Leptin augments coronary vasoconstriction and smooth muscle proliferation via a Rho kinase dependent pathway

Basic Research in Cardiology

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Table I. Complete list of protein changes detected in leptin-treated coronary arteries

Accession Number (gi)	Protein Name	Control MEAN	Control SEM	Leptin MEAN	Leptin SEM	Ratio (Leptin/Control)	*P* value
113205812	calsarcin 1 [Sus scrofa]	0.258	0.258	1.490	0.281	5.784	0.02224
115496760	ras-related protein Rab-21 [Bos taurus]	0.258	0.258	1.231	0.215	4.780	0.00024
478507295	PREDICTED: sorbin and SH3 domain-containing protein 1 isoform 1 [Ceratotherium simum simum]	1.291	0.975	5.667	0.915	4.391	0.00710
344285965	PREDICTED: LIM and SH3 domain protein 1 isoform X1 [Loxodonta africana]	1.004	0.421	3.247	0.778	3.234	0.04793
149733215	PREDICTED: eukaryotic translation initiation factor 6 isoform X1 [Equus caballus]	1.260	0.258	1.994	0.052	1.582	0.04877
343488453	adipose specific 2 [Sus scrofa]	3.586	1.391	5.547	1.081	1.547	0.01758
311275365	PREDICTED: non-muscle caldesmon isoform X1 [Sus scrofa]	34.882	3.369	52.065	4.141	1.493	0.00491
21956645	myotrophin [Homo sapiens]	4.024	0.424	5.947	0.589	1.478	0.02820
51592139	protein S100-A11 [Sus scrofa]	4.309	0.562	6.181	0.802	1.435	0.03670
160333553	60S ribosomal protein L12 [Mus musculus]	6.139	1.680	8.180	1.548	1.333	0.01125
471405033	PREDICTED: tropomyosin alpha-4 chain isoform 3 [Trichechus manatus latirostris]	83.834	6.385	109.518	7.208	1.306	0.01805
471405030	PREDICTED: tropomyosin alpha-4 chain isoform 2 [Trichechus manatus latirostris]	96.952	7.387	123.493	7.044	1.274	0.02291
528768836	hypothetical protein CB1_000172007 [Camelus ferus]	92.690	7.586	116.227	7.239	1.254	0.02265
545503914	PREDICTED: tubulin alpha chain-like [Canis lupus familiaris]	17.534	0.968	20.608	1.172	1.175	0.01756
73971272	PREDICTED: tropomyosin beta chain isoform 1 [Canis lupus familiaris]	185.488	11.935	215.973	5.359	1.164	0.03469
338726213	PREDICTED: tubulin alpha-1A chain-like [Equus caballus]	75.314	3.450	82.436	3.646	1.095	0.00926
426222300	PREDICTED: transitional endoplasmic reticulum ATPase [Ovis aries]	10.398	1.452	11.243	1.614	1.081	0.03649
545871305	PREDICTED: LOW QUALITY PROTEIN: myoferlin [Sus scrofa]	1.984	0.550	0.261	0.261	-7.590	0.02799
194207963	PREDICTED: delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial [Equus caballus]	1.476	0.448	0.243	0.243	-6.080	0.00918
148222591	ATPase inhibitor, mitochondrial precursor [Sus scrofa]	1.267	0.272	0.259	0.259	-4.894	0.00003
115496434	sorcin [Bos taurus]	1.260	0.258	0.261	0.261	-4.821	0.00003
311277187	PREDICTED: translocon-associated protein subunit delta isoformX1 [Sus scrofa]	2.483	0.425	0.954	0.551	-2.603	0.04270
298160970	cAMP-dependent protein kinase type II-alpha regulatory subunit [Sus scrofa]	1.267	0.272	0.493	0.285	-2.569	0.04252
350586839	PREDICTED: LOW QUALITY PROTEIN: chondroitin sulfate proteoglycan 4 [Sus scrofa]	4.764	0.933	1.976	0.384	-2.411	0.02713
12082136	heat shock protein 90 alpha [Equus caballus]	16.304	0.884	6.962	2.030	-2.342	0.02046
256838109	phosphate carrier protein, mitochondrial [Sus scrofa]	5.769	0.721	2.487	0.280	-2.319	0.01566
617574582	PREDICTED: fibrillin-1 [Erinaceus europaeus]	31.725	6.279	14.566	8.410	-2.178	0.01951

392513702	protein disulfide isomerase family A, member 4 precursor [Sus scrofa]	5.769	0.721	2.706	0.399	-2.132	0.03800
132574	RecName: Full=Ribonuclease inhibitor; AltName: Full=Ribonuclease/angiogenin inhibitor 1 [Sus scrofa]	5.783	0.492	2.724	0.433	-2.123	0.00433
586989063	PREDICTED: LOW QUALITY PROTEIN: fibrillin-1 [Felis catus]	45.016	9.359	21.334	12.353	-2.110	0.03330
47522608	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 precursor [Sus scrofa]	7.757	0.711	3.934	0.724	-1.972	0.01836
239781822	Chain A, Structure Of Glutamate Dehydrogenase Complexed With Bithionol	4.519	0.253	2.471	0.227	-1.828	0.00041
545877383	PREDICTED: integrin alpha-1 [Sus scrofa]	11.781	0.983	6.486	0.868	-1.816	0.04630
210060948	Chain A, Crystal Structure Of Porcine Aldehyde Reductase Ternary Complex	6.535	0.654	3.676	0.745	-1.778	0.00017
281350257	hypothetical protein PANDA_012129 [Ailuropoda melanoleuca]	1.755	0.245	0.997	0.026	-1.760	0.04256
335287187	PREDICTED: ATP synthase subunit b, mitochondrial [Sus scrofa]	3.020	0.069	1.736	0.238	-1.740	0.01894
149756873	PREDICTED: calreticulin [Equus caballus]	9.489	1.636	5.628	1.584	-1.686	0.01366
545881093	PREDICTED: prostacyclin synthase isoform X1 [Sus scrofa]	12.396	1.539	7.377	1.684	-1.680	0.02832
311253435	PREDICTED: collagen alpha-1(XIV) chain isoform X1 [Sus scrofa]	78.779	3.063	47.471	4.658	-1.660	0.01278
545884624	PREDICTED: LOW QUALITY PROTEIN: ubiquitin-like modifier activating enzyme 1 [Sus scrofa]	12.607	1.346	7.704	1.591	-1.637	0.03853
281348600	hypothetical protein PANDA_019876 [Ailuropoda melanoleuca]	2.766	0.254	1.724	0.440	-1.604	0.04743
548527697	PREDICTED: LOW QUALITY PROTEIN: neuroblast differentiation-associated protein AHNAK [Capra hircus]	26.261	2.876	17.150	2.095	-1.531	0.00744
154147607	calpain-2 catalytic subunit [Sus scrofa]	12.114	1.105	7.959	0.335	-1.522	0.03649
1170740	RecName: Full=L-lactate dehydrogenase A chain; Short=LDH-A; AltName: Full=LDH muscle subunit; Short=LDH-M [Sus scrofa]	16.064	1.286	10.635	1.669	-1.510	0.02359
301786567	PREDICTED: transmembrane protein 109-like [Ailuropoda melanoleuca]	7.509	0.498	5.013	0.520	-1.498	0.02765
114052480	dermatopontin precursor [Bos taurus]	7.035	0.922	4.725	0.207	-1.489	0.04980
126722693	alpha-crystallin B chain [Oryctolagus cuniculus]	27.360	1.370	18.690	1.113	-1.464	0.01028
304365428	protein disulfide-isomerase A3 precursor [Sus scrofa]	20.767	1.652	14.538	2.162	-1.429	0.04491
343183420	lumican precursor [Sus scrofa]	34.624	4.503	24.337	3.975	-1.423	0.00826
426251878	PREDICTED: LOW QUALITY PROTEIN: neuroblast differentiation-associated protein AHNAK [Ovis aries]	27.025	3.273	19.104	1.750	-1.415	0.01529
431892845	Moesin [Pteropus alecto]	34.832	2.058	25.027	1.669	-1.392	0.03728
329744642	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]	38.195	3.502	27.918	2.370	-1.368	0.00487
528757271	hypothetical protein CB1_001341009 [Camelus ferus]	18.356	0.507	13.443	1.192	-1.366	0.01312
47169448	Chain A, Structure Of Pig Muscle Pgk Complexed With Mgatp	32.384	1.055	24.059	1.313	-1.346	0.00197

335282386	PREDICTED: elongation factor 2 [Sus scrofa]	26.117	1.288	19.803	2.247	-1.319	0.03958
470629372	PREDICTED: LOW QUALITY PROTEIN: neuroblast differentiation-associated protein AHNAK [Tursiops truncatus]	24.972	2.460	19.120	2.026	-1.306	0.00849
301761876	PREDICTED: 78 kDa glucose-regulated protein-like [Ailuropoda melanoleuca]	28.360	1.661	22.023	1.574	-1.288	0.01731
149725667	PREDICTED: T-complex protein 1 subunit zeta isoformX1 [Equus caballus]	7.347	0.884	5.732	0.620	-1.282	0.01049
545806957	PREDICTED: LOW QUALITY PROTEIN: AHNAK nucleoprotein [Sus scrofa]	33.820	3.865	26.585	2.561	-1.272	0.02246
545819748	PREDICTED: elongation factor 1-delta isoform X4 [Sus scrofa]	4.047	0.633	3.269	0.545	-1.238	0.01977
13399613	Chain A, X-Ray Structure Of Full-Length Annexin 1	57.789	3.069	46.700	2.254	-1.237	0.00267
54020966	annexin A2 [Sus scrofa]	81.978	4.401	68.049	4.666	-1.205	0.02374
511902194	PREDICTED: WD repeat-containing protein 1 isoform X2 [Mustela putorius furo]	24.342	1.691	20.421	2.096	-1.192	0.00872
347300323	thioredoxin-dependent peroxide reductase, mitochondrial [Sus scrofa]	7.023	0.292	5.983	0.156	-1.174	0.02274
545870537	PREDICTED: vinculin isoform X1 [Sus scrofa]	119.348	4.302	106.039	5.949	-1.126	0.02628
335289881	PREDICTED: EH domain-containing protein 2 [Sus scrofa]	26.506	2.799	23.891	2.757	-1.109	0.00404
357575888	heat shock protein 70kDa protein 8 [Capra hircus]	18.079	0.613	17.123	0.848	-1.056	0.03843
346644882	reticulocalbin 2, EF-hand calcium binding domain precursor [Sus scrofa]	1.476	0.448	0.000	0.000	0.000	0.04580
335299041	PREDICTED: cytochrome b-c1 complex subunit 1, mitochondrial isoform X1 [Sus scrofa]	1.476	0.448	0.000	0.000	0.000	0.04580
488618959	MULTISPECIES: nitrogen regulatory protein P-II 1 [Pseudomonas]	0.23493	0.23493	1.9427	1.9427	8.269271698	0.391002219
634880411	PREDICTED: synaptopodin-2 isoform X1 [Orycteropus afer afer]	0.488805	0.282635309	4.01695	1.272730077	8.217898753	0.082955279
602719972	PREDICTED: synemin isoform X1 [Lipotes vexillifer]	0.260075	0.260075	1.231365	0.214574573	4.734653465	0.085621219
545855913	PREDICTED: collagen alpha-2(IV) chain [Sus scrofa]	1.007805	0.729026877	4.7238	1.128609755	4.687216277	0.055005478
620976181	PREDICTED: filamin-A isoform X1 [Ornithorhynchus anatinus]	78.0625	78.0625	322.545	1.938136992	4.131881505	0.050705015
28189705	similar to cytoplasmic dynein light chain 1 [Bos taurus]	0.260075	0.260075	1.04305	0.739402621	4.010573873	0.391899516
281341251	hypothetical protein PANDA_002907 [Ailuropoda melanoleuca]	0.488805	0.282635309	1.490165	0.281379967	3.048587883	0.172658966
297481810	PREDICTED: LOW QUALITY PROTEIN: laminin subunit alpha-5 [Bos taurus]	0.77405	0.496985842	2.34755	1.727765035	3.032814418	0.391903963
545824615	PREDICTED: SUN domain-containing protein 2 isoform X1 [Sus scrofa]	0.253875	0.253875	0.744475	0.468041151	2.93244707	0.499101166
47522718	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 [Sus scrofa]	0.5177	0.298900928	1.5040775	0.673491777	2.905307128	0.375166859
478512633	PREDICTED: laminin subunit alpha-5 [Ceratotherium simum simum]	1.507725	0.660919619	4.323375	1.424801544	2.867482465	0.225458215
350595384	PREDICTED: glycine--tRNA ligase isoform X1 [Sus scrofa]	0.260075	0.260075	0.7271	0.4533045	2.795732	0.392505995

395504892	PREDICTED: 40S ribosomal protein S14-like [Sarcophilus harrisii]	1.006505	0.022838214	2.734865	1.038651828	2.717189681	0.189377295
296475388	TPA: cellular retinoic acid-binding protein 1 [Bos taurus]	1.02545	0.414620763	2.705575	0.398691356	2.638427032	0.091648916
157832116	Chain A, Structural Basis Of The 70-Kilodalton Heat Shock Cognate Protein Atp Hydrolytic Activity, Ii. Structure Of The Active Site With Adp Or Atp Bound To Wild Type And Mutant Atpase Fragment	6.343	6.343	16.4375	5.524842705	2.591439382	0.263224284
149642096	PREDICTED: cellular nucleic acid-binding protein isoform X2 [Ornithorhynchus anatinus]	0.492555	0.284979855	1.231365	0.214574573	2.49995432	0.05436688
154426164	Ribosomal protein L3 [Bos taurus]	0.51395	0.29677235	1.2746025	0.503264533	2.480012647	0.058569339
149720998	PREDICTED: small nuclear ribonucleoprotein Sm D1 [Equus caballus]	0.5115	0.295330535	1.24875	0.606877259	2.441348974	0.444372388
530667993	unconventional myosin-Ic isoform b [Camelus ferus]	6.751625	4.408863673	16.311525	2.625003491	2.415940607	0.248428968
149635990	PREDICTED: 40S ribosomal protein S21 [Ornithorhynchus anatinus]	0.77405	0.496985842	1.7602775	0.276514646	2.274113429	0.090337268
114052148	tubulin beta-6 chain [Bos taurus]	7.2135	7.2135	15.48925	8.949716507	2.147258612	0.340052857
262073079	collagen alpha-1(IV) chain precursor [Bos taurus]	1.52423	0.315995655	3.269	0.545039697	2.14468945	0.050983207
194211182	PREDICTED: nexilin isoformX1 [Equus caballus]	1.0292	0.420730989	2.2013	0.563231313	2.138845705	0.070796767
281341175	hypothetical protein PANDA_015940 [Ailuropoda melanoleuca]	1.1936	0.887967981	2.5213	1.457648164	2.112349196	0.27468909
343780946	D-dopachrome decarboxylase [Sus scrofa]	0.5115	0.295330535	1.037825	0.732001647	2.028983382	0.597589397
281346938	hypothetical protein PANDA_001588 [Ailuropoda melanoleuca]	0.74643	0.249601883	1.49279	0.286403496	1.99990622	0.054829328
118403848	ubiquitin-conjugating enzyme E2 D2 [Sus scrofa]	1.25793	0.493812054	2.508565	0.673823561	1.99420079	0.094704976
139948705	leiomodin-1 [Bos taurus]	3.077675	1.250675031	6.11965	1.316191158	1.988400335	0.195584174
156523084	matrin-3 [Bos taurus]	0.77405	0.496985842	1.5334025	0.676427546	1.981012209	0.058559222
440904073	Copper transport protein ATOX1, partial [Bos mutus]	0.771575	0.257242212	1.5174425	0.325417898	1.966681787	0.076545378
296477149	TPA: elongin B-like [Bos taurus]	0.51395	0.29677235	0.988525	0.383544768	1.923387489	0.3837056
148230268	galectin-3 [Sus scrofa]	1.02545	0.414620763	1.969775	0.364531449	1.92088839	0.173083485
153791684	calcium/calmodulin-dependent protein kinase type II subunit gamma [Oryctolagus cuniculus]	1.521755	0.523685429	2.74355	0.887189261	1.802885484	0.312661824
586534588	PREDICTED: laminin subunit alpha-5 [Pteropus alecto]	1.965175	0.6423131	3.54175	0.950173974	1.802256796	0.237217836
545873981	PREDICTED: sorbin and SH3 domain-containing protein 2 isoform X5 [Sus scrofa]	14.2028	2.675584398	25.43625	5.634251405	1.79093207	0.065176462
505842687	PREDICTED: polypyrimidine tract-binding protein 1 isoform X1 [Sorex araneus]	1.546925	0.667458936	2.746175	0.501940352	1.775247669	0.113055905
313507265	Chain A, Refined Structure Of Porcine Cytosolic Adenylate Kinase At 2.1 Angstroms Resolution	1.52423	0.315995655	2.69425	0.785646225	1.767613812	0.117340448
311268187	PREDICTED: thioredoxin domain-containing protein 17 isoform 1 [Sus scrofa]	2.008125	0.842543258	3.505775	0.684877165	1.745795207	0.21637304
444706336	Leiomodin-1 [Tupaia chinensis]	2.262	0.882158292	3.9369	0.589139998	1.740450928	0.07525657
301753613	PREDICTED: transcriptional activator protein Pur-alpha-like, partial [Ailuropoda melanoleuca]	1.2818	0.765856263	2.228575	0.196507703	1.738629271	0.354120077
545840976	PREDICTED: poly [ADP-ribose] polymerase 6 isoform X2 [Sus scrofa]	39.84425	23.22938314	69.26025	4.596551994	1.738274657	0.240371352

667266325	PREDICTED: keratin, type I cytoskeletal 14 isoform X1 [Galeopterus variegatus]	4.5088	1.899073927	7.75565	2.686317118	1.720113999	0.357797129
126322035	PREDICTED: translocon-associated protein subunit alpha isoform X1 [Monodelphis domestica]	1.2893	0.496579616	2.192615	0.867171251	1.70062437	0.238883247
148792972	heart fatty acid-binding protein [Sus scrofa]	2.54968	0.536871863	4.290875	0.849298426	1.682907267	0.09331917
335306675	PREDICTED: B-cell receptor-associated protein 31 isoform X1 [Sus scrofa]	1.49905	0.274579389	2.498675	0.310198215	1.666838998	0.124311312
667266322	PREDICTED: keratin, type I cytoskeletal 19-like [Galeopterus variegatus]	3.038475	0.447276975	5.039175	1.165114839	1.658455311	0.07505649
194207535	PREDICTED: 40S ribosomal protein S8 [Equus caballus]	0.765375	0.486800411	1.2647	0.479258418	1.652392618	0.606466474
350587194	PREDICTED: tryptophan--tRNA ligase, cytoplasmic isoformX1 [Sus scrofa]	0.755105	0.494271511	1.231365	0.214574573	1.630720231	0.505692042
149715179	PREDICTED: dynactin subunit 2 isoformX2 [Equus caballus]	1.543175	0.51449313	2.5073525	0.642497106	1.624801141	0.435830313
118403762	extracellular superoxide dismutase precursor [Sus scrofa]	0.765375	0.486800411	1.231365	0.214574573	1.608838805	0.407883873
297591965	leukotriene A-4 hydrolase [Sus scrofa]	1.991625	0.559199179	3.179925	0.780884647	1.596648465	0.072458048
281342866	hypothetical protein PANDA_018340 [Ailuropoda melanoleuca]	1.546925	0.667458936	2.426765	1.093417258	1.56876707	0.235371407
117938498	fatty acid binding protein 4 [Sus scrofa]	3.610275	1.374065461	5.569275	2.012289828	1.542617945	0.27818017
545856478	PREDICTED: septin-9-like isoform X1 [Sus scrofa]	1.776955	1.148670405	2.74009	0.607741772	1.542014288	0.413519855
350579892	PREDICTED: coronin-1B [Sus scrofa]	0.9851	0.569954481	1.5174425	0.325417898	1.540394376	0.593919161
13385872	interleukin enhancer-binding factor 2 [Mus musculus]	1.266605	0.272091248	1.9425	0.637802136	1.533627295	0.459408797
347300340	thrombospondin 1 precursor [Sus scrofa]	6.63105	1.665915133	10.111	1.144890851	1.524796224	0.12336597
14043072	heterogeneous nuclear ribonucleoproteins A2/B1 isoform B1 [Homo sapiens]	4.847925	1.113695348	7.37835	1.106500442	1.521960426	0.24418042
350584744	PREDICTED: cysteine and glycine-rich protein 2 isoform X1 [Sus scrofa]	7.57495	1.409203281	11.51795	1.434208517	1.520531489	0.110276528
472359333	PREDICTED: laminin subunit beta-2-like [Odobenus rosmarus divergens]	7.206	1.839846774	10.825975	2.669073601	1.502355676	0.437927026
170763498	protein SET isoform 2 [Homo sapiens]	0.520175	0.520175	0.779025	0.49602796	1.497620993	0.396468174
560938097	PREDICTED: protein DJ-1 [Camelus ferus]	0.939725	0.939725	1.4049	1.4049	1.495011839	0.825346305
14277700	40S ribosomal protein S12 [Homo sapiens]	1.53043	0.677161461	2.2804775	0.527140986	1.490089387	0.468677593
48374073	chitinase-3-like protein 1 precursor [Sus scrofa]	1.002755	0.415149412	1.4841	0.61443455	1.480022538	0.593770093
126722987	glycogenin-1 [Oryctolagus cuniculus]	1.037875	0.735630862	1.5334025	0.676427546	1.477444297	0.420607147
126308801	PREDICTED: 60S ribosomal protein L38 isoform X1 [Monodelphis domestica]	2.053375	0.932604761	3.026165	0.755481182	1.47375175	0.064054278
126022833	cystatin B protein [Sus scrofa]	2.553455	0.686771089	3.76195	0.67617061	1.473278362	0.13238317
511922328	PREDICTED: collagen alpha-1(VI) chain isoform X2 [Mustela putorius furo]	10.528875	2.510794796	15.4846	3.977013079	1.470679441	0.194501553
119936498	proteasome 26S non-ATPase subunit 11 [Bos taurus]	0.495005	0.286527772	0.7271	0.4533045	1.468874052	0.720305909
301779149	PREDICTED: keratin, type I cytoskeletal 10-like [Ailuropoda melanoleuca]	19.756	4.691383946	28.9255	1.708215272	1.464137477	0.175508717
478537935	PREDICTED: plectin isoform 1 [Ceratotherium simum simum]	2.846175	1.655408299	4.1299	1.782206708	1.451035161	0.190155206
545869589	PREDICTED: smoothelin isoform X1 [Sus scrofa]	11.674325	2.585582511	16.8645	3.274509289	1.444580308	0.431351248

593727743	PREDICTED: collagen alpha-1(VI) chain [Physeter catodon]	10.03385	2.572626917	14.4561	3.006271031	1.440733118	0.120999911
154757413	EIF6 protein [Bos taurus]	1.031675	0.424761675	1.481475	0.612096669	1.435990016	0.384936899
110331767	EH-domain containing 1 [Bos taurus]	1.5507	0.987519575	2.223325	0.86807199	1.433755723	0.468684667
194038973	PREDICTED: purine nucleoside phosphorylase isoform X1 [Sus scrofa]	1.0292	0.420730989	1.471575	0.492221644	1.429824135	0.546759582
148225172	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 [Sus scrofa]	1.7554	0.245396186	2.47869	0.60705176	1.412037143	0.418220519
555956323	PREDICTED: tropomyosin alpha-1 chain-like isoform X1 [Bos mutus]	129.185	43.75929339	180.0475	2.951077134	1.393718311	0.345376335
466017989	PREDICTED: PRKC apoptosis WT1 regulator protein [Orcinus orca]	1.26038	0.257869159	1.75419	0.504653041	1.391794538	0.179006114
545862279	PREDICTED: LOW QUALITY PROTEIN: laminin subunit beta-2 [Sus scrofa]	13.027775	1.841860835	18.108	4.103866043	1.389953388	0.371397769
47523866	aldose 1-epimerase [Sus scrofa]	2.530725	0.333771692	3.50315	0.529351843	1.384247597	0.113946917
586449585	PREDICTED: keratin, type I cytoskeletal 10 [Chrysochloris asiatica]	15.651725	3.877080995	21.64425	2.396142747	1.382866745	0.292309369
444727517	Sorting nexin-12 [Tupaia chinensis]	2.533175	0.544161567	3.489825	0.672972286	1.377648603	0.452985295
350590267	PREDICTED: dual specificity protein phosphatase 3 isoform 2 [Sus scrofa]	3.441575	1.070507723	4.72725	0.22616664	1.373571693	0.292557331
617600588	PREDICTED: chloride intracellular channel protein 4 [Erinaceus europaeus]	3.064955	0.86015343	4.1957	0.520227274	1.368927113	0.172684508
14165469	40S ribosomal protein S15a [Homo sapiens]	2.03198	0.430648594	2.773425	0.540247647	1.364887942	0.2403883
545868396	PREDICTED: palladin [Sus scrofa]	10.2162	2.653495347	13.8811	2.065347778	1.358734167	0.3753886
545810360	PREDICTED: perilipin-4 [Sus scrofa]	0.767825	0.487251147	1.04045	0.600719382	1.355061375	0.359980012
345786437	PREDICTED: KN motif and ankyrin repeat domain-containing protein 2 isoformX1 [Canis lupus familiaris]	1.804575	0.881584626	2.44415	0.578219936	1.35441863	0.463770462
350595800	PREDICTED: SH3 domain-binding glutamic acid-rich-like protein-like [Sus scrofa]	12.750675	3.233066558	17.18675	0.299844508	1.347909032	0.259086153
444722654	T-complex protein 1 subunit delta [Tupaia chinensis]	3.32618	1.166880068	4.470475	0.844149992	1.344026781	0.338577461
4506715	40S ribosomal protein S28 [Homo sapiens]	2.78705	0.524948767	3.743375	0.508904969	1.343131627	0.061700102
335287916	PREDICTED: integrin alpha-5 isoform 1 [Sus scrofa]	3.816275	0.696689782	5.12245	1.341187982	1.342264381	0.484314315
545197429	PREDICTED: histone H2A type 1-E-like [Equus caballus]	9.501725	3.376317058	12.72675	4.289769018	1.339414685	0.651800203
281351987	hypothetical protein PANDA_004938 [Ailuropoda melanoleuca]	1.5028	0.654351418	2.01039	0.438221025	1.337762843	0.615573943
194043123	PREDICTED: coronin-1C isoform X1 [Sus scrofa]	5.036325	0.447751429	6.735	0.53687657	1.337284627	0.064926766
162287374	polymerase I and transcript release factor isoform 2 [Bos taurus]	21.03875	2.966046453	28.04	3.038197602	1.332778801	0.141552484
118403904	protein DJ-1 [Sus scrofa]	4.279925	0.280834181	5.70325	0.561162995	1.332558398	0.187209781
113205682	protein S100-A6 [Sus scrofa]	2.81108	0.898576623	3.728615	0.981256383	1.326399462	0.13910146
554546398	PREDICTED: uncharacterized protein LOC102248938 [Myotis brandtii]	35.76475	5.856715624	46.956	9.839650815	1.312912854	0.455225418
114051526	coactosin-like protein [Bos taurus]	1.518005	0.30559001	1.98834	0.572781263	1.309837583	0.184420273
350593998	PREDICTED: EF-hand domain-containing protein D1 [Sus scrofa]	3.04225	0.458667978	3.977525	0.560609215	1.307428712	0.112362335
149722119	PREDICTED: 26S protease regulatory subunit 6B isoform 1 [Equus caballus]	0.775325	0.493746702	1.0105525	0.732411783	1.303392126	0.746981565

162951821	heterogeneous nuclear ribonucleoprotein A/B [Sus scrofa]	1.49155	0.64528063	1.939875	0.766142521	1.300576581	0.770070384
157829918	Chain A, Destrin, Nmr, Minimized Average Structure	10.606525	1.126258448	13.71595	2.590878938	1.293161521	0.202319846
556775761	PREDICTED: vimentin [Pantholops hodgsonii]	227.3375	76.87556898	293.21	16.73376228	1.289756419	0.438023043
545207279	PREDICTED: ATP synthase subunit gamma, mitochondrial isoform X2 [Equus caballus]	4.054975	0.649595464	5.2016	0.365836806	1.282769931	0.183054568
556727629	PREDICTED: fatty acid-binding protein, heart isoform X2 [Pantholops hodgsonii]	2.553455	0.686771089	3.275075	0.690901406	1.282605333	0.527725063
350585312	PREDICTED: basal cell adhesion molecule isoform X1 [Sus scrofa]	4.521075	0.268415149	5.785075	1.017279163	1.279579525	0.285037185
545837210	PREDICTED: thioredoxin domain-containing protein 5, partial [Sus scrofa]	0.771575	0.257242212	0.9859	0.570631168	1.277775978	0.677580829
545560279	PREDICTED: LOW QUALITY PROTEIN: transcriptional activator protein Pur-beta [Canis lupus familiaris]	10.62235	2.169090589	13.5705	1.778259519	1.277542163	0.336544375
126320832	PREDICTED: T-complex protein 1 subunit epsilon [Monodelphis domestica]	2.530725	0.333771692	3.225775	0.180396491	1.274644618	0.07329543
281353832	hypothetical protein PANDA_008751 [Ailuropoda melanoleuca]	4.3013	0.800031619	5.479	0.28951373	1.273800944	0.214683206
554534292	PREDICTED: keratin, type I cytoskeletal 14 [Myotis brandtii]	6.32065	1.332417433	8.04195	2.764583091	1.272329586	0.559425712
655884340	PREDICTED: LOW QUALITY PROTEIN: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6 [Oryctolagus cuniculus]	0.771575	0.257242212	0.9812525	0.397217845	1.271752584	0.759416369
301783431	PREDICTED: hypothetical protein LOC100468944 [Ailuropoda melanoleuca]	79.379	27.65839025	100.915	33.65308047	1.271306013	0.708948754
197099010	60S ribosomal protein L23 [Pongo abelii]	2.025755	0.724461265	2.5738275	1.247158156	1.270552214	0.685368718
545197486	PREDICTED: histone H2A type 1-like [Equus caballus]	90.69825	17.86586175	115.07925	20.66740418	1.268814448	0.514641686
149728615	PREDICTED: alpha/beta hydrolase domain-containing protein 14B [Equus caballus]	2.547255	0.678922227	3.23185	0.477150405	1.268757937	0.567034803
126722859	40S ribosomal protein S4 [Bos taurus]	1.807	0.778259677	2.28395	1.13690856	1.263945766	0.744415125
149744781	PREDICTED: SH3 domain-binding glutamic acid-rich-like protein-like isoform X1 [Equus caballus]	11.428775	1.953120849	14.41075	0.292990152	1.260918165	0.206290878
545880563	PREDICTED: protein-glutamine gamma-glutamyltransferase 2 [Sus scrofa]	61.02275	8.481504057	76.54025	6.999119699	1.254290408	0.17770027
18777767	dynein light chain roadblock-type 1 [Rattus norvegicus]	1.00898	0.425388436	1.2612425	0.664493351	1.250017344	0.794736677
126337523	PREDICTED: importin-5 isoform X1 [Monodelphis domestica]	1.006505	0.022838214	1.2560175	0.272412578	1.247899911	0.410953137
505768901	PREDICTED: lysine--tRNA ligase isoform X2 [Sorex araneus]	1.006505	0.022838214	1.2560175	0.272412578	1.247899911	0.410953137
602708825	PREDICTED: plectin [Lipotes vexillifer]	3.5637	1.016711115	4.431925	1.706692667	1.243630216	0.394339605
301785528	PREDICTED: PDZ and LIM domain protein 7-like [Ailuropoda melanoleuca]	14.794075	2.775250332	18.359	2.312263141	1.24096978	0.378847811
560978056	PREDICTED: plectin [Vicugna pacos]	3.8816	2.249625966	4.8163	2.341130354	1.240802762	0.59853346
335310350	PREDICTED: carbonyl reductase [NADPH] 1-like, partial [Sus scrofa]	2.785925	0.790052329	3.438725	0.814821902	1.234320737	0.476211292
148230364	heterogeneous nuclear ribonucleoprotein D0 [Bos taurus]	1.9941	0.370857468	2.4601	0.601350429	1.233689384	0.467889234

149716550	PREDICTED: platelet-activating factor acetylhydrolase IB subunit beta [Equus caballus]	1.807	0.778259677	2.228575	0.196507703	1.233301051	0.574429779
350586422	PREDICTED: adenylyl cyclase-associated protein 2, partial [Sus scrofa]	1.006505	0.022838214	1.2400525	0.235500938	1.232038092	0.431761829
21465643	Chain B, Crystal Structure Of The Mammalian 20s Proteasome At 2.75 A Resolution	4.84925	1.189176013	5.96205	0.685215042	1.229478785	0.47872135
431921648	Keratin, type II cytoskeletal 1 [Pteropus alecto]	40.3265	3.482752037	49.4775	4.352721074	1.226922743	0.235063617
28603770	F-actin-capping protein subunit beta [Bos taurus]	4.843	1.102504975	5.940025	0.429002064	1.226517654	0.456361893
411147409	laminin subunit gamma-1 precursor [Sus scrofa]	17.15375	2.850962743	20.92625	4.452607782	1.219922757	0.616231791
311259322	PREDICTED: LOW QUALITY PROTEIN: chloride intracellular channel protein 1 [Sus scrofa]	0.769125	0.492675365	0.9366	0.9366	1.21774744	0.784314392
335305150	PREDICTED: zyxin isoform X1 [Sus scrofa]	6.354525	1.42574826	7.73685	1.421199159	1.217533962	0.200222494
444517659	Galectin-1, partial [Tupaia chinensis]	7.32945	1.213690126	8.915725	0.731589322	1.216424834	0.464394676
213021130	proteasome subunit alpha type-6 [Ovis aries]	2.247975	0.190682268	2.732825	0.231111461	1.215683004	0.166515154
548458608	PREDICTED: F-actin-capping protein subunit alpha-1 [Capra hircus]	0.772875	0.772875	0.9366	0.9366	1.211838913	0.391002219
2497487	RecName: Full=UMP-CMP kinase; AltName: Full=Deoxycytidylate kinase; Short=CK; Short=dCMP kinase; AltName: Full=Nucleoside-diphosphate kinase; AltName: Full=Uridine monophosphate/cytidine monophosphate kinase; Short=UMP/CMP kinase; Short=UMP/CMPK [Sus scrofa]	2.060875	0.732242628	2.487375	0.279825405	1.206950931	0.464925018
162139823	prelamin-A/C [Sus scrofa]	42.78225	2.773033338	51.59225	2.348401917	1.205926523	0.057785816
126722963	calumenin isoform 2 precursor [Oryctolagus cuniculus]	1.235225	0.466896884	1.48754	0.661190142	1.204266429	0.836218043
146231742	ubiquitin-conjugating enzyme E2N-like [Bos taurus]	4.5614	0.92941628	5.481625	0.306983529	1.20174179	0.349888496
555994603	PREDICTED: LOW QUALITY PROTEIN: ribosomal protein S19 [Bos mutus]	6.86095	1.157153891	8.244225	1.137794251	1.201615665	0.492356667
311277155	PREDICTED: biglycan [Sus scrofa]	42.489	5.491151564	51.003	7.521545331	1.200381275	0.195546575
47523692	thioredoxin [Sus scrofa]	9.36775	1.271172542	11.2335	0.791395655	1.199167356	0.366628784
301771378	PREDICTED: proteasome activator complex subunit 1-like [Ailuropoda melanoleuca]	1.0292	0.420730989	1.22874	0.474321155	1.193878741	0.712578513
504179152	PREDICTED: histone H1.1-like [Ochotona princeps]	74.49175	16.13945952	88.91375	12.81406797	1.193605332	0.61338643
47522760	long-chain 3-ketoacyl-CoA thiolase [Sus scrofa]	2.252875	0.870224313	2.686975	0.685112653	1.192687122	0.757444135
18087731	dynein light chain 2, cytoplasmic [Mus musculus]	2.547255	0.678922227	3.03485	0.65082687	1.191419783	0.640460409
655854442	PREDICTED: LOW QUALITY PROTEIN: profilin-2 [Oryctolagus cuniculus]	2.526975	0.323941611	3.0102	0.462202501	1.191226664	0.179612141
586533349	PREDICTED: glycogen phosphorylase, brain form isoform X1 [Pteropus alecto]	1.266605	0.272091248	1.50875	0.505311959	1.191176413	0.633578133
585195860	PREDICTED: serine/threonine-protein phosphatase 2A activator [Leptonychotes weddellii]	1.035425	0.597816427	1.231365	0.214574573	1.189236304	0.721837265
521021546	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 [Myotis brandtii]	1.26038	0.257869159	1.4988525	0.295117345	1.189206827	0.656472165
126339314	PREDICTED: cullin-associated NEDD8-dissociated protein 1-like [Monodelphis domestica]	4.57515	1.044120078	5.43575	0.503897401	1.188103122	0.480778418

157831033	Chain A, Crevice-Forming Mutants In The Rigid Core Of Bovine Pancreatic Trypsin Inhibitor: Crystal Structures Of F22a, Y23a, N43g, And F45a	4.296425	0.791842561	5.078575	1.396028434	1.182046702	0.682662587
327272802	PREDICTED: 40S ribosomal protein S16 [Anolis carolinensis]	4.298875	0.67442198	5.072525	1.276541563	1.179965689	0.466138671
6919844	RecName: Full=Transforming growth factor-beta-induced protein ig-h3; Short=Beta ig-h3; AltName: Full=Kerato-epithelin; AltName: Full=RGD-containing collagen-associated protein; Short=RGD-CAP; Flags: Precursor [Sus scrofa]	5.492475	0.787387546	6.476775	1.365782247	1.179208827	0.264589329
149727536	PREDICTED: UTP--glucose-1-phosphate uridylyltransferase isoformX2 [Equus caballus]	1.26413	0.266483331	1.490165	0.281379967	1.178806768	0.46830929
126307067	PREDICTED: astrocytic phosphoprotein PEA-15 [Monodelphis domestica]	2.7846	0.302121832	3.275075	0.690901406	1.176138404	0.532130403
528763338	hypothetical protein CB1_000606063 [Camelus ferus]	32.53325	3.242089177	38.063	3.665989203	1.169972259	0.344357648
545873945	PREDICTED: PDZ and LIM domain protein 3 isoform X1 [Sus scrofa]	8.075125	1.646544249	9.44065	0.517864309	1.169102645	0.528783167
126310923	PREDICTED: proteasome subunit alpha type-5 [Monodelphis domestica]	2.765675	0.254137441	3.23185	0.477150405	1.168557405	0.264359223
545867751	PREDICTED: collagen alpha-2(VI) chain [Sus scrofa]	21.704775	6.061201247	25.34625	2.881351199	1.16777299	0.538906978
121118	RecName: Full=Gelsolin; AltName: Full=Actin-depolymerizing factor; Short=ADF; AltName: Full=Brevin; Flags: Precursor, partial [Sus scrofa]	44.84425	2.934915058	52.36625	4.569996105	1.167736109	0.165225148
281349702	hypothetical protein PANDA_003128 [Ailuropoda melanoleuca]	7.0822	1.303380129	8.25775	0.793135023	1.165986558	0.149295125
148352329	septin-7 isoform 2 [Homo sapiens]	7.0947	1.193249007	8.184575	0.440119371	1.153618194	0.275939425
664708095	PREDICTED: phosphoglucomutase-like protein 5 [Equus przewalskii]	29.19225	1.914739598	33.58775	3.19927399	1.150570785	0.215533548
478515717	PREDICTED: histone H2B type 1-B-like [Ceratotherium simum simum]	38.324	5.578462512	43.975	9.855226135	1.147453293	0.666416865
115495141	serine/threonine-protein phosphatase 2A catalytic subunit beta isoform [Bos taurus]	1.514255	0.511249894	1.735625	0.237868656	1.146190701	0.656661828
432112608	Keratin, type II cytoskeletal 5 [Myotis davidii]	17.22625	6.130506102	19.7375	7.452410354	1.145780422	0.826868341
164448580	peptidyl-prolyl cis-trans isomerase FKBP2 isoform 1 [Bos taurus]	1.518005	0.30559001	1.738225	0.647947138	1.145071986	0.696446641
344266889	PREDICTED: keratin, type II cytoskeletal 1 [Loxodonta africana]	37.066	4.242677948	42.40425	4.785517342	1.144020126	0.535495959
545806931	PREDICTED: elongation factor 1-gamma [Sus scrofa]	1.270355	0.500408155	1.44955	0.602617002	1.141058995	0.827928896
511910681	PREDICTED: keratin, type II cytoskeletal 1 [Mustela putorius furo]	40.87075	4.620846899	46.6275	4.730145338	1.140852566	0.520209353
311276332	PREDICTED: 3-hydroxyacyl-CoA dehydrogenase type-2 isoform 2 [Sus scrofa]	6.066675	0.80607318	6.9126	0.733766235	1.139437995	0.613744691
281350953	hypothetical protein PANDA_001716 [Ailuropoda melanoleuca]	1.781855	0.508344511	2.0297925	1.411841398	1.139145722	0.867830067
329664122	ras-related protein Rab-5B [Bos taurus]	8.787175	1.093297272	9.995375	1.16939645	1.137495839	0.544999332
126722713	elongation factor 1-beta [Oryctolagus cuniculus]	1.52423	0.315995655	1.733	0.23271051	1.136967518	0.494165352

305855180	catechol O-methyltransferase [Sus scrofa]	1.511805	0.662680133	1.71705	0.444685448	1.135761557	0.826407178
114051185	programmed cell death protein 5 [Bos taurus]	3.29855	0.531040636	3.746	0.294198303	1.135650513	0.163879593
47716872	galectin-1 [Sus scrofa]	25.35725	4.964055992	28.762	1.29962065	1.134271264	0.606390857
47523734	protein phosphatase 1 regulatory subunit 14A [Sus scrofa]	6.995275	0.671803234	7.934475	0.381744023	1.134262055	0.118943323
545812163	PREDICTED: histidine triad nucleotide-binding protein 1-like [Sus scrofa]	1.746725	0.636188829	1.978475	0.386112759	1.132676867	0.668194913
187370723	hydroxyacyl-coenzyme A dehydrogenase/3-ketoacyl-coenzyme A thiolase/enoyl-coenzyme A hydratase alpha subunit [Sus scrofa]	9.649425	1.506336614	10.9256	1.548132761	1.132253994	0.375670977
505850104	PREDICTED: alpha-actinin-3 [Sorex araneus]	25.796	3.67551849	29.2065	3.130216433	1.13221042	0.242941591
335289705	PREDICTED: flavin reductase (NADPH) [Sus scrofa]	3.307225	1.011296314	3.743375	0.508904969	1.131877934	0.518734721
114051487	cytochrome c [Bos taurus]	2.014325	0.73071291	2.274415	0.67958931	1.129120177	0.839672126
126723252	heterogeneous nuclear ribonucleoprotein K [Oryctolagus cuniculus]	6.85325	1.764151906	7.6903	1.130701459	1.122139131	0.528616568
28603774	rho GDP-dissociation inhibitor 1 [Bos taurus]	7.04315	0.438239973	7.898575	0.859352338	1.121454889	0.254294058
586457760	PREDICTED: lysozyme C [Chrysochloris asiatica]	2.2682	0.655242506	2.5419025	0.703916363	1.120669474	0.84071795
586480648	PREDICTED: 60S ribosomal protein L31-like [Chrysochloris asiatica]	2.039505	0.741451968	2.2778775	0.671850465	1.116877625	0.851154337
194211402	PREDICTED: calcium-binding protein 39 isoform X1 [Equus caballus]	1.778105	0.279648381	1.98574	0.379294633	1.116773194	0.334446264
345090969	septin 2 [Sus scrofa]	3.7722	0.258303149	4.211675	0.692266973	1.116503632	0.458639266
311275457	PREDICTED: filamin-C isoformX1 [Sus scrofa]	65.54525	3.79476333	73.08825	6.104492081	1.115080803	0.180313109
488529388	PREDICTED: myosin-9 [Dasypus novemcinctus]	92.7255	3.382146323	103.36725	5.366208708	1.114766165	0.15265488
82465299	filamin-A [Sus scrofa]	51.5625	5.209627794	57.47075	3.4937609	1.114584242	0.074065937
126723197	calpain small subunit 1 [Oryctolagus cuniculus]	5.795475	0.796268028	6.44165	0.524789179	1.111496469	0.614146065
118403788	glutathione S-transferase mu 2 [Sus scrofa]	4.254775	0.42590501	4.72725	0.22616664	1.111045825	0.105667983
340007404	alpha-actinin-1 [Sus scrofa]	115.883	10.83522738	128.3	11.54508914	1.107151178	0.158117808
655864464	PREDICTED: LOW QUALITY PROTEIN: bromodomain adjacent to zinc finger domain protein 1A [Oryctolagus cuniculus]	11.902125	1.713106564	13.16915	1.343422714	1.106453679	0.425037782
478491393	PREDICTED: dihydropyrimidinase-related protein 3 isoform 1 [Ceratotherium simum simum]	26.24275	2.576637388	28.86525	1.658964204	1.099932362	0.343598809
346986388	profilin-1 [Sus scrofa]	55.1165	5.299464258	60.622	2.5720382	1.099888418	0.325798338
311248247	PREDICTED: ATP synthase subunit delta, mitochondrial-like isoform 1 [Sus scrofa]	2.2731	0.285413869	2.496075	0.302489772	1.098092913	0.477569494
149751402	PREDICTED: NAD(P)H-hydrate epimerase [Equus caballus]	2.03818	0.445316912	2.237275	0.230898511	1.097682737	0.775376708
149758330	PREDICTED: guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 isoform X1 [Equus caballus]	6.554325	0.577703881	7.187375	0.45924546	1.096585079	0.094199315
472382549	PREDICTED: uncharacterized protein LOC101365636 [Odobenus rosmarus divergens]	5.54535	0.919003479	6.076975	1.702173882	1.095868611	0.822312031
149612407	PREDICTED: pyruvate kinase PKM [Ornithorhynchus anatinus]	20.91425	2.089622987	22.90625	1.76328313	1.095246064	0.458722057
545887975	PREDICTED: LanC lantibiotic synthetase component C-like 1 [Sus scrofa]	2.288305	0.776752311	2.50594	0.516808759	1.095107514	0.725868444
528754126	actin, cytoplasmic 1 [Camelus ferus]	79.59875	2.410559388	87.14725	1.665239641	1.094831891	0.119447522

586531235	PREDICTED: EH domain-containing protein 4 [Pteropus alecto]	4.797625	0.347182316	5.2495	1.151910002	1.094187228	0.660667028
114051223	prohibitin-2 [Bos taurus]	2.4891	0.603217499	2.721525	0.428321167	1.093377124	0.781981315
335294000	PREDICTED: 3-hydroxybutyrate dehydrogenase type 2-like isoform 1 [Sus scrofa]	2.285855	0.649321367	2.496075	0.302489772	1.091965588	0.820826869
545859588	PREDICTED: unconventional myosin-Ic [Sus scrofa]	22.6025	3.578101976	24.67525	4.355374962	1.091704457	0.680428527
586993676	PREDICTED: myosin-9 [Felis catus]	111.4875	0.917990332	121.61	4.62177996	1.090794932	0.107402993
555986717	PREDICTED: filamin-A isoform X2 [Bos mutus]	553.145	15.28308788	603.2	8.217488465	1.090491643	0.056319923
471418286	PREDICTED: filamin-A isoform 2 [Trichechus manatus latirostris]	533.665	14.77285433	580.8575	9.062945966	1.088430945	0.05469397
586564248	PREDICTED: filamin-A isoform X2 [Pteropus alecto]	581.04	16.09713691	631.38	10.19054055	1.086637753	0.070615551
74008809	PREDICTED: filamin-A isoform 2 [Canis lupus familiaris]	587.8475	16.28637538	637.7625	9.773937602	1.084911478	0.084979188
47523318	ubiquitin carboxyl-terminal hydrolase isozyme L1 [Sus scrofa]	2.280955	1.063155807	2.4726	0.983311205	1.084019632	0.806931595
343887360	proteasome (prosome, macropain) subunit, alpha type [Sus scrofa]	2.045705	0.952006097	2.217265	0.71017819	1.083863509	0.613353384
667246325	PREDICTED: ATP-dependent RNA helicase DDX3X isoform X1 [Galeopterus variegatus]	5.0301	0.427819275	5.433125	0.779684414	1.080122662	0.668850776
270289750	non-specific lipid-transfer protein [Sus scrofa]	3.0158	0.413913848	3.25305	0.315878179	1.07866901	0.263941308
334311991	PREDICTED: 14-3-3 protein theta isoform X1 [Monodelphis domestica]	7.865	1.092542705	8.47325	0.342982314	1.0773363	0.578377479
655895781	PREDICTED: calpain-2 catalytic subunit-like [Oryctolagus cuniculus]	1.545775	1.545775	1.665125	0.976256742	1.077210461	0.920044005
335296245	PREDICTED: cysteine and glycine-rich protein 1-like isoform 1 [Sus scrofa]	78.18575	8.355059948	84.20575	2.018870038	1.076996128	0.431408645
505794832	PREDICTED: filamin-A [Sorex araneus]	515.105	12.19733065	554.6625	6.919574138	1.076795022	0.051417459
338729679	PREDICTED: LOW QUALITY PROTEIN: filamin-A [Equus caballus]	571.795	13.09164969	615.625	9.973953161	1.076653346	0.075390125
281345571	hypothetical protein PANDA_005634 [Ailuropoda melanoleuca]	11.3304	0.946796772	12.19175	0.524172741	1.076021147	0.472052855
671031328	PREDICTED: myosin light chain kinase, smooth muscle [Ursus maritimus]	13.8345	1.377487114	14.871	1.6063071	1.074921392	0.68482649
291405834	PREDICTED: prohibitin [Oryctolagus cuniculus]	6.003675	0.83774931	6.451575	0.36082733	1.074604305	0.701972403
472390487	PREDICTED: filamin-A [Odobenus rosmarus divergens]	541.91	16.02267716	582.3225	16.95934913	1.074574191	0.138609386
47523632	proteasome activator complex subunit 2 [Sus scrofa]	2.27555	0.666016897	2.44415	0.578219936	1.074091978	0.884541193
470614409	PREDICTED: tubulin beta chain-like [Tursiops truncatus]	57.8905	2.149199483	62.1595	3.771517212	1.073742669	0.366724161
13775198	SH3 domain-binding glutamic acid-rich-like protein 3 [Homo sapiens]	3.273425	0.271492935	3.514475	0.57458207	1.073638467	0.504061753
15553463	beta-actin [Oryctolagus cuniculus]	145.2225	7.911307704	155.43	4.416267278	1.070288695	0.232248219
301777322	PREDICTED: 2-oxoglutarate dehydrogenase, mitochondrial-like [Ailuropoda melanoleuca]	0.729925	0.454899845	0.779025	0.49602796	1.067267185	0.947583602
2959454	desmin [Sus scrofa]	266.23	12.03574191	284.055	4.324766853	1.066953386	0.320722843
478521049	PREDICTED: collagen alpha-1(I) chain isoform 1 [Ceratotherium simum simum]	6.886825	2.101836437	7.339525	1.668548676	1.06573421	0.892126711
4506413	ras-related protein Rap-1A precursor [Homo sapiens]	16.085	0.318292057	17.1235	0.969327301	1.064563258	0.269964172
47523488	glutathione peroxidase 1 [Sus scrofa]	3.057405	0.845092517	3.250425	0.304534859	1.06313197	0.83461508

433552070	Chain A, Refined Crystal Structure Of Cytoplasmic Malate Dehydrogenase At 2.5-Angstroms Resolution	6.76035	0.526783196	7.186525	1.317226897	1.063040375	0.711633973
545894385	PREDICTED: myosin-11-like, partial [Sus scrofa]	95.7635	7.036972177	101.47575	1.979858092	1.059649553	0.458999714
545876122	PREDICTED: collagen alpha-3(VI) chain isoformX2 [Sus scrofa]	104.42875	21.03854809	110.433	18.63254408	1.05749614	0.802750381
395508878	PREDICTED: T-complex protein 1 subunit eta [Sarcophilus harrisii]	3.050875	0.765929017	3.225775	0.180396491	1.057327816	0.833519327
560923515	PREDICTED: talin-1 [Camelus ferus]	117.6355	8.139623266	124.305	5.194696815	1.05669632	0.1941455
347658971	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d [Sus scrofa]	7.04805	0.465216019	7.444125	0.800026893	1.056196395	0.762877979
149755988	PREDICTED: mitochondrial fission 1 protein [Equus caballus]	3.30475	0.691726775	3.4872	0.292256602	1.055208412	0.827192145
148226851	ATP synthase subunit f, mitochondrial [Sus scrofa]	4.045	0.464390775	4.2636	0.700496054	1.054042027	0.756295952
311252459	PREDICTED: poly(rC)-binding protein 1 isoform X1 [Sus scrofa]	3.79245	0.799463856	3.98015	0.376086831	1.049493072	0.778053669
545830727	PREDICTED: alpha-actinin-4 isoformX2 [Sus scrofa]	96.687	11.04387244	101.31425	14.44063508	1.047858037	0.421831439
471411352	PREDICTED: guanine nucleotide-binding protein subunit beta-2-like 1 [Trichechus manatus latirostris]	3.074905	1.279364888	3.214475	0.700794358	1.04539002	0.831336635
311270662	PREDICTED: phosphatidylethanolamine-binding protein 1 [Sus scrofa]	27.20875	1.511887142	28.338	0.586505044	1.041503193	0.370896738
335309939	PREDICTED: nucleolin-like [Sus scrofa]	4.2886	0.681954887	4.4632	0.453699908	1.040712587	0.814924039
514483031	PDZ and LIM domain protein 1 [Sus scrofa]	13.91705	1.545335401	14.481	0.658148286	1.040522237	0.711837576
135490	RecName: Full=Tubulin beta chain; AltName: Full=Beta-tubulin [Sus scrofa]	44.465	0.686831857	46.14625	2.071913221	1.037810638	0.369871172
126341423	PREDICTED: ras-related protein Rab-5A [Monodelphis domestica]	3.6078	1.369417366	3.743375	0.508904969	1.037578303	0.909219577
594108752	PREDICTED: tropomyosin alpha-3 chain-like, partial [Bubalus bubalis]	50.8085	2.246384076	52.70225	0.635189391	1.037272307	0.515079117
116242946	RecName: Full=Actin, cytoplasmic 1; AltName: Full=Beta-actin; Contains: RecName: Full=Actin, cytoplasmic 1, N-terminally processed [Bos grunniens]	759.3025	23.07020386	786.86	18.24283649	1.036293177	0.464742184
335280610	PREDICTED: LOW QUALITY PROTEIN: talin-1 [Sus scrofa]	117.1105	8.127525059	121.3175	5.80936367	1.035923337	0.346893093
488564479	PREDICTED: myosin-11 isoform 1 [Dasypus novemcinctus]	409.3675	37.44154341	423.8775	17.93602073	1.035444924	0.588460147
254692804	ras suppressor protein 1 [Ovis aries]	17.72525	2.257565185	18.33625	1.228852607	1.0344706	0.721147869
545867698	PREDICTED: collagen alpha-1(XVIII) chain, partial [Sus scrofa]	7.309425	0.571176437	7.559875	1.363032084	1.034263981	0.87260921
465965068	PREDICTED: cysteine-rich protein 2 [Orcinus orca]	11.363625	1.175958286	11.74215	0.829644476	1.033310233	0.455974522
585701676	PREDICTED: polyubiquitin-B-like [Elephantulus edwardii]	18.70025	2.212612045	19.28325	2.46988422	1.031176054	0.774019783
311264396	PREDICTED: prolargin isoform X1 [Sus scrofa]	37.17225	3.766579845	38.28075	1.591595498	1.029820632	0.695980185
359320104	PREDICTED: creatine kinase B-type [Canis lupus familiaris]	25.561	1.390363681	26.29925	1.627417349	1.02888189	0.822472656
560905580	PREDICTED: myosin-11 isoform X1 [Camelus ferus]	481.145	46.07585096	493.52	22.18909304	1.025719897	0.721919941
194207324	PREDICTED: cell division control protein 42 homolog [Equus caballus]	7.27155	1.070757061	7.45485	0.426121885	1.025207831	0.809061989
545834675	PREDICTED: tubulointerstitial nephritis antigen-like 1 isoform X1 [Sus scrofa]	4.2156	0.924222595	4.314675	1.423889032	1.023501993	0.960395363

426234055	PREDICTED: actin, alpha cardiac muscle 1, partial [Ovis aries]	1167.65	34.35356604	1194.55	50.87464169	1.023037725	0.697189911
118085932	PREDICTED: 60S ribosomal protein L15 isoform X3 [Gallus gallus]	1.002755	0.415149412	1.02449	0.427279593	1.021675285	0.248971411
118419977	beta-actin, partial [Eubalaena glacialis]	810.49	23.64800238	828.025	18.31451542	1.02163506	0.643088375
47523544	tenascin precursor [Sus scrofa]	1.940025	1.008668479	1.981075	0.715483137	1.021159521	0.953802824
346421409	transgelin [Sus scrofa]	405.495	31.37650647	413.9625	34.1881535	1.020881885	0.760187956
478535539	PREDICTED: myosin-11 isoform 1 [Ceratotherium simum simum]	453.2575	42.0935746	462.49	17.09522399	1.020369216	0.78111452
311252403	PREDICTED: sepiapterin reductase [Sus scrofa]	8.532275	0.838412871	8.701475	0.973888362	1.019830584	0.806245496
335294283	PREDICTED: protein kinase C delta-binding protein-like [Sus scrofa]	11.85065	1.388487591	12.073625	2.305460306	1.018815424	0.871722529
149720909	PREDICTED: haloacid dehalogenase-like hydrolase domain-containing protein 2 isoform X1 [Equus caballus]	0.765375	0.486800411	0.779025	0.49602796	1.017834395	0.986172946
344293080	PREDICTED: heat shock cognate 71 kDa protein [Loxodonta africana]	28.618	1.096090781	29.089	0.67896183	1.016458173	0.468032315
511958474	PREDICTED: myosin-11 isoform X2 [Mustela putorius furo]	466.81	42.26036027	474.3125	21.64961831	1.016071849	0.791903312
594051609	PREDICTED: myosin-11 isoform X3 [Bubalus bubalis]	493.7775	44.42864642	501.3925	21.90392825	1.015421926	0.825630595
349732238	transaldolase [Sus scrofa]	6.598425	0.978898528	6.69705	0.527990206	1.014946749	0.933594724
594051607	PREDICTED: myosin-11 isoform X2 [Bubalus bubalis]	503.525	45.21178027	510.3625	21.18454837	1.013579266	0.845497809
395510320	PREDICTED: beta-actin-like protein 2 [Sarcophilus harrisii]	574.9525	21.8765759	582.335	8.8715552	1.012840191	0.797849738
488567906	PREDICTED: LOW QUALITY PROTEIN: calponin 1, basic, smooth muscle [Dasypus novemcinctus]	17.7025	3.378650754	17.922	1.908153863	1.012399379	0.963187102
291405401	PREDICTED: 14-3-3 protein epsilon isoform X1 [Oryctolagus cuniculus]	7.60865	1.172556644	7.69365	1.272191288	1.011171496	0.930927139
146198759	15 kDa selenoprotein precursor [Sus scrofa]	0.74888	0.25054158	0.7570025	0.496569994	1.010846197	0.989658351
311265878	PREDICTED: inter-alpha-trypsin inhibitor heavy chain H5-like [Sus scrofa]	4.33775	1.108388318	4.3799425	1.991135008	1.009726817	0.985849628
585679399	PREDICTED: myosin regulatory light polypeptide 9 isoform X2 [Elephantulus edwardii]	34.9375	5.604046343	35.23025	2.684309016	1.008379249	0.945990554
110331787	actin related protein 2/3 complex subunit 1B [Bos taurus]	0.74643	0.249601883	0.7517525	0.491872881	1.007130608	0.994560992
545502107	PREDICTED: myosin-11 isoform X31 [Canis lupus familiaris]	478.2975	43.36256669	481.6825	20.076938	1.007077185	0.910067121
593743500	PREDICTED: myosin-11 isoform X4 [Physeter catodon]	477.3425	42.71058619	479.9275	19.3345767	1.005415399	0.934532054
426247306	PREDICTED: phosphatidylethanolamine-binding protein 1 [Ovis aries]	18.335	1.399986607	18.43075	1.306623982	1.005222253	0.960720388
410985147	PREDICTED: myosin-11 [Felis catus]	469.2275	39.96916778	471.6775	19.50757305	1.005221348	0.927346831
115495671	neuroplastin precursor [Bos taurus]	0.9838	0.384508229	0.988525	0.383544768	1.004802805	0.995465867
11321591	high mobility group protein B2 [Homo sapiens]	0.51525	0.51525	0.5176	0.5176	1.004560893	0.997951554
335295652	PREDICTED: laminin subunit beta-1 isoform X1 [Sus scrofa]	1.76535	0.64901617	1.772775	0.889970588	1.004205965	0.996249334
350578365	PREDICTED: LOW QUALITY PROTEIN: laminin subunit alpha-4 [Sus scrofa]	6.491125	1.256216695	6.516825	0.977218464	1.003959252	0.985502692
14141193	40S ribosomal protein S9 [Homo sapiens]	1.5407	0.662667047	1.54469	0.678638135	1.002589732	0.997158433
296472241	TPA: alpha-actinin-2 [Bos taurus]	22.3635	8.05206591	22.404	8.195667097	1.001810987	0.984826227

134104894	Chain A, Structure Of Camp-Dependent Protein Kinase Complexed With A- 443654	2.48665	0.599551312	2.489975	0.288166978	1.00133714	0.996983515
151556324	CLTLB protein [Bos taurus]	0	0	0.7271	0.4533045	#DIV/0!	0.207050872
602714922	PREDICTED: chaperonin CPN60-1, mitochondrial-like, partial [Lipotes vexillifer]	0	0	0.485675	0.485675	#DIV/0!	0.391002219
305855162	ELAV-like protein 1 [Sus scrofa]	0	0	0.4683	0.4683	#DIV/0!	0.391002219
335283403	PREDICTED: lamin-B1 isoform X1 [Sus scrofa]	0	0	0.4683	0.4683	#DIV/0!	0.391002219
153792600	fatty acid synthase [Sus scrofa]	6.160875	2.882075284	0.5176	0.5176	-11.90277241	0.098587972
667247687	PREDICTED: delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial [Galeopterus variegatus]	1.24765	0.474066188	0.24284	0.24284	-5.137745017	0.099491641
212549619	ERO1-like protein alpha precursor [Sus scrofa]	1.238975	0.471775848	0.2588	0.2588	-4.78738408	0.261005804
1304179	fibrinogen A-alpha-chain [Sus scrofa]	1.237675	0.466545088	0.261425	0.261425	-4.734340633	0.084691496
291409329	PREDICTED: LOW QUALITY PROTEIN: prolow-density lipoprotein receptor-related protein 1 [Oryctolagus cuniculus]	3.28095	0.66484621	0.763065	0.254884778	-4.299699239	0.069659192
545880794	PREDICTED: adenosine deaminase [Sus scrofa]	0.98755	0.38462955	0.2341525	0.2341525	-4.217550528	0.187408776
158429133	Chain A, C28s Mutant Of Succinyl-Coa:3-Ketoacid Coa Transferase From Pig Heart	4.20285	1.332005033	0.9972175	0.026036997	-4.214577061	0.095570026
115496662	cAMP-dependent protein kinase type I-alpha regulatory subunit [Bos taurus]	1.01273	0.425424122	0.24284	0.24284	-4.170359084	0.222501527
194037005	PREDICTED: ribonuclease UK114 isoform 1 [Sus scrofa]	1.023	0.59066107	0.2588	0.2588	-3.952859351	0.393940074
342349319	calnexin precursor [Sus scrofa]	2.702625	1.171195403	0.7384175	0.247188426	-3.660022954	0.19165605
343790920	fumarate hydratase [Sus scrofa]	1.75165	0.637018328	0.4955775	0.286987013	-3.534563212	0.18470584
11514531	Chain A, Fructose-1,6-Bisphosphatase (Mutant Y57w) ProductZN COMPLEX (R-State)	1.746725	0.636188829	0.4955775	0.286987013	-3.524625311	0.072520899
545806760	PREDICTED: atlastin-3 [Sus scrofa]	0.775325	0.493746702	0.2341525	0.2341525	-3.311196763	0.18217009
343790922	phospholipase C, delta 1 [Sus scrofa]	0.77405	0.496985842	0.2341525	0.2341525	-3.305751594	0.467192101
149725788	PREDICTED: elongation factor Tu, mitochondrial [Equus caballus]	0.77405	0.496985842	0.2341525	0.2341525	-3.305751594	0.467192101
350592528	PREDICTED: endoplasmic reticulum resident protein 29 [Sus scrofa]	0.772875	0.772875	0.2341525	0.2341525	-3.300733496	0.391002219
444526054	Dihydrolipoyl dehydrogenase, mitochondrial [Tupaia chinensis]	3.237975	0.69689868	0.9859	0.570631168	-3.284283396	0.093472785
47522940	dihydrolipoyl dehydrogenase, mitochondrial precursor [Sus scrofa]	4.523525	0.66128086	1.46814	0.618515023	-3.081126459	0.096019624
545855978	PREDICTED: lysosome-associated membrane glycoprotein 1 isoform X1 [Sus scrofa]	2.97415	0.75157072	0.96994	0.383071264	-3.06632369	0.140625466
12082134	heat shock protein 90 beta [Equus caballus]	12.534	1.056477717	4.177775	2.412228448	-3.000161569	0.053270731
545805333	PREDICTED: 14 kDa phosphohistidine phosphatase isoform X2 [Sus scrofa]	0.769125	0.492675365	0.2588	0.2588	-2.97188949	0.498788177
545843364	PREDICTED: LOW QUALITY PROTEIN: cytoplasmic dynein 1 heavy chain 1 [Sus scrofa]	7.75825	4.647166563	2.67125	2.67125	-2.904351895	0.49233898
602717035	PREDICTED: tubulointerstitial nephritis antigen-like isoform X1 [Lipotes vexillifer]	3.725475	1.285504361	1.294	1.294	-2.879037867	0.188312399
56711370	LIM and cysteine-rich domains protein 1 [Sus scrofa]	4.493775	1.679479704	1.675015	1.030566864	-2.682826721	0.184931023

545889716	PREDICTED: cytochrome P450 1B1-like, partial [Sus scrofa]	5.94365	2.765693128	2.257875	1.132381063	-2.632408791	0.111360356
809283	Chain B, Structure Determination Of Aquomet Porcine Hemoglobin At 2.8 Angstrom Resolution	87.1385	38.53431268	33.2095	8.282494818	-2.623902799	0.216870632
261245058	hemoglobin subunit beta [Sus scrofa]	86.90725	38.71527665	33.16875	7.653926524	-2.620154513	0.225976476
122465	RecName: Full=Hemoglobin subunit alpha; AltName: Full=Alpha-globin; AltName: Full=Hemoglobin alpha chain [Sus scrofa]	39.1875	11.97332431	15.188975	3.372778098	-2.579996346	0.131069506
449081295	RecName: Full=Aminopeptidase N; Short=AP-N; Short=pAPN; AltName: Full=Alanyl aminopeptidase; AltName: Full=Aminopeptidase M; Short=AP-M; AltName: Full=Microsomal aminopeptidase; AltName: Full=gp130; AltName: CD_antigen=CD13 [Sus scrofa]	4.330225	0.924797876	1.6837	0.793919705	-2.571850686	0.17785867
157834775	Chain A, Crystallographic Refinement And Atomic Models Of Two Different Forms Of Citrate Synthase At 2.7 And 1.7 Angstroms Resolution	4.47815	1.27738105	1.75419	0.504653041	-2.552830651	0.185699335
229368698	ribosomal protein S6 (predicted) [Dasypus novemcinctus]	1.279325	0.637614484	0.5176	0.5176	-2.471647991	0.445736625
431891794	Syntenin-1 [Pteropus alecto]	1.7616	0.496069352	0.7357925	0.2461123	-2.394153243	0.0870198
47522770	clusterin precursor [Sus scrofa]	2.9704	1.041802217	1.269925	0.77265852	-2.33903577	0.106090262
311265713	PREDICTED: integrin alpha-8 [Sus scrofa]	5.181775	1.428679098	2.231175	0.471601867	-2.322442211	0.16969718
335293373	PREDICTED: UDP-glucose 6-dehydrogenase isoform 1 [Sus scrofa]	4.5387	1.002657048	1.95584	0.881408161	-2.320588596	0.205792828
264681430	3-ketoacyl-CoA thiolase, mitochondrial [Sus scrofa]	1.76405	0.886581106	0.763065	0.254884778	-2.311795194	0.269627441
149750911	PREDICTED: 40S ribosomal protein S2 [Equus caballus]	1.788375	1.05135134	0.779025	0.49602796	-2.295658034	0.479719854
126327421	PREDICTED: high mobility group protein B1 isoform X2 [Monodelphis domestica]	2.243075	0.863086333	0.9859	0.570631168	-2.275154681	0.343963829
114052342	vesicle-associated membrane protein 3 [Bos taurus]	2.7846	0.302121832	1.23399	0.477445212	-2.256582306	0.060640028
262072947	dihydrolipoamide dehydrogenase [Sus scrofa]	2.250425	0.467062645	0.9998425	0.427784253	-2.250779498	0.197948978
164359	apolipoprotein A-I [Sus scrofa]	2.238	0.739217547	0.9972175	0.026036997	-2.244244611	0.186946687
25777713	S-phase kinase-associated protein 1 isoform b [Homo sapiens]	0.520175	0.520175	0.2341525	0.2341525	-2.221522299	0.684174184
335284501	PREDICTED: cytochrome b-c1 complex subunit 2, mitochondrial-like [Sus scrofa]	2.18115	1.152394615	0.987325	0.687045318	-2.209150989	0.12445382
126272971	PREDICTED: annexin A8-like [Monodelphis domestica]	0.51525	0.51525	0.2341525	0.2341525	-2.200488998	0.391002219
14141157	heterogeneous nuclear ribonucleoprotein H3 isoform a [Homo sapiens]	1.031675	0.424761675	0.4769925	0.275483085	-2.162874678	0.456668256
149727574	PREDICTED: spectrin beta chain, non-erythrocytic 1 isoform X1 [Equus caballus]	4.018225	1.254886736	1.939875	0.766142521	-2.071383465	0.241379766
15431303	60S ribosomal protein L9 [Homo sapiens]	1.539425	0.657842919	0.744475	0.468041151	-2.067799456	0.495705299
429836835	signal peptidase complex catalytic subunit SEC11A isoform 6 [Homo sapiens]	1.01273	0.425424122	0.4929525	0.28531688	-2.054417008	0.154625988
545815836	PREDICTED: fumarylacetoacetate hydrolase domain-containing protein 2-like [Sus scrofa]	1.543175	0.51449313	0.7543775	0.252656581	-2.045627024	0.058477265
117661065	RPL35 [Sus scrofa]	1.02545	0.414620763	0.50164	0.289915006	-2.04419504	0.477810785
298160991	actin-related protein 2/3 complex subunit 2 [Sus scrofa]	2.5345	0.683189397	1.2400525	0.235500938	-2.043865078	0.206727527

149698113	PREDICTED: peptidyl-prolyl cis-trans isomerase D [Equus caballus]	2.014325	0.73071291	0.9972175	0.026036997	-2.019945498	0.270492921
149720524	PREDICTED: malectin [Equus caballus]	0.98755	0.38462955	0.4955775	0.286987013	-1.992725658	0.491216636
295442674	2,4-dienoyl-CoA reductase 1 [Sus scrofa]	0.520175	0.520175	0.261425	0.261425	-1.98976762	0.719397173
115496280	annexin A7 [Bos taurus]	5.40275	2.193686865	2.748775	0.278616177	-1.96551191	0.353795202
545822821	PREDICTED: pre-B-cell leukemia transcription factor-interacting protein 1 [Sus scrofa]	1.52913	0.907275105	0.779025	0.49602796	-1.962876673	0.230846412
156523130	surfeit locus protein 4 [Bos taurus]	1.48505	0.859604348	0.76044	0.493036547	-1.952882542	0.20488549
221136947	delta-sarcoglycan [Sus scrofa]	0.50775	0.50775	0.261425	0.261425	-1.942239648	0.391002219
545845559	PREDICTED: fibrinogen beta chain isoform X2 [Sus scrofa]	0.46985	0.46985	0.24284	0.24284	-1.934813046	0.391002219
178056753	glycogen phosphorylase, liver form [Sus scrofa]	4.784925	0.663816362	2.489975	0.288166978	-1.92167592	0.081124968
641692928	PREDICTED: dihydrolipoyl dehydrogenase, mitochondrial isoform X1 [Eptesicus fuscus]	3.751925	0.727702031	1.98574	0.379294633	-1.889434166	0.18441278
13386338	ras-related protein Rap-2b precursor [Mus musculus]	2.2731	0.285413869	1.206715	0.585047036	-1.883709078	0.271383643
585169082	PREDICTED: heat shock protein HSP 90-beta-like [Leptonychotes weddellii]	3.216875	1.155460439	1.713	0.997613332	-1.877918856	0.51026988
432106259	Calpain-2 catalytic subunit [Myotis davidii]	5.83305	0.860200994	3.2072	0.408862658	-1.818735969	0.069826564
13937391	guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 [Mus musculus]	2.846175	1.655408299	1.568525	1.568525	-1.814555076	0.685301003
560901208	PREDICTED: myosin-10 isoform X5 [Camelus ferus]	100.2375	34.02913712	55.46175	32.70720111	-1.807326671	0.187828002
115496898	histone H1.0 [Bos taurus]	1.79705	0.641654173	0.9972175	0.026036997	-1.802064244	0.293040893
545819203	PREDICTED: very long-chain specific acyl-CoA dehydrogenase, mitochondrial-like isoform X3 [Sus scrofa]	1.780555	0.510645139	0.9972175	0.026036997	-1.785523218	0.207928031
521035382	Spectrin alpha chain, brain [Myotis brandtii]	9.282	1.36351891	5.20365	1.376197988	-1.783747946	0.079628982
47523726	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Sus scrofa]	6.96365	1.303275255	3.97145	0.758591401	-1.753427589	0.206486857
15718687	40S ribosomal protein S3 isoform 1 [Homo sapiens]	3.0839	1.108603285	1.7602775	0.276514646	-1.75193968	0.375746643
281348394	hypothetical protein PANDA_006316 [Ailuropoda melanoleuca]	1.78705	1.123608558	1.02709	0.739631315	-1.739915684	0.304683022
47522630	aspartate aminotransferase, mitochondrial precursor [Sus scrofa]	12.930525	3.151648554	7.446175	0.536719305	-1.736532515	0.211204304
335285324	PREDICTED: prenylcysteine oxidase 1 isoform X1 [Sus scrofa]	3.445325	1.072457766	1.994425	0.052079529	-1.727477844	0.279273618
225735713	thy-1 membrane glycoprotein precursor [Sus scrofa]	2.526975	0.323941611	1.465515	0.448395934	-1.724291461	0.206306058
281338460	hypothetical protein PANDA_002264 [Ailuropoda melanoleuca]	2.9844	0.895018232	1.735625	0.237868656	-1.719495859	0.175885816
833798	albumin [Sus scrofa]	12.107375	3.564518792	7.057025	1.219459758	-1.715648591	0.239224044
300796787	integrin alpha-7 [Bos taurus]	5.15045	1.792714262	3.002925	0.599757772	-1.715144401	0.256087414
545826025	PREDICTED: ATP synthase subunit beta, mitochondrial [Sus scrofa]	43.737	7.773384816	25.5665	2.387925617	-1.710715194	0.094175489
21703344	GTP-binding protein SAR1a [Mus musculus]	2.547255	0.678922227	1.490165	0.281379967	-1.709377821	0.186016784
1942990	Chain E, Structure Of Bovine Heart Cytochrome C Oxidase At The Fully Oxidized State	2.51425	0.661907303	1.471575	0.492221644	-1.708543567	0.077002703
149726611	PREDICTED: transmembrane emp24 domain-containing protein 9 [Equus caballus]	2.50805	0.273854041	1.4829025	0.477698068	-1.691311465	0.105311968

545857842	PREDICTED: membrane primary amine oxidase [Sus scrofa]	81.58075	13.95086903	48.797	8.107382634	-1.671839457	0.108289056
545497341	PREDICTED: LOW QUALITY PROTEIN: oligoribonuclease, mitochondrial [Canis lupus familiaris]	2.4602	0.784363305	1.4742	0.250836351	-1.668837336	0.272196413
343887367	collagen, type I, alpha 2 precursor [Sus scrofa]	5.182925	1.764956559	3.10799	1.659086836	-1.667613152	0.45305447
466065834	PREDICTED: fibrillin-1 isoform 1 [Orcinus orca]	48.58975	10.31637562	29.29875	11.5011143	-1.658423994	0.126457917
149725016	PREDICTED: microfibril-associated glycoprotein 4 [Equus caballus]	13.1784	2.036812705	7.967025	1.111136312	-1.654118068	0.069421647
126337145	PREDICTED: cytoplasmic FMR1-interacting protein 1 isoform 1 [Monodelphis domestica]	1.2439	0.47465323	0.7543775	0.252656581	-1.6489092	0.484483449
545887597	PREDICTED: glucose-6-phosphate 1-dehydrogenase X-like isoform X1 [Sus scrofa]	0.771575	0.257242212	0.4683	0.4683	-1.647608371	0.550591044
284156668	plasma membrane Ca2+-ATPase isoform 4xb [Bos taurus]	1.99035	0.367210191	1.212775	0.453808675	-1.641153553	0.283772312
114052937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor [Bos taurus]	2.013025	0.045698512	1.22874	0.474321155	-1.638283933	0.185806354
126309291	PREDICTED: mitochondrial 2-oxoglutarate/malate carrier protein [Monodelphis domestica]	1.245175	0.470836696	0.763065	0.254884778	-1.631807251	0.518306661
255683404	isocitrate dehydrogenase [NADP], mitochondrial [Sus scrofa]	5.206925	1.169421069	3.201125	0.544746723	-1.626592214	0.257010539
545547690	PREDICTED: sideroflexin-3 isoform X1 [Canis lupus familiaris]	2.01055	0.421055864	1.2426775	0.487193157	-1.617917762	0.243460632
655862912	PREDICTED: fibrillin-1 [Oryctolagus cuniculus]	29.81475	12.44987049	18.47175	10.6884779	-1.614072841	0.066145988
585187220	PREDICTED: serpin H1 isoform X1 [Leptonychotes weddellii]	11.484975	1.412163712	7.13815	1.107834764	-1.608956803	0.087063905
593735466	PREDICTED: fibrillin-1-like [Physeter catodon]	35.98725	15.1869706	22.37725	12.99154659	-1.608206996	0.069876657
110331811	COP9 complex subunit 7a [Bos taurus]	0.74888	0.25054158	0.4683	0.4683	-1.599145847	0.722146909
343962597	cytosolic non-specific dipeptidase [Sus scrofa]	1.549375	0.671897232	0.96994	0.383071264	-1.597392622	0.43624171
545802439	PREDICTED: nidogen-2 [Sus scrofa]	9.238175	1.226801942	5.837325	2.251454489	-1.582604189	0.190963744
159794954	Chain A, Structure Of Full Length Grp94 With Amp-Pnp Bound	10.018525	1.279717349	6.379575	1.700233566	-1.570406336	0.30329757
545869779	PREDICTED: sushi domain-containing protein 2 [Sus scrofa]	1.968925	0.644454028	1.2586425	0.278335495	-1.564324262	0.452746172
350580983	PREDICTED: receptor expression-enhancing protein 5 [Sus scrofa]	4.54625	0.570810051	2.92234	1.239204197	-1.55568825	0.33775244
350578417	PREDICTED: CD109 antigen isoformX1 [Sus scrofa]	0.765375	0.486800411	0.4955775	0.286987013	-1.544410309	0.341969737
48976131	fibrillin-1 precursor [Sus scrofa]	53.63	11.4266967	34.78075	10.50586383	-1.541944898	0.102293382
47523464	dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor [Sus scrofa]	3.001925	0.912549263	1.96715	0.361753541	-1.526027502	0.189842154
395521751	PREDICTED: aflatoxin B1 aldehyde reductase member 2-like [Sarcophilus harrisii]	1.52048	0.30981711	0.9972175	0.026036997	-1.52472254	0.164268007
504147195	PREDICTED: tumor protein D54 [Ochotona princeps]	1.518005	0.30559001	0.9998425	0.427784253	-1.518244123	0.210424098
21730305	Chain A, Crystal Structure Of Pig Phosphoglucose Isomerase	15.48825	2.453532908	10.220175	0.918438378	-1.515458395	0.16336746
655884414	PREDICTED: aconitate hydratase, mitochondrial [Oryctolagus cuniculus]	7.90645	2.328599812	5.2408	1.383647987	-1.508634178	0.244033665

114050997	PRA1 family protein 2 [Bos taurus]	1.539425	0.657842919	1.021865	0.422961049	-1.50648569	0.478776288
172072653	lactadherin precursor [Sus scrofa]	42.047	3.425272666	28.00125	4.809285851	-1.501611535	0.061125083
126310931	PREDICTED: guanine nucleotide-binding protein G(k) subunit alpha [Monodelphis domestica]	7.3107	1.098899855	4.8743	1.883068447	-1.499846132	0.461689393
223872	calmodulin	3.369875	2.381825983	2.257875	1.132381063	-1.492498478	0.480047268
2392156	Chain A, Refinement And Comparison Of The Crystal Structures Of Pig Cytosolic Aspartate Aminotransferase And Its Complex With 2-Methylaspartate	6.288025	0.887146472	4.222975	0.166821933	-1.489003605	0.076628192
178056860	caveolin-2 [Sus scrofa]	3.022	0.434286156	2.043725	0.845922297	-1.478672522	0.101384505
358009193	prolyl 4-hydroxylase beta polypeptide [Sus scrofa]	19.397	2.969282152	13.1419	1.583372364	-1.475966184	0.226457793
47523548	glutaredoxin-1 [Sus scrofa]	0.771575	0.257242212	0.52285	0.52285	-1.475710051	0.655834607
47522680	neutral alpha-glucosidase AB precursor [Sus scrofa]	2.5056	0.265739368	1.699665	0.682442689	-1.474172852	0.222411534
154425761	FAH protein [Bos taurus]	0.729925	0.454899845	0.4955775	0.286987013	-1.472877602	0.768747872
545805668	PREDICTED: LOW QUALITY PROTEIN: nucleosome assembly protein 1-like 4 [Sus scrofa]	1.778105	0.279648381	1.212775	0.453808675	-1.466145823	0.444821955
347582591	cytoskeleton-associated protein 4 [Sus scrofa]	6.8309	0.954907606	4.675325	0.723264584	-1.46105351	0.069109656
4507143	sorting nexin-3 isoform a [Homo sapiens]	1.75915	0.251989287	1.206715	0.585047036	-1.457800723	0.433243947
113205888	aldehyde dehydrogenase, mitochondrial precursor [Sus scrofa]	5.6019	1.288399404	3.91695	1.293181577	-1.430168881	0.056634917
478510027	PREDICTED: extended synaptotagmin-1 isoform 1 [Ceratotherium simum simum]	6.0226	0.54357822	4.211675	0.692266973	-1.429977384	0.123765089
342349344	protein Niban-like [Sus scrofa]	4.28825	1.952386539	3.027	1.421145283	-1.416666667	0.226421458
291389298	PREDICTED: coatomer subunit zeta-1 [Oryctolagus cuniculus]	1.02545	0.414620763	0.7271	0.4533045	-1.410328703	0.658777445
134085902	rho GTPase-activating protein 1 [Canis lupus familiaris]	1.02545	0.414620763	0.729725	0.453906417	-1.405255404	0.556722786
48675953	rab GDP dissociation inhibitor beta [Sus scrofa]	13.5266	1.503639505	9.6501	0.864387847	-1.401705682	0.07609482
281353806	hypothetical protein PANDA_017913 [Ailuropoda melanoleuca]	1.034125	0.735652952	0.7384175	0.247188426	-1.400461121	0.779669575
281338468	hypothetical protein PANDA_002275 [Ailuropoda melanoleuca]	4.3126	0.822716234	3.08415	1.347842199	-1.398310718	0.525413753
304365440	protein disulfide-isomerase A6 precursor [Sus scrofa]	11.6906	1.764954625	8.375425	1.08108163	-1.395821705	0.174062673
115497826	Golgi-associated plant pathogenesis-related protein 1 [Bos taurus]	2.78085	0.507267473	1.994425	0.052079529	-1.394311644	0.186706
301773598	PREDICTED: LOW QUALITY PROTEIN: serine/threonine-protein kinase WNK4-like [Ailuropoda melanoleuca]	1.01273	0.425424122	0.7271	0.4533045	-1.392834548	0.565376584
311272309	PREDICTED: ADP/ATP translocase 1 isoform 2 [Sus scrofa]	9.071125	0.908330103	6.51945	0.781017914	-1.391394213	0.070693095
472381913	PREDICTED: cytosol aminopeptidase [Odobenus rosmarus divergens]	3.74085	0.57168406	2.696875	0.662856404	-1.387105446	0.276631903
15431301	60S ribosomal protein L7 [Homo sapiens]	3.52485	0.667746846	2.5506	0.894868148	-1.381968948	0.448410546
126131205	progesterone receptor membrane component 2 [Sus scrofa]	2.03573	0.439500937	1.4742	0.250836351	-1.380904898	0.362304787
149640868	PREDICTED: EGF-containing fibulin-like extracellular matrix protein 1 [Ornithorhynchus anatinus]	1.004055	0.42126092	0.7271	0.4533045	-1.38090359	0.601226645
113205608	60S ribosomal protein L6 [Sus scrofa]	2.80385	1.917220735	2.033	0.936582491	-1.379168716	0.670400232

311268489	PREDICTED: fatty aldehyde dehydrogenase isoform X1 [Sus scrofa]	0.98755	0.38462955	0.7198275	0.463565445	-1.371925913	0.378173608
149723798	PREDICTED: ATP-citrate synthase isoformX1 [Equus caballus]	3.757	0.936019527	2.74355	0.887189261	-1.369393669	0.348024802
149642985	alpha-parvin [Bos taurus]	9.102825	1.802629588	6.664525	0.895888239	-1.365862533	0.207311423
47523722	hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor [Sus scrofa]	5.7852	0.272266888	4.236325	0.766835718	-1.365617605	0.071489812
149730823	PREDICTED: 60 kDa heat shock protein, mitochondrial [Equus caballus]	14.7845	1.509893953	10.87875	1.224176794	-1.359025623	0.182320414
504148889	PREDICTED: myosin-11 isoform X2 [Ochotona princeps]	411.165	33.35275913	302.7425	102.9036882	-1.358134388	0.310995941
555989153	PREDICTED: myosin-11-like, partial [Bos mutus]	326.11	28.57932382	240.64	81.08109737	-1.355177859	0.314296069
47523746	dihydropteridine reductase [Sus scrofa]	3.017125	0.422087938	2.228575	0.196507703	-1.353835971	0.064844498
55742742	decorin precursor [Sus scrofa]	39.3584	10.31585058	29.135	4.924637905	-1.350897546	0.414573314
346421386	ATP synthase subunit g, mitochondrial [Sus scrofa]	5.0388	0.459212638	3.730025	0.227161977	-1.350875664	0.152236076
281346955	hypothetical protein PANDA_001608 [Ailuropoda melanoleuca]	2.013025	0.045698512	1.49279	0.286403496	-1.348498449	0.149497727
281350720	hypothetical protein PANDA_002799 [Ailuropoda melanoleuca]	8.24785	0.964772127	6.151575	1.363082215	-1.340770453	0.348158449
219521974	copine-1 [Sus scrofa]	3.28715	0.895517209	2.4601	0.601350429	-1.336185521	0.073716604
545895236	PREDICTED: vacuolar protein sorting-associated protein 35, partial [Sus scrofa]	2.292055	0.51141417	1.715625	0.798022611	-1.335988342	0.518727324
311260217	PREDICTED: BAG family molecular chaperone regulator 2 isoform X1 [Sus scrofa]	0.9838	0.384508229	0.7384175	0.247188426	-1.332308619	0.631033022
585690381	gi|585690381-DECOY	1.01273	0.425424122	0.76044	0.493036547	-1.33176845	0.402741576
178056732	guanine nucleotide-binding protein G(i) subunit alpha-2 [Sus scrofa]	11.386975	1.512229177	8.553625	1.615784648	-1.331245525	0.288724258
157428118	programmed cell death protein 6 [Bos taurus]	5.273725	0.461286259	3.964175	0.330128648	-1.330346163	0.16807527
545531227	PREDICTED: LOW QUALITY PROTEIN: neuroblast differentiation-associated protein AHNAK [Canis lupus familiaris]	31.3815	4.313939895	23.59825	2.132760511	-1.329823186	0.053492617
507696166	PREDICTED: integral membrane protein 2B-like [Echinops telfairi]	1.006505	0.022838214	0.7570025	0.496569994	-1.329592703	0.645789549
47522764	integrin beta-1 precursor [Sus scrofa]	36.688	4.262646674	27.66775	0.99726454	-1.326020367	0.155336418
77736431	ras-related protein Rab-5C [Bos taurus]	6.3029	0.557684369	4.765225	0.832048735	-1.322686757	0.126649183
281338419	hypothetical protein PANDA_002213 [Ailuropoda melanoleuca]	3.55995	0.706283409	2.705575	0.398691356	-1.315783151	0.292963937
297591959	farnesyl pyrophosphate synthase precursor [Sus scrofa]	1.262855	0.496499091	0.96125	0.66273479	-1.313763329	0.795599411
545822151	PREDICTED: 4-trimethylaminobutyraldehyde dehydrogenase [Sus scrofa]	3.2445	0.7291109	2.477475	0.631923106	-1.309599491	0.541985267
344306519	PREDICTED: myosin-11 [Loxodonta africana]	441.7825	41.03352925	337.4625	113.9211557	-1.309130644	0.355796909
157279907	parathymosin [Bos taurus]	8.350075	0.985246293	6.388425	1.371325516	-1.307063165	0.334332752
301757033	PREDICTED: 40S ribosomal protein S10-like isoform 1 [Ailuropoda melanoleuca]	3.585105	1.014817463	2.746175	0.501940352	-1.305490364	0.311123918
157831091	Chain A, Atomic Structure Of Fkbp12, An Immunophilin Binding Protein	7.093425	0.845100347	5.481625	0.306983529	-1.294036896	0.127449517
504150368	PREDICTED: annexin A6 isoform X1 [Ochotona princeps]	27.26825	6.783413231	21.0745	1.196573546	-1.293897839	0.446971547

194221910	PREDICTED: translationally-controlled tumor protein [Equus caballus]	0.9838	0.384508229	0.76044	0.493036547	-1.293724686	0.670805317
90109258	Chain A, Structure Of Calmodulin Bound To A Calcineurin Peptide: A New Way Of Making An Old Binding Mode	7.389725	2.12033643	5.74245	1.410394471	-1.286859267	0.188854332
194036227	PREDICTED: selenium-binding protein 1 [Sus scrofa]	4.532175	1.375649999	3.522575	1.255626926	-1.286608518	0.253229016
126308210	PREDICTED: importin subunit beta-1 [Monodelphis domestica]	3.818725	0.922915765	2.969015	1.136452575	-1.286192559	0.434592888
488517430	PREDICTED: adenylyl cyclase-associated protein 1 isoform 1 [Dasypus novemcinctus]	13.65175	1.552568806	10.62155	1.050188149	-1.285287929	0.192257436
194042189	PREDICTED: annexin A11 isoform X1 [Sus scrofa]	6.7514	1.025966667	5.25475	0.794020831	-1.284818498	0.436706849
157074012	EF-hand domain-containing protein D2 [Bos taurus]	3.768425	0.241325373	2.94315	0.984443289	-1.280405348	0.503506406
545884676	PREDICTED: RNA binding motif (RNP1, RRM) protein 3 isoform X2 [Sus scrofa]	5.036325	0.447751429	3.943	0.635752693	-1.277282526	0.096377669
545803430	PREDICTED: annexin A1 isoform X1 [Sus scrofa]	42.4065	14.55719377	33.27175	11.27568706	-1.274549731	0.090754502
118138612	CD81 [Sus scrofa]	3.7735	0.878846205	2.964375	0.34109145	-1.27294961	0.257322884
562861819	PREDICTED: fibromodulin [Tupaia chinensis]	14.096	0.930436367	11.0783	1.869069597	-1.272397389	0.16743862
543113	smooth muscle protein SM22 homolog - bovine (fragments)	340.115	30.10638872	267.6225	90.81072829	-1.270875954	0.339347464
48675943	amine oxidase [flavin-containing] A [Sus scrofa]	2.809755	0.674483335	2.2112	0.958878571	-1.270692384	0.497805534
194038270	PREDICTED: fibulin-5 isoformX1 [Sus scrofa]	9.249525	0.72096609	7.28425	1.792910865	-1.269797852	0.452921438
350585077	PREDICTED: uncharacterized protein LOC100739300 [Sus scrofa]	1.26413	0.266483331	0.9972175	0.026036997	-1.267657256	0.419460284
671004321	PREDICTED: 60S ribosomal protein L22 isoform X1 [Ursus maritimus]	2.54348	0.670350678	2.01039	0.438221025	-1.265167455	0.480455973
114051892	UDP-N-acetylhexosamine pyrophosphorylase [Bos taurus]	1.26038	0.257869159	0.9972175	0.026036997	-1.263896793	0.356654368
47522916	glutathione S-transferase omega-1 [Sus scrofa]	3.76465	0.631341176	2.98555	0.57279261	-1.260956943	0.431948136
545184513	PREDICTED: annexin A6 isoform X1 [Equus caballus]	35.884	9.844227996	28.5245	1.348607955	-1.258006275	0.494243173
593737926	PREDICTED: adenylyl cyclase-associated protein 1 isoform X1 [Physeter catodon]	8.081	0.722991917	6.435625	0.488448301	-1.255666699	0.178612314
291383155	PREDICTED: S-methyl-5'-thioadenosine phosphorylase [Oryctolagus cuniculus]	1.518005	0.30559001	1.212775	0.453808675	-1.251679001	0.662192658
431902724	ADP/ATP translocase 3 [Pteropus alecto]	12.86985	1.597732619	10.302225	1.881533302	-1.249230142	0.317927805
291393841	PREDICTED: musculoskeletal embryonic nuclear protein 1 [Oryctolagus cuniculus]	2.54103	0.895801147	2.0350425	0.751407858	-1.248637313	0.736945541
146674796	laminin receptor precursor [Oryctolagus cuniculus]	5.56515	1.344358871	4.470475	0.844149992	-1.244867715	0.285429436
296488587	TPA: calcium channel, voltage-dependent, alpha 2/delta subunit 1 [Bos taurus]	1.241425	0.212719461	0.9998425	0.427784253	-1.241620555	0.65356975
545878421	PREDICTED: annexin A6-like [Sus scrofa]	38.04	11.12689298	30.67275	2.40523822	-1.240188767	0.499768779
327343034	versican [Sus scrofa]	4.302925	1.84010039	3.476475	1.295912266	-1.237726433	0.478333944
311257410	PREDICTED: heat shock protein beta-6 [Sus scrofa]	5.8306	0.951029413	4.715925	0.408492981	-1.236364022	0.144482594
545815606	PREDICTED: asporin isoform X1 [Sus scrofa]	22.2115	3.459335256	17.989	2.559373068	-1.234726777	0.351739383
731514756	PREDICTED: 60S ribosomal protein L8 [Loxodonta africana]	1.26038	0.257869159	1.021865	0.422961049	-1.233411458	0.659027211
528979844	PREDICTED: alpha-enolase isoform X3 [Bos taurus]	31.031	4.314268092	25.19225	2.368035838	-1.231767706	0.067641133
164518958	L-lactate dehydrogenase B chain [Sus scrofa]	14.8275	0.832979842	12.04095	1.970627067	-1.23142277	0.360367085

126302599	RecName: Full=Protein S100-A10; AltName: Full=Calpactin I light chain; AltName: Full=Calpactin-1 light chain; AltName: Full=Cellular ligand of annexin II; AltName: Full=S100 calcium-binding protein A10; AltName: Full=p10 protein; AltName: Full=p11 [Sus scrofa]	1.543175	0.51449313	1.2560175	0.272412578	-1.228625397	0.597065538
602700845	PREDICTED: LOW QUALITY PROTEIN: dicarbonyl/L-xylulose reductase [Lipotes vexillifer]	1.521755	0.523685429	1.2400525	0.235500938	-1.227169817	0.701070815
395545191	PREDICTED: annexin A5 [Sarcophilus harrisii]	16.65225	1.559841892	13.5795	1.318435721	-1.226278582	0.116014441
22770997	thioredoxin reductase [Sus scrofa]	1.507725	0.660919619	1.231365	0.214574573	-1.22443386	0.735560948
591335618	PREDICTED: annexin A6 isoform X1 [Panthera tigris altaica]	34.9115	8.917363189	28.51475	1.57800942	-1.224331267	0.478112118
157954416	cadherin-13 precursor [Equus caballus]	1.237675	0.466545088	1.0131775	0.423395831	-1.22157766	0.775930589
311258421	PREDICTED: 6-phosphogluconate dehydrogenase, decarboxylating [Sus scrofa]	1.779405	0.781191281	1.456825	0.801627728	-1.221426733	0.247554694
545834105	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein [Sus scrofa]	62.70375	6.625930367	51.3585	12.65520162	-1.220903064	0.584729897
156120603	phosphatidylinositol-binding clathrin assembly protein [Bos taurus]	1.75425	0.877758545	1.43824	0.805013202	-1.219719935	0.550789744
545833443	PREDICTED: alpha-enolase isoform X1 [Sus scrofa]	34.02675	5.219888415	27.9025	2.776656668	-1.219487501	0.151990668
189571595	plasminogen activator inhibitor 1 RNA-binding protein [Felis catus]	1.52423	0.315995655	1.24995	0.474778126	-1.219432777	0.61394988
21070334	ribosomal protein L7a, partial [Equus caballus]	1.5407	0.662667047	1.2647	0.479258418	-1.218233573	0.821283941
545204976	PREDICTED: collagen alpha-1(XVIII) chain isoform X1 [Equus caballus]	4.048775	0.478114447	3.3235525	1.18946319	-1.218207024	0.624313588
126352304	elongation factor 1-alpha 1 [Equus caballus]	27.91775	3.407284901	22.968	3.384888797	-1.215506357	0.442729277
311273021	PREDICTED: fibronectin isoformX2 [Sus scrofa]	23.835	2.730666982	19.6285	5.731291892	-1.214305729	0.270310187
731493073	PREDICTED: ras-related protein Rab-1A isoform X1 [Loxodonta africana]	10.84795	1.254217757	8.939	0.555047824	-1.21355297	0.234607685
350586352	PREDICTED: serpin peptidase inhibitor, clade B (ovalbumin), member 1 isoform X1 [Sus scrofa]	4.54245	0.700823813	3.743375	0.508904969	-1.213463786	0.235018698
281344360	hypothetical protein PANDA_004987 [Ailuropoda melanoleuca]	1.52048	0.30981711	1.2560175	0.272412578	-1.210556382	0.353848941
115495993	ras-related protein Rab-1B [Bos taurus]	11.10555	1.170138155	9.18185	0.421808759	-1.209511155	0.198134515
153792484	peptidyl-prolyl cis-trans isomerase B [Equus caballus]	11.2724	1.635838315	9.3441	1.994401958	-1.206365514	0.597177309
213972608	ras-related protein Rab-6A [Rattus norvegicus]	3.60405	1.229805801	2.991625	0.078099641	-1.204713158	0.649041657
426254625	PREDICTED: transforming growth factor beta-1-induced transcript 1 protein isoform 1 [Ovis aries]	6.569525	0.732492732	5.4596	0.938418858	-1.203297861	0.21488821
16758368	ras-related protein Rab-14 [Rattus norvegicus]	6.875	1.412245207	5.715775	0.413041169	-1.202811517	0.362175913
335309772	PREDICTED: acyl-coenzyme A thioesterase 2, mitochondrial-like, partial [Sus scrofa]	1.476375	0.447637378	1.231365	0.214574573	-1.198974309	0.695834925
346986361	electron-transfer-flavoprotein, alpha polypeptide [Sus scrofa]	3.813825	0.690208199	3.189825	0.850135217	-1.195622017	0.340832216
335302965	PREDICTED: lupus La protein homolog isoform X1 [Sus scrofa]	1.514255	0.511249894	1.267325	0.482633891	-1.19484347	0.640784595
14043070	heterogeneous nuclear ribonucleoprotein A1 isoform b [Homo sapiens]	3.543475	0.700971963	2.966975	0.346777345	-1.194305648	0.569768461

504154327	PREDICTED: transgelin-2 [Ochotona princeps]	25.27875	2.843072674	21.1675	2.542380823	-1.194224637	0.208550173
641725986	PREDICTED: cytoplasmic dynein 1 heavy chain 1 [Eptesicus fuscus]	20.9735	3.671036854	17.56675	3.692807093	-1.193931718	0.587030187
311252243	PREDICTED: macrophage-capping protein isoformX2 [Sus scrofa]	10.019775	0.638930331	8.401375	1.355657548	-1.192635134	0.474303413
311247250	PREDICTED: barrier-to-autointegration factor-like isoformX1 [Sus scrofa]	3.279625	0.299872232	2.7514	0.513954192	-1.191984081	0.488300872
126723018	voltage-dependent anion-selective channel protein 1 [Oryctolagus cuniculus]	8.32845	1.348713311	6.996425	0.525597083	-1.190386519	0.358354165
311266781	PREDICTED: galactokinase isoform X1 [Sus scrofa]	2.029505	0.600574037	1.705725	0.599835004	-1.189819578	0.757599425
311254975	PREDICTED: NADH-cytochrome b5 reductase 3-like isoform X1 [Sus scrofa]	14.91325	1.332566782	12.538775	1.260928897	-1.189370572	0.200156128
505855867	PREDICTED: N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 [Sorex araneus]	13.90805	1.832291771	11.69625	0.389147867	-1.189103345	0.279579974
114689	RecName: Full=ATP synthase-coupling factor 6, mitochondrial; Short=ATPase subunit F6 [Sus scrofa]	1.774355	0.496834648	1.49279	0.286403496	-1.188616617	0.573588726
530668313	putative cation-transporting ATPase 13A2 isoform 2 [Camelus ferus]	1.784305	0.513784861	1.5014775	0.299885513	-1.188366126	0.743544712
312283580	superoxide dismutase [Mn], mitochondrial [Sus scrofa]	17.41775	2.881808529	14.69275	1.360848227	-1.185465621	0.227723188
343478174	T-complex protein 1 subunit alpha [Sus scrofa]	1.784305	0.513784861	1.506125	0.656599068	-1.184699145	0.3051032
584056604	PREDICTED: LOW QUALITY PROTEIN: neuroblast differentiation-associated protein AHNAK [Myotis davidii]	30.0005	3.168081294	25.3445	2.734845684	-1.183708497	0.057801799
505856264	PREDICTED: neuroblast differentiation-associated protein AHNAK [Sorex araneus]	17.64575	1.893072695	14.9289	2.590286987	-1.181985947	0.174634577
617600724	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein [Erinaceus europaeus]	20.35875	2.159093536	17.230775	5.806827288	-1.181534203	0.71339185
511901993	PREDICTED: neuroblast differentiation-associated protein AHNAK [Mustela putorius furo]	20.48825	3.155894416	17.3825	1.043363192	-1.178671077	0.241518847
109110241	PREDICTED: actin-related protein 2/3 complex subunit 5-like protein-like [Macaca mulatta]	1.7554	0.245396186	1.490165	0.281379967	-1.177990357	0.58143468
154757562	SYNCRIP protein [Bos taurus]	1.75915	0.251989287	1.4962275	0.667163524	-1.175723612	0.639290834
194038586	PREDICTED: transmembrane emp24 domain-containing protein 10 [Sus scrofa]	5.253475	0.99852019	4.4731	0.600232165	-1.174459547	0.603456822
350587966	PREDICTED: PDZ and LIM domain protein 5 isoformX3 [Sus scrofa]	5.805425	0.819899504	4.950075	0.602292625	-1.172795362	0.086345087
10880989	ras-related protein Rab-18 isoform 1 [Homo sapiens]	2.03198	0.430648594	1.735625	0.237868656	-1.17074829	0.576095035
440904790	Annexin A6, partial [Bos mutus]	35.3525	9.466361291	30.2635	1.278272304	-1.16815636	0.591966354
149636177	PREDICTED: actin-related protein 2/3 complex subunit 5 [Ornithorhynchus anatinus]	2.013025	0.045698512	1.724315	0.440218891	-1.167434604	0.532588548
999617	Chain A, Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine Heart And The Consensus Structure For Dicarboxylic Acid Oxidoreductases	25.472	1.84719684	21.8555	1.610095313	-1.165473222	0.153098556
149724885	PREDICTED: proteasome subunit beta type-6 isoform X1 [Equus caballus]	2.013025	0.045698512	1.733	0.23271051	-1.161583958	0.32917887
545210896	PREDICTED: LOW QUALITY PROTEIN: ezrin [Equus caballus]	8.2309	3.061077394	7.08665	2.446743859	-1.161465573	0.829448341

116734835	ras-related protein Rab-2A [Bos taurus]	2.251725	0.464107722	1.9425	0.637802136	-1.159189189	0.494636811
335306783	PREDICTED: rab GDP dissociation inhibitor alpha isoform 1 [Sus scrofa]	11.507475	1.254662495	9.927475	0.919872108	-1.159154266	0.410417609
149728225	PREDICTED: ras-related protein Rab-7a [Equus caballus]	8.626525	1.380220672	7.446175	0.536719305	-1.158517628	0.470918575
149633630	PREDICTED: proteasome subunit alpha type-4 [Ornithorhynchus anatinus]	1.77188	0.494633373	1.5307775	0.901102677	-1.157503295	0.845743891
296472904	TPA: ras-related C3 botulinum toxin substrate 1 precursor [Bos taurus]	1.9941	0.370857468	1.724315	0.440218891	-1.156459232	0.659725704
113205874	ATP synthase subunit O, mitochondrial precursor [Sus scrofa]	6.32055	0.847729361	5.472925	0.607163225	-1.154876049	0.428793679
426232103	PREDICTED: annexin A5 [Ovis aries]	44.821	5.657344342	38.898	3.34266311	-1.15227004	0.330048421
350276172	leucine-rich repeat-containing protein 59 [Sus scrofa]	2.016775	0.426276881	1.75159	0.264678814	-1.151396731	0.642268063
148237282	60S ribosomal protein L14 [Sus scrofa]	2.054675	0.723480567	1.784925	0.648649853	-1.151126798	0.824912129
242247459	ADP-ribosylation factor 3 [Ovis aries]	8.7908	1.029774279	7.644275	1.368185374	-1.149984793	0.561456455
335293906	PREDICTED: annexin A5 [Sus scrofa]	60.41675	6.827392101	52.5405	4.137811851	-1.149908166	0.288460397
602681137	PREDICTED: alpha-enolase isoform X1 [Lipotes vexillifer]	33.29575	4.63001266	28.957	2.092199202	-1.149834237	0.211755742
162952052	transketolase [Sus scrofa]	8.598725	1.938131341	7.49245	1.534712017	-1.14765197	0.602870314
47523308	heat shock 70 kDa protein 1B [Sus scrofa]	22.63725	2.829066141	19.73075	1.527812563	-1.147308136	0.492521939
149243025	Chain B, Crystal Structure Of Bovine Arp23 COMPLEX CO-Crystallized With Atp And Crosslinked With Glutaraldehyde	2.806005	0.788056688	2.44879	1.15592546	-1.145874085	0.812545983
194220990	PREDICTED: 40S ribosomal protein S7 [Equus caballus]	4.55895	0.706137947	3.9862	0.428605234	-1.143683207	0.549420249
335290008	PREDICTED: ras-related protein R-Ras [Sus scrofa]	6.007725	0.644001473	5.253525	0.541551388	-1.143560752	0.504894879
545858631	PREDICTED: integrin alpha-3 isoform X2 [Sus scrofa]	6.232375	0.787990863	5.479	0.28951373	-1.137502281	0.487641237
1943418	Chain A, Structure Of Porcine Class Pi Glutathione S-Transferase	16.314	0.273635098	14.36875	1.411642623	-1.1353806	0.200787588
586540023	PREDICTED: integrin alpha-3 isoform X1 [Pteropus alecto]	4.774925	0.242478292	4.207025	0.393963671	-1.134988501	0.410024298
264681432	annexin A4 [Sus scrofa]	22.183	3.933064009	19.55525	1.70141732	-1.134375679	0.468396688
594104235	PREDICTED: myosin light polypeptide 6 isoform X2 [Bubalus bubalis]	77.29325	6.303694596	68.233	4.927540073	-1.13278399	0.46467675
591326005	PREDICTED: serine/threonine-protein phosphatase PP1-beta catalytic subunit [Panthera tigris altaica]	7.8901	1.453529685	6.969175	0.561391773	-1.132142614	0.424763401
545802444	PREDICTED: fermitin family homolog 2, partial [Sus scrofa]	18.916	2.127934249	16.7564	2.525696721	-1.128882099	0.370481388
115304856	ARP3 actin-related protein 3 homolog (yeast) [Bos taurus]	7.55055	0.907522617	6.6918	0.508468388	-1.128328701	0.164120212
349732194	armadillo repeat containing 10 [Sus scrofa]	3.068705	1.129586937	2.721525	0.428321167	-1.127568183	0.668504137
560949121	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein [Vicugna pacos]	44.06	6.217470185	39.0955	9.404167281	-1.126983924	0.760242864
338709914	PREDICTED: serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform-like isoform 1 [Equus caballus]	5.011175	0.531500601	4.4519	0.928777973	-1.125626137	0.587353944
346716222	histidine triad nucleotide-binding protein 2, mitochondrial isoform 1 precursor [Sus scrofa]	2.78085	0.507267473	2.471425	0.226513217	-1.125201048	0.696698187
466023053	PREDICTED: basement membrane-specific heparan sulfate proteoglycan core protein [Orcinus orca]	37.8465	4.851946079	33.63825	9.204221109	-1.125103119	0.769080254
311253953	PREDICTED: myelin protein P0 [Sus scrofa]	6.48625	0.699930423	5.7865025	1.863403395	-1.120927538	0.625764461
335306431	PREDICTED: plastin-3 isoformX1 [Sus scrofa]	14.7305	1.542793219	13.1515	1.068186742	-1.12006235	0.444717897

512011889	PREDICTED: neuroblast differentiation-associated protein AHNAK [Mustela putorius furo]	26.722	3.43361816	23.8585	1.274346793	-1.120020119	0.318463806
620979001	PREDICTED: vesicle-associated membrane protein 2 [Ornithorhynchus anatinus]	2.7846	0.302121832	2.487375	0.279825405	-1.119493442	0.289147949
77735497	actin-related protein 2/3 complex subunit 3 [Bos taurus]	5.5251	0.250144255	4.957375	1.214130377	-1.114521294	0.655745917
281427374	T-complex protein 1 subunit beta [Sus scrofa]	8.57595	0.76917748	7.729625	0.909055137	-1.109491081	0.098073633
560910590	PREDICTED: fructose-bisphosphate aldolase A isoform X1 [Camelus ferus]	23.21675	2.357071431	20.94525	1.355244343	-1.10844941	0.366209047
410948265	PREDICTED: stress-70 protein, mitochondrial [Felis catus]	8.803375	0.665753145	7.945175	1.058247385	-1.108015242	0.489185811
143811426	RecName: Full=Neurofilament light polypeptide; Short=NF-L; AltName: Full=68 kDa neurofilament protein; AltName: Full=Neurofilament triplet L protein [Sus scrofa]	1.87945	1.87945	1.699875	1.699875	-1.105640121	0.391002219
545799434	PREDICTED: collagen alpha-1(XII) chain [Sus scrofa]	8.565225	3.732980296	7.7482	0.94495428	-1.105447072	0.86527439
431895484	Alpha-centractin [Pteropus alecto]	3.273425	0.271492935	2.964375	0.34109145	-1.104254691	0.627075641
28395033	rho-related GTP-binding protein RhoC precursor [Homo sapiens]	5.76005	0.368109419	5.22485	1.011797057	-1.102433563	0.686818778
112980819	mitochondrial succinate dehydrogenase complex subunit A [Sus scrofa]	3.0068	0.699462558	2.7276	0.636884405	-1.10236105	0.258090622
297591975	ATP synthase subunit alpha, mitochondrial [Sus scrofa]	30.6055	1.535635835	27.81175	1.319570408	-1.100452147	0.153177958
554570166	PREDICTED: 14-3-3 protein zeta/delta [Myotis brandtii]	26.96975	1.310907915	24.5185	1.713250541	-1.099975529	0.328273634
253706	14-3-3 protein zeta chain [cattle, brain, Peptide, 245 aa]	27.22975	1.469812764	24.78575	1.323308315	-1.098605045	0.341554376
47523870	peroxiredoxin-6 [Sus scrofa]	11.13345	1.459503775	10.1417	0.979137268	-1.097789325	0.650866097
335300581	PREDICTED: T-complex protein 1 subunit theta isoform 1 [Sus scrofa]	3.79735	0.547565352	3.466	0.465421021	-1.095600115	0.547043947
281352800	hypothetical protein PANDA_015972 [Ailuropoda melanoleuca]	4.026075	0.091369072	3.6781	0.746652755	-1.09460727	0.679662553
47523806	four and a half LIM domains 1 protein, isoform C [Sus scrofa]	12.703025	2.449252964	11.61115	1.446306925	-1.094036766	0.496633493
297307137	ran-specific GTPase-activating protein [Sus scrofa]	0.7778	0.497606888	0.71114	0.449957229	-1.093736817	0.930636518
335288532	PREDICTED: ubiquitin carboxyl-terminal hydrolase 5 isoform 1 [Sus scrofa]	0.5115	0.295330535	0.4683	0.4683	-1.092248559	0.916695964
291399010	PREDICTED: peroxiredoxin-1 [Oryctolagus cuniculus]	10.61445	1.184793499	9.722625	1.664877478	-1.091726771	0.625025575
129077	RecName: Full=Mimecan; AltName: Full=Osteoglycin; Contains: RecName: Full=Corneal keratan sulfate proteoglycan 25 core protein; Short=KSPG25 protein; Contains: RecName: Full=Osteoinductive factor; Short=OIF; Flags: Precursor [Bos taurus]	12.602925	3.311465211	11.547525	2.995020168	-1.091396208	0.704597335
444721919	Annexin A5 [Tupaia chinensis]	34.3385	4.392873291	31.46975	3.073403119	-1.09115897	0.668391307
545865248	PREDICTED: lipoma-preferred partner [Sus scrofa]	4.318825	1.105182554	3.974925	0.920838033	-1.086517356	0.438931126
329664500	pyruvate kinase PKM [Bos taurus]	41.747	2.332906663	38.48775	2.554871894	-1.084682789	0.200318345
115503718	RecName: Full=Caveolin-1 [Rhinolophus ferrumequinum]	5.992375	1.313140292	5.527075	1.521508476	-1.084185577	0.624502275
149709439	PREDICTED: dnaJ homolog subfamily B member 4 isoform X1 [Equus caballus]	0.769125	0.492675365	0.71114	0.449957229	-1.081538094	0.895967902

124231	RecName: Full=Eukaryotic translation initiation factor 5A-1; Short=eIF-5A-1; Short=eIF-5A1; AltName: Full=Eukaryotic initiation factor 5A isoform 1; Short=eIF-5A; AltName: Full=eIF-4D [Oryctolagus cuniculus]	4.252325	0.730659539	3.9456	0.477273346	-1.077738494	0.657162971
149621306	PREDICTED: 40S ribosomal protein S25 [Ornithorhynchus anatinus]	3.302325	0.540064123	3.065575	1.268882478	-1.077228579	0.872469409
284004958	14-3-3 protein eta [Oryctolagus cuniculus]	9.3125	0.34698797	8.6517	0.93249808	-1.076378053	0.639626178
440909750	GTP-binding nuclear protein Ran, partial [Bos mutus]	5.290175	0.316279777	4.915525	0.779313672	-1.076217698	0.625781682
298104076	enoyl-CoA hydratase, mitochondrial [Sus scrofa]	4.8001	0.555259124	4.465825	0.179310589	-1.074851791	0.675676155
194038728	PREDICTED: poly [ADP-ribose] polymerase 6 isoformX1 [Sus scrofa]	78.8525	5.559857919	73.535	4.335161608	-1.072312504	0.142445178
281350286	hypothetical protein PANDA_006098 [Ailuropoda melanoleuca]	9.53835	0.810240225	8.903025	1.218434581	-1.071360577	0.616516687
545860373	PREDICTED: myosin-10, partial [Sus scrofa]	131.5275	10.48401035	122.775	8.552002202	-1.071288943	0.515237189
115496488	vesicle-trafficking protein SEC22b precursor [Bos taurus]	1.0292	0.420730989	0.96125	0.66273479	-1.070689207	0.863126164
347300176	peroxiredoxin-2 [Sus scrofa]	19.12525	0.857227739	17.919	0.83041867	-1.067316815	0.308175688
281351805	hypothetical protein PANDA_010030 [Ailuropoda melanoleuca]	5.7725	0.936667664	5.424475	0.933278941	-1.064158283	0.638223917
281342576	hypothetical protein PANDA_020401 [Ailuropoda melanoleuca]	12.32615	1.917343246	11.5866	1.773281303	-1.063828043	0.32116651
47523764	peptidyl-prolyl cis-trans isomerase A [Sus scrofa]	47.32375	2.983907711	44.6705	2.458892993	-1.059396022	0.612418637
194218821	PREDICTED: protein canopy homolog 4 [Equus caballus]	0.771575	0.257242212	0.729725	0.453906417	-1.057350372	0.920470443
116175251	macrophage migration inhibitory factor [Sus scrofa]	12.1135	1.10487175	11.479525	0.745783945	-1.055226588	0.697340924
545853401	PREDICTED: vimentin isoform X1 [Sus scrofa]	384.66	18.8224011	365.59	23.13139749	-1.052162258	0.171569586
194206522	PREDICTED: acidic leucine-rich nuclear phosphoprotein 32 family member A isoform X1 [Equus caballus]	0.492555	0.284979855	0.4683	0.4683	-1.051793722	0.951078813
113205886	nucleoside diphosphate kinase B [Sus scrofa]	8.84505	0.896445779	8.412575	0.998034687	-1.05140816	0.767507612
344281491	PREDICTED: dihydropyrimidinase-related protein 2 isoform X2 [Loxodonta africana]	11.966	1.901592164	11.383025	0.978228229	-1.051214418	0.759338806
440907381	Cofilin-1, partial [Bos mutus]	23.26025	2.407803196	22.19125	4.155642938	-1.04817214	0.777088432
27806689	clathrin heavy chain 1 [Bos taurus]	24.925	1.541399364	23.78375	2.764160854	-1.047984443	0.516480751
298677090	superoxide dismutase [Cu-Zn] [Sus scrofa]	10.62725	1.818888071	10.1411	1.037453859	-1.047938587	0.815802279
157428070	erythrocyte band 7 integral membrane protein [Bos taurus]	7.074475	0.704268342	6.752375	0.810698179	-1.047701735	0.803385053
281341352	hypothetical protein PANDA_012739 [Ailuropoda melanoleuca]	1.26413	0.266483331	1.206715	0.585047036	-1.047579586	0.886152766
148887343	RecName: Full=ATP synthase subunit e, mitochondrial; Short=ATPase subunit e [Sus scrofa]	6.521675	0.607422133	6.2261	0.241377267	-1.047473539	0.6609292
488544468	PREDICTED: pyruvate kinase isozymes M1/M2 isoform 2 [Dasypus novemcinctus]	44.54275	3.604126255	42.54575	3.422490184	-1.046937708	0.63949077
149751396	PREDICTED: T-complex protein 1 subunit gamma isoform 1 [Equus caballus]	1.53043	0.677161461	1.46289	0.616771422	-1.046168885	0.866973354
13385408	60S ribosomal protein L11 [Mus musculus]	1.80325	0.652334318	1.724315	0.440218891	-1.045777599	0.893870769
545859794	PREDICTED: myb-binding protein 1A isoform X1 [Sus scrofa]	0.767825	0.487251147	0.7357925	0.2461123	-1.043534692	0.966551466

593763768	PREDICTED: peptidyl-prolyl cis-trans isomerase A-like [Physeter catodon]	39.798	1.926682425	38.22775	1.784565417	-1.041076182	0.638995453
126303044	PREDICTED: ras-related protein Rab-10 [Monodelphis domestica]	8.823675	0.437710782	8.476725	0.700804323	-1.040929722	0.707554362
229506	aldolase C	12.1045	0.891411474	11.63365	1.221566285	-1.04047311	0.742859698
28461233	tubulin-specific chaperone A [Bos taurus]	0.765375	0.486800411	0.7357925	0.2461123	-1.040204949	0.969623824
335284210	PREDICTED: heat shock protein beta-1-like isoform 1 [Sus scrofa]	37.3635	2.919394015	36.0625	1.782036873	-1.036076256	0.703369425
350578838	PREDICTED: synemin [Sus scrofa]	1.52668	0.531811205	1.4742	0.250836351	-1.035598969	0.945763145
585697890	PREDICTED: heterogeneous nuclear ribonucleoprotein L-like [Elephantulus edwardii]	2.01055	0.421055864	1.9425	0.637802136	-1.035032175	0.854062683
488520727	PREDICTED: transgelin [Dasypus novemcinctus]	301.895	26.23473223	291.6825	24.23206463	-1.035012385	0.669083906
335292694	PREDICTED: heat shock-related 70 kDa protein 2 [Sus scrofa]	22.8735	1.718820453	22.106	1.128577645	-1.034719081	0.695449464
109131908	PREDICTED: small nuclear ribonucleoprotein Sm D2-like [Macaca mulatta]	1.031675	0.424761675	0.9972175	0.026036997	-1.034553646	0.938684944
298104130	acylphosphatase-1 isoform 1 [Sus scrofa]	2.060875	0.732242628	1.994425	0.052079529	-1.033317874	0.932963789
545840440	PREDICTED: LOW QUALITY PROTEIN: IQ motif containing GTPase activating protein 1 [Sus scrofa]	14.6655	1.600583461	14.203125	2.891620684	-1.032554455	0.773900075
126345443	PREDICTED: poly(rC)-binding protein 2-like isoform X1 [Monodelphis domestica]	1.5407	0.662667047	1.49279	0.286403496	-1.032094266	0.92180872
301779207	PREDICTED: integrin-linked protein kinase-like [Ailuropoda melanoleuca]	2.832475	0.978844125	2.746175	0.501940352	-1.031425528	0.913259084
432092845	Translational activator GCN1 [Myotis davidii]	9.145625	1.612784673	8.88705	1.113779168	-1.029095707	0.848024234
281353009	hypothetical protein PANDA_006420 [Ailuropoda melanoleuca]	1.26413	0.266483331	1.22874	0.474321155	-1.028801862	0.938255035
130490906	voltage-dependent anion-selective channel protein 2 [Oryctolagus cuniculus]	10.26505	0.888265863	9.990575	0.603009309	-1.027473394	0.790414175
126282483	PREDICTED: proteasome subunit alpha type-3 [Monodelphis domestica]	1.26413	0.266483331	1.231365	0.214574573	-1.026608682	0.57592442
634882188	PREDICTED: mimecan [Orycteropus afer afer]	13.4109	3.425828519	13.0673	2.901392486	-1.026294644	0.923011558
586489477	PREDICTED: calponin-1 [Chrysochloris asiatica]	154.2825	18.7091343	150.4475	9.184022698	-1.02549062	0.781386303
593739773	PREDICTED: carbonyl reductase [NADPH] 1 [Physeter catodon]	2.520775	0.515735353	2.4601	0.601350429	-1.024663632	0.957143961
114051331	obg-like ATPase 1 [Bos taurus]	1.734	0.436085808	1.6924	0.708494431	-1.024580477	0.917659381
147903595	F-actin-capping protein subunit alpha-2 [Sus scrofa]	4.32775	0.816516186	4.23895	0.485938498	-1.020948584	0.844063067
560963606	PREDICTED: LOW QUALITY PROTEIN: collagen alpha-1(XV) chain [Vicugna pacos]	3.068705	1.129586937	3.007575	0.454057949	-1.020325345	0.959334485
395516598	PREDICTED: actin-related protein 2/3 complex subunit 4 [Sarcophilus harrisii]	8.5801	0.963841224	8.416175	0.883941371	-1.019477375	0.908160292
335298275	PREDICTED: glyoxalase domain-containing protein 4 [Sus scrofa]	1.75915	0.251989287	1.72694	0.442984409	-1.018651488	0.956992512
350583750	PREDICTED: hsc70-interacting protein isoform 1 [Sus scrofa]	1.006505	0.022838214	0.988525	0.383544768	-1.018188716	0.963741837
349501107	ribosomal protein, large, P2 [Sus scrofa]	6.2892	0.650889283	6.181475	0.801956763	-1.01742707	0.938272005

345792633	PREDICTED: phosphoglycerate mutase 1 isoform 4 [Canis lupus familiaris]	8.330075	1.050608637	8.193275	0.306577993	-1.01669662	0.909452389
190360743	charged multivesicular body protein 4b [Bos taurus]	1.26038	0.257869159	1.2400525	0.235500938	-1.016392451	0.963270496
350583566	PREDICTED: serine--tRNA ligase, cytoplasmic [Sus scrofa]	1.514255	0.511249894	1.490165	0.281379967	-1.016165995	0.97447564
586458037	PREDICTED: 14-3-3 protein gamma [Chrysochloris asiatica]	13.616	1.476003218	13.405	0.565725788	-1.015740395	0.849944079
335281609	PREDICTED: stress-induced-phosphoprotein 1 [Sus scrofa]	0.9851	0.569954481	0.96994	0.383071264	-1.015629833	0.972224381
14249144	ras-related protein Rab-11B [Rattus norvegicus]	3.582655	1.094292459	3.5278	0.71725886	-1.015549351	0.963578787
350589409	PREDICTED: protein phosphatase 1 regulatory subunit 12B-like isoform X1 [Sus scrofa]	5.0288	0.417662701	4.9614	0.314754105	-1.013584875	0.915710816
223950631	guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 [Sus scrofa]	4.330225	0.924797876	4.272275	0.710396558	-1.013564202	0.942349406
47523106	calponin-1 [Sus scrofa]	170.96	19.97253239	168.97	7.270521531	-1.011777239	0.908010134
262263205	triosephosphate isomerase 1 [Sus scrofa]	33.11025	3.886751115	32.8385	0.966145736	-1.008275348	0.933895635
444729185	Myosin regulatory light polypeptide 9 [Tupaia chinensis]	40.485	6.164606678	40.20525	2.324142902	-1.006958047	0.960768187
217038350	ribosomal protein L17 (predicted) [Oryctolagus cuniculus]	0.50775	0.50775	0.504265	0.291532728	-1.006911049	0.993585989
545800035	PREDICTED: tropomyosin alpha-1 chain isoform X2 [Sus scrofa]	153.7025	8.311183605	152.8775	3.155805167	-1.005396478	0.941642608
47523046	acyl-CoA-binding protein [Sus scrofa]	2.745425	0.735028595	2.732825	0.231111461	-1.004610614	0.989576269
528766928	tropomyosin 3, gamma isoform 19-like protein [Camelus ferus]	69.4605	4.226390452	69.151	0.675619099	-1.004475713	0.948874313
634836482	PREDICTED: gelsolin isoform X5 [Orycteropus afer afer]	11.86605	0.862325269	11.8228	1.907464549	-1.003658186	0.986787531
466033133	PREDICTED: tropomyosin alpha-4 chain isoform 6 [Orcinus orca]	164.835	9.696101021	164.4525	3.434834724	-1.0023259	0.973819965
280937	transforming protein ras - rabbit	1.7554	0.245396186	1.75159	0.264678814	-1.002175167	0.992177908
545857759	PREDICTED: synaptic vesicle membrane protein VAT-1 homolog [Sus scrofa]	1.4953	0.267328035	1.49279	0.286403496	-1.001681415	0.994846711
264670244	nucleophosmin [Bos taurus]	1.26038	0.257869159	1.2586425	0.278335495	-1.001380456	0.961912311
311264072	PREDICTED: cell surface glycoprotein MUC18 isoform X1 [Sus scrofa]	2.5105	0.660855291	2.5094	0.911915227	-1.000438352	0.998498186
149702854	PREDICTED: 60S ribosomal protein L23a-like [Equus caballus]	0.5177	0.298900928	0.5176	0.5176	-1.000193199	0.999825232
114373	RecName: Full=Sodium/potassium-transporting ATPase subunit alpha-1; Short=Sodium pump subunit alpha-1; AltName: Full=Na(+)/K(+) ATPase alpha-1 subunit; Flags: Precursor [Equus caballus]	0.98755	0.38462955	0	0	0	0.082670109
545812125	PREDICTED: alpha-aminoadipic semialdehyde dehydrogenase-like [Sus scrofa]	0.98755	0.38462955	0	0	0	0.082670109
157785569	coatomer subunit alpha [Bos taurus]	1.80945	0.889706962	0	0	0	0.134854524
560933266	PREDICTED: PRA1 family protein 3 [Camelus ferus]	2.4437	1.247518516	0	0	0	0.145015048
350594715	PREDICTED: adipocyte plasma membrane-associated protein [Sus scrofa]	1.68615	1.032698938	0	0	0	0.201024176
178056488	tenascin-X precursor [Sus scrofa]	0.729925	0.454899845	0	0	0	0.206926313
350582175	PREDICTED: mitochondrial inner membrane protein, partial [Sus scrofa]	0.765375	0.486800411	0	0	0	0.213938092

194220950	PREDICTED: ATP-dependent RNA helicase DDX1 [Equus caballus]	0.7778	0.497606888	0	0	0	0.21597607
126328613	PREDICTED: non-histone chromosomal protein HMG-17 [Monodelphis domestica]	0.7778	0.497606888	0	0	0	0.21597607
350579447	PREDICTED: protein NipSnap homolog 3A [Sus scrofa]	0.769125	0.492675365	0	0	0	0.21641467
1236646	ch4 and secrete domains of swine IgM [Sus scrofa]	0.50775	0.50775	0	0	0	0.391002219
560926081	PREDICTED: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 isoform X1 [Camelus ferus]	0.520175	0.520175	0	0	0	0.391002219
149725681	PREDICTED: ribosome maturation protein SBDS [Equus caballus]	0.51525	0.51525	0	0	0	0.391002219
115496153	DDRGK domain-containing protein 1 precursor [Bos taurus]	0.51525	0.51525	0	0	0	0.391002219
27807043	phosphatidylinositol 4-kinase alpha [Bos taurus]	0.51525	0.51525	0	0	0	0.391002219
667277536	PREDICTED: keratin, type II cytoskeletal 78 [Galeopterus variegatus]	1.8034	1.8034	0	0	0	0.391002219
225382135	fascin [Sus scrofa]	0.46985	0.46985	0	0	0	0.391002219
118151180	phosphatidate cytidylyltransferase 2 [Bos taurus]	0.46985	0.46985	0	0	0	0.391002219
556736937	PREDICTED: elongation factor Tu, mitochondrial-like [Pantholops hodgsonii]	0.7048	0.7048	0	0	0	0.391002219
519028151	nitrogen regulatory protein P-II 1 [Methylotenera sp. 1P/1]	0.939725	0.939725	0	0	0	0.391002219
335297640	PREDICTED: 2',3'-cyclic-nucleotide 3'-phosphodiesterase [Sus scrofa]	1.17465	1.17465	0	0	0	0.391002219
558701311	MHC class I antigen [Sus scrofa]	1.409575	1.409575	0	0	0	0.391002219
640484928	MULTISPECIES: molecular chaperone GroEL [Mesorhizobium]	2.3493	2.3493	0	0	0	0.391002219