130.6927	23660.47023	22628.83463	22324.01055	25693.98309	19.49384573	14.4988	14.2971	14.5302	14.4659	14.4463	14.6491	0.08811	0.08811	0.09287	0.08811	0.08811	0.09287	5	7	11
IPI00231927.10	ADP/ATP_translocase_1	YFAGNLASGGAAGATSLCFVYPLDFAR	99.99999962	0.138422462	0.997658493	0.99643308	0.91586083	0.977979004	0.613231168	0.05726735	0.536181803	0.816356065	0.816424512	0.69405981	0.274848013	1.247518963	-1.075484461	-1.026904375	-1.027641077	1.047307312	1.137649499	12722.95884	15872.13242	11829.97924	11511.78121	12389.62375	14095.04925	25.85017431	13.6351	13.9542	13.5302	13.4908	13.5968	13.7829	0.116	0.116	0.1223	0.116	0.116	0.1223	12	15	75
IPI00364286.3	PREDICTED:_similar_to_T-complex_protein_1_subunit_eta	INALTAASEAACLIVSVDETIKNPR	99.9937225	0.088319438	0.997658493	0.99643308	0.525414564	0.977979004	0.384065202	0.027959411	0.857415271	0.607848038	0.161080595	0.497595627	0.073750265	1.089395407	1.007049268	-1.019742119	1.056868878	-1.026930555	1.07358083	7154.201034	7793.753743	7204.632914	7614.352306	7015.696321	7531.917077	8.482442541	12.8046	12.9281	12.8147	12.8945	12.7764	12.8788	0.03863	0.03863	0.04072	0.03863	0.03863	0.04072	2	3	22
IPI00562994.2	PREDICTED:_similar_to_transcription_elongation_factor_A_(SII)-like_3_isoform_1	RPAEDYVPR	99.9982741	0.135794857	0.997658493	0.99643308	0.498231465	0.977979004	0.673644494	0.054789821	0.415505643	0.956927692	0.136288489	0.386338835	0.359595405	-1.093230085	1.038998667	-1.002465098	-1.073075664	-1.041559901	-1.044023281	8802.230826	8051.581227	9145.506097	8522.703856	8780.585818	8410.335267	10.1704374	13.1037	12.9751	13.1588	13.0571	13.1001	13.0379	0.04628	0.04628	0.04878	0.04628	0.04628	0.04878	6	6	71
IPI00367441.3	50_kDa_protein	IGGIGTVPVGR	99.99988808	0.108618199	0.997658493	0.99643308	0.83893122	0.977979004	0.979042717	0.03686812	0.520963224	0.960886948	0.628175776	0.552249512	0.915346921	1.209031593	-1.060593498	-1.004375711	1.045347219	1.055972866	-1.009770952	30271.30684	36598.96633	28541.85595	29836.14974	30139.42541	29847.78415	20.0084035	14.8857	15.1595	14.8008	14.8648	14.8794	14.8653	0.09039	0.09039	0.09528	0.09039	0.09039	0.09528	2	2	47
51243733	heat_shock_protein_90_[Rattus_norvegicus]	NPDDITQEEYGEFYK	99.99999946	0.204155235	0.997658493	0.99643308	0.943668993	0.977979004	0.4228421	0.100094395	0.850951689	0.571904129	0.878931047	0.461111176	0.103898344	1.07680446	-1.008612148	1.025461299	-1.006975347	1.034292724	-1.078061324	13903.44098	14971.28726	13784.72489	13689.2377	14257.44066	13225.07388	9.907294875	13.7632	13.8699	13.7508	13.7408	13.7994	13.691	0.04509	0.04509	0.04753	0.04509	0.04509	0.04753	15	15	33
IPI00763758.1	PREDICTED:_similar_to_3-oxoacid_CoA_transferase_1	KSTGCDFAVSPNLMPMQQIST	99.998595	0.469115163	0.997658493	0.99643308	0.400146534	0.977979004	0.916967389	0.342840972	0.976123662	0.240269288	0.073169652	0.265274123	0.774080518	-1.037503817	-1.001189008	-1.046745857	1.074936335	-1.045502746	1.011466437	6009.378428	5792.150667	6002.241717	6452.027714	5741.009995	5806.838921	8.615734283	12.553	12.4999	12.5513	12.6555	12.4871	12.5035	0.03923	0.03923	0.04136	0.03923	0.03923	0.04136	3	3	119
IPI00231126.1	Isoform_RTN1-S_of_Reticulon-1	HQAQVDQYLGLVR	99.988772	0.465384377	0.997658493	0.86359048	0.733834025	0.757639751	0.38112535	0.337204223	0.345856353	0.107994027	0.40898106	0.014000723	0.070460149	1.041554616	-1.041936082	1.071159369	-1.036600903	1.116079596	-1.083021697	12978.69069	13518.0152	12456.32138	12016.50639	13902.24613	12836.53519	9.419471953	13.6639	13.7226	13.6046	13.5527	13.763	13.648	0.04288	0.04288	0.0452	0.04288	0.04288	0.0452	2	4	73
IPI00327448.1	Isoform_1_of_Discs_large_homolog_2	YGDILHVINASDDEWWQAR	99.99999998	0.835054027	0.997658493	0.860437254	0.599602934	0.757639751	0.146792151	0.749162756	0.32071131	0.103252471	0.229562266	0.011595238	0.006733465	-1.008331091	1.026942328	-1.043733921	1.032764734	-1.071854543	1.077721722	10350.39061	10264.87302	10629.25423	10977.51892	9916.694669	10687.43726	5.776183929	13.3374	13.3254	13.3758	13.4223	13.2756	13.3836	0.02633	0.02633	0.02775	0.02633	0.02633	0.02775	4	4	104
IPI00190392.3	51_kDa_protein	LAGPQLVQMFIGDGAK	99.99999087	0.030758203	0.997658493	0.319486977	0.954046054	0.806688502	0.847855771	0.00597214	0.564080738	0.004016408	0.897819465	0.022612905	0.619818649	1.077821619	1.015712651	1.081878998	-1.003471751	1.065142782	-1.013494241	11844.09594	12765.82265	12030.19808	11988.57672	12813.87865	12643.26735	5.850168139	13.5319	13.64	13.5544	13.5494	13.6454	13.6261	0.02667	0.02667	0.02811	0.02667	0.02667	0.02811	3	3	106
IPI00189813.1	Actin,_alpha_skeletal_muscle	SYELPDGQVITIGNER	100	0.17298045	0.997658493	0.99643308	0.271569898	0.977979004	0.902279665	0.077890625	0.336225015	0.850547228	0.027423568	0.253393964	0.740384913	1.090499705	-1.049208122	1.00916308	1.118856912	1.0588221	1.016622336	20585.36399	22448.33336	19619.90529	21951.86664	20773.98931	21119.30153	10.80226846	14.3293	14.4543	14.26	14.4221	14.3425	14.3663	0.04914	0.04914	0.0518	0.04914	0.04914	0.0518	20	47	15
IPI00189925.1	Alpha-soluble_NSF_attachment_protein	LDQWLTTMLLR	99.99999984	0.564904209	0.997658493	0.99643308	0.797906375	0.977979004	0.45250857	0.435137642	0.343942756	0.680400098	0.557166623	0.583372429	0.126963899	1.040557933	-1.050853062	-1.021160153	-1.031161796	1.029077621	-1.083882951	11732.77786	12208.63508	11165.00327	10827.59593	11489.655	10600.45735	11.33920347	13.5183	13.5756	13.4467	13.4024	13.488	13.3718	0.05157	0.05157	0.05436	0.05157	0.05157	0.05436	2	2	17
IPI00363719.3	Heterogeneous_nuclear_ribonucleoprotein_D-like	GFGFVLFK	99.99986628	0.128225748	0.997658493	0.99643308	0.333651543	0.982193145	0.343015874	0.049385231	0.454875609	0.51901646	0.041188464	0.904166099	0.044110559	-1.122520858	1.045433533	1.037996164	-1.131500127	-1.007165122	-1.129466027	11349.22312	10110.4786	11864.85842	10485.95412	11780.45005	10430.1057	12.89627993	13.4703	13.3036	13.5344	13.3562	13.5241	13.3485	0.05859	0.05859	0.06176	0.05859	0.05859	0.06176	3	3	82
IPI00391300.3	234_kDa_protein	SLEAEILQLQEELASSER	99.99999526	0.127795487	0.997658493	0.99643308	0.838783791	0.988483763	0.443669775	0.049073467	0.451934859	0.394729962	0.61830488	0.938603474	0.119133007	-1.061003872	-1.02314509	-1.02553868	-1.015248432	-1.002339443	1.049001096	10299.25721	9707.08743	10066.27242	9915.082957	10042.77792	10534.88504	6.577865833	13.3303	13.2448	13.2972	13.2754	13.2939	13.3629	0.02998	0.02998	0.0316	0.02998	0.02998	0.0316	7	8	133
IPI00191103.2	PREDICTED:_similar_to_NADH_dehydrogenase_(ubiquinone)_1_alpha_subcomplex,_2	KAHPDLPILIR	99.9959257	0.832692474	0.997658493	0.639633748	0.966345081	0.888247413	0.662721482	0.742946194	0.847318652	0.019220173	0.921684869	0.035529897	0.321135895	1.010785327	-1.00648946	-1.081795464	-1.003307843	-1.074820459	1.034051469	14262.8323	14416.6616	14170.87029	14124.15052	13184.40756	13633.356	7.285076291	13.8	13.8154	13.7906	13.7859	13.6865	13.7349	0.03319	0.03319	0.03499	0.03319	0.03319	0.03499	3	3	83
IPI00206226.1	Adenylyl_cyclase-associated_protein_2	GIVAPSVEAFDKLINSMVAEFLK	99.9979136	0.311280174	0.997658493	0.99643308	0.629773213	0.977979004	0.661535969	0.188872228	0.208254317	0.688879587	0.260546175	0.381658899	0.314513101	1.076691946	-1.075363073	-1.022597411	1.067012282	1.051599643	-1.059622715	7647.705011	8234.222392	7111.74226	7588.31634	7478.705623	7057.894773	12.45843128	12.9008	13.0074	12.796	12.8896	12.8686	12.785	0.05662	0.05662	0.05968	0.05662	0.05662	0.05968	3	3	48
3642631	cytoskeletal_beta-actin_[Mus_musculus]	GYSFTTTAER	99.99987343	0.073874881	0.997658493	0.99643308	0.879103848	0.977979004	0.569356066	0.02035629	0.290046518	0.396600823	0.7213675	0.813632927	0.233986818	1.126629445	1.056241799	1.043508075	-1.018524607	-1.012202804	-1.063578944	14534.95592	16375.50895	15352.42765	15073.2025	15167.34353	14260.66548	11.17570834	13.8272	13.9993	13.9062	13.8797	13.8887	13.7998	0.05083	0.05083	0.05358	0.05083	0.05083	0.05358	8	13	26
IPI00367152.1	NADH_dehydrogenase_[ubiquinone]_flavoprotein_2,_mitochondrial_precursor	VYEVATFYTMYNR	99.99999982	0.031695156	0.997658493	0.99643308	0.788902735	0.977979004	0.453249617	0.006194139	0.745881838	0.415970865	0.492489186	0.638683674	0.133491151	-1.081804645	-1.009266507	-1.022852631	-1.01976258	-1.013461383	-1.044099686	21755.70834	20110.57028	21555.95987	21138.21423	21269.64109	20371.27428	6.167583101	14.4091	14.2957	14.3958	14.3676	14.3765	14.3142	0.02811	0.02811	0.02963	0.02811	0.02811	0.02963	9	11	134
IPI00417225.1	Isoform_1_of_Synaptopodin	TARPFGMQSPGTTSQIEQSPMMGR	99.99998262	0.882626904	0.997658493	0.99643308	0.169558539	0.977979004	0.119761122	0.80697317	0.865355185	0.2453147	0.007348331	0.334891227	0.002483236	1.012445028	-1.008856128	-1.060966992	1.155311236	-1.051653415	1.178848839	17260.34232	17475.14777	17108.82438	19766.01703	16268.50077	19178.10324	11.29732794	14.0752	14.093	14.0625	14.2707	13.9898	14.2272	0.05138	0.05138	0.05416	0.05138	0.05138	0.05416	3	3	38
IPI00200847.1	T-complex_protein_1_subunit_alpha	SQNVMAAASIANIVK	99.67511	0.292178655	0.997658493	0.99643308	0.243871572	0.977979004	0.45250857	0.173063273	0.548847186	0.495211593	0.020624567	0.209037304	0.129531409	1.099585558	1.043526121	-1.048335864	1.183626299	-1.093965858	1.114894413	12313.32756	13539.55715	12849.27894	15208.74447	11745.59411	13095.09725	15.45799947	13.5879	13.7249	13.6494	13.8926	13.5198	13.6767	0.07011	0.07011	0.0739	0.07011	0.07011	0.0739	2	2	104
IPI00679210.2	Isoform_Tau-G_of_Microtubule-associated_protein_tau	IGSLDNITHVPGGGNK	99.99976325	0.734898948	0.997658493	0.846402451	0.63922298	0.757639751	0.406234571	0.62779162	0.420734338	0.082436016	0.279066489	0.012882897	0.088675203	-1.015221528	-1.026162838	1.056384227	-1.035421718	1.084022237	-1.056762847	12890.67113	12697.39734	12562.01321	12132.26746	13617.50166	12886.05263	6.934270921	13.654	13.6322	13.6168	13.5666	13.7332	13.6535	0.0316	0.0316	0.03331	0.0316	0.0316	0.03331	8	10	73
IPI00563431.2	Glyceraldehyde_3-phosphate_dehydrogenase_(Fragment)	VGVNGFGR	99.9934479	0.118068559	0.997658493	0.99643308	0.638878253	0.982193145	0.80914378	0.041299724	0.617389891	0.523847073	0.275995405	0.903308744	0.54755415	-1.337541137	1.074406058	1.093300267	-1.170248694	1.017585725	-1.090297972	13073.70292	9774.430526	14046.46562	12002.97493	14293.4829	13109.70328	31.84584392	13.6744	13.2548	13.7779	13.5511	13.8031	13.6783	0.1418	0.1418	0.1495	0.1418	0.1418	0.1495	3	3	36
IPI00199872.1	Guanine_nucleotide-binding_protein_G(s)_subunit_alpha	LLLLGAGESGK	99.9999872	0.110436999	0.997658493	0.99643308	0.560474035	0.988483763	0.715156691	0.037864114	0.597620805	0.554400341	0.195255061	0.96183691	0.430728659	1.214449564	-1.051013766	-1.055758618	1.130797976	-1.004514548	1.077236323	19067.22496	23156.18304	18141.74617	20514.64985	18060.21247	19455.11688	20.60383488	14.2188	14.4991	14.147	14.3244	14.1405	14.2479	0.09302	0.09302	0.09806	0.09302	0.09302	0.09806	2	2	35
IPI00464920.4	XLalphas_protein	LLLLGAGESGK	99.9999872	0.110436999	0.997658493	0.99643308	0.560474035	0.988483763	0.715156691	0.037864114	0.597620805	0.554400341	0.195255061	0.96183691	0.430728659	1.214449564	-1.051013766	-1.055758618	1.130797976	-1.004514548	1.077236323	19067.22496	23156.18304	18141.74617	20514.64985	18060.21247	19455.11688	20.60383488	14.2188	14.4991	14.147	14.3244	14.1405	14.2479	0.09302	0.09302	0.09806	0.09302	0.09302	0.09806	2	2	35
551295	pyruvate_kinase_M_[Mus_musculus]	FGVEQDVDMVFASFIR	100	0.618684709	0.997658493	0.795267491	0.945991925	0.977979004	0.370871244	0.493533631	0.277172145	0.047526798	0.882205041	0.384370618	0.064134742	1.015318932	-1.02518758	-1.045763123	1.003378536	-1.020070028	1.043775272	19299.97457	19595.62956	18825.79827	18889.40191	18455.39792	19263.28799	4.93283686	14.2363	14.2582	14.2004	14.2053	14.1718	14.2336	0.02249	0.02249	0.02371	0.02249	0.02249	0.02371	25	31	16
28972786	mKIAA1576_protein_[Mus_musculus]	ACGLNFIDLMVR	100	0.568363266	0.997658493	0.795267491	0.786739785	0.92052399	0.421432785	0.439750779	0.921373371	0.058193567	0.482423175	0.052491953	0.099104477	-1.028305094	-1.003659807	1.071905921	-1.026400417	1.075828889	-1.063802136	10069.98743	9792.801275	10033.26761	9775.198297	10794.07915	10146.69814	8.029056445	13.2978	13.2575	13.2925	13.2549	13.398	13.3087	0.03657	0.03657	0.03855	0.03657	0.03657	0.03855	6	6	73
IPI00190632.3	46_kDa_protein	ACGLNFIDLMVR	100	0.568363266	0.997658493	0.795267491	0.786739785	0.92052399	0.421432785	0.439750779	0.921373371	0.058193567	0.482423175	0.052491953	0.099104477	-1.028305094	-1.003659807	1.071905921	-1.026400417	1.075828889	-1.063802136	10069.98743	9792.801275	10033.26761	9775.198297	10794.07915	10146.69814	8.029056445	13.2978	13.2575	13.2925	13.2549	13.398	13.3087	0.03657	0.03657	0.03855	0.03657	0.03657	0.03855	6	6	73
473729	cytochrome_c_oxidase_subunit_Vb_[Rattus_norvegicus]	ASGGGVPTDEEQATGLER	99.99998558	0.032788784	0.997658493	0.99643308	0.667740008	0.977979004	0.451022894	0.006632703	0.861819699	0.707169055	0.302200049	0.841578406	0.124740046	-1.1920454	-1.010699901	-1.023739592	-1.068761523	-1.012901645	-1.10470225	22531.38562	18901.44923	22292.85429	20858.58613	22008.90324	19922.92787	13.95630715	14.4596	14.2062	14.4443	14.3484	14.4258	14.2821	0.06336	0.06336	0.06679	0.06336	0.06336	0.06679	4	5	107
IPI00231971.4	Fatty_acid-binding_protein,_heart	SLGVGFATR	99.999876	0.247086905	0.997658493	0.99643308	0.682649423	0.977979004	0.870908519	0.130498079	0.855428591	0.318961653	0.318371424	0.429481541	0.668857743	-1.134545351	1.015576067	1.086185595	1.088773412	1.069526578	-1.036977449	15951.6815	14059.97697	16200.14596	17638.2882	17326.48667	16708.64364	18.52759243	13.9614	13.7793	13.9837	14.1064	14.0807	14.0283	0.08381	0.08381	0.08835	0.08381	0.08381	0.08835	2	2	21
12834081	unnamed_protein_product_[Mus_musculus]	LIAVIGDEDTVTGFLLGGIGELNK	99.99999998	0.469115163	0.997658493	0.99643308	0.541686564	0.977979004	0.342414031	0.238211323	0.709439336	0.597449596	0.175370951	0.88723103	0.477222616	-1.034355721	1.013662428	1.018907992	1.051020554	1.005174863	1.026270754	9498.548814	9183.058231	9628.322052	10119.56438	9678.147299	9932.399529	7.895210301	13.2135	13.1648	13.2331	13.3049	13.2405	13.2779	0.03596	0.03596	0.03791	0.03596	0.03596	0.03791	5	7	43
1703221	AINX_RAT_Alpha-internexin_(Alpha-Inx)	VGESFEETLEETVVSTK	100	0.368027631	0.997658493	0.99643308	0.507654338	0.977979004	0.91254317	0.238211323	0.138993205	0.346797334	0.149895701	0.565429263	0.76132173	-1.033228694	1.04320009	1.026351589	-1.041994162	-1.016415915	1.008631512	16667.75949	16131.72339	17387.8082	16687.04954	17106.98144	17254.64055	6.131677148	14.0248	13.9776	14.0858	14.0264	14.0623	14.0747	0.02795	0.02795	0.02946	0.02795	0.02795	0.02946	28	35	80
IPI00231734.4	Fructose-bisphosphate_aldolase_A	FSNEEIAMATVTALR	100	0.494216669	0.997658493	0.99643308	0.843117632	0.977979004	0.426869209	0.369719927	0.176930697	0.874861516	0.639805834	0.229927513	0.109542722	-1.046192684	1.0727079	1.007929665	-1.024429511	-1.064268607	1.087063819	18506.44768	17689.33004	19852.01253	19378.60284	18653.19761	20277.21622	11.19422293	14.1759	14.1106	14.277	14.2422	14.1871	14.3076	0.05091	0.05091	0.05367	0.05091	0.05091	0.05367	33	52	90
55825	unnamed_protein_product_[Rattus_norvegicus]	FGDLSSASAIMGNPQVK	100	0.957181136	0.997658493	0.99643308	0.560474035	0.977979004	0.454871916	0.936396631	0.780543801	0.275617556	0.196863626	0.182073372	0.137926198	-1.004182318	-1.015088764	1.059023912	1.072408785	1.075003273	1.083908079	17303.63142	17231.56354	17046.42199	18280.73269	18324.95943	19862.57158	11.67792677	14.0788	14.0728	14.0572	14.158	14.1615	14.2778	0.0531	0.0531	0.05597	0.0531	0.0531	0.05597	18	25	32
IPI00764950.1	PREDICTED:_similar_to_ubiquinol-cytochrome_c_reductase_complex_7.2kDa_protein_isoform_a	AFDQGADAVYDYINEGK	100	0.504990663	0.997658493	0.99643308	0.877572362	0.977979004	0.48309073	0.379243012	0.374961724	0.713958332	0.716099048	0.59411836	0.156797448	-1.063437679	1.06584309	1.025890055	-1.026397672	-1.038944753	1.107793735	13828.55014	13003.63003	14739.0646	14359.99418	14186.57206	15715.79565	15.60177591	13.7554	13.6666	13.8474	13.8098	13.7922	13.9399	0.07075	0.07075	0.07458	0.07075	0.07075	0.07458	2	3	79
IPI00215107.2	40S_ribosomal_protein_SA	AIVAIENPADVSVISSR	100	0.601707784	0.997658493	0.99643308	0.454617724	0.991296718	0.390747044	0.476299895	0.840725882	0.862678318	0.107857378	0.9739718	0.079219692	-1.021815063	1.006261135	1.005242155	1.05186083	-1.001013666	1.056886844	15197.98619	14873.51942	15293.14283	16086.25791	15277.65639	16146.75405	6.733477037	13.8916	13.8605	13.9006	13.9735	13.8991	13.979	0.03068	0.03068	0.03234	0.03068	0.03068	0.03234	4	4	101
IPI00212647.2	Glyceraldehyde-3-phosphate_dehydrogenase	WGDAGAEYVVESTGVFTTMEK	100	0.241981068	0.997658493	0.99643308	0.950116019	0.977979004	0.486972084	0.125000506	0.733004176	0.782229752	0.888222747	0.542280535	0.164735699	-1.079517795	1.017441368	-1.013727707	-1.007146331	-1.031408505	1.073628939	17585.83869	16290.45743	17892.55976	17765.60089	17347.69462	18624.98696	11.0057104	14.1021	13.9917	14.1271	14.1168	14.0825	14.185	0.05006	0.05006	0.05277	0.05006	0.05006	0.05277	41	63	5
IPI00207944.5	Myelin-oligodendrocyte_glycoprotein_precursor	ALVGDEAELPCR	99.99999962	0.247086905	0.997658493	0.99643308	0.603432408	0.977979004	0.924766593	0.130744271	0.963519804	0.663853172	0.231718045	0.705878322	0.796286626	1.097852229	1.002875013	1.026932289	-1.078521674	1.02398831	-1.016341432	11990.89102	13164.22643	12025.36498	11149.85936	12313.83317	12115.84295	13.65871656	13.5497	13.6843	13.5538	13.4447	13.588	13.5646	0.06203	0.06203	0.06538	0.06203	0.06203	0.06538	2	2	64
IPI00198693.1	Vacuolar_ATPase_NG38	QQAAMGSQGNLSAEVEQATR	99.99949094	0.360449564	0.997658493	0.99643308	0.668421481	0.977979004	0.849367056	0.232335491	0.147110992	0.822704577	0.304800196	0.09683047	0.635193226	1.041078638	-1.05166234	1.00753033	1.036108918	1.059581704	1.016467862	13011.16291	13545.64377	12371.99662	12818.73604	13109.14126	13325.02079	7.459311757	13.6675	13.7255	13.5948	13.646	13.6783	13.7019	0.03398	0.03398	0.03582	0.03398	0.03398	0.03582	4	5	78
508538	alpha-internexin	FANLNEQAAR	99.99999127	0.332281068	0.997658493	0.99643308	0.619530286	0.977979004	0.933287832	0.208862386	0.165072999	0.370721909	0.24710408	0.598937476	0.823426522	-1.040168517	1.045789383	1.028339694	-1.037923088	-1.016968798	1.007156724	15118.1547	14534.33212	15810.40567	15232.73338	15546.59858	15657.8613	6.928821216	13.884	13.8272	13.9486	13.8949	13.9243	13.9346	0.03157	0.03157	0.03328	0.03157	0.03157	0.03328	18	23	80
IPI00231102.9	Myelin_proteolipid_protein	TSASIGSLCADAR	99.99999999	0.131487826	0.997658493	0.99643308	0.674180112	0.988483763	0.70028075	0.051543228	0.756920991	0.683143982	0.309737606	0.929926484	0.405762675	1.281265347	1.040561276	1.052377016	-1.140053788	1.01135516	-1.11304901	11741.08189	15043.44136	12217.31516	10716.43749	12356.04473	11101.07876	28.35682016	13.5193	13.8768	13.5766	13.3875	13.5929	13.4384	0.1269	0.1269	0.1337	0.1269	0.1269	0.1337	5	9	54
IPI00776479.1	36_kDa_protein	DIVAINDPFIDLNY	99.9964486	0.175457495	0.997658493	0.99643308	0.733834025	0.977979004	0.673644494	0.080610186	0.557319134	0.987264409	0.412749001	0.546984336	0.359196351	-1.268266022	1.08429864	-1.002141478	-1.119790871	-1.086620642	1.135145162	13838.70653	10911.51721	15005.29067	13400.08305	13809.13457	15675.3723	30.49833794	13.7564	13.4136	13.8732	13.71	13.7533	13.9362	0.1361	0.1361	0.1434	0.1361	0.1361	0.1434	7	9	11
IPI00366110.3	47_kDa_protein	FYEEVHDLERK	99.6231	0.634363686	0.997658493	0.99643308	0.41449023	0.977979004	0.03637813	0.514015833	0.569799517	0.331526005	0.07840234	0.703962245	0.000328759	-1.024329562	1.021730633	1.036508858	-1.069808856	1.014463915	-1.155547284	14149.48523	13813.41099	14456.96251	13513.59397	14666.06678	12691.87941	8.193807085	13.7885	13.7538	13.8195	13.7221	13.8402	13.6316	0.03732	0.03732	0.03934	0.03732	0.03732	0.03934	2	2	24
IPI00454375.1	Pkm2_protein	FGVEQDVDMVFASFIR	100	0.841713319	0.997658493	0.639633748	0.907783534	0.977979004	0.160426354	0.758022966	0.315044383	0.022994843	0.791587242	0.211180808	0.008800531	1.006684738	-1.022675481	-1.051693387	1.005887818	-1.0283745	1.062016049	20373.51644	20509.70806	19921.78048	20039.07629	19372.10663	20573.48814	4.813098805	14.3144	14.324	14.2821	14.2905	14.2417	14.3285	0.02195	0.02195	0.02313	0.02195	0.02195	0.02313	37	50	16
IPI00568632.1	Isoform_Tau-A_of_Microtubule-associated_protein_tau	IGSLDNITHVPGGGNK	99.99976325	0.494216669	0.997658493	0.846402451	0.507654338	0.977979004	0.348219477	0.368344815	0.819201753	0.087285849	0.148996212	0.148519806	0.052266976	-1.027640881	1.007116844	1.053758198	-1.046255112	1.046311761	-1.063238818	13712.67776	13343.77409	13810.19824	13199.64709	14449.77284	13590.33605	6.726062055	13.7432	13.7039	13.7534	13.6882	13.8188	13.7303	0.03065	0.03065	0.03231	0.03065	0.03065	0.03231	11	14	73
IPI00211756.1	Prohibitin	FDAGELITQR	99.99999966	0.081246355	0.997658493	0.99643308	0.792374134	0.977979004	0.725898654	0.024513186	0.933591672	0.741981948	0.527947566	0.686486315	0.447983169	-1.063164966	-1.002277313	1.00879059	-1.017412023	1.011087923	-1.020988298	13864.38279	13040.66936	13832.88099	13596.1446	13986.2589	13698.74555	5.917872421	13.7591	13.6707	13.7558	13.7309	13.7717	13.7418	0.02697	0.02697	0.02843	0.02697	0.02697	0.02843	12	15	128
IPI00230907.4	Macrophage_migration_inhibitory_factor	PMFIVNTNVPR	99.99999994	0.126343985	0.997658493	0.99643308	0.333651543	0.977979004	0.494377841	0.046733819	0.52789658	0.65168774	0.042117967	0.847277504	0.170065977	-1.112387776	1.034724221	1.024022163	-1.118429594	-1.010451002	-1.077594917	16048.46734	14427.04396	16605.73787	14847.36989	16433.98625	15250.61597	11.73062916	13.9701	13.8165	14.0194	13.8579	14.0044	13.8966	0.05333	0.05333	0.05622	0.05333	0.05333	0.05622	7	8	82
IPI00210570.1	Isoform_1_of_Homer_protein_homolog_1	NKDLEGQLSELEQR	99.988714	0.103480936	0.997658493	0.99643308	0.765696444	0.977979004	0.697837817	0.034541915	0.675118273	0.641290873	0.455042458	0.384172866	0.397193203	-1.100855564	-1.019354798	1.020961062	-1.034823103	1.040721557	-1.039588242	14900.65758	13535.52416	14617.7338	14125.82861	15212.99068	14633.66942	9.922426636	13.8631	13.7245	13.8354	13.786	13.893	13.837	0.04516	0.04516	0.0476	0.04516	0.04516	0.0476	2	2	117
IPI00206624.1	78_kDa_glucose-regulated_protein_precursor	IINEPTAAAIAYGLDK	100	0.136547984	0.997658493	0.99643308	0.903404554	0.977979004	0.985692829	0.055867632	0.812112858	0.504088916	0.779059214	0.679202747	0.942251171	-1.059609778	1.007293073	1.02011568	1.008614178	1.012729768	-1.002216441	13743.29426	12970.14669	13843.5251	13962.77569	14019.74995	13988.74475	6.626953931	13.7464	13.6629	13.7569	13.7693	13.7752	13.772	0.0302	0.0302	0.03183	0.0302	0.0302	0.03183	11	11	100
IPI00778786.1	62_kDa_protein	SQIHDIVLVGGSTR	100	0.28341012	0.997658493	0.99643308	0.876899711	0.977979004	0.613231168	0.163664136	0.767414704	0.230580405	0.71295409	0.381076685	0.276129235	-1.048233964	1.010236638	1.041275964	1.012752112	1.030724807	-1.038422616	23472.78697	22392.69837	23713.06938	24015.4611	24441.64886	23537.2849	7.465919508	14.5187	14.4507	14.5334	14.5517	14.5771	14.5227	0.03401	0.03401	0.03585	0.03401	0.03401	0.03585	20	40	114
IPI00339197.3	Isoform_M2_of_Pyruvate_kinase_isozymes_M1/M2	FGVEQDVDMVFASFIR	100	0.763969153	0.997658493	0.685064733	0.794117156	0.977979004	0.147881653	0.666181102	0.300531902	0.033023311	0.530924042	0.282486911	0.007374576	1.009830696	-1.024520307	-1.050622058	1.014720529	-1.025477046	1.066736637	20092.76312	20290.28897	19611.87395	19900.5711	19124.63475	20400.94855	5.045038092	14.2944	14.3085	14.2594	14.2805	14.2231	14.3163	0.023	0.023	0.02425	0.023	0.023	0.02425	38	51	16
IPI00421625.5	Myosin_regulatory_light_chain_2-B,_smooth_muscle_isoform	ELLTTMGDRFTDEEVDELYR	99.99989994	0.448477828	0.997658493	0.86359048	0.638878253	0.977979004	0.956374612	0.319316214	0.458682273	0.112316853	0.275948595	0.412827108	0.856911652	-1.061340608	1.046461265	1.100355107	-1.069270417	1.051501039	-1.011083652	12300.32419	11589.422	12871.81281	12037.93971	13534.72455	13386.35485	13.29746482	13.5864	13.5005	13.6519	13.5553	13.7244	13.7085	0.0604	0.0604	0.06367	0.0604	0.0604	0.06367	3	3	84
IPI00198720.1	Isocitrate_dehydrogenase_[NAD]_subunit_alpha,_mitochondrial_precursor	DMANPTALLLSAVMMLR	100	0.038232272	0.997658493	0.795267491	0.733834025	0.977979004	0.799607172	0.007996007	0.845583147	0.056784215	0.413250211	0.094989646	0.530939163	-1.082502995	-1.005795963	-1.057589287	-1.024652402	-1.051494862	-1.018799493	19053.5937	17601.42353	18943.75617	18488.02201	18016.06156	17683.6185	6.43283097	14.2178	14.1034	14.2094	14.1743	14.137	14.1101	0.02932	0.02932	0.0309	0.02932	0.02932	0.0309	14	21	130
IPI00373143.1	21_kDa_protein	QNYHQDSEAAINR	99.986249	0.140809205	0.997658493	0.99643308	0.638878253	0.977979004	0.993109576	0.059864028	0.783736758	0.494006316	0.275319741	0.69478124	0.965238853	-1.130787966	1.018274322	1.044992283	-1.075054866	1.02623847	-1.002878702	9556.774128	8451.428931	9731.417699	9052.019579	9986.755214	9958.08884	14.35996618	13.2223	13.045	13.2484	13.144	13.2858	13.2817	0.06518	0.06518	0.0687	0.06518	0.06518	0.0687	3	4	84
IPI00230941.4	Vimentin	VEVERDNLAEDIMR	99.975047	0.175457495	0.997658493	0.99643308	0.467884871	0.977979004	0.538949881	0.080475041	0.9543261	0.67860036	0.11454136	0.645185988	0.210652411	-1.067554778	1.0021706	-1.015398281	-1.062335018	-1.017602305	1.04890784	21711.44908	20337.55038	21758.57596	20481.84009	21382.19996	22427.95717	8.213411289	14.4062	14.3119	14.4093	14.3221	14.3841	14.453	0.03741	0.03741	0.03943	0.03741	0.03741	0.03943	3	3	133
IPI00476155.3	54_kDa_protein	IVFEDGNISVSK	99.99999981	0.085747313	0.997658493	0.99643308	0.658666867	0.977979004	0.70956869	0.026361174	0.977076501	0.747679978	0.29282447	0.776080159	0.4208756	1.087449169	-1.001088482	-1.011931333	1.040853843	-1.010831062	1.031041747	14578.99666	15853.9178	14563.14494	15158.10538	14407.10075	14854.32232	8.214283586	13.8316	13.9526	13.83	13.8878	13.8145	13.8586	0.03741	0.03741	0.03944	0.03741	0.03741	0.03944	9	11	62
IPI00191707.3	Pyruvate_dehydrogenase_E1_component_alpha_subunit,_somatic_form,_mitochondrial_precursor	YHGHSMSDPGVSYR	99.99999871	0.039035383	0.997658493	0.99643308	0.577643504	0.977979004	0.602776182	0.008208584	0.480702868	0.274479762	0.215274782	0.716801779	0.262465972	-1.067996442	-1.017618767	-1.026785967	-1.031327688	-1.009028482	-1.028248106	18992.37054	17783.17774	18663.54196	18096.61679	18496.91284	17988.76432	5.35552754	14.2131	14.1182	14.1879	14.1434	14.175	14.1348	0.02442	0.02442	0.02574	0.02442	0.02442	0.02574	11	13	134
IPI00231434.5	FK506-binding_protein_1A	GWEEGVAQMSVGQR	100	0.190389371	0.997658493	0.99643308	0.243213193	0.977979004	0.697837817	0.090013696	0.366206303	0.898824202	0.019341114	0.434738378	0.396366735	-1.097129516	1.051538711	1.00687964	-1.142337497	-1.044353932	-1.04827611	17755.20719	16183.32834	18670.28768	16343.93315	17877.35662	17054.05326	12.04200363	14.116	13.9822	14.1885	13.9965	14.1258	14.0578	0.05474	0.05474	0.0577	0.05474	0.05474	0.0577	7	11	51
IPI00763477.1	PREDICTED:_similar_to_splicing_factor,_arginine/serine-rich_1	SHEGETAYIR	99.99982989	0.204857991	0.997658493	0.99643308	0.706612353	0.977979004	0.962930205	0.10067307	0.340070929	0.479947898	0.358470921	0.787973984	0.872689888	-1.083906643	1.04884671	1.034896549	-1.046958731	-1.013479763	1.008008024	6718.325124	6198.250714	7046.493201	6730.440269	6952.771486	7008.449448	10.81133837	12.7139	12.5976	12.7827	12.7165	12.7634	12.7749	0.04918	0.04918	0.05184	0.04918	0.04918	0.05184	3	3	80
IPI00569103.3	Isoform_3_of_Myelin_basic_protein_S	YLATASTMDHAR	99.99999999	0.039657352	0.997658493	0.99643308	0.779512133	0.977979004	0.847997354	0.008384697	0.250912322	0.559286718	0.466816409	0.558366775	0.622187773	1.423943508	1.166298112	1.0787333	-1.101997789	-1.081173735	1.067882667	22883.50652	32584.82056	26688.99044	24218.73321	24685.20051	26360.90269	29.44611103	14.482	14.9919	14.704	14.5638	14.5914	14.6861	0.1316	0.1316	0.1387	0.1316	0.1316	0.1387	10	20	115
IPI00562798.1	NAD-dependent_deacetylase_sirtuin-2	LLDELTLEGVTR	99.9999999	0.079607598	0.997658493	0.99643308	0.780681315	0.977979004	0.453249617	0.023472869	0.935861371	0.79175696	0.469667081	0.735842854	0.13166221	1.156916902	1.005200894	-1.016709049	1.047832911	-1.021996845	1.103248034	9389.288855	10862.62697	9438.121549	9889.574372	9234.981104	10188.47475	14.03026402	13.1968	13.4071	13.2043	13.2717	13.1729	13.3147	0.0637	0.0637	0.06714	0.0637	0.0637	0.06714	8	8	22
126897	MDHM_MOUSE_Malate_dehydrogenase,_mitochondrial_precursor	VAVLGASGGIGQPLSLLLK	100	0.445502935	0.997658493	0.869092652	0.271569898	0.977979004	0.119761122	0.315670651	0.545891609	0.120183098	0.027593322	0.356721752	0.002910125	1.035391476	-1.021671455	-1.055733431	1.083225993	-1.033339462	1.116500912	26650.53255	27593.73423	26085.22772	28256.19671	25243.61905	28184.52369	7.687189793	14.7019	14.7521	14.6709	14.7863	14.6236	14.7826	0.03502	0.03502	0.03691	0.03502	0.03502	0.03691	22	30	22
IPI00196656.2	Ba1-667	SAGWIIPIGLLFCNLPEPR	99.99968733	0.1910604	0.997658493	0.99643308	0.271569898	0.977979004	0.365553516	0.091108324	0.799269629	0.386593925	0.027622538	0.55491036	0.061412991	1.061165975	-1.009097416	-1.030570161	1.083610528	-1.021279159	1.070087163	9142.477265	9701.685804	9060.054185	9817.570098	8871.280787	9493.043689	7.722946493	13.1584	13.244	13.1453	13.2612	13.1149	13.2127	0.03518	0.03518	0.03708	0.03518	0.03518	0.03708	4	4	22
IPI00209114.1	Isoform_1_of_Limbic_system-associated_membrane_protein_precursor	EFEGEEEYLEILGITR	100	0.324262391	0.997658493	0.99643308	0.886734314	0.977979004	0.343015874	0.200486804	0.977528087	0.200516577	0.73705083	0.202670128	0.045284	1.05606829	1.001224216	-1.056064418	-1.014698527	-1.05735855	1.092722741	16229.96308	17139.94935	16249.83207	16014.44333	15368.34572	16793.34085	9.42869784	13.9864	14.0651	13.9881	13.9671	13.9077	14.0356	0.04292	0.04292	0.04524	0.04292	0.04292	0.04524	4	4	16
IPI00201713.5	Isoform_B_of_AP-1_complex_subunit_beta-1	LASQANIAQVLAELK	99.9999997	0.210427148	0.997658493	0.99643308	0.691591891	0.977979004	0.697837817	0.104131377	0.337852724	0.702089267	0.332783801	0.185524052	0.398764467	1.059671354	-1.035437214	1.013567999	1.035820917	1.049486026	-1.031103455	9001.423219	9538.55033	8693.354938	9004.758888	9123.554524	8848.340564	7.847091784	13.1359	13.2196	13.0857	13.1365	13.1554	13.1112	0.03575	0.03575	0.03768	0.03575	0.03575	0.03768	8	8	67
IPI00211317.1	Dynein_light_chain_2,_cytoplasmic	NADMSEDMQQDAVDCATQAMEK	100	0.109379305	0.997658493	0.99643308	0.416332803	0.977979004	0.248149304	0.037251466	0.9021917	0.654874148	0.083818315	0.754698039	0.019144322	-1.096161814	1.0546402	1.019496535	-1.080885761	1.013956258	-1.112593811	15658.0838	14284.46384	15743.63987	14565.49844	15963.36217	14347.87971	9.625596402	13.9346	13.8022	13.9425	13.8303	13.9625	13.8085	0.04381	0.04381	0.04618	0.04381	0.04381	0.04618	8	11	82
13123946	ACTN4_MOUSE_Alpha-actinin-4_(Non-muscle_alpha-actinin_4)_(F-actin_cross-linking_protein)	VGWEQLLTTIAR	99.99999998	0.471137912	0.997658493	0.99643308	0.842694959	0.988483763	0.849720293	0.345680616	0.213681753	0.233111355	0.637723471	0.932852398	0.640490125	1.036033067	-1.049288498	-1.045898827	1.018266857	1.003240917	-1.01811503	12515.74364	12966.72427	11927.8384	12145.72252	11966.49553	11753.57909	8.332096031	13.6115	13.6625	13.542	13.5682	13.5467	13.5208	0.03795	0.03795	0.04	0.03795	0.03795	0.04	8	9	28
IPI00382148.1	Aa2-258	SHCAEPFTEYWTCLDYSSMQLFR	99.99917896	0.908474472	0.997658493	0.456464817	0.416332803	0.977979004	0.384065202	0.852220781	0.281526447	0.007825111	0.084693987	0.114634146	0.074256383	-1.007413746	-1.045097657	-1.115334211	1.073845891	-1.067205733	1.076637362	11933.64726	11845.82532	11418.69105	12261.91446	10699.61554	11519.60586	8.839407182	13.5427	13.5321	13.4791	13.5819	13.3853	13.4918	0.04025	0.04025	0.04243	0.04025	0.04025	0.04243	2	2	59
IPI00557327.1	20_kDa_protein	SHCAEPFTEYWTCLDYSSMQLFR	99.99917896	0.908474472	0.997658493	0.456464817	0.416332803	0.977979004	0.384065202	0.852220781	0.281526447	0.007825111	0.084693987	0.114634146	0.074256383	-1.007413746	-1.045097657	-1.115334211	1.073845891	-1.067205733	1.076637362	11933.64726	11845.82532	11418.69105	12261.91446	10699.61554	11519.60586	8.839407182	13.5427	13.5321	13.4791	13.5819	13.3853	13.4918	0.04025	0.04025	0.04243	0.04025	0.04025	0.04243	2	2	59
IPI00368806.3	PREDICTED:_similar_to_N-ethylmaleimide_sensitive_fusion_protein_attachment_protein_beta	LDQWLTTMLLR	99.99999984	0.312831382	0.997658493	0.99643308	0.898510823	0.977979004	0.533584354	0.191586185	0.62070943	0.991136357	0.763990916	0.613124313	0.204108375	1.029798242	-1.011415161	1.000247756	-1.006905412	1.011665745	-1.029757459	13504.88871	13907.31065	13352.46814	13260.89659	13508.23463	13117.87871	4.965398415	13.7212	13.7636	13.7048	13.6949	13.7216	13.6792	0.02264	0.02264	0.02386	0.02264	0.02264	0.02386	10	10	128
45476974	DDAH1_MOUSE_NG,NG-dimethylarginine_dimethylaminohydrolase_1_(Dimethylarginine_dimethylaminohydrolase_1)_(Dimethylarginine_	SFCSMAGPNLIAIGSSESAQK	100	0.218247419	0.997658493	0.99643308	0.666252843	0.977979004	0.994839219	0.109747274	0.951219758	0.588780172	0.299242705	0.641740096	0.982304027	-1.068105157	-1.002560526	-1.022270889	1.044585272	-1.019660023	1.000927606	14840.42535	13894.16132	14802.52311	15462.49762	14517.11627	14530.58244	9.072740984	13.8572	13.7622	13.8536	13.9165	13.8255	13.8268	0.04131	0.04131	0.04354	0.04131	0.04131	0.04354	5	8	119
IPI00194873.1	Isoform_D_of_Plasma_membrane_calcium-transporting_ATPase_1	YGDLLPADGILIQGNDLK	99.99996639	0.484170148	0.997658493	0.99643308	0.629509094	0.977979004	0.454871916	0.358773225	0.598294899	0.591722632	0.259717466	0.296125881	0.136994234	1.043618168	-1.025431123	1.025196915	-1.055465966	1.051268824	-1.074175574	11383.60248	11880.13437	11101.28435	10517.89893	11670.43414	10864.54991	10.33803267	13.4747	13.5363	13.4384	13.3606	13.5106	13.4073	0.04704	0.04704	0.04958	0.04704	0.04704	0.04958	4	5	64

SUPPLEMENTAL TABLE A. All priority 1 proteins measured in the nucleus accumbens shell of P, NP and W rats

IPI00368347.2	Similar_to_ubiquitin-protein_ligase_(EC_6.3.2.19)_E1-mouse	IYDDDFFQNLDGVANALDNVDAR	100	0.299218459	0.997658493	0.99643308	0.23197177	0.977979004	0.260206946	0.179189111	0.529068059	0.23413125	0.016428318	0.592885212	0.023208816	1.057590968	-1.027134377	-1.050748052	1.110449711	-1.022989859	1.103873596	12452.32471	13169.46615	12123.36476	13462.38689	11850.91392	13081.91097	9.214828472	13.6041	13.6849	13.5655	13.7166	13.5327	13.6753	0.04195	0.04195	0.04422	0.04195	0.04195	0.04422	11	13	22
37590235	Malate_dehydrogenase_1,_NAD_(soluble)_[Rattus_norvegicus]	VIVVGNPANTNCLTASK	99.99999997	0.135794857	0.997658493	0.99643308	0.879103848	0.977979004	0.377188892	0.05496783	0.810413706	0.209875769	0.721220998	0.324520703	0.066385245	-1.044873723	-1.005553983	-1.028792853	-1.008275244	-1.023110514	1.044016063	22206.45341	21252.76282	22083.80035	21902.55139	21584.96081	22535.0458	5.002554488	14.4387	14.3754	14.4307	14.4188	14.3977	14.4599	0.02281	0.02281	0.02404	0.02281	0.02281	0.02404	17	20	133
IPI00198291.1	Vacuolar_ATP_synthase_subunit_F	LIAVIGDEDTVTGFLLGGIGELNK	99.99999998	0.418994477	0.997658493	0.99643308	0.765226641	0.977979004	0.837394717	0.291141305	0.452093625	0.53332617	0.451791034	0.883514849	0.600840215	-1.038171734	1.027719387	1.02227294	1.027738297	-1.005327781	1.019179382	9793.989956	9433.882312	10065.47335	10344.67244	10012.13091	10204.15739	7.866881765	13.2577	13.2036	13.2971	13.3366	13.2895	13.3169	0.03583	0.03583	0.03777	0.03583	0.03583	0.03777	7	9	43
IPI00421832.1	Dermcidin	LGKDAVEDLESVGK	99.9986665	0.474076133	0.997658493	0.86359048	0.797906375	0.977979004	0.661535969	0.349461835	0.636965837	0.112889897	0.555485035	0.278634433	0.314048325	-1.077443091	1.039285232	1.135870255	-1.049344199	1.092934066	-1.086016176	8935.78617	8293.511043	9286.830602	8850.128117	10149.89371	9345.987604	17.80443664	13.1254	13.0178	13.181	13.1115	13.3092	13.1901	0.08059	0.08059	0.08495	0.08059	0.08059	0.08495	4	5	70
IPI00558079.2	PREDICTED:_similar_to_glyceraldehyde-3-phosphate_dehydrogenase	VIHDNFGIVEGLMTTVHAITATQK	99.99999992	0.194012633	0.998795589	0.99643308	0.725790696	0.977979004	0.673446244	0.093347793	0.997654108	0.405326186	0.387364863	0.41621424	0.3531468	1.048655178	1.000084364	-1.023591742	1.025204448	-1.023678096	1.027113832	19476.68169	20424.3231	19478.32482	19969.26525	19027.78314	19543.69926	6.220775436	14.2495	14.318	14.2496	14.2855	14.2158	14.2544	0.02835	0.02835	0.02989	0.02835	0.02835	0.02989	23	23	62
IPI00204641.1	PREDICTED:_similar_to_NADH_dehydrogenase_(ubiquinone)_1_beta_subcomplex,_9	QAEEEFWQNQHPQPYIFPDSPGGTSYER	99.99988611	0.370250272	0.997658493	0.99643308	0.607397898	0.977979004	0.837394717	0.241206717	0.173259323	0.871840128	0.234629131	0.129976864	0.597593071	-1.049052706	1.058976622	-1.006570175	-1.051169922	-1.065934283	1.022287029	17547.15098	16726.66291	18582.02267	17677.46801	17432.01565	17821.13687	9.050872272	14.0989	14.0299	14.1816	14.1096	14.0895	14.1213	0.04121	0.04121	0.04344	0.04121	0.04121	0.04344	3	3	103
IPI00764841.2	PREDICTED:_similar_to_solute_carrier_family_25_(mitochondrial_carrier;_adenine_nucleotide_translocator),_mer	GNLANVIR	99.9975958	0.26742745	0.997658493	0.99643308	0.911527876	0.977979004	0.537446148	0.148195299	0.39329291	0.529486218	0.811520246	0.807679754	0.208822812	1.226254004	-1.130771041	-1.091953927	-1.034811819	1.035548307	1.19924298	14999.38936	18393.06125	13264.74487	12818.50925	13736.28409	16473.14227	31.83862126	13.8726	14.1669	13.6953	13.6459	13.7457	14.0078	0.1418	0.1418	0.1494	0.1418	0.1418	0.1494	3	3	75
IPI00471901.3	Adaptor_protein_complex_AP-2,_alpha_2_subunit	VGGYILGEFGNLIAGDPR	99.99999992	0.131450262	0.997658493	0.99643308	0.279701276	0.977979004	0.611308062	0.051077816	0.57129083	0.896074998	0.03014168	0.660319171	0.271770099	1.053170197	-1.015301818	-1.003411004	1.061217146	1.011850392	1.030048389	13273.31177	13979.05637	13073.26702	13873.57512	13228.19036	13625.67617	5.805715678	13.6962	13.771	13.6743	13.7601	13.6913	13.734	0.02646	0.02646	0.0279	0.02646	0.02646	0.0279	13	13	78
IPI00364363.3	30_kDa_protein	YGKIETIEVMEDR	99.9964883	0.235579056	0.997658493	0.99643308	0.903404554	0.977979004	0.708668856	0.120616477	0.333283969	0.409689897	0.784671384	0.07999776	0.418168073	-1.047543539	1.029973213	-1.024765362	-1.008340114	-1.055480872	1.024985879	18934.06737	18074.73071	19501.5822	19340.28205	18476.49041	18938.14176	6.588679228	14.2087	14.1417	14.2513	14.2393	14.1734	14.209	0.03003	0.03003	0.03165	0.03003	0.03003	0.03165	4	4	103
IPI00777829.1	54_kDa_protein	LDIDSAPITAR	99.99999731	0.561364984	0.997658493	0.959908311	0.630797204	0.977979004	0.119761122	0.429845188	0.620767323	0.160389149	0.26257259	0.378424362	0.002851348	-1.063005427	-1.040050672	-1.115563181	1.093472496	-1.072604644	1.280285048	24351.04791	22907.7362	23413.32837	25601.8306	21828.47939	27946.67578	17.29846853	14.5717	14.4835	14.515	14.644	14.4139	14.7704	0.07834	0.07834	0.08258	0.07834	0.07834	0.08258	2	2	97
IPI00421428.6	Phosphoglycerate_mutase_1	YADLTEDQLPSCESLKDTIAR	99.99999941	0.564791543	0.997658493	0.99643308	0.797906375	0.977979004	0.343015874	0.434405381	0.391405735	0.751061987	0.552980582	0.245468745	0.043914349	1.032187991	-1.036355082	1.012908316	1.024980866	1.04973268	-1.089071484	15659.16418	16163.20122	15109.84454	15487.30154	15861.29761	14564.05556	9.010696391	13.9347	13.9804	13.8832	13.9188	13.9532	13.8301	0.04103	0.04103	0.04324	0.04103	0.04103	0.04324	10	20	126
IPI00199203.1	PREDICTED:_similar_to_glyceraldehyde-3-phosphate_dehydrogenase	DGRGAAQNIIPASTGAAK	99.99999835	0.923303688	0.998795589	0.99643308	0.271569898	0.977979004	0.119761122	0.875819498	0.996845953	0.609092753	0.026846973	0.615877296	0.002584621	1.010552319	1.000272814	-1.034987334	1.169362093	-1.035269693	1.242867492	17685.8012	17872.4274	17690.62612	20686.74759	17087.93973	21238.0448	15.03017863	14.1103	14.1254	14.1107	14.3364	14.0607	14.3744	0.06819	0.06819	0.07188	0.06819	0.06819	0.07188	3	5	38
IPI00363402.3	41_kDa_protein	LISWYDNEYGYSNR	100	0.164813431	0.997658493	0.99643308	0.71532686	0.977979004	0.686505831	0.073836417	0.715514532	0.867390545	0.368450512	0.598520698	0.375812906	-1.371494851	1.067362371	-1.029481282	-1.175154579	-1.098829582	1.172237884	28389.02245	20699.32849	30301.37431	25785.01148	27576.04527	32325.68495	40.21526353	14.793	14.3373	14.8871	14.6542	14.7511	14.9804	0.1766	0.1766	0.1862	0.1766	0.1766	0.1862	4	7	11
IPI00231819.5	myelin_basic_protein_isoform_1	YLATASTMDHAR	99.99999999	0.046230241	0.997658493	0.99643308	0.733834025	0.977979004	0.915790782	0.010702812	0.253677582	0.504749073	0.405978839	0.618862588	0.766799376	1.390578951	1.159140533	1.087245891	-1.113147245	-1.066125467	1.038879538	18557.15954	25805.19544	21510.3558	19323.90876	20176.19545	20960.6366	28.39477774	14.1797	14.6554	14.3927	14.2381	14.3004	14.3554	0.127	0.127	0.1339	0.127	0.127	0.1339	13	27	115
IPI00368053.2	Similar_to_RIKEN_cDNA_2700085E05	ESQSILTPLVSLDTPGK	99.99998485	0.384647147	0.997658493	0.99643308	0.71532686	0.977979004	0.979042717	0.253431988	0.635497642	0.410296319	0.36835586	0.741884364	0.920031557	-1.048253486	1.02019115	1.034452352	1.038777555	1.016378951	1.004238443	11653.78302	11117.33295	11889.0863	12350.116	12055.28325	12106.37888	9.143657869	13.5085	13.4405	13.5374	13.5922	13.5574	13.5635	0.04163	0.04163	0.04388	0.04163	0.04163	0.04388	2	2	43
IPI00464820.4	PREDICTED:_similar_to_neuronal_guanine_nucleotide_exchange_factor	NLIEQIGLLYQEYR	99.99973336	0.469115163	0.997658493	0.99643308	0.091880843	0.983633917	0.146792151	0.341576007	0.464392729	0.388132008	0.001580995	0.912812275	0.00658855	1.149788865	-1.116412192	-1.134915635	1.645738731	-1.016574025	1.526398779	10074.27207	11583.28585	9023.792595	14850.80498	8876.670438	13549.33892	33.39515428	13.2984	13.4998	13.1395	13.8583	13.1158	13.7259	0.1483	0.1483	0.1564	0.1483	0.1483	0.1564	2	2	109
IPI00231714.3	Dihydrolipoamide_S-acetyltransferase	VAPTPAGVFIDIPISNIR	99.99999943	0.047029537	0.997658493	0.99643308	0.903404554	0.977979004	0.359553375	0.011053281	0.562305944	0.764684511	0.774298177	0.772757928	0.059586421	-1.064196502	-1.014246558	-1.007129898	-1.007016831	1.007066278	-1.047827182	19354.49514	18186.95616	19082.63329	18949.66668	19217.47648	18340.31109	5.283157464	14.2404	14.1506	14.22	14.2099	14.2301	14.1627	0.02409	0.02409	0.02539	0.02409	0.02409	0.02539	11	11	134
113607	ALDOA_MOUSE_Fructose-bisphosphate_aldolase_A_(Muscle-type_aldolase)_(Aldolase_1)	FSNEEIAMATVTALR	100	0.469115163	0.997658493	0.99643308	0.875711929	0.977979004	0.42839358	0.342960351	0.161872689	0.94651412	0.705573611	0.14369031	0.110647942	-1.047713463	1.073580086	-1.003288301	-1.019189778	-1.077110341	1.084593074	18897.61057	18037.0027	20288.09839	19906.10465	18835.67321	20429.04071	10.92220425	14.2059	14.1387	14.3083	14.2809	14.2012	14.3183	0.04968	0.04968	0.05237	0.04968	0.04968	0.05237	30	47	90
IPI00471584.5	Heat_shock_protein_HSP_90-beta	NPDDITQEEYGEFYK	99.99999946	0.247086905	0.997658493	0.99643308	0.919964679	0.977979004	0.412212281	0.130201779	0.820032414	0.455274668	0.824657942	0.341063151	0.091393351	1.06991893	-1.010378946	1.033617341	-1.010106221	1.0443452	-1.080762241	15296.70774	16366.23718	15139.57491	14988.10184	15810.94238	14629.43632	9.851872296	13.9009	13.9984	13.886	13.8715	13.9486	13.8366	0.04484	0.04484	0.04726	0.04484	0.04484	0.04726	13	13	33
2137113	I49069_A+U-rich_RNA-binding_protein_-_mouse_(fragment)	IFVGGLSPDTPEEK	99.99999999	0.260209032	0.997658493	0.99643308	0.333651543	0.983712483	0.353175547	0.141851095	0.387401877	0.320679125	0.043968809	0.917382155	0.057315346	-1.065246791	1.038678362	1.043402743	-1.094047375	1.004548454	-1.08832006	14065.30378	13203.7983	14609.32669	13353.46807	14675.77654	13484.79834	9.496759249	13.7799	13.6887	13.8346	13.7049	13.8411	13.719	0.04323	0.04323	0.04557	0.04323	0.04323	0.04557	5	5	53
33516945	HNRPD_MOUSE_Heterogeneous_nuclear_ribonucleoprotein_D0_(hnRNP_D0)_(AU-rich_element_RNA-binding_	IFVGGLSPDTPEEK	99.99999999	0.260209032	0.997658493	0.99643308	0.333651543	0.983712483	0.353175547	0.141851095	0.387401877	0.320679125	0.043968809	0.917382155	0.057315346	-1.065246791	1.038678362	1.043402743	-1.094047375	1.004548454	-1.08832006	14065.30378	13203.7983	14609.32669	13353.46807	14675.77654	13484.79834	9.496759249	13.7799	13.6887	13.8346	13.7049	13.8411	13.719	0.04323	0.04323	0.04557	0.04323	0.04323	0.04557	5	5	53
IPI00230859.4	Alcohol_dehydrogenase	ILQNIQVFDFTFSPEEMK	100	0.741506034	0.997658493	0.795267491	0.808701932	0.757639751	0.998192766	0.638918876	0.58634021	0.049916495	0.572848351	0.015556134	0.997051975	1.01004338	1.011982457	-1.043419626	1.01242059	-1.055922357	-1.000080766	10441.33315	10546.19942	10566.44597	10697.68746	10006.8399	10006.03176	4.737148677	13.35	13.3644	13.3672	13.385	13.2887	13.2886	0.0216	0.0216	0.02277	0.0216	0.0216	0.02277	6	7	83
IPI00327830.2	Fatty_acid-binding_protein,_epidermal	KTETVCTFTDGALVQHQK	99.99993496	0.285594458	0.997658493	0.99643308	0.486148755	0.977979004	0.590127084	0.166361389	0.668281593	0.553359054	0.127787673	0.881550826	0.254201002	-1.031901273	-1.009954801	-1.013436792	1.036211634	-1.00344767	1.026855105	12552.76912	12164.69971	12429.04049	12879.11636	12386.33649	12718.97286	5.005680521	13.6157	13.5704	13.6014	13.6527	13.5965	13.6347	0.02282	0.02282	0.02406	0.02282	0.02282	0.02406	6	7	124
IPI00362452.2	PREDICTED:_similar_to_Glyceraldehyde-3-phosphate_dehydrogenase	LISWYDNEYGYSNR	100	0.270977138	0.997658493	0.99643308	0.990640456	0.977979004	0.519423329	0.152676262	0.868663067	0.77781415	0.982715332	0.660143291	0.190554158	-1.118660965	1.01327764	-1.022155248	1.001729437	-1.035727057	1.111011943	19696.82082	17607.4981	19958.34811	19992.86482	19269.8916	21409.07971	17.40518227	14.2657	14.1039	14.2847	14.2872	14.2341	14.3859	0.07881	0.07881	0.08308	0.07881	0.07881	0.08308	12	19	72
IPI00231900.4	Fatty_acid-binding_protein,_brain	LTDSQNFDEYMK	99.99930046	0.967209953	0.997658493	0.683449136	0.875711929	0.977979004	0.898633842	0.951734594	0.338419713	0.030462304	0.70429867	0.235879392	0.727123155	1.002093092	1.034714711	1.07948262	1.013569966	1.043265943	1.012468817	18580.96091	18619.85256	19225.9936	19486.88969	20057.82435	20307.92168	7.698471194	14.1815	14.1846	14.2308	14.2502	14.2919	14.3098	0.03507	0.03507	0.03697	0.03507	0.03507	0.03697	3	3	32
IPI00196202.1	NEDD8_precursor	TLTGKEIEIDIEPTDKVER	99.99953628	0.120487706	0.997658493	0.99643308	0.541686564	0.977979004	0.520988984	0.042923527	0.082089337	0.372749854	0.175815982	0.373393747	0.197065527	-1.09323134	-1.081381956	-1.039373066	1.062436301	1.040417528	1.059358186	9871.300468	9029.470804	9128.412414	9698.35672	9497.360273	10061.10635	9.626559385	13.269	13.1404	13.1561	13.2435	13.2133	13.2965	0.04382	0.04382	0.04619	0.04382	0.04382	0.04619	3	3	0
IPI00372183.3	PREDICTED:_similar_to_Heat_shock_70_kDa_protein_4L	GCALQCAILSPAFK	100	0.213661392	0.997658493	0.577998545	0.733834025	0.244428157	0.386695018	0.106433009	0.400228826	0.012632904	0.423469958	0.001454432	0.07701967	-1.069103385	1.036077427	-1.110791191	-1.034286751	-1.150865679	1.078297645	20094.78774	18795.92566	20819.75597	20129.57813	18090.51773	19506.96267	9.113288317	14.2945	14.1981	14.3457	14.297	14.1429	14.2517	0.04149	0.04149	0.04374	0.04149	0.04149	0.04374	4	5	0
IPI00211360.1	Synaptophysin	LHQVYFDAPSCVK	99.99970823	0.121895949	0.997658493	0.99643308	0.630431568	0.977979004	0.837394717	0.043870264	0.664691045	0.397772832	0.261539039	0.211218238	0.600787346	1.074304205	-1.01566234	1.030027674	1.041296196	1.046160318	-1.018946576	24100.16573	25890.90938	23728.52155	24708.41923	24823.83765	24362.25631	7.770661925	14.5568	14.6602	14.5343	14.5927	14.5994	14.5724	0.0354	0.0354	0.03731	0.0354	0.0354	0.03731	4	7	0
IPI00365985.4	93_kDa_protein	ELISNASDALDKIR	99.99995037	0.325822904	0.997658493	0.99643308	0.423679834	0.977979004	0.260206946	0.202196385	0.453439091	0.227333415	0.090546433	0.057256859	0.021319114	1.054263201	-1.032258972	1.051250969	1.075179044	1.085163245	-1.104937072	12034.52768	12687.55967	11658.43844	12534.9087	12651.30889	11449.80036	9.167181887	13.5549	13.6311	13.5091	13.6137	13.627	13.483	0.04174	0.04174	0.04399	0.04174	0.04174	0.04399	2	2	0
IPI00193721.1	Non-inducible_carbony_reductase	FHQLDIDNPQSIR	99.9936669	0.079206356	0.997658493	0.99643308	0.837948891	0.977979004	0.962983009	0.023025029	0.873179815	0.295378362	0.615772728	0.239739924	0.877371919	-1.161315776	1.010577914	-1.069818673	-1.033673339	-1.081135122	-1.01022354	21442.6061	18464.06166	21669.42413	20963.51266	20043.2154	19840.37652	14.34972055	14.3882	14.1724	14.4034	14.3556	14.2908	14.2762	0.06513	0.06513	0.06866	0.06513	0.06513	0.06866	2	3	0
IPI00189819.1	Actin,_cytoplasmic_1	SYELPDGQVITIGNER	100	0.153653791	0.997658493	0.99643308	0.544217174	0.977979004	0.838326544	0.067080855	0.540396828	0.695701121	0.178503233	0.322373553	0.607427462	1.076353846	-1.025222806	1.015593664	1.056672359	1.041209786	-1.021112154	20058.62106	21590.17392	19565.13348	20673.93575	20371.40844	19950.2164	8.814111868	14.2919	14.3981	14.256	14.3355	14.3143	14.2841	0.04013	0.04013	0.0423	0.04013	0.04013	0.0423	37	78	0
IPI00764461.1	PREDICTED:_similar_to_Actin,_cytoplasmic_2	SYELPDGQVITIGNER	100	0.153653791	0.997658493	0.99643308	0.544217174	0.977979004	0.838326544	0.067080855	0.540396828	0.695701121	0.178503233	0.322373553	0.607427462	1.076353846	-1.025222806	1.015593664	1.056672359	1.041209786	-1.021112154	20058.62106	21590.17392	19565.13348	20673.93575	20371.40844	19950.2164	8.814111868	14.2919	14.3981	14.256	14.3355	14.3143	14.2841	0.04013	0.04013	0.0423	0.04013	0.04013	0.0423	37	78	0
IPI00365600.2	cAMP-dependent_protein_kinase_type_II-beta_regulatory_subunit	NLDPEQMSQVLDAMFEK	100	0.942430729	0.997658493	0.99643308	0.792374134	0.977979004	0.429427724	0.912272946	0.75158455	0.470575383	0.527233695	0.309781926	0.111405821	1.00501297	1.01487707	-1.033374858	-1.029977973	-1.048748447	-1.078045164	11553.75265	11611.67127	11725.63863	11384.35864	11180.60166	10371.18113	10.1255257	13.4961	13.5033	13.5174	13.4748	13.4487	13.3403	0.04608	0.04608	0.04857	0.04608	0.04608	0.04857	15	18	0
IPI00212566.3	Isoform_3_of_Ras_GTPase-activating_protein_SynGAP	GKEEVASALVHILQSTGK	99.9919149	0.184798221	0.997658493	0.99643308	0.199585822	0.977979004	0.392793357	0.08616877	0.471138384	0.865057304	0.011192344	0.578087801	0.080803205	-1.122063335	1.050333217	1.011308434	-1.194758313	-1.038588409	-1.128016523	8709.974229	7762.462207	9148.375256	7657.092785	8808.470394	7808.813273	14.80324271	13.0885	12.9223	13.1593	12.9026	13.1047	12.9309	0.06717	0.06717	0.0708	0.06717	0.06717	0.0708	2	2	0
42542422	Heat_shock_protein_8_[Mus_musculus]	SQIHDIVLVGGSTR	100	0.292065533	0.997658493	0.99643308	0.719614739	0.977979004	0.666788291	0.171713038	0.893079225	0.297157925	0.380466774	0.37758784	0.326244179	-1.049501804	1.00484978	1.037398047	1.032191548	1.032391177	-1.036136803	21956.2296	20920.62111	22062.71248	22772.94534	22777.3497	21982.95595	7.807674875	14.4223	14.3526	14.4293	14.475	14.4753	14.4241	0.03557	0.03557	0.03749	0.03557	0.03557	0.03749	34	66	0
IPI00369383.3	PREDICTED:_similar_to_Nucleophosmin	GPSSVEDIK	99.9956818	0.126828827	0.997658493	0.99643308	0.706612353	0.977979004	0.761781252	0.048126142	0.969407979	0.806654753	0.355927695	0.782137999	0.488410609	-1.281230757	1.004859544	-1.030578707	-1.124315981	-1.035586849	1.091750686	14678.09362	11456.24513	14749.42246	13118.57406	14242.57413	15549.34007	27.9004454	13.8414	13.4838	13.8484	13.6793	13.7979	13.9246	0.1249	0.1249	0.1317	0.1249	0.1249	0.1317	2	2	0
IPI00208636.1	Glutathione_s-transferase_M5	FKLDLDFPNLPYLMDGK	99.99979619	0.859588437	0.997658493	0.99643308	0.521054574	0.977979004	0.81097989	0.779032721	0.460808236	0.308590412	0.158025168	0.797595551	0.552393159	1.01460884	-1.040036008	-1.054298118	-1.078610641	-1.013713092	-1.032101121	16613.62045	16856.32618	15974.08198	14809.8687	15757.99119	15267.87528	11.53651832	14.0201	14.041	13.9634	13.8543	13.9438	13.8982	0.05246	0.05246	0.0553	0.05246	0.05246	0.0553	2	2	0
IPI00393034.3	PREDICTED:_similar_to_Pyruvate_dehydrogenase_E1_component_alpha_subunit,_somatic_form,_mitochondrial	YHGHSMSDPGVSYR	99.99999871	0.052009711	0.997658493	0.99643308	0.691591891	0.988483763	0.391797307	0.01266065	0.407709449	0.436809309	0.330771502	0.942911256	0.083524919	-1.056327222	-1.018362641	-1.016766418	1.021632448	1.001569901	-1.039214502	18655.36918	17660.59683	18318.98426	17931.09086	18347.74325	17655.3957	4.747231695	14.1873	14.1082	14.1611	14.1302	14.1633	14.1078	0.02165	0.02165	0.02282	0.02165	0.02165	0.02282	13	15	0
4433295	mouse_PFK-M_[Mus_musculus]	IVEIVDAITTTAQSHQR	99.926397	0.126343985	0.997658493	0.99643308	0.940752994	0.983712483	0.948495187	0.047239148	0.659906768	0.730930043	0.873018779	0.9159466	0.846599704	1.09269204	-1.020030629	-1.015194419	1.007223406	1.004763826	1.008750636	9527.384983	10410.49773	9340.293037	9407.761763	9384.788568	9466.911437	9.776183983	13.2179	13.3458	13.1893	13.1996	13.1961	13.2087	0.04449	0.04449	0.0469	0.04449	0.04449	0.0469	3	3	0
IPI00231265.2	myelin_basic_protein_isoform_4	YLATASTMDHAR	99.99999999	0.052277618	0.997658493	0.99643308	0.733834025	0.977979004	0.900010096	0.012785612	0.263163805	0.532263959	0.426881736	0.60581626	0.73345925	1.409763892	1.167393918	1.087339096	-1.115798768	-1.073624522	1.047957494	21047.96538	29672.66159	24571.26675	22021.2349	22886.27566	23983.84409	30.45119038	14.3614	14.8568	14.5847	14.4266	14.4822	14.5498	0.1359	0.1359	0.1432	0.1359	0.1359	0.1432	10	21	0
203033	F1-ATPase_beta_subunit	DQEGQDVLLFIDNIFR	100	0.09136995	0.997658493	0.99643308	0.783271466	0.977979004	0.605003344	0.029342807	0.815284557	0.994155519	0.476229051	0.809758208	0.266201471	-1.088834123	1.009204883	-1.000279604	-1.028398084	-1.00948706	-1.044835937	22096.88029	20294.07402	22300.27948	21684.48175	22090.70365	21142.7487	8.508506904	14.4316	14.3088	14.4448	14.4044	14.4312	14.3679	0.03875	0.03875	0.04084	0.03875	0.03875	0.04084	22	52	0
IPI00365742.1	Adaptin_ear-binding_coat-associated_protein_1	ASGTGGLSLLPPPPGGK	99.99986226	0.052504436	0.997658493	0.99643308	0.682649423	0.977979004	0.977852791	0.012972646	0.307450799	0.718609393	0.319089845	0.500725701	0.909682482	-1.099633631	-1.039861807	-1.01346238	-1.038886819	1.02604875	1.004332364	19098.69545	17368.23511	18366.57074	17679.08726	18844.99694	18926.64032	8.26785505	14.2212	14.0842	14.1648	14.1098	14.2019	14.2081	0.03766	0.03766	0.03969	0.03766	0.03766	0.03969	5	5	0
IPI00363988.3	47_kDa_protein	IGAEVYHNLK	99.99995377	0.052921026	0.997658493	0.307157315	0.473411924	0.977979004	0.454871916	0.013184896	0.061164954	0.003443313	0.120111368	0.289608297	0.137043684	-1.090278345	-1.068451496	-1.108741859	1.056195055	-1.037709117	1.053638277	30290.90836	27782.72952	28350.28867	29943.43469	27320.07284	28785.47449	7.540556933	14.8866	14.7619	14.7911	14.87	14.7377	14.8131	0.03435	0.03435	0.03621	0.03435	0.03435	0.03621	5	8	0
IPI00778615.1	34_kDa_protein	LISWYDNEYGYSNR	100	0.253547667	0.997658493	0.99643308	0.784965667	0.977979004	0.670153176	0.136481087	0.623551439	0.977077994	0.479053333	0.603979673	0.336156568	-1.227813258	1.07126448	-1.003925465	-1.10450854	-1.075469691	1.14492928	19751.0293	16086.34634	21158.57613	19156.55277	19673.80049	22525.11023	31.05535578	14.2696	13.9735	14.369	14.2256	14.264	14.4592	0.1384	0.1384	0.1459	0.1384	0.1384	0.1459	4	5	0
IPI00332042.8	Retinal_dehydrogenase_1	REPIGVCGQIIPWNFPLLM	99.99973107	0.473017345	0.997658493	0.99643308	0.984163624	0.977979004	0.862332749	0.347600175	0.972497909	0.288240244	0.962931425	0.285571306	0.656358412	1.038188764	1.001408282	-1.043338416	-1.001898929	-1.044807731	-1.018346292	10701.34686	11110.01807	10716.41738	10696.10624	10256.83201	10072.04729	8.858820178	13.3855	13.4396	13.3875	13.3848	13.3243	13.2981	0.04034	0.04034	0.04252	0.04034	0.04034	0.04252	2	2	0
IPI00209828.5	PREDICTED:_similar_to_Myosin_regulatory_light_chain_2,_smooth_muscle_isoform	ATSNVFAMFDQSQIQEFK	99.99975965	0.750019037	0.997658493	0.795267491	0.679460331	0.977979004	0.603463344	0.650587942	0.593954925	0.054487018	0.31530353	0.173961975	0.264834199	-1.023550184	1.028558782	1.105744496	-1.054667388	1.07504259	-1.060955965	9822.14547	9596.15427	10102.65398	9578.995322	10860.7833	10236.78989	11.46219705	13.2618	13.2282	13.3024	13.2257	13.4068	13.3215	0.05212	0.05212	0.05494	0.05212	0.05212	0.05494	2	2	0
IPI00231118.4	Calbindin	ELQNLIQELLQAR	99.99996352	0.395716721	0.997658493	0.99643308	0.117623759	0.977979004	0.149954502	0.266373884	0.194972449	0.416517998	0.002763561	0.608208163	0.007722135	-1.055443745	1.06693044	1.040119734	-1.167744909	-1.025776557	-1.146555221	13690.88619	12971.68727	14607.22322	12508.91621	14240.16089	12419.95207	10.77053101	13.7409	13.6631	13.8344	13.6107	13.7977	13.6004	0.049	0.049	0.05165	0.049	0.049	0.05165	5	5	0
IPI00197696.1	Malate_dehydrogenase,_mitochondrial_precursor	VAVLGASGGIGQPLSLLLK	100	0.596143063	0.997658493	0.846402451	0.333651543	0.977979004	0.119761122	0.46745063	0.599227705	0.098189786	0.044613978	0.271992577	0.003843494	1.026505948	-1.01960422	-1.062028666	1.078495126	-1.04160874	1.117529534	25597.82867	26276.32339	25105.65194	27076.32324	24102.76622	26935.5531	8.00412069	14.6437	14.6815	14.6157	14.7247	14.5569	14.7172	0.03646	0.03646	0.03843	0.03646	0.03646	0.03843	25	34	0
IPI00566583.1	Malate_dehydrogenase,_mitochondrial	VAVLGASGGIGQPLSLLLK	100	0.596143063	0.997658493	0.846402451	0.333651543	0.977979004	0.119761122	0.46745063	0.599227705	0.098189786	0.044613978	0.271992577	0.003843494	1.026505948	-1.01960422	-1.062028666	1.078495126	-1.04160874	1.117529534	25597.82867	26276.32339	25105.65194	27076.32324	24102.76622	26935.5531	8.00412069	14.6437	14.6815	14.6157	14.7247	14.5569	14.7172	0.03646	0.03646	0.03843	0.03646	0.03646	0.03843	25	34	0
IPI00189722.1	Tropomodulin-2	SNDPVALAFAEMLK	99.99999946	0.616419765	0.997658493	0.846402451	0.796416454	0.977979004	0.927911986	0.490317893	0.528042226	0.090386429	0.534323894	0.301241206	0.803599688	-1.019763697	1.018556209	1.049807481	1.018270903	1.030681932	-1.007260842	14567.12437	14284.80383	14837.43498	15108.52831	15292.67614	15182.43885	6.305392208	13.8304	13.8022	13.857	13.8831	13.9006	13.8901	0.02874	0.02874	0.03029	0.02874	0.02874	0.03029	6	6	0
IPI00211024.3	Solute_carrier_family_12_member_5	NGDENYMEFLEVLTEQLDR	100	0.296542966	0.997658493	0.99643308	0.686643596	0.977979004	0.535693726	0.177247967	0.806486781	0.298785517	0.325272351	0.441656859	0.206930834	-1.06447964	1.011622897	1.049113518	-1.047712723	1.037059878	-1.061816877	9090.732426	8540.071678	9196.393069	8777.590331	9537.210274	8981.972766	10.24165765	13.1502	13.06	13.1669	13.0996	13.2194	13.1328	0.0466	0.0466	0.04912	0.0466	0.0466	0.04912	4	4	0
IPI00764212.1	PREDICTED:_similar_to_nuclear_membrane_binding_protein_NUCLING	ELEGQLK	93.7266	0.394040776	0.997658493	0.99643308	0.966345081	0.977979004	0.613231168	0.263444404	0.564343697	0.205194037	0.924378095	0.506688232	0.274169734	1.052987351	-1.027593786	-1.060343915	1.00448552	-1.031870696	1.053225045	17738.67794	18678.60348	17262.34449	17339.77507	16729.17407	17619.58511	10.23887349	14.1146	14.1891	14.0753	14.0818	14.0301	14.1049	0.04659	0.04659	0.04911	0.04659	0.04659	0.04911	2	2	0
IPI00392259.2	28_kDa_protein	LISWYDNEYGYSNR	100	0.156373688	0.997658493	0.99643308	0.733834025	0.977979004	0.725884166	0.068983136	0.726863975	0.854518633	0.424194839	0.597992005	0.442167155	-1.344289109	1.059171888	-1.029794297	-1.140943602	-1.090729169	1.135159347	40950.08813	30462.26281	43373.18214	38015.18505	39765.30873	45139.96189	36.78746189	15.3216	14.8947	15.4045	15.2143	15.2792	15.4621	0.1625	0.1625	0.1713	0.1625	0.1625	0.1713	2	3	0
IPI00200773.1	Skeletal_muscle-specific_alpha-actinin_3	LMLLLEVISGER	99.9984143	0.440557624	0.997658493	0.99643308	0.243213193	0.977979004	0.241480862	0.310728179	0.16815059	0.318161061	0.019203017	0.678669918	0.0176626	1.055338342	-1.078481451	-1.054463828	1.139563093	1.022777095	1.141648139	12999.99887	13719.39726	12053.98466	13736.27605	12328.53941	14074.85408	11.80608325	13.6662	13.7439	13.5572	13.7457	13.5897	13.7808	0.05368	0.05368	0.05658	0.05368	0.05368	0.05658	2	2	0
IPI00195673.1	Tubulin,_beta_6	GHYTEGAELVDSVLDVVRK	100	0.140204014	0.997658493	0.99643308	0.606111691	0.977979004	0.979161445	0.058691237	0.893734693	0.669219451	0.233439589	0.583017958	0.923092362	1.10289783	1.007012308	-1.022008699	1.064769166	-1.029175339	-1.005054974	24234.39378	26728.06031	24404.33282	25984.98109	23712.51224	23593.24897	11.36620565	14.5648	14.7061	14.5748	14.6654	14.5334	14.5261	0.05169	0.05169	0.05448	0.05169	0.05169	0.05448	19	44	0
IPI00763398.1	PREDICTED:_similar_to_Zinc_finger_protein_469	CILDKPPK	90.1178	0.636782192	0.997658493	0.99643308	0.813181576	0.977979004	0.482325939	0.516703265	0.194904936	0.744295118	0.581203155	0.324843923	0.15544676	1.038604889	-1.081415259	-1.019206377	1.033641179	1.06103659	-1.089719899	12389.50182	12867.79716	11456.74773	11842.16623	12156.02855	11155.18636	13.02763999	13.5968	13.6515	13.4839	13.5316	13.5694	13.4454	0.05918	0.05918	0.06239	0.05918	0.05918	0.06239	2	2	0
IPI00567818.2	41_kDa_protein	LISWYDNEYGYSNR	100	0.530460136	0.997658493	0.99643308	0.83893122	0.977979004	0.369763067	0.402543463	0.736256365	0.741061893	0.62230539	0.510907064	0.063387954	-1.047650484	1.019373891	-1.018492254	1.02847854	-1.038224412	1.113486544	18126.1364	17301.70194	18477.31019	19003.51701	17797.02921	19816.75256	12.38007737	14.1458	14.0786	14.1735	14.214	14.1193	14.2744	0.05627	0.05627	0.05931	0.05627	0.05627	0.05931	12	21	0
26345918	unnamed_protein_product_[Mus_musculus]	NPDDITNEEYGEFYK	99.99999976	0.277550879	0.997658493	0.99643308	0.607960717	0.977979004	0.45250857	0.1579661	0.832350761	0.572832413	0.236930977	0.735535207	0.126862692	1.059776818	1.008898007	1.023264895	-1.051081489	1.014240179	-1.066730902	17529.06332	18576.89495	17685.03704	16825.56227	17936.87513	16814.80785	9.080856775	14.0975	14.1812	14.1102	14.0384	14.1306	14.0374	0.04134	0.04134	0.04358	0.04134	0.04134	0.04358	16	16	0
IPI00207201.1	Disks_large_homolog_1	ILAGGPADLSGELR	99.99999985	0.208340764	0.997658493	0.99643308	0.855934899	0.977979004	0.469196089	0.102860812	0.580158627	0.473078554	0.665863393	0.883843045	0.145347841	-1.096265353	-1.032163771	-1.040818247	1.025007313	-1.00838479	1.087711684	11774.01902	10740.11779	11407.12294	11692.38443	11312.27191	12304.49032	12.42530622	13.5233	13.3907	13.4776	13.5133	13.4656	13.5869	0.05647	0.05647	0.05952	0.05647	0.05647	0.05952	2	2	0
IPI00231677.4	14-3-3_protein_eta	NSVVEASEAAYK	99.99999958	0.576115962	0.997658493	0.99643308	0.972747387	0.977979004	0.418299862	0.447724405	0.671236298	0.950643455	0.934949202	0.628016936	0.094061326	1.026344915	-1.015019266	1.002116452	1.002868339	1.017167506	-1.061372214	11691.93552	11999.95856	11518.92965	11551.96985	11716.68094	11039.18191	7.61174042	13.5132	13.5507	13.4917	13.4959	13.5163	13.4303	0.03468	0.03468	0.03655	0.03468	0.03468	0.03655	16	28	0
56206607	novel_protein_similar_to_stathmin_1_Stmn1_[Mus_musculus]	ASGQAFELILSPR	99.9999015	0.469115163	0.997658493	0.99643308	0.149698425	0.977979004	0.811601962	0.341607642	0.159268994	0.707338154	0.005397083	0.078395941	0.555599155	-1.025961293	-1.039956089	1.010131777	1.082932523	1.050492692	1.016408889	14365.02522	14001.52747	13813.10747	14958.66332	14510.56845	14748.67076	5.976535859	13.8103	13.7733	13.7538	13.8687	13.8248	13.8483	0.02724	0.02724	0.02872	0.02724	0.02724	0.02872	5	5	0
IPI00199394.2	2',3'-cyclic-nucleotide_3'-phosphodiesterase	ATGAEEYAQQDVVR	100	0.215362902	0.997658493	0.99643308	0.467884871	0.977979004	0.764419202	0.107804516	0.433063478	0.93154346	0.113686825	0.483294738	0.492563831	1.130278858	1.062633726	1.006481091	-1.131689345	-1.055791048	1.054577943	11134.8063	12585.43615	11832.22071	10455.36106	11206.972	11818.62547	16.85253245	13.4428	13.6195	13.5304	13.352	13.4521	13.5288	0.07635	0.07635	0.08048	0.07635	0.07635	0.08048	30	45	0
IPI00211593.1	Superoxide_dismutase_[Mn],_mitochondrial_precursor	GDVTTQVALQPALK	100	0.795684045	0.997658493	0.929766668	0.638878253	0.773591433	0.837394717	0.702930019	0.328005304	0.134948991	0.273392507	0.017023142	0.595841273	1.010202209	1.027216971	-1.041012626	-1.030562428	-1.069345837	-1.014619125	19712.0459	19913.15232	20248.54809	19648.05579	18935.45324	18662.62203	5.924001076	14.2668	14.2814	14.3055	14.2621	14.2088	14.1879	0.027	0.027	0.02846	0.027	0.027	0.02846	3	4	0
IPI00389152.4	PREDICTED:_similar_to_cytochrome_c_oxidase,_subunit_VIb_polypeptide_1	SLCPVSWVSAWDDR	99.99999996	0.126607778	0.997658493	0.99643308	0.656666972	0.977979004	0.735808484	0.04761521	0.863021652	0.721830856	0.291175903	0.604034313	0.461314972	-1.082228331	-1.006962647	1.014039937	-1.043598123	1.021100338	-1.030146121	30253.07042	27954.42472	30043.88545	28788.74998	30677.8216	29780.06806	8.726151994	14.8848	14.7708	14.8748	14.8132	14.9049	14.8621	0.03973	0.03973	0.04188	0.03973	0.03973	0.04188	5	5	0
IPI00213571.1	Isoform_1_of_Cytosolic_acyl_coenzyme_A_thioester_hydrolase	LMDEVAGIVAAR	99.935347	0.533151891	0.997658493	0.99643308	0.486148755	0.977979004	0.168325627	0.405195437	0.930558709	0.593223543	0.126064384	0.544047062	0.010003352	-1.035696312	1.003767078	-1.022718105	-1.069040428	-1.026570764	-1.121652759	26254.84454	25349.94499	26353.74858	24651.77919	25671.63366	22887.32717	9.365918253	14.6803	14.6297	14.6857	14.5894	14.6479	14.4823	0.04264	0.04264	0.04494	0.04264	0.04264	0.04494	2	2	0
IPI00358767.2	PREDICTED:_similar_to_SH3-domain_GRB2-like_2	ALYDFEPENEGELGFK	99.99999933	0.343397384	0.997658493	0.99643308	0.342215144	0.977979004	0.993109576	0.217812055	0.425073215	0.656539079	0.051584934	0.71389756	0.959514828	-1.043528664	-1.028614121	-1.015393861	1.072419161	1.013019835	1.001791526	18004.36927	17253.35383	17503.52138	18771.11172	17731.41434	17763.18063	7.648508778	14.1361	14.0746	14.0954	14.1962	14.114	14.1166	0.03484	0.03484	0.03673	0.03484	0.03484	0.03673	14	16	0
IPI00203358.1	Isoform_Gamma-1_of_Serine/threonine-protein_phosphatase_PP1-gamma_catalytic_subunit	EIFLSQPILLELEAPLK	99.99988757	0.647454701	0.997658493	0.846402451	0.377717662	0.996058404	0.516390929	0.526103191	0.098281075	0.087933149	0.067824585	0.992644705	0.188147156	1.032478664	-1.090474447	-1.090994267	1.100708978	-1.000476691	1.071021473	11141.04638	11502.89267	10216.69642	11245.60947	10211.82852	10937.08763	11.23276942	13.4436	13.4897	13.3186	13.4571	13.318	13.4169	0.05109	0.05109	0.05385	0.05109	0.05109	0.05385	3	3	0
IPI00781570.2	Pgam1_protein	YADLTEDQLPSCESLKDTIAR	99.99999941	0.627250404	0.997658493	0.99643308	0.86551567	0.977979004	0.343015874	0.505445295	0.423090143	0.735025815	0.686477571	0.260074506	0.045088419	1.024761645	-1.030720968	1.012488619	1.015327406	1.04359325	-1.079984615	15993.59377	16389.62146	15516.89958	15754.7334	16193.33167	14994.03922	8.169653747	13.9652	14.0005	13.9216	13.9435	13.9831	13.8721	0.03721	0.03721	0.03922	0.03721	0.03721	0.03922	13	23	0
IPI00365813.3	PREDICTED:_similar_to_Voltage-dependent_anion-selective_channel_protein_1	VTQSNFAVGYK	99.99995854	0.384647147	0.997658493	0.99643308	0.733834025	0.977979004	0.348219477	0.255845302	0.660200506	0.314457009	0.406521391	0.1584653	0.052929361	1.086725223	-1.033431736	1.076298413	-1.064213791	1.112280937	-1.158709235	12215.34587	13274.72446	11820.17684	11106.95703	13147.35737	11346.5544	16.29316514	13.5764	13.6964	13.529	13.4392	13.6825	13.47	0.07385	0.07385	0.07784	0.07385	0.07385	0.07784	4	5	0
IPI00209836.4	Paralemmin	EIDVLEFGESAPAAPK	99.9998932	0.309826607	0.997658493	0.99643308	0.367357043	0.977979004	0.260206946	0.186604139	0.979225917	0.304702314	0.061228434	0.330245793	0.021924031	-1.066561614	1.00129517	1.051179348	-1.099268768	1.049819653	-1.123976728	15617.64782	14642.98697	15637.87533	14225.70693	16416.94885	14606.12879	10.79766339	13.9309	13.8379	13.9328	13.7962	14.0029	13.8343	0.04912	0.04912	0.05178	0.04912	0.04912	0.05178	6	6	0
IPI00193151.1	Dihydropteridine_reductase	MTDSFTEQADQVTAEVGK	99.99999174	0.313726202	0.997658493	0.99643308	0.189267082	0.977979004	0.43434326	0.192538252	0.123013099	0.253301435	0.009950041	0.659347032	0.113177444	1.052206117	1.064051861	1.045532671	-1.111777468	-1.017712684	-1.065888218	16717.58358	17590.3437	17788.37593	15999.94283	17478.77982	16398.32351	8.635044219	14.0291	14.1025	14.1186	13.9658	14.0933	14.0013	0.03932	0.03932	0.04145	0.03932	0.03932	0.04145	4	4	0
IPI00213735.2	Sideroflexin-1	NILLTNEQLENAR	99.99927893	0.397080303	0.997658493	0.99643308	0.855934899	0.977979004	0.609075496	0.268653188	0.705652967	0.864444756	0.666727054	0.832320146	0.270081477	-1.059377999	1.020333155	1.008890051	-1.023221044	-1.011342271	1.060864317	13162.90455	12425.12545	13430.54793	13125.75422	13279.92344	14088.19691	11.57394323	13.6842	13.601	13.7132	13.6801	13.697	13.7822	0.05263	0.05263	0.05547	0.05263	0.05263	0.05547	2	2	0
54041237	KAP3_MOUSE_cAMP-dependent_protein_kinase_type_II-beta_regulatory_subunit	NLDPEQMSQVLDAMFEK	100	0.887674197	0.997658493	0.99643308	0.813181576	0.977979004	0.453898305	0.812602322	0.726185261	0.528773066	0.582261104	0.336871519	0.134872639	1.010989583	1.016731657	-1.029514497	-1.02642986	-1.046739981	-1.07419859	11523.56893	11650.20815	11716.37734	11414.68872	11193.20706	10420.05376	10.28373272	13.4923	13.5081	13.5162	13.4786	13.4503	13.3471	0.04679	0.04679	0.04932	0.04679	0.04679	0.04932	14	17	0
26341378	unnamed_protein_product_[Mus_musculus]	DFLPLYFGWFLTK	99.99999998	0.178185015	0.997658493	0.997244055	0.555941486	0.977979004	0.761781252	0.082270567	0.505518584	0.996104348	0.187431701	0.502505089	0.487646096	1.141116864	1.052659668	-1.000365569	-1.107654775	-1.053044488	1.05496278	9756.858588	11133.71587	10270.65153	9272.430145	9753.293091	10289.36119	16.77508965	13.2522	13.4426	13.3262	13.1787	13.2517	13.3289	0.076	0.076	0.08011	0.076	0.076	0.08011	17	24	0
IPI00212741.7	6-phosphofructokinase,_liver_type	LPLMECVQVTK	99.99969015	0.283070069	0.997658493	0.99643308	0.792374134	0.977979004	0.38112535	0.162823304	0.900296913	0.379434232	0.521618858	0.464466124	0.070345189	-1.12052434	-1.010451562	-1.07385782	-1.054730544	-1.062750418	1.164843232	19221.82089	17154.3091	19023.00082	18035.88692	17899.78201	20850.43994	18.12001642	14.2305	14.0663	14.2155	14.1386	14.1277	14.3478	0.082	0.082	0.08644	0.082	0.082	0.08644	2	2	0
55153885	Similar_to_glyceraldehyde-3-phosphate_dehydrogenase_[Mus_musculus]	LISWYDNEYGYSNR	100	0.335170349	0.997658493	0.99643308	0.974820419	0.977979004	0.426572047	0.211061557	0.883121321	0.598036062	0.944306567	0.509580414	0.106756626	-1.059680293	1.006972562	-1.02458175	1.003306976	-1.03172571	1.080255622	20858.79311	19684.04363	21004.23234	21073.69282	20358.34925	21992.22124	10.26317712	14.3484	14.2647	14.3584	14.3632	14.3133	14.4247	0.0467	0.0467	0.04923	0.0467	0.0467	0.04923	28	45	0
IPI00231358.5	Profilin-1	TFVSITPAEVGVLVGK	99.9999995	0.409342926	0.997658493	0.99643308	0.797906375	0.988483763	0.38112535	0.281655662	0.198148518	0.213244566	0.541949471	0.938949469	0.070998208	-1.027262833	1.033665627	1.031646805	-1.015716861	-1.001956892	-1.047935219	14890.26116	14495.0841	15391.55113	15153.38745	15361.49035	14658.81676	5.532797129	13.8621	13.8233	13.9099	13.8874	13.907	13.8395	0.02522	0.02522	0.02659	0.02522	0.02522	0.02659	4	4	0
IPI00421874.3	Voltage-dependent_anion-selective_channel_protein_1	GALVLGYEGWLAGYQMNFETSK	99.99999989	0.267835528	0.997658493	0.99643308	0.911527876	0.977979004	0.587595758	0.1493757	0.482659602	0.468705939	0.811162674	0.162281253	0.247924531	1.082926602	-1.040341733	1.040537455	-1.013522212	1.082514539	-1.067540315	13277.76924	14378.84952	12762.89206	12592.61209	13816.01621	12941.91519	12.21830859	13.6967	13.8117	13.6397	13.6203	13.7541	13.6598	0.05554	0.05554	0.05854	0.05554	0.05554	0.05854	12	15	0
47132509	septin_5_[Mus_musculus]	MESPIPILPLPTPDAETEK	99.99999929	0.956183718	0.997658493	0.739211837	0.486148755	0.977979004	0.569356066	0.93432809	0.752790259	0.041395863	0.12637071	0.091567808	0.234307125	-1.003535574	-1.01396274	-1.093238624	1.070399132	-1.078184218	1.054109137	13383.33177	13336.18071	13199.03704	14128.23779	12241.91267	12904.31201	9.552838704	13.7081	13.7031	13.6881	13.7863	13.5795	13.6556	0.04348	0.04348	0.04584	0.04348	0.04348	0.04584	9	9	0
IPI00197123.1	Isoform_Long_of_Hyaluronan_and_proteoglycan_link_protein_1_precursor	QACLDQDAVIASFDQLYDAWR	99.9985801	0.441916625	0.997658493	0.991204521	0.507654338	0.977979004	0.670153176	0.312624447	0.278179094	0.186421902	0.150265684	0.836568743	0.336720451	1.054304009	-1.060131561	-1.071907644	1.080908953	-1.011108133	1.053023552	9794.677046	10326.56727	9239.114656	9986.641749	9137.612833	9622.121522	11.63596776	13.2578	13.3341	13.1735	13.2858	13.1576	13.2321	0.05291	0.05291	0.05577	0.05291	0.05291	0.05577	2	2	0
IPI00215093.1	Similar_to_oxoglutarate_dehydrogenase	FLDTAFDLDAFKK	99.987576	0.068127065	0.997658493	0.99643308	0.63922298	0.977979004	0.808612793	0.018219124	0.984491224	0.235317088	0.277024904	0.255763887	0.544311926	1.092833318	1.000730954	1.044688072	1.041951925	1.043925011	-1.023093955	5675.70971	6202.604674	5679.85839	5918.139382	5929.346232	5795.505097	8.155342995	12.4706	12.5987	12.4716	12.5309	12.5337	12.5007	0.03714	0.03714	0.03915	0.03714	0.03714	0.03915	2	2	0
IPI00554039.1	PREDICTED:_similar_to_glyceraldehyde-3-phosphate_dehydrogenase	LISWYDNEYGYSNR	100	0.312831382	0.997658493	0.99643308	0.998662363	0.977979004	0.45250857	0.191631567	0.772431857	0.615926138	0.997785303	0.437812398	0.128704327	-1.053982943	1.011940248	-1.020258307	-1.000113885	-1.032440445	1.065061621	18960.68137	17989.55239	19187.07662	19184.89175	18584.197	19793.31498	8.903905001	14.2107	14.1349	14.2278	14.2277	14.1818	14.2727	0.04054	0.04054	0.04273	0.04054	0.04054	0.04273	44	72	0
IPI00210641.2	10_kDa_protein	FQYDSTHGKFNGTVK	97.7234	0.135794857	0.997658493	0.99643308	0.797906375	0.988483763	0.959191605	0.055093913	0.673792828	0.700855222	0.555832647	0.962416019	0.866443518	-1.425358796	1.081727254	1.072264146	-1.116300489	-1.008825351	-1.031860355	8599.811995	6033.436645	9302.651016	8333.464968	9221.270068	8936.548458	42.09225267	13.0701	12.5588	13.1834	13.0247	13.1707	13.1255	0.1843	0.1843	0.1942	0.1843	0.1843	0.1942	2	2	0
IPI00200391.1	Serine/threonine-protein_phosphatase_2A_catalytic_subunit_alpha_isoform	ELDQWIEQLNECK	99.99996953	0.292178655	0.997658493	0.99643308	0.090063224	0.977979004	0.146792151	0.173303682	0.430550425	0.806958044	0.001160605	0.581009968	0.005916552	-1.035369159	1.020761292	1.006202351	-1.093007767	-1.014469198	-1.077068706	28914.42672	27926.6834	29514.72757	27003.2185	29093.76414	27011.98537	5.63394179	14.8195	14.7694	14.8491	14.7208	14.8284	14.7213	0.02568	0.02568	0.02707	0.02568	0.02568	0.02707	2	2	0
IPI00191913.1	NADH_dehydrogenase_(Ubiquinone)_flavoprotein_1	GAGAYICGEETALIESIEGK	99.9941483	0.414926456	0.997658493	0.99643308	0.706612353	0.977979004	0.894800678	0.286892007	0.490788911	0.210076822	0.359429268	0.590664309	0.717418813	1.079157269	-1.051774825	-1.094007288	1.069570376	-1.040153521	1.026822226	14494.65632	15642.01373	13781.14019	14739.8993	13249.14054	13604.51199	15.93092166	13.8232	13.9331	13.7504	13.8474	13.6936	13.7318	0.07223	0.07223	0.07613	0.07223	0.07223	0.07613	2	2	0
IPI00476899.1	PREDICTED:_similar_to_eukaryotic_translation_elongation_factor_1_beta_2	SSILLDVKPWDDETDMTKLEECVR	99.9999871	0.6520394	0.997658493	0.99643308	0.407868352	0.977979004	0.730123281	0.531318963	0.93939157	0.641465316	0.075047777	0.596787071	0.452905514	-1.032784478	-1.004026113	1.024265146	1.100245654	1.028388953	1.040573123	12060.02479	11677.19408	12011.66446	13215.78163	12352.66305	12853.84916	11.48339579	13.5579	13.5114	13.5521	13.69	13.5925	13.6499	0.05222	0.05222	0.05504	0.05222	0.05222	0.05504	2	2	0
225480	1304282A_tubulin_Mbeta_1	KLAVNMVPFPR	99.99999995	0.908474472	0.997658493	0.991204521	0.69806763	0.867565465	0.713885578	0.851597255	0.381137944	0.183910751	0.33906142	0.032719612	0.428238762	1.006354624	1.031047706	-1.04641841	1.033963946	-1.078907301	1.028023906	30433.93128	30627.32746	31378.83504	32444.58411	29083.90277	29898.94731	7.544393103	14.8934	14.9025	14.9375	14.9857	14.8279	14.8678	0.03437	0.03437	0.03623	0.03437	0.03437	0.03623	7	9	0
IPI00191130.1	Synaptotagmin-5	MDVGGLSDPYVK	99.99926702	0.062108055	0.997658493	0.99643308	0.792374134	0.977979004	0.69561724	0.016467507	0.786782935	0.238540593	0.505893702	0.378284369	0.384050621	1.09822408	1.010614937	1.046101179	1.026356745	1.035113515	-1.034680453	15438.51197	16954.94559	15602.39079	16013.61902	16150.24557	15608.92112	8.467384368	13.9142	14.0494	13.9295	13.967	13.9793	13.9301	0.03856	0.03856	0.04065	0.03856	0.03856	0.04065	2	2	0
IPI00471835.1	Heat-shock_protein_105_kDa	LLTETEDWLYEEGEDQAK	100	0.280530761	0.997658493	0.99643308	0.615789539	0.977979004	0.931974488	0.160623898	0.816147969	0.989645736	0.243500778	0.806361093	0.813746867	-1.031050831	-1.005171446	1.000280196	1.026380895	1.005453092	1.005240457	9863.197068	9566.159851	9812.452497	10071.31377	9865.960701	9917.662845	4.806819816	13.2678	13.2237	13.2604	13.298	13.2682	13.2758	0.02192	0.02192	0.0231	0.02192	0.02192	0.0231	10	10	0
1000439	grp75_[Rattus_sp.]	VQQTVQDLFGR	99.99999982	0.083970664	0.997658493	0.99643308	0.903404554	0.977979004	0.985692829	0.025623048	0.8571772	0.640793939	0.78445735	0.783679806	0.944012103	-1.060083533	-1.004729508	-1.011988607	1.007198186	-1.007224929	1.001842668	16205.00836	15286.53908	16128.72742	16244.825	16013.03439	16042.5411	5.682412244	13.9842	13.9	13.9773	13.9877	13.967	13.9696	0.0259	0.0259	0.0273	0.0259	0.0259	0.0273	16	19	0
202837	aldolase_A	FSNEEIAMATVTALR	100	0.454985324	0.997658493	0.99643308	0.868162741	0.977979004	0.426869209	0.32706945	0.182812933	0.685313952	0.694027373	0.086578459	0.109766368	-1.050345845	1.071296152	-1.020437512	-1.020383227	-1.09319078	1.086535672	18744.17559	17845.71785	20080.56317	19679.43282	18368.76375	19958.31706	11.13588706	14.1942	14.1233	14.2935	14.2644	14.165	14.2847	0.05065	0.05065	0.05339	0.05065	0.05065	0.05339	33	52	0
IPI00201444.1	Dynein_light_chain_1,_cytoplasmic	YNPTWHCIVGR	99.99996897	0.138396984	0.997658493	0.99643308	0.554634429	0.977979004	0.670153176	0.057021032	0.865503114	0.713889423	0.1857233	0.851141163	0.344650205	-1.075392759	1.006552009	1.013861899	-1.052800518	1.007262307	-1.037268536	15213.24065	14146.68317	15312.91794	14544.93769	15424.12505	14869.94401	8.364976187	13.893	13.7882	13.9025	13.8282	13.9129	13.8601	0.0381	0.0381	0.04016	0.0381	0.0381	0.04016	4	6	0
IPI00192409.1	Glyceraldehyde-3-phosphate_dehydrogenase_type_2	VPTPNVSVVDLTCR	100	0.439123468	0.997658493	0.846402451	0.618473049	0.977979004	0.119761122	0.309142921	0.411861902	0.08560016	0.245975567	0.383775671	0.003969226	-1.045116712	-1.037193337	-1.078199875	1.053163086	-1.03953606	1.142347053	27893.53185	26689.39414	26893.28099	28323.01081	25870.46474	29553.04916	9.629615228	14.7676	14.704	14.715	14.7897	14.659	14.851	0.04383	0.04383	0.0462	0.04383	0.04383	0.0462	6	11	0
IPI00230838.4	ATP_synthase_D_chain,_mitochondrial	NCAQFVTGSQAR	100	0.135559745	0.997658493	0.99643308	0.849985868	0.988483763	0.799607172	0.054223898	0.762172038	0.80519316	0.649736822	0.950054496	0.528334592	-1.164089967	-1.024404829	-1.019307269	-1.036865686	1.005001005	1.05160443	16386.02809	14076.25575	15995.65682	15426.93238	16075.65118	16905.16168	17.37882063	14.0002	13.781	13.9654	13.9132	13.9726	14.0452	0.0787	0.0787	0.08295	0.0787	0.0787	0.08295	8	11	0
IPI00208256.1	Heat_shock_protein_86	NPDDITNEEYGEFYK	99.99999976	0.27961848	0.997658493	0.99643308	0.674180112	0.977979004	0.45250857	0.159462425	0.782956585	0.520737688	0.309683965	0.725923616	0.127221898	1.055588829	1.010840907	1.024810058	-1.040758219	1.013819337	-1.062214162	16629.49109	17553.90503	16809.76985	16151.46491	17042.06973	16043.91124	8.490395535	14.0215	14.0995	14.037	13.9794	14.0568	13.9697	0.03867	0.03867	0.04076	0.03867	0.03867	0.04076	20	20	0
IPI00231411.6	ATP_synthase_epsilon_chain,_mitochondrial	FSQICAK	99.982246	0.285594458	0.997658493	0.795267491	0.853810813	0.977979004	0.146792151	0.16646077	0.222278387	0.053958529	0.656702488	0.497033657	0.006134029	-1.059316983	-1.053495406	-1.084336754	1.019038553	-1.029275257	1.128097913	12098.731	11421.25652	11484.36996	11703.01575	11157.72471	12587.00595	9.201232118	13.5626	13.4794	13.4874	13.5146	13.4458	13.6196	0.04189	0.04189	0.04416	0.04189	0.04189	0.04416	2	2	0
IPI00567681.1	36_kDa_protein	LEKPAKYDDLKK	99.977778	0.217016172	0.997658493	0.99643308	0.46981881	0.977979004	0.613231168	0.108880114	0.690025509	0.69548306	0.117052001	0.436505564	0.275675411	-1.424994607	1.093583711	-1.08921476	-1.42690695	-1.191147519	1.278572683	7649.516336	5368.101956	8365.386463	5862.601248	7022.964266	8979.370261	51.55446354	12.9012	12.3902	13.0302	12.5173	12.7779	13.1324	0.2215	0.2215	0.2335	0.2215	0.2215	0.2335	3	4	0
IPI00339040.2	Ubiquitin-conjugating_enzyme_E2_variant_2	WTGMIIGPPR	99.99997816	0.720198551	0.997658493	0.99643308	0.225498692	0.977979004	0.38112535	0.606296568	0.472369167	0.822886851	0.014248274	0.615736382	0.068252485	-1.014441159	-1.020778583	-1.006240094	1.074711545	1.014448331	1.054325995	16587.95966	16351.82042	16250.30142	17464.38654	16485.09115	17380.62056	6.189013245	14.0178	13.9972	13.9882	14.0921	14.0089	14.0852	0.02821	0.02821	0.02973	0.02821	0.02821	0.02973	2	2	0
IPI00231051.1	Isoform_MAP2b_of_Microtubule-associated_protein_2	TTATSGESAQAPSAFK	100	0.385925201	0.997658493	0.99643308	0.855934899	0.977979004	0.993109576	0.257577506	0.443990247	0.34937396	0.665368512	0.883086539	0.962587274	-1.045124391	1.031027521	1.037081016	1.017380864	1.005871323	-1.001868873	13423.62292	12844.03429	13840.12466	14080.67797	13921.38449	13895.41573	8.637642648	13.7125	13.6488	13.7566	13.7814	13.765	13.7623	0.03933	0.03933	0.04146	0.03933	0.03933	0.04146	47	60	0
IPI00202238.1	PREDICTED:_similar_to_NADH-ubiquinone_oxidoreductase_PDSW_subunit_(Complex_I-PDSW)_(CI-PDSW)_i	AYDLVVDWPVTLVR	99.99999998	0.102240972	0.997658493	0.99643308	0.940752994	0.977979004	0.353175547	0.033885579	0.878533759	0.903422265	0.871734042	0.698431325	0.055856154	-1.047059454	-1.009167763	1.00400595	-1.005480779	1.013210439	-1.068107544	12889.66945	12000.89009	12772.57353	12702.95146	12941.30483	12116.10657	7.341513199	13.6539	13.5509	13.6408	13.6329	13.6597	13.5646	0.03345	0.03345	0.03526	0.03345	0.03345	0.03526	9	10	0
IPI00362992.3	PREDICTED:_similar_to_Succinate_semialdehyde_dehydrogenase_(NAD(+)-dependent_succinic_semialdehyde_	LGTVADCGVPEAR	99.99999985	0.395716271	0.997658493	0.99643308	0.377717662	0.92052399	0.941936591	0.266309302	0.235564299	0.365324505	0.068205018	0.041625789	0.834286695	1.029960261	-1.032920294	1.024282193	1.051551878	1.058001864	-1.005691229	10683.05661	11003.12377	10342.57597	10875.75518	10942.46465	10880.541	5.879445149	13.383	13.4256	13.3363	13.4088	13.4177	13.4095	0.0268	0.0268	0.02825	0.0268	0.0268	0.02825	9	10	0
IPI00391854.2	Isoform_Short_of_Clathrin_coat_assembly_protein_AP180	GLGSDLDSSLASLVGNLGISGTTSK	99.99999983	0.877096629	0.997658493	0.795267491	0.797906375	0.773591433	0.453249617	0.798909279	0.655675528	0.046575548	0.551424136	0.018457509	0.132371397	-1.00634514	-1.011446274	1.015648259	1.015331065	1.063685713	-1.039560465	15439.3864	15342.03901	15264.66288	15498.68642	16236.80382	15618.91239	5.527521286	13.9143	13.9052	13.8979	13.9199	13.987	13.931	0.0252	0.0252	0.02656	0.0252	0.0252	0.02656	12	15	0
IPI00390302.3	57_kDa_protein	YIDQEELNK	99.99962702	0.771949882	0.997658493	0.846402451	0.271569898	0.977979004	0.266373442	0.677997975	0.415979765	0.09740942	0.026598955	0.414281854	0.025571847	1.019074322	1.03885746	1.07937582	-1.111936557	1.03900281	-1.112790759	17096.76696	17422.8762	17761.1039	15973.12706	18453.83685	16583.38435	10.14454904	14.0614	14.0887	14.1164	13.9634	14.1716	14.0175	0.04616	0.04616	0.04866	0.04616	0.04616	0.04866	2	2	0
IPI00188330.1	PREDICTED:_similar_to_NADH_dehydrogenase_(ubiquinone)_Fe-S_protein_8	ILMWTELFR	99.99999871	0.332281068	0.997658493	0.99643308	0.788902735	0.977979004	0.932261716	0.208618502	0.511343528	0.409524063	0.489607826	0.882934497	0.82039031	1.048404221	-1.025545497	-1.031350489	1.026899034	-1.005660395	-1.008742324	9857.214599	10334.34539	9611.679468	9870.224363	9557.579796	9474.748479	8.316184748	13.267	13.3352	13.2306	13.2689	13.2224	13.2099	0.03787	0.03787	0.03992	0.03787	0.03787	0.03992	3	3	0
IPI00194958.1	Isoform_2_of_Phosphatidylinositol-binding_clathrin_assembly_protein	NTLFNLSNFLDK	99.99954524	0.292178655	0.997658493	0.99643308	0.333651543	0.977979004	0.915790782	0.172658876	0.266497976	0.798148069	0.044215366	0.386660478	0.76666533	1.047398034	1.039405761	1.008646348	-1.073530916	-1.030495736	1.010316917	13090.42928	13710.88989	13606.26762	12674.31372	13203.61369	13339.83427	7.499359577	13.6762	13.743	13.732	13.6296	13.6886	13.7035	0.03417	0.03417	0.03601	0.03417	0.03417	0.03601	3	3	0
IPI00206171.1	Isoform_MAP2x_of_Microtubule-associated_protein_2	TTATSGESAQAPSAFK	100	0.398320625	0.997658493	0.99643308	0.86551567	0.977979004	0.970183966	0.270858025	0.436948194	0.325276502	0.684342768	0.855366506	0.892569249	-1.043988533	1.031622123	1.0391595	1.016379782	1.007306336	-1.005408002	13490.75579	12922.32181	13917.36212	14145.32548	14019.04704	13943.63981	8.665406514	13.7197	13.6576	13.7646	13.788	13.7751	13.7673	0.03946	0.03946	0.04159	0.03946	0.03946	0.04159	46	59	0
IPI00212052.3	NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_4,_mitochondrial_precursor	ERWENPLMGWASTADPLSNMVLTFSAK	99.9938368	0.327528873	0.997658493	0.99643308	0.149698425	0.977979004	0.195033964	0.204378017	0.560052659	0.833997412	0.005594987	0.432218371	0.013564462	-1.151993662	1.024048869	-1.008341004	-1.124259765	-1.032590464	-1.109092771	18216.76403	17316.41994	18654.85659	16593.01274	18066.07483	16289.05652	8.835235824	14.153	14.0799	14.1873	14.0183	14.141	13.9916	0.04023	0.04023	0.04241	0.04023	0.04023	0.04241	4	4	0
IPI00357945.1	PREDICTED:_similar_to_Glycogen_phosphorylase,_brain_form	VIFLENYR	99.9946165	0.439123468	0.997658493	0.99643308	0.607960717	0.977979004	0.994839229	0.308725916	0.213069032	0.257448314	0.236456485	0.884358762	0.978010793	1.056511253	-1.07171694	-1.063145015	1.068019052	1.0080628	1.001522829	28210.73857	29804.96275	26322.938	28113.39929	26535.17458	26575.58312	12.0006733	14.784	14.8633	14.684	14.779	14.6956	14.6978	0.05455	0.05455	0.0575	0.05455	0.05455	0.0575	2	2	0
IPI00562632.1	33_kDa_protein	DGRGAAQNIIPASTGAAK	99.99999835	0.771949882	0.997658493	0.99643308	0.149698425	0.977979004	0.178834944	0.678433668	0.737344145	0.577306644	0.005816853	0.835481111	0.011241054	1.031138758	-1.025803675	-1.042109629	1.242779896	-1.015895785	1.219726328	26740.59187	27573.26068	26067.94314	32396.71566	25660.05641	31298.24638	16.5566691	14.7067	14.751	14.67	14.9836	14.6472	14.9338	0.07502	0.07502	0.07908	0.07502	0.07502	0.07908	2	4	0
12853094	unnamed_protein_product_[Mus_musculus]	FSNEEIAMATVTALR	100	0.542424787	0.997658493	0.99643308	0.699730801	0.977979004	0.673446244	0.414722494	0.150884669	0.890005132	0.342268323	0.191799922	0.352958206	-1.036863229	1.068171097	1.006137744	-1.044309566	-1.061654931	1.043308726	16872.75496	16272.88392	18022.98918	17258.28218	16976.31561	17711.5382	9.869030445	14.0424	13.9902	14.1376	14.075	14.0512	14.1124	0.04492	0.04492	0.04735	0.04492	0.04492	0.04735	19	27	0
IPI00364134.1	PREDICTED:_similar_to_Protein_NipSnap1	GWDENVYYTVPLVR	99.99999758	0.205652834	0.997658493	0.99643308	0.450498174	0.977979004	0.994153085	0.10129871	0.312202735	0.587570368	0.101916445	0.626664293	0.973725431	1.070321002	1.04364	1.022482409	-1.072177401	-1.020692377	1.00138617	11567.51974	12380.95932	12072.3263	11259.63511	11827.58545	11843.98049	9.128460033	13.4978	13.5958	13.5594	13.4589	13.5299	13.5319	0.04156	0.04156	0.04381	0.04156	0.04156	0.04381	3	3	0
IPI00193568.3	Isoform_4_of_Dynamin-1-like_protein	TLESVDPLGGLNTIDILTAIR	99.99999507	0.373536852	0.997658493	0.99643308	0.333651543	0.977979004	0.730123281	0.244186376	0.274622125	0.580304618	0.043896601	0.576167502	0.453093647	1.055229552	-1.053134241	-1.025719401	1.101682259	1.026727427	1.036080721	12336.64804	13017.99559	11714.22176	12905.35029	12027.31276	12461.26688	10.23156489	13.5907	13.6682	13.516	13.6557	13.554	13.6052	0.04656	0.04656	0.04908	0.04656	0.04656	0.04908	4	4	0
IPI00365935.3	19_kDa_protein	HLNEIDLFHCIDPNDSK	99.99997733	0.741506034	0.997658493	0.99643308	0.344566778	0.977979004	0.182066285	0.639573696	0.915240954	0.91904239	0.054343103	0.837315639	0.011988486	-1.028375148	1.006548091	-1.006085155	-1.127649688	-1.012673092	-1.172223955	10817.67364	10519.19006	10888.50875	9655.932037	10752.24456	9172.517347	13.34081531	13.4011	13.3607	13.4105	13.2372	13.3924	13.1631	0.0606	0.0606	0.06387	0.0606	0.0606	0.06387	2	2	0
IPI00325135.3	14-3-3_protein_epsilon	AAFDDAIAELDTLSEESYK	100	0.494216669	0.997658493	0.99643308	0.984163624	0.977979004	0.494461272	0.370146726	0.759277494	0.981562609	0.967499768	0.742238607	0.172822598	1.047128652	-1.016252657	1.001183602	-1.002144992	1.017455496	-1.075019187	18189.19203	19046.42412	17898.29714	17859.98761	18210.7208	16939.90304	11.42765568	14.1508	14.2172	14.1275	14.1244	14.1525	14.0481	0.05197	0.05197	0.05478	0.05197	0.05197	0.05478	17	31	0
IPI00569616.2	36_kDa_protein	MAYMASKE	99.969402	0.190389371	0.997658493	0.99643308	0.669782509	0.977979004	0.924766593	0.090081371	0.583877645	0.983878329	0.30618629	0.597399328	0.79125914	-1.17864628	1.055369485	1.001934182	-1.106325189	-1.053332149	1.026353628	19269.42973	16348.78085	20336.36813	18381.90826	19306.70031	19815.50191	21.52334002	14.234	13.9969	14.3118	14.166	14.2368	14.2743	0.09708	0.09708	0.1023	0.09708	0.09708	0.1023	9	13	0
IPI00782125.1	13_kDa_protein	TITLEVEPSDTIENVK	99.99999994	0.375688535	0.997658493	0.99643308	0.336582112	0.977979004	0.071235349	0.246022321	0.803417762	0.316341473	0.046411751	0.465903657	0.000976942	-1.083523284	1.017730251	1.071621702	-1.154097166	1.052952589	-1.278295702	27414.71277	25301.45237	27900.7825	24175.41895	29378.20117	22982.32022	15.3776801	14.7427	14.6269	14.768	14.5613	14.8425	14.4882	0.06975	0.06975	0.07352	0.06975	0.06975	0.07352	2	2	0
IPI00561110.2	PREDICTED:_similar_to_Glyceraldehyde-3-phosphate_dehydrogenase	DGRGAAQNIIPASTGAAK	99.99999835	0.916887014	0.997658493	0.99643308	0.189267082	0.977979004	0.146792151	0.867637083	0.485578366	0.279544795	0.009780445	0.719397821	0.005832694	1.007696748	-1.033586441	-1.05129636	1.134455356	-1.017134434	1.144819379	25085.47979	25278.55639	24270.32591	27533.60122	23861.47308	27317.0768	10.26326634	14.6146	14.6256	14.5669	14.7489	14.5424	14.7375	0.0467	0.0467	0.04923	0.0467	0.0467	0.04923	3	6	0
IPI00210264.3	Glutathione_transferase_omega-1	TYRDYLSLYLQDSPEACDYGL	99.99999886	0.927462268	0.997658493	0.99643308	0.855934899	0.977979004	0.923770784	0.882944079	0.022668514	0.302484904	0.661983148	0.187643563	0.785469101	-1.004926384	-1.083448361	-1.035194755	1.015116696	1.04661307	1.009380001	8851.939055	8808.544784	8170.153165	8293.658888	8550.989088	8631.19806	7.436885494	13.1118	13.1047	12.9961	13.0178	13.0619	13.0753	0.03388	0.03388	0.03571	0.03388	0.03388	0.03571	4	6	0
IPI00763565.1	PREDICTED:_similar_to_polyubiquitin	TLSDYNIQK	99.99988854	0.744003168	0.997658493	0.846402451	0.430171333	0.977979004	0.119761122	0.643669027	0.661583815	0.086141141	0.093681025	0.212441465	0.003454342	-1.051758394	1.05027913	1.208913641	-1.209578656	1.151040334	-1.406981229	31380.46028	29836.18715	32958.24252	27247.70511	37936.26647	26962.88032	24.61263925	14.9376	14.8648	15.0084	14.7338	15.2113	14.7187	0.1106	0.1106	0.1166	0.1106	0.1106	0.1166	3	3	0
IPI00208672.2	Isoform_Crk-I_of_Proto-oncogene_C-crk	IGDQEFDSLPALLEFYK	99.99984592	0.155279398	0.997658493	0.99643308	0.512587348	0.977979004	0.40581774	0.068322935	0.42993599	0.720868194	0.152311669	0.25738352	0.087641283	-1.072634136	-1.031263451	1.013623256	-1.057827728	1.045312617	-1.069685013	11817.20013	11016.99054	11458.95369	10832.53292	11978.18886	11197.86547	8.437366745	13.5286	13.4274	13.4842	13.4031	13.5481	13.4509	0.03842	0.03842	0.0405	0.03842	0.03842	0.0405	2	2	0
IPI00362160.1	Tubulin_beta-3_chain	GHYTEGAELVDSVLDVVRK	100	0.190890095	0.998997816	0.99643308	0.666252843	0.977979004	0.993109576	0.090754605	0.998997816	0.622729852	0.297146469	0.631124613	0.964847999	1.095233619	1.000068446	-1.026468584	1.058773683	-1.026538841	-1.002404366	24105.30594	26400.94146	24106.95585	25523.81042	23483.725	23427.39695	11.8439155	14.5571	14.6883	14.5572	14.6396	14.5194	14.5159	0.05385	0.05385	0.05676	0.05385	0.05385	0.05676	30	69	0
IPI00194047.3	Isocitrate_dehydrogenase_[NAD]_subunit_gamma,_mitochondrial_precursor	HTVTMIPGDGIGPELMLHVK	99.99964549	0.293124447	0.997658493	0.99643308	0.966345081	0.977979004	0.45250857	0.174534671	0.544713841	0.405147867	0.923415602	0.836660274	0.128983753	1.041581545	-1.018711421	-1.025149758	-1.002941513	-1.006320079	1.048022521	15109.94951	15738.24456	14832.41397	14788.91219	14739.26067	15447.07713	6.624862926	13.8832	13.942	13.8565	13.8522	13.8474	13.915	0.03019	0.03019	0.03182	0.03019	0.03019	0.03182	4	4	0
IPI00199305.1	Vacuolar_ATP_synthase_subunit_B,_brain_isoform	AVVQVFEGTSGIDAK	100	0.190464311	0.997658493	0.99643308	0.679460331	0.977979004	0.752607186	0.090334502	0.839478816	0.626886752	0.31604612	0.786396041	0.4758051	1.062344999	-1.007356839	-1.017285404	1.037123708	-1.009856055	1.02619912	13271.19723	14098.59	13174.27619	13663.35418	13045.69709	13387.48287	7.848413894	13.696	13.7833	13.6854	13.738	13.6713	13.7086	0.03575	0.03575	0.03768	0.03575	0.03575	0.03768	20	27	0
17380501	SPTA2_RAT_Spectrin_alpha_chain,_brain_(Spectrin,_non-erythroid_alpha_chain)_(Alpha-II_spectrin)_(Fodrin_alp	LSDDNTIGQEEIQQR	100	0.259347012	0.997658493	0.99643308	0.875711929	0.977979004	0.647257068	0.140491981	0.942559036	0.476034057	0.705561811	0.444106798	0.303604851	-1.038957268	-1.001901121	1.018499033	-1.010015769	1.020435323	-1.027630913	14178.79614	13647.14082	14151.89168	14011.55518	14441.09015	14052.79849	5.713993202	13.7914	13.7363	13.7887	13.7743	13.8179	13.7786	0.02605	0.02605	0.02746	0.02605	0.02605	0.02746	112	145	0
8850209	actin-like_[Mus_musculus]	KDLYANTVLSGGTTMYPGLADR	100	0.247086905	0.997658493	0.99643308	0.780681315	0.977979004	0.589134502	0.130604982	0.749271464	0.6473667	0.468608402	0.445300305	0.250041779	1.077577466	-1.01618696	1.022632847	1.037161294	1.039186164	-1.059857528	22387.14526	24123.88326	22030.53782	22849.2211	22893.83009	21600.85622	10.90923368	14.4504	14.5582	14.4272	14.4799	14.4827	14.3988	0.04962	0.04962	0.05231	0.04962	0.04962	0.05231	26	58	0
IPI00566874.2	44_kDa_protein	IGAEVYHNLK	99.99995377	0.140594471	0.997658493	0.749294352	0.57026792	0.977979004	0.444862176	0.059508432	0.350771429	0.04281682	0.2049175	0.285366633	0.120471327	-1.087589912	-1.043061412	-1.094715554	1.059166819	-1.049521669	1.073247114	28691.55166	26380.85491	27507.05887	29134.56405	26209.13859	28128.88235	9.768531507	14.8083	14.6872	14.7475	14.8304	14.6778	14.7798	0.04446	0.04446	0.04687	0.04446	0.04446	0.04687	3	8	0
IPI00191335.1	Isoform_IA_of_Synapsin-1	TNTGSAMLEQIAMSDR	100	0.265492465	0.997658493	0.99643308	0.733834025	0.977979004	0.852901543	0.146284114	0.964754439	0.470228696	0.413164088	0.455188641	0.645280939	1.055568501	1.001674127	-1.027032084	-1.031566407	-1.028751466	1.017596321	16676.07177	17602.73608	16703.98962	16192.83985	16237.14782	16522.86189	8.213006965	14.0255	14.1035	14.0279	13.9831	13.987	14.0122	0.03741	0.03741	0.03943	0.03741	0.03741	0.03943	25	36	0
57829	heavy_neurofilament_polypeptide_(854_AA)_[Rattus_sp.]	AQLEGHTVQSTLQSEEWFR	99.99985277	0.959297485	0.997658493	0.846402451	0.091880843	0.977979004	0.837394717	0.941453587	0.041431634	0.071135868	0.001821886	0.767014194	0.596354967	-1.003362124	1.102640793	1.087401321	-1.165984415	-1.014014579	-1.025215138	16091.28141	16037.36181	17742.90328	15217.10158	17497.68066	17067.32569	10.19633073	13.974	13.9691	14.115	13.8934	14.0949	14.0589	0.0464	0.0464	0.04891	0.0464	0.0464	0.04891	4	4	0
IPI00190240.1	Ribosomal_protein_S27a	TITLEVEPSDTIENVK	99.99999994	0.534503678	0.997658493	0.991204521	0.342215144	0.977979004	0.126890551	0.406833657	0.749044207	0.187202605	0.052469288	0.331986296	0.004495551	-1.0922283	1.035470949	1.151415619	-1.239993108	1.111972885	-1.379777466	23551.28361	21562.60152	24386.67	19666.77866	27117.31579	19653.39808	23.92095063	14.5235	14.3962	14.5738	14.2635	14.7269	14.2625	0.1076	0.1076	0.1134	0.1076	0.1076	0.1134	5	6	0
IPI00199114.5	Acidic_leucine-rich_nuclear_phosphoprotein_32_family_member_A	SLDLFNCEVTNLNAYRENVFK	99.981395	0.280530761	0.997658493	0.991204521	0.521054574	0.977979004	0.837394717	0.160601253	0.544598549	0.182376807	0.158400591	0.483584405	0.600251545	-1.078365392	-1.03377038	-1.074266731	1.08104869	-1.039173449	-1.029129997	7101.769859	6585.680429	6869.774949	7426.561211	6610.806845	6423.684923	11.89412074	12.794	12.6851	12.746	12.8585	12.6906	12.6492	0.05407	0.05407	0.057	0.05407	0.05407	0.057	2	2	0
IPI00366104.1	PREDICTED:_similar_to_toll_interacting_protein	GPVYIGELPQDFLR	99.9955246	0.176650095	0.997658493	0.99643308	0.656666972	0.977979004	0.260206946	0.081359987	0.395974131	0.680198438	0.290912659	0.213518726	0.023790349	1.067275584	1.032738097	-1.015300922	1.040974524	-1.048539942	1.091604711	13559.75138	14471.99157	14003.67183	14577.46562	13355.40142	14578.8191	8.205112027	13.727	13.821	13.7735	13.8315	13.7051	13.8316	0.03737	0.03737	0.03939	0.03737	0.03737	0.03939	2	2	0
IPI00209258.4	Spectrin_alpha_chain,_brain	LSDDNTIGQEEIQQR	100	0.265492465	0.997658493	0.99643308	0.884024126	0.977979004	0.66199794	0.145929501	0.941762293	0.477319774	0.73146682	0.444717451	0.320028718	-1.038081907	-1.001911379	1.018288261	-1.009015389	1.020234596	-1.026460568	14148.39161	13629.35961	14121.40026	13995.22784	14407.14109	14035.74725	5.665983059	13.7884	13.7344	13.7856	13.7726	13.8145	13.7768	0.02583	0.02583	0.02723	0.02583	0.02583	0.02723	111	144	0
IPI00195123.1	ATP_synthase_O_subunit,_mitochondrial_precursor	GEVPCTVTTAFPLDEAVLSELK	99.99999995	0.384647147	0.997658493	0.99643308	0.87217354	0.977979004	0.670153176	0.25376721	0.77137684	0.305875492	0.699732372	0.478160298	0.342690183	1.044011924	-1.011263348	-1.039349513	-1.014982126	-1.027773345	1.037402213	17733.67977	18514.17313	17536.16385	17277.31297	17062.28708	17700.45437	8.360095996	14.1142	14.1763	14.098	14.0766	14.0585	14.1115	0.03807	0.03807	0.04013	0.03807	0.03807	0.04013	11	13	0
IPI00211936.2	Alpha-internexin	VGESFEETLEETVVSTK	100	0.619795629	0.997658493	0.99643308	0.538897987	0.977979004	0.957767968	0.495128165	0.136608234	0.311386184	0.169983822	0.607406101	0.860349284	-1.019509003	1.044653851	1.029167003	-1.041026819	-1.015047945	1.005121663	17900.21901	17557.68606	18699.53273	17962.58502	18422.31476	18516.66764	6.29482059	14.1277	14.0998	14.1907	14.1327	14.1692	14.1765	0.02869	0.02869	0.03024	0.02869	0.02869	0.03024	25	31	0
IPI00476086.2	ATPase,_H+_transporting,_V0_subunit_D_isoform_1	LLFEGAGSNPGDK	99.99986218	0.126343985	0.997658493	0.99643308	0.788902735	0.977979004	0.849720293	0.046481663	0.852709011	0.834199964	0.497940298	0.697138039	0.640931878	1.081348553	-1.007377786	1.008099198	1.02725269	1.015536738	1.01865363	14062.09858	15206.02995	13959.11125	14339.53458	14175.9903	14440.42398	8.589861197	13.7795	13.8924	13.7689	13.8077	13.7912	13.8178	0.03912	0.03912	0.04123	0.03912	0.03912	0.04123	7	7	0
IPI00201032.1	Isoform_1_of_Heterogeneous_nuclear_ribonucleoprotein_D0	IFVGGLSPDTPEEK	99.99999999	0.271094468	0.997658493	0.99643308	0.240152764	0.977979004	0.621993365	0.153052191	0.458561126	0.731854801	0.01838884	0.682426601	0.282323972	-1.052306618	1.027343937	1.012186769	-1.091920695	-1.014974675	-1.040024667	13665.2682	12986.01374	14038.93043	12857.09713	13831.80367	13299.49578	7.874347866	13.7382	13.6647	13.7771	13.6503	13.7557	13.6991	0.03587	0.03587	0.03781	0.03587	0.03587	0.03781	5	5	0
IPI00200466.2	ADP/ATP_translocase_2	YFAGNLASGGAAGATSLCFVYPLDFAR	99.99999962	0.252744602	0.997658493	0.99643308	0.966312395	0.990285572	0.426869209	0.134131639	0.55380794	0.568897906	0.914334022	0.969913983	0.109129786	1.144030799	-1.055630301	-1.052002104	-1.009868693	1.003448849	1.15961285	11530.83753	13191.63327	10923.17785	10816.43379	10960.85025	12710.3428	19.96690744	13.4932	13.6873	13.4151	13.4009	13.4201	13.6337	0.0902	0.0902	0.09508	0.0902	0.0902	0.09508	13	16	0
IPI00568873.2	20_kDa_protein	TLSDYNIQKESTLHLVLR	99.99988936	0.630515243	0.997658493	0.959908311	0.377717662	0.977979004	0.146792151	0.510176905	0.729254729	0.164084326	0.06772563	0.309751847	0.006226358	-1.080605926	1.042681279	1.179388865	-1.251178251	1.131111577	-1.408452551	27124.02938	25100.75943	28281.71763	22604.06749	31989.77823	22712.71276	26.59332916	14.7273	14.6154	14.7876	14.4643	14.9653	14.4712	0.1193	0.1193	0.1257	0.1193	0.1193	0.1257	4	5	0
IPI00365217.1	Cytidylate_kinase	SVDEVFGDVMK	99.9987237	0.350991518	0.997658493	0.99643308	0.706612353	0.994226451	0.421432785	0.224233438	0.381797792	0.360511106	0.349738699	0.987408899	0.100830754	-1.040237542	1.029491933	1.030030004	-1.031581246	1.000522657	-1.056588175	15773.32747	15163.19766	16238.51338	15741.38096	16247.00055	15376.85254	7.180853486	13.9452	13.8883	13.9871	13.9423	13.9879	13.9085	0.03272	0.03272	0.03449	0.03272	0.03272	0.03449	2	2	0
IPI00198118.1	112_kDa_protein	KVAELEEEQSQGSSSYSDWVK	99.99998236	0.464190051	0.997658493	0.99643308	0.577643504	0.977979004	0.670153176	0.335808346	0.979542973	0.660842838	0.214655965	0.650809017	0.339326384	-1.022832502	-1.000615351	1.010307382	1.030446686	1.010929076	-1.023291695	14723.16369	14394.50121	14714.10935	15162.10522	14874.92097	14536.34486	5.199815146	13.8458	13.8132	13.8449	13.8882	13.8606	13.8274	0.02371	0.02371	0.02499	0.02371	0.02371	0.02499	6	6	0
IPI00197900.5	Translation_elongation_factor_1-delta_subunit	GVVQDLQQAISK	99.9941556	0.123608993	0.997658493	0.99643308	0.557987386	0.977979004	0.485775688	0.044781772	0.819304643	0.925666808	0.190175193	0.749610456	0.162665459	1.096291576	1.010601652	-1.004200116	1.062866751	-1.014846296	1.067213167	8253.755158	9048.522251	8341.258597	8865.646421	8219.233426	8771.674132	10.02174109	13.0108	13.1435	13.026	13.114	13.0048	13.0986	0.04561	0.04561	0.04807	0.04561	0.04561	0.04807	2	2	0
IPI00197885.1	Tubulin_beta_chain	GHYTEGAELVDSVLDVVRK	100	0.211037253	0.997658493	0.99643308	0.541686564	0.977979004	0.967192189	0.104674477	0.936982735	0.625095883	0.173126543	0.691521562	0.885395364	1.088864247	-1.00421669	-1.025664878	1.075896419	-1.021358127	1.007701	26326.53704	28666.02494	26215.99232	28205.69227	25667.77668	26585.44424	11.56574746	14.6842	14.8071	14.6782	14.7837	14.6477	14.6587	0.05259	0.05259	0.05543	0.05259	0.05259	0.05543	35	81	0
201006	Cu/Zn-superoxide_dismutase	VISLSGEHSIIGR	99.99999154	0.164813431	0.997658493	0.99643308	0.879103848	0.977979004	0.774104485	0.073677931	0.977457407	0.786978818	0.721159284	0.770870931	0.503557007	-1.135051895	1.002024769	-1.019028994	1.025915183	-1.021092292	-1.049196712	23812.20464	20978.95677	23860.41887	24478.76599	23367.5438	22271.84238	15.61119612	14.5394	14.3567	14.5423	14.5792	14.5122	14.4429	0.07079	0.07079	0.07462	0.07079	0.07079	0.07462	4	8	0
IPI00471530.1	Leucine_aminopeptidase_3	GSEEPPVFLEIHYTGSPNATEAPLVFVGK	99.9938474	0.87730717	0.997658493	0.99643308	0.117623759	0.977979004	0.260206946	0.800104139	0.218328544	0.556467998	0.002629754	0.505871743	0.022218843	-1.014406183	-1.074597876	-1.033825129	1.200160997	1.039438727	1.145792941	10399.71465	10252.02213	9677.773312	11614.88606	10059.45238	11526.04952	12.61634323	13.3443	13.3236	13.2405	13.5037	13.2963	13.4926	0.05733	0.05733	0.06043	0.05733	0.05733	0.06043	2	2	0
IPI00369217.1	TNF_receptor-associated_protein_1	GVVDSEDIPLNLSR	99.99999459	0.988639936	0.997658493	0.99643308	0.817753948	0.982193145	0.666788291	0.979600943	0.192130521	0.222705804	0.593455722	0.9047402	0.3290418	-1.00126553	-1.069116494	-1.06263373	1.027538434	1.006100657	-1.051093264	12796.52586	12780.35193	11969.25306	12298.86754	12042.27336	11456.9028	11.04061274	13.6435	13.6416	13.547	13.5862	13.5558	13.4839	0.05022	0.05022	0.05293	0.05022	0.05022	0.05293	2	2	0
IPI00390850.3	111_kDa_protein	MALDIEIAAYR	99.99999157	0.990065019	0.997658493	0.795267491	0.149698425	0.977979004	0.808231386	0.984407504	0.035963831	0.058481729	0.00514424	0.788134413	0.542491643	1.000788603	1.092862639	1.080755342	-1.128043686	-1.011202625	-1.025607061	14466.82578	14478.23437	15810.2534	14015.63929	15635.09924	15244.7266	8.9940617	13.8205	13.8216	13.9486	13.7747	13.9325	13.896	0.04095	0.04095	0.04317	0.04095	0.04095	0.04317	7	7	0
IPI00200659.1	Succinate_dehydrogenase_[ubiquinone]_flavoprotein_subunit,_mitochondrial_precursor	LGANSLLDLVVFGR	99.99999992	0.932837436	0.997658493	0.99643308	0.082790115	0.806688502	0.80914378	0.897656139	0.087089265	0.573842883	0.000851556	0.025814032	0.548368299	-1.002912833	1.041141968	-1.012817749	-1.08530189	-1.054487064	-1.014065914	12327.48725	12291.68363	12834.66433	11825.89328	12171.47633	12002.64811	5.035043513	13.5896	13.5854	13.6478	13.5297	13.5712	13.5511	0.02296	0.02296	0.0242	0.02296	0.02296	0.0242	6	7	0
IPI00331981.7	Dihydropyrimidinase-related_protein_5	IIPGADADVVVWDPEATK	99.99985845	0.605905998	0.997658493	0.99643308	0.352646721	0.977979004	0.506065569	0.481262479	0.626083712	0.348754543	0.056020451	0.164351443	0.182761966	1.02132813	1.015094626	-1.028529381	-1.06156258	-1.044054648	1.042136443	13369.88889	13655.04361	13571.70236	12784.64653	12999.03448	13546.76756	6.659686568	13.7067	13.7371	13.7283	13.6421	13.6661	13.7257	0.03035	0.03035	0.03199	0.03035	0.03035	0.03199	9	11	0
IPI00205056.1	CaM_kinase-like_vesicle-associated_protein	ATPATEESTVPAAQSSAAPAAK	99.99999483	0.487484454	0.997658493	0.99643308	0.367357043	0.977979004	0.658793859	0.362131308	0.435090894	0.230049303	0.063258937	0.689058552	0.311703609	1.033241915	-1.02890289	-1.04414348	1.071818381	-1.014812467	1.038037359	8744.328315	9035.00653	8498.691568	9109.053834	8374.642455	8693.19174	7.965864227	13.0941	13.1413	13.053	13.1531	13.0318	13.0857	0.03628	0.03628	0.03825	0.03628	0.03628	0.03825	4	4	0
8048915	beta_2_globin_[rats,_Sprague-Dawley,_Peptide,_146_aa]	YFDSFGDLSSASAIMGNPK	100	0.932837436	0.997658493	0.99643308	0.554634429	0.977979004	0.503151385	0.895330728	0.493810356	0.497213891	0.185055844	0.181412864	0.181022434	-1.007516644	-1.040918132	1.03948479	1.081300159	1.082018566	1.08209624	19407.3653	19262.57538	18644.46847	20160.26672	20173.66104	21829.84275	12.71660242	14.2443	14.2335	14.1865	14.2992	14.3002	14.414	0.05778	0.05778	0.06091	0.05778	0.05778	0.06091	16	26	0
IPI00199688.2	Mitogen-activated_protein_kinase_1	VADPDHDHTGFLTEYVATR	99.9996226	0.618684709	0.997658493	0.99643308	0.416332803	0.977979004	0.569356066	0.493179105	0.746412615	0.39804122	0.080517865	0.253567945	0.232838551	-1.028289928	-1.013592976	1.035046275	1.076833956	1.049115634	-1.051411344	16164.45685	15719.74636	15947.68042	17173.00379	16730.96085	15912.85937	9.057316873	13.9805	13.9403	13.9611	14.0679	14.0302	13.9579	0.04124	0.04124	0.04347	0.04124	0.04124	0.04347	4	4	0
IPI00769218.1	PREDICTED:_similar_to_glyceraldehyde-3-phosphate_dehydrogenase	LISWYDNEYGYSNR	100	0.30883246	0.997658493	0.99643308	0.876899711	0.977979004	0.609075496	0.185420182	0.628065885	0.770756185	0.70982143	0.443351849	0.269946153	-1.058674626	1.021500627	-1.012522515	-1.016465587	-1.034292383	1.04987781	18355.89002	17338.55669	18750.55316	18446.81551	18128.87097	19033.09934	9.521754327	14.164	14.0817	14.1946	14.1711	14.146	14.2162	0.04334	0.04334	0.04569	0.04334	0.04334	0.04569	42	66	0
1170099	GSTP2_MOUSE_Glutathione_S-transferase_P_2_(GST_YF-YF)_(GST-piA)_(GST_class-pi)_(Gst_P2)	FEDGDLTLYQSNAILR	100	0.400143834	0.997658493	0.99643308	0.23197177	0.977979004	0.520988984	0.273469729	0.163614342	0.202302372	0.017232189	0.876546444	0.197678106	1.040442256	1.053376153	1.047341562	-1.09477676	-1.005761817	-1.049193304	15388.03754	16010.36449	16209.39178	14806.11607	16116.53128	15360.8789	8.022440058	13.9095	13.9667	13.9845	13.8539	13.9763	13.907	0.03654	0.03654	0.03852	0.03654	0.03654	0.03852	2	2	0
IPI00360666.3	PREDICTED:_similar_to_Serine/threonine-protein_kinase_ATR	EILTKAIHMK	99.07962	0.311280174	0.997658493	0.99643308	0.733834025	0.977979004	0.647257068	0.188902529	0.572521863	0.831239273	0.413985963	0.441023677	0.303945115	1.065399967	-1.028155405	1.010244361	1.04108207	1.0386882	-1.052071561	45911.21426	48913.80617	44653.96382	46488.44111	46381.54529	44085.92249	10.67070226	15.4866	15.578	15.4465	15.5046	15.5013	15.428	0.04854	0.04854	0.05117	0.04854	0.04854	0.05117	2	2	0
IPI00188524.2	Neurofilament_triplet_H_protein	MALDIEIAAYR	99.99999157	0.940758258	0.997658493	0.728765365	0.17731616	0.988483763	0.69561724	0.908503689	0.050091646	0.037268821	0.008511176	0.940665874	0.389545655	1.005123659	1.095481662	1.099213173	-1.13240752	1.003406274	-1.040238343	13866.03392	13937.07875	15189.98589	13413.88645	15241.72715	14652.14895	9.919380952	13.7593	13.7666	13.8908	13.7114	13.8957	13.8388	0.04514	0.04514	0.04759	0.04514	0.04514	0.04759	7	7	0
IPI00196994.1	Rho_GDP_dissociation_inhibitor_(GDI)_alpha	SIQEIQELDKDDESLR	99.99999999	0.24587381	0.997658493	0.99643308	0.719614739	0.977979004	0.490453166	0.128416379	0.754665702	0.419584653	0.381132156	0.273797114	0.167322433	1.050252193	-1.010295399	1.026156024	1.029219127	1.03672071	-1.046719537	15730.40729	16520.89475	15570.10683	16025.05175	16141.8522	15421.37281	7.105170777	13.9413	14.012	13.9265	13.968	13.9785	13.9126	0.03237	0.03237	0.03413	0.03237	0.03237	0.03413	8	10	0
IPI00563613.1	Neurocan_core_protein_precursor	SGSGPIQAALAELVALPCFFTLQPR	99.990186	0.135346768	0.997658493	0.99643308	0.83893122	0.977979004	0.962983009	0.053703028	0.871237302	0.94337119	0.621467222	0.817168519	0.875391351	1.205199628	-1.015949185	1.00677163	1.049437276	1.022828818	-1.015426226	7274.300661	8766.984453	7160.102853	7514.078837	7323.559534	7212.300949	21.38071616	12.8286	13.0979	12.8058	12.8754	12.8383	12.8162	0.09646	0.09646	0.1017	0.09646	0.09646	0.1017	2	3	0
IPI00231965.4	ADP-ribosylation_factor_5	LGEIVTTIPTIGFNVETVEYK	99.99999785	0.398144613	0.997658493	0.99643308	0.57026792	0.988483763	0.686505831	0.269910848	0.841213658	0.899144922	0.204504663	0.938617774	0.373243417	-1.049062651	1.008924569	1.005485325	-1.058340497	-1.003420482	1.040429582	14324.07443	13654.16491	14451.91063	13655.25619	14402.64663	14984.93961	9.626321487	13.8062	13.7371	13.819	13.7372	13.814	13.8712	0.04382	0.04382	0.04619	0.04382	0.04382	0.04619	9	10	0
IPI00768167.1	PREDICTED:_similar_to_beta_tubulin_1,_class_VI	KLAVNMVPFPR	99.99999995	0.932837436	0.997658493	0.991204521	0.803761658	0.867565465	0.826974443	0.896276652	0.373059942	0.184647171	0.564929623	0.031747357	0.571793758	1.004552685	1.032525222	-1.047718838	1.020848651	-1.081796125	1.020477054	25617.08474	25733.71126	26450.28611	27001.73889	24450.3428	24951.01378	7.764795207	14.6448	14.6514	14.691	14.7208	14.5776	14.6068	0.03537	0.03537	0.03728	0.03537	0.03537	0.03728	6	8	0
IPI00230865.6	Glia_maturation_factor_beta	NTEDLTEEWLR	99.99994227	0.741506034	0.997658493	0.99643308	0.284423747	0.977979004	0.633473404	0.639813778	0.571888931	0.835102858	0.032180515	0.716407901	0.29231851	-1.016038048	-1.01995219	-1.007096611	1.079442032	1.012764991	1.037635462	15779.11521	15530.04363	15470.44593	16699.44959	15667.92603	16257.59566	7.569036767	13.9457	13.9228	13.9172	14.0275	13.9355	13.9888	0.03448	0.03448	0.03635	0.03448	0.03448	0.03635	7	10	0
IPI00476991.1	Neural_cell_adhesion_molecule_1,_140_kDa_isoform_precursor	LEGQMGEDGNSIK	99.9999859	0.311280174	0.997658493	0.99643308	0.599602934	0.988483763	0.995931319	0.188328368	0.671266384	0.697446564	0.229092665	0.963228179	0.987718912	1.074327626	1.023865447	1.021247909	-1.069561003	-1.002563079	-1.000855013	13752.54209	14774.73589	14080.75266	13164.98322	14044.75484	14032.75666	12.06983798	13.7474	13.8508	13.7814	13.6844	13.7777	13.7765	0.05487	0.05487	0.05783	0.05487	0.05487	0.05783	7	9	0
IPI00655259.1	Tubulin,_beta_2b	GHYTEGAELVDSVLDVVRK	100	0.236412223	0.997658493	0.99643308	0.502800017	0.977979004	0.878427415	0.121313244	0.977685333	0.624901193	0.140813518	0.654138433	0.67965184	1.086214624	-1.001517313	-1.026160981	1.084021316	-1.024606333	1.022654523	25402.9148	27593.01754	25364.42902	27495.58174	24755.29206	25316.11139	11.78127282	14.6327	14.752	14.6305	14.7469	14.5954	14.6278	0.05356	0.05356	0.05646	0.05356	0.05356	0.05646	36	87	0
IPI00215470.2	A-kinase_anchor_protein_5	ATVGQAEEPIVGQAEETVLR	99.99999997	0.27061826	0.997658493	0.99643308	0.342215144	0.977979004	0.849367056	0.152164781	0.526540978	0.610621392	0.050464893	0.26107959	0.634765964	-1.076517956	1.033793408	-1.026331942	-1.110021749	-1.061015196	-1.025220864	8823.00522	8195.873712	9121.164633	8217.104432	8596.639019	8385.158085	11.3815104	13.1071	13.0007	13.155	13.0044	13.0696	13.0336	0.05176	0.05176	0.05456	0.05176	0.05176	0.05456	9	10	0
IPI00231644.1	Isoform_Short_of_Succinate_semialdehyde_dehydrogenase	LGTVADCGVPEAR	99.99999985	0.440557624	0.997658493	0.99643308	0.342215144	0.977979004	0.994153085	0.311159556	0.296835562	0.388691168	0.052638814	0.062996066	0.971743836	1.029751191	-1.031522277	1.025230838	1.060145292	1.057548449	1.001048757	10346.03426	10653.8411	10029.86992	10633.11937	10607.07338	10618.19762	6.41628062	13.3368	13.3791	13.292	13.3763	13.3727	13.3743	0.02924	0.02924	0.03082	0.02924	0.02924	0.03082	8	9	0
IPI00197579.1	Tubulin_beta-5_chain	GHYTEGAELVDSVLDVVRK	100	0.230736601	0.997658493	0.99643308	0.50424441	0.977979004	0.898224099	0.117346043	0.966194623	0.645406556	0.142340993	0.685011291	0.724899967	1.085732898	-1.002262548	-1.024195607	1.082266274	-1.021883547	1.018954531	26685.6143	28973.44934	26625.37312	28815.74336	26055.19308	26549.05705	11.58868262	14.7038	14.8224	14.7005	14.8146	14.6693	14.6964	0.05269	0.05269	0.05554	0.05269	0.05269	0.05554	36	85	0
IPI00400573.1	Tubulin,_beta_2c	GHYTEGAELVDSVLDVVRK	100	0.221160806	0.998795589	0.99643308	0.486148755	0.977979004	0.931974488	0.111717802	0.990063948	0.674876998	0.127440635	0.673961805	0.811383549	1.089265686	1.000679632	-1.022543192	1.087741015	-1.023238146	1.013108041	27633.32404	30100.03168	27652.10453	30078.32826	27024.11423	27378.34744	11.85810785	14.7541	14.8775	14.7551	14.8764	14.722	14.7407	0.05391	0.05391	0.05683	0.05391	0.05391	0.05683	34	77	0
IPI00231978.4	ATP_synthase_e_chain,_mitochondrial	ELAEAEDVSIFK	99.99999882	0.191420745	0.997658493	0.99643308	0.450498174	0.977979004	0.931989435	0.091663191	0.853115192	0.874588142	0.10095809	0.734888587	0.819085572	-1.103899064	-1.011056944	1.009165452	-1.103718613	1.020323738	1.013678255	25556.77084	23151.36563	25277.28135	22901.92542	25791.01021	26143.78621	12.91564072	14.6414	14.4988	14.6256	14.4832	14.6546	14.6742	0.05868	0.05868	0.06185	0.05868	0.05868	0.06185	4	4	0
202229	beta-tubulin	MAATFIGNSTAIQELFK	100	0.143984005	0.997658493	0.99643308	0.667622878	0.977979004	0.977970118	0.061871984	0.811806272	0.930181103	0.300621045	0.746482159	0.912917929	1.100066747	1.012363079	-1.00440964	1.055148634	-1.016827236	-1.005658328	22859.53234	25147.01137	23142.14655	24418.40431	22759.17257	22631.11828	11.20978684	14.4805	14.6181	14.4982	14.5757	14.4742	14.466	0.05098	0.05098	0.05374	0.05098	0.05098	0.05374	24	47	0
IPI00565128.2	35_kDa_protein	RVIISAPSADAPMFVM	99.99924787	0.384647147	0.997658493	0.99643308	0.360181899	0.977979004	0.670153176	0.254526876	0.379197004	0.576747435	0.058511083	0.735048165	0.340303024	-1.060257725	1.047364705	1.028935531	-1.106200485	-1.017910913	-1.051496743	15255.98896	14388.94393	15978.58437	14444.56461	15697.42909	14928.65213	11.39254497	13.8971	13.8127	13.9639	13.8182	13.9382	13.8658	0.05181	0.05181	0.05461	0.05181	0.05181	0.05461	9	11	0
IPI00566635.2	Discs_large_homolog_4	ILAGGPADLSGELR	99.99999985	0.579720673	0.997658493	0.99643308	0.483603981	0.994226451	0.131663761	0.451850856	0.874792774	0.856462462	0.123802619	0.985247887	0.004815132	1.047685649	-1.010048001	-1.011233517	1.103810033	-1.001173722	1.204379282	19558.00223	20490.63826	19363.43838	21373.55755	19340.73772	23293.58381	13.80641773	14.2555	14.3227	14.241	14.3835	14.2394	14.5076	0.06269	0.06269	0.06608	0.06269	0.06269	0.06608	5	5	0
IPI00192034.2	PREDICTED:_similar_to_Dihydropyrimidinase-related_protein_2	THNSALEYNIFEGMECR	100	0.834460072	0.997658493	0.99643308	0.706612353	0.977979004	0.460688749	0.747676225	0.415594138	0.821687647	0.351341224	0.30263581	0.141628884	1.006400799	1.016772505	-1.004478737	-1.019244252	-1.021326361	-1.030711747	22043.85778	22184.95609	22413.58848	21990.39969	21945.56934	21291.66511	4.413477074	14.4281	14.4373	14.4521	14.4246	14.4216	14.378	0.02013	0.02013	0.02121	0.02013	0.02013	0.02121	42	77	0
IPI00464440.2	Sideroflexin_1	SSMSVTSLEDELQASIQK	99.99984603	0.565055215	0.997658493	0.99643308	0.765397355	0.99715038	0.488323473	0.435899737	0.892106582	0.885113141	0.453115234	0.99601078	0.165750939	-1.037795613	-1.006638505	-1.006884024	-1.037375102	-1.0002439	1.070619648	11557.44605	11136.53392	11481.22786	11067.57607	11478.42827	12289.03084	10.5944566	13.4965	13.443	13.487	13.4341	13.4866	13.5851	0.0482	0.0482	0.05081	0.0482	0.0482	0.05081	3	3	0
12963569	protein_phosphatase-1_regulatory_subunit_7_[Mus_musculus]	AIENIDTLTNLESLFLGK	100	0.576115962	0.997658493	0.99643308	0.833824109	0.977979004	0.931989435	0.447452959	0.215122266	0.369857966	0.611788661	0.709590187	0.817272274	1.03336496	-1.056836733	-1.039547117	1.022747605	1.016631873	-1.010282428	22118.67703	22856.66581	20929.13345	21405.2211	21277.22414	21060.66933	9.609493779	14.433	14.4803	14.3532	14.3857	14.377	14.3623	0.04374	0.04374	0.04611	0.04374	0.04374	0.04611	2	2	0
IPI00361415.3	Pyridoxal_phosphate_phosphatase	TPGTGSLAAAVETASGR	99.99997337	0.368514106	0.997658493	0.99643308	0.881159734	0.977979004	0.712613435	0.2392183	0.753569066	0.417741824	0.724061541	0.63362083	0.42593923	-1.028814486	1.007766434	1.019680812	-1.008739025	1.011822559	-1.019865758	13366.67416	12992.3075	13470.48555	13353.78648	13629.74115	13364.2502	5.338960606	13.7064	13.6654	13.7175	13.705	13.7345	13.7061	0.02434	0.02434	0.02566	0.02434	0.02434	0.02566	4	4	0
IPI00205912.3	Non-POU_domain-containing_octamer-binding_protein	NLPQYVSNELLEEAFSVFGQVER	99.9999909	0.409342926	0.997658493	0.99643308	0.49686884	0.977979004	0.418299862	0.282095753	0.583577519	0.377668726	0.133306746	0.162247711	0.094909586	-1.050917979	-1.026233937	1.041496183	1.074219441	1.068818728	-1.083131301	13434.18423	12783.28519	13090.762	14062.35104	13991.6516	12917.77976	10.2441025	13.7136	13.642	13.6763	13.7796	13.7723	13.6571	0.04661	0.04661	0.04914	0.04661	0.04661	0.04914	3	3	0
IPI00231771.4	Protein_S100-B	AMVALIDVFHQYSGR	100	0.882626904	0.997658493	0.959908311	0.668421481	0.977979004	0.944410779	0.806833834	0.454786412	0.167449659	0.304239607	0.544803235	0.838142373	-1.011561655	1.036853757	1.067675865	1.05112885	1.029726572	1.009914521	14664.873	14497.26067	15205.32866	15982.75963	15657.33096	15812.56589	10.48770042	13.8401	13.8235	13.8923	13.9642	13.9346	13.9488	0.04772	0.04772	0.0503	0.04772	0.04772	0.0503	4	7	0
51771457	PREDICTED:_similar_to_eukaryotic_translation_initiation_factor_4A,_isoform_1_isoform_1_[Mus_musculus]	MFVLDEADEMLSR	99.99997938	0.446302616	0.997658493	0.99643308	0.532363335	0.977979004	0.983012577	0.316763677	0.317636255	0.98168079	0.16609736	0.328424256	0.93151468	1.06460742	-1.066310615	-1.001429978	1.093488443	1.064787992	-1.00551004	13017.81961	13858.86735	12208.28099	13349.61417	12999.23099	12927.99722	13.9154078	13.6682	13.7585	13.5756	13.7045	13.6661	13.6582	0.06318	0.06318	0.0666	0.06318	0.06318	0.0666	2	2	0
IPI00364431.2	PREDICTED:_similar_to_succinate-Coenzyme_A_ligase,_ADP-forming,_beta_subunit	ILACDDLDEAAK	99.99983925	0.1910604	0.997658493	0.99643308	0.90918008	0.977979004	0.979042717	0.091272283	0.964576139	0.780099133	0.803307566	0.751922631	0.918868074	1.059998547	1.001553885	-1.009549207	-1.008748256	-1.01111793	1.003567602	9002.866933	9543.025872	9016.856349	8938.658678	8917.709872	8949.52471	7.583301067	13.1362	13.2202	13.1384	13.1258	13.1225	13.1276	0.03455	0.03455	0.03642	0.03455	0.03455	0.03642	6	6	0
IPI00197770.1	Aldehyde_dehydrogenase,_mitochondrial_precursor	HEPVGVCGQIIPWNFPLLMQAWK	99.99991158	0.737973862	0.997658493	0.795267491	0.638878253	0.977979004	0.314955746	0.634235822	0.731772892	0.055608168	0.273790131	0.124557064	0.035994942	-1.012344819	-1.009118047	-1.051476147	1.02956072	-1.041975367	1.058340223	12139.77797	11991.74209	12030.08707	12385.70511	11545.46206	12219.02689	5.737134863	13.5675	13.5498	13.5544	13.5964	13.495	13.5768	0.02615	0.02615	0.02757	0.02615	0.02615	0.02757	6	6	0
IPI00362949.1	Ubiquinol-cytochrome_c_reductase_iron-sulfur_subunit,_mitochondrial_precursor	GVAGALRPLLQSAVPATSEPPVLDVK	99.99983727	0.106421825	0.997658493	0.99643308	0.984163624	0.977979004	0.673446244	0.035879358	0.473929128	0.217975638	0.971791281	0.624493551	0.348865675	-1.076160967	-1.025573374	-1.043405536	-1.001244645	-1.017387506	1.0336463	18240.50012	16949.60204	17785.66077	17763.55146	17481.69765	18069.89209	7.630025251	14.1549	14.049	14.1184	14.1166	14.0936	14.1413	0.03476	0.03476	0.03664	0.03476	0.03476	0.03664	6	6	0
IPI00231685.4	Neuron-specific_calcium-binding_protein_hippocalcin	LSLEEFIR	99.99987438	0.494216669	0.997658493	0.99643308	0.450498174	0.977979004	0.182066285	0.370521297	0.736542073	0.54021717	0.103183403	0.352400165	0.011833845	-1.042920556	-1.016298598	1.02909928	-1.082512907	1.045872155	-1.132805782	13698.02842	13134.29708	13478.35022	12450.98338	14096.63119	12443.9965	10.43101826	13.7417	13.6811	13.7184	13.604	13.7831	13.6032	0.04746	0.04746	0.05003	0.04746	0.04746	0.05003	4	4	0
IPI00210225.1	Isoform_Long_of_Discs_large_homolog_3	YGDILHVINASDDEWWQAR	99.99999998	0.164813431	0.997658493	0.99643308	0.454617724	0.977979004	0.832460662	0.073473947	0.855816513	0.570170162	0.106753728	0.463352786	0.583198155	-1.116778936	1.011407629	-1.035152704	-1.107337139	-1.046961342	-1.034894257	11024.94116	9872.089102	11150.7096	10069.84161	10650.54568	10291.43374	13.58140128	13.4285	13.2691	13.4448	13.2978	13.3786	13.3292	0.06168	0.06168	0.06501	0.06168	0.06168	0.06501	4	4	0
IPI00358524.3	PREDICTED:_similar_to_ectonucleotide_pyrophosphatase/phosphodiesterase_6	NVPTDINFANAVSDALDSLK	99.9954219	0.233114146	0.997658493	0.99643308	0.62797337	0.977979004	0.731856923	0.119088027	0.677632911	0.480651102	0.255495451	0.272332928	0.455842312	1.09393358	-1.024631023	1.041064917	1.069213181	1.06670741	-1.044701425	9705.485944	10617.15698	9472.17655	10127.77602	10104.04092	9671.702052	12.71892104	13.2446	13.3741	13.2095	13.306	13.3026	13.2396	0.05779	0.05779	0.06092	0.05779	0.05779	0.06092	2	2	0
IPI00203250.1	Isoform_2_of_Dihydropyrimidinase-related_protein_3	IVNDDQSFYADIYMEDGLIK	100	0.721189845	0.997658493	0.99643308	0.934974476	0.977979004	0.944410779	0.612393205	0.980915979	0.191407453	0.859773083	0.21175448	0.838636772	1.012767113	-1.000614786	-1.033491756	-1.004550045	-1.03285677	-1.005246868	22675.22016	22964.71726	22661.28832	22558.64547	21940.39772	21825.88022	5.569435019	14.4688	14.4871	14.4679	14.4614	14.4213	14.4138	0.02539	0.02539	0.02676	0.02539	0.02539	0.02676	8	12	0
1657657	brain_beta-spectrin_[Mus_musculus]	EIEELQSQAQALSQEGK	99.99995664	0.731762939	0.997658493	0.959908311	0.57026792	0.977979004	0.832460662	0.622207574	0.309839456	0.14803539	0.205296451	0.688159894	0.581871699	-1.020564741	1.044221214	1.062155445	-1.055609932	1.017174743	-1.023655064	13699.28866	13423.24315	14305.08783	13551.49037	14550.77404	14214.52846	9.202246867	13.7418	13.7124	13.8042	13.7262	13.8288	13.7951	0.04189	0.04189	0.04416	0.04189	0.04189	0.04416	2	2	0
IPI00207072.1	NADH_dehydrogenase_[ubiquinone]_iron-sulfur_protein_6,_mitochondrial_precursor	VYINLDKETK	99.965214	0.395783959	0.997658493	0.99643308	0.577643504	0.92052399	0.618548028	0.267251308	0.396465526	0.230909075	0.216533793	0.046973874	0.279937165	-1.056007105	1.04361088	-1.060675371	-1.064447985	-1.106932356	1.056023214	19201.37268	18182.99572	20038.76143	18825.49614	18102.96837	19117.15483	10.89799904	14.2289	14.1503	14.2905	14.2004	14.1439	14.2226	0.04957	0.04957	0.05225	0.04957	0.04957	0.05225	2	3	0
IPI00364916.2	PREDICTED:_similar_to_Alpha-2_catenin	VLTEAVDDITSVDDFLSVSENHILEDVNK	99.99979338	0.494216669	0.997658493	0.99643308	0.599602934	0.977979004	0.440189179	0.3700168	0.258972276	0.828234509	0.228245085	0.181734688	0.11721609	1.038676493	1.050436853	-1.009192749	1.05397359	-1.060093255	1.071095069	12176.17073	12647.10231	12790.29847	13480.63679	12065.25785	12923.03819	9.404139001	13.5718	13.6265	13.6428	13.7186	13.5586	13.6577	0.04281	0.04281	0.04512	0.04281	0.04281	0.04512	2	2	0
IPI00561103.2	Protein	GSYGDLGGPIITTQVTIPK	100	0.407901803	0.997658493	0.99643308	0.341387261	0.977979004	0.182066285	0.280170267	0.388753627	0.49430082	0.049159766	0.842896075	0.012068394	-1.031969069	1.02608418	1.020047068	-1.061493559	-1.005918464	-1.080111807	13658.69832	13235.56948	14014.97426	13203.07048	13932.51517	12899.14163	6.454607213	13.7375	13.6921	13.7747	13.6886	13.7662	13.655	0.02942	0.02942	0.03101	0.02942	0.02942	0.03101	6	6	0
IPI00765366.1	PREDICTED:_similar_to_tubulin,_beta_4	MAATFIGNSTAIQELFK	100	0.189264771	0.997658493	0.99643308	0.629348071	0.977979004	0.996576476	0.088684064	0.813883427	0.83403919	0.258931778	0.660624576	0.990838037	1.087622284	1.011839147	-1.010247198	1.058417286	-1.022207663	-1.000574099	23765.91991	25848.34411	24047.28814	25452.06544	23524.85607	23511.35822	10.85760576	14.5366	14.6578	14.5536	14.6355	14.5219	14.5211	0.04939	0.04939	0.05206	0.04939	0.04939	0.05206	34	74	0
IPI00566286.1	PREDICTED:_similar_to_heat_shock_protein_1,_alpha	HIYFITGETK	99.99999659	0.462177574	0.997658493	0.99643308	0.973913878	0.977979004	0.418312577	0.333824259	0.722807761	0.491511087	0.938328513	0.751987198	0.096500534	1.050880523	1.01881561	1.035874817	1.004071929	1.016744156	-1.092505546	10051.01491	10562.41581	10240.13089	10281.82797	10411.59324	9530.014081	11.41275755	13.2951	13.3667	13.3219	13.3278	13.3459	13.2183	0.0519	0.0519	0.05471	0.0519	0.0519	0.05471	4	6	0
126608	LYSOZYME_Spiked_Standard_(HEN)	NTDGSTDYGILQINSR	100	0.516102423	0.997658493	0.99643308	0.450498174	0.977979004	0.670153176	0.389288685	0.247898922	0.505954043	0.103562457	0.607583065	0.333429244	1.051076528	1.071318182	1.039180034	1.102605819	-1.030926448	1.0592435	26027.8111	27357.22131	27884.06727	30745.13483	27047.58164	28649.97504	12.88331622	14.6678	14.7396	14.7672	14.9081	14.7232	14.8062	0.05853	0.05853	0.0617	0.05853	0.05853	0.0617	13	21	0
IPI00208193.1	Nucleic_acid_binding_factor_pRM10	FGEVVDCTIK	99.9984862	0.896465088	0.997658493	0.846402451	0.993116531	0.977979004	0.670153176	0.827834116	0.510716217	0.091526371	0.98857657	0.316666887	0.343711395	-1.010188044	1.032057759	1.082991657	-1.000685693	1.04935179	-1.046580833	17242.43534	17068.5403	17795.18917	17782.9955	18673.41362	17842.30422	10.39762683	14.0737	14.0591	14.1192	14.1182	14.1887	14.123	0.04731	0.04731	0.04987	0.04731	0.04731	0.04987	2	2	0
IPI00209115.2	Slc25a3_protein	IQTQPGYANTLR	99.99999711	0.260702672	0.997658493	0.99643308	0.966345081	0.977979004	0.837394717	0.142418145	0.669844964	0.592962273	0.923560069	0.345342424	0.600353758	1.127274929	-1.036070961	1.044213702	-1.007999765	1.081879494	1.044523917	8489.54116	9570.046904	8193.976549	8128.946888	8864.895202	9259.59506	18.13254293	13.0515	13.2243	13.0003	12.9889	13.1139	13.1767	0.08206	0.08206	0.08649	0.08206	0.08206	0.08649	6	6	0
IPI00203344.1	G-septin_alpha	VVNVIPVIAK	99.9975472	0.253547667	0.997658493	0.99643308	0.876899711	0.988483763	0.985692829	0.135675463	0.659625782	0.682928793	0.711115734	0.965743896	0.938638052	-1.052375045	1.015447315	1.013931999	-1.012970202	-1.001494495	-1.002680505	13370.99583	12705.54247	13577.54181	13403.6932	13557.28052	13521.03731	7.542367378	13.7068	13.6332	13.7289	13.7103	13.7268	13.7229	0.03436	0.03436	0.03622	0.03436	0.03436	0.03622	2	2	0
IPI00551812.1	ATP_synthase_subunit_beta,_mitochondrial_precursor	DQEGQDVLLFIDNIFR	100	0.164813431	0.997658493	0.99643308	0.949009336	0.977979004	0.829230725	0.073656653	0.890013686	0.886825895	0.886103575	0.781982557	0.578092277	-1.06986781	1.005295691	-1.005304893	-1.005485784	-1.010628678	-1.021500227	23228.30677	21711.38018	23351.31672	23223.91533	23105.73333	22619.41085	8.286172512	14.5036	14.4062	14.5112	14.5033	14.496	14.4653	0.03774	0.03774	0.03978	0.03774	0.03774	0.03978	32	73	0
IPI00371236.3	PREDICTED:_similar_to_Tu_translation_elongation_factor,_mitochondrial	LLDAVDTYIPVPTR	99.99999999	0.734815425	0.997658493	0.99643308	0.705475595	0.977979004	0.121958101	0.626345329	0.629439313	0.266454789	0.345962011	0.12045499	0.004181421	1.016751151	1.017058249	-1.038836044	1.033697807	-1.056556768	1.110055325	25657.75263	26087.54952	26095.42897	26974.78769	24698.55834	27416.7662	7.595139066	14.6471	14.6711	14.6715	14.7193	14.5921	14.7428	0.0346	0.0346	0.03647	0.0346	0.0346	0.03647	4	4	0
IPI00199755.3	PREDICTED:_hypothetical_protein	AALAIQGK	99.9979684	0.311280174	0.997658493	0.99643308	0.813181576	0.977979004	0.673644494	0.18919644	0.915532547	0.383957661	0.578505649	0.340896451	0.354623832	1.110091349	-1.008633401	1.071362575	-1.04612579	1.080612077	1.078242837	18978.29481	21067.64088	18815.85003	17986.22136	20332.63479	21923.51782	17.6904224	14.2121	14.3627	14.1997	14.1346	14.3115	14.4202	0.08009	0.08009	0.08442	0.08009	0.08009	0.08442	2	2	0
IPI00365851.1	ATPase,_H+_transporting,_V1_subunit_D	AVELLVELASLQTSFVTLDEAIK	99.973318	0.119187666	0.997658493	0.99643308	0.572971917	0.977979004	0.907196794	0.042226487	0.178109468	0.285578004	0.207905954	0.754121804	0.748566955	1.09049422	1.060075583	1.045905872	-1.056012025	-1.013547787	1.01386693	12240.34669	13348.02732	12975.69265	12287.44782	12802.25048	12979.77839	9.321778754	13.5794	13.7043	13.6635	13.5849	13.6441	13.664	0.04244	0.04244	0.04473	0.04244	0.04244	0.04473	4	4	0
1934981	glucocorticoid_receptor_[Rattus_norvegicus]	CIIDKIR	91.7315	0.697597358	0.997658493	0.99643308	0.333651543	0.977979004	0.66199794	0.578806494	0.506757961	0.83180558	0.042739783	0.384905623	0.319712711	-1.039993388	-1.049394848	1.015096691	1.161610307	1.065237237	1.075145491	21172.79793	20358.58899	20176.19772	23436.87923	21492.43712	23107.49686	15.79355784	14.3699	14.3133	14.3004	14.5165	14.3915	14.4961	0.07161	0.07161	0.07548	0.07161	0.07161	0.07548	2	2	0
IPI00326099.3	Isoform_A_of_Glucocorticoid_receptor	CIIDKIR	91.7315	0.697597358	0.997658493	0.99643308	0.333651543	0.977979004	0.66199794	0.578806494	0.506757961	0.83180558	0.042739783	0.384905623	0.319712711	-1.039993388	-1.049394848	1.015096691	1.161610307	1.065237237	1.075145491	21172.79793	20358.58899	20176.19772	23436.87923	21492.43712	23107.49686	15.79355784	14.3699	14.3133	14.3004	14.5165	14.3915	14.4961	0.07161	0.07161	0.07548	0.07161	0.07161	0.07548	2	2	0
IPI00210119.1	STOP_protein	AVAIETQPAQGESDAVAR	99.99999992	0.242832763	0.997658493	0.99643308	0.733834025	0.977979004	0.533584354	0.125995514	0.710148337	0.375970804	0.421918447	0.622345037	0.203872154	1.059060154	1.01426811	1.033500562	-1.031164603	1.018961902	-1.049992405	10467.94338	11086.18173	10617.30115	10296.41739	10818.62537	10303.52726	8.265129955	13.3537	13.4365	13.3741	13.3299	13.4012	13.3309	0.03764	0.03764	0.03968	0.03764	0.03764	0.03968	6	6	0
IPI00205036.1	Alpha-2-globin_chain	AADHVEDLPGALSTLSDLHAHK	100	0.454985324	0.997658493	0.99643308	0.560474035	0.977979004	0.47023366	0.326665294	0.344719712	0.608337396	0.193839749	0.653338894	0.147787722	-1.072744051	-1.071945113	-1.037238719	1.100654752	1.033460373	1.112987662	23649.25211	22045.56818	22061.99909	24282.64413	22800.2018	25376.3433	15.95736904	14.5295	14.4282	14.4293	14.5676	14.4768	14.6312	0.07234	0.07234	0.07626	0.07234	0.07234	0.07626	16	29	0
IPI00230835.4	14-3-3_protein_gamma	TAFDDAIAELDTLNEDSYK	100	0.399465485	0.997658493	0.99643308	0.686643596	0.977979004	0.590127084	0.272205668	0.797632337	0.752360836	0.325904262	0.573510213	0.252631703	1.053923512	-1.012610207	1.015124858	1.049403236	1.027925793	-1.057858959	14360.62367	15134.99894	14181.78838	14882.41462	14577.82606	13780.50064	10.61192682	13.8098	13.8856	13.7918	13.8613	13.8315	13.7503	0.04828	0.04828	0.05089	0.04828	0.04828	0.05089	15	35	0
IPI00367666.3	34_kDa_protein	RVIISAPSADAPMFVM	99.99924787	0.246767949	0.997658493	0.99643308	0.776508778	0.977979004	0.901207579	0.129165395	0.701646112	0.948048224	0.46413039	0.655335734	0.737445287	-1.080225672	1.020005674	-1.003282254	-1.038651149	-1.023353591	1.017481691	19204.40269	17778.13951	19588.59971	18859.65247	19141.57519	19476.20229	11.22644634	14.2291	14.1178	14.2577	14.203	14.2244	14.2494	0.05106	0.05106	0.05382	0.05106	0.05106	0.05382	12	20	0
IPI00195851.1	Aldolase_A-like_1	TPSALAILENANVLAR	100	0.744003168	0.997658493	0.99643308	0.849985868	0.977979004	0.476387421	0.643635836	0.16571124	0.992200568	0.651471694	0.168554814	0.150266204	-1.019883169	1.063017567	1.000415669	-1.019946239	-1.062575888	1.06552862	17170.35288	16835.60764	18252.38674	17895.44002	17177.49006	18303.10728	9.481932265	14.0676	14.0392	14.1558	14.1273	14.0682	14.1598	0.04316	0.04316	0.0455	0.04316	0.04316	0.0455	19	28	0
IPI00287835.6	Hemoglobin_subunit_alpha-1/2	AADHVEDLPGALSTLSDLHAHK	100	0.454985324	0.997658493	0.99643308	0.519786998	0.977979004	0.469675267	0.326218686	0.355489585	0.592683573	0.155639078	0.684669888	0.146947348	-1.070264726	-1.067828044	-1.037568295	1.106741653	1.029164103	1.109205003	23465.41988	21924.87457	21974.90505	24320.54275	22615.78346	25085.54014	15.41069647	14.5182	14.4203	14.4236	14.5699	14.465	14.6146	0.06989	0.06989	0.07368	0.06989	0.06989	0.07368	17	31	0
IPI00370387.3	PREDICTED:_similar_to_prohibitin	AAELIANSLATAGDGLIELR	99.99999938	0.126343985	0.997658493	0.99643308	0.903404554	0.994226451	0.970372282	0.047182172	0.653567048	0.660370578	0.773450616	0.983111501	0.894644942	-1.067707786	-1.015058605	-1.014343995	-1.009626993	1.000704504	-1.004415944	11338.45195	10619.43361	11170.24366	11063.73318	11178.11315	11128.96824	7.215508656	13.4689	13.3744	13.4474	13.4336	13.4484	13.442	0.03288	0.03288	0.03465	0.03288	0.03288	0.03465	4	5	0
IPI00360356.1	PREDICTED:_similar_to_cytoplasmic_beta-actin	SYELPDGQVITIGNER	100	0.384647147	0.997658493	0.99643308	0.507654338	0.977979004	0.849367056	0.255312111	0.459221112	0.797266566	0.148831678	0.323383697	0.630283102	1.05697944	-1.037598885	1.01251748	1.075229604	1.050587009	-1.024255907	25222.30597	26659.45884	24308.33951	26137.04627	25538.02569	24933.24716	10.80417179	14.6224	14.7024	14.5692	14.6738	14.6404	14.6058	0.04915	0.04915	0.05181	0.04915	0.04915	0.05181	11	18	0
461586	ATP5I_MOUSE_ATP_synthase_e_chain,_mitochondrial	YSALIIGMAYGAK	99.99986218	0.247086905	0.997658493	0.99643308	0.536459109	0.977979004	0.959191605	0.130067184	0.887987228	0.809722865	0.168496813	0.707633191	0.863849821	-1.093264771	-1.008465773	1.014128294	-1.086730204	1.022713674	1.010316353	22191.56858	20298.4393	22005.27691	20249.07087	22505.0976	22737.26812	13.0171194	14.4377	14.3091	14.4256	14.3056	14.458	14.4728	0.05914	0.05914	0.06234	0.05914	0.05914	0.06234	3	3	0
IPI00231302.4	Neurofilament_triplet_L_protein	SAYSGLQSSSYLMSAR	100	0.893475939	0.997658493	0.86359048	0.525414564	0.977979004	0.974941498	0.82301898	0.162601217	0.114566489	0.16318917	0.884758077	0.903843336	-1.009731382	1.064701426	1.071587492	-1.064606405	1.006467603	1.005387686	13693.12066	13561.15191	14579.08509	13694.34283	14673.37682	14752.43237	9.655494619	13.7412	13.7272	13.8316	13.7413	13.8409	13.8487	0.04395	0.04395	0.04633	0.04395	0.04395	0.04633	24	30	0
IPI00212658.3	Guanine_nucleotide-binding_protein_G(I)/G(S)/G(T)_subunit_beta_2	IYAMHWGTDSR	99.99999995	0.267573173	0.997658493	0.99643308	0.911527876	0.977979004	0.711959443	0.148923583	0.501976334	0.731060039	0.810486826	0.735419286	0.423920994	1.062956	1.029370026	1.01450514	1.010372724	-1.014652351	-1.035110625	14420.71042	15328.58067	14844.24706	14998.22235	14629.88485	14133.64379	9.338637282	13.8159	13.9039	13.8576	13.8725	13.8366	13.7868	0.04251	0.04251	0.04481	0.04251	0.04251	0.04481	12	16	0
IPI00366416.2	PREDICTED:_similar_to_cytochrome_c-1	ALAEEVEVQDGPNEDGNMFMRPGK	99.99919091	0.697597358	0.997658493	0.99643308	0.727515376	0.977979004	0.624688993	0.578235669	0.61727774	0.982074107	0.394351737	0.632708144	0.286286041	1.035778273	-1.032985167	-1.001419557	-1.057009037	1.031520865	-1.072023665	10208.92859	10574.18642	9882.938221	9349.908916	10194.45698	9509.544719	14.11920171	13.3175	13.3683	13.2707	13.1907	13.3155	13.2152	0.0641	0.0641	0.06756	0.0641	0.0641	0.06756	2	2	0
2494630	G3PT_MOUSE_Glyceraldehyde-3-phosphate_dehydrogenase,_testis-specific_(Spermatogenic_cell-specific_glyce	VPTPNVSVVDLTCR	100	0.253547667	0.997658493	0.99643308	0.498231465	0.977979004	0.827199838	0.136126258	0.70910635	0.521853569	0.137510978	0.320616964	0.573977159	-1.092839873	1.022858744	-1.038542689	-1.095142303	-1.06228247	1.034677723	34119.49476	31220.94608	34899.42355	31867.47829	32853.24245	33992.5181	13.17025099	15.0583	14.9302	15.0909	14.9598	15.0037	15.0529	0.05983	0.05983	0.06306	0.05983	0.05983	0.06306	4	6	0
IPI00210212.5	38_kDa_protein	GFGFVTFDDHDPVDKIVLQK	99.99944418	0.908474472	0.997658493	0.846402451	0.416332803	0.141883765	0.300507042	0.852484508	0.052444737	0.097098283	0.082249935	0.000648612	0.033588048	1.004605874	1.051424275	-1.042421643	-1.04578525	-1.096027421	1.056695044	14338.35833	14404.39901	15075.69802	14415.67284	13754.85479	14534.68688	5.502650833	13.8076	13.8142	13.8799	13.8154	13.7477	13.8272	0.02509	0.02509	0.02644	0.02509	0.02509	0.02644	5	8	0
33859560	guanosine_diphosphate_(GDP)_dissociation_inhibitor_1_[Mus_musculus]	TDDYLDQPCLETINR	100	0.292903014	0.997658493	0.99643308	0.984163624	0.977979004	0.482636899	0.174068077	0.732232318	0.359613596	0.971434607	0.219215909	0.156098563	1.064239528	-1.016095287	1.042640772	-1.001671524	1.059422375	-1.069081372	16238.15733	17281.2889	15980.93952	15954.27157	16930.5649	15836.55402	10.12791142	13.9871	14.0769	13.9641	13.9617	14.0473	13.951	0.04609	0.04609	0.04858	0.04609	0.04609	0.04858	22	35	0
IPI00358033.1	NADH_dehydrogenase_(Ubiquinone)_Fe-S_protein_1	GLLTYTSWEDALSR	100	0.131487826	0.997658493	0.846402451	0.903404554	0.977979004	0.837394717	0.051500295	0.551792989	0.085345589	0.781774646	0.272910187	0.602061269	-1.042479142	-1.012927116	-1.037284923	1.005988822	-1.024046949	1.01131391	21026.06686	20169.29262	20757.72929	20882.04363	20270.29065	20499.62689	4.669656204	14.3599	14.2999	14.3414	14.35	14.3071	14.3233	0.02129	0.02129	0.02244	0.02129	0.02129	0.02244	23	25	0
IPI00211779.1	Peroxiredoxin-1	TIAQDYGVLK	99.99999982	0.910396276	0.997658493	0.99643308	0.79823953	0.977979004	0.469675267	0.856496537	0.213060292	0.552412105	0.558311534	0.500418842	0.147075455	1.004694702	1.0339434	1.015532017	-1.015722011	-1.01812979	1.039742767	10954.26506	11005.69207	11326.09006	11150.77742	11124.40689	11566.5216	5.767603859	13.4192	13.426	13.4674	13.4449	13.4414	13.4977	0.02629	0.02629	0.02771	0.02629	0.02629	0.02771	7	8	0
IPI00190869.1	GTPase_NRas_precursor	SALTIQLIQNHFVDEYDPTIEDSYRK	99.99989088	0.956183718	0.997658493	0.99643308	0.792374134	0.988483763	0.300507042	0.933243247	0.660426711	0.688454303	0.522773299	0.960783047	0.033656789	-1.00419229	-1.022819477	-1.020242143	1.033402015	1.002526198	1.117862868	11509.39116	11461.34189	11252.61243	11628.47236	11281.03876	12610.65434	11.14819781	13.4905	13.4845	13.458	13.5054	13.4616	13.6224	0.0507	0.0507	0.05345	0.0507	0.0507	0.05345	2	2	0
IPI00190701.5	Apolipoprotein_E_precursor	IKGWFEPLVEDMQR	99.99999922	0.132411747	0.997658493	0.99643308	0.864387973	0.977979004	0.897756662	0.052359388	0.627126228	0.842689104	0.680643787	0.769513737	0.723335368	-1.048139294	-1.011959079	-1.004733816	1.010120114	1.007191221	-1.00869632	13883.89474	13246.23055	13719.81834	13858.66447	13818.48059	13699.34669	5.298368593	13.7611	13.6933	13.744	13.7585	13.7543	13.7418	0.02416	0.02416	0.02546	0.02416	0.02416	0.02546	10	10	0
IPI00230787.4	Carbonic_anhydrase_2	IVLKEPITVSSEQMSHFR	99.99993221	0.665564226	0.997658493	0.99643308	0.354988387	0.977979004	0.725898654	0.54607529	0.516160065	0.663330547	0.056798142	0.285178136	0.444226291	1.024339752	1.026938449	-1.017478536	-1.08243855	-1.044887829	1.031844399	8577.58233	8786.358557	8808.649096	8137.782139	8430.234181	8698.689922	8.867025411	13.0664	13.101	13.1047	12.9904	13.0414	13.0866	0.04037	0.04037	0.04256	0.04037	0.04037	0.04256	5	7	0
IPI00392830.3	77_kDa_protein	HIYFITGETK	99.99999659	0.576758968	0.997658493	0.99643308	0.467884871	0.977979004	0.348219477	0.448883266	0.535337599	0.364215983	0.114237449	0.79057036	0.051602059	1.02999117	1.025139495	1.036085528	-1.066002875	1.010677604	-1.082495023	19765.56791	20358.36041	20262.46429	19007.88898	20478.81886	18918.16444	8.675793452	14.2707	14.3133	14.3065	14.2143	14.3218	14.2075	0.03951	0.03951	0.04164	0.03951	0.03951	0.04164	7	7	0
IPI00365393.2	PREDICTED:_similar_to_tubulin_polymerization-promoting_protein	TITFEQFQEALEELAK	100	0.155279398	0.997658493	0.99643308	0.933949271	0.988483763	0.994153085	0.068284024	0.899426512	0.843481126	0.856367053	0.947524389	0.974838111	1.061807562	1.004212008	1.006412323	-1.006038111	1.002191086	-1.00104942	14337.98852	15224.18463	14398.38023	14311.96301	14429.92832	14414.80115	7.21214138	13.8076	13.8941	13.8136	13.8049	13.8168	13.8153	0.03286	0.03286	0.03464	0.03286	0.03286	0.03464	6	6	0
IPI00203214.5	Elongation_factor_2	KIWCFGPDGTGPNILTDITK	99.9942576	0.420693285	0.997658493	0.99643308	0.557987386	0.977979004	0.343015874	0.29336189	0.937433372	0.446564354	0.191309961	0.507314209	0.041605608	1.051288651	-1.00382568	-1.036799509	1.066190181	-1.032848162	1.106425269	8086.997553	8501.76875	8056.177194	8589.417019	7799.962751	8630.075881	10.5652744	12.9814	13.0535	12.9759	13.0683	12.9293	13.0752	0.04807	0.04807	0.05067	0.04807	0.04807	0.05067	4	4	0
IPI00210920.1	Aspartate_aminotransferase,_mitochondrial_precursor	ASAELALGENSEVLK	100	0.395783959	0.997658493	0.99643308	0.877154628	0.977979004	0.440189179	0.267323794	0.972041142	0.480415276	0.714755714	0.470480031	0.116571439	1.054478161	1.001713219	-1.034196414	-1.018021682	-1.035968219	1.080656783	16573.2578	17476.1384	16601.65142	16307.75819	16025.25165	17317.7969	10.60823424	14.0166	14.0931	14.019	13.9933	13.9681	14.08	0.04826	0.04826	0.05087	0.04826	0.04826	0.05087	20	30	0
IPI00326260.3	Isoform_2_of_Neuroplastin_precursor	IVTSEEVIIR	99.9998078	0.140594471	0.997658493	0.99643308	0.966345081	0.977979004	0.348219477	0.059296365	0.6029097	0.474429191	0.919850777	0.859498662	0.051799413	1.094385013	1.02547264	1.03427693	1.004870925	1.008585592	1.100383823	11432.26642	12511.30103	11723.47643	11780.58061	11824.12942	13011.08073	10.48789638	13.4808	13.6109	13.5171	13.5241	13.5294	13.6675	0.04772	0.04772	0.0503	0.04772	0.04772	0.0503	3	4	0
IPI00192626.2	Isoform_1_of_Beta-adducin	MLDNLGYR	99.99974706	0.140594471	0.997658493	0.99643308	0.888968762	0.977979004	0.686505831	0.059612056	0.252610662	0.305542156	0.742669903	0.881615291	0.375206226	1.045845818	1.02805298	1.024380133	1.007924981	-1.003585433	1.021621071	12251.68782	12813.37647	12595.38417	12695.20234	12550.3856	12821.73838	5.208466498	13.5807	13.6454	13.6206	13.632	13.6154	13.6463	0.02375	0.02375	0.02503	0.02375	0.02375	0.02503	7	7	0
IPI00325884.5	Guanine_deaminase	FQSTDVAEEVYTR	100	0.420693285	0.997658493	0.99643308	0.807856171	0.977979004	0.872410761	0.293764111	0.454311726	0.911452635	0.570577273	0.5216806	0.673085074	-1.03319713	1.02413633	1.003446839	-1.018222174	-1.020618422	1.013513841	14318.53383	13858.47233	14664.13069	14401.70039	14367.88751	14562.05286	6.893339858	13.8056	13.7585	13.84	13.814	13.8106	13.8299	0.03141	0.03141	0.03311	0.03141	0.03141	0.03311	26	35	0
IPI00231816.4	Visinin-like_protein_1	VEMLEIIEAIYK	99.99993517	0.908474472	0.997658493	0.846402451	0.367357043	0.977979004	0.503151385	0.853446875	0.242698429	0.086573699	0.06465484	0.606295111	0.180436812	1.006687262	1.044552374	1.064722908	-1.072110464	1.019310218	-1.051353522	12780.12721	12865.59127	13349.51221	12451.6201	13607.29421	12942.64386	8.040933538	13.6416	13.6512	13.7045	13.604	13.7321	13.6598	0.03663	0.03663	0.03861	0.03663	0.03663	0.03861	7	7	0
IPI00324986.1	Rab_GDP_dissociation_inhibitor_alpha	TDDYLDQPCLETINR	100	0.311280174	0.997658493	0.99643308	0.990640456	0.977979004	0.494461272	0.189490484	0.697603766	0.374146833	0.982081866	0.212133937	0.172227139	1.061283756	-1.018121249	1.040920672	1.001037828	1.059783455	-1.065688729	16070.68834	17055.56049	15784.65076	15801.03251	16728.31171	15697.18366	10.02891363	13.9721	14.058	13.9462	13.9477	14.03	13.9382	0.04564	0.04564	0.04811	0.04564	0.04564	0.04811	24	37	0
IPI00199482.2	Similar_to_glutathione_transferase_GSTM7-7	PMTLGYWDIR	99.99999245	0.326142987	0.997658493	0.99643308	0.792374134	0.977979004	0.72175173	0.202971983	0.600515781	0.80272751	0.526187057	0.778696023	0.435859718	1.05432896	1.022459398	1.010356076	-1.027265821	-1.011979263	-1.033657238	20135.01435	21228.92874	20587.23465	20040.80562	20343.5341	19681.12189	9.194146582	14.2974	14.3737	14.3295	14.2907	14.3123	14.2645	0.04186	0.04186	0.04412	0.04186	0.04186	0.04412	5	6	0
7533042	AF245172_1_guanine_deaminase_[Rattus_norvegicus]	FQSTDVAEEVYTR	100	0.418903536	0.997658493	0.99643308	0.797370437	0.977979004	0.907196794	0.290599368	0.471133976	0.911576608	0.536744214	0.53971855	0.748037269	-1.033846468	1.023524661	1.003485099	-1.020118687	-1.019969964	1.01039763	14551.39794	14075.00861	14893.71464	14599.98217	14602.111	14753.93834	6.97974429	13.8289	13.7808	13.8624	13.8337	13.8339	13.8488	0.0318	0.0318	0.03352	0.0318	0.0318	0.03352	27	36	0
IPI00327185.3	nucleosome_assembly_protein_1-like_1	GIPEFWLTVFK	99.9945508	0.761257401	0.997658493	0.99643308	0.291125272	0.988483763	0.149954502	0.662076437	0.245582882	0.256636619	0.03327146	0.953963651	0.007883322	-1.014103013	1.03919053	1.037219159	-1.074208588	-1.001900631	-1.094687509	11429.25501	11270.30969	11877.17357	11056.67344	11854.64227	10829.24777	7.133199399	13.4804	13.4602	13.5359	13.4326	13.5332	13.4026	0.0325	0.0325	0.03426	0.0325	0.0325	0.03426	3	3	0
IPI00230897.4	Hemoglobin_subunit_beta-1	YFDSFGDLSSASAIMGNPK	100	0.994214891	0.997658493	0.99643308	0.416332803	0.977979004	0.418299862	0.990806154	0.212292954	0.871545451	0.083496456	0.274399584	0.09513334	-1.000675971	-1.078659148	-1.009528601	1.111609991	1.068478047	1.107299956	20146.08236	20132.47338	18676.96797	20761.50419	19955.93027	22097.20071	13.10579576	14.2982	14.2972	14.189	14.3416	14.2845	14.4316	0.05954	0.05954	0.06276	0.05954	0.05954	0.06276	18	31	0
IPI00215134.1	Isoform_Long_of_Clathrin_coat_assembly_protein_AP180	GLGSDLDSSLASLVGNLGISGTTSK	99.99999983	0.987191505	0.997658493	0.846402451	0.715782389	0.92052399	0.704501025	0.977037535	0.779831503	0.086160732	0.371388806	0.052601371	0.411805735	-1.000753586	-1.007547612	1.046612842	1.024421932	1.054512269	-1.022387227	16468.14637	16455.74556	16344.7823	16743.95346	17235.77347	16858.3615	5.829005278	14.0074	14.0063	13.9965	14.0314	14.0731	14.0412	0.02657	0.02657	0.02801	0.02657	0.02657	0.02801	11	14	0
IPI00387852.2	94_kDa_protein	GLGSDLDSSLASLVGNLGISGTTSK	99.99999983	0.987191505	0.997658493	0.846402451	0.715782389	0.92052399	0.704501025	0.977037535	0.779831503	0.086160732	0.371388806	0.052601371	0.411805735	-1.000753586	-1.007547612	1.046612842	1.024421932	1.054512269	-1.022387227	16468.14637	16455.74556	16344.7823	16743.95346	17235.77347	16858.3615	5.829005278	14.0074	14.0063	13.9965	14.0314	14.0731	14.0412	0.02657	0.02657	0.02801	0.02657	0.02657	0.02801	11	14	0
IPI00213551.1	Isoform_1_of_Brevican_core_protein_precursor	CEVQHGIDDSSDAVEVK	99.99999529	0.959297485	0.997658493	0.99643308	0.416332803	0.977979004	0.655416804	0.941756046	0.963610085	0.538855948	0.081899829	0.580396531	0.309356732	-1.002267098	-1.001453859	-1.019264986	1.05783212	-1.01778527	1.03306828	14603.2234	14570.19134	14582.02319	15425.33251	14327.20989	14800.98608	6.905325235	13.834	13.8307	13.8319	13.913	13.8065	13.8534	0.03147	0.03147	0.03317	0.03147	0.03147	0.03317	5	5	0
IPI00359278.2	Protein_C2orf32_homolog	VVYTGIYDTEGVAPTK	100	0.844525469	0.997658493	0.99643308	0.198010279	0.977979004	0.725898654	0.762485852	0.584185644	0.351303764	0.010862278	0.148630378	0.447128777	1.012489285	-1.023385022	1.039171821	1.11727706	1.063472877	1.032675286	12527.70095	12684.16297	12241.43472	13677.0742	13018.43381	13443.81486	9.154419488	13.6128	13.6307	13.5795	13.7395	13.6683	13.7147	0.04168	0.04168	0.04393	0.04168	0.04168	0.04393	5	5	0
IPI00213553.1	ProSAAS_precursor	GEAAGAVQELAR	99.99999991	0.819362758	0.997658493	0.959908311	0.933949271	0.977979004	0.628057626	0.728530543	0.825094217	0.165139276	0.854836943	0.256164927	0.288547618	-1.018475459	1.012043784	1.076651445	-1.009959273	1.0638388	-1.059497572	14256.9943	13998.36802	14428.70245	14286.4201	15349.81351	14487.82347	11.77124959	13.7994	13.773	13.8167	13.8024	13.9059	13.8226	0.05352	0.05352	0.05641	0.05352	0.05352	0.05641	6	6	0
IPI00193595.3	Eukaryotic_initiation_factor_4A-II	MFVLDEADEMLSR	99.99997938	0.360449564	0.997658493	0.99643308	0.733408131	0.977979004	0.80914378	0.232250931	0.580620374	0.897972638	0.398974023	0.498655964	0.547846441	1.053228245	-1.024810641	1.005543798	1.038200941	1.030491984	-1.027025804	9646.581074	10160.05165	9413.037579	9772.62447	9700.059772	9444.80629	9.616205573	13.2358	13.3106	13.2004	13.2545	13.2438	13.2053	0.04377	0.04377	0.04614	0.04377	0.04377	0.04614	4	4	0
31980648	ATP_synthase,_H+_transporting_mitochondrial_F1_complex,_beta_subunit_[Mus_musculus]	DQEGQDVLLFIDNIFR	100	0.252744602	0.997658493	0.99643308	0.950644423	0.977979004	0.894800678	0.134414407	0.868660591	0.915949291	0.890653499	0.788686329	0.719931059	-1.059697996	1.006531602	-1.004052148	1.00542705	-1.010610217	-1.014223583	22252.44509	20998.85549	22397.78919	22519.3431	22162.63879	21851.82752	8.542077577	14.4417	14.358	14.4511	14.4589	14.4358	14.4155	0.0389	0.0389	0.041	0.0389	0.0389	0.041	30	66	0
IPI00285606.5	CDC42_protein	CVVVGDGAVGK	99.99999838	0.370250272	0.997658493	0.99643308	0.792374134	0.977979004	0.84424164	0.241614749	0.64832251	0.924052735	0.525283108	0.71620931	0.614607914	-1.107144529	1.04133361	1.008265771	-1.058087259	-1.032796749	1.045737598	20942.22724	18915.53152	21807.8451	20610.63009	21115.33088	22081.09539	19.39386094	14.3541	14.2073	14.4126	14.3311	14.366	14.4305	0.08766	0.08766	0.09241	0.08766	0.08766	0.09241	3	3	0
IPI00373076.1	PREDICTED:_similar_to_ATPase,_H+_transporting,_V1_subunit_A,_isoform_1_isoform_1	TALVANTSNMPVAAR	100	0.407480734	0.997658493	0.99643308	0.498231465	0.977979004	0.808231386	0.27941536	0.767660702	0.948209128	0.136256096	0.816323856	0.543131492	1.058293074	-1.015941736	-1.003388995	1.08392793	1.012510343	-1.033135205	17467.41685	18485.64628	17193.32541	18636.32562	17408.4198	16850.08866	11.62963625	14.0924	14.1741	14.0696	14.1858	14.0875	14.0405	0.05288	0.05288	0.05574	0.05288	0.05288	0.05574	23	30	0
IPI00371462.3	PREDICTED:_similar_to_OTU_domain,_ubiquitin_aldehyde_binding_1	AFGFSHLEALLDDSKELQR	99.99998776	0.525774937	0.997658493	0.99643308	0.342215144	0.977979004	0.569356066	0.398387181	0.386064393	0.75780245	0.052302806	0.245005118	0.234776064	1.033045064	-1.034883553	1.011905965	1.081023015	1.047204841	-1.048282562	14802.95027	15292.11471	14303.97674	15462.92807	14979.19369	14289.27107	8.552867692	13.8536	13.9005	13.8041	13.9165	13.8707	13.8026	0.03895	0.03895	0.04106	0.03895	0.03895	0.04106	3	4	0
IPI00202627.1	Secernin_1	DGLVVFGK	99.97738	0.932837436	0.997658493	0.869092652	0.576914427	0.977979004	0.825701789	0.897512307	0.820449016	0.119518007	0.213080363	0.082799452	0.56902649	-1.004888273	-1.008868729	1.061446491	1.050003258	1.070860173	-1.022431715	12963.80111	12900.73877	12849.83936	13492.37319	13760.3812	13458.48431	8.439139335	13.6622	13.6552	13.6495	13.7199	13.7482	13.7162	0.03843	0.03843	0.04051	0.03843	0.03843	0.04051	3	3	0
IPI00197568.1	Rab_GDP_dissociation_inhibitor_beta	KFDLGQDVIDFTGHSLALYR	99.99999977	0.470124215	0.997658493	0.99643308	0.718361311	0.977979004	0.520988984	0.344399568	0.449940799	0.36220084	0.375189851	0.103743394	0.191852388	1.030094943	-1.024601584	1.028977496	1.028968485	1.054291972	-1.043119549	14462.64009	14897.89243	14115.37941	14524.28056	14881.73119	14266.56341	6.956824835	13.82	13.8628	13.785	13.8262	13.8613	13.8004	0.0317	0.0317	0.03341	0.0317	0.0317	0.03341	9	10	0
984679	beta-globin_[Rattus_norvegicus]	YFDSFGDLSSASAIMGNPK	100	0.989382285	0.997658493	0.99643308	0.450498174	0.977979004	0.418299862	0.981865075	0.102366972	0.397719159	0.100386879	0.408752768	0.094999193	1.001347602	-1.105975942	-1.051563554	1.106640748	1.05174427	1.108508031	20389.7637	20417.241	18435.99207	20402.02005	19389.94901	21493.9142	13.24165401	14.3156	14.3175	14.1702	14.3164	14.243	14.3916	0.06015	0.06015	0.0634	0.06015	0.06015	0.0634	18	31	0
IPI00421723.1	Tubulin_cofactor_a	MKAEDGENYAIKK	99.994205	0.169170218	0.997658493	0.846402451	0.628717364	0.977979004	0.696071914	0.075981595	0.738365933	0.092489308	0.257235219	0.188522041	0.390595783	-1.060839539	-1.011317595	-1.057501089	-1.039136698	-1.045666658	1.029439562	12820.58536	12085.32007	12677.11096	12199.65669	12123.47249	12480.38221	7.303613306	13.6462	13.561	13.6299	13.5746	13.5655	13.6074	0.03328	0.03328	0.03508	0.03328	0.03328	0.03508	2	2	0
IPI00210536.1	Isoform_L-MAG_of_Myelin-associated_glycoprotein_precursor	LREDEGTWVQVSLLHFVPTR	99.99998994	0.173761429	0.997658493	0.99643308	0.923529101	0.977979004	0.73259831	0.07892257	0.626906351	0.924700007	0.832635949	0.693324628	0.457141345	1.078633071	1.021445551	1.004019405	-1.009258758	-1.017356384	1.033042376	9944.345067	10726.29946	10157.60702	10064.42297	9984.315414	10314.22092	9.465352701	13.2797	13.3889	13.3103	13.297	13.2854	13.3323	0.04309	0.04309	0.04542	0.04309	0.04309	0.04542	4	4	0

SUPPLEMENTAL TABLE A. All priority 1 proteins measured in the nucleus accumbens shell of P, NP and W rats

IPI00198567.1	LIM_and_SH3_domain_protein_1	MGPSGGEGIEPERR	99.957866	0.800707901	0.997658493	0.99643308	0.367357043	0.988483763	0.957172872	0.708283332	0.606749388	0.629664448	0.064553431	0.963698783	0.858720805	-1.016042559	-1.022762669	-1.020731822	1.085537008	1.001989599	1.007805152	16605.62245	16343.43199	16236.04669	17624.82954	16268.34992	16395.32686	9.480415318	14.0194	13.9964	13.9869	14.1053	13.9898	14.001	0.04315	0.04315	0.04549	0.04315	0.04315	0.04549	2	2	0
3334470	MAG_MOUSE_Myelin-associated_glycoprotein_precursor_(Siglec-4a)	LREDEGTWVQVSLLHFVPTR	99.99998994	0.173761429	0.997658493	0.99643308	0.923529101	0.977979004	0.735808484	0.079235212	0.627999201	0.921640407	0.831937004	0.697229764	0.461667266	1.078869635	1.021417543	1.004191524	-1.009315872	-1.017154117	1.032766659	9905.311137	10684.8555	10117.45857	10024.07556	9946.829485	10272.75385	9.483331389	13.274	13.3833	13.3046	13.2912	13.28	13.3265	0.04317	0.04317	0.0455	0.04317	0.04317	0.0455	4	4	0
IPI00339124.2	Sodium/potassium-transporting_ATPase_subunit_beta-1	SYEAYVLNIIR	99.9999997	0.601707784	0.997658493	0.99643308	0.789502069	0.988483763	0.666788291	0.477240231	0.732802292	0.787585184	0.499867596	0.936843855	0.327228931	1.071171445	-1.034445714	-1.026351077	-1.069335887	1.007886811	1.102502545	16223.69965	17378.3638	15683.47129	14666.55284	15807.16386	17427.43838	21.72370196	13.9858	14.085	13.937	13.8402	13.9483	14.0891	0.09797	0.09797	0.1033	0.09797	0.09797	0.1033	13	18	0
IPI00188880.1	Striatin	GPLLGHTDAVWGLAYSAAHQR	99.9988653	0.399465485	0.997658493	0.99643308	0.718821841	0.977979004	0.872410761	0.272549594	0.684680274	0.85615452	0.376379652	0.560621876	0.672441329	-1.053912666	-1.020064838	1.008663296	1.044360802	1.028901961	1.020900723	11349.89302	10769.29179	11126.63882	11620.22544	11448.2205	11687.49658	10.61758105	13.4704	13.3946	13.4417	13.5044	13.4828	13.5127	0.0483	0.0483	0.05092	0.0483	0.0483	0.05092	2	2	0
IPI00554155.3	PREDICTED:_similar_to_nucleolar_protein_1	QQLVGQQHSK	99.18913	0.720198551	0.997658493	0.99643308	0.377716762	0.977979004	0.864332588	0.609905287	0.296437218	0.458836789	0.068063459	0.7440099	0.659856193	-1.030935267	1.06642764	1.045291343	-1.120332161	-1.020220484	1.02735969	7433.009986	7209.967707	7926.767295	7075.372439	7769.660988	7982.236506	13.33023435	12.8597	12.8158	12.9525	12.7886	12.9236	12.9626	0.06055	0.06055	0.06382	0.06055	0.06055	0.06382	2	2	0
IPI00191444.3	31_kDa_protein	NLSDLIDLVPSLCEDLLSSVDQPLK	99.99997061	0.287569668	0.997658493	0.99643308	0.800808209	0.977979004	0.712613435	0.168225612	0.66936258	0.797894454	0.56193856	0.499530714	0.425754389	-1.035068585	-1.010942548	1.006368814	1.014901969	1.017381053	-1.020551957	7405.524675	7154.622201	7325.366498	7434.528884	7452.689081	7302.606234	5.519565729	12.8544	12.8047	12.8387	12.86	12.8635	12.8342	0.02516	0.02516	0.02652	0.02516	0.02516	0.02652	5	6	0
IPI00213436.2	PREDICTED:_similar_to_NADH-ubiquinone_oxidoreductase_MLRQ_subunit	FYSVNVDYSK	99.99999428	0.51786338	0.997658493	0.99643308	0.863165572	0.977979004	0.348219477	0.391208793	0.922079436	0.610174968	0.678694758	0.552742522	0.050389111	1.035310209	-1.004061084	1.020798973	1.017325714	1.024944523	1.0861025	19544.42996	20234.54788	19465.37942	19802.63101	19950.93403	21668.75933	8.992262063	14.2545	14.3045	14.2486	14.2734	14.2842	14.4033	0.04094	0.04094	0.04316	0.04094	0.04094	0.04316	4	5	0
IPI00231253.4	3-hydroxyacyl-CoA_dehydrogenase_type-2	VVTIAPGLFATPLLTTLPDKVR	99.917287	0.908474472	0.997658493	0.99643308	0.525414564	0.988483763	0.609075496	0.851674923	0.643640294	0.701258312	0.16332887	0.92873643	0.269045479	1.008381604	1.021462028	1.017281453	1.066653312	-1.004109556	1.052304717	8071.632258	8139.285484	8244.865857	8794.413475	8211.121788	8640.602191	9.956567455	12.9786	12.9907	13.0093	13.1024	13.0034	13.0769	0.04531	0.04531	0.04776	0.04531	0.04531	0.04776	2	2	0
IPI00387868.2	Ischemia_responsive_94_kDa_protein	GCALQCAILSPAFK	100	0.601707784	0.997658493	0.99643308	0.788902735	0.977979004	0.932942733	0.476877168	0.770499123	0.639592583	0.491206419	0.869416344	0.822055825	-1.021159347	1.008843217	1.013859803	1.021033421	1.004972612	-1.006809608	12020.91013	11771.82598	12127.21364	12382.29043	12187.51757	12105.08668	6.541373853	13.5533	13.5231	13.566	13.596	13.5731	13.5633	0.02981	0.02981	0.03142	0.02981	0.02981	0.03142	10	10	0
IPI00361267.4	36_kDa_protein	DGRGAAQNIIPASTGAAK	99.99999835	0.720495749	0.997658493	0.99643308	0.502800017	0.977979004	0.38112535	0.610980395	0.498222053	0.966590622	0.140308713	0.472898859	0.068481153	1.022482741	1.030912673	-1.001830137	1.069126244	-1.032799385	1.086587533	19399.97825	19836.14295	19999.68345	21382.18644	19364.53849	21041.26612	9.737560322	14.2438	14.2758	14.2877	14.3841	14.2411	14.3609	0.04432	0.04432	0.04672	0.04432	0.04432	0.04672	11	13	0
IPI00201969.1	Vesicle_amine_transport_protein_1_homolog	ACGLNFADLMGR	99.99999441	0.942438635	0.997658493	0.99643308	0.186627414	0.977979004	0.910343272	0.913357671	0.182909524	0.739323324	0.009384693	0.310460969	0.755782417	1.00548968	1.017910598	1.016891942	-1.148888928	-1.054104722	1.01621519	15255.66834	15339.41708	16352.71257	14233.50175	15513.3662	15764.91839	11.23171858	13.8971	13.905	13.9972	13.797	13.9212	13.9444	0.05108	0.05108	0.05384	0.05108	0.05108	0.05384	2	2	0
IPI00231506.4	Phosphoglycerate_mutase_2	HYGGLTGLNKAETAAK	99.99924451	0.434942942	0.997658493	0.99643308	0.471474337	0.977979004	0.857920499	0.305205676	0.557780933	0.968204606	0.118213146	0.532147065	0.651039099	1.048573464	-1.028150456	1.001836192	1.077620891	1.030038379	1.021639669	14374.56047	15072.78266	13980.98925	15066.20609	14400.95492	14712.58681	10.26867069	13.8112	13.8797	13.7712	13.879	13.8139	13.8448	0.04672	0.04672	0.04925	0.04672	0.04672	0.04925	3	4	0
IPI00373024.4	Nectin-like_protein_3	AYLTVLGVPEKPQISGFSSPVMEGDLMQLTCK	99.99904735	0.287569668	0.997658493	0.99643308	0.815642478	0.977979004	0.343015874	0.168597988	0.60124097	0.821595603	0.590059073	0.458773928	0.045846409	1.07448552	1.028189009	-1.011730207	-1.02907421	-1.040249879	1.114221978	12240.30604	13152.03159	12585.34814	12229.77703	12098.38942	13480.29139	11.54427119	13.5794	13.683	13.6195	13.5781	13.5625	13.7186	0.05249	0.05249	0.05533	0.05249	0.05249	0.05533	4	4	0
IPI00214454.2	Glycine_cleavage_system_H_protein,_mitochondrial_precursor	MTLSDPSELDELMSEEAYEK	100	0.30883246	0.997658493	0.99643308	0.788902735	0.977979004	0.996781381	0.185652427	0.749455002	0.791105446	0.497526143	0.564287588	0.993363845	-1.069175506	-1.016585133	1.013365481	1.035622096	1.030172283	1.000428276	11600.53605	10849.98299	11411.27848	11817.77214	11755.5828	11760.61744	11.18555742	13.5019	13.4054	13.4782	13.5287	13.5211	13.5217	0.05087	0.05087	0.05362	0.05087	0.05087	0.05362	2	2	0
IPI00388289.1	Cell_division_cycle_42	CVVVGDGAVGK	99.99999838	0.627250404	0.997658493	0.99643308	0.783271466	0.977979004	0.780724823	0.506101468	0.469169149	0.750167366	0.474106523	0.677960535	0.511263227	-1.053336379	1.059862945	1.025154058	-1.059177171	-1.033857241	1.054153005	16865.35939	16011.37084	17874.96948	16876.27902	17289.59162	18225.87496	17.48498879	14.0418	13.9668	14.1257	14.0427	14.0776	14.1537	0.07917	0.07917	0.08345	0.07917	0.07917	0.08345	4	4	0
IPI00187698.2	32_kDa_protein	AIENIDTLTNLESLFLGK	100	0.919446795	0.997658493	0.99643308	0.974820419	0.978543127	0.315622627	0.871110163	0.812605498	0.704422935	0.942949014	0.894703889	0.036431869	-1.004416037	1.006637509	1.010361691	1.001998564	1.003699626	-1.061439203	15775.95152	15706.59063	15880.66454	15912.40307	15939.41706	15016.79702	6.048298472	13.9454	13.9391	13.955	13.9579	13.9603	13.8743	0.02757	0.02757	0.02906	0.02757	0.02757	0.02906	4	4	0
IPI00231192.4	Hemoglobin_subunit_beta-2	FGDLSSASAIMGNPQVK	100	0.784311359	0.997658493	0.99643308	0.617018123	0.977979004	0.554444403	0.690193996	0.243475114	0.82398549	0.244691759	0.340427629	0.219243158	1.022676906	-1.070159579	-1.012584697	1.069970164	1.056859326	1.074091968	19368.34548	19807.55962	18226.89161	19364.91533	19127.63006	20544.8338	12.55859503	14.2414	14.2738	14.1436	14.2412	14.2234	14.3265	0.05707	0.05707	0.06016	0.05707	0.05707	0.06016	15	22	0
IPI00206054.1	Contactin-1_precursor	IKTDGAAPNVAPSDVGGGGGTNR	99.99997841	0.284389622	0.997658493	0.99643308	0.736310101	0.977979004	0.776665617	0.165108489	0.843383697	0.596331464	0.429774856	0.47639746	0.507717409	1.044399458	-1.006314349	1.016580837	1.025548272	1.022999884	1.021370051	10806.27392	11286.06662	10738.46749	11012.81677	10985.45099	11220.21064	6.907767398	13.3996	13.4623	13.3905	13.4269	13.4233	13.4538	0.03148	0.03148	0.03318	0.03148	0.03148	0.03318	14	14	0
IPI00205634.4	PREDICTED:_similar_to_ankyrin_2_isoform_2	ELGDDSLPSSQFLDGMNYLR	99.99998761	0.712372332	0.997658493	0.99643308	0.788902735	0.977979004	0.325774813	0.598392759	0.947852147	0.293655095	0.489065888	0.277138098	0.038348349	-1.018656467	1.00235786	-1.037694823	-1.025281922	-1.040141562	1.079127359	11717.84263	11503.23295	11745.47166	11455.84585	11292.18569	12185.70651	7.811040519	13.5164	13.4898	13.5198	13.4838	13.463	13.5729	0.03558	0.03558	0.03751	0.03558	0.03558	0.03751	8	8	0
IPI00214448.1	Mu-crystallin_homolog	GFLGVMPAYSAAEDALTTK	99.99999973	0.67537681	0.997658493	0.99643308	0.813638662	0.977979004	0.946581826	0.554966773	0.614912159	0.776291387	0.585645026	0.820462296	0.841646469	1.020262051	-1.017709714	-1.009689691	-1.019209472	1.007943057	1.004988686	15375.16693	15686.69936	15107.61538	14822.87576	15227.61604	15334.03706	7.55970408	13.9083	13.9373	13.883	13.8555	13.8944	13.9044	0.03444	0.03444	0.0363	0.03444	0.03444	0.0363	11	11	0
IPI00212811.1	Cathepsin_B_precursor	HEAGDVMGGHAIR	99.99988519	0.311280174	0.997658493	0.99643308	0.548262079	0.977979004	0.902380455	0.189614094	0.792968418	0.907639194	0.181083132	0.707497395	0.741498911	-1.073079628	1.014487371	-1.006205986	-1.076709971	-1.020783265	1.018245705	10835.12777	10097.22623	10992.10029	10208.97046	10768.29986	10964.77508	11.90817065	13.4034	13.3017	13.4242	13.3175	13.3945	13.4206	0.05414	0.05414	0.05706	0.05414	0.05414	0.05706	5	5	0
IPI00369496.3	61_kDa_protein	IPCVDAGLISPLVQLLNSKDQEVLLQTGR	99.9986319	0.928097019	0.997658493	0.938007139	0.315028161	0.988483763	0.405470553	0.884917712	0.169810971	0.141505077	0.036363251	0.951620818	0.086198525	-1.005439519	-1.054792391	-1.057259355	1.085805339	-1.002338814	1.069314179	7708.412643	7666.709429	7307.990374	7935.054967	7290.938223	7796.30362	8.354260596	12.9122	12.9044	12.8353	12.954	12.8319	12.9286	0.03805	0.03805	0.04011	0.03805	0.03805	0.04011	2	2	0
IPI00206664.1	acid_phosphatase_1,_soluble	SVLFVCLGNICR	99.99986126	0.734898948	0.997658493	0.99643308	0.954046054	0.977979004	0.490453166	0.6290735	0.662698935	0.776792386	0.898326149	0.872467758	0.167594853	1.014367763	1.013320315	1.008401637	1.003880495	-1.004877698	-1.043117304	15231.27696	15450.11634	15434.16237	15494.05456	15359.24461	14724.3695	6.571832209	13.8947	13.9153	13.9138	13.9194	13.9068	13.8459	0.02995	0.02995	0.03157	0.02995	0.02995	0.03157	2	2	0
IPI00373134.2	PREDICTED:_similar_to_fumarylacetoacetate_hydrolase_domain_containing_2A	TEDLIAWVSQFVTLYPGDILLTGTPPGVGMFR	99.84973	0.201425078	0.997658493	0.795267491	0.450498174	0.977979004	0.931974488	0.097850729	0.002632418	0.055443835	0.102155858	0.21597302	0.813574362	1.070714912	1.140630212	1.082658124	-1.071747452	-1.05354607	-1.009919321	3931.413687	4209.423262	4484.289226	4184.091335	4256.376967	4214.571281	9.082242579	11.9408	12.0394	12.1307	12.0307	12.0554	12.0412	0.04135	0.04135	0.04359	0.04135	0.04135	0.04359	2	2	0
IPI00206406.2	protein_phospatase_3,_regulatory_subunit_B,_alpha_isoform,type_1	IYDMDKDGYISNGELFQVLK	99.99999943	0.535927591	0.997658493	0.99643308	0.367357043	0.977979004	0.260548875	0.408529947	0.690849332	0.497159408	0.061800353	0.791595803	0.024417152	-1.058914554	1.028630951	1.04809713	-1.144239132	1.018924357	-1.177761959	15700.44515	14826.92357	16149.96382	14114.15094	16455.59151	13971.9163	15.45339915	13.9385	13.8559	13.9792	13.7849	14.0063	13.7702	0.07009	0.07009	0.07388	0.07009	0.07009	0.07388	4	7	0
IPI00213408.4	Actin_related_protein_2/3_complex,_subunit_5-like	ALAVGGLGSIIR	99.9999988	0.855428256	0.997658493	0.99643308	0.231514459	0.977979004	0.699167779	0.773307144	0.213537537	0.588446222	0.015610689	0.469044987	0.400323494	1.008503057	-1.038558581	-1.016048599	1.078000833	1.022154434	1.02580379	14139.80169	14260.03324	13614.83305	14676.80137	13916.46198	14275.55944	6.545632161	13.7875	13.7997	13.7329	13.8412	13.7645	13.8013	0.02983	0.02983	0.03144	0.02983	0.02983	0.03144	3	3	0
IPI00365323.2	PREDICTED:_similar_to_coactosin-like_1	FALITWGEDVSGLQR	100	0.476758746	0.997658493	0.99643308	0.984163624	0.977979004	0.520988984	0.351984172	0.906525916	0.532361233	0.967773379	0.468768231	0.193066004	-1.029460455	-1.003754858	1.019623492	1.001290264	1.023452033	-1.042772932	7624.76351	7406.562803	7596.240705	7606.041859	7774.387994	7455.494629	6.921143602	12.8965	12.8546	12.8911	12.8929	12.9245	12.8641	0.03154	0.03154	0.03324	0.03154	0.03154	0.03324	4	4	0
IPI00627068.1	Splicing_factor_proline/glutamine_rich	NLSPYVSNELLEEAFSQFGPIER	99.99999939	0.600662032	0.997658493	0.99643308	0.655810826	0.977979004	0.666788291	0.473664917	0.448757386	0.894986834	0.288556763	0.376307677	0.327738376	1.040182413	-1.043731138	1.007266264	1.061974246	1.051315164	-1.056967138	14541.39095	15125.69912	13932.12335	14795.55618	14647.05254	13857.62339	12.25052117	13.8279	13.8847	13.7661	13.8529	13.8383	13.7584	0.05568	0.05568	0.05869	0.05568	0.05568	0.05869	4	4	0
IPI00212346.1	Neurabin-1	IQVNDQIVEVDGISLVGVTQNFAATVLR	99.9985087	0.596143063	0.997658493	0.99643308	0.54769755	0.977979004	0.985692829	0.468057468	0.622208022	0.839253349	0.180270737	0.490702484	0.943410245	-1.026347894	-1.01828307	1.007279283	1.050896542	1.02569544	1.00261056	6711.373013	6539.081973	6590.871644	6926.324221	6760.226994	6777.874975	7.96780397	12.7124	12.6749	12.6863	12.7579	12.7229	12.7266	0.03629	0.03629	0.03826	0.03629	0.03629	0.03826	2	2	0
2493437	CANB1_MOUSE_Calcineurin_subunit_B_isoform_1_(Protein_phosphatase_2B_regulatory_subunit_1)_(Protein_p	IYDMDKDGYISNGELFQVLK	99.99999943	0.484170148	0.997658493	0.99643308	0.360181899	0.977979004	0.34532203	0.358931871	0.681843776	0.545803066	0.058461588	0.858188285	0.048147757	-1.063732114	1.028675886	1.041422087	-1.141893473	1.012390881	-1.148880053	14910.53645	14017.19122	15338.1093	13432.1718	15528.16199	13515.91227	15.0092839	13.864	13.7749	13.9048	13.7134	13.9226	13.7224	0.06809	0.06809	0.07178	0.06809	0.06809	0.07178	5	9	0
IPI00212655.3	Guanine_nucleotide-binding_protein_G(I)/G(S)/G(T)_subunit_beta_1	LLLAGYDDFNCNVWDALK	100	0.627250404	0.997658493	0.99643308	0.498231465	0.977979004	0.849367056	0.505907805	0.487026863	0.684049532	0.137796588	0.764072696	0.631867994	1.022766899	1.024464555	1.013847759	1.053419087	-1.010471785	1.016779335	15357.18259	15706.81802	15732.88923	16573.32581	15569.84516	15831.0968	7.525191901	13.9066	13.9391	13.9415	14.0166	13.9265	13.9505	0.03428	0.03428	0.03614	0.03428	0.03428	0.03614	20	29	0
IPI00567272.2	37_kDa_protein	GAAQNIIPASTGAAK	99.9999718	0.487587317	0.997658493	0.99643308	0.718361311	0.977979004	0.454871916	0.362764964	0.67400309	0.376934292	0.37507879	0.202597107	0.138281062	-1.046373245	1.021690047	-1.044979807	-1.046426045	-1.067645469	1.079346568	27638.7629	26413.86622	28238.24897	26985.42252	26449.08802	28547.73239	11.07310856	14.7544	14.689	14.7854	14.7199	14.6909	14.8011	0.05036	0.05036	0.05309	0.05036	0.05036	0.05309	2	3	0
IPI00205332.3	Electron_transfer_flavoprotein_subunit_alpha,_mitochondrial_precursor	TIVAINKDPEAPIFQVADYGIVADLFK	99.99997522	0.624175914	0.997658493	0.99643308	0.63922298	0.977979004	0.861432408	0.500054075	0.421794204	0.859734919	0.279050775	0.527009278	0.65468863	-1.025088249	1.030817129	1.006500378	-1.041855748	-1.024159704	1.017005402	14301.51704	13951.49837	14742.24874	14149.99031	14394.48231	14639.26627	8.171848264	13.8039	13.7681	13.8477	13.7885	13.8132	13.8376	0.03722	0.03722	0.03923	0.03722	0.03722	0.03923	3	3	0
IPI00200845.1	Actin-related_protein_2/3_complex_subunit_1A	TLESSIQGLR	99.967599	0.974683592	0.997658493	0.99643308	0.868162741	0.977979004	0.366287193	0.960810764	0.811166265	0.629643379	0.691453971	0.479462639	0.062373476	-1.003796143	1.019113807	-1.037928406	1.03196672	-1.05776717	1.162024168	14451.11688	14396.46583	14727.33274	15198.11726	13923.03823	16178.90691	17.28681694	13.8189	13.8134	13.8462	13.8916	13.7652	13.9818	0.07829	0.07829	0.08252	0.07829	0.07829	0.08252	2	2	0
IPI00212553.2	Protein_bassoon	LQLEQIQQLQQQLQQQLEEQKQR	99.99936629	0.504990663	0.997658493	0.99643308	0.966312395	0.977979004	0.580472536	0.379752978	0.898226851	0.563067869	0.914407615	0.663222713	0.243441513	1.036574873	1.005368824	1.023880874	-1.004509598	1.018413193	-1.050379049	11522.86983	11944.31733	11584.73409	11532.72613	11798.04603	11232.17952	9.085636137	13.4922	13.544	13.4999	13.4934	13.5263	13.4554	0.04137	0.04137	0.0436	0.04137	0.04137	0.0436	3	3	0
IPI00555259.4	Matrin-3	YQLLQLVEPFGVISNHLILNK	99.999878	0.296382326	0.997658493	0.99643308	0.88970951	0.977979004	0.959191605	0.176813228	0.641782715	0.97930002	0.747907483	0.659916615	0.867109211	1.059410012	1.020470587	1.001099507	1.014090451	-1.019349804	-1.00730868	7540.682826	7988.67488	7695.045027	7803.471683	7548.973862	7494.201142	9.4458672	12.8805	12.9637	12.9097	12.9299	12.8821	12.8716	0.043	0.043	0.04532	0.043	0.043	0.04532	3	4	0
IPI00202342.3	21_kDa_protein	TPGTGSLAAAVETASGR	99.99997337	0.275132498	0.997658493	0.99643308	0.679460331	0.977979004	0.902762239	0.155960822	0.35873046	0.912730648	0.315002725	0.416640142	0.742844357	-1.061406289	-1.040167726	-1.004569259	1.04409439	1.035436548	-1.01412695	12740.96181	12003.84994	12248.94937	12789.05932	12683.00985	12506.3335	9.2761536	13.6372	13.5512	13.5804	13.6426	13.6306	13.6104	0.04223	0.04223	0.04451	0.04223	0.04223	0.04451	2	2	0
IPI00364777.1	Leucine_zipper-EF-hand-containing_transmembrane_protein_1,_mitochondrial_precursor	AMYLPDTLSPADQLK	99.99999973	0.40730283	0.997658493	0.99643308	0.87575432	0.977979004	0.700280075	0.27882788	0.96980813	0.655371478	0.707609491	0.691605981	0.405162576	-1.077426707	-1.00266617	-1.031062056	-1.026755049	-1.028320379	1.060518154	13122.09266	12179.10468	13087.19995	12746.17541	12726.77292	13496.97372	15.32622683	13.6797	13.5721	13.6759	13.6378	13.6356	13.7203	0.06952	0.06952	0.07328	0.06952	0.06952	0.07328	5	5	0
IPI00569956.2	35_kDa_protein	LEKPAKYDDIK	99.942235	0.369516722	0.997658493	0.99643308	0.597976693	0.977979004	0.691634953	0.240291445	0.783671608	0.918147694	0.225522638	0.861409213	0.380201614	-1.130132239	1.029630163	1.010692164	-1.138578482	-1.018737653	-1.098173444	15064.47759	13329.83616	15510.84052	13622.98758	15225.54946	13864.43057	23.33768574	13.8789	13.7024	13.921	13.7338	13.8942	13.7591	0.1051	0.1051	0.1107	0.1051	0.1051	0.1107	2	3	0
IPI00211216.3	Eukaryotic_translation_initiation_factor_5A-1	RNDFQLIGIQDGYLSLLQDSGEVR	99.99994514	0.665564226	0.997658493	0.99643308	0.83893122	0.977979004	0.700280075	0.546142988	0.049147667	0.318452308	0.624579925	0.305915713	0.402621159	1.020681296	1.072224607	1.034523057	-1.017188291	-1.036443411	-1.029642795	7314.252189	7465.520403	7842.521176	7709.999462	7566.762537	7348.920006	7.544989173	12.8365	12.866	12.9371	12.9125	12.8855	12.8433	0.03437	0.03437	0.03623	0.03437	0.03437	0.03623	5	6	0
IPI00203347.1	G-septin_beta_(Fragment)	AIGHVIEEGGVK	99.9981368	0.398144613	0.997658493	0.99643308	0.792374134	0.977979004	0.970372282	0.270283314	0.80672481	0.859022765	0.522164884	0.676474055	0.894960493	-1.042346253	-1.009447851	1.006666061	1.024947369	1.016176893	-1.005086559	13191.13235	12655.23074	13067.67094	13393.67494	13279.06525	13211.86233	8.337222624	13.6873	13.6274	13.6737	13.7093	13.6969	13.6895	0.03797	0.03797	0.04002	0.03797	0.03797	0.04002	3	3	0
51092266	hypoxanthine_guanine_phosphoribosyl_transferase_[Rattus_norvegicus]	VIGGDDLSTLTGK	99.99994689	0.240287534	0.997658493	0.99643308	0.498231465	0.977979004	0.38112535	0.123576446	0.565052078	0.708724568	0.13740194	0.831810909	0.069679491	1.094895425	1.035056958	1.021993582	1.093934332	-1.012782248	1.116516583	6831.017584	7479.249902	7070.492278	7734.654245	6981.256129	7794.688236	13.00525178	12.7379	12.8687	12.7876	12.9171	12.7693	12.9283	0.05908	0.05908	0.06228	0.05908	0.05908	0.06228	2	2	0
IPI00389231.1	PREDICTED:_NADH_dehydrogenase_(ubiquinone)_Fe-S_protein_6	EVNENFAIDLIAQQPVNEVDHR	99.971455	0.860070621	0.997658493	0.99643308	0.853810813	0.977979004	0.670153176	0.781128256	0.614582311	0.242723613	0.65583166	0.103598984	0.33912124	1.010233241	1.019154327	-1.044016393	-1.016930011	-1.064013825	1.036794203	16356.77236	16524.15515	16670.07533	16392.54928	15667.16046	16243.62115	8.164847806	13.9976	14.0123	14.025	14.0008	13.9355	13.9876	0.03719	0.03719	0.0392	0.03719	0.03719	0.0392	4	5	0
IPI00324459.3	Proenkephalin_A_precursor	ELLGTGDNR	99.9917388	0.76451765	0.997658493	0.99643308	0.336424812	0.977979004	0.758577321	0.667533125	0.323560171	0.529205762	0.045369289	0.705450515	0.483755594	1.024265079	1.058473822	1.035782379	-1.124031208	-1.021907539	-1.041037563	20343.80103	20837.44496	21533.38082	19157.28022	21071.75062	20241.10499	12.45800407	14.3123	14.3469	14.3943	14.2256	14.363	14.305	0.05662	0.05662	0.05968	0.05662	0.05662	0.05968	2	3	0
IPI00207657.1	PREDICTED:_similar_to_Ubiquitin_carboxyl-terminal_hydrolase_5_(Ubiquitin_thiolesterase_5)_(Ubiquitin-specific-	IGEWELIQESGVPLKPLFGPGYTGIR	99.999997	0.628452959	0.997658493	0.99643308	0.727515376	0.977979004	0.453249617	0.507789991	0.968782915	0.71260868	0.394936919	0.690927688	0.133533692	-1.022378934	-1.0013417	1.012367477	1.029680076	1.01372577	-1.053341784	14116.29713	13807.30437	14097.38267	14515.79406	14290.88011	13567.18239	7.431092155	13.7851	13.7531	13.7831	13.8253	13.8028	13.7278	0.03386	0.03386	0.03569	0.03386	0.03386	0.03569	5	6	0
IPI00421539.3	Aconitate_hydratase,_mitochondrial_precursor	WVIGDENYGEGSSR	100	0.346306149	0.997658493	0.795267491	0.576914427	0.92052399	0.597243234	0.220844378	0.845649939	0.059077014	0.212236483	0.04303674	0.258691641	-1.061017202	1.009653694	-1.09663261	-1.063982707	-1.107219166	1.057680593	17414.45789	16412.98356	17582.57174	16525.24202	15879.93803	16795.90226	10.71817816	14.088	14.0025	14.1019	14.0124	13.9549	14.0358	0.04876	0.04876	0.0514	0.04876	0.04876	0.0514	32	44	0
IPI00372027.3	PREDICTED:_similar_to_coiled-coil-helix-coiled-coil-helix_domain_containing_3	AVANEQLTR	99.967456	0.809100741	0.997658493	0.99643308	0.733834025	0.977979004	0.440189179	0.716632085	0.302997618	0.518405971	0.411565034	0.685352529	0.116864939	1.017058505	-1.050786679	-1.030595849	1.040205923	1.019591414	1.078889016	7428.231094	7554.94561	7069.209426	7353.433513	7207.705236	7776.314011	10.39170504	12.8588	12.8832	12.7873	12.8442	12.8153	12.9249	0.04728	0.04728	0.04984	0.04728	0.04728	0.04984	2	2	0
55976533	MATR3_MOUSE_Matrin-3	YQLLQLVEPFGVISNHLILNK	99.999878	0.355374751	0.997658493	0.99643308	0.88196112	0.977979004	0.962983009	0.227845984	0.614865673	0.831554068	0.726820125	0.478257691	0.87796897	1.052096997	1.012878637	-1.008936421	1.015131558	-1.031010574	1.006619224	8341.720606	8776.299203	8524.226082	8653.210899	8267.835748	8322.562404	9.325831016	13.0261	13.0994	13.0574	13.079	13.0133	13.0228	0.04245	0.04245	0.04475	0.04245	0.04245	0.04475	4	5	0
IPI00422092.1	Ras-related_C3_botulinum_toxin_substrate_1_precursor	CVVVGDGAVGK	99.99999838	0.83404542	0.997658493	0.99643308	0.614073752	0.977979004	0.603416065	0.746351502	0.432047372	0.531976415	0.241418709	0.858294179	0.263434214	1.011397422	1.028759154	1.022170634	-1.043342605	-1.006445616	1.041311534	15361.3349	15536.41451	15803.11389	15146.61993	15701.90544	16350.57523	7.804904915	13.907	13.9234	13.9479	13.8867	13.9387	13.9971	0.03555	0.03555	0.03748	0.03555	0.03555	0.03748	9	10	0
IPI00396910.1	ATP_synthase_subunit_alpha,_mitochondrial_precursor	NVQAEEMVEFSSGLK	100	0.253547667	0.997658493	0.86359048	0.930552243	0.977979004	0.520988984	0.136305802	0.738964374	0.111701558	0.847672591	0.220583465	0.192725089	-1.047454055	-1.010602	-1.050827536	1.006095712	-1.039803539	1.042418462	23287.26368	22232.25312	23042.9622	23183.42546	22160.88072	23100.91121	6.859473019	14.5073	14.4404	14.492	14.5008	14.4357	14.4957	0.03126	0.03126	0.03295	0.03126	0.03126	0.03295	41	67	0
51315739	BSN_MOUSE_Protein_bassoon	HREEEQLLVQR	99.965704	0.700196305	0.997658493	0.99643308	0.890444404	0.977979004	0.390800613	0.58336355	0.798495663	0.354594428	0.751026251	0.51693153	0.07994664	1.029172365	1.013830087	1.049866954	-1.017220132	1.035545274	-1.100312131	10630.66429	10940.78591	10777.6873	10595.23593	11160.78314	10143.28828	11.68939685	13.3759	13.4174	13.3958	13.3711	13.4462	13.3082	0.05315	0.05315	0.05602	0.05315	0.05315	0.05602	2	2	0
IPI00382312.3	Low_molecular_mass_ubiquinone-binding_protein	VAPPFVLFYLIYTWGNQEFAQSK	99.910628	0.31421831	0.997658493	0.99643308	0.733834025	0.977979004	0.724613902	0.193523014	0.947474393	0.285990767	0.415845947	0.269770703	0.439737122	1.05460209	-1.002748638	1.044468897	1.034594351	1.047339763	-1.032811786	3686.720648	3888.023302	3676.614965	3803.805073	3850.665047	3728.331821	9.042918593	11.8481	11.9248	11.8442	11.8932	11.9109	11.8643	0.04117	0.04117	0.0434	0.04117	0.04117	0.0434	2	3	0
3955096	vacuolar_adenosine_triphosphatase_subunit_Ac116_[Mus_musculus]	SEEMTLAQLFLQSEAAYCCVSELGELGK	99.99999764	0.720198551	0.997658493	0.99643308	0.367357043	0.977979004	0.733022461	0.606698926	0.406933144	0.968276576	0.06264082	0.38560829	0.458243755	-1.029653054	1.049657919	-1.002257183	-1.116595225	-1.052027189	-1.044270266	13986.84289	13584.03477	14681.4004	13148.36394	13955.34312	13363.72736	12.66621663	13.7718	13.7296	13.8417	13.6826	13.7685	13.706	0.05756	0.05756	0.06067	0.05756	0.05756	0.06067	7	10	0
26328615	unnamed_protein_product_[Mus_musculus]	GLLPEELTPLILETQK	99.984864	0.888682341	0.997658493	0.99643308	0.676746044	0.977979004	0.837394717	0.81555648	0.271215479	0.660594865	0.312463316	0.498111352	0.604596389	-1.008140829	1.040303698	1.01538958	-1.0369045	-1.024536511	1.018682684	14181.47671	14066.96	14753.04266	14227.96667	14399.72369	14668.74918	7.744466156	13.7917	13.78	13.8487	13.7964	13.8138	13.8405	0.03528	0.03528	0.03719	0.03528	0.03528	0.03719	3	3	0
IPI00204239.1	Guanine_nucleotide-binding_protein_G(I)/G(S)/G(T)_subunit_beta_3	LLVSASQDGK	99.99999634	0.703271862	0.997658493	0.99643308	0.849985868	0.977979004	0.353175547	0.588337146	0.936423155	0.260513006	0.651817735	0.240471654	0.055564015	1.040567262	-1.006030855	1.08660686	1.034632897	1.093160029	-1.158245632	10580.8746	11010.11171	10517.4454	10881.69501	11497.25092	9926.435811	16.43603811	13.3692	13.4265	13.3605	13.4096	13.489	13.2771	0.07449	0.07449	0.07851	0.07449	0.07449	0.07851	2	3	0
17865719	LMNB1_MOUSE_Lamin-B1	SLEGDLEDLKDQIAQLEASLSAAK	99.9949024	0.27061826	0.997658493	0.959908311	0.367357043	0.977979004	0.725884166	0.152047075	0.477922848	0.151075519	0.062859533	0.484871916	0.442007946	1.136082383	1.066579479	1.136433836	1.186981187	1.065493813	1.07235789	5152.133754	5853.248393	5495.160137	6522.6517	5855.059125	6278.71885	19.81605161	12.331	12.515	12.4239	12.6712	12.5155	12.6163	0.08954	0.08954	0.09438	0.08954	0.08954	0.09438	2	2	0
IPI00201964.3	35_kDa_protein	GLIDGVVEADLVEALQEFGPISYVVVMPK	99.99998036	0.837496246	0.997658493	0.99643308	0.788902735	0.977979004	0.34532203	0.752310913	0.314772882	0.448959521	0.498586529	0.786317617	0.048087804	-1.015774732	1.05279451	1.038353876	-1.035144231	-1.013907238	-1.108049539	3890.080589	3829.668595	4095.455488	3956.410486	4039.280255	3645.39681	11.06472275	11.9256	11.903	11.9998	11.95	11.9799	11.8319	0.05033	0.05033	0.05305	0.05033	0.05033	0.05305	2	3	0
IPI00231293.6	6-phosphofructokinase,_muscle_type	IFANTPDSGCVLGMR	99.99988435	0.703271862	0.997658493	0.943743986	0.450498174	0.977979004	0.412212281	0.587841935	0.797252274	0.143449086	0.104000721	0.2403663	0.091005331	-1.025149572	-1.012156637	-1.069999481	-1.080508436	-1.057148115	1.08391663	14803.81285	14440.63701	14626.00976	13536.22912	13835.34582	14996.36141	10.21079498	13.8537	13.8178	13.8362	13.7245	13.7561	13.8723	0.04646	0.04646	0.04898	0.04646	0.04646	0.04898	5	5	0
IPI00213677.1	ADP-ribosylation_factor_2	NISFTVWDVGGQDK	100	0.568370311	0.997658493	0.99643308	0.41449023	0.983201098	0.827199838	0.440405796	0.878294621	0.966083022	0.078634718	0.911017959	0.573221584	-1.033246504	1.006673128	1.001798994	-1.08061959	-1.004865382	1.024803911	16465.73041	15935.91688	16575.60834	15338.98561	16495.35216	16904.5014	9.427330465	14.0072	13.96	14.0168	13.9049	14.0098	14.0451	0.04291	0.04291	0.04524	0.04291	0.04291	0.04524	13	16	0
IPI00208382.1	Palmitoyl-protein_thioesterase_1_precursor	LQHGYNAIGFSQGGQFLR	99.9986296	0.927202091	0.997658493	0.99643308	0.792374134	0.977979004	0.38112535	0.881464401	0.692336281	0.732964805	0.522880255	0.467595188	0.070985261	1.005697575	1.01562013	-1.013090448	1.025373883	-1.028915053	1.074444256	12390.92394	12461.52215	12584.47178	12903.78869	12230.81706	13141.33113	8.493197494	13.597	13.6052	13.6194	13.6555	13.5782	13.6818	0.03868	0.03868	0.04077	0.03868	0.03868	0.04077	3	3	0
IPI00231229.8	Glutathione_S-transferase_P	EAALVDMVNDGVEDLR	100	0.276820566	0.997658493	0.99643308	0.686643596	0.977979004	0.72175173	0.157234082	0.192782661	0.619436337	0.323395986	0.40855092	0.436350474	1.046119033	1.043509929	1.015820773	-1.032702927	-1.027257915	1.025642389	15300.16447	16005.79326	15965.87354	15460.27723	15542.22489	15940.76467	7.033615916	13.9013	13.9663	13.9627	13.9163	13.9239	13.9604	0.03205	0.03205	0.03378	0.03205	0.03205	0.03378	7	7	0
126741	MAP2_MOUSE_Microtubule-associated_protein_2_(MAP_2)	DLATDLSLIEVK	99.99999976	0.950652774	0.997658493	0.99643308	0.572971917	0.977979004	0.974941498	0.923696467	0.845414866	0.194119283	0.20888919	0.283168974	0.902930386	1.003570527	1.007483131	1.04992162	1.049602547	1.042123275	-1.004673844	14382.91719	14434.27179	14490.54645	15209.31446	15100.93572	15030.68464	8.294930061	13.8121	13.8172	13.8228	13.8927	13.8824	13.8756	0.03778	0.03778	0.03982	0.03778	0.03778	0.03982	20	22	0
IPI00231674.4	ADP-ribosylation_factor_3	NISFTVWDVGGQDK	100	0.983119806	0.997658493	0.99643308	0.476152552	0.991110251	0.916053663	0.970760585	0.813199037	0.780255269	0.121350879	0.971854395	0.768438159	1.001385883	1.009217537	1.010600731	-1.062729792	1.001370561	1.011499273	14847.67628	14868.25343	14984.53529	14100.04256	15005.07251	15177.61993	8.422913537	13.8579	13.8599	13.8712	13.7834	13.8732	13.8897	0.03836	0.03836	0.04043	0.03836	0.03836	0.04043	18	21	0
IPI00210071.1	CORO1A_protein	KSDLFQEDLYPPTAGPDPALTAEEWLSGR	99.99859	0.928097019	0.997658493	0.99643308	0.706612353	0.977979004	0.386695018	0.885669727	0.461440537	0.22779469	0.357645625	0.657493928	0.077780941	1.005021494	-1.026778048	-1.043215788	1.033619875	-1.016009049	1.066179348	15711.42927	15790.32412	15301.68015	15816.12072	15060.57468	16057.27369	7.76310768	13.9395	13.9468	13.9014	13.9491	13.8785	13.9709	0.03536	0.03536	0.03728	0.03536	0.03536	0.03728	5	5	0
IPI00196684.2	cAMP-dependent_protein_kinase_type_II-alpha_regulatory_subunit	GQYFGELALVTNKPR	99.99965856	0.916887014	0.997658493	0.99643308	0.930552243	0.977979004	0.485775688	0.866915944	0.905297933	0.933169238	0.843724417	0.841038853	0.160508322	-1.008252037	1.006011972	-1.004120545	-1.009982496	-1.01015729	-1.073988205	15288.64997	15163.52004	15380.56491	15228.54601	15225.91092	14176.9815	10.94441876	13.9002	13.8883	13.9088	13.8945	13.8942	13.7913	0.04978	0.04978	0.05247	0.04978	0.04978	0.05247	5	6	0
IPI00324741.2	Protein_disulfide-isomerase_A3_precursor	SDVLELTDENFESR	100	0.601707784	0.997658493	0.99643308	0.934974476	0.977979004	0.871808051	0.476013136	0.571746219	0.711635682	0.860176518	0.836574308	0.670545289	1.023697624	-1.019257289	-1.012199452	1.005951007	1.006972773	1.01444277	13611.713	13934.27826	13354.54075	13434.01372	13447.65893	13641.88038	7.304482222	13.7326	13.7664	13.705	13.7136	13.7151	13.7358	0.03328	0.03328	0.03508	0.03328	0.03328	0.03508	7	8	0
IPI00212320.1	Neuromodulin	QADVPAAVTDAAATTPAAEDAAK	100	0.927202091	0.997658493	0.99643308	0.638878253	0.977979004	0.704501025	0.881636731	0.93711145	0.570954182	0.274618728	0.528641007	0.411687027	1.010393879	-1.005644988	1.040195615	-1.081547861	1.046067507	-1.060519036	14150.45847	14297.53662	14071.02769	13010.08322	14719.24485	13879.28396	15.54530962	13.7886	13.8035	13.7804	13.6673	13.8454	13.7606	0.0705	0.0705	0.07431	0.0705	0.0705	0.07431	3	3	0
IPI00372388.1	Chaperonin_subunit_3	ILQMEEEYIQQLCEDIIQLKPDVVITEK	99.9988496	0.484170148	0.997658493	0.99643308	0.797906375	0.977979004	0.643190497	0.359115916	0.404670379	0.708713923	0.550625322	0.233364155	0.29844039	1.045434178	1.042322838	-1.018202778	-1.030083003	-1.061296009	1.05318594	13441.20209	14051.89206	14010.07191	13600.91553	13200.90888	13903.01163	10.76918946	13.7144	13.7785	13.7742	13.7314	13.6883	13.7631	0.04899	0.04899	0.05164	0.04899	0.04899	0.05164	2	2	0
IPI00189723.1	Tropomodulin-1	TLNVESNFISGAGILCLVEALPHNTSLVELK	99.5794	0.454627406	0.997658493	0.99643308	0.908565709	0.977979004	0.448976523	0.32482145	0.802800143	0.206327664	0.799958427	0.140547558	0.123660962	1.047600377	-1.012137431	1.061696327	1.012317306	1.074582593	-1.078119487	6763.935877	7085.901771	6682.823569	6765.137952	7181.245878	6660.899803	10.48955823	12.7236	12.7907	12.7062	12.7239	12.81	12.7015	0.04772	0.04772	0.05031	0.04772	0.04772	0.05031	2	2	0
IPI00364895.4	82_kDa_protein	SLEDALNQTATVTR	99.99987198	0.660860724	0.997658493	0.99643308	0.814837379	0.997548061	0.704501025	0.54001762	0.294714335	0.283213565	0.588545398	0.997548061	0.412233743	1.040214842	1.071982475	1.071765129	1.036390805	-1.000202792	1.055781714	12094.94534	12581.34166	12965.56944	13437.39695	12962.94066	13686.03571	14.36532726	13.5621	13.619	13.6624	13.714	13.6621	13.7404	0.0652	0.0652	0.06873	0.0652	0.0652	0.06873	4	4	0
91997	JT0439_aspartate_transaminase_(EC_2.6.1.1),_cytosolic_-_rat	NLDYVATSINEAVTK	100	0.784346963	0.997658493	0.99643308	0.691591891	0.806688502	0.603463344	0.691121724	0.15289167	0.375017858	0.33324867	0.024209676	0.264652503	-1.010444956	-1.039519435	1.023542982	1.026439047	1.063992822	-1.030587163	14657.9372	14506.4183	14100.68605	14473.49475	15003.02875	14557.74852	5.820033421	13.8394	13.8244	13.7835	13.8211	13.873	13.8295	0.02653	0.02653	0.02796	0.02653	0.02653	0.02796	27	36	0
IPI00198884.3	58_kDa_protein	NLSFNITEDELKEVFEDAVEIR	99.99995307	0.720198551	0.997658493	0.99643308	0.469497133	0.977979004	0.7054999	0.608106432	0.845384219	0.437797593	0.115898721	0.574439399	0.414177617	1.031873207	1.012321212	1.048703802	1.105066539	1.035939769	-1.052779312	6255.892699	6455.28806	6332.97288	6998.356419	6560.578461	6231.674944	13.66216992	12.611	12.6563	12.6287	12.7728	12.6796	12.6054	0.06204	0.06204	0.0654	0.06204	0.06204	0.0654	2	2	0
IPI00417750.3	TOM70	ILLDLVEEAVADFDACIR	99.99941531	0.651928753	0.997658493	0.821454277	0.630797204	0.977979004	0.520988984	0.530483739	0.459715729	0.06199788	0.263142986	0.271386936	0.196861386	-1.023788175	-1.028899284	-1.073592117	-1.044218372	-1.043437521	1.051273887	10251.30915	10013.1154	9963.374756	9541.466632	9548.606943	10038.20113	8.339009462	13.3235	13.2896	13.2824	13.22	13.2211	13.2932	0.03798	0.03798	0.04003	0.03798	0.03798	0.04003	3	3	0
IPI00203237.1	Rat_brain_4.1(S)	HKQEFLDKPEDVLLK	99.3839	0.989382285	0.997658493	0.99643308	0.799542028	0.977979004	0.66199794	0.98259795	0.830540067	0.20129464	0.560136301	0.146288378	0.316965449	-1.000953879	1.009659367	-1.057917128	-1.02655518	-1.068135938	1.046195023	12529.03522	12517.09542	12650.05777	12322.82299	11843.11595	12390.20896	9.750254091	13.613	13.6116	13.6269	13.589	13.5318	13.5969	0.04438	0.04438	0.04678	0.04438	0.04438	0.04678	3	3	0
IPI00210881.1	DnaJ_homolog_subfamily_C_member_5	YVSPEDLEAQLQSDER	99.99995122	0.860070621	0.997658493	0.99643308	0.577643504	0.977979004	0.755856757	0.781435593	0.638008376	0.771261655	0.216486685	0.850977471	0.480972312	-1.021010388	1.036915999	1.022027572	-1.100576868	-1.014567539	1.055878176	8564.021811	8387.791065	8880.17123	8068.65153	8752.666417	9241.74945	16.78758172	13.0641	13.0341	13.1164	12.9781	13.0955	13.174	0.07606	0.07606	0.08017	0.07606	0.07606	0.08017	5	7	0
IPI00558932.2	48_kDa_protein	SSTYDLQESNVGLK	99.99946357	0.661719911	0.997658493	0.99643308	0.541686564	0.994226451	0.864935633	0.54147595	0.482063546	0.459356191	0.173655558	0.986106818	0.661305073	-1.029263881	-1.034728608	-1.035601898	1.068771662	-1.00084398	1.021472135	16648.61516	16175.26414	16089.8375	17196.36236	16076.26945	16421.46127	10.52247196	14.0231	13.9815	13.9739	14.0698	13.9726	14.0033	0.04787	0.04787	0.05046	0.04787	0.04787	0.05046	5	5	0
IPI00370681.1	Capping_protein_(Actin_filament)_muscle_Z-line,_alpha_2	FTVTPSTTQVVGILK	99.99965158	0.81696115	0.997658493	0.99643308	0.333651543	0.977979004	0.589134502	0.725461501	0.132438526	0.861462272	0.042429007	0.18037743	0.251139622	-1.014403521	-1.065674933	-1.007128845	1.09043312	1.058131677	-1.049478445	19864.87952	19582.81799	18640.6557	20326.38835	19724.26827	18794.35292	9.075532325	14.2779	14.2573	14.1862	14.3111	14.2677	14.198	0.04132	0.04132	0.04355	0.04132	0.04132	0.04355	5	5	0
IPI00421513.6	Aspartate_aminotransferase,_cytoplasmic	NLDYVATSINEAVTK	100	0.816364191	0.997658493	0.99643308	0.706612353	0.806688502	0.616048134	0.723998414	0.1434564	0.387841117	0.358843271	0.023546451	0.278101729	-1.0089384	-1.038993425	1.022066975	1.024125868	1.061920867	-1.028626783	14224.84573	14098.82479	13690.98725	14021.29421	14538.74506	14134.13037	5.608922384	13.7961	13.7833	13.7409	13.7753	13.8276	13.7869	0.02557	0.02557	0.02695	0.02557	0.02557	0.02695	25	34	0
IPI00195860.1	Cytochrome_c_oxidase_polypeptide_VIIa-liver/heart,_mitochondrial_precursor	GGTSDALLYR	99.99980306	0.420423143	0.997658493	0.99643308	0.49686884	0.977979004	0.965573146	0.292614507	0.741430959	0.927944884	0.134007485	0.808747581	0.881706221	-1.058811819	-1.018488105	-1.00489636	-1.087699432	-1.013525519	-1.008292444	20257.34874	19132.15208	19889.62723	18285.95901	20158.64477	19992.85513	12.06274617	14.3062	14.2237	14.2797	14.1584	14.2991	14.2872	0.05483	0.05483	0.0578	0.05483	0.05483	0.0578	2	4	0
IPI00779050.1	24_kDa_protein	FDAGELITQR	99.99999966	0.384647147	0.997658493	0.99643308	0.733834025	0.977979004	0.924766593	0.25575362	0.966250809	0.806681282	0.425293067	0.77912739	0.791874676	-1.056392637	1.002087457	-1.011811275	-1.040201342	-1.013923388	-1.013094357	11354.96457	10748.81078	11378.66757	10938.90876	11222.41356	11077.36262	10.70540358	13.471	13.3919	13.474	13.4172	13.4541	13.4353	0.0487	0.0487	0.05134	0.0487	0.0487	0.05134	3	4	0
7305619	ubiquitin_specific_protease_5_(isopeptidase_T)_[Mus_musculus]	IGEWELIQESGVPLKPLFGPGYTGIR	99.999997	0.844525469	0.997658493	0.99643308	0.628717364	0.977979004	0.520988984	0.762106911	0.827021097	0.712956075	0.256739923	0.564642992	0.197170844	-1.011219348	-1.008307165	1.013654173	1.044141311	1.022074766	-1.050439237	14780.47344	14616.48599	14658.70119	15305.75548	14982.28858	14262.87981	8.211885077	13.8514	13.8353	13.8395	13.9018	13.871	13.8	0.0374	0.0374	0.03942	0.0374	0.0374	0.03942	6	7	0
IPI00331896.1	RSA-14-44	LVIVGDGACGK	99.9999999	0.940964954	0.997658493	0.99643308	0.638878253	0.977979004	0.673644494	0.909778687	0.644585796	0.270698895	0.271940008	0.538220121	0.3610004	1.005183782	1.021881462	1.051849767	-1.053164664	1.029326596	-1.043929538	11222.34868	11280.52289	11467.91008	10889.00005	11804.22485	11307.49195	10.1792573	13.4541	13.4615	13.4853	13.4106	13.527	13.465	0.04632	0.04632	0.04883	0.04632	0.04632	0.04883	4	4	0
IPI00363930.4	49_kDa_protein	STLMDTLFNTK	99.99932598	0.950652774	0.997658493	0.99643308	0.507654338	0.977979004	0.979042717	0.924577726	0.719315363	0.596621466	0.149725577	0.383087068	0.920637697	-1.004930115	-1.019377382	1.027913685	1.080755276	1.047831961	1.005331762	15529.77007	15453.58214	15234.56411	16464.83553	15963.26318	16048.3755	11.59876169	13.9227	13.9157	13.8951	14.0071	13.9625	13.9701	0.05274	0.05274	0.05559	0.05274	0.05274	0.05559	4	4	0
IPI00367445.3	PREDICTED:_similar_to_3-oxoacid_CoA_transferase_1_isoform_1	DLTAVSNNAGVDNFGLGLLLR	99.9999878	0.910396276	0.997658493	0.99643308	0.83893122	0.977979004	0.810151214	0.857333179	0.604906569	0.814789076	0.621009374	0.771933902	0.550902825	-1.008096032	1.024155902	1.010563754	1.023070054	-1.013450065	-1.027909957	9673.567684	9595.879141	9907.241436	10135.80203	9775.756874	9510.32414	10.00493899	13.2398	13.2282	13.2743	13.3072	13.255	13.2153	0.04553	0.04553	0.04799	0.04553	0.04553	0.04799	3	3	0
IPI00202658.1	3-hydroxyisobutyrate_dehydrogenase,_mitochondrial_precursor	TPILLGSVAHQIYR	99.99988717	0.767016456	0.997658493	0.99643308	0.792374134	0.977979004	0.697837817	0.67146812	0.570538559	0.458980984	0.526536717	0.200336355	0.393863221	-1.012646129	-1.017430145	1.022223953	1.019486662	1.040041465	-1.026365845	9849.229627	9726.230462	9680.497154	9869.137728	10068.11845	9809.483128	6.594967712	13.2658	13.2477	13.2409	13.2687	13.2975	13.26	0.03005	0.03005	0.03168	0.03005	0.03005	0.03168	3	3	0
117119	CX6C2_RAT_Cytochrome_c_oxidase_polypeptide_VIc-2	NYDSMKDFEEMR	99.99995449	0.932087614	0.997658493	0.99643308	0.416332803	0.977979004	0.799607172	0.891608381	0.654461996	0.934298588	0.082846977	0.597821123	0.530353404	-1.010579368	1.036182765	-1.006386444	-1.149851416	-1.042800288	1.05114124	19188.71407	18987.83478	19883.0148	17291.81224	19066.9441	20042.05126	17.31197412	14.228	14.2128	14.2792	14.0778	14.2188	14.2907	0.0784	0.0784	0.08264	0.0784	0.0784	0.08264	4	5	0
IPI00230832.6	Cytochrome_c_oxidase_polypeptide_VIc-2	NYDSMKDFEEMR	99.99995449	0.932087614	0.997658493	0.99643308	0.416332803	0.977979004	0.799607172	0.891608381	0.654461996	0.934298588	0.082846977	0.597821123	0.530353404	-1.010579368	1.036182765	-1.006386444	-1.149851416	-1.042800288	1.05114124	19188.71407	18987.83478	19883.0148	17291.81224	19066.9441	20042.05126	17.31197412	14.228	14.2128	14.2792	14.0778	14.2188	14.2907	0.0784	0.0784	0.08264	0.0784	0.0784	0.08264	4	5	0
IPI00197616.4	CAP,_adenylate_cyclase-associated_protein_1	GAVPYVQAFDSLLANPVAEYLK	100	0.762901768	0.997658493	0.99643308	0.519827808	0.977979004	0.569356066	0.664378454	0.88607486	0.334878022	0.156839476	0.425385407	0.234900046	-1.015782843	-1.005322536	-1.035547873	-1.05439255	-1.030065313	1.045305083	9250.477011	9106.746658	9201.501687	8726.827296	8932.930336	9337.637488	8.037389886	13.1753	13.1527	13.1677	13.0912	13.1249	13.1888	0.03661	0.03661	0.03859	0.03661	0.03661	0.03859	8	8	0
IPI00776533.1	44_kDa_protein	VTNGELLAQYMAEAASELGPNTPYGK	99.99999289	0.365384746	0.997658493	0.99643308	0.930552243	0.977979004	0.725898654	0.23593415	0.176279836	0.590100889	0.849323949	0.40289211	0.44769107	1.038492399	1.045366147	1.017220725	-1.006198092	-1.027668943	1.025068451	11031.14253	11455.75766	11531.58296	11460.54941	11221.10679	11502.40256	7.052202255	13.4293	13.4838	13.4933	13.4844	13.4539	13.4896	0.03213	0.03213	0.03387	0.03213	0.03213	0.03387	5	5	0
IPI00230942.4	Glutathione_S-transferase_Yb-3	PMTLGYWDIR	99.99999245	0.368027631	0.997658493	0.99643308	0.940752994	0.977979004	0.885563065	0.238481905	0.797659667	0.674435479	0.872035344	0.878604577	0.697578739	1.043654071	1.009531597	1.015252062	-1.005976685	1.005666454	-1.014488533	15449.95975	16124.41338	15597.22254	15504.55668	15685.60349	15461.58776	8.024915458	13.9153	13.977	13.929	13.9204	13.9372	13.9164	0.03655	0.03655	0.03853	0.03655	0.03655	0.03853	12	15	0
IPI00359981.2	PREDICTED:_similar_to_NADH_dehydrogenase_(ubiquinone)_1_alpha_subcomplex,_13	IALMPLLQAEK	99.9975609	0.974683592	0.997658493	0.99643308	0.993116531	0.977979004	0.485775688	0.961316503	0.959124217	0.816070636	0.988304231	0.860939771	0.162563274	1.00432306	-1.004694322	-1.020908429	-1.001340385	-1.016138348	1.137488648	11170.89296	11219.1854	11118.69821	11103.81483	10942.11062	12446.52661	19.98745412	13.4475	13.4537	13.4407	13.4388	13.4176	13.6035	0.0903	0.0903	0.09518	0.0903	0.0903	0.09518	4	4	0
350611	0709230A_transaminase,Glu_oxaloacetic	ASAELALGENSEVLK	100	0.699062415	0.998795589	0.99643308	0.90918008	0.977979004	0.519332024	0.581619929	0.991664406	0.578280871	0.805273786	0.581280256	0.18992714	1.033478329	1.000640724	-1.033780522	-1.015233792	-1.03444289	1.084411996	15792.15929	16320.85439	15802.27771	15565.16128	15276.12385	16565.61195	13.33832688	13.9469	13.9944	13.9478	13.926	13.899	14.0159	0.06058	0.06058	0.06386	0.06058	0.06058	0.06386	10	16	0
IPI00364395.3	PREDICTED:_similar_to_leishmanolysin-like	GQREELAEVVLEALVIR	98.9913	0.684795684	0.997658493	0.99643308	0.792374134	0.977979004	0.390747044	0.56348902	0.933606803	0.759396676	0.51237981	0.829859881	0.079489113	-1.043480197	1.006316044	1.022795355	-1.05086641	1.016375881	-1.144001581	22953.46712	21997.03184	23098.44222	21980.37923	23476.69956	20521.56216	16.47970371	14.4864	14.425	14.4955	14.4239	14.5189	14.3249	0.07468	0.07468	0.07872	0.07468	0.07468	0.07872	2	2	0
120517	FRIH_MOUSE_Ferritin_heavy_chain_(Ferritin_H_subunit)	SIKELGDHVTNLR	99.974633	0.735573766	0.997658493	0.991204521	0.781118785	0.977979004	0.924766593	0.630491799	0.625675671	0.186462016	0.471349393	0.420296757	0.796884584	1.020561752	1.021433137	1.057926849	-1.031851779	1.03572795	1.011242318	13590.65756	13870.1053	13881.94799	13453.43224	14377.92153	14539.56269	9.426004042	13.7303	13.7597	13.7609	13.7157	13.8116	13.8277	0.04291	0.04291	0.04523	0.04291	0.04291	0.04523	2	2	0
IPI00372080.2	SH3-domain_GRB2-like_endophilin_B2	SQTTYYAQCYR	99.9961273	0.394946302	0.997658493	0.99643308	0.966345081	0.977979004	0.774104485	0.264952548	0.271319413	0.883735837	0.923544886	0.337125487	0.505158469	1.056214585	1.057004156	1.007157513	-1.004820069	-1.049492401	1.034025914	13101.4168	13837.9075	13848.252	13781.82267	13195.19035	13644.16876	10.88411446	13.6774	13.7563	13.7574	13.7505	13.6877	13.736	0.04951	0.04951	0.05219	0.04951	0.04951	0.05219	3	3	0
IPI00202120.5	V-H+ATPase_subunit_a1-IV	SEEMTLAQLFLQSEAAYCCVSELGELGK	99.99999764	0.832692474	0.997658493	0.99643308	0.576914427	0.977979004	0.994153085	0.744189159	0.478561906	0.992398274	0.213433222	0.484295448	0.970653308	-1.018653538	1.042179195	1.000539488	-1.075631744	-1.041617255	1.00214196	13142.06881	12901.41183	13696.3907	12733.34557	13149.15881	13177.32377	12.64761329	13.6819	13.6552	13.7415	13.6363	13.6827	13.6858	0.05747	0.05747	0.06058	0.05747	0.05747	0.06058	10	13	0
126745	MAP1B_MOUSE_Microtubule-associated_protein_1B_(MAP_1B)_(MAP1.2)_(MAP1(X))_[Contains:_MAP1_light_	SSYYVVSGNDPAAEEPSR	100	0.519316492	0.997658493	0.99643308	0.423679834	0.977979004	0.893304386	0.39290002	0.864479818	0.394256766	0.088296865	0.318285102	0.70970263	1.021693381	-1.004399449	1.021630141	1.045460282	1.026124751	-1.009625643	18225.08477	18620.44847	18145.25565	18970.14409	18619.29593	18441.78193	5.574534838	14.1536	14.1846	14.1473	14.2114	14.1845	14.1707	0.02541	0.02541	0.02679	0.02541	0.02541	0.02679	9	9	0
IPI00395241.1	Dephosphin_long_form_(Fragment)	TGLFTPDLAFEATVK	99.99991563	0.41119906	0.997658493	0.99643308	0.71532686	0.977979004	0.769772884	0.283844837	0.248983599	0.305210037	0.368699902	0.875099961	0.498812829	-1.031891676	-1.035335107	-1.03047553	1.027376418	1.004715859	1.020494264	22504.38039	21808.85932	21736.32501	22331.38773	21838.83046	22286.40121	6.489211142	14.4579	14.4126	14.4078	14.4468	14.4146	14.4439	0.02957	0.02957	0.03117	0.02957	0.02957	0.03117	2	2	0
IPI00392151.3	59_kDa_protein	TKVHAELADVLTEAVVDSILAIR	99.979005	0.888682341	0.997658493	0.99643308	0.627206744	0.988483763	0.686505831	0.815489582	0.902988798	0.831466495	0.253749929	0.932029318	0.375108609	1.015995005	1.008550461	1.01457699	1.083527819	1.005975436	1.064162369	4851.957662	4929.564751	4893.444138	5302.182852	4922.684598	5238.535702	15.21593007	12.2444	12.2672	12.2566	12.3724	12.2652	12.3549	0.06902	0.06902	0.07275	0.06902	0.06902	0.07275	2	2	0
IPI00203346.4	PREDICTED:_similar_to_AP-2_complex_subunit_alpha-1_(Adapter-related_protein_complex_2_alpha-1_subunit)_	VGGYILGEFGNLIAGDPR	99.99999992	0.999466799	0.997658493	0.99643308	0.423679834	0.977979004	0.454871916	0.999466799	0.351266534	0.536378625	0.089659713	0.739156114	0.137319296	1.00002803	-1.041163445	-1.026322637	1.076991109	1.014460178	1.066862099	17098.20055	17098.67982	16422.20597	17686.56982	16659.67399	17773.57477	9.354396174	14.0616	14.0616	14.0034	14.1104	14.0241	14.1174	0.04258	0.04258	0.04489	0.04258	0.04258	0.04489	6	6	0
IPI00189653.1	Secretogranin-2_precursor	GMMEALPDGLSVEDILNVLGMENVANQK	99.99999646	0.914999308	0.997658493	0.99643308	0.788902735	0.977979004	0.920058762	0.862713633	0.861873617	0.721580087	0.49329856	0.862638208	0.781261326	-1.008279049	1.008559695	1.017144171	1.034203236	1.008511619	-1.013698627	8477.098487	8407.492441	8549.659863	8842.085893	8622.431311	8505.911997	10.63895286	13.0494	13.0375	13.0617	13.1102	13.0739	13.0543	0.0484	0.0484	0.05102	0.0484	0.0484	0.05102	5	7	0
IPI00369207.4	PREDICTED:_similar_to_Septin-8	SLSLGGHVGFDSLPDQLVSK	99.85861	0.697940373	0.997658493	0.99643308	0.706612353	0.977979004	0.852458285	0.579888744	0.656341458	0.808945831	0.358686228	0.496960743	0.643971344	1.051603412	-1.042407711	1.022194055	1.089742947	1.065542965	-1.044084359	19928.46273	20956.83941	19117.72383	20833.40471	20370.75613	19510.64199	20.40554504	14.2825	14.3551	14.2226	14.3466	14.3142	14.252	0.09215	0.09215	0.09713	0.09215	0.09215	0.09713	2	2	0
IPI00558210.3	PREDICTED:_similar_to_transcription_elongation_factor_A_(SII)-like_5	RPAEDYVPR	99.9982741	0.827956925	0.997658493	0.99643308	0.849985868	0.977979004	0.785391084	0.737118222	0.379287703	0.965497544	0.649288727	0.402280437	0.515216551	1.016272133	1.04453906	1.002081054	1.022731154	-1.042369833	1.032721289	8991.704136	9138.018342	9392.186188	9605.681422	9010.416354	9305.248791	10.72562732	13.1344	13.1577	13.1972	13.2297	13.1374	13.1838	0.04879	0.04879	0.05143	0.04879	0.04879	0.05143	3	3	0
IPI00373419.2	Non-erythrocyte_beta-spectrin	DASVAEAWLLGQEPYLSSR	100	0.734815425	0.997658493	0.99643308	0.886734314	0.977979004	0.979042717	0.626482637	0.862534538	0.853884633	0.737085429	0.7246555	0.916665698	1.009833838	-1.003579729	1.00370622	-1.006955144	1.007299216	1.00216152	13046.21311	13174.50746	12999.67779	12909.88767	13094.56525	13122.86941	4.471622279	13.6713	13.6855	13.6662	13.6562	13.6767	13.6798	0.02039	0.02039	0.02149	0.02039	0.02039	0.02149	42	46	0
IPI00777695.1	87_kDa_protein	SLEDALNQTATVTR	99.99987198	0.600662032	0.997658493	0.99643308	0.792374134	0.983874203	0.752607186	0.47351967	0.39580941	0.329132687	0.511367378	0.918657398	0.477367987	1.039348367	1.048144305	1.054068114	1.036982205	1.005651712	1.040088305	12507.98657	13000.15541	13110.17489	13595.01806	13184.26982	13712.80485	11.9952935	13.6106	13.6662	13.6784	13.7308	13.6865	13.7432	0.05453	0.05453	0.05748	0.05453	0.05453	0.05748	5	5	0
IPI00203614.2	Isoform_1_of_Brain-specific_angiogenesis_inhibitor_1-associated_protein_2	SNLVISDPIPGAKPLPVPPELAPFVGR	99.99997958	0.450247158	0.997658493	0.99643308	0.554634429	0.977979004	0.774104485	0.321090545	0.173267991	0.317629517	0.183926081	0.691815552	0.503992617	-1.039321798	-1.056133654	-1.039612335	1.054711857	1.015891808	1.026973788	17997.53188	17316.61157	17040.9605	17973.30309	17311.77217	17778.73624	8.624833659	14.1355	14.0799	14.0567	14.1336	14.0795	14.1179	0.03928	0.03928	0.0414	0.03928	0.03928	0.0414	4	4	0
IPI00373621.3	PREDICTED:_similar_to_Copine-6	DIVQFVPFR	99.9950021	0.454627406	0.997658493	0.99643308	0.733834025	0.977979004	0.849367056	0.325523435	0.251964492	0.343743809	0.406559991	0.820191053	0.637026654	-1.059548607	-1.071782366	-1.057230181	1.051346174	1.013764443	-1.028810063	8070.906347	7617.30636	7530.359338	7917.014478	7634.01054	7420.233154	13.07918901	12.9785	12.8951	12.8785	12.9507	12.8982	12.8572	0.05942	0.05942	0.06263	0.05942	0.05942	0.06263	2	2	0
IPI00331848.3	SH3P13	SMFNFLENDVEQVSQLAVFVEAALDYHR	99.9933549	0.769160192	0.997658493	0.970109364	0.933949271	0.991296718	0.752607186	0.674223848	0.196481825	0.174246606	0.857098588	0.97430306	0.474504686	1.018366136	1.05957974	1.061097741	-1.008036274	1.001432645	-1.032376684	5309.951264	5407.474549	5626.316781	5581.462615	5634.377293	5457.675848	9.648780815	12.3745	12.4007	12.458	12.4464	12.46	12.4141	0.04392	0.04392	0.04629	0.04392	0.04392	0.04629	2	2	0
IPI00194222.1	Cytochrome_c_oxidase_subunit_4_isoform_1,_mitochondrial_precursor	DYPLPDVAHVK	99.99904606	0.737973862	0.997658493	0.99643308	0.975215569	0.978543127	0.469196089	0.633681376	0.978573906	0.871180806	0.946237735	0.895786337	0.145852956	1.064334182	-1.003612641	-1.021421543	1.009095541	-1.017744796	1.2181036	14849.04305	15804.34409	14795.59189	14930.1658	14537.6247	17708.33298	29.70910891	13.8581	13.948	13.8529	13.8659	13.8275	14.1121	0.1327	0.1327	0.1399	0.1327	0.1327	0.1399	3	3	0
IPI00370372.2	PREDICTED:_similar_to_NADH_dehydrogenase_(ubiquinone)_1_beta_subcomplex_8	SQHERDPWYEWDHPDLR	99.9900431	0.908474472	0.997658493	0.99643308	0.797906375	0.977979004	0.893774223	0.844554777	0.921949386	0.470958743	0.556282129	0.545572135	0.713217744	1.007726258	-1.003958701	-1.028771261	-1.02404893	-1.024714722	1.014940133	19482.7719	19633.30082	19405.94955	18950.2171	18937.90451	19220.83931	8.750421116	14.2499	14.261	14.2442	14.2099	14.209	14.2304	0.03985	0.03985	0.042	0.03985	0.03985	0.042	2	2	0
IPI00190669.2	Isoform_1_of_Tenascin-R_precursor	VGFGNLEDEFWLGLDNIHR	99.99999968	0.586219504	0.997658493	0.99643308	0.57026792	0.977979004	0.725898654	0.458256161	0.883185075	0.366038703	0.20406813	0.462685095	0.447470716	1.028141684	1.005649872	1.034445754	1.050300718	1.028634103	1.029636747	13151.62257	13521.73138	13225.92755	13891.20121	13604.64013	14007.83741	8.318715883	13.683	13.723	13.6911	13.7619	13.7318	13.7739	0.03789	0.03789	0.03994	0.03789	0.03789	0.03994	12	12	0
IPI00231513.4	Hippocalcin-like_protein_4	LAPEELEDLVQNTEFSEQELK	99.99999997	0.947538371	0.997658493	0.99643308	0.982798955	0.977979004	0.69561724	0.919382946	0.348724523	0.612667588	0.95921178	0.654690993	0.387807256	1.0038945	1.03782745	1.019656816	-1.002019883	-1.017820343	-1.034788043	12297.22611	12345.11765	12762.39881	12736.67222	12538.95042	12117.40945	8.561474866	13.586	13.5917	13.6396	13.6367	13.6141	13.5648	0.03899	0.03899	0.0411	0.03899	0.03899	0.0411	3	3	0
IPI00555287.2	Non-erythroid_spectrin_beta	DASVAEAWLLGQEPYLSSR	100	0.685829628	0.997658493	0.99643308	0.940752994	0.977979004	0.985692829	0.565123613	0.857803413	0.880103335	0.869391809	0.744528408	0.940999052	1.011331541	-1.003606999	1.002954528	-1.003309688	1.006572183	1.001488258	13545.29036	13698.77938	13496.60812	13452.08592	13585.3103	13605.52875	4.354024102	13.7255	13.7418	13.7203	13.7155	13.7298	13.7319	0.01985	0.01985	0.02093	0.01985	0.01985	0.02093	44	48	0
IPI00370158.3	RAS-related_C3_botulinum_substrate_2	CVVVGDGAVGK	99.99999838	0.990690043	0.997658493	0.99643308	0.792374134	0.977979004	0.993109576	0.986161175	0.507295475	0.411585959	0.527382532	0.890760724	0.965869999	-1.000846142	1.033848754	1.040987352	-1.032232094	1.006904876	-1.002145937	15143.08468	15130.28231	15655.65924	15166.80146	15763.75962	15730.00403	10.88316115	13.8864	13.8852	13.9344	13.8886	13.9443	13.9412	0.04951	0.04951	0.05218	0.04951	0.04951	0.05218	5	5	0
IPI00197555.6	Suclg1_protein	LIGPNCPGIINPGECK	99.99997991	0.694415682	0.998795589	0.99643308	0.950769805	0.977979004	0.69561724	0.57299214	0.256078268	0.782963942	0.892093726	0.783447598	0.387754561	1.01915093	1.000232008	-1.0093028	1.004694822	-1.009536966	1.030379021	15931.44387	16236.54584	15935.14009	16009.95274	15784.60287	16264.12365	7.488415753	13.9596	13.987	13.9599	13.9667	13.9462	13.9894	0.03412	0.03412	0.03596	0.03412	0.03412	0.03596	3	4	0
IPI00357972.3	Similar_to_lipin_3	AESHMQWAWGRLPK	95.9959	0.720198551	0.997658493	0.99643308	0.963866333	0.977979004	0.93573341	0.608738091	0.256072068	0.821064248	0.909889819	0.17668902	0.82665363	1.025779936	1.060046073	-1.011298578	-1.005791742	-1.072023086	1.011239127	16020.47022	16433.47693	16982.43654	16884.64503	15841.48398	16019.52843	11.08540387	13.9676	14.0044	14.0518	14.0434	13.9514	13.9675	0.05042	0.05042	0.05315	0.05042	0.05042	0.05315	2	2	0
IPI00656341.1	Microtubule-associated_protein_RP/EB_family_member_2	SDKDLETQVIQLNEQVHSLK	99.9963114	0.964478514	0.997658493	0.99643308	0.541686564	0.977979004	0.883229884	0.947944596	0.592779226	0.948116342	0.17280993	0.637135328	0.690305742	1.002373919	-1.02018361	-1.002366066	1.052666399	1.017775486	-1.014989266	14022.5337	14055.82205	13745.1078	14469.01314	13989.43377	13782.83914	8.094954865	13.7755	13.7789	13.7466	13.8207	13.772	13.7506	0.03687	0.03687	0.03886	0.03687	0.03687	0.03886	2	2	0
IPI00188111.1	Chaperonin_subunit_6a	TKVHAELADVLTEAVVDSILAIR	99.979005	0.896465088	0.997658493	0.99643308	0.718821841	0.977979004	0.697837817	0.827806072	0.904065707	0.913708702	0.3770734	0.821234725	0.396426044	1.011654219	1.00661701	-1.005787996	1.049710081	-1.012443306	1.047663545	7016.14349	7097.911165	7062.569384	7413.65028	6975.767773	7308.25759	11.89316473	12.7765	12.7932	12.786	12.856	12.7681	12.8353	0.05407	0.05407	0.05699	0.05407	0.05407	0.05699	3	3	0
12857982	unnamed_protein_product_[Mus_musculus]	SVLFVCLGNICR	99.99986126	0.908474472	0.997658493	0.99643308	0.796416454	0.977979004	0.725898654	0.849942356	0.735299315	0.836048808	0.535191857	0.891200782	0.446933123	1.00512272	1.00942885	1.00560516	1.017384921	-1.003802377	-1.021384306	15432.20401	15511.25886	15577.71194	15848.52924	15518.70399	15193.79523	6.014532274	13.9137	13.921	13.9272	13.9521	13.9217	13.8912	0.02741	0.02741	0.0289	0.02741	0.02741	0.0289	3	3	0
22137336	Sh3glb2_protein_[Mus_musculus]	SQTTYYAQCYR	99.9961273	0.78769303	0.997658493	0.99643308	0.892326425	0.977979004	0.569356066	0.694970308	0.71445328	0.876136474	0.754238006	0.605032219	0.232728065	1.017056664	1.016344179	-1.006741317	1.013965579	-1.023195677	1.054650849	12924.05717	13144.49847	13135.29027	13318.73221	12837.51541	13539.09653	9.613277979	13.6578	13.6822	13.6812	13.7012	13.6481	13.7248	0.04376	0.04376	0.04612	0.04376	0.04376	0.04612	4	4	0
21165521	unnamed_protein_product_[Mus_musculus]	MFDVGGQR	99.99942534	0.95812209	0.997658493	0.99643308	0.83893122	0.977979004	0.66199794	0.93841215	0.713172303	0.837594913	0.627345259	0.571052455	0.319093102	-1.007803745	-1.038752156	1.020839214	1.051518705	1.060398934	-1.109021358	19422.44426	19272.0501	18697.8618	19661.15143	19827.19273	17878.09819	22.6712903	14.2454	14.2342	14.1906	14.2631	14.2752	14.1259	0.1021	0.1021	0.1077	0.1021	0.1021	0.1077	2	2	0
28916703	peroxiredoxin_5_related_sequence_1_protein_[Mus_musculus]	DFTPVCTTELGR	99.9999277	0.695262015	0.997658493	0.99643308	0.993335324	0.977979004	0.745741615	0.574485071	0.92030672	0.571135647	0.989929603	0.5151462	0.468751872	1.016073578	-1.002919204	1.016216044	-1.000367792	1.019182585	-1.021387439	18793.03405	19095.10534	18738.33304	18731.44376	19097.78271	18697.88288	6.316749362	14.1979	14.2209	14.1937	14.1932	14.2211	14.1906	0.02879	0.02879	0.03035	0.02879	0.02879	0.03035	2	2	0
IPI00366856.4	PREDICTED:_similar_to_destrin	YALYDASFETK	99.99999998	0.734898948	0.997658493	0.99643308	0.783271466	0.977979004	0.807907053	0.628428439	0.64753016	0.981747619	0.4755499	0.663567852	0.541066895	-1.078055042	-1.075667975	-1.003555355	1.120746925	1.071857142	-1.102510476	19272.77456	17877.35673	17917.02924	20080.45543	19204.49576	17418.87825	35.57610986	14.2343	14.1258	14.129	14.2935	14.2292	14.0884	0.1575	0.1575	0.166	0.1575	0.1575	0.166	3	3	0
IPI00366218.1	Chaperonin_containing_TCP1,_subunit_2	LSSFIGAIAIGDLVK	100	0.876296528	0.997658493	0.99643308	0.88970951	0.977979004	0.907672112	0.79717947	0.943203881	0.668718686	0.747245753	0.625870519	0.75034279	1.006867467	1.00195056	-1.011467064	1.008858062	-1.013439991	1.008745158	10025.31642	10094.16495	10044.8714	10133.84949	9911.658795	9998.33782	5.929489065	13.2914	13.3012	13.2942	13.3069	13.2749	13.2875	0.02703	0.02703	0.02849	0.02703	0.02703	0.02849	8	9	0
IPI00372009.3	PREDICTED:_similar_to_Microtubule-associated_protein_1B	SSYYVVSGNDPAAEEPSR	100	0.600662032	0.997658493	0.99643308	0.633504755	0.977979004	0.69561724	0.473028296	0.804454429	0.330513985	0.267882011	0.482587134	0.389201018	1.019256915	1.006769512	1.026259104	1.030828743	1.019358544	-1.023820843	16905.04616	17230.58518	17019.48507	17544.1744	17348.95752	16945.30605	5.905687203	14.0452	14.0727	14.0549	14.0987	14.0826	14.0486	0.02692	0.02692	0.02838	0.02692	0.02692	0.02838	13	13	0
IPI00392657.1	C-terminal-binding_protein_1	AFGFNVLFYDPYLSDGIER	99.99988145	0.95315102	0.997658493	0.99643308	0.886579721	0.977979004	0.834834254	0.928096765	0.473742211	0.863885344	0.734594626	0.581978008	0.585815123	1.004122505	1.034210326	1.007846953	-1.016014572	-1.026158111	-1.025888431	7373.280376	7403.676761	7625.522697	7505.328079	7431.13816	7243.612402	10.17111348	12.8481	12.854	12.8966	12.8737	12.8594	12.8225	0.04628	0.04628	0.04879	0.04628	0.04628	0.04879	3	3	0
IPI00364061.4	Hnrpl_protein	GLIDGVVEADLVEALQEFGPISYVVVMPK	99.99998036	0.623766512	0.997658493	0.99643308	0.903404554	0.977979004	0.621993365	0.499013209	0.411894637	0.239234098	0.782819541	0.741533602	0.283301146	1.025375275	1.031776283	1.044795438	1.010532978	1.012618196	-1.041849903	6107.702838	6262.68748	6301.782929	6368.159472	6381.30006	6124.970632	8.244303008	12.5764	12.6126	12.6215	12.6367	12.6396	12.5805	0.03755	0.03755	0.03958	0.03755	0.03755	0.03958	4	5	0
IPI00208286.1	Ubiquitin_carboxyl-terminal_hydrolase_isozyme_L3	WLPLEANPEVTNQFLK	99.99999863	0.935732347	0.997658493	0.99643308	0.981742185	0.996058404	0.729388931	0.901511279	0.967181171	0.973407935	0.957058382	0.993059481	0.450970756	-1.003731884	1.001273089	1.001003796	1.001666439	-1.000269023	-1.023648884	16030.43332	15970.83203	16050.84149	16077.58924	16046.52461	15675.80921	6.705286894	13.9685	13.9632	13.9704	13.9728	13.97	13.9363	0.03056	0.03056	0.03221	0.03056	0.03056	0.03221	2	2	0
42559420	PCBP1_MOUSE_Poly(rC)-binding_protein_1_(Alpha-CP1)_(hnRNP-E1)	LVVPATQCGSLIGK	99.987854	0.720198551	0.997658493	0.99643308	0.797906375	0.977979004	0.996576476	0.609754374	0.750027113	0.954018686	0.548247174	0.707936085	0.992020698	1.017081452	1.010912539	-1.001912784	1.020689433	-1.012846197	-1.000340572	11557.69675	11755.11899	11683.82057	11925.55219	11535.63158	11531.70421	7.384990562	13.4966	13.521	13.5122	13.5418	13.4938	13.4933	0.03365	0.03365	0.03547	0.03365	0.03365	0.03547	3	3	0
IPI00358845.4	PREDICTED:_similar_to_Proline_synthetase_co-transcribed_bacterial_homolog_protein	ELGVGLALR	99.84311	0.901636804	0.997658493	0.99643308	0.825556919	0.977979004	0.927911986	0.83465807	0.795721345	0.981109546	0.601005437	0.778012269	0.804897368	1.00651706	1.008312936	-1.000736996	1.016880378	-1.009056059	1.007929909	11123.03465	11195.52414	11215.49972	11404.8216	11114.84305	11202.98274	6.932329573	13.4413	13.4506	13.4532	13.4774	13.4402	13.4516	0.03159	0.03159	0.0333	0.03159	0.03159	0.0333	2	2	0
IPI00782359.1	Isoform_II_of_Vacuolar_proton_translocating_ATPase_116_kDa_subunit_a_isoform_1	DLNPDVNVFQR	99.99997652	0.936284608	0.997658493	0.99643308	0.699730801	0.977979004	0.880480913	0.903113382	0.50950763	0.981411922	0.341058375	0.495154141	0.683955667	1.007244812	1.041090975	-1.001382506	-1.05998836	-1.042530289	1.02513001	15525.74342	15638.22451	16163.71135	15248.95175	15504.30862	15893.93204	13.25325809	13.9224	13.9328	13.9805	13.8964	13.9204	13.9562	0.0602	0.0602	0.06346	0.0602	0.0602	0.06346	10	12	0
IPI00204503.1	Type_II_brain_4.1_minor_isoform	LMDGSEILSLLESAR	100	0.711462769	0.997658493	0.99643308	0.972077312	0.983201098	0.993109576	0.596815626	0.674866034	0.75146196	0.930972329	0.911286961	0.958886311	1.015724233	1.012785783	1.009376667	-1.002624799	-1.003377447	-1.001561234	10316.05697	10478.26905	10447.95584	10420.60386	10412.78721	10396.55575	6.561574997	13.3326	13.3551	13.3509	13.3472	13.3461	13.3438	0.0299	0.0299	0.03152	0.0299	0.0299	0.03152	5	5	0
6671700	chaperonin_subunit_2_(beta)_[Mus_musculus]	LSSFIGAIAIGDLVK	100	0.916380118	0.997658493	0.99643308	0.933949271	0.977979004	0.927911986	0.865062831	0.694857657	0.935639977	0.856826666	0.753661861	0.804624301	1.003804332	1.009051581	1.001805796	-1.004150466	-1.007232725	-1.005695868	10498.49945	10538.43923	10593.52747	10549.74113	10517.45759	10457.89082	4.974858348	13.3579	13.3634	13.3709	13.3649	13.3605	13.3523	0.02268	0.02268	0.02391	0.02268	0.02268	0.02391	7	7	0