Supporting Information - Tables

Proteomic profiling of cardiomyocyte-specific cathepsin A overexpression links cathepsin A to the oxidative stress response

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Table S-1. Proteins identified via MaxQuant in replicate 1.

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P54923	[Protein ADP-ribosylarginine] hydrolase	Adprh	3	3	3	14.1	14.1	14.1	40.068	362	7.8799E-06	1.0146	1.0041	68.614	2	55650000	24267000	31383000
Q8BGK2	[Protein ADP-ribosylarginine] hydrolase-like protein 1	Adprhl1	9	9	9	30.6	30.6	30.6	39.885	353	5.823E-272	0.91397	0.90883	60.821	15	2948600000	1569400000	1379300000
A2AJQ0	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1	Pdp1	6	6	6	18.8	18.8	18.8	67.615	597	3.302E-183	0.97198	0.8921	23.685	4	394530000	202730000	191800000
Q8BFP9	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial	Pdk1	10	10	9	28.1	28.1	26	48.994	434	1.156E-288	1.4411	1.4652	68.031	13	2354400000	832500000	1521900000
Q9JK42	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial	Pdk2	9	8	8	31.7	29.5	29.5	46.04	407	0	1.3221	1.1297	43.745	10	2123300000	1027200000	1096100000
O70571	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial	Pdk4	9	9	9	29.9	29.9	29.9	46.596	412	9.438E-137	2.0682	2.1784	96.066	6	583510000	206650000	376860000
F6ZHD8	1,4-alpha-glucan-branching enzyme	Gbe1	7	7	7	15.1	15.1	15.1	80.336	702	6.178E-130	1.3579	1.5395	67.712	7	631570000	276390000	355180000
Q9DCT1	1,5-anhydro-D-fructose reductase	Akr1e2	3	3	3	12.3	12.3	12.3	34.46	301	0.00019505	1.1717	0.33666	78.822	3	152890000	77628000	75266000
Q64433	10 kDa heat shock protein, mitochondrial	Hspe1	8	8	8	62.7	62.7	62.7	10.963	102	7.846E-177	0.4639	0.45059	126.38	36	5.2038E+10	3.5014E+10	1.7024E+10
Q9DAK9	14 kDa phosphohistidine phosphatase	Phpt1	4	4	4	40.3	40.3	40.3	13.996	124	1.4298E-22	0.53597	0.56922	40.161	8	962500000	674130000	288370000
Q9CQV8	14-3-3 protein beta/alpha	Ywhab	7	5	5	33.7	26.4	26.4	28.086	246	0	0.6578	0.68066	30.612	11	2106000000	1316800000	789120000
P62259	14-3-3 protein epsilon	Ywhae	10	8	8	44.3	37.3	37.3	29.174	255	5.855E-281	0.59368	0.57	76.543	19	1915900000	980730000	935130000
P68510	14-3-3 protein eta	Ywhah	6	4	4	29.7	22.4	22.4	28.211	246	6.021E-230	0.6445	0.77583	10.034	6	1098700000	698400000	400280000
P61982	14-3-3 protein gamma;14-3-3 protein gamma, N-terminally processed	Ywhag	6	4	4	25.1	17.8	17.8	28.302	247	0	0.63409	0.68498	102.8	12	4772900000	2892500000	1880400000
F6VW30	14-3-3 protein theta	Ywhaq	11	11	9	31	31	25.1	34.348	303	0	0.50914	0.54586	34.166	26	8873800000	5511300000	3362600000
P63101	14-3-3 protein zeta/delta	Ywhaz	10	8	8	42	34.7	34.7	27.771	245	0	0.50077	0.49116	57.823	30	1.6006E+10	1.096E+10	5046600000
P58871	182 kDa tankyrase-1-binding protein	Tnks1bp1	4	4	4	4.5	4.5	4.5	181.82	1720	3.0067E-19	0.81824	1.0266	34.422	5	87772000	52176000	35596000
Q8R3B1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1	Plcd1	6	6	6	11.9	11.9	11.9	85.872	756	1.246E-79	1.3457	1.3896	47.537	5	233680000	86782000	146890000
Q62077	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	Plcg1	2	2	2	2.6	2.6	2.6	149.67	1302	3.8821E-05	1.3263	1.1371	12.779	2	19576000	8996500	10580000
Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial	Decr1	11	11	11	46	46	46	36.213	335	0	0.9459	0.99097	52.537	48	1.5765E+10	9020100000	6745100000
P62334	26S protease regulatory subunit 10B	Psmc6	6	6	6	20.8	20.8	20.8	44.172	389	2.01E-126	1.1674	1.3727	30.888	10	832560000	419760000	412790000
P62192	26S protease regulatory subunit 4	Psmc1	10	10	10	30.9	30.9	30.9	49.184	440	1.7619E-46	1.4426	1.3089	49.435	14	1233500000	510480000	723000000
B7ZCF1	26S protease regulatory subunit 6A	Psmc3	11	11	11	34.1	34.1	34.1	50.395	451	8.5316E-93	0.73841	0.88724	50.562	10	1306300000	761120000	545200000
P54775	26S protease regulatory subunit 6B	Psmc4	4	4	4	11	11	11	47.408	418	1.2138E-81	0.96109	1.013	49.091	9	738800000	372980000	365820000
Q8BVQ9	26S protease regulatory subunit 7	Psmc2	11	11	11	30.3	30.3	30.3	52.866	475	3.598E-285	1.1102	1.1601	60.775	17	1122600000	555590000	567050000
P62196	26S protease regulatory subunit 8	Psmc5	6	6	6	17	17	17	45.626	406	1.238E-197	1.7665	1.6497	34.603	4	158720000	50607000	108120000
Q3TXS7	26S proteasome non-ATPase regulatory subunit 1	Psmd1	9	9	9	13.7	13.7	13.7	105.73	953	6.15E-122	0.98082	0.97533	44.164	10	936090000	461640000	474460000
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	Psmd11	13	13	11	37.4	37.4	31	47.436	422	2.3142E-56	0.96629	0.87102	105.93	15	1722700000	910410000	812320000
Q9D8W5	26S proteasome non-ATPase regulatory subunit 12	Psmd12	8	8	8	22.6	22.6	22.6	52.895	456	1.8505E-55	1.2497	1.2807	61.247	8	569250000	273630000	295610000
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	Psmd13	8	8	8	27.7	27.7	27.7	42.809	376	3.464E-174	0.92406	0.85865	32.132	8	595620000	326940000	268680000
O35593	26S proteasome non-ATPase regulatory subunit 14	Psmd14	4	4	4	19	19	19	34.577	310	3.5583E-20	1.0332	1.0329	29.441	3	255020000	138770000	116260000
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	Psmd2	14	14	14	21	21	21	100.2	908	1.1868E-87	1.122	1.0902	59.191	21	1742700000	850690000	892040000
P14685	26S proteasome non-ATPase regulatory subunit 3	Psmd3	9	9	9	21.7	21.7	21.7	60.718	530	1.29E-134	1.2359	1.1301	52.984	10	518990000	226270000	292730000
O35226	26S proteasome non-ATPase regulatory subunit 4	Psmd4	7	7	6	30.3	30.3	27.7	40.703	376	2.99E-160	0.55002	0.55244	50.329	9	1687100000	1087100000	600020000
F7AI87	26S proteasome non-ATPase regulatory subunit 4 (Fragment)	Psmd4	3	2	2	19.6	14.4	14.4	21.316	194	1.071E-146	0.5972	0.61723	8.8941	5	201700000	141460000	60239000
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5	Psmd5	4	4	4	10.5	10.5	10.5	55.971	504	6.1356E-73	1.2051	1.2346	26.462	4	454890000	231510000	223370000
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	Psmd6	8	8	8	21.3	21.3	21.3	45.536	389	1.8423E-40	1.2274	1.1809	121.54	7	535540000	243900000	291630000
P26516	26S proteasome non-ATPase regulatory subunit 7	Psmd7	3	3	3	14.6	14.6	14.6	36.539	321	1.6364E-64	1.0366	0.87085	7.8785	3	325040000	164620000	160420000
Q9CX56	26S proteasome non-ATPase regulatory subunit 8	Psmd8	6	6	6	22.4	22.4	22.4	39.93	353	1.3855E-18	0.68867	0.65027	45.884	13	1010400000	596150000	414200000
Q3UHX2	28 kDa heat- and acid-stable phosphoprotein	Pdap1	3	3	3	17.1	17.1	17.1	20.605	181	2.0362E-77	0.38377	0.37663	42.035	5	317640000	244770000	72876000
Q8VE22	28S ribosomal protein S23, mitochondrial	Mrps23	3	3	3	24.9	24.9	24.9	20.348	177	1.9263E-22	0.68829	0.68444	130.33	5	327730000	118600000	209130000
Q8BK72	28S ribosomal protein S27, mitochondrial	Mrps27	6	6	6	14.9	14.9	14.9	47.778	415	5.0675E-10	0.68642	0.61105	15.026	3	113330000	62228000	51106000
Q9CY16	28S ribosomal protein S28, mitochondrial	Mrps28	2	2	2	10.2	10.2	10.2	20.52	186	0.0007918	0.37947	0.42696	5.1369	2	112340000	80330000	32005000
G3X9M0	28S ribosomal protein S29, mitochondrial	Dap3	3	3	3	10.6	10.6	10.6	45.287	396	1.4152E-15	0.73959	0.70271	26.345	3	113890000	61821000	52072000
Q9D0G0	28S ribosomal protein S30, mitochondrial	Mrps30	3	3	3	10.4	10.4	10.4	49.939	442	3.5135E-46	1.3757	1.6174	26.291	3	182490000	82707000	99784000
Q61733	28S ribosomal protein S31, mitochondrial	Mrps31	4	4	4	18.5	18.5	18.5	43.88	384	8.5146E-82	0.30521	0.32587	47.012	6	426130000	325690000	100440000
Q8BJZ4	28S ribosomal protein S35, mitochondrial	Mrps35	3	3	3	7.8	7.8	7.8	35.975	320	3.8811E-06	0.64086	0.55133	16.048	2	49825000	34751000	15074000
Q9CQX8	28S ribosomal protein S36, mitochondrial	Mrps36	4	4	1	69.6	69.6	23.5	11.101	102	2.079E-284	0.43729	0.45344	43.648	12	1.1226E+10	8017000000	3209100000
Q99N87	28S ribosomal protein S5, mitochondrial	Mrps5	3	3	3	6.7	6.7	6.7	48.206	432	1.0499E-05	0.56465	0.54241	18.43	4	117020000	74414000	42611000
Q9CXI0	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	Coq5	7	7	7	27.2	27.2	27.2	37.335	327	1.776E-222	0.97548	0.95277	46.327	8	459220000	233520000	225710000
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	Ogdh	33	33	31	42.6	42.6	40.4	116.45	1023	0	1.7696	1.7972	57.399	104	3.0026E+10	1.1392E+10	1.8634E+10
Q3U3J1	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	Bckdha	7	7	7	23.3	23.3	23.3	50.773	446	0	1.0783	0.94102	63.94	7	394780000	192950000	201840000
Q6P3A8	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	Bckdhb	5	5	5	20.8	20.8	20.8	42.88	390	3.2368E-41	1.282	1.131	84.149	10	1782400000	907590000	874810000
Q9Z0S1	3(2),5-bisphosphate nucleotidase 1	Bpnt1	8	8	8	37	37	37	33.196	308	4.4349E-55	1.0137	0.63915	113.47	7	555180000	300010000	255180000
Q99N96	39S ribosomal protein L1, mitochondrial	Mrpl1	3	3	3	17	17	17	37.596	336	2.0293E-21	0.62068	0.69054	19.058	3	242470000	145100000	97373000
Q3TBW2	39S ribosomal protein L10, mitochondrial	Mrpl10	2	2	2	14.5	14.5	14.5	29.395	262	0.00024401	1.3679	1.6562	50.595	3	121310000	49306000	72005000
Q9CQF0	39S ribosomal protein L11, mitochondrial	Mrpl11	2	2	2	10.4	10.4	10.4	20.68	192	4.7761E-08	0.88773	0.57945	82.929	2	73855000	41852000	32004000
Q9DB15	39S ribosomal protein L12, mitochondrial	Mrpl12	2	2	2	11.4	11.4	11.4	21.708	201	1.0543E-08	0.48884	0.47668	7.8377	3	440110000	311090000	129020000
Q9CPR5	39S ribosomal protein L15, mitochondrial	Mrpl15	2	2	2	8.8	8.8	8.8	33.541	295	0.0049556	1.492	1.4756	37.553	2	175660000	78584000	97077000
Q99N95	39S ribosomal protein L3, mitochondrial	Mrpl3	2	2	2	6.6	6.6	6.6	39.109	348	6.934E-21	1.2007	1.0724	42.286	2	91055000	38066000	52990000
Q921S7	39S ribosomal protein L37, mitochondrial	Mrpl37	1	1	1	3.8	3.8	3.8	48.34	423	6.4335E-06	1.7218	1.7521	9.4346	2	79494000	32009000	47485000
Q9JKF7	39S ribosomal protein L39, mitochondrial	Mrpl39	5	5	5	14.9	14.9	14.9	38.549	336	2.0758E-12	1.0192	1.2296	38.339	3	201880000	101460000	100420000
Q9D0Q7	39S ribosomal protein L45, mitochondrial	Mrpl45	4	4	4	19.6	19.6	19.6	35.41	306	3.8503E-14	1.6903	1.5256	54.745	3	110550000	50645000	59904000
Q9CQ40	39S ribosomal protein L49, mitochondrial	Mrpl49	2	2	2	13.3	13.3	13.3	19.133	166	0.0018876	0.81802	0.97658	75.201	2	233510000	147860000	85650000
Q8VDT9	39S ribosomal protein L50, mitochondrial	Mrpl50	2	2	2	16.4	16.4	16.4	18.213	159	0.0016605	0.65831	0.66013	27.197	2	145730000	86042000	59686000
A2AFQ2	3-hydroxyacyl-CoA dehydrogenase type-2	Hsd17b10	13	13	5	60.9	60.9	20.7	28.374	271	2.278E-234	1.3248	1.387	39.171	28	7099200000	3191800000	3907300000
Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial	Hibadh	9	9	9	40	40	40	35.44	335	5.226E-85	0.99562	1.0025	38.407	23	3078100000	1646800000	1431200000
Q8QZS1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	Hibch	15	15	15	47.3	47.3	47.3	43.037	385	8.525E-212	0.90068	0.96337	109.4	18	8958200000	4850300000	4107900000
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	Acaa1a	6	6	6	24.3	24.3	24.3	43.953	424	1.3413E-81	0.92754	1.0876	38.725	4	365700000	191690000	174010000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	Acaa2	16	16	16	57.4	57.4	57.4	41.829	397	0	0.84418	0.8553	102.19	50	2.0771E+10	1.1156E+10	9614300000
Q9D404	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	Oxsm	3	3	3	11.8	11.8	11.8	48.627	459	2.1738E-25	1.344	1.4303	101.4	6	482310000	189130000	293180000
P62281	40S ribosomal protein S11	Rps11	3	3	3	22.8	22.8	22.8	18.431	158	4.7103E-09	0.88943	0.98893	135.11	3	384860000	233440000	151420000
Q6ZWZ6	40S ribosomal protein S12	Rps12	5	5	5	47	47	47	14.515	132	2.1315E-97	0.57051	0.549	56.091	9	1665900000	1100600000	565220000
P62301	40S ribosomal protein S13	Rps13	3	3	3	24.5	24.5	24.5	17.222	151	1.7251E-59	0.39491	0.37651	293.6	2	78240000	44747000	33492000
P62264	40S ribosomal protein S14	Rps14	2	2	2	15.2	15.2	15.2	16.273	151	0.0013714	2.5609	2.9209	45.158	2	200870000	58399000	142470000
D3Z722	40S ribosomal protein S19	Rps19	2	2	2	7.5	7.5	7.5	23.104	212	1.9153E-13	3.35	3.8911	120.98	3	90882000	26241000	64640000
D3YWJ3	40S ribosomal protein S2	Rps2	1	1	1	4.3	4.3	4.3	32.105	302	2.6395E-08	3.8656	3.4376	38.543	3	303080000	62808000	240270000
Q9CQR2	40S ribosomal protein S21	Rps21	2	2	2	22.9	22.9	22.9	9.1413	83	0.014409	1.1433	1.339	38.822	2	458790000	189710000	269080000
P62858	40S ribosomal protein S28	Rps28	1	1	1	17.4	17.4	17.4	7.8409	69	0.00042197	1.593	1.7067	5.986	2	365890000	122420000	243470000
D3Z6C3	40S ribosomal protein S3a	Gm10119	2	2	2	8.7	8.7	8.7	29.824	264	5.8185E-11	2.8647	1.0885	117.21	2	314570000	80408000	234160000
Q91V55	40S ribosomal protein S5	Rps5	2	2	2	13.7	13.7	13.7	22.876	204	4.7766E-08	3.9019	3.8552	28.758	5	418500000	83400000	335100000
P62754	40S ribosomal protein S6	Rps6	2	2	2	8	8	8	28.68	249	6.7959E-05	2.5016	3.0792	16.645	2	234760000	85008000	149750000
P14206	40S ribosomal protein SA	Rpsa	5	5	5	27.5	27.5	27.5	32.838	295	5.0104E-82	2.0706	2.101	62.819	4	662530000	216440000	446090000
P61922	4-aminobutyrate aminotransferase, mitochondrial	Abat	6	6	6	13	13	13	56.451	500	2.1832E-19	0.9694	1.0572	17.495	7	233630000	112500000	121130000
Q3U367	4-trimethylaminobutyraldehyde dehydrogenase	Aldh9a1	5	5	5	15.1	15.1	15.1	55.887	518	8.9153E-24	1.3031	0.34837	110.23	5	795630000	352650000	442980000
Q9JM14	5(3)-deoxyribonucleotidase, cytosolic type	Nt5c	1	1	1	9	9	9	23.076	200	1.0025E-05	1.0633	1.0847	1.041	2	341270000	154270000	186990000
P70290	55 kDa erythrocyte membrane protein	Mpp1	4	4	3	13.5	13.5	10.5	52.227	466	3.9158E-09	0.75552	0.78687	37.292	4	180780000	109920000	70857000
Q8BRK8	5-AMP-activated protein kinase catalytic subunit alpha-2	Prkaa2	2	2	2	5.1	5.1	5.1	62.022	552	0.0054901	0.22604	0.25024	38.654	2	22098000	17438000	4659200
O54950	5-AMP-activated protein kinase subunit gamma-1	Prkag1	3	3	3	11.8	11.8	11.8	37.52	330	1.1166E-07	2.1057	0.92858	195.18	2	323150000	116300000	206860000
Q3UHB1	5-nucleotidase domain-containing protein 3	Nt5dc3	4	4	4	7.1	7.1	7.1	63.17	546	7.8572E-09	1.3364	1.5889	44.324	5	266980000	115190000	151790000
Q8K010	5-oxoprolinase	Oplah	10	10	10	11.5	11.5	11.5	137.61	1288	3.1833E-82	1.1212	1.3924	82.199	15	1009700000	445240000	564500000
P63038	60 kDa heat shock protein, mitochondrial	Hspd1	33	33	33	60	60	60	60.955	573	0	0.45899	0.46563	94.093	102	9.8417E+10	6.6471E+10	3.1946E+10
E9Q3T0	60S acidic ribosomal protein P1	Gm10073	1	1	1	14	14	14	11.433	114	8.182E-11	1.0085	1.1523	47.865	2	243280000	135520000	107750000
P14115	60S ribosomal protein L27a	Rpl27a	2	2	2	14.2	14.2	14.2	16.605	148	0.00023552	3.6002	3.9734	32.658	2	204030000	53419000	150610000
P62889	60S ribosomal protein L30	Rpl30	1	1	1	13.9	13.9	13.9	12.784	115	0.00083495	2.7984	2.8409	13.538	2	85934000	16174000	69761000
Q9JJI8	60S ribosomal protein L38	Rpl38	1	1	1	10	10	10	8.2038	70	0.0029142	0.64236	0.7492	22.824	2	68755000	42809000	25946000
P47911	60S ribosomal protein L6	Rpl6	2	2	2	8.1	8.1	8.1	33.509	296	1.1619E-08	3.8596	3.9426	18.006	2	44599000	10573000	34026000
F6XI62	60S ribosomal protein L7	Rpl7	1	1	1	3.6	3.6	3.6	32.416	279	5.0421E-06	4.0976	3.77	17.565	2	31960000	6742200	25218000
P12382	6-phosphofructokinase, liver type	Pfkl	9	7	6	16.9	14.4	11.9	85.359	780	2.914E-157	1.8121	1.6154	78.502	10	1411000000	403610000	1007400000
P47857	6-phosphofructokinase, muscle type	Pfkm	16	16	14	31.4	31.4	28.8	85.268	780	0	1.5094	1.7404	60.39	28	6174400000	2257000000	3917400000
Q8C605	6-phosphofructokinase;6-phosphofructokinase type C	Pfkp	5	3	3	10.6	7	7	85.546	784	4.2657E-27	1.3919	1.3765	24.613	4	135240000	62117000	73126000
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	Pgd	7	7	7	21.3	21.3	21.3	53.247	483	8.3244E-44	1.1252	1.1124	63.542	13	1955300000	971980000	983370000
Q9CQ60	6-phosphogluconolactonase	Pgls	6	6	6	35.4	35.4	35.4	27.254	257	9.4325E-29	0.79751	0.91661	32.676	10	1502600000	870460000	632130000
Q9R1Z7	6-pyruvoyl tetrahydrobiopterin synthase	Pts	3	3	3	23.6	23.6	23.6	16.188	144	1.8062E-07	0.50187	0.10745	96.229	3	453120000	306050000	147070000
P20029	78 kDa glucose-regulated protein	Hspa5	26	26	24	41.1	41.1	39.4	72.421	655	2.295E-281	0.7592	0.74577	45.546	44	7101900000	3960300000	3141600000
Q6PE15	Abhydrolase domain-containing protein 10, mitochondrial	Abhd10	2	2	2	9.4	9.4	9.4	33.04	297	6.376E-169	0.93919	0.95801	33.714	2	91586000	49698000	41888000
Q8K4F5	Abhydrolase domain-containing protein 11	Abhd11	2	2	2	13	13	13	33.56	307	1.0654E-28	0.78425	0.71394	17.447	2	94965000	53109000	41856000
E9QN99	Abhydrolase domain-containing protein 14B	Abhd14b	4	4	4	21.9	21.9	21.9	22.45	210	3.1986E-25	0.66919	0.73664	79.313	4	620700000	152310000	468380000
Q80X81	Acetyl-CoA acetyltransferase, cytosolic	Acat3	4	4	4	20.7	20.7	20.7	41.47	397	2.0128E-06	1.1186	1.173	33.2	4	193200000	86024000	107180000
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	Acat1	16	16	16	50	50	50	44.816	424	0	0.71824	0.65099	50.08	58	2.7783E+10	1.5834E+10	1.1949E+10
E9Q4Z2	Acetyl-CoA carboxylase 2	Acacb	11	11	7	6.1	6.1	4	275.75	2448	1.9294E-51	1.4839	1.5528	150.52	10	2930700000	171820000	2758900000
Q99NB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	Acss1	19	19	19	42.1	42.1	42.1	74.622	682	0	1.3796	1.4263	46.911	31	9886300000	4279000000	5607300000
A2AQN4	Acetyl-coenzyme A synthetase, cytoplasmic	Acss2	1	1	1	2.5	2.5	2.5	80.386	714	6.091E-07	1.641	1.7592	164.43	2	374280000	44605000	329670000
P70158	Acid sphingomyelinase-like phosphodiesterase 3a	Smpdl3a	2	2	2	7	7	7	49.857	445	1.8856E-07	0.6275	0.73886	15.833	2	58594000	32487000	26107000
O35381	Acidic leucine-rich nuclear phosphoprotein 32 family member A	Anp32a	7	7	7	23.1	23.1	23.1	28.537	247	2.6193E-58	0.46366	0.4793	101.05	10	2135300000	1437000000	698280000
Q99KI0	Aconitate hydratase, mitochondrial	Aco2	41	41	41	54.7	54.7	54.7	85.462	780	0	1.3105	1.2632	59.223	190	1.5543E+11	6.3476E+10	9.1951E+10
P62737	Actin, aortic smooth muscle	Acta2	15	15	8	57	57	39	42.009	377	0	0.77845	0.79448	73.501	47	1.7048E+10	9964500000	7083200000
E9QK41	Actin-binding LIM protein 1	Ablim1	2	2	2	4.3	4.3	4.3	96.834	861	1.1039E-28	3.0792	3.1129	30.381	2	132290000	37765000	94528000
Q9Z2N8	Actin-like protein 6A	Actl6a	2	2	2	10	10	10	47.447	429	1.5054E-07	1.4926	1.263	23.128	3	98220000	35058000	63162000
P61161	Actin-related protein 2	Actr2	5	5	5	19.3	19.3	19.3	44.76	394	2.1089E-56	1.086	0.89703	52.034	4	388050000	195360000	192690000
Q9R0Q6	Actin-related protein 2/3 complex subunit 1A	Arpc1a	2	2	2	8.1	8.1	8.1	41.626	370	0.00052327	1.0153	1.0287	65.363	2	154360000	66753000	87610000
Q9WV32	Actin-related protein 2/3 complex subunit 1B	Arpc1b	1	1	1	4.8	4.8	4.8	41.063	372	1.3274E-49	0.48822	0.42763	141.33	2	185000000	152840000	32154000
Q9CVB6	Actin-related protein 2/3 complex subunit 2	Arpc2	6	6	6	17.7	17.7	17.7	34.357	300	3.5375E-18	0.87654	1.0544	54.783	6	744250000	306160000	438100000
Q9JM76	Actin-related protein 2/3 complex subunit 3	Arpc3	2	2	2	11.2	11.2	11.2	20.524	178	3.8921E-07	0.85651	0.83511	20.335	4	197490000	103240000	94252000
P59999	Actin-related protein 2/3 complex subunit 4	Arpc4	1	1	1	6.5	6.5	6.5	19.667	168	4.1922E-09	2.2691	2.4593	52.628	2	512460000	140770000	371690000
Q9CPW4	Actin-related protein 2/3 complex subunit 5	Arpc5	2	2	2	21.2	21.2	21.2	16.288	151	4.1051E-07	0.51973	0.28586	99.992	2	298700000	195680000	103020000
A3KGQ6	Actin-related protein 2/3 complex subunit 5	Arpc5l	2	2	2	20.3	20.3	20.3	17.109	153	1.4433E-07	0.63691	0.72898	7.1078	2	140620000	84872000	55753000
Q99JY9	Actin-related protein 3	Actr3	9	9	6	27.5	27.5	22	47.357	418	8.2933E-81	1.5173	1.8698	45.77	13	1179400000	389380000	790020000
P11031	Activated RNA polymerase II transcriptional coactivator p15	Sub1	2	2	2	18.9	18.9	18.9	14.427	127	0.00058324	0.17327	0.098138	265.03	2	113980000	94372000	19610000
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	Ahsa1	7	7	7	22.8	22.8	22.8	38.117	338	3.4529E-30	0.43236	0.43392	93.707	10	793420000	509540000	283880000
Q9CR21	Acyl carrier protein, mitochondrial;Acyl carrier protein	Ndufab1	3	3	3	15.4	15.4	15.4	17.37	156	3.7372E-20	0.53982	0.49639	41.423	11	1309100000	924110000	384950000
Q8R146	Acylamino-acid-releasing enzyme	Apeh	5	5	5	7.2	7.2	7.2	81.58	732	6.285E-14	0.98286	0.95835	54.877	4	278060000	132980000	145090000
D3Z7X0	Acyl-CoA dehydrogenase family member 10	Acad12	11	11	11	22.5	22.5	22.5	61.389	555	1.6348E-64	1.9851	1.9599	71.82	13	2003400000	722190000	1281300000
Q8JZN5	Acyl-CoA dehydrogenase family member 9, mitochondrial	Acad9	10	10	10	22.7	22.7	22.7	68.721	625	2.4849E-77	1.0418	0.9073	98.153	9	1195800000	625270000	570550000
Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial	Acsf2	6	6	6	13.7	13.7	13.7	67.95	615	5.1788E-57	1.1741	0.89314	120.09	4	248380000	118460000	129920000
Q3URE1	Acyl-CoA synthetase family member 3, mitochondrial	Acsf3	6	6	6	16.1	16.1	16.1	65.076	583	3.168E-14	1.2343	1.1212	78.901	7	1008100000	681320000	326800000
Q4VWZ5	Acyl-CoA-binding protein	Dbi	3	3	1	32.6	32.6	11.9	15.228	135	1.0012E-96	0.54282	0.54391	69.037	15	1.7648E+10	1.1954E+10	5694100000
O55137	Acyl-coenzyme A thioesterase 1	Acot1	13	13	6	32	32	12.4	46.135	419	6.492E-172	0.91859	0.63863	137.38	19	7760400000	1616800000	6143600000
Q9CQR4	Acyl-coenzyme A thioesterase 13	Acot13	5	5	5	40.7	40.7	40.7	15.183	140	7.901E-207	1.0475	0.85436	132.07	11	4578500000	2206000000	2372500000
Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial	Acot2	12	5	5	32.5	14.3	14.3	49.656	453	0	1.3074	1.4376	43.082	13	2753200000	1252700000	1500500000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial	Acot9	6	6	6	13.4	13.4	13.4	50.56	439	1.9119E-13	1.1873	0.93287	94.796	5	487980000	217420000	270560000
Q9ESW4	Acylglycerol kinase, mitochondrial	Agk	2	2	2	9.5	9.5	9.5	46.975	421	4.6959E-05	0.31937	0.32199	148.3	3	294400000	242360000	52048000
E9QJT5	Acylphosphatase;Acylphosphatase-1	Acyp1	3	3	3	18.5	18.5	18.5	17.344	157	3.0436E-43	0.45586	0.40672	171.07	4	1132800000	754020000	378810000
P56375	Acylphosphatase-2	Acyp2	5	5	5	40.6	40.6	40.6	11.877	106	2.062E-196	0.47623	0.5512	146.38	9	4508300000	3050100000	1458200000
P97823	Acyl-protein thioesterase 1	Lypla1	4	4	4	26.5	26.5	26.5	24.687	230	2.4899E-23	0.75124	0.58655	165.27	4	1742100000	983720000	758410000
Q8R0F8	Acylpyruvase FAHD1, mitochondrial	Fahd1	2	2	2	20.7	20.7	20.7	25.172	227	5.7367E-06	2.2976	3.1241	42.232	3	1260400000	396010000	864440000
Q64010	Adapter molecule crk	Crk	7	7	7	38.5	38.5	38.5	33.814	304	4.953E-79	0.51917	0.50738	22.102	13	990940000	656090000	334850000
P08030	Adenine phosphoribosyltransferase	Aprt	2	2	2	11.1	11.1	11.1	19.724	180	0.0019075	0.76362	0.87001	119.95	3	54514000	34723000	19791000
P55264	Adenosine kinase	Adk	8	8	8	29.9	29.9	29.9	40.148	361	7.6685E-85	0.70952	0.66285	112.07	10	2363600000	1865600000	498040000
P50247	Adenosylhomocysteinase	Ahcy	9	9	9	25.5	25.5	25.5	47.688	432	2.4608E-66	0.91378	0.82568	43.377	9	2413400000	1295300000	1118100000
E9PV16	Adenosylhomocysteinase	Ahcyl2	2	2	2	3.1	3.1	3.1	69.97	643	6.9457E-07	1.9945	2.0386	38.386	3	65217000	27466000	37751000
Q9WTP6	Adenylate kinase 2, mitochondrial	Ak2	7	7	7	38.5	38.5	38.5	26.468	239	0	0.8454	0.97576	78.491	12	2261100000	1223000000	1038100000
Q9R0Y5	Adenylate kinase isoenzyme 1	Ak1	11	11	11	51.5	51.5	51.5	21.539	194	0	0.37068	0.37849	41.981	37	3.0748E+10	2.2262E+10	8486000000
Q9WUR9	Adenylate kinase isoenzyme 4, mitochondrial	Ak4	6	6	6	26	26	26	25.061	223	7.8684E-47	1.001	1.0051	57.257	6	535230000	292490000	242740000
P54822	Adenylosuccinate lyase	Adsl	7	7	7	20.5	20.5	20.5	54.866	484	2.0331E-29	1.3872	1.1423	61.497	9	475260000	227660000	247600000
J3QN31	Adenylosuccinate synthetase isozyme 1	Adssl1	8	8	8	20.4	20.4	20.4	52.779	480	2.4644E-33	1.1444	1.0226	52.296	10	1793900000	851840000	942090000
P40124	Adenylyl cyclase-associated protein 1	Cap1	9	9	9	28.3	28.3	28.3	51.564	474	2.808E-229	0.55425	0.51411	35.546	8	514600000	353320000	161280000
Q60994	Adiponectin	Adipoq	4	4	4	21.1	21.1	21.1	26.809	247	3.9456E-95	0.5039	0.50489	108.04	7	1969000000	1605400000	363620000
P48962	ADP/ATP translocase 1	Slc25a4	17	17	10	54.4	54.4	29.5	32.904	298	1.017E-118	1.9682	2.4032	80.307	36	1.4027E+10	4556600000	9470200000
P51881	ADP/ATP translocase 2	Slc25a5	9	2	2	32.9	8.1	8.1	32.931	298	4.1999E-42	2.1003	1.597	103.5	4	1222100000	440460000	781680000
Q3V132	ADP/ATP translocase 4	Slc25a31	4	1	1	9.7	2.8	2.8	35.257	320	1.5859E-20	2.3889	2.5421	1.3618	2	161570000	62279000	99287000
Q8BVU5	ADP-ribose pyrophosphatase, mitochondrial	Nudt9	4	4	4	11.4	11.4	11.4	38.604	350	2.2949E-15	0.44777	0.33843	65.653	4	409930000	283620000	126310000
P61205	ADP-ribosylation factor 3	Arf3	4	4	4	30.9	30.9	30.9	20.601	181	9.3183E-22	0.82671	0.79584	155.56	4	1056900000	621340000	435540000
Q8R0H9	ADP-ribosylation factor-binding protein GGA1	Gga1	2	2	2	4.4	4.4	4.4	69.971	635	5.7139E-11	0.85685	0.87384	73.514	2	109820000	53027000	56790000
Q9WUL7	ADP-ribosylation factor-like protein 3	Arl3	2	2	2	12.6	12.6	12.6	20.486	182	1.0125E-07	0.91637	0.35188	194.6	2	233020000	135640000	97376000
Q9JKX6	ADP-sugar pyrophosphatase	Nudt5	1	1	1	6	6	6	23.984	218	6.9155E-19	0.53307	0.44802	26.84	2	191320000	106480000	84839000
Q9CPW2	Adrenodoxin-like protein, mitochondrial	Fdx1l	2	2	2	19	19	19	18.766	174	4.1359E-42	0.55317	0.60878	18.384	2	227320000	134350000	92970000
E9Q9C3	Afadin	Mllt4	3	3	3	2.5	2.5	2.5	207.31	1827	5.2707E-56	0.73136	0.62568	52.741	4	104180000	60722000	43459000
O89020	Afamin	Afm	11	11	11	23.4	23.4	23.4	69.378	608	1.536E-124	0.41429	0.39792	75.048	12	905910000	640140000	265760000
Q8CG76	Aflatoxin B1 aldehyde reductase member 2	Akr7a2	5	5	5	21	21	21	40.612	367	4.1979E-61	1.671	1.6103	18.226	5	788470000	315550000	472920000
M0QWP1	Agrin	Agrn	6	6	6	4.4	4.4	4.4	216.65	2034	2.2685E-55	0.97474	1.0542	45.255	2	42320000	22442000	19878000
O08715	A-kinase anchor protein 1, mitochondrial	Akap1	4	4	4	10.3	10.3	10.3	92.194	857	2.2922E-95	0.75346	0.67254	40.008	4	55678000	27806000	27872000
Q9WTQ5	A-kinase anchor protein 12	Akap12	11	11	11	12.7	12.7	12.7	180.69	1684	9.609E-239	0.71314	0.68919	71.718	12	545050000	333830000	211230000
F7AA26	A-kinase anchor protein 2	Gm20459	9	9	9	11.4	11.4	11.4	125.98	1137	2.171E-110	0.41826	0.4246	74.4	9	690730000	475930000	214810000
Q64362	AKT-interacting protein	Aktip	1	1	1	5.8	5.8	5.8	32.941	292	4.9943E-22	0.42807	0.36299	69.228	2	20709000	14501000	6207800
Q8QZR5	Alanine aminotransferase 1	Gpt	8	8	8	22.4	22.4	22.4	55.142	496	3.7337E-40	1.1289	1.1532	28.833	10	759860000	368500000	391360000
Q8BGQ7	Alanine--tRNA ligase, cytoplasmic	Aars	4	4	4	5.7	5.7	5.7	106.91	968	1.5174E-27	0.6334	0.71941	34.864	3	140630000	52564000	88062000
Q3THG9	Alanyl-tRNA editing protein Aarsd1	Aarsd1	5	5	5	20.1	20.1	20.1	44.97	412	1.1471E-33	0.49287	0.50283	95.715	5	202170000	152850000	49319000
Q9JII6	Alcohol dehydrogenase [NADP(+)]	Akr1a1	3	3	3	14.8	14.8	14.8	36.586	325	3.5239E-14	1.4105	1.4066	24.383	6	312300000	129010000	183290000
P00329	Alcohol dehydrogenase 1	Adh1	4	4	4	13.9	13.9	13.9	39.771	375	1.8304E-13	0.82916	0.90503	59.088	3	290290000	177030000	113260000
P28474	Alcohol dehydrogenase class-3	Adh5	6	6	6	22.7	22.7	22.7	39.547	374	1.019E-178	0.88569	0.91152	76.557	9	1802200000	981240000	820980000
Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	Aldh1b1	8	8	8	20.8	20.8	20.8	57.552	519	1.4618E-94	0.93039	0.79753	57.637	13	1883300000	997800000	885510000
P47738	Aldehyde dehydrogenase, mitochondrial	Aldh2	18	18	18	46.6	46.6	46.6	56.537	519	4.352E-259	0.87918	0.7887	72.251	34	1.0104E+10	5487400000	4617000000
Q8K157	Aldose 1-epimerase	Galm	2	2	2	8.8	8.8	8.8	37.798	342	2.5414E-07	0.93276	0.87729	20.365	2	210880000	110880000	100000000
P45376	Aldose reductase	Akr1b1	10	10	10	40.8	40.8	40.8	35.732	316	1.335E-178	0.85089	0.7939	131.96	17	1.6645E+10	1.0106E+10	6539300000
P09242	Alkaline phosphatase, tissue-nonspecific isozyme	Alpl	2	2	2	4.8	4.8	4.8	57.514	524	0.0028707	0.60262	0.55596	88.717	2	27279000	18177000	9102600
Q8R2R3	Alpha- and gamma-adaptin-binding protein p34	Aagab	1	1	1	6.3	6.3	6.3	34.51	316	0.0070663	0.91111	0.81162	7.4388	2	13207000	6818800	6388200
P07758	Alpha-1-antitrypsin 1-1;Alpha-1-antitrypsin 1-3	Serpina1a	11	11	4	30.5	30.5	16	46.002	413	0	0.43718	0.46713	34.344	29	4.1828E+10	3.071E+10	1.1117E+10
P22599	Alpha-1-antitrypsin 1-2	Serpina1b	11	4	2	28.3	13.8	6.1	45.974	413	0	0.40638	0.372	18.554	3	1325800000	922550000	403250000
Q00897	Alpha-1-antitrypsin 1-4	Serpina1d	11	3	3	26.4	9.4	9.4	45.998	413	0	0.67559	0.70268	68.854	6	522430000	327840000	194590000
Q00898	Alpha-1-antitrypsin 1-5	Serpina1e	7	1	1	19.1	4.6	4.6	45.891	413	0	0.55721	0.35592	46.886	4	191690000	102100000	89586000
Q61234	Alpha-1-syntrophin	Snta1	5	5	5	19.1	19.1	19.1	53.664	503	2.295E-150	1.0722	0.67075	165.52	3	174680000	96191000	78488000
Q61247	Alpha-2-antiplasmin	Serpinf2	6	6	6	14.9	14.9	14.9	54.971	491	1.7603E-44	0.39893	0.3454	46.157	8	853110000	592760000	260350000
P29699	Alpha-2-HS-glycoprotein	Ahsg	6	6	6	27	27	27	37.325	345	1.583E-230	0.26925	0.2595	49.072	12	1845000000	1376500000	468560000
D3YW52	Alpha-2-macroglobulin	Pzp	31	31	31	32.3	32.3	32.3	167.28	1507	0	0.40864	0.40066	60.316	38	1.0308E+10	7487400000	2820600000
P55302	Alpha-2-macroglobulin receptor-associated protein	Lrpap1	2	2	2	5.6	5.6	5.6	42.215	360	0.00014895	0.67133	0.56387	50.276	3	210020000	143450000	66576000
Q7TPR4	Alpha-actinin-1	Actn1	11	8	5	13.9	10	6.1	103.07	892	5.1188E-41	3.1622	3.7319	77.881	5	196070000	26113000	169960000
Q9JI91	Alpha-actinin-2	Actn2	19	19	15	32	32	25.3	103.83	894	2.698E-159	4.6204	4.6202	129.61	19	2155900000	779230000	1376600000
P57780	Alpha-actinin-4	Actn4	10	6	5	13.5	8.2	7	104.98	912	6.664E-48	1.575	1.6364	97.491	5	279330000	155220000	124110000
Q9QYC0	Alpha-adducin	Add1	5	5	4	11.7	11.7	10.6	80.646	735	2.1489E-22	0.64115	0.67964	34.116	5	131280000	87120000	44157000
Q9DBF1	Alpha-aminoadipic semialdehyde dehydrogenase	Aldh7a1	8	8	8	21.2	21.2	21.2	58.861	539	0	1.1134	1.0551	38.254	9	600910000	303980000	296920000
P61164	Alpha-centractin	Actr1a	4	4	3	17.6	17.6	15.2	42.613	376	1.2109E-15	1.8775	2.0021	81.214	3	245440000	87383000	158050000
P23927	Alpha-crystallin B chain	Cryab	4	4	4	32	32	32	20.069	175	3.6595E-89	0.65686	0.82664	50.122	13	2954400000	1800900000	1153500000
P60840	Alpha-endosulfine	Ensa	3	3	3	26.4	26.4	26.4	13.335	121	2.2819E-56	0.38358	0.35264	81.508	3	55004000	42800000	12204000
P17182	Alpha-enolase;Enolase	Eno1	14	12	5	48.8	45.4	19.1	47.14	434	0	0.64273	0.63746	110.11	27	9420700000	5512900000	3907800000
Q9CY02	Alpha-hemoglobin-stabilizing protein	Ahsp	1	1	1	18.6	18.6	18.6	11.832	102	1.334E-07	0.51465	0.48705	9.647	2	108430000	73883000	34544000
A2AKV6	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3	Alkbh3	2	2	2	8.7	8.7	8.7	33.301	287	0.00055047	1.158	1.0935	100.46	2	23314000	6716100	16598000
O09174	Alpha-methylacyl-CoA racemase	Amacr	2	2	2	7.1	7.1	7.1	41.704	381	2.1494E-08	1.622	1.4757	4.1359	2	91393000	33091000	58301000
Q9EPC1	Alpha-parvin	Parva	2	2	2	7.5	7.5	7.5	42.329	372	4.0082E-10	0.43538	0.50231	70.297	3	118330000	79876000	38457000
D3YUT2	Alpha-protein kinase 3	Alpk3	3	3	3	3	3	3	180.11	1680	3.0783E-19	0.72617	0.78392	68.868	4	183050000	129370000	53671000
P82350	Alpha-sarcoglycan	Sgca	6	6	6	22.2	22.2	22.2	43.286	387	3.0941E-55	1.3233	1.2429	62.941	6	443940000	188580000	255360000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9DB05	Alpha-soluble NSF attachment protein	Napa	3	3	3	15.3	15.3	15.3	33.189	295	3.6444E-27	0.61705	0.65387	36.112	5	162630000	102650000	59976000
O55042	Alpha-synuclein	Snca	4	4	4	37.9	37.9	37.9	14.485	140	5.9454E-31	0.31561	0.33379	25.465	7	747300000	570450000	176850000
Q6PAM1	Alpha-taxilin	Txlna	2	2	2	6.1	6.1	6.1	62.368	554	3.0551E-06	0.49234	0.41105	7.5886	2	9265100	6453900	2811200
Q8BW75	Amine oxidase [flavin-containing] B	Maob	6	6	6	15.6	15.6	15.6	58.557	520	8.6894E-41	1.0613	1.1446	13.252	5	630910000	309060000	321850000
Q3UZG4	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	Aimp1	5	5	5	25.7	25.7	25.7	35.166	319	2.1237E-40	0.98254	1.1969	23.517	6	910690000	485260000	425420000
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	Aimp2	3	3	3	19.4	19.4	19.4	35.377	320	6.186E-142	1.4315	1.4628	40.405	5	197690000	75860000	121830000
Q99JW2	Aminoacylase-1	Acy1	2	2	2	4.7	4.7	4.7	45.78	408	0.0002814	0.82345	0.79292	17.677	3	241860000	129060000	112800000
Q8VCT3	Aminopeptidase B	Rnpep	4	4	4	8.6	8.6	8.6	72.415	650	3.7697E-23	1.2017	0.84226	81.037	4	260750000	116780000	143970000
P97449	Aminopeptidase N	Anpep	5	5	5	7.6	7.6	7.6	109.65	966	1.025E-183	0.53016	0.63638	12.685	4	336870000	214000000	122870000
O08739	AMP deaminase 3	Ampd3	3	3	3	4.6	4.6	4.6	88.651	766	5.3332E-06	1.4988	1.0781	223.85	2	51930000	24290000	27640000
Q60709	Amyloid-like protein 2	Aplp2	2	2	2	2.7	2.7	2.7	85.247	751	0.015156	2.2126	1.8022	106.53	2	23815000	7692600	16122000
Q8BFR6	AN1-type zinc finger protein 1	Zfand1	2	2	2	6	6	6	30.202	268	0.0096239	0.3931	0.40437	94.892	2	38057000	24596000	13462000
Q8WTY4	Anamorsin	Ciapin1	6	6	6	32.4	32.4	32.4	33.429	309	0	0.45431	0.4764	18.43	14	2820800000	1927700000	893060000
P09470	Angiotensin-converting enzyme	Ace	12	12	12	11.4	11.4	11.4	150.92	1312	3.2144E-58	0.70607	0.76386	35.31	13	959280000	516730000	442550000
Q3UTR7	Angiotensinogen;Angiotensin-1;Angiotensin-2;Angiotensin-3	Agt	2	2	2	5.6	5.6	5.6	52.67	482	1.5191E-07	0.51585	0.46829	11.818	2	62636000	40058000	22578000
S4R2H6	Ankyrin-2	Ank2	16	16	12	13.8	13.8	11.7	202.96	1851	1.1819E-74	1.2031	1.1189	83.508	20	1034600000	395660000	638960000
S4R2K9	Ankyrin-3 (Fragment)	Ank3	9	6	6	5.1	4	4	284.64	2622	8.3799E-22	0.89283	0.85921	38.892	5	188610000	110220000	78386000
P10107	Annexin A1	Anxa1	10	10	9	41.6	41.6	39.6	38.734	346	9.947E-256	0.8511	0.93484	71.683	12	891790000	456480000	435310000
P97384	Annexin A11;Annexin	Anxa11	9	9	9	22.5	22.5	22.5	54.079	503	4.307E-213	0.98043	0.94894	39.159	11	1611100000	891530000	719610000
P07356	Annexin A2;Annexin	Anxa2	15	15	15	46.9	46.9	46.9	38.676	339	0	1.0116	1.0398	44.521	23	2579600000	1358800000	1220800000
O35639	Annexin A3	Anxa3	9	9	9	25.1	25.1	25.1	36.384	323	3.9117E-39	0.67795	0.81609	15.237	8	714430000	432130000	282300000
P97429	Annexin A4;Annexin	Anxa4	12	11	11	38.9	36.7	36.7	35.915	319	1.536E-111	1.0222	0.96044	58.731	12	903010000	464150000	438860000
P48036	Annexin A5	Anxa5	12	12	12	44.8	44.8	44.8	35.752	319	0	0.64236	0.64056	66.622	33	9464000000	5840600000	3623400000
Q07076	Annexin A7	Anxa7	6	6	6	14.3	14.3	14.3	49.925	463	8.3006E-81	0.90875	0.96297	97.22	7	1208200000	624890000	583360000
F8WIT2	Annexin;Annexin A6	Anxa6	25	25	24	44.1	44.1	44.1	75.288	667	0	0.61595	0.59407	83.777	45	9416500000	6045200000	3371200000
Q6PB70	Anoctamin-8	Ano8	2	2	2	2.3	2.3	2.3	119.1	1060	0.0031685	0.8397	0.89252	93.626	2	159560000	81769000	77790000
P32261	Antithrombin-III	Serpinc1	13	13	13	32.3	32.3	32.3	52.003	465	5.517E-190	0.43915	0.48067	80.49	16	4958000000	3102500000	1855500000
O35643	AP-1 complex subunit beta-1	Ap1b1	10	10	6	12.6	12.6	8	103.93	943	3.6707E-74	0.92389	1.1168	78.713	10	634150000	347980000	286170000
Q8CBB7	AP-1 complex subunit gamma-1	Ap1g1	3	3	3	5.6	5.6	5.6	91.721	825	3.3337E-08	1.2498	1.3163	19.492	3	256810000	81713000	175100000
P35585	AP-1 complex subunit mu-1	Ap1m1	2	2	2	7.1	7.1	7.1	48.542	423	7.7784E-08	1.116	0.73173	81.464	2	107620000	45736000	61883000
P17427	AP-2 complex subunit alpha-2	Ap2a2	5	5	4	6.5	6.5	4.6	104.02	938	8.1646E-18	1.8926	1.7045	77.94	5	400700000	102410000	298290000
H3BIY9	AP-2 complex subunit beta	Ap2b1	9	5	5	11.1	6.5	6.5	104.83	942	1.1219E-56	1.0169	0.99104	41.128	5	294540000	140050000	154490000
P84091	AP-2 complex subunit mu	Ap2m1	4	4	4	12.2	12.2	12.2	49.654	435	9.9743E-14	1.4748	1.3539	49.086	4	196760000	78508000	118250000
Q3UHJ0	AP2-associated protein kinase 1	Aak1	5	5	5	9.5	9.5	9.5	103.35	959	3.3117E-19	0.85231	0.77683	31.048	7	218650000	126030000	92618000
Q9Z1T1	AP-3 complex subunit beta-1	Ap3b1	5	5	5	5.4	5.4	5.4	122.74	1105	9.2907E-07	0.89787	0.92803	23.919	3	187100000	113220000	73876000
O54774	AP-3 complex subunit delta-1	Ap3d1	2	2	2	3.6	3.6	3.6	135.08	1199	4.097E-10	2.5626	2.3702	57.206	3	137970000	41215000	96755000
Q00623	Apolipoprotein A-I;Truncated apolipoprotein A-I	Apoa1	8	8	8	26.5	26.5	26.5	30.615	264	3.1856E-47	0.44512	0.46543	22.634	10	5476900000	3611700000	1865200000
P06728	Apolipoprotein A-IV	Apoa4	10	10	10	37.5	37.5	37.5	45.029	395	8.7734E-55	0.47045	0.45954	79.366	8	560670000	355430000	205240000
P08226	Apolipoprotein E	Apoe	2	2	2	8.4	8.4	8.4	35.866	311	1.1097E-19	0.72956	0.72915	30.655	2	64670000	35662000	29008000
Q9DCZ4	Apolipoprotein O	Apoo	2	2	2	8.5	8.5	8.5	24.136	212	2.7352E-10	3.2767	4.0149	36.628	3	210530000	65440000	145090000
Q78IK4	Apolipoprotein O-like	Apool	6	6	6	32.1	32.1	32.1	29.26	265	1.357E-65	1.6606	1.1701	59.936	6	341770000	142490000	199280000
O35841	Apoptosis inhibitor 5	Api5	2	2	2	5.2	5.2	5.2	56.784	504	8.9556E-05	0.56748	0.54873	21.573	2	695460000	449240000	246230000
Q9EPB4	Apoptosis-associated speck-like protein containing a CARD	Pycard	6	6	6	46.1	46.1	46.1	21.458	193	5.2722E-81	0.34371	0.3389	39.65	8	761510000	569940000	191570000
Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial	Aifm1	8	8	8	20.3	20.3	20.3	66.765	612	1.6018E-64	1.4334	1.3282	152.1	12	2204900000	1365100000	839760000
Q02013	Aquaporin-1	Aqp1	1	1	1	7.4	7.4	7.4	28.793	269	7.474E-167	1.1039	1.2274	27.146	3	208160000	108900000	99254000
Q8K2K6	Arf-GAP domain and FG repeat-containing protein 1	Agfg1	4	4	4	11.8	11.8	11.8	58.042	561	4.3707E-45	0.79809	0.69278	21.709	5	286150000	175840000	110300000
Q9D0I9	Arginine--tRNA ligase, cytoplasmic	Rars	6	6	6	12.6	12.6	12.6	75.673	660	5.0335E-22	1.4713	1.6227	53.337	8	571350000	237620000	333730000
Q91YI0	Argininosuccinate lyase	Asl	5	5	5	12.9	12.9	12.9	51.739	464	1.2357E-07	1.5215	1.5841	11.158	3	126330000	51310000	75022000
Q91WU5	Arsenite methyltransferase	As3mt	8	8	8	28.5	28.5	28.5	41.793	376	5.666E-91	0.4198	0.43106	57.404	10	2012400000	1331100000	681370000
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	Nars	4	4	4	7.5	7.5	7.5	64.279	559	1.7588E-09	1.4228	1.3711	22.49	4	308760000	139950000	168820000
P05201	Aspartate aminotransferase, cytoplasmic	Got1	17	17	17	58.8	58.8	58.8	46.247	413	0	0.94217	1.0154	29.478	80	3.8281E+10	1.8596E+10	1.9685E+10
P05202	Aspartate aminotransferase, mitochondrial	Got2	17	17	17	47.7	47.7	47.7	47.411	430	5.553E-251	1.2723	1.3521	36.518	46	2.8914E+10	1.3196E+10	1.5718E+10
Q922B2	Aspartate--tRNA ligase, cytoplasmic	Dars	8	8	8	19.8	19.8	19.8	57.147	501	4.1483E-66	1.1512	1.1817	141.55	9	1188000000	740740000	447230000
Q8BIP0	Aspartate--tRNA ligase, mitochondrial	Dars2	2	2	2	2.9	2.9	2.9	74.101	653	0.00041476	0.50204	0.33679	53.885	2	54381000	35668000	18713000
Q91XE4	Aspartoacylase-2	Acy3	6	6	6	34.6	34.6	34.6	35.286	318	8.492E-162	1.0291	0.9998	28.642	8	903960000	511140000	392820000
Q9Z2W0	Aspartyl aminopeptidase	Dnpep	8	8	8	20.3	20.3	20.3	52.206	473	8.7251E-32	1.2746	1.1015	95.322	5	445370000	164370000	281000000
Q8BSY0	Aspartyl/asparaginyl beta-hydroxylase	Asph	5	5	5	8.4	8.4	8.4	83.041	741	2.0748E-27	0.91838	0.80326	73.304	4	159420000	78748000	80675000
Q99MQ4	Asporin	Aspn	3	3	3	11.3	11.3	11.3	42.572	373	0.0011306	1.4655	1.2311	20.611	3	285260000	122530000	162730000
Q62048	Astrocytic phosphoprotein PEA-15	Pea15	3	3	3	22.3	22.3	22.3	15.054	130	4.6221E-12	0.46007	0.37934	68.082	6	181590000	93473000	88117000
P28658	Ataxin-10	Atxn10	3	3	3	7.2	7.2	7.2	53.706	475	7.0827E-20	0.27983	0.2872	152.57	2	57663000	43013000	14650000
E9QM77	Ataxin-2	Atxn2	5	5	5	4.4	4.4	4.4	136.46	1286	1.3896E-34	1.0711	0.88607	33.326	3	38387000	22223000	16165000
Q7TQH0	Ataxin-2-like protein	Atxn2l	2	2	2	1.9	1.9	1.9	110.65	1049	0.017622	0.61851	0.58325	18.874	2	29638000	17435000	12203000
H3BLL2	ATP synthase mitochondrial F1 complex assembly factor 1	Atpaf1	7	7	7	26.7	26.7	26.7	38.796	348	4.985E-118	0.52883	0.53575	113.27	6	1139000000	748660000	390340000
Q91YY4	ATP synthase mitochondrial F1 complex assembly factor 2	Atpaf2	6	6	6	23.5	23.5	23.5	33.289	289	1.2723E-20	1.3814	1.4149	99.371	4	142760000	55737000	87021000
Q03265	ATP synthase subunit alpha, mitochondrial;ATP synthase subunit alpha	Atp5a1	22	22	22	49.7	49.7	49.7	59.752	553	0	1.1136	1.0909	87.974	115	5.577E+10	2.4143E+10	3.1627E+10
Q9CQQ7	ATP synthase subunit b, mitochondrial	Atp5f1	3	3	3	14.8	14.8	14.8	28.948	256	6.0865E-20	1.5333	1.4853	20.98	4	1040700000	397780000	642880000
P56480	ATP synthase subunit beta, mitochondrial	Atp5b	25	25	25	64.8	64.8	64.8	56.3	529	0	0.58293	0.59682	79.311	217	2.6889E+11	1.6915E+11	9.9733E+10
Q9DCX2	ATP synthase subunit d, mitochondrial	Atp5h	9	9	9	70.8	70.8	70.8	18.749	161	3.037E-136	0.7631	0.80814	78.404	22	7790300000	4521900000	3268400000
Q9D3D9	ATP synthase subunit delta, mitochondrial	Atp5d	1	1	1	8.3	8.3	8.3	17.6	168	1.7958E-49	0.52725	0.54135	15.445	6	3979700000	2495000000	1484700000
Q06185	ATP synthase subunit e, mitochondrial	Atp5i	2	2	2	33.8	33.8	33.8	8.2355	71	2.6927E-07	0.74239	0.66126	57.931	3	374600000	199350000	175240000
P56135	ATP synthase subunit f, mitochondrial	Atp5j2	1	1	1	13.6	13.6	13.6	10.344	88	3.1379E-05	1.7736	1.8573	22.586	2	62543000	23308000	39235000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9CPQ8	ATP synthase subunit g, mitochondrial	Atp5l	3	3	3	28.2	28.2	28.2	11.424	103	1.8986E-05	1.7502	2.0895	47.138	5	3566000000	1213400000	2352600000
Q91VR2	ATP synthase subunit gamma, mitochondrial	Atp5c1	6	6	6	16.8	16.8	16.8	32.886	298	1.5121E-23	1.4344	1.4551	68.811	5	4903400000	1955800000	2947600000
Q9DB20	ATP synthase subunit O, mitochondrial	Atp5o	8	8	8	45.1	45.1	45.1	23.363	213	3.657E-224	1.7357	1.4853	94.866	27	5778400000	1985900000	3792500000
P97450	ATP synthase-coupling factor 6, mitochondrial	Atp5j	6	6	6	44.4	44.4	44.4	12.496	108	0	0.72442	0.69359	29.374	16	2192300000	1179500000	1012800000
O54984	ATPase Asna1	Asna1	2	2	2	8	8	8	38.822	348	1.0934E-09	0.98088	1.3138	2.0284	2	61117000	31514000	29603000
Q9D5T0	ATPase family AAA domain-containing protein 1	Atad1	2	2	2	4.7	4.7	4.7	40.744	361	2.1892E-05	1.2564	1.0007	20.345	2	188410000	89433000	98972000
P61222	ATP-binding cassette sub-family E member 1	Abce1	5	5	5	8.3	8.3	8.3	67.314	599	4.2744E-14	0.94149	0.6927	63.389	3	172710000	90389000	82326000
Q6P542	ATP-binding cassette sub-family F member 1	Abcf1	5	5	5	9.9	9.9	9.9	94.944	837	4.4141E-43	1.177	1.2379	44.784	5	94952000	43919000	51033000
Q3V117	ATP-citrate synthase	Acly	4	4	4	4.9	4.9	4.9	120.79	1101	1.0859E-12	2.0032	1.559	64.271	4	188380000	65272000	123110000
K3W4M4	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	Carkd	9	9	9	39.5	39.5	39.5	38.911	365	0	1.067	1.353	72.399	9	973940000	473760000	500180000
Q91VR5	ATP-dependent RNA helicase DDX1	Ddx1	5	5	5	7.7	7.7	7.7	82.499	740	2.6594E-12	2.1879	2.0838	64.284	5	142510000	48578000	93929000
Q61655	ATP-dependent RNA helicase DDX19A	Ddx19a	4	4	4	9.4	9.4	9.4	53.932	478	1.1425E-28	0.83069	0.86199	22.131	4	172360000	96725000	75640000
Q62095	ATP-dependent RNA helicase DDX3Y	Ddx3y	4	4	4	8.4	8.4	8.4	73.427	658	2.0914E-10	2.5599	1.6708	32.099	2	53692000	16006000	37686000
Q80YD1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	Supv3l1	6	6	6	10	10	10	87.004	779	5.6953E-15	0.6411	0.54025	78.536	4	147060000	98250000	48811000
P18293	Atrial natriuretic peptide receptor 1	Npr1	1	1	1	1.2	1.2	1.2	119.11	1057	0.06424	0.72439	0.7192	23.935	2	314410000	175870000	138540000
Q99J83	Autophagy protein 5	Atg5	4	4	4	15.6	15.6	15.6	32.402	275	1.1486E-23	0.82165	0.75466	16.225	4	119580000	65962000	53618000
Q91YN9	BAG family molecular chaperone regulator 2	Bag2	2	2	2	8.6	8.6	8.6	23.473	210	3.5714E-15	0.75863	0.39162	88.205	2	135480000	73901000	61579000
Q9JLV1	BAG family molecular chaperone regulator 3	Bag3	13	13	13	36.2	36.2	36.2	61.859	577	6.441E-190	0.81022	0.76559	53.593	24	2550000000	1377100000	1172900000
O70318	Band 4.1-like protein 2	Epb41l2	14	14	14	20.3	20.3	20.3	109.94	988	1.1826E-55	0.65597	0.61202	67.124	13	331210000	198670000	132530000
Q9WV92	Band 4.1-like protein 3	Epb41l3	2	2	2	3.6	3.6	3.6	103.34	929	2.6846E-11	0.32419	0.34009	36.929	2	37354000	29648000	7706400
Q9R069	Basal cell adhesion molecule	Bcam	4	4	4	11.3	11.3	11.3	67.669	622	6.139E-60	0.69926	0.95391	225	5	5314500000	154800000	5159700000
E9PZ16	Basement membrane-specific heparan sulfate proteoglycan core protein	Hspg2	45	45	45	19.7	19.7	19.7	469.78	4383	0	2.6109	2.6833	63.501	52	4636500000	1375400000	3261100000
Q9CQC6	Basic leucine zipper and W2 domain-containing protein 1	Bzw1	4	4	2	6.7	6.7	3.3	48.043	419	4.0916E-07	0.095511	0.076337	91.14	4	105420000	83324000	22095000
Q91VK1	Basic leucine zipper and W2 domain-containing protein 2	Bzw2	4	2	2	7.2	3.8	3.8	48.063	419	1.1696E-06	0.58176	0.65297	1.8658	2	182680000	121060000	61620000
P18572	Basigin	Bsg	6	6	6	20.3	20.3	20.3	42.444	389	1.0282E-75	0.65141	0.66702	36.811	12	1566200000	933330000	632890000
P59017	Bcl-2-like protein 13	Bcl2l13	6	6	6	20	20	20	46.719	434	6.1199E-89	0.81381	0.8712	38.642	10	1406400000	804950000	601440000
Q01339	Beta-2-glycoprotein 1	Apoh	6	6	6	22.6	22.6	22.6	38.618	345	2.0187E-19	0.68513	0.75206	31.2	5	195890000	119740000	76145000
J3QNU6	Beta-arrestin-1	Arrb1	3	3	3	7.9	7.9	7.9	47.106	419	2.664E-97	0.51144	0.37893	3.7569	2	79684000	53279000	26405000
P21550	Beta-enolase;Enolase	Eno3	21	21	18	50.2	50.2	44.2	47.024	434	0	0.65184	0.66696	94.488	73	4.7141E+10	2.774E+10	1.9402E+10
P23780	Beta-galactosidase	Glb1	5	5	5	9.3	9.3	9.3	73.12	647	1.2914E-10	3.4137	3.7072	71.775	4	160400000	48511000	111890000
A8DUK4	Beta-globin	Hbb-b1	14	14	5	89.8	89.8	24.5	15.748	147	0	0.34792	0.33343	73.961	299	5.8606E+11	4.3725E+11	1.4881E+11
P12265	Beta-glucuronidase	Gusb	2	2	2	3.2	3.2	3.2	74.194	648	0.005177	1.9511	2.1462	37.254	2	63652000	31137000	32516000
P29416	Beta-hexosaminidase subunit alpha	Hexa	3	3	3	6.6	6.6	6.6	60.612	528	1.0871E-07	2.2331	2.5073	21.145	2	157070000	54045000	103020000
P20060	Beta-hexosaminidase subunit beta	Hexb	3	3	3	5.4	5.4	5.4	61.115	536	6.5462E-06	2.2089	2.4436	72.136	3	33668000	13526000	20143000
Q99KR3	Beta-lactamase-like protein 2	Lactb2	5	5	5	22.2	22.2	22.2	32.754	288	1.4934E-96	0.7502	0.83524	22.109	6	555260000	319500000	235760000
Q9ES46	Beta-parvin	Parvb	6	6	6	26.8	26.8	26.8	41.669	365	7.5823E-52	0.422	0.37339	60.477	7	358630000	241130000	117500000
P82349	Beta-sarcoglycan	Sgcb	2	2	2	12.2	12.2	12.2	34.872	320	1.5733E-20	1.2453	1.304	17.19	3	137170000	63312000	73863000
Q8VBT1	Beta-taxilin	Txlnb	10	10	10	20.7	20.7	20.7	77.206	685	2.641E-168	0.6057	0.61454	61.394	16	1592000000	980060000	611900000
Q8VC30	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)	Dak	2	2	2	5.2	5.2	5.2	59.69	578	4.0224E-12	0.65274	0.63314	38.393	3	144710000	90635000	54078000
Q9DBL7	Bifunctional coenzyme A synthase	Coasy	2	2	2	5.7	5.7	5.7	62.022	563	1.1918E-10	0.91618	0.73666	84.946	2	100330000	53742000	46583000
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	Eprs	15	15	15	15.7	15.7	15.7	170.08	1512	2.601E-215	1.9308	2.1875	61.334	16	1431500000	476860000	954600000
Q9EQQ9	Bifunctional protein NCOAT	Mgea5	3	3	3	6	6	6	103.16	916	6.9911E-13	0.98877	0.7928	44.57	4	68092000	30835000	37257000
Q9CWJ9	Bifunctional purine biosynthesis protein PURH	Atic	12	12	12	28.5	28.5	28.5	64.217	592	2.711E-101	0.9186	0.84846	62.049	16	1736000000	963950000	772050000
Q9CY64	Biliverdin reductase A	Blvra	5	5	5	21	21	21	33.524	295	1.3518E-19	0.965	0.99147	67.311	6	622160000	315360000	306800000
Q8CIF4	Biotinidase	Btd	2	2	2	4.4	4.4	4.4	58.154	520	5.5747E-07	0.63978	0.7199	38.095	4	84652000	55945000	28707000
P56380	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	Nudt2	4	4	4	36.1	36.1	36.1	16.989	147	3.431E-13	1.3224	1.4408	153.88	5	666150000	348370000	317770000
P15327	Bisphosphoglycerate mutase;Phosphoglycerate mutase	Bpgm	9	9	9	37.8	37.8	37.8	29.978	259	1.161E-123	0.67938	0.66087	60.815	10	1262300000	654420000	607890000
Q8R016	Bleomycin hydrolase	Blmh	4	4	4	9.9	9.9	9.9	52.511	455	9.5256E-12	0.98105	0.78319	83.414	5	389560000	196820000	192740000
Q9D8S9	BolA-like protein 1	Bola1	3	3	3	37.2	37.2	37.2	14.379	137	7.473E-16	0.90681	0.67981	67.915	3	1061900000	487410000	574500000
E9PX89	BolA-like protein 3	Bola3	3	3	3	27.2	27.2	27.2	15.231	136	8.463E-147	0.48306	0.52853	18.426	4	240450000	163280000	77171000
Q91XV3	Brain acid soluble protein 1	Basp1	3	3	3	26.1	26.1	26.1	22.086	226	1.8048E-29	0.60185	0.55896	15.917	5	64469000	39094000	25375000
Q9D023	Brain protein 44	Brp44	4	4	4	25.2	25.2	25.2	14.286	127	1.7419E-05	1.2512	0.80911	100.52	6	497580000	215180000	282410000
O35855	Branched-chain-amino-acid aminotransferase, mitochondrial	Bcat2	10	10	10	32.8	32.8	32.8	44.127	393	2.238E-127	1.084	1.0181	48.033	16	4081900000	2051500000	2030400000
S4R270	Bridging integrator 2	Bin2	3	3	3	9.3	9.3	9.3	54.766	505	8.5125E-29	0.33712	0.2972	38.905	4	117250000	86033000	31221000
Q8K2Q7	BRO1 domain-containing protein BROX	Brox	1	1	1	4.6	4.6	4.6	46.201	411	3.7124E-47	2.0184	2.1057	54.755	2	13803000	5173600	8629400
Q6WVG3	BTB/POZ domain-containing protein KCTD12	Kctd12	8	8	8	31.5	31.5	31.5	35.892	327	1.3338E-47	0.60027	0.71909	44.952	7	423650000	262880000	160770000
Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	Mthfd1	5	5	5	7.3	7.3	7.3	101.2	935	2.6728E-37	0.91679	1.0429	39.212	3	127190000	67530000	59665000
P08607	C4b-binding protein	C4bpa	4	4	4	8.3	8.3	8.3	51.523	469	6.2481E-06	0.39567	0.4367	72.959	4	105200000	74351000	30851000
Q9WTR5	Cadherin-13	Cdh13	10	10	10	19.9	19.9	19.9	78.185	714	4.218E-109	0.42288	0.47751	23.773	15	2647900000	1841500000	806370000
P15116	Cadherin-2	Cdh2	3	3	3	8.1	8.1	8.1	99.795	906	1.002E-91	1.2535	1.1298	45.002	7	289690000	179250000	110440000
Q63810	Calcineurin subunit B type 1	Ppp3r1	2	2	2	20	20	20	19.3	170	1.0431E-05	0.40794	0.45167	44.039	2	51905000	37518000	14387000
Q8BFS6	Calcineurin-like phosphoesterase domain-containing protein 1	Cpped1	3	3	3	13.8	13.8	13.8	35.247	312	2.0585E-20	0.53762	0.39216	115.07	3	370450000	232760000	137690000
Q91YS8	Calcium/calmodulin-dependent protein kinase type 1	Camk1	8	8	8	37.4	37.4	37.4	41.624	374	2.089E-128	0.6967	0.75048	36.795	11	646280000	364180000	282090000
Q5SVJ0	Calcium/calmodulin-dependent protein kinase type II subunit beta	Camk2b	4	2	2	10.8	6.2	6.2	72.902	666	2.6859E-47	0.78722	0.75256	68.813	2	43742000	20843000	22899000
E9Q1T1	Calcium/calmodulin-dependent protein kinase type II subunit delta	Camk2d	4	4	2	13.5	13.5	7.7	60.004	533	1.0533E-57	1.379	1.5539	25.803	8	853060000	371020000	482040000
Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1	Slc25a12	12	12	12	29.4	29.4	29.4	74.569	677	2.368E-232	1.9569	2.1643	53.127	22	3598700000	1242400000	2356400000
Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	Slc25a13	11	11	11	24.6	24.6	24.6	74.466	676	1.9022E-94	2.2613	2.5143	67.816	15	1555500000	501070000	1054400000
Q06138	Calcium-binding protein 39	Cab39	8	8	8	21.1	21.1	21.1	39.842	341	2.9288E-14	0.62566	0.57761	63.189	8	493620000	250840000	242780000
J3QPI4	Calcium-regulated heat stable protein 1	Carhsp1	2	2	2	18.2	18.2	18.2	16.048	148	8.8348E-09	0.41817	0.45271	50.55	2	215210000	149830000	65382000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9CXW3	Calcyclin-binding protein	Cacybp	2	2	2	13.1	13.1	13.1	26.51	229	0.0018827	0.78613	0.84203	65.416	2	163860000	100670000	63189000
Q3UKW2	Calmodulin	Calm1	4	4	4	32.5	32.5	32.5	21.56	197	0	0.4685	0.46843	18.616	11	3193300000	2244600000	948680000
P35564	Calnexin	Canx	5	5	5	12.2	12.2	12.2	67.277	591	1.1596E-61	1.6475	1.5451	19.97	6	487570000	167410000	320160000
O88456	Calpain small subunit 1	Capns1	3	3	3	16.4	16.4	16.4	28.463	269	1.489E-125	0.7145	0.67796	14.634	4	71653000	39669000	31985000
O35350	Calpain-1 catalytic subunit	Capn1	12	12	12	22.7	22.7	22.7	82.105	713	5.6885E-38	1.4675	1.51	40	13	626970000	278200000	348760000
O08529	Calpain-2 catalytic subunit	Capn2	18	18	18	34.7	34.7	34.7	79.871	700	2.769E-103	1.2209	1.1645	59.041	17	1366000000	652350000	713670000
P51125	Calpastatin	Cast	13	13	13	27	27	27	84.921	788	0	0.49276	0.50602	32.724	17	1773300000	1208900000	564420000
Q08091	Calponin-1	Cnn1	3	3	3	11.1	11.1	11.1	33.355	297	2.2715E-25	0.36262	0.38571	62.989	4	321690000	243920000	77772000
Q08093	Calponin-2	Cnn2	3	3	3	13.4	13.4	13.4	33.155	305	3.5381E-86	0.48516	0.43444	49.661	4	220940000	154670000	66271000
Q9DAW9	Calponin-3	Cnn3	4	4	4	13	13	13	36.428	330	2.8136E-33	0.58115	0.6622	50.084	4	211770000	112410000	99364000
P14211	Calreticulin	Calr	7	7	7	23.6	23.6	23.6	47.994	416	1.932E-177	0.67508	0.69126	22.234	14	3034200000	1885500000	1148600000
F6QYE1	Calsequestrin-2;Calsequestrin	Casq2	6	6	6	15.3	15.3	15.3	48.435	418	1.335E-142	1.1634	1.2523	45.123	7	671850000	301040000	370800000
O35887	Calumenin	Calu	5	5	5	21.9	21.9	21.9	37.063	315	1.7584E-45	0.72951	0.40081	74.975	3	257260000	142640000	114620000
P05132	cAMP-dependent protein kinase catalytic subunit alpha	Prkaca	4	4	4	11.4	11.4	11.4	40.57	351	1.435E-09	1.4433	1.6022	61.759	5	1372000000	598780000	773230000
P63248	cAMP-dependent protein kinase inhibitor alpha	Pkia	1	1	1	22.4	22.4	22.4	7.9604	76	9.8005E-10	0.47003	0.41537	10.278	2	593100000	422160000	170950000
Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit	Prkar1a	7	7	7	25.5	25.5	25.5	43.185	381	1.446E-125	1.2454	1.1909	44.578	10	5631800000	2641100000	2990700000
Q8K1M3	cAMP-dependent protein kinase type II-alpha regulatory subunit	Prkar2a	8	8	8	30.1	30.1	30.1	45.589	402	3.732E-190	1.0762	0.9579	37.276	13	972120000	453050000	519070000
B2RX12	Canalicular multispecific organic anion transporter 2	Abcc3	2	2	2	1.2	1.2	1.2	169.12	1523	0.018491	0.92379	0.85631	106.94	2	184230000	79025000	105200000
F8WIA1	CAP-Gly domain-containing linker protein 1	Clip1	29	29	25	25.7	25.7	22.5	161.23	1437	1.601E-259	0.47054	0.3854	71.006	26	2534000000	1484000000	1050000000
Q60865	Caprin-1	Caprin1	3	3	3	5.8	5.8	5.8	78.168	707	9.2649E-08	0.8744	0.65757	94.277	3	197410000	105890000	91529000
Q3UZA1	CapZ-interacting protein	Rcsd1	4	4	4	17.2	17.2	17.2	44.114	412	2.5498E-30	0.38463	0.38913	126.37	4	541660000	181160000	360500000
P13634	Carbonic anhydrase 1	Ca1	5	5	5	29.1	29.1	29.1	28.33	261	7.516E-101	0.33338	0.38601	84.178	8	1591800000	1168300000	423480000
P00920	Carbonic anhydrase 2	Ca2	8	8	8	41.9	41.9	41.9	29.032	260	6.79E-163	0.52372	0.54715	47.451	16	4728100000	3003000000	1725100000
P16015	Carbonic anhydrase 3	Ca3	7	7	7	41.2	41.2	41.2	29.366	260	3.871E-115	0.64624	0.76882	61.797	9	1005800000	567870000	437950000
P48758	Carbonyl reductase [NADPH] 1	Cbr1	5	5	5	29.2	29.2	29.2	30.641	277	9.372E-155	0.99204	1.3118	45.904	13	1529900000	767360000	762510000
P08074	Carbonyl reductase [NADPH] 2	Cbr2	2	2	2	12.3	12.3	12.3	25.958	244	3.4058E-33	1.1791	0.95981	44.425	4	152670000	71799000	80868000
Q91VT4	Carbonyl reductase family member 4	Cbr4	6	6	6	39.4	39.4	39.4	25.414	236	3.5817E-46	1.2543	1.2258	74.581	6	507910000	208600000	299320000
P23953	Carboxylesterase 1C	Ces1c	10	8	5	19.3	15.5	10.6	61.055	554	4.17E-111	0.39658	0.46544	73.056	9	1635300000	1302700000	332690000
Q8VCT4	Carboxylesterase 1D	Ces1d	10	10	8	23.2	23.2	19.5	61.787	565	3.286E-154	0.95286	0.86833	79.191	17	3761900000	1928500000	1833400000
Q8R1G2	Carboxymethylenebutenolidase homolog	Cmbl	5	5	5	20	20	20	27.902	245	3.5382E-21	1.0943	0.96955	71.716	5	780350000	383480000	396870000
Q9JHH6	Carboxypeptidase B2	Cpb2	2	2	2	7.1	7.1	7.1	48.87	422	0.0011231	0.38727	0.35991	22.828	2	77382000	54307000	23075000
Q9DBB9	Carboxypeptidase N subunit 2	Cpn2	3	3	3	7.3	7.3	7.3	60.478	547	9.0077E-51	0.39369	0.36745	96.085	4	135570000	82282000	53289000
Q9WVJ3	Carboxypeptidase Q	Cpq	2	2	2	7.7	7.7	7.7	51.813	470	2.7656E-06	0.49796	0.5031	26.104	3	317110000	196010000	121090000
Q80ZM8	Cardiolipin synthase	Crls1	1	1	1	6.6	6.6	6.6	32.502	303	0.00065679	1.2261	1.2051	15.431	2	10558000	4174000	6383900
E9QLJ0	Cardiomyopathy-associated protein 5	Cmya5	19	19	19	9.4	9.4	9.4	405.57	3676	4.056E-171	0.88465	0.96095	83.764	24	1953400000	1164800000	788650000
P47934	Carnitine O-acetyltransferase	Crat	13	13	13	22.7	22.7	22.7	70.839	626	1.41E-236	1.7204	1.7069	95.146	16	1549300000	596480000	952770000
Q924X2	Carnitine O-palmitoyltransferase 1, muscle isoform	Cpt1b	10	10	9	13.2	13.2	11.9	88.216	772	3.2536E-26	2.4006	2.2625	79.503	12	3531000000	766600000	2764400000
P52825	Carnitine O-palmitoyltransferase 2, mitochondrial	Cpt2	9	9	9	18.7	18.7	18.7	73.98	658	0	2.0268	2.2255	63.254	17	4550700000	1559100000	2991600000
Q80UY1	Carnosine N-methyltransferase	Carnmt1	4	4	4	11	11	11	46.338	400	3.3414E-10	0.99628	0.93132	55.42	4	107330000	46510000	60819000
G3UZX4	Casein kinase II subunit beta	Csnk2b	1	1	1	4.3	4.3	4.3	29.207	257	0.00015182	1.159	1.2446	1.7459	2	51403000	25254000	26149000
E9PY58	Caseinolytic peptidase B protein homolog	Clpb	4	4	4	7.8	7.8	7.8	79.509	707	1.2336E-14	1.1753	1.3116	21.7	4	154460000	71156000	83299000
P24270	Catalase	Cat	10	10	10	26.9	26.9	26.9	59.795	527	1.557E-297	1.1954	1.0306	58.87	14	4509100000	1042700000	3466300000
O88587	Catechol O-methyltransferase	Comt	5	5	5	24.9	24.9	24.9	29.486	265	9.4264E-13	0.28962	0.32952	215.3	4	532610000	447940000	84672000
P26231	Catenin alpha-1	Ctnna1	7	7	5	10.8	10.8	7.9	100.11	906	2.351E-100	0.48957	0.47509	27.511	6	293150000	194540000	98615000
P10605	Cathepsin B;Cathepsin B light chain;Cathepsin B heavy chain	Ctsb	5	5	5	21.5	21.5	21.5	37.279	339	1.726E-201	1.5734	1.8016	12.522	5	697810000	258850000	438960000
P18242	Cathepsin D	Ctsd	6	6	6	18.8	18.8	18.8	44.953	410	3.3695E-63	1.4315	1.5559	64.507	8	729510000	297840000	431670000
Q9WUU7	Cathepsin Z	Ctsz	4	4	4	14.1	14.1	14.1	33.996	306	1.6656E-25	5.343	5.5726	83.748	3	161680000	28945000	132740000
Q07113	Cation-independent mannose-6-phosphate receptor	Igf2r	4	4	4	1.9	1.9	1.9	273.81	2483	0.00022427	0.6655	0.70182	127.78	2	405600000	262800000	142800000
P49817	Caveolin-1;Caveolin	Cav1	2	2	2	19.7	19.7	19.7	20.538	178	1.8457E-15	0.7146	0.76198	30.512	4	703290000	416840000	286450000
Q8K1J6	CCA tRNA nucleotidyltransferase 1, mitochondrial	Trnt1	3	3	3	6.9	6.9	6.9	49.895	434	5.0355E-06	0.62817	0.60134	50.343	2	84762000	54749000	30013000
Q9JLQ0	CD2-associated protein	Cd2ap	4	4	4	7.5	7.5	7.5	70.449	637	3.5511E-10	0.36751	0.33055	58.605	4	91494000	66902000	24592000
Q8CJ53	Cdc42-interacting protein 4	Trip10	3	3	3	5.6	5.6	5.6	68.489	603	5.1709E-05	0.93671	1.071	1.4537	2	42638000	23088000	19550000
Q8VDP4	Cell cycle and apoptosis regulator protein 2	Ccar2	2	2	2	3.9	3.9	3.9	103	922	0.0022305	0.44445	0.40396	87.223	2	145020000	120300000	24718000
P60766	Cell division control protein 42 homolog	Cdc42	3	2	2	18.8	13.1	13.1	21.258	191	4.494E-13	0.82444	0.91142	51.423	6	321000000	264120000	56873000
Q8R2Y2	Cell surface glycoprotein MUC18	Mcam	5	5	5	11.7	11.7	11.7	71.545	648	1.0069E-21	0.59199	0.67803	15.553	5	499580000	304370000	195210000
P53996	Cellular nucleic acid-binding protein	Cnbp	3	3	3	23.6	23.6	23.6	19.592	178	3.8758E-42	0.85671	0.79609	72.718	4	905650000	374240000	531410000
E9PZD8	Ceruloplasmin	Cp	18	18	18	23	23	23	124.21	1086	0	0.54634	0.58425	41.604	21	2486000000	1621900000	864080000
Q60936	Chaperone activity of bc1 complex-like, mitochondrial	Adck3	6	6	6	13.5	13.5	13.5	71.742	645	5.303E-58	1.0402	1.1108	49.446	9	904010000	501830000	402190000
Q99LU0	Charged multivesicular body protein 1b-1	Chmp1b1	1	1	1	4	4	4	22.124	199	0.04735	0.4909	0.54081	39.748	2	139060000	89086000	49977000
Q9CQ10	Charged multivesicular body protein 3	Chmp3	3	3	3	12.9	12.9	12.9	25.219	224	2.2337E-06	0.34561	0.20589	33.359	2	105840000	74819000	31023000
Q9D8B3	Charged multivesicular body protein 4b	Chmp4b	3	3	3	21.9	21.9	21.9	24.936	224	6.878E-110	0.33904	0.40041	19.539	4	156100000	113630000	42473000
O35744	Chitinase-3-like protein 3;Chitinase-3-like protein 4	Chi3l3	3	3	3	14.1	14.1	14.1	44.458	398	4.7831E-10	0.4415	0.48631	91.604	4	189430000	122600000	66830000
Q9Z1Q5	Chloride intracellular channel protein 1	Clic1	5	5	5	30.7	30.7	30.7	27.013	241	4.6213E-84	0.85494	0.98546	34.887	6	198500000	101200000	97298000
Q9QYB1	Chloride intracellular channel protein 4	Clic4	10	10	10	49.8	49.8	49.8	28.729	253	0	0.58874	0.65758	71.717	13	1603200000	928700000	674460000
Q8BXK9	Chloride intracellular channel protein 5	Clic5	3	3	3	20.7	20.7	20.7	28.287	251	8.9367E-22	1.3604	1.0846	71.734	5	349700000	157260000	192440000
Q8VHY0	Chondroitin sulfate proteoglycan 4	Cspg4	3	3	3	2.3	2.3	2.3	252.31	2327	4.4235E-17	0.59882	0.62814	26.473	4	361670000	234620000	127050000
P23198	Chromobox protein homolog 3	Cbx3	3	3	3	14.2	14.2	14.2	20.855	183	5.5342E-15	0.34797	0.36192	3.6158	2	116560000	89280000	27281000
Q8R4N0	Citrate lyase subunit beta-like protein, mitochondrial	Clybl	14	14	14	41.7	41.7	41.7	37.548	338	2.107E-276	0.85092	0.73154	123.79	18	3715000000	1846800000	1868200000
Q9CZU6	Citrate synthase, mitochondrial	Cs	11	11	5	22	22	9.1	51.736	464	1.002E-147	1.391	1.4136	31.505	60	1.4926E+10	6457700000	8468500000
Q58A65	C-Jun-amino-terminal kinase-interacting protein 4	Spag9	13	13	2	15	15	1.9	146.22	1321	3.541E-183	0.77217	0.77255	27.816	14	394160000	215880000	178280000
Q5SXR6	Clathrin heavy chain 1	Cltc	17	17	17	16	16	16	191.98	1679	0	2.4822	2.6914	89.402	20	3275400000	1047400000	2228000000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q5SUH6	Clathrin interactor 1	Clint1	2	2	2	5.8	5.8	5.8	69.758	641	8.6604E-08	0.64177	0.67133	41.579	2	60817000	37838000	22978000
B1AWD9	Clathrin light chain A	Clta	2	2	2	11.7	11.7	11.7	27.061	248	2.342E-218	0.80841	0.82018	3.0108	3	185000000	106810000	78193000
Q6IRU5	Clathrin light chain B	Cltb	6	6	6	20.5	20.5	20.5	25.171	229	6.47E-12	0.69972	0.7253	21.509	6	615220000	369130000	246090000
H3BJW3	Cleavage and polyadenylation specificity factor subunit 6	Cpsf6	2	2	2	6.1	6.1	6.1	63.413	588	9.8142E-26	1.3368	1.4539	59.486	3	55041000	27119000	27922000
F7DCH5	CLIP-associating protein 2	Clasp2	3	3	2	4.2	4.2	2.8	142.85	1307	4.1935E-06	0.4975	0.48886	20.085	4	194660000	125640000	69024000
Q06890	Clusterin;Clusterin beta chain;Clusterin alpha chain	Clu	8	8	8	24.8	24.8	24.8	51.655	448	4.0663E-83	0.47036	0.42938	39.197	10	675380000	430790000	244580000
Q1ERP8	CMRF35-like molecule 9	Cd300lg	2	2	2	10	10	10	36.756	331	6.2843E-30	0.54699	0.64877	6.668	2	124730000	87598000	37133000
Q9EQS3	C-Myc-binding protein	Mycbp	2	2	2	30.1	30.1	30.1	11.97	103	1.0352E-10	0.72369	0.86799	21.076	3	1052000000	84278000	967730000
Q9CQI6	Coactosin-like protein	Cotl1	3	3	3	24.6	24.6	24.6	15.944	142	4.039E-180	0.57368	0.63717	46.642	2	129230000	82522000	46703000
Q3U3V1	Coagulation factor X	F10	1	1	1	3.2	3.2	3.2	55.255	493	7.6902E-05	0.75736	0.73928	11.026	2	84032000	41942000	42090000
Q8BH61	Coagulation factor XIII A chain	F13a1	4	4	4	6	6	6	83.206	732	4.4333E-08	0.64237	0.21664	29.046	2	122250000	71809000	50436000
Q9JIF7	Coatomer subunit beta	Copb1	2	2	2	3	3	3	107.06	953	1.9363E-07	1.515	1.4596	19.249	3	172510000	68831000	103680000
O89079	Coatomer subunit epsilon	Cope	2	2	2	11	11	11	34.567	308	1.3193E-21	1.177	1.1634	30.806	4	204200000	87158000	117040000
Q9QZE5	Coatomer subunit gamma-1	Copg1	2	2	2	4	4	4	97.512	874	7.8651E-06	1.3724	1.004	15.887	2	33589000	15173000	18416000
Q9D273	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	Mmab	4	4	4	23.6	23.6	23.6	26.273	237	3.1077E-15	0.73553	0.71464	32.603	5	291630000	177460000	114170000
F8WGL3	Cofilin-1	Cfl1	9	9	8	41.4	41.4	36.6	24.576	227	1.459E-142	0.49071	0.43527	51.872	13	2246600000	1385700000	860870000
P45591	Cofilin-2	Cfl2	7	6	6	55.4	48.8	48.8	18.709	166	1.623E-43	0.66835	0.63998	106.02	10	1621500000	978160000	643380000
E9Q2S9	Coiled-coil domain-containing protein 43	Ccdc43	3	3	3	18.5	18.5	18.5	25.035	222	1.435E-12	0.2802	0.29684	39.836	2	27428000	20377000	7050500
F8WJI3	Coiled-coil domain-containing protein 58	Ccdc58	2	2	2	14.9	14.9	14.9	15.601	134	0.00055586	0.11292	0.11234	181.8	2	72972000	64350000	8622500
B2RPU8	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	2410018M08Rik	4	4	4	6.2	6.2	6.2	84.266	756	1.046E-145	0.71765	0.78496	65.012	7	1318800000	758100000	560680000
Q9CRB9	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3	Chchd3	2	2	2	16.3	16.3	16.3	26.334	227	5.5951E-18	1.6841	1.4141	72.936	3	669900000	254120000	415780000
Q91YQ3	Cold shock domain-containing protein C2	Csdc2	2	2	2	13	13	13	16.853	154	0.00019969	0.34806	0.32589	68.962	2	51390000	38135000	13255000
Q91W50	Cold shock domain-containing protein E1	Csde1	11	11	11	16.5	16.5	16.5	88.79	798	3.815E-116	0.67962	0.77344	107.57	10	827390000	229570000	597820000
Q04857	Collagen alpha-1(VI) chain	Col6a1	5	5	5	5.6	5.6	5.6	108.49	1025	1.4566E-10	0.55762	0.66857	54.529	4	151230000	98685000	52546000
O35206	Collagen alpha-1(XV) chain;Endostatin	Col15a1	4	4	4	3.6	3.6	3.6	140.47	1367	1.2714E-27	1.3865	1.3275	32.437	5	402670000	164800000	237870000
Q02788	Collagen alpha-2(VI) chain	Col6a2	5	5	5	5.4	5.4	5.4	110.33	1034	9.099E-14	0.57407	0.57266	31.744	4	181490000	114650000	66837000
E9Q6A6	Collagen alpha-6(VI) chain	Col6a6	5	5	3	3.5	3.5	1.6	246.42	2265	6.6339E-53	0.98457	0.93631	101.82	4	551320000	86412000	464900000
Q63829	COMM domain-containing protein 3	Commd3	3	3	3	21	21	21	22.037	195	8.0526E-06	0.67932	0.76544	7.6554	2	56922000	31165000	25757000
Q8K2Q0	COMM domain-containing protein 9	Commd9	2	2	2	15.7	15.7	15.7	21.85	198	0.00090105	0.74874	0.59582	48.316	3	107440000	74770000	32673000
E9Q6C2	Complement C1s-B subcomponent	C1s	2	2	2	3.5	3.5	3.5	77.499	694	0.0013491	1.1428	1.2037	226.88	2	75614000	18258000	57355000
P01027	Complement C3	C3	34	34	34	24.8	24.8	24.8	186.48	1663	2.505E-238	0.86854	0.9155	39.311	47	7711100000	4144700000	3566400000
P01029	Complement C4-B	C4b	9	9	8	8.6	8.6	7.9	192.91	1738	1.352E-161	0.54274	0.49837	39.277	14	961560000	618920000	342640000
P06684	Complement C5	C5	4	4	4	3.2	3.2	3.2	188.88	1680	1.4919E-16	0.90253	1.0382	107.23	3	88822000	50286000	38536000
Q8R5L1	Complement component 1 Q subcomponent-binding protein	C1qbp	6	6	6	24.7	24.7	24.7	31.025	279	3.53E-77	0.73451	0.55751	57.719	10	925020000	541700000	383320000
Q8K182	Complement component C8 alpha chain	C8a	3	3	3	7.2	7.2	7.2	66.08	587	1.2211E-12	0.49491	0.33831	50.771	3	228770000	154620000	74154000
Q8BH35	Complement component C8 beta chain	C8b	4	4	4	8.1	8.1	8.1	66.229	589	1.2314E-13	0.50634	0.58061	71.08	4	161650000	85630000	76017000
Q8VCG4	Complement component C8 gamma chain	C8g	2	2	2	10.4	10.4	10.4	22.508	202	4.6516E-07	0.67163	0.64928	7.2028	2	120070000	74196000	45871000
P06683	Complement component C9	C9	2	2	2	4.9	4.9	4.9	62.002	548	8.9762E-05	1.0413	1.0393	92.406	2	35993000	22018000	13975000
B8JJN0	Complement factor B	Gm20547	12	12	11	13.1	13.1	11.8	142.32	1276	2.017E-163	0.57053	0.68247	83.282	16	1203400000	792490000	410930000
P03953	Complement factor D	Cfd	2	2	2	16.6	16.6	16.6	28.057	259	1.5944E-15	0.36133	0.36929	28.259	4	323390000	263460000	59926000
E9Q8I0	Complement factor H	Cfh	7	7	7	9.4	9.4	9.4	141.27	1252	1.6284E-70	0.61807	0.63993	33.87	9	734030000	450510000	283520000
Q61129	Complement factor I	Cfi	6	6	6	10.1	10.1	10.1	67.26	603	1.767E-269	0.41258	0.43924	88.979	4	400820000	331950000	68868000
A2AQ17	Complex I intermediate-associated protein 30, mitochondrial	Ndufaf1	2	2	2	8.8	8.8	8.8	37.782	328	1.9312E-06	0.55178	0.57498	89.436	2	82579000	49064000	33515000
Q8C0L8	Conserved oligomeric Golgi complex subunit 5	Cog5	2	2	2	5.1	5.1	5.1	91.39	829	0.0022659	1.1132	0.96819	12.477	2	8171000	4675100	3496000
Q6A0A9	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	2	2	2	3.3	3.3	3.3	121.64	1112	6.5727E-26	1.3747	1.6695	48.465	2	67380000	32425000	34955000
G3UXW9	COP9 signalosome complex subunit 1	Gps1	4	4	4	9.5	9.5	9.5	58.86	526	8.3818E-12	1.1554	1.1307	67.111	4	237000000	109430000	127560000
P61202	COP9 signalosome complex subunit 2	Cops2	5	5	5	14	14	14	51.596	443	4.0003E-21	0.74451	0.54398	56.26	2	477980000	259020000	218960000
O88543	COP9 signalosome complex subunit 3	Cops3	6	6	6	22.7	22.7	22.7	47.832	423	1.434E-116	1.2013	1.1816	129.52	7	1517800000	204530000	1313300000
O88544	COP9 signalosome complex subunit 4	Cops4	10	10	10	37.2	37.2	37.2	46.284	406	1.64E-100	0.59017	0.55393	31.156	11	1057400000	674220000	383230000
O35864	COP9 signalosome complex subunit 5	Cops5	4	4	4	18	18	18	37.548	334	3.0444E-33	0.8686	0.80577	58.75	2	48630000	30917000	17713000
O88545	COP9 signalosome complex subunit 6	Cops6	5	5	5	19.1	19.1	19.1	35.88	324	2.4868E-39	0.89591	0.90697	5.5207	2	93902000	45256000	48646000
Q9CZ04	COP9 signalosome complex subunit 7a	Cops7a	6	6	6	28.7	28.7	28.7	30.224	275	8.575E-163	0.51232	0.36955	64.703	6	602150000	431180000	170970000
Q8VBV7	COP9 signalosome complex subunit 8	Cops8	3	3	3	23.9	23.9	23.9	23.255	209	7.8372E-68	0.69458	0.82167	18.861	4	173520000	106070000	67449000
Q9D8X1	Copper homeostasis protein cutC homolog	Cutc	3	3	3	15.4	15.4	15.4	29.003	272	3.27E-107	0.56378	0.5386	13.897	2	177360000	108530000	68824000
O08997	Copper transport protein ATOX1	Atox1	3	3	3	47.1	47.1	47.1	7.3384	68	1.126E-150	0.47949	0.50939	40.568	8	1588000000	1045900000	542150000
P36552	Coproporphyrinogen-III oxidase, mitochondrial	Cpox	6	6	6	19.2	19.2	19.2	49.714	443	2.1541E-25	1.2287	1.2273	64.182	4	241050000	108080000	132970000
Q3UMF0	Cordon-bleu protein-like 1	Cobll1	13	13	13	19.2	19.2	19.2	137.38	1273	1.781E-150	0.52222	0.56377	53.922	16	766750000	459140000	307610000
O89053	Coronin-1A	Coro1a	2	2	2	5.4	5.4	5.4	50.989	461	4.6263E-09	1.0957	1.138	15.182	4	203570000	95020000	108550000
Q9WUM3	Coronin-1B	Coro1b	2	2	2	7	7	7	53.912	484	7.9872E-25	0.30406	0.32958	201.55	2	126410000	88556000	37852000
Q9WUM4	Coronin-1C	Coro1c	4	4	4	12	12	12	53.12	474	2.6035E-08	3.2531	2.9878	202.71	3	397320000	50723000	346600000
Q06770	Corticosteroid-binding globulin	Serpina6	3	3	3	9.8	9.8	9.8	44.769	397	2.8742E-38	0.33815	0.37922	47.898	4	304120000	225300000	78817000
E9QMV2	Costars family protein ABRACL	3110003A17Rik	2	2	2	27.2	27.2	27.2	9.0583	81	2.2513E-07	0.45444	0.41068	128.12	4	1321700000	704710000	617010000
Q9CPZ8	COX assembly mitochondrial protein homolog	Cmc1	2	2	2	17.9	17.9	17.9	12.552	106	1.8291E-10	0.51683	0.53426	42.317	2	182950000	119380000	63577000
Q04447	Creatine kinase B-type	Ckb	11	11	11	39.4	39.4	39.4	42.713	381	0	0.61491	0.69992	28.063	16	3723300000	2312500000	1410800000
P07310	Creatine kinase M-type	Ckm	23	23	23	61.9	61.9	61.9	43.044	381	0	0.63002	0.63933	72.098	129	1.2006E+11	7.054E+10	4.9517E+10
Q6P8J7	Creatine kinase S-type, mitochondrial	Ckmt2	18	18	18	50.1	50.1	50.1	47.473	419	0	1.2597	1.2561	45.246	119	3.2436E+10	1.4375E+10	1.806E+10
P47941	Crk-like protein	Crkl	6	6	6	28.7	28.7	28.7	33.83	303	2.0386E-34	0.52728	0.56555	73.292	8	415850000	264350000	151500000
O88712	C-terminal-binding protein 1	Ctbp1	4	4	4	13.4	13.4	13.4	47.744	441	1.3844E-10	0.81223	0.87025	9.2234	3	201890000	117270000	84625000
Q9Z0H4	CUGBP Elav-like family member 2;CUGBP Elav-like family member 1	Celf2	2	2	2	5.1	5.1	5.1	54.27	508	1.7761E-06	1.011	1.1846	7.7553	3	142300000	68020000	74282000
Q9JLV5	Cullin-3	Cul3	5	5	5	6.8	6.8	6.8	88.947	768	5.6218E-15	0.72905	0.64344	35.731	3	52880000	28430000	24450000
G3X914	Cullin-5	Cul5	2	2	2	2.9	2.9	2.9	99.04	855	0.0085321	1.1321	1.3509	32.163	2	17573000	8080200	9492900

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	Cand1	11	11	11	11	11	11	136.33	1230	1.6961E-30	1.0321	0.91475	50.29	12	430560000	220860000	209700000
Q6ZQ73	Cullin-associated NEDD8-dissociated protein 2	Cand2	5	5	5	6	6	6	135.63	1235	1.945E-40	0.67317	0.75139	16.843	2	57921000	33508000	24413000
Q60772	Cyclin-dependent kinase 4 inhibitor C	Cdkn2c	2	2	2	14.9	14.9	14.9	18.066	168	0.00017872	0.93863	0.99691	159.09	2	69616000	40597000	29020000
P49615	Cyclin-dependent kinase 5	Cdk5	2	2	2	5.1	5.1	5.1	33.288	292	0.00031628	1.1476	0.99374	46.461	2	63807000	28663000	35144000
P46414	Cyclin-dependent kinase inhibitor 1B	Cdkn1b	3	3	3	20.8	20.8	20.8	22.193	197	3.1145E-61	0.43104	0.48597	74.154	5	98327000	54130000	44197000
P97315	Cysteine and glycine-rich protein 1	Csrp1	5	5	5	43	43	43	20.583	193	4.754E-175	0.51002	0.50057	72.987	4	1276900000	872200000	404720000
P50462	Cysteine and glycine-rich protein 3	Csrp3	10	10	10	55.2	55.2	55.2	20.895	194	0	0.46835	0.4501	44.706	41	3.9655E+10	2.7132E+10	1.2523E+10
Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	Chordc1	2	2	2	12.1	12.1	12.1	37.35	331	9.622E-28	0.9153	0.88722	50.413	2	144100000	99236000	44864000
Q9Z1J3	Cysteine desulfurase, mitochondrial	Nfs1	9	9	9	27.9	27.9	27.9	50.569	459	5.2255E-83	1.6638	1.6706	74.911	8	351950000	139700000	212250000
P63254	Cysteine-rich protein 1	Crip1	1	1	1	13	13	13	8.5497	77	1.6792E-05	0.52771	0.22444	38.666	2	57533000	37212000	20321000
Q9DCT8	Cysteine-rich protein 2	Crip2	3	3	3	33.7	33.7	33.7	22.727	208	9.091E-164	0.51269	0.70603	36.648	6	711980000	396180000	315800000
Q9ER72	Cysteine--tRNA ligase, cytoplasmic	Cars	3	3	3	3.5	3.5	3.5	94.859	831	6.5778E-07	0.65712	0.28757	48.042	3	280560000	223790000	56771000
P56395	Cytochrome b5	Cyb5a	2	2	2	25.4	25.4	25.4	15.241	134	5.144E-130	1.301	1.0251	21.919	5	1959400000	813990000	1145400000
Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	Uqcrc1	15	15	14	36.5	36.5	36.5	52.851	480	0	1.3797	1.4853	37.265	40	1.2432E+10	5486200000	6946000000
Q9CPX8	Cytochrome b-c1 complex subunit 10	Uqcr11	1	1	1	21.4	21.4	21.4	6.5386	56	3.9351E-09	2.1557	2.5354	28.167	2	83012000	28120000	54892000
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	Uqcrc2	15	15	15	40.4	40.4	40.4	48.234	453	0	1.5467	1.6127	140.34	30	9303300000	3832200000	5471100000
P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	Uqcrh	5	5	5	61.8	61.8	61.8	10.435	89	0	0.6733	0.70139	27.672	14	1686400000	1037400000	648990000
Q9CQB4	Cytochrome b-c1 complex subunit 7	Uqcrb	7	7	7	52.3	52.3	52.3	13.561	111	3.6602E-84	0.91716	0.99686	57.191	12	6433400000	3347300000	3086100000
Q9CQ69	Cytochrome b-c1 complex subunit 8	Uqcrq	2	2	2	25.6	25.6	25.6	9.7681	82	3.5364E-06	2.9793	2.8957	65.687	2	670130000	236400000	433730000
Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochondrial	Uqcrfs1	9	9	9	44.9	44.9	44.9	29.367	274	0	0.94098	1.0163	34.125	17	4183100000	2354200000	1828900000
Q8BGD8	Cytochrome c oxidase assembly factor 6 homolog	1810063B05Rik	3	3	3	51.9	51.9	51.9	9.2983	79	5.9558E-27	1.7456	0.65417	25.639	2	266080000	71771000	194300000
P00405	Cytochrome c oxidase subunit 2	Mtco2	4	4	4	23.3	23.3	23.3	25.976	227	3.6672E-42	1.9108	1.8792	77.048	11	1904700000	675590000	1229100000
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	Cox4i1	9	9	9	53.8	53.8	53.8	19.53	169	5.112E-99	1.2873	1.4596	38.598	20	4700000000	2371700000	2328300000
P12787	Cytochrome c oxidase subunit 5A, mitochondrial	Cox5a	4	4	4	32.9	32.9	32.9	16.101	146	4.2735E-82	0.59947	0.58238	28.656	19	4070700000	2605500000	1465200000
Q9D881	Cytochrome c oxidase subunit 5B, mitochondrial	Cox5b	6	6	6	38.8	38.8	38.8	13.847	129	1.798E-249	0.56365	0.4068	90.38	7	4146800000	2698400000	1448400000
P56391	Cytochrome c oxidase subunit 6B1	Cox6b1	6	6	6	74.4	74.4	74.4	10.071	86	3.9271E-71	0.64207	0.61432	93.995	14	2176600000	1408800000	767800000
Q9CPQ1	Cytochrome c oxidase subunit 6C	Cox6c	1	1	1	9.2	9.2	9.2	8.4689	76	0.0011538	1.6582	1.9038	18.073	3	71799000	27397000	44403000
P56392	Cytochrome c oxidase subunit 7A1, mitochondrial	Cox7a1	1	1	1	16.2	16.2	16.2	8.9863	80	1.1988E-06	1.2908	1.1258	12.77	3	1.4915E+10	6813100000	8101700000
P62897	Cytochrome c, somatic	Cycs	12	12	9	76.2	76.2	45.7	11.605	105	0	0.93868	1.0164	58.265	32	6446000000	2882200000	3563800000
Q9D0M3	Cytochrome c1, heme protein, mitochondrial	Cyc1	8	8	8	34.5	34.5	34.5	35.327	325	3.967E-170	2.0261	2.0715	52.334	12	3983000000	1198600000	2784400000
P28271	Cytoplasmic aconitate hydratase	Aco1	13	13	13	21.5	21.5	21.5	98.124	889	4.0121E-57	1.3743	1.584	42.405	12	1069900000	437900000	631960000
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	Dync1h1	22	22	22	6.4	6.4	6.4	532.04	4644	9.219E-110	1.515	1.4027	52.954	21	805600000	359830000	445770000
A2BFF9	Cytoplasmic dynein 1 intermediate chain 2	Dync1i2	5	5	5	13.9	13.9	13.9	71.424	638	3.372E-124	0.94291	0.85964	53.397	9	291120000	162840000	128280000
Q8R1Q8	Cytoplasmic dynein 1 light intermediate chain 1	Dync1li1	6	6	5	21.2	21.2	18.7	56.614	523	6.648E-85	0.65071	0.63253	51.319	5	284010000	146900000	137110000
Q6PDL0	Cytoplasmic dynein 1 light intermediate chain 2	Dync1li2	6	5	5	21.1	18.5	18.5	54.218	492	5.1903E-50	0.70343	0.75619	7.9378	5	184930000	118050000	66881000
Q45VK7	Cytoplasmic dynein 2 heavy chain 1	Dync2h1	3	3	3	0.7	0.7	0.7	492.33	4306	0.0027848	0.96049	1.0064	40.202	2	100890000	38923000	61965000
Q99M51	Cytoplasmic protein NCK1	Nck1	3	3	2	7.7	7.7	5.6	42.89	377	2.5807E-05	0.66592	0.71666	263.8	4	310140000	70141000	240000000
Q8BMK4	Cytoskeleton-associated protein 4	Ckap4	2	2	2	3.8	3.8	3.8	63.691	575	2.9897E-06	1.215	1.164	22.024	2	46369000	20712000	25656000
A2AGT5	Cytoskeleton-associated protein 5	Ckap5	3	3	3	1.7	1.7	1.7	225.63	2032	2.2673E-14	0.88976	0.93525	79.025	2	32860000	16726000	16134000
Q9CPY7	Cytosol aminopeptidase	Lap3	12	12	12	28.9	28.9	28.9	56.141	519	2.9E-87	1.1125	1.1234	38.191	12	1304300000	612400000	691950000
Q9D020	Cytosolic 5-nucleotidase 3	Nt5c3	12	12	12	40.5	40.5	40.5	37.252	331	2.001E-151	0.56264	0.47717	59.702	20	3172800000	1946900000	1225900000
Q9D1A2	Cytosolic non-specific dipeptidase	Cndp2	9	9	9	30.7	30.7	30.7	52.767	475	5.7791E-52	1.073	1.155	26.031	11	1162400000	615040000	547370000
E9Q9M1	Cytosolic purine 5-nucleotidase	Nt5c2	4	4	4	7.5	7.5	7.5	67.703	586	1.0447E-05	1.1507	1.0149	44.259	3	65550000	33235000	32315000
E9QN44	D-2-hydroxyglutarate dehydrogenase, mitochondrial	D2hgdh	8	8	8	24.6	24.6	24.6	61.072	557	4.177E-157	1.4493	1.5334	25.6	11	933490000	391360000	542120000
Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	Bdh1	4	4	4	15.5	15.5	15.5	38.299	343	1.4561E-53	1.977	2.1793	71.755	5	766910000	279660000	487250000
Q8K3H0	DCC-interacting protein 13-alpha	Appl1	5	5	5	12.2	12.2	12.2	79.327	707	1.196E-239	0.77578	0.72335	23.88	7	347280000	203860000	143420000
Q8BZJ7	DCN1-like protein 2	Dcun1d2	3	3	3	13.5	13.5	13.5	30.068	259	3.3612E-42	0.66128	0.69853	48.115	4	133820000	79493000	54329000
Q9QY93	dCTP pyrophosphatase 1	Dctpp1	3	3	3	23.5	23.5	23.5	18.795	170	1.2396E-07	0.44727	0.40949	51.926	3	135700000	84355000	51342000
O35215	D-dopachrome decarboxylase	Ddt	5	5	5	64.4	64.4	64.4	13.077	118	0	0.63761	0.66746	33.838	9	7724700000	4842600000	2882100000
G3X8X0	DEAH (Asp-Glu-Ala-His) box polypeptide 16, isoform CRA_a (Protein Dhx16)	Dhx16	2	2	2	3.8	3.8	3.8	119.07	1044	0.013093	0.48597	0.52525	94.434	2	48383000	39523000	8860300
P28654	Decorin	Dcn	3	3	3	9	9	9	39.809	354	2.3384E-41	0.67376	0.74328	6.2219	4	310690000	203950000	106750000
Q3U0B3	Dehydrogenase/reductase SDR family member 11	Dhrs11	4	4	4	24.2	24.2	24.2	28.274	260	9.664E-142	1.3489	1.3951	69.648	7	716650000	155790000	560860000
Q99LB2	Dehydrogenase/reductase SDR family member 4	Dhrs4	7	7	7	30.5	30.5	30.5	29.884	279	1.2961E-88	1.4569	1.3572	42.742	9	3082200000	1395000000	1687200000
O35459	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Ech1	14	14	14	54.7	54.7	54.7	36.118	327	0	1.0062	0.96265	108.8	37	6325500000	3525200000	2800300000
Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	Aldh4a1	10	10	10	28.5	28.5	28.5	61.84	562	1.02E-136	1.5688	1.7916	39.49	13	1814700000	782460000	1032300000
P10518	Delta-aminolevulinic acid dehydratase	Alad	7	7	7	25.2	25.2	25.2	36.023	330	2.322E-136	0.86154	0.93458	65.009	8	334290000	191710000	142580000
Q9QX60	Deoxyguanosine kinase, mitochondrial	Dguok	2	2	2	12.6	12.6	12.6	32.281	277	2.022E-229	1.3752	0.91144	23.818	4	364380000	156580000	207800000
Q99LN9	Deoxyhypusine hydroxylase	Dohh	3	3	3	21.2	21.2	21.2	32.905	302	9.7995E-32	0.62336	0.62211	40.097	5	231400000	130480000	100910000
Q8VCG1	Deoxyuridine triphosphatase, isoform CRA_b	Dut	4	4	4	31.5	31.5	31.5	21.251	200	1.2412E-21	0.54487	0.57189	36.147	4	334740000	188900000	145840000
O55111	Desmoglein-2	Dsg2	1	1	1	1.2	1.2	1.2	122.38	1122	2.4772E-08	0.51481	0.64262	20.567	2	38263000	26276000	11987000
E9Q557	Desmoplakin	Dsp	2	2	2	1	1	1	332.91	2883	0.00092385	1.3221	1.1671	139.88	2	49181000	20148000	29033000
Q9R0P5	Destrin	Dstn	6	5	5	38.2	31.5	31.5	18.521	165	2.208E-79	0.57668	0.52023	114.57	10	2348100000	1502900000	845120000
Q9JIQ3	Diablo homolog, mitochondrial	Diablo	3	3	3	17.3	17.3	17.3	26.82	237	1.674E-243	0.46901	0.54688	32.802	4	122310000	90177000	32135000
Q8C2K1	Differentially expressed in FDCP 6	Def6	2	2	2	2.9	2.9	2.9	73.453	630	0.00028418	0.048362	0.051594	37.507	2	130140000	127930000	2204500
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	Dld	12	12	12	33.2	33.2	33.2	54.272	509	0	0.9432	0.82675	113.24	36	1.299E+10	6836000000	6153800000
Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	Dlat	19	19	19	34.1	34.1	34.1	67.941	642	1.578E-271	0.66784	0.71289	81.004	78	2.6145E+10	1.5047E+10	1.1098E+10
Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	Dlst	11	11	11	28.2	28.2	28.2	48.994	454	0	0.87575	0.96626	36.05	23	5003200000	2668700000	2334500000
Q8BVI4	Dihydropteridine reductase	Qdpr	4	4	4	26.1	26.1	26.1	25.57	241	8.311E-167	1.0174	0.99943	25.69	4	626600000	333040000	293560000
O08553	Dihydropyrimidinase-related protein 2	Dpysl2	16	16	15	45.3	45.3	42.5	62.277	572	0	0.9399	0.861	95.424	28	4835300000	2563700000	2271600000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
E9PWE8	Dihydropyrimidinase-related protein 3	Dpysl3	11	10	10	24	21.7	21.7	73.884	683	2.642E-213	0.74463	0.74762	96.995	11	1266500000	686070000	580430000
P31428	Dipeptidase 1	Dpep1	6	6	6	25.1	25.1	25.1	45.722	410	2.5611E-71	0.57608	0.53646	85.644	6	639030000	360770000	278260000
P97821	Dipeptidyl peptidase 1	Ctsc	3	3	3	9.7	9.7	9.7	52.376	462	5.6029E-38	1.4884	1.8231	48.937	4	274500000	107700000	166800000
Q99KK7	Dipeptidyl peptidase 3	Dpp3	8	8	8	19.6	19.6	19.6	82.897	738	5.455E-237	1.9149	1.991	72.164	11	937440000	337690000	599750000
Q8BVG4	Dipeptidyl peptidase 9	Dpp9	2	2	2	2.2	2.2	2.2	98	862	0.011403	0.97789	1.1876	38.851	2	50191000	23200000	26991000
Q9JI46	Diphosphoinositol polyphosphate phosphohydrolase 1	Nudt3	4	4	3	30.4	30.4	26.2	19.029	168	4.8143E-26	0.66143	0.66567	1.8623	2	107090000	63418000	43674000
Q3UH60	Disco-interacting protein 2 homolog B	Dip2b	2	2	2	2.2	2.2	2.2	171.12	1574	8.7337E-08	0.68064	0.59229	14.445	3	31431000	17917000	13514000
E9Q9H0	Disks large homolog 1	Dlg1	4	4	4	6.6	6.6	6.6	100.82	912	2.9616E-21	1.0275	1.1044	20.015	4	252050000	120470000	131580000
Q3U1J4	DNA damage-binding protein 1	Ddb1	8	8	8	10.4	10.4	10.4	126.85	1140	3.1262E-61	1.3539	1.0918	49.357	10	526890000	208250000	318640000
P28352	DNA-(apurinic or apyrimidinic site) lyase	Apex1	3	3	3	13.9	13.9	13.9	35.49	317	2.9702E-06	0.93389	0.977	34.601	5	177230000	94717000	82518000
Q9JKB3	DNA-binding protein A	Csda	5	1	1	16.3	5.3	5.3	38.813	361	1.312E-104	0.48701	0.50921	4.7905	2	161510000	110520000	50983000
P63037	DnaJ homolog subfamily A member 1	Dnaja1	2	2	2	6	6	6	44.868	397	7.2026E-06	2.4123	2.3418	47.375	2	168860000	67630000	101230000
Q9QYJ0	DnaJ homolog subfamily A member 2	Dnaja2	3	3	3	10	10	10	45.745	412	1.4203E-11	1.7362	1.6774	43.562	2	821550000	326700000	494850000
Q99M87	DnaJ homolog subfamily A member 3, mitochondrial	Dnaja3	2	2	2	7.7	7.7	7.7	52.443	480	1.8307E-08	1.0052	0.97802	29.044	3	138910000	61736000	77175000
Q9JMC3	DnaJ homolog subfamily A member 4	Dnaja4	2	2	2	6.3	6.3	6.3	44.901	397	1.4626E-09	1.0597	1.0046	37.682	2	141620000	69420000	72204000
Q9D832	DnaJ homolog subfamily B member 4	Dnajb4	4	4	4	15.1	15.1	15.1	37.781	337	8.0572E-14	0.92042	0.96089	76.495	7	384730000	220930000	163800000
Q6NZB0	DnaJ homolog subfamily C member 8	Dnajc8	2	2	2	10.3	10.3	10.3	29.812	253	3.8139E-06	0.46987	0.31504	56.313	3	229990000	157050000	72948000
Q9D113	DNL-type zinc finger protein	Dnlz	2	2	2	12.4	12.4	12.4	19.403	177	0.0013403	1.3745	1.2582	152.7	2	145200000	55075000	90126000
Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Rpn1	2	2	2	3.1	3.1	3.1	68.527	608	0.002225	2.1084	1.8879	25.457	2	69533000	21142000	48392000
Q8K0W9	DPH3 homolog	Dph3	2	2	2	50	50	50	9.2862	82	1.0751E-55	0.61487	0.65632	81.414	2	66250000	38820000	27430000
Q62418	Drebrin-like protein	Dbnl	9	9	9	33.9	33.9	33.9	48.699	436	2.717E-102	0.60182	0.55422	18.29	10	613510000	391080000	222430000
P31938	Dual specificity mitogen-activated protein kinase kinase 1	Map2k1	3	3	2	13	13	7.4	43.474	393	1.1114E-13	0.77853	0.79389	61.564	3	147830000	90385000	57445000
P47809	Dual specificity mitogen-activated protein kinase kinase 4	Map2k4	5	5	5	15.9	15.9	15.9	44.113	397	1.0535E-37	0.9586	1.0047	39.113	8	309910000	158560000	151350000
Q6NT99	Dual specificity protein phosphatase 23	Dusp23	3	3	3	26.7	26.7	26.7	16.637	150	4.0302E-06	1.7802	1.678	33.166	2	63822000	20455000	43366000
B1AQF4	Dual specificity protein phosphatase 3	Dusp3	2	2	2	14.3	14.3	14.3	23.223	210	1.082E-22	0.79141	0.78223	5.0009	4	388950000	233530000	155420000
O08788	Dynactin subunit 1	Dctn1	3	3	3	4	4	4	141.67	1281	1.5123E-19	1.3625	1.2361	50.489	3	172210000	79289000	92925000
Q99KJ8	Dynactin subunit 2	Dctn2	5	5	5	18.2	18.2	18.2	44.116	402	2.3185E-29	0.49337	0.51389	18.25	7	927080000	634720000	292360000
Q9Z0Y1	Dynactin subunit 3	Dctn3	2	2	2	8.6	8.6	8.6	20.978	186	0.00077148	0.34964	0.35053	106.5	2	102100000	68504000	33598000
Q8K1M6	Dynamin-1-like protein	Dnm1l	19	19	1	38	38	3.1	82.657	742	0	0.75965	0.77445	38.077	32	4271800000	2452900000	1818900000
E9PUD2	Dynamin-1-like protein	Dnm1l	19	1	1	39.6	3.2	3.2	79.532	712	0	0.82415	0.89132	6.3961	2	200600000	110200000	90406000
F8WIV5	Dynamin-2	Dnm2	7	7	7	9.4	9.4	9.4	98.096	870	1.4191E-29	0.91256	0.83921	56.581	8	498280000	253180000	245100000
P58281	Dynamin-like 120 kDa protein, mitochondrial	Opa1	10	10	10	13.2	13.2	13.2	111.34	960	2.4201E-84	1.3035	1.1972	54.79	11	485010000	227550000	257460000
Q9D0M5	Dynein light chain 2, cytoplasmic;Dynein light chain 1, cytoplasmic	Dynll2	3	3	3	33.7	33.7	33.7	10.35	89	2.7836E-12	0.4003	0.39323	34.166	3	357020000	234920000	122100000
A2AVR9	Dynein light chain roadblock-type 1	Dynlrb1	1	1	1	15.4	15.4	15.4	11.928	104	0.00010096	0.46795	0.43526	29.715	2	118970000	77318000	41652000
E9Q423	Dysferlin	Dysf	5	5	5	3.6	3.6	3.6	239.13	2099	2.0425E-09	1.1729	1.2639	6.9109	4	119100000	35842000	83254000
S4R1P5	Dystonin	Dst	7	7	7	1.3	1.3	1.3	870.52	7717	1.1654E-23	0.91638	0.85513	18.643	5	87812000	44067000	43745000
Q9D2N4	Dystrobrevin alpha	Dtna	3	3	3	3.6	3.6	3.6	84.066	746	2.7941E-06	1.1931	1.3967	73.502	3	81782000	41331000	40451000
Q62165	Dystroglycan;Alpha-dystroglycan;Beta-dystroglycan	Dag1	4	4	4	5.3	5.3	5.3	96.904	893	8.9302E-31	0.37024	0.34897	13.342	4	775210000	549770000	225440000
P11531	Dystrophin	Dmd	11	11	11	3.7	3.7	3.7	425.83	3678	7.8012E-27	0.92549	0.93041	79.155	9	476900000	238420000	238490000
Q9ERU9	E3 SUMO-protein ligase RanBP2	Ranbp2	1	1	1	0.7	0.7	0.7	341.12	3053	2.6686E-07	1.19	1.0748	3.3537	2	30023000	14858000	15165000
A2AFQ0	E3 ubiquitin-protein ligase HUWE1	Huwe1	18	18	18	6.2	6.2	6.2	482.69	4378	0	0.94586	0.99165	49.871	16	576160000	300170000	275990000
P46935	E3 ubiquitin-protein ligase NEDD4	Nedd4	4	4	4	4.3	4.3	4.3	102.71	887	1.2733E-09	0.78972	0.78922	62.345	4	213320000	112300000	101020000
A2A5Z6	E3 ubiquitin-protein ligase SMURF2	Smurf2	3	3	3	4.5	4.5	4.5	86.174	748	0.0024299	0.66412	0.71184	80.6	2	67868000	33532000	34336000
A2AN08	E3 ubiquitin-protein ligase UBR4	Ubr4	5	5	5	1.8	1.8	1.8	572.28	5180	1.0261E-47	1.0143	1.009	74.665	5	112620000	63109000	49512000
Q8BL66	Early endosome antigen 1	Eea1	13	13	13	11.3	11.3	11.3	160.91	1411	1.241E-178	0.563	0.54689	76.851	13	695520000	450430000	245090000
D3Z4J9	Echinoderm microtubule-associated protein-like 1	Eml1	13	13	12	18.4	18.4	17.4	88.327	800	3.4795E-62	1.5589	1.483	114.93	17	1718100000	965410000	752700000
E9QK48	Echinoderm microtubule-associated protein-like 2	Eml2	9	9	9	15.1	15.1	15.1	90.791	841	1.4013E-61	1.2251	1.3038	17.683	12	1151300000	499310000	652010000
Q8R2G4	Ecto-ADP-ribosyltransferase 3	Art3	6	6	6	19.1	19.1	19.1	42.014	371	1.7069E-52	0.56585	0.62564	16.041	6	665300000	421560000	243740000
Q8CDV7	Ectonucleoside triphosphate diphosphohydrolase 1	Entpd1	4	4	4	10.2	10.2	10.2	60.589	539	9.2257E-45	0.80264	0.95724	82.159	5	158180000	96781000	61400000
O55026	Ectonucleoside triphosphate diphosphohydrolase 2	Entpd2	2	2	2	4.8	4.8	4.8	54.319	495	1.0599E-19	0.8892	1.1323	9.0308	2	75229000	38689000	36540000
Q8BGN3	Ectonucleotide pyrophosphatase/phosphodiesterase family member 6	Enpp6	2	2	2	4.8	4.8	4.8	50.618	440	0.00020418	1.0147	0.07512	361.4	2	1.0652E+10	5201800000	5450200000
Q91VK2	Eef1d protein (Elongation factor 1-delta)	Eef1d	5	1	0	31.2	13.4	0	30.634	276	2.8545E-57	0.64005	0.65702	4.127	2	59173000	34210000	24963000
Q8BPB5	EGF-containing fibulin-like extracellular matrix protein 1	Efemp1	3	3	3	10.8	10.8	10.8	54.952	493	3.388E-268	0.73518	0.75826	3.0873	3	102680000	58696000	43988000
Q91YE3	Egl nine homolog 1	Egln1	3	3	3	10.2	10.2	10.2	43.11	400	3.5624E-09	1.104	1.0054	55.523	4	66432000	32235000	34197000
E9QP49	EH domain-binding protein 1-like protein 1	Ehbp1l1	10	10	10	11.1	11.1	11.1	184.8	1718	8.219E-281	1.1418	1.2105	35.758	8	481630000	261780000	219850000
Q9WVK4	EH domain-containing protein 1	Ehd1	11	9	7	30	26.6	21.2	60.602	534	5.9191E-51	0.93869	0.83706	78.648	13	1381800000	718950000	662840000
Q8BH64	EH domain-containing protein 2	Ehd2	13	13	12	30.4	30.4	28.7	61.174	543	1.5301E-81	1.0443	1.0222	38.898	21	1109100000	545730000	563330000
Q9EQP2	EH domain-containing protein 4	Ehd4	14	14	12	32.9	32.9	29.2	61.48	541	6.17E-140	0.96434	0.976	71.369	17	2105700000	1060400000	1045300000
E9PVA8	eIF-2-alpha kinase activator GCN1	Gcn1l1	3	3	3	1.4	1.4	1.4	293.02	2671	0.00044019	0.59156	0.57422	82.692	4	110220000	75718000	34504000
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	Etfa	20	20	20	66.1	66.1	66.1	35.009	333	0	0.56671	0.55431	106.79	96	8.2847E+10	5.5483E+10	2.7364E+10
Q9DCW4	Electron transfer flavoprotein subunit beta	Etfb	15	15	15	48.6	48.6	48.6	27.623	255	1.333E-255	0.58114	0.54024	78.934	59	8.7346E+10	5.642E+10	3.0926E+10
Q921G7	Electron transfer flavoprotein-ubiquinone oxidoreductase	Etfdh	16	16	16	33.3	33.3	33.3	68.09	616	2.542E-204	1.2253	1.2336	69.42	28	7952300000	4259600000	3692700000
F8VPM7	ELKS/Rab6-interacting/CAST family member 1	Erc1	2	2	2	3.1	3.1	3.1	128.33	1120	2.51E-153	0.65676	0.69132	15.759	3	124230000	73259000	50974000
P10126	Elongation factor 1-alpha 1	Eef1a1	14	9	9	33.8	24.2	24.2	50.113	462	1.784E-149	0.62518	0.65189	46.325	15	1354000000	951700000	402260000
P62631	Elongation factor 1-alpha 2	Eef1a2	14	14	9	42.3	42.3	32.8	50.454	463	0	0.87298	0.81404	95.686	37	8901400000	4657600000	4243800000
O70251	Elongation factor 1-beta	Eef1b	4	4	4	34.7	34.7	34.7	24.693	225	3.0637E-57	0.45001	0.32626	140.9	4	600740000	416200000	184540000
Q80T06	Elongation factor 1-delta	Eef1d	6	6	1	29.5	29.5	8.5	31.292	281	0	0.85091	0.91108	24.906	8	2306900000	1188900000	1118000000
F6ZFU0	Elongation factor 1-delta (Fragment)	Eef1d	5	1	1	12.7	3.8	3.8	61.391	552	2.7665E-80	0.71973	0.68539	12.237	2	69683000	39605000	30078000
Q9D8N0	Elongation factor 1-gamma	Eef1g	10	10	10	22.9	22.9	22.9	50.06	437	1.04E-114	1.2245	1.2837	47.665	12	2208500000	1323000000	885550000
P58252	Elongation factor 2	Eef2	18	18	17	24.7	24.7	23.5	95.313	858	1.153E-295	1.1619	1.261	105.45	39	8793400000	3651300000	5142000000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8K0D5	Elongation factor G, mitochondrial	Gfm1	13	13	13	20.1	20.1	20.1	83.549	751	7.0179E-64	1.1805	1.2971	78.925	19	2651600000	1334400000	1317200000
Q9CZR8	Elongation factor Ts, mitochondrial	Tsfm	6	6	6	35.5	35.5	35.5	35.334	324	1.001E-243	1.1094	1.2742	13.574	9	1035100000	460930000	574180000
Q8BFR5	Elongation factor Tu, mitochondrial;Elongation factor Tu	Tufm	14	14	14	39.4	39.4	39.4	49.508	452	0	0.47532	0.48149	44.765	26	3105400000	2161500000	943930000
O08600	Endonuclease G, mitochondrial	Endog	2	2	2	9.2	9.2	9.2	32.19	294	3.821E-12	1.2171	1.3569	1.3194	2	96688000	43376000	53312000
Q62419	Endophilin-A2;Endophilin-A1	Sh3gl1	2	2	2	6.2	6.2	6.2	41.518	368	2.1858E-05	0.63324	0.49492	59.881	2	28322000	18455000	9867500
Q9JK48	Endophilin-B1	Sh3glb1	2	2	2	7.1	7.1	7.1	40.855	365	3.3686E-51	0.63792	0.63255	12.986	4	218510000	134660000	83851000
A2AWI7	Endophilin-B2	Sh3glb2	5	5	5	14.6	14.6	14.6	44.907	404	1.6497E-36	0.53941	0.54682	25.182	3	117310000	78644000	38662000
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	Erap1	6	6	6	7.5	7.5	7.5	106.6	930	4.9183E-22	0.75962	0.76406	84.332	7	486880000	163540000	323330000
P57759	Endoplasmic reticulum resident protein 29	Erp29	3	3	3	19.5	19.5	19.5	28.823	262	1.4408E-08	0.82559	0.62745	91.893	4	580540000	296700000	283840000
Q9D1Q6	Endoplasmic reticulum resident protein 44	Erp44	5	5	5	14.8	14.8	14.8	46.852	406	3.7466E-33	0.45411	0.42285	75.337	4	587530000	377930000	209610000
P08113	Endoplasmin	Hsp90b1	22	20	20	29.9	28.2	28.2	92.475	802	0	0.66834	0.69325	29.64	30	5015600000	3028900000	1986700000
Q9JMG1	Endothelial differentiation-related factor 1	Edf1	3	3	3	22.3	22.3	22.3	16.369	148	7.1246E-14	0.49557	0.27877	103.06	2	130180000	88272000	41907000
G5E896	Enhancer of mRNA-decapping protein 4	Edc4	2	2	2	2.1	2.1	2.1	152.48	1406	1.5373E-08	2.7183	3.4636	220.45	2	30059000	11433000	18627000
B0QZL1	Enolase	Eno1	10	1	1	64.7	6.3	6.3	23.935	221	1.696E-107	0.9049	0.26623	165.74	2	1455900000	807300000	648580000
P42125	Enoyl-CoA delta isomerase 1, mitochondrial	Eci1	8	8	8	32.5	32.5	32.5	32.25	289	1.893E-122	1.4006	1.3913	132.69	30	4.1902E+10	2.3689E+10	1.8213E+10
Q9WUR2	Enoyl-CoA delta isomerase 2, mitochondrial	Eci2	11	11	3	37.1	37.1	12.3	43.267	391	1.991E-253	1.029	0.99688	121.27	17	4556000000	2213700000	2342300000
Q3TLP5	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	Echdc2	7	7	7	32.1	32.1	32.1	31.852	296	3.02E-199	1.0815	1.0765	22.669	13	3622000000	1782900000	1839100000
Q9D7J9	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	Echdc3	4	4	4	22.3	22.3	22.3	32.402	300	1.0397E-85	2.4204	2.9826	71.883	3	627890000	178880000	449020000
Q8BH95	Enoyl-CoA hydratase, mitochondrial	Echs1	11	11	11	41.7	41.7	41.7	31.474	290	8.286E-285	0.59975	0.59363	32.749	47	2.2191E+10	1.421E+10	7980500000
Q01279	Epidermal growth factor receptor	Egfr	6	6	6	5	5	5	134.85	1210	1.7167E-92	0.34555	0.28116	72.509	5	236250000	147860000	88389000
H3BK65	Epidermal growth factor receptor substrate 15	Eps15	3	3	3	4.9	4.9	4.9	102.23	933	3.8046E-60	0.67319	0.89507	26.902	2	50176000	35772000	14403000
Q60902	Epidermal growth factor receptor substrate 15-like 1	Eps15l1	8	8	8	13.9	13.9	13.9	99.307	907	4.123E-294	0.73223	0.63757	176.72	3	318530000	120730000	197800000
Q9Z0J0	Epididymal secretory protein E1	Npc2	2	2	2	18.8	18.8	18.8	16.442	149	5.5667E-06	1.4936	1.482	55.775	2	170490000	56899000	113590000
Q5M8N4	Epimerase family protein SDR39U1	Sdr39u1	5	5	5	20.8	20.8	20.8	32.994	308	6.8505E-19	1.2785	1.2058	57.66	5	443680000	188510000	255170000
Q9D379	Epoxide hydrolase 1	Ephx1	2	2	2	7	7	7	52.576	455	3.938E-07	1.4064	1.4495	30.658	2	54575000	19271000	35304000
P34914	Epoxide hydrolase 2	Ephx2	19	19	19	47.8	47.8	47.8	62.515	554	0	1.1367	1.2399	45.841	32	9700600000	4308500000	5392100000
Q80VP1	Epsin-1	Epn1	2	2	2	9.4	9.4	9.4	60.211	575	4.7631E-78	0.70948	0.85662	19.071	5	334540000	190180000	144360000
P54116	Erythrocyte band 7 integral membrane protein	Stom	5	5	5	30.3	30.3	30.3	31.375	284	2.2794E-65	3.8534	3.9128	62.396	6	442090000	82977000	359110000
Q9D172	ES1 protein homolog, mitochondrial	D10Jhu81e	6	6	6	39.1	39.1	39.1	28.09	266	0	0.45603	0.46484	27.814	18	7038700000	4251700000	2787000000
P50171	Estradiol 17-beta-dehydrogenase 8	Hsd17b8	7	7	7	37.8	37.8	37.8	26.588	259	2.2926E-70	1.311	0.97675	100.12	7	1170600000	501930000	668690000
Q922E4	Ethanolamine-phosphate cytidylyltransferase	Pcyt2	3	3	3	10.1	10.1	10.1	45.234	404	2.1838E-05	0.96607	0.50496	14.564	2	70298000	33785000	36513000
P60843	Eukaryotic initiation factor 4A-I	Eif4a1	6	3	3	24.4	12.3	12.3	46.153	406	1.558E-298	0.63567	0.62808	17.211	2	78467000	50030000	28438000
P10630	Eukaryotic initiation factor 4A-II	Eif4a2	7	7	4	21.1	21.1	9.1	46.402	407	0	0.52927	0.58299	33.893	4	326030000	224260000	101770000
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	Gspt1	5	5	5	7.9	7.9	7.9	68.625	636	1.04E-20	0.42793	0.1607	127.76	4	467960000	297460000	170510000
Q8BWY3	Eukaryotic peptide chain release factor subunit 1	Etf1	3	3	3	7.3	7.3	7.3	49.03	437	3.5698E-12	1.1563	1.0463	6.3825	2	127840000	59909000	67928000
P48024	Eukaryotic translation initiation factor 1	Eif1	4	4	4	35.4	35.4	35.4	12.746	113	6.6992E-41	0.41341	0.44901	19.539	3	534370000	380000000	154360000
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	Eif2s1	9	9	9	38.1	38.1	38.1	36.108	315	4.11E-140	1.1014	0.99561	48.797	8	512940000	268260000	244680000
Q99L45	Eukaryotic translation initiation factor 2 subunit 2	Eif2s2	5	5	5	20.5	20.5	20.5	38.092	331	1.8534E-16	0.98083	1.0906	49.764	3	167250000	87419000	79827000
Q9Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	Eif2s3x	5	5	1	18.6	18.6	3.8	51.065	472	1.2609E-53	1.2494	1.3713	14.58	6	582650000	263380000	319270000
Q8BJW6	Eukaryotic translation initiation factor 2A	Eif2a	2	2	2	8.1	8.1	8.1	64.403	581	3.2E-10	2.4531	2.6518	9.3775	3	41310000	11285000	30025000
P23116	Eukaryotic translation initiation factor 3 subunit A	Eif3a	9	9	9	7.4	7.4	7.4	161.93	1344	5.0673E-45	1.4473	1.4087	38.881	6	188280000	77423000	110850000
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B	Eif3b	11	11	11	20.3	20.3	20.3	91.369	803	7.2681E-93	1.2592	1.3577	23.676	12	702330000	313600000	388720000
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	Eif3c	7	7	7	9.1	9.1	9.1	105.53	911	1.1672E-22	1.6999	1.7281	21.094	7	255310000	103480000	151830000
O70194	Eukaryotic translation initiation factor 3 subunit D	Eif3d	3	3	3	9.7	9.7	9.7	63.988	548	1.7356E-15	1.9538	1.9829	33.66	4	274890000	90931000	183960000
Q9DCH4	Eukaryotic translation initiation factor 3 subunit F	Eif3f	4	4	4	16.1	16.1	16.1	37.984	361	3.306E-38	0.81221	0.77793	11.992	6	532150000	313180000	218970000
Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G	Eif3g	6	6	6	19.4	19.4	19.4	35.638	320	4.7559E-33	0.53952	0.51842	248.23	7	1934200000	1599900000	334280000
Q9QZD9	Eukaryotic translation initiation factor 3 subunit I	Eif3i	4	4	4	17.8	17.8	17.8	36.46	325	1.3964E-36	1.145	1.1436	28.779	3	212900000	107450000	105450000
Q66JS6	Eukaryotic translation initiation factor 3 subunit J	Eif3j	3	3	3	12.5	12.5	12.5	29.485	263	1.0216E-09	0.63944	0.67962	158.67	3	492200000	299270000	192930000
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L	Eif3l	8	8	8	16.8	16.8	16.8	66.612	564	8.2108E-46	1.2851	1.1058	52.082	7	382750000	155240000	227510000
Q99JX4	Eukaryotic translation initiation factor 3 subunit M	Eif3m	3	3	3	11.2	11.2	11.2	42.516	374	2.8924E-07	0.6828	0.60044	28.167	3	68960000	41198000	27762000
Q6NZJ6	Eukaryotic translation initiation factor 4 gamma 1	Eif4g1	9	9	8	8.2	8.2	7.5	176.07	1600	1.117E-43	0.81732	0.7587	48.128	8	268190000	157840000	110350000
G3XA17	Eukaryotic translation initiation factor 4 gamma 2	Eif4g2	8	8	8	13.4	13.4	13.4	102.1	906	1.886E-46	0.57255	0.44226	85.374	7	487140000	182520000	304620000
A2AMI2	Eukaryotic translation initiation factor 4 gamma 3	Eif4g3	5	4	4	4.1	3.3	3.3	174.82	1579	1.1728E-12	0.58804	0.66949	83.083	3	375990000	322740000	53252000
Q8BGD9	Eukaryotic translation initiation factor 4B	Eif4b	5	5	5	10.8	10.8	10.8	68.839	611	4.2766E-22	0.38949	0.33889	72.951	4	152180000	122950000	29237000
P63073	Eukaryotic translation initiation factor 4E	Eif4e	3	3	3	11.5	11.5	11.5	25.053	217	1.1201E-05	0.67552	0.61539	44.486	4	108990000	67154000	41833000
Q9DBB5	Eukaryotic translation initiation factor 4E type 3	Eif4e3	4	4	4	24.6	24.6	24.6	22.836	207	1.5148E-21	0.5498	0.57118	54.193	3	301680000	178210000	123460000
Q60876	Eukaryotic translation initiation factor 4E-binding protein 1	Eif4ebp1	2	2	2	54.7	54.7	54.7	12.325	117	1.2017E-32	0.29434	0.36499	24.323	3	147490000	112070000	35422000
Q9WUK2	Eukaryotic translation initiation factor 4H	Eif4h	5	5	5	21.4	21.4	21.4	27.341	248	8.173E-272	0.49691	0.45928	65.827	8	675860000	531690000	144170000
P59325	Eukaryotic translation initiation factor 5	Eif5	5	5	5	16.6	16.6	16.6	48.968	429	1.3256E-27	0.52928	0.42052	48.742	7	291380000	195690000	95690000
P63242	Eukaryotic translation initiation factor 5A-1	Eif5a	4	4	4	32.5	32.5	32.5	16.832	154	1.9437E-23	0.47408	0.43473	39.271	8	2615700000	1801700000	814030000
Q05D44	Eukaryotic translation initiation factor 5B	Eif5b	4	4	4	4.9	4.9	4.9	137.61	1216	1.9242E-17	0.73419	0.68373	36.664	4	90038000	50016000	40022000
O35382	Exocyst complex component 4	Exoc4	2	2	2	2.9	2.9	2.9	110.54	975	0.00003392	0.8054	0.71867	16.387	2	28949000	15070000	13879000
Q6P5F9	Exportin-1	Xpo1	5	5	5	6.3	6.3	6.3	123.09	1071	3.4544E-12	0.9792	0.87387	73.915	6	267020000	143680000	123330000
Q9ERK4	Exportin-2	Cse1l	3	3	3	4.8	4.8	4.8	110.45	971	2.3717E-24	0.72836	0.52018	26.92	4	82676000	48674000	34002000
Q3U7R1	Extended synaptotagmin-1	Esyt1	2	2	2	2.6	2.6	2.6	121.55	1092	1.6336E-05	1.7975	1.9406	50.027	2	60577000	25198000	35379000
O09164	Extracellular superoxide dismutase [Cu-Zn]	Sod3	3	3	3	19.1	19.1	19.1	27.392	251	1.03E-106	0.45823	0.44904	10.205	5	454690000	300480000	154210000
P26040	Ezrin	Ezr	7	4	4	13	8.5	8.5	69.406	586	2.7747E-15	0.57438	0.59514	33.3	5	449590000	271390000	178200000
P47754	F-actin-capping protein subunit alpha-2	Capza2	3	3	3	17.1	17.1	17.1	32.967	286	3.0282E-33	0.78028	0.75797	31.902	6	367930000	215060000	152870000
P47757	F-actin-capping protein subunit beta	Capzb	3	3	3	10.5	10.5	10.5	31.345	277	3.2054E-12	0.50269	0.54547	19.761	3	155630000	97031000	58599000
Q8R123	FAD synthase	Flad1	8	8	8	28	28	28	54.766	492	1.011E-72	1.0856	1.2744	31.924	12	560240000	281660000	278590000
P56213	FAD-linked sulfhydryl oxidase ALR	Gfer	2	2	2	15.2	15.2	15.2	22.876	198	3.0954E-15	0.60626	0.68948	24.808	5	177950000	104020000	73930000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q91WJ8	Far upstream element-binding protein 1	Fubp1	5	3	3	6.8	5.5	5.5	68.539	651	1.9729E-15	0.48802	0.58431	77.965	3	199980000	128190000	71790000
Q3U0V1	Far upstream element-binding protein 2	Khsrp	7	7	5	14.3	14.3	12.2	76.775	748	1.9211E-56	0.51218	0.52262	128.09	12	2323700000	578470000	1745200000
Q920E5	Farnesyl pyrophosphate synthase	Fdps	2	2	2	7.4	7.4	7.4	40.581	353	6.8599E-09	0.89223	0.94651	18.371	4	205110000	107980000	97128000
P54731	FAS-associated factor 1	Faf1	5	5	5	8.6	8.6	8.6	73.862	649	5.3792E-30	0.56795	0.63539	25.109	2	119100000	75809000	43293000
P19096	Fatty acid synthase	Fasn	18	18	18	11.5	11.5	11.5	272.43	2504	4.4892E-98	2.2753	2.2954	65.185	16	935340000	336020000	599320000
P04117	Fatty acid-binding protein, adipocyte	Fabp4	8	8	8	60.6	60.6	60.6	14.65	132	8.872E-254	0.37241	0.35262	178.63	21	3.6962E+10	2.7739E+10	9222800000
Q05816	Fatty acid-binding protein, epidermal	Fabp5	7	7	7	57.8	57.8	57.8	15.137	135	0	0.44754	0.48198	73.898	9	3111400000	1733700000	1377700000
P11404	Fatty acid-binding protein, heart	Fabp3	8	8	8	55.6	55.6	55.6	14.819	133	2.1828E-93	0.46645	0.47565	46.213	20	7.1406E+10	4.9277E+10	2.2129E+10
Q8CIB5	Fermitin family homolog 2	Fermt2	10	10	10	19.7	19.7	19.7	77.8	680	1.298E-133	1.1377	1.2292	58.064	13	1607100000	722250000	884810000
P09528	Ferritin heavy chain	Fth1	9	9	9	55.5	55.5	55.5	21.066	182	2.523E-263	0.39209	0.40155	81.852	22	6961000000	4323300000	2637700000
P29391	Ferritin light chain 1;Ferritin;Ferritin light chain 2	Ftl1	6	6	6	51.4	51.4	51.4	20.802	183	2.009E-220	0.3335	0.39108	75.12	13	3275200000	2391800000	883370000
Q544X6	Ferrochelatase;Ferrochelatase, mitochondrial	Fech	3	3	3	12.6	12.6	12.6	47.421	422	2.5551E-09	2.15	2.1796	38.878	4	436700000	155030000	281670000
Q9QXC1	Fetuin-B	Fetub	6	6	6	24.5	24.5	24.5	42.712	388	4.212E-136	0.30379	0.32699	40.932	10	782950000	622060000	160880000
Q6P9Q4	FH1/FH2 domain-containing protein 1	Fhod1	2	2	2	1.9	1.9	1.9	129.6	1197	0.0054728	14.005	12.953	138.65	3	2469300000	104170000	2365200000
Q76LL6	FH1/FH2 domain-containing protein 3	Fhod3	6	6	6	6.8	6.8	6.8	175.65	1578	4.2419E-12	1.6355	2.0286	30.361	4	392750000	143200000	249550000
A2AQ53	Fibrillin-1	Fbn1	9	9	8	3.6	3.6	3.3	312.3	2873	2.5496E-46	0.28635	0.253	19.464	4	136910000	115620000	21289000
E9PV24	Fibrinogen alpha chain	Fga	12	12	12	20.4	20.4	20.4	87.428	789	4.536E-276	1.0422	1.0751	63.996	19	1539200000	775380000	763870000
Q8K0E8	Fibrinogen beta chain;Fibrinopeptide B;Fibrinogen beta chain	Fgb	13	13	13	32.6	32.6	32.6	54.752	481	2.794E-172	1.1159	1.1022	46.659	16	1396900000	639100000	757830000
Q8VCM7	Fibrinogen gamma chain	Fgg	9	9	9	28.9	28.9	28.9	49.391	436	3.432E-132	1.2344	1.0648	31.198	10	910770000	476570000	434200000
P61148	Fibroblast growth factor 1	Fgf1	4	4	4	28.4	28.4	28.4	17.417	155	1.1046E-25	0.36085	0.35279	39.339	4	464360000	332820000	131540000
Q08879	Fibulin-1	Fbln1	7	7	7	18.2	18.2	18.2	78.032	705	6.54E-108	0.42803	0.46591	27.633	5	279850000	198780000	81075000
Q9WVH9	Fibulin-5	Fbln5	5	5	5	20.5	20.5	20.5	50.193	448	5.888E-101	1.0976	1.0978	29.99	5	209130000	91728000	117400000
Q8BTM8	Filamin-A	Flna	42	42	40	24.3	24.3	23.6	281.22	2647	0	0.69296	0.81074	49.673	51	4030500000	2445300000	1585200000
Q059P4	Filamin-A-interacting protein 1	Filip1	2	2	2	3.4	3.4	3.4	137.91	1214	0.00028995	1.0764	0.91212	22.178	2	35576000	18465000	17111000
Q80X90	Filamin-B	Flnb	16	13	13	8.5	7.1	7.1	277.82	2602	2.864E-136	0.72651	0.83037	93.191	9	433570000	225290000	208280000
Q71FD7	Filamin-binding LIM protein 1	Fblim1	7	7	7	34.7	34.7	34.7	41.026	375	7.7175E-59	0.6939	0.68386	48.336	10	561320000	307790000	253530000
D3Z576	Filamin-C	Flnc	40	38	37	22.3	21.6	21	292.34	2737	0	0.86235	0.90084	47.305	47	5687800000	2492600000	3195200000
Q923D2	Flavin reductase (NADPH)	Blvrb	6	6	6	58.3	58.3	58.3	22.197	206	4.27E-217	0.60391	0.6758	50.504	13	2173500000	1371600000	801840000
A2AEY2	Four and a half LIM domains protein 1	Fhl1	4	4	4	13.6	13.6	13.6	36.261	323	2.3894E-16	0.37486	0.24485	65.467	3	217860000	145700000	72154000
O70433	Four and a half LIM domains protein 2	Fhl2	14	14	14	58.1	58.1	58.1	32.072	279	0	0.33914	0.33393	55.092	25	4829400000	3830200000	999270000
Q61584	Fragile X mental retardation syndrome-related protein 1	Fxr1	2	2	2	2.8	2.8	2.8	76.221	677	1.4961E-10	1.3572	0.88363	61.051	3	224100000	118070000	106020000
P70695	Fructose-1,6-bisphosphatase isozyme 2	Fbp2	7	7	7	30.4	30.4	30.4	36.947	339	1.4575E-88	0.93395	1.0388	34.447	12	1492200000	754790000	737390000
A6ZI44	Fructose-bisphosphate aldolase;Fructose-bisphosphate aldolase A	Aldoa	21	21	20	60.3	60.3	58.6	45.12	418	0	1.0677	1.0627	67.53	87	8.9365E+10	4.5397E+10	4.3968E+10
P97807	Fumarate hydratase, mitochondrial	Fh	17	17	17	47.7	47.7	47.7	54.356	507	0	0.65581	0.72535	84.981	59	2.3565E+10	1.4834E+10	8730700000
P35505	Fumarylacetoacetase	Fah	6	6	6	21.7	21.7	21.7	46.175	419	2.2832E-44	1.9759	2.132	67.707	5	627970000	219670000	408300000
Q3TC72	Fumarylacetoacetate hydrolase domain-containing protein 2A	Fahd2	7	7	7	33.5	33.5	33.5	34.69	313	1.746E-292	0.97645	1.1041	29.933	9	1301000000	628010000	673030000
Q9D6K8	FUN14 domain-containing protein 2	Fundc2	3	3	3	19.9	19.9	19.9	16.564	151	5.0039E-14	1.2158	1.206	80.007	2	86735000	36622000	50114000
O35601	FYN-binding protein	Fyb	2	2	2	4.5	4.5	4.5	90.054	819	8.7206E-14	0.37655	0.4145	88.241	2	37055000	25594000	11460000
Q8VDC1	FYVE and coiled-coil domain-containing protein 1	Fyco1	3	3	3	2.8	2.8	2.8	162.33	1437	3.7877E-37	0.59936	0.63973	121.28	2	150950000	107300000	43654000
Q9R0N0	Galactokinase	Galk1	3	3	3	8.2	8.2	8.2	42.295	392	1.6172E-07	0.78401	0.69429	37.703	3	155550000	92902000	62650000
P16045	Galectin-1	Lgals1	5	5	5	43.7	43.7	43.7	14.866	135	1.2243E-36	0.68554	0.62807	151.28	10	8266900000	2959600000	5307300000
Q9D7X8	Gamma-glutamylcyclotransferase	Ggct	5	5	5	30.9	30.9	30.9	21.166	188	1.65E-36	0.75836	0.75452	59.819	7	468900000	294070000	174830000
P82348	Gamma-sarcoglycan	Sgcg	2	2	2	11.3	11.3	11.3	32.081	291	2.1957E-09	1.4917	1.3911	2.6246	2	126250000	46679000	79571000
Q9Z0F7	Gamma-synuclein	Sncg	6	6	6	60.2	60.2	60.2	13.159	123	7.275E-146	0.48954	0.53626	50.617	8	593310000	396430000	196880000
P23242	Gap junction alpha-1 protein	Gja1	3	3	3	16	16	16	43.004	382	2.6476E-28	0.46698	0.33979	35.103	3	224700000	144890000	79811000
A2A7A7	GDH/6PGL endoplasmic bifunctional protein	H6pd	2	2	2	3.4	3.4	3.4	89.909	797	2.5845E-07	1.2747	1.5762	58.569	2	37070000	13259000	23812000
Q8VHI3	GDP-fucose protein O-fucosyltransferase 2	Pofut2	4	4	4	12.1	12.1	12.1	49.429	429	8.7111E-22	0.99051	0.89392	62.094	4	39176000	20042000	19133000
P23591	GDP-L-fucose synthase	Tsta3	4	4	4	10.9	10.9	10.9	35.877	321	8.8369E-10	1.4099	1.5175	27.852	3	96805000	41373000	55432000
P13020	Gelsolin	Gsn	5	5	5	10.1	10.1	10.1	85.941	780	4.9919E-26	0.31242	0.34737	102.65	7	283820000	199140000	84677000
Q9Z1Z0	General vesicular transport factor p115	Uso1	9	9	9	15.5	15.5	15.5	106.98	959	2.1E-111	1.5056	1.6761	29.923	8	173160000	65584000	107570000
A0JNY3	Gephyrin	Gphn	4	4	4	8.3	8.3	8.3	83.665	772	1.4272E-43	0.68445	0.65638	55.651	5	138640000	67090000	71546000
Q9WTN0	Geranylgeranyl pyrophosphate synthase	Ggps1	2	2	2	6.7	6.7	6.7	34.706	300	1.9291E-14	0.67065	0.69125	39.446	3	49279000	30213000	19065000
Q9JHK4	Geranylgeranyl transferase type-2 subunit alpha	Rabggta	3	3	3	5.3	5.3	5.3	64.989	567	3.6459E-06	1.1183	1.2865	11.725	3	177830000	87195000	90637000
Q9CQI3	Glia maturation factor beta;Glia maturation factor gamma	Gmfb	2	2	2	26.8	26.8	26.8	16.723	142	1.1809E-17	0.51329	0.74012	26.149	3	62952000	43215000	19737000
E9PYV1	Glucocorticoid receptor	Nr3c1	2	2	2	5.9	5.9	5.9	87.319	793	3.493E-06	0.53951	0.47978	62.792	2	10803000	6637700	4165100
O88958	Glucosamine-6-phosphate isomerase 1	Gnpda1	4	4	3	18.7	18.7	14.9	32.549	289	7.2195E-15	1.1755	1.0812	112.6	4	591990000	270370000	321620000
Q00612	Glucose-6-phosphate 1-dehydrogenase X	G6pdx	5	5	5	10.3	10.3	10.3	59.262	515	8.5488E-13	1.2183	1.2577	41.653	6	149920000	80617000	69298000
P06745	Glucose-6-phosphate isomerase	Gpi	17	17	17	34.2	34.2	34.2	62.766	558	0	0.82745	0.83575	77.929	36	1.0697E+10	5096500000	5600000000
O08795	Glucosidase 2 subunit beta	Prkcsh	4	4	4	8.4	8.4	8.4	58.792	521	3.0376E-38	0.46737	0.56108	61.274	3	88029000	61625000	26404000
P26443	Glutamate dehydrogenase 1, mitochondrial	Glud1	8	8	8	19.9	19.9	19.9	61.336	558	2.19E-155	3.383	3.547	91.371	9	1703900000	331690000	1372200000
P97494	Glutamate--cysteine ligase catalytic subunit	Gclc	4	4	4	7.4	7.4	7.4	72.571	637	1.2438E-08	0.74753	0.74456	39.421	2	46205000	25263000	20942000
O09172	Glutamate--cysteine ligase regulatory subunit	Gclm	4	4	4	19	19	19	30.534	274	4.7869E-46	0.56116	0.60243	21.521	4	259000000	158450000	100560000
D3Z7P3	Glutaminase kidney isoform, mitochondrial	Gls	3	3	3	8.5	8.5	8.5	73.963	674	1.0079E-12	0.65918	0.60052	32.414	4	84074000	48001000	36073000
P15105	Glutamine synthetase	Glul	3	3	3	13.9	13.9	13.9	42.119	373	1.2429E-98	3.2594	2.7125	54.144	5	572480000	111520000	460960000
Q8BML9	Glutaminyl-tRNA synthetase (Protein Qars)	Qars	1	1	1	1.5	1.5	1.5	87.676	775	0.014735	1.44	1.5126	16.968	2	122390000	45705000	76687000
P16406	Glutamyl aminopeptidase	Enpep	3	3	3	3.6	3.6	3.6	107.96	945	3.5332E-06	0.75909	0.75735	76.679	2	31973000	15324000	16649000
Q9CZN8	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	Qrsl1	4	4	4	10.7	10.7	10.7	56.782	525	6.9823E-14	1.4663	1.4129	52.202	4	128000000	56254000	71743000
Q99JT1	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	Pet112	3	3	3	9.5	9.5	9.5	62.118	557	1.1198E-68	0.79972	0.97589	61.257	3	116930000	72173000	44756000
Q9QUH0	Glutaredoxin-1	Glrx	2	2	2	23.4	23.4	23.4	11.871	107	6.0434E-22	0.41183	0.11872	147.4	2	406340000	264030000	142310000
Q9CQM9	Glutaredoxin-3	Glrx3	8	8	8	29.7	29.7	29.7	37.778	337	2.3735E-29	0.48869	0.42319	97.331	9	2699100000	1916000000	783140000
Q80Y14	Glutaredoxin-related protein 5, mitochondrial	Glrx5	3	3	3	27	27	27	16.292	152	9.5552E-56	0.54924	0.64947	25.583	5	1766200000	1163500000	602690000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q60759	Glutaryl-CoA dehydrogenase, mitochondrial	Gcdh	4	4	4	16.9	16.9	16.9	48.605	438	1.2812E-80	1.9276	1.9123	29.924	5	512830000	181640000	331180000
P11352	Glutathione peroxidase 1	Gpx1	5	5	5	33.8	33.8	33.8	22.347	201	2.8495E-53	0.84357	0.87631	92.275	4	534530000	316780000	217750000
P46412	Glutathione peroxidase 3;Glutathione peroxidase	Gpx3	3	3	3	17.3	17.3	17.3	25.442	226	9.4902E-14	1.031	0.93584	68.496	4	627720000	342140000	285580000
P47791	Glutathione reductase, mitochondrial	Gsr	3	3	3	13.2	13.2	13.2	53.662	500	1.4874E-32	1.0813	1.1867	2.0221	3	452300000	226890000	225410000
P30115	Glutathione S-transferase A3	Gsta3	2	2	2	8.1	8.1	8.1	25.36	221	0.00013414	0.84742	0.77044	9.7348	3	229830000	136250000	93581000
P24472	Glutathione S-transferase A4	Gsta4	2	2	2	7.2	7.2	7.2	25.564	222	0.00018403	0.29795	0.27163	164.86	3	1335000000	999270000	335720000
Q9DCM2	Glutathione S-transferase kappa 1	Gstk1	10	10	10	52.2	52.2	52.2	25.704	226	9.711E-140	0.78017	0.75131	88.03	13	1871100000	1045800000	825260000
P10649	Glutathione S-transferase Mu 1	Gstm1	10	9	6	47.7	39.9	25.2	25.97	218	3.888E-258	0.56269	0.60525	55.924	14	2087000000	1366900000	720150000
P15626	Glutathione S-transferase Mu 2	Gstm2	11	11	8	50	50	34.9	25.716	218	6.5507E-75	0.62168	0.65446	53.246	20	5320600000	3545100000	1775600000
P48774	Glutathione S-transferase Mu 5	Gstm5	8	8	8	40.2	40.2	40.2	26.635	224	4.3294E-79	0.87328	0.87082	25.952	8	738660000	409720000	328940000
Q80W21	Glutathione S-transferase Mu 7	Gstm7	6	4	4	30.3	18.3	18.3	25.709	218	1.0929E-51	0.64068	0.57188	84.986	6	644370000	296520000	347850000
O09131	Glutathione S-transferase omega-1	Gsto1	4	4	4	14.2	14.2	14.2	27.497	240	2.1341E-08	0.88539	0.98886	57.268	3	1689600000	707540000	982060000
P19157	Glutathione S-transferase P 1	Gstp1	7	7	7	45.2	45.2	45.2	23.609	210	5.968E-243	0.60075	0.64034	76.34	13	1.2862E+10	7953000000	4909100000
P51855	Glutathione synthetase	Gss	4	4	4	11.4	11.4	11.4	52.246	474	5.3701E-63	1.2149	1.3683	9.8033	7	463740000	175520000	288220000
P16858	Glyceraldehyde-3-phosphate dehydrogenase	Gapdh	15	15	1	56.2	56.2	6	35.81	333	0	0.78823	0.79286	50.46	99	8.3631E+10	4.3958E+10	3.9673E+10
D3Z0Z9	Glyceraldehyde-3-phosphate dehydrogenase	Gm5069	7	1	1	30.9	4.5	4.5	36.487	337	2.8255E-93	0.087554	0.089997	163.53	2	142220000	133920000	8303500
Q64516	Glycerol kinase	Gk	5	5	4	10.9	10.9	8.6	61.227	559	2.7348E-11	0.79513	0.41219	80.919	4	160100000	81128000	78974000
P13707	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	Gpd1	8	8	8	28.1	28.1	28.1	37.572	349	4.1776E-58	0.52422	0.54713	17.301	8	929480000	606690000	322790000
Q3ULJ0	Glycerol-3-phosphate dehydrogenase 1-like protein	Gpd1l	7	7	7	18.8	18.8	18.8	38.225	351	2.4741E-37	0.4623	0.49833	16.315	7	658330000	463300000	195020000
Q8C0L9	Glycerophosphocholine phosphodiesterase GPCPD1	Gpcpd1	3	3	3	7.4	7.4	7.4	76.578	675	1.257E-08	1.3295	1.3745	71.848	3	102590000	52363000	50227000
Q91WK5	Glycine cleavage system H protein, mitochondrial	Gcsh	2	2	2	17.6	17.6	17.6	18.637	170	1.1984E-48	0.63465	0.58045	48.026	4	533450000	332590000	200860000
Q9CZD3	Glycine--tRNA ligase	Gars	9	9	9	15.8	15.8	15.8	81.877	729	5.312E-231	0.62416	0.63544	32.998	17	1710100000	1025000000	685110000
Q9Z1E4	Glycogen [starch] synthase, muscle	Gys1	11	11	11	21.1	21.1	21.1	83.926	738	6.71E-282	1.4819	1.4719	53.174	15	1698200000	747700000	950470000
Q8CI94	Glycogen phosphorylase, brain form	Pygb	28	20	20	42.6	32.4	32.4	96.729	843	0	1.9079	1.8478	101.35	34	1.5193E+10	5032400000	1.0161E+10
Q9WUB3	Glycogen phosphorylase, muscle form;Phosphorylase	Pygm	33	33	24	41.7	41.7	30.2	97.285	842	0	2.1191	2.2155	52.431	57	1.8326E+10	5901200000	1.2425E+10
Q2NL51	Glycogen synthase kinase-3 alpha	Gsk3a	5	5	5	13.5	13.5	13.5	51.66	490	1.9549E-11	0.78395	0.72807	41.382	6	118610000	67956000	50656000
E9QAQ5	Glycogen synthase kinase-3 beta	Gsk3b	4	4	4	16.4	16.4	16.4	47.989	433	1.4863E-25	1.3316	1.6823	85.454	7	393950000	151430000	242530000
K3W4S6	Glycogenin-1	Gyg1	3	3	3	11.7	11.7	11.7	41.926	377	1.0886E-09	0.8219	0.68166	38.418	4	605630000	337080000	268560000
O70310	Glycylpeptide N-tetradecanoyltransferase 1	Nmt1	3	3	3	8.3	8.3	8.3	56.888	496	4.8868E-23	1.5385	1.4926	19.849	3	14672000	5998000	8673900
Q9CPV4	Glyoxalase domain-containing protein 4	Glod4	12	12	12	47.7	47.7	47.7	33.316	298	2.567E-189	0.7001	0.63822	77.973	16	1695800000	995620000	700140000
Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	Grhpr	7	7	7	30.2	30.2	30.2	35.328	328	1.468E-88	1.493	1.7802	53.111	12	3179500000	1303300000	1876100000
Q9QZF2	Glypican-1;Secreted glypican-1	Gpc1	3	3	3	8.1	8.1	8.1	61.359	557	3.4407E-11	1.9513	1.9579	33.587	3	325550000	137590000	187970000
Q9DCZ1	GMP reductase 1	Gmpr	5	5	4	24.3	24.3	22.3	37.482	345	1.456E-232	0.88345	0.64111	62.085	6	755920000	435310000	320610000
Q3THK7	GMP synthase [glutamine-hydrolyzing]	Gmps	6	6	6	14.7	14.7	14.7	76.723	693	1.1489E-23	0.84208	0.71716	51.486	7	452630000	227450000	225180000
Q99JX3	Golgi reassembly-stacking protein 2	Gorasp2	3	3	3	10.9	10.9	10.9	47.038	451	6.705E-117	0.86939	0.97231	16.632	6	390820000	199160000	191670000
Q91VW5	Golgin subfamily A member 4	Golga4	9	9	9	4.6	4.6	4.6	257.56	2238	3.9073E-24	0.73895	0.73295	26.046	8	138790000	75380000	63412000
Q6IR34	G-protein-signaling modulator 1	Gpsm1	4	4	4	10.7	10.7	10.7	74.361	673	6.856E-212	0.47031	0.52744	51.752	2	128720000	78108000	50610000
Q9QYY0	GRB2-associated-binding protein 1	Gab1	3	3	3	6.3	6.3	6.3	76.812	695	2.0361E-12	0.4057	0.29622	67.525	2	69259000	50249000	19010000
Q8C5Q4	G-rich sequence factor 1	Grsf1	3	3	3	10.9	10.9	10.9	53.076	479	1.2641E-11	0.61723	0.46713	30.343	3	135190000	77501000	57688000
A2AEW8	GRIP1-associated protein 1	Gripap1	4	4	4	5.6	5.6	5.6	95.912	837	0	0.66687	0.61734	21.655	5	124870000	78346000	46526000
Q9JLM9	Growth factor receptor-bound protein 14	Grb14	2	2	2	6.3	6.3	6.3	60.572	538	9.4681E-13	1.0942	1.1604	14.89	3	114700000	68173000	46529000
Q60631	Growth factor receptor-bound protein 2	Grb2	6	6	6	27.6	27.6	27.6	25.238	217	4.9119E-17	0.49391	0.38304	81.024	7	967540000	441160000	526380000
Q99LP6	GrpE protein homolog 1, mitochondrial	Grpel1	7	7	7	42.9	42.9	42.9	24.307	217	4.206E-106	0.41473	0.30573	62.301	12	2824800000	1978700000	846030000
Q9WTP7	GTP:AMP phosphotransferase, mitochondrial	Ak3	5	5	5	28.2	28.2	28.2	25.426	227	4.1606E-21	1.1574	1.1744	49.504	6	952350000	551980000	400370000
D3YTN4	GTPase IMAP family member 4	Gimap4	4	4	4	18.6	18.6	18.6	38.044	328	1.5393E-24	0.89027	1.0642	43.975	5	401620000	205080000	196550000
P62827	GTP-binding nuclear protein Ran	Ran	5	5	5	30.6	30.6	30.6	24.423	216	2.018E-108	1.0051	0.94735	66.13	9	1393000000	695820000	697210000
Q61635	GTP-binding protein	Ifi47	2	2	2	6	6	6	46.784	420	0.021464	0.095354	0.076271	254.98	2	1253000000	1240600000	12347000
Q9CQC9	GTP-binding protein SAR1b	Sar1b	3	3	2	17.2	17.2	11.6	22.382	198	2.5957E-09	2.9122	0.7181	213.12	2	472180000	176270000	295910000
Q9R111	Guanine deaminase	Gda	5	5	5	16.3	16.3	16.3	51.012	454	5.405E-39	0.88149	0.80948	65.911	6	427600000	247700000	179910000
E9PXE2	Guanine nucleotide exchange factor DBS	Mcf2l	1	1	1	1.2	1.2	1.2	132.39	1175	0.02229	0.70317	0.7132	33.427	2	533900000	332960000	200940000
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	Gnai2	6	6	6	22.5	22.5	22.5	40.489	355	1.1519E-75	1.2648	1.1606	38.341	5	259980000	111140000	148840000
E9QKR0	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	Gnb2	6	6	3	23	23	11.5	41.408	382	9.4476E-82	1.3481	0.49431	87.121	4	386510000	151490000	235020000
Q6R0H7	Guanine nucleotide-binding protein G(s) subunit alpha isoforms Xlas	Gnas	5	5	5	4.8	4.8	4.8	121.5	1133	8.1741E-51	1.2279	1.2698	79.804	5	316420000	143420000	173000000
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	Gnb2l1	8	8	8	43.8	43.8	43.8	35.076	317	2.21E-173	2.7465	2.2538	69.38	9	792570000	235690000	556880000
Q9ESX5	H/ACA ribonucleoprotein complex subunit 4	Dkc1	1	1	1	3.5	3.5	3.5	57.401	509	9.9116E-29	0.69777	0.60662	10.895	3	14298000	8407200	5890600
P01899	H-2 class I histocompatibility antigen, D-B alpha chain	H2-D1	2	2	1	4.7	4.7	2.8	40.836	362	1.1134E-05	1.3284	1.2341	28.345	3	59395000	25542000	33853000
P01898	H-2 class I histocompatibility antigen, Q10 alpha chain	H2-Q10	4	4	3	13.2	13.2	9.8	37.251	325	1.8062E-09	1.213	1.2464	67.651	4	168060000	96567000	71494000
Q3UGR5	Haloacid dehalogenase-like hydrolase domain-containing protein 2	Hdhd2	2	2	2	9.3	9.3	9.3	28.73	259	3.0486E-05	0.81619	0.7044	51.838	2	48171000	23862000	24309000
Q9CYW4	Haloacid dehalogenase-like hydrolase domain-containing protein 3	Hdhd3	2	2	2	7.6	7.6	7.6	28.027	251	0.00033213	0.82446	0.83323	8.1637	2	158940000	95698000	63240000
Q61646	Haptoglobin;Haptoglobin alpha chain;Haptoglobin beta chain	Hp	7	7	7	22.5	22.5	22.5	38.752	347	8.37E-229	0.10786	0.073954	141.13	8	1716300000	1555200000	161100000
Q69ZS7	HBS1-like protein	Hbs1l	2	2	2	4.3	4.3	4.3	75.1	682	1.3407E-09	0.84407	0.79946	22.709	2	55833000	31140000	24693000
Q61696	Heat shock 70 kDa protein 1A;Heat shock 70 kDa protein 1B	Hspa1a	11	8	6	22.8	15.3	12.3	70.078	641	1.736E-267	0.73871	0.77607	48.095	10	358150000	228030000	130120000
Q3U2G2	Heat shock 70 kDa protein 4	Hspa4	23	23	21	38.7	38.7	35.2	94.208	842	0	0.59846	0.59457	69.1	32	4457100000	2369100000	2088100000
P48722	Heat shock 70 kDa protein 4L	Hspa4l	15	13	13	22.6	19	19	94.381	838	9.43E-127	0.90496	0.79939	67.493	13	811970000	423200000	388770000
P63017	Heat shock cognate 71 kDa protein	Hspa8	24	22	16	45	43.3	29.6	70.87	646	0	0.7104	0.75369	51.594	52	2.6556E+10	1.5628E+10	1.0928E+10
Q61699	Heat shock protein 105 kDa	Hsph1	14	13	13	26.1	24.5	24.5	96.406	858	8.9251E-78	0.55074	0.59167	40.234	17	949250000	589440000	359820000
Q9CQN1	Heat shock protein 75 kDa, mitochondrial	Trap1	13	13	13	25.5	25.5	25.5	80.208	706	7.1322E-89	0.77662	0.6581	56.087	21	2102800000	1222500000	880270000
P14602	Heat shock protein beta-1	Hspb1	7	7	7	48.3	48.3	48.3	23.014	209	2.073E-91	0.35505	0.43326	100.38	14	3899100000	2818200000	1081000000
P35385	Heat shock protein beta-7	Hspb7	4	4	4	29.6	29.6	29.6	18.634	169	4.1111E-26	1.0256	1.156	47.479	7	830290000	420110000	410180000
Q9JK92	Heat shock protein beta-8	Hspb8	1	1	1	4.6	4.6	4.6	21.533	196	0.0087201	0.73691	0.40863	126.45	2	109650000	61197000	48452000
P07901	Heat shock protein HSP 90-alpha	Hsp90aa1	14	8	8	24.6	15.4	15.4	84.787	733	0	0.46378	0.41123	48.617	12	2182300000	1483800000	698480000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P11499	Heat shock protein HSP 90-beta	Hsp90ab1	30	30	22	43.9	43.9	33	83.28	724	0	0.5473	0.59928	56.182	48	2.3985E+10	1.4737E+10	9248500000
P17156	Heat shock-related 70 kDa protein 2	Hspa2	10	2	2	16.7	3.5	3.5	69.641	633	9.035E-163	0.76173	0.81796	4.312	2	73068000	43293000	29776000
P97825	Hematological and neurological expressed 1 protein	Hn1	2	2	2	27.9	27.9	27.9	16.08	154	1.8683E-86	0.40965	0.38478	64.573	3	396380000	295540000	100840000
Q9R257	Heme-binding protein 1	Hebp1	2	2	2	17.9	17.9	17.9	21.067	190	0.00093212	1.2478	1.4215	23.185	2	102450000	50727000	51728000
Q91VB8	Hemoglobin subunit alpha	Hba-a1	11	11	11	90.1	90.1	90.1	15.112	142	0	0.35931	0.30869	95.654	109	2.2834E+11	1.7237E+11	5.5971E+10
P02088	Hemoglobin subunit beta-1	Hbb-b1	12	3	2	88.4	23.1	15	15.84	147	0	3.1209	3.0656	265.24	4	792440000	329920000	462520000
P02089	Hemoglobin subunit beta-2	Hbb-b2	7	2	2	59.9	21.8	21.8	15.878	147	0	3.9465	4.2068	50.067	6	165590000	35598000	129990000
Q91X72	Hemopexin	Hpx	24	24	24	52.6	52.6	52.6	51.317	460	0	0.23636	0.26437	70.307	47	1.276E+10	1.0265E+10	2494800000
P49182	Heparin cofactor 2	Serpind1	4	4	4	7.9	7.9	7.9	54.496	478	1.4078E-08	0.50052	0.53579	133.88	4	402710000	290600000	112120000
P27656	Hepatic triacylglycerol lipase	Lipc	1	1	1	1.8	1.8	1.8	57.388	510	0.036019	2.177	1.8275	2.4583	2	1535300000	435350000	1099900000
P51859	Hepatoma-derived growth factor	Hdgf	10	10	10	53.2	53.2	53.2	26.268	237	2.051E-193	0.39506	0.51803	63.403	10	1401400000	727710000	673660000
Q20BD0	Heterogeneous nuclear ribonucleoprotein A/B	Hnrnpab	5	5	5	20.2	20.2	20.2	36.21	332	1.5224E-46	0.51183	0.29701	125.34	5	964540000	620820000	343720000
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0	Hnrnpa0	2	2	2	11.8	11.8	11.8	30.53	305	4.6399E-25	0.67476	0.72713	71.676	2	207850000	129530000	78318000
Q5EBP8	Heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	2	2	2	7.2	7.2	7.2	38.833	373	7.5972E-07	0.82514	0.78295	38.045	2	352400000	205440000	146960000
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	Hnrnpa3	3	3	3	12.4	12.4	12.4	39.652	379	1.896E-142	0.83187	0.76882	13.708	4	160350000	84143000	76210000
Q60668	Heterogeneous nuclear ribonucleoprotein D0	Hnrnpd	7	7	6	16.6	16.6	14.4	38.354	355	6.7337E-29	0.4817	0.47369	42.192	9	2806900000	1426200000	1380700000
D3YTQ3	Heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	4	3	3	11.2	9.3	9.3	46.27	420	2.3716E-34	0.6058	0.63325	29.829	3	282460000	180090000	102370000
Q8C2Q7	Heterogeneous nuclear ribonucleoprotein H	Hnrnph1	3	3	1	11.4	11.4	4.4	51.217	472	2.492E-109	0.68845	0.68838	13.433	8	468880000	283370000	185510000
P61979	Heterogeneous nuclear ribonucleoprotein K	Hnrnpk	10	10	10	28.7	28.7	28.7	50.976	463	0	0.60692	0.58577	35.88	10	2265700000	1308300000	957460000
Q921F4	Heterogeneous nuclear ribonucleoprotein L-like	Hnrpll	2	2	2	5.9	5.9	5.9	64.124	591	9.857E-10	0.8085	0.89085	7.4625	2	65871000	36679000	29192000
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	Hnrnpm	2	2	2	4.7	4.7	4.7	77.648	729	1.3949E-05	0.68887	0.4456	56.134	2	112680000	66920000	45760000
Q7TMK9	Heterogeneous nuclear ribonucleoprotein Q	Syncrip	8	8	7	14.6	14.6	13.3	69.632	623	2.828E-88	0.75378	0.74584	39.8	9	1159400000	658610000	500760000
Q8VEK3	Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	6	6	6	9.8	9.8	9.8	87.917	800	6.1523E-22	1.3249	1.2379	71.949	8	543860000	221400000	322460000
Q8VDM6	Heterogeneous nuclear ribonucleoprotein U-like protein 1	Hnrnpul1	4	4	4	6.3	6.3	6.3	96.001	859	2.5356E-09	2.3253	2.0125	51.643	3	1698900000	40568000	1658300000
Q00PI9	Heterogeneous nuclear ribonucleoprotein U-like protein 2	Hnrnpul2	3	3	3	6.8	6.8	6.8	84.939	745	9.5273E-16	1.3449	1.5263	57.112	4	113800000	44595000	69207000
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	Hnrnpa2b1	6	6	6	20.4	20.4	20.4	37.402	353	7.9184E-80	0.70471	0.81744	41.13	9	1962100000	1152300000	809880000
Q9Z204	Heterogeneous nuclear ribonucleoproteins C1/C2	Hnrnpc	4	4	4	15.7	15.7	15.7	34.384	313	3.6324E-11	1.0831	1.1725	191.18	3	329780000	86525000	243260000
Q8BMS4	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	Coq3	5	5	5	18.6	18.6	18.6	40.956	370	8.488E-232	0.89579	0.8499	116.92	7	6301900000	711020000	5590900000
P17710	Hexokinase-1	Hk1	18	15	15	22	20	20	108.3	974	5.181E-257	1.2317	1.1015	89.476	12	1509000000	804800000	704180000
O08528	Hexokinase-2	Hk2	25	25	22	33.7	33.7	31.6	102.53	917	0	1.5787	1.5644	72.847	35	1.1396E+10	4275300000	7120400000
P63158	High mobility group protein B1	Hmgb1	3	3	2	14	14	8.4	24.893	215	3.8133E-25	0.4931	0.51678	116.11	3	333900000	103340000	230560000
P30681	High mobility group protein B2	Hmgb2	3	2	2	18.1	12.4	12.4	24.162	210	7.3371E-13	0.32959	0.33756	27.03	2	157820000	116190000	41625000
Q91VF2	Histamine N-methyltransferase	Hnmt	3	3	3	14.2	14.2	14.2	33.664	295	1.1105E-42	0.87277	0.77773	42.389	4	313850000	162620000	151230000
G5E8J6	Histidine rich calcium binding protein, isoform CRA	Hrc	5	5	5	8.8	8.8	8.8	85.171	738	2.853E-103	0.57044	0.64455	16.666	6	771140000	488230000	282920000
P70349	Histidine triad nucleotide-binding protein 1	Hint1	6	6	6	58.7	58.7	58.7	13.777	126	4.167E-126	0.56207	0.69767	52.135	11	5519800000	3505600000	2014100000
Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochondrial	Hint2	4	4	4	39.9	39.9	39.9	17.32	163	4.213E-112	0.7527	0.7942	33.43	18	4222200000	2350200000	1871900000
Q9ESB3	Histidine-rich glycoprotein	Hrg	3	3	3	5	5	5	59.162	525	2.378E-06	0.38416	0.40682	29.077	4	365440000	253640000	111800000
Q61035	Histidine--tRNA ligase, cytoplasmic	Hars	7	7	6	16.1	16.1	14.1	57.432	509	1.3408E-43	0.64265	0.57846	114.64	7	611100000	389820000	221280000
P43274	Histone H1.4	Hist1h1e	5	5	3	22.8	22.8	13.2	21.977	219	1.3199E-10	0.89784	0.93209	19.749	2	207040000	110510000	96523000
Q8CBB6	Histone H2B	Gm13646	3	3	3	24.6	24.6	24.6	14.888	134	4.8394E-42	1.692	1.5811	182.19	3	640570000	243260000	397310000
D3YUP1	Histone-arginine methyltransferase CARM1	Carm1	2	2	2	4.1	4.1	4.1	70.322	651	1.5686E-05	0.80302	0.70786	57.333	2	46164000	30416000	15747000
Q6S9I3	HMW kininogen-II (Protein Kng2)	Kng2	6	4	4	13.4	10.4	10.4	71.272	644	1.8358E-81	0.51138	0.42879	14.228	3	53660000	39678000	13982000
Q8R1H0	Homeodomain-only protein	Hopx	2	2	2	35.6	35.6	35.6	8.2821	73	1.388E-53	0.55515	0.56874	11.246	3	356710000	234250000	122470000
B1AUX2	Host cell factor 1;HCF N-terminal chain 16	Hcfc1	4	4	4	3.8	3.8	3.8	215.05	2090	1.0198E-19	0.64825	0.68968	27.551	4	108280000	63272000	45011000
Q99L47	Hsc70-interacting protein	St13	6	6	6	16.4	16.4	16.4	41.655	371	2.865E-285	0.49096	0.40618	45.856	8	1319600000	867090000	452530000
Q61081	Hsp90 co-chaperone Cdc37	Cdc37	6	6	6	21.6	21.6	21.6	44.593	379	4.1303E-98	0.59008	0.70506	42.024	10	1454600000	887450000	567130000
Q8VD75	Huntingtin-interacting protein 1	Hip1	3	3	3	4.6	4.6	4.6	115.2	1029	1.1723E-12	0.63493	0.6317	38.642	2	58366000	39067000	19299000
Q8R0N6	Hydroxyacid-oxoacid transhydrogenase, mitochondrial	Adhfe1	6	6	6	14.6	14.6	14.6	49.937	465	7.186E-28	0.6078	0.5752	37.692	8	405580000	220370000	185210000
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Hadh	14	14	14	52.2	52.2	52.2	34.463	314	0	1.0443	1.0484	90.394	32	1.8995E+10	8760900000	1.0234E+10
G5E8T9	Hydroxyacylglutathione hydrolase, mitochondrial	Hagh	4	4	4	16.8	16.8	16.8	34.103	309	6.821E-46	0.80001	0.78288	14.389	4	547580000	321560000	226020000
P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	Hmgcl	6	6	6	24.9	24.9	24.9	34.238	325	3.4124E-83	0.97237	0.93014	97.243	10	1978800000	1028500000	950360000
Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2	Hsdl2	17	17	17	49.6	49.6	49.6	54.208	490	0	1.0323	1.0741	82.564	22	6323700000	3071800000	3251800000
P00493	Hypoxanthine-guanine phosphoribosyltransferase	Hprt1	4	4	4	21.6	21.6	21.6	24.57	218	8.0666E-14	0.96627	0.29865	71.163	3	284870000	145580000	139300000
Q9JKR6	Hypoxia up-regulated protein 1	Hyou1	10	10	10	15	15	15	111.18	999	7.644E-177	1.0724	1.0571	63.116	14	706770000	349070000	357700000
P01869	Ig gamma-1 chain C region, membrane-bound form	Ighg1	4	4	4	9.7	9.7	9.7	43.386	393	2.9677E-20	0.21782	0.19662	23.941	6	372560000	297490000	75070000
P01865	Ig gamma-2A chain C region, membrane-bound form	Igh-1a	7	7	6	26.9	26.9	22.9	43.949	398	3.901E-160	0.1102	0.12007	121.64	8	826140000	735710000	90432000
P01867	Ig gamma-2B chain C region	Igh-3	6	6	6	22.8	22.8	22.8	44.259	404	5.501E-154	0.4478	0.44083	32.194	11	1358400000	946770000	411630000
P03987	Ig gamma-3 chain C region		2	2	2	6.8	6.8	6.8	43.929	398	3.8448E-06	0.67253	0.50582	42.457	3	180390000	96118000	84268000
P06330	Ig heavy chain V region AC38 205.12		1	1	1	16.1	16.1	16.1	12.934	118	2.1184E-39	0.26433	0.29391	30.888	2	19617000	16391000	3226300
P01837	Ig kappa chain C region		3	3	3	29.2	29.2	29.2	11.778	106	1.017E-168	0.41418	0.363	66.207	4	585860000	358750000	227110000
P01665	Ig kappa chain V-III region PC 7043		2	2	1	38.7	38.7	22.5	12.002	111	3.2418E-49	0.58886	0.65474	41.358	3	872680000	578500000	294180000
P01675	Ig kappa chain V-VI region XRPC 44		2	2	2	29.9	29.9	29.9	11.627	107	1.0844E-15	0.19734	0.19323	9.8339	3	241860000	204730000	37125000
P01843	Ig lambda-1 chain C region		2	2	2	34.3	34.3	34.3	11.575	105	1.285E-100	0.21977	0.27486	104.12	5	235000000	148790000	86207000
P01872	Ig mu chain C region secreted form	Igh-6	12	12	12	29.7	29.7	29.7	49.971	454	2.762E-263	0.20563	0.21114	70.21	15	3813900000	3163000000	650950000
Q61249	Immunoglobulin-binding protein 1	Igbp1	3	3	3	10.3	10.3	10.3	38.97	340	3.882E-11	0.36092	0.39868	71.601	4	219030000	158940000	60094000
Q60960	Importin subunit alpha-1	Kpna1	2	2	2	4.6	4.6	4.6	60.182	538	2.8113E-06	1.4596	1.3	98.941	2	60167000	13104000	47063000
P52293	Importin subunit alpha-2	Kpna2	2	2	2	4.9	4.9	4.9	57.927	529	0.00051717	1.3506	1.3548	11.5	2	23612000	10066000	13546000
O35344	Importin subunit alpha-3	Kpna3	4	4	3	13.2	13.2	7.9	57.772	521	5.2484E-40	1.1771	1.1706	108.1	3	226680000	92289000	134400000
P70168	Importin subunit beta-1	Kpnb1	13	13	13	21.1	21.1	21.1	97.183	876	1.445E-52	1.287	1.2592	40.6	18	2260500000	420510000	1840000000
Q8BKC5	Importin-5	Ipo5	11	11	11	15	15	15	123.59	1097	9.6309E-70	1.26	1.3698	55.82	13	1015200000	531150000	484070000
Q9EPL8	Importin-7	Ipo7	9	9	9	11	11	11	119.49	1038	8.0174E-28	1.2001	1.0143	56.504	11	456040000	183680000	272360000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P40936	Indolethylamine N-methyltransferase	Inmt	4	4	4	23.5	23.5	23.5	29.459	264	2.694E-135	0.42685	0.32654	53.772	8	441450000	310730000	130730000
Q920Q8	Influenza virus NS1A-binding protein homolog	Ivns1abp	5	5	5	9.3	9.3	9.3	71.58	642	2.8348E-12	2.8117	2.5565	54.203	2	21248000	5299500	15949000
Q9DBD0	Inhibitor of carbonic anhydrase	Ica	8	8	8	12.1	12.1	12.1	76.765	700	1.4563E-50	0.82476	0.83174	55.115	9	437100000	222560000	214540000
Q9D819	Inorganic pyrophosphatase	Ppa1	13	13	13	61.6	61.6	61.6	32.667	289	5.42E-267	0.52069	0.45098	63.939	11	2135100000	1358800000	776290000
Q91VM9	Inorganic pyrophosphatase 2, mitochondrial	Ppa2	13	13	13	46.4	46.4	46.4	38.114	330	7.133E-236	0.89649	0.80761	64.264	24	4205500000	2203200000	2002300000
P70227	Inositol 1,4,5-trisphosphate receptor type 3	Itpr3	2	2	2	0.8	0.8	0.8	304.27	2670	0.0022094	0.34036	0.21101	327.12	3	2.0199E+10	1.4632E+10	5566900000
E9Q9J4	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2	Ppip5k2	2	2	2	2.1	2.1	2.1	140.37	1242	0.0012821	1.1945	1.1391	8.9457	2	19004000	10811000	8193100
Q924B0	Inositol monophosphatase 1	Impa1	3	3	3	18.8	18.8	18.8	30.429	277	1.1059E-13	0.67394	0.72542	7.2993	2	126960000	84181000	42779000
Q91UZ5	Inositol monophosphatase 2	Impa2	3	3	3	17.9	17.9	17.9	31.716	290	7.5708E-47	0.83382	0.79792	12.884	3	289900000	153020000	136880000
P49442	Inositol polyphosphate 1-phosphatase	Inpp1	2	2	2	7.1	7.1	7.1	43.346	396	6.8191E-25	0.91145	0.65734	38.767	2	196930000	89042000	107880000
Q9Z0Y7	Insulin receptor substrate 4	Irs4	1	1	1	0.7	0.7	0.7	130.15	1216	0.044734	1.198	1.0539	15.517	2	99167000	44147000	55020000
F6RPJ9	Insulin-degrading enzyme	Ide	7	7	7	8.3	8.3	8.3	114.15	987	4.2923E-17	1.804	1.7196	41.731	5	336540000	143060000	193490000
F8WH23	Insulin-like growth factor-binding protein 7	Igfbp7	4	4	4	17.7	17.7	17.7	29.1	282	1.198E-175	0.61593	0.55805	19.253	3	162520000	99910000	62608000
Q61739	Integrin alpha-6	Itga6	4	4	4	4.3	4.3	4.3	122.16	1091	9.9362E-41	0.57411	0.6656	14.157	4	127650000	79120000	48534000
G3X9Q1	Integrin alpha-7	Itga7	9	9	9	13.5	13.5	13.5	124.61	1136	1.5773E-46	0.75581	0.81139	30.888	6	262050000	162650000	99403000
P09055	Integrin beta-1	Itgb1	10	10	10	16.4	16.4	16.4	88.231	798	2.017E-71	0.60667	0.55401	85.411	9	1151200000	707120000	444060000
O55222	Integrin-linked protein kinase	Ilk	6	6	6	19.9	19.9	19.9	51.373	452	2.6971E-87	0.82233	0.71782	36.703	6	573090000	326590000	246490000
A6X935	Inter alpha-trypsin inhibitor, heavy chain 4	Itih4	12	12	12	15.1	15.1	15.1	104.66	942	3.1752E-64	0.31193	0.33662	45.575	8	372520000	270000000	102520000
Q61702	Inter-alpha-trypsin inhibitor heavy chain H1	Itih1	8	8	8	16.6	16.6	16.6	101.07	907	2.3922E-58	0.6205	0.60239	26.819	7	258280000	154430000	103850000
G3X977	Inter-alpha-trypsin inhibitor heavy chain H2	Itih2	5	5	5	8.1	8.1	8.1	106.36	950	1.887E-138	0.46979	0.47375	48.973	5	576350000	401450000	174900000
Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	Itih3	4	4	4	6.3	6.3	6.3	99.357	889	1.6064E-37	0.48162	0.56699	114.81	3	271660000	171300000	100360000
E9Q1P8	Interferon regulatory factor 2-binding protein 2	Irf2bp2	2	2	2	6	6	6	59.291	570	6.6654E-11	0.42111	0.52497	32.397	2	34595000	23707000	10888000
P70671	Interferon regulatory factor 3	Irf3	2	2	2	7.9	7.9	7.9	46.852	419	9.6984E-07	0.61248	0.56184	42.326	2	45381000	27777000	17604000
P15092	Interferon-activable protein 204	Ifi204	3	2	2	6.7	5.6	5.6	71.65	640	1.3624E-28	0.75879	0.71061	10.891	3	13835000	8251100	5584400
Q08619	Interferon-activable protein 205-B	Ifi205b	4	4	1	15.1	15.1	8.5	46.977	425	6.513E-32	1.2239	1.0536	46.951	6	207380000	87491000	119890000
Q3UVZ1	Interleukin-1 receptor accessory protein	Il1rap	5	5	5	8.9	8.9	8.9	78.639	685	6.1996E-12	0.3431	0.32555	48.435	6	233030000	168070000	64960000
I3ITR1	Iron-sulfur cluster assembly 1 homolog, mitochondrial	Isca1	1	1	1	11.6	11.6	11.6	14.218	129	3.691E-60	0.58105	0.51745	9.3502	3	385680000	243430000	142250000
Q9DCB8	Iron-sulfur cluster assembly 2 homolog, mitochondrial	Isca2	7	7	7	56.5	56.5	56.5	16.718	154	3.76E-139	0.53462	0.493	76.364	8	1739800000	1147100000	592620000
Q9D7P6	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	Iscu	2	2	2	18.5	18.5	18.5	18.098	168	3.2117E-53	0.58104	0.39373	34.892	6	357170000	209670000	147500000
Q8K3A0	Iron-sulfur cluster co-chaperone protein HscB, mitochondrial	Hscb	6	6	6	28.6	28.6	28.6	26.645	234	0	0.45292	0.61158	259.02	3	1135200000	204850000	930390000
Q9DB29	Isoamyl acetate-hydrolyzing esterase 1 homolog	Iah1	2	2	2	11.2	11.2	11.2	27.974	249	0.00037579	1.5551	1.543	16.92	3	300750000	139500000	161250000
Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	Acad8	6	6	6	20.6	20.6	20.6	45.019	413	1.689E-170	2.5072	2.731	64.755	9	1180700000	314160000	866500000
Q91V64	Isochorismatase domain-containing protein 1	Isoc1	5	5	5	21.5	21.5	21.5	32.032	297	1.7854E-21	0.70132	0.85373	97.441	6	3293400000	1364500000	1928900000
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	Isoc2a	4	4	4	43.7	43.7	43.7	22.417	206	3.5031E-38	1.4844	1.3258	70.903	8	2916100000	1217500000	1698600000
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Idh3a	16	16	16	44.8	44.8	44.8	39.638	366	0	0.7097	0.71494	59.82	52	1.7617E+10	1.0529E+10	7088300000
P70404	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	Idh3g	9	9	9	38.2	38.2	38.2	42.785	393	0	1.339	1.2899	41.1	28	1.1005E+10	4724500000	6280100000
Q91VA7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	Idh3b	6	6	6	25.5	25.5	25.5	42.194	384	7.438E-282	0.87152	0.95247	35.709	27	3966700000	2017000000	1949700000
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	Idh1	13	12	12	33.3	31.6	31.6	46.674	414	1.318E-260	1.2157	1.104	99.365	13	2242100000	776150000	1465900000
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	Idh2	27	27	26	53.5	53.5	52	50.906	452	0	1.5781	1.5756	63.255	99	3.5981E+10	1.1848E+10	2.4133E+10
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic	Iars	7	7	7	7.1	7.1	7.1	144.27	1262	8.8639E-10	1.5471	1.6802	10.564	7	355330000	146700000	208640000
Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	Iars2	14	14	14	16.5	16.5	16.5	112.8	1012	8.352E-141	1.1651	1.1071	54.546	18	2164400000	864650000	1299700000
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	Ivd	10	10	10	32.3	32.3	32.3	46.325	424	0	1.0784	1.1336	67.738	20	1.0863E+10	5624800000	5237800000
Q9CX00	IST1 homolog	Ist1	2	2	2	4.1	4.1	4.1	39.468	362	0.0016997	0.36631	0.28299	11.044	2	43288000	29495000	13793000
Q02257	Junction plakoglobin	Jup	5	5	4	6.7	6.7	5.4	81.8	745	1.9769E-19	1.1255	1.3194	105.89	5	319570000	152100000	167470000
Q9ET78	Junctophilin-2	Jph2	4	4	4	9.9	9.9	9.9	74.691	696	1.9395E-19	1.3348	1.6044	82.738	5	240810000	110130000	130680000
A2CG49	Kalirin	Kalrn	2	2	2	0.9	0.9	0.9	337	2964	0.0022603	0.5376	0.67034	21.358	3	2537600000	1748500000	789080000
A2AUC9	Kelch-like protein 41	Kbtbd10	6	6	6	13.9	13.9	13.9	68.189	606	2.897E-125	0.76593	0.84167	43.198	8	461440000	264220000	197220000
E9Q1Q9	Ketohexokinase	Khk	2	2	2	8.5	8.5	8.5	37.724	343	3.0616E-06	0.41571	0.42342	0.061072	2	51758000	34967000	16791000
F8VQC7	Kinectin	Ktn1	14	14	14	15.1	15.1	15.1	152.54	1327	1.67E-130	1.2201	1.0621	50.96	14	870010000	382010000	488000000
Q61768	Kinesin-1 heavy chain	Kif5b	13	13	11	17.9	17.9	15	109.55	963	6.157E-161	0.73057	0.52228	58.179	16	775760000	472410000	303340000
F8VQ75	Kinesin-like protein KIF13A	Kif13a	7	7	5	6.4	6.4	5.1	195.7	1749	1.124E-33	0.53002	0.60012	32.545	6	151650000	91276000	60370000
O08677	Kininogen-1	Kng1	13	13	11	25.1	25.1	22.2	73.101	661	0	0.33278	0.3439	68.115	27	9865600000	7406500000	2459100000
Q8BX02	KN motif and ankyrin repeat domain-containing protein 2	Kank2	2	2	2	5.2	5.2	5.2	90.244	843	5.7089E-11	2.2371	2.3599	33.1	2	40823000	9697300	31126000
Q8BTY1	Kynurenine--oxoglutarate transaminase 1	Ccbl1	7	7	7	24.1	24.1	24.1	47.563	424	1.4279E-63	1.0267	0.98276	15.946	10	1024800000	525840000	498990000
Q71RI9	Kynurenine--oxoglutarate transaminase 3	Ccbl2	5	5	5	15.8	15.8	15.8	51.126	455	1.1333E-38	1.4143	1.6342	13.385	6	687940000	291740000	396210000
Q91YP0	L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2hgdh	6	6	6	14.9	14.9	14.9	50.898	464	7.0701E-16	1.5978	1.7007	31.885	6	216360000	93350000	123010000
Q3V384	Lactation elevated protein 1	Lace1	4	4	4	13.8	13.8	13.8	54.313	480	2.672E-109	0.68039	0.57312	30.464	4	280450000	183590000	96861000
Q9CPU0	Lactoylglutathione lyase	Glo1	9	9	9	46.7	46.7	46.7	20.809	184	1.1202E-97	0.66033	0.65429	55.725	15	1675700000	1066100000	609640000
Q99KP3	Lambda-crystallin homolog	Cryl1	3	3	3	13.2	13.2	13.2	35.208	319	8.8729E-23	0.89363	0.82956	7.1204	2	116210000	63508000	52698000
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta	Tmpo	4	4	4	11.5	11.5	11.5	75.167	693	3.966E-56	0.85182	0.93043	34.237	4	258130000	131290000	126840000
Q60675	Laminin subunit alpha-2	Lama2	57	57	57	27.4	27.4	27.4	343.81	3118	0	0.85111	0.81297	57.705	85	8128200000	4359500000	3768700000
P97927	Laminin subunit alpha-4	Lama4	17	17	17	12.2	12.2	12.2	201.82	1816	5.981E-141	0.8494	0.77114	53.249	14	1193500000	674330000	519150000
Q61001	Laminin subunit alpha-5	Lama5	6	6	6	1.7	1.7	1.7	404.05	3718	3.9458E-15	1.3588	1.448	24.209	4	75861000	32921000	42940000
E9QN70	Laminin subunit beta-1	Lamb1	23	23	23	17.7	17.7	17.7	202.44	1834	1.686E-244	0.92678	0.87966	61.739	32	4841100000	2520800000	2320300000
Q61292	Laminin subunit beta-2	Lamb2	18	18	18	13.6	13.6	13.6	196.58	1799	0	1.3013	1.4443	43.045	13	972990000	420260000	552730000
F8VQJ3	Laminin subunit gamma-1	Lamc1	36	36	3	32.8	32.8	2.6	177.19	1607	0	0.89311	0.87218	27.235	41	4578700000	2513700000	2065000000
Q9CQF6	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	Aasdhppt	2	2	2	6.8	6.8	6.8	35.764	309	0.00019648	1.088	1.0437	19.908	2	29111000	15333000	13778000
O89112	LanC-like protein 1	Lancl1	3	3	3	10.5	10.5	10.5	45.341	399	4.0064E-17	2.2723	2.3233	22.256	3	191410000	54494000	136910000
Q9Z1R2	Large proline-rich protein BAG6	Bag6	6	6	6	8.2	8.2	8.2	121.04	1154	3.4459E-77	0.96689	1.1544	38.566	7	430180000	213920000	216260000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8C0M9	L-asparaginase	Asrgl1	7	7	7	31.6	31.6	31.6	33.95	326	7.358E-130	0.52477	0.48194	40.262	12	1907600000	1305000000	602600000
Q8K4G1	Latent-transforming growth factor beta-binding protein 4	Ltbp4	6	6	6	5.8	5.8	5.8	178.64	1666	1.1126E-61	0.91541	0.93688	24.665	8	108470000	52552000	55917000
Q9ERE7	LDLR chaperone MESD	Mesdc2	1	1	1	8.9	8.9	8.9	25.206	224	2.5063E-50	0.4443	0.47823	12.104	2	342140000	250030000	92115000
Q9Z2I0	LETM1 and EF-hand domain-containing protein 1, mitochondrial	Letm1	5	5	5	11.2	11.2	11.2	82.988	738	4.133E-140	0.9191	0.89031	55.013	9	1372800000	673700000	699090000
Q9JHQ5	Leucine zipper transcription factor-like protein 1	Lztfl1	2	2	2	10.7	10.7	10.7	34.773	299	1.8415E-11	0.40968	0.38901	14.695	4	326960000	235490000	91475000
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	Lrpprc	38	38	38	34.3	34.3	34.3	156.61	1392	0	1.0666	1.1039	64.209	54	8982800000	4512300000	4470500000
Q8CI70	Leucine-rich repeat-containing protein 20	Lrrc20	2	2	2	9.2	9.2	9.2	20.809	184	0.0059681	0.22961	0.17842	25.006	2	165410000	139450000	25962000
Q8BMJ2	Leucine--tRNA ligase, cytoplasmic	Lars	5	5	5	5	5	5	134.19	1178	7.0843E-12	1.5159	0.74616	63.259	4	198220000	84887000	113330000
Q8C129	Leucyl-cystinyl aminopeptidase	Lnpep	5	5	5	6.4	6.4	6.4	117.3	1025	2.043E-13	0.92632	0.99023	96.951	4	93991000	36448000	57543000
P42703	Leukemia inhibitory factor receptor	Lifr	4	4	4	5.5	5.5	5.5	122.57	1092	1.673E-138	0.3649	0.35165	69.338	7	285190000	200340000	84853000
Q9D154	Leukocyte elastase inhibitor A	Serpinb1a	2	2	2	5.5	5.5	5.5	42.574	379	2.5369E-07	0.51777	0.45266	11.47	2	127750000	79028000	48719000
P24527	Leukotriene A-4 hydrolase	Lta4h	11	11	11	22.9	22.9	22.9	69.05	611	0	0.8101	0.77882	92.713	15	2387500000	1346400000	1041200000
D3YU59	LIM and calponin homology domains-containing protein 1	Limch1	7	7	7	10.8	10.8	10.8	120.99	1083	9.2993E-27	1.0255	1.0255	68.346	9	468510000	239870000	228640000
Q8VEE1	LIM and cysteine-rich domains protein 1	Lmcd1	3	3	3	10.1	10.1	10.1	40.996	365	1.4239E-18	0.64966	0.72353	6.3299	4	267510000	159200000	108310000
Q9D7B2	LIM and senescent cell antigen-like-containing domain protein 1	Lims1	5	5	5	16.9	16.9	16.9	45.593	396	1.4713E-12	0.7681	0.89121	153.47	6	717940000	415340000	302600000
Q61792	LIM and SH3 domain protein 1	Lasp1	3	3	3	14.8	14.8	14.8	29.994	263	8.3256E-32	0.63584	0.5913	38.52	4	231290000	130930000	100360000
Q9JKS4	LIM domain-binding protein 3	Ldb3	18	18	5	39.1	39.1	13.7	76.431	723	0	1.1065	0.8156	125.83	33	1.1193E+10	6723000000	4470100000
E9PYJ9	LIM domain-binding protein 3	Ldb3	14	1	1	32.5	2.1	2.1	72.312	679	0	0.5223	0.61559	32.565	3	83498000	56202000	27296000
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	Dbt	9	9	9	27.2	27.2	27.2	53.246	482	5.981E-121	0.73806	0.73182	34.775	15	2042200000	1149200000	893020000
Q8BFW7	Lipoma-preferred partner homolog	Lpp	4	4	4	9.8	9.8	9.8	65.89	613	2.1525E-07	0.7114	0.73756	39.722	3	367610000	232500000	135100000
P11152	Lipoprotein lipase	Lpl	5	5	5	11.6	11.6	11.6	53.109	474	7.0073E-30	1.0909	1.1716	52.822	8	796070000	374530000	421540000
Q99M04	Lipoyl synthase, mitochondrial;Lipoyl synthase, mitochondrial A	Lias	5	5	5	14.2	14.2	14.2	41.879	373	1.0566E-13	0.6747	0.45653	120.57	6	296100000	210280000	85824000
G3X9J4	LisH domain and HEAT repeat-containing protein KIAA1468	2310035C23Rik	2	2	2	2	2	2	134.57	1216	5.3755E-07	0.86909	1.0167	48.492	2	29101000	15139000	13962000
P16125	L-lactate dehydrogenase B chain;L-lactate dehydrogenase	Ldhb	17	17	15	47.9	47.9	40.4	36.572	334	0	0.64363	0.59438	70.128	65	1.2117E+11	7.3153E+10	4.8016E+10
G5E8N5	L-lactate dehydrogenase;L-lactate dehydrogenase A chain	Ldha	14	12	12	41	34.1	34.1	39.758	361	0	0.82059	0.79095	83.444	27	8856500000	4326500000	4530000000
Q8CGK3	Lon protease homolog, mitochondrial	Lonp1	17	17	16	22.3	22.3	21.6	105.84	949	2.863E-222	0.57472	0.58127	50.645	20	2297900000	1436800000	861140000
P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadl	12	12	12	30.2	30.2	30.2	47.907	430	2.063E-201	1.3191	1.315	111.09	28	2.2755E+10	9174200000	1.3581E+10
D3Z041	Long-chain-fatty-acid--CoA ligase 1	Acsl1	16	16	16	28.8	28.8	28.8	78.034	699	3.049E-107	1.8058	1.7245	69.515	21	5544900000	2019200000	3525700000
Q9D358	Low molecular weight phosphotyrosine protein phosphatase	Acp1	1	1	1	11.4	11.4	11.4	18.192	158	1.3953E-20	1.1464	1.1857	7.7581	2	150160000	60578000	89586000
P51885	Lumican	Lum	8	8	8	31.4	31.4	31.4	38.265	338	1.844E-274	0.27038	0.25614	137.98	14	5676500000	4435100000	1241400000
P32067	Lupus La protein homolog	Ssb	4	4	4	10.8	10.8	10.8	47.756	415	2.3396E-12	1.0033	1.1106	78.211	5	232050000	120970000	111080000
Q8K215	LYR motif-containing protein 4	Lyrm4	2	2	2	24.2	24.2	24.2	10.854	91	5.6853E-20	1.3077	1.4865	52.382	2	196880000	80570000	116310000
Q9DA03	LYR motif-containing protein 7	Lyrm7	2	2	2	34.6	34.6	34.6	12.047	104	2.1418E-56	0.3972	0.40424	77.327	2	206640000	160180000	46458000
Q8BP40	Lysophosphatidic acid phosphatase type 6	Acp6	8	8	8	26.8	26.8	26.8	47.624	418	2.572E-150	0.51824	0.49629	44.925	9	1232000000	824060000	407990000
P70699	Lysosomal alpha-glucosidase	Gaa	2	2	2	2.9	2.9	2.9	106.25	953	2.6209E-12	2.5028	2.9743	79.863	2	85597000	28717000	56879000
O09159	Lysosomal alpha-mannosidase	Man2b1	3	3	3	3.2	3.2	3.2	114.65	1013	5.4952E-09	0.63728	0.59461	44.468	3	67643000	34382000	33261000
P10619	Lysosomal protective protein	CTSA	10	10	10	20.6	20.6	20.6	54.465	480	0	5.1477	4.9871	183.23	65	7.7761E+10	1127500000	7.6634E+10
O35448	Lysosomal thioesterase PPT2	Ppt2	2	2	2	7.3	7.3	7.3	34.366	302	0.000134	0.19231	0.17673	124.92	2	33042000	29306000	3736000
P11438	Lysosome-associated membrane glycoprotein 1	Lamp1	2	2	2	5.7	5.7	5.7	43.865	406	1.8181E-14	3.4539	0.64948	39.842	2	282090000	74892000	207200000
P17047	Lysosome-associated membrane glycoprotein 2	Lamp2	3	3	3	6.5	6.5	6.5	45.681	415	6.1003E-06	1.1188	0.76745	201.73	2	133310000	50539000	82776000
Q8R2P8	Lysyl-tRNA synthetase;Lysine--tRNA ligase	Kars	7	7	7	17	17	17	71.29	624	2.517E-174	1.1855	1.1896	47.367	9	1169200000	468590000	700590000
Q9DAR7	m7GpppX diphosphatase	Dcps	8	8	8	37.3	37.3	37.3	38.988	338	1.7306E-76	0.85344	0.83215	59.195	8	359630000	198750000	160880000
Q61830	Macrophage mannose receptor 1	Mrc1	7	7	7	5.8	5.8	5.8	164.98	1456	1.0695E-25	0.59017	0.6264	136.53	6	240050000	160210000	79843000
P34884	Macrophage migration inhibitory factor	Mif	2	2	2	24.3	24.3	24.3	12.504	115	1.63E-243	0.65491	0.62805	26.461	18	1237500000	739890000	497640000
Q99LB4	Macrophage-capping protein	Capg	6	6	6	23.2	23.2	23.2	38.768	349	4.51E-157	1.1909	1.1474	85.697	5	822870000	421770000	401100000
Q9D967	Magnesium-dependent phosphatase 1	Mdp1	3	3	3	26.8	26.8	26.8	18.582	164	5.67E-27	1.5929	1.606	50.504	2	165880000	69259000	96616000
E9PVW0	Major urinary protein 17	Mup13	5	5	2	29.8	29.8	8.9	26.848	235	8.2974E-62	0.32907	0.30431	46.136	5	611980000	464000000	147980000
P11589	Major urinary protein 2	Mup2	4	1	1	32.2	5	5	20.663	180	3.4452E-62	0.54559	0.45109	66.13	2	133270000	103770000	29494000
E9Q3X0	Major vault protein	Mvp	4	4	4	6.3	6.3	6.3	96.856	870	1.67E-12	1.1833	1.2387	51.888	6	348340000	194580000	153770000
P14152	Malate dehydrogenase, cytoplasmic	Mdh1	16	16	16	41.3	41.3	41.3	36.511	334	0	0.59492	0.61877	93.657	49	9.0323E+10	5.5399E+10	3.4924E+10
P08249	Malate dehydrogenase, mitochondrial	Mdh2	19	19	19	60.1	60.1	60.1	35.611	338	0	0.75741	0.71963	80.311	204	8.0909E+10	4.643E+10	3.4479E+10
Q9WVL0	Maleylacetoacetate isomerase	Gstz1	4	4	4	28.7	28.7	28.7	24.275	216	9.6957E-73	1.0511	1.1587	73.812	4	680470000	321840000	358630000
Q9DB27	Malignant T-cell-amplified sequence 1	Mcts1	2	2	2	19.3	19.3	19.3	20.555	181	2.2612E-13	1.1557	0.88174	110.19	4	209670000	74354000	135320000
Q99J39	Malonyl-CoA decarboxylase, mitochondrial	Mlycd	11	11	11	34.8	34.8	34.8	54.735	492	1.741E-192	1.7623	1.8375	36.956	13	1291300000	501240000	790090000
Q8R3F5	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	Mcat	2	2	2	9.2	9.2	9.2	41.928	381	9.722E-07	0.91656	1.0521	144.14	2	30569000	15968000	14601000
Q99M71	Mammalian ependymin-related protein 1	Epdr1	3	3	3	12.9	12.9	12.9	25.485	224	5.7134E-07	2.4361	1.4082	117.26	2	175050000	78320000	96729000
Q922H4	Mannose-1-phosphate guanyltransferase alpha	Gmppa	1	1	1	3.3	3.3	3.3	46.244	420	2.1355E-05	1.2506	1.1035	4.4516	2	23116000	9871000	13245000
Q8BTZ7	Mannose-1-phosphate guanyltransferase beta	Gmppb	3	3	3	11.4	11.4	11.4	39.916	360	1.0819E-07	0.81159	0.90219	142.16	4	338490000	235090000	103400000
Q924M7	Mannose-6-phosphate isomerase	Mpi	11	11	11	36.2	36.2	36.2	46.575	423	8.038E-238	0.646	0.59713	76.008	23	4087200000	2497700000	1589500000
P41317	Mannose-binding protein C	Mbl2	2	2	2	11.5	11.5	11.5	25.957	244	1.8678E-38	0.6719	0.69393	10.443	2	49767000	30632000	19135000
P49138	MAP kinase-activated protein kinase 2	Mapkapk2	5	5	5	17.6	17.6	17.6	44.049	386	1.6822E-16	0.80125	0.70968	64.874	7	421990000	231780000	190220000
A2AJI0	MAP7 domain-containing protein 1	Map7d1	3	3	3	4.1	4.1	4.1	93.275	846	5.4042E-10	0.91624	0.86809	29.226	5	127350000	66466000	60880000
Q9CZH7	Matrix-remodeling-associated protein 7	Mxra7	1	1	1	9.6	9.6	9.6	19.457	178	0.00068477	0.9222	0.92116	12.109	2	19724000	9582500	10141000
Q61908	Mature T-cell proliferation 1 neighbor protein	Mtcp1	1	1	1	20.6	20.6	20.6	7.743	68	0.00038551	0.53609	0.55049	9.1368	2	109510000	70537000	38978000
D3Z3N4	MCG11326, isoform CRA_a (Protein Hnrnph3)	Hnrnph3	1	1	1	4.9	4.9	4.9	36.869	346	3.4099E-90	0.90386	0.92368	28.911	4	132570000	70312000	62260000
Q792Z1	MCG140784 (Protein Try10) (Trypsin 10) (Trypsinogen 10)	Try10	1	1	1	4.1	4.1	4.1	26.221	246	0.0029009	0.24323	0.13449	36.289	2	112800000	82795000	30002000
G5E895	MCG142264, isoform CRA_b (Protein Akr1b10)	Akr1b10	5	5	3	29.4	29.4	22.2	35.848	316	0	1.0793	0.93485	25.592	13	3740600000	1811600000	1929100000
G3X8U3	MCG6895 (Protein 2210016F16Rik)	2210016F16Rik	7	7	7	24.3	24.3	24.3	38.615	338	2.5392E-16	1.0111	0.99233	45.141	9	474240000	238360000	235880000
P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadm	17	17	17	38.7	38.7	38.7	46.481	421	0	1.0515	1.0696	68.684	41	5501000000	2682600000	2818400000
Q8BJ34	Meiosis arrest female protein 1	Marf1	2	2	2	0.9	0.9	0.9	192.06	1730	0.00031516	1.4731	1.5425	176.97	3	656460000	272530000	383930000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O70423	Membrane primary amine oxidase	Aoc3	2	2	2	4.8	4.8	4.8	84.533	765	3.183E-184	0.85102	0.8592	20.772	2	94668000	52425000	42243000
Q3UI33	Methionine aminopeptidase;Methionine aminopeptidase 2	Metap2	7	7	7	23	23	23	54.117	488	6.8464E-65	1.1176	1.0018	81.121	7	879110000	428640000	450470000
Q78J03	Methionine-R-sulfoxide reductase B2, mitochondrial	Msrb2	8	8	8	46.9	46.9	46.9	19.157	175	6.407E-109	0.40202	0.37	40.934	9	1270000000	803200000	466820000
Q8BU85	Methionine-R-sulfoxide reductase B3, mitochondrial	Msrb3	3	3	3	19.4	19.4	19.4	26.832	253	1.3765E-21	0.6893	0.77044	18.116	2	83401000	52536000	30865000
E9QB02	Methionine--tRNA ligase, cytoplasmic	Mars	4	4	4	5.8	5.8	5.8	102.37	910	1.4276E-16	1.2328	1.2893	35.733	3	226560000	95270000	131290000
Q499X9	Methionine--tRNA ligase, mitochondrial	Mars2	5	5	5	10.1	10.1	10.1	65.804	586	7.0945E-13	1.5228	1.445	52.016	5	207410000	79088000	128320000
Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	Mccc2	10	10	10	25	25	25	61.378	563	7.6769E-39	1.3339	1.4584	30.809	10	857610000	347700000	509910000
Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	Mccc1	10	10	10	21.5	21.5	21.5	79.343	717	3.9445E-80	0.78034	0.73547	59.48	10	1268500000	686480000	582030000
Q9JLZ3	Methylglutaconyl-CoA hydratase, mitochondrial	Auh	5	5	5	17.8	17.8	17.8	33.395	314	3.721E-283	1.2178	1.0903	78.818	10	2512300000	1019800000	1492400000
Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Aldh6a1	18	18	18	48.4	48.4	48.4	57.915	535	0	1.16	1.0026	101.81	29	8130100000	3756400000	4373700000
Q8C7H1	Methylmalonic aciduria type A homolog, mitochondrial	Mmaa	3	3	3	10.6	10.6	10.6	45.932	415	2.3061E-14	1.4446	1.4787	54.576	3	97343000	48236000	49107000
Q9D1I5	Methylmalonyl-CoA epimerase, mitochondrial	Mcee	2	2	2	18	18	18	19.017	178	2.4484E-45	0.55403	0.4774	40.894	6	414320000	264510000	149810000
P16332	Methylmalonyl-CoA mutase, mitochondrial	Mut	11	11	11	21	21	21	82.843	748	1.614E-187	1.2005	0.99467	100.16	12	2112100000	901220000	1210900000
Q9CQT1	Methylthioribose-1-phosphate isomerase	Mri1	3	3	3	10	10	10	39.41	369	5.2444E-29	0.67078	0.73973	32.299	3	161420000	102810000	58616000
E9PVY8	Microtubule-actin cross-linking factor 1	Macf1	7	7	7	1.4	1.4	1.4	831.87	7355	3.774E-25	1.1053	1.0233	127.13	5	106040000	42475000	63568000
F7CK47	Microtubule-associated protein	Mtap4	20	20	15	20.1	20.1	16.4	152.67	1441	4.177E-155	0.68662	0.64528	63.381	21	1439500000	906280000	533200000
A2ARP8	Microtubule-associated protein 1A;MAP1 light chain LC2	Mtap1a	4	4	4	1.6	1.6	1.6	325.88	3014	2.6838E-30	0.24481	0.23665	142.43	2	43952000	39120000	4832100
P27546	Microtubule-associated protein 4;Microtubule-associated protein	Map4	18	13	13	22.4	17.7	17.7	117.43	1125	8.396E-254	0.66969	0.71251	36.59	18	1491000000	913910000	577090000
Q7TSJ2	Microtubule-associated protein 6	Map6	3	3	3	4.9	4.9	4.9	96.449	906	1.0407E-05	0.40482	0.34782	2.4793	2	38908000	29150000	9758000
Q61166	Microtubule-associated protein RP/EB family member 1	Mapre1	4	4	2	14.9	14.9	11.2	30.016	268	8.009E-20	0.7676	0.95513	40.986	4	326240000	195380000	130860000
Q8R001	Microtubule-associated protein RP/EB family member 2	Mapre2	4	4	4	17.5	17.5	17.5	36.946	326	1.7369E-14	0.754	0.81861	42.383	5	439600000	274030000	165570000
A2A5Y6	Microtubule-associated protein;Microtubule-associated protein tau	Mapt	11	11	11	22.4	22.4	22.4	78.085	749	6.376E-174	0.55058	0.48876	140.8	12	2800300000	1593100000	1207100000
Q62000	Mimecan	Ogn	4	4	4	15.1	15.1	15.1	34.012	298	3.8101E-13	0.20057	0.18415	76.907	3	129130000	103540000	25593000
Q59J78	Mimitin, mitochondrial	Ndufaf2	1	1	1	9.5	9.5	9.5	19.628	168	1.5652E-09	0.99032	1.064	35.454	3	153470000	80057000	73409000
Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	Aldh1l2	5	5	5	9.4	9.4	9.4	101.59	923	4.053E-103	0.58289	0.72235	47.604	5	128580000	66733000	61843000
Q9CR62	Mitochondrial 2-oxoglutarate/malate carrier protein	Slc25a11	8	8	8	29	29	29	34.155	314	4.707E-118	1.6604	1.9345	30.655	9	4011100000	1366800000	2644300000
Q8VCF0	Mitochondrial antiviral-signaling protein	Mavs	7	7	7	32.4	32.4	32.4	53.398	503	1.1253E-96	0.71258	0.75902	33.731	10	403010000	249290000	153720000
Q9Z2Z6	Mitochondrial carnitine/acylcarnitine carrier protein	Slc25a20	3	3	3	15.3	15.3	15.3	33.026	301	4.7731E-14	1.5136	1.274	1.4005	2	36245000	13965000	22280000
Q791V5	Mitochondrial carrier homolog 2	Mtch2	3	3	3	14.9	14.9	14.9	33.499	303	1.5107E-24	2.1447	2.5184	13.623	7	795170000	256940000	538240000
Q9CZP5	Mitochondrial chaperone BCS1	Bcs1l	2	2	2	6.9	6.9	6.9	47.406	418	0.00025791	0.27947	0.30915	248.98	2	119340000	107190000	12142000
Q9CRB8	Mitochondrial fission process protein 1	Mtfp1	2	2	2	19.9	19.9	19.9	18.314	166	3.8108E-05	1.309	1.5745	49.681	3	361780000	139990000	221790000
P62075	Mitochondrial import inner membrane translocase subunit Tim13	Timm13	5	5	5	61.1	61.1	61.1	10.458	95	3.5202E-89	0.69027	0.74665	23.333	5	600330000	344010000	256320000
G3X8S1	Mitochondrial import inner membrane translocase subunit TIM14	Dnajc19	1	1	1	5.7	5.7	5.7	17.025	157	0.02517	1.3452	1.5267	13.653	2	64514000	23219000	41295000
O35857	Mitochondrial import inner membrane translocase subunit TIM44	Timm44	6	6	6	17.5	17.5	17.5	51.091	452	1.0616E-34	0.77822	0.6752	51.406	8	616870000	310510000	306360000
Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	Timm8a1	3	3	3	38.1	38.1	38.1	11.042	97	7.4287E-15	0.50405	0.61044	104.92	4	730410000	496890000	233510000
Q9WV96	Mitochondrial import inner membrane translocase subunit Tim9 B	Fxc1	2	2	2	27	27	27	11.314	100	2.1363E-13	1.8917	2.0677	114.25	2	98139000	43634000	54505000
Q9CYG7	Mitochondrial import receptor subunit TOM34	Tomm34	4	4	4	15.9	15.9	15.9	34.278	309	1.0258E-37	0.84868	0.8288	12.389	4	120310000	68442000	51865000
Q9QYA2	Mitochondrial import receptor subunit TOM40 homolog	Tomm40	1	1	1	3	3	3	37.895	361	8.4872E-09	1.8047	1.9663	5.7549	2	67649000	24836000	42813000
Q9CZW5	Mitochondrial import receptor subunit TOM70	Tomm70a	3	3	3	5.4	5.4	5.4	67.589	611	2.1177E-10	1.3226	1.5787	50.543	2	81008000	31934000	49073000
Q8CAQ8	Mitochondrial inner membrane protein	Immt	14	14	14	24.4	24.4	24.4	83.899	757	5.618E-248	1.6692	1.5821	46.4	18	2202200000	834860000	1367400000
A6H611	Mitochondrial intermediate peptidase	Mipep	5	5	5	8.2	8.2	8.2	80.851	711	3.2897E-08	1.1511	1.2661	77.597	5	419200000	198230000	220970000
Q8VEA4	Mitochondrial intermembrane space import and assembly protein 40	Chchd4	2	2	2	26.6	26.6	26.6	15.525	139	4.8119E-28	0.58528	0.42731	31.074	3	98200000	61725000	36475000
Q9D6Y7	Mitochondrial peptide methionine sulfoxide reductase	Msra	8	8	8	48.1	48.1	48.1	25.988	233	6.92E-252	0.82918	0.83661	68.958	8	912930000	486960000	425970000
Q3UFY8	Mitochondrial ribonuclease P protein 1	Rg9mtd1	4	4	4	13.3	13.3	13.3	48.385	414	4.1105E-59	0.98276	1.0089	76.022	4	144410000	54635000	89774000
Q9DAT5	Mitochondrial tRNA-specific 2-thiouridylase 1	Trmu	3	3	3	9.4	9.4	9.4	47.24	417	4.7356E-09	0.75592	0.73408	128.97	2	27244000	18578000	8665700
Q9DC61	Mitochondrial-processing peptidase subunit alpha	Pmpca	9	9	9	18.3	18.3	18.3	58.278	524	5.7001E-77	1.1804	1.1122	78.017	12	1788700000	869120000	919610000
Q9CXT8	Mitochondrial-processing peptidase subunit beta	Pmpcb	8	7	7	21.5	20	20	54.614	489	3.0498E-29	1.8328	1.8104	45.468	8	784490000	325220000	459270000
Q811U4	Mitofusin-1	Mfn1	2	2	2	2.8	2.8	2.8	83.725	741	0.0017633	4.5062	4.0586	123.11	2	163950000	18658000	145290000
P63085	Mitogen-activated protein kinase 1	Mapk1	3	3	3	13.1	13.1	13.1	41.275	358	6.5239E-09	1.3033	1.4491	68.096	3	255000000	90339000	164660000
P47811	Mitogen-activated protein kinase 14	Mapk14	5	5	5	20.8	20.8	20.8	41.287	360	2.1858E-09	1.2459	1.2318	138.26	4	252510000	102670000	149850000
D3Z3G6	Mitogen-activated protein kinase 3	Mapk3	1	1	1	5	5	5	42.401	380	9.9768E-08	1.4413	1.4037	49.281	2	101020000	41196000	59820000
Q9ESL4	Mitogen-activated protein kinase kinase kinase kinase MLT	Mltk	1	1	1	1.9	1.9	1.9	91.719	802	0.016011	1.0265	0.86321	5.1319	2	126080000	63473000	62603000
P10404	MLV-related proviral Env polyprotein	Fv4	2	2	2	3.7	3.7	3.7	69.612	641	0.0090412	0.5337	0.15838	143.3	2	333200000	223890000	109310000
P26041	Moesin	Msn	13	13	10	25.1	25.1	20.6	67.766	577	2.7732E-66	0.69921	0.70773	26.195	14	3441800000	2129900000	1311900000
P53986	Monocarboxylate transporter 1	Slc16a1	3	3	3	7.7	7.7	7.7	53.267	493	2.6026E-22	1.183	1.1233	15.067	4	109380000	49435000	59941000
Q922Q1	MOSC domain-containing protein 2, mitochondrial	Marc2	2	2	2	7.4	7.4	7.4	38.194	338	6.7885E-18	1.7435	1.3331	54.544	2	39187000	14488000	24699000
Q8BKY8	mTERF domain-containing protein 3, mitochondrial	Mterfd3	3	3	3	9.1	9.1	9.1	43.452	385	1.8869E-09	0.70369	0.83168	41.876	2	86474000	55258000	31216000
Q9DCL9	Multifunctional protein ADE2	Paics	9	9	9	29.6	29.6	29.6	47.006	425	1.012E-223	0.89954	0.96121	99.825	13	1971600000	866920000	1104700000
A6H6E2	Multimerin-2	Mmrn2	5	5	5	6.8	6.8	6.8	105.21	943	6.7146E-59	0.52545	0.44394	97.473	4	268330000	169860000	98468000
Q9Z2L6	Multiple inositol polyphosphate phosphatase 1	Minpp1	3	3	3	9.1	9.1	9.1	54.537	481	1.6299E-17	0.77742	0.53127	15.65	3	204570000	116390000	88185000
P28665	Murinoglobulin-1;Murinoglobulin-2	Mug1	24	24	24	21.2	21.2	21.2	165.3	1476	0	0.31481	0.30197	80.295	33	5827800000	4300800000	1527000000
A2AMM0	Muscle-related coiled-coil protein	Murc	4	4	4	17.4	17.4	17.4	41.008	362	1.9423E-46	0.77425	0.86444	34.363	3	543890000	315570000	228320000
V9GWW6	Muscular LMNA-interacting protein	2310046A06Rik	6	6	6	10.8	10.8	10.8	103.45	967	1.645E-192	1.0646	1.0838	35.18	4	1007000000	533280000	473680000
O35682	Myeloid-associated differentiation marker	Myadm	1	1	1	5.3	5.3	5.3	35.284	320	0.0011022	1.4082	1.3957	6.47	2	15270000	6707300	8562300
E9PZ54	Myocardial zonula adherens protein	Gcom1	4	4	4	10	10	10	63.506	550	1.0185E-18	0.47234	0.26732	45.375	4	122120000	81450000	40667000
P04247	Myoglobin	Mb	12	12	12	81.8	81.8	81.8	17.069	154	0	0.61357	0.57596	44.169	52	1.4137E+10	8806400000	5330600000
Q14BI5	Myomesin 2 (Protein Myom2)	Myom2	36	36	36	34.6	34.6	34.6	164.74	1463	0	1.2991	1.2312	40.678	54	7871300000	3401300000	4470000000
Q62234	Myomesin-1	Myom1	46	46	46	36	36	36	185.46	1667	0	1.1523	1.1126	53.425	59	1.0346E+10	4917000000	5428600000
P09542	Myosin light chain 3	Myl3	11	11	10	61.3	61.3	57.4	22.421	204	0	0.55602	0.63199	82.011	40	2.7986E+10	1.7848E+10	1.0137E+10
Q9CZ19	Myosin light chain 4	Myl4	6	6	6	40.4	40.4	40.4	21.189	193	3.8307E-65	0.92243	0.86019	46.464	6	1093600000	503130000	590470000
B1B1A8	Myosin light chain kinase, smooth muscle	Mylk	6	6	6	4.5	4.5	4.5	213.61	1950	4.539E-30	0.51831	0.53672	56.904	6	149570000	89690000	59884000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9QVP4	Myosin regulatory light chain 2, atrial isoform	Myl7	6	6	6	48.6	48.6	48.6	19.45	175	1.254E-119	0.85776	0.56468	42.82	11	1868800000	975580000	893220000
E9Q8Y0	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	Myl2	6	6	1	38.1	38.1	11.9	19.808	176	0	0.56843	0.55966	47.328	16	3004600000	1930500000	1074100000
Q02566	Myosin-6	Myh6	44	44	12	29.8	29.8	9.2	223.56	1938	0	1.0317	1.0739	76.119	61	9447300000	4125000000	5322300000
Q3UIK0	Myosin-binding protein C, cardiac-type	Mybpc3	50	50	50	52.4	52.4	52.4	141.39	1278	0	1.3378	1.2871	40.671	96	4.1672E+10	1.8258E+10	2.3414E+10
P54265	Myotonin-protein kinase	Dmpk	2	2	2	5.7	5.7	5.7	69.601	631	1.0562E-14	1.1161	0.97621	13.932	4	23047000	12091000	10956000
Q9JJW5	Myozenin-2	Myoz2	5	5	5	23.5	23.5	23.5	29.761	264	3.3757E-20	1.2243	1.4417	28.718	8	603070000	280170000	322900000
P26645	Myristoylated alanine-rich C-kinase substrate	Marcks	5	5	5	36.6	36.6	36.6	29.661	309	1.371E-75	0.66202	0.65156	35.422	5	151710000	93054000	58658000
Q64191	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	Aga	4	4	4	19.4	19.4	19.4	37.022	346	1.1556E-07	1.1716	1.2048	3.1707	2	31242000	11891000	19350000
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	Ddah1	4	3	3	18.9	16.1	16.1	31.381	285	1.0026E-14	0.33164	0.20739	52.298	3	114990000	75454000	39532000
Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	Ddah2	7	7	6	36.1	36.1	33.3	29.645	285	9.001E-227	0.57439	0.59733	53.49	9	699500000	405880000	293620000
P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	Slc9a3r1	3	3	3	14.1	14.1	14.1	38.6	355	1.678E-70	0.32547	0.2775	34.566	3	145830000	109330000	36497000
Q9JHL1	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	Slc9a3r2	4	4	4	18.7	18.7	18.7	37.402	337	3.5326E-13	0.72099	0.6629	58.936	6	574640000	323840000	250800000
Q9D997	N-acetyl-D-glucosamine kinase	Nagk	4	4	4	13.9	13.9	13.9	39.346	361	4.4911E-22	1.0657	1.033	33.687	5	263560000	118730000	144820000
Q4PLS0	NACHT (Protein Nlrp2)	Nlrp2	1	1	1	0.9	0.9	0.9	118.64	1046	0.02766	0.29151	0.31098	51.395	2	51595000	40038000	11557000
Q8C5H8	NAD kinase domain-containing protein 1	Nadkd1	5	5	5	16.2	16.2	16.2	50.858	452	4.0472E-19	1.2178	1.1057	78.414	6	785520000	488260000	297250000
Q61941	NAD(P) transhydrogenase, mitochondrial	Nnt	18	18	18	24.5	24.5	24.5	113.84	1086	1.721E-116	1.7263	1.7831	98.902	23	3829600000	1406500000	2423100000
Q64669	NAD(P)H dehydrogenase [quinone] 1	Nqo1	4	4	4	19.3	19.3	19.3	30.959	274	1.7309E-40	0.96701	1.059	120.22	4	1350300000	169410000	1180900000
Q8K4Z3	NAD(P)H-hydrate epimerase	Apoa1bp	5	5	5	24.8	24.8	24.8	30.972	282	2.722E-103	1.6503	1.8726	103.13	9	1943500000	777020000	1166500000
Q8VDQ8	NAD-dependent protein deacetylase sirtuin-2	Sirt2	4	4	4	19.5	19.5	19.5	43.256	389	3.4356E-61	0.80692	0.79757	17.191	3	209950000	97526000	112430000
Q8R104	NAD-dependent protein deacetylase sirtuin-3	Sirt3	3	3	3	10.8	10.8	10.8	36.614	334	6.3094E-08	2.2423	2.2073	0.024448	2	210160000	66954000	143200000
Q8K2C6	NAD-dependent protein deacylase sirtuin-5, mitochondrial	Sirt5	6	6	6	24.5	24.5	24.5	34.134	310	1.167E-232	1.458	1.4869	40.866	10	890830000	414640000	476190000
Q9JKL4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	Ndufaf3	3	3	3	21.1	21.1	21.1	20.733	185	1.8428E-57	1.0212	1.0317	47.033	3	109360000	59277000	50086000
A2APY7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 5	Ndufaf5	4	4	4	13.1	13.1	13.1	38.404	343	4.3402E-17	1.0431	1.2262	90.698	3	117920000	53178000	64742000
Q9D1H6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	Ndufaf4	4	4	4	30.1	30.1	30.1	20.082	173	8.4591E-16	0.96078	1.0314	77.598	4	429740000	215980000	213760000
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10	Ndufa10	6	6	6	26.2	26.2	26.2	40.603	355	2.7163E-81	1.8056	1.4826	116.28	8	1893900000	599240000	1294600000
G5E814	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	Ndufa11	2	2	2	25.9	25.9	25.9	15.115	143	2.7691E-10	1.5041	1.7662	34.666	3	323820000	120020000	203800000
Q7TMF3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	Ndufa12	5	5	5	38.6	38.6	38.6	17.086	145	3.9349E-27	1.5601	1.0784	44.592	5	393090000	183070000	210020000
Q9ERS2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Ndufa13	5	5	5	41	41	41	16.859	144	2.2863E-26	1.334	1.2699	16.782	7	987950000	437950000	550000000
Q9CQ91	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	Ndufa3	2	2	2	41.7	41.7	41.7	9.3308	84	2.0749E-11	1.0289	0.90345	54.192	2	191750000	81815000	109940000
Q62425	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	Ndufa4	5	5	5	47.6	47.6	47.6	9.3267	82	1.6376E-20	1.3784	1.3886	65.609	4	1361600000	581780000	779820000
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Ndufa5	6	6	6	64.7	64.7	64.7	13.36	116	1.885E-175	0.52791	0.52431	102.27	15	3333300000	1825500000	1507800000
Q9Z1P6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	Ndufa7	4	4	4	39.8	39.8	39.8	12.575	113	5.3932E-79	0.94563	1.1491	22.803	4	428130000	223470000	204650000
Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	Ndufa8	2	2	2	22.1	22.1	22.1	19.992	172	4.0715E-65	1.4231	1.5318	31.838	2	590220000	311290000	278930000
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9	Ndufa9	8	8	8	28.4	28.4	28.4	42.525	377	1.628E-49	1.3564	1.3183	62.24	17	3138800000	1230700000	1908100000
Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Ndufb10	5	5	5	44.9	44.9	44.9	21.024	176	1.5516E-20	1.0515	1.2162	51.81	7	1092300000	531180000	561120000
O09111	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11	Ndufb11	4	4	4	38.4	38.4	38.4	17.444	151	1.8999E-19	1.0296	1.0365	32.948	8	459090000	210990000	248090000
Q9CPU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2	Ndufb2	1	1	1	8.6	8.6	8.6	11.967	105	3.2239E-07	1.4362	1.3457	10.497	3	557860000	181290000	376560000
Q9CQZ6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	Ndufb3	2	2	2	17.3	17.3	17.3	11.692	104	0.0024945	1.0814	1.057	0.83329	2	439620000	220620000	219000000
Q9CQC7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	Ndufb4	1	1	1	19.4	19.4	19.4	15.081	129	5.4681E-36	1.2339	1.3558	9.1263	3	451520000	191230000	260290000
Q9CQH3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5	Ndufb5	3	3	3	16.9	16.9	16.9	21.71	189	2.2074E-15	0.85568	0.8339	100.12	3	130940000	93464000	37471000
Q3UIU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	Ndufb6	2	2	2	19.5	19.5	19.5	15.515	128	1.1131E-08	1.5586	1.7437	15.605	8	1477900000	593550000	884320000
Q9D6J5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8	Ndufb8	3	3	3	19.9	19.9	19.9	21.876	186	6.3877E-07	1.0354	0.97703	22.944	2	243020000	116290000	126730000
Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	Ndufb9	4	4	4	38	38	38	21.984	179	2.0623E-27	1.3436	1.1768	57.699	7	1137100000	454060000	683000000
Q9CQ54	NADH dehydrogenase [ubiquinone] 1 subunit C2	Ndufc2	2	2	2	18.3	18.3	18.3	14.164	120	1.4009E-39	1.1539	1.0228	59.571	4	1260200000	591220000	669020000
Q9CWG8	NADH dehydrogenase [ubiquinone] complex I, assembly factor 7	Ndufaf7	2	2	2	6.4	6.4	6.4	48.384	436	3.0835E-07	0.74235	0.66675	34.051	2	247320000	88488000	158830000
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	Ndufv1	11	11	11	41.4	41.4	41.4	50.834	464	0	1.332	1.2528	44.237	27	4113400000	1797800000	2315600000
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	Ndufv2	9	9	9	51.6	51.6	51.6	27.285	248	2.818E-289	0.56233	0.59351	70.719	29	1.4246E+10	8759600000	5486400000
Q3U422	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	Ndufv3	4	4	4	14.3	14.3	14.3	50.498	468	5.5186E-32	0.52431	0.52891	39.152	7	164310000	113360000	50953000
Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	Ndufs2	12	12	12	33.7	33.7	33.7	52.625	463	4.1491E-88	1.7569	1.6496	27.915	17	2543200000	897830000	1645300000
Q9DCT2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	Ndufs3	8	8	8	30.8	30.8	30.8	30.149	263	1.1659E-51	1.0677	1.0617	123.37	21	6590500000	2551700000	4038800000
E9QPX3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	Ndufs4	6	6	6	30.9	30.9	30.9	19.803	175	7.3043E-45	0.40731	0.37789	44.74	11	4871100000	3106300000	1764800000
Q99LY9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	Ndufs5	2	2	2	23.6	23.6	23.6	12.648	106	1.5962E-47	1.0078	0.99262	1.7361	2	159560000	78889000	80670000
P52503	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	Ndufs6	4	4	4	44	44	44	13.02	116	5.3774E-71	0.50053	0.42037	47.985	9	8506800000	5709200000	2797500000
Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	Ndufs7	4	4	4	24.6	24.6	24.6	24.683	224	2.2187E-68	1.4684	1.3012	21.903	3	580150000	250410000	329730000
Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	Ndufs8	3	3	3	17.9	17.9	17.9	24.038	212	3.7269E-52	1.0123	1.2305	24.122	8	2305400000	1098300000	1207000000
F2Z456	NADH-cytochrome b5 reductase 3	Cyb5r3	2	2	2	7	7	7	34.929	313	2.3447E-09	1.4652	1.2992	34.495	3	359130000	150130000	209000000
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Ndufs1	20	20	20	37.8	37.8	37.8	79.776	727	0	1.1173	1.211	39.579	35	1.2813E+10	6017600000	6795200000
P03899	NADH-ubiquinone oxidoreductase chain 3	Mtnd3	1	1	1	13	13	13	13.219	115	6.669E-13	1.7532	1.928	9.627	2	186540000	68857000	117690000
P06801	NADP-dependent malic enzyme	Me1	9	9	9	19.8	19.8	19.8	63.953	572	1.5317E-95	1.7938	1.9024	32.501	10	1135800000	420740000	715100000
Q8BMF3	NADP-dependent malic enzyme, mitochondrial;Malic enzyme	Me3	13	13	12	33.4	33.4	32	67.098	604	1.077E-187	1.5018	1.6178	52.307	21	3357400000	1283200000	2074200000
Q61578	NADPH:adrenodoxin oxidoreductase, mitochondrial	Fdxr	3	3	3	8.5	8.5	8.5	54.201	494	1.9504E-12	1.1287	1.1955	11.939	2	64270000	31161000	33109000
G3X8Y3	N-alpha-acetyltransferase 15, NatA auxiliary subunit	Naa15	5	5	5	4.9	4.9	4.9	101.09	865	1.0359E-07	1.0162	0.80834	25.096	2	142730000	94136000	48591000
Q6ZWM4	N-alpha-acetyltransferase 38, NatC auxiliary subunit	Naa38	2	2	2	27.1	27.1	27.1	10.403	96	3.2883E-07	0.4577	0.51131	8.5665	2	206020000	141070000	64953000
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	Naca	80	80	80	56.5	56.5	56.5	220.5	2187	0	0.48388	0.48306	72.409	139	2.3428E+10	1.5686E+10	7742000000
P05125	Natriuretic peptides A	Nppa	2	2	2	10.5	10.5	10.5	16.572	152	1.0051E-06	0.20453	0.18569	101.55	2	220740000	144250000	76489000
B7ZCI2	Nebulette	Nebl	12	12	9	14.7	14.7	10.7	116.01	1014	2.877E-228	1.0956	1.3232	66.876	13	2156900000	1184100000	972840000
Q8C878	NEDD8-activating enzyme E1 catalytic subunit	Uba3	8	8	8	25.8	25.8	25.8	51.737	462	2.5994E-36	0.77626	0.74417	17.19	8	705740000	391480000	314270000
Q8VBW6	NEDD8-activating enzyme E1 regulatory subunit	Nae1	5	5	5	12	12	12	60.273	534	1.1131E-50	0.79105	0.78867	36.273	8	491840000	277800000	214030000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P61082	NEDD8-conjugating enzyme Ubc12	Ube2m	5	5	2	31.1	31.1	11.5	20.9	183	6.803E-138	0.39632	0.39833	71.257	8	613870000	490350000	123520000
Q9CQ45	Neudesin	Nenf	3	3	3	24.6	24.6	24.6	18.904	171	2.9599E-10	0.35912	0.31927	38.095	3	286800000	198910000	87894000
P06837	Neuromodulin	Gap43	1	1	1	7.5	7.5	7.5	23.632	227	0.0026606	0.60087	0.50593	9.2296	2	12307000	7876300	4430800
Q8BLF1	Neutral cholesterol ester hydrolase 1	Nceh1	3	3	3	8.6	8.6	8.6	45.739	408	1.6357E-08	0.57876	0.55802	141.72	3	358930000	258850000	100080000
O08692	Neutrophilic granule protein (NGP)	Ngp	3	3	3	29.3	29.3	29.3	19.331	167	1.7625E-34	0.29772	0.37186	68.3	3	214940000	158510000	56426000
Q9QZ23	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	Nfu1	3	1	1	15.7	5.9	5.9	28.567	255	7.7941E-47	0.44065	0.4047	11.721	4	1258500000	853130000	405380000
D3Z285	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial (Fragment)	Nfu1	3	3	1	20.1	20.1	7.5	22.028	199	8.3374E-85	0.46321	0.42298	48.282	6	834440000	574980000	259460000
Q8BZW8	NHL repeat-containing protein 2	Nhlrc2	4	4	4	10.8	10.8	10.8	78.429	725	5.1784E-20	0.73847	0.79112	14.009	2	165620000	100920000	64695000
Q99KQ4	Nicotinamide phosphoribosyltransferase	Nampt	17	17	17	43.6	43.6	43.6	55.446	491	0	1.4173	1.2592	74.462	24	4059900000	1697000000	2362900000
Q8CC86	Nicotinate phosphoribosyltransferase	Naprt1	2	2	2	5.9	5.9	5.9	58.265	538	8.1418E-07	1.0767	1.0317	49.353	2	209060000	107130000	101930000
P10493	Nidogen-1	Nid1	20	20	19	21.7	21.7	20.9	136.54	1245	3.971E-230	1.187	1.1963	68.818	27	3938900000	2077900000	1861000000
O88322	Nidogen-2	Nid2	5	4	4	6.2	5.5	5.5	153.91	1403	3.0504E-30	1.2297	1.5141	53.936	3	91178000	49368000	41810000
Q9EQ80	NIF3-like protein 1	Nif3l1	2	2	2	8.2	8.2	8.2	41.745	376	3.2954E-16	0.8851	0.56584	73.716	2	56042000	29967000	26075000
O08804	NK13 (Protein Serpinb6b)	Serpinb6b	7	7	7	24.1	24.1	24.1	42.535	377	2.5611E-57	0.54231	0.66048	41.075	7	630970000	400170000	230790000
P32020	Non-specific lipid-transfer protein	Scp2	5	5	5	9	9	9	59.125	547	3.3312E-61	0.46016	0.52034	51.877	11	3525200000	2245700000	1279500000
Q9CZ44	NSFL1 cofactor p47	Nsfl1c	11	11	11	40.3	40.3	40.3	40.709	370	0	0.53838	0.572	132.51	13	3746400000	1142900000	2603500000
B1AU75	Nuclear autoantigenic sperm protein	Nasp	6	6	6	11.8	11.8	11.8	84.012	773	3.3964E-98	0.52455	0.50715	81.426	4	171130000	112520000	58617000
Q5F2E7	Nuclear fragile X mental retardation-interacting protein 2	Nufip2	1	1	1	4	4	4	75.656	692	0.00062377	1.0549	1.0165	6.1705	2	5112300	2719500	2392800
O35685	Nuclear migration protein nudC	Nudc	5	5	5	16.6	16.6	16.6	38.358	332	1.818E-17	0.49276	0.3819	50.859	2	52581000	36077000	16504000
P60670	Nuclear protein localization protein 4 homolog	Nploc4	5	5	5	11.7	11.7	11.7	68.016	608	7.3282E-17	1.1221	1.3361	31.972	5	309290000	134500000	174790000
D3YUV1	Nuclear receptor-binding protein	Nrbp1	3	3	3	9.2	9.2	9.2	60.85	543	2.6342E-14	0.70444	0.60954	31.423	4	128140000	75259000	52882000
P61971	Nuclear transport factor 2	Nutf2	4	4	4	63	63	63	14.478	127	3.8066E-58	1.0419	1.1738	64.485	7	479290000	184770000	294520000
P62960	Nuclease-sensitive element-binding protein 1	Ybx1	8	8	4	43.8	43.8	31.4	35.73	322	0	0.44798	0.39512	85.877	14	2037400000	1338300000	699020000
Q02819	Nucleobindin-1	Nucb1	4	4	4	9.6	9.6	9.6	53.408	459	4.7322E-27	0.77636	0.75859	102.56	5	185630000	111810000	73821000
Q99ME9	Nucleolar GTP-binding protein 1	Gtpbp4	2	2	2	2.4	2.4	2.4	74.112	634	0.01568	0.34017	0.33717	95.247	2	48934000	44020000	4914000
Q9D1X0	Nucleolar protein 3	Nol3	6	6	6	41.4	41.4	41.4	24.567	220	2.034E-139	0.58718	0.69492	21.913	9	1062600000	673310000	389320000
P09405	Nucleolin	Ncl	5	5	5	7.9	7.9	7.9	76.722	707	5.7064E-31	0.8232	0.62675	49.646	5	395290000	197440000	197840000
Q61937	Nucleophosmin	Npm1	3	3	3	13.4	13.4	13.4	32.56	292	7.4289E-15	0.78326	0.89728	15.879	3	429180000	223500000	205690000
F6ZDS4	Nucleoprotein TPR (NPC-associated intranuclear protein)	Tpr	8	8	8	4	4	4	273.99	2431	3.847E-134	0.54592	0.62064	254.07	5	2901800000	2537800000	364010000
Q9WV85	Nucleoside diphosphate kinase 3	Nme3	2	2	2	16	16	16	19.099	169	4.07E-09	0.15191	0.16657	138.48	2	85976000	65546000	20430000
E9PZF0	Nucleoside diphosphate kinase;Nucleoside diphosphate kinase B	Gm20390	10	10	6	59.9	59.9	27.7	30.2	267	1.62E-208	0.53638	0.49655	54.204	35	9.6751E+10	6.3107E+10	3.3645E+10
P11930	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	Nudt19	3	3	3	14.3	14.3	14.3	40.32	357	6.0349E-33	1.4072	1.355	48.481	4	274060000	133690000	140370000
Q3ULU4	Nucleoside diphosphate-linked moiety X motif 6	Nudt6	2	2	2	6.7	6.7	6.7	35.211	313	7.6919E-06	1.9668	1.9785	108.95	2	96654000	44256000	52398000
Q9CR24	Nucleoside diphosphate-linked moiety X motif 8, mitochondrial	Nudt8	5	5	5	32.4	32.4	32.4	23.252	210	1.408E-18	1.6218	1.8101	30.313	5	592240000	208330000	383910000
E9PW66	Nucleosome assembly protein 1-like 1	Nap1l1	2	1	1	6.5	4.1	4.1	48.542	418	1.2355E-42	0.92318	1.0917	8.2478	2	273030000	150080000	122940000
Q78ZA7	Nucleosome assembly protein 1-like 4	Nap1l4	7	7	6	26.4	26.4	23.7	42.679	375	1.093E-116	0.67266	0.6861	62.753	14	1360000000	819030000	540920000
Q8R1N4	NudC domain-containing protein 3	Nudcd3	5	5	5	14	14	14	40.89	363	8.0193E-14	0.55951	0.4793	58.385	5	207920000	136020000	71902000
Q922B1	O-acetyl-ADP-ribose deacetylase MACROD1	Macrod1	5	5	5	26.6	26.6	26.6	35.294	323	1.808E-125	1.0997	1.0185	53.345	21	3895600000	1759900000	2135700000
Q9CZ30	Obg-like ATPase 1	Ola1	7	7	7	28	28	28	44.729	396	8.6784E-64	0.62526	0.66613	78.308	8	397420000	242950000	154470000
A2AAJ9	Obscurin	Obscn	23	23	23	4	4	4	966.36	8891	1.059E-292	2.0255	2.0327	35.764	20	717080000	248030000	469050000
Q9CRD0	OCIA domain-containing protein 1	Ociad1	3	3	3	17.4	17.4	17.4	27.61	247	4.486E-112	0.50478	0.45609	54.695	3	235160000	152990000	82168000
Q9D8S4	Oligoribonuclease, mitochondrial	Rexo2	1	1	1	7.6	7.6	7.6	26.738	237	5.2066E-75	0.69082	0.69863	0.222	2	45404000	28667000	16738000
Q9JHW2	Omega-amidase NIT2	Nit2	10	10	10	59.8	59.8	59.8	30.501	276	5.725E-199	1.1198	1.1491	51.599	11	1817500000	857490000	959990000
Q99PG2	Opioid growth factor receptor	Ogfr	2	2	2	6	6	6	70.678	633	9.0309E-26	0.63512	0.65641	15.515	5	92149000	58868000	33281000
P29758	Ornithine aminotransferase, mitochondrial	Oat	12	12	12	36.4	36.4	36.4	48.354	439	3.143E-244	1.0252	0.92176	74.16	18	3309600000	1600300000	1709300000
Q62422	Osteoclast-stimulating factor 1	Ostf1	1	1	1	11.6	11.6	11.6	23.782	215	1.6129E-16	0.61421	0.80692	44.195	3	321120000	202160000	118960000
B2RRE7	OTU domain-containing protein 4	Otud4	2	2	2	3	3	3	123.05	1107	1.1646E-05	0.99772	0.84767	4.7612	2	28734000	14080000	14654000
B2RUR8	OTU domain-containing protein 7B	Otud7b	3	3	3	5.7	5.7	5.7	91.982	840	5.2077E-05	9.4063	9.7532	4.9519	2	271030000	18919000	252110000
D3YXF5	Oxidation resistance protein 1	C7	6	6	6	13	13	13	93.337	845	7.502E-101	0.59894	0.53034	11.698	4	110750000	74366000	36380000
Q4KMM3	Oxidation resistance protein 1	Oxr1	4	4	4	7.7	7.7	7.7	95.911	866	3.1512E-32	0.96087	0.96592	54.662	4	92780000	47058000	45722000
Q8VE38	Oxidoreductase NAD-binding domain-containing protein 1	Oxnad1	6	6	6	19.3	19.3	19.3	34.727	311	2.1219E-61	0.96978	1.0439	100.63	5	413150000	122180000	290970000
Q3B7Z2	Oxysterol-binding protein 1	Osbp	4	4	4	8.1	8.1	8.1	88.796	805	1.4034E-12	1.0543	1.0502	29.04	4	199770000	85782000	113990000
Q9ET54	Palladin	Palld	2	2	2	1.6	1.6	1.6	152.13	1408	0.0017628	0.88416	0.88779	124.08	2	87417000	43855000	43562000
Q3UVT7	Palmdelphin	Palmd	8	8	8	24.5	24.5	24.5	62.616	551	4.1477E-33	0.67845	0.66234	36.434	7	395540000	241190000	154350000
O88531	Palmitoyl-protein thioesterase 1	Ppt1	3	3	3	18.6	18.6	18.6	34.49	306	1.81E-130	0.59261	0.64712	7.2543	4	383920000	256980000	126940000
Q80YV4	Pantothenate kinase 4	Pank4	2	2	2	2.4	2.4	2.4	91.521	820	1.7574E-09	1.2701	0.61372	153.15	2	121020000	60572000	60445000
Q9Z0P4	Paralemmin-1	Palm	4	4	4	15.4	15.4	15.4	41.614	383	4.729E-297	0.49013	0.43548	69.905	6	388580000	253830000	134750000
Q99JF8	PC4 and SFRS1-interacting protein	Psip1	2	2	2	5.3	5.3	5.3	59.696	528	4.0076E-07	0.9464	1.0936	36.92	2	27891000	16136000	11755000
O70400	PDZ and LIM domain protein 1	Pdlim1	10	10	10	49.8	49.8	49.8	35.774	327	4.7737E-93	0.54889	0.63764	33.079	7	838230000	535490000	302740000
Q8CI51	PDZ and LIM domain protein 5	Pdlim5	8	8	3	19.1	19.1	7.6	63.299	591	2.277E-201	0.47484	0.44453	86.336	12	2313900000	1570200000	743710000
E9Q8P5	PDZ and LIM domain protein 5	Pdlim5	7	2	2	43.5	15.1	15.1	26.355	239	0	0.80971	0.70605	70.453	15	3307800000	2265800000	1042000000
Q8VI59	Pecanex-like protein 3	Pcnxl3	1	1	1	1.1	1.1	1.1	221.57	2028	1.487E-09	0.26934	0.2776	23.427	5	952380000	815620000	136760000
A3KG59	Peptidase M20 domain-containing protein 2	Pm20d2	4	4	4	19.7	19.7	19.7	46.481	431	7.7633E-85	0.72571	0.6444	54.902	5	323060000	190860000	132200000
P97467	Peptidyl-glycine alpha-amidating monooxygenase	Pam	6	6	6	6.4	6.4	6.4	108.96	979	9.0578E-12	0.66144	0.70371	44.648	8	286160000	161580000	124580000
P17742	Peptidyl-prolyl cis-trans isomerase A	Ppia	6	6	6	48.8	48.8	48.8	17.971	164	4.308E-272	0.55998	0.61174	71.571	10	1595200000	960460000	634720000
P24369	Peptidyl-prolyl cis-trans isomerase B	Ppib	4	4	4	21.8	21.8	21.8	23.713	216	3.4218E-36	0.66308	0.62236	30.299	6	807540000	500320000	307220000
Q9CR16	Peptidyl-prolyl cis-trans isomerase D	Ppid	7	7	7	27	27	27	40.742	370	6.613E-39	0.45873	0.45184	67.468	8	988830000	690550000	298280000
Q99KR7	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	Ppif	4	4	4	39.3	39.3	39.3	21.737	206	0	0.54657	0.55391	46.628	8	781240000	482220000	299020000
P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A	Fkbp1a	3	3	3	39.8	39.8	39.8	11.922	108	1.5618E-43	0.79931	0.97078	39.875	4	450540000	242510000	208040000
Q62446	Peptidyl-prolyl cis-trans isomerase FKBP3	Fkbp3	8	8	8	40.2	40.2	40.2	25.147	224	3.1649E-96	0.42759	0.36589	141.86	7	2495700000	1860000000	635690000
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4	Fkbp4	11	11	11	35.8	35.8	35.8	51.572	458	1.841E-243	0.75123	0.52078	77.246	13	2506400000	955370000	1551000000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O54998	Peptidyl-prolyl cis-trans isomerase FKBP7	Fkbp7	3	3	3	12.8	12.8	12.8	24.913	218	3.174E-12	0.39312	0.33251	53.622	3	232200000	163120000	69082000
Q9CWW6	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	Pin4	3	3	3	25.2	25.2	25.2	13.815	131	3.398E-09	0.48219	0.26744	46.827	3	150540000	91805000	58737000
Q9DBG5	Perilipin-3	Plin3	10	10	10	26.3	26.3	26.3	47.262	437	2.118E-103	1.1978	1.1984	46.284	11	1234800000	545880000	688900000
O88492	Perilipin-4	Plin4	15	15	15	30.5	30.5	30.5	139.41	1403	0	0.78244	0.90164	55.215	26	3187700000	1842900000	1344800000
Q8BVZ1	Perilipin-5	Plin5	3	3	3	10.6	10.6	10.6	50.474	463	2.4826E-59	0.58663	0.32179	74.632	3	113010000	69714000	43291000
Q62009	Periostin	Postn	5	5	5	8.4	8.4	8.4	93.142	838	6.2177E-43	0.67462	0.61262	29.206	5	239930000	152970000	86955000
P35700	Peroxiredoxin-1	Prdx1	8	8	7	43.7	43.7	39.7	22.176	199	1.581E-114	0.48446	0.44762	103.68	10	1.171E+10	8209100000	3501300000
Q61171	Peroxiredoxin-2	Prdx2	11	11	11	65.7	65.7	65.7	21.778	198	0	0.4826	0.4637	67.203	38	2.98E+10	2.2987E+10	6813000000
O08807	Peroxiredoxin-4	Prdx4	5	4	4	18.2	15.3	15.3	31.052	274	1.5048E-38	0.50074	0.56827	22.817	5	4714700000	3102200000	1612500000
H3BJQ7	Peroxiredoxin-5, mitochondrial	Prdx5	10	10	10	40.4	40.4	40.4	22.677	213	0	0.50792	0.51782	35.558	71	3.2316E+10	2.1896E+10	1.042E+10
O08709	Peroxiredoxin-6	Prdx6	11	11	11	51.8	51.8	51.8	24.87	224	9.743E-154	0.64868	0.71793	50.651	19	2.4634E+10	1.5958E+10	8675600000
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1;Acyl-coenzyme A oxidase	Acox1	9	9	9	20.6	20.6	20.6	74.648	661	6.8105E-37	1.6231	1.6416	48.266	10	540440000	227130000	313320000
Q8VCI5	Peroxisomal biogenesis factor 19	Pex19	4	4	4	24.4	24.4	24.4	32.733	299	5.167E-173	0.56317	0.59093	0.29288	2	108860000	76200000	32664000
Q9DC50	Peroxisomal carnitine O-octanoyltransferase	Crot	4	4	4	9.8	9.8	9.8	70.264	612	5.7528E-09	1.5072	1.8274	28.937	3	69729000	27035000	42694000
Q99P30	Peroxisomal coenzyme A diphosphatase NUDT7	Nudt7	2	2	2	13.6	13.6	13.6	26.856	236	1.394E-06	0.94637	1.1008	24.104	2	79247000	37731000	41516000
P51660	Peroxisomal multifunctional enzyme type 2	Hsd17b4	6	6	6	11.7	11.7	11.7	79.481	735	1.8775E-30	1.4488	1.2288	84.791	5	701060000	290850000	410210000
Q149B8	PGC-1 and ERR-induced regulator in muscle protein 1	Perm1	9	9	9	18.2	18.2	18.2	85.156	807	1.442E-211	0.76951	0.81728	83.77	12	1572500000	924360000	648160000
Q8C0C7	Phenylalanine--tRNA ligase alpha subunit	Farsa	4	4	4	11.2	11.2	11.2	57.598	508	1.9224E-24	1.1029	0.98153	9.2326	3	105820000	62507000	43310000
Q9WUA2	Phenylalanine--tRNA ligase beta subunit	Farsb	4	4	4	6.8	6.8	6.8	65.696	589	3.2106E-09	1.4583	1.4414	93.845	5	343420000	141480000	201940000
Q99M01	Phenylalanine--tRNA ligase, mitochondrial	Fars2	3	3	3	10	10	10	52.336	451	3.3559E-07	0.90474	0.88173	24.761	4	150750000	88173000	62574000
Q8BVF2	Phosducin-like protein 3	Pdcl3	2	2	2	13.8	13.8	13.8	27.581	240	4.7634E-27	6.3897	7.2215	268.86	2	321740000	21341000	300400000
G5E902	Phosphate carrier protein, mitochondrial	Slc25a3	8	8	8	23.5	23.5	23.5	39.736	358	2.0153E-30	1.7334	1.8146	49.814	9	1843800000	736120000	1107600000
Q99L43	Phosphatidate cytidylyltransferase 2	Cds2	1	1	1	4.3	4.3	4.3	51.313	444	1.7795E-07	1.5937	1.9447	11.725	2	72764000	28393000	44371000
P70296	Phosphatidylethanolamine-binding protein 1	Pebp1	11	11	11	73.3	73.3	73.3	20.83	187	0	0.49503	0.5072	68.04	46	1.889E+10	1.2521E+10	6368800000
P53810	Phosphatidylinositol transfer protein alpha isoform	Pitpna	4	4	4	11.8	11.8	11.8	31.893	271	1.4566E-06	0.47322	0.4212	13.796	3	118180000	82060000	36116000
Q7M6Y3	Phosphatidylinositol-binding clathrin assembly protein	Picalm	9	9	9	19.5	19.5	19.5	71.543	660	7.4139E-76	0.86056	0.9187	50.763	9	381400000	248900000	132500000
Q9CYR6	Phosphoacetylglucosamine mutase	Pgm3	3	3	3	8.3	8.3	8.3	59.452	542	1.6772E-09	0.72806	0.14654	119.88	3	176530000	104990000	71539000
Q8K212	Phosphofurin acidic cluster sorting protein 1	Pacs1	4	4	4	5.8	5.8	5.8	104.83	961	5.6519E-07	0.81713	0.84504	41.289	4	89378000	51823000	37556000
Q9D0F9	Phosphoglucomutase-1	Pgm1	17	17	17	42.2	42.2	42.2	61.417	562	0	0.91456	0.80876	107.66	43	1.7275E+10	9527900000	7747400000
Q7TSV4	Phosphoglucomutase-2	Pgm2	5	5	5	10.6	10.6	10.6	68.747	620	4.1243E-47	0.86534	1.0351	32.903	7	417080000	215870000	201210000
Q8BZF8	Phosphoglucomutase-like protein 5	Pgm5	11	11	11	26.3	26.3	26.3	62.219	567	3.3404E-89	1.1023	1.1689	55.195	9	581350000	261950000	319400000
P09411	Phosphoglycerate kinase 1	Pgk1	16	16	16	51.1	51.1	51.1	44.55	417	0	0.56636	0.58513	79.236	43	2.209E+10	1.344E+10	8650100000
Q9DBJ1	Phosphoglycerate mutase 1	Pgam1	6	5	5	32.3	28	28	28.832	254	8.934E-174	1.2883	1.2803	38.565	9	1608200000	898000000	710170000
O70250	Phosphoglycerate mutase 2	Pgam2	7	7	6	29.6	29.6	25.3	28.827	253	1.632E-192	1.2793	1.1318	40.938	11	1.0607E+10	5104400000	5502600000
Q8CHP8	Phosphoglycolate phosphatase	Pgp	4	4	4	18.1	18.1	18.1	34.54	321	2.3132E-73	1.4228	1.4072	46.133	6	1020200000	328950000	691280000
Q9Z239	Phospholemman	Fxyd1	1	1	1	13	13	13	10.323	92	1.3479E-27	1.0453	1.2164	7.18	3	200120000	104990000	95135000
P27612	Phospholipase A-2-activating protein	Plaa	11	11	11	20.2	20.2	20.2	87.22	794	1.4718E-97	0.91486	0.83971	71.713	13	587440000	303940000	283490000
Q8VCI0	Phospholipase B-like 1	Plbd1	2	2	2	5.6	5.6	5.6	62.998	550	1.367E-07	3.4188	3.1643	10.712	2	56167000	13375000	42792000
O35405	Phospholipase D3	Pld3	3	3	3	6.4	6.4	6.4	54.388	488	1.327E-06	0.56135	0.68747	98.727	3	267270000	183690000	83582000
Q9Z2M7	Phosphomannomutase 2	Pmm2	3	3	3	13.6	13.6	13.6	27.656	242	2.1124E-14	0.88833	0.94083	90.501	5	873500000	499370000	374120000
Q8VDG5	Phosphopantothenate--cysteine ligase	Ppcs	6	6	6	19.3	19.3	19.3	33.794	311	3.4989E-64	0.89252	0.52892	90.638	5	529210000	280970000	248240000
B1AT82	Phosphoribosyl pyrophosphate synthase-associated protein 1	Prpsap1	3	3	3	13.2	13.2	13.2	42.467	385	9.9084E-71	1.6548	1.6188	87.296	4	148700000	66461000	82244000
Q5SUR0	Phosphoribosylformylglycinamidine synthase	Pfas	2	2	2	2.7	2.7	2.7	144.63	1337	6.1269E-08	0.88786	0.86376	46.518	2	83790000	48040000	35750000
Q8BQ30	Phostensin	Ppp1r18	1	1	1	4.2	4.2	4.2	65.629	594	0.001808	0.73666	0.61968	2.2872	2	13527000	7586400	5941000
Q9DB26	Phytanoyl-CoA dioxygenase domain-containing protein 1	Phyhd1	3	3	3	18.9	18.9	18.9	32.517	291	0	0.62056	0.57165	26.284	4	504400000	324000000	180400000
P26262	Plasma kallikrein;Plasma kallikrein heavy chain	Klkb1	5	5	5	11	11	11	71.382	638	9.0226E-19	0.51882	0.5929	34.327	4	162650000	92117000	70529000
G5E829	Plasma membrane calcium-transporting ATPase 1	Atp2b1	3	3	3	4.1	4.1	4.1	134.75	1220	7.5219E-37	1.1279	1.129	8.4909	2	62351000	30381000	31970000
P97290	Plasma protease C1 inhibitor	Serping1	4	4	4	12.1	12.1	12.1	55.584	504	9.4238E-34	0.56297	0.48803	45.201	8	642550000	430460000	212090000
P20918	Plasminogen	Plg	5	5	5	7.5	7.5	7.5	90.807	812	4.4257E-35	1.1024	1.1351	31.391	4	225070000	109340000	115740000
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein	Serbp1	4	4	4	12.8	12.8	12.8	44.714	407	1.658E-103	0.74528	0.72233	71.237	6	748710000	419110000	329600000
Q3V0K9	Plastin-1	Pls1	5	2	2	11.6	6	6	70.407	630	5.4188E-43	0.20223	0.18262	15.114	2	26747000	22146000	4601500
Q61233	Plastin-2	Lcp1	15	15	13	34.1	34.1	30.6	70.148	627	1.13E-189	1.287	1.2286	37.526	22	2063000000	898590000	1164400000
B1AX58	Plastin-3	Pls3	8	6	4	16.9	13.5	9.4	71.745	639	3.7672E-34	0.51255	0.47992	23.451	8	902590000	599690000	302900000
B1ARB3	Platelet endothelial cell adhesion molecule	Pecam1	3	3	3	5.5	5.5	5.5	81.917	732	7.9002E-21	0.68232	0.46846	43.884	3	114580000	72321000	42254000
Q08857	Platelet glycoprotein 4	Cd36	5	5	5	15.7	15.7	15.7	52.697	472	1.327E-135	0.76152	0.77362	23.479	7	1156400000	741770000	414640000
O35930	Platelet glycoprotein Ib alpha chain	Gp1ba	2	2	2	3.3	3.3	3.3	80.054	734	0.00010192	0.26321	0.25712	59.469	2	86338000	66089000	20249000
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	Pafah1b1	9	9	9	29.3	29.3	29.3	46.67	410	4.3515E-53	1.3938	1.2367	32.018	8	1387600000	629830000	757740000
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	Pafah1b2	2	2	2	12.2	12.2	12.2	25.581	229	3.0546E-65	0.50667	0.49158	30.969	3	294330000	202590000	91743000
Q61205	Platelet-activating factor acetylhydrolase IB subunit gamma	Pafah1b3	2	2	2	7.3	7.3	7.3	25.853	232	0.0009977	0.5499	0.57745	22.919	2	84887000	54167000	30720000
Q9JHK5	Pleckstrin	Plek	3	3	3	16.3	16.3	16.3	39.9	350	8.7807E-09	0.76275	0.75781	12.646	3	350120000	220490000	129630000
Q80TI1	Pleckstrin homology domain-containing family H member 1	Plekhh1	2	2	2	1.7	1.7	1.7	150.91	1356	0.0063121	1.2222	0.23502	234.5	2	1257100000	580440000	676650000
Q8K124	Pleckstrin homology domain-containing family O member 2	Plekho2	2	2	2	8.1	8.1	8.1	53.872	495	4.9727E-29	0.87301	1.0495	39.935	2	34814000	23311000	11503000
Q9QXS1	Plectin	Plec	7	7	7	2.3	2.3	2.3	534.18	4691	9.2802E-17	1.106	1.0468	27.55	5	206250000	137480000	68767000
Q2EMV9	Poly [ADP-ribose] polymerase 14	Parp14	4	4	4	2.5	2.5	2.5	203.8	1817	0.00045655	0.67493	0.7455	38.209	3	297010000	169180000	127830000
P60335	Poly(rC)-binding protein 1	Pcbp1	9	6	6	41.3	30.3	30.3	37.497	356	1.811E-116	0.63939	0.52644	24.63	8	2554400000	1619500000	934880000
Q61990	Poly(rC)-binding protein 2	Pcbp2	9	9	6	31.5	31.5	20.7	38.221	362	1.0384E-79	0.5775	0.63816	111.14	12	2307700000	1025100000	1282700000
Q6PHQ9	Polyadenylate-binding protein	Pabpc4	7	7	4	13.6	13.6	7.6	72.242	660	2.606E-110	1.2802	1.2524	24.374	9	1173700000	530140000	643580000
O54724	Polymerase I and transcript release factor	Ptrf	8	8	8	23.7	23.7	23.7	43.953	392	0	0.70004	0.63253	32.48	12	1510400000	920970000	589470000
P0CG50	Polyubiquitin-C	Ubc	3	3	3	41.7	41.7	41.7	82.549	734	5.071E-110	0.96239	0.83079	33.24	6	2918800000	1515200000	1403600000
Q6P3F7	Popeye domain-containing protein 2	Popdc2	2	2	2	5.9	5.9	5.9	41.847	371	0.0002361	1.0933	1.3385	37.12	2	114690000	56482000	58207000
P22907	Porphobilinogen deaminase	Hmbs	3	3	3	9.7	9.7	9.7	39.344	361	2.0848E-53	0.87589	0.93823	50.613	5	389030000	207270000	181770000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8R5J9	PRA1 family protein 3	Arl6ip5	1	1	1	5.9	5.9	5.9	21.557	188	0.015725	2.0208	1.8855	5.1692	2	19109000	5973900	13135000
O70591	Prefoldin subunit 2	Pfdn2	3	3	3	26	26	26	16.534	154	2.1738E-30	0.62139	0.62733	56.533	2	255560000	167560000	88002000
P61759	Prefoldin subunit 3	Vbp1	2	2	2	10.7	10.7	10.7	22.435	196	2.6467E-05	0.50849	0.28578	68.87	2	140180000	95148000	45033000
Q9WU28	Prefoldin subunit 5	Pfdn5	3	3	3	26	26	26	17.356	154	1.4953E-30	0.71277	0.63316	80.004	5	500890000	322420000	178470000
P48678	Prelamin-A/C;Lamin-A/C	Lmna	6	6	6	10.5	10.5	10.5	74.237	665	4.4352E-27	0.49453	0.39618	67.847	6	230360000	144980000	85381000
Q9CQF9	Prenylcysteine oxidase	Pcyox1	2	2	2	7.3	7.3	7.3	56.494	505	1.5955E-08	1.3705	1.2636	11.096	2	25980000	13054000	12927000
Q8K411	Presequence protease, mitochondrial	Pitrm1	13	13	13	16.3	16.3	16.3	117.37	1036	8.705E-165	1.39	1.2524	37.992	15	886030000	398830000	487200000
Q9D6Z0	Probable alpha-ketoglutarate-dependent dioxygenase ABH7	Alkbh7	2	2	2	15.8	15.8	15.8	24.97	221	1.6271E-13	1.7453	1.9088	21.013	2	156760000	70496000	86268000
Q6NSR8	Probable aminopeptidase NPEPL1	Npepl1	5	5	5	14.9	14.9	14.9	55.939	524	3.1287E-14	1.2301	1.2272	31.582	3	233590000	102130000	131460000
Q6Q899	Probable ATP-dependent RNA helicase DDX58	Ddx58	2	2	2	3.7	3.7	3.7	105.97	926	3.8667E-08	0.39144	0.41025	99.316	2	67046000	48014000	19032000
Q9WV35	Probable C->U-editing enzyme APOBEC-2	Apobec2	6	6	6	38.8	38.8	38.8	25.66	224	2.392E-106	0.72151	0.74138	44.921	14	1508000000	962470000	545530000
G3X975	Probable cysteine--tRNA ligase, mitochondrial	Cars2	8	8	8	18.1	18.1	18.1	61.342	552	1.0174E-24	1.1023	1.1929	72.014	6	329990000	189190000	140800000
Q7TNG8	Probable D-lactate dehydrogenase, mitochondrial	Ldhd	2	2	2	5.6	5.6	5.6	51.847	484	0.00013176	0.58652	0.53481	16.196	2	216690000	138760000	77926000
Q8BZA9	Probable fructose-2,6-bisphosphatase TIGAR	Tigar	3	3	3	19.3	19.3	19.3	29.19	269	3.7018E-67	1.2155	1.2134	16.311	5	211050000	92456000	118600000
Q9CXJ1	Probable glutamate--tRNA ligase, mitochondrial	Ears2	4	4	4	8.4	8.4	8.4	58.326	523	8.5097E-18	0.81665	0.81194	79.026	2	73815000	37519000	36296000
Q8VDC0	Probable leucine--tRNA ligase, mitochondrial	Lars2	4	4	4	5.7	5.7	5.7	101.48	902	4.1326E-10	1.0016	0.95388	54.658	5	122300000	66289000	56016000
Q9WVQ5	Probable methylthioribulose-1-phosphate dehydratase	Apip	7	7	7	44.4	44.4	44.4	26.949	241	5.9818E-42	0.68784	0.57799	30.094	9	1045400000	618330000	427100000
P86049	Probable RNA-binding protein 46	Rbm46	2	2	2	2.3	2.3	2.3	60.077	533	0.00049958	1.0925	1.1971	71.753	2	167910000	78964000	88946000
Q8BLY2	Probable threonine--tRNA ligase 2, cytoplasmic	Tarsl2	4	4	4	5.4	5.4	5.4	91.317	790	7.1181E-11	1.329	1.3528	30.912	5	126140000	55775000	70362000
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	Usp9x	11	11	11	5.7	5.7	5.7	290.71	2559	6.1323E-40	1.2991	1.3103	51.018	9	271290000	121260000	150030000
Q9WU78	Programmed cell death 6-interacting protein	Pdcd6ip	14	14	14	26.2	26.2	26.2	96.023	869	0	0.86073	0.59468	63.61	14	1029800000	563430000	466390000
P56812	Programmed cell death protein 5	Pdcd5	4	4	4	34.1	34.1	34.1	14.275	126	6.8008E-33	0.43444	0.4575	39.015	3	90007000	64385000	25623000
P12815	Programmed cell death protein 6	Pdcd6	3	3	3	23.6	23.6	23.6	21.867	191	9.3105E-07	1.0056	1.2167	26.452	2	135050000	60561000	74486000
P67778	Prohibitin	Phb	3	3	3	16.2	16.2	16.2	29.82	272	5.1393E-21	1.9298	2.3161	3.742	3	599970000	176990000	422980000
O35129	Prohibitin-2	Phb2	9	9	9	39.8	39.8	39.8	33.296	299	7.129E-115	2.0762	1.6487	83.833	11	1573900000	502920000	1071000000
Q9JK53	Prolargin	Prelp	2	2	2	6.9	6.9	6.9	43.292	378	2.1833E-10	0.85833	0.79271	5.7464	2	230930000	118350000	112580000
P17918	Proliferating cell nuclear antigen	Pcna	4	4	4	20.3	20.3	20.3	28.785	261	7.9078E-30	2.793	3.3619	209.23	2	253630000	84553000	169080000
P50580	Proliferation-associated protein 2G4	Pa2g4	9	9	9	34.5	34.5	34.5	43.698	394	1.4051E-79	0.68731	0.61163	50.842	6	355920000	193270000	162650000
Q9Z2Y8	Proline synthase co-transcribed bacterial homolog protein	Prosc	5	5	5	21.5	21.5	21.5	30.048	274	4.3993E-57	0.55795	0.57248	39.118	8	589050000	341980000	247070000
E9QKI4	Proline-rich AKT1 substrate 1	Akt1s1	2	2	2	9.5	9.5	9.5	35.581	328	4.2699E-09	0.57761	0.71906	14.387	5	73031000	40501000	32530000
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	Lrp1	9	9	9	1.6	1.6	1.6	504.74	4545	2.8353E-16	0.48471	0.54307	40.954	8	148330000	108610000	39724000
Q9QUR6	Prolyl endopeptidase	Prep	11	11	11	23.5	23.5	23.5	80.751	710	6.0047E-83	1.264	1.3826	54.833	12	1577600000	756840000	820810000
Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondrial	Pcca	17	17	17	32.6	32.6	32.6	79.921	724	1.973E-281	0.86941	0.94527	57.205	23	3791100000	2118600000	1672600000
Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial	Pccb	14	14	14	39.2	39.2	39.2	58.408	541	0	1.0969	1.0471	74.517	18	1397200000	677690000	719530000
Q8BWM0	Prostaglandin E synthase 2;Prostaglandin E synthase 2 truncated form	Ptges2	2	2	2	9.1	9.1	9.1	43.323	384	3.6985E-25	0.84928	0.93012	135.06	2	51052000	23202000	27849000
Q9R0Q7	Prostaglandin E synthase 3	Ptges3	3	3	3	20.6	20.6	20.6	18.721	160	2.7861E-08	0.64621	0.51132	43.937	3	773680000	433880000	339800000
Q8VDQ1	Prostaglandin reductase 2	Ptgr2	7	7	7	31.1	31.1	31.1	38.015	351	1.0335E-80	0.89108	0.84862	48.209	10	1127000000	565780000	561220000
Q9DB60	Prostamide/prostaglandin F synthase	Fam213b	2	2	2	11.9	11.9	11.9	21.67	201	3.1748E-22	2.0247	1.7956	40.736	2	679890000	215800000	464090000
Q9JKV1	Proteasomal ubiquitin receptor ADRM1	Adrm1	3	3	3	8.8	8.8	8.8	42.06	407	1.0355E-27	1.1745	1.1446	26.68	3	143240000	65080000	78163000
P97371	Proteasome activator complex subunit 1	Psme1	13	13	13	55.8	55.8	55.8	28.673	249	2.783E-108	0.55431	0.53188	45.479	15	3482800000	2317200000	1165600000
P97372	Proteasome activator complex subunit 2	Psme2	6	6	6	31.4	31.4	31.4	27.057	239	8.9247E-42	0.59912	0.63073	45.402	5	541550000	350600000	190950000
P61290	Proteasome activator complex subunit 3	Psme3	4	4	4	18.5	18.5	18.5	29.506	254	1.5753E-39	0.28449	0.26631	82.323	3	49002000	28909000	20093000
Q5SSW2	Proteasome activator complex subunit 4	Psme4	4	4	4	2.3	2.3	2.3	211.19	1843	8.2191E-09	0.98112	0.87737	24.459	4	140850000	73197000	67655000
Q9JK23	Proteasome assembly chaperone 1	Psmg1	3	3	3	11.8	11.8	11.8	33.104	289	1.8384E-06	1.4641	1.4562	56.087	4	168740000	42560000	126180000
Q9R1P4	Proteasome subunit alpha type-1	Psma1	7	7	7	35.4	35.4	35.4	29.546	263	1.4713E-32	1.3428	1.0528	47.133	8	700160000	324750000	375420000
P49722	Proteasome subunit alpha type-2	Psma2	5	5	5	35	35	35	25.926	234	2.6271E-48	1.6407	1.8673	42.223	6	652550000	230620000	421920000
O70435	Proteasome subunit alpha type-3	Psma3	5	5	5	18.4	18.4	18.4	28.405	255	2.2428E-15	1.0022	0.89776	28.067	9	1205400000	592970000	612480000
Q9R1P0	Proteasome subunit alpha type-4;Proteasome subunit alpha type	Psma4	5	5	5	34.1	34.1	34.1	29.47	261	9.207E-98	0.74613	0.77517	73.733	9	2368400000	1429500000	938900000
Q9Z2U1	Proteasome subunit alpha type-5;Proteasome subunit alpha type	Psma5	6	6	6	33.2	33.2	33.2	26.411	241	0	0.64205	0.68994	74.907	8	788550000	413330000	375220000
Q9QUM9	Proteasome subunit alpha type-6	Psma6	6	6	6	26	26	26	27.372	246	1.4401E-14	0.90313	1.0828	41.522	6	1513900000	820100000	693840000
Q9Z2U0	Proteasome subunit alpha type-7	Psma7	6	6	6	27.8	27.8	27.8	27.855	248	2.596E-165	0.81963	0.75102	92.364	7	1006200000	583760000	422400000
O09061	Proteasome subunit beta type-1	Psmb1	3	3	3	20	20	20	26.372	240	6.3766E-16	1.0593	1.0478	21.126	5	444390000	195190000	249200000
Q9R1P3	Proteasome subunit beta type-2	Psmb2	2	2	2	12.9	12.9	12.9	22.906	201	1.712E-07	1.8509	2.097	27.855	2	37421000	13906000	23515000
Q9R1P1	Proteasome subunit beta type-3;Proteasome subunit beta type	Psmb3	4	4	4	30.7	30.7	30.7	22.965	205	3.3154E-38	1.351	1.2707	19.242	8	1192400000	521510000	670920000
P99026	Proteasome subunit beta type-4	Psmb4	2	2	2	11.4	11.4	11.4	29.116	264	1.7508E-62	1.712	1.8989	10.971	2	88668000	29085000	59583000
O55234	Proteasome subunit beta type-5	Psmb5	4	4	4	15.2	15.2	15.2	28.532	264	3.0358E-92	1.643	1.4962	25.181	5	494830000	174260000	320570000
Q6PDI5	Proteasome-associated protein ECM29 homolog	Ecm29	8	8	8	5.7	5.7	5.7	203.7	1840	4.2858E-66	0.56555	0.62402	60.165	11	342140000	204610000	137530000
Q9CPR6	Protein 1700011A15Rik (RIKEN cDNA 1700011A15)	1700011A15Rik	1	1	1	6.4	6.4	6.4	18.193	171	0.00043498	0.099076	0.099497	105.85	2	232480000	216000000	16475000
A2A841	Protein 4.1	Epb4.1	3	3	3	5.1	5.1	5.1	97.239	869	3.4927E-33	0.59762	0.59424	21.978	4	134390000	83265000	51122000
F8VPN4	Protein Agl	Agl	26	26	26	23	23	23	174.29	1532	4.954E-302	2.527	2.4215	63.608	29	3020000000	938290000	2081700000
E9Q616	Protein Ahnak	Ahnak	99	99	99	41.5	41.5	41.5	604.25	5656	0	0.59573	0.53183	77.199	120	1.8588E+10	1.1387E+10	7201000000
E9PYB0	Protein Ahnak2 (Fragment)	Ahnak2	4	4	2	13.1	13.1	2.2	182.7	1739	2.5947E-34	0.686	0.75285	25.192	4	666110000	371310000	294810000
F7DBB3	Protein Ahnak2 (Fragment)	Ahnak2	3	1	1	7.6	1	1	166.49	1576	3.4228E-36	0.7781	0.68186	7.5967	2	44197000	26867000	17329000
Q07456	Protein AMBP	Ambp	2	2	2	7.2	7.2	7.2	39.029	349	6.6767E-39	0.30018	0.2903	27.233	5	481900000	365820000	116070000
Q9JIF0	Protein arginine N-methyltransferase 1	Prmt1	3	3	3	10.8	10.8	10.8	42.435	371	5.6414E-34	2.1481	1.8042	195.58	3	413210000	161030000	252180000
Q921C5	Protein bicaudal D homolog 2	Bicd2	4	4	4	7.6	7.6	7.6	93.39	820	3.2589E-31	0.30806	0.31699	45.993	4	98515000	79901000	18613000
O35127	Protein C10	Grcc10	2	2	2	26.2	26.2	26.2	13.194	126	1.9009E-38	0.4316	0.52368	87.015	4	369460000	252140000	117330000
E9QA15	Protein Cald1	Cald1	5	5	5	8.3	8.3	8.3	89.272	768	2.5126E-20	0.48201	0.48697	48.848	5	277070000	179550000	97523000
Q9QXT0	Protein canopy homolog 2	Cnpy2	2	2	2	17	17	17	20.767	182	7.642E-100	1.8465	1.9494	144.83	2	120490000	27557000	92929000
Q4VAA2	Protein CDV3	Cdv3	5	5	5	39.1	39.1	39.1	29.729	281	2.1048E-85	0.45125	0.37227	54.137	12	758180000	584030000	174160000
E9PWQ3	Protein Col6a3	Col6a3	7	7	7	2.5	2.5	2.5	353.93	3284	3.7606E-20	0.94037	0.83773	112.08	5	269100000	179580000	89518000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
E9Q3H6	Protein Coq10a	Coq10a	4	4	4	19.3	19.3	19.3	28.927	259	1.969E-24	3.0451	3.4864	44.518	4	1059800000	257400000	802410000
A2ADY9	Protein DDI1 homolog 2	Ddi2	2	2	2	7	7	7	44.59	399	2.6263E-06	0.36766	0.32072	3.5734	2	54431000	40766000	13665000
Q7TNV0	Protein DEK	Dek	4	4	4	15	15	15	43.158	380	1.98E-124	0.6397	0.66589	84.736	4	73872000	49033000	24838000
E9PV41	Protein diaphanous homolog 1	Diap1	1	1	1	1.1	1.1	1.1	140.4	1264	3.1429E-06	0.8074	0.76654	5.5243	2	32765000	18299000	14466000
P09103	Protein disulfide-isomerase	P4hb	13	13	13	26.5	26.5	26.5	57.058	509	5.746E-232	0.6432	0.65872	78.109	18	2255200000	1379200000	875990000
P27773	Protein disulfide-isomerase A3	Pdia3	17	17	17	38.2	38.2	38.2	56.678	505	0	1.0629	1.049	41.372	24	3653700000	1721000000	1932800000
P08003	Protein disulfide-isomerase A4	Pdia4	9	9	9	18.2	18.2	18.2	71.982	638	9.5161E-87	0.63373	0.62671	114.86	7	983480000	622310000	361170000
Q3TML0	Protein disulfide-isomerase A6	Pdia6	5	5	5	15.3	15.3	15.3	48.689	445	1.7836E-50	0.87554	0.88126	34.586	6	698190000	360390000	337790000
Q99LX0	Protein DJ-1	Park7	9	9	9	55	55	55	20.021	189	0	0.44538	0.50279	86.686	11	5967400000	4307400000	1660000000
E9Q9R9	Protein Dlg5	Dlg5	2	2	2	1.2	1.2	1.2	214.38	1921	0.004436	0.39529	0.18324	95.404	2	158560000	114280000	44283000
E9Q8T7	Protein Dnah1	Dnahc1	1	1	1	0.2	0.2	0.2	487.06	4250	0.035702	1.668	2.1233	8.7219	3	6905700000	2678900000	4226700000
Q9DCM0	Protein ETHE1, mitochondrial	Ethe1	5	5	5	29.1	29.1	29.1	27.738	254	2.0737E-37	1.2955	1.2431	79.351	10	5001600000	1283100000	3718500000
Q61160	Protein FADD	Fadd	1	1	1	8.3	8.3	8.3	22.96	205	1.2911E-14	0.5276	0.53812	38.628	2	206980000	140590000	66388000
Q8VE88	Protein FAM114A2	Fam114a2	3	3	3	9.3	9.3	9.3	54.044	497	5.0951E-11	0.42269	0.4595	66.414	3	173480000	113810000	59666000
Q9CR98	Protein FAM136A	Fam136a	2	2	2	29	29	29	15.674	138	1.783E-138	0.51287	0.47053	10.906	4	504950000	319790000	185170000
Q9D6U8	Protein FAM162A	Fam162a	3	3	3	22.6	22.6	22.6	17.725	155	1.0733E-30	0.85388	0.74357	26.601	3	847890000	448810000	399080000
Q9CQB2	Protein FAM195A	Fam195a	3	3	3	38.1	38.1	38.1	17.871	160	5.2922E-05	0.76745	0.87325	16.496	3	88772000	56725000	32047000
Q3UGS4	Protein FAM195B	Fam195b	1	1	1	18.6	18.6	18.6	11.101	97	0.063764	0.66373	0.68902	18.763	2	129690000	76084000	53604000
Q921M7	Protein FAM49B	Fam49b	3	3	3	12	12	12	36.776	324	5.7269E-12	0.54336	0.6842	26.038	5	267400000	181910000	85486000
Q9CWE0	Protein FAM54B	Fam54b	2	2	2	8.7	8.7	8.7	31.726	289	0.0055116	0.86633	0.66034	12.442	2	66847000	34012000	32835000
Q76LS9	Protein FAM63A	Fam63a	1	1	1	3.8	3.8	3.8	51.225	468	4.3613E-10	0.9483	0.93592	9.7318	2	104810000	52884000	51926000
D3YWJ4	Protein farnesyltransferase subunit beta	Fntb	1	1	1	1.9	1.9	1.9	52.784	471	0.052488	1.5247	1.5726	15.576	2	33020000	12517000	20503000
Q61239	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	Fnta	7	7	7	23.9	23.9	23.9	44.013	377	6.551E-38	0.54092	0.50078	77.855	7	187810000	93430000	94383000
L7N1X8	Protein Gbp6	Gbp10	8	8	4	14.7	14.7	9.2	70.451	611	5.4299E-65	0.76327	0.80122	69.726	6	302370000	171950000	130430000
E9Q035	Protein Gm20425	Gm20425	34	2	2	41.4	3.4	3.4	107.8	978	0	2.2117	1.9514	16.841	2	43507000	15596000	27911000
E9PVZ8	Protein Golgb1	Golgb1	4	4	4	1.6	1.6	1.6	370.15	3238	1.1917E-06	0.06829	0.07593	132.94	3	151460000	140840000	10623000
Q8BUK6	Protein Hook homolog 3	Hook3	2	2	2	3.8	3.8	3.8	83.217	718	2.1037E-05	1.1713	1.0819	70.327	2	61987000	22089000	39898000
F6TQW2	Protein Ighg2c	Ighg2c	5	4	4	23.6	19.6	19.6	44.095	403	5.367E-222	0.8129	0.89184	25.018	10	2114200000	1368500000	745670000
O55091	Protein IMPACT	Impact	3	3	3	14.5	14.5	14.5	36.276	318	3.2213E-06	0.49395	0.53037	40.077	2	25789000	16147000	9642600
E9QAS7	Protein Inpp5a	Inpp5a	2	2	2	4.7	4.7	4.7	48.812	422	0.00067849	1.3363	1.2685	30.918	2	33434000	15315000	18119000
Q5SW19	Protein KIAA0664	Kiaa0664	15	15	15	14.6	14.6	14.6	148.07	1315	1.321E-146	1.1548	1.2662	55.155	15	1019200000	479740000	539420000
Q99JB8	Protein kinase C and casein kinase II substrate protein 3	Pacsin3	3	3	3	10.1	10.1	10.1	48.584	424	2.5251E-30	0.99014	1.1659	16.658	6	491940000	241930000	250010000
Q9WVE8	Protein kinase C and casein kinase substrate in neurons protein 2	Pacsin2	7	7	7	18.5	18.5	18.5	55.832	486	3.712E-149	0.56312	0.651	51.938	8	1245200000	812060000	433100000
E9PYF4	Protein Lmo7	Lmo7	8	8	8	7.4	7.4	7.4	192.55	1699	6.8243E-40	1.4408	1.3362	22.895	6	164730000	65919000	98812000
Q8K2F8	Protein LSM14 homolog A	Lsm14a	3	3	3	8.4	8.4	8.4	50.545	462	9.9748E-24	0.45075	0.44255	7.2641	2	37183000	25212000	11971000
Q7TQ95	Protein lunapark	Lnp	2	2	2	11.8	11.8	11.8	47.499	425	4.9177E-10	1.1905	0.99535	33.385	2	33772000	18735000	15037000
Q80WJ7	Protein LYRIC	Mtdh	3	3	3	6.2	6.2	6.2	63.845	579	8.152E-06	1.3129	1.3329	47.84	2	94996000	45396000	49601000
Q8K3C3	Protein LZIC	Lzic	7	7	7	43.2	43.2	43.2	21.536	190	2.241E-270	0.46028	0.49329	63.479	9	799310000	530540000	268770000
Q91VH6	Protein MEMO1	Memo1	4	4	4	19.9	19.9	19.9	33.692	297	5.0715E-15	2.0251	2.0441	21.093	5	234170000	78370000	155800000
Q9QYG0	Protein NDRG2	Ndrg2	9	9	9	34.5	34.5	34.5	40.789	371	3.627E-166	0.60466	0.67132	87.283	26	1.0965E+10	7106200000	3859000000
O55126	Protein NipSnap homolog 2	Gbas	5	5	5	20.6	20.6	20.6	32.932	281	1.7301E-32	1.4572	1.0877	117.99	5	1089500000	441590000	647860000
E9Q7L0	Protein Ogdhl	Ogdhl	19	17	17	27.3	25.1	25.1	116.6	1029	5.061E-239	2.3746	2.5578	59.615	30	4523500000	1289300000	3234200000
Q9D0B6	Protein PBDC1	Pbdc1	3	3	3	16.2	16.2	16.2	22.223	198	1.5193E-06	0.75025	0.79247	105.76	4	147750000	76851000	70901000
Q8CFX3	Protein Pcdh1 (Protocadherin 1)	Pcdh1	3	3	3	4.3	4.3	4.3	112.41	1038	5.0823E-10	0.21782	0.19945	35.976	2	55241000	48211000	7030000
A6H644	Protein phosphatase 1 regulatory subunit 12B	Ppp1r12b	7	7	6	9.2	9.2	7.7	110.97	992	3.6999E-49	1.3055	1.1188	34.966	7	479160000	185960000	293200000
Q8R4S0	Protein phosphatase 1 regulatory subunit 14C	Ppp1r14c	2	2	2	22.6	22.6	22.6	17.754	164	3.325E-170	0.41884	0.47926	10.572	6	1005100000	714520000	290560000
Q99MR9	Protein phosphatase 1 regulatory subunit 3A	Ppp1r3a	9	9	9	12.6	12.6	12.6	121.43	1089	1.562E-167	0.74443	0.80684	23.973	12	399950000	223760000	176190000
Q3UM45	Protein phosphatase 1 regulatory subunit 7	Ppp1r7	6	6	6	23.8	23.8	23.8	41.291	361	0	0.86293	0.94646	33.889	8	530490000	278700000	251780000
P49443	Protein phosphatase 1A	Ppm1a	4	3	3	14.7	12	12	42.432	382	6.7458E-16	0.69425	0.70218	15.8	4	153450000	86338000	67116000
Q99NF7	Protein phosphatase 1B	Ppm1b	4	4	3	12.2	12.2	10.1	52.11	477	7.9286E-54	0.71839	0.71089	7.6138	5	486460000	292160000	194300000
Q8CGA0	Protein phosphatase 1F	Ppm1f	3	3	3	8.2	8.2	8.2	49.61	452	6.6097E-12	0.9096	0.99543	154.58	3	170510000	86522000	83991000
Q8BXN7	Protein phosphatase 1K, mitochondrial	Ppm1k	3	3	3	9.1	9.1	9.1	40.918	372	5.1993E-06	0.81056	0.77988	26.882	5	132110000	70310000	61798000
Q9DCL8	Protein phosphatase inhibitor 2	Ppp1r2	4	4	4	20.9	20.9	20.9	23.119	206	2.5115E-63	0.41075	0.44083	41.545	3	104000000	79031000	24969000
Q8BVQ5	Protein phosphatase methylesterase 1	Ppme1	2	2	2	5.2	5.2	5.2	42.256	386	0.00027935	0.42249	0.4375	27.561	2	38001000	24360000	13641000
Q6NVE9	Protein phosphatase PTC7 homolog	Pptc7	3	3	3	11.9	11.9	11.9	33.048	310	1.0629E-10	0.7584	0.86862	41.947	5	88513000	46704000	41810000
Q3UKG2	Protein Prob1 (Fragment)	Gm1614	4	4	4	8.4	8.4	8.4	106.42	1006	2.7878E-13	1.2068	1.1712	43.285	4	212170000	120180000	91998000
Q7TSC1	Protein PRRC2A	Prrc2a	7	7	7	6.1	6.1	6.1	229.2	2158	5.7103E-26	0.61382	0.56113	139.25	6	332780000	65905000	266880000
Q3TLH4	Protein PRRC2C	Prrc2c	5	5	5	3	3	3	310.89	2846	5.9278E-42	0.64969	0.71155	32.098	4	160260000	106710000	53546000
Q8BIW1	Protein prune homolog	Prune	7	7	7	20.9	20.9	20.9	50.239	454	1.2531E-79	0.75554	0.75534	92.086	8	342080000	201720000	140360000
Q52KR3	Protein prune homolog 2	Prune2	5	5	5	3	3	3	339.51	3084	5.3576E-29	1.4599	1.2509	44.459	6	129650000	64522000	65126000
Q9QYS9	Protein quaking	Qki	4	4	4	16.7	16.7	16.7	37.67	341	5.8488E-14	0.46618	0.45687	66.82	4	262590000	145870000	116720000
E9Q912	Protein Rap1gds1	Rap1gds1	5	5	5	12.9	12.9	12.9	66.076	607	3.6346E-91	0.58877	0.60621	27.159	8	378440000	240320000	138120000
H3BL40	Protein Rgsl1	Rgsl1	2	2	2	1.8	1.8	1.8	125.04	1073	0.0044634	0.76448	0.68889	46.561	3	7074700000	4093600000	2981100000
P56565	Protein S100-A1	S100a1	4	4	4	40.4	40.4	40.4	10.505	94	7.1727E-50	0.71234	0.89846	37.65	5	3248900000	1995400000	1253600000
P08207	Protein S100-A10	S100a10	2	2	2	17.5	17.5	17.5	11.186	97	2.4546E-17	0.5423	0.60297	42.369	4	1264800000	858760000	406050000
P50543	Protein S100-A11	S100a11	4	4	4	38.8	38.8	38.8	11.083	98	1.63E-153	0.34916	0.32263	119.04	6	934860000	680330000	254530000
P31725	Protein S100-A9	S100a9	2	2	2	19.5	19.5	19.5	13.049	113	4.8202E-06	0.23246	0.21251	42.394	2	409250000	340520000	68732000
Q9D1M0	Protein SEC13 homolog	Sec13	1	1	1	5.3	5.3	5.3	35.565	322	7.2511E-28	0.70308	0.61551	67.31	3	77693000	47827000	29866000
A2AIX1	Protein Sec16a	Sec16a	4	4	4	2.6	2.6	2.6	256.47	2377	1.7676E-06	0.61525	0.76966	71.6	3	85416000	58852000	26565000
G3X972	Protein Sec24c	Sec24c	5	5	5	7	7	7	118.58	1096	6.2615E-47	1.4711	1.4459	23.377	3	155850000	83896000	71957000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O08797	Protein Serpinb9	Serpinb9	2	2	2	9.6	9.6	9.6	42.259	374	6.5126E-08	0.54566	0.574	0.42192	2	129370000	92574000	36799000
Q9EQU5	Protein SET	Set	5	5	5	19.4	19.4	19.4	33.377	289	1.1575E-33	0.47979	0.23781	87.646	5	1763700000	415310000	1348400000
Q3UJB0	Protein Sf3b2 (Splicing factor 3b, subunit 2)	Sf3b2	3	3	3	3.3	3.3	3.3	98.197	878	6.7331E-06	0.7782	0.90064	80.376	3	682760000	464530000	218230000
Q6NZR5	Protein Skiv2l (Superkiller viralicidic activity 2-like (S. cerevisiae))	Skiv2l	2	2	2	2	2	2	137.52	1244	0.0001675	0.74195	0.93675	81.591	2	2860000000	1440800000	1419100000
Q7TNB8	Protein strawberry notch homolog 2;Protein strawberry notch homolog 1	Sbno2	2	2	2	1.9	1.9	1.9	149.29	1349	0.020213	0.81178	0.62273	116.18	2	1564500000	663800000	900730000
Q91YM4	Protein TBRG4	Tbrg4	3	3	3	5.7	5.7	5.7	71.513	630	6.1752E-07	1.3986	1.5476	44.959	4	301830000	150290000	151540000
Q9Z1A1	Protein Tfg	Tfg	6	6	6	29.7	29.7	29.7	43.02	397	8.6221E-81	0.60456	0.75554	18.09	4	260890000	163750000	97144000
E9Q0S6	Protein Tns1	Tns1	15	15	14	12.1	12.1	11.4	201.38	1888	2.0162E-85	1.3705	1.341	59.984	8	485650000	203340000	282310000
O35452	Protein Tnxb (Tenascin X)	Tnxb	5	5	5	5	5	5	435.47	4006	1.7568E-15	0.82797	0.79646	141.26	8	421950000	269650000	152310000
Q01405	Protein transport protein Sec23A	Sec23a	6	6	6	10.6	10.6	10.6	86.161	765	3.832E-92	1.5258	1.5502	81.875	4	226760000	119720000	107050000
Q3UPL0	Protein transport protein Sec31A	Sec31a	9	9	9	10.2	10.2	10.2	133.57	1230	1.6956E-24	1.2294	1.288	55.262	10	581950000	299230000	282720000
Q3TZ89	Protein transport protein Sec31B	Sec31b	2	2	2	1.3	1.3	1.3	125.63	1158	0.00063717	1.3415	1.1788	34.774	2	1.2534E+10	5112800000	7421600000
Q8R121	Protein Z-dependent protease inhibitor	Serpina10	3	3	3	8.9	8.9	8.9	51.797	448	6.9673E-23	0.37596	0.33421	25.299	2	62077000	45673000	16404000
Q9D1G3	Protein-cysteine N-palmitoyltransferase HHAT-like protein	Hhatl	4	4	4	10.3	10.3	10.3	56.43	503	4.3593E-13	1.383	1.3365	30.35	4	561230000	245270000	315960000
P21981	Protein-glutamine gamma-glutamyltransferase 2	Tgm2	14	14	14	28.3	28.3	28.3	77.06	686	0	0.79797	0.80504	57.558	17	2009700000	1178000000	831740000
E0CYV0	Protein-L-isoaspartate O-methyltransferase	Pcmt1	5	5	5	29.4	29.4	29.4	30.441	286	7.111E-94	0.70655	0.70464	31.657	6	627230000	350560000	276670000
P19221	Prothrombin;Activation peptide fragment 1	F2	8	8	8	19.1	19.1	19.1	70.268	618	8.9563E-37	0.54695	0.57848	56.839	10	947160000	567070000	380090000
P26350	Prothymosin alpha;Thymosin alpha	Ptma	2	2	2	12.6	12.6	12.6	12.254	111	0	0.16988	0.13525	37.94	2	28121000	23173000	4948200
P51175	Protoporphyrinogen oxidase	Ppox	2	2	2	7.5	7.5	7.5	50.87	477	2.4852E-05	1.3353	1.1868	143.32	3	80333000	57646000	22687000
Q9CZL5	Pterin-4-alpha-carbinolamine dehydratase 2	Pcbd2	2	2	2	19.1	19.1	19.1	14.83	136	1.3609E-46	0.6463	0.70309	5.9765	3	637540000	394590000	242950000
P23492	Purine nucleoside phosphorylase	Pnp	6	6	6	30.4	30.4	30.4	32.277	289	1.9197E-41	0.88476	0.84779	18.284	9	531310000	296460000	234860000
Q6W8Q3	Purkinje cell protein 4-like protein 1	Pcp4l1	2	2	2	39.7	39.7	39.7	7.5023	68	1.7733E-08	1.5293	1.5376	254.32	2	324960000	142870000	182080000
Q11011	Puromycin-sensitive aminopeptidase	Npepps	16	16	16	20.8	20.8	20.8	103.32	920	2.267E-183	0.97217	0.8638	64.643	19	2233400000	1220900000	1012400000
O88696	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	Clpp	3	3	3	16.5	16.5	16.5	29.8	272	1.151E-52	1.0713	0.96941	12.025	3	198570000	99275000	99290000
Q6P8M1	Putative deoxyribonuclease TATDN1	Tatdn1	2	2	2	11.9	11.9	11.9	33.365	295	3.9421E-47	0.77899	0.77678	42.976	2	68431000	39555000	28877000
Q8BU04	Putative E3 ubiquitin-protein ligase UBR7	Ubr7	2	2	2	5.9	5.9	5.9	48.064	425	0.00026835	0.7894	0.68974	17.937	3	7110700	4122500	2988300
O88851	Putative hydrolase RBBP9	Rbbp9	5	5	5	43	43	43	20.911	186	6.5957E-20	0.57829	0.58934	64.791	8	466730000	266640000	200080000
Q3UIZ8	Putative myosin light chain kinase 3	Mylk3	6	6	6	16.7	16.7	16.7	86.371	795	1.934E-160	0.72138	0.69372	56.371	7	704700000	361030000	343670000
Q3TCN2	Putative phospholipase B-like 2	Plbd2	4	4	4	10.6	10.6	10.6	66.289	594	1.978E-133	2.0425	1.9905	144.15	3	134430000	28655000	105780000
Q8CAK1	Putative transferase CAF17 homolog, mitochondrial	Iba57	6	6	6	32.4	32.4	32.4	38.399	358	1.973E-119	1.5532	1.6579	24.733	10	1046900000	420670000	626200000
Q8K183	Pyridoxal kinase	Pdxk	4	4	4	14.7	14.7	14.7	35.015	312	1.1255E-44	1.1611	1.3788	35.615	6	757720000	357360000	400360000
Q99K01	Pyridoxal-dependent decarboxylase domain-containing protein 1	Pdxdc1	2	2	2	3.8	3.8	3.8	87.334	787	0.0069715	0.48021	0.52484	55.452	2	47351000	32252000	15099000
Q91XF0	Pyridoxine-5-phosphate oxidase	Pnpo	1	1	1	3.1	3.1	3.1	30.114	261	0.00077395	1.4329	1.6942	45.559	2	215830000	127020000	88813000
E9QPD7	Pyruvate carboxylase;Pyruvate carboxylase, mitochondrial	Pcx	13	13	13	14.5	14.5	14.5	129.83	1179	7.749E-58	1.2279	1.3459	38.312	12	912050000	503930000	408120000
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form	Pdha1	11	11	11	36.9	36.9	36.9	43.231	390	4.299E-146	1.0387	1.2132	74.828	17	8489300000	3859500000	4629800000
Q9D051	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	Pdhb	14	14	14	46.5	46.5	46.5	38.937	359	0	1.0315	1.0215	84.815	66	2.5748E+10	1.2247E+10	1.3502E+10
Q7TSQ8	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	Pdpr	7	7	7	10.1	10.1	10.1	99.229	878	2.0355E-28	1.8972	1.7047	50.495	6	173340000	59279000	114060000
Q8BKZ9	Pyruvate dehydrogenase protein X component, mitochondrial	Pdhx	10	10	10	34.1	34.1	34.1	53.998	501	9.127E-248	0.61659	0.65005	48.127	20	4685600000	2912100000	1773500000
P52480	Pyruvate kinase isozymes M1/M2	Pkm2	18	18	18	43.3	43.3	43.3	57.844	531	0	0.96063	0.99009	76.699	44	1.7589E+10	9454000000	8135400000
P47199	Quinone oxidoreductase	Cryz	3	3	3	14.8	14.8	14.8	35.268	331	7.8109E-42	0.99599	1.0458	29.78	2	388080000	201020000	187060000
P50396	Rab GDP dissociation inhibitor alpha	Gdi1	13	9	9	39.8	27.1	27.1	50.521	447	1.264E-265	0.69826	0.64023	68.315	12	1780700000	1303100000	477650000
Q61598	Rab GDP dissociation inhibitor beta	Gdi2	18	18	14	52.8	52.8	40	50.537	445	0	0.97312	1.0135	55.356	31	5057000000	2471700000	2585300000
A6H6A9	Rab GTPase-activating protein 1-like	Rabgap1l	4	4	4	4.8	4.8	4.8	92.403	815	3.9859E-17	0.41007	0.43202	55.829	4	70190000	49299000	20890000
O35551	Rab GTPase-binding effector protein 1	Rabep1	4	4	4	6.6	6.6	6.6	99.523	862	1.7194E-26	1.2833	1.0987	188.08	2	479840000	77893000	401950000
Q91WG2	Rab GTPase-binding effector protein 2	Rabep2	4	4	4	8.5	8.5	8.5	62.132	554	1.964E-11	0.7553	0.70912	107.37	4	44386000	19268000	25117000
Q9QXG2	Rab proteins geranylgeranyltransferase component A 1	Chm	2	2	2	4.4	4.4	4.4	73.976	665	9.1545E-25	0.83097	0.84534	31.862	3	119750000	65182000	54566000
Q68EF0	Rab-3A-interacting protein	Rab3ip	2	2	2	7.5	7.5	7.5	47.133	428	3.4503E-80	0.95687	0.97065	2.3064	2	73393000	40242000	33150000
P31750	RAC-alpha serine/threonine-protein kinase	Akt1	3	3	3	6.7	6.7	6.7	55.707	480	4.854E-08	0.43187	0.42087	121.07	3	1142000000	452050000	689930000
P26043	Radixin	Rdx	8	5	5	15.3	10.8	10.8	68.542	583	1.4096E-49	0.61734	0.67029	24.66	5	413520000	267910000	145610000
Q9CQ22	Ragulator complex protein LAMTOR1	Lamtor1	2	2	2	27.3	27.3	27.3	17.749	161	1.1989E-17	2.295	1.7278	24.871	2	61771000	16089000	45682000
Q9CT10	Ran-binding protein 3	Ranbp3	3	3	3	8.6	8.6	8.6	52.572	491	4.4626E-20	0.49348	0.2523	80.149	2	121440000	82348000	39097000
P34022	Ran-specific GTPase-activating protein	Ranbp1	3	3	3	22.2	22.2	22.2	23.596	203	2.8211E-46	0.42728	0.31225	135.86	3	685360000	483050000	202310000
Q60790	Ras GTPase-activating protein 3	Rasa3	2	2	2	3.5	3.5	3.5	95.986	834	5.3554E-05	2.0466	2.2328	101.03	2	146730000	21695000	125030000
P97855	Ras GTPase-activating protein-binding protein 1	G3bp1	6	6	6	18.3	18.3	18.3	51.828	465	1.5398E-34	1.0441	0.93278	9.8848	9	920270000	507310000	412960000
P97379	Ras GTPase-activating protein-binding protein 2	G3bp2	6	6	6	19.3	19.3	19.3	54.087	482	2.7822E-18	0.87228	0.799	19.511	7	226420000	121630000	104790000
Q9JKF1	Ras GTPase-activating-like protein IQGAP1	Iqgap1	5	5	5	4.2	4.2	4.2	188.74	1657	1.095E-35	1.3244	1.4443	48.137	7	624490000	273530000	350950000
Q01730	Ras suppressor protein 1	Rsu1	4	4	4	21.7	21.7	21.7	31.55	277	5.6982E-23	1.086	1.2389	32.559	3	333050000	175620000	157440000
Q3TLP8	Ras-related C3 botulinum toxin substrate 1	Rac1	4	4	3	20.9	20.9	15.6	23.432	211	7.0284E-13	1.3446	0.66565	137.19	5	1002700000	453170000	549550000
Q80X95	Ras-related GTP-binding protein A;Ras-related GTP-binding protein B	Rraga	3	3	3	9.9	9.9	9.9	36.566	313	1.977E-07	3.6943	4.1492	70.494	3	237270000	55254000	182020000
Q99K70	Ras-related GTP-binding protein C	Rragc	1	1	1	9.5	9.5	9.5	44.12	398	7.2262E-16	2.068	1.8639	14.24	2	33972000	18317000	15655000
P61027	Ras-related protein Rab-10	Rab10	3	2	2	15	9.5	9.5	22.541	200	2.1142E-06	1.7948	2.0318	77.669	2	363950000	113510000	250440000
P46638	Ras-related protein Rab-11B;Ras-related protein Rab-11A	Rab11b	6	6	6	32.1	32.1	32.1	24.489	218	1.3842E-56	1.0466	1.1088	32.98	8	876350000	436390000	439970000
Q91V41	Ras-related protein Rab-14	Rab14	6	6	6	45.1	45.1	45.1	23.897	215	7.557E-110	1.1202	0.91902	41.129	7	476190000	209460000	266730000
P62821	Ras-related protein Rab-1A	Rab1A	4	2	2	25.4	16.1	16.1	22.677	205	3.5411E-35	1.1388	1.2727	24.578	6	338250000	154200000	184050000
Q9D1G1	Ras-related protein Rab-1B	Rab1b	5	5	3	32.8	32.8	23.4	22.187	201	1.6648E-27	1.064	0.73699	125.09	8	2130300000	1016700000	1113600000
P35282	Ras-related protein Rab-21	Rab21	7	7	7	37.8	37.8	37.8	24.106	222	1.1647E-89	0.94717	0.96047	72.804	8	494370000	253760000	240600000
P53994	Ras-related protein Rab-2A	Rab2a	3	3	3	19.3	19.3	19.3	23.547	212	3.3515E-17	1.2291	1.1876	70.055	2	33469000	10763000	22706000
P63011	Ras-related protein Rab-3A	Rab3a	2	2	2	14.1	14.1	14.1	24.97	220	2.1074E-29	0.82004	0.90782	10.68	2	67164000	35698000	31466000
Q8C266	Ras-related protein Rab-5C	Rab5c	5	5	5	24.8	24.8	24.8	25.352	234	4.4782E-07	1.4692	1.3724	166.47	3	416160000	190660000	225500000
P35279	Ras-related protein Rab-6A	Rab6a	2	2	2	9.1	9.1	9.1	23.59	208	3.7119E-05	1.1198	1.1944	18.501	2	88607000	43483000	45125000
P51150	Ras-related protein Rab-7a	Rab7a	7	7	7	38.6	38.6	38.6	23.489	207	6.0322E-27	1.3078	1.1815	71.244	8	877520000	407050000	470470000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P63321	Ras-related protein Ral-A;Ras-related protein Ral-B	Rala	2	2	2	12.1	12.1	12.1	23.553	206	2.055E-06	1.1311	0.63591	53.846	2	63997000	33300000	30697000
P62835	Ras-related protein Rap-1A	Rap1a	2	1	1	12.5	7.1	7.1	20.987	184	2.5996E-10	1.6917	1.6487	4.5079	2	39662000	14817000	24845000
P61226	Ras-related protein Rap-2b	Rap2b	2	2	2	12	12	12	20.504	183	0.0098415	1.3948	1.3755	0.60164	2	13048000	5550600	7497800
P62071	Ras-related protein R-Ras2;Ras-related protein R-Ras	Rras2	2	2	2	13.7	13.7	13.7	23.399	204	1.1022E-10	0.82665	0.89017	9.6513	3	173540000	89266000	84277000
G3X8R0	Receptor expression-enhancing protein 5	Reep5	2	2	2	9	9	9	21.447	189	0.00011658	2.2644	1.9016	155.49	3	1294400000	225090000	1069300000
Q9CSU0	Regulation of nuclear pre-mRNA domain-containing protein 1B	Rprd1b	3	3	3	14.4	14.4	14.4	36.883	326	3.9712E-07	0.80148	0.72695	64.648	2	57252000	36680000	20572000
Q9CQE5	Regulator of G-protein signaling 10	Rgs10	2	2	2	16	16	16	21.151	181	5.201E-06	0.61807	0.57106	0.59516	2	64999000	40980000	24020000
Q9DCV4	Regulator of microtubule dynamics protein 1	Fam82b	8	8	8	32.5	32.5	32.5	35	305	5.382E-188	0.4778	0.51331	119.21	12	2173200000	1473800000	699390000
Q9EPU0	Regulator of nonsense transcripts 1	Upf1	3	3	3	3.8	3.8	3.8	123.97	1124	3.5642E-10	1.0762	0.89082	0.64607	2	46083000	25311000	20773000
Q99P72	Reticulon-4	Rtn4	8	8	8	10.9	10.9	10.9	126.61	1162	1.7027E-42	0.71779	0.72743	262.55	6	729260000	675250000	54008000
Q924D0	Reticulon-4-interacting protein 1, mitochondrial	Rtn4ip1	8	8	8	30.1	30.1	30.1	43.371	396	2.3931E-68	1.1789	1.0269	59.872	11	1402500000	675630000	726890000
P24549	Retinal dehydrogenase 1	Aldh1a1	12	12	12	32.7	32.7	32.7	54.467	501	1.847E-126	0.84222	0.81584	82.753	17	1279300000	699030000	580230000
Q62148	Retinal dehydrogenase 2	Aldh1a2	3	3	3	10.4	10.4	10.4	56.625	518	1.1215E-32	1.3262	1.5577	15.751	3	94089000	42143000	51946000
O55057	Retinal rod rhodopsin-sensitive cGMP 3,5-cyclic phosphodiesterase subunit delta	Pde6d	2	2	2	17.3	17.3	17.3	17.348	150	8.5291E-05	1.642	1.8336	172.58	2	245560000	114190000	131360000
Q920A5	Retinoid-inducible serine carboxypeptidase	Scpep1	1	1	1	3.8	3.8	3.8	50.964	452	0.00017789	1.2777	1.3598	14.278	3	90880000	38576000	52304000
Q9ERI6	Retinol dehydrogenase 14	Rdh14	2	2	2	9.9	9.9	9.9	36.365	334	7.8368E-13	3.1565	3.2634	74.637	2	56321000	16870000	39451000
Q00915	Retinol-binding protein 1	Rbp1	3	3	3	25.9	25.9	25.9	15.846	135	6.7925E-18	0.33458	0.35032	26.161	3	135940000	96457000	39486000
Q99PT1	Rho GDP-dissociation inhibitor 1	Arhgdia	5	5	5	30.4	30.4	30.4	23.407	204	4.97E-153	0.64381	0.59475	20.593	10	6704800000	4269000000	2435900000
Q61599	Rho GDP-dissociation inhibitor 2	Arhgdib	3	3	3	30.5	30.5	30.5	22.851	200	0	0.54322	0.6917	14.403	6	1212800000	790590000	422230000
A2AH25	Rho GTPase-activating protein 1	Arhgap1	2	2	2	5.8	5.8	5.8	54.437	479	1.9267E-06	1.5533	1.3633	67.482	3	33761000	17291000	16470000
A6X8Z5	Rho GTPase-activating protein 31	Arhgap31	2	2	2	1.8	1.8	1.8	155.27	1425	5.7742E-05	0.27489	0.24345	87.427	2	15676000	10050000	5625800
E9PUF7	Rho guanine nucleotide exchange factor 1	Arhgef1	2	2	2	3.9	3.9	3.9	108.69	976	6.4153E-06	1.1617	1.1248	9.8499	2	14046000	6116800	7929100
P70335	Rho-associated protein kinase 1	Rock1	5	4	4	4.4	3.7	3.7	158.17	1354	4.316E-77	0.97041	0.96136	47.292	4	139010000	66633000	72378000
F8VPK5	Rho-associated protein kinase 2	Rock2	11	11	10	10.4	10.4	9.7	160.61	1388	8.3426E-48	0.90223	0.82579	39.668	9	441560000	247400000	194160000
Q91VI7	Ribonuclease inhibitor	Rnh1	16	16	16	50.7	50.7	50.7	49.816	456	0	0.83859	0.91796	38.93	29	3735800000	2094700000	1641100000
P52760	Ribonuclease UK114	Hrsp12	5	5	5	44.4	44.4	44.4	14.255	135	2.4482E-26	0.53149	0.54627	54.639	8	423840000	230070000	193770000
Q9CW46	Ribonucleoprotein PTB-binding 1	Raver1	2	2	2	4.9	4.9	4.9	79.381	748	1.0315E-06	0.60853	0.5257	7.4196	2	41616000	23746000	17870000
P70122	Ribosome maturation protein SBDS	Sbds	3	3	3	14.4	14.4	14.4	28.78	250	4.0777E-09	0.62532	0.65192	62.286	3	252840000	153250000	99587000
Q99PL5	Ribosome-binding protein 1	Rrbp1	8	8	8	6.8	6.8	6.8	172.88	1605	4.9964E-61	0.89317	0.92264	42.481	9	653590000	345720000	307870000
Q9D6S7	Ribosome-recycling factor, mitochondrial	Mrrf	6	6	6	39.3	39.3	39.3	29.05	262	4.6558E-89	0.47158	0.46652	117.32	9	1846800000	1288500000	558290000
Q8R2Q4	Ribosome-releasing factor 2, mitochondrial	Gfm2	9	9	9	17.6	17.6	17.6	86.108	779	3.7515E-83	0.80355	0.81776	25.774	10	709500000	401030000	308470000
Q9JI75	Ribosyldihydronicotinamide dehydrogenase [quinone]	Nqo2	2	2	2	14.3	14.3	14.3	26.248	231	9.0332E-12	1.0821	1.0412	53.179	4	154420000	72681000	81738000
Q9D7H3	RNA 3-terminal phosphate cyclase	Rtcd1	3	3	3	9	9	9	39.254	366	4.2106E-05	0.41209	0.29293	25.434	2	40163000	29047000	11116000
Q9WV02	RNA-binding motif protein, X chromosome	Rbmx	2	2	2	6.9	6.9	6.9	42.3	391	1.3895E-06	0.8769	0.75837	35.53	2	278890000	157130000	121750000
Q8R4X3	RNA-binding protein 12	Rbm12	4	4	4	4.2	4.2	4.2	102.8	992	3.4908E-10	0.43658	0.45313	80.347	4	127110000	90355000	36754000
Q62176	RNA-binding protein 38;RNA-binding protein 24	Rbm38	2	2	2	11.8	11.8	11.8	25.363	237	4.6876E-06	0.67361	0.76571	45.793	3	510360000	323770000	186590000
Q5SUS9	RNA-binding protein EWS	Ewsr1	2	2	2	4.4	4.4	4.4	69.036	661	4.8754E-14	0.80031	0.76737	24.878	2	443300000	277190000	166110000
P56959	RNA-binding protein FUS	Fus	3	3	2	7.5	7.5	5.8	52.673	518	4.5173E-25	1.7859	1.7867	95.022	2	738260000	312230000	426030000
Q920Q6	RNA-binding protein Musashi homolog 2	Msi2	4	4	4	14.7	14.7	14.7	36.938	346	2.1046E-17	1.1532	1.1012	52.592	3	148390000	78567000	69828000
Q9WVB0	RNA-binding protein with multiple splicing	Rbpms	4	4	4	24.9	24.9	24.9	21.816	197	6.027E-184	0.79709	0.98348	29.117	6	737930000	408700000	329230000
Q8CJ40	Rootletin	Crocc	2	2	2	1	1	1	226.94	2009	0.0034841	0.050055	0.05519	82.736	2	2949200000	2857300000	91892000
P60122	RuvB-like 1	Ruvbl1	3	3	3	8.6	8.6	8.6	50.213	456	1.209E-09	0.50686	0.55612	27.938	3	33224000	23015000	10209000
Q9CPR1	RWD domain-containing protein 4	Rwdd4	2	2	2	10.6	10.6	10.6	21.137	188	8.1867E-06	1.9191	2.1499	164.19	2	115670000	34823000	80850000
E9Q401	Ryanodine receptor 2	Ryr2	15	15	15	3.8	3.8	3.8	564.81	4966	9.36E-29	2.3084	1.9434	51.553	10	305600000	106310000	199290000
Q3THS6	S-adenosylmethionine synthase isoform type-2	Mat2a	4	4	4	14.9	14.9	14.9	43.688	395	4.7418E-17	0.71317	0.78878	29.609	4	535230000	318360000	216870000
Q9D1J3	SAP domain-containing ribonucleoprotein	Sarnp	1	1	1	9	9	9	23.532	210	1.5607E-76	0.24426	0.24438	18.903	4	176900000	138360000	38546000
Q7TQ48	Sarcalumenin	Srl	30	30	30	48	48	48	99.183	910	0	0.54097	0.53356	37.688	84	2.303E+10	1.496E+10	8069900000
Q3URD3	Sarcolemmal membrane-associated protein	Slmap	5	5	5	6.7	6.7	6.7	96.932	845	1.0984E-27	0.81295	0.9039	36.169	7	361530000	192710000	168820000
O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	Atp2a2	26	26	26	34.7	34.7	34.7	114.86	1044	0	1.6125	1.5194	97.791	49	2.0416E+10	9552900000	1.0863E+10
S4R1M2	Scaffold attachment factor B1;Scaffold attachment factor B2	Safb	5	5	5	8.7	8.7	8.7	105.32	939	9.8562E-71	1.0929	0.69711	63.957	4	224310000	59891000	164420000
A2AD39	SCL-interrupting locus protein homolog	Stil	2	2	2	2.1	2.1	2.1	138.76	1262	0.019472	1.5697	1.7099	220.49	2	288300000	116020000	172280000
G3X928	SEC23-interacting protein	Sec23ip	4	4	4	4.8	4.8	4.8	110.76	998	1.0845E-09	1.1818	1.2868	4.0122	3	85771000	35631000	50140000
Q8VCA8	Secernin-2	Scrn2	5	5	5	21.2	21.2	21.2	46.6	425	2.4892E-22	1.3361	1.6333	28.138	5	617600000	269680000	347920000
Q3TMH2	Secernin-3	Scrn3	3	3	3	12.2	12.2	12.2	47.661	418	2.698E-21	0.9163	0.95986	50.958	3	693870000	352350000	341530000
Q921H9	Sel1 repeat-containing protein 1	Selrc1	2	2	2	14.7	14.7	14.7	25.617	231	4.7323E-19	0.42402	0.25375	9.0268	2	74036000	54444000	19592000
Q8BH69	Selenide, water dikinase 1	Sephs1	3	3	3	9.9	9.9	9.9	42.906	392	4.482E-06	1.2975	0.39789	71.309	3	669600000	74713000	594890000
P97364	Selenide, water dikinase 2	Sephs2	2	2	2	9.1	9.1	9.1	47.851	452	3.8073E-08	0.74852	0.68251	9.6055	2	30875000	17715000	13159000
P17563	Selenium-binding protein 1;Selenium-binding protein 2	Selenbp1	19	19	17	64	64	57.6	52.513	472	0	1.0689	0.92348	74.131	33	7006900000	3610900000	3396000000
Q91XH5	Sepiapterin reductase	Spr	12	12	12	53.1	53.1	53.1	27.928	262	9.582E-208	0.95746	1.0065	35.908	20	4007200000	2127500000	1879800000
Q8C1B7	Septin-11	Sept11	6	6	2	18.1	18.1	7	49.694	431	2.1354E-68	0.72661	0.6822	65.158	7	415650000	240420000	175230000
P42208	Septin-2	Sept2	6	6	6	29.6	29.6	29.6	41.525	361	8.459E-109	0.88205	0.89989	51.691	7	421710000	229400000	192310000
P28661	Septin-4	Sept4	1	1	1	2.9	2.9	2.9	54.935	478	4.5617E-05	1.3072	1.1614	6.4621	2	21826000	9135700	12690000
Q9R1T4	Septin-6	Sept6	5	2	2	15.7	9	9	49.619	434	5.4203E-26	0.65678	0.56582	25.973	3	35358000	23597000	11761000
E9Q1G8	Septin-7	Sept7	5	5	4	18.1	18.1	16	50.648	437	1.5979E-88	1.2229	1.1563	140.17	5	775010000	399670000	375340000
B1AQZ0	Septin-8	Sept8	4	2	2	9.7	4.1	4.1	55.874	484	1.4191E-53	0.87624	1.0474	29.271	2	177050000	100420000	76624000
Q80UG5	Septin-9	Sint1	3	3	3	7.9	7.9	7.9	65.574	583	1.1272E-19	0.84379	0.9212	18.026	4	154800000	73794000	81003000
Q64337	Sequestosome-1	Sqstm1	2	2	2	9.5	9.5	9.5	48.162	442	5.3463E-10	1.0228	0.77552	40.392	3	73864000	34359000	39505000
P54797	Ser/Thr-rich protein T10 in DGCR region	T10	6	6	6	28.6	28.6	28.6	30.947	276	2.878E-215	1.093	0.96623	18.373	6	179450000	88968000	90480000
Q3U3G8	Serine hydrolase-like protein	Serhl	3	3	3	12.8	12.8	12.8	36.353	321	2.1637E-67	2.5911	2.5309	26.887	4	185370000	48910000	136460000
Q9CZN7	Serine hydroxymethyltransferase	Shmt2	5	5	5	9.5	9.5	9.5	55.758	504	9.4525E-25	1.3014	0.86111	43.553	5	499810000	139630000	360180000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P50431	Serine hydroxymethyltransferase, cytosolic	Shmt1	2	2	2	6.3	6.3	6.3	52.6	478	5.5434E-27	0.82989	0.97344	93.137	2	116160000	72251000	43905000
Q9JIY5	Serine protease HTRA2, mitochondrial	Htra2	4	4	4	12.7	12.7	12.7	49.348	458	2.9259E-08	1.6988	1.8495	96.255	4	214550000	142040000	72513000
P07759	Serine protease inhibitor A3K	Serpina3k	14	14	9	38	38	24.6	46.879	418	0	0.41362	0.4748	86.412	59	2.604E+10	1.9118E+10	6921200000
Q03734	Serine protease inhibitor A3M	Serpina3m	8	3	2	23.2	9.8	6.9	47.064	418	8.531E-137	0.30977	0.28884	9.9815	2	84314000	62498000	21816000
Q91WP6	Serine protease inhibitor A3N	Serpina3n	7	5	5	20.3	14.1	14.1	46.717	418	2.587E-120	0.54287	0.57758	116.23	7	528220000	323730000	204490000
Q8BTI8	Serine/arginine repetitive matrix protein 2	Srrm2	1	1	1	0.8	0.8	0.8	294.84	2703	1.7986E-13	0.85702	0.778	43.131	4	33666000	22159000	11508000
P84104	Serine/arginine-rich splicing factor 3	Srsf3	2	2	2	10.4	10.4	10.4	19.329	164	8.1302E-08	0.78817	0.83448	87.278	3	174170000	100060000	74106000
A2A837	Serine/arginine-rich splicing factor 4	Srsf4	2	2	2	5	5	5	56.455	496	6.1989E-11	0.66314	0.63146	57.874	2	17129000	11382000	5747700
Q99KH8	Serine/threonine-protein kinase 24	Stk24	4	4	4	9	9	9	47.953	431	3.4761E-06	0.29232	0.28544	58.259	4	104600000	72688000	31910000
E9QPK4	Serine/threonine-protein kinase ATR	Atr	3	3	3	1.3	1.3	1.3	301.02	2641	0.0026972	1.1342	1.1157	5.7899	2	267690000	123760000	143930000
Q6P9R2	Serine/threonine-protein kinase OSR1	Oxsr1	6	6	5	13.9	13.9	12	58.213	527	1.6894E-35	0.58522	0.56152	45.696	6	1123900000	667910000	456010000
Q8CIN4	Serine/threonine-protein kinase PAK 2;PAK-2p27;PAK-2p34	Pak2	5	5	5	17	17	17	57.93	524	1.8175E-32	0.53832	0.46853	28.486	4	386310000	172840000	213470000
P83741	Serine/threonine-protein kinase WNK1	Wnk1	5	5	5	3.3	3.3	3.3	250.93	2377	2.331E-24	0.99572	0.8406	23.763	3	56943000	32181000	24762000
E9QM73	Serine/threonine-protein kinase WNK2	Wnk2	2	2	2	2.1	2.1	2.1	234.04	2213	6.1687E-05	0.80139	0.87919	3.9977	2	32114000	17506000	14608000
Q6P1F6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	Ppp2r2a	2	2	2	4.9	4.9	4.9	51.691	447	1.0628E-05	0.82048	0.79757	18.89	2	120940000	70309000	50631000
Q6PD03	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	Ppp2r5a	6	6	6	15.2	15.2	15.2	56.346	486	1.1475E-15	1.0793	1.0166	60.99	7	352000000	191700000	160310000
Q61151	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	Ppp2r5e	2	2	1	5.6	5.6	3	54.713	467	4.7431E-06	1.2485	1.1184	72.858	3	66005000	34523000	31482000
Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	Ppp2r1a	13	13	13	31.6	31.6	31.6	65.322	589	6.334E-124	0.82355	0.96606	40.086	23	7136500000	4043700000	3092800000
P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	Ppp2ca	7	7	1	29.1	29.1	4.2	35.608	309	4.0412E-65	1.3536	1.4262	53.505	9	1049100000	445950000	603180000
P63328	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	Ppp3ca	3	3	3	6.3	6.3	6.3	58.643	521	1.3052E-07	1.3065	1.1272	25.719	3	153920000	71903000	82015000
Q60676	Serine/threonine-protein phosphatase 5	Ppp5c	6	6	6	12.6	12.6	12.6	56.876	499	0	1.1026	1.1015	32.602	7	253490000	121650000	131840000
Q9CQR6	Serine/threonine-protein phosphatase 6 catalytic subunit	Ppp6c	3	3	3	12.5	12.5	12.5	35.159	305	4.0121E-07	1.2376	1.2773	29.384	2	50614000	20084000	30530000
G5E8R4	Serine/threonine-protein phosphatase 6 regulatory subunit 3	Ppp6r3	7	7	7	10.7	10.7	10.7	97.862	873	3.2496E-94	0.77327	0.83734	45.037	3	18147000	10590000	7557000
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	Ppp1cb	7	7	3	33.6	33.6	15.9	37.186	327	3.602E-120	1.6808	1.7059	58.358	8	1071100000	346370000	724740000
Q9Z1Z2	Serine-threonine kinase receptor-associated protein	Strap	6	6	6	26.6	26.6	26.6	38.442	350	2.1116E-94	0.60554	0.46713	77.974	4	334880000	207420000	127460000
Q8C483	Serine--tRNA ligase, cytoplasmic	Sars	4	4	4	11.8	11.8	11.8	61.166	536	1.5798E-33	1.2876	0.78805	96.545	4	297460000	136620000	160840000
Q9JJL8	Serine--tRNA ligase, mitochondrial	Sars2	3	3	3	9.8	9.8	9.8	58.316	518	1.5095E-53	0.9904	0.77617	73.533	3	119440000	68520000	50917000
Q921I1	Serotransferrin	Tf	34	34	2	57.7	57.7	4.3	76.723	697	0	0.56229	0.53055	60.079	109	4.4786E+10	2.9181E+10	1.5605E+10
F8WIV2	Serpin B6	Serpinb6a	10	10	9	30.6	30.6	28.8	44.774	399	0	0.90549	0.93557	92.585	11	1345200000	766850000	578340000
P19324	Serpin H1	Serpinh1	6	6	6	20.9	20.9	20.9	46.533	417	1.117E-169	0.61731	0.61998	66.909	10	873510000	584090000	289420000
Q99MR6	Serrate RNA effector molecule homolog	Srrt	5	5	5	6.4	6.4	6.4	100.45	875	4.9933E-17	1.2992	0.79721	60.362	3	86064000	41100000	44964000
P07724	Serum albumin	Alb	49	49	47	66.1	66.1	64.6	68.692	608	0	0.38529	0.36226	74.676	253	2.734E+11	2.0262E+11	7.0781E+10
Q63918	Serum deprivation-response protein	Sdpr	6	6	6	19.4	19.4	19.4	46.763	418	5.0055E-75	0.60202	0.68183	19.596	6	2068000000	1315300000	752700000
P52430	Serum paraoxonase/arylesterase 1	Pon1	2	2	2	6.5	6.5	6.5	39.565	355	1.2538E-06	1.0727	1.0674	85.94	2	62755000	33799000	28956000
P97443	SET and MYND domain-containing protein 1	Smyd1	7	7	7	22.4	22.4	22.4	56.495	490	7.1901E-48	0.4324	0.52561	15.899	7	696320000	446230000	250080000
H3BKH6	S-formylglutathione hydrolase	Esd	7	7	7	38.6	38.6	38.6	32.829	295	5.742E-195	1.6795	1.8936	46.883	12	2769600000	1094200000	1675400000
Q9WUZ7	SH3 domain-binding glutamic acid-rich protein	Sh3bgr	7	7	7	40.7	40.7	40.7	23.102	214	2.517E-238	0.4259	0.44788	127.89	12	1329100000	949280000	379830000
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	Sh3bgrl	5	5	5	54.4	54.4	54.4	12.811	114	2.335E-99	0.48764	0.41694	45.041	5	530140000	357930000	172220000
Q91VW3	SH3 domain-binding glutamic acid-rich-like protein 3	Sh3bgrl3	2	2	2	20.4	20.4	20.4	10.477	93	1.6877E-06	0.74853	0.73618	29.531	2	136660000	69809000	66854000
Q8R550	SH3 domain-containing kinase-binding protein 1	Sh3kbp1	3	3	3	5.2	5.2	5.2	78.169	709	6.8431E-67	0.42842	0.45655	17.963	3	143450000	95908000	47540000
Q9DBL1	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Acadsb	12	12	12	33.3	33.3	33.3	47.874	432	2.8901E-83	1.246	1.219	78.931	16	1427800000	691720000	736110000
Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	Acads	14	14	14	43.9	43.9	43.9	44.889	412	1.923E-190	1.6438	1.6218	86.195	26	1.2242E+10	4713300000	7528400000
P42232	Signal transducer and activator of transcription 5B	Stat5b	2	2	2	3.4	3.4	3.4	90.001	786	2.1633E-07	0.69734	0.811	50.235	3	67462000	36845000	30617000
Q9CYR0	Single-stranded DNA-binding protein, mitochondrial	Ssbp1	2	2	2	15.1	15.1	15.1	17.319	152	4.7736E-12	0.48532	0.45356	138.49	4	526940000	377730000	149210000
F8WHU5	Sister chromatid cohesion protein PDS5 homolog B	Pds5b	1	1	1	0.5	0.5	0.5	164.76	1449	0.0054914	0.30805	0.18797	37.235	2	114430000	84027000	30406000
Q8CI08	SLAIN motif-containing protein 2	Slain2	3	3	3	6	6	6	62.377	581	1.1938E-05	0.70729	0.72764	25.431	2	31568000	18745000	12824000
Q8BJU0	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	Sgta	5	5	5	20	20	20	34.322	315	7.6317E-44	0.56815	0.66244	61.951	8	679400000	445630000	233780000
Q9DC77	Small muscular protein	Smpx	5	5	5	65.9	65.9	65.9	9.2525	85	3.31E-149	0.39466	0.43674	33.634	9	571340000	436780000	134560000
G3UZA7	Small ubiquitin-related modifier 3	Sumo3	1	1	1	10.6	10.6	10.6	12.713	113	0.0024909	0.40113	0.19036	99.025	2	144380000	103860000	40519000
Q9CQ65	S-methyl-5-thioadenosine phosphorylase	Mtap	5	5	5	27.9	27.9	27.9	31.062	283	2.4414E-35	1.1204	1.03	24.964	7	510990000	248670000	262320000
D3YVS1	Smoothelin	Smtn	5	5	5	16.1	16.1	16.1	47.573	436	2.1279E-41	1.3013	1.2207	45.786	8	410540000	195140000	215410000
G3X9J1	Sodium/calcium exchanger 1	Slc8a1	5	5	5	8.6	8.6	8.6	108.04	970	2.135E-112	0.98195	1.1516	29.715	4	112540000	61878000	50667000
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	Atp1a1	22	22	11	26.3	26.3	14.1	112.98	1023	0	1.1433	1.1818	35.664	28	4123300000	1962700000	2160600000
Q6PIE5	Sodium/potassium-transporting ATPase subunit alpha-2	Atp1a2	15	4	4	16.9	4.5	4.5	112.22	1020	0	1.1625	0.6753	66.157	4	206560000	100990000	105570000
Q9WV27	Sodium/potassium-transporting ATPase subunit alpha-4	Atp1a4	8	2	2	8.4	3	3	114.89	1032	7.584E-133	0.9455	0.98983	27.938	2	138150000	70079000	68073000
P14094	Sodium/potassium-transporting ATPase subunit beta-1	Atp1b1	6	6	6	25	25	25	35.194	304	4.4907E-73	0.68927	0.58339	44.402	6	568980000	342110000	226870000
Q8R0Y8	Solute carrier family 25 member 42	Slc25a42	2	2	2	12.3	12.3	12.3	35.24	318	8.319E-25	2.0728	2.1573	2.8894	2	198740000	70264000	128480000
Q62417	Sorbin and SH3 domain-containing protein 1	Sorbs1	7	6	6	8.3	7.4	7.4	143.07	1290	6.221E-108	0.64566	0.59424	21.591	4	126300000	80850000	45450000
B9EKP8	Sorbin and SH3 domain-containing protein 2	Sorbs2	9	9	7	9.3	9.3	7.7	136.2	1214	1.3296E-29	0.86381	0.88974	68.508	7	480770000	264740000	216030000
Q64442	Sorbitol dehydrogenase	Sord	6	6	6	20.7	20.7	20.7	38.249	357	1.7986E-59	0.87489	0.83589	54.018	8	841500000	467740000	373760000
Q6P069	Sorcin	Sri	5	5	5	32.3	32.3	32.3	21.627	198	0	0.86405	0.63713	38.243	4	449670000	217740000	231930000
Q8BGH2	Sorting and assembly machinery component 50 homolog	Samm50	3	3	3	9	9	9	51.863	469	1.8102E-11	2.2844	1.9204	22.331	3	149290000	50498000	98794000
Q9WV80	Sorting nexin-1	Snx1	4	4	4	8.4	8.4	8.4	58.951	522	1.1681E-10	0.42783	0.38106	49.543	3	145020000	100930000	44088000
Q8C788	Sorting nexin-18	Snx18	2	2	2	4.4	4.4	4.4	67.789	615	0.010331	0.64717	0.68965	55.214	2	34020000	17981000	16039000
Q9CWK8	Sorting nexin-2	Snx2	8	8	8	19.7	19.7	19.7	58.47	519	1.54E-179	0.66244	0.71804	169.35	7	605980000	239210000	366770000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O70492	Sorting nexin-3	Snx3	4	4	3	25.9	25.9	21.6	18.757	162	2.1289E-10	0.47385	0.47112	36.619	3	389910000	263920000	125990000
Q9D8U8	Sorting nexin-5	Snx5	5	5	5	14.9	14.9	14.9	46.797	404	1.9239E-22	0.60059	0.44071	136.46	6	565580000	453140000	112440000
Q6P8X1	Sorting nexin-6	Snx6	2	2	2	5.7	5.7	5.7	46.648	406	5.7129E-10	1.6318	1.6332	302.32	2	97057000	22249000	74808000
Q8R1X6	Spartin	Spg20	2	2	2	5.4	5.4	5.4	72.654	671	0.00024159	0.84446	0.68844	6.0614	2	61120000	33392000	27728000
P16546	Spectrin alpha chain, brain	Sptan1	52	52	2	28	28	0.9	284.59	2472	0	0.86659	0.8843	71.507	62	9765800000	4350500000	5415300000
P08032	Spectrin alpha chain, erythrocyte	Spta1	3	3	3	1.8	1.8	1.8	279.86	2415	8.0368E-07	0.40305	0.41022	90.821	2	119810000	107930000	11878000
Q62261	Spectrin beta chain, brain 1	Sptbn1	34	34	32	21.5	21.5	20.8	274.22	2363	0	1.5957	1.4169	75.276	34	2995100000	1296500000	1698600000
Q3UGX2	Spectrin beta chain, erythrocyte	Spnb1	6	5	5	2.8	2.4	2.4	268.09	2329	8.8713E-22	0.72761	0.64653	40.768	2	47467000	25640000	21827000
Q7TNE3	Sperm-associated antigen 7	Spag7	4	4	4	19.8	19.8	19.8	25.921	227	1.2669E-31	0.70287	0.64461	99.587	4	113620000	58586000	55030000
P97355	Spermine synthase	Sms	4	4	4	14.2	14.2	14.2	41.313	366	6.193E-112	0.79669	0.97029	78.779	4	435840000	254280000	181550000
Q9WTX5	S-phase kinase-associated protein 1	Skp1	3	3	3	13.5	13.5	13.5	18.672	163	2.2236E-32	1.1949	0.76717	82.399	9	2896900000	612770000	2284100000
Q9CR46	Spindle and kinetochore-associated protein 2	Ska2	2	2	2	17.5	17.5	17.5	13.725	120	0.0094809	0.39068	0.51458	61.654	2	678730000	462860000	215860000
Q9Z1N5	Spliceosome RNA helicase Ddx39b	Ddx39b	9	9	9	30.6	30.6	30.6	49.035	428	8.0498E-31	0.9771	1.0931	27.289	9	1130100000	571100000	559020000
Q64213	Splicing factor 1	Sf1	3	3	3	5.7	5.7	5.7	70.402	653	2.6318E-18	0.43592	0.39972	13.167	3	293320000	197980000	95344000
Q8K4Z5	Splicing factor 3A subunit 1	Sf3a1	6	6	6	11	11	11	88.544	791	8.3984E-18	0.44116	0.41395	25.277	7	493870000	377200000	116670000
Q9D554	Splicing factor 3A subunit 3	Sf3a3	3	3	3	10.2	10.2	10.2	58.841	501	2.5544E-19	0.61469	0.52054	67.686	4	185430000	106560000	78875000
G5E866	Splicing factor 3B subunit 1	Sf3b1	3	3	3	3.5	3.5	3.5	145.83	1304	8.6271E-06	0.60554	0.84077	111.91	3	408970000	351860000	57110000
Q91WK1	SPRY domain-containing protein 4	Spryd4	3	3	3	22.2	22.2	22.2	23.275	207	6.026E-40	0.9716	0.85652	35.296	5	374300000	168470000	205830000
Q9D8T7	SRA stem-loop-interacting RNA-binding protein, mitochondrial	Slirp	2	2	2	20.5	20.5	20.5	12.605	112	0.0011779	0.73622	0.68749	28.643	3	108750000	66050000	42700000
Q60598	Src substrate cortactin	Cttn	3	3	3	10.3	10.3	10.3	61.249	546	2.0576E-85	0.56052	0.46687	25.878	2	73118000	52198000	20920000
G3X973	Stabilin-1	Stab1	3	3	3	1.8	1.8	1.8	276.47	2571	3.9568E-05	1.3906	1.2234	56.556	3	57810000	45377000	12432000
Q78PY7	Staphylococcal nuclease domain-containing protein 1	Snd1	7	7	7	12.7	12.7	12.7	102.09	910	1.2468E-19	2.9353	3.2785	33.931	7	558170000	136370000	421790000
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	Stk39	4	3	3	11	9.2	9.2	60.319	556	9.145E-150	0.59875	0.59754	66.173	4	427040000	249680000	177350000
O54988	STE20-like serine/threonine-protein kinase	Slk	10	10	10	14.3	14.3	14.3	141.46	1233	3.6562E-98	0.81612	0.75178	24.357	10	642630000	338020000	304610000
Q9WUD1	STIP1 homology and U box-containing protein 1	Stub1	2	2	2	9.2	9.2	9.2	34.909	304	1.1109E-05	0.83851	0.85571	28.077	2	129290000	69333000	59961000
P38647	Stress-70 protein, mitochondrial	Hspa9	28	28	28	48.3	48.3	48.3	73.46	679	0	0.60241	0.63104	84.339	82	3.3475E+10	2.1184E+10	1.2292E+10
Q60864	Stress-induced-phosphoprotein 1	Stip1	19	19	19	42.2	42.2	42.2	62.581	543	0	0.45885	0.49117	98.418	24	7256200000	5075700000	2180500000
E9QQ25	Striated muscle-specific serine/threonine-protein kinase	Speg	3	3	3	1.5	1.5	1.5	354.31	3262	0.00004647	2.0015	2.0214	10.359	2	33225000	6896700	26329000
Q9CXV1	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit	Sdhd	2	2	2	10.7	10.7	10.7	17.014	159	4.2872E-07	1.0597	0.97259	71.794	3	1294400000	623880000	670550000
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit	Sdha	20	20	20	46.1	46.1	46.1	72.585	664	0	1.3892	1.5423	60.754	35	6039600000	2623800000	3415800000
Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit	Sdhb	8	8	8	31.9	31.9	31.9	31.814	282	7.947E-141	1.634	2.08	108.76	10	3593100000	1459300000	2133900000
Q9CZB0	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	Sdhc	4	4	4	29	29	29	18.382	169	1.3395E-15	1.2778	1.257	25.813	5	1040200000	476200000	564040000
Q8BWF0	Succinate-semialdehyde dehydrogenase, mitochondrial	Aldh5a1	11	11	11	28.9	28.9	28.9	55.968	523	3.968E-233	1.0709	1.0398	52.066	14	2868300000	1387600000	1480700000
Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	Suclg1	6	6	6	24.6	24.6	24.6	36.154	346	7.398E-187	1.127	1.2373	41.537	16	8516300000	3965400000	4550900000
Q9Z2I9	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	Sucla2	20	20	20	46	46	46	50.113	463	0	0.65503	0.67401	80.955	53	2.6223E+10	1.6133E+10	1.009E+10
Q9Z2I8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Suclg2	15	15	15	41.3	41.3	41.3	46.839	433	0	0.39651	0.40995	126.89	14	4036000000	2929500000	1106500000
Q9D0K2	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	Oxct1	11	11	11	28.5	28.5	28.5	55.988	520	0	1.0306	1.2304	76.441	20	6213700000	2899800000	3313900000
J3QPG5	Sulfated glycoprotein 1	Psap	8	8	8	15.4	15.4	15.4	61.363	557	1.105E-107	1.2358	0.46517	158.39	8	3133300000	1004200000	2129100000
Q8BND5	Sulfhydryl oxidase 1	Qsox1	3	3	3	5.6	5.6	5.6	82.784	748	9.5725E-09	0.52694	0.49451	7.4774	2	65548000	48155000	17393000
Q9R112	Sulfide:quinone oxidoreductase, mitochondrial	Sqrdl	4	4	4	12.9	12.9	12.9	50.282	450	4.1125E-27	1.4941	1.5288	17.478	5	134050000	55686000	78367000
Q8R086	Sulfite oxidase, mitochondrial	Suox	7	7	7	23.3	23.3	23.3	60.755	546	5.912E-221	0.66827	0.71712	26.612	12	1383400000	866400000	517010000
Q9D0B5	Sulfurtransferase	2610029I01Rik	3	3	3	20.4	20.4	20.4	17.271	157	2.0994E-40	0.44671	0.31984	45.856	3	238950000	178660000	60287000
Q3UW66	Sulfurtransferase;3-mercaptopyruvate sulfurtransferase	Mpst	9	9	9	41.4	41.4	41.4	33.097	297	1.2587E-85	1.0544	0.80446	54.96	13	1976700000	818690000	1158000000
Q9Z1F9	SUMO-activating enzyme subunit 2	Uba2	3	3	3	5.5	5.5	5.5	70.568	638	3.6122E-22	0.58602	0.54005	144.98	3	253760000	117340000	136420000
P08228	Superoxide dismutase [Cu-Zn]	Sod1	4	4	4	28.6	28.6	28.6	15.942	154	6.259E-206	1.1144	1.0403	82.712	13	2194900000	788190000	1406700000
P09671	Superoxide dismutase [Mn], mitochondrial	Sod2	6	6	6	31.5	31.5	31.5	24.603	222	7.9943E-37	0.60734	0.5722	46.838	23	2.7131E+10	1.5707E+10	1.1424E+10
Q8K4L3	Supervillin	Svil	5	5	5	4.3	4.3	4.3	243.16	2170	4.8775E-21	1.0143	1.0265	13.626	5	177310000	91957000	85352000
Q9CX34	Suppressor of G2 allele of SKP1 homolog	Sugt1	9	9	9	27.7	27.7	27.7	38.158	336	3.092E-119	0.65369	0.54889	45.854	10	461420000	282600000	178820000
Q9D5V6	Synapse-associated protein 1	Syap1	2	2	2	8.2	8.2	8.2	41.349	365	1.4381E-06	1.1051	1.1895	75.916	2	121810000	41004000	80802000
Q64332	Synapsin-2	Syn2	3	3	2	4.9	4.9	4.9	63.372	586	7.4179E-15	0.88591	0.87623	117.66	6	185570000	141810000	43755000
Q62465	Synaptic vesicle membrane protein VAT-1 homolog	Vat1	4	4	4	12.6	12.6	12.6	43.096	406	1.087E-14	1.6076	1.4975	11.91	3	188600000	74509000	114090000
Q9CQW1	Synaptobrevin homolog YKT6	Ykt6	3	3	3	22.2	22.2	22.2	22.314	198	2.1294E-40	0.89136	0.63141	60.314	2	189780000	111080000	78698000
D3Z656	Synaptojanin-1	Synj1	2	2	2	2.2	2.2	2.2	176.33	1607	7.9356E-05	0.98359	0.86958	0.83475	2	34913000	17120000	17793000
B2RQK7	Synaptopodin 2-like protein	Synpo2l	3	3	3	5.6	5.6	5.6	103.27	978	3.1376E-10	1.9392	2.1422	11.245	2	143260000	49564000	93701000
E9Q1U2	Synaptopodin-2	Synpo2	2	2	2	2.9	2.9	2.9	135.76	1257	0.00054407	0.7067	0.6715	103.8	2	144350000	69808000	74540000
Q9ERB0	Synaptosomal-associated protein 29	Snap29	3	3	3	23.1	23.1	23.1	29.572	260	5.2974E-15	0.86452	1.2466	19.984	2	15421000	8567600	6853600
Q9ER00	Syntaxin-12	Stx12	2	2	2	9.5	9.5	9.5	31.195	274	9.3566E-29	0.90764	0.79946	28.045	3	43677000	24566000	19111000
O70439	Syntaxin-7	Stx7	4	4	4	19.2	19.2	19.2	29.82	261	1.5501E-12	1.5119	1.5534	14.646	4	96896000	46012000	50884000
P26039	Talin-1	Tln1	46	46	42	29.3	29.3	27.4	269.82	2541	0	0.65098	0.70277	59.121	71	8141100000	4518000000	3623000000
E9PUM4	Talin-2	Tln2	19	15	15	10.9	9	9	271.66	2542	7.549E-152	0.74841	0.7962	66.301	12	618100000	368320000	249780000
Q3UDC3	Target of Myb protein 1	Tom1	6	6	6	20.7	20.7	20.7	57.145	516	5.8508E-28	0.71113	0.66203	23.29	6	175630000	111910000	63716000
Q925I4	Taste receptor type 1 member 2	Tas1r2	1	1	1	2.1	2.1	2.1	95.734	843	0.024757	17.816	19.692	6.5817	2	1311600000	79179000	1232500000
Q9DBG9	Tax1-binding protein 3	Tax1bp3	1	1	1	13.7	13.7	13.7	13.722	124	1.2965E-14	0.53457	0.47533	10.996	2	241970000	165560000	76401000
P11983	T-complex protein 1 subunit alpha	Tcp1	10	10	10	25.9	25.9	25.9	60.448	556	2.544E-100	0.83538	0.74209	57.503	10	906000000	491050000	414950000
P80314	T-complex protein 1 subunit beta	Cct2	12	12	12	26.9	26.9	26.9	57.477	535	1.946E-201	0.90565	0.9323	61.7	13	2073100000	1133600000	939510000
P80315	T-complex protein 1 subunit delta	Cct4	10	10	10	28.9	28.9	28.9	58.066	539	4.015E-126	1.112	1.1991	30.536	13	1394300000	581470000	812840000
P80316	T-complex protein 1 subunit epsilon	Cct5	10	10	10	20.7	20.7	20.7	59.623	541	2.9359E-34	0.93891	0.87322	34.381	10	1988000000	1078300000	909700000
P80313	T-complex protein 1 subunit eta	Cct7	10	10	10	20.6	20.6	20.6	59.652	544	1.493E-172	1.264	1.395	77.657	11	1721600000	768860000	952750000
P80318	T-complex protein 1 subunit gamma	Cct3	10	10	10	24.6	24.6	24.6	60.629	545	9.5574E-53	1.5349	1.5411	38.907	6	329330000	137080000	192240000
P42932	T-complex protein 1 subunit theta	Cct8	12	12	12	26.8	26.8	26.8	59.555	548	5.144E-139	0.6749	0.70124	30.498	16	1540000000	962680000	577350000
P80317	T-complex protein 1 subunit zeta	Cct6a	9	9	9	23.4	23.4	23.4	58.004	531	5.534E-122	1.0294	0.91852	62.409	12	1356200000	656880000	699360000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
A6H6E9	Tetratricopeptide repeat protein 23-like	Ttc23l	1	1	1	1.7	1.7	1.7	51.532	458	0.023461	0.99184	1.0483	21.096	2	49974000	25309000	24665000
Q8C1A5	Thimet oligopeptidase	Thop1	10	10	10	17.3	17.3	17.3	78.025	687	6.675E-131	0.83249	0.83532	85.53	8	277370000	138150000	139220000
O55060	Thiopurine S-methyltransferase	Tpmt	1	1	1	4.2	4.2	4.2	27.585	240	0.0050191	0.69989	0.6266	5.5301	2	7569100	4440000	3129100
P10639	Thioredoxin	Txn	3	3	3	31.4	31.4	31.4	11.675	105	2.8313E-10	0.47144	0.46168	158.38	4	1424900000	969560000	455320000
Q9CQU0	Thioredoxin domain-containing protein 12	Txndc12	3	3	3	24.1	24.1	24.1	19.048	170	3.1109E-30	1.257	1.3774	118.88	2	193620000	58590000	135030000
Q9CQM5	Thioredoxin domain-containing protein 17	Txndc17	1	1	1	11.4	11.4	11.4	14.015	123	1.0393E-26	0.79815	0.8445	10.767	3	314250000	170800000	143460000
Q91W90	Thioredoxin domain-containing protein 5	Txndc5	6	6	6	17	17	17	46.415	417	1.912E-92	0.75567	0.69955	37.84	10	612070000	376500000	235570000
Q9JMH6	Thioredoxin reductase 1, cytoplasmic	Txnrd1	7	7	6	20.2	20.2	17.8	67.101	613	4.787E-30	0.8312	0.86588	100.99	9	1353500000	726840000	626660000
Q9JLT4	Thioredoxin reductase 2, mitochondrial	Txnrd2	4	3	3	9.2	6.3	6.3	56.62	524	2.2231E-16	1.2892	1.2098	55.781	9	1090300000	449310000	640960000
P97493	Thioredoxin, mitochondrial;Thioredoxin	Txn2	2	2	2	18.7	18.7	18.7	18.255	166	9.1629E-52	0.61528	0.75794	66.181	4	1200600000	757540000	443080000
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	Prdx3	6	6	6	32.3	32.3	32.3	28.127	257	0	0.44621	0.49583	54.035	29	2.6387E+10	1.7776E+10	8611100000
Q8CDN6	Thioredoxin-like protein 1	Txnl1	9	9	9	41.2	41.2	41.2	32.237	289	5.767E-119	0.5376	0.48056	48.989	11	1476100000	982810000	493280000
P52196	Thiosulfate sulfurtransferase	Tst	5	5	5	20.2	20.2	20.2	33.466	297	8.2666E-16	1.1493	0.95167	81.183	6	677470000	361210000	316260000
Q9D0R2	Threonine--tRNA ligase, cytoplasmic	Tars	5	5	5	8.2	8.2	8.2	83.355	722	3.6727E-25	1.2001	1.2711	1.0938	3	157860000	73710000	84152000
Q3UQ84	Threonine--tRNA ligase, mitochondrial	Tars2	3	3	3	5.4	5.4	5.4	81.699	723	1.2987E-05	2.0631	2.153	60.888	2	58984000	19461000	39523000
Q80YQ1	Thrombospondin-1	Thbs1	10	10	10	12	12	12	129.69	1171	1.033E-266	0.49087	0.4416	50.399	7	1330200000	915200000	414990000
P97770	THUMP domain-containing protein 3	Thumpd3	1	1	1	2	2	2	56.431	505	0.0006533	1.3503	1.2578	13.105	2	17931000	8379900	9551200
P97930	Thymidylate kinase	Dtymk	5	5	5	26.9	26.9	26.9	23.914	212	3.3785E-13	0.49589	0.4837	33.866	3	250740000	166600000	84146000
P39447	Tight junction protein ZO-1	Tjp1	11	11	11	8	8	8	194.74	1745	4.8547E-35	1.1783	1.2052	51.356	10	162010000	84437000	77572000
Q9Z0U1	Tight junction protein ZO-2	Tjp2	3	3	3	2.7	2.7	2.7	131.28	1167	0.00013002	0.77799	0.86734	10.205	2	130450000	112950000	17496000
Q8BH58	TIP41-like protein	Tiprl	2	2	2	13.3	13.3	13.3	31.253	271	1.6902E-10	0.39476	0.38102	56.87	5	303780000	177920000	125850000
A2ASS6	Titin	Ttn	332	332	332	13.8	13.8	13.8	3906.4	35213	0	2.3055	2.3293	82.015	341	3.7525E+10	1.4175E+10	2.335E+10
Q9QZ06	Toll-interacting protein	Tollip	4	4	4	25.5	25.5	25.5	30.345	274	6.8845E-50	0.93857	0.96133	12.961	6	307210000	146950000	160260000
Q5SRX1	TOM1-like protein 2	Tom1l2	9	9	9	26.4	26.4	26.4	55.662	507	1.0016E-37	0.65462	0.55215	46.689	11	960740000	444790000	515950000
O55013	Trafficking protein particle complex subunit 3	Trappc3	2	2	2	11.7	11.7	11.7	20.302	180	3.4464E-11	0.64654	0.761	7.4546	3	188970000	111750000	77220000
Q9DBB8	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	Dhdh	6	6	6	19.2	19.2	19.2	36.3	333	4.7738E-31	1.2863	1.2431	14.661	11	1156200000	502910000	653270000
Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial	Mecr	6	6	6	30.8	30.8	30.8	40.342	373	7.0832E-35	1.0656	1.2819	15.21	5	452430000	228100000	224340000
Q93092	Transaldolase	Taldo1	9	9	9	25.2	25.2	25.2	37.387	337	3.2997E-16	0.49653	0.44194	142.25	8	3116000000	1420300000	1695800000
P83940	Transcription elongation factor B polypeptide 1	Tceb1	2	2	2	18.8	18.8	18.8	12.473	112	7.0443E-10	0.56009	0.47262	18.707	2	407010000	270060000	136950000
P62869	Transcription elongation factor B polypeptide 2	Tceb2	7	7	7	53.4	53.4	53.4	13.17	118	4.1049E-49	0.53755	0.64319	28.129	8	1039600000	636090000	403560000
O55201	Transcription elongation factor SPT5	Supt5h	2	2	2	3	3	3	120.66	1082	0.00074138	0.54046	0.59189	13.065	2	49841000	31241000	18600000
P40630	Transcription factor A, mitochondrial	Tfam	3	3	3	10.7	10.7	10.7	27.987	243	1.8856E-08	0.69976	0.68194	117.61	3	130810000	78698000	52108000
Q64152	Transcription factor BTF3	Btf3	4	4	4	27	27	27	22.031	204	3.706E-102	0.52337	0.5829	36.192	6	504500000	343480000	161020000
Q9CQH7	Transcription factor BTF3 homolog 4	Btf3l4	2	2	2	19	19	19	17.27	158	7.8417E-70	0.50319	0.72556	30.07	3	71182000	53183000	17999000
Q62318	Transcription intermediary factor 1-beta	Trim28	2	2	2	3.1	3.1	3.1	88.846	834	8.7726E-07	0.60418	0.68384	1.1632	2	125820000	79665000	46160000
P42669	Transcriptional activator protein Pur-alpha	Pura	2	2	2	10.9	10.9	10.9	34.883	321	5.513E-63	1.4266	1.7937	34.965	4	342340000	143070000	199260000
O35295	Transcriptional activator protein Pur-beta	Purb	2	2	2	16	16	16	33.901	324	7.298E-63	0.94337	1.3258	41.33	2	46920000	22017000	24903000
Q8VHR5	Transcriptional repressor p66-beta	Gatad2b	2	2	2	5.7	5.7	5.7	65.41	594	1.0309E-08	0.84729	0.65286	53.619	2	28834000	15706000	13128000
E9Q8T1	Transforming acidic coiled-coil-containing protein 2	Tacc2	35	35	35	24	24	24	305.23	2879	0	0.68651	0.67606	48.763	41	2267100000	1422200000	844860000
P04202	Transforming growth factor beta-1;Latency-associated peptide	Tgfb1	1	1	1	4.9	4.9	4.9	44.309	390	0.00071757	0.51595	0.46564	5.9405	2	6810300	4952400	1857900
Q9QUI0	Transforming protein RhoA;Rho-related GTP-binding protein RhoC	Rhoa	3	3	3	22.8	22.8	22.8	21.782	193	2.5893E-55	0.97913	1.0028	49.391	2	197580000	101980000	95593000
P37804	Transgelin	Tagln	7	7	7	38.8	38.8	38.8	22.576	201	7.15E-111	0.52241	0.50724	69.245	8	4471900000	2735300000	1736600000
Q9WVA4	Transgelin-2	Tagln2	8	8	8	48.2	48.2	48.2	22.395	199	7.93E-116	0.62624	0.5435	49.79	12	2193700000	1440700000	752950000
Q01853	Transitional endoplasmic reticulum ATPase	Vcp	30	30	30	50.5	50.5	50.5	89.321	806	0	0.81765	0.85731	34.62	60	1.4572E+10	8099300000	6472200000
P40142	Transketolase	Tkt	12	12	12	25.4	25.4	25.4	67.63	623	3.971E-162	1.1766	1.3655	66.387	16	2146700000	1024700000	1122000000
Q9CXA2	Trans-L-3-hydroxyproline dehydratase	L3hypdh	4	4	4	17.5	17.5	17.5	37.804	354	4.991E-36	0.77512	0.8901	40.355	4	164960000	90857000	74107000
Q8C3X4	Translation factor Guf1, mitochondrial	Guf1	2	2	2	5.1	5.1	5.1	72.462	651	0.00036729	0.84743	0.93116	78.601	2	135580000	83615000	51966000
Q99LD9	Translation initiation factor eIF-2B subunit beta	Eif2b2	3	3	3	12.8	12.8	12.8	38.897	351	1.0816E-12	0.92467	0.8913	51.279	3	230090000	111450000	118640000
Q91YJ5	Translation initiation factor IF-2, mitochondrial	Mtif2	4	4	4	7.2	7.2	7.2	81.288	727	4.1198E-69	0.2884	0.11305	96.966	3	117160000	90291000	26869000
Q8K0Z7	Translational activator of cytochrome c oxidase 1	Taco1	5	5	5	30.3	30.3	30.3	32.314	294	9.4851E-88	0.77758	0.73268	95.108	7	836540000	511700000	324840000
P63028	Translationally-controlled tumor protein	Tpt1	5	5	5	34.3	34.3	34.3	19.462	172	1.2138E-47	0.55777	0.66416	68.785	13	1727500000	1152300000	575230000
Q62348	Translin	Tsn	2	2	2	14	14	14	26.201	228	2.721E-21	0.69551	0.67306	14.775	2	100620000	53790000	46831000
P58021	Transmembrane 9 superfamily member 2	Tm9sf2	1	1	1	2.3	2.3	2.3	75.329	662	5.3683E-06	1.8092	1.395	35.545	2	44114000	18059000	26055000
O70472	Transmembrane protein 131	Tmem131	1	1	1	0.7	0.7	0.7	204.65	1877	0.028523	0.27592	0.24206	45.592	2	65699000	60523000	5176300
G3X9F4	Transmembrane protein 143	Tmem143	4	4	4	13.5	13.5	13.5	51.579	458	2.4207E-13	2.0505	1.8835	46.49	3	200280000	66849000	133430000
Q9D938	Transmembrane protein 160	Tmem160	2	2	2	9.6	9.6	9.6	19.587	188	0.00013332	2.0436	1.8387	32.514	2	57094000	16570000	40524000
Q5F285	Transmembrane protein 256	Tmem256	1	1	1	24.8	24.8	24.8	11.655	113	4.374E-116	2.2794	2.355	17.099	3	184980000	56822000	128160000
Q9DAM7	Transmembrane protein 263	Tmem263	1	1	1	22.6	22.6	22.6	11.549	115	1.1242E-21	0.66529	0.95929	6.362	2	30649000	19909000	10741000
Q9CZX7	Transmembrane protein 55A	Tmem55a	2	2	2	14.4	14.4	14.4	28.038	257	2.2002E-09	1.1254	1.1879	92.73	2	32804000	11033000	21771000
Q7TNI2	Transmembrane protein 59-like	Tmem59l	1	1	1	2.1	2.1	2.1	37.661	337	0.001042	2.4791	2.83	143.07	2	615310000	79411000	535900000
Q4VAE3	Transmembrane protein 65	Tmem65	4	4	4	17.1	17.1	17.1	24.918	234	2.4478E-10	0.88289	0.78461	175.87	3	236700000	144920000	91787000
Q6P2B1	Transportin-3	Tnpo3	3	3	3	3.8	3.8	3.8	104.17	923	2.0672E-06	1.0765	1.1316	82.417	3	77968000	34390000	43578000
P07309	Transthyretin	Ttr	5	5	5	46.9	46.9	46.9	15.776	147	4.4138E-93	0.57991	0.56272	191.44	6	4669000000	2896100000	1772800000
H3BL37	Treacle protein	Tcof1	2	2	2	2.6	2.6	2.6	138.55	1356	6.0554E-06	0.21587	0.20671	157.9	2	112170000	73522000	38644000
E9Q9K5	Triadin	Trdn	2	2	2	2.7	2.7	2.7	77.843	693	0.0048858	0.53978	0.65557	43.201	2	146960000	89739000	57218000
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	Hadha	26	26	26	46	46	46	82.669	763	0	1.5453	1.6609	62.863	77	3.5311E+10	1.3626E+10	2.1685E+10
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	Hadhb	17	17	17	46.1	46.1	46.1	51.386	475	1.153E-255	1.3439	1.3213	44.687	37	7084100000	3221600000	3862400000
Q64737	Trifunctional purine biosynthetic protein adenosine-3	Gart	13	13	13	19.5	19.5	19.5	107.5	1010	3.273E-240	0.78551	0.75601	22.981	13	2032300000	1132600000	899690000
P17751	Triosephosphate isomerase	Tpi1	15	15	15	68.9	68.9	68.9	32.191	299	4.145E-303	0.51927	0.48097	97.37	75	4.6112E+10	2.9448E+10	1.6664E+10
G3X8Y1	Tripartite motif-containing protein 54	Trim55	2	2	2	4.6	4.6	4.6	60.137	545	9.9348E-07	1.2067	1.3286	24.466	3	89920000	38595000	51326000
Q1XH17	Tripartite motif-containing protein 72	Trim72	13	13	13	48	48	48	52.816	477	4.779E-228	0.47578	0.492	31.805	28	6416300000	4228900000	2187300000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O89023	Tripeptidyl-peptidase 1	Tpp1	1	1	1	3.7	3.7	3.7	61.341	562	4.7444E-18	1.7878	1.9088	19.848	2	232770000	86998000	145770000
Q64514	Tripeptidyl-peptidase 2	Tpp2	13	13	13	15.8	15.8	15.8	139.88	1262	9.0423E-88	1.6039	1.8982	98.64	14	1219800000	260470000	959310000
O55055	tRNA (cytosine(38)-C(5))-methyltransferase	Trdmt1	1	1	1	2.7	2.7	2.7	46.794	415	0.029606	0.084401	0.16115	27.743	2	931670000	857880000	73789000
Q99LF4	tRNA-splicing ligase RtcB homolog	D10Wsu52e	5	5	5	11.1	11.1	11.1	55.249	505	4.967E-38	1.5334	1.4679	44.145	5	153080000	58074000	95004000
P49813	Tropomodulin-1	Tmod1	9	9	9	39.6	39.6	39.6	40.466	359	2.811E-174	1.1545	1.1849	52.105	12	809300000	514560000	294730000
P58771	Tropomyosin alpha-1 chain	Tpm1	13	13	3	35.9	35.9	4.9	32.68	284	0	0.5185	0.59528	127.3	19	1.2484E+10	8278100000	4206200000
E9Q5J9	Tropomyosin alpha-3 chain	Tpm3	7	2	0	18.2	4.6	0	33.28	285	0	0.48854	0.0981	263.31	3	4242800000	2978400000	1264400000
P19123	Troponin C, slow skeletal and cardiac muscles	Tnnc1	4	4	4	26.7	26.7	26.7	18.42	161	6.308E-186	0.78628	0.77998	115.85	19	2.8533E+10	1.7089E+10	1.1444E+10
P48787	Troponin I, cardiac muscle	Tnni3	6	6	6	38.9	38.9	38.9	24.258	211	9.2932E-50	0.90567	0.8548	145.64	9	4874000000	2666100000	2207900000
J3QQ13	Troponin T, cardiac muscle	Tnnt2	11	11	11	29.8	29.8	29.8	35.943	302	0	0.59535	0.5407	64.087	27	7247200000	4405900000	2841300000
P32921	Tryptophan--tRNA ligase, cytoplasmic;T1-TrpRS;T2-TrpRS	Wars	4	4	4	12.7	12.7	12.7	54.357	481	2.9661E-57	1.3769	1.4514	27.092	6	675520000	273790000	401730000
P68368	Tubulin alpha-4A chain	Tuba4a	9	9	3	31	31	10	49.924	448	2.714E-155	1.0925	0.89342	81.885	12	1633100000	728730000	904330000
P68372	Tubulin beta-4B chain	Tubb4b	12	12	4	40.2	40.2	14.4	49.83	445	2.425E-208	1.0995	0.92951	38.222	12	545760000	251400000	294360000
Q7TQD2	Tubulin polymerization-promoting protein	Tppp	3	3	3	25.2	25.2	25.2	23.574	218	1.472E-147	0.33588	0.33285	15.957	3	196340000	151660000	44674000
Q9CRB6	Tubulin polymerization-promoting protein family member 3	Tppp3	8	8	8	39.2	39.2	39.2	18.965	176	1.174E-191	0.37235	0.36504	67.471	13	1300200000	970160000	330050000
Q9D1E6	Tubulin-folding cofactor B	Tbcb	4	4	4	19.3	19.3	19.3	27.385	244	1.052E-107	0.51659	0.53906	47.08	3	151270000	91319000	59953000
P48428	Tubulin-specific chaperone A	Tbca	2	2	2	16.7	16.7	16.7	12.758	108	4.4427E-07	0.19637	0.23269	98.811	2	448720000	425100000	23626000
Q3UDE2	Tubulin--tyrosine ligase-like protein 12	Ttll12	2	2	2	3.6	3.6	3.6	74.042	639	0.0059953	1.4919	1.5244	62.741	2	42650000	17562000	25088000
A2AUD5	Tumor protein D54	Tpd52l2	2	2	2	12.7	12.7	12.7	25.067	229	3.9466E-05	0.57755	0.37434	42.426	2	100750000	62189000	38565000
Q9Z0P5	Twinfilin-2	Twf2	4	4	4	19.8	19.8	19.8	39.47	349	8.0745E-32	0.65043	0.77339	79.42	3	165490000	93904000	71585000
P35235	Tyrosine-protein phosphatase non-receptor type 11	Ptpn11	14	14	14	30.3	30.3	30.3	68.46	597	0	0.75754	0.51916	62.443	13	1236100000	796840000	439270000
Q6PB44	Tyrosine-protein phosphatase non-receptor type 23	Ptpn23	3	3	3	2.9	2.9	2.9	185.21	1692	3.0449E-16	0.76022	0.6285	26.086	3	51607000	31272000	20336000
A2A7S7	Tyrosine--tRNA ligase, cytoplasmic	Yars	11	11	11	22	22	22	63.001	564	1.0815E-28	0.76581	0.78744	101.53	11	730090000	396290000	333810000
Q62189	U1 small nuclear ribonucleoprotein A	Snrpa	2	2	2	7	7	7	31.835	287	0.00046505	0.61076	0.44769	31.672	2	68521000	39048000	29473000
Q6P4T2	U5 small nuclear ribonucleoprotein 200 kDa helicase	Snrnp200	2	2	2	1.5	1.5	1.5	244.54	2136	0.00046784	1.1639	1.0848	19.513	2	63768000	34362000	29407000
Q8VC85	U6 snRNA-associated Sm-like protein LSm1	Lsm1	2	2	2	17.3	17.3	17.3	15.236	133	1.1118E-12	0.50565	0.50827	9.5671	3	97810000	61153000	36657000
O35900	U6 snRNA-associated Sm-like protein LSm2	Lsm2	3	3	3	35.8	35.8	35.8	10.834	95	2.314E-14	0.48246	0.47641	30.774	4	234450000	158520000	75931000
Q8R317	Ubiquilin-1	Ubqln1	4	3	3	10.3	7.7	7.7	61.976	582	3.6357E-52	0.61902	0.57756	93.02	2	88560000	55252000	33308000
Q9QZM0	Ubiquilin-2	Ubqln2	4	4	3	10.3	10.3	8	67.35	638	1.282E-105	0.58097	0.53761	71.487	4	142970000	97265000	45708000
Q8R1S0	Ubiquinone biosynthesis monooxygenase COQ6	Coq6	8	8	8	23.1	23.1	23.1	51.392	476	1.9706E-47	1.1665	1.254	46.26	10	615180000	265570000	349610000
Q8BGB8	Ubiquinone biosynthesis protein COQ4 homolog, mitochondrial	Coq4	2	2	2	9	9	9	30.084	266	0.00059795	0.57341	0.41248	83.654	2	221540000	138680000	82852000
P97478	Ubiquinone biosynthesis protein COQ7 homolog	Coq7	3	3	3	27.2	27.2	27.2	24.041	217	5.365E-127	0.73246	0.91085	58.2	3	543890000	358810000	185080000
Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondrial	Coq9	6	6	6	21.7	21.7	21.7	35.082	313	0	0.72222	0.65816	60.328	17	2864700000	1685500000	1179200000
Q9JMA1	Ubiquitin carboxyl-terminal hydrolase 14	Usp14	12	12	12	34.1	34.1	34.1	56.001	493	2.607E-170	0.66032	0.69131	43.794	16	1710400000	1017800000	692610000
Q8R5H1	Ubiquitin carboxyl-terminal hydrolase 15	Usp15	6	6	6	8.4	8.4	8.4	112.32	981	2.3609E-24	0.94145	0.89495	48.546	8	329700000	179250000	150450000
Q3UJD6	Ubiquitin carboxyl-terminal hydrolase 19	Usp19	3	3	3	4.9	4.9	4.9	150.55	1360	3.0659E-17	0.76242	0.84826	48.395	5	30190000	15354000	14836000
P35123	Ubiquitin carboxyl-terminal hydrolase 4	Usp4	6	6	5	8.6	8.6	7.2	108.34	962	1.2865E-14	0.81795	0.79818	67.853	6	195490000	107220000	88266000
P56399	Ubiquitin carboxyl-terminal hydrolase 5	Usp5	10	10	10	16.7	16.7	16.7	95.832	858	2.3275E-84	0.63933	0.69802	35.102	15	2021900000	1215500000	806420000
Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	Uchl1	4	4	4	21.1	21.1	21.1	24.838	223	2.188E-23	0.34508	0.3363	79.206	3	1060100000	412270000	647850000
Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3	Uchl3	9	9	9	52.2	52.2	52.2	26.151	230	1.577E-272	0.56947	0.60965	109.64	13	2444000000	1226100000	1217900000
Q9ES00	Ubiquitin conjugation factor E4 B	Ube4b	1	1	1	1.5	1.5	1.5	133.32	1173	7.1021E-05	1.0678	1.0706	17.756	2	21872000	10104000	11767000
P70362	Ubiquitin fusion degradation protein 1 homolog	Ufd1l	2	2	2	9.1	9.1	9.1	34.481	307	8.6905E-05	1.2367	1.1633	10.891	2	110000000	51209000	58787000
Q7TQI3	Ubiquitin thioesterase OTUB1	Otub1	5	5	5	27.3	27.3	27.3	31.27	271	5.4411E-56	0.59516	0.67311	59.63	8	943660000	612160000	331510000
Q80X50	Ubiquitin-associated protein 2-like	Ubap2l	5	5	5	7.3	7.3	7.3	116.8	1107	5.0777E-19	0.6252	0.77881	117.66	3	346970000	234210000	112760000
P62254	Ubiquitin-conjugating enzyme E2 G1	Ube2g1	3	3	3	30.6	30.6	30.6	19.509	170	3.8198E-25	0.30513	0.25884	61.809	3	120780000	79645000	41133000
P61087	Ubiquitin-conjugating enzyme E2 K	Ube2k	4	4	4	24	24	24	22.406	200	5.8107E-10	0.70031	0.48746	128.92	4	486800000	287450000	199350000
P68037	Ubiquitin-conjugating enzyme E2 L3	Ube2l3	4	4	4	51.9	51.9	51.9	17.861	154	1.396E-178	0.54099	0.59948	21.992	14	2939100000	1934100000	1005000000
P61089	Ubiquitin-conjugating enzyme E2 N	Ube2n	4	4	4	36.8	36.8	36.8	17.138	152	2.751E-111	0.46651	0.56429	48.873	6	1896300000	1217400000	678830000
Q6ZPJ3	Ubiquitin-conjugating enzyme E2 O	Ube2o	8	8	8	8.6	8.6	8.6	140.83	1288	2.8732E-25	0.71522	0.7374	43.218	6	224540000	126470000	98074000
Q6ZWZ2	Ubiquitin-conjugating enzyme E2 R2	Ube2r2	2	2	2	10.1	10.1	10.1	27.166	238	0.0039036	2.52	0.92196	333.33	2	323040000	135370000	187670000
Q9D2M8	Ubiquitin-conjugating enzyme E2 variant 2	Ube2v2	3	3	1	24.1	24.1	11	16.367	145	4.3181E-07	0.59501	0.73735	70.259	3	532990000	313640000	219350000
P61961	Ubiquitin-fold modifier 1	Ufm1	2	2	2	50.6	50.6	50.6	9.1175	85	3.3146E-14	0.45114	0.53429	104.72	5	1103200000	903420000	199830000
Q02053	Ubiquitin-like modifier-activating enzyme 1	Uba1	21	21	21	30.2	30.2	30.2	117.81	1058	0	1.098	1.0946	50.799	38	5776800000	2939100000	2837800000
Q64339	Ubiquitin-like protein ISG15	Isg15	3	3	3	21.7	21.7	21.7	17.897	161	1.3901E-13	0.57298	0.62683	12.336	2	132890000	84009000	48885000
Q922Y1	UBX domain-containing protein 1	Ubxn1	3	3	3	12.5	12.5	12.5	33.572	297	3.0069E-14	0.51951	0.60016	15.004	3	145380000	82771000	62609000
Q8VCH8	UBX domain-containing protein 4	Ubxn4	3	3	3	8.5	8.5	8.5	56.471	506	2.0581E-33	0.59742	0.30948	204	2	123070000	91976000	31092000
Q99PL6	UBX domain-containing protein 6	Ubxn6	2	2	2	8.8	8.8	8.8	49.795	442	1.178E-08	0.37337	0.37022	16.912	2	34457000	26073000	8384200
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	Uggt1	4	4	4	2.9	2.9	2.9	176.43	1551	3.5799E-08	1.2953	0.69616	149.93	4	361330000	265630000	95697000
Q3UHZ7	UDP-N-acetylhexosamine pyrophosphorylase	Uap1	3	3	3	6.9	6.9	6.9	58.582	522	9.6402E-08	0.63233	0.69331	52.02	5	127790000	80493000	47299000
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	Uap1l1	6	6	5	11.2	11.2	9.9	56.613	507	8.9493E-10	1.2621	1.5362	94.231	6	455240000	299100000	156130000
Q9DBP5	UMP-CMP kinase	Cmpk1	5	5	5	35.2	35.2	35.2	22.165	196	2.4268E-81	0.39966	0.37606	123.36	5	907540000	639640000	267900000
Q3U5Q7	UMP-CMP kinase 2, mitochondrial	Cmpk2	3	3	3	9.6	9.6	9.6	50.036	447	1.9206E-05	1.2344	1.2154	52.528	3	85720000	37281000	48439000
A2AMZ4	Uncharacterized protein C17orf89 homolog		2	2	2	39.2	39.2	39.2	7.7849	74	1.123E-157	0.7271	0.51491	19.908	3	482470000	292280000	190190000
Q9CQF4	Uncharacterized protein C6orf203 homolog	1700021F05Rik	4	4	4	22.1	22.1	22.1	27.847	240	5.3336E-59	0.44082	0.36391	47.731	6	335610000	235570000	100040000
Q6PIU9	Uncharacterized protein FLJ45252 homolog		5	5	5	23.2	23.2	23.2	37.704	354	2.7258E-52	0.44564	0.459	43.15	7	289500000	183020000	106490000
Q8CC88	Uncharacterized protein KIAA0564 homolog	Kiaa0564	11	11	11	8	8	8	213.42	1905	1.883E-55	1.6875	1.8501	97.27	8	394060000	150670000	243390000
E9QA74	Unconventional myosin-XVIIIa	Myo18a	1	1	1	1.1	1.1	1.1	186.53	1642	0.018984	1.3496	1.1815	15.918	3	23531000	9733700	13797000
E9QMK9	UPF0317 protein C14orf159 homolog, mitochondrial	9030617O03Rik	5	5	5	13	13	13	69.921	647	4.278E-42	0.68119	0.98266	41.893	9	938120000	538340000	399770000
D3YZD8	UPF0366 protein C11orf67 homolog	1810020D17Rik	5	5	5	30	30	30	16.358	150	1.4474E-18	0.36683	0.40785	91.131	6	631330000	469340000	161990000
I1E4X5	UPF0505 protein C16orf62 homolog	9030624J02Rik	3	3	3	3.5	3.5	3.5	111.98	991	2.3651E-06	1.1099	1.0828	114.86	3	29894000	12403000	17491000
Q9CPT4	UPF0556 protein C19orf10 homolog	D17Wsu104e	3	3	3	21.7	21.7	21.7	17.982	166	1.072E-21	0.61044	0.62601	50.286	3	701240000	157650000	543590000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence coverage [%]	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9CQE8	UPF0568 protein C14orf166 homolog		3	3	3	17.2	17.2	17.2	28.152	244	1.1262E-13	0.75759	0.57993	26.867	4	173590000	88662000	84933000
Q9DCS2	UPF0585 protein C16orf13 homolog	0610011F06Rik	2	2	2	13.7	13.7	13.7	22.687	204	9.1279E-31	1.1866	1.4457	65.723	4	231510000	116570000	114940000
Q8BHG2	UPF0587 protein C1orf123 homolog	0610037L13Rik	3	3	3	28.1	28.1	28.1	18.02	160	1.525E-06	0.62792	0.28846	170.82	2	189860000	118220000	71640000
Q8VE95	UPF0598 protein C8orf82 homolog		4	4	4	28.9	28.9	28.9	24.33	218	3.0898E-44	1.3032	1.5016	48.07	6	466710000	211360000	255350000
Q78IK2	Up-regulated during skeletal muscle growth protein 5	Usmg5	3	3	3	44.8	44.8	44.8	6.3814	58	2.5333E-54	1.1604	0.38243	143.94	4	1569400000	722440000	846990000
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	Ugp2	8	8	8	21.1	21.1	21.1	56.979	508	0	1.7486	1.9324	29.422	13	4104000000	1471500000	2632500000
P54726	UV excision repair protein RAD23 homolog A	Rad23a	4	3	3	18.7	16.5	16.5	39.706	363	7.87E-147	0.37936	0.41126	16.259	7	442480000	328470000	114010000
P54728	UV excision repair protein RAD23 homolog B	Rad23b	6	6	5	16.8	16.8	14.9	43.512	416	1.1863E-44	0.55608	0.53429	21.184	12	1029900000	659670000	370260000
Q8BX70	Vacuolar protein sorting-associated protein 13C	Vps13c	4	4	4	1.6	1.6	1.6	420.08	3748	3.2131E-15	2.4075	2.3598	55.708	4	81332000	24322000	57011000
Q9D1C8	Vacuolar protein sorting-associated protein 28 homolog	Vps28	2	2	2	11.8	11.8	11.8	25.452	221	5.4112E-16	0.46079	0.46606	113.44	3	3979000000	39881000	3939100000
Q9QZ88	Vacuolar protein sorting-associated protein 29	Vps29	4	4	4	24.7	24.7	24.7	20.495	182	1.1641E-07	1.6654	1.523	89.927	4	842960000	275280000	567680000
Q9EQH3	Vacuolar protein sorting-associated protein 35	Vps35	11	11	11	19.1	19.1	19.1	91.712	796	6.877E-134	1.6144	1.5547	85.79	12	1053500000	445830000	607650000
Q9CR26	Vacuolar protein sorting-associated protein VTA1 homolog	Vta1	5	5	5	23.6	23.6	23.6	33.913	309	8.238E-212	0.5409	0.62183	39.241	8	438380000	288570000	149800000
Q8R164	Valacyclovir hydrolase	Bphl	5	5	5	17.9	17.9	17.9	32.851	291	6.673E-23	1.4569	1.2159	75.746	7	895090000	394090000	501000000
Q9Z1Q9	Valine--tRNA ligase	Vars	12	12	12	12.4	12.4	12.4	140.21	1263	2.7373E-38	1.9416	1.8862	51.548	13	971460000	331520000	639940000
P70460	Vasodilator-stimulated phosphoprotein	Vasp	4	4	4	15.7	15.7	15.7	39.666	375	4.1944E-78	0.65527	0.62095	60.183	5	310500000	191470000	119030000
Q62059	Versican core protein	Vcan	2	2	2	0.6	0.6	0.6	366.78	3357	0.0010795	0.72155	0.90236	75.941	2	73393000	30295000	43099000
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadvl	28	28	28	55	55	55	70.875	656	0	1.2077	1.2038	71.219	53	1.7463E+10	8036000000	9426900000
P98156	Very low-density lipoprotein receptor	Vldlr	2	2	2	2.3	2.3	2.3	96.372	873	1.5586E-05	1.4049	1.5435	3.6499	2	36268000	16899000	19369000
Q8BH80	Vesicle-associated membrane protein-associated protein B	Vapb	4	4	4	20.2	20.2	20.2	26.918	243	6.1589E-24	0.75463	0.6708	72.935	6	1380900000	761920000	618980000
P46460	Vesicle-fusing ATPase	Nsf	3	3	3	4.3	4.3	4.3	82.613	744	8.7751E-08	0.54089	0.66277	17.225	3	197640000	120840000	76801000
O08547	Vesicle-trafficking protein SEC22b	Sec22b	2	2	2	15.3	15.3	15.3	24.74	215	6.0458E-09	2.5585	1.7963	39.475	2	47463000	12002000	35460000
Q8VDJ3	Vigilin	Hdlbp	11	11	11	13.1	13.1	13.1	141.74	1268	1.8223E-52	1.7798	1.5124	51.874	9	714720000	275230000	439490000
P20152	Vimentin	Vim	9	9	9	23.8	23.8	23.8	53.687	466	3.502E-113	0.41632	0.46281	74.776	10	595330000	379530000	215800000
Q64727	Vinculin	Vcl	26	26	26	33.3	33.3	33.3	116.72	1066	0	0.59958	0.59908	82.56	43	5649300000	3376100000	2273200000
P21614	Vitamin D-binding protein	Gc	13	13	13	39.7	39.7	39.7	53.6	476	0	0.51859	0.63292	51.566	21	2156500000	1482600000	673940000
P29788	Vitronectin	Vtn	1	1	1	3.8	3.8	3.8	54.848	478	9.2431E-08	0.80081	0.8375	10.803	2	106490000	64303000	42183000
Q60932	Voltage-dependent anion-selective channel protein 1	Vdac1	10	10	10	48	48	48	32.351	296	2.583E-304	1.5008	1.6116	47.09	11	6727100000	2840900000	3886200000
Q60930	Voltage-dependent anion-selective channel protein 2	Vdac2	7	7	7	38.3	38.3	38.3	31.732	295	0	2.0774	1.8458	62.474	7	618150000	217320000	400830000
J3QMG3	Voltage-dependent anion-selective channel protein 3	Vdac3	6	6	6	29.6	29.6	29.6	30.851	284	3.128E-191	1.4855	1.2976	36.254	10	1701000000	668850000	1032200000
O08532	Voltage-dependent calcium channel subunit alpha-2/delta-1	Cacna2d1	9	9	9	9.9	9.9	9.9	124.63	1103	1.8154E-48	0.27775	0.31959	67.337	7	281060000	213640000	67427000
Q8R2Z5	von Willebrand factor A domain-containing protein 1	Vwa1	1	1	1	3.9	3.9	3.9	44.708	415	0.010856	1.4265	1.672	18.414	2	55726000	24980000	30746000
Q99KC8	von Willebrand factor A domain-containing protein 5A	Vwa5a	8	8	8	12	12	12	87.142	793	7.1891E-57	0.83008	0.85518	63.059	11	917680000	621840000	295830000
Q9Z1G4	V-type proton ATPase 116 kDa subunit a isoform 1	Atp6v0a1	2	2	2	4.4	4.4	4.4	96.466	839	1.7585E-05	2.4001	1.9607	5.938	2	42708000	12897000	29811000
P50516	V-type proton ATPase catalytic subunit A	Atp6v1a	7	7	7	17.7	17.7	17.7	68.325	617	1.869E-115	1.4709	1.6653	33.782	9	572600000	211670000	360930000
P62814	V-type proton ATPase subunit B, brain isoform	Atp6v1b2	6	6	6	16	16	16	56.55	511	9.0603E-70	1.3325	1.6347	20.758	3	191600000	69904000	121700000
Q9Z1G3	V-type proton ATPase subunit C 1	Atp6v1c1	5	5	5	12.8	12.8	12.8	43.887	382	2.4427E-10	0.76804	0.72585	76.586	6	264070000	165430000	98632000
Q9CR51	V-type proton ATPase subunit G 1	Atp6v1g1	1	1	1	14.4	14.4	14.4	13.724	118	1.8299E-49	0.72593	0.6839	14.236	2	41891000	24205000	17686000
Q8BVE3	V-type proton ATPase subunit H	Atp6v1h	4	4	4	13.9	13.9	13.9	55.854	483	8.8794E-50	2.0314	2.2226	88.775	3	121880000	41362000	80518000
P0C7L0	WAS/WASL-interacting protein family member 3	Wipf3	2	2	2	6	6	6	49.452	485	3.6027E-06	0.30267	0.32395	39.803	2	50243000	39637000	10605000
O88342	WD repeat-containing protein 1	Wdr1	17	17	17	47.2	47.2	47.2	66.406	606	0	0.74621	0.69064	76.925	25	4571700000	2781400000	1790300000
Q923D5	WW domain-binding protein 11	Wbp11	2	2	2	4.1	4.1	4.1	69.874	641	1.7121E-08	0.26068	0.30564	78.745	2	62489000	56956000	5532600
Q3UE92	Xaa-Pro aminopeptidase 1	Xpnpep1	6	6	6	12.5	12.5	12.5	74.559	666	2.7099E-28	0.90812	0.90034	107.03	4	426930000	297010000	129910000
Q11136	Xaa-Pro dipeptidase	Pepd	2	2	2	6.1	6.1	6.1	55.028	493	2.4128E-38	2.6718	2.6489	150.95	2	181540000	20888000	160660000
Q00519	Xanthine dehydrogenase/oxidase	Xdh	11	11	11	12.4	12.4	12.4	146.56	1335	5.506E-103	1.6156	1.5836	23.464	13	783930000	330320000	453610000
E9QQ93	Xin actin-binding repeat-containing protein 1	Xirp1	5	5	5	7.2	7.2	7.2	123.69	1132	4.4572E-12	0.64386	0.70343	39.013	3	183830000	133980000	49846000
Q4U4S6	Xin actin-binding repeat-containing protein 2	Xirp2	3	3	3	1	1	1	428.25	3784	3.2406E-06	0.48603	0.44291	255.73	2	65923000	53623000	12301000
P46938	Yorkie homolog	Yap1	2	2	2	11.3	11.3	11.3	52.383	488	2.0006E-07	0.60934	0.50728	27.864	3	58367000	35618000	22750000
D3Z4T9	Zinc finger Ran-binding domain-containing protein 2	Zranb2	2	2	2	9.1	9.1	9.1	38.363	340	4.8264E-10	0.93028	1.0254	16.803	2	22352000	12195000	10157000
Q64726	Zinc-alpha-2-glycoprotein	Azgp1	5	5	5	22.5	22.5	22.5	35.332	307	5.1543E-40	0.51729	0.49783	102.7	6	644850000	278320000	366530000
Q8BGC4	Zinc-binding alcohol dehydrogenase domain-containing protein 2	Zadh2	9	9	9	30.8	30.8	30.8	40.528	377	2.6238E-54	0.86735	0.7679	119.22	8	1156200000	869420000	286780000
Q62523	Zyxin	Zyx	7	7	7	17.2	17.2	17.2	60.545	564	3.3865E-82	0.43568	0.40864	107.89	8	2037700000	1403100000	634610000
D3Z7P5		Gls	1	1	1	5.8	5.8	5.8	30.364	274	2.7332E-20	0.77226	0.70499	6.0266	2	40667000	22231000	18437000

Table S-2. Proteins identified via MaxQuant in replicate 2.

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8BGK2	[Protein ADP-ribosylarginine] hydrolase-like protein 1	Adprhl1	11	11	11	43.1	43.1	43.1	39.885	353	0	1.3022	1.0218	28.393	16	3083100000	1394200000	1688900000
A2AJQ0	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial	Pdp1	6	6	6	16.2	16.2	16.2	67.615	597	4.737E-217	1.1578	0.8354	36.053	8	593550000	272680000	320870000
Q8BFP9	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial	Pdk1	12	12	12	37.6	37.6	37.6	48.994	434	8.178E-289	0.65707	0.43057	47.022	16	1721200000	935310000	785900000
Q9JK42	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial	Pdk2	12	12	12	44.7	44.7	44.7	46.04	407	2.573E-191	0.93212	0.65701	34.534	17	1679600000	883780000	795840000
O70571	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial	Pdk4	9	9	9	34.5	34.5	34.5	46.596	412	2.119E-141	0.56702	0.44883	72.321	12	1403500000	738630000	664900000
Q99JT9	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	Adi1	3	3	3	19.6	19.6	19.6	21.523	179	1.4918E-06	1.9285	1.834	1.5806	2	53162000	17779000	35383000
F6ZHD8	1,4-alpha-glucan-branching enzyme	Gbe1	10	10	10	20.2	20.2	20.2	80.336	702	9.4738E-60	0.63954	0.4754	48.902	12	1844800000	1074300000	770520000
Q9DCT1	1,5-anhydro-D-fructose reductase	Akr1e2	3	3	3	15.6	15.6	15.6	34.46	301	3.8684E-07	1.0813	0.78017	19.023	2	83488000	36927000	46561000
Q64433	10 kDa heat shock protein, mitochondrial	Hspe1	9	9	9	66.7	66.7	66.7	10.963	102	3.8137E-47	1.9277	1.3909	35.413	21	2.0729E+10	6754200000	1.3975E+10
Q9DAK9	14 kDa phosphohistidine phosphatase	Phpt1	4	4	4	40.3	40.3	40.3	13.996	124	7.2751E-26	3.2324	2.3139	18.428	4	597920000	164410000	433510000
Q9CQV8	14-3-3 protein beta/alpha	Ywhab	8	6	5	34.1	26.8	23.2	28.086	246	0	1.8091	1.7007	29.547	6	1204400000	449720000	754640000
P62259	14-3-3 protein epsilon	Ywhae	11	11	9	42	42	34.9	29.174	255	1.015E-303	1.6572	1.2011	36.784	18	1.2446E+10	5021200000	7424900000
P68510	14-3-3 protein eta	Ywhah	6	4	4	27.6	20.3	20.3	28.211	246	5.993E-128	1.9681	1.3155	53.753	5	1190800000	439570000	751250000
P61982	14-3-3 protein gamma	Ywhag	6	3	3	28.7	17.8	17.8	28.302	247	9.726E-168	1.1424	0.62901	54.95	3	1414900000	732390000	682510000
F6VW30	14-3-3 protein theta	Ywhaq	10	8	8	31	25.1	25.1	34.348	303	7.477E-225	2.0863	1.9858	32.543	13	1095400000	387600000	707830000
P63101	14-3-3 protein zeta/delta	Ywhaz	9	7	7	40.4	33.1	33.1	27.771	245	0	2.0303	1.693	33.267	17	6269100000	2207200000	4061900000
P58871	182 kDa tankyrase-1-binding protein	Tnks1bp1	2	2	2	1.9	1.9	1.9	181.82	1720	3.3807E-05	1.2713	1.2419	8.783	2	54610000	25523000	29087000
Q9D517	1-acyl-sn-glycerol-3-phosphate acyltransferase gamma	Agpat3	3	3	3	6.9	6.9	6.9	43.295	376	9.5551E-07	0.45543	0.49737	59.77	3	61979000	34393000	27586000
Q8R3B1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1	Plcd1	5	5	5	9	9	9	85.872	756	1.2639E-18	1.145	0.83229	44.857	5	277700000	145860000	131840000
Q62077	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	Plcg1	4	4	4	4.1	4.1	4.1	149.67	1302	5.4491E-30	1.0468	0.75269	275.02	4	279830000	221670000	58163000
Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial	Decr1	19	19	19	60.6	60.6	60.6	36.213	335	0	1.5786	1.1564	56.452	62	2.2731E+10	9658100000	1.3073E+10
P62334	26S protease regulatory subunit 10B	Psmc6	7	7	7	25.2	25.2	25.2	44.172	389	7.5527E-44	0.80471	0.61905	25.117	9	927600000	510470000	417130000
P62192	26S protease regulatory subunit 4	Psmc1	11	11	11	33.9	33.9	33.9	49.184	440	5.691E-107	0.76441	0.52454	29.901	14	1906500000	1151700000	754780000
B7ZCF1	26S protease regulatory subunit 6A	Psmc3	10	10	10	27.1	27.1	27.1	50.395	451	0	1.2475	0.81275	31.804	7	1172100000	542730000	629380000
P54775	26S protease regulatory subunit 6B	Psmc4	6	6	6	20.8	20.8	20.8	47.408	418	9.6333E-50	0.96533	0.6595	43.362	8	617340000	342970000	274370000
Q8BVQ9	26S protease regulatory subunit 7	Psmc2	13	13	13	37.7	37.7	37.7	52.866	475	1.271E-275	0.94728	0.72677	24.879	17	1634100000	861120000	773010000
P62196	26S protease regulatory subunit 8	Psmc5	6	6	6	20	20	20	45.626	406	7.27E-113	0.636	0.45489	15.55	5	1064800000	636200000	428630000
Q3TXS7	26S proteasome non-ATPase regulatory subunit 1	Psmd1	16	16	16	23	23	23	105.73	953	1.953E-250	1.0806	0.70208	57.444	17	1190200000	678670000	511510000
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	Psmd11	8	8	8	25.1	25.1	25.1	47.436	422	1.7631E-81	1.1855	0.92977	26.241	13	1932800000	952960000	979820000
Q9D8W5	26S proteasome non-ATPase regulatory subunit 12	Psmd12	10	10	10	29.2	29.2	29.2	52.895	456	1.572E-150	0.80439	0.80214	42.201	9	652340000	378980000	273370000
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	Psmd13	14	14	14	48.1	48.1	48.1	42.809	376	6.632E-106	1.1874	0.93989	30.03	21	2663500000	1271000000	1392400000
O35593	26S proteasome non-ATPase regulatory subunit 14	Psmd14	4	4	4	14.8	14.8	14.8	34.577	310	2.5367E-33	0.66888	0.4808	63.478	4	329670000	187830000	141840000
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	Psmd2	18	18	18	28.5	28.5	28.5	100.2	908	0	0.88726	0.80701	61.172	23	2670700000	1562000000	1108700000
P14685	26S proteasome non-ATPase regulatory subunit 3	Psmd3	10	10	10	20.8	20.8	20.8	60.718	530	1.649E-100	0.62304	0.46782	47.04	15	1170800000	778350000	392500000
O35226	26S proteasome non-ATPase regulatory subunit 4	Psmd4	5	5	4	23.4	23.4	20.7	40.703	376	7.5419E-79	1.7	1.2012	24.593	4	628430000	229770000	398660000
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5	Psmd5	7	7	7	21.2	21.2	21.2	55.971	504	5.2496E-66	1.0712	0.80945	56.932	11	1603100000	322430000	1280700000
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	Psmd6	6	6	6	17	17	17	45.536	389	2.5945E-22	0.44222	0.31114	102.98	7	738240000	433330000	304910000
P26516	26S proteasome non-ATPase regulatory subunit 7	Psmd7	5	5	5	24.9	24.9	24.9	36.539	321	9.7573E-70	1.0128	0.75013	27.776	7	1567200000	758320000	808840000
Q9CX56	26S proteasome non-ATPase regulatory subunit 8	Psmd8	4	4	4	19.5	19.5	19.5	39.93	353	9.761E-118	1.5413	1.7875	71.309	8	839650000	379270000	460380000
Q9CR00	26S proteasome non-ATPase regulatory subunit 9	Psmd9	3	3	3	18.9	18.9	18.9	24.72	222	1.6621E-39	2.3709	1.6219	40.367	3	342650000	93276000	249370000
Q3UHX2	28 kDa heat- and acid-stable phosphoprotein	Pdap1	3	3	3	16.6	16.6	16.6	20.605	181	8.9431E-33	2.9869	1.9147	27.629	5	396570000	95687000	300890000
Q5U5I3	28S ribosomal protein S18a, mitochondrial	Mrps18a	1	1	1	8.2	8.2	8.2	22.236	196	0.00042496	1.2005	0.93915	29.418	2	27670000	12130000	15540000
Q99N84	28S ribosomal protein S18b, mitochondrial	Mrps18b	1	1	1	8.7	8.7	8.7	28.702	254	3.2272E-05	1.9552	1.3298	25.597	2	52553000	21095000	31458000
Q9CXW2	28S ribosomal protein S22, mitochondrial	Mrps22	3	3	3	12.5	12.5	12.5	41.192	359	8.5723E-14	1.1279	0.69148	59.633	2	306950000	143510000	163440000
Q8VE22	28S ribosomal protein S23, mitochondrial	Mrps23	3	3	3	19.8	19.8	19.8	20.348	177	3.0401E-10	0.89434	0.57252	71.191	3	146320000	60388000	85929000
Q8BK72	28S ribosomal protein S27, mitochondrial	Mrps27	3	3	3	6.7	6.7	6.7	47.778	415	2.7436E-13	0.55681	0.6282	31.666	3	154610000	93025000	61588000
G3X9M0	28S ribosomal protein S29, mitochondrial	Dap3	3	3	3	9.8	9.8	9.8	45.287	396	8.4296E-16	0.83848	0.73462	41.425	2	254320000	99164000	155160000
Q9D0G0	28S ribosomal protein S30, mitochondrial	Mrps30	3	3	3	11.1	11.1	11.1	49.939	442	5.0952E-61	0.52687	0.37418	29.199	4	256730000	166600000	90127000
Q9CQX8	28S ribosomal protein S36, mitochondrial	Mrps36	4	4	1	69.6	69.6	23.5	11.101	102	1.789E-191	3.2111	2.0039	53.805	9	2398700000	643340000	1755300000
Q99N87	28S ribosomal protein S5, mitochondrial	Mrps5	3	3	3	7.6	7.6	7.6	48.206	432	2.4312E-06	0.87661	0.92528	44.876	4	147730000	82041000	65689000
Q80X85	28S ribosomal protein S7, mitochondrial	Mrps7	4	4	4	23.6	23.6	23.6	28.062	242	1.1286E-14	0.51875	0.50138	38.558	4	205270000	121600000	83666000
Q9D7N3	28S ribosomal protein S9, mitochondrial	Mrps9	4	4	4	13.3	13.3	13.3	44.929	390	1.3111E-06	1.6546	1.8965	71.636	3	137860000	56522000	81338000
Q6PDY2	2-aminoethanethiol dioxygenase	Ado	2	2	2	16	16	16	28.372	256	3.6156E-05	1.0324	0.74777	61.603	2	51766000	16662000	35104000
Q5RJG7	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase-like protein	Ispd	2	2	2	6.9	6.9	6.9	49.135	447	1.0398E-31	3.0341	2.1034	39.046	2	51250000	13145000	38106000
Q9CXI0	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	Coq5	5	5	5	20.5	20.5	20.5	37.335	327	7.6367E-53	0.86022	0.7883	104.55	4	1007400000	342580000	664840000
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	Ogdh	41	41	34	46.2	46.2	40.6	116.45	1023	0	0.69051	0.49189	52.145	111	5.7445E+10	3.4909E+10	2.2537E+10
Q3U3J1	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	Bckdha	9	9	9	31.8	31.8	31.8	50.773	446	5.131E-146	1.0966	0.66844	54.552	12	1876500000	862930000	1013600000
Q6P3A8	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	Bckdhb	8	8	8	26.7	26.7	26.7	42.88	390	9.223E-119	0.95302	0.78342	30.147	10	1628000000	859750000	768230000
Q9Z0S1	3(2),5-bisphosphate nucleotidase 1	Bpnt1	8	8	8	36	36	36	33.196	308	2.0902E-93	1.3954	0.74933	53.633	7	782170000	395120000	387060000
Q99N96	39S ribosomal protein L1, mitochondrial	Mrpl1	4	4	4	21.4	21.4	21.4	37.596	336	3.8451E-08	0.84692	0.75119	63.325	3	86157000	38793000	47364000
Q3TBW2	39S ribosomal protein L10, mitochondrial	Mrpl10	4	4	4	27.5	27.5	27.5	29.395	262	7.756E-21	0.83561	0.64372	14.501	4	291220000	156750000	134460000
Q9D1P0	39S ribosomal protein L13, mitochondrial	Mrpl13	3	3	3	18.5	18.5	18.5	20.677	178	0.00026473	0.25153	0.17281	52.055	3	106770000	81428000	25342000
Q9D338	39S ribosomal protein L19, mitochondrial	Mrpl19	2	2	2	7.9	7.9	7.9	33.578	292	5.2232E-05	1.0771	0.81714	31.185	4	175380000	92834000	82544000
O35972	39S ribosomal protein L23, mitochondrial	Mrpl23	1	1	1	10.3	10.3	10.3	17.121	146	0.0000438	0.68073	0.51506	22.873	3	52534000	29718000	22817000
Q99N95	39S ribosomal protein L3, mitochondrial	Mrpl3	4	4	4	16.4	16.4	16.4	39.109	348	7.4004E-22	0.79656	0.56923	18.019	6	306230000	166690000	139550000
Q921S7	39S ribosomal protein L37, mitochondrial	Mrpl37	7	7	7	21	21	21	48.34	423	1.4815E-23	0.60721	0.42138	66.781	7	517190000	368080000	149100000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9JKF7	39S ribosomal protein L39, mitochondrial	Mrpl39	4	4	4	16.1	16.1	16.1	38.549	336	1.4217E-10	0.84057	0.73665	88.577	3	220270000	80877000	139400000
Q9EQI8	39S ribosomal protein L46, mitochondrial	Mrpl46	3	3	3	14.1	14.1	14.1	32.131	283	7.2912E-14	0.67234	0.512	30.019	2	226630000	146050000	80578000
Q9CQ40	39S ribosomal protein L49, mitochondrial	Mrpl49	2	2	2	22.3	22.3	22.3	19.133	166	2.3031E-05	1.5938	1.1331	20.6	3	184540000	74267000	110280000
A2AFQ2	3-hydroxyacyl-CoA dehydrogenase type-2	Hsd17b10	11	11	11	59	59	59	28.374	271	1.715E-295	0.99027	0.87324	44.712	21	2.7637E+10	1.5357E+10	1.2281E+10
Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial	Hibadh	8	8	8	34.3	34.3	34.3	35.44	335	3.3148E-49	1.2206	0.8849	26.063	13	1238200000	529960000	708200000
Q8QZS1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	Hibch	14	14	14	44.7	44.7	44.7	43.037	385	1.598E-220	1.322	0.93027	57.305	23	8458400000	3775400000	4683000000
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	Acaa1a	9	9	9	38.7	38.7	38.7	43.953	424	4.945E-128	1.252	0.8362	21.424	7	1148600000	517670000	630900000
Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	Acaa2	15	15	15	59.4	59.4	59.4	41.829	397	0	1.0027	0.81996	71.002	37	2.8586E+10	1.209E+10	1.6496E+10
Q9D404	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	Oxsm	6	6	6	25.1	25.1	25.1	48.627	459	7.849E-129	1.0043	0.70499	31.145	11	1189000000	504390000	684570000
P63325	40S ribosomal protein S10	Rps10	5	5	5	37.6	37.6	37.6	18.916	165	1.3505E-21	0.29334	0.21516	36.804	8	421510000	327110000	94399000
Q6ZWZ6	40S ribosomal protein S12	Rps12	4	4	4	25.8	25.8	25.8	14.515	132	3.0983E-57	2.0102	1.5581	45.331	5	466430000	172090000	294340000
P62301	40S ribosomal protein S13	Rps13	4	4	4	23.8	23.8	23.8	17.222	151	2.6769E-19	0.14458	0.10874	53.737	3	280080000	252270000	27816000
P62264	40S ribosomal protein S14	Rps14	3	3	3	21.9	21.9	21.9	16.273	151	9.998E-13	0.56314	0.35679	27.916	3	211960000	140740000	71223000
P14131	40S ribosomal protein S16	Rps16	3	3	3	22.6	22.6	22.6	16.445	146	7.2197E-09	0.25931	0.3133	90.245	3	345280000	291150000	54128000
F6YVP7	40S ribosomal protein S18	Gm17352	3	3	3	18.4	18.4	18.4	17.671	152	8.0695E-08	0.3633	0.25723	39.315	4	505930000	328930000	176990000
D3Z722	40S ribosomal protein S19	Rps19	6	6	6	18.9	18.9	18.9	23.104	212	6.8185E-28	0.22881	0.17379	47.834	7	546060000	425810000	120250000
D3YWJ3	40S ribosomal protein S2	Rps2	5	5	1	16.6	16.6	2.3	32.105	302	1.8175E-13	0.17003	0.18829	83.526	6	360160000	288100000	72065000
P62849	40S ribosomal protein S24	Rps24	3	3	3	20.3	20.3	20.3	15.423	133	4.7462E-19	0.15011	0.10175	106.64	3	175100000	150370000	24724000
Q6ZWU9	40S ribosomal protein S27	Rps27	2	2	2	22.6	22.6	22.6	9.461	84	0.0052489	0.3921	0.25112	26.663	2	142920000	98464000	44452000
P62908	40S ribosomal protein S3	Rps3	9	9	9	43.6	43.6	43.6	26.674	243	5.6336E-67	0.25835	0.19028	67.703	8	552310000	430870000	121440000
D3Z6C3	40S ribosomal protein S3a	Gm10119	5	5	5	18.9	18.9	18.9	29.824	264	1.3665E-07	0.37742	0.259	32.084	4	662400000	503780000	158620000
P62702	40S ribosomal protein S4, X isoform	Rps4x	6	6	6	27.8	27.8	27.8	29.597	263	6.7019E-59	0.41082	0.28997	136.61	4	179380000	119460000	59920000
Q91V55	40S ribosomal protein S5	Rps5	2	2	2	12.3	12.3	12.3	22.876	204	3.9417E-09	0.12337	0.10991	21.868	2	50127000	43025000	7102600
J3QJZ3	40S ribosomal protein S7	Rps7	3	3	3	19.6	19.6	19.6	22.084	194	6.8028E-09	0.29304	0.29357	16.424	3	342040000	264770000	77275000
P62242	40S ribosomal protein S8	Rps8	4	4	4	24	24	24	24.205	208	2.1451E-17	0.26579	0.21786	60.511	8	869210000	691440000	177770000
Q6ZWN5	40S ribosomal protein S9	Rps9	3	3	3	11.9	11.9	11.9	22.591	194	0.00041025	0.71617	0.50939	99.533	3	378870000	205880000	172990000
P14206	40S ribosomal protein SA	Rpsa	6	6	6	32.2	32.2	32.2	32.838	295	5.2478E-34	0.526	0.3704	37.068	8	1331900000	846600000	485300000
P61922	4-aminobutyrate aminotransferase, mitochondrial	Abat	4	4	4	9.8	9.8	9.8	56.451	500	5.1747E-24	1.8684	1.4396	26.114	6	216890000	81696000	135190000
Q3U367	4-trimethylaminobutyraldehyde dehydrogenase	Aldh9a1	4	4	4	13.1	13.1	13.1	55.887	518	1.3743E-15	0.80456	0.57814	84.61	5	662730000	355210000	307530000
P70290	55 kDa erythrocyte membrane protein	Mpp1	3	3	3	10.1	10.1	10.1	52.227	466	4.2495E-09	1.1914	0.8032	11.375	4	139700000	68542000	71160000
Q5EG47	5-AMP-activated protein kinase catalytic subunit alpha-1	Prkaa1	2	2	2	5	5	5	63.928	559	9.2159E-07	0.44373	0.31166	5.0025	2	54309000	37343000	16965000
Q8BRK8	5-AMP-activated protein kinase catalytic subunit alpha-2	Prkaa2	3	3	3	6.2	6.2	6.2	62.022	552	3.3978E-05	0.97521	0.69275	50.37	3	116810000	53758000	63055000
Q3UHB1	5-nucleotidase domain-containing protein 3	Nt5dc3	7	7	7	14.5	14.5	14.5	63.17	546	1.1156E-49	0.70591	0.56353	19.973	6	332720000	186620000	146100000
Q8K010	5-oxoprolinase	Oplah	16	16	16	19.3	19.3	19.3	137.61	1288	8.698E-164	0.66465	0.48763	36.208	19	1210200000	742660000	467530000
P63038	60 kDa heat shock protein, mitochondrial	Hspd1	25	25	25	58.5	58.5	58.5	60.955	573	0	2.4334	1.6868	62.031	62	4.2566E+10	1.0929E+10	3.1637E+10
E9Q070	60S acidic ribosomal protein P0	Gm8730	3	3	3	6.3	6.3	6.3	34.216	317	7.1138E-14	0.11759	0.14228	283.05	3	276840000	175730000	101120000
P99027	60S acidic ribosomal protein P2	Rplp2	5	5	5	73.9	73.9	73.9	11.651	115	9.5974E-26	1.1545	0.9565	192.02	5	1187000000	179310000	1007700000
Q6ZWV3	60S ribosomal protein L10	Rpl10	3	3	3	15	15	15	24.604	214	0.00001852	0.33416	0.32304	61.815	4	741110000	416510000	324600000
P35979	60S ribosomal protein L12	Rpl12	6	6	6	49.1	49.1	49.1	17.804	165	1.868E-122	0.18543	0.15052	38.709	6	290440000	260720000	29713000
P47963	60S ribosomal protein L13	Rpl13	2	2	2	9	9	9	24.305	211	3.6674E-56	0.27972	0.21583	6.991	2	191960000	140090000	51868000
E9Q5A0	60S ribosomal protein L13a	Rpl13a	3	3	3	7.6	7.6	7.6	48.342	423	4.0017E-15	0.36303	0.4279	6.628	2	235320000	159790000	75528000
Q6ZWZ7	60S ribosomal protein L17	Rpl17	3	3	3	21.7	21.7	21.7	21.397	184	3.849E-33	0.27075	0.27934	97.441	3	175100000	129580000	45521000
P35980	60S ribosomal protein L18	Rpl18	3	3	3	16	16	16	21.644	188	7.6269E-13	0.075597	0.058958	60.549	2	288640000	245680000	42966000
P62717	60S ribosomal protein L18a	Rpl18a	3	3	3	18.2	18.2	18.2	20.732	176	4.2572E-21	0.093724	0.064302	108.21	4	835220000	691680000	143540000
P62830	60S ribosomal protein L23	Rpl23	3	3	3	27.1	27.1	27.1	14.865	140	6.2162E-08	0.75999	0.81225	59.396	3	398280000	197400000	200880000
P14115	60S ribosomal protein L27a	Rpl27a	4	4	4	27.7	27.7	27.7	16.605	148	9.9792E-22	0.18266	0.14882	80.69	3	200290000	159370000	40917000
P62889	60S ribosomal protein L30	Rpl30	3	3	3	40.9	40.9	40.9	12.784	115	1.1624E-11	0.14259	0.094718	8.1865	2	85355000	74541000	10814000
P62900	60S ribosomal protein L31	Rpl31	1	1	1	11.2	11.2	11.2	14.463	125	1.4654E-20	0.41362	0.27727	87.18	2	184240000	150150000	34087000
Q9JJI8	60S ribosomal protein L38	Rpl38	2	2	2	18.6	18.6	18.6	8.2038	70	4.8318E-05	1.3675	0.90923	44.003	2	158070000	57482000	100590000
Q9D8E6	60S ribosomal protein L4	Rpl4	8	8	8	23.9	23.9	23.9	47.153	419	2.4542E-31	0.11941	0.11031	58.135	9	1041100000	944850000	96214000
P47962	60S ribosomal protein L5	Rpl5	8	8	8	32	32	32	34.4	297	1.1931E-45	0.2904	0.16813	106.05	5	530390000	354640000	175750000
E9PUX4	60S ribosomal protein L6	Gm5428	3	3	3	11.5	11.5	11.5	33.59	296	4.1044E-37	0.75004	0.48316	211.66	3	346990000	195620000	151380000
F6XI62	60S ribosomal protein L7	Rpl7	4	4	4	10	10	10	32.416	279	8.8304E-13	0.67994	0.38001	227.76	2	413120000	222410000	190710000
L7N202	60S ribosomal protein L7a	Rpl7a	3	3	3	12	12	12	29.964	266	1.5065E-09	0.081936	0.058315	86.757	2	188330000	182190000	6134700
P62918	60S ribosomal protein L8	Rpl8	4	4	4	24.9	24.9	24.9	28.024	257	1.7152E-75	0.12868	0.087884	92.655	3	152380000	136120000	16254000
P51410	60S ribosomal protein L9	Rpl9	4	4	4	21.4	21.4	21.4	21.881	192	2.9758E-41	0.18644	0.12446	2.0023	2	269610000	227880000	41736000
P70265	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2	Pfkfb2	8	8	8	15.8	15.8	15.8	59.925	519	2.2708E-18	0.36908	0.27997	61.349	7	541520000	387800000	153720000
Q8C605	6-phosphofructokinase	Pfkp	14	13	12	21.6	20.4	18	85.546	784	4.371E-131	0.52757	0.40022	61.462	14	1305700000	963100000	342620000
P12382	6-phosphofructokinase, liver type	Pfkl	13	9	9	22.8	16.7	16.7	85.359	780	1.8385E-59	0.50595	0.34063	45.947	17	2039400000	1344700000	694690000
P47857	6-phosphofructokinase, muscle type	Pfkm	22	22	19	36.4	36.4	32.7	85.268	780	0	0.8735	0.62325	35.202	34	2.0383E+10	1.1647E+10	8736500000
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	Pgd	13	13	13	31.1	31.1	31.1	53.247	483	1.509E-157	0.90596	0.61673	36.576	15	2360900000	1301600000	1059300000
Q9CQ60	6-phosphogluconolactonase	Pgls	3	3	3	16	16	16	27.254	257	5.1731E-35	1.6948	1.2632	63.267	5	415970000	161110000	254860000
Q9R1Z7	6-pyruvoyl tetrahydrobiopterin synthase	Pts	2	2	2	15.3	15.3	15.3	16.188	144	1.86E-08	1.8399	1.6494	23.564	2	263400000	122270000	141130000
P20029	78 kDa glucose-regulated protein	Hspa5	23	22	22	40.9	39.2	39.2	72.421	655	0	1.2488	0.91034	57.131	36	9594700000	4233900000	5360700000
Q6PE15	Abhydrolase domain-containing protein 10, mitochondrial	Abhd10	5	5	5	25.3	25.3	25.3	33.04	297	2.054E-170	1.3185	0.9357	4.6352	6	277500000	110720000	166780000
Q8K4F5	Abhydrolase domain-containing protein 11	Abhd11	6	6	6	32.6	32.6	32.6	33.56	307	8.53E-116	1.0229	0.81434	25.356	8	1126800000	502580000	624210000
E9QN99	Abhydrolase domain-containing protein 14B	Abhd14b	3	3	3	21.9	21.9	21.9	22.45	210	3.2884E-30	1.3233	0.9646	31.817	4	272240000	130850000	141400000
J3QNK8	Abl interactor 1	Abi1	2	2	2	7.5	7.5	7.5	52.345	481	0.0013874	3.9381	3.5039	49.148	2	34602000	7703600	26899000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	Acat1	19	19	19	65.6	65.6	65.6	44.816	424	0	2.084	1.5933	73.565	39	5.4505E+10	1.6143E+10	3.8361E+10
Q99NB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	Acss1	22	22	22	47.5	47.5	47.5	74.622	682	0	0.96235	0.65684	28.518	44	1.0496E+10	5598100000	4898100000
Q9WV54	Acid ceramidase	Asah1	6	6	6	20.6	20.6	20.6	44.669	394	5.1499E-21	0.33044	0.26928	17.674	7	475730000	355400000	120330000
O35381	Acidic leucine-rich nuclear phosphoprotein 32 family member A	Anp32a	7	7	6	26.7	26.7	23.5	28.537	247	2.0571E-23	1.6963	1.2479	44.773	9	1934000000	793120000	1140900000
Q9EST5	Acidic leucine-rich nuclear phosphoprotein 32 family member B	Anp32b	2	1	1	7.4	4.4	4.4	31.078	272	1.1686E-13	1.1108	0.85706	2.7025	2	104940000	50107000	54836000
Q99KI0	Aconitate hydratase, mitochondrial	Aco2	45	45	45	56.7	56.7	56.7	85.462	780	0	0.99237	0.71081	51.207	262	2.1398E+11	1.0866E+11	1.0532E+11
P62737	Actin, aortic smooth muscle	Acta2	15	15	1	56	56	5.8	42.009	377	0	1.1389	0.72759	40.685	65	2.5514E+10	1.2442E+10	1.3073E+10
E9QK41	Actin-binding LIM protein 1	Ablim1	5	5	5	9.2	9.2	9.2	96.834	861	1.1553E-91	0.88212	0.64856	63.313	6	316130000	198110000	118020000
Q9Z2N8	Actin-like protein 6A	Actl6a	2	2	2	11.2	11.2	11.2	47.447	429	4.2813E-08	0.91006	0.60234	113.38	2	106520000	47845000	58676000
Q9QZB7	Actin-related protein 10	Actr10	3	3	3	8.6	8.6	8.6	46.207	417	3.1516E-42	0.55934	0.42109	59.756	2	63520000	49691000	13829000
P61161	Actin-related protein 2	Actr2	6	6	6	23.1	23.1	23.1	44.76	394	5.193E-230	0.55699	0.41769	42.924	7	443430000	289130000	154310000
Q9WV32	Actin-related protein 2/3 complex subunit 1B	Arpc1b	7	7	7	26.1	26.1	26.1	41.063	372	1.213E-75	0.56597	0.48675	42.921	6	442940000	261470000	181470000
Q9CVB6	Actin-related protein 2/3 complex subunit 2	Arpc2	8	8	8	19	19	19	34.357	300	2.7007E-26	1.2211	0.73278	48.836	9	1359700000	604910000	754780000
Q9JM76	Actin-related protein 2/3 complex subunit 3	Arpc3	3	3	3	16.3	16.3	16.3	20.524	178	5.9837E-05	0.81315	0.80798	104.26	2	218670000	105500000	113160000
A3KGQ6	Actin-related protein 2/3 complex subunit 5	Arpc5l	3	3	3	37.9	37.9	37.9	17.109	153	3.261E-23	1.972	1.4371	77.595	4	1066200000	384680000	681540000
Q99JY9	Actin-related protein 3	Actr3	12	12	12	41.9	41.9	41.9	47.357	418	8.102E-131	0.85674	0.60665	30.167	20	1759400000	967170000	792270000
P11031	Activated RNA polymerase II transcriptional coactivator p15	Sub1	2	2	2	18.9	18.9	18.9	14.427	127	3.7502E-15	0.4574	0.42907	182.61	2	351600000	275740000	75854000
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	Ahsa1	8	8	8	26	26	26	38.117	338	8.2465E-37	1.0915	0.71099	121.16	11	1653400000	1229000000	424370000
Q9CR21	Acyl carrier protein, mitochondrial	Ndufab1	3	3	3	15.4	15.4	15.4	17.37	156	1.1973E-42	2.1139	1.9338	158.57	4	3268300000	959290000	2309000000
Q8R146	Acylamino-acid-releasing enzyme	Apeh	9	9	9	18.4	18.4	18.4	81.58	732	5.028E-116	0.56809	0.39529	62.92	8	714830000	479540000	235290000
Q80XL6	Acyl-CoA dehydrogenase family member 11	Acad11	2	2	2	3.3	3.3	3.3	87.365	779	0.00054895	0.25087	0.19024	52.613	2	31585000	25995000	5590200
Q8JZN5	Acyl-CoA dehydrogenase family member 9, mitochondrial	Acad9	9	9	9	23	23	23	68.721	625	1.495E-230	1.2471	1.0876	27.957	12	1644700000	716040000	928660000
Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial	Acsf2	13	13	13	31.2	31.2	31.2	67.95	615	1.599E-249	0.98664	0.75533	27.357	10	1337500000	680160000	657360000
Q3URE1	Acyl-CoA synthetase family member 3, mitochondrial	Acsf3	9	9	9	25.4	25.4	25.4	65.076	583	8.5004E-62	0.83396	0.52777	95.597	8	812650000	460160000	352490000
Q4VWZ5	Acyl-CoA-binding protein	Dbi	5	5	5	40	40	40	15.228	135	1.13E-110	2.9944	1.7622	31.11	11	5088800000	1483400000	3605400000
O55137	Acyl-coenzyme A thioesterase 1	Acot1	13	3	3	32	10.5	10.5	46.135	419	0	2.366	2.2206	95.168	2	169600000	41385000	128220000
Q9CQR4	Acyl-coenzyme A thioesterase 13	Acot13	6	6	6	62.1	62.1	62.1	15.183	140	1.656E-133	1.2165	1.079	66.665	15	995240000	470740000	524500000
Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial	Acot2	17	17	7	46.1	46.1	26.3	49.656	453	0	1.1497	0.9514	36.822	62	2.1361E+10	9799400000	1.1562E+10
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial	Acot9	3	3	3	10	10	10	50.56	439	3.7316E-45	1.0619	1.0675	50.388	5	755600000	336580000	419020000
E9QJT5	Acylphosphatase	Acyp1	1	1	1	8.3	8.3	8.3	17.344	157	5.8002E-36	2.9041	3.2248	17.613	3	603180000	172680000	430500000
P56375	Acylphosphatase-2	Acyp2	6	6	6	59.4	59.4	59.4	11.877	106	9.566E-140	2.7831	1.8235	57.584	9	8901000000	2233400000	6667600000
P97823	Acyl-protein thioesterase 1	Lypla1	5	5	5	40.9	40.9	40.9	24.687	230	1.8788E-60	1.4997	1.1313	51.997	11	400510000	185810000	214700000
Q8R0F8	Acylpyruvase FAHD1, mitochondrial	Fahd1	5	5	5	30.8	30.8	30.8	25.172	227	3.8666E-21	1.214	1.1125	26.486	8	404490000	169500000	234990000
Q64010	Adapter molecule crk	Crk	4	4	2	17.8	17.8	8.6	33.814	304	3.6433E-65	2.459	1.6465	4.5118	2	458470000	144280000	314190000
P08030	Adenine phosphoribosyltransferase	Aprt	3	3	3	25.6	25.6	25.6	19.724	180	1.7246E-13	0.84166	0.45184	229.93	3	1150800000	1060500000	90243000
P55264	Adenosine kinase	Adk	5	5	5	22.7	22.7	22.7	40.148	361	3.148E-156	1.9858	1.369	59.178	10	3599900000	1198700000	2401200000
P50247	Adenosylhomocysteinase	Ahcy	12	12	12	30.6	30.6	30.6	47.688	432	2.463E-179	1.1647	0.85429	65.892	23	4223900000	2150200000	2073700000
Q9WTP6	Adenylate kinase 2, mitochondrial	Ak2	8	8	8	44.8	44.8	44.8	26.468	239	1.226E-168	1.7188	1.3924	52.115	15	3671600000	1345700000	2325900000
Q9R0Y5	Adenylate kinase isoenzyme 1	Ak1	12	12	12	68	68	68	21.539	194	0	2.7993	2.0466	67.571	50	2.3208E+10	5592400000	1.7616E+10
Q9WUR9	Adenylate kinase isoenzyme 4, mitochondrial	Ak4	5	5	5	25.1	25.1	25.1	25.061	223	6.2647E-38	0.70963	0.48614	26.272	7	818500000	479810000	338680000
P54822	Adenylosuccinate lyase	Adsl	9	9	9	24.4	24.4	24.4	54.866	484	1.1771E-73	0.81912	0.60388	48.377	13	896900000	476090000	420810000
P28650	Adenylosuccinate synthetase isozyme 1	Adssl1	12	12	12	34.4	34.4	34.4	50.254	457	7.107E-225	0.92229	0.7108	38.007	14	998250000	542470000	455780000
P40124	Adenylyl cyclase-associated protein 1	Cap1	7	7	7	24.3	24.3	24.3	51.564	474	1.68E-146	1.5445	1.0347	19.307	11	1528000000	623050000	904900000
Q9CYT6	Adenylyl cyclase-associated protein 2	Cap2	7	7	7	23.1	23.1	23.1	52.861	476	1.029E-52	1.4976	1.1321	29.198	8	394020000	170080000	223940000
Q60994	Adiponectin	Adipoq	5	5	5	21.9	21.9	21.9	26.809	247	3.6742E-86	2.6095	1.6069	57.53	7	2920800000	882680000	2038100000
P48962	ADP/ATP translocase 1	Slc25a4	16	16	10	47.3	47.3	26.8	32.904	298	0	0.4281	0.28858	100.27	37	5.8813E+10	3.9754E+10	1.9059E+10
P51881	ADP/ATP translocase 2	Slc25a5	10	4	4	35.2	14.8	14.8	32.931	298	3.602E-101	0.40034	0.29232	77.708	4	1427700000	989370000	438360000
Q3V132	ADP/ATP translocase 4	Slc25a31	3	1	1	9.1	2.8	2.8	35.257	320	3.9698E-19	0.37707	0.27388	3.9614	3	63629000	48783000	14846000
P61205	ADP-ribosylation factor 3	Arf3	3	2	2	26	16	16	20.601	181	0	1.2882	0.97889	21.814	2	300330000	132720000	167610000
P84084	ADP-ribosylation factor 5	Arf5	4	4	3	28.3	28.3	18.3	20.529	180	0	1.2814	0.95679	20.712	5	777280000	259980000	517300000
P62331	ADP-ribosylation factor 6	Arf6	1	1	1	12	12	12	20.082	175	1.6821E-14	1.0024	0.67334	17.6	2	117310000	54163000	63149000
Q8R0H9	ADP-ribosylation factor-binding protein GGA1	Gga1	3	3	3	8	8	8	69.971	635	7.7236E-13	1.2295	0.9209	56.159	5	183520000	66647000	116870000
Q9WUL7	ADP-ribosylation factor-like protein 3	Arl3	3	3	3	24.7	24.7	24.7	20.486	182	3.4482E-19	1.2633	1.1809	13.077	3	179220000	73180000	106040000
E9Q9C3	Afadin	Mllt4	5	5	5	4.2	4.2	4.2	207.31	1827	3.2455E-19	1.0655	0.8317	69.291	6	258990000	109070000	149920000
O89020	Afamin	Afm	5	5	5	12.8	12.8	12.8	69.378	608	1.5186E-68	2.3844	1.5075	21.853	5	594980000	218200000	376780000
Q8JZQ2	AFG3-like protein 2	Afg3l2	3	3	3	5.4	5.4	5.4	89.518	802	1.923E-06	0.70713	0.43024	76.386	3	358340000	197240000	161100000
Q8CG76	Aflatoxin B1 aldehyde reductase member 2	Akr7a2	4	4	4	16.9	16.9	16.9	40.612	367	2.7184E-94	0.79235	0.60001	25.262	6	506440000	300300000	206140000
M0QWP1	Agrin	Agrn	5	5	5	4.1	4.1	4.1	216.65	2034	2.434E-236	1.2658	1.0521	15.852	4	142370000	56352000	86023000
O08715	A-kinase anchor protein 1, mitochondrial	Akap1	5	5	5	10.3	10.3	10.3	92.194	857	2.2922E-12	1.1638	0.71658	30.686	4	376570000	178730000	197840000
Q9WTQ5	A-kinase anchor protein 12	Akap12	17	17	17	19.5	19.5	19.5	180.69	1684	4.156E-157	2.2739	2.0083	25.475	15	584160000	158880000	425290000
F7AA26	A-kinase anchor protein 2	Gm20459	10	10	10	13.6	13.6	13.6	125.98	1137	1.2732E-75	2.4244	1.9078	60.003	9	615110000	202060000	413050000
Q8QZR5	Alanine aminotransferase 1	Gpt	9	9	8	25.6	25.6	24	55.142	496	1.2893E-45	1.5677	0.951	55.252	12	1415200000	648510000	766720000
H7BWY3	Alanine--glyoxylate aminotransferase 2, mitochondrial	Agxt2	2	2	2	4.4	4.4	4.4	60.1	541	0.0075412	1.0338	0.75002	24.799	3	8074000000	3952100000	4121800000
Q8BGQ7	Alanine--tRNA ligase, cytoplasmic	Aars	6	6	6	9	9	9	106.91	968	2.8379E-90	0.87376	0.75667	39.321	6	260930000	134640000	126280000
A2A4P4	Alanyl-tRNA editing protein Aarsd1	Aarsd1	7	7	7	23.6	23.6	23.6	60.506	543	6.2398E-73	1.7759	1.1901	28.79	7	520670000	180620000	340050000
Q9JII6	Alcohol dehydrogenase [NADP(+)]	Akr1a1	6	6	6	24.6	24.6	24.6	36.586	325	5.024E-200	0.65612	0.45691	20.689	9	1022300000	596300000	426040000
P00329	Alcohol dehydrogenase 1	Adh1	4	4	4	12.3	12.3	12.3	39.771	375	1.4686E-13	1.0191	0.87549	37.875	4	221770000	118920000	102850000
P28474	Alcohol dehydrogenase class-3	Adh5	10	10	10	42.5	42.5	42.5	39.547	374	3.667E-239	1.5906	1.2369	46.896	20	3370300000	1265200000	2105100000

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Q571I9	Aldehyde dehydrogenase family 16 member A1	Aldh16a1	2	2	2	3.7	3.7	3.7	84.755	802	0.00051865	0.39957	0.29591	10.871	2	21433000	15302000	6131500
Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	Aldh1b1	11	11	11	33.1	33.1	33.1	57.552	519	1.172E-79	1.6962	1.1387	37.5	16	2056600000	845030000	1211600000
P47738	Aldehyde dehydrogenase, mitochondrial	Aldh2	19	19	19	42	42	42	56.537	519	4.081E-179	1.5931	1.1701	65.634	38	1.072E+10	4507700000	6212100000
G3X8P9	Aldehyde oxidase	Aox1	3	3	3	4	4	4	146.65	1333	2.8015E-06	0.30944	0.31505	57.238	3	121830000	88605000	33225000
Q8K157	Aldose 1-epimerase	Galm	5	5	5	19.9	19.9	19.9	37.798	342	1.7089E-18	1.2196	1.0196	44.529	4	345120000	154940000	190170000
P45376	Aldose reductase	Akr1b1	11	11	11	38.3	38.3	38.3	35.732	316	3.772E-230	1.6179	1.056	46.207	20	1.7731E+10	6335100000	1.1396E+10
Q60590	Alpha-1-acid glycoprotein 1	Orm1	1	1	1	7.2	7.2	7.2	23.895	207	2.3263E-22	2.3167	1.7293	26.97	2	267100000	80297000	186810000
P07758	Alpha-1-antitrypsin 1-1	Serpina1a	10	4	4	31	16.5	16.5	46.002	413	0	2.2566	1.8243	16.311	9	1.0531E+10	3451000000	7079800000
P22599	Alpha-1-antitrypsin 1-2	Serpina1b	11	4	3	30.8	13.8	8.5	45.974	413	0	1.9566	1.4378	26.859	20	3124800000	1052400000	2072400000
Q00897	Alpha-1-antitrypsin 1-4	Serpina1d	13	13	6	32.2	32.2	15.3	45.998	413	0	2.028	1.6199	55.06	31	2.0789E+10	8444200000	1.2345E+10
Q00898	Alpha-1-antitrypsin 1-5	Serpina1e	9	4	4	31.2	16.7	16.7	45.891	413	0	1.6288	1.3438	27.274	4	356660000	139260000	217410000
Q61234	Alpha-1-syntrophin	Snta1	6	6	6	20.7	20.7	20.7	53.664	503	9.5156E-98	0.71186	0.41873	27.604	9	1080500000	642480000	438010000
Q61247	Alpha-2-antiplasmin	Serpinf2	4	4	4	10.6	10.6	10.6	54.971	491	5.6827E-73	1.9254	1.1762	33.916	4	332760000	103820000	228950000
P29699	Alpha-2-HS-glycoprotein	Ahsg	6	6	6	25.8	25.8	25.8	37.325	345	0	1.9386	1.1739	27.569	13	3500700000	1198900000	2301900000
D3YW52	Alpha-2-macroglobulin	Pzp	27	27	27	28.3	28.3	28.3	167.28	1507	0	1.9043	1.2878	52.041	40	7887400000	2803100000	5084300000
P55302	Alpha-2-macroglobulin receptor-associated protein	Lrpap1	5	5	5	16.7	16.7	16.7	42.215	360	3.7862E-20	1.9211	1.3229	40.25	6	649590000	201350000	448240000
Q7TPR4	Alpha-actinin-1	Actn1	17	9	5	24	14	8.7	103.07	892	3.171E-123	0.44587	0.42796	75.528	9	647290000	488940000	158350000
Q9JI91	Alpha-actinin-2	Actn2	28	28	20	40.9	40.9	31	103.83	894	0	0.23288	0.16285	76.483	32	4152300000	3146400000	1006000000
P57780	Alpha-actinin-4	Actn4	15	5	4	20.2	7.6	6.4	104.98	912	3.853E-121	0.37436	0.42942	50.682	5	231630000	159070000	72568000
Q9QYC0	Alpha-adducin	Add1	7	7	7	15.6	15.6	15.6	80.646	735	2.0894E-21	1.1483	0.88726	43.786	8	450460000	201020000	249430000
Q9DBF1	Alpha-aminoadipic semialdehyde dehydrogenase	Aldh7a1	7	7	7	19.3	19.3	19.3	58.861	539	1.4538E-88	0.68395	0.5971	18.61	10	796460000	471480000	324980000
P61164	Alpha-centractin	Actr1a	4	4	3	18.4	18.4	13.3	42.613	376	9.2371E-12	0.6217	0.71314	49.023	3	52418000	29786000	22632000
P23927	Alpha-crystallin B chain	Cryab	7	7	7	45.1	45.1	45.1	20.069	175	2.7727E-84	0.88578	0.57794	56.516	20	2348200000	1484000000	864140000
P60840	Alpha-endosulfine	Ensa	3	3	3	33.1	33.1	33.1	13.335	121	7.6224E-08	2.5073	2.876	65.903	3	438910000	125390000	313520000
P17182	Alpha-enolase	Eno1	14	12	7	50.5	47.2	27	47.14	434	7.233E-293	1.5996	1.2693	70.87	20	8319000000	4211900000	4107100000
Q91W89	Alpha-mannosidase 2C1	Man2c1	4	4	4	5.3	5.3	5.3	115.69	1039	3.1671E-29	0.72933	0.67589	25.548	5	171710000	99970000	71740000
O09174	Alpha-methylacyl-CoA racemase	Amacr	3	3	3	11.3	11.3	11.3	41.704	381	7.6311E-20	1.0739	0.97625	32.272	7	346360000	158810000	187550000
Q9QWR8	Alpha-N-acetylgalactosaminidase	Naga	3	3	3	8.9	8.9	8.9	47.234	415	3.3144E-14	0.40492	0.32928	46.445	3	199830000	150190000	49636000
D3YUT2	Alpha-protein kinase 3	Alpk3	2	2	2	1.5	1.5	1.5	180.11	1680	0.0074186	0.33716	0.22721	149.1	2	182340000	169930000	12406000
P82350	Alpha-sarcoglycan	Sgca	5	5	5	15.8	15.8	15.8	43.286	387	3.6202E-19	0.59791	0.44852	53.755	5	231300000	147360000	83935000
Q9DB05	Alpha-soluble NSF attachment protein	Napa	3	3	3	14.9	14.9	14.9	33.189	295	1.4885E-15	1.5637	0.84119	49.207	5	163220000	60459000	102760000
O55042	Alpha-synuclein	Snca	5	5	5	43.6	43.6	43.6	14.485	140	1.2268E-47	2.4082	1.9606	45.959	8	912970000	285200000	627770000
Q8BW75	Amine oxidase [flavin-containing] B	Maob	2	2	2	7.5	7.5	7.5	58.557	520	3.2736E-06	0.74996	0.53105	31.71	2	68456000	44657000	23799000
Q3UZG4	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	Aimp1	2	2	2	13.5	13.5	13.5	35.166	319	2.3248E-86	1.0624	0.7907	5.2503	3	420270000	203340000	216920000
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	Aimp2	3	3	3	19.4	19.4	19.4	35.377	320	1.692E-104	0.6504	0.49981	14.365	4	94235000	56715000	37520000
Q99JW2	Aminoacylase-1	Acy1	6	6	6	22.5	22.5	22.5	45.78	408	1.119E-151	1.3301	1.0391	39.419	7	352270000	133080000	219180000
Q8VCT3	Aminopeptidase B	Rnpep	11	11	11	22.9	22.9	22.9	72.415	650	2.2292E-59	0.98433	0.73287	45.237	12	806360000	410770000	395590000
P97449	Aminopeptidase N	Anpep	5	5	5	6.9	6.9	6.9	109.65	966	4.1427E-56	1.2227	0.92245	49.175	6	164880000	76771000	88104000
O08739	AMP deaminase 3	Ampd3	5	5	5	6.3	6.3	6.3	88.651	766	1.8441E-08	0.30313	0.24813	45.346	4	244940000	189430000	55503000
Q8WTY4	Anamorsin	Ciapin1	7	7	7	32.4	32.4	32.4	33.429	309	1.7613E-56	2.5476	1.5922	131.9	8	2022300000	654130000	1368200000
P09470	Angiotensin-converting enzyme	Ace	6	6	6	5.2	5.2	5.2	150.92	1312	2.4223E-15	1.0752	0.7988	31.647	6	287330000	145290000	142040000
S4R291	Ankyrin-2	Ank2	18	18	15	7.5	7.5	6.5	432.25	3954	0	0.72029	0.46593	32.351	18	841420000	485420000	356000000
F8WIT2	Annexin	Anxa6	28	1	1	48.3	3.6	3.6	75.288	667	0	1.8676	1.4926	18.484	3	256090000	83777000	172310000
P10107	Annexin A1	Anxa1	14	14	14	52	52	52	38.734	346	1.505E-198	1.7889	1.283	32.071	17	2043600000	789950000	1253600000
P97384	Annexin A11	Anxa11	11	11	11	25.8	25.8	25.8	54.079	503	3.578E-183	1.3472	0.79428	41.667	15	2243400000	1004600000	1238800000
P07356	Annexin A2	Anxa2	18	18	18	57.5	57.5	57.5	38.676	339	0	1.4822	1.0963	41.041	30	6978100000	2820900000	4157300000
O35639	Annexin A3	Anxa3	9	9	9	26.3	26.3	26.3	36.384	323	4.4976E-90	1.5937	1.2175	37.423	12	1259800000	477490000	782310000
P97429	Annexin A4	Anxa4	9	9	9	29.5	29.5	29.5	35.915	319	5.155E-79	1.0152	0.74246	36.933	14	1569500000	719080000	850410000
P48036	Annexin A5	Anxa5	17	17	17	53.9	53.9	53.9	35.752	319	0	1.726	1.4009	59.763	30	1.1697E+10	4660400000	7036400000
P14824	Annexin A6	Anxa6	29	29	2	48.7	48.7	5.5	75.884	673	0	1.9262	1.3134	41.996	48	1.7311E+10	5900500000	1.141E+10
Q07076	Annexin A7	Anxa7	7	7	7	17.1	17.1	17.1	49.925	463	3.3859E-91	0.91322	0.66512	27.68	9	1210400000	596510000	613930000
P32261	Antithrombin-III	Serpinc1	11	11	11	29.2	29.2	29.2	52.003	465	5.1908E-74	1.8611	1.388	57.368	12	3470800000	1035500000	2435300000
O35643	AP-1 complex subunit beta-1	Ap1b1	17	17	9	24.7	24.7	15.2	103.93	943	6.6368E-77	0.7682	0.55544	35.473	14	1175100000	712500000	462570000
P35585	AP-1 complex subunit mu-1	Ap1m1	2	2	2	6.9	6.9	6.9	48.542	423	2.2259E-05	0.68966	0.51706	8.8786	4	186930000	106410000	80520000
P17426	AP-2 complex subunit alpha-1	Ap2a1	11	6	6	15.7	8.4	8.4	107.66	977	8.2844E-46	0.65005	0.53559	61.992	5	283240000	129880000	153360000
P17427	AP-2 complex subunit alpha-2	Ap2a2	15	15	10	22	22	14.4	104.02	938	4.0334E-50	0.68055	0.47908	40.164	13	603670000	338500000	265170000
H3BIY9	AP-2 complex subunit beta	Ap2b1	13	5	5	17.1	7.5	7.5	104.83	942	1.737E-140	0.58057	0.36526	32.525	6	704170000	445230000	258940000
P84091	AP-2 complex subunit mu	Ap2m1	6	6	6	13.8	13.8	13.8	49.654	435	1.7393E-31	0.3887	0.31491	40.087	6	369630000	258480000	111150000
Q3UHJ0	AP2-associated protein kinase 1	Aak1	8	8	8	15.2	15.2	15.2	103.35	959	5.5216E-28	1.7585	1.4388	51.438	8	577090000	237370000	339710000
Q9Z1T1	AP-3 complex subunit beta-1	Ap3b1	3	3	3	3.8	3.8	3.8	122.74	1105	7.6285E-19	0.85108	0.54499	130.19	3	367810000	127510000	240300000
O54774	AP-3 complex subunit delta-1	Ap3d1	3	3	3	5.2	5.2	5.2	135.08	1199	9.6059E-98	0.50059	0.34943	119.51	4	354650000	202930000	151710000
Q00623	Apolipoprotein A-I	Apoa1	8	8	8	34.5	34.5	34.5	30.615	264	6.2853E-45	0.90314	0.69722	40.146	8	4598900000	2142300000	2456600000
P06728	Apolipoprotein A-IV	Apoa4	4	4	4	13.4	13.4	13.4	45.029	395	5.7577E-07	3.0361	1.9616	71.842	4	155930000	54367000	101560000
O35841	Apoptosis inhibitor 5	Api5	3	3	3	7.5	7.5	7.5	56.784	504	1.3354E-08	1.024	0.97327	53.182	3	198870000	70385000	128480000
Q9EPB4	Apoptosis-associated speck-like protein containing a CARD	Pycard	2	2	2	16.6	16.6	16.6	21.458	193	1.0879E-22	2.6287	2.0579	16.374	5	250360000	73598000	176770000
Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial	Aifm1	9	9	9	18.3	18.3	18.3	66.765	612	5.1767E-62	0.81678	0.61045	112.17	11	2798700000	2354000000	444660000
Q02013	Aquaporin-1	Aqp1	1	1	1	7.4	7.4	7.4	28.793	269	5.765E-124	0.99475	0.78214	11.599	3	76033000	40823000	35209000
Q8K2K6	Arf-GAP domain and FG repeat-containing protein 1	Agfg1	4	4	4	11.8	11.8	11.8	58.042	561	2.995E-59	1.8379	1.1064	66.844	5	214600000	56662000	157930000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9D0I9	Arginine--tRNA ligase, cytoplasmic	Rars	10	10	10	20.3	20.3	20.3	75.673	660	1.8553E-54	0.47786	0.38808	56.569	11	670950000	435510000	235440000
Q9D7A8	Armadillo repeat-containing protein 1	Armc1	2	2	2	12.8	12.8	12.8	31.246	282	1.5657E-08	1.4912	1.0799	108.86	2	179670000	88702000	90963000
Q91WU5	Arsenite methyltransferase	As3mt	10	10	10	35.1	35.1	35.1	41.793	376	6.001E-148	2.6126	1.7138	31.765	15	2909200000	915490000	1993800000
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	Nars	7	7	7	15.7	15.7	15.7	64.279	559	1.0211E-15	0.83353	0.57962	36.481	9	676300000	379810000	296490000
P05201	Aspartate aminotransferase, cytoplasmic	Got1	20	20	20	63.2	63.2	63.2	46.247	413	0	1.2785	0.82648	47.886	59	8.5405E+10	3.9398E+10	4.6007E+10
P05202	Aspartate aminotransferase, mitochondrial	Got2	20	20	20	59.3	59.3	59.3	47.411	430	0	0.81739	0.63067	51.4	57	6.5869E+10	3.636E+10	2.951E+10
Q922B2	Aspartate--tRNA ligase, cytoplasmic	Dars	16	16	16	36.9	36.9	36.9	57.147	501	0	0.86035	0.60108	67.638	15	3135700000	1673100000	1462600000
Q8BIP0	Aspartate--tRNA ligase, mitochondrial	Dars2	4	4	4	5.5	5.5	5.5	74.101	653	9.9752E-10	0.93731	0.90205	39.978	2	184330000	84696000	99637000
Q91XE4	Aspartoacylase-2	Acy3	7	7	7	33.3	33.3	33.3	35.286	318	6.0738E-55	1.2567	0.78029	34.362	11	1312100000	595860000	716190000
Q9Z2W0	Aspartyl aminopeptidase	Dnpep	8	8	8	25.8	25.8	25.8	52.206	473	4.6693E-38	0.65382	0.48739	54.66	13	662800000	380640000	282160000
Q62048	Astrocytic phosphoprotein PEA-15	Pea15	3	3	3	22.3	22.3	22.3	15.054	130	1.3809E-24	2.8597	1.6455	21.422	6	249380000	63619000	185760000
P28658	Ataxin-10	Atxn10	5	5	5	11.6	11.6	11.6	53.706	475	5.3509E-14	1.1101	0.72258	35.823	3	1745600000	786900000	958700000
Q7TQH0	Ataxin-2-like protein	Atxn2l	3	3	3	4.8	4.8	4.8	110.65	1049	4.1425E-09	2.4118	2.0322	31.413	3	125670000	38654000	87019000
Q91YH5	Atlastin-3	Atl3	2	2	2	5	5	5	60.574	541	0.010967	0.99077	1.068	182.56	2	34508000	15143000	19364000
H3BLL2	ATP synthase mitochondrial F1 complex assembly factor 1	Atpaf1	9	9	9	31.3	31.3	31.3	38.796	348	1.4563E-57	2.03	1.185	43.507	10	1424000000	478840000	945190000
Q91YY4	ATP synthase mitochondrial F1 complex assembly factor 2	Atpaf2	6	6	6	29.1	29.1	29.1	33.289	289	2.4513E-61	1.3649	0.92362	24.594	7	1071700000	448640000	623100000
Q03265	ATP synthase subunit alpha, mitochondrial	Atp5a1	22	22	22	49.7	49.7	49.7	59.752	553	0	0.87675	0.64387	44.684	113	6.8957E+10	3.312E+10	3.5837E+10
Q9CQQ7	ATP synthase subunit b, mitochondrial	Atp5f1	6	6	6	25.8	25.8	25.8	28.948	256	1.2352E-22	0.514	0.43889	134.62	5	947190000	585140000	362050000
P56480	ATP synthase subunit beta, mitochondrial	Atp5b	26	26	26	60.5	60.5	60.5	56.3	529	0	1.7168	1.2142	46.681	189	7.749E+10	2.8422E+10	4.9068E+10
Q9DCX2	ATP synthase subunit d, mitochondrial	Atp5h	11	11	11	71.4	71.4	71.4	18.749	161	1.19E-281	1.3122	1.0918	41.894	17	2419000000	1075500000	1343500000
Q9D3D9	ATP synthase subunit delta, mitochondrial	Atp5d	3	3	3	28.6	28.6	28.6	17.6	168	1.8294E-38	1.8843	1.4496	36.77	7	1.9015E+10	6318200000	1.2697E+10
Q06185	ATP synthase subunit e, mitochondrial	Atp5i	1	1	1	16.9	16.9	16.9	8.2355	71	3.4614E-35	2.9338	2.1473	3.4435	2	1048600000	287350000	761200000
P56382	ATP synthase subunit epsilon, mitochondrial	Atp5e	2	2	2	30.8	30.8	30.8	5.8378	52	0.00063627	1.1186	1.204	5.0252	2	1875500000	950110000	925390000
P56135	ATP synthase subunit f, mitochondrial	Atp5j2	2	2	2	26.1	26.1	26.1	10.344	88	2.2973E-05	0.58007	0.43389	20.979	5	166230000	103550000	62680000
Q9CPQ8	ATP synthase subunit g, mitochondrial	Atp5l	1	1	1	14.6	14.6	14.6	11.424	103	1.5022E-19	0.41532	0.22289	1.2727	2	1352600000	993180000	359430000
Q91VR2	ATP synthase subunit gamma, mitochondrial	Atp5c1	6	6	6	21.5	21.5	21.5	32.886	298	3.1191E-63	0.56505	0.38652	109.41	17	4731500000	3936100000	795460000
Q9DB20	ATP synthase subunit O, mitochondrial	Atp5o	9	9	9	53.5	53.5	53.5	23.363	213	1.457E-303	0.46971	0.34442	38.492	23	2962600000	2122400000	840240000
Q9CRA7	ATP synthase subunit s, mitochondrial	Atp5s	2	2	2	10	10	10	23.275	200	1.2661E-09	0.47572	0.57547	5.5074	2	118990000	77906000	41080000
P97450	ATP synthase-coupling factor 6, mitochondrial	Atp5j	5	5	5	38	38	38	12.496	108	4.144E-190	2.0644	1.4651	46.316	7	1614300000	610720000	1003600000
O54984	ATPase Asna1	Asna1	4	4	4	15.5	15.5	15.5	38.822	348	1.7566E-19	0.87738	0.52755	12.929	3	322210000	182390000	139810000
Q9CXJ4	ATP-binding cassette sub-family B member 8, mitochondrial	Abcb8	2	2	2	4.5	4.5	4.5	77.999	717	1.0291E-15	0.9779	0.72467	123.15	2	57654000	24269000	33385000
P61222	ATP-binding cassette sub-family E member 1	Abce1	4	4	4	9.5	9.5	9.5	67.314	599	4.1077E-24	0.29264	0.2725	120.35	4	444030000	381080000	62957000
Q6P542	ATP-binding cassette sub-family F member 1	Abcf1	5	5	5	8	8	8	94.944	837	7.314E-34	0.57829	0.68107	95.783	4	179810000	83634000	96179000
Q99LE6	ATP-binding cassette sub-family F member 2	Abcf2	2	2	2	4.5	4.5	4.5	71.781	628	6.7055E-13	0.63306	0.44314	32.84	2	104320000	67855000	36463000
Q3V117	ATP-citrate synthase	Acly	7	7	7	8.4	8.4	8.4	120.79	1101	3.5225E-21	0.35517	0.32987	36.771	7	220810000	153410000	67395000
K3W4M4	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	Carkd	4	4	4	19.5	19.5	19.5	38.911	365	1.786E-107	1.0329	0.69089	16.687	5	1109900000	564690000	545180000
Q9JHS4	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	Clpx	3	3	3	6.2	6.2	6.2	69.228	634	1.9479E-08	1.5904	1.5957	35.523	4	262400000	104990000	157410000
E9QNN1	ATP-dependent RNA helicase A	Dhx9	4	4	4	4.3	4.3	4.3	149.69	1384	3.6903E-30	0.59524	0.47648	73.632	4	138350000	85570000	52781000
Q91VR5	ATP-dependent RNA helicase DDX1	Ddx1	8	8	8	13.1	13.1	13.1	82.499	740	1.2974E-38	0.55845	0.335	45.895	7	282800000	210920000	71878000
Q8BZY3	ATP-dependent RNA helicase DDX19A	Ddx19b	2	2	2	4.3	4.3	4.3	55.674	494	0.011156	1.0688	0.89376	162.5	2	28259000	16369000	11890000
Q62167	ATP-dependent RNA helicase DDX3X	Ddx3x	2	2	2	4.7	4.7	4.7	73.101	662	8.443E-07	0.41526	0.30534	88.941	3	111290000	80185000	31105000
Q80YD1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	Supv3l1	6	6	6	9.2	9.2	9.2	87.004	779	3.089E-15	1.2511	0.8798	86.2	3	175460000	100860000	74599000
Q9JLV1	BAG family molecular chaperone regulator 3	Bag3	14	14	14	41.9	41.9	41.9	61.859	577	1.149E-201	1.6798	1.3347	33.611	20	3633500000	1384100000	2249500000
O70318	Band 4.1-like protein 2	Epb41l2	8	8	8	14.7	14.7	14.7	109.94	988	4.102E-114	1.7102	1.3294	28.403	6	174710000	69542000	105170000
Q9R069	Basal cell adhesion molecule	Bcam	6	6	6	16.4	16.4	16.4	67.669	622	8.028E-221	1.7641	1.6719	160.11	5	978290000	165040000	813250000
E9PZ16	Basement membrane-specific heparan sulfate proteoglycan core protein	Hspg2	60	60	60	24.3	24.3	24.3	469.78	4383	0	0.51024	0.37637	59.812	89	1.4413E+10	7118600000	7294400000
Q9CQC6	Basic leucine zipper and W2 domain-containing protein 1	Bzw1	4	4	2	7.4	7.4	4.1	48.043	419	2.0446E-08	1.2217	1.0462	16.998	4	175370000	74640000	100730000
P18572	Basigin	Bsg	7	7	7	20.3	20.3	20.3	42.444	389	4.5205E-86	1.6268	1.3459	35.77	9	989510000	396770000	592740000
P59017	Bcl-2-like protein 13	Bcl2l13	8	8	8	27.4	27.4	27.4	46.719	434	1.067E-218	1.0826	0.77196	46.415	12	1370600000	650560000	720050000
Q01339	Beta-2-glycoprotein 1	Apoh	4	4	4	18.3	18.3	18.3	38.618	345	3.9269E-12	1.9764	1.7734	76.605	6	264210000	98923000	165280000
J3QNU6	Beta-arrestin-1	Arrb1	2	2	2	7.6	7.6	7.6	47.106	419	2.8259E-07	1.0223	0.7391	8.4234	2	45485000	19857000	25628000
P21550	Beta-enolase	Eno3	17	17	14	44.2	44.2	36.9	47.024	434	0	1.6276	1.286	38.292	34	2.603E+10	9481400000	1.6549E+10
P23780	Beta-galactosidase	Glb1	7	7	7	13.1	13.1	13.1	73.12	647	6.6368E-25	0.14973	0.12196	39.928	6	523450000	462790000	60663000
P12265	Beta-glucuronidase	Gusb	5	5	5	8.6	8.6	8.6	74.194	648	4.0751E-19	0.5834	0.44558	101.22	3	176790000	113820000	62972000
P29416	Beta-hexosaminidase subunit alpha	Hexa	3	3	3	7.2	7.2	7.2	60.612	528	2.8933E-18	0.26806	0.17238	21.701	2	110890000	87878000	23008000
P20060	Beta-hexosaminidase subunit beta	Hexb	4	4	4	9.7	9.7	9.7	61.115	536	1.1428E-05	0.31626	0.22488	13.778	3	133540000	104540000	29005000
Q8K2I4	Beta-mannosidase	Manba	4	4	4	5.2	5.2	5.2	100.83	879	1.9531E-09	0.39372	0.42474	50.883	2	101370000	72458000	28917000
Q9ES46	Beta-parvin	Parvb	9	9	8	31.8	31.8	28.2	41.669	365	1.5529E-76	1.528	1.363	36.413	9	593780000	203380000	390400000
P82349	Beta-sarcoglycan	Sgcb	3	3	3	15.3	15.3	15.3	34.872	320	1.3341E-11	0.5659	0.54598	28.492	2	72325000	50252000	22073000
Q8VBT1	Beta-taxilin	Txlnb	13	13	13	27.7	27.7	27.7	77.206	685	7.449E-302	1.9144	1.9906	111.06	15	3302800000	1317200000	1985600000
Q9DBL7	Bifunctional coenzyme A synthase	Coasy	2	2	2	5.3	5.3	5.3	62.022	563	1.1454E-10	1.3231	0.89651	74.116	2	116000000	53984000	62020000
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	Eprs	30	30	30	28.4	28.4	28.4	170.08	1512	0	0.70371	0.49988	63.729	37	4045200000	2241800000	1803500000
G5E8N7	Bifunctional polynucleotide phosphatase/kinase	Pnkp	2	2	2	6.7	6.7	6.7	57.214	522	2.4832E-26	2.0717	1.4934	21.875	2	136350000	41467000	94880000
Q9EQQ9	Bifunctional protein NCOAT	Mgea5	4	4	4	7.2	7.2	7.2	103.16	916	2.47E-12	0.76351	0.54371	97.512	3	135150000	71793000	63357000
Q9CWJ9	Bifunctional purine biosynthesis protein PURH	Atic	7	7	7	18.8	18.8	18.8	64.217	592	0	1.3042	0.96603	40.32	12	1115800000	407350000	708470000
Q9CY64	Biliverdin reductase A	Blvra	5	5	5	25.8	25.8	25.8	33.524	295	3.2237E-44	1.1334	0.80222	38.348	6	779270000	414610000	364660000
P56380	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	Nudt2	5	5	5	50.3	50.3	50.3	16.989	147	1.063E-103	2.0378	1.2589	15.415	5	246690000	101720000	144970000
P15327	Bisphosphoglycerate mutase	Bpgm	6	6	6	32	32	32	29.978	259	1.32E-120	1.2099	0.76594	30.422	7	923690000	416550000	507130000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8R016	Bleomycin hydrolase	Blmh	4	4	4	13.8	13.8	13.8	52.511	455	1.5057E-34	1.0598	0.82334	18.062	7	842600000	429740000	412850000
Q9ES83	Blood vessel epicardial substance	Bves	2	2	2	5.6	5.6	5.6	41.015	358	0.0023283	0.4744	0.44966	187.28	2	181680000	85286000	96398000
Q9D8S9	BolA-like protein 1	Bola1	5	5	5	45.3	45.3	45.3	14.379	137	4.5789E-25	2.1469	1.638	43.473	4	574680000	200160000	374520000
E9PX89	BolA-like protein 3	Bola3	4	4	4	32.4	32.4	32.4	15.231	136	9.3494E-83	2.9914	2.0031	33.593	6	825220000	231120000	594100000
Q91XV3	Brain acid soluble protein 1	Basp1	3	3	3	26.1	26.1	26.1	22.086	226	5.2236E-19	2.3951	2.0111	20.795	3	51464000	17356000	34108000
Q9D023	Brain protein 44	Brp44	4	4	3	26.8	26.8	26.8	14.286	127	2.829E-09	0.43036	0.49243	75.565	4	929220000	698790000	230430000
E9Q0V4	Brain protein 44-like protein	Brp44l	1	1	1	4.8	4.8	4.8	18.36	167	0.043843	1.0347	0.91377	19.754	2	352350000	167280000	185060000
O35855	Branched-chain-amino-acid aminotransferase, mitochondrial	Bcat2	16	16	16	43	43	43	44.127	393	0	1.1608	0.74382	71.922	33	7587700000	3468200000	4119500000
D3Z7P0	BRCA1-A complex subunit BRE	Bre	2	2	2	7	7	7	43.749	385	8.5675E-07	0.55431	0.53165	23.396	3	108470000	68281000	40184000
Q8BXV2	BRI3-binding protein	Bri3bp	1	1	1	5.5	5.5	5.5	28.263	253	0.00011481	0.56601	0.57949	7.4564	2	22906000	13670000	9235800
Q3TCJ1	BRISC complex subunit Abro1	Fam175b	1	1	1	3.1	3.1	3.1	46.942	415	3.7207E-16	0.40076	0.4347	23.549	2	36021000	24757000	11264000
Q3UH70	Bromodomain-containing protein 4	Brd4	2	2	2	1.7	1.7	1.7	156.05	1401	0.0003746	1.77	1.1726	25.84	2	657790000	270760000	387020000
Q6WVG3	BTB/POZ domain-containing protein KCTD12	Kctd12	5	5	4	20.8	20.8	17.4	35.892	327	6.2076E-86	1.236	0.89166	106.94	4	344300000	164600000	179700000
Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	Mthfd1	5	5	5	6.6	6.6	6.6	101.2	935	1.1833E-74	1.1795	1.0559	30.469	3	194550000	78034000	116520000
Q9WTR5	Cadherin-13	Cdh13	6	6	6	12	12	12	78.185	714	4.749E-83	2.8389	1.7373	16.613	9	2711500000	639070000	2072400000
P15116	Cadherin-2	Cdh2	3	3	3	7.5	7.5	7.5	99.795	906	4.9789E-85	1.816	1.113	64.389	7	880760000	237800000	642960000
Q63810	Calcineurin subunit B type 1	Ppp3r1	2	2	2	21.2	21.2	21.2	19.3	170	4.7188E-07	2.7185	2.0617	7.4717	3	164170000	43438000	120730000
Q8BFS6	Calcineurin-like phosphoesterase domain-containing protein 1	Cpped1	5	5	5	31.7	31.7	31.7	35.247	312	1.741E-149	2.3411	1.9009	20.923	6	505660000	178510000	327140000
Q91YS8	Calcium/calmodulin-dependent protein kinase type 1	Camk1	3	3	3	15	15	15	41.624	374	1.7554E-09	1.8451	0.99132	187.21	3	451960000	315830000	136140000
E9Q1T1	Calcium/calmodulin-dependent protein kinase type II subunit delta	Camk2d	4	2	2	12.9	7.1	7.1	60.004	533	4.3937E-70	1.2713	0.81801	20.71	5	573400000	230900000	342500000
Q923T9	Calcium/calmodulin-dependent protein kinase type II subunit gamma	Camk2g	6	6	4	16.4	16.4	10.6	59.606	529	4.5957E-76	0.90672	0.79864	22.39	8	865280000	448420000	416870000
Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1	Slc25a12	11	11	9	22.3	22.3	19.8	74.569	677	5.861E-159	0.61447	0.42413	30.621	20	2558100000	1661300000	896770000
Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	Slc25a13	11	9	9	21.6	19.1	19.1	74.466	676	5.6029E-64	0.52869	0.54943	23.177	9	1185600000	770440000	415200000
Q06138	Calcium-binding protein 39	Cab39	4	4	4	13.2	13.2	13.2	39.842	341	3.4387E-10	1.8454	1.2216	47.688	3	117790000	48475000	69314000
Q9DB16	Calcium-binding protein 39-like	Cab39l	1	1	1	3.3	3.3	3.3	39.105	337	7.4285E-05	1.3007	1.06	6.214	2	61352000	26645000	34707000
Q8K1N1	Calcium-independent phospholipase A2-gamma	Pnpla8	2	2	2	4.1	4.1	4.1	87.38	776	6.9767E-05	0.97771	0.66068	197.33	2	30994000	19936000	11058000
Q9CXW3	Calcyclin-binding protein	Cacybp	2	2	2	13.5	13.5	13.5	26.51	229	0.001175	1.4104	1.0562	109.79	2	61411000	24078000	37333000
Q3UKW2	Calmodulin	Calm1	4	4	4	21.3	21.3	21.3	21.56	197	9.183E-68	2.2972	1.7128	38.401	4	2612600000	632320000	1980300000
P35564	Calnexin	Canx	12	12	12	26.2	26.2	26.2	67.277	591	7.857E-157	0.6649	0.529	69.705	14	967220000	601580000	365640000
O88456	Calpain small subunit 1	Capns1	4	4	4	25.3	25.3	25.3	28.463	269	0	1.5076	1.1151	10.552	7	706860000	283190000	423670000
O35350	Calpain-1 catalytic subunit	Capn1	20	20	20	35.3	35.3	35.3	82.105	713	6.694E-124	0.66846	0.46388	104.89	20	1444600000	741350000	703280000
O08529	Calpain-2 catalytic subunit	Capn2	14	14	14	22	22	22	79.871	700	4.0272E-72	0.79931	0.55547	29.394	15	1587000000	874040000	713000000
P51125	Calpastatin	Cast	11	11	11	29.7	29.7	29.7	84.921	788	0	2.0573	1.4157	66.412	14	1016300000	317190000	699100000
Q08091	Calponin-1	Cnn1	2	2	2	8.1	8.1	8.1	33.355	297	1.8177E-12	2.9498	2.7228	19.992	3	540450000	161500000	378960000
Q9DAW9	Calponin-3	Cnn3	4	4	4	14.8	14.8	14.8	36.428	330	6.6737E-54	1.6835	1.5934	32.064	4	124180000	38537000	85643000
P14211	Calreticulin	Calr	14	14	14	39.7	39.7	39.7	47.994	416	2.673E-175	1.3865	1.2389	68.188	16	7617600000	2284500000	5333100000
F6QYE1	Calsequestrin-2	Casq2	6	6	6	16	16	16	48.435	418	3.5981E-73	0.64052	0.37118	41.942	10	1630800000	991730000	639030000
O35887	Calumenin	Calu	2	2	2	7.3	7.3	7.3	37.063	315	3.9156E-05	1.0815	1.0712	22.286	2	142710000	69317000	73390000
P05132	cAMP-dependent protein kinase catalytic subunit alpha	Prkaca	7	7	1	19.1	19.1	4.6	40.57	351	1.368E-191	0.41186	0.3315	56.974	9	1035500000	715230000	320250000
Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit	Prkar1a	11	11	11	28.1	28.1	28.1	43.185	381	1.0517E-78	1.2648	0.88664	97.457	12	3603500000	1092700000	2510900000
Q8K1M3	cAMP-dependent protein kinase type II-alpha regulatory subunit	Prkar2a	8	8	8	30.6	30.6	30.6	45.589	402	6.854E-138	1.055	0.74764	54.302	13	999990000	450490000	549500000
F8WIA1	CAP-Gly domain-containing linker protein 1	Clip1	23	23	13	20.3	20.3	11.1	161.23	1437	0	2.8853	2.209	46.011	20	2405200000	696540000	1708600000
Q60865	Caprin-1	Caprin1	3	3	3	6.5	6.5	6.5	78.168	707	4.7624E-36	1.3041	0.8463	54.44	4	304210000	127250000	176960000
Q3UZA1	CapZ-interacting protein	Rcsd1	6	6	6	29.6	29.6	29.6	44.114	412	5.269E-61	4.1462	3.7683	73.662	4	847250000	339090000	508160000
P13634	Carbonic anhydrase 1	Ca1	7	7	7	41.8	41.8	41.8	28.33	261	1.688E-86	2.2305	1.5862	35.24	9	2467700000	817260000	1650400000
P00920	Carbonic anhydrase 2	Ca2	9	9	9	45.4	45.4	45.4	29.032	260	1.57E-186	1.2627	0.85627	30.645	21	4311000000	1987400000	2323600000
P16015	Carbonic anhydrase 3	Ca3	6	6	6	36.5	36.5	36.5	29.366	260	1.3945E-35	0.7	0.489	24.335	7	419550000	232040000	187510000
P48758	Carbonyl reductase [NADPH] 1	Cbr1	9	9	9	48	48	48	30.641	277	1.925E-126	1.3939	0.81905	42.06	11	1631900000	641380000	990500000
Q91VT4	Carbonyl reductase family member 4	Cbr4	9	9	9	47.5	47.5	47.5	25.414	236	1.45E-158	0.90866	0.64275	70.655	14	3001100000	1406100000	1595000000
P23953	Carboxylesterase 1C	Ces1c	9	8	5	19.1	16.6	10.1	61.055	554	2.282E-255	2.8269	2.4653	26.321	10	3206500000	1002200000	2204300000
Q8VCT4	Carboxylesterase 1D	Ces1d	9	9	8	25.1	25.1	22.7	61.787	565	1.218E-181	1.7249	1.2267	74.595	17	2699400000	1062200000	1637100000
Q8R1G2	Carboxymethylenebutenolidase homolog	Cmbl	3	3	3	13.5	13.5	13.5	27.902	245	1.3038E-79	1.1416	0.82305	19.91	3	848320000	397840000	450480000
Q9JJN5	Carboxypeptidase N catalytic chain	Cpn1	2	2	2	5.3	5.3	5.3	51.845	457	5.3468E-09	2.7377	1.9542	112.71	2	180930000	31005000	149920000
Q9DBB9	Carboxypeptidase N subunit 2	Cpn2	3	3	3	5.3	5.3	5.3	60.478	547	0.00011034	1.4947	1.4329	30.968	2	101110000	49719000	51396000
Q9WVJ3	Carboxypeptidase Q	Cpq	3	3	3	12.6	12.6	12.6	51.813	470	5.1081E-96	3.0776	2.0218	11.837	3	169100000	43912000	125180000
P47934	Carnitine O-acetyltransferase	Crat	13	13	13	22.8	22.8	22.8	70.839	626	5.449E-182	0.87774	0.65531	40.664	25	6109000000	3375800000	2733200000
Q924X2	Carnitine O-palmitoyltransferase 1, muscle isoform	Cpt1b	11	11	11	15.9	15.9	15.9	88.216	772	0	0.51764	0.39963	27.193	13	1931100000	1317100000	614020000
P52825	Carnitine O-palmitoyltransferase 2, mitochondrial	Cpt2	11	11	11	20.7	20.7	20.7	73.98	658	0	0.57692	0.43178	38.807	18	3558200000	2229100000	1329100000
Q60737	Casein kinase II subunit alpha	Csnk2a1	2	2	2	9	9	9	45.133	391	0.012408	0.73272	0.39456	4.9058	3	238240000	148490000	89754000
E9PY58	Caseinolytic peptidase B protein homolog	Clpb	4	4	4	6.1	6.1	6.1	79.509	707	6.7317E-10	0.75352	0.45644	9.7371	3	216290000	126650000	89646000
O08738	Caspase-6	Casp6	2	2	2	7.6	7.6	7.6	31.595	276	0.0005344	0.94676	1.1385	132.27	3	223430000	165260000	58172000
Q91WM2	Cat eye syndrome critical region protein 5 homolog	Cecr5	4	4	4	15.5	15.5	15.5	46.306	419	2.1226E-71	0.73652	0.57945	85.617	4	206330000	162890000	43437000
P24270	Catalase	Cat	12	12	12	27.7	27.7	27.7	59.795	527	2.196E-149	1.042	0.6729	67.356	21	3174600000	1130200000	2044500000
O88587	Catechol O-methyltransferase	Comt	6	6	6	31.3	31.3	31.3	29.486	265	1.0002E-14	1.1495	0.87483	57.523	6	159940000	81447000	78490000
P26231	Catenin alpha-1	Ctnna1	8	8	6	12.6	12.6	9.7	100.11	906	2.848E-110	1.419	1.1438	64.343	8	404000000	172500000	231510000
Q02248	Catenin beta-1	Ctnnb1	4	2	2	4.5	2.2	2.2	85.47	781	7.1556E-10	0.47827	0.31401	90.747	2	34169000	23867000	10302000
P10605	Cathepsin B	Ctsb	10	10	10	32.7	32.7	32.7	37.279	339	3.691E-282	0.7325	0.566	87.842	20	2676900000	1471600000	1205200000
P18242	Cathepsin D	Ctsd	8	8	8	26.1	26.1	26.1	44.953	410	0	0.60207	0.40186	92.94	7	6009300000	3589300000	2420000000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9WUU7	Cathepsin Z	Ctsz	5	5	5	20.6	20.6	20.6	33.996	306	5.86E-110	0.34343	0.26173	134.33	4	468240000	326840000	141400000
P24668	Cation-dependent mannose-6-phosphate receptor	M6pr	2	2	2	7.9	7.9	7.9	31.172	278	2.2332E-14	1.1681	0.80758	7.5968	3	93657000	46866000	46791000
P49817	Caveolin-1	Cav1	1	1	1	11.8	11.8	11.8	20.538	178	9.6808E-37	1.0871	0.58474	8.7948	2	83675000	42397000	41278000
Q8K1J6	CCA tRNA nucleotidyltransferase 1, mitochondrial	Trnt1	2	2	2	6.9	6.9	6.9	49.895	434	5.1276E-05	0.91822	0.79973	12.968	2	73845000	40181000	33664000
Q9JLQ0	CD2-associated protein	Cd2ap	3	3	3	7.5	7.5	7.5	70.449	637	7.8415E-10	1.5106	1.7786	103.42	4	105560000	59414000	46143000
Q8CJ53	Cdc42-interacting protein 4	Trip10	3	3	3	7.5	7.5	7.5	68.489	603	1.0203E-10	1.7552	1.3435	37.101	3	226130000	86062000	140070000
Q91WS0	CDGSH iron-sulfur domain-containing protein 1	Cisd1	3	3	3	24.1	24.1	24.1	12.097	108	2.2731E-41	0.78979	0.45639	25.603	7	996470000	578220000	418250000
Q8BI72	CDKN2A-interacting protein	Cdkn2aip	1	1	1	3.6	3.6	3.6	59.744	563	4.1744E-13	1.6484	1.3854	11.904	3	65158000	21527000	43630000
P60766	Cell division control protein 42 homolog	Cdc42	2	1	1	14.7	8.9	8.9	21.258	191	0.00038779	0.59106	0.50236	13.012	2	37609000	23667000	13942000
Q8R2Y2	Cell surface glycoprotein MUC18	Mcam	2	2	2	3.7	3.7	3.7	71.545	648	7.2026E-06	2.0958	1.4965	98.003	2	305080000	114890000	190190000
P53996	Cellular nucleic acid-binding protein	Cnbp	2	2	2	15.2	15.2	15.2	19.592	178	3.1517E-53	3.6488	2.9438	37.93	3	1567400000	417190000	1150200000
B2RX88	Centrosome and spindle pole associated protein 1	Cspp1	2	2	2	1.8	1.8	1.8	138.31	1205	0.0031991	0.28022	0.19935	224.88	2	173220000	146260000	26951000
E9PZD8	Ceruloplasmin	Cp	11	11	11	16.9	16.9	16.9	124.21	1086	2.7366E-86	1.5013	1.3828	41.105	10	861270000	394300000	466970000
P0C605	cGMP-dependent protein kinase 1	Prkg1	3	3	3	5.1	5.1	5.1	76.35	671	0.0017125	0.88686	0.7475	45.543	2	86424000	54074000	32349000
Q60936	Chaperone activity of bc1 complex-like, mitochondrial	Adck3	10	10	10	19.8	19.8	19.8	71.742	645	4.778E-164	0.68752	0.51225	76.061	18	2791200000	1671600000	1119600000
Q9D8B3	Charged multivesicular body protein 4b	Chmp4b	3	3	3	14.7	14.7	14.7	24.936	224	8.6252E-37	2.5011	2.2526	80.111	4	427460000	69205000	358250000
Q9Z1Q5	Chloride intracellular channel protein 1	Clic1	5	5	5	27.8	27.8	27.8	27.013	241	8.3401E-52	1.1914	1.0201	16.181	6	489240000	228780000	260460000
Q9QYB1	Chloride intracellular channel protein 4	Clic4	8	8	8	36.8	36.8	36.8	28.729	253	8.049E-160	1.715	1.5715	19.044	12	1.895E+10	8790300000	1.016E+10
Q8BXK9	Chloride intracellular channel protein 5	Clic5	5	5	5	35.9	35.9	35.9	28.287	251	1.0345E-51	1.282	0.90577	20.529	9	754360000	328870000	425490000
Q8VHY0	Chondroitin sulfate proteoglycan 4	Cspg4	7	7	7	5.2	5.2	5.2	252.31	2327	2.5042E-42	1.8495	1.5151	41.75	6	121730000	43010000	78716000
Q8R4N0	Citrate lyase subunit beta-like protein, mitochondrial	Clybl	15	15	15	46.2	46.2	46.2	37.548	338	0	1.3912	1.1724	109.32	19	3788500000	1600500000	2188000000
Q80X68	Citrate synthase	Csl	10	2	2	24.7	4.9	4.9	52.325	466	7.52E-120	1.1627	0.8835	49.202	4	58259000	37621000	20638000
Q9CZU6	Citrate synthase, mitochondrial	Cs	16	16	8	35.3	35.3	15.5	51.736	464	1.498E-172	1.0308	0.72637	46.434	43	9.0536E+10	4.6197E+10	4.4339E+10
K3W4S4	C-Jun-amino-terminal kinase-interacting protein 3	Mapk8ip3	2	1	1	1.3	0.7	0.7	148.64	1345	0.0001353	0.91947	0.67279	18.273	2	18893000	10747000	8146300
Q58A65	C-Jun-amino-terminal kinase-interacting protein 4	Spag9	10	10	9	11.1	11.1	10.5	146.22	1321	2.0694E-49	1.218	1.2023	25.062	11	468190000	212260000	255920000
Q5SXR6	Clathrin heavy chain 1	Cltc	33	33	33	25.5	25.5	25.5	191.98	1679	0	0.31399	0.22043	45.224	39	3800900000	2912300000	888580000
Q5SUH6	Clathrin interactor 1	Clint1	4	4	4	8.6	8.6	8.6	69.758	641	5.0584E-08	1.3966	1.2175	37.978	4	228500000	106420000	122070000
B1AWD9	Clathrin light chain A	Clta	3	3	3	14.5	14.5	14.5	27.061	248	0	0.83066	0.81525	3.0668	2	68659000	39353000	29306000
Q6IRU5	Clathrin light chain B	Cltb	6	6	6	19.7	19.7	19.7	25.171	229	5.3694E-14	1.1915	0.93028	37.277	7	654700000	299860000	354840000
E9QKH0	CLIP-associating protein 1	Clasp1	5	5	4	5.5	5.5	4.3	169.31	1536	3.5779E-44	1.3952	1.1363	47.217	6	185210000	86905000	98308000
Q06890	Clusterin	Clu	4	4	4	11.6	11.6	11.6	51.655	448	4.6301E-47	1.6107	1.3346	21.617	6	310590000	129320000	181260000
Q9CQI6	Coactosin-like protein	Cotl1	3	3	3	30.3	30.3	30.3	15.944	142	9.9168E-35	0.50072	0.47089	92.996	2	342380000	255790000	86592000
Q8BH61	Coagulation factor XIII A chain	F13a1	3	3	3	4.4	4.4	4.4	83.206	732	2.98E-08	0.48639	0.39217	53.638	4	214600000	146970000	67628000
F8WHL2	Coatomer subunit alpha	Copa	2	2	2	2.4	2.4	2.4	139.41	1233	0.0017983	0.26774	0.14903	0.84449	2	159950000	127270000	32682000
O55029	Coatomer subunit beta	Copb2	3	3	3	4.3	4.3	4.3	102.45	905	4.7376E-16	0.27081	0.32605	83.41	2	38931000	30423000	8508300
Q5XJY5	Coatomer subunit delta	Arcn1	5	5	5	15.5	15.5	15.5	57.229	511	5.1384E-14	0.81762	0.5973	67.878	4	138470000	79590000	58880000
Q9QZE5	Coatomer subunit gamma-1	Copg1	3	3	3	6.4	6.4	6.4	97.512	874	8.8574E-14	0.64576	0.5602	17.995	2	21794000	15281000	6513100
P61924	Coatomer subunit zeta-1	Copz1	1	1	1	10.7	10.7	10.7	20.198	177	4.7833E-19	1.1791	0.79042	11.653	3	176840000	82538000	94302000
Q9JHH9	Coatomer subunit zeta-2	Copz2	1	1	1	9.3	9.3	9.3	22.934	205	1.2937E-88	1.0918	0.73083	2.308	2	118310000	62836000	55472000
Q9D273	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	Mmab	4	4	4	18.1	18.1	18.1	26.273	237	1.2048E-80	2.4058	1.8415	47.125	5	831750000	221160000	610590000
F8WGL3	Cofilin-1	Cfl1	6	6	6	30.4	30.4	30.4	24.576	227	6.88E-205	2.9871	2.0302	49.68	7	7201600000	2022600000	5179000000
P45591	Cofilin-2	Cfl2	6	6	6	42.8	42.8	42.8	18.709	166	1.256E-130	1.9119	1.9177	24.61	9	3670300000	1279100000	2391200000
Q8R3Q6	Coiled-coil domain-containing protein 58	Ccdc58	2	2	2	18.8	18.8	18.8	16.665	144	1.2429E-42	1.6285	0.91052	123.69	2	108750000	44512000	64235000
B2RPU8	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	2410018M08Rik	3	3	3	4.5	4.5	4.5	84.266	756	2.1298E-16	2.8387	1.4329	29.753	6	1766100000	530950000	1235200000
Q9CRB9	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	Chchd3	4	4	4	18.1	18.1	18.1	26.334	227	6.903E-14	0.61787	0.3499	56.44	4	325650000	212720000	112930000
Q91W50	Cold shock domain-containing protein E1	Csde1	7	7	7	10.3	10.3	10.3	88.79	798	2.1404E-14	0.95609	0.93675	64.843	5	154540000	83726000	70816000
P02463	Collagen alpha-1(IV) chain	Col4a1	4	4	4	4.4	4.4	4.4	160.68	1669	6.1725E-77	1.1316	0.79174	70.517	3	73307000	25225000	48082000
Q04857	Collagen alpha-1(VI) chain	Col6a1	1	1	1	2.8	2.8	2.8	108.49	1025	1.1876E-26	1.0087	1.2166	9.3119	2	128370000	63812000	64556000
O35206	Collagen alpha-1(XV) chain	Col15a1	10	10	10	9	9	9	140.47	1367	6.1962E-88	1.0882	0.75073	43.448	12	1405200000	621940000	783310000
E9Q6A6	Collagen alpha-6(VI) chain	Col6a6	4	4	4	3	3	3	246.42	2265	8.7928E-33	1.444	1.0792	65.114	4	238040000	105820000	132220000
P01027	Complement C3	C3	37	37	37	26.8	26.8	26.8	186.48	1663	0	0.90702	0.63686	67.254	46	6642100000	3467300000	3174900000
P01029	Complement C4-B	C4b	6	6	6	6	6	6	192.91	1738	2.5375E-79	1.1916	0.98685	69.749	7	539100000	228780000	310310000
P06684	Complement C5	C5	7	7	7	6.1	6.1	6.1	188.88	1680	1.5497E-62	0.56871	0.58514	106.61	5	169180000	101390000	67790000
Q8R5L1	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1qbp	6	6	6	32.6	32.6	32.6	31.025	279	6.231E-275	1.8405	1.6627	51.379	8	4386900000	1765200000	2621700000
O89103	Complement component C1q receptor	Cd93	7	7	7	16	16	16	69.354	644	1.4777E-33	1.6692	1.0449	25.134	5	311630000	107290000	204340000
Q8K182	Complement component C8 alpha chain	C8a	2	2	2	5.1	5.1	5.1	66.08	587	6.2648E-05	0.74925	0.72437	27.015	2	53209000	28607000	24602000
Q8BH35	Complement component C8 beta chain	C8b	2	2	2	3.9	3.9	3.9	66.229	589	0.00054648	0.95598	0.70037	8.2251	2	54326000	24968000	29358000
Q8VCG4	Complement component C8 gamma chain	C8g	2	2	2	13.9	13.9	13.9	22.508	202	1.4882E-05	0.68518	0.5211	14.981	3	168390000	99947000	68439000
P06683	Complement component C9	C9	4	4	4	9.9	9.9	9.9	62.002	548	2.2441E-11	0.85531	0.69479	101.14	2	80923000	50534000	30390000
B8JJN0	Complement factor B	Gm20547	9	9	8	7.8	7.8	6.7	142.32	1276	5.3604E-53	1.5474	1.1506	14.679	9	518650000	199420000	319230000
E9Q8I0	Complement factor H	Cfh	8	8	8	9.6	9.6	9.6	141.27	1252	5.5013E-65	1.353	0.9004	51.02	7	448540000	190270000	258270000
Q61129	Complement factor I	Cfi	3	3	3	5.8	5.8	5.8	67.26	603	1.1831E-10	1.5099	1.1604	51.915	3	290410000	121280000	169130000
Q6A0A9	Constitutive coactivator of PPAR-gamma-like protein 1	FAM120A	1	1	1	1.8	1.8	1.8	121.64	1112	1.6481E-12	1.0653	0.57314	12.208	2	74121000	36146000	37975000
G3UXW9	COP9 signalosome complex subunit 1	Gps1	5	5	5	12.2	12.2	12.2	58.86	526	3.1543E-29	0.70505	0.54137	67.568	5	333670000	197600000	136070000
P61202	COP9 signalosome complex subunit 2	Cops2	6	6	6	15.6	15.6	15.6	51.596	443	4.3509E-13	1.485	1.0871	35.554	8	838430000	340390000	498040000
O88543	COP9 signalosome complex subunit 3	Cops3	5	5	5	22.7	22.7	22.7	47.832	423	5.303E-109	1.1336	0.98916	59.892	5	570750000	184200000	386550000
O88544	COP9 signalosome complex subunit 4	Cops4	7	7	7	24.9	24.9	24.9	46.284	406	3.2169E-78	1.5707	1.1754	52.589	9	819460000	375480000	443970000
O35864	COP9 signalosome complex subunit 5	Cops5	6	6	6	26.9	26.9	26.9	37.548	334	2.1872E-73	1.2739	1.0412	36.615	6	366940000	148310000	218630000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O88545	COP9 signalosome complex subunit 6	Cops6	7	7	7	28.4	28.4	28.4	35.88	324	5.665E-28	1.1864	0.9839	87.243	8	866000000	340330000	525660000
Q9CZ04	COP9 signalosome complex subunit 7a	Cops7a	5	5	5	28.7	28.7	28.7	30.224	275	1.7119E-29	2.0927	1.8394	55.783	4	407020000	149190000	257830000
Q8VBV7	COP9 signalosome complex subunit 8	Cops8	3	3	3	23.9	23.9	23.9	23.255	209	2.6323E-46	2.042	1.2827	29.961	5	1075000000	320140000	754850000
Q8C166	Copine-1	Cpne1	3	3	3	5.2	5.2	5.2	58.886	536	9.9998E-08	1.0835	1.0144	33.991	3	246460000	115370000	131080000
Q8BT60	Copine-3	Cpne3	3	3	3	8.6	8.6	8.6	59.584	533	4.6387E-26	1.2066	0.8318	16.339	2	392690000	175700000	216990000
Q9WU84	Copper chaperone for superoxide dismutase	Ccs	3	3	3	18.6	18.6	18.6	28.911	274	2.0277E-10	2.1469	1.6955	28.32	4	126940000	37420000	89522000
Q9D8X1	Copper homeostasis protein cutC homolog	Cutc	3	3	3	17.3	17.3	17.3	29.003	272	1.1952E-11	1.2545	0.84048	25.668	3	196500000	80981000	115520000
O08997	Copper transport protein ATOX1	Atox1	2	2	2	47.1	47.1	47.1	7.3384	68	1.125E-149	2.3171	2.1446	34.672	4	1450100000	509760000	940390000
P36552	Coproporphyrinogen-III oxidase, mitochondrial	Cpox	7	7	7	24.4	24.4	24.4	49.714	443	2.9557E-35	0.98383	0.65854	94.011	7	1700700000	1255400000	445240000
Q3UMF0	Cordon-bleu protein-like 1	Cobll1	9	9	9	12.5	12.5	12.5	137.38	1273	9.515E-293	3.6294	3.0638	55.903	8	352050000	91902000	260150000
O89053	Coronin-1A	Coro1a	1	1	1	6.3	6.3	6.3	50.989	461	3.4068E-25	0.70225	0.51582	3.3153	2	70263000	41676000	28587000
Q9WUM3	Coronin-1B	Coro1b	6	6	6	22.9	22.9	22.9	53.912	484	7.0566E-88	0.71784	0.54532	54.179	6	296410000	178210000	118200000
Q9WUM4	Coronin-1C	Coro1c	6	6	6	20.7	20.7	20.7	53.12	474	8.865E-117	0.67041	0.54839	61.243	8	1203100000	457140000	745950000
Q9D2V7	Coronin-7	Coro7	3	3	3	5.2	5.2	5.2	100.81	922	2.2999E-16	0.57092	0.45645	10.656	3	75933000	44830000	31103000
Q06770	Corticosteroid-binding globulin	Serpina6	1	1	1	2.8	2.8	2.8	44.769	397	0.00020935	3.5716	2.2696	28.454	2	180490000	41489000	139000000
E9QMV2	Costars family protein ABRACL	3110003A17Rik	1	1	1	16	16	16	9.0583	81	6.7536E-21	3.9954	4.3196	67.599	6	663030000	99135000	563900000
Q04447	Creatine kinase B-type	Ckb	10	10	10	47	47	47	42.713	381	1.45E-183	1.6162	1.0355	30.121	32	9046400000	3340200000	5706200000
P07310	Creatine kinase M-type	Ckm	25	25	25	61.4	61.4	61.4	43.044	381	0	2.0798	1.3894	49.203	116	1.0984E+11	3.1984E+10	7.7855E+10
Q6P8J7	Creatine kinase S-type, mitochondrial	Ckmt2	21	21	18	48.2	48.2	40.6	47.473	419	0	1.1792	0.79306	43.563	114	6.0552E+10	2.7821E+10	3.2731E+10
P47941	Crk-like protein	Crkl	5	5	5	27.1	27.1	27.1	33.83	303	2.0861E-38	2.5716	1.649	30.441	8	903020000	275240000	627790000
O88712	C-terminal-binding protein 1	Ctbp1	5	5	5	17.2	17.2	17.2	47.744	441	1.5291E-50	1.6389	1.0591	39.666	6	795830000	351070000	444760000
P70698	CTP synthase 1	Ctps	4	4	4	11.3	11.3	11.3	66.682	591	9.0327E-27	0.59544	0.62921	58.743	5	202090000	91925000	110160000
P28659	CUGBP Elav-like family member 1	Celf1	2	2	1	4.7	4.7	2.7	52.107	486	7.7892E-17	1.6324	1.2311	20.495	2	105950000	40365000	65589000
Q9WTX6	Cullin-1	Cul1	6	6	6	9.7	9.7	9.7	89.69	776	2.9986E-43	0.60913	0.47765	36.995	4	118080000	73102000	44981000
Q9JLV5	Cullin-3	Cul3	4	4	4	5.9	5.9	5.9	88.947	768	4.8735E-14	0.73303	0.62187	33.637	4	132610000	70842000	61768000
Q3TCH7	Cullin-4A	Cul4a	3	3	3	5.3	5.3	5.3	87.752	759	4.7202E-91	1.395	0.79221	8.2156	3	239130000	104630000	134500000
G3X914	Cullin-5	Cul5	5	5	5	6.2	6.2	6.2	99.04	855	1.299E-13	0.60646	0.62297	24.827	9	196310000	115990000	80321000
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	Cand1	12	12	12	12.9	12.9	12.9	136.33	1230	2.6981E-78	0.64104	0.52887	31.563	12	937890000	541970000	395920000
Q6ZQ73	Cullin-associated NEDD8-dissociated protein 2	Cand2	4	4	4	5.8	5.8	5.8	135.63	1235	2.408E-38	0.72284	0.57008	35.671	4	130540000	77044000	53497000
Q3TZR9	Cyclic AMP-dependent transcription factor ATF-7	Atf7	2	2	2	6	6	6	51.779	483	1.9239E-05	2.2692	1.7892	2.2517	2	9450700	3577200	5873500
P46414	Cyclin-dependent kinase inhibitor 1B	Cdkn1b	1	1	1	6.6	6.6	6.6	22.193	197	5.9097E-07	3.1233	2.3227	8.7955	2	80618000	27078000	53540000
Q62426	Cystatin-B	Cstb	3	3	3	39.8	39.8	39.8	11.045	98	1.84E-39	1.5224	1.3342	66.777	3	307670000	143980000	163700000
P21460	Cystatin-C	Cst3	2	2	2	25	25	25	15.531	140	1.2174E-15	1.6902	1.1545	7.2215	2	224530000	84173000	140360000
P97315	Cysteine and glycine-rich protein 1	Csrp1	4	4	4	30.6	30.6	30.6	20.583	193	1.653E-43	1.9821	1.0653	80.196	4	326560000	90428000	236140000
P50462	Cysteine and glycine-rich protein 3	Csrp3	10	10	10	55.2	55.2	55.2	20.895	194	0	1.969	1.3725	39.969	28	3380400000	1070500000	2309900000
Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	Chordc1	6	6	6	32.6	32.6	32.6	37.35	331	1.8679E-37	1.3381	0.99525	20.468	5	416260000	217760000	198500000
Q9Z1J3	Cysteine desulfurase, mitochondrial	Nfs1	12	12	12	34.4	34.4	34.4	50.569	459	1.355E-267	0.57186	0.45844	32.729	13	840390000	527530000	312860000
P63254	Cysteine-rich protein 1	Crip1	1	1	1	13	13	13	8.5497	77	0.0011822	0.75205	0.5619	9.7456	2	385460000	229720000	155740000
Q9DCT8	Cysteine-rich protein 2	Crip2	3	3	3	29.3	29.3	29.3	22.727	208	2.628E-160	2.9574	1.8648	19.612	9	1904100000	414800000	1489300000
Q9ER72	Cysteine--tRNA ligase, cytoplasmic	Cars	7	7	7	8.8	8.8	8.8	94.859	831	1.5143E-12	0.52592	0.28232	54.413	5	152860000	104730000	48126000
P56395	Cytochrome b5	Cyb5a	3	3	3	34.3	34.3	34.3	15.241	134	2.6331E-13	1.2537	0.93617	2.3538	2	336530000	149690000	186840000
Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	Uqcrc1	17	17	17	47.9	47.9	47.9	52.851	480	0	0.84368	0.55527	70.037	40	7309400000	4257000000	3052300000
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	Uqcrc2	14	14	14	37.3	37.3	37.3	48.234	453	1.006E-144	0.75873	0.55807	41.932	27	1.4519E+10	8025000000	6494200000
P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	Uqcrh	4	4	4	57.3	57.3	57.3	10.435	89	0	1.9862	1.3907	32.008	11	1545300000	473470000	1071800000
Q9CQB4	Cytochrome b-c1 complex subunit 7	Uqcrb	9	9	9	56.8	56.8	56.8	13.561	111	7.5698E-32	1.1525	0.79347	54.122	14	5008000000	2339900000	2668200000
Q9CQ69	Cytochrome b-c1 complex subunit 8	Uqcrq	2	2	2	18.3	18.3	18.3	9.7681	82	7.1596E-05	0.46464	0.31361	21.637	2	1305800000	876490000	429300000
Q8R1I1	Cytochrome b-c1 complex subunit 9	Uqcr10	2	2	2	37.5	37.5	37.5	7.4454	64	3.627E-147	0.74979	0.49012	13.728	3	1092700000	668130000	424540000
Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochondrial	Uqcrfs1	10	10	10	44.9	44.9	44.9	29.367	274	3.34E-119	1.4306	0.97765	47.039	14	3291800000	1432000000	1859800000
P00397	Cytochrome c oxidase subunit 1	Mtco1	2	2	2	7.8	7.8	7.8	56.861	514	7.0807E-45	0.51046	0.3134	25.47	4	372440000	246550000	125900000
P00405	Cytochrome c oxidase subunit 2	Mtco2	5	5	5	40.5	40.5	40.5	25.976	227	3.321E-117	0.66638	0.46329	28.107	19	3764100000	2191600000	1572500000
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	Cox4i1	6	6	6	36.7	36.7	36.7	19.53	169	3.873E-102	0.83256	0.63049	35.596	14	5266300000	3008900000	2257300000
P12787	Cytochrome c oxidase subunit 5A, mitochondrial	Cox5a	6	6	6	34.2	34.2	34.2	16.101	146	1.785E-49	1.6633	0.94424	123.14	14	1.0634E+10	3802100000	6831500000
Q9D881	Cytochrome c oxidase subunit 5B, mitochondrial	Cox5b	2	2	2	22.5	22.5	22.5	13.847	129	7.9638E-80	1.4879	1.5302	21.658	3	468080000	197160000	270920000
P56391	Cytochrome c oxidase subunit 6B1	Cox6b1	5	5	5	62.8	62.8	62.8	10.071	86	1.4874E-43	2.0645	1.4845	32.737	20	1.1349E+10	3698000000	7650700000
Q9CPQ1	Cytochrome c oxidase subunit 6C	Cox6c	3	3	3	34.2	34.2	34.2	8.4689	76	3.5355E-08	0.53692	0.40072	25.311	7	2868300000	1870700000	997610000
P48771	Cytochrome c oxidase subunit 7A2, mitochondrial	Cox7a2	2	2	2	27.7	27.7	27.7	9.2908	83	7.4783E-22	0.9863	0.75623	37.036	3	473670000	247370000	226300000
J3QNB4	Cytochrome c oxidase subunit 7C, mitochondrial	Cox7c	1	1	1	14.3	14.3	14.3	7.3757	63	0.00067649	0.92143	0.81559	44.382	2	800010000	429480000	370530000
P62897	Cytochrome c, somatic	Cycs	12	12	8	73.3	73.3	41.9	11.605	105	0	1.3947	1.4291	59.03	41	2.383E+10	1.0444E+10	1.3386E+10
Q9D0M3	Cytochrome c1, heme protein, mitochondrial	Cyc1	7	7	7	32.3	32.3	32.3	35.327	325	4.411E-222	0.62735	0.45243	21.713	14	2071600000	1320600000	750960000
Q9CX80	Cytoglobin	Cygb	2	2	2	8.9	8.9	8.9	21.465	190	0.00592	2.5031	1.7794	3.7838	2	42343000	10255000	32087000
A2A517	Cytohesin-1	Cyth1	3	3	3	11.1	11.1	11.1	52.492	460	1.8352E-11	2.4047	1.3379	19.136	4	199400000	59772000	139630000
P28271	Cytoplasmic aconitate hydratase	Aco1	16	16	16	22.4	22.4	22.4	98.124	889	1.1823E-74	0.66968	0.45455	39.416	19	1874100000	1091500000	782630000
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	Dync1h1	40	40	40	11.1	11.1	11.1	532.04	4644	0	0.55473	0.4775	68.914	39	3209100000	1386100000	1823000000
A2BFF9	Cytoplasmic dynein 1 intermediate chain 2	Dync1i2	4	4	4	11.4	11.4	11.4	71.424	638	1.1258E-98	1.1406	0.90998	47.124	4	171580000	86186000	85394000
Q8R1Q8	Cytoplasmic dynein 1 light intermediate chain 1	Dync1li1	4	4	4	14.7	14.7	14.7	56.614	523	2.0751E-18	1.8026	1.5007	43.952	4	393980000	167300000	226680000
Q6PDL0	Cytoplasmic dynein 1 light intermediate chain 2	Dync1li2	6	6	6	20.9	20.9	20.9	54.218	492	4.5179E-41	1.3575	1.3236	28.305	6	272380000	100130000	172250000
Q7TMB8	Cytoplasmic FMR1-interacting protein 1	Cyfip1	3	3	2	2.4	2.4	1.4	145.24	1253	1.7194E-07	0.52378	0.3775	33.711	3	123000000	79971000	43031000
Q99M51	Cytoplasmic protein NCK1	Nck1	2	2	2	5.6	5.6	5.6	42.89	377	0.00015475	2.7593	1.8283	110.93	2	199600000	47744000	151860000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8BMK4	Cytoskeleton-associated protein 4	Ckap4	2	2	2	4.5	4.5	4.5	63.691	575	1.9476E-05	0.33176	0.21527	23.711	2	35376000	28494000	6882200
A2AGT5	Cytoskeleton-associated protein 5	Ckap5	4	4	4	2.6	2.6	2.6	225.63	2032	2.5241E-16	1.007	0.60428	64.877	4	110710000	60868000	49839000
Q9CPY7	Cytosol aminopeptidase	Lap3	14	14	14	42	42	42	56.141	519	3.504E-157	0.97537	0.7735	68.946	20	1207600000	612780000	594810000
Q9D020	Cytosolic 5-nucleotidase 3	Nt5c3	8	8	8	27.8	27.8	27.8	37.252	331	4.5137E-28	2.8161	2.0546	36.511	9	2307200000	648910000	1658300000
E9PYH2	Cytosolic acyl coenzyme A thioester hydrolase	Acot7	3	3	3	10.4	10.4	10.4	42.826	384	0.00017161	1.619	1.0178	15.812	3	199500000	78605000	120900000
Q9D1A2	Cytosolic non-specific dipeptidase	Cndp2	15	15	15	38.7	38.7	38.7	52.767	475	5.7744E-74	0.95702	0.64945	66.272	18	2431700000	1121800000	1309900000
E9Q9M1	Cytosolic purine 5-nucleotidase	Nt5c2	5	5	5	15.5	15.5	15.5	67.703	586	2.4652E-32	0.34193	0.23617	89.552	4	308850000	235480000	73367000
Q3UGB5	DAZ-associated protein 1	Dazap1	3	3	3	11.6	11.6	11.6	43.157	406	2.0369E-66	2.3023	1.6488	3.5288	3	492400000	135570000	356830000
Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	Bdh1	6	6	6	21.6	21.6	21.6	38.299	343	2.2516E-72	1.102	0.7027	28.554	6	504150000	278990000	225160000
Q8K3H0	DCC-interacting protein 13-alpha	Appl1	3	3	3	9.3	9.3	9.3	79.327	707	1.5634E-68	0.99438	0.75443	96.388	2	66800000	30805000	35995000
Q8BZJ7	DCN1-like protein 2	Dcun1d2	3	3	3	13.9	13.9	13.9	30.068	259	9.2822E-12	1.5909	1.1296	22.993	5	344190000	145950000	198240000
O35215	D-dopachrome decarboxylase	Ddt	4	4	1	51.7	51.7	12.7	13.077	118	3.534E-119	1.9065	1.1673	26.209	12	5072700000	1743300000	3329400000
P28654	Decorin	Dcn	4	4	4	15.8	15.8	15.8	39.809	354	7.3133E-17	0.41874	0.47379	29.404	5	337870000	247590000	90282000
Q3U0B3	Dehydrogenase/reductase SDR family member 11	Dhrs11	4	4	4	28.8	28.8	28.8	28.274	260	1.58E-124	1.0339	0.77103	27.996	9	769770000	387070000	382700000
Q99LB2	Dehydrogenase/reductase SDR family member 4	Dhrs4	6	6	6	25.8	25.8	25.8	29.884	279	8.527E-135	0.90309	0.6497	82.622	9	4627500000	2061400000	2566100000
O35459	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Ech1	14	14	14	49.5	49.5	49.5	36.118	327	0	1.603	1.15	54.461	49	1.0363E+10	4946600000	5416800000
Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	Aldh4a1	14	14	14	36.5	36.5	36.5	61.84	562	0	1.0161	0.68449	74.3	26	6757700000	3185800000	3571900000
P10518	Delta-aminolevulinic acid dehydratase	Alad	9	9	9	39.4	39.4	39.4	36.023	330	1.3686E-68	1.0712	0.84437	117.63	8	986490000	598570000	387920000
P82347	Delta-sarcoglycan	Sgcd	2	2	2	8.7	8.7	8.7	32.133	289	8.512E-07	0.62979	0.64961	5.5097	2	184330000	100020000	84316000
Q9CQJ6	Density-regulated protein	Denr	5	5	5	36.4	36.4	36.4	22.166	198	1.2424E-57	2.4774	1.6628	46.86	5	379790000	118550000	261240000
Q99LN9	Deoxyhypusine hydroxylase	Dohh	2	2	2	10.9	10.9	10.9	32.905	302	0.00077344	2.815	2.2059	9.3146	2	86942000	25726000	61216000
Q9R0P5	Destrin	Dstn	7	7	7	46.7	46.7	46.7	18.521	165	2.3607E-81	2.0412	2.2112	33.601	9	3750100000	1361100000	2389000000
P32233	Developmentally-regulated GTP-binding protein 1	Drg1	3	3	3	9.8	9.8	9.8	40.512	367	5.8686E-08	0.49226	0.46251	34.493	3	82244000	54395000	27849000
Q9JIQ3	Diablo homolog, mitochondrial	Diablo	3	3	3	21.1	21.1	21.1	26.82	237	1.064E-244	1.892	1.279	17.646	4	248880000	87786000	161100000
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	Dld	18	18	18	48.1	48.1	48.1	54.272	509	0	1.1477	0.77185	42.829	43	3.5479E+10	1.6184E+10	1.9295E+10
Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	Dlat	14	14	14	31.5	31.5	31.5	67.941	642	0	1.7563	1.351	96.668	32	1.6849E+10	6609700000	1.0239E+10
Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	Dlst	11	11	11	27.3	27.3	27.3	48.994	454	3.159E-239	1.6495	1.1334	56.187	16	1.9529E+10	7901600000	1.1627E+10
Q8BVI4	Dihydropteridine reductase	Qdpr	6	6	6	34.9	34.9	34.9	25.57	241	2.384E-106	1.3573	0.7552	36.79	8	1561100000	702630000	858520000
O08553	Dihydropyrimidinase-related protein 2	Dpysl2	18	18	17	48.8	48.8	46.5	62.277	572	0	1.4126	1.0747	27.653	38	6589400000	2854000000	3735400000
E9PWE8	Dihydropyrimidinase-related protein 3	Dpysl3	11	11	10	24.9	24.9	23.9	73.884	683	8.382E-207	1.7144	1.2169	54.073	13	1592900000	525670000	1067200000
P31428	Dipeptidase 1	Dpep1	5	5	5	22.2	22.2	22.2	45.722	410	5.9151E-17	1.3542	1.0575	34.087	6	463120000	207500000	255620000
P97821	Dipeptidyl peptidase 1	Ctsc	3	3	3	9.7	9.7	9.7	52.376	462	2.6345E-25	0.70171	0.47016	73.992	3	277340000	180080000	97256000
Q99KK7	Dipeptidyl peptidase 3	Dpp3	6	6	6	13	13	13	82.897	738	1.0621E-67	0.83725	0.73428	56.779	6	386050000	200020000	186030000
Q9JI46	Diphosphoinositol polyphosphate phosphohydrolase 1	Nudt3	3	3	3	30.4	30.4	30.4	19.029	168	3.8803E-26	1.9657	1.1703	16.298	6	634530000	222510000	412020000
Q8CI75	DIS3-like exonuclease 2	Dis3l2	2	2	2	3.3	3.3	3.3	97.774	870	3.3049E-06	1.0268	0.84795	78.782	2	179980000	102300000	77687000
P98078	Disabled homolog 2	Dab2	2	2	2	5.1	5.1	5.1	82.311	766	3.4243E-07	1.2653	0.73549	19.601	2	126910000	63336000	63570000
Q8BPM0	Disheveled-associated activator of morphogenesis 1	Daam1	2	2	2	2	2	2	123.37	1077	1.0619E-21	1.534	1.0488	105.6	2	318270000	95454000	222820000
Q3U1J4	DNA damage-binding protein 1	Ddb1	15	15	15	16.9	16.9	16.9	126.85	1140	1.5415E-68	0.7303	0.442	66.706	13	838650000	448430000	390220000
Q64511	DNA topoisomerase 2-beta	Top2b	2	2	2	1.2	1.2	1.2	181.91	1612	0.0091164	0.72935	0.6445	143.41	2	120780000	67028000	53749000
P28352	DNA-(apurinic or apyrimidinic site) lyase	Apex1	3	3	3	15.1	15.1	15.1	35.49	317	3.4681E-56	0.99522	0.75584	83.254	4	136540000	62932000	73604000
P63037	DnaJ homolog subfamily A member 1	Dnaja1	2	2	2	8.1	8.1	8.1	44.868	397	4.7835E-07	1.0412	0.80648	35.072	2	46764000	26344000	20419000
Q9QYJ0	DnaJ homolog subfamily A member 2	Dnaja2	3	3	3	9.2	9.2	9.2	45.745	412	6.6698E-73	0.70779	0.58427	69.486	2	53380000	32042000	21338000
Q9JMC3	DnaJ homolog subfamily A member 4	Dnaja4	7	7	7	23.7	23.7	23.7	44.901	397	2.9252E-61	0.85967	0.64794	30.382	8	602830000	326860000	275970000
Q9D832	DnaJ homolog subfamily B member 4	Dnajb4	7	7	7	24.9	24.9	24.9	37.781	337	6.2503E-21	0.82121	0.61878	75.421	8	588840000	287920000	300920000
P60904	DnaJ homolog subfamily C member 5	Dnajc5	1	1	1	7.6	7.6	7.6	22.101	198	0.015046	0.41581	0.23626	4.454	2	85437000	61221000	24217000
Q6NZB0	DnaJ homolog subfamily C member 8	Dnajc8	2	2	2	18.2	18.2	18.2	29.812	253	9.1452E-27	2.7203	1.8834	17.505	4	200940000	48664000	152280000
Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Rpn1	3	3	3	4.8	4.8	4.8	68.527	608	4.7419E-14	0.22563	0.13348	79.131	2	200700000	122380000	78318000
Q62418	Drebrin-like protein	Dbnl	5	5	5	17	17	17	48.699	436	8.2612E-66	1.6056	1.3775	13.322	5	153220000	49549000	103670000
Q9DD18	D-tyrosyl-tRNA(Tyr) deacylase 1	Dtd1	2	2	2	14.8	14.8	14.8	23.384	209	3.673E-38	2.265	1.7217	6.6228	2	56797000	17280000	39517000
P31938	Dual specificity mitogen-activated protein kinase kinase 1	Map2k1	3	2	2	13	7.4	7.4	43.474	393	5.8348E-15	1.1179	1.0656	33.893	2	160480000	82662000	77823000
Q63932	Dual specificity mitogen-activated protein kinase kinase 2	Map2k2	3	3	2	20.2	20.2	14.7	44.402	401	1.2309E-31	1.0651	0.86843	6.8053	4	302440000	139400000	163030000
P47809	Dual specificity mitogen-activated protein kinase kinase 4	Map2k4	3	3	3	12.6	12.6	12.6	44.113	397	1.649E-40	1.0448	0.85051	41.34	2	76193000	37153000	39040000
B1AQF4	Dual specificity protein phosphatase 3	Dusp3	5	5	5	35.2	35.2	35.2	23.223	210	1.583E-146	1.1187	0.7749	46.39	9	860760000	406790000	453980000
O08788	Dynactin subunit 1	Dctn1	15	15	15	16.9	16.9	16.9	141.67	1281	3.7766E-60	0.7118	0.68525	62.028	17	977210000	546380000	430830000
Q99KJ8	Dynactin subunit 2	Dctn2	14	14	14	46.8	46.8	46.8	44.116	402	5.186E-114	1.5988	1.0275	52.367	17	2833500000	1180700000	1652900000
Q9Z0Y1	Dynactin subunit 3	Dctn3	4	4	4	28	28	28	20.978	186	1.2367E-10	1.0776	0.89742	65.979	4	105450000	63661000	41793000
Q8K1M6	Dynamin-1-like protein	Dnm1l	19	19	1	36	36	3.1	82.657	742	0	1.1727	0.88306	65.461	24	2791500000	1419000000	1372500000
F8WIV5	Dynamin-2	Dnm2	7	7	6	12.1	12.1	9.9	98.096	870	7.5881E-19	0.91878	0.69601	44.458	11	677350000	343150000	334200000
P58281	Dynamin-like 120 kDa protein, mitochondrial	Opa1	13	13	13	15.4	15.4	15.4	111.34	960	3.9116E-75	0.72928	0.63042	36.185	10	338450000	193700000	144750000
P63168	Dynein light chain 1, cytoplasmic	Dynll1	1	1	1	12.4	12.4	12.4	10.366	89	0.003711	1.1169	0.77487	15.709	2	279070000	139410000	139660000
A2AVR9	Dynein light chain roadblock-type 1	Dynlrb1	3	3	3	47.1	47.1	47.1	11.928	104	2.3057E-37	1.8722	1.7013	97.983	3	311070000	91473000	219590000
P51807	Dynein light chain Tctex-type 1	Dynlt1	1	1	1	15.9	15.9	15.9	12.483	113	1.3063E-18	1.3617	1.3111	11.344	2	91305000	36803000	54502000
E9Q423	Dysferlin	Dysf	3	3	3	1.9	1.9	1.9	239.13	2099	4.7103E-09	0.29062	0.30021	182.82	3	7243300000	1065600000	6177700000
S4R1P5	Dystonin	Dst	20	20	18	3.8	3.8	3.5	870.52	7717	2.18E-173	1.0717	1.0406	135.75	12	1017700000	247360000	770380000
Q9D2N4	Dystrobrevin alpha	Dtna	5	5	5	8.3	8.3	8.3	84.066	746	1.8593E-19	0.42169	0.32949	32.393	5	353490000	246460000	107030000
Q62165	Dystroglycan	Dag1	5	5	5	8.4	8.4	8.4	96.904	893	1.4212E-64	2.3928	1.53	14.453	5	1046300000	315420000	730840000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P11531	Dystrophin	Dmd	12	12	12	4.7	4.7	4.7	425.83	3678	3.939E-134	0.59534	0.45638	63.63	7	281850000	167070000	114780000
Q9ERU9	E3 SUMO-protein ligase RanBP2	Ranbp2	2	2	2	1.1	1.1	1.1	341.12	3053	1.7478E-14	0.84615	0.6148	41.75	3	69509000	37916000	31594000
F8WIE5	E3 ubiquitin-protein ligase HECTD1	Hectd1	4	4	4	2.5	2.5	2.5	289.23	2610	3.987E-11	0.90946	0.69549	13.094	4	143440000	71310000	72134000
A2AFQ0	E3 ubiquitin-protein ligase HUWE1	Huwe1	12	12	12	4.1	4.1	4.1	482.69	4378	6.258E-167	1.0778	0.82048	28.609	13	425190000	206840000	218350000
P46935	E3 ubiquitin-protein ligase NEDD4	Nedd4	12	12	10	15.3	15.3	14	102.71	887	2.2963E-52	0.8256	0.57491	75.85	11	2311300000	681530000	1629800000
Q5XPI3	E3 ubiquitin-protein ligase RNF123	Rnf123	4	4	4	3.1	3.1	3.1	148.65	1314	1.415E-12	0.42877	0.32697	30.502	4	129870000	93186000	36688000
F7A6H4	E3 ubiquitin-protein ligase RNF213	Rnf213	2	2	2	0.3	0.3	0.3	584.78	5152	0.00037982	0.67958	0.45783	8.439	2	458460000	318270000	140200000
A2AN08	E3 ubiquitin-protein ligase UBR4	Ubr4	12	12	12	3.1	3.1	3.1	572.28	5180	1.4256E-24	0.75779	0.44583	105.46	9	189600000	109240000	80361000
Q8BL66	Early endosome antigen 1	Eea1	11	11	11	10	10	10	160.91	1411	1.8883E-63	1.9617	1.2258	26.014	11	611580000	222160000	389410000
D3Z4J9	Echinoderm microtubule-associated protein-like 1	Eml1	13	13	11	18.2	18.2	17	88.327	800	1.1605E-34	0.85746	0.67052	81.386	16	1799900000	981990000	817900000
E9QK48	Echinoderm microtubule-associated protein-like 2	Eml2	13	13	13	22	22	22	90.791	841	3.342E-100	0.92196	0.74684	34.246	12	1307800000	711520000	596320000
Q8R2G4	Ecto-ADP-ribosyltransferase 3	Art3	9	9	9	30.5	30.5	30.5	42.014	371	3E-103	1.3072	0.87741	49.52	12	998580000	439920000	558660000
Q8BTJ4	Ectonucleotide pyrophosphatase/phosphodiesterase family member 4	Enpp4	4	4	4	9.4	9.4	9.4	51.611	456	2.4835E-08	0.46246	0.35647	37.262	3	200250000	133300000	66946000
Q8BGN3	Ectonucleotide pyrophosphatase/phosphodiesterase family member 6	Enpp6	2	2	2	7	7	7	50.618	440	0.00031182	1.3761	1.1068	28.665	3	3525400000	1462100000	2063300000
Q8C845	EF-hand domain-containing protein D2	Efhd2	4	4	4	18.3	18.3	18.3	26.8	240	1.231E-129	0.7047	0.63781	20.955	5	190160000	104270000	85885000
Q8BPB5	EGF-containing fibulin-like extracellular matrix protein 1	Efemp1	4	4	4	13.6	13.6	13.6	54.952	493	2.409E-215	1.7577	1.3239	22.152	3	93988000	28905000	65083000
Q91YE3	Egl nine homolog 1	Egln1	4	4	4	12.2	12.2	12.2	43.11	400	2.1015E-09	1.7671	1.349	31.532	4	106830000	42937000	63894000
Q69ZW3	EH domain-binding protein 1	Ehbp1	2	2	2	2.7	2.7	2.7	139.1	1231	0.0004529	1.6815	1.1906	21.971	2	64521000	23418000	41104000
E9QP49	EH domain-binding protein 1-like protein 1	Ehbp1l1	12	12	12	10.9	10.9	10.9	184.8	1718	2.181E-281	1.3487	0.92125	30.894	12	435460000	203300000	232150000
Q9WVK4	EH domain-containing protein 1	Ehd1	17	16	13	44.6	42.9	37.8	60.602	534	3.145E-156	0.9283	0.72986	38.926	22	3112500000	1640500000	1472000000
Q8BH64	EH domain-containing protein 2	Ehd2	23	23	20	52.1	52.1	48.4	61.174	543	0	0.68581	0.46864	76.907	33	2957300000	1660100000	1297200000
Q9EQP2	EH domain-containing protein 4	Ehd4	17	12	12	37.5	30.5	30.5	61.48	541	1.17E-163	0.70317	0.55404	71.504	16	2440900000	1356500000	1084500000
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	Etfa	18	18	18	62.2	62.2	62.2	35.009	333	0	2.4918	1.7269	110.63	52	6.7746E+10	1.6927E+10	5.0819E+10
Q9DCW4	Electron transfer flavoprotein subunit beta	Etfb	12	12	12	57.3	57.3	57.3	27.623	255	0	2.1649	1.6314	43.045	48	1.7286E+10	4818400000	1.2468E+10
Q921G7	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	Etfdh	15	15	15	32.3	32.3	32.3	68.09	616	2.646E-191	0.92342	0.69016	34.434	29	9235200000	5091000000	4144200000
P10126	Elongation factor 1-alpha 1	Eef1a1	13	7	7	37.2	24	24	50.113	462	0	1.9716	1.3734	61.962	20	3508100000	1271000000	2237100000
P62631	Elongation factor 1-alpha 2	Eef1a2	22	22	16	57.2	57.2	44.1	50.454	463	0	1.7508	1.2517	88.011	79	1.504E+10	5314600000	9724900000
O70251	Elongation factor 1-beta	Eef1b	6	6	6	45.8	45.8	45.8	24.693	225	6.6203E-60	1.7673	1.4574	53.761	9	922090000	392760000	529330000
P57776	Elongation factor 1-delta	Eef1d	6	6	1	33.5	33.5	8.5	31.293	281	4.202E-242	1.6723	1.2448	67.833	10	609390000	328750000	280640000
Q9D8N0	Elongation factor 1-gamma	Eef1g	12	12	12	29.1	29.1	29.1	50.06	437	1.426E-128	0.76149	0.59302	79.44	18	4567800000	2512400000	2055400000
P58252	Elongation factor 2	Eef2	26	26	25	37.5	37.5	36.4	95.313	858	0	0.98162	0.68472	44.806	41	1.0028E+10	5075100000	4952900000
Q8K0D5	Elongation factor G, mitochondrial	Gfm1	14	14	14	27.4	27.4	27.4	83.549	751	1.992E-153	0.92844	0.65285	37.771	26	3000100000	1529200000	1470900000
Q9CZR8	Elongation factor Ts, mitochondrial	Tsfm	7	7	7	38.3	38.3	38.3	35.334	324	6.74E-298	1.2626	0.84109	28.737	17	1760600000	868100000	892510000
Q8BFR5	Elongation factor Tu, mitochondrial	Tufm	17	17	17	49.3	49.3	49.3	49.508	452	1.688E-270	1.4757	1.0711	38.753	32	8057800000	3349800000	4708000000
O08600	Endonuclease G, mitochondrial	Endog	3	3	3	13.6	13.6	13.6	32.19	294	3.4797E-30	0.4223	0.34103	24.366	4	295760000	211080000	84687000
Q9JK48	Endophilin-B1	Sh3glb1	1	1	1	3.6	3.6	3.6	40.855	365	3.3461E-15	1.8008	1.385	8.7939	2	38489000	11663000	26826000
A2AWI7	Endophilin-B2	Sh3glb2	2	2	2	5.7	5.7	5.7	44.907	404	0.0019652	3.9934	2.3793	52.343	2	182080000	27608000	154480000
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	Erap1	3	3	3	3.8	3.8	3.8	106.6	930	9.4302E-12	2.6269	2.1993	86.583	3	145020000	69438000	75582000
P08113	Endoplasmin	Hsp90b1	23	21	21	32.5	30.8	30.8	92.475	802	0	1.1703	0.85725	40.972	32	4182300000	1900100000	2282200000
B0QZL1	Enolase	Eno1	7	1	1	46.2	6.3	6.3	23.935	221	7.075E-137	1.2535	1.2224	37.577	2	1531900000	707830000	824080000
P42125	Enoyl-CoA delta isomerase 1, mitochondrial	Eci1	9	9	9	32.5	32.5	32.5	32.25	289	2.398E-131	1.0631	0.75186	38.668	47	3.1138E+10	1.545E+10	1.5687E+10
Q9WUR2	Enoyl-CoA delta isomerase 2, mitochondrial	Eci2	12	12	12	36.8	36.8	36.8	43.267	391	0	1.3413	0.95529	49.078	22	3240300000	1402800000	1837500000
Q3TLP5	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	Echdc2	8	8	8	41.2	41.2	41.2	31.852	296	9.534E-248	1.1601	0.77733	43.886	15	2818400000	1427400000	1391100000
Q9D7J9	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	Echdc3	5	5	1	23.7	23.7	7.7	32.402	300	1.271E-83	0.60052	0.39126	61.335	5	614960000	410820000	204150000
Q8BH95	Enoyl-CoA hydratase, mitochondrial	Echs1	17	17	17	53.8	53.8	53.8	31.474	290	9.175E-291	2.6913	2.0474	44.411	30	3.0127E+10	8307600000	2.182E+10
Q01279	Epidermal growth factor receptor	Egfr	3	3	3	3.5	3.5	3.5	134.85	1210	4.2391E-11	1.2568	0.85367	4.3238	2	112730000	44999000	67729000
Q60902	Epidermal growth factor receptor substrate 15-like 1	Eps15l1	4	4	4	9.6	9.6	9.6	99.307	907	1.874E-40	1.0036	0.77237	57.81	3	112230000	55198000	57028000
Q5M8N4	Epimerase family protein SDR39U1	Sdr39u1	4	4	4	21.4	21.4	21.4	32.994	308	2.96E-167	0.66039	0.43198	19.065	7	579260000	351810000	227450000
Q9D379	Epoxide hydrolase 1	Ephx1	3	3	3	13	13	13	52.576	455	8.911E-07	0.41722	0.30968	65.533	3	94227000	67051000	27177000
P34914	Epoxide hydrolase 2	Ephx2	24	24	24	54.2	54.2	54.2	62.515	554	0	1.1182	0.75037	42.725	41	1.4288E+10	6924200000	7364000000
Q80VP1	Epsin-1	Epn1	4	4	4	11.1	11.1	11.1	60.211	575	9.629E-107	1.5451	1.0557	5.4231	5	511980000	192410000	319570000
Q8R180	ERO1-like protein alpha	Ero1l	4	4	4	14.2	14.2	14.2	54.084	464	4.8078E-11	1.4984	0.87094	90.412	3	134460000	72620000	61843000
P54116	Erythrocyte band 7 integral membrane protein	Stom	4	4	4	22.9	22.9	22.9	31.375	284	1.3148E-87	0.2899	0.22563	36.62	6	291630000	219720000	71904000
Q9D172	ES1 protein homolog, mitochondrial	D10Jhu81e	10	10	10	52.6	52.6	52.6	28.09	266	0	2.3284	1.6664	44.921	38	6807600000	2213300000	4594200000
Q91V76	Ester hydrolase C11orf54 homolog		2	2	2	9.5	9.5	9.5	34.995	315	0.0023165	0.34639	0.24296	106.07	2	229030000	155430000	73599000
P50171	Estradiol 17-beta-dehydrogenase 8	Hsd17b8	9	9	9	54.4	54.4	54.4	26.588	259	1.201E-219	0.89559	0.66603	24.947	10	2568900000	1439100000	1129800000
Q922E4	Ethanolamine-phosphate cytidylyltransferase	Pcyt2	2	2	2	9.4	9.4	9.4	45.234	404	2.266E-08	1.0137	0.74062	48.732	3	126920000	52654000	74263000
P60843	Eukaryotic initiation factor 4A-I	Eif4a1	16	16	8	43.1	43.1	23.9	46.153	406	2.394E-157	0.95103	0.68012	51.91	15	1708300000	1011200000	697180000
P10630	Eukaryotic initiation factor 4A-II	Eif4a2	13	5	5	31.9	12.8	12.8	46.402	407	4.247E-125	1.229	0.98814	35.457	6	1481000000	763030000	717960000
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	Gspt1	2	2	2	4.7	4.7	4.7	68.625	636	1.6929E-18	10.36	5.5556	212.24	2	1973800000	90920000	1882800000
Q8BWY3	Eukaryotic peptide chain release factor subunit 1	Etf1	3	3	3	6.4	6.4	6.4	49.03	437	9.8492E-08	0.43546	0.48445	93.599	3	239290000	142910000	96379000
Q9D1M4	Eukaryotic translation elongation factor 1 epsilon-1	Eef1e1	2	2	2	20.1	20.1	20.1	19.859	174	1.0582E-38	2.5804	1.4225	33.25	2	264940000	42307000	222630000
P48024	Eukaryotic translation initiation factor 1	Eif1	4	4	4	49.6	49.6	49.6	12.746	113	3.3861E-41	3.0748	2.425	32.309	6	445490000	98488000	347000000
Q60872	Eukaryotic translation initiation factor 1A	Eif1a	3	3	3	18.1	18.1	18.1	16.502	144	2.4299E-31	0.74733	0.42118	14.129	2	216970000	121640000	95332000
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	Eif2s1	4	4	4	15.2	15.2	15.2	36.108	315	2.7657E-15	0.75967	0.56107	27.084	7	405430000	230350000	175090000
Q99L45	Eukaryotic translation initiation factor 2 subunit 2	Eif2s2	4	4	4	14.2	14.2	14.2	38.092	331	2.4499E-30	1.4878	1.0763	33.709	4	340220000	154390000	185820000
Q9Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	Eif2s3x	7	7	7	21.6	21.6	21.6	51.065	472	1.8318E-64	0.85654	0.52044	131.74	10	1705900000	792780000	913090000
P23116	Eukaryotic translation initiation factor 3 subunit A	Eif3a	10	10	10	10.2	10.2	10.2	161.93	1344	8.2473E-33	0.40698	0.30206	88.44	8	633880000	384440000	249440000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B	Eif3b	11	11	11	22.4	22.4	22.4	91.369	803	8.011E-110	0.65769	0.54206	89.001	14	1363900000	872680000	491260000
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	Eif3c	12	12	12	14.4	14.4	14.4	105.53	911	4.623E-204	0.43288	0.32157	55.185	16	1011700000	635660000	376070000
O70194	Eukaryotic translation initiation factor 3 subunit D	Eif3d	7	7	7	18.8	18.8	18.8	63.988	548	2.219E-191	0.50711	0.41061	62.749	8	414130000	285370000	128760000
P60229	Eukaryotic translation initiation factor 3 subunit E	Eif3e	3	3	3	7.6	7.6	7.6	52.22	445	1.5563E-21	0.39628	0.29066	22.801	3	279630000	195700000	83926000
Q9DCH4	Eukaryotic translation initiation factor 3 subunit F	Eif3f	4	4	4	16.1	16.1	16.1	37.984	361	4.8777E-29	1.0049	0.74629	12.749	6	458030000	232420000	225610000
Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G	Eif3g	3	3	3	13.4	13.4	13.4	35.638	320	1.3587E-20	1.8241	1.2357	9.5029	2	206490000	71318000	135170000
Q91WK2	Eukaryotic translation initiation factor 3 subunit H	Eif3h	5	5	5	10.8	10.8	10.8	39.832	352	9.2313E-16	0.61711	0.74656	147.66	3	321380000	85465000	235920000
Q9QZD9	Eukaryotic translation initiation factor 3 subunit I	Eif3i	5	5	5	21.2	21.2	21.2	36.46	325	2.4398E-31	0.67216	0.54636	27.234	6	527240000	320650000	206590000
Q66JS6	Eukaryotic translation initiation factor 3 subunit J	Eif3j	3	3	3	17.1	17.1	17.1	29.485	263	3.631E-100	1.9976	1.507	14.002	3	228750000	96528000	132220000
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L	Eif3l	10	10	10	18.8	18.8	18.8	66.612	564	1.6762E-41	0.39012	0.36107	55.272	9	515390000	373960000	141430000
Q99JX4	Eukaryotic translation initiation factor 3 subunit M	Eif3m	2	2	2	7.2	7.2	7.2	42.516	374	9.5494E-24	1.3326	0.97819	18.688	3	114150000	51130000	63018000
Q6NZJ6	Eukaryotic translation initiation factor 4 gamma 1	Eif4g1	6	6	6	5.4	5.4	5.4	176.07	1600	0	0.98877	0.94606	20.694	6	610090000	316250000	293840000
G3XA17	Eukaryotic translation initiation factor 4 gamma 2	Eif4g2	8	8	8	11.6	11.6	11.6	102.1	906	7.799E-38	1.1415	1.0182	89.842	8	457760000	154420000	303340000
Q8BGD9	Eukaryotic translation initiation factor 4B	Eif4b	4	4	4	11	11	11	68.839	611	1.5565E-25	3.6914	2.4769	45.454	5	337230000	90957000	246270000
P63073	Eukaryotic translation initiation factor 4E	Eif4e	5	5	5	23	23	23	25.053	217	1.9616E-30	1.578	1.1651	38.213	9	1047100000	412760000	634370000
Q9WUK2	Eukaryotic translation initiation factor 4H	Eif4h	4	4	4	18.1	18.1	18.1	27.341	248	6.907E-125	6.5044	4.7947	28.099	5	487370000	61593000	425780000
P59325	Eukaryotic translation initiation factor 5	Eif5	5	5	5	15.9	15.9	15.9	48.968	429	2.0353E-33	2.3817	1.7066	18.228	8	651970000	200580000	451390000
P63242	Eukaryotic translation initiation factor 5A-1	Eif5a	7	7	7	35.7	35.7	35.7	16.832	154	1.597E-111	1.6645	1.0999	64.143	4	1072400000	418080000	654280000
Q05D44	Eukaryotic translation initiation factor 5B	Eif5b	10	10	10	12.9	12.9	12.9	137.61	1216	4.5062E-38	1.0517	0.90495	66.399	7	174840000	78967000	95874000
Q6KAR6	Exocyst complex component 3	Exoc3	2	2	2	2.4	2.4	2.4	86.454	755	1.2611E-05	1.5009	1.4621	42.236	2	97231000	45055000	52177000
Q6P5F9	Exportin-1	Xpo1	7	7	7	9.8	9.8	9.8	123.09	1071	4.9938E-39	0.70268	0.6009	32.35	6	580810000	257270000	323540000
Q9ERK4	Exportin-2	Cse1l	2	2	2	3.3	3.3	3.3	110.45	971	5.5156E-19	1.3081	0.87897	44.913	3	57644000	26096000	31547000
Q3U7R1	Extended synaptotagmin-1	Esyt1	4	4	4	5.2	5.2	5.2	121.55	1092	1.848E-12	0.35653	0.27802	48.329	2	82799000	62707000	20092000
Q61508	Extracellular matrix protein 1	Ecm1	3	3	3	7.3	7.3	7.3	62.832	559	6.9949E-09	1.8088	1.207	69.247	3	113690000	49340000	64345000
O09164	Extracellular superoxide dismutase [Cu-Zn]	Sod3	4	4	4	24.7	24.7	24.7	27.392	251	6.464E-25	1.3376	1.0464	49.505	5	453820000	192320000	261500000
P26040	Ezrin	Ezr	13	7	7	26.1	15	15	69.406	586	3.8357E-72	1.4417	1.0301	47.292	7	885050000	296510000	588550000
P47754	F-actin-capping protein subunit alpha-2	Capza2	6	6	6	29.4	29.4	29.4	32.967	286	8.4922E-10	1.7529	1.2256	109.93	6	346280000	148660000	197610000
Q8R123	FAD synthase	Flad1	8	8	8	29.3	29.3	29.3	54.766	492	8.892E-93	1.0311	0.78823	21.664	16	1052100000	523510000	528590000
P56213	FAD-linked sulfhydryl oxidase ALR	Gfer	4	4	4	25.8	25.8	25.8	22.876	198	3.4622E-13	2.309	1.6357	15.581	5	359810000	124870000	234940000
Q91WJ8	Far upstream element-binding protein 1	Fubp1	4	4	4	9.7	9.7	9.7	68.539	651	3.525E-301	2.5758	1.3841	42.577	3	302040000	93397000	208650000
Q3U0V1	Far upstream element-binding protein 2	Khsrp	7	7	7	18.4	18.4	18.4	76.775	748	4.654E-101	3.1636	2.4768	32.949	7	379850000	90210000	289640000
P54731	FAS-associated factor 1	Faf1	5	5	5	8.6	8.6	8.6	73.862	649	7.9768E-23	0.79547	0.63351	82.861	4	191640000	97975000	93665000
Q61553	Fascin	Fscn1	7	7	7	20.7	20.7	20.7	54.507	493	7.9655E-27	1.2798	0.83894	62.34	5	503690000	225680000	278010000
P19096	Fatty acid synthase	Fasn	17	17	17	11.1	11.1	11.1	272.43	2504	1.36E-259	0.41492	0.29298	125.73	12	1286600000	569450000	717140000
P04117	Fatty acid-binding protein, adipocyte	Fabp4	11	11	11	63.6	63.6	63.6	14.65	132	4.136E-146	2.3956	1.5915	72.207	24	3994700000	1122300000	2872400000
Q05816	Fatty acid-binding protein, epidermal	Fabp5	8	8	8	73.3	73.3	73.3	15.137	135	0	1.9115	1.2344	73.028	7	2134900000	499660000	1635300000
P11404	Fatty acid-binding protein, heart	Fabp3	8	8	8	55.6	55.6	55.6	14.819	133	2.076E-189	4.0758	2.9791	51.919	37	8.4162E+10	1.6629E+10	6.7532E+10
Q8BJL1	F-box only protein 30	Fbxo30	1	1	1	1.9	1.9	1.9	82.687	746	0.035105	1.8002	1.3441	0.81151	2	19238000	7605300	11633000
P62932	F-box only protein 40	Fbxo40	2	2	2	3.4	3.4	3.4	79.95	710	2.934E-27	0.42537	0.28472	52.479	2	3253000000	3215500000	37499000
Q9QZN4	F-box only protein 6	Fbxo6	3	3	3	13.9	13.9	13.9	34.492	295	5.1447E-17	1.0987	0.78011	168.95	2	138160000	58011000	80149000
Q3U7U3	F-box only protein 7	Fbxo7	2	2	2	7.5	7.5	7.5	57.648	523	1.1406E-19	1.1896	0.7975	57.21	3	171820000	78698000	93118000
Q8CIB5	Fermitin family homolog 2	Fermt2	10	10	10	21.6	21.6	21.6	77.8	680	6.308E-136	0.81316	0.56411	39.12	15	1020000000	517430000	502590000
Q8K1B8	Fermitin family homolog 3	Fermt3	2	2	2	3	3	3	75.634	665	0.0012537	0.88708	0.69452	20.614	2	53563000	28730000	24833000
Q9CPX4	Ferritin	Ftl1	12	12	12	73.8	73.8	73.8	20.772	183	1.146E-228	2.7673	1.9127	125.62	15	2131400000	631180000	1500200000
P09528	Ferritin heavy chain	Fth1	8	8	8	47.8	47.8	47.8	21.066	182	1.393E-126	3.1573	2.9966	51.8	18	3277800000	756270000	2521600000
Q544X6	Ferrochelatase	Fech	11	11	11	37.2	37.2	37.2	47.421	422	0	0.65014	0.42798	32.263	12	2625700000	1596300000	1029400000
Q9QXC1	Fetuin-B	Fetub	5	5	5	22.4	22.4	22.4	42.712	388	3.41E-107	2.3977	1.7825	24.965	5	364310000	106740000	257570000
Q76LL6	FH1/FH2 domain-containing protein 3	Fhod3	9	9	9	9.6	9.6	9.6	175.65	1578	6.4573E-37	0.90618	0.86077	49.067	6	134170000	73420000	60750000
Q8K0E8	Fibrinogen beta chain	Fgb	17	17	17	48	48	48	54.752	481	2.973E-232	0.77117	0.51674	52.61	22	1729200000	1041400000	687740000
Q8VCM7	Fibrinogen gamma chain	Fgg	14	14	14	33.7	33.7	33.7	49.391	436	0	0.68028	0.54469	40.771	18	1972200000	1132800000	839400000
P61148	Fibroblast growth factor 1	Fgf1	3	3	3	20	20	20	17.417	155	2.3992E-07	2.677	1.5731	15.831	3	543010000	155220000	387790000
Q9WVH9	Fibulin-5	Fbln5	3	3	3	8.9	8.9	8.9	50.193	448	1.6345E-31	0.29334	0.18454	82.219	2	110030000	84510000	25521000
Q8BTM8	Filamin-A	Flna	31	27	27	19	17.5	17.5	281.22	2647	3.197E-224	1.6848	1.2329	37.79	29	2712100000	979100000	1733000000
Q80X90	Filamin-B	Flnb	14	10	10	8	6.3	6.3	277.82	2602	7.2198E-48	2.0355	1.4274	33.021	10	448640000	156680000	291970000
Q71FD7	Filamin-binding LIM protein 1	Fblim1	6	6	6	29.6	29.6	29.6	41.026	375	3.4231E-31	1.7756	1.2897	47.198	10	719640000	308600000	411050000
D3Z576	Filamin-C	Flnc	39	39	34	21.6	21.6	19.1	292.34	2737	0	1.4223	1.0104	54.317	43	5510100000	2702900000	2807200000
Q923D2	Flavin reductase (NADPH)	Blvrb	9	9	9	50.5	50.5	50.5	22.197	206	5.9702E-21	1.5958	1.0234	44.129	11	1686900000	638620000	1048300000
Q5SS83	Flotillin-2	Flot2	4	4	4	11.7	11.7	11.7	47.116	428	3.7064E-08	1.2509	0.88144	33.471	4	107250000	51610000	55644000
A2AEX6	Four and a half LIM domains protein 1	Fhl1	2	2	2	7.8	7.8	7.8	35.08	309	1.6941E-07	0.50064	0.39953	56.133	2	109960000	47499000	62462000
O70433	Four and a half LIM domains protein 2	Fhl2	13	13	13	57.3	57.3	57.3	32.072	279	0	1.8054	1.2037	53.457	21	2426700000	1010700000	1416000000
Q61584	Fragile X mental retardation syndrome-related protein 1	Fxr1	4	4	4	8.1	8.1	8.1	76.221	677	3.9533E-28	1.3804	0.93343	66.483	5	227190000	116590000	110600000
P70695	Fructose-1,6-bisphosphatase isozyme 2	Fbp2	4	4	4	18.3	18.3	18.3	36.947	339	1.3004E-55	1.4573	1.1246	35.157	10	1119400000	411080000	708310000
A6ZI44	Fructose-bisphosphate aldolase	Aldoa	22	22	18	61.5	61.5	51.4	45.12	418	0	1.2642	0.83647	69.22	85	7.1185E+10	3.1576E+10	3.9608E+10
P97807	Fumarate hydratase, mitochondrial	Fh	20	20	20	59.4	59.4	59.4	54.356	507	0	2.0899	1.5213	61.579	57	3.1447E+10	1.0983E+10	2.0464E+10
P35505	Fumarylacetoacetase	Fah	6	6	6	17.9	17.9	17.9	46.175	419	2.1899E-25	1.4261	1.0267	36.876	6	574090000	256140000	317950000
Q3TC72	Fumarylacetoacetate hydrolase domain-containing protein 2A	Fahd2	10	10	10	50.2	50.2	50.2	34.69	313	0	0.98427	0.71143	33.362	14	2041500000	1003400000	1038100000
Q8VDC1	FYVE and coiled-coil domain-containing protein 1	Fyco1	5	5	5	4.2	4.2	4.2	162.33	1437	1.2799E-57	0.83999	0.69141	16.779	4	115840000	64319000	51520000
Q9R0N0	Galactokinase	Galk1	3	3	3	8.2	8.2	8.2	42.295	392	1.2012E-22	0.87034	0.76476	173.42	3	943790000	782290000	161500000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q03249	Galactose-1-phosphate uridylyltransferase	Galt	4	4	4	17.7	17.7	17.7	43.232	379	2.3787E-13	1.0087	0.54246	19.983	3	176150000	88447000	87706000
P16045	Galectin-1	Lgals1	5	5	5	43.7	43.7	43.7	14.866	135	7.6145E-34	2.3681	1.71	68.226	12	5857500000	1815700000	4041800000
P16110	Galectin-3	Lgals3	3	3	3	13.3	13.3	13.3	27.515	264	2.4497E-10	0.18549	0.13248	18.68	3	440390000	357850000	82538000
Q8VED9	Galectin-related protein A	Lgalsla	2	2	2	23.8	23.8	23.8	18.955	172	4.529E-36	2.451	1.9823	12.272	2	46602000	11678000	34924000
Q9QYB5	Gamma-adducin	Add3	2	2	2	4.7	4.7	4.7	78.776	706	6.4563E-11	2.5902	2.0523	16.589	3	173710000	44930000	128780000
P17183	Gamma-enolase	Eno2	5	3	3	15.7	9.7	9.7	47.296	434	3.4542E-22	2.3429	1.9906	52.32	5	2069100000	655520000	1413600000
P82348	Gamma-sarcoglycan	Sgcg	3	3	3	13.7	13.7	13.7	32.081	291	9.7469E-29	1.0725	0.89172	58.452	4	417430000	182070000	235360000
Q9Z0F7	Gamma-synuclein	Sncg	5	5	5	43.9	43.9	43.9	13.159	123	4.5969E-53	2.2323	2.0621	33.583	7	656340000	221550000	434790000
P23242	Gap junction alpha-1 protein	Gja1	2	2	2	12	12	12	43.004	382	9.8496E-13	3.6861	2.5012	90.114	2	49443000	12548000	36895000
P23591	GDP-L-fucose synthase	Tsta3	2	2	2	8.1	8.1	8.1	35.877	321	9.5427E-15	0.92413	0.65402	21.238	4	256550000	139900000	116650000
Q9Z1Z0	General vesicular transport factor p115	Uso1	13	13	13	18.9	18.9	18.9	106.98	959	2.477E-185	0.52994	0.39166	36.855	15	536210000	346920000	189290000
Q9JHK4	Geranylgeranyl transferase type-2 subunit alpha	Rabggta	5	5	5	14.8	14.8	14.8	64.989	567	2.7698E-57	0.39199	0.33644	37.412	4	191080000	122580000	68500000
P53612	Geranylgeranyl transferase type-2 subunit beta	Rabggtb	2	2	2	6.5	6.5	6.5	37.803	339	1.0093E-17	0.58982	0.43468	27.319	2	133110000	79143000	53970000
Q9CQI3	Glia maturation factor beta	Gmfb	2	2	2	26.8	26.8	26.8	16.723	142	3.325E-22	1.6487	1.6758	35.829	3	254990000	90197000	164790000
O88958	Glucosamine-6-phosphate isomerase 1	Gnpda1	6	6	4	27.7	27.7	19.7	32.549	289	3.1451E-34	0.85704	0.67826	30.845	5	401350000	222380000	178970000
Q00612	Glucose-6-phosphate 1-dehydrogenase X	G6pdx	4	4	4	8.7	8.7	8.7	59.262	515	1.0275E-10	0.63391	0.37927	24.435	6	243100000	149850000	93247000
P06745	Glucose-6-phosphate isomerase	Gpi	21	21	14	45.7	45.7	32.1	62.766	558	0	1.0563	0.76409	57.053	45	2.5733E+10	1.2783E+10	1.295E+10
P26443	Glutamate dehydrogenase 1, mitochondrial	Glud1	12	12	12	30.5	30.5	30.5	61.336	558	3.756E-219	0.44249	0.36598	111.59	12	1192000000	673290000	518710000
O09172	Glutamate--cysteine ligase regulatory subunit	Gclm	3	3	3	16.1	16.1	16.1	30.534	274	9.3166E-23	1.3077	0.8316	49.113	3	150430000	76810000	73616000
D3Z7P3	Glutaminase kidney isoform, mitochondrial	Gls	6	6	6	15.1	15.1	15.1	73.963	674	5.4853E-14	1.1533	0.88151	18.472	5	263550000	121730000	141820000
P15105	Glutamine synthetase	Glul	7	7	7	26.8	26.8	26.8	42.119	373	1.4134E-86	0.48531	0.42767	28.91	10	1037200000	710430000	326820000
Q9CZN8	Glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial	Qrsl1	3	3	3	7.4	7.4	7.4	56.782	525	2.961E-08	0.47085	0.56952	36.681	3	63492000	42786000	20706000
Q99JT1	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial	Pet112	2	2	2	6.6	6.6	6.6	62.118	557	6.4181E-11	0.88232	0.64096	16.153	2	120730000	63939000	56788000
Q8CBY0	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial	Gatc	2	2	2	23.9	23.9	23.9	16.667	155	5.6998E-17	2.158	1.5879	92.819	3	182710000	18581000	164130000
Q9CQM9	Glutaredoxin-3	Glrx3	9	9	9	35	35	35	37.778	337	3.389E-161	2.0079	1.4255	48.216	17	2533100000	921060000	1612100000
Q80Y14	Glutaredoxin-related protein 5, mitochondrial	Glrx5	1	1	1	12.5	12.5	12.5	16.292	152	2.1967E-48	2.6153	1.7984	14.049	4	927770000	288440000	639330000
Q60759	Glutaryl-CoA dehydrogenase, mitochondrial	Gcdh	7	7	7	27.9	27.9	27.9	48.605	438	8.9282E-93	0.70306	0.54544	24.915	11	1043500000	609780000	433680000
Q76LV0	Glutathione peroxidase	Gpx4	4	4	4	18.2	18.2	18.2	29.211	253	5.9517E-48	0.72435	0.54199	29.717	5	698570000	396340000	302230000
P11352	Glutathione peroxidase 1	Gpx1	4	4	4	31.8	31.8	31.8	22.347	201	3.0667E-24	0.72771	0.4873	57.229	6	966950000	610740000	356210000
P46412	Glutathione peroxidase 3	Gpx3	3	3	1	15	15	5.3	25.442	226	8.8132E-14	0.91285	0.631	13.775	5	592840000	311240000	281600000
P47791	Glutathione reductase, mitochondrial	Gsr	6	6	6	21.8	21.8	21.8	53.662	500	1.338E-113	1.2987	0.82897	46.157	9	1215100000	471840000	743250000
P30115	Glutathione S-transferase A3	Gsta3	4	3	3	15.8	12.2	12.2	25.36	221	2.0854E-16	1.6565	1.1697	17.64	3	363030000	138500000	224530000
P24472	Glutathione S-transferase A4	Gsta4	5	5	4	28.4	28.4	24.8	25.564	222	2.9405E-39	3.779	2.5077	29.276	8	5062400000	934190000	4128200000
Q9DCM2	Glutathione S-transferase kappa 1	Gstk1	11	11	11	55.8	55.8	55.8	25.704	226	3.084E-123	1.4485	0.94933	33.427	11	1775500000	823930000	951620000
P10649	Glutathione S-transferase Mu 1	Gstm1	15	15	8	62.8	62.8	30.7	25.97	218	1.31E-135	1.9023	1.3256	45.219	30	1.2517E+10	4492400000	8024900000
P15626	Glutathione S-transferase Mu 2	Gstm2	13	11	8	61.9	50.5	43.1	25.716	218	3.2514E-79	2.1374	1.9795	27.226	14	6362200000	2105200000	4257100000
P48774	Glutathione S-transferase Mu 5	Gstm5	8	8	8	41.1	41.1	41.1	26.635	224	8.151E-62	1.125	0.87294	45.451	9	1022300000	488770000	533510000
Q80W21	Glutathione S-transferase Mu 7	Gstm7	9	5	5	49.5	30.3	30.3	25.709	218	6.3523E-45	2.6641	2.557	50.971	5	465720000	142260000	323450000
O09131	Glutathione S-transferase omega-1	Gsto1	12	12	12	51.2	51.2	51.2	27.497	240	1.4859E-53	0.94904	0.72073	61.443	20	4684500000	2266400000	2418100000
P19157	Glutathione S-transferase P 1	Gstp1	8	8	8	50.5	50.5	50.5	23.609	210	4.046E-186	1.8779	1.5768	36.329	16	5189700000	1961100000	3228600000
Q64471	Glutathione S-transferase theta-1	Gstt1	3	3	3	13.8	13.8	13.8	27.374	240	4.269E-25	1.4659	1.0145	47.688	3	260980000	113910000	147070000
P51855	Glutathione synthetase	Gss	4	4	4	15.2	15.2	15.2	52.246	474	5.8248E-66	1.493	1.0408	45.17	7	452490000	258110000	194380000
P16858	Glyceraldehyde-3-phosphate dehydrogenase	Gapdh	20	20	1	61	61	6	35.81	333	0	1.7243	1.2775	54.562	100	8.1416E+10	3.4808E+10	4.6608E+10
Q64516	Glycerol kinase	Gk	4	4	4	9.7	9.7	9.7	61.227	559	1.4516E-29	1.3566	0.99957	53.406	4	270330000	107370000	162960000
P13707	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	Gpd1	12	12	12	41	41	41	37.572	349	1.8834E-61	1.5705	1.1824	57.313	13	2148700000	757190000	1391500000
Q3ULJ0	Glycerol-3-phosphate dehydrogenase 1-like protein	Gpd1l	9	9	9	28.8	28.8	28.8	38.225	351	1.2179E-98	1.7192	1.3623	66.264	10	1735600000	747780000	987790000
Q8C0L9	Glycerophosphocholine phosphodiesterase GPCPD1	Gpcpd1	3	3	3	6.5	6.5	6.5	76.578	675	1.3448E-08	0.965	0.75895	32.643	3	155510000	78319000	77191000
Q91WK5	Glycine cleavage system H protein, mitochondrial	Gcsh	2	2	2	17.6	17.6	17.6	18.637	170	1.568E-124	1.9935	1.3369	28.283	3	261730000	99239000	162490000
Q9CZD3	Glycine--tRNA ligase	Gars	10	10	10	18.8	18.8	18.8	81.877	729	5.27E-217	2.1499	1.5114	60.169	14	1241500000	426130000	815410000
Q9Z1E4	Glycogen [starch] synthase, muscle	Gys1	19	19	19	35.2	35.2	35.2	83.926	738	0	0.60629	0.46685	34.002	31	4492500000	2616500000	1876000000
Q8CI94	Glycogen phosphorylase, brain form	Pygb	41	41	31	52	52	40.5	96.729	843	0	0.52764	0.34863	62.195	79	3.434E+10	2.3246E+10	1.1094E+10
Q9ET01	Glycogen phosphorylase, liver form	Pygl	10	4	4	12.4	6	6	97.462	850	6.5188E-40	0.29057	0.26396	14.215	2	21574000	18613000	2960300
Q9WUB3	Glycogen phosphorylase, muscle form	Pygm	39	30	29	49.5	38	36.7	97.285	842	0	0.42929	0.29247	50.54	85	2.7948E+10	1.9477E+10	8471100000
Q2NL51	Glycogen synthase kinase-3 alpha	Gsk3a	5	5	5	18.2	18.2	18.2	51.66	490	3.2388E-21	0.84376	0.76029	65.291	7	432080000	202620000	229460000
E9QAQ5	Glycogen synthase kinase-3 beta	Gsk3b	6	6	6	25.9	25.9	25.9	47.989	433	1.6749E-97	0.58418	0.53561	119.13	7	990520000	863180000	127340000
K3W4S6	Glycogenin-1	Gyg1	6	6	6	24.4	24.4	24.4	41.926	377	3.644E-104	1.4657	1.0577	13.926	6	3439500000	1985200000	1454300000
O70310	Glycylpeptide N-tetradecanoyltransferase 1	Nmt1	4	4	4	12.1	12.1	12.1	56.888	496	2.5648E-16	0.68872	0.63282	45.349	4	292600000	179960000	112640000
Q9CPV4	Glyoxalase domain-containing protein 4	Glod4	6	6	6	22.5	22.5	22.5	33.316	298	1.863E-52	0.98711	0.84486	47.298	6	942630000	488880000	453750000
Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	Grhpr	9	9	9	35.4	35.4	35.4	35.328	328	3.847E-217	0.93509	0.61624	66.152	13	4440400000	2429000000	2011400000
Q9QZF2	Glypican-1	Gpc1	6	6	6	17.2	17.2	17.2	61.359	557	1.052E-49	0.35909	0.25979	56.942	5	328220000	216730000	111490000
Q9DCZ1	GMP reductase 1	Gmpr	4	4	4	23.2	23.2	23.2	37.482	345	5.477E-249	1.5654	1.1301	34.944	4	270740000	108600000	162140000
Q3THK7	GMP synthase [glutamine-hydrolyzing]	Gmps	11	11	11	25	25	25	76.723	693	1.739E-137	1.339	1.1063	37.393	15	971970000	412810000	559160000
Q99JX3	Golgi reassembly-stacking protein 2	Gorasp2	4	4	4	15.5	15.5	15.5	47.038	451	2.216E-107	1.1344	0.86451	7.5737	5	176200000	81234000	94968000
E9QP99	Golgin subfamily A member 3	Golga3	5	5	5	5.5	5.5	5.5	167.29	1487	2.1389E-76	1.3276	1.1052	72.876	4	114690000	62982000	51711000
Q91VW5	Golgin subfamily A member 4	Golga4	8	8	8	5.6	5.6	5.6	257.56	2238	3.804E-38	0.99413	0.99513	26.878	7	124140000	69714000	54429000
Q6IR34	G-protein-signaling modulator 1	Gpsm1	5	5	5	13.4	13.4	13.4	74.361	673	4.45E-182	2.7229	1.7871	63.289	6	545220000	194030000	351190000
Q9QYY0	GRB2-associated-binding protein 1	Gab1	4	4	4	7.9	7.9	7.9	76.812	695	1.2924E-05	0.72943	0.50663	128.17	2	57241000	33012000	24229000
Q8C5Q4	G-rich sequence factor 1	Grsf1	4	4	4	17.1	17.1	17.1	53.076	479	3.606E-138	1.69	1.2375	31.366	5	278230000	92933000	185300000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9JLM9	Growth factor receptor-bound protein 14	Grb14	3	3	3	10.6	10.6	10.6	60.572	538	5.5945E-06	1.0693	0.80357	63.436	3	94803000	50893000	43910000
Q60631	Growth factor receptor-bound protein 2	Grb2	2	2	2	8.8	8.8	8.8	25.238	217	1.7517E-55	2.4554	2.734	27.121	3	337990000	93277000	244710000
Q99LP6	GrpE protein homolog 1, mitochondrial	Grpel1	5	5	5	33.6	33.6	33.6	24.307	217	2.893E-216	2.3173	1.7709	27.643	5	886730000	289690000	597050000
Q9WTP7	GTP:AMP phosphotransferase, mitochondrial	Ak3	7	7	7	39.2	39.2	39.2	25.426	227	2.989E-119	1.045	0.63828	16.513	7	926240000	482520000	443720000
D3YTN4	GTPase IMAP family member 4	Gimap4	6	6	6	21	21	21	38.044	328	7.514E-35	2.0128	1.5112	34.915	6	235920000	75342000	160580000
P62827	GTP-binding nuclear protein Ran	Ran	5	5	5	30.6	30.6	30.6	24.423	216	1.898E-135	1.0146	0.77678	20.474	8	3814600000	2006300000	1808200000
O08582	GTP-binding protein 1	Gtpbp1	2	2	2	3.4	3.4	3.4	72.3	668	0.00095565	0.88913	0.64894	19.372	2	42130000	22789000	19341000
Q9CQC9	GTP-binding protein SAR1b	Sar1b	4	4	2	19.7	19.7	11.6	22.382	198	6.1967E-19	0.26328	0.18275	73.724	5	345210000	259000000	86204000
Q9R111	Guanine deaminase	Gda	4	4	4	12.6	12.6	12.6	51.012	454	7.945E-106	1.645	1.6376	26.021	4	247380000	89174000	158210000
E9PXE2	Guanine nucleotide exchange factor DBS	Mcf2l	1	1	1	1.2	1.2	1.2	132.39	1175	0.027288	1.8844	1.2604	24.498	3	549620000	207150000	342470000
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	Gnai2	5	5	4	19.2	19.2	16.1	40.489	355	2.842E-150	0.85954	0.62544	17.974	5	482710000	280730000	201970000
P62874	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	Gnb1	4	4	2	15.3	15.3	9.1	37.377	340	3.7411E-57	0.49566	0.53518	46.98	6	406960000	287720000	119230000
Q6R0H7	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	Gnas	4	3	3	5	4.1	4.1	121.5	1133	2.3858E-22	0.82576	0.64681	61.994	4	236370000	122700000	113680000
P21278	Guanine nucleotide-binding protein subunit alpha-11	Gna11	3	3	2	13.9	13.9	8.4	42.024	359	9.5254E-23	0.46374	0.41006	59.879	2	83759000	48588000	35171000
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	Gnb2l1	9	9	9	38.8	38.8	38.8	35.076	317	2.2243E-88	0.36248	0.26221	89.211	10	2115000000	1197700000	917340000
Q9D114	Guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase MESH1	Hddc3	2	2	2	17.3	17.3	17.3	20.262	179	9.4736E-22	1.6446	1.4208	66.143	2	102260000	46927000	55333000
Q9ERL9	Guanylate cyclase soluble subunit alpha-3	Gucy1a3	2	2	2	4.6	4.6	4.6	77.587	691	1.3157E-05	1.5086	1.3396	50.459	2	52776000	19291000	33485000
Q564G0	Guanylate kinase	Guk1	7	7	7	50.7	50.7	50.7	24.032	219	4.6638E-44	1.9628	1.3983	33.521	6	938620000	309190000	629430000
Q9ESX5	H/ACA ribonucleoprotein complex subunit 4	Dkc1	2	2	2	7.5	7.5	7.5	57.401	509	7.172E-111	2.3478	1.6221	113.49	3	62405000	28833000	33571000
Q3UGR5	Haloacid dehalogenase-like hydrolase domain-containing protein 2	Hdhd2	4	4	4	20.8	20.8	20.8	28.73	259	9.6821E-13	0.90964	0.80252	1.0281	2	210140000	104050000	106090000
Q9CYW4	Haloacid dehalogenase-like hydrolase domain-containing protein 3	Hdhd3	2	2	2	4.8	4.8	4.8	28.027	251	2.5069E-07	0.86356	0.64149	35.802	3	156510000	90270000	66237000
Q3TC93	HCLS1-binding protein 3	Hs1bp3	2	2	2	9.9	9.9	9.9	43.691	395	5.9964E-05	1.9047	2.0912	28.865	2	39037000	16437000	22600000
Q61696	Heat shock 70 kDa protein 1A	Hspa1a	14	9	8	32	23.4	22.2	70.078	641	0	0.89236	0.69393	95.662	12	1410000000	570400000	839560000
Q3U2G2	Heat shock 70 kDa protein 4	Hspa4	27	27	25	44.3	44.3	40.7	94.208	842	0	1.6045	1.3131	37.455	48	7571300000	3150500000	4420900000
P48722	Heat shock 70 kDa protein 4L	Hspa4l	11	9	9	18.6	15	15	94.381	838	1.0765E-68	1.303	0.82822	94.483	10	575590000	266310000	309280000
P63017	Heat shock cognate 71 kDa protein	Hspa8	27	27	17	47.2	47.2	30.3	70.87	646	0	1.449	1.0858	45.738	68	3.4217E+10	1.4349E+10	1.9868E+10
Q61699	Heat shock protein 105 kDa	Hsph1	9	8	8	16.8	15.2	15.2	96.406	858	1.7612E-60	1.1494	0.77019	82.275	9	630770000	332660000	298110000
Q9CQN1	Heat shock protein 75 kDa, mitochondrial	Trap1	15	15	15	30.2	30.2	30.2	80.208	706	0	1.1085	0.80792	36.692	20	2746300000	1363700000	1382600000
P14602	Heat shock protein beta-1	Hspb1	7	7	7	48.3	48.3	48.3	23.014	209	8.494E-196	1.3581	0.94223	93.278	19	8083000000	3708400000	4374600000
Q99PR8	Heat shock protein beta-2	Hspb2	4	4	4	31.3	31.3	31.3	20.374	182	2.5332E-17	1.6757	1.1619	18.054	3	276880000	110050000	166830000
Q9QZ57	Heat shock protein beta-3	Hspb3	2	2	2	10.4	10.4	10.4	17.229	154	0.00077856	1.7367	1.2952	35.525	2	216760000	79162000	137590000
Q5EBG6	Heat shock protein beta-6	Hspb6	4	4	4	40.7	40.7	40.7	17.521	162	4.6729E-72	3.8045	2.5081	39.476	10	1474400000	244170000	1230300000
P35385	Heat shock protein beta-7	Hspb7	5	5	5	49.1	49.1	49.1	18.634	169	8.632E-135	1.5621	1.0671	42.851	13	1589300000	590060000	999270000
P07901	Heat shock protein HSP 90-alpha	Hsp90aa1	25	14	14	38.9	25	25	84.787	733	0	1.204	0.78289	61.159	18	6963000000	3304500000	3658500000
P11499	Heat shock protein HSP 90-beta	Hsp90ab1	31	31	18	43.6	43.6	27.9	83.28	724	0	1.5611	1.1492	63.488	54	1.5346E+10	6292000000	9054100000
P17156	Heat shock-related 70 kDa protein 2	Hspa2	12	2	2	19.6	4.9	4.9	69.641	633	4.698E-234	1.4138	1.2154	165.04	2	75847000	37987000	37860000
P97825	Hematological and neurological expressed 1 protein	Hn1	2	2	2	27.3	27.3	27.3	16.08	154	3.788E-117	3.2768	2.842	13.466	2	500600000	105860000	394740000
Q9R257	Heme-binding protein 1	Hebp1	3	3	3	25.3	25.3	25.3	21.067	190	1.2298E-13	1.0195	0.79638	6.3605	2	43744000	22471000	21273000
Q91VB8	Hemoglobin subunit alpha	Hba-a1	12	12	10	93	93	86.6	15.112	142	0	1.9518	1.2018	42.318	163	2.454E+11	7.1064E+10	1.7433E+11
P02088	Hemoglobin subunit beta-1	Hbb-b1	14	4	1	83.7	26.5	8.8	15.84	147	0	4.8461	2.5991	261.98	9	3.9292E+10	252830000	3.9039E+10
P02089	Hemoglobin subunit beta-2	Hbb-b2	10	3	3	68	28.6	28.6	15.878	147	0	18.085	16.81	210.82	7	2.0781E+10	84443000	2.0697E+10
P04443	Hemoglobin subunit beta-H0	Hbb-bh0	1	1	1	6.8	6.8	6.8	16.384	147	0.0022801	0.64811	0.47429	152.88	2	120740000	65596000	55149000
Q91X72	Hemopexin	Hpx	22	22	22	48.3	48.3	48.3	51.317	460	1.517E-265	2.2895	1.5117	75.75	35	1.4731E+10	4961000000	9770100000
P49182	Heparin cofactor 2	Serpind1	2	2	2	2.9	2.9	2.9	54.496	478	0.00091776	1.1374	1.0057	15.65	2	123910000	56488000	67420000
G3UW70	Hepatitis B virus X-interacting protein homolog	Hbxip	1	1	1	13.8	13.8	13.8	15.354	145	2.7185E-62	1.0042	0.60624	4.5864	2	700760000	351880000	348880000
P51859	Hepatoma-derived growth factor	Hdgf	6	6	6	44.7	44.7	44.7	26.268	237	3.741E-137	2.6996	2.0261	37.265	8	1533500000	422430000	1111100000
Q3UMU9	Hepatoma-derived growth factor-related protein 2	Hdgfrp2	3	3	2	6.6	6.6	4	74.29	669	2.0833E-08	2.2743	1.3366	103.49	2	168630000	78207000	90423000
Q3TEA8	Heterochromatin protein 1-binding protein 3	Hp1bp3	4	4	4	9	9	9	60.866	554	7.2177E-11	0.58924	0.44822	17.739	3	83970000	59830000	24139000
Q20BD0	Heterogeneous nuclear ribonucleoprotein A/B	Hnrnpab	6	6	6	19	19	19	36.21	332	2.8408E-65	2.1872	1.474	59.874	10	2107000000	781800000	1325200000
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0	Hnrnpa0	4	4	4	14.4	14.4	14.4	30.53	305	3.7021E-31	0.96249	0.63678	41.647	6	900730000	466790000	433940000
Q5EBP8	Heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	6	6	6	21.7	21.7	21.7	38.833	373	1.337E-151	1.9214	1.072	54.176	6	701810000	235330000	466480000
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	Hnrnpa3	9	9	9	23.7	23.7	23.7	39.652	379	2.239E-213	1.1519	0.63096	38.707	12	1866000000	915580000	950410000
Q60668	Heterogeneous nuclear ribonucleoprotein D0	Hnrnpd	5	5	4	13.5	13.5	11.3	38.354	355	1.5385E-18	2.5788	1.8167	37.226	4	553040000	174060000	378980000
D3YTQ3	Heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	4	3	3	11.2	9.3	9.3	46.27	420	6.0362E-35	2.173	2.4926	35.27	3	338920000	100810000	238110000
Q9Z2X1	Heterogeneous nuclear ribonucleoprotein F	Hnrnpf	3	2	2	12	8	8	45.729	415	4.477E-105	1.6729	1.3363	18.008	5	314920000	117420000	197500000
Q8C2Q7	Heterogeneous nuclear ribonucleoprotein H	Hnrnph1	5	5	2	17.6	17.6	7	51.217	472	2.017E-135	1.4927	1.197	2.7086	3	285150000	115920000	169230000
P70333	Heterogeneous nuclear ribonucleoprotein H2	Hnrnph2	3	1	1	11.1	3.8	3.8	49.279	449	1.117E-161	2.2219	1.6264	80.37	2	138590000	29460000	109130000
P61979	Heterogeneous nuclear ribonucleoprotein K	Hnrnpk	12	12	12	40.8	40.8	40.8	50.976	463	0	1.8063	1.3782	31.019	16	8486800000	2507600000	5979200000
G5E924	Heterogeneous nuclear ribonucleoprotein L	Hnrnpl	4	4	4	11.2	11.2	11.2	66.821	615	3.9182E-53	1.0416	0.96296	31.908	5	300420000	146080000	154340000
Q921F4	Heterogeneous nuclear ribonucleoprotein L-like	Hnrpll	1	1	1	2.9	2.9	2.9	64.124	591	7.566E-08	0.91695	0.9021	5.9187	2	58648000	30797000	27851000
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	Hnrnpm	3	3	3	6.7	6.7	6.7	77.648	729	2.7425E-17	1.169	0.88752	26.18	3	176380000	82638000	93740000
Q7TMK9	Heterogeneous nuclear ribonucleoprotein Q	Syncrip	9	9	7	24.7	24.7	21.7	69.632	623	7.928E-139	1.8004	1.5633	63.923	9	1180600000	453380000	727260000
Q8VEK3	Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	9	9	9	17.2	17.2	17.2	87.917	800	1.1388E-66	0.72108	0.64203	62.761	9	1256400000	718910000	537490000
Q8VDM6	Heterogeneous nuclear ribonucleoprotein U-like protein 1	Hnrnpul1	2	2	2	3.8	3.8	3.8	96.001	859	0.00024247	0.55737	0.42019	15.89	2	27178000	17700000	9477500
Q00PI9	Heterogeneous nuclear ribonucleoprotein U-like protein 2	Hnrnpul2	5	5	5	11.3	11.3	11.3	84.939	745	7.4229E-28	0.84336	0.64033	9.8495	4	130700000	69110000	61588000
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	Hnrnpa2b1	7	7	7	15.3	15.3	15.3	37.402	353	1.875E-75	1.3523	0.87238	40.359	16	2224600000	930650000	1293900000
Q9Z204	Heterogeneous nuclear ribonucleoproteins C1/C2	Hnrnpc	5	5	5	10.9	10.9	10.9	34.384	313	1.0448E-22	1.1069	1.3384	27.909	3	214130000	84248000	129880000
Q8BMS4	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	Coq3	6	6	6	23	23	23	40.956	370	8.453E-204	0.99819	0.71275	28.349	7	2111400000	1058200000	1053200000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P17710	Hexokinase-1	Hk1	25	21	20	28.9	25.8	24.8	108.3	974	3.044E-217	0.74857	0.51902	37.493	25	5437300000	3347100000	2090300000
P63158	High mobility group protein B1	Hmgb1	5	5	4	27.4	27.4	21.9	24.893	215	0	2.8549	1.8499	38.123	5	2105400000	587240000	1518100000
P30681	High mobility group protein B2	Hmgb2	3	2	2	12.9	7.1	7.1	24.162	210	2.034E-09	2.8369	2.209	9.0004	3	430730000	118680000	312050000
P62748	Hippocalcin-like protein 1	Hpcal1	2	2	2	11.9	11.9	11.9	22.338	193	2.4286E-06	0.69449	0.4478	154.27	2	106870000	74010000	32856000
P70349	Histidine triad nucleotide-binding protein 1	Hint1	5	5	5	47.6	47.6	47.6	13.777	126	2.956E-123	2.3861	1.783	51.889	15	1.3832E+10	3370100000	1.0461E+10
Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochondrial	Hint2	3	3	3	31.9	31.9	31.9	17.32	163	9.84E-170	1.8904	1.3339	42.878	17	4316600000	1825300000	2491300000
Q9ESB3	Histidine-rich glycoprotein	Hrg	4	4	4	7.4	7.4	7.4	59.162	525	2.2532E-09	1.038	0.74842	19.735	6	265000000	118670000	146330000
Q61035	Histidine--tRNA ligase, cytoplasmic	Hars	4	4	4	12	12	12	57.432	509	1.8703E-23	1.5066	1.3607	62.099	6	550230000	177890000	372350000
P10922	Histone H1.0	H1f0	2	2	2	10.8	10.8	10.8	20.861	194	1.9985E-08	0.29341	0.30999	20.212	2	356310000	279420000	76885000
P43275	Histone H1.1	Hist1h1a	3	2	2	18.8	14.6	14.6	21.785	213	1.0877E-10	0.46294	0.56676	37.111	2	59843000	39108000	20735000
P43277	Histone H1.3	Hist1h1d	4	4	2	14.9	14.9	5.9	22.099	221	3.0853E-16	0.43098	0.3974	33.795	4	764200000	574850000	189350000
Q8CBB6	Histone H2B	Gm13646	1	1	1	11.2	11.2	11.2	14.888	134	7.4465E-63	0.27764	0.20798	3.3895	4	196950000	156100000	40853000
P62806	Histone H4	Hist1h4a	4	4	4	43.7	43.7	43.7	11.367	103	4.1039E-18	0.18401	0.13132	79.246	3	279430000	225430000	54000000
D3YUP1	Histone-arginine methyltransferase CARM1	Carm1	3	3	3	6.1	6.1	6.1	70.322	651	4.4037E-09	0.98028	0.73934	66.603	3	108040000	55391000	52651000
Q60973	Histone-binding protein RBBP7	Rbbp7	2	2	1	8.2	8.2	6.4	47.789	425	1.1013E-12	1.1089	0.85124	15.787	3	387340000	144420000	242910000
Q91WC0	Histone-lysine N-methyltransferase setd3	Setd3	4	4	4	10.9	10.9	10.9	67.175	594	4.3447E-46	0.9056	0.74169	41.483	7	191950000	95470000	96483000
Q8R1H0	Homeodomain-only protein	Hopx	4	4	4	78.1	78.1	78.1	8.2821	73	1.967E-201	2.482	1.8781	105.41	3	800280000	166980000	633290000
Q9Z2Y3	Homer protein homolog 1	Homer1	4	4	4	12.6	12.6	12.6	41.412	366	6.0779E-36	1.619	1.3892	9.037	3	84323000	38708000	45614000
B1AUX2	Host cell factor 1	Hcfc1	4	4	4	3.6	3.6	3.6	215.05	2090	6.522E-33	1.774	1.1342	71.63	4	155290000	51277000	104010000
Q99L47	Hsc70-interacting protein	St13	7	7	7	18.3	18.3	18.3	41.655	371	0	1.5947	1.6798	29.918	8	1825700000	695480000	1130200000
Q99P31	Hsp70-binding protein 1	Hspbp1	3	3	3	13.7	13.7	13.7	39.166	357	4.1839E-11	0.77608	0.59172	45.04	3	151490000	84385000	67106000
Q61081	Hsp90 co-chaperone Cdc37	Cdc37	4	4	4	17.4	17.4	17.4	44.593	379	2.0003E-96	1.7256	1.2016	22.381	5	394200000	164370000	229830000
Q9CZP7	Hsp90 co-chaperone Cdc37-like 1	Cdc37l1	4	4	4	14.9	14.9	14.9	38.439	335	1.0523E-10	1.9987	1.123	47.608	4	221750000	104140000	117610000
Q8VD75	Huntingtin-interacting protein 1	Hip1	2	2	2	3.2	3.2	3.2	115.2	1029	0.001091	0.99608	0.6644	113.54	2	40384000	21186000	19198000
Q6P9N1	Hyccin	Fam126a	3	3	3	14.8	14.8	14.8	57.306	521	4.3695E-05	0.45896	0.3644	71.335	2	36045000	28409000	7635100
Q80W93	Hydrocephalus-inducing protein	Hydin	2	2	2	0.4	0.4	0.4	581.52	5154	0.0024878	1.3017	0.88061	33.535	2	220390000	93516000	126870000
Q8R0N6	Hydroxyacid-oxoacid transhydrogenase, mitochondrial	Adhfe1	9	9	9	35.7	35.7	35.7	49.937	465	1.92E-122	1.0769	0.86014	61.75	17	1310200000	648500000	661690000
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Hadh	14	14	14	54.8	54.8	54.8	34.463	314	0	1.4078	0.91505	59.269	48	3.9845E+10	1.6434E+10	2.341E+10
G5E8T9	Hydroxyacylglutathione hydrolase, mitochondrial	Hagh	6	6	6	27.8	27.8	27.8	34.103	309	9.358E-99	1.1636	0.76846	41.433	10	1146500000	541830000	604670000
P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	Hmgcl	7	7	7	29.2	29.2	29.2	34.238	325	3.439E-115	1.5235	1.2702	22.925	9	1841900000	692970000	1148900000
Q8JZK9	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	Hmgcs1	3	3	3	8.3	8.3	8.3	57.568	520	4.9169E-14	2.777	2.4029	5.4388	4	73887000	20628000	53259000
Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2	Hsdl2	18	18	18	50	50	50	54.208	490	0	1.2348	0.85547	73.786	33	1.1504E+10	5255400000	6249000000
P00493	Hypoxanthine-guanine phosphoribosyltransferase	Hprt1	5	5	5	25.7	25.7	25.7	24.57	218	4.1037E-26	1.2796	1.5296	22.257	3	490200000	196010000	294200000
Q9JKR6	Hypoxia up-regulated protein 1	Hyou1	12	12	12	16.7	16.7	16.7	111.18	999	5.0457E-71	0.89438	0.69185	47.234	11	925440000	458900000	466540000
P01869	Ig gamma-1 chain C region, membrane-bound form	Ighg1	3	3	3	13	13	13	43.386	393	5.4615E-17	0.98396	0.7472	22.172	2	413280000	184800000	228480000
P01865	Ig gamma-2A chain C region, membrane-bound form	Igh-1a	5	5	5	22.6	22.6	22.6	43.949	398	3.9179E-95	0.19892	0.22818	139.18	5	325590000	286530000	39055000
P01867	Ig gamma-2B chain C region	Igh-3	4	4	4	15.6	15.6	15.6	44.259	404	3.7732E-22	0.60376	0.41963	22.45	6	584090000	363050000	221040000
P03987	Ig gamma-3 chain C region		2	2	2	6.8	6.8	6.8	43.929	398	7.8054E-09	1.4659	0.98335	39.625	4	391950000	183100000	208840000
P06330	Ig heavy chain V region AC38 205.12		2	2	2	24.6	24.6	24.6	12.934	118	5.9668E-10	2.0911	1.8908	7.3628	2	100240000	32417000	67826000
P01872	Ig mu chain C region secreted form	Igh-6	7	7	7	22	22	22	49.971	454	1.131E-123	7.4592	6.7556	67.058	7	717460000	117510000	599950000
Q61249	Immunoglobulin-binding protein 1	Igbp1	5	5	5	22.1	22.1	22.1	38.97	340	2.5061E-16	1.3628	0.98164	38.6	5	336060000	149930000	186120000
Q60960	Importin subunit alpha-1	Kpna1	3	3	3	7.2	7.2	7.2	60.182	538	1.6346E-08	0.3133	0.22844	141.57	2	56707000	44978000	11728000
O35344	Importin subunit alpha-3	Kpna3	4	3	3	15.9	10.6	10.6	57.772	521	4.6518E-28	1.1444	0.7676	47.561	3	190670000	101090000	89588000
O35343	Importin subunit alpha-4	Kpna4	7	7	6	25.9	25.9	20.5	57.922	521	1.1275E-57	1.1569	0.78637	82.342	6	657140000	225410000	431730000
P70168	Importin subunit beta-1	Kpnb1	11	11	11	17.7	17.7	17.7	97.183	876	3.3413E-92	0.79909	0.56188	104.34	16	2272200000	707420000	1564800000
Q8BKC5	Importin-5	Ipo5	13	13	13	18.1	18.1	18.1	123.59	1097	1.254E-282	0.79188	0.57197	39.082	16	1379800000	870070000	509740000
Q9EPL8	Importin-7	Ipo7	8	8	8	9.2	9.2	9.2	119.49	1038	6.1436E-20	0.7618	0.59157	26.687	8	397040000	218470000	178570000
P40936	Indolethylamine N-methyltransferase	Inmt	7	7	7	34.5	34.5	34.5	29.459	264	1.795E-71	1.1699	0.70102	32.606	11	1201500000	599290000	602210000
Q920Q8	Influenza virus NS1A-binding protein homolog	Ivns1abp	5	5	5	9	9	9	71.58	642	5.8759E-36	0.50662	0.34741	47.143	5	352860000	169730000	183130000
Q9DBD0	Inhibitor of carbonic anhydrase	Ica	8	8	8	14.4	14.4	14.4	76.765	700	4.1609E-78	1.5795	1.3752	40.961	10	510010000	204030000	305980000
Q9D819	Inorganic pyrophosphatase	Ppa1	13	13	13	66.4	66.4	66.4	32.667	289	4.338E-150	1.9515	1.7826	41.864	17	2667000000	992820000	1674100000
Q91VM9	Inorganic pyrophosphatase 2, mitochondrial	Ppa2	11	11	11	45.5	45.5	45.5	38.114	330	0	1.9144	1.5628	49.487	22	3485600000	1287500000	2198100000
Q9D892	Inosine triphosphate pyrophosphatase	Itpa	4	4	4	30.8	30.8	30.8	21.897	198	9.359E-76	1.239	1.1808	13.515	3	241360000	119910000	121450000
P24547	Inosine-5-monophosphate dehydrogenase 2	Impdh2	5	5	5	12.3	12.3	12.3	55.814	514	4.8238E-15	1.3194	0.94525	41.1	3	194280000	74267000	120010000
Q924B0	Inositol monophosphatase 1	Impa1	4	4	4	23.8	23.8	23.8	30.429	277	3.1629E-13	1.4226	1.1865	27.332	4	578520000	213030000	365490000
Q91UZ5	Inositol monophosphatase 2	Impa2	5	5	5	23.1	23.1	23.1	31.716	290	2.638E-113	1.3745	1.2013	62.346	5	789400000	377980000	411420000
P49442	Inositol polyphosphate 1-phosphatase	Inpp1	4	4	4	15.7	15.7	15.7	43.346	396	5.2698E-29	1.2999	1.3372	49.404	3	258350000	111900000	146450000
Q9JHU9	Inositol-3-phosphate synthase 1	Isyna1	2	2	2	3.8	3.8	3.8	60.931	557	2.5816E-06	0.82911	0.68157	31.039	3	198010000	134540000	63472000
F6RPJ9	Insulin-degrading enzyme	Ide	3	3	3	3.9	3.9	3.9	114.15	987	1.1849E-08	1.1434	1.0841	41.682	5	427810000	240290000	187520000
E9Q5D9	Insulin-like growth factor-binding protein 7	Igfbp7	2	2	2	11.2	11.2	11.2	32.803	313	0.0076055	1.5648	0.97253	23.005	2	29094000	11667000	17427000
Q3V3R4	Integrin alpha-1	Itga1	2	2	2	2.2	2.2	2.2	130.81	1179	0.0037509	3.8915	2.9191	12.932	2	75111000	17715000	57396000
Q61739	Integrin alpha-6	Itga6	3	3	3	3.1	3.1	3.1	122.16	1091	4.1784E-40	1.5838	1.0969	18.025	4	85483000	29822000	55661000
Q61738	Integrin alpha-7	Itga7	10	10	10	10.9	10.9	10.9	129.33	1179	4.6664E-97	1.0948	0.82936	51.923	18	1023800000	481130000	542720000
P09055	Integrin beta-1	Itgb1	5	5	5	9.6	9.6	9.6	88.231	798	2.0245E-45	1.4252	0.85397	62.186	7	633900000	283670000	350230000
O55222	Integrin-linked protein kinase	Ilk	3	3	3	11.1	11.1	11.1	51.373	452	2.7574E-71	0.62944	0.44302	35.484	3	237390000	122630000	114760000
F8WJ05	Inter-alpha-trypsin inhibitor heavy chain H1	Itih1	9	9	9	17.6	17.6	17.6	101.63	911	2.013E-99	1.4342	1.2363	44.841	11	689140000	248270000	440870000
G3X977	Inter-alpha-trypsin inhibitor heavy chain H2	Itih2	3	3	3	5.8	5.8	5.8	106.36	950	6.9364E-15	1.4591	1.012	34.281	4	373910000	153960000	219950000
Q61704	Inter-alpha-trypsin inhibitor heavy chain H3	Itih3	2	2	2	3.1	3.1	3.1	99.357	889	0.0014724	3.348	2.0949	60.669	2	45820000	9289200	36531000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8CGE8	Interferon-activable protein 205-A	Ifi205a	4	4	2	13.4	13.4	6.7	45.176	404	1.9543E-08	1.765	1.1689	66.053	4	265830000	108880000	156950000
Q9Z0E6	Interferon-induced guanylate-binding protein 2	Gbp2	3	3	3	8.3	8.3	8.3	66.739	589	3.499E-101	1.374	0.96896	62.009	3	230340000	123140000	107200000
Q9CXY6	Interleukin enhancer-binding factor 2	Ilf2	4	4	4	14.6	14.6	14.6	43.062	390	4.6284E-18	0.88365	0.589	53.621	3	304550000	163940000	140610000
Q3UVZ1	Interleukin-1 receptor accessory protein	Il1rap	3	3	3	4.7	4.7	4.7	78.639	685	5.8933E-06	1.2483	0.79061	349.86	3	6204400000	6038000000	166430000
P14719	Interleukin-1 receptor-like 1	Il1rl1	2	2	2	5.6	5.6	5.6	64.801	567	0.0099269	11.032	7.091	412.27	2	6963400000	88368000	6875100000
Q6PHB0	Interleukin-20 receptor subunit alpha	Il20ra	1	1	1	1.8	1.8	1.8	61.977	546	0.00086483	0.043509	0.034159	208.61	3	7631400000	7506000000	125420000
E9Q0N0	Intersectin-1	Itsn1	6	6	6	4.4	4.4	4.4	194.89	1719	1.3098E-20	1.419	1.715	38.853	5	109830000	39669000	70161000
Q9DCB8	Iron-sulfur cluster assembly 2 homolog, mitochondrial	Isca2	5	5	5	48.1	48.1	48.1	16.718	154	5.4E-167	3.2799	2.1699	1.4101	2	664700000	152880000	511820000
Q8K3A0	Iron-sulfur cluster co-chaperone protein HscB, mitochondrial	Hscb	4	4	4	23.9	23.9	23.9	26.645	234	2.2777E-25	1.9526	1.6922	101.75	2	48037000	16078000	31959000
Q9DB29	Isoamyl acetate-hydrolyzing esterase 1 homolog	Iah1	3	3	3	15.7	15.7	15.7	27.974	249	0.00014714	0.64401	0.57204	22.585	6	547380000	320200000	227180000
Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	Acad8	9	9	9	28.3	28.3	28.3	45.019	413	1.026E-193	0.43602	0.31949	58.955	14	1962100000	1297100000	665050000
Q91V64	Isochorismatase domain-containing protein 1	Isoc1	5	5	5	22.9	22.9	22.9	32.032	297	9.8519E-20	1.7823	1.5189	34.25	7	1005500000	361260000	644260000
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	Isoc2a	6	6	6	57.8	57.8	57.8	22.417	206	1.703E-212	1.012	0.79907	54.228	17	977120000	306840000	670280000
Q9DCC7	Isochorismatase domain-containing protein 2B, mitochondrial	Isoc2b	3	3	3	23.8	23.8	23.8	23.151	210	4.3901E-08	0.7663	0.6681	60.559	7	112630000	61713000	50912000
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Idh3a	13	13	13	33.3	33.3	33.3	39.638	366	0	1.6087	1.1516	49.477	56	2.33E+10	9924500000	1.3375E+10
P70404	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	Idh3g	10	10	10	40.7	40.7	40.7	42.785	393	0	0.93724	0.64251	51.79	30	1.2197E+10	6943800000	5252800000
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	Idh1	16	14	14	35.5	31.6	31.6	46.674	414	2.904E-229	1.0974	0.93062	41.548	15	2016900000	1009700000	1007200000
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	Idh2	34	34	32	55.3	55.3	53.8	50.906	452	0	0.81406	0.5514	54.862	168	8.5251E+10	5.0335E+10	3.4916E+10
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic	Iars	14	14	14	15	15	15	144.27	1262	6.3365E-45	0.62083	0.45697	57.488	17	968510000	644340000	324170000
Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	Iars2	18	18	18	23.2	23.2	23.2	112.8	1012	0	0.68803	0.49489	30.102	19	3021900000	1886000000	1135900000
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	Ivd	18	18	18	46	46	46	46.325	424	2.3E-254	1.3534	1.1578	42.521	28	1.1036E+10	4757300000	6278400000
Q02257	Junction plakoglobin	Jup	4	4	2	7.5	7.5	5.1	81.8	745	2.4558E-23	0.53039	0.44222	59.72	4	102460000	67053000	35402000
Q9ET78	Junctophilin-2	Jph2	5	5	5	7.8	7.8	7.8	74.691	696	2.9625E-47	1.622	1.2921	17.264	3	255930000	94757000	161180000
E9Q1Q9	Ketohexokinase	Khk	2	2	2	8.5	8.5	8.5	37.724	343	6.5341E-28	2.1011	1.5619	59.333	2	142720000	36905000	105810000
Q6ZPU9	KIF1-binding protein	Kbp	1	1	1	3.4	3.4	3.4	71.051	617	3.0129E-10	1.1423	0.8865	2.5757	2	46002000	19725000	26277000
F8VQC7	Kinectin	Ktn1	18	18	18	21.1	21.1	21.1	152.54	1327	1.291E-230	0.73389	0.55368	69.624	16	1422300000	734900000	687400000
Q8CD76	Kinesin light chain 1	Klc1	6	6	6	12	12	12	69.494	616	2.9963E-21	0.64259	0.41292	170.85	4	216160000	127190000	88977000
Q61768	Kinesin-1 heavy chain	Kif5b	22	22	22	28.8	28.8	28.8	109.55	963	0	1.8786	1.5579	56.401	30	1762900000	664770000	1098200000
F8VQ75	Kinesin-like protein KIF13A	Kif13a	5	5	3	3.9	3.9	2.6	195.7	1749	6.6461E-23	1.3012	1.0926	97.81	5	207500000	71441000	136060000
O08677	Kininogen-1	Kng1	8	8	8	19.1	19.1	19.1	73.101	661	0	1.9907	1.4234	80.744	10	2030500000	646110000	1384400000
Q8BTY1	Kynurenine--oxoglutarate transaminase 1	Ccbl1	7	7	7	27.8	27.8	27.8	47.563	424	1.45E-231	0.98894	0.72819	29.756	8	751380000	384680000	366700000
Q71RI9	Kynurenine--oxoglutarate transaminase 3	Ccbl2	6	6	6	17.6	17.6	17.6	51.126	455	7.5041E-25	0.66055	0.55555	36.392	9	1154700000	675180000	479540000
Q91YP0	L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2hgdh	3	3	3	8.6	8.6	8.6	50.898	464	1.0105E-50	0.3441	0.25932	56.85	2	81590000	57097000	24493000
Q3V384	Lactation elevated protein 1	Lace1	6	6	6	18.8	18.8	18.8	54.313	480	1.5138E-83	0.85097	0.55949	66.344	9	741670000	390140000	351530000
Q9CPU0	Lactoylglutathione lyase	Glo1	9	9	9	52.2	52.2	52.2	20.809	184	1.2605E-50	3.6804	2.4131	50.816	8	3915900000	979670000	2936300000
Q99KP3	Lambda-crystallin homolog	Cryl1	4	4	4	16.9	16.9	16.9	35.208	319	1.1636E-09	0.89207	0.73125	33.837	4	272280000	147700000	124580000
Q61033	Lamina-associated polypeptide 2, isoforms alpha/zeta	Tmpo	7	7	2	17.9	17.9	4.5	75.167	693	3.635E-225	2.0086	1.3898	56.136	9	605210000	214580000	390630000
Q60675	Laminin subunit alpha-2	Lama2	70	70	70	32.2	32.2	32.2	343.81	3118	0	1.8676	1.3452	58.977	96	9855900000	3701700000	6154300000
P97927	Laminin subunit alpha-4	Lama4	15	15	15	12.8	12.8	12.8	201.82	1816	0	1.3753	1.0061	39.229	18	1335000000	560410000	774580000
Q61001	Laminin subunit alpha-5	Lama5	3	3	3	1.4	1.4	1.4	404.05	3718	5.1496E-30	1.24	0.76821	17.99	2	116240000	51461000	64776000
E9QN70	Laminin subunit beta-1	Lamb1	20	20	20	15	15	15	202.44	1834	0	1.3529	1.0522	36.959	27	3129300000	1298600000	1830700000
Q61292	Laminin subunit beta-2	Lamb2	20	20	20	15.1	15.1	15.1	196.58	1799	0	1.2947	0.89724	64.951	24	1745500000	765830000	979650000
F8VQJ3	Laminin subunit gamma-1	Lamc1	34	34	33	27.4	27.4	26.9	177.19	1607	0	1.8036	1.2556	64.999	44	6542400000	2545900000	3996500000
Q9CQF6	L-aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	Aasdhppt	2	2	2	5.5	5.5	5.5	35.764	309	0.0072014	0.7978	0.61878	48.981	2	30399000	14881000	15518000
Q9JJK2	LanC-like protein 2	Lancl2	4	4	4	12.4	12.4	12.4	50.777	450	1.1837E-36	0.83113	0.6537	62.152	3	70592000	42063000	28529000
Q9Z1R2	Large proline-rich protein BAG6	Bag6	9	9	9	11.9	11.9	11.9	121.04	1154	2.471E-131	1.3137	0.9534	106.79	7	630640000	379090000	251550000
Q8C0M9	L-asparaginase	Asrgl1	5	5	5	26.1	26.1	26.1	33.95	326	5.419E-256	2.3848	1.7559	32.314	8	1035000000	344280000	690680000
Q8K4G1	Latent-transforming growth factor beta-binding protein 4	Ltbp4	5	5	5	5.5	5.5	5.5	178.64	1666	1.751E-56	2.008	1.6906	17.69	4	72037000	24010000	48027000
Q9ERE7	LDLR chaperone MESD	Mesdc2	2	2	2	15.2	15.2	15.2	25.206	224	0.0028573	4.1887	3.8332	71.686	2	430650000	134640000	296010000
O89017	Legumain	Lgmn	1	1	1	2.8	2.8	2.8	49.372	435	5.1676E-27	0.40868	0.30934	48.371	2	39728000	33316000	6412300
Q9Z2I0	LETM1 and EF-hand domain-containing protein 1, mitochondrial	Letm1	8	8	8	19.8	19.8	19.8	82.988	738	9.5052E-63	1.086	1.1023	57.671	7	707330000	329170000	378150000
Q9JHQ5	Leucine zipper transcription factor-like protein 1	Lztfl1	2	2	2	10.7	10.7	10.7	34.773	299	3.8522E-39	0.81288	0.5449	79.183	3	198210000	87355000	110860000
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	Lrpprc	47	47	47	40.4	40.4	40.4	156.61	1392	0	1.091	0.74272	66.465	63	1.4274E+10	7122300000	7151800000
E9PV22	Leucine-rich repeat-containing protein 47	Lrrc47	5	5	5	10.3	10.3	10.3	65.903	603	2.0493E-58	0.92101	0.7245	31.467	5	211880000	114920000	96961000
Q922Q8	Leucine-rich repeat-containing protein 59	Lrrc59	3	3	3	10.4	10.4	10.4	34.877	307	1.2041E-14	0.39996	0.38711	55.253	2	60788000	44494000	16294000
Q8BMJ2	Leucine--tRNA ligase, cytoplasmic	Lars	6	6	6	6.5	6.5	6.5	134.19	1178	2.5955E-28	0.58088	0.4009	29.305	7	307140000	197400000	109750000
Q8C129	Leucyl-cystinyl aminopeptidase	Lnpep	8	8	8	11	11	11	117.3	1025	8.8977E-58	1.7435	1.4729	58.967	8	521150000	199030000	322120000
P42703	Leukemia inhibitory factor receptor	Lifr	1	1	1	1.5	1.5	1.5	122.57	1092	1.8864E-05	1.6273	1.5291	22.805	2	20380000	8159900	12220000
Q61735	Leukocyte surface antigen CD47	Cd47	1	1	1	4.6	4.6	4.6	33.097	303	0.001901	1.2053	1.244	26.172	2	30884000	14961000	15923000
P24527	Leukotriene A-4 hydrolase	Lta4h	17	17	17	34.7	34.7	34.7	69.05	611	0	1.2119	1.1666	44.918	21	1524300000	687490000	836820000
D3YU59	LIM and calponin homology domains-containing protein 1	Limch1	6	6	6	8.5	8.5	8.5	120.99	1083	1.832E-15	1.7905	1.3068	23.488	7	204510000	67303000	137210000
Q8VEE1	LIM and cysteine-rich domains protein 1	Lmcd1	5	5	5	15.1	15.1	15.1	40.996	365	2.0646E-67	1.5419	1.034	76.45	3	264220000	139840000	124380000
E9QP62	LIM and senescent cell antigen-like-containing domain protein 1	Lims1	8	8	6	24.8	24.8	19.1	44.34	387	2.6241E-51	0.5283	0.58751	68.023	8	426440000	231480000	194970000
Q9JKS4	LIM domain-binding protein 3	Ldb3	20	20	3	37.8	37.8	4.8	76.431	723	0	2.3577	1.5069	72.828	41	1.8534E+10	5326500000	1.3208E+10
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenas	Dbt	11	11	11	31.5	31.5	31.5	53.246	482	5.3636E-82	1.0313	0.68936	36.145	17	3011200000	1566800000	1444400000
Q8BFW7	Lipoma-preferred partner homolog	Lpp	6	6	6	12.7	12.7	12.7	65.89	613	1.6749E-21	1.7454	1.5765	37.283	6	205610000	86545000	119060000
Q9ESE1	Lipopolysaccharide-responsive and beige-like anchor protein	Lrba	2	2	2	0.8	0.8	0.8	317.06	2856	0.0000183	0.71964	0.46592	92.055	2	40308000	25974000	14334000
P11152	Lipoprotein lipase	Lpl	6	6	6	16.7	16.7	16.7	53.109	474	2.2913E-36	0.67459	0.446	35.714	6	723580000	404950000	318630000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q99M04	Lipoyl synthase, mitochondrial	Lias	2	2	2	6.2	6.2	6.2	41.879	373	0.002208	0.40109	0.35344	9.7613	2	9513400	6392300	3121100
G3X9J4	LisH domain and HEAT repeat-containing protein KIAA1468	2310035C23Rik	5	5	5	6.3	6.3	6.3	134.57	1216	2.3061E-13	0.91984	0.71905	120.66	4	386700000	298450000	88250000
G5E8N5	L-lactate dehydrogenase	Ldha	15	13	13	46.3	39.3	39.3	39.758	361	0	0.89492	0.76241	80.447	23	1.087E+10	6242700000	4627500000
P16125	L-lactate dehydrogenase B chain	Ldhb	17	17	15	50	50	44.6	36.572	334	0	1.7118	1.2764	54.66	50	7.1256E+10	2.7333E+10	4.3923E+10
Q8CGK3	Lon protease homolog, mitochondrial	Lonp1	22	22	22	29	29	29	105.84	949	1.45E-295	1.6277	1.1394	36.777	33	5216200000	2137100000	3079000000
P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadl	20	20	20	42.6	42.6	42.6	47.907	430	0	0.91909	0.6425	46.998	92	2.3975E+10	1.2598E+10	1.1377E+10
D3Z041	Long-chain-fatty-acid--CoA ligase 1	Acsl1	25	25	25	43.5	43.5	43.5	78.034	699	2.227E-299	0.55506	0.46079	78.959	33	6531600000	3866100000	2665500000
Q9D358	Low molecular weight phosphotyrosine protein phosphatase	Acp1	3	3	1	25.9	25.9	11.4	18.192	158	3.025E-94	0.95734	0.88618	44.427	2	218000000	123320000	94680000
P51885	Lumican	Lum	7	7	7	27.5	27.5	27.5	38.265	338	0	2.8042	2.826	33.847	12	6190000000	2035500000	4154500000
P32067	Lupus La protein homolog	Ssb	6	6	6	15.4	15.4	15.4	47.756	415	2.3438E-11	1.3599	0.96273	22.621	4	190840000	85509000	105330000
Q91V16	LYR motif-containing protein 5	Lyrm5	3	3	3	27.9	27.9	27.9	10.391	86	0.00003349	0.88651	0.72575	9.1386	4	206750000	118180000	88575000
P46737	Lys-63-specific deubiquitinase BRCC36	Brcc3	3	3	3	12.4	12.4	12.4	33.34	291	1.807E-10	0.86345	0.58348	18.734	3	183950000	107100000	76844000
Q8BP40	Lysophosphatidic acid phosphatase type 6	Acp6	8	8	8	27.3	27.3	27.3	47.624	418	4.786E-111	2.0866	2.2662	44.34	11	1126600000	383490000	743110000
P70699	Lysosomal alpha-glucosidase	Gaa	6	6	6	9.9	9.9	9.9	106.25	953	9.9325E-48	0.80736	0.63533	47.34	9	499920000	264670000	235250000
G3X8T3	Lysosomal protective protein	Ctsa	7	6	6	17.7	17.7	17.7	55.726	492	5.3475E-81	0.2631	0.15975	81.462	7	1244900000	902180000	342760000
P10619	Lysosomal protective protein	CTSA	23	23	22	47.1	47.1	47.1	54.465	480	0	0.086628	0.0675	218.74	117	3.0631E+11	3.0281E+11	3501600000
P11438	Lysosome-associated membrane glycoprotein 1	Lamp1	2	2	2	5.4	5.4	5.4	43.865	406	1.6012E-16	0.25219	0.22141	37.038	2	720650000	569900000	150750000
P17047	Lysosome-associated membrane glycoprotein 2	Lamp2	2	2	2	4.6	4.6	4.6	45.681	415	1.6422E-05	0.26999	0.23352	55.387	2	49596000	38990000	10607000
P08905	Lysozyme C-2	Lyz2	2	2	2	21.6	21.6	21.6	16.689	148	1.8584E-33	0.39155	0.27953	56.419	2	115310000	81956000	33359000
Q8R2P8	Lysyl-tRNA synthetase	Kars	11	11	11	21	21	21	71.29	624	4.682E-186	0.9462	0.70682	45.566	11	1573400000	872720000	700690000
Q9DAR7	m7GpppX diphosphatase	Dcps	4	4	4	18.9	18.9	18.9	38.988	338	2.5789E-19	1.3077	0.81497	49.58	4	285960000	127640000	158310000
Q61830	Macrophage mannose receptor 1	Mrc1	6	6	6	5.6	5.6	5.6	164.98	1456	2.9513E-31	1.3836	1.2357	33.016	5	92249000	43929000	48320000
P34884	Macrophage migration inhibitory factor	Mif	2	2	2	26.1	26.1	26.1	12.504	115	1.05E-124	1.8049	1.2976	13.53	4	9185600000	3309600000	5876000000
Q99LB4	Macrophage-capping protein	Capg	5	5	5	24.4	24.4	24.4	38.768	349	7.873E-200	0.79191	0.55479	30.944	7	1105000000	584920000	520050000
Q9D967	Magnesium-dependent phosphatase 1	Mdp1	3	3	3	28.7	28.7	28.7	18.582	164	5.1151E-70	0.96101	0.69801	12.988	3	137650000	68128000	69525000
A2BIN1	Major urinary protein 2	Mup10	4	4	1	29.4	29.4	6.1	20.681	180	5.0097E-19	1.1697	0.6681	42.322	4	698190000	315690000	382500000
E9Q3X0	Major vault protein	Mvp	8	8	8	14.1	14.1	14.1	96.856	870	2.1995E-59	0.56972	0.38487	46.128	10	1022300000	687850000	334500000
P14152	Malate dehydrogenase, cytoplasmic	Mdh1	12	12	12	35.6	35.6	35.6	36.511	334	0	1.9462	1.409	47.372	57	4.809E+10	1.4521E+10	3.3569E+10
P08249	Malate dehydrogenase, mitochondrial	Mdh2	23	23	23	67.2	67.2	67.2	35.611	338	0	1.9192	1.3039	36.988	112	4.6336E+10	1.6343E+10	2.9993E+10
Q9WVL0	Maleylacetoacetate isomerase	Gstz1	4	4	4	27.8	27.8	27.8	24.275	216	6.0202E-14	0.84354	0.6976	56.061	6	969320000	528500000	440810000
Q9DB27	Malignant T-cell-amplified sequence 1	Mcts1	4	4	4	30.4	30.4	30.4	20.555	181	5.8812E-14	0.72676	0.50047	35.115	4	242290000	134800000	107490000
Q99J39	Malonyl-CoA decarboxylase, mitochondrial	Mlycd	12	12	12	39.2	39.2	39.2	54.735	492	1.176E-287	0.81318	0.64772	28.495	23	3746700000	2106300000	1640300000
Q8R3F5	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial	Mcat	2	2	2	5.5	5.5	5.5	41.928	381	0.0012057	0.26159	0.19482	5.3832	3	166080000	134300000	31778000
Q99M71	Mammalian ependymin-related protein 1	Epdr1	2	2	2	8.9	8.9	8.9	25.485	224	0.0027174	0.36641	0.32906	44.537	2	151930000	118060000	33871000
Q922H4	Mannose-1-phosphate guanyltransferase alpha	Gmppa	3	3	3	10	10	10	46.244	420	2.0736E-23	0.74553	0.55395	47.031	3	182140000	135010000	47132000
Q8BTZ7	Mannose-1-phosphate guanyltransferase beta	Gmppb	3	3	3	14.2	14.2	14.2	39.916	360	6.31E-08	1.8569	1.4611	201.43	4	1143100000	979450000	163640000
Q924M7	Mannose-6-phosphate isomerase	Mpi	6	6	6	18.7	18.7	18.7	46.575	423	2.331E-171	2.0804	1.5814	17.046	12	2138000000	617060000	1521000000
P49138	MAP kinase-activated protein kinase 2	Mapkapk2	2	2	2	8.8	8.8	8.8	44.049	386	1.537E-08	2.1209	1.307	28.624	2	152860000	48343000	104520000
A2AJI0	MAP7 domain-containing protein 1	Map7d1	4	4	4	7.4	7.4	7.4	93.275	846	1.3559E-18	0.80388	0.61018	31.145	4	124560000	71689000	52867000
Q8K310	Matrin-3	Matr3	4	4	4	7.3	7.3	7.3	94.629	846	1.8939E-10	1.1452	1.0295	30.166	3	99392000	47375000	52016000
P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadm	18	18	18	40.1	40.1	40.1	46.481	421	1.629E-174	0.96885	0.75449	45.471	55	3.7912E+10	1.8054E+10	1.9858E+10
Q8BJ34	Meiosis arrest female protein 1	Marf1	1	1	1	0.4	0.4	0.4	192.06	1730	0.007211	1.1825	0.83374	30.426	2	609280000	302950000	306320000
Q9D4I2	Meiosis inhibitor protein 1	Mei1	1	1	1	0.8	0.8	0.8	146.75	1325	0.023538	0.025491	0.01852	21.69	2	275490000	270730000	4756300
Q8BI84	Melanoma inhibitory activity protein 3	Mia3	3	3	3	2.8	2.8	2.8	213.67	1930	5.6958E-19	2.3691	1.6482	54.258	2	59665000	15955000	43710000
Q99LB6	Methionine adenosyltransferase 2 subunit beta	Mat2b	4	4	4	18.9	18.9	18.9	37.392	334	2.4497E-14	1.2318	0.75646	48.763	4	182240000	76122000	106120000
Q3UI33	Methionine aminopeptidase	Metap2	4	4	4	14.8	14.8	14.8	54.117	488	7.1614E-43	1.1709	0.89337	61.483	7	615540000	353050000	262500000
Q8BP48	Methionine aminopeptidase 1	Metap1	2	2	2	8.3	8.3	8.3	43.221	386	6.7182E-15	0.6933	0.43918	23.163	2	128670000	72646000	56024000
Q78J03	Methionine-R-sulfoxide reductase B2, mitochondrial	Msrb2	6	6	6	38.3	38.3	38.3	19.157	175	5.4061E-56	2.1295	1.5444	63.797	8	1867800000	775400000	1092400000
Q8BU85	Methionine-R-sulfoxide reductase B3, mitochondrial	Msrb3	3	3	3	17.8	17.8	17.8	26.832	253	4.5791E-17	2.4678	1.8302	30.559	3	186480000	51359000	135120000
E9QB02	Methionine--tRNA ligase, cytoplasmic	Mars	2	2	2	4.4	4.4	4.4	102.37	910	6.9693E-06	0.46123	0.35438	69.098	3	112080000	82600000	29478000
Q499X9	Methionine--tRNA ligase, mitochondrial	Mars2	8	8	8	17.7	17.7	17.7	65.804	586	1.674E-27	0.6041	0.46268	140.2	9	1460500000	1295800000	164690000
Q9Z2D6	Methyl-CpG-binding protein 2	Mecp2	3	3	3	10.3	10.3	10.3	52.307	484	7.1312E-08	1.1799	1.137	22.152	3	53618000	24968000	28651000
Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	Mccc2	13	13	13	30.4	30.4	30.4	61.378	563	0	0.53509	0.39091	38.219	21	2912300000	1933300000	979010000
Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	Mccc1	13	13	13	29.7	29.7	29.7	79.343	717	2.478E-245	0.84985	0.56187	45.842	14	2455400000	1285700000	1169700000
Q9JLZ3	Methylglutaconyl-CoA hydratase, mitochondrial	Auh	6	6	6	21.7	21.7	21.7	33.395	314	0	1.1205	0.74842	12.227	7	1802300000	847450000	954830000
Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Aldh6a1	20	20	20	53.8	53.8	53.8	57.915	535	0	1.1823	0.71975	46.866	41	3.0281E+10	1.331E+10	1.6971E+10
Q8C7H1	Methylmalonic aciduria type A homolog, mitochondrial	Mmaa	1	1	1	5.1	5.1	5.1	45.932	415	3.4946E-27	0.94753	0.63495	20.481	2	134810000	75181000	59625000
Q9D1I5	Methylmalonyl-CoA epimerase, mitochondrial	Mcee	2	2	2	18	18	18	19.017	178	4.5477E-39	2.8283	1.8223	45.511	4	841740000	196090000	645640000
P16332	Methylmalonyl-CoA mutase, mitochondrial	Mut	12	12	12	22.7	22.7	22.7	82.843	748	3.562E-135	1.2725	1.0275	45.714	15	3363600000	1586000000	1777600000
Q9CQT1	Methylthioribose-1-phosphate isomerase	Mri1	3	3	3	13	13	13	39.41	369	1.3168E-19	0.84527	0.63567	90.136	2	38025000	22309000	15716000
Q91YR5	Methyltransferase-like protein 13	Mettl13	1	1	1	1.6	1.6	1.6	78.756	698	0.014562	1.2427	0.894	24.197	2	137680000	64188000	73489000
Q8BGT6	MICAL-like protein 1	Micall1	3	3	3	4.6	4.6	4.6	94.078	870	1.0738E-06	3.9972	2.9814	28.368	3	55872000	11730000	44142000
Q9CPU4	Microsomal glutathione S-transferase 3	Mgst3	1	1	1	9.2	9.2	9.2	16.958	153	2.6787E-08	0.49399	0.46376	20.774	2	104240000	75365000	28878000
E9PVY8	Microtubule-actin cross-linking factor 1	Macf1	13	11	11	2.5	2.1	2.1	831.87	7355	6.4928E-41	1.1531	0.9208	33.609	7	240100000	109300000	130800000
A2A5Y6	Microtubule-associated protein	Mapt	8	8	8	22	22	22	78.085	749	1.134E-110	1.8358	1.3684	66.943	8	447080000	159140000	287940000
F7CK47	Microtubule-associated protein	Mtap4	19	19	15	21.6	21.6	16.1	152.67	1441	2.214E-293	2.473	1.8281	56.02	21	3156100000	992570000	2163600000
P14873	Microtubule-associated protein 1B	Map1b	3	3	3	1.9	1.9	1.9	270.25	2464	6.3147E-12	2.6042	2.3386	221.09	2	222460000	31279000	191180000
P27546	Microtubule-associated protein 4	Map4	13	9	9	22.1	15.1	15.1	117.43	1125	2.666E-296	2.1738	1.5894	36.621	21	4807900000	1628500000	3179500000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q61166	Microtubule-associated protein RP/EB family member 1	Mapre1	5	4	3	25.4	22.4	19	30.016	268	2.745E-181	1.4963	1.2023	49.264	2	98781000	45302000	53479000
Q8R001	Microtubule-associated protein RP/EB family member 2	Mapre2	7	7	6	29.4	29.4	27	36.946	326	5.9066E-56	1.3736	1.134	31.478	9	1396900000	628670000	768210000
Q59J78	Mimitin, mitochondrial	Ndufaf2	2	2	2	15.5	15.5	15.5	19.628	168	7.5557E-10	1.0729	0.78896	6.1996	2	119380000	59215000	60164000
Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	Aldh1l2	6	6	6	9.2	9.2	9.2	101.59	923	3.4485E-21	2.6881	2.5125	48.293	5	280570000	97387000	183180000
Q9CR62	Mitochondrial 2-oxoglutarate/malate carrier protein	Slc25a11	9	9	9	28.7	28.7	28.7	34.155	314	1.956E-34	0.55525	0.34924	35.445	9	1963200000	1262700000	700490000
Q8VCF0	Mitochondrial antiviral-signaling protein	Mavs	7	7	7	33	33	33	53.398	503	9.527E-118	1.7847	1.2337	31.574	12	777060000	299280000	477780000
Q9Z2Z6	Mitochondrial carnitine/acylcarnitine carrier protein	Slc25a20	6	6	6	19.9	19.9	19.9	33.026	301	3.1491E-30	0.78352	0.62988	40.217	5	715180000	363270000	351910000
Q791V5	Mitochondrial carrier homolog 2	Mtch2	3	3	3	19.1	19.1	19.1	33.499	303	1.261E-30	0.56179	0.46517	22.425	4	369340000	246690000	122650000
Q9CQ92	Mitochondrial fission 1 protein	Fis1	2	2	2	16.4	16.4	16.4	17.008	152	3.4824E-37	1.3635	1.3929	9.3367	3	103270000	43187000	60085000
E0CYB9	Mitochondrial fission factor	Mff	1	1	1	10.1	10.1	10.1	35.878	316	1.8793E-05	1.165	1.3364	5.3844	2	143890000	69905000	73990000
Q9CRB8	Mitochondrial fission process protein 1	Mtfp1	5	5	5	45.2	45.2	45.2	18.314	166	7.8526E-12	1.1509	0.94535	104.37	5	299760000	87410000	212350000
P62075	Mitochondrial import inner membrane translocase subunit Tim13	Timm13	4	4	4	49.5	49.5	49.5	10.458	95	9.2749E-13	1.9804	1.3597	14.334	5	1084100000	405510000	678610000
Q9CQV1	Mitochondrial import inner membrane translocase subunit TIM16	Pam16	2	2	2	32	32	32	13.784	125	5.4808E-58	1.0644	0.57226	4.8453	2	103670000	49613000	54053000
O35857	Mitochondrial import inner membrane translocase subunit TIM44	Timm44	3	3	3	8	8	8	51.091	452	7.5861E-24	1.1367	0.64532	31.218	3	111500000	52830000	58671000
Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	Timm8a1	2	2	2	22.7	22.7	22.7	11.042	97	1.8362E-34	2.6791	1.9627	38.199	4	564800000	176060000	388740000
P62077	Mitochondrial import inner membrane translocase subunit Tim8 B	Timm8b	3	3	3	34.9	34.9	34.9	9.2864	83	9.9349E-22	2.2533	1.6704	32.1	4	399480000	139110000	260370000
Q9WV98	Mitochondrial import inner membrane translocase subunit Tim9	Timm9	3	3	3	52.8	52.8	52.8	10.344	89	5.598E-184	2.031	1.384	43.747	4	725400000	281140000	444260000
Q9CYG7	Mitochondrial import receptor subunit TOM34	Tomm34	3	3	3	9.7	9.7	9.7	34.278	309	1.5717E-58	1.0893	0.93097	34.842	2	80288000	40463000	39825000
Q8CAQ8	Mitochondrial inner membrane protein	Immt	16	16	16	24.4	24.4	24.4	83.899	757	0	0.49204	0.36065	74.459	16	1461200000	925320000	535870000
A6H611	Mitochondrial intermediate peptidase	Mipep	4	4	4	7.5	7.5	7.5	80.851	711	3.8141E-11	0.70923	0.59559	26.203	4	192510000	106700000	85818000
Q9D6Y7	Mitochondrial peptide methionine sulfoxide reductase	Msra	6	6	6	36.5	36.5	36.5	25.988	233	4.001E-99	2.1099	1.3881	32.861	7	2202500000	639790000	1562700000
Q3UFY8	Mitochondrial ribonuclease P protein 1	Rg9mtd1	2	2	2	7.2	7.2	7.2	48.385	414	9.4251E-39	2.281	1.7359	61.059	2	102340000	35817000	66526000
Q9DC61	Mitochondrial-processing peptidase subunit alpha	Pmpca	15	15	2	33.4	33.4	6.9	58.278	524	4.2582E-74	0.86452	0.57971	30.976	22	3009800000	1559600000	1450200000
Q9CXT8	Mitochondrial-processing peptidase subunit beta	Pmpcb	4	4	4	10.8	10.8	10.8	54.614	489	1.1475E-92	0.78238	0.53442	141.3	4	733950000	316580000	417370000
Q811U4	Mitofusin-1	Mfn1	2	2	2	3.1	3.1	3.1	83.725	741	0.00016452	0.8737	0.65371	230.94	2	105360000	38096000	67265000
P63085	Mitogen-activated protein kinase 1	Mapk1	4	4	4	15.1	15.1	15.1	41.275	358	3.5947E-09	0.92089	0.63382	6.6391	3	194650000	112380000	82268000
P47811	Mitogen-activated protein kinase 14	Mapk14	6	6	6	22.5	22.5	22.5	41.287	360	5.6744E-17	0.9395	0.58107	35.737	4	250300000	135290000	115010000
D3Z3G6	Mitogen-activated protein kinase 3	Mapk3	2	2	2	9.5	9.5	9.5	42.401	380	6.8633E-10	0.74243	0.5167	1.0872	2	430970000	248230000	182750000
Q9WTU6	Mitogen-activated protein kinase 9	Mapk9	2	2	2	6.9	6.9	6.9	48.189	423	4.257E-08	1.1381	0.98255	34.812	2	15925000	7831700	8093100
Q3U1V8	Mitogen-activated protein kinase kinase kinase 9	Map3k9	3	3	2	2.5	2.5	1.8	118.8	1077	0.0014775	0.59239	0.45552	72.526	3	508270000	306360000	201900000
Q9ESL4	Mitogen-activated protein kinase kinase kinase MLT	Mltk	3	3	3	4.6	4.6	4.6	91.719	802	7.2383E-07	1.0002	0.67624	6.5771	4	409890000	220490000	189410000
Q9WVA3	Mitotic checkpoint protein BUB3	Bub3	4	4	4	14.4	14.4	14.4	36.954	326	2.3809E-14	0.87451	0.69665	20.81	3	168110000	89107000	78999000
P10404	MLV-related proviral Env polyprotein	Fv4	2	2	2	3.7	3.7	3.7	69.612	641	0.0085974	0.64104	0.53506	135.7	2	92212000	45807000	46405000
P26041	Moesin	Msn	20	20	12	34.1	34.1	20.5	67.766	577	1.129E-183	1.4591	1.1671	42.363	22	3764000000	1503200000	2260800000
P53986	Monocarboxylate transporter 1	Slc16a1	2	2	2	4.7	4.7	4.7	53.267	493	5.4044E-55	0.74961	0.6179	6.8692	4	214420000	131520000	82892000
D3YYS6	Monoglyceride lipase	Mgll	2	2	2	7.3	7.3	7.3	36.654	331	0.00012057	0.47717	0.30947	19.248	2	103870000	56630000	47237000
Q8BKY8	mTERF domain-containing protein 3, mitochondrial	Mterfd3	4	4	4	14.3	14.3	14.3	43.452	385	1.3334E-14	0.82673	0.72452	64.768	3	99052000	52774000	46278000
Q9DCL9	Multifunctional protein ADE2	Paics	10	10	10	31.8	31.8	31.8	47.006	425	1.081E-109	1.7927	1.4319	39.631	14	2064400000	572830000	1491600000
A6H6E2	Multimerin-2	Mmrn2	5	5	5	8.9	8.9	8.9	105.21	943	1.5267E-15	2.357	1.5185	35.378	4	241390000	78685000	162710000
Q9Z2L6	Multiple inositol polyphosphate phosphatase 1	Minpp1	2	2	2	6.9	6.9	6.9	54.537	481	3.5972E-06	1.8466	1.0252	21.814	2	105610000	41579000	64029000
P28665	Murinoglobulin-1	Mug1	24	24	24	25.6	25.6	25.6	165.3	1476	0	2.0087	1.5871	40.613	33	5817900000	2116500000	3701400000
G3X9Q0	Muscleblind-like protein 1	Mbnl1	2	2	2	10.8	10.8	10.8	40.894	381	2.6611E-09	1.4488	1.0494	7.9965	3	275870000	110850000	165020000
A2AMM0	Muscle-related coiled-coil protein	Murc	2	2	2	8.8	8.8	8.8	41.008	362	3.4142E-50	1.6186	1.4141	20.904	6	264720000	106880000	157830000
Q8R4U1	Myb-related transcription factor, partner of profilin	Mypop	1	1	1	3.3	3.3	3.3	41.89	393	0.048983	0.12843	0.078851	11.295	2	2091900000	1960100000	131810000
Q5SUV2	MYCBP-associated protein	Mycbpap	1	1	1	0.8	0.8	0.8	106.45	932	0.042645	0.66906	0.52283	18.319	4	127940000	71605000	56333000
E9PZ54	Myocardial zonula adherens protein	Gcom1	4	4	4	9.5	9.5	9.5	63.506	550	1.4114E-13	1.9967	1.3607	42.44	6	230290000	78969000	151320000
P04247	Myoglobin	Mb	13	13	13	78.6	78.6	78.6	17.069	154	0	3.1924	2.1681	37.846	79	8.8719E+10	1.9337E+10	6.9382E+10
Q62234	Myomesin-1	Myom1	50	50	50	39.2	39.2	39.2	185.46	1667	0	1.1882	0.91719	38.944	82	1.3079E+10	6689000000	6390300000
Q5DTJ9	Myopalladin	Mypn	2	2	2	1.9	1.9	1.9	144.11	1315	1.0168E-11	1.5184	1.3085	14.728	2	81835000	38072000	43763000
P09542	Myosin light chain 3	Myl3	11	11	8	61.3	61.3	50	22.421	204	3.317E-106	1.7991	1.373	72.877	26	2.5747E+10	8098200000	1.7649E+10
P09541	Myosin light chain 4	Myl4	6	5	5	32.6	26.9	26.9	21.159	193	1.165E-147	1.633	1.2309	25.371	4	1092100000	364270000	727860000
B1B1A8	Myosin light chain kinase, smooth muscle	Mylk	8	8	8	5.5	5.5	5.5	213.61	1950	4.5034E-25	3.0043	2.0764	25.878	5	227420000	73456000	153960000
Q60605	Myosin light polypeptide 6	Myl6	4	4	4	34.4	34.4	34.4	16.93	151	6.6709E-52	1.7064	1.4408	32.017	6	742030000	294750000	447280000
Q3THE2	Myosin regulatory light chain 12B	Myl12b	1	1	1	5.8	5.8	5.8	19.779	172	5.1105E-05	1.5891	1.1875	5.6559	2	65650000	28448000	37202000
Q9QVP4	Myosin regulatory light chain 2, atrial isoform	Myl7	4	4	4	33.7	33.7	33.7	19.45	175	1.5863E-25	1.559	1.4322	13.047	7	1383600000	571320000	812240000
P51667	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	Myl2	11	11	4	74.1	74.1	35.5	18.864	166	0	1.8053	1.2416	69.785	17	8023500000	2833100000	5190400000
Q02566	Myosin-6	Myh6	60	60	22	40.9	40.9	16.6	223.56	1938	0	0.56356	0.46068	64.52	83	1.2279E+10	8459100000	3820200000
Q3UIK0	Myosin-binding protein C, cardiac-type	Mybpc3	62	62	62	52.1	52.1	52.1	141.39	1278	0	1.2175	0.89953	53.773	142	5.1425E+10	2.4624E+10	2.6801E+10
P54265	Myotonin-protein kinase	Dmpk	3	3	3	7.4	7.4	7.4	69.601	631	1.4635E-09	0.94973	0.7333	35.918	5	79411000	43518000	35893000
P62774	Myotrophin	Mtpn	2	2	2	20.3	20.3	20.3	12.861	118	1.9631E-49	2.6278	1.7586	41.625	3	464000000	134430000	329570000
Q9JJW5	Myozenin-2	Myoz2	4	4	4	25.8	25.8	25.8	29.761	264	8.46E-43	2.1258	1.5867	79.052	5	391160000	116130000	275030000
Q64191	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	Aga	3	3	3	11.6	11.6	11.6	37.022	346	1.0716E-28	1.8729	1.2791	27.176	5	415910000	148280000	267630000
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	Ddah1	3	2	2	11.9	9.1	9.1	31.381	285	7.7413E-06	3.8483	3.7027	32.164	2	73242000	16436000	56805000
Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	Ddah2	8	8	7	41.1	41.1	38.2	29.645	285	0	2.1141	1.6926	94.4	8	974170000	386470000	587700000
Q9JHL1	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	Slc9a3r2	4	4	4	18.7	18.7	18.7	37.402	337	4.7256E-11	1.7443	0.98414	58.892	3	270460000	109110000	161360000
Q9D997	N-acetyl-D-glucosamine kinase	Nagk	6	6	6	26.3	26.3	26.3	39.346	361	1.5058E-57	0.75469	0.55183	41.192	6	428550000	276530000	152020000
Q68FH4	N-acetylgalactosamine kinase	Galk2	2	2	2	4.1	4.1	4.1	50.503	458	3.224E-09	0.51746	0.42058	60.413	2	139630000	89186000	50439000
Q8BFR4	N-acetylglucosamine-6-sulfatase	Gns	2	2	2	3.9	3.9	3.9	61.174	544	0.00032235	1.1008	0.84893	27.167	2	56355000	26936000	29419000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8C5H8	NAD kinase domain-containing protein 1	Nadkd1	8	8	8	27.7	27.7	27.7	50.858	452	6.2202E-41	0.73699	0.57857	24.997	10	713620000	425710000	287910000
Q61941	NAD(P) transhydrogenase, mitochondrial	Nnt	22	22	22	29.7	29.7	29.7	113.84	1086	3.292E-247	0.83377	0.68012	37.299	31	5775700000	3190500000	2585200000
Q64669	NAD(P)H dehydrogenase [quinone] 1	Nqo1	7	7	7	29.2	29.2	29.2	30.959	274	1.4533E-32	0.74388	0.47218	109.72	8	2355900000	869840000	1486100000
Q8K4Z3	NAD(P)H-hydrate epimerase	Apoa1bp	7	7	7	30.9	30.9	30.9	30.972	282	1.006E-129	0.84357	0.60694	45.258	13	3829200000	2160900000	1668400000
Q8VDQ8	NAD-dependent protein deacetylase sirtuin-2	Sirt2	3	3	3	16.5	16.5	16.5	43.256	389	4.961E-48	0.59138	0.51562	31.941	4	116500000	82030000	34468000
Q8K2C6	NAD-dependent protein deacylase sirtuin-5, mitochondrial	Sirt5	10	10	10	40.3	40.3	40.3	34.134	310	2.41E-257	1.411	0.90442	27.335	12	1661100000	616400000	1044700000
Q9JKL4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3	Ndufaf3	3	3	3	20.5	20.5	20.5	20.733	185	6.9567E-63	0.71824	0.55088	8.0096	2	58383000	31553000	26830000
Q9D1H6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 4	Ndufaf4	1	1	1	8.1	8.1	8.1	20.082	173	3.1874E-39	0.71993	0.47779	12.791	2	83008000	45023000	37984000
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	Ndufa10	12	12	12	46.8	46.8	46.8	40.603	355	1.983E-219	0.31204	0.27842	51.664	27	8519800000	6526800000	1993000000
G5E814	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	Ndufa11	4	4	4	50.3	50.3	50.3	15.115	143	1.0519E-13	0.82309	0.52782	35.857	4	300060000	156980000	143080000
Q7TMF3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	Ndufa12	5	5	5	43.4	43.4	43.4	17.086	145	9.4105E-15	0.73506	0.56167	14.622	7	827870000	488690000	339180000
Q9ERS2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Ndufa13	5	5	5	42.4	42.4	42.4	16.859	144	1.3376E-17	0.44512	0.36406	49.948	9	2151800000	1441500000	710320000
Q62425	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	Ndufa4	5	5	5	47.6	47.6	47.6	9.3267	82	2.2143E-39	0.90856	0.54182	34.696	11	5001400000	2803300000	2198200000
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Ndufa5	4	4	4	45.7	45.7	45.7	13.36	116	1.1048E-78	1.5358	1.7319	84.394	4	1201700000	513300000	688390000
Q9CQZ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	Ndufa6	2	2	2	25.2	25.2	25.2	15.283	131	1.766E-169	0.57904	0.36714	25.479	4	1799600000	1155100000	644500000
Q9Z1P6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	Ndufa7	3	3	3	30.1	30.1	30.1	12.575	113	3.7338E-07	1.3831	0.83982	22.378	3	346760000	168320000	178430000
Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	Ndufa8	3	3	3	28.5	28.5	28.5	19.992	172	2.0339E-08	0.6544	0.50082	45.808	4	344020000	231590000	112430000
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	Ndufa9	10	10	10	35.8	35.8	35.8	42.525	377	1.336E-131	0.578	0.40082	54.349	13	2862000000	1770900000	1091100000
Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Ndufb10	5	5	5	46.6	46.6	46.6	21.024	176	1.1163E-64	0.95146	0.55686	23.93	7	1450700000	828570000	622120000
O09111	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	Ndufb11	4	4	4	38.4	38.4	38.4	17.444	151	4.3699E-33	1.0796	0.72338	27.855	6	640240000	305980000	334270000
Q9CPU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial	Ndufb2	1	1	1	8.6	8.6	8.6	11.967	105	0.00002313	0.38072	0.29516	7.9218	2	260240000	176390000	83850000
Q9CQZ6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	Ndufb3	3	3	3	27.9	27.9	27.9	11.692	104	4.5187E-10	0.94184	0.87383	44.001	3	1182900000	568980000	613910000
Q9CQC7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	Ndufb4	2	2	2	27.1	27.1	27.1	15.081	129	9.0471E-19	0.61874	0.47079	50.972	3	470630000	279030000	191600000
Q9CQH3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	Ndufb5	3	3	3	15.3	15.3	15.3	21.71	189	6.8883E-16	0.52463	0.37666	29.375	2	352420000	239180000	113230000
Q3UIU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	Ndufb6	2	2	2	19.5	19.5	19.5	15.515	128	5.0587E-28	0.66974	0.44791	12.28	5	683920000	411790000	272130000
Q9CR61	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	Ndufb7	3	3	3	27	27	27	16.331	137	1.585E-27	0.42607	0.49224	19.724	5	250220000	161570000	88652000
Q9D6J5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	Ndufb8	5	5	5	33.9	33.9	33.9	21.876	186	7.0298E-17	0.70701	0.50833	42.173	4	276280000	152210000	124070000
Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	Ndufb9	4	4	4	35.2	35.2	35.2	21.984	179	7.74E-151	0.6261	0.44745	49.931	4	372640000	220200000	152440000
Q9CQ54	NADH dehydrogenase [ubiquinone] 1 subunit C2	Ndufc2	4	4	4	33.3	33.3	33.3	14.164	120	1.0499E-40	0.65602	0.50323	46.791	6	1106500000	677260000	429210000
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	Ndufv1	14	14	14	47.6	47.6	47.6	50.834	464	0	0.71185	0.52612	44.177	27	4950600000	2821600000	2129000000
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	Ndufv2	7	7	7	42.3	42.3	42.3	27.285	248	1.331E-119	1.9051	1.2861	47.843	10	1738300000	529630000	1208600000
Q8BK30	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	Ndufv3	2	2	2	16.3	16.3	16.3	11.813	104	1.7237E-16	1.9685	2.3322	35.853	3	1077000000	333410000	743550000
Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	Ndufs2	12	12	12	32.4	32.4	32.4	52.625	463	8.97E-86	0.51759	0.36148	60.175	21	2577600000	1702800000	874860000
Q9DCT2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	Ndufs3	8	8	8	24.3	24.3	24.3	30.149	263	5.685E-101	1.0197	0.68337	50.98	18	5398900000	2504300000	2894600000
E9QPX3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	Ndufs4	3	3	3	18.9	18.9	18.9	19.803	175	1.1507E-17	2.0881	1.2844	85.903	3	1272900000	430530000	842410000
Q99LY9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	Ndufs5	2	2	2	19.8	19.8	19.8	12.648	106	8.8988E-30	1.044	0.75382	28.255	2	152230000	72233000	80002000
P52503	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	Ndufs6	4	4	4	42.2	42.2	42.2	13.02	116	9.6101E-67	1.8555	1.3851	30.416	7	3896200000	1231400000	2664800000
Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	Ndufs7	4	4	4	14.7	14.7	14.7	24.683	224	9.2426E-46	0.60735	0.46733	21.582	6	760330000	489970000	270360000
Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	Ndufs8	3	3	3	18.9	18.9	18.9	24.038	212	1.8985E-50	0.9694	0.63312	27.494	6	1397400000	661680000	735750000
F2Z456	NADH-cytochrome b5 reductase 3	Cyb5r3	5	5	5	20.4	20.4	20.4	34.929	313	8.4534E-30	0.67065	0.48063	7.5547	2	90301000	51802000	38499000
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Ndufs1	18	18	18	31.9	31.9	31.9	79.776	727	8.803E-176	0.91417	0.57326	50.101	29	9113500000	4950600000	4162900000
P03921	NADH-ubiquinone oxidoreductase chain 5	Mtnd5	3	3	3	9.4	9.4	9.4	68.44	607	3.2197E-09	0.65679	0.43376	9.058	3	62833000	35701000	27132000
P06801	NADP-dependent malic enzyme	Me1	16	16	16	36.7	36.7	36.7	63.953	572	2.731E-221	0.5413	0.43143	64.968	25	2753000000	1928100000	824910000
Q8BMF3	NADP-dependent malic enzyme, mitochondrial	Me3	15	15	15	37.7	37.7	37.7	67.098	604	0	0.87511	0.55019	39.773	34	4335900000	2563000000	1772900000
Q61578	NADPH:adrenodoxin oxidoreductase, mitochondrial	Fdxr	6	6	6	19	19	19	54.201	494	1.5431E-11	0.92394	0.6993	114.79	4	141710000	78818000	62897000
Q8BWZ3	N-alpha-acetyltransferase 25, NatB auxiliary subunit	Naa25	3	3	3	3.1	3.1	3.1	111.71	972	9.658E-07	0.71035	0.59847	46.859	4	112420000	77677000	34743000
A2A9Q2	Nardilysin	Nrd1	3	3	3	3.3	3.3	3.3	140.62	1229	3.6551E-05	1.5361	1.2214	54.737	2	34861000	15462000	19400000
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	Naca	59	59	59	45.2	45.2	45.2	220.5	2187	0	2.6993	2.0349	60.777	114	2.2666E+10	6405400000	1.6261E+10
P05125	Natriuretic peptides A	Nppa	3	3	3	15.8	15.8	15.8	16.572	152	5.0807E-07	2.143	1.4536	49.003	9	4435300000	1341900000	3093400000
Q80XB4	Nebulin-related-anchoring protein	Nrap	12	12	12	8.2	8.2	8.2	195.75	1728	2.2759E-47	0.71886	0.52366	45.796	9	700330000	394610000	305720000
Q6A037	NEDD4-binding protein 1	N4bp1	2	2	2	1.9	1.9	1.9	99.146	893	0.0088623	1.9417	1.4813	85.675	3	1431000000	563260000	867730000
Q8C878	NEDD8-activating enzyme E1 catalytic subunit	Uba3	7	7	7	27.9	27.9	27.9	51.737	462	5.507E-48	1.734	1.1001	53.818	6	738450000	383480000	354970000
Q8VBW6	NEDD8-activating enzyme E1 regulatory subunit	Nae1	6	6	6	16.9	16.9	16.9	60.273	534	1.0914E-76	1.4399	1.0663	66.67	4	269910000	98473000	171430000
F6YXS3	NEDD8-conjugating enzyme Ubc12	Ube2m	2	2	2	15.2	15.2	15.2	15.173	138	1.2686E-09	2.0322	1.9397	49.485	2	654880000	217880000	437000000
P19426	Negative elongation factor E	Rdbp	1	1	1	5.3	5.3	5.3	42.554	375	6.924E-09	1.8762	1.582	12.999	2	21665000	7185400	14480000
Q9CQ45	Neudesin	Nenf	3	3	3	20.5	20.5	20.5	18.904	171	4.1379E-10	3.5929	2.3862	32.87	2	279450000	66865000	212580000
Q91YP2	Neurolysin, mitochondrial	Nln	4	4	4	9.7	9.7	9.7	80.428	704	3.6422E-12	1.2353	0.73422	39.688	5	874620000	284380000	590240000
Q7TPW1	Nexilin	Nexn	1	1	1	2.3	2.3	2.3	72.107	607	1.9885E-13	0.47159	0.48541	31.935	2	22336000	14247000	8089000
Q9QZ23	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	Nfu1	4	4	2	21.6	21.6	12.2	28.567	255	5.3665E-42	2.9773	2.4362	31.167	7	2666200000	726770000	1939500000
Q8BZW8	NHL repeat-containing protein 2	Nhlrc2	7	7	7	15.2	15.2	15.2	78.429	725	3.283E-37	1.3694	0.92588	51.223	7	458370000	188400000	269980000
Q8R1F1	Niban-like protein 1	Fam129b	4	4	4	10	10	10	84.818	749	5.1033E-38	0.44682	0.51254	50.407	5	134960000	93978000	40985000
P57716	Nicastrin	Ncstn	2	2	2	3.2	3.2	3.2	78.491	708	2.7115E-05	0.97996	1.1735	63.43	3	67343000	38993000	28350000
Q99JR6	Nicotinamide mononucleotide adenylyltransferase 3	Nmnat3	5	5	5	30.6	30.6	30.6	27.702	245	8.2392E-51	0.39778	0.33219	57.504	7	383240000	278890000	104350000
Q99KQ4	Nicotinamide phosphoribosyltransferase	Nampt	18	18	18	44.2	44.2	44.2	55.446	491	1.095E-294	0.71379	0.56942	49.599	21	6196700000	3143200000	3053500000
Q8CC86	Nicotinate phosphoribosyltransferase	Naprt1	3	3	3	8.2	8.2	8.2	58.265	538	1.1337E-13	2.1301	1.8549	30.698	4	185440000	57290000	128150000
P10493	Nidogen-1	Nid1	23	23	22	27	27	26.2	136.54	1245	0	1.1113	0.78222	47.286	33	5189800000	2595700000	2594100000
O88322	Nidogen-2	Nid2	7	6	6	6.8	6.1	6.1	153.91	1403	9.3928E-52	0.94165	0.71484	25.259	4	247710000	129100000	118610000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9EQ80	NIF3-like protein 1	Nif3l1	5	5	5	22.3	22.3	22.3	41.745	376	4.5029E-14	0.85455	0.58769	50.661	5	313750000	172320000	141430000
Q8VDK1	Nitrilase homolog 1	Nit1	5	5	5	21.4	21.4	21.4	35.705	323	3.2562E-17	0.57364	0.40714	53.576	5	380800000	210200000	170600000
O35309	N-myc-interactor	Nmi	2	2	2	8.9	8.9	8.9	35.235	314	0.00051587	3.2497	2.4329	87.476	2	74374000	21193000	53181000
Q99K48	Non-POU domain-containing octamer-binding protein	Nono	5	5	4	11.2	11.2	9.5	54.54	473	7.8164E-11	0.19559	0.1326	44.808	6	449540000	357050000	92490000
P32020	Non-specific lipid-transfer protein	Scp2	5	5	5	9.1	9.1	9.1	59.125	547	2.272E-124	2.2179	1.8873	110.03	8	2154900000	755610000	1399300000
Q9CZ44	NSFL1 cofactor p47	Nsfl1c	8	8	8	29.2	29.2	29.2	40.709	370	2.184E-187	2.5431	1.814	57.683	11	1671600000	419110000	1252500000
Q8CCP0	Nuclear export mediator factor Nemf	Nemf	2	2	2	1.9	1.9	1.9	121.19	1064	0.00054303	1.2486	0.97304	136.4	2	161910000	48810000	113100000
Q5F2E7	Nuclear fragile X mental retardation-interacting protein 2	Nufip2	2	2	2	4.2	4.2	4.2	75.656	692	4.0982E-05	1.2661	0.98866	108.62	2	128610000	71029000	57585000
Q63850	Nuclear pore glycoprotein p62	Nup62	3	3	3	7.2	7.2	7.2	53.254	526	2.1031E-30	2.3225	1.6384	5.1905	2	83496000	26409000	57087000
P60670	Nuclear protein localization protein 4 homolog	Nploc4	5	5	5	13.3	13.3	13.3	68.016	608	1.303E-30	0.69509	0.56886	37.845	6	429120000	262100000	167020000
P61971	Nuclear transport factor 2	Nutf2	4	4	4	50.4	50.4	50.4	14.478	127	2.4768E-14	1.0978	0.787	19.983	3	599310000	370580000	228730000
P62960	Nuclease-sensitive element-binding protein 1	Ybx1	5	5	2	27.3	27.3	16.1	35.73	322	1.139E-224	4.0696	2.5823	43.731	6	661740000	170790000	490960000
Q02819	Nucleobindin-1	Nucb1	4	4	4	12.4	12.4	12.4	53.408	459	2.5552E-23	1.3519	0.9716	10.23	5	262180000	125290000	136890000
Q9D1X0	Nucleolar protein 3	Nol3	5	5	5	36.8	36.8	36.8	24.567	220	1.9706E-84	2.9967	1.9332	19.316	6	944040000	238200000	705840000
P09405	Nucleolin	Ncl	12	12	12	19.4	19.4	19.4	76.722	707	9.2084E-95	0.6066	0.7246	50.789	12	1033600000	652420000	381150000
Q61937	Nucleophosmin	Npm1	6	6	6	28.4	28.4	28.4	32.56	292	1.5805E-98	1.2879	1.0023	28.125	8	965840000	434890000	530950000
E9PZF0	Nucleoside diphosphate kinase	Gm20390	12	12	6	65.5	65.5	26.2	30.2	267	1.522E-179	2.0261	1.2381	107.63	36	2.3936E+10	7960100000	1.5976E+10
Q9WV85	Nucleoside diphosphate kinase 3	Nme3	3	3	3	27.2	27.2	27.2	19.099	169	1.0484E-23	1.2248	0.95671	29.033	2	99719000	38763000	60956000
Q8JZU0	Nucleoside diphosphate-linked moiety X motif 13	Nudt13	2	2	2	11.1	11.1	11.1	39.136	352	1.3713E-46	1.287	0.99876	17.831	3	151720000	59010000	92706000
P11930	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	Nudt19	3	3	3	12.3	12.3	12.3	40.32	357	1.7021E-34	0.78741	0.55383	20.618	3	147050000	87855000	59198000
Q9CR24	Nucleoside diphosphate-linked moiety X motif 8, mitochondrial	Nudt8	4	4	4	25.2	25.2	25.2	23.252	210	2.7791E-48	0.97482	0.5769	41.888	3	398090000	216990000	181100000
E9PW66	Nucleosome assembly protein 1-like 1	Nap1l1	2	1	1	6.5	4.1	4.1	48.542	418	1.2794E-16	0.94321	0.63172	1.9833	2	405110000	212510000	192600000
Q78ZA7	Nucleosome assembly protein 1-like 4	Nap1l4	8	8	7	32.3	32.3	29.6	42.679	375	3.975E-159	1.5049	1.1553	39.484	10	687780000	302360000	385420000
Q8R1N4	NudC domain-containing protein 3	Nudcd3	3	3	3	11.3	11.3	11.3	40.89	363	8.2125E-07	1.4775	1.2557	82.437	2	71653000	32259000	39394000
Q922B1	O-acetyl-ADP-ribose deacetylase MACROD1	Macrod1	7	7	7	28.2	28.2	28.2	35.294	323	1.527E-203	1.7806	1.2979	10.857	18	1500700000	508430000	992300000
Q9CZ30	Obg-like ATPase 1	Ola1	7	7	7	25.5	25.5	25.5	44.729	396	2.6E-83	1.4011	1.3644	34.983	7	959290000	371160000	588130000
E9QQ96	Obscurin	Obscn	36	36	29	9.8	9.8	8.4	815.63	7496	0	0.78726	0.57362	47.249	41	2600700000	1437700000	1163000000
Q9CRD0	OCIA domain-containing protein 1	Ociad1	4	4	4	19.8	19.8	19.8	27.61	247	5.7987E-11	1.5754	0.98388	14.516	4	275420000	109030000	166390000
Q9D8S4	Oligoribonuclease, mitochondrial	Rexo2	4	4	4	16.9	16.9	16.9	26.738	237	1.2373E-56	2.1802	1.715	32.944	3	152270000	33029000	119240000
Q9JHW2	Omega-amidase NIT2	Nit2	11	11	11	65.2	65.2	65.2	30.501	276	9.745E-143	1.1383	0.7666	39.742	16	2223900000	997090000	1226800000
Q99PG2	Opioid growth factor receptor	Ogfr	2	2	2	6	6	6	70.678	633	4.8172E-14	2.2923	1.7775	115.86	3	119110000	45181000	73932000
P29758	Ornithine aminotransferase, mitochondrial	Oat	15	15	15	43.3	43.3	43.3	48.354	439	1.355E-279	1.1833	0.83896	80.372	22	3642900000	1931400000	1711500000
Q62422	Osteoclast-stimulating factor 1	Ostf1	2	2	2	15.3	15.3	15.3	23.782	215	5.7549E-09	1.6842	1.0498	17.795	3	333020000	136300000	196720000
B2RRE7	OTU domain-containing protein 4	Otud4	4	4	4	4.8	4.8	4.8	123.05	1107	3.5442E-17	0.57817	0.36014	88.608	2	119200000	71215000	47981000
Q4KMM3	Oxidation resistance protein 1	Oxr1	3	3	3	4.5	4.5	4.5	95.911	866	2.2738E-18	1.4882	1.3206	23.29	4	92639000	38713000	53927000
Q8VE38	Oxidoreductase NAD-binding domain-containing protein 1	Oxnad1	7	7	7	23.5	23.5	23.5	34.727	311	1.3552E-26	0.83323	0.90262	32.962	7	1219700000	650490000	569170000
G5E8A0	Oxysterol-binding protein	Osbpl11	1	1	1	1.5	1.5	1.5	84.332	757	0.037074	1.2464	0.92342	17.637	2	43456000	21680000	21777000
Q3B7Z2	Oxysterol-binding protein 1	Osbp	5	5	4	11.6	11.6	9.6	88.796	805	3.797E-207	1.3386	1.0142	74.274	6	492300000	244560000	247740000
Q91XL9	Oxysterol-binding protein-related protein 1	Osbpl1a	2	2	2	2.5	2.5	2.5	107.79	950	6.0854E-28	1.1564	0.92239	14.209	4	248780000	117660000	131130000
Q9JJX6	P2X purinoceptor 4	P2rx4	3	3	3	10.1	10.1	10.1	43.437	388	2.7598E-17	0.27861	0.21962	43.675	2	36720000	26671000	10049000
Q3UVT7	Palmdelphin	Palmd	4	4	4	13.8	13.8	13.8	62.616	551	3.3535E-35	1.9638	1.4641	38.128	7	278600000	84299000	194300000
O88531	Palmitoyl-protein thioesterase 1	Ppt1	3	3	3	18.6	18.6	18.6	34.49	306	2.4561E-42	1.0837	0.72933	62.556	7	469730000	196680000	273040000
Q80YV4	Pantothenate kinase 4	Pank4	4	4	4	6	6	6	91.521	820	8.683E-09	0.88376	0.78776	24.315	3	101430000	55865000	45565000
Q9Z0P4	Paralemmin-1	Palm	5	5	5	20.4	20.4	20.4	41.614	383	1.0911E-86	2.841	1.9032	20.319	7	627600000	154970000	472630000
D3Z1Z1	Paraplegin	Spg7	2	2	2	3.3	3.3	3.3	86.007	781	1.6706E-07	0.74448	0.59393	45.414	2	255030000	116660000	138370000
Q99JF8	PC4 and SFRS1-interacting protein	Psip1	3	3	3	8.7	8.7	8.7	59.696	528	3.9482E-36	1.5394	1.6646	42.4	4	69043000	26603000	42439000
E9PVP0	PCTP-like protein	Stard10	3	3	3	11.3	11.3	11.3	40.116	364	3.4218E-12	0.92164	0.65024	64.295	2	81193000	43006000	38187000
O70400	PDZ and LIM domain protein 1	Pdlim1	9	9	9	47.4	47.4	47.4	35.774	327	1.627E-258	2.3795	1.5202	33.097	12	2736900000	869670000	1867200000
Q8CI51	PDZ and LIM domain protein 5	Pdlim5	12	12	5	27.6	27.6	11.5	63.299	591	0	1.969	1.3786	96.664	21	1.163E+10	3730100000	7899800000
Q8R5M0	PDZ domain-containing protein GIPC3	Gipc3	2	2	2	10.8	10.8	10.8	32.108	297	0.0062732	2.33	1.6689	67.807	2	136670000	52332000	84338000
Q8VI59	Pecanex-like protein 3	Pcnxl3	1	1	1	1.1	1.1	1.1	221.57	2028	4.4559E-05	2.1612	1.3021	35.57	2	1303900000	291850000	1012000000
Q8BFY6	Peflin	Pef1	3	3	3	11.6	11.6	11.6	29.227	275	4.2753E-05	2.5197	1.7918	3.1203	3	122360000	32252000	90109000
Q14C51	Pentatricopeptide repeat-containing protein 3, mitochondrial	Ptcd3	2	2	2	7.7	7.7	7.7	77.795	685	3.586E-06	1.0827	0.72599	25.483	3	221990000	94364000	127630000
A3KG59	Peptidase M20 domain-containing protein 2	Pm20d2	4	4	4	20	20	20	46.481	431	7.8891E-74	1.769	1.0749	25.974	7	553300000	220610000	332690000
P97467	Peptidyl-glycine alpha-amidating monooxygenase	Pam	3	3	3	2.7	2.7	2.7	108.96	979	4.0448E-05	1.0289	1.0525	64.139	3	143260000	48853000	94403000
P17742	Peptidyl-prolyl cis-trans isomerase A	Ppia	8	8	8	59.8	59.8	59.8	17.971	164	7.952E-142	2.2969	1.5985	96.96	16	6901000000	2039700000	4861300000
P24369	Peptidyl-prolyl cis-trans isomerase B	Ppib	6	6	6	33.3	33.3	33.3	23.713	216	2.2837E-17	1.7083	1.2173	38.836	8	1622800000	645260000	977560000
Q9CR16	Peptidyl-prolyl cis-trans isomerase D	Ppid	6	6	6	31.1	31.1	31.1	40.742	370	3.5287E-37	1.7348	1.3122	106.48	7	424600000	140460000	284150000
Q99KR7	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	Ppif	4	4	4	31.1	31.1	31.1	21.737	206	0	3.3832	2.7176	37.611	5	3547500000	929880000	2617700000
Q62446	Peptidyl-prolyl cis-trans isomerase FKBP3	Fkbp3	6	6	6	33.5	33.5	33.5	25.147	224	2.65E-121	5.1235	2.9226	51.122	9	3550600000	778260000	2772300000
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4	Fkbp4	10	10	10	32.3	32.3	32.3	51.572	458	9.912E-143	3.0789	2.1769	35.455	13	2544200000	753870000	1790300000
Q9CWW6	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	Pin4	2	2	2	32.1	32.1	32.1	13.815	131	4.4161E-09	3.0559	3.6369	13.841	3	88604000	31119000	57485000
Q8R035	Peptidyl-tRNA hydrolase ICT1, mitochondrial	Ict1	3	3	3	17.5	17.5	17.5	23.477	206	1.6368E-08	1.4899	1.1488	4.4764	2	124330000	53495000	70839000
Q9R0L6	Pericentriolar material 1 protein	Pcm1	2	2	2	1.3	1.3	1.3	228.84	2025	0.0010925	0.40607	0.29836	226.22	2	408810000	393200000	15601000
P43883	Perilipin-2	Plin2	6	6	6	20	20	20	46.646	425	2.7974E-16	2.0607	1.3674	145.71	5	349710000	220530000	129180000
Q9DBG5	Perilipin-3	Plin3	11	11	11	34.6	34.6	34.6	47.262	437	1.248E-126	1.1204	0.82259	34.569	14	1532600000	624780000	907840000
O88492	Perilipin-4	Plin4	14	14	14	19.2	19.2	19.2	139.41	1403	1.168E-244	1.4352	1.1839	48.763	12	1401100000	783810000	617240000
Q8BVZ1	Perilipin-5	Plin5	4	4	4	17.9	17.9	17.9	50.474	463	5.9376E-24	1.3893	1.0457	12.201	4	37447000	13451000	23996000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q62009	Periostin	Postn	4	4	4	6.7	6.7	6.7	93.142	838	7.2508E-07	1.3967	1.0988	44.775	3	83887000	37729000	46158000
Q3UQ28	Peroxidasin homolog	Pxdn	4	4	4	2.8	2.8	2.8	165.1	1475	5.223E-25	1.3908	1.2484	155.78	2	45547000	15510000	30037000
P35700	Peroxiredoxin-1	Prdx1	11	11	11	43.7	43.7	43.7	22.176	199	1.061E-118	1.9874	1.6438	43.587	13	1.8462E+10	6721500000	1.1741E+10
Q61171	Peroxiredoxin-2	Prdx2	11	11	11	69.2	69.2	69.2	21.778	198	2.64E-263	2.538	2.0408	71.457	22	1.4985E+10	4288200000	1.0697E+10
O08807	Peroxiredoxin-4	Prdx4	6	6	6	37.6	37.6	37.6	31.052	274	4.8172E-54	2.0225	1.3644	31.874	8	6809800000	2364200000	4445600000
H3BJQ7	Peroxiredoxin-5, mitochondrial	Prdx5	11	11	11	40.8	40.8	40.8	22.677	213	3.501E-178	2.2896	1.6637	39.417	51	1.8683E+10	4731000000	1.3952E+10
Q6GT24	Peroxiredoxin-6	Prdx6	11	11	11	52.2	52.2	52.2	24.826	224	9.743E-141	1.8573	1.3781	50.327	16	1.3323E+10	4586700000	8735800000
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	Acox1	10	10	10	22.8	22.8	22.8	74.648	661	1.6726E-37	0.66173	0.44973	41.819	9	813490000	487010000	326480000
Q8VCI5	Peroxisomal biogenesis factor 19	Pex19	4	4	4	24.4	24.4	24.4	32.733	299	3.4251E-74	2.7563	2.4156	17.552	5	247270000	74596000	172670000
Q9DC50	Peroxisomal carnitine O-octanoyltransferase	Crot	3	3	3	8	8	8	70.264	612	2.4494E-18	1.0972	0.80591	20.367	2	95086000	42851000	52235000
Q99P30	Peroxisomal coenzyme A diphosphatase NUDT7	Nudt7	4	4	4	22.9	22.9	22.9	26.856	236	1.2223E-16	1.3054	1.0626	37.481	4	428420000	144540000	283880000
P51660	Peroxisomal multifunctional enzyme type 2	Hsd17b4	7	7	7	13.6	13.6	13.6	79.481	735	6.4662E-28	0.98175	0.73602	46.185	6	731340000	410410000	320930000
F8WI88	PEST proteolytic signal-containing nuclear protein	Pcnp	2	2	2	12.7	12.7	12.7	20.165	189	0.00011294	1.4658	1.6224	111.27	2	34012000	17882000	16130000
Q8C0C7	Phenylalanine--tRNA ligase alpha subunit	Farsa	5	5	5	14	14	14	57.598	508	5.2799E-21	1.1265	0.81784	50.087	6	129120000	72827000	56292000
Q9WUA2	Phenylalanine--tRNA ligase beta subunit	Farsb	5	5	5	10.9	10.9	10.9	65.696	589	4.1154E-17	0.47089	0.34877	35.189	5	341190000	221070000	120130000
Q8BVF2	Phosducin-like protein 3	Pdcl3	2	2	2	11.7	11.7	11.7	27.581	240	9.7712E-11	1.7856	1.8557	39.348	3	182400000	42323000	140080000
G5E902	Phosphate carrier protein, mitochondrial	Slc25a3	10	10	10	29.3	29.3	29.3	39.736	358	2.465E-193	0.55068	0.38589	37.012	16	5715500000	3811800000	1903700000
Q99L43	Phosphatidate cytidylyltransferase 2	Cds2	1	1	1	4.3	4.3	4.3	51.313	444	6.488E-19	0.50352	0.40135	3.6088	2	77667000	46474000	31193000
P70296	Phosphatidylethanolamine-binding protein 1	Pebp1	10	10	10	73.3	73.3	73.3	20.83	187	0	3.0099	2.3797	42.157	22	9150000000	2378200000	6771700000
Q9EP69	Phosphatidylinositide phosphatase SAC1	Sacm1l	3	3	3	4.4	4.4	4.4	66.943	587	8.0768E-09	0.95819	0.65529	220.77	2	97919000	30593000	67326000
Q6P549	Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2	Inppl1	4	4	4	6.1	6.1	6.1	138.97	1257	2.0271E-13	0.76275	0.59845	68.474	4	87227000	47932000	39295000
Q80XI4	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta	Pip4k2b	3	3	2	9.9	9.9	5.8	47.318	416	6.8365E-07	1.0777	0.78637	15.823	2	35623000	15022000	20601000
J3QPW1	Phosphatidylinositol transfer protein alpha isoform	Pitpna	2	2	2	11	11	11	32.021	272	4.8005E-17	1.5169	1.0777	45.372	2	181320000	78019000	103300000
Q7M6Y3	Phosphatidylinositol-binding clathrin assembly protein	Picalm	4	4	4	6.8	6.8	6.8	71.543	660	5.5131E-07	1.6631	1.5432	85.619	3	215890000	87692000	128200000
Q9CYR6	Phosphoacetylglucosamine mutase	Pgm3	3	3	3	8.1	8.1	8.1	59.452	542	8.1002E-08	1.2355	0.88378	57.293	4	322850000	144760000	178090000
Q8K212	Phosphofurin acidic cluster sorting protein 1	Pacs1	2	2	2	2.5	2.5	2.5	104.83	961	0.00017023	1.1698	0.93411	30.556	2	65502000	28590000	36911000
Q9D0F9	Phosphoglucomutase-1	Pgm1	22	22	22	50	50	50	61.417	562	0	1.451	0.91347	66.184	45	1.1911E+10	4949700000	6961800000
Q7TSV4	Phosphoglucomutase-2	Pgm2	2	2	2	5.2	5.2	5.2	68.747	620	2.0596E-20	1.4615	1.0891	32.897	3	221170000	89717000	131450000
Q8BZF8	Phosphoglucomutase-like protein 5	Pgm5	11	11	11	24.5	24.5	24.5	62.219	567	1.1779E-88	1.0089	0.75347	25.28	9	320420000	164240000	156180000
P09411	Phosphoglycerate kinase 1	Pgk1	20	20	20	58.3	58.3	58.3	44.55	417	0	1.8892	1.5483	69.693	47	1.849E+10	6520400000	1.197E+10
Q9DBJ1	Phosphoglycerate mutase 1	Pgam1	9	7	7	43.7	35.4	35.4	28.832	254	1.506E-266	1.5683	1.2475	64.206	12	1521000000	665030000	855970000
O70250	Phosphoglycerate mutase 2	Pgam2	13	13	11	48.2	48.2	39.9	28.827	253	4.05E-114	0.7213	0.58527	67.461	16	2.223E+10	1.2474E+10	9755800000
Q8CHP8	Phosphoglycolate phosphatase	Pgp	5	5	5	23.4	23.4	23.4	34.54	321	1.035E-191	1.1204	0.73505	40.691	8	887570000	379450000	508120000
P27612	Phospholipase A-2-activating protein	Plaa	8	8	8	16	16	16	87.22	794	3.3707E-56	0.89207	0.91707	26.411	5	135060000	78596000	56467000
Q9Z2M7	Phosphomannomutase 2	Pmm2	5	5	4	24	24	21.1	27.656	242	1.5186E-10	1.2665	0.94478	39.042	6	950560000	446280000	504270000
Q8VDG5	Phosphopantothenate--cysteine ligase	Ppcs	5	5	5	18.3	18.3	18.3	33.794	311	4.0509E-09	1.2121	0.65144	43.949	5	567480000	281570000	285910000
B1AT82	Phosphoribosyl pyrophosphate synthase-associated protein 1	Prpsap1	4	4	4	17.7	17.7	17.7	42.467	385	9.9535E-56	0.90549	0.54508	33.191	3	161080000	85373000	75711000
Q8R574	Phosphoribosyl pyrophosphate synthase-associated protein 2	Prpsap2	2	2	2	10.6	10.6	10.6	40.88	369	2.0523E-05	1.5893	0.99663	85.976	2	326180000	81258000	244920000
Q7TSH2	Phosphorylase b kinase regulatory subunit beta	Phkb	4	4	4	4.3	4.3	4.3	123.89	1085	3.2647E-13	0.69908	0.51871	65.68	3	96363000	67923000	28440000
Q9DB26	Phytanoyl-CoA dioxygenase domain-containing protein 1	Phyhd1	3	3	3	19.9	19.9	19.9	32.517	291	0	2.8262	1.7359	21.474	5	465780000	125880000	339900000
O35386	Phytanoyl-CoA dioxygenase, peroxisomal	Phyh	5	5	5	14.8	14.8	14.8	38.607	338	2.3244E-10	1.4153	1.4941	81.129	3	144330000	66418000	77913000
P26262	Plasma kallikrein	Klkb1	7	7	7	14.6	14.6	14.6	71.382	638	8.2672E-23	1.5044	1.7413	31.215	5	157100000	46769000	110330000
P97290	Plasma protease C1 inhibitor	Serping1	3	3	3	9.9	9.9	9.9	55.584	504	1.3356E-88	2.0061	1.2506	15.589	7	609490000	211710000	397790000
P20918	Plasminogen	Plg	8	8	8	14.2	14.2	14.2	90.807	812	3.5501E-37	0.6836	0.47447	46.85	12	391240000	223460000	167780000
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein	Serbp1	2	2	2	7.1	7.1	7.1	44.714	407	5.3994E-06	2.0419	1.7908	58.113	2	137350000	52247000	85101000
Q61233	Plastin-2	Lcp1	17	17	15	35.4	35.4	32.5	70.148	627	1.264E-222	0.52976	0.49426	48.893	22	2268700000	1376300000	892410000
B1AX58	Plastin-3	Pls3	9	7	7	19.1	16.3	16.3	71.745	639	4.0957E-51	1.9946	1.5124	39.052	6	852520000	281380000	571130000
B1ARB3	Platelet endothelial cell adhesion molecule	Pecam1	4	4	4	10.7	10.7	10.7	81.917	732	1.3548E-60	1.462	1.0438	19.704	2	53485000	17418000	36067000
Q08857	Platelet glycoprotein 4	Cd36	6	6	6	17.4	17.4	17.4	52.697	472	4.9394E-66	1.9416	1.487	31.613	11	3354700000	1304400000	2050300000
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	Pafah1b1	10	10	10	30.5	30.5	30.5	46.67	410	1.912E-103	0.72468	0.57658	26.739	13	1446200000	850340000	595810000
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	Pafah1b2	2	2	2	12.2	12.2	12.2	25.581	229	4.9858E-48	2.1503	1.5838	37.51	6	1162500000	305270000	857280000
Q9JHK5	Pleckstrin	Plek	1	1	1	4	4	4	39.9	350	3.4023E-09	1.8459	1.0312	28.72	2	218050000	77967000	140080000
Q80TI1	Pleckstrin homology domain-containing family H member 1	Plekhh1	2	2	2	1.6	1.6	1.6	150.91	1356	0.0026623	1.4341	1.2559	55.763	2	817520000	295420000	522110000
Q9QXS1	Plectin	Plec	10	10	10	3.3	3.3	3.3	534.18	4691	2.228E-59	0.60978	0.43748	111.53	10	584420000	345180000	239240000
B2RXS4	Plexin-B2	Plxnb2	2	2	2	2.2	2.2	2.2	206.23	1842	4.9582E-05	1.1783	0.98934	40.328	2	88069000	41803000	46266000
P60335	Poly(rC)-binding protein 1	Pcbp1	8	8	5	39.9	39.9	28.9	37.497	356	1.972E-106	1.4797	1.1209	28.236	11	1396600000	539720000	856920000
Q61990	Poly(rC)-binding protein 2	Pcbp2	8	5	5	31.5	20.7	20.7	38.221	362	2.0913E-68	1.3981	1.0735	15.456	4	794170000	346950000	447230000
Q3UEB3	Poly(U)-binding-splicing factor PUF60	Puf60	2	2	2	6.7	6.7	6.7	60.248	564	1.7977E-09	1.924	1.4495	9.7688	3	291550000	86883000	204670000
P29341	Polyadenylate-binding protein 1	Pabpc1	5	4	4	10.5	7.9	7.9	70.67	636	1.7028E-50	1.275	0.89498	95.819	3	960300000	198060000	762240000
O54724	Polymerase I and transcript release factor	Ptrf	11	11	11	28.6	28.6	28.6	43.953	392	2.212E-185	1.0363	0.76484	60.651	22	1741000000	849200000	891790000
Q922I7	Polypyrimidine tract-binding protein 1	Ptbp1	5	5	5	19.1	19.1	19.1	59.321	555	2.257E-146	0.66152	0.47282	28.548	4	248630000	150790000	97846000
Q8K1R3	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	Pnpt1	6	6	6	9.8	9.8	9.8	85.682	783	5.969E-47	0.63715	0.48137	53.253	5	243510000	161100000	82409000
Q8R5J9	PRA1 family protein 3	Arl6ip5	2	2	2	9.6	9.6	9.6	21.557	188	0.00045068	0.27704	0.20327	27.094	2	162350000	126990000	35355000
P61759	Prefoldin subunit 3	Vbp1	3	3	3	17.9	17.9	17.9	22.435	196	1.7378E-09	3.7494	2.9658	37.099	3	93550000	17367000	76182000
Q9WU28	Prefoldin subunit 5	Pfdn5	3	3	3	26.6	26.6	26.6	17.356	154	1.2515E-41	1.8294	1.7552	43.791	3	139710000	42521000	97186000
P48678	Prelamin-A/C	Lmna	4	4	4	10.2	10.2	10.2	74.237	665	1.9657E-82	1.1878	0.89317	10.993	3	66727000	29998000	36729000
Q99KP6	Pre-mRNA-processing factor 19	Prpf19	4	4	4	10.9	10.9	10.9	55.238	504	1.0569E-71	0.63612	0.42336	28.556	3	113510000	67864000	45648000
E9QJV4	Pre-mRNA-processing factor 39	Prpf39	2	2	2	4.5	4.5	4.5	77.923	665	0.010546	1.906	1.8965	174.57	2	168010000	38045000	129960000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9CQF9	Prenylcysteine oxidase	Pcyox1	2	2	2	7.3	7.3	7.3	56.494	505	3.2478E-13	0.61428	0.40845	77.759	3	108900000	61980000	46921000
Q8K411	Presequence protease, mitochondrial	Pitrm1	20	20	20	28.5	28.5	28.5	117.37	1036	0	0.9463	0.67449	57.831	25	3723000000	1915000000	1808000000
Q6NSR8	Probable aminopeptidase NPEPL1	Npepl1	5	5	5	14.3	14.3	14.3	55.939	524	1.4166E-13	1.1343	0.7073	23.634	4	212740000	102910000	109830000
Q569Z5	Probable ATP-dependent RNA helicase DDX46	Ddx46	2	2	2	2.9	2.9	2.9	117.45	1032	0.0005221	0.2879	0.24289	5.5025	2	60006000	50934000	9072200
Q8BTS0	Probable ATP-dependent RNA helicase DDX5	Ddx5	4	4	3	7.2	7.2	5.4	69.265	615	2.9592E-09	0.41791	0.32993	111.75	3	104360000	65907000	38454000
P54823	Probable ATP-dependent RNA helicase DDX6	Ddx6	3	3	3	9.9	9.9	9.9	54.191	483	2.3675E-39	0.78745	0.62393	125.28	3	103080000	67881000	35198000
Q9WV35	Probable C->U-editing enzyme APOBEC-2	Apobec2	7	7	7	48.2	48.2	48.2	25.66	224	9.496E-103	2.1203	1.5045	35.118	9	1664500000	509520000	1155000000
Q8BYM8	Probable cysteine--tRNA ligase, mitochondrial	Cars2	5	5	5	13.4	13.4	13.4	61.271	551	7.9515E-61	0.88836	0.62754	58.582	8	458000000	259070000	198930000
Q7TNG8	Probable D-lactate dehydrogenase, mitochondrial	Ldhd	3	3	3	11.8	11.8	11.8	51.847	484	7.7854E-33	2.3543	1.6672	1.1661	2	159800000	48364000	111440000
Q8BHA3	Probable D-tyrosyl-tRNA(Tyr) deacylase 2	Dtd2	2	2	2	22.6	22.6	22.6	18.236	168	1.0917E-06	1.173	0.91603	26.689	3	88579000	39299000	49280000
Q6PAV2	Probable E3 ubiquitin-protein ligase HERC4	Herc4	7	7	7	7.9	7.9	7.9	118.41	1057	4.6108E-12	0.68768	0.38461	66.955	5	372440000	176510000	195930000
Q8BZA9	Probable fructose-2,6-bisphosphatase TIGAR	Tigar	4	4	4	27.5	27.5	27.5	29.19	269	8.0482E-75	1.1934	0.76215	30.62	6	640350000	288660000	351690000
Q9CXJ1	Probable glutamate--tRNA ligase, mitochondrial	Ears2	2	2	2	6.3	6.3	6.3	58.326	523	3.5215E-07	0.79796	0.63974	5.9709	2	145850000	83317000	62533000
Q80T32	Probable G-protein coupled receptor 133	Gpr133	1	1	1	1.2	1.2	1.2	99.276	903	0.021553	0.95799	0.79003	30.591	2	246430000	119470000	126960000
Q8VDC0	Probable leucine--tRNA ligase, mitochondrial	Lars2	5	5	5	7.1	7.1	7.1	101.48	902	1.6348E-52	0.67936	0.45825	47.406	3	112770000	62042000	50724000
Q9WVQ5	Probable methylthioribulose-1-phosphate dehydratase	Apip	5	5	5	27.4	27.4	27.4	26.949	241	1.0952E-73	1.5091	0.89346	43.793	7	805640000	365100000	440540000
A2APY7	Probable methyltransferase C20orf7 homolog, mitochondrial	Ndufaf5	3	3	3	9.6	9.6	9.6	38.404	343	1.6716E-09	1.1386	0.91333	6.5091	2	146970000	60465000	86506000
Q9CXA2	Probable proline racemase	L3hypdh	4	4	4	18.4	18.4	18.4	37.804	354	1.2418E-13	1.6073	0.86413	19.426	4	224170000	80239000	143930000
A8Y5T6	Probable proline--tRNA ligase, mitochondrial	Pars2	2	2	2	4.1	4.1	4.1	57.735	511	1.7914E-07	0.45276	0.4719	22.941	2	30912000	19955000	10957000
P86049	Probable RNA-binding protein 46	Rbm46	2	2	2	2.3	2.3	2.3	60.077	533	0.00071923	0.57463	0.42963	91.828	2	1802200000	883570000	918650000
Q8BLY2	Probable threonine--tRNA ligase 2, cytoplasmic	Tarsl2	4	4	4	7.3	7.3	7.3	91.317	790	2.9692E-20	0.58409	0.46755	20.451	6	276700000	182650000	94043000
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	Usp9x	5	5	5	2.3	2.3	2.3	290.71	2559	5.1318E-18	0.47469	0.35841	61.033	3	93386000	66664000	26722000
P49935	Pro-cathepsin H	Ctsh	2	2	2	11.1	11.1	11.1	37.17	333	1.501E-106	0.32457	0.35451	123.5	3	28694000	19260000	9434400
Q9WU78	Programmed cell death 6-interacting protein	Pdcd6ip	14	14	14	23.2	23.2	23.2	96.023	869	2.6222E-88	1.1777	1.2185	57.309	18	2148200000	1032400000	1115900000
D3Z7Q5	Programmed cell death protein 5	Pdcd5	3	3	3	17.1	17.1	17.1	21.985	205	6.8636E-16	2.2773	1.9013	32.201	3	939460000	271130000	668330000
P12815	Programmed cell death protein 6	Pdcd6	2	2	2	19.9	19.9	19.9	21.867	191	1.4888E-34	1.4006	1.0125	85.906	6	393750000	191500000	202250000
P67778	Prohibitin	Phb	4	4	4	20.6	20.6	20.6	29.82	272	6.5449E-17	0.73383	0.54238	47.984	3	385450000	212220000	173240000
O35129	Prohibitin-2	Phb2	9	9	9	38.5	38.5	38.5	33.296	299	1.2043E-82	0.56123	0.42015	28.794	13	1082000000	689410000	392540000
Q9JK53	Prolargin	Prelp	2	2	2	5.3	5.3	5.3	43.292	378	4.0442E-05	1.0086	0.71771	4.7801	2	99504000	51637000	47867000
P17918	Proliferating cell nuclear antigen	Pcna	2	2	2	10.3	10.3	10.3	28.785	261	4.8311E-61	22.164	14.792	69.641	3	1886100000	82463000	1803600000
P50580	Proliferation-associated protein 2G4	Pa2g4	7	7	7	23.4	23.4	23.4	43.698	394	2.381E-112	1.5912	1.2179	68.658	8	854280000	399150000	455130000
Q9Z2Y8	Proline synthase co-transcribed bacterial homolog protein	Prosc	6	6	6	29.9	29.9	29.9	30.048	274	1.031E-111	1.7031	1.3322	28.425	6	2120000000	735650000	1384400000
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	Lrp1	5	5	5	1.5	1.5	1.5	504.74	4545	5.7622E-25	1.1482	0.70702	26.016	2	101410000	42056000	59353000
Q9QUR6	Prolyl endopeptidase	Prep	18	18	18	34.5	34.5	34.5	80.751	710	2.4452E-95	0.82064	0.53767	67.06	20	2084600000	1167200000	917460000
Q9D820	Prolyl-tRNA synthetase associated domain-containing protein 1	Prorsd1	2	2	2	14.8	14.8	14.8	18.862	169	2.4051E-09	2.4059	1.5821	52.793	2	265800000	81792000	184010000
Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondrial	Pcca	19	19	19	33.8	33.8	33.8	79.921	724	0	1.3845	1.0135	100.78	32	6740700000	3417200000	3323500000
Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial	Pccb	16	16	16	45.5	45.5	45.5	58.408	541	0	1.1494	0.79249	56.939	25	5387500000	2528400000	2859000000
Q8BWM0	Prostaglandin E synthase 2	Ptges2	3	3	3	13	13	13	43.323	384	9.4556E-36	0.61622	0.53001	51.701	3	99453000	69809000	29644000
Q9R0Q7	Prostaglandin E synthase 3	Ptges3	5	5	5	35.6	35.6	35.6	18.721	160	4.704E-35	1.0049	0.74174	43.667	7	1459000000	727960000	731070000
Q8VDQ1	Prostaglandin reductase 2	Ptgr2	6	6	6	24.5	24.5	24.5	38.015	351	1.1729E-42	1.8552	1.6323	47.45	9	1368500000	522020000	846440000
O09114	Prostaglandin-H2 D-isomerase	Ptgds	2	2	2	13.8	13.8	13.8	21.066	189	2.0635E-49	0.5713	0.50438	9.8047	2	326270000	207930000	118340000
Q9DB60	Prostamide/prostaglandin F synthase	Fam213b	4	4	4	16.9	16.9	16.9	21.67	201	2.8193E-22	0.73075	0.39638	71.82	5	568370000	323010000	245350000
P97371	Proteasome activator complex subunit 1	Psme1	5	5	5	29.3	29.3	29.3	28.673	249	4.433E-114	2.288	2.1147	72.516	5	964810000	352640000	612170000
P97372	Proteasome activator complex subunit 2	Psme2	3	3	3	17.6	17.6	17.6	27.057	239	1.1206E-09	1.766	1.8942	60.829	3	183840000	50768000	133080000
Q9JK23	Proteasome assembly chaperone 1	Psmg1	1	1	1	4.8	4.8	4.8	33.104	289	3.3735E-05	0.89282	0.89161	16.571	2	43411000	23681000	19731000
Q9R1P4	Proteasome subunit alpha type-1	Psma1	5	5	5	27.8	27.8	27.8	29.546	263	8.8282E-80	0.75586	0.51767	55.709	5	247430000	148700000	98731000
P49722	Proteasome subunit alpha type-2	Psma2	5	5	5	29.5	29.5	29.5	25.926	234	6.588E-244	0.88863	0.661	16.197	8	1819300000	1038300000	781010000
O70435	Proteasome subunit alpha type-3	Psma3	6	6	6	23.1	23.1	23.1	28.405	255	1.9266E-72	0.85607	0.56327	51.769	10	1602600000	809780000	792780000
Q9R1P0	Proteasome subunit alpha type-4	Psma4	7	7	7	41.8	41.8	41.8	29.47	261	1.1E-172	1.5581	1.2981	47.591	11	2293300000	973460000	1319900000
Q9Z2U1	Proteasome subunit alpha type-5	Psma5	8	8	8	42.7	42.7	42.7	26.411	241	2.308E-228	1.5246	1.0723	49.953	9	1392600000	607270000	785320000
Q9QUM9	Proteasome subunit alpha type-6	Psma6	7	7	7	31.3	31.3	31.3	27.372	246	2.7309E-35	1.4029	1.1296	26.155	9	1197100000	537700000	659410000
Q9Z2U0	Proteasome subunit alpha type-7	Psma7	9	9	9	37.9	37.9	37.9	27.855	248	1.173E-170	1.4564	1.103	50.541	15	1975800000	849780000	1126100000
O09061	Proteasome subunit beta type-1	Psmb1	8	8	8	40.4	40.4	40.4	26.372	240	1.141E-120	0.93636	0.67552	39.226	17	3068600000	1695100000	1373500000
Q9R1P1	Proteasome subunit beta type-3	Psmb3	3	3	3	22.9	22.9	22.9	22.965	205	1.2812E-51	0.76814	0.53661	30.771	5	763100000	403990000	359110000
P99026	Proteasome subunit beta type-4	Psmb4	4	4	4	29.2	29.2	29.2	29.116	264	3.4003E-64	0.66438	0.47514	10.369	5	309680000	154750000	154930000
O55234	Proteasome subunit beta type-5	Psmb5	6	6	6	25	25	25	28.532	264	2.7531E-85	0.64068	0.45852	47.236	8	894070000	544190000	349880000
Q60692	Proteasome subunit beta type-6	Psmb6	3	3	3	13	13	13	25.378	238	3.0766E-09	1.4503	1.2263	19.472	3	948070000	408250000	539820000
P70195	Proteasome subunit beta type-7	Psmb7	3	3	3	9	9	9	29.891	277	8.1954E-31	0.9283	0.85425	24.272	4	242620000	130500000	112120000
Q6PDI5	Proteasome-associated protein ECM29 homolog	Ecm29	11	11	11	8.7	8.7	8.7	203.7	1840	1.6467E-26	0.84187	0.69633	69.667	11	306790000	165490000	141300000
A2A841	Protein 4.1	Epb4.1	2	2	1	3.3	3.3	1.6	97.239	869	5.0627E-07	1.2073	1.06	76.732	2	60639000	27874000	32766000
Q07456	Protein AMBP	Ambp	3	3	3	11.5	11.5	11.5	39.029	349	1.0637E-28	1.6663	1.0763	30.863	2	75766000	20813000	54953000
Q9JIF0	Protein arginine N-methyltransferase 1	Prmt1	4	4	4	14.3	14.3	14.3	42.435	371	2.8869E-22	1.5078	1.1255	8.8286	2	130570000	48721000	81847000
Q8CIG8	Protein arginine N-methyltransferase 5	Prmt5	3	3	3	4.9	4.9	4.9	72.679	637	2.6333E-09	0.56595	0.41387	72.911	2	54921000	39142000	15779000
Q8CJG0	Protein argonaute-2	Eif2c2	3	3	3	4.4	4.4	4.4	97.303	860	1.6111E-05	0.43821	0.32698	7.8681	3	88155000	60547000	27608000
Q921C5	Protein bicaudal D homolog 2	Bicd2	3	3	3	6.7	6.7	6.7	93.39	820	6.0997E-33	2.3754	1.8706	121.52	3	163240000	86740000	76502000
Q4VAA2	Protein CDV3	Cdv3	5	5	5	35.6	35.6	35.6	29.729	281	5.8138E-46	2.2492	1.4195	53.726	7	520210000	105220000	414990000
O88668	Protein CREG1	Creg1	2	2	2	13.2	13.2	13.2	24.452	220	1.1772E-16	0.43526	0.24993	6.5814	4	703670000	503300000	200360000
A2ADY9	Protein DDI1 homolog 2	Ddi2	4	4	4	16	16	16	44.59	399	1.8153E-24	1.6877	1.3143	32.671	4	165450000	60503000	104940000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q7TNV0	Protein DEK	Dek	4	4	4	11.6	11.6	11.6	43.158	380	3.1749E-17	1.6198	1.2996	61.449	4	883330000	386820000	496510000
E9PV41	Protein diaphanous homolog 1	Diap1	3	3	3	3	3	3	140.4	1264	7.3346E-16	1.0083	0.54227	21.743	3	116660000	53494000	63166000
P09103	Protein disulfide-isomerase	P4hb	22	22	22	40.3	40.3	40.3	57.058	509	2.642E-297	1.2376	1.0252	58.047	29	8696400000	3634000000	5062500000
P27773	Protein disulfide-isomerase A3	Pdia3	25	25	25	51.7	51.7	51.7	56.678	505	0	0.99575	0.72237	82.861	38	7327400000	3961600000	3365800000
P08003	Protein disulfide-isomerase A4	Pdia4	6	6	6	11.9	11.9	11.9	71.982	638	1.52E-235	1.2335	0.90993	24.482	5	349470000	149610000	199860000
Q922R8	Protein disulfide-isomerase A6	Pdia6	3	3	3	9.5	9.5	9.5	48.1	440	2.8751E-76	0.77852	0.49386	188.31	4	346150000	198490000	147660000
Q99LX0	Protein DJ-1	Park7	10	10	10	59.8	59.8	59.8	20.021	189	0	2.521	1.6877	83.948	19	7860500000	2580600000	5279900000
E9QKR1	Protein enabled homolog	Enah	5	5	5	10.6	10.6	10.6	83.983	785	3.219E-106	1.3014	1.008	135.85	4	445980000	71633000	374350000
Q9DCM0	Protein ETHE1, mitochondrial	Ethe1	5	5	5	32.3	32.3	32.3	27.738	254	4.6789E-89	1.7838	1.1275	15.974	7	1854400000	704460000	1150000000
Q61160	Protein FADD	Fadd	2	2	2	17.6	17.6	17.6	22.96	205	6.3101E-10	0.71023	0.60289	101.14	2	89273000	45815000	43458000
Q8VE88	Protein FAM114A2	Fam114a2	3	3	3	9.7	9.7	9.7	54.044	497	1.3329E-09	1.1154	0.67258	44.584	2	69993000	32066000	37927000
Q9CR98	Protein FAM136A	Fam136a	3	3	3	34.1	34.1	34.1	15.674	138	9.9715E-38	2.4062	1.7162	1.0982	2	292420000	86149000	206270000
Q9D6U8	Protein FAM162A	Fam162a	1	1	1	11	11	11	17.725	155	0.00096957	1.6304	1.088	4.6484	2	81029000	30710000	50319000
Q921M7	Protein FAM49B	Fam49b	3	3	3	12.7	12.7	12.7	36.776	324	8.9814E-16	2.0822	1.5603	14.77	3	247290000	70989000	176300000
Q8K2I1	Protein farnesyltransferase subunit beta	Fntb	2	2	2	8	8	8	48.819	437	7.0959E-09	0.90219	0.63541	7.3984	2	97792000	48196000	49596000
Q61239	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	Fnta	6	6	6	21	21	21	44.013	377	1.1983E-17	1.9139	2.0214	62.188	5	159780000	83428000	76355000
J3QPI0	Protein Gm8298	Gm8298	1	1	1	3.2	3.2	3.2	45.876	401	0.033271	1.3524	0.81034	59.361	2	146310000	70046000	76267000
Q8BUK6	Protein Hook homolog 3	Hook3	3	3	3	6.4	6.4	6.4	83.217	718	1.338E-11	0.83388	0.65058	63.788	4	111640000	61763000	49882000
O55091	Protein IMPACT	Impact	3	3	3	14.8	14.8	14.8	36.276	318	5.5222E-12	1.245	0.92109	38.468	3	245800000	116640000	129160000
Q8C1D8	Protein IWS1 homolog	Iws1	2	2	2	3.3	3.3	3.3	85.247	766	0.0091424	0.61912	0.51609	68.561	2	95808000	57761000	38047000
Q5SW19	Protein KIAA0664	Kiaa0664	15	15	15	16.3	16.3	16.3	148.07	1315	0	1.1552	0.88189	144.01	17	2770300000	2000300000	769990000
Q99JB8	Protein kinase C and casein kinase II substrate protein 3	Pacsin3	2	2	2	6.4	6.4	6.4	48.584	424	8.9798E-15	1.5293	1.0877	42.132	2	197370000	93222000	104150000
Q9WVE8	Protein kinase C and casein kinase substrate in neurons protein 2	Pacsin2	11	11	11	27.8	27.8	27.8	55.832	486	5.046E-233	2.1357	1.4391	26.863	15	1886600000	631850000	1254700000
P28867	Protein kinase C delta type	Prkcd	1	1	1	1.3	1.3	1.3	77.546	674	0.032182	1.4283	1.0524	14.776	2	119040000	50732000	68308000
Q8K3C3	Protein LZIC	Lzic	7	7	7	47.9	47.9	47.9	21.536	190	8.135E-131	2.7884	2.5665	147.65	9	3433500000	1454500000	1979000000
Q91VH6	Protein MEMO1	Memo1	5	5	5	27.3	27.3	27.3	33.692	297	1.2074E-25	0.74189	0.54552	23.014	8	492300000	281050000	211250000
Q9CWG8	Protein midA homolog, mitochondrial	Ndufaf7	2	2	2	6.4	6.4	6.4	48.384	436	0.0018381	0.86662	0.59445	18.067	3	764510000	410880000	353630000
Q9QYG0	Protein NDRG2	Ndrg2	11	11	11	46.6	46.6	46.6	40.789	371	0	2.1106	1.5828	62.546	36	4601400000	1566300000	3035100000
Q3UW53	Protein Niban	Fam129a	2	2	2	3.3	3.3	3.3	102.65	926	7.6225E-06	1.7183	1.2445	18.652	2	154720000	44675000	110050000
O55126	Protein NipSnap homolog 2	Gbas	7	7	7	32.4	32.4	32.4	32.932	281	8.819E-245	0.66139	0.50255	29.467	11	3319800000	2081000000	1238700000
A6H644	Protein phosphatase 1 regulatory subunit 12B	Ppp1r12b	5	5	5	6.2	6.2	6.2	110.97	992	4.6076E-45	0.98474	0.66892	29.887	6	1018000000	495040000	522930000
Q3UMT1	Protein phosphatase 1 regulatory subunit 12C	Ppp1r12c	2	2	2	6.4	6.4	6.4	84.684	782	3.0658E-16	1.0906	0.9207	26.615	3	81254000	35731000	45523000
Q62084	Protein phosphatase 1 regulatory subunit 14B	Ppp1r14b	2	2	2	30.6	30.6	30.6	15.957	147	2.1E-12	1.9713	1.7856	48.747	2	76754000	27222000	49531000
Q8R4S0	Protein phosphatase 1 regulatory subunit 14C	Ppp1r14c	2	2	2	22.6	22.6	22.6	17.754	164	1.0316E-50	3.3876	1.9347	9.6293	3	1688700000	442580000	1246100000
Q99MR9	Protein phosphatase 1 regulatory subunit 3A	Ppp1r3a	14	14	14	20.5	20.5	20.5	121.43	1089	0	2.0542	1.5282	67.087	11	976630000	319770000	656860000
Q3UM45	Protein phosphatase 1 regulatory subunit 7	Ppp1r7	5	5	5	21.6	21.6	21.6	41.291	361	2.395E-145	1.0343	0.83643	19.357	10	502590000	252510000	250080000
P49443	Protein phosphatase 1A	Ppm1a	6	5	5	18.1	15.4	15.4	42.432	382	5.8139E-32	1.6906	1.2276	31.491	7	649800000	256790000	393010000
Q99NF7	Protein phosphatase 1B	Ppm1b	7	7	6	20.8	20.8	18.7	52.11	477	5.6904E-26	1.5858	1.1993	66.013	7	1039500000	409350000	630160000
Q8CGA0	Protein phosphatase 1F	Ppm1f	3	3	3	8.2	8.2	8.2	49.61	452	5.1859E-09	1.1624	0.85276	69.929	3	211420000	74108000	137310000
Q61074	Protein phosphatase 1G	Ppm1g	2	2	2	5.4	5.4	5.4	58.727	542	8.7794E-09	2.4271	1.5633	20.392	2	62095000	20393000	41702000
Q9DCL8	Protein phosphatase inhibitor 2	Ppp1r2	5	5	5	35.4	35.4	35.4	23.119	206	1.4999E-45	3.592	2.5847	60.984	6	469890000	113660000	356230000
Q6NVE9	Protein phosphatase PTC7 homolog	Pptc7	4	4	4	18.7	18.7	18.7	33.048	310	7.1275E-73	1.6534	1.4147	25.06	4	244070000	92551000	151520000
Q7TSC1	Protein PRRC2A	Prrc2a	3	3	3	3.2	3.2	3.2	229.2	2158	3.3885E-19	2.4724	1.6624	28.126	3	116860000	27296000	89567000
Q3TLH4	Protein PRRC2C	Prrc2c	5	5	5	3.4	3.4	3.4	310.89	2846	1.5615E-92	2.6075	1.9041	50.704	6	149750000	41381000	108370000
Q8BIW1	Protein prune homolog	Prune	6	6	6	18.7	18.7	18.7	50.239	454	2.7265E-48	1.8932	1.4971	32.919	7	286380000	109360000	177020000
Q52KR3	Protein prune homolog 2	Prune2	8	8	8	4.5	4.5	4.5	339.51	3084	1.206E-155	0.87019	0.62464	72.734	8	265220000	123420000	141790000
Q9QYS9	Protein quaking	Qki	7	7	7	27.3	27.3	27.3	37.67	341	1.5245E-19	2.7356	2.038	64.712	9	765130000	263470000	501660000
P56565	Protein S100-A1	S100a1	2	2	2	37.2	37.2	37.2	10.505	94	2.026E-144	2.3405	2.0379	95.963	7	434020000	86198000	347820000
P08207	Protein S100-A10	S100a10	1	1	1	17.5	17.5	17.5	11.186	97	1.8601E-35	1.5546	1.6995	24.681	2	100610000	37597000	63011000
P50543	Protein S100-A11	S100a11	2	2	2	27.6	27.6	27.6	11.083	98	4.2771E-30	2.1827	1.9958	9.024	3	435590000	145560000	290030000
P97352	Protein S100-A13	S100a13	3	3	3	25.5	25.5	25.5	11.158	98	0.0002009	1.6858	1.2921	44.332	2	408380000	172300000	236090000
P27005	Protein S100-A8	S100a8	1	1	1	22.5	22.5	22.5	10.294	89	1.0871E-61	1.0831	0.82647	10.191	3	251380000	112600000	138770000
P31725	Protein S100-A9	S100a9	2	2	2	17.7	17.7	17.7	13.049	113	9.7313E-12	1.007	0.85703	28.246	2	858230000	473070000	385160000
Q9D1M0	Protein SEC13 homolog	Sec13	2	2	2	8.7	8.7	8.7	35.565	322	8.2386E-28	1.3886	1.6778	13.628	3	236430000	104940000	131490000
Q9EQU5	Protein SET	Set	3	3	3	13.5	13.5	13.5	33.377	289	1.0855E-84	1.8475	1.2177	25.771	2	244570000	86588000	157980000
Q91YM4	Protein TBRG4	Tbrg4	2	2	2	6	6	6	71.513	630	0.0015301	0.81604	0.68616	26.436	3	101940000	48777000	53166000
Q01405	Protein transport protein Sec23A	Sec23a	8	8	5	13.2	13.2	7.7	86.161	765	5.7442E-52	0.60661	0.45978	35.721	12	554600000	342230000	212360000
Q3UPL0	Protein transport protein Sec31A	Sec31a	11	11	11	10.4	10.4	10.4	133.57	1230	6.286E-119	0.58487	0.40826	45.647	11	1295600000	794070000	501520000
Q3TZ89	Protein transport protein Sec31B	Sec31b	3	3	3	3	3	3	125.63	1158	8.9935E-08	0.78923	0.53299	63.035	6	3.6506E+10	1.9634E+10	1.6872E+10
Q80WQ2	Protein VAC14 homolog	Vac14	3	3	3	4.5	4.5	4.5	88.047	782	3.5259E-06	0.5983	0.49934	49.3	4	609170000	213860000	395310000
Q9D1G3	Protein-cysteine N-palmitoyltransferase HHAT-like protein	Hhatl	3	3	3	6.4	6.4	6.4	56.43	503	1.3084E-22	0.73696	0.58417	22.451	4	222290000	136630000	85654000
P21981	Protein-glutamine gamma-glutamyltransferase 2	Tgm2	12	12	12	24.8	24.8	24.8	77.06	686	6.34E-189	0.77201	0.55189	23.834	15	2035000000	1118800000	916170000
E0CYV0	Protein-L-isoaspartate O-methyltransferase	Pcmt1	9	9	9	35	35	35	30.441	286	2.4311E-60	1.139	0.99838	36.757	13	2311400000	1054900000	1256500000
P19221	Prothrombin	F2	8	8	8	22.2	22.2	22.2	70.268	618	3.2723E-85	1.5676	1.0663	77.326	12	954990000	318950000	636040000
Q9CZL5	Pterin-4-alpha-carbinolamine dehydratase 2	Pcbd2	2	2	2	19.1	19.1	19.1	14.83	136	2.1304E-10	2.0246	1.3015	2.438	2	536600000	176510000	360090000
P23492	Purine nucleoside phosphorylase	Pnp	6	6	6	26.6	26.6	26.6	32.277	289	1.3867E-30	0.88968	0.6869	29.587	10	874750000	471310000	403430000
Q6W8Q3	Purkinje cell protein 4-like protein 1	Pcp4l1	2	2	2	39.7	39.7	39.7	7.5023	68	1.5437E-09	3.5625	3.8367	30.278	4	954890000	228310000	726570000
Q11011	Puromycin-sensitive aminopeptidase	Npepps	17	17	17	24.6	24.6	24.6	103.32	920	3.638E-182	1.0928	0.85987	26.629	20	3133300000	1670100000	1463200000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O88696	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	Clpp	2	2	2	12.1	12.1	12.1	29.8	272	3.497E-15	1.2446	0.93813	133.56	4	263880000	149320000	114550000
Q6P8M1	Putative deoxyribonuclease TATDN1	Tatdn1	3	3	3	15.6	15.6	15.6	33.365	295	8.078E-151	1.0902	0.79128	61.774	5	306760000	183720000	123040000
O88851	Putative hydrolase RBBP9	Rbbp9	3	3	3	32.8	32.8	32.8	20.911	186	1.848E-109	2.2625	1.6219	28.935	3	380260000	121800000	258450000
E9QLT0	Putative hydroxypyruvate isomerase	Hyi	2	2	2	18.7	18.7	18.7	29.395	267	4.8776E-18	0.8808	0.70071	53.288	3	133540000	71263000	62273000
Q3UIZ8	Putative myosin light chain kinase 3	Mylk3	9	9	9	20	20	20	86.371	795	8.2144E-82	1.4817	1.0146	63.757	10	1162200000	506050000	656190000
Q3TCN2	Putative phospholipase B-like 2	Plbd2	9	9	9	22.2	22.2	22.2	66.289	594	4.7327E-85	0.34905	0.22725	88.543	10	604390000	455050000	149330000
Q8CAK1	Putative transferase CAF17 homolog, mitochondrial	Iba57	8	8	8	31	31	31	38.399	358	1.323E-57	0.71178	0.4688	45.297	9	907920000	540550000	367370000
Q8K183	Pyridoxal kinase	Pdxk	4	4	4	19.6	19.6	19.6	35.015	312	1.7702E-88	1.1096	0.84883	18.966	6	403310000	183490000	219820000
Q91XF0	Pyridoxine-5-phosphate oxidase	Pnpo	2	2	2	12.3	12.3	12.3	30.114	261	7.1866E-35	1.5384	1.0385	9.7704	2	192380000	70243000	122140000
Q9DCC4	Pyrroline-5-carboxylate reductase 3	Pycrl	1	1	1	6.9	6.9	6.9	28.721	274	9.1951E-09	1.9909	1.2981	22.868	2	245170000	96694000	148470000
E9QPD7	Pyruvate carboxylase	Pcx	12	12	12	16.2	16.2	16.2	129.83	1179	2.146E-126	0.72889	0.49945	31.955	16	759730000	463660000	296070000
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	Pdha1	17	17	17	44.9	44.9	44.9	43.231	390	0	0.66905	0.45412	93.077	52	3.5141E+10	1.8364E+10	1.6777E+10
Q9D051	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	Pdhb	14	14	14	40.1	40.1	40.1	38.937	359	0	1.2409	0.76788	54.094	26	5563000000	2453800000	3109100000
Q7TSQ8	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	Pdpr	11	11	11	16.9	16.9	16.9	99.229	878	5.7719E-49	0.46484	0.29782	58.34	11	371920000	229820000	142090000
Q8BKZ9	Pyruvate dehydrogenase protein X component, mitochondrial	Pdhx	11	11	11	31.5	31.5	31.5	53.998	501	0	1.9522	1.3217	43.858	22	5146200000	1782000000	3364200000
P52480	Pyruvate kinase isozymes M1/M2	Pkm2	22	22	22	42	42	42	57.844	531	0	1.0989	0.81072	74.402	44	1.4162E+10	7404400000	6758000000
P47199	Quinone oxidoreductase	Cryz	3	3	3	15.7	15.7	15.7	35.268	331	4.5163E-26	1.3617	1.1197	12.894	4	299790000	132960000	166830000
Q3UNZ8	Quinone oxidoreductase-like protein 2		1	1	1	7.7	7.7	7.7	37.808	350	6.9435E-09	0.58978	0.43166	4.8998	2	19615000	11086000	8528300
P50396	Rab GDP dissociation inhibitor alpha	Gdi1	16	11	11	44.3	31.5	31.5	50.521	447	0	1.5256	1.1578	42.892	16	1405900000	576090000	829840000
Q61598	Rab GDP dissociation inhibitor beta	Gdi2	25	25	20	60	60	47.4	50.537	445	0	1.1241	0.80279	49.584	32	4959300000	2328800000	2630400000
E9QKE4	Rab3 GTPase-activating protein non-catalytic subunit	Rab3gap2	2	2	2	1.2	1.2	1.2	154.64	1387	0.0032689	0.55812	0.41744	36.098	2	38006000	24338000	13668000
Q68EF0	Rab-3A-interacting protein	Rab3ip	2	2	2	7.5	7.5	7.5	47.133	428	1.172E-150	1.0012	0.73495	7.6101	3	251110000	128260000	122850000
Q5U3K5	Rab-like protein 1	Parf	2	2	2	4.4	4.4	4.4	79.83	725	6.2979E-09	0.60876	0.49597	3.7219	2	42159000	24178000	17981000
P31750	RAC-alpha serine/threonine-protein kinase	Akt1	4	4	3	11.2	11.2	8.5	55.707	480	1.6413E-07	0.87401	0.68084	57.421	4	284940000	168090000	116840000
P26043	Radixin	Rdx	15	7	7	29.7	14.8	14.8	68.542	583	9.3104E-90	2.0963	2.0411	25.157	10	1070100000	386640000	683450000
Q9CQ22	Ragulator complex protein LAMTOR1	Lamtor1	2	2	2	27.3	27.3	27.3	17.749	161	5.7567E-55	0.35809	0.35777	31.99	3	196050000	146240000	49808000
O88653	Ragulator complex protein LAMTOR3	Lamtor3	2	2	2	21.8	21.8	21.8	13.553	124	3.6302E-06	1.1961	0.72193	20.006	3	327720000	158010000	169710000
P34022	Ran-specific GTPase-activating protein	Ranbp1	4	4	4	36.9	36.9	36.9	23.596	203	6.2716E-36	2.4551	1.8921	77.622	5	796710000	204790000	591920000
P97855	Ras GTPase-activating protein-binding protein 1	G3bp1	9	9	9	29.2	29.2	29.2	51.828	465	2.1568E-79	1.1638	0.99885	31.446	12	738230000	357200000	381030000
P97379	Ras GTPase-activating protein-binding protein 2	G3bp2	3	3	3	7.9	7.9	7.9	54.087	482	5.6183E-05	1.1347	0.89239	154.98	3	526120000	484340000	41783000
Q9JKF1	Ras GTPase-activating-like protein IQGAP1	Iqgap1	10	10	10	9.3	9.3	9.3	188.74	1657	3.77E-181	0.7436	0.48816	30.927	10	539960000	327960000	212000000
Q01730	Ras suppressor protein 1	Rsu1	2	2	2	9	9	9	31.55	277	4.7594E-22	0.73989	0.48692	26.327	3	433160000	247570000	185590000
Q3U0S6	Ras-interacting protein 1	Rasip1	3	3	3	7.2	7.2	7.2	103.56	961	1.2938E-24	0.75252	0.60771	84.336	2	19321000	12477000	6843500
Q3TLP8	Ras-related C3 botulinum toxin substrate 1	Rac1	8	8	7	29.4	29.4	24.2	23.432	211	5.0448E-18	0.66462	0.60675	57.567	7	1758700000	1081300000	677340000
Q80X95	Ras-related GTP-binding protein A	Rraga	4	4	4	15.7	15.7	15.7	36.566	313	2.0356E-12	0.42718	0.29758	55.71	4	294850000	223820000	71029000
Q99K70	Ras-related GTP-binding protein C	Rragc	4	4	4	16.3	16.3	16.3	44.12	398	1.7331E-93	0.43116	0.35495	52.477	6	521530000	370390000	151140000
P61027	Ras-related protein Rab-10	Rab10	3	3	3	16.5	16.5	16.5	22.541	200	4.0909E-17	0.79677	0.54037	18.557	4	219360000	136720000	82638000
P46638	Ras-related protein Rab-11B	Rab11b	2	2	2	14.7	14.7	14.7	24.489	218	8.1078E-83	1.3039	1.1045	24.291	2	135340000	63651000	71685000
Q91V41	Ras-related protein Rab-14	Rab14	4	4	4	34.4	34.4	34.4	23.897	215	2.029E-107	0.80519	0.49101	100.11	4	330700000	220020000	110670000
P35293	Ras-related protein Rab-18	Rab18	1	1	1	6.8	6.8	6.8	23.035	206	0.014746	0.99621	0.78506	26.87	2	26050000	12232000	13818000
P62821	Ras-related protein Rab-1A	Rab1A	2	1	1	12.2	8.3	8.3	22.677	205	7.9289E-39	0.99981	0.94844	4.562	2	80668000	38822000	41846000
Q9D1G1	Ras-related protein Rab-1B	Rab1b	3	3	2	20.4	20.4	16.4	22.187	201	8.6268E-68	0.99283	0.82039	46.001	4	379070000	202240000	176830000
P35282	Ras-related protein Rab-21	Rab21	4	4	4	19.8	19.8	19.8	24.106	222	5.0238E-45	0.93412	1.026	50.54	5	278910000	147830000	131080000
P53994	Ras-related protein Rab-2A	Rab2a	6	6	6	38.2	38.2	38.2	23.547	212	3.7539E-83	0.52418	0.37176	31.784	7	578630000	377070000	201560000
Q8C266	Ras-related protein Rab-5C	Rab5c	4	4	2	20.9	20.9	12	25.352	234	2.6958E-34	0.71606	0.56951	40.372	6	701620000	422580000	279040000
P51150	Ras-related protein Rab-7a	Rab7a	5	5	5	29.5	29.5	29.5	23.489	207	1.239E-36	0.35562	0.29815	49.569	6	577020000	412040000	164980000
P55258	Ras-related protein Rab-8A	Rab8a	2	2	2	10.6	10.6	10.6	23.668	207	0.00033126	0.39163	0.3688	22.217	2	37165000	26714000	10451000
P63321	Ras-related protein Ral-A	Rala	2	2	2	10.2	10.2	10.2	23.553	206	9.523E-08	0.62138	0.59626	49.636	2	94401000	58793000	35608000
Q99JI6	Ras-related protein Rap-1b	Rap1b	4	4	2	21.2	21.2	15.2	20.825	184	2.5878E-16	0.58517	0.67124	66.195	3	218410000	139560000	78846000
P62071	Ras-related protein R-Ras2	Rras2	2	2	1	13.7	13.7	5.9	23.399	204	1.887E-26	0.95425	0.65197	6.7003	4	352990000	174740000	178250000
P28828	Receptor-type tyrosine-protein phosphatase mu	Ptprm	2	2	2	1.2	1.2	1.2	163.65	1452	0.000963	0.84294	0.79507	99.533	2	103560000	52243000	51315000
Q9CSU0	Regulation of nuclear pre-mRNA domain-containing protein 1B	Rprd1b	2	2	2	9.2	9.2	9.2	36.883	326	3.1481E-05	1.4208	1.2704	31.899	2	47361000	18846000	28515000
Q6PFB2	Regulator of chromosome condensation	Rcc1	3	3	3	10.6	10.6	10.6	46.374	434	3.1891E-17	0.93794	0.69821	38.434	4	133380000	70620000	62757000
Q9CQE5	Regulator of G-protein signaling 10	Rgs10	3	3	3	24.3	24.3	24.3	21.151	181	0.00055295	0.18299	0.11997	189.69	2	63339000	56812000	6527200
Q9DCV4	Regulator of microtubule dynamics protein 1	Fam82b	6	6	6	28.2	28.2	28.2	35	305	5.574E-211	2.0572	1.7448	53.245	6	1414500000	497540000	916960000
Q9EPU0	Regulator of nonsense transcripts 1	Upf1	8	8	8	8.1	8.1	8.1	123.97	1124	2.5896E-25	0.42022	0.32369	48.756	6	216210000	153720000	62486000
Q99P72	Reticulon-4	Rtn4	10	10	10	13.7	13.7	13.7	126.61	1162	3.2667E-90	0.8724	0.64654	123.36	13	968990000	634790000	334190000
Q924D0	Reticulon-4-interacting protein 1, mitochondrial	Rtn4ip1	9	9	9	37.6	37.6	37.6	43.371	396	3.2737E-69	0.79882	0.63375	62.826	12	1434400000	978560000	455800000
P24549	Retinal dehydrogenase 1	Aldh1a1	9	9	9	28.1	28.1	28.1	54.467	501	9.216E-199	1.0951	0.82456	49.646	11	1882900000	983780000	899080000
Q9EPC5	Retinoid-binding protein 7	Rbp7	2	2	2	20.1	20.1	20.1	15.427	134	0.000176	1.5585	1.7386	112.59	3	61246000	20774000	40472000
Q920A5	Retinoid-inducible serine carboxypeptidase	Scpep1	3	3	3	8.2	8.2	8.2	50.964	452	5.5842E-17	0.45789	0.44169	6.4467	3	149920000	97316000	52606000
Q00915	Retinol-binding protein 1	Rbp1	3	3	3	25.2	25.2	25.2	15.846	135	2.0997E-15	4.6908	3.5322	42.927	3	111880000	22852000	89027000
Q99PT1	Rho GDP-dissociation inhibitor 1	Arhgdia	7	7	7	46.6	46.6	46.6	23.407	204	0	1.397	0.83216	38.997	10	5425800000	2307600000	3118200000
Q61599	Rho GDP-dissociation inhibitor 2	Arhgdib	3	3	3	36	36	36	22.851	200	8.2666E-23	1.6763	1.1856	69.541	6	840670000	377360000	463310000
B7ZCJ1	Rho GTPase-activating protein 21	Arhgap21	1	1	1	0.9	0.9	0.9	216.98	1955	6.1545E-19	1.2515	1.0143	15.068	2	19259000	9534400	9725100
F8VPK5	Rho-associated protein kinase 2	Rock2	5	5	4	4.5	4.5	3.7	160.61	1388	4.957E-35	1.3563	1.0253	54.289	5	431340000	204690000	226660000
Q62159	Rho-related GTP-binding protein RhoC	Rhoc	4	4	4	16.6	16.6	16.6	22.006	193	1.303E-195	0.81657	0.68218	20.888	4	1068100000	609250000	458890000
P84096	Rho-related GTP-binding protein RhoG	Rhog	2	1	1	14.7	8.9	8.9	21.308	191	4.1326E-05	0.39785	0.32016	42.121	2	28076000	15215000	12861000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8CFV9	Riboflavin kinase	Rfk	1	1	1	4.5	4.5	4.5	17.437	155	0.0019818	1.9458	1.5225	30.246	2	102620000	36248000	66376000
Q91VI7	Ribonuclease inhibitor	Rnh1	14	14	14	52.6	52.6	52.6	49.816	456	0	1.5601	1.0372	46.816	22	3767700000	1576200000	2191600000
Q9CQ01	Ribonuclease T2	Rnaset2	2	2	2	9.7	9.7	9.7	29.608	259	1.6743E-06	0.47467	0.41381	25.22	2	148710000	104160000	44549000
P52760	Ribonuclease UK114	Hrsp12	5	5	5	45.9	45.9	45.9	14.255	135	8.439E-285	1.7721	1.2447	52.759	6	473160000	208930000	264230000
G3UXL2	Ribose-phosphate pyrophosphokinase	Prps1l3	5	5	1	24.5	24.5	6.3	34.824	318	2.2883E-26	1.4053	1.0121	12.645	6	937010000	339970000	597040000
Q5XJF6	Ribosomal protein	Rpl10a	3	3	3	21.7	21.7	21.7	24.831	217	1.1512E-19	0.11198	0.096051	9.1354	2	123960000	115810000	8155800
Q99PL5	Ribosome-binding protein 1	Rrbp1	14	14	14	11.7	11.7	11.7	172.88	1605	0	1.3121	1.2455	50.377	15	889200000	385930000	503270000
Q9D6S7	Ribosome-recycling factor, mitochondrial	Mrrf	6	6	6	39.3	39.3	39.3	29.05	262	2.383E-265	2.7869	1.9914	44.131	13	2088300000	499030000	1589200000
Q8R2Q4	Ribosome-releasing factor 2, mitochondrial	Gfm2	11	11	11	22.2	22.2	22.2	86.108	779	3.668E-206	1.2844	0.94346	42.786	14	893630000	350380000	543250000
Q9JI75	Ribosyldihydronicotinamide dehydrogenase [quinone]	Nqo2	7	7	7	48.1	48.1	48.1	26.248	231	6.6806E-43	1.498	1.1256	120.55	9	1020400000	493320000	527070000
Q9ET26	RING finger protein 114	Rnf114	3	3	3	17	17	17	25.745	229	9.5924E-18	2.4458	2.2686	86.289	2	87134000	27024000	60109000
Q9D706	RNA polymerase II-associated protein 3	Rpap3	1	1	1	2.6	2.6	2.6	74.095	660	3.9862E-05	1.7845	1.2736	12.847	2	40169000	14011000	26158000
E9PZ21	RNA-binding motif, single-stranded-interacting protein 1	Rbms1	2	2	2	5.8	5.8	5.8	45.02	417	0.00065492	0.23119	0.16476	288.79	2	32840000	19879000	12961000
Q62176	RNA-binding protein 38	Rbm38	5	5	5	28.3	28.3	28.3	25.363	237	6.3581E-20	2.1935	1.9373	44.877	6	569290000	202220000	367070000
Q8VH51	RNA-binding protein 39	Rbm39	3	3	3	10.2	10.2	10.2	59.406	530	1.4836E-05	1.1029	0.7921	10.448	2	56917000	24353000	32564000
Q5SUS9	RNA-binding protein EWS	Ewsr1	3	3	3	7.3	7.3	7.3	69.036	661	4.4728E-83	1.8503	1.9697	9.1353	2	298800000	103520000	195280000
P56959	RNA-binding protein FUS	Fus	3	3	3	8.1	8.1	8.1	52.673	518	5.7356E-15	1.166	1.0949	18.699	2	22103000	9664800	12438000
Q920Q6	RNA-binding protein Musashi homolog 2	Msi2	4	4	4	18.8	18.8	18.8	36.938	346	3.3979E-50	1.2038	1.0466	12.224	3	236070000	113440000	122620000
Q9WVB0	RNA-binding protein with multiple splicing	Rbpms	6	6	5	35.5	35.5	32	21.816	197	4.828E-160	1.983	1.1213	38.824	8	1404400000	491150000	913240000
Q9CPR1	RWD domain-containing protein 4	Rwdd4	2	2	2	10.6	10.6	10.6	21.137	188	0.00033631	3.0531	2.0643	21.805	2	141900000	30934000	110960000
E9Q401	Ryanodine receptor 2	Ryr2	29	29	29	6.7	6.7	6.7	564.81	4966	4.747E-105	0.32554	0.25843	51.871	22	490660000	371120000	119540000
Q497V5	S1 RNA-binding domain-containing protein 1	Srbd1	3	3	3	2.8	2.8	2.8	114.09	1015	0.0019067	0.67924	0.49013	89.043	3	143390000	93566000	49824000
Q3THS6	S-adenosylmethionine synthase isoform type-2	Mat2a	3	3	3	10.4	10.4	10.4	43.688	395	8.9261E-10	1.3639	0.88193	5.8033	3	592850000	258570000	334270000
F8WJE0	SAM domain and HD domain-containing protein 1	Samhd1	5	5	5	10.9	10.9	10.9	75.892	658	3.3642E-18	0.61525	0.46115	9.8892	3	250710000	149080000	101630000
Q7TQ48	Sarcalumenin	Srl	27	27	27	42.5	42.5	42.5	99.183	910	0	1.6786	1.3458	43.949	69	1.4219E+10	6163700000	8055300000
O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	Atp2a2	35	35	35	41.4	41.4	41.4	114.86	1044	0	0.54346	0.42289	53.274	52	2.2875E+10	1.5014E+10	7860700000
S4R1M2	Scaffold attachment factor B1	Safb	3	3	3	4.9	4.9	4.9	105.32	939	2.346E-152	1.8683	1.3642	93.542	2	42480000	17440000	25040000
Q8BRF7	Sec1 family domain-containing protein 1	Scfd1	2	2	2	5.9	5.9	5.9	72.322	639	0.00001356	0.35826	0.29807	35.171	2	71304000	53038000	18266000
G3X928	SEC23-interacting protein	Sec23ip	2	2	2	1.8	1.8	1.8	110.76	998	7.9912E-05	0.91406	0.68439	14.179	2	109310000	59119000	50195000
Q8VCA8	Secernin-2	Scrn2	6	6	6	29.4	29.4	29.4	46.6	425	9.396E-106	0.82402	0.60213	31.268	10	1027400000	531170000	496270000
Q3TMH2	Secernin-3	Scrn3	7	7	7	23.7	23.7	23.7	47.661	418	3.0969E-70	1.494	0.90629	19.42	8	907880000	413430000	494450000
Q8K021	Secretory carrier-associated membrane protein 1	Scamp1	1	1	1	6.8	6.8	6.8	38.028	338	1.0966E-09	0.85687	0.57188	43.522	2	83585000	46387000	37198000
Q921H9	Sel1 repeat-containing protein 1	Selrc1	3	3	3	21.6	21.6	21.6	25.617	231	3.0628E-26	1.8894	1.4955	3.0722	3	160090000	66664000	93430000
Q8BH69	Selenide, water dikinase 1	Sephs1	2	2	2	9.7	9.7	9.7	42.906	392	1.1472E-26	1.6775	1.059	37.029	2	95867000	43933000	51934000
P17563	Selenium-binding protein 1	Selenbp1	21	21	21	67.2	67.2	67.2	52.513	472	0	1.1043	0.80741	36.099	36	7837400000	3949900000	3887600000
Q91XH5	Sepiapterin reductase	Spr	12	12	12	56.5	56.5	56.5	27.928	262	0	1.1056	0.89255	21.178	21	6543800000	3188800000	3355100000
Q8C1B7	Septin-11	Sept11	7	7	6	18.6	18.6	16.7	49.694	431	1.454E-104	1.6757	1.4121	42.963	9	556230000	214420000	341810000
P42208	Septin-2	Sept2	7	7	7	31.9	31.9	31.9	41.525	361	1.988E-157	1.0558	0.85063	51.439	10	1180000000	530940000	649090000
P28661	Septin-4	Sept4	1	1	1	2.9	2.9	2.9	54.935	478	9.646E-14	1.0882	0.82533	3.533	2	49778000	23773000	26005000
E9Q1G8	Septin-7	Sept7	7	7	7	21.1	21.1	21.1	50.648	437	2.9691E-59	1.1818	0.89954	42.095	7	567360000	244980000	322380000
B1AQZ0	Septin-8	Sept8	5	4	4	12.2	10.5	10.5	55.874	484	6.1537E-15	2.1229	1.7155	72.563	3	185340000	69629000	115720000
Q80UG5	Septin-9	Sept9	6	6	6	16.8	16.8	16.8	65.574	583	1.4859E-42	1.238	0.98151	45.01	6	213920000	108660000	105260000
P54797	Ser/Thr-rich protein T10 in DGCR region	T10	8	8	8	36.2	36.2	36.2	30.947	276	3.609E-236	1.0767	0.8258	53.408	17	1681400000	844050000	837310000
Q8R238	Serine dehydratase-like	Sdsl	2	2	2	11.2	11.2	11.2	34.732	329	0.0011002	1.5091	1.0898	57.207	2	138740000	63910000	74834000
Q3U3G8	Serine hydrolase-like protein	Serhl	6	6	6	19.9	19.9	19.9	36.353	321	6.7199E-19	0.73208	0.5097	20.403	9	1193800000	648620000	545200000
Q9CZN7	Serine hydroxymethyltransferase	Shmt2	5	5	5	15.1	15.1	15.1	55.758	504	2.6232E-25	0.98201	0.74134	108.54	8	1127300000	326340000	800960000
Q9JIY5	Serine protease HTRA2, mitochondrial	Htra2	5	5	5	17.2	17.2	17.2	49.348	458	8.7533E-22	1.2305	0.88191	36.96	4	287330000	139820000	147510000
P07759	Serine protease inhibitor A3K	Serpina3k	9	9	4	23.2	23.2	12.4	46.879	418	4.022E-253	1.4922	0.98678	55.672	36	1.9879E+10	4478800000	1.54E+10
G3X8T9	Serine protease inhibitor A3N	Serpina3n	6	3	3	18.4	12	12	46.766	418	4.9238E-40	0.27818	0.1776	138.42	2	61456000	48146000	13310000
P84104	Serine/arginine-rich splicing factor 3	Srsf3	2	2	1	13.4	13.4	4.9	19.329	164	0.0012856	1.3159	0.9867	10.866	3	231280000	94515000	136770000
Q9Z2W1	Serine/threonine-protein kinase 25	Stk25	3	3	2	7.3	7.3	5.6	48.157	426	5.1033E-05	1.2443	1.3381	9.3513	2	102310000	44872000	57433000
Q9JI11	Serine/threonine-protein kinase 4	Stk4	1	1	1	3.3	3.3	3.3	55.541	487	0.014119	2.6897	1.5339	12.364	3	1.4383E+10	3489400000	1.0893E+10
Q9JLN9	Serine/threonine-protein kinase mTOR	Mtor	2	2	2	1.3	1.3	1.3	288.79	2549	0.0021206	0.31643	0.24111	49.051	2	26535000	18938000	7597500
Q8K1R7	Serine/threonine-protein kinase Nek9	Nek9	2	2	2	2.3	2.3	2.3	107.14	984	8.5036E-09	0.79804	0.5898	11.548	2	32281000	18431000	13851000
Q6P9R2	Serine/threonine-protein kinase OSR1	Oxsr1	5	5	4	13.3	13.3	12	58.213	527	4.2338E-22	2.0028	1.5016	97.623	7	1543100000	788450000	754690000
Q8CIN4	Serine/threonine-protein kinase PAK 2	Pak2	5	5	5	14.1	14.1	14.1	57.93	524	2.3385E-15	1.7883	1.7392	34.54	4	431330000	165440000	265880000
P83741	Serine/threonine-protein kinase WNK1	Wnk1	5	5	4	2.9	2.9	2.5	250.93	2377	1.215E-10	1.345	1.058	19.933	5	185380000	84107000	101270000
Q6P1F6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	Ppp2r2a	6	6	3	15.2	15.2	5.1	51.691	447	9.0655E-38	1.0643	0.73776	46.595	3	250230000	137210000	113020000
Q60996	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	Ppp2r5c	2	2	2	4.8	4.8	4.8	60.824	524	0.010399	0.57322	0.43765	18.144	2	28603000	18361000	10243000
Q6PD03	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	Ppp2r5a	4	4	4	9.3	9.3	9.3	56.346	486	1.6974E-08	1.4975	1.1384	115.8	3	64843000	27705000	37138000
Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	Ppp2r1a	14	14	14	32.6	32.6	32.6	65.322	589	2.796E-274	1.4559	1.0812	22.363	18	6190500000	2741800000	3448800000
P58389	Serine/threonine-protein phosphatase 2A activator	Ppp2r4	4	4	4	23.5	23.5	23.5	36.71	323	1.105E-37	1.7056	1.0916	8.3333	4	393520000	147670000	245850000
P62715	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	Ppp2cb	8	8	1	35	35	4.2	35.575	309	8.059E-68	0.82557	0.59315	33.722	15	900090000	480870000	419210000
P63328	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	Ppp3ca	4	4	1	9.4	9.4	5	58.643	521	2.3824E-12	0.72604	0.5546	180.93	4	764370000	617850000	146520000
Q60676	Serine/threonine-protein phosphatase 5	Ppp5c	8	8	8	19.6	19.6	19.6	56.876	499	6.834E-177	1.2213	0.93498	30.053	9	379650000	167940000	211710000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
G5E8R4	Serine/threonine-protein phosphatase 6 regulatory subunit 3	Ppp6r3	4	4	4	6.5	6.5	6.5	97.862	873	1.1298E-38	1.3253	1.0069	14.945	3	69411000	27466000	41945000
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	Ppp1ca	9	9	3	29.1	29.1	11.2	37.54	330	1.828E-215	0.59284	0.44615	32.232	13	1974600000	1262000000	712550000
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	Ppp1cb	9	3	3	33	12.2	12.2	37.186	327	3.295E-198	0.81888	0.58022	13.389	2	179300000	93026000	86275000
Q9Z1Z2	Serine-threonine kinase receptor-associated protein	Strap	7	7	7	27.4	27.4	27.4	38.442	350	5.0384E-40	1.7089	1.284	76.792	7	1067500000	582810000	484710000
Q8C483	Serine--tRNA ligase, cytoplasmic	Sars	13	13	13	27.4	27.4	27.4	61.166	536	3.95E-274	1.1187	0.67808	38.14	13	1188100000	627710000	560410000
Q9JJL8	Serine--tRNA ligase, mitochondrial	Sars2	3	3	3	7.5	7.5	7.5	58.316	518	8.0594E-46	1.1876	0.86753	38.04	4	113080000	45775000	67307000
Q921I1	Serotransferrin	Tf	41	41	2	58.8	58.8	4.4	76.723	697	0	1.5111	1.1187	48.215	85	2.5893E+10	9845000000	1.6048E+10
F8WIV2	Serpin B6	Serpinb6a	10	10	10	33.3	33.3	33.3	44.774	399	0	1.4805	1.0898	33.785	11	2963300000	1375700000	1587600000
P19324	Serpin H1	Serpinh1	9	9	9	31.9	31.9	31.9	46.533	417	8.582E-116	0.97552	0.92227	45.824	13	1212200000	601630000	610560000
P07724	Serum albumin	Alb	58	58	57	78.1	78.1	78.1	68.692	608	0	2.9746	2.1837	50.886	239	1.0305E+11	2.263E+10	8.0416E+10
Q63918	Serum deprivation-response protein	Sdpr	9	9	9	34	34	34	46.763	418	0	1.3673	0.91596	158.69	6	1335200000	663620000	671580000
P97443	SET and MYND domain-containing protein 1	Smyd1	12	12	12	35.3	35.3	35.3	56.495	490	2.3142E-69	1.0454	0.7563	62.624	11	504000000	283950000	220050000
H3BKH6	S-formylglutathione hydrolase	Esd	10	10	10	51.5	51.5	51.5	32.829	295	0	0.76084	0.51378	124.12	18	9312800000	7366400000	1946500000
Q9WUZ7	SH3 domain-binding glutamic acid-rich protein	Sh3bgr	9	9	9	63.1	63.1	63.1	23.102	214	0	4.1363	2.7763	59.088	15	2987900000	587500000	2400400000
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	Sh3bgrl	3	3	3	45.6	45.6	45.6	12.811	114	3.8472E-20	1.9368	1.9444	45.17	3	226870000	72681000	154190000
Q8R550	SH3 domain-containing kinase-binding protein 1	Sh3kbp1	5	5	5	8.3	8.3	8.3	78.169	709	7.186E-13	1.5504	1.8742	18.873	3	278590000	98140000	180450000
Q9DBL1	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Acadsb	8	8	8	28.2	28.2	28.2	47.874	432	1.245E-136	1.0845	0.86322	55.466	8	1404100000	680930000	723180000
Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	Acads	17	17	17	57	57	57	44.889	412	4.012E-234	0.97789	0.6682	45.126	43	1.6425E+10	8380900000	8043900000
Q9D104	Signal recognition particle 19 kDa protein	Srp19	2	2	2	27.8	27.8	27.8	16.094	144	3.9256E-06	0.479	0.38658	20.571	2	67411000	48506000	18905000
E9PXC0	Signal recognition particle 54 kDa protein	Srp54c	2	2	2	6.7	6.7	6.7	55.815	504	0.0003373	0.58043	0.43922	93.384	3	147880000	97117000	50766000
P49962	Signal recognition particle 9 kDa protein	Srp9	2	2	2	23.3	23.3	23.3	10.194	86	2.6863E-05	0.63349	0.43918	38.377	2	130180000	77037000	53141000
P42227	Signal transducer and activator of transcription 3	Stat3	3	3	3	7.1	7.1	7.1	88.053	770	6.12E-192	0.59465	0.51318	5.3763	2	39966000	24119000	15847000
Q9CYR0	Single-stranded DNA-binding protein, mitochondrial	Ssbp1	3	3	3	25	25	25	17.319	152	1.009E-105	2.2109	1.681	15.351	6	357440000	128270000	229170000
Q8BJU0	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	Sgta	4	4	4	17.1	17.1	17.1	34.322	315	4.4891E-41	2.4487	1.6433	12.732	5	421590000	126930000	294650000
Q9DC77	Small muscular protein	Smpx	3	3	3	65.9	65.9	65.9	9.2525	85	9.3923E-67	4.4843	4.6406	26.758	6	1063900000	208420000	855520000
G3UZA7	Small ubiquitin-related modifier 3	Sumo3	1	1	1	10.6	10.6	10.6	12.713	113	1.1384E-10	1.8685	1.4405	49.448	2	155880000	60991000	94886000
Q9CQ65	S-methyl-5-thioadenosine phosphorylase	Mtap	5	5	5	30	30	30	31.062	283	9.1515E-63	1.1505	0.80074	35.252	9	745960000	355600000	390360000
G3X9J1	Sodium/calcium exchanger 1	Slc8a1	5	5	5	9.6	9.6	9.6	108.04	970	2.723E-121	0.72239	0.67624	33.013	4	133310000	71703000	61611000
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	Atp1a1	23	23	20	28.6	28.6	25.2	112.98	1023	0	0.75869	0.56195	53.621	29	4868600000	2946400000	1922200000
Q9WV27	Sodium/potassium-transporting ATPase subunit alpha-4	Atp1a4	5	2	2	6.4	3	3	114.89	1032	1.1861E-98	0.77408	0.46463	11.411	2	199750000	115450000	84298000
P14094	Sodium/potassium-transporting ATPase subunit beta-1	Atp1b1	7	7	7	33.2	33.2	33.2	35.194	304	2.2301E-47	0.87654	0.94851	69.062	6	1029900000	518430000	511500000
P97370	Sodium/potassium-transporting ATPase subunit beta-3	Atp1b3	4	4	4	18	18	18	31.775	278	2.3462E-22	1.3824	0.86888	107.3	2	71933000	19200000	52733000
Q9WVL3	Solute carrier family 12 member 7	Slc12a7	3	3	3	3.8	3.8	3.8	119.48	1083	7.2913E-21	0.93228	0.70899	24.236	4	154140000	81818000	72317000
P14142	Solute carrier family 2, facilitated glucose transporter member 4	Slc2a4	2	2	2	3.7	3.7	3.7	54.755	509	2.7082E-07	0.65728	0.71901	56.166	3	248990000	152020000	96965000
Q8R0Y8	Solute carrier family 25 member 42	Slc25a42	2	2	2	12.3	12.3	12.3	35.24	318	2.0536E-06	0.61221	0.5462	16.796	2	61242000	37178000	24064000
D3Z5J3	Sorbin and SH3 domain-containing protein 1	Sorbs1	7	6	6	13.3	12.2	12.2	103.98	938	2.5223E-27	1.2625	0.96871	63.877	5	176180000	72120000	104060000
B9EKP8	Sorbin and SH3 domain-containing protein 2	Sorbs2	11	11	9	12.9	12.9	10.6	136.2	1214	3.194E-151	1.7215	1.1617	130.17	9	2755900000	427830000	2328100000
Q64442	Sorbitol dehydrogenase	Sord	5	5	5	21.8	21.8	21.8	38.249	357	2.8781E-37	1.1921	1.081	24.225	6	534250000	230410000	303840000
Q6P069	Sorcin	Sri	4	4	4	25.3	25.3	25.3	21.627	198	6.8374E-25	1.8499	1.1176	25.634	4	182480000	63867000	118610000
Q8BGH2	Sorting and assembly machinery component 50 homolog	Samm50	4	4	4	13.2	13.2	13.2	51.863	469	3.7715E-14	0.58085	0.4366	35.585	3	110760000	75735000	35023000
Q9WV80	Sorting nexin-1	Snx1	5	4	4	11.9	10	10	58.951	522	1.8909E-20	2.1318	1.4109	19.868	3	219860000	86192000	133670000
Q8C080	Sorting nexin-16	Snx16	2	2	2	6.7	6.7	6.7	38.817	344	7.1724E-06	0.62693	0.52441	71.409	2	17403000	8819600	8583500
Q9CWK8	Sorting nexin-2	Snx2	10	10	9	23.1	23.1	21.2	58.47	519	3.842E-61	2.1553	2.024	76.796	10	463440000	171860000	291580000
O70492	Sorting nexin-3	Snx3	4	4	4	38.9	38.9	38.9	18.757	162	1.6919E-18	1.9307	1.3145	63.097	4	501510000	138100000	363410000
Q9D8U8	Sorting nexin-5	Snx5	2	2	2	6.2	6.2	6.2	46.797	404	1.0447E-05	0.71023	0.62998	146.66	2	392140000	250150000	141990000
Q6P8X1	Sorting nexin-6	Snx6	2	2	2	7.1	7.1	7.1	46.648	406	1.9778E-12	1.4802	0.99947	26.917	4	256400000	95514000	160890000
P16546	Spectrin alpha chain, brain	Sptan1	52	2	1	28.4	1.3	0.7	284.59	2472	0	1.0017	1.1046	45.484	2	142790000	67586000	75206000
Q62261	Spectrin beta chain, brain 1	Sptbn1	46	46	45	28.1	28.1	27.7	274.22	2363	0	0.86906	0.65985	53.686	58	5064300000	2686700000	2377600000
Q8C9J3	Sperm flagellar protein 2	Spef2	2	2	2	1.5	1.5	1.5	199.14	1734	0.0044133	0.91006	0.63981	354.91	2	165130000	20189000	144940000
P97355	Spermine synthase	Sms	6	6	6	22.7	22.7	22.7	41.313	366	1.1131E-23	1.0135	1.0385	20.385	5	367860000	182220000	185640000
Q9WTX5	S-phase kinase-associated protein 1	Skp1	5	5	5	25.8	25.8	25.8	18.672	163	1.1617E-54	1.9837	1.6571	56.683	6	1248100000	348820000	899230000
Q9Z1N5	Spliceosome RNA helicase Ddx39b	Ddx39b	11	11	11	31.3	31.3	31.3	49.035	428	1.241E-113	1.0227	0.76219	49.54	15	2349100000	922820000	1426200000
Q64213	Splicing factor 1	Sf1	3	3	3	6.1	6.1	6.1	70.402	653	1.0253E-37	2.9664	2.2218	22.772	2	176710000	40600000	136110000
Q8K4Z5	Splicing factor 3A subunit 1	Sf3a1	6	6	6	10.4	10.4	10.4	88.544	791	7.0057E-18	2.0622	1.7858	112.71	6	637520000	395420000	242100000
Q9D554	Splicing factor 3A subunit 3	Sf3a3	2	2	2	7.8	7.8	7.8	58.841	501	7.4932E-15	1.4429	1.1547	31.388	2	73955000	31689000	42266000
P26369	Splicing factor U2AF 65 kDa subunit	U2af2	2	2	2	6.1	6.1	6.1	53.516	475	7.091E-50	1.5128	1.1029	8.8622	4	251760000	106150000	145610000
Q8VIJ6	Splicing factor, proline- and glutamine-rich	Sfpq	3	2	2	5.2	4	4	75.441	699	1.6463E-22	3.0408	2.0841	365.24	2	805780000	76006000	729770000
Q91WK1	SPRY domain-containing protein 4	Spryd4	3	3	3	20.8	20.8	20.8	23.275	207	1.7214E-27	1.182	0.80554	12.651	4	439940000	209010000	230930000
Q60598	Src substrate cortactin	Cttn	2	2	2	5.5	5.5	5.5	61.249	546	1.2008E-15	1.8657	1.7441	34.856	2	115940000	36624000	79311000
O54781	SRSF protein kinase 2	Srpk2	3	3	3	5.9	5.9	5.9	76.756	681	4.9978E-06	1.7278	1.3769	136.15	2	271390000	55304000	216090000
Q78PY7	Staphylococcal nuclease domain-containing protein 1	Snd1	13	13	13	19.3	19.3	19.3	102.09	910	4.9947E-94	0.42137	0.27063	42.555	13	1107400000	761870000	345490000
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	Stk39	4	3	3	11.7	10.4	10.4	60.319	556	1.2422E-98	1.9268	1.2082	51.778	4	520030000	212590000	307440000
O54988	STE20-like serine/threonine-protein kinase	Slk	9	9	9	9.7	9.7	9.7	141.46	1233	1.064E-184	2.0163	1.5474	93.258	8	241470000	92066000	149410000
Q9WUD1	STIP1 homology and U box-containing protein 1	Stub1	4	4	4	16.1	16.1	16.1	34.909	304	2.5266E-07	1.3674	1.1495	32.027	4	130710000	53887000	76823000
P38647	Stress-70 protein, mitochondrial	Hspa9	29	29	29	46.4	46.4	46.4	73.46	679	0	1.8979	1.4833	63.527	43	1.0314E+10	3515300000	6799100000
Q60864	Stress-induced-phosphoprotein 1	Stip1	19	19	19	39.4	39.4	39.4	62.581	543	0	2.013	1.5139	54.347	26	6178400000	2283700000	3894700000
E9QQ25	Striated muscle-specific serine/threonine-protein kinase	Speg	4	4	4	1.5	1.5	1.5	354.31	3262	1.2182E-07	0.83999	0.71626	69.602	4	151030000	79879000	71152000
Q9ERG2	Striatin-3	Strn3	3	3	3	4.8	4.8	4.8	87.149	796	2.5041E-08	1.0143	0.61881	83.24	2	169150000	52046000	117110000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q7TN29	Stromal membrane-associated protein 2	Smap2	2	2	1	4.4	4.4	2.6	46.577	428	0.0041992	0.7228	0.57562	93.898	2	65196000	45663000	19533000
Q9CXV1	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial	Sdhd	2	2	2	10.7	10.7	10.7	17.014	159	2.7136E-05	1.1147	0.80436	17.692	4	705740000	338960000	366790000
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Sdha	19	19	19	40.8	40.8	40.8	72.585	664	0	0.77913	0.58249	32.008	40	7339800000	4347200000	2992600000
Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	Sdhb	10	10	10	40.8	40.8	40.8	31.814	282	1.44E-224	0.69129	0.46696	70.476	11	2262700000	1478900000	783840000
Q8C6I2	Succinate dehydrogenase assembly factor 2, mitochondrial	Sdhaf2	1	1	1	11.6	11.6	11.6	19.431	164	3.7007E-07	3.3488	3.1175	19.953	2	114550000	25717000	88836000
Q9CZB0	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	Sdhc	3	3	3	21.3	21.3	21.3	18.382	169	1.6088E-14	0.58996	0.4031	31.705	5	492150000	307820000	184340000
Q8BWF0	Succinate-semialdehyde dehydrogenase, mitochondrial	Aldh5a1	10	10	10	24.9	24.9	24.9	55.968	523	8.4912E-93	1.071	0.85865	26.032	14	4559000000	2137400000	2421500000
Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	Suclg1	9	9	9	30.9	30.9	30.9	36.154	346	0	1.0183	0.73749	40.69	26	1.6133E+10	7438400000	8694500000
Q9Z2I9	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	Sucla2	27	27	27	56.2	56.2	56.2	50.113	463	0	2.3602	1.614	54.265	56	3.393E+10	9574400000	2.4355E+10
Q9Z2I8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Suclg2	17	17	17	42.3	42.3	42.3	46.839	433	0	1.7033	1.181	71.732	28	1.048E+10	4283600000	6195900000
Q9D0K2	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	Oxct1	16	16	16	34.2	34.2	34.2	55.988	520	4.62E-301	1.2807	1.0028	58.662	29	1.0338E+10	4771800000	5565900000
J3QPG5	Sulfated glycoprotein 1	Psap	9	9	9	20.1	20.1	20.1	61.363	557	1.684E-120	0.88386	0.73805	63.033	10	2985500000	1399100000	1586400000
Q9R112	Sulfide:quinone oxidoreductase, mitochondrial	Sqrdl	6	6	6	16.4	16.4	16.4	50.282	450	3.8687E-62	0.5064	0.41358	48.659	4	223360000	111340000	112010000
Q8R086	Sulfite oxidase, mitochondrial	Suox	9	9	9	28.4	28.4	28.4	60.755	546	0	1.5432	1.1558	36.597	10	638620000	231480000	407140000
Q9D0B5	Sulfurtransferase	2610029I01Rik	3	3	3	33.8	33.8	33.8	17.271	157	1.0823E-15	3.1153	2.3702	38.711	3	151370000	41369000	110000000
Q3UW66	Sulfurtransferase	Mpst	8	8	8	37.7	37.7	37.7	33.097	297	3.397E-204	0.53932	0.42718	59.232	15	1993900000	1103300000	890570000
Q9Z1F9	SUMO-activating enzyme subunit 2	Uba2	5	5	5	14.1	14.1	14.1	70.568	638	5.5189E-25	1.0858	0.89282	72.511	4	130800000	61278000	69522000
P63280	SUMO-conjugating enzyme UBC9	Ube2i	2	2	2	13.9	13.9	13.9	18.007	158	7.8542E-05	1.4365	1.3307	41.493	2	180690000	79736000	100950000
P08228	Superoxide dismutase [Cu-Zn]	Sod1	4	4	4	32.5	32.5	32.5	15.942	154	5.3121E-38	1.9533	1.3453	58.009	11	1.7376E+10	5733200000	1.1643E+10
P09671	Superoxide dismutase [Mn], mitochondrial	Sod2	8	8	8	41.4	41.4	41.4	24.603	222	0	2.3343	1.3396	35.828	34	6.8965E+10	2.016E+10	4.8805E+10
Q8K4L3	Supervillin	Svil	6	6	6	4.9	4.9	4.9	243.16	2170	1.6026E-80	1.1662	0.82704	77.997	7	384920000	172380000	212540000
Q9CX34	Suppressor of G2 allele of SKP1 homolog	Sugt1	6	6	6	21.4	21.4	21.4	38.158	336	0	1.4665	1.1458	84.479	6	509200000	216250000	292950000
Q6P9Z1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3	Smarcd3	2	2	2	3.3	3.3	3.3	54.985	483	0.0040588	0.042535	0.033566	248.75	3	1037100000	959260000	77864000
Q9D5V6	Synapse-associated protein 1	Syap1	3	3	3	12.6	12.6	12.6	41.349	365	1.14E-09	2.467	2.5535	259.6	2	325370000	44174000	281200000
Q64332	Synapsin-2	Syn2	2	2	2	4.9	4.9	4.9	63.372	586	1.4491E-40	1.5898	1.2478	12.251	3	136050000	59375000	76673000
Q62465	Synaptic vesicle membrane protein VAT-1 homolog	Vat1	5	5	5	15	15	15	43.096	406	1.024E-14	0.52639	0.48427	72.91	5	440190000	275950000	164240000
Q9CQW1	Synaptobrevin homolog YKT6	Ykt6	2	2	2	11.1	11.1	11.1	22.314	198	4.5407E-05	0.58127	0.52675	53.87	2	240680000	153290000	87393000
E9PVN6	Synaptojanin-2-binding protein	Gm20498	2	2	2	12.1	12.1	12.1	20.443	182	5.8108E-08	0.65842	0.4	1.0969	2	58983000	34613000	24370000
E9Q3E2	Synaptopodin	Synpo	2	2	2	2.7	2.7	2.7	117.51	1100	2.6691E-05	1.2175	0.91716	39.287	3	119700000	55067000	64632000
B2RQK7	Synaptopodin 2-like protein	Synpo2l	4	4	4	5.2	5.2	5.2	103.27	978	3.1539E-13	1.4868	1.1457	13.889	4	175930000	70301000	105630000
E9Q1U2	Synaptopodin-2	Synpo2	3	3	3	4	4	4	135.76	1257	2.4247E-10	1.3353	0.89505	53.627	3	272190000	129600000	142590000
Q9ER00	Syntaxin-12	Stx12	2	2	2	11.7	11.7	11.7	31.195	274	3.3243E-23	1.0689	0.83027	16.787	4	176600000	86001000	90604000
O08599	Syntaxin-binding protein 1	Stxbp1	2	2	2	8.8	8.8	8.8	67.568	594	2.2412E-12	0.50739	0.34122	11.794	2	29341000	18818000	10523000
P26039	Talin-1	Tln1	41	41	37	23.8	23.8	22.1	269.82	2541	0	1.6704	1.1857	36.681	49	7628800000	2876800000	4752000000
E9PUM4	Talin-2	Tln2	20	16	16	12.2	10.4	10.4	271.66	2542	0	0.93151	0.67847	48.492	13	771420000	476410000	295010000
Q921F2	TAR DNA-binding protein 43	Tardbp	2	2	2	8.7	8.7	8.7	44.547	414	5.0625E-26	1.1788	0.88129	83.645	5	314520000	136840000	177680000
Q3UDC3	Target of Myb protein 1	Tom1	11	11	11	34.5	34.5	34.5	57.145	516	9.269E-121	1.3431	0.90229	18.876	15	1748900000	707110000	1041800000
Q3UUG6	TBC1 domain family member 24	Tbc1d24	4	4	4	10.3	10.3	10.3	63.235	561	6.324E-23	0.63047	0.55785	14.171	4	59186000	34837000	24349000
Q8BYJ6	TBC1 domain family member 4	Tbc1d4	4	4	4	4.6	4.6	4.6	147.45	1307	6.1114E-16	0.96591	0.84237	59.098	4	60880000	30751000	30128000
P11983	T-complex protein 1 subunit alpha	Tcp1	8	8	8	19.1	19.1	19.1	60.448	556	4.8718E-28	0.856	0.61023	43.829	8	1276800000	679880000	596920000
P80314	T-complex protein 1 subunit beta	Cct2	15	15	15	36.3	36.3	36.3	57.477	535	7.542E-135	0.88065	0.65612	56.509	16	2495700000	1654100000	841570000
P80315	T-complex protein 1 subunit delta	Cct4	11	11	11	24.9	24.9	24.9	58.066	539	8.724E-197	0.82135	0.4664	36.037	16	1813700000	905620000	908080000
P80316	T-complex protein 1 subunit epsilon	Cct5	14	14	14	33.3	33.3	33.3	59.623	541	1.055E-99	0.874	0.63971	66.659	24	4093500000	1762800000	2330700000
P80313	T-complex protein 1 subunit eta	Cct7	13	13	13	30.3	30.3	30.3	59.652	544	1.92E-247	0.54748	0.46106	25.275	20	2081900000	1337800000	744080000
P80318	T-complex protein 1 subunit gamma	Cct3	11	11	11	23.7	23.7	23.7	60.629	545	1.1461E-97	0.55249	0.39676	112.55	12	1963800000	630670000	1333100000
P42932	T-complex protein 1 subunit theta	Cct8	13	13	13	33.2	33.2	33.2	59.555	548	3.783E-196	1.2262	0.90651	50.646	18	2788100000	1179500000	1608600000
P80317	T-complex protein 1 subunit zeta	Cct6a	6	6	6	17.9	17.9	17.9	58.004	531	1.59E-115	0.87358	0.64382	20.339	8	900050000	527590000	372460000
Q6X6Z7	Tektin-3	Tekt3	1	1	1	2.7	2.7	2.7	56.672	490	0.0051035	2.3356	1.6772	10.838	2	288640000	91398000	197240000
Q8VBT9	Tether containing UBX domain for GLUT4	Aspscr1	2	2	2	5.5	5.5	5.5	59.795	550	0.00019474	1.8577	1.3041	79.343	2	148130000	62675000	85452000
Q91Z38	Tetratricopeptide repeat protein 1	Ttc1	2	2	2	13	13	13	33.263	292	0.00014002	2.1553	1.4434	18.597	2	77633000	26338000	51295000
A3KMP2	Tetratricopeptide repeat protein 38	Ttc38	4	4	4	8.8	8.8	8.8	52.223	465	2.0982E-16	1.3562	1.2303	35.488	3	253830000	109390000	144440000
Q8C1A5	Thimet oligopeptidase	Thop1	8	8	8	13.7	13.7	13.7	78.025	687	2.6075E-64	1.2466	0.99935	25.753	8	636670000	297190000	339480000
P10639	Thioredoxin	Txn	4	4	4	46.7	46.7	46.7	11.675	105	2.1858E-17	2.4395	2.5007	44.565	3	5699800000	1714000000	3985900000
Q9CQU0	Thioredoxin domain-containing protein 12	Txndc12	3	3	3	25.9	25.9	25.9	19.048	170	3.1572E-26	2.3823	1.8861	63.747	3	101730000	31102000	70626000
Q9CQM5	Thioredoxin domain-containing protein 17	Txndc17	1	1	1	11.4	11.4	11.4	14.015	123	1.2549E-28	2.579	1.9922	3.5396	2	98617000	29156000	69461000
Q91W90	Thioredoxin domain-containing protein 5	Txndc5	6	6	6	18.2	18.2	18.2	46.415	417	8.866E-111	1.6826	1.3127	41.776	8	521800000	215100000	306700000
Q9JMH6	Thioredoxin reductase 1, cytoplasmic	Txnrd1	12	12	11	30.7	30.7	28.2	67.101	613	5.9488E-74	1.2686	0.92308	69.481	16	1532400000	729850000	802600000
Q9JLT4	Thioredoxin reductase 2, mitochondrial	Txnrd2	10	9	9	24.4	21.6	21.6	56.62	524	3.901E-223	1.2296	0.80981	33.294	17	2562400000	1199700000	1362700000
P97493	Thioredoxin, mitochondrial	Txn2	4	4	4	22.3	22.3	22.3	18.255	166	2.746E-102	2.2955	2.6331	37.071	5	549210000	188250000	360960000
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	Prdx3	3	3	3	21	21	21	28.127	257	2.574E-223	2.0544	1.7648	37.078	14	9151400000	3394000000	5757500000
Q8CDN6	Thioredoxin-like protein 1	Txnl1	9	9	9	45	45	45	32.237	289	1.217E-126	2.7123	1.8009	40.707	12	1989800000	552060000	1437800000
P52196	Thiosulfate sulfurtransferase	Tst	4	4	4	17.2	17.2	17.2	33.466	297	9.1814E-18	1.5049	1.271	55.483	4	202110000	88702000	113410000
Q8BH55	Threonine synthase-like 1	Thnsl1	5	5	5	10.4	10.4	10.4	83.099	747	5.0615E-15	1.3117	1.0696	124.52	5	208050000	60310000	147740000
Q80W22	Threonine synthase-like 2	Thnsl2	4	4	4	10.8	10.8	10.8	54.187	483	2.6483E-11	0.94886	0.70109	27.605	4	164570000	85460000	79109000
Q9D0R2	Threonine--tRNA ligase, cytoplasmic	Tars	5	5	5	6.9	6.9	6.9	83.355	722	3.3469E-26	0.61508	0.46612	20.765	6	263280000	173760000	89520000
Q3UQ84	Threonine--tRNA ligase, mitochondrial	Tars2	4	4	4	8.3	8.3	8.3	81.699	723	1.5855E-14	0.56828	0.44159	13.608	3	94803000	60014000	34789000
Q80YQ1	Thrombospondin-1	Thbs1	9	9	9	8.8	8.8	8.8	129.69	1171	2.388E-190	2.9997	2.2405	50.394	7	393860000	113490000	280360000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q99J36	THUMP domain-containing protein 1	Thumpd1	2	2	2	7.4	7.4	7.4	38.884	350	4.4816E-06	3.6293	2.9122	0.85414	2	33830000	9163600	24666000
P39447	Tight junction protein ZO-1	Tjp1	6	6	6	5.3	5.3	5.3	194.74	1745	2.592E-113	1.027	1.017	72.562	4	136810000	58339000	78474000
Q9Z0U1	Tight junction protein ZO-2	Tjp2	4	4	4	3.8	3.8	3.8	131.28	1167	5.2726E-59	0.16934	0.13003	201.48	3	411130000	371740000	39394000
Q8BH58	TIP41-like protein	Tiprl	4	4	4	21.8	21.8	21.8	31.253	271	2.2875E-25	1.5888	1.0464	68.609	8	673680000	258460000	415210000
Q99LJ1	Tissue alpha-L-fucosidase	Fuca1	1	1	1	3.8	3.8	3.8	52.28	452	0.0008718	0.35391	0.23075	32.633	2	42406000	32331000	10074000
A2ASS6	Titin	Ttn	566	566	566	23.7	23.7	23.7	3906.4	35213	0	0.6344	0.48636	61.783	680	8.2927E+10	4.9228E+10	3.3698E+10
Q9QZ06	Toll-interacting protein	Tollip	3	3	3	14.2	14.2	14.2	30.345	274	4.7625E-38	1.23	0.88107	22.343	6	352740000	171840000	180900000
Q5SRX1	TOM1-like protein 2	Tom1l2	9	9	9	27.6	27.6	27.6	55.662	507	1.733E-147	1.6591	1.0922	55.347	10	469830000	180100000	289730000
Q9DBB8	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	Dhdh	2	2	2	10.2	10.2	10.2	36.3	333	5.4518E-18	0.88655	0.75472	16.936	3	447650000	245720000	201920000
Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial	Mecr	7	7	7	39.1	39.1	39.1	40.342	373	1.833E-232	1.0017	0.78344	73.838	8	626040000	307040000	319000000
Q93092	Transaldolase	Taldo1	6	6	6	16.3	16.3	16.3	37.387	337	4.1749E-14	2.5586	2.8119	64.304	7	7052500000	2033400000	5019100000
P83940	Transcription elongation factor B polypeptide 1	Tceb1	4	4	4	48.2	48.2	48.2	12.473	112	0	1.8195	1.3753	47.858	6	392540000	168680000	223860000
P62869	Transcription elongation factor B polypeptide 2	Tceb2	4	4	4	33.9	33.9	33.9	13.17	118	1.308E-28	1.4278	1.1543	50.818	5	809220000	317330000	491890000
P40630	Transcription factor A, mitochondrial	Tfam	2	2	2	7.8	7.8	7.8	27.987	243	1.1881E-07	1.4194	1.3649	11.018	2	188830000	79899000	108930000
Q64152	Transcription factor BTF3	Btf3	3	3	3	26.5	26.5	26.5	22.031	204	1.744E-103	2.1099	1.5267	11.977	5	504990000	173270000	331720000
Q9CQH7	Transcription factor BTF3 homolog 4	Btf3l4	2	2	2	29.7	29.7	29.7	17.27	158	1.4418E-27	1.9533	1.7251	41.158	3	358140000	174860000	183270000
E9PXW9	Transcription factor GATA-4	Gata4	1	1	1	4.3	4.3	4.3	44.679	442	0.00081201	1.1815	1.0271	28.678	2	13479000	7090400	6388700
P42669	Transcriptional activator protein Pur-alpha	Pura	4	4	4	20.6	20.6	20.6	34.883	321	6.769E-224	0.56455	0.40629	29.046	6	720060000	447080000	272980000
Q62351	Transferrin receptor protein 1	Tfrc	2	2	2	3.4	3.4	3.4	85.73	763	0.00026832	1.0325	0.7572	73.355	2	72720000	40731000	31988000
P82198	Transforming growth factor-beta-induced protein ig-h3	Tgfbi	2	2	2	3.4	3.4	3.4	74.596	683	1.0413E-10	0.65831	0.48928	73.336	2	46147000	26550000	19596000
P37804	Transgelin	Tagln	8	8	8	42.3	42.3	42.3	22.576	201	1.7747E-32	2.0041	1.8026	33.102	7	2559000000	900980000	1658000000
Q9WVA4	Transgelin-2	Tagln2	7	7	7	38.7	38.7	38.7	22.395	199	1.963E-182	2.0642	2.2924	118.61	8	2116700000	708790000	1407900000
Q9JJH7	Transient receptor potential cation channel subfamily M member 5	Trpm5	1	1	1	0.8	0.8	0.8	130.84	1158	0.0053607	1.3821	1.0544	76.236	4	127950000	55925000	72020000
Q01853	Transitional endoplasmic reticulum ATPase	Vcp	29	29	29	46.5	46.5	46.5	89.321	806	0	1.1165	0.77558	55.14	51	1.5047E+10	7396200000	7650500000
P40142	Transketolase	Tkt	11	11	11	33.9	33.9	33.9	67.63	623	5.729E-112	1.1381	0.86814	37.107	15	2076100000	1008200000	1068000000
Q8C3X4	Translation factor Guf1, mitochondrial	Guf1	2	2	2	6	6	6	72.462	651	5.3218E-18	0.68736	0.45931	11.154	2	89725000	51700000	38025000
Q8CHW4	Translation initiation factor eIF-2B subunit epsilon	Eif2b5	3	3	3	4.9	4.9	4.9	80.085	717	8.9259E-06	0.22332	0.26449	65.689	2	57710000	50235000	7474500
Q91YJ5	Translation initiation factor IF-2, mitochondrial	Mtif2	2	2	2	3.4	3.4	3.4	81.288	727	1.3971E-20	0.99631	0.62813	73.082	2	62767000	28805000	33962000
Q8K0Z7	Translational activator of cytochrome c oxidase 1	Taco1	4	4	4	22.8	22.8	22.8	32.314	294	7.48E-141	0.86719	0.86964	23.453	5	490410000	261480000	228930000
P63028	Translationally-controlled tumor protein	Tpt1	2	2	2	15.7	15.7	15.7	19.462	172	0.00084891	2.5955	2.1789	14.731	2	25216000	8027000	17189000
Q62348	Translin	Tsn	2	2	2	9.2	9.2	9.2	26.201	228	3.7141E-12	2.0304	1.5097	2.275	3	312290000	82202000	230090000
Q8VHE0	Translocation protein SEC63 homolog	Sec63	2	2	2	2.9	2.9	2.9	87.869	760	0.00053804	0.83963	0.54155	88.066	2	165650000	69933000	95718000
Q8BFY9	Transportin-1	Tnpo1	4	4	3	8.9	8.9	6.1	102.36	898	4.833E-15	0.63987	0.50971	9.8636	3	75627000	52989000	22639000
Q6P2B1	Transportin-3	Tnpo3	2	2	2	3.6	3.6	3.6	104.17	923	0.0029756	0.46061	0.42951	52.586	2	53639000	35776000	17863000
P07309	Transthyretin	Ttr	5	5	5	55.8	55.8	55.8	15.776	147	0	2.2148	1.6351	22.995	21	1.0733E+10	3133800000	7599500000
H3BL37	Treacle protein	Tcof1	4	4	4	5.2	5.2	5.2	138.55	1356	2.0481E-07	2.9898	1.8985	92.455	2	65755000	17242000	48513000
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	Hadha	27	27	27	51	51	51	82.669	763	0	0.59574	0.42881	43.643	86	5.601E+10	3.6263E+10	1.9748E+10
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	Hadhb	21	21	21	53.1	53.1	53.1	51.386	475	0	0.71856	0.52786	44.627	54	1.6523E+10	1.0033E+10	6490700000
Q64737	Trifunctional purine biosynthetic protein adenosine-3	Gart	12	12	12	17.6	17.6	17.6	107.5	1010	0	1.4915	1.0783	42.396	13	2669300000	1049200000	1620100000
P17751	Triosephosphate isomerase	Tpi1	16	16	16	55.2	55.2	55.2	32.191	299	7.466E-236	2.1365	1.9076	62.727	64	3.6199E+10	1.1876E+10	2.4323E+10
Q1XH17	Tripartite motif-containing protein 72	Trim72	14	14	14	54.9	54.9	54.9	52.816	477	0	1.2111	0.82478	44.149	23	5303200000	2479900000	2823300000
O89023	Tripeptidyl-peptidase 1	Tpp1	2	2	2	3.7	3.7	3.7	61.341	562	1.0647E-07	0.55056	0.33113	74.545	2	1575300000	811150000	764110000
Q64514	Tripeptidyl-peptidase 2	Tpp2	15	15	15	13.9	13.9	13.9	139.88	1262	6.666E-45	0.71869	0.55842	54.279	14	947940000	526960000	420980000
Q99LF4	tRNA-splicing ligase RtcB homolog	D10Wsu52e	8	8	8	21	21	21	55.249	505	2.6038E-32	0.43813	0.41834	31.253	8	593330000	361860000	231470000
P49813	Tropomodulin-1	Tmod1	6	6	6	27.6	27.6	27.6	40.466	359	1.409E-107	1.0377	0.80566	55.862	8	538400000	271390000	267010000
P58771	Tropomyosin alpha-1 chain	Tpm1	20	20	9	47.2	47.2	23.2	32.68	284	0	2.1515	1.7967	73.826	30	9369800000	3292800000	6077000000
E9Q5J9	Tropomyosin alpha-3 chain	Tpm3	11	2	0	23.5	4.6	0	33.28	285	2.626E-130	3.1532	2.9119	108.29	2	270480000	76167000	194310000
Q6IRU2	Tropomyosin alpha-4 chain	Tpm4	9	9	9	40.3	40.3	40.3	28.467	248	3.3145E-97	1.9009	1.3182	97.574	9	598110000	245210000	352900000
P19123	Troponin C, slow skeletal and cardiac muscles	Tnnc1	5	5	5	37.3	37.3	37.3	18.42	161	2.537E-101	1.1997	1.2834	54.174	9	1.4584E+10	5921000000	8663000000
P48787	Troponin I, cardiac muscle	Tnni3	6	6	6	38.9	38.9	38.9	24.258	211	1.856E-118	1.5791	1.2457	19.977	10	4010900000	1535900000	2475000000
J3QQ13	Troponin T, cardiac muscle	Tnnt2	15	15	15	38.1	38.1	38.1	35.943	302	1.781E-252	2.2649	1.6594	102.82	36	1.4618E+10	4106200000	1.0512E+10
P32921	Tryptophan--tRNA ligase, cytoplasmic	Wars	7	7	7	21.6	21.6	21.6	54.357	481	1.3552E-52	0.80015	0.75844	27.748	13	1113100000	622990000	490110000
P68369	Tubulin alpha-1A chain	Tuba1a	13	1	0	40.8	2.9	0	50.135	451	2.386E-251	0.63413	0.76723	27.043	2	161380000	101060000	60325000
P68368	Tubulin alpha-4A chain	Tuba4a	12	2	2	40	7.8	7.8	49.924	448	0	0.50326	0.36088	14.416	6	728920000	500480000	228440000
Q7TMM9	Tubulin beta-2A chain	Tubb2a	16	2	2	44.3	5.4	5.4	49.906	445	0	0.6507	0.48394	9.1773	2	46807000	31968000	14839000
P68372	Tubulin beta-4B chain	Tubb4b	20	20	3	60.7	60.7	9.9	49.83	445	0	0.34961	0.28005	69.426	32	4281300000	2982200000	1299100000
P99024	Tubulin beta-5 chain	Tubb5	16	2	1	50.2	6.8	3.4	49.67	444	0	0.54458	0.36527	25.634	2	350970000	234050000	116920000
Q7TQD2	Tubulin polymerization-promoting protein	Tppp	4	4	4	31.7	31.7	31.7	23.574	218	9.8722E-49	3.3548	2.8731	3.055	3	328560000	74743000	253820000
Q9CRB6	Tubulin polymerization-promoting protein family member 3	Tppp3	5	5	5	31.8	31.8	31.8	18.965	176	2.8413E-29	2.1365	1.7004	54.961	4	526190000	165980000	360210000
Q9D1E6	Tubulin-folding cofactor B	Tbcb	3	3	3	11.1	11.1	11.1	27.385	244	7.6138E-07	1.4977	1.776	6.1719	3	297230000	113810000	183410000
Q8C5W3	Tubulin-specific chaperone cofactor E-like protein	Tbcel	2	2	2	4.2	4.2	4.2	48.031	424	0.0042873	0.92807	0.90712	2.6142	2	35716000	19005000	16712000
Q3UDE2	Tubulin--tyrosine ligase-like protein 12	Ttll12	5	5	5	11	11	11	74.042	639	1.6372E-11	0.63414	0.46577	74.989	4	69815000	40739000	29076000
F8WHQ1	Tumor protein D52	Tpd52	1	1	1	7.7	7.7	7.7	26.927	247	2.6593E-47	0.95746	1.0983	8.4759	2	110300000	62445000	47854000
A2AUD5	Tumor protein D54	Tpd52l2	3	3	3	17.5	17.5	17.5	25.067	229	2.8696E-07	0.69343	0.48286	45.068	2	284760000	153390000	131370000
Q61187	Tumor susceptibility gene 101 protein	Tsg101	2	2	2	7.2	7.2	7.2	44.123	391	0.00054175	0.30332	0.33981	8.9481	2	38488000	26846000	11642000
Q9Z0P5	Twinfilin-2	Twf2	4	4	4	20.6	20.6	20.6	39.47	349	2.8425E-98	1.3806	0.9638	39.914	5	501470000	218420000	283050000
P41241	Tyrosine-protein kinase CSK	Csk	2	2	2	5.1	5.1	5.1	50.716	450	0.0042612	0.22395	0.14635	184.98	2	148500000	130220000	18270000
P35235	Tyrosine-protein phosphatase non-receptor type 11	Ptpn11	11	11	11	26.5	26.5	26.5	68.46	597	2.566E-102	1.228	0.96923	60.277	14	910690000	435820000	474860000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q6PB44	Tyrosine-protein phosphatase non-receptor type 23	Ptpn23	4	4	4	3.3	3.3	3.3	185.21	1692	7.065E-06	0.11038	0.081024	168.88	3	568910000	530440000	38473000
A2A7S7	Tyrosine--tRNA ligase, cytoplasmic	Yars	11	11	11	22.2	22.2	22.2	63.001	564	7.5257E-66	1.1992	0.98204	47.134	11	702590000	315280000	387310000
Q8BYL4	Tyrosine--tRNA ligase, mitochondrial	Yars2	4	4	4	10.8	10.8	10.8	52.597	472	7.5894E-08	0.69182	0.5446	26.306	4	146890000	85675000	61219000
Q62376	U1 small nuclear ribonucleoprotein 70 kDa	Snrnp70	1	1	1	2.5	2.5	2.5	51.991	448	0.018296	1.9884	1.3388	5.9779	2	210050000	65565000	144480000
Q9DAW6	U4/U6 small nuclear ribonucleoprotein Prp4	Prpf4	2	2	2	4.8	4.8	4.8	58.369	521	4.4167E-06	0.51343	0.54213	34.936	2	22508000	14508000	8000200
O35901	U6 snRNA-associated Sm-like protein LSm2	Lsm2	1	1	1	14.5	14.5	14.5	14.857	131	6.5365E-13	1.695	1.1492	6.7365	2	286280000	95789000	190490000
Q8R317	Ubiquilin-1	Ubqln1	4	2	2	10.1	5	5	61.976	582	1.1236E-17	1.6711	1.0545	85.333	2	74221000	27853000	46369000
Q9QZM0	Ubiquilin-2	Ubqln2	5	5	3	12.9	12.9	8.2	67.35	638	4.0667E-43	1.8932	1.415	67.174	4	96492000	25783000	70709000
Q8R1S0	Ubiquinone biosynthesis monooxygenase COQ6	Coq6	12	12	12	26.1	26.1	26.1	51.392	476	2.606E-170	0.55782	0.40187	50.507	20	2770400000	1736200000	1034200000
P97478	Ubiquinone biosynthesis protein COQ7 homolog	Coq7	3	3	3	27.2	27.2	27.2	24.041	217	3.057E-108	0.93013	0.50071	47.491	4	850810000	442590000	408220000
Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondrial	Coq9	7	7	7	26.2	26.2	26.2	35.082	313	2.271E-276	1.8482	1.2327	41.76	14	4313400000	1698200000	2615100000
Q9JMA1	Ubiquitin carboxyl-terminal hydrolase 14	Usp14	9	9	9	33.1	33.1	33.1	56.001	493	1.72E-256	2.2338	1.6495	39.952	12	1164800000	290320000	874480000
Q8R5H1	Ubiquitin carboxyl-terminal hydrolase 15	Usp15	4	3	3	4.6	3.7	3.7	112.32	981	1.4331E-09	1.0838	0.8176	6.4752	2	47593000	22205000	25388000
P35123	Ubiquitin carboxyl-terminal hydrolase 4	Usp4	5	5	4	6.4	6.4	5.5	108.34	962	7.509E-14	1.1729	0.69702	37.795	5	171070000	80588000	90479000
Q8BY87	Ubiquitin carboxyl-terminal hydrolase 47	Usp47	3	3	3	3.8	3.8	3.8	157.45	1376	2.6367E-21	0.96244	0.72833	47.64	3	199820000	113760000	86057000
P56399	Ubiquitin carboxyl-terminal hydrolase 5	Usp5	12	12	12	23	23	23	95.832	858	5.93E-70	1.363	0.9201	22.289	17	2624900000	1192300000	1432600000
Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	Uchl1	7	7	7	46.6	46.6	46.6	24.838	223	5.498E-175	3.4034	2.5046	77.586	6	1275100000	208820000	1066200000
Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3	Uchl3	6	6	6	42.2	42.2	42.2	26.151	230	7.6845E-31	2.0402	1.6104	52.279	8	598800000	243060000	355740000
Q9WUP7	Ubiquitin carboxyl-terminal hydrolase isozyme L5	Uchl5	5	5	5	22.5	22.5	22.5	37.616	329	1.5597E-21	1.3914	1.1633	19.435	4	218520000	102000000	116520000
P70362	Ubiquitin fusion degradation protein 1 homolog	Ufd1l	2	2	2	9.1	9.1	9.1	34.481	307	4.5335E-18	1.0227	0.87122	14.172	2	56920000	27719000	29201000
Q7TQI3	Ubiquitin thioesterase OTUB1	Otub1	5	5	5	30.6	30.6	30.6	31.27	271	7.393E-117	1.6598	1.1227	47.418	5	619050000	252150000	366900000
P62983	Ubiquitin-40S ribosomal protein S27a	Rps27a	4	4	1	34	34	12.2	17.951	156	1.6388E-17	0.71004	0.62485	74.955	4	412290000	188870000	223420000
Q8VDI7	Ubiquitin-associated domain-containing protein 1	Ubac1	2	2	2	7.8	7.8	7.8	45.53	409	2.772E-10	2.2489	1.8848	18.556	2	91852000	30562000	61290000
Q80X50	Ubiquitin-associated protein 2-like	Ubap2l	7	7	7	11.7	11.7	11.7	116.8	1107	0	2.7189	2.1587	35.13	6	341580000	109920000	231670000
P61079	Ubiquitin-conjugating enzyme E2 D3	Ube2d3	1	1	1	12.2	12.2	12.2	16.687	147	1.2118E-05	0.8923	0.68817	22.355	2	80488000	35321000	45167000
P62254	Ubiquitin-conjugating enzyme E2 G1	Ube2g1	2	2	2	14.7	14.7	14.7	19.509	170	4.4938E-16	2.3037	1.65	13.646	3	145820000	32615000	113210000
P61087	Ubiquitin-conjugating enzyme E2 K	Ube2k	4	4	4	28.5	28.5	28.5	22.406	200	3.659E-14	1.489	1.1015	20.777	5	394740000	163140000	231600000
P68037	Ubiquitin-conjugating enzyme E2 L3	Ube2l3	4	4	4	41.6	41.6	41.6	17.861	154	4.363E-107	1.9241	1.5594	36.942	14	1869400000	653440000	1216000000
P61089	Ubiquitin-conjugating enzyme E2 N	Ube2n	5	5	5	40.1	40.1	40.1	17.138	152	1.21E-177	1.7517	1.1585	40.813	9	2358500000	900740000	1457800000
Q6ZPJ3	Ubiquitin-conjugating enzyme E2 O	Ube2o	7	7	7	7.7	7.7	7.7	140.83	1288	4.1732E-33	1.2045	0.94179	34.427	8	327340000	146120000	181230000
E9PY39	Ubiquitin-conjugating enzyme E2 variant 1	Gm20431	3	3	3	9.7	9.7	9.7	42.096	371	4.9989E-19	1.6099	1.184	30.35	4	1446400000	560740000	885640000
P61961	Ubiquitin-fold modifier 1	Ufm1	3	3	3	58.8	58.8	58.8	9.1175	85	7.4136E-26	2.0976	1.8113	25.101	7	900570000	226700000	673870000
Q9CR09	Ubiquitin-fold modifier-conjugating enzyme 1	Ufc1	3	3	3	15	15	15	19.481	167	1.4796E-07	1.0243	0.81046	19.718	3	166910000	83801000	83110000
Q02053	Ubiquitin-like modifier-activating enzyme 1	Uba1	22	22	18	28	28	24.1	117.81	1058	0	0.94845	0.62571	41.698	30	6862600000	3565500000	3297100000
Q8C7R4	Ubiquitin-like modifier-activating enzyme 6	Uba6	2	2	2	2.6	2.6	2.6	117.96	1053	6.1328E-05	1.0569	0.83123	9.0249	2	42933000	22901000	20032000
Q64339	Ubiquitin-like protein ISG15	Isg15	2	2	2	11.8	11.8	11.8	17.897	161	8.3063E-21	1.2641	0.85159	94.201	2	119030000	47063000	71971000
Q9CPX6	Ubiquitin-like-conjugating enzyme ATG3	Atg3	2	2	2	6.4	6.4	6.4	35.796	314	0.00089552	0.7759	0.82172	47.069	2	76294000	35579000	40716000
E9QKT1	Ubiquitin-protein ligase E3A	Ube3a	5	5	5	7.9	7.9	7.9	99.818	870	3.1556E-30	1.1555	0.86324	27.068	4	180860000	83958000	96901000
Q922Y1	UBX domain-containing protein 1	Ubxn1	5	5	5	23.9	23.9	23.9	33.572	297	1.5792E-41	2.9841	2.2803	23.887	3	84687000	21432000	63255000
Q8VCH8	UBX domain-containing protein 4	Ubxn4	2	2	2	4.5	4.5	4.5	56.471	506	4.2413E-24	0.0087708	0.0054248	6.8961	2	664120000	661240000	2881200
Q99PL6	UBX domain-containing protein 6	Ubxn6	2	2	2	8.4	8.4	8.4	49.795	442	3.4892E-07	1.7085	1.2301	53.025	2	59058000	20999000	38059000
O70475	UDP-glucose 6-dehydrogenase	Ugdh	3	3	3	12.4	12.4	12.4	54.831	493	4.3424E-10	0.71864	0.64257	8.7642	2	35400000	18578000	16822000
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	Uggt1	5	5	5	4.3	4.3	4.3	176.43	1551	1.7914E-10	0.88488	0.67229	66.146	3	88402000	55669000	32733000
Q3UHZ7	UDP-N-acetylhexosamine pyrophosphorylase	Uap1	1	1	1	1.9	1.9	1.9	58.582	522	0.0086056	1.3894	1.3393	32.546	2	65971000	29325000	36647000
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	Uap1l1	7	7	7	16.8	16.8	16.8	56.613	507	2.9534E-27	0.65018	0.54931	131.21	8	2753900000	2359600000	394290000
Q9DBP5	UMP-CMP kinase	Cmpk1	7	7	7	44.4	44.4	44.4	22.165	196	1.466E-111	2.7053	2.2113	38.417	10	3204500000	962580000	2241900000
Q3U5Q7	UMP-CMP kinase 2, mitochondrial	Cmpk2	2	2	2	6	6	6	50.036	447	1.5417E-07	1.2565	1.2428	27.859	2	48527000	24439000	24088000
A2AMZ4	Uncharacterized protein C17orf89 homolog		2	2	2	39.2	39.2	39.2	7.7849	74	4.0608E-57	3.0911	1.8841	62.81	2	166850000	35254000	131590000
Q149B8	Uncharacterized protein C1orf170 homolog	Perm1	10	10	10	24	24	24	85.156	807	3.61E-244	2.2624	1.5279	41.574	11	1122500000	355640000	766840000
Q9CQF4	Uncharacterized protein C6orf203 homolog	1700021F05Rik	4	4	4	16.7	16.7	16.7	27.847	240	1.444E-186	3.5709	2.8751	81.392	5	565460000	153390000	412070000
Q6PIU9	Uncharacterized protein FLJ45252 homolog		7	7	7	29.7	29.7	29.7	37.704	354	2.0831E-44	1.9853	1.451	17.079	4	273240000	85467000	187770000
Q8CC88	Uncharacterized protein KIAA0564 homolog	Kiaa0564	21	21	21	14.3	14.3	14.3	213.42	1905	2.527E-103	0.46781	0.4283	98.752	18	2395400000	706080000	1689300000
Q9WTI7	Unconventional myosin-Ic	Myo1c	3	3	3	3.9	3.9	3.9	121.94	1063	3.2959E-06	0.32457	0.23805	236.37	3	647910000	534450000	113470000
E9QA74	Unconventional myosin-XVIIIa	Myo18a	2	2	2	1.6	1.6	1.6	186.53	1642	6.1586E-14	1.3266	0.91151	7.6277	2	93444000	61037000	32407000
E9QMK9	UPF0317 protein C14orf159 homolog, mitochondrial	9030617O03Rik	9	9	9	22.7	22.7	22.7	69.921	647	1.7075E-67	1.4795	1.0194	52.612	16	2126200000	907720000	1218500000
A6H630	UPF0364 protein C6orf211 homolog	Armt1	3	3	3	14.4	14.4	14.4	50.548	439	5.3756E-08	1.22	0.99321	54.019	3	192190000	78825000	113360000
D3YZD8	UPF0366 protein C11orf67 homolog	1810020D17Rik	2	2	2	18	18	18	16.358	150	7.4109E-08	3.0745	1.8453	4.1792	2	90060000	21826000	68233000
Q5F285	UPF0451 protein C17orf61 homolog	Tmem256	1	1	1	24.8	24.8	24.8	11.655	113	2.7951E-30	0.39904	0.24273	2.2128	2	134740000	95303000	39440000
I1E4X5	UPF0505 protein C16orf62 homolog	9030624J02Rik	5	5	5	7.2	7.2	7.2	111.98	991	3.3627E-12	0.78955	0.67328	87.328	4	63660000	34615000	29044000
Q9D0A3	UPF0552 protein C15orf38 homolog	Arpin	2	2	2	8.4	8.4	8.4	25.193	226	0.00013479	2.3861	2.3725	118.15	2	75172000	33335000	41837000
Q9CQE8	UPF0568 protein C14orf166 homolog		5	5	5	23.4	23.4	23.4	28.152	244	3.0106E-10	1.0873	0.72134	32.085	5	197810000	106580000	91230000
Q8BHG2	UPF0587 protein C1orf123 homolog	0610037L13Rik	2	2	2	15.6	15.6	15.6	18.02	160	0.0038337	1.4096	0.82931	78.28	2	455490000	190900000	264590000
Q8VE95	UPF0598 protein C8orf82 homolog		6	6	6	40.4	40.4	40.4	24.33	218	5.3793E-87	1.0655	0.77514	33.14	9	1950500000	871860000	1078700000
Q9CWU4	UPF0690 protein C1orf52 homolog		1	1	1	10	10	10	20.101	180	0.00035142	3.0831	1.7843	11.246	2	41711000	10029000	31682000
Q78IK2	Up-regulated during skeletal muscle growth protein 5	Usmg5	4	4	4	44.8	44.8	44.8	6.3814	58	3.796E-127	0.80425	0.7723	43.353	7	1170500000	631740000	538740000
P70697	Uroporphyrinogen decarboxylase	Urod	3	3	3	10.6	10.6	10.6	40.691	367	1.4821E-18	0.69339	0.53223	26.638	5	218860000	136290000	82570000
P51163	Uroporphyrinogen-III synthase	Uros	5	5	5	38.5	38.5	38.5	28.504	265	2.2422E-41	2.3298	1.6904	16.334	4	200950000	57285000	143660000
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	Ugp2	17	17	17	44.3	44.3	44.3	56.979	508	0	0.41271	0.3015	86.803	29	1.8506E+10	1.6486E+10	2019900000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P54726	UV excision repair protein RAD23 homolog A	Rad23a	2	2	2	18.2	18.2	18.2	39.706	363	8.0367E-20	3.4208	2.7248	54.811	2	52615000	8439500	44175000
P54728	UV excision repair protein RAD23 homolog B	Rad23b	4	4	4	20.7	20.7	20.7	43.512	416	3.0938E-85	2.0545	1.7959	20.152	6	531240000	172190000	359050000
Q8BX70	Vacuolar protein sorting-associated protein 13C	Vps13c	14	14	14	5.1	5.1	5.1	420.08	3748	1.0973E-43	0.3495	0.28297	93.89	11	373200000	226020000	147180000
P40336	Vacuolar protein sorting-associated protein 26A	Vps26a	3	3	3	11.3	11.3	11.3	38.113	327	2.3734E-29	0.79324	0.59299	40.889	4	267460000	158580000	108880000
Q9D1C8	Vacuolar protein sorting-associated protein 28 homolog	Vps28	2	2	2	13.1	13.1	13.1	25.452	221	1.3801E-10	2.2993	1.9348	17.31	3	25883000	7820400	18063000
Q9QZ88	Vacuolar protein sorting-associated protein 29	Vps29	6	6	6	38.5	38.5	38.5	20.495	182	9.378E-149	0.80146	0.65537	23.265	7	1157900000	608460000	549410000
Q9EQH3	Vacuolar protein sorting-associated protein 35	Vps35	13	13	13	19.8	19.8	19.8	91.712	796	5.796E-159	0.53384	0.38514	30.348	18	1639500000	1041600000	597980000
P46467	Vacuolar protein sorting-associated protein 4B	Vps4b	3	3	3	9	9	9	49.419	444	4.0326E-15	0.904	0.73244	52.711	2	51384000	29456000	21929000
Q9CR26	Vacuolar protein sorting-associated protein VTA1 homolog	Vta1	3	3	3	17.5	17.5	17.5	33.913	309	1.762E-183	2.3556	1.6762	44.364	3	132230000	41716000	90518000
A2A4J8	Vacuolar protein-sorting-associated protein 25	Vps25	3	3	3	17.4	17.4	17.4	21.594	184	2.2865E-11	0.89745	0.67761	62.388	5	235140000	120750000	114400000
Q9CZ28	Vacuolar-sorting protein SNF8	Snf8	3	3	3	13.2	13.2	13.2	28.886	258	5.0758E-11	1.1724	1.009	0.40938	2	53209000	19419000	33790000
Q8R164	Valacyclovir hydrolase	Bphl	8	8	8	29.2	29.2	29.2	32.851	291	4.9174E-66	0.70099	0.61704	29.422	14	1681400000	1005500000	675860000
Q9Z1Q9	Valine--tRNA ligase	Vars	11	11	11	10.4	10.4	10.4	140.21	1263	4.3363E-43	0.4788	0.36239	85.23	8	373090000	228350000	144740000
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadvl	33	33	33	54.4	54.4	54.4	70.875	656	0	1.1882	0.83738	60.712	51	2.0293E+10	9408900000	1.0884E+10
B0QZN5	Vesicle-associated membrane protein 2	Vamp2	1	1	1	10.4	10.4	10.4	17.862	163	4.5547E-14	0.85598	0.77539	23.299	3	227030000	116830000	110200000
Q9WV55	Vesicle-associated membrane protein-associated protein A	Vapa	3	2	2	15.7	10.8	10.8	27.855	249	2.6667E-08	0.58615	0.45814	53.759	2	59240000	37270000	21970000
Q8BH80	Vesicle-associated membrane protein-associated protein B	Vapb	3	3	2	15.2	15.2	10.3	26.918	243	2.252E-12	1.1911	0.82345	46.434	2	166650000	80702000	85946000
P46460	Vesicle-fusing ATPase	Nsf	8	8	8	11.7	11.7	11.7	82.613	744	8.2083E-70	1.4293	1.0692	25.654	6	235240000	107060000	128170000
Q8VDJ3	Vigilin	Hdlbp	11	11	11	12.6	12.6	12.6	141.74	1268	6.807E-147	0.70903	0.57214	71.723	12	1213100000	640880000	572220000
P20152	Vimentin	Vim	5	5	5	13.5	13.5	13.5	53.687	466	4.1052E-61	1.93	1.4912	62.64	6	305150000	127160000	177990000
Q64727	Vinculin	Vcl	25	25	25	29.7	29.7	29.7	116.72	1066	1.537E-291	1.6261	1.3	52.504	37	5410800000	2080800000	3329900000
P21614	Vitamin D-binding protein	Gc	18	18	18	48.3	48.3	48.3	53.6	476	0	1.9747	1.6342	34.913	22	2008800000	630180000	1378600000
P29788	Vitronectin	Vtn	2	2	2	7.5	7.5	7.5	54.848	478	2.0251E-16	0.81512	0.55446	12.474	3	135590000	78922000	56669000
Q60932	Voltage-dependent anion-selective channel protein 1	Vdac1	12	12	12	49	49	49	32.351	296	0	0.69052	0.57041	50.028	17	2883500000	1748300000	1135200000
Q60930	Voltage-dependent anion-selective channel protein 2	Vdac2	8	8	8	42.4	42.4	42.4	31.732	295	2.785E-303	0.63624	0.50324	131.31	11	2519500000	1647900000	871610000
J3QMG3	Voltage-dependent anion-selective channel protein 3	Vdac3	5	5	5	28.5	28.5	28.5	30.851	284	2.026E-130	0.65105	0.39239	35.172	8	675560000	445460000	230100000
O08532	Voltage-dependent calcium channel subunit alpha-2/delta-1	Cacna2d1	6	6	6	7.2	7.2	7.2	124.63	1103	1.6598E-39	2.1192	1.5512	103.55	3	213940000	134760000	79184000
P54285	Voltage-dependent L-type calcium channel subunit beta-3	Cacnb3	2	2	2	4.1	4.1	4.1	54.571	484	0.0091062	1.9401	1.4911	216.62	2	1340900000	126270000	1214700000
Q8R2Z5	von Willebrand factor A domain-containing protein 1	Vwa1	2	2	2	14	14	14	44.708	415	3.447E-59	0.82783	0.6137	58.63	2	131950000	94185000	37767000
Q99KC8	von Willebrand factor A domain-containing protein 5A	Vwa5a	13	13	13	20.7	20.7	20.7	87.142	793	1.955E-288	1.0115	0.86456	41.532	13	1061300000	559660000	501680000
Q9Z1G4	V-type proton ATPase 116 kDa subunit a isoform 1	Atp6v0a1	2	2	2	3.3	3.3	3.3	96.466	839	1.1206E-06	0.43097	0.30103	84.037	2	70366000	50769000	19598000
P50516	V-type proton ATPase catalytic subunit A	Atp6v1a	9	9	9	21.7	21.7	21.7	68.325	617	2.2224E-59	0.66678	0.45002	29.947	10	713230000	418120000	295110000
P62814	V-type proton ATPase subunit B, brain isoform	Atp6v1b2	9	9	9	27.2	27.2	27.2	56.55	511	2.071E-53	0.5649	0.47534	63.999	11	364040000	236280000	127760000
Q9Z1G3	V-type proton ATPase subunit C 1	Atp6v1c1	3	3	3	11.8	11.8	11.8	43.887	382	1.1361E-17	0.76124	0.72668	0.97322	2	111790000	62128000	49662000
P51863	V-type proton ATPase subunit d 1	Atp6v0d1	2	2	2	9.7	9.7	9.7	40.301	351	5.6366E-12	0.52244	0.37507	17.092	2	65060000	46971000	18089000
Q8BVE3	V-type proton ATPase subunit H	Atp6v1h	8	8	8	25.7	25.7	25.7	55.854	483	8.4563E-48	0.52304	0.36937	80.467	10	705790000	422440000	283350000
Q6PGL7	WASH complex subunit FAM21	Fam21	3	3	3	4.1	4.1	4.1	145.31	1334	3.5843E-24	1.3284	0.82059	26.566	2	76903000	34140000	42763000
O88342	WD repeat-containing protein 1	Wdr1	15	15	15	41.1	41.1	41.1	66.406	606	0	1.4485	1.0459	38.476	23	4108900000	1739000000	2369900000
Q8C6G8	WD repeat-containing protein 26	Wdr26	2	2	2	5.6	5.6	5.6	70.543	641	0.00022476	0.35727	0.30363	26.083	2	22393000	17014000	5378800
Q3UE92	Xaa-Pro aminopeptidase 1	Xpnpep1	7	7	7	10.7	10.7	10.7	74.559	666	1.0866E-23	1.0695	0.8146	42.722	6	604930000	288230000	316700000
Q11136	Xaa-Pro dipeptidase	Pepd	3	3	3	7.3	7.3	7.3	55.028	493	6.0802E-30	0.81756	0.56121	54.341	5	495830000	233530000	262300000
Q00519	Xanthine dehydrogenase/oxidase	Xdh	16	16	16	19	19	19	146.56	1335	2.337E-117	0.73896	0.55326	51.269	19	1336900000	763780000	573120000
E9QQ93	Xin actin-binding repeat-containing protein 1	Xirp1	7	7	7	11.5	11.5	11.5	123.69	1132	7.9193E-23	1.9641	1.5368	85.538	6	402390000	39355000	363040000
B2RUF0	Y-box-binding protein 2	Ybx2	5	2	2	22.3	12.3	12.3	38.08	359	1.871E-123	8.9673	7.0192	77.676	3	27430000	3583400	23847000
P46938	Yorkie homolog	Yap1	3	3	3	14.5	14.5	14.5	52.383	488	1.8432E-62	2.7165	2.0298	51.195	4	99869000	23089000	76780000
Q8BYK6	YTH domain family protein 3	Ythdf3	2	2	2	3.8	3.8	3.8	63.961	585	0.0084482	0.55044	0.47979	39.24	2	60262000	35970000	24293000
Q3TIV5	Zinc finger CCCH domain-containing protein 15	Zc3h15	1	1	1	4.9	4.9	4.9	48.327	426	3.6838E-09	1.5988	1.194	4.3556	2	85693000	32318000	53374000
Q8R1N0	Zinc finger protein 830	Znf830	2	2	2	10.5	10.5	10.5	40.658	363	0.00011774	3.8483	3.4629	38.911	2	19500000	4309900	15191000
Q64726	Zinc-alpha-2-glycoprotein	Azgp1	3	3	3	10.7	10.7	10.7	35.332	307	7.9592E-07	1.819	1.2159	38.08	3	295250000	105270000	189980000
Q8BGC4	Zinc-binding alcohol dehydrogenase domain-containing protein 2	Zadh2	5	5	5	16.4	16.4	16.4	40.528	377	2.1021E-63	0.99497	0.61093	29.768	7	2067100000	1103600000	963500000
Q62523	Zyxin	Zyx	4	4	4	10.8	10.8	10.8	60.545	564	1.7841E-26	2.4292	1.7909	42.281	7	897250000	286240000	611010000
Q8BGD8	Cytochrome c oxidase assembly factor 6 homolog	1810063B05Rik	2	2	2	30.4	30.4	30.4	9.2983	79	2.7385E-18	3.0288	2.5056	42.078	4	92398000	21695000	70703000
G3X8U3	MCG6895	2210016F16Rik	5	5	5	16	16	16	38.615	338	2.5172E-17	0.91746	0.65598	42.288	6	328970000	186050000	142920000
V9GXP3	Muscular LMNA-interacting protein	2310046A06Rik	8	8	5	30.7	30.7	18.7	50.902	460	8.543E-204	2.1558	1.9123	59.192	7	855060000	304770000	550290000
E9Q4Z2	Acetyl-CoA carboxylase 2	Acacb	7	7	7	4.5	4.5	4.5	275.75	2448	1.2394E-28	0.52183	0.3522	49.271	10	337750000	226580000	111180000
D3Z7X0	MCG142036	Acad12	17	17	5	32.8	32.8	10.6	61.389	555	7.876E-102	0.49134	0.38682	34.376	30	2834800000	1990100000	844690000
F8VPN4	Protein Agl	Agl	44	44	44	35.9	35.9	35.9	174.29	1532	0	0.45535	0.30879	51.844	61	7948900000	5270900000	2678000000
E9Q616	Protein Ahnak	Ahnak	114	114	114	51	51	51	604.25	5656	0	1.7989	1.3578	51.791	128	2.1497E+10	8188200000	1.3309E+10
F7DBB3	Protein Ahnak2	Ahnak2	5	5	2	9.7	9.7	2	166.49	1576	1.2071E-32	0.96937	0.7783	24.541	9	2536900000	1326800000	1210100000
G5E895	MCG142264, isoform CRA_b	Akr1b10	8	8	5	33.5	33.5	24.4	35.848	316	0	1.025	0.68886	25.324	15	4422900000	2117200000	2305700000
S4R2K9	Ankyrin-3	Ank3	5	2	2	2.9	1.4	1.4	284.64	2622	3.4278E-13	1.6516	1.3046	33.062	2	38241000	13615000	24626000
D3YXF5	Oxidation resistance protein 1	C7	4	4	4	7.6	7.6	7.6	93.337	845	2.4369E-10	1.4385	1.4298	56.061	3	60346000	26105000	34241000
E9QA15	Protein Cald1	Cald1	7	7	7	12.8	12.8	12.8	89.272	768	1.945E-124	1.8199	1.9547	37.464	4	105320000	28274000	77046000
E9Q6J4	Protein Ceacam3	Ceacam3	1	1	1	1.3	1.3	1.3	78.534	709	0.017674	2.1395	1.554	28.017	2	1326600000	354700000	971920000
E9QLJ0	Cardiomyopathy-associated protein 5	Cmya5	19	19	5	9.4	9.4	2.9	405.57	3676	1.532E-187	1.645	1.3937	114.06	24	1934500000	1118800000	815690000
E9PWQ3	Protein Col6a3	Col6a3	9	9	9	4	4	4	353.93	3284	7.499E-57	0.60488	0.44912	57.798	10	384200000	275200000	109000000
E9Q3H6	Protein Coq10a	Coq10a	7	7	7	29.7	29.7	29.7	28.927	259	1.7227E-46	0.81401	0.50754	68.574	12	1358200000	694300000	663890000
E9Q0T8	Protein Dnah7a	Dnahc7b	2	2	2	0.5	0.5	0.5	460.9	4024	0.0036678	0.041829	0.037088	334.53	2	1102900000	1055600000	47389000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q8VCG1	Deoxyuridine triphosphatase, isoform CRA_b	Dut	5	5	5	38.5	38.5	38.5	21.251	200	2.954E-136	3.2369	2.1256	19.786	11	1203700000	317300000	886390000
Q91VK2	Eef1d protein	Eef1d	6	1	1	38.8	13.4	13.4	30.634	276	9.265E-260	1.4998	1.145	5.8034	3	194360000	66748000	127610000
E9PV24	Fibrinogen alpha chain	Fga	11	11	11	19.5	19.5	19.5	87.428	789	6.201E-174	0.79364	0.69464	39.742	13	1700300000	1011700000	688620000
Q6DFZ1	Golgi-specific brefeldin A-resistance factor 1	Gbf1	4	4	4	2.6	2.6	2.6	206.78	1861	4.0551E-25	0.48435	0.32103	94.524	3	171460000	64251000	107210000
L7N1X8	Protein Gbp6	Gbp10	4	4	2	7.4	7.4	4.3	70.451	611	1.4402E-15	1.3359	1.0597	69.068	5	230250000	121910000	108350000
Q8BTS3	Guanylate-binding protein 9	Gbp9	4	2	2	5.3	2.3	2.3	71.341	619	5.7357E-14	2.0054	1.3991	79.764	2	70634000	25258000	45376000
D3Z7P5	Deleted.	Gls	1	1	1	5.8	5.8	5.8	30.364	274	1.1604E-12	1.8733	1.4733	3.2095	2	50560000	20136000	30424000
Q3UKG2	Protein Prob1	Gm1614	4	4	4	5.8	5.8	5.8	106.42	1006	4.8003E-08	0.80987	0.62402	28.588	2	107080000	57662000	49414000
E9Q035	Protein Gm20425	Gm20425	40	1	1	40.7	1.9	1.9	107.8	978	0	0.56533	0.4143	10.855	3	85324000	52000000	33324000
E9PVZ8	Protein Golgb1	Golgb1	6	6	6	2.3	2.3	2.3	370.15	3238	1.0533E-21	6.1615	4.2278	94.663	2	186290000	67018000	119270000
A8DUK4	Beta-globin	Hbb-b1	17	17	7	89.8	89.8	39.5	15.748	147	0	1.8637	1.2581	63.855	202	1.7772E+11	7.0274E+10	1.0744E+11
E9Q5B5	Hexokinase	Hk2	31	31	1	37.8	37.8	1.3	99.213	889	0	1.0267	0.77854	59.397	56	1.5559E+10	6164800000	9393900000
D3Z3N4	MCG11326, isoform CRA_a	Hnrnph3	2	2	2	8.4	8.4	8.4	36.869	346	1.6202E-08	0.63691	0.61519	4.2976	2	71310000	40891000	30420000
G5E8J6	Histidine rich calcium binding protein, isoform CRA_a	Hrc	4	4	4	8.4	8.4	8.4	85.171	738	1.2099E-87	1.9627	1.4262	71.614	4	253360000	82950000	170410000
Q91VA7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	Idh3b	10	10	10	36.7	36.7	36.7	42.194	384	1.179E-299	0.76502	0.55443	30.558	23	1.0323E+10	5697400000	4625400000
F6TQW2	Protein Ighg2c	Ighg2c	3	3	3	16.6	16.6	16.6	44.095	403	9.727E-136	1.662	1.1314	22.509	3	425330000	124390000	300940000
E9Q1P8	Interferon regulatory factor 2-binding protein 2	Irf2bp2	3	3	2	11.1	11.1	8.2	59.291	570	7.9177E-54	2.4956	1.9006	37.93	3	78065000	23858000	54207000
A6X935	Inter alpha-trypsin inhibitor, heavy chain 4	Itih4	6	6	6	10.1	10.1	10.1	104.66	942	3.4821E-62	2.2987	2.1212	29.709	7	365300000	127450000	237850000
A2AUC9	Kelch-like protein 41	Kbtbd10	12	12	12	23.9	23.9	23.9	68.189	606	5.6316E-51	0.96174	0.6754	87.794	17	1307800000	778040000	529720000
A2RTH5	Leucine carboxyl methyltransferase 1	Lcmt1	4	4	4	11.4	11.4	11.4	38.192	332	0.0001725	1.067	0.53535	43.321	3	374970000	217260000	157720000
E9PYJ9	LIM domain-binding protein 3	Ldb3	19	2	2	39	4	4	72.312	679	0	3.187	2.6648	51.302	3	296460000	84805000	211650000
E9PYF4	Protein Lmo7	Lmo7	6	6	6	6.3	6.3	6.3	192.55	1699	3.2569E-91	1.6232	1.2612	74.957	7	197330000	68749000	128580000
Q91XL1	Leucine-rich HEV glycoprotein	Lrg1	1	1	1	4.1	4.1	4.1	37.431	342	0.0025011	1.9518	1.4112	22.1	4	390020000	143710000	246310000
Q14BI5	Myomesin 2	Myom2	42	42	42	36.1	36.1	36.1	164.74	1463	0	0.80914	0.6431	40.895	77	1.5998E+10	8923500000	7074500000
Q99J77	N-acetylneuraminic acid synthase	Nans	4	4	4	24.5	24.5	24.5	40.024	359	2.7015E-90	0.90188	0.57932	48.82	4	168950000	89262000	79691000
Q3U422	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	Ndufv3	2	2	2	6.4	6.4	6.4	50.498	468	4.0419E-07	1.124	1.2683	1.994	2	231290000	114790000	116490000
B7ZCI2	Nebulette	Nebl	20	20	4	24.3	24.3	5.3	116.01	1014	0	1.0583	0.8386	51.538	24	2373000000	1069200000	1303800000
O08692	Neutrophilic granule protein	Ngp	2	2	2	22.8	22.8	22.8	19.331	167	8.6005E-06	0.68796	0.47547	2.2115	2	210850000	110670000	100170000
E9Q5C9	Protein Nolc1	Nolc1	2	2	2	3.3	3.3	3.3	73.697	702	5.7355E-05	1.641	1.2194	55.933	2	113990000	55943000	58046000
E9Q7L0	Protein Ogdhl	Ogdhl	21	14	14	28	22.3	22.3	116.6	1029	1.908E-295	1.427	1.0545	22.549	25	2422000000	1011100000	1410900000
E9Q5F1	Olfactory receptor	Olfr430	1	1	1	2.2	2.2	2.2	35.782	317	0.049369	0.19318	0.23348	104.48	2	55631000	42381000	13250000
Q6PHQ9	Polyadenylate-binding protein	Pabpc4	6	6	5	12	12	9.4	72.242	660	4.281E-104	1.4548	0.82544	62.914	11	1799800000	679250000	1120600000
Q8CFX3	Protein Pcdh1	Pcdh1	4	4	4	7	7	7	112.41	1038	1.9306E-13	1.2873	0.9682	80.12	3	137500000	76702000	60797000
E9Q8P5	PDZ and LIM domain protein 5	Pdlim5	11	4	4	56.1	16.3	16.3	26.355	239	0	2.1097	1.4136	45.982	10	1534800000	605720000	929100000
E9Q3L2	Phosphatidylinositol 4-kinase alpha	Pi4ka	4	4	4	2.9	2.9	2.9	231.35	2044	5.623E-131	0.38101	0.25538	181.49	3	572730000	550430000	22299000
Q9CQ73	Plakophilin 2	Pkp2	4	4	4	6.4	6.4	6.4	88.103	795	2.0523E-24	0.5427	0.33419	115.94	3	102980000	59387000	43592000
Q91UZ1	Phosphoinositide phospholipase C	Plcb4	3	3	3	2.8	2.8	2.8	134.53	1175	3.4878E-06	0.60099	0.65307	40.583	3	47083000	27677000	19406000
B2RXC8	3222402P14Rik protein	Ppp2r3a	3	3	3	2	2	2	130.26	1150	0.0016309	0.85598	1.0357	22.309	3	103000000	56802000	46198000
F7AI87	26S proteasome non-ATPase regulatory subunit 4	Psmd4	3	2	2	19.6	14.4	14.4	21.316	194	2.213E-144	1.9586	1.354	59.783	4	177490000	72367000	105130000
Q8BML9	Glutaminyl-tRNA synthetase	Qars	10	10	10	17	17	17	87.676	775	2.1936E-71	0.4538	0.31566	69.4	12	626190000	410010000	216190000
E9Q912	Protein Rap1gds1	Rap1gds1	6	6	6	14.7	14.7	14.7	66.076	607	5.6849E-48	1.5711	1.1973	21.373	6	373910000	123780000	250130000
G5E867	MCG116540, isoform CRA_b	Raph1	3	3	3	6.5	6.5	6.5	76.269	679	2.3342E-08	1.9284	1.5015	59.374	4	87563000	31291000	56272000
E9PYG6	Protein Rasa1	Rasa1	3	3	3	5	5	5	115.43	1038	1.0644E-05	1.2364	0.95799	13.036	2	213700000	89887000	123810000
G3X8R0	Receptor expression-enhancing protein	Reep5	4	4	4	15.3	15.3	15.3	21.447	189	7.8032E-10	0.28009	0.35129	143.15	5	491110000	217840000	273270000
E9PWZ3	Protein Rpl3l	Rpl3l	2	2	2	5.9	5.9	5.9	46.512	407	7.0307E-13	0.30212	0.27938	44.131	2	61386000	49557000	11829000
Q80ZX0	Protein Sec24b	Sec24b	4	4	4	6.1	6.1	6.1	135.55	1251	5.2338E-13	0.50798	0.34088	14.77	3	88675000	39502000	49173000
G3X972	Protein Sec24c	Sec24c	5	5	5	6.9	6.9	6.9	118.58	1096	9.8668E-19	1.0006	0.85015	38.7	5	300870000	135760000	165110000
Q6NXL1	Protein Sec24d	Sec24d	2	2	2	2.8	2.8	2.8	112.67	1032	0.0026078	0.57788	0.57271	44.26	2	33845000	21576000	12269000
O08804	NK13	Serpinb6b	7	7	7	23.1	23.1	23.1	42.535	377	3.614E-132	1.7029	1.2901	45.732	10	1453000000	503260000	949690000
Q3UWK8	MCG20280	Serpinb6d	1	1	1	2.7	2.7	2.7	43.315	375	0.048432	2.2087	1.6355	207.33	4	905710000	26280000	879430000
O08797	Protein Serpinb9	Serpinb9	6	6	6	19.8	19.8	19.8	42.259	374	1.215E-36	1.8785	1.4519	59.349	9	959100000	525590000	433510000
Q6NZR5	Protein Skiv2l	Skiv2l	3	3	3	3.9	3.9	3.9	137.52	1244	9.7991E-13	1.4711	1.1455	20.866	4	99823000	38982000	60841000
D3YVS1	Smoothelin	Smtn	3	3	1	12.6	12.6	5.7	47.573	436	5.5904E-70	2.6097	2.0834	59.339	3	283160000	94542000	188620000
E9Q447	Spectrin alpha chain, non-erythrocytic 1	Spna2	54	54	3	29.7	29.7	2	285.34	2478	0	1.3414	0.9612	46.686	63	7789200000	3339800000	4449300000
E9Q8T1	Transforming acidic coiled-coil-containing protein 2	Tacc2	28	28	28	19.6	19.6	19.6	305.23	2879	0	2.4106	1.6844	67.2	25	2208500000	801970000	1406500000
Q9Z1A1	Protein Tfg	Tfg	4	4	4	17.1	17.1	17.1	43.02	397	1.167E-156	2.9365	2.244	30.607	5	554320000	149450000	404870000
Q6XPS7	L-threonine aldolase	Tha1	4	4	4	13.2	13.2	13.2	43.496	400	2.1617E-12	1.3091	0.97775	29.993	3	82819000	45595000	37225000
D3YZZ5	Protein Tmed7	Tmed7	2	2	2	10.3	10.3	10.3	25.2	224	0.00031537	0.62314	0.41086	55.971	2	121080000	77314000	43764000
E9Q0S6	Protein Tns1	Tns1	21	21	21	17.3	17.3	17.3	201.38	1888	6.718E-104	0.86126	0.68273	57.567	22	1222200000	596800000	625370000
O35452	Protein Tnxb	Tnxb	13	13	13	6	6	6	435.47	4006	4.9633E-48	0.79881	0.59982	33.12	12	271150000	141060000	130090000
F6ZDS4	Nucleoprotein TPR	Tpr	9	9	9	5.5	5.5	5.5	273.99	2431	6.182E-191	1.9235	1.3922	33.969	8	332590000	126250000	206330000
G3X8Y1	MCG19772	Trim55	2	2	2	4.4	4.4	4.4	60.137	545	0.00030996	1.4474	1.251	69.155	2	83953000	35720000	48233000
G5E870	E3 ubiquitin-protein ligase TRIP12	Trip12	2	2	2	0.9	0.9	0.9	224.13	2025	0.00536	0.44383	0.26204	48.402	2	2243600000	1374700000	868960000
B1ART2	Protein Vps13d	Vps13d	2	2	2	0.8	0.8	0.8	490.96	4390	0.0047607	0.91746	0.75043	30.211	2	24524000	10621000	13902000

Table S-3. Proteins identified via MaxQuant in replicate 3.

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O55028	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial	Bckdk	2	2	2	9.5	9.5	9.5	46.587	412	2.7751E-06	2.8122	2.9732	27.196	2	89219000	22733000	66486000
P54923	[Protein ADP-ribosylarginine] hydrolase	Adprh	2	2	2	12.2	12.2	12.2	40.068	362	5.8725E-28	1.5531	3.4983	131.48	2	62850000	29386000	33464000
Q8BGK2	[Protein ADP-ribosylarginine] hydrolase-like protein 1	Adprhl1	10	10	10	33.4	33.4	33.4	39.885	353	2.899E-145	1.6078	1.9473	77.797	11	1683500000	749180000	934340000
A2AJQ0	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial	Pdp1	6	6	6	16.8	16.8	16.8	67.615	597	6.0296E-31	1.6688	2.795	66.14	6	397940000	133630000	264310000
Q8BFP9	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial	Pdk1	9	9	8	22.6	22.6	22.6	48.994	434	2.787E-120	1.9418	2.0742	31.484	7	527310000	176630000	350680000
Q9JK42	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial	Pdk2	9	9	9	31.7	31.7	31.7	46.04	407	0	1.4316	1.4833	41.011	15	2457000000	1012400000	1444600000
O70571	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial	Pdk4	6	6	6	21.1	21.1	21.1	46.596	412	9.8933E-32	2.522	2.5764	98.009	7	687120000	188780000	498330000
Q99JT9	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	Adi1	3	3	3	22.9	22.9	22.9	21.523	179	4.1405E-10	0.77822	0.80179	71.214	3	42558000	24934000	17625000
F6ZHD8	1,4-alpha-glucan-branching enzyme	Gbe1	9	9	9	18.7	18.7	18.7	80.336	702	2.2844E-54	2.2161	2.8522	74.023	12	821940000	293820000	528120000
Q9DCT1	1,5-anhydro-D-fructose reductase	Akr1e2	5	5	5	28.9	28.9	28.9	34.46	301	2.1603E-13	1.4077	1.8621	27	5	541560000	258070000	283490000
Q64433	10 kDa heat shock protein, mitochondrial	Hspe1	9	9	9	71.6	71.6	71.6	10.963	102	7.9635E-33	0.46945	0.55504	86.469	56	4.5941E+10	2.982E+10	1.6122E+10
Q9DAK9	14 kDa phosphohistidine phosphatase	Phpt1	6	6	6	48.4	48.4	48.4	13.996	124	1.5181E-67	0.66764	1.0455	153.05	8	2417000000	1613500000	803450000
Q9CQV8	14-3-3 protein beta/alpha	Ywhab	7	5	4	29.3	22	18.3	28.086	246	0	0.82088	1.4092	89.409	11	2341000000	1272400000	1068600000
P62259	14-3-3 protein epsilon	Ywhae	13	13	11	45.5	45.5	38.4	29.174	255	2.9385E-75	0.71032	0.97155	104.19	27	5771800000	3301700000	2470100000
P68510	14-3-3 protein eta	Ywhah	6	4	4	24	16.7	16.7	28.211	246	2.306E-124	0.55055	0.52178	73.259	4	189110000	111530000	77571000
P61982	14-3-3 protein gamma	Ywhag	5	2	2	24.3	13.4	13.4	28.302	247	8.1312E-49	0.84461	1.1138	51.452	3	497630000	248960000	248670000
F6VW30	14-3-3 protein theta	Ywhaq	8	6	6	24.1	18.2	18.2	34.348	303	4.7763E-79	0.64813	0.75756	48.469	8	563960000	330550000	233410000
P63101	14-3-3 protein zeta/delta	Ywhaz	10	8	8	41.6	34.3	34.3	27.771	245	0	0.67465	1.0882	57.781	14	1.0724E+10	5898000000	4825800000
P58871	182 kDa tankyrase-1-binding protein	Tnks1bp1	5	5	5	5.8	5.8	5.8	181.82	1720	5.182E-42	0.72022	0.71548	33.112	5	275410000	175550000	99867000
Q8R3B1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1	Plcd1	4	4	4	7.7	7.7	7.7	85.872	756	8.4537E-11	1.3365	2.5925	44.859	3	217770000	77153000	140620000
Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial	Decr1	16	16	16	57.9	57.9	57.9	36.213	335	0	0.91748	1.0007	49.443	73	5.3419E+10	2.9184E+10	2.4235E+10
P62334	26S protease regulatory subunit 10B	Psmc6	8	8	8	27.8	27.8	27.8	44.172	389	4.4881E-26	1.5867	2.1046	86.448	10	762830000	290350000	472480000
P62192	26S protease regulatory subunit 4	Psmc1	7	7	7	19.8	19.8	19.8	49.184	440	2.6856E-39	1.6254	4.5861	72.466	9	1312100000	513770000	798350000
B7ZCF1	26S protease regulatory subunit 6A	Psmc3	14	14	14	37.3	37.3	37.3	50.395	451	7.255E-107	0.91023	1.1927	96.612	16	2494300000	1359200000	1135100000
P54775	26S protease regulatory subunit 6B	Psmc4	7	7	7	23.2	23.2	23.2	47.408	418	3.3188E-40	1.2307	1.4416	88.249	7	739160000	445100000	294060000
Q8BVQ9	26S protease regulatory subunit 7	Psmc2	11	11	11	27.8	27.8	27.8	52.866	475	1.5415E-52	1.1652	1.6196	62.683	13	708990000	318380000	390610000
P62196	26S protease regulatory subunit 8	Psmc5	7	7	7	24.4	24.4	24.4	45.626	406	6.0272E-29	1.7241	1.7313	35.669	6	780390000	342190000	438200000
Q3TXS7	26S proteasome non-ATPase regulatory subunit 1	Psmd1	12	12	12	20.3	20.3	20.3	105.73	953	2.923E-200	1.2374	1.4485	103.26	9	555870000	261360000	294510000
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	Psmd11	11	11	11	28.4	28.4	28.4	47.436	422	1.4695E-84	0.91092	1.1162	58.552	15	2581900000	1309200000	1272700000
Q9D8W5	26S proteasome non-ATPase regulatory subunit 12	Psmd12	7	7	7	16.2	16.2	16.2	52.895	456	4.7916E-57	1.2973	1.4773	41.18	8	657530000	307940000	349590000
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	Psmd13	6	6	6	24.2	24.2	24.2	42.809	376	2.714E-134	1.1169	1.3277	57.706	10	711190000	376470000	334720000
O35593	26S proteasome non-ATPase regulatory subunit 14	Psmd14	3	3	3	10.6	10.6	10.6	34.577	310	1.2706E-65	1.1376	1.1857	47.766	4	455630000	225580000	230060000
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	Psmd2	12	12	12	19.8	19.8	19.8	100.2	908	4.9903E-42	1.4043	1.7381	64.513	16	3317000000	1501900000	1815000000
P14685	26S proteasome non-ATPase regulatory subunit 3	Psmd3	7	7	7	17.5	17.5	17.5	60.718	530	9.0137E-87	1.6552	2.037	23.942	5	213910000	87817000	126090000
O35226	26S proteasome non-ATPase regulatory subunit 4	Psmd4	4	4	3	18.4	18.4	15.7	40.703	376	6.82E-170	0.72781	0.73842	35.769	4	1429600000	817870000	611700000
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5	Psmd5	3	3	3	8.1	8.1	8.1	55.971	504	5.3833E-08	1.3804	1.7296	42.849	3	471610000	192630000	278980000
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	Psmd6	11	11	11	29	29	29	45.536	389	1.3899E-36	2.3793	2.507	83.09	14	1273300000	338120000	935190000
P26516	26S proteasome non-ATPase regulatory subunit 7	Psmd7	2	2	2	11.2	11.2	11.2	36.539	321	2.8938E-95	1.105	1.689	52.295	5	881960000	408590000	473370000
Q9CX56	26S proteasome non-ATPase regulatory subunit 8	Psmd8	7	7	7	24.9	24.9	24.9	39.93	353	1.9245E-46	0.80875	0.82228	98.308	8	986460000	566680000	419780000
Q3UHX2	28 kDa heat- and acid-stable phosphoprotein	Pdap1	2	2	2	17.7	17.7	17.7	20.605	181	1.5506E-07	0.52	1.2052	101.6	2	137120000	100520000	36601000
Q9CQE3	28S ribosomal protein S17, mitochondrial	Mrps17	1	1	1	20	20	20	13.382	120	0.0018511	2.0035	1.7918	9.6279	2	44953000	14840000	30114000
Q9CXW2	28S ribosomal protein S22, mitochondrial	Mrps22	2	2	2	7.8	7.8	7.8	41.192	359	0.00025331	1.3515	1.5501	11.351	2	278190000	118330000	159860000
Q8BK72	28S ribosomal protein S27, mitochondrial	Mrps27	2	2	2	6	6	6	47.778	415	8.1902E-06	2.654	2.3957	9.6759	2	113600000	36689000	76911000
Q9D0G0	28S ribosomal protein S30, mitochondrial	Mrps30	3	3	3	6.3	6.3	6.3	49.939	442	9.4265E-05	3.3942	3.8741	36.366	3	73016000	19726000	53291000
Q9CQX8	28S ribosomal protein S36, mitochondrial	Mrps36	5	5	2	69.6	69.6	44.1	11.101	102	6.135E-184	0.35244	0.46037	107.9	13	3.1539E+10	2.5075E+10	6463700000
Q9CXI0	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	Coq5	2	2	2	7.6	7.6	7.6	37.335	327	1.2936E-08	2.3774	2.6901	32.891	2	432330000	125940000	306390000
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	Ogdh	41	41	36	48.2	48.2	44.8	116.45	1023	0	2.0885	2.2842	72.096	122	6.5084E+10	2.0242E+10	4.4842E+10
Q3U3J1	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	Bckdha	8	8	8	28.5	28.5	28.5	50.773	446	0	1.4984	1.6336	75.473	17	2402500000	947120000	1455400000
Q6P3A8	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	Bckdhb	6	6	6	19.2	19.2	19.2	42.88	390	3.041E-133	1.4615	2.0046	52.14	9	1339900000	546520000	793370000
Q9Z0S1	3(2),5-bisphosphate nucleotidase 1	Bpnt1	4	4	4	17.9	17.9	17.9	33.196	308	2.8915E-18	0.8064	1.3976	51.216	5	322600000	182560000	140040000
Q9DB15	39S ribosomal protein L12, mitochondrial	Mrpl12	3	3	3	18.4	18.4	18.4	21.708	201	7.7567E-22	0.55171	2.5199	111.8	3	193380000	126580000	66797000
Q9D1P0	39S ribosomal protein L13, mitochondrial	Mrpl13	3	3	3	29.8	29.8	29.8	20.677	178	2.4219E-06	3.0727	3.8358	42.316	3	175320000	39119000	136200000
Q9CPR5	39S ribosomal protein L15, mitochondrial	Mrpl15	2	2	2	9.8	9.8	9.8	33.541	295	0.00015408	4.4442	4.2828	32.041	2	100780000	18315000	82462000
O35972	39S ribosomal protein L23, mitochondrial	Mrpl23	1	1	1	10.3	10.3	10.3	17.121	146	0.00024621	1.8472	1.6826	49.152	2	8458900	2716800	5742000
Q921S7	39S ribosomal protein L37, mitochondrial	Mrpl37	3	3	3	10.2	10.2	10.2	48.34	423	5.8493E-05	2.7861	3.1632	7.5826	3	75713000	20351000	55363000
Q9CPW3	39S ribosomal protein L54, mitochondrial	Mrpl54	2	2	2	30.4	30.4	30.4	15.422	135	1.7703E-26	1.2831	1.601	65.313	2	80834000	33216000	47617000
Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial	Hibadh	7	7	7	32.2	32.2	32.2	35.44	335	5.7635E-71	1.1802	1.0464	27.761	11	977340000	435880000	541460000
Q8QZS1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	Hibch	13	13	13	40	40	40	43.037	385	1.727E-110	0.92623	1.0004	120.48	27	7647700000	4159600000	3488100000
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	Acaa1a	10	10	10	34.9	34.9	34.9	43.953	424	1.5794E-28	1.1161	1.2606	35.107	14	1833100000	906650000	926430000
Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	Acaa2	14	14	14	50.1	50.1	50.1	41.829	397	0	2.4362	2.449	83.24	22	7032300000	2916300000	4116000000
Q9D404	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	Oxsm	6	6	6	25.7	25.7	25.7	48.627	459	5.082E-122	1.5671	1.6684	87.624	15	1061400000	387870000	673500000
P63325	40S ribosomal protein S10	Rps10	2	2	2	17.6	17.6	17.6	18.916	165	1.2836E-56	4.475	4.3045	55.465	2	105200000	14824000	90372000
Q6ZWZ6	40S ribosomal protein S12	Rps12	4	4	4	40.2	40.2	40.2	14.515	132	0	1.0778	0.97766	25.033	6	1098900000	525720000	573190000
P62264	40S ribosomal protein S14	Rps14	2	2	2	20.5	20.5	20.5	16.273	151	2.7904E-08	4.2078	10.173	83.706	2	156490000	30742000	125740000
F6YVP7	40S ribosomal protein S18	Gm17352	2	2	2	13.2	13.2	13.2	17.671	152	0.0036694	5.5732	6.8467	110.46	2	167190000	28104000	139080000
D3Z722	40S ribosomal protein S19	Rps19	3	3	3	14.6	14.6	14.6	23.104	212	1.4904E-12	3.5242	3.6183	45.286	4	322020000	80105000	241920000
P62858	40S ribosomal protein S28	Rps28	2	2	2	30.4	30.4	30.4	7.8409	69	8.7262E-10	1.8785	3.0743	36.323	3	433010000	139180000	293830000
D3Z6C3	40S ribosomal protein S3a	Gm10119	2	2	2	8.7	8.7	8.7	29.824	264	4.7245E-08	3.4212	11.182	113.85	2	282190000	78558000	203640000
P62702	40S ribosomal protein S4, X isoform	Rps4x	2	2	2	13.3	13.3	13.3	29.597	263	1.4928E-12	2.1841	1.9869	45.715	2	77767000	22666000	55101000
Q91V55	40S ribosomal protein S5	Rps5	2	2	2	13.7	13.7	13.7	22.876	204	7.1968E-07	3.8875	4.7438	8.0225	2	16687000	3268800	13418000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P62242	40S ribosomal protein S8	Rps8	3	3	3	17.3	17.3	17.3	24.205	208	6.7696E-14	0.27489	1.2516	342.83	2	2751100000	2624900000	126220000
P14206	40S ribosomal protein SA	Rpsa	6	6	6	29.5	29.5	29.5	32.838	295	4.9687E-96	2.0505	2.2217	47.77	11	1333500000	444510000	888980000
P61922	4-aminobutyrate aminotransferase, mitochondrial	Abat	6	6	6	16.6	16.6	16.6	56.451	500	7.7228E-45	1.2402	1.4023	25.95	5	249390000	114750000	134640000
Q3U367	4-trimethylaminobutyraldehyde dehydrogenase	Aldh9a1	4	4	4	16	16	16	55.887	518	3.9047E-11	1.9932	2.1863	39.993	4	457020000	122910000	334110000
Q9JM14	5(3)-deoxyribonucleotidase, cytosolic type	Nt5c	2	2	2	15.5	15.5	15.5	23.076	200	3.5841E-59	1.4459	1.7926	40.377	3	339190000	135990000	203210000
Q8VC19	5-aminolevulinate synthase, nonspecific, mitochondrial	Alas1	2	2	2	5.6	5.6	5.6	71.017	642	0.0016312	1.2974	1.6728	39.325	3	224630000	101700000	122930000
Q8BRK8	5-AMP-activated protein kinase catalytic subunit alpha-2	Prkaa2	1	1	1	2.2	2.2	2.2	62.022	552	0.0059	2.0876	1.9825	4.3771	2	69210000	28773000	40437000
Q3UHB1	5-nucleotidase domain-containing protein 3	Nt5dc3	4	4	4	7.3	7.3	7.3	63.17	546	2.4912E-08	1.1912	1.2078	33.317	3	101860000	39995000	61866000
Q8K010	5-oxoprolinase	Oplah	8	8	8	8.9	8.9	8.9	137.61	1288	1.2082E-49	1.7452	1.6657	53.547	7	684360000	250070000	434290000
P63038	60 kDa heat shock protein, mitochondrial	Hspd1	37	37	37	66.8	66.8	66.8	60.955	573	0	0.50858	0.62424	90.885	101	8.9736E+10	5.9121E+10	3.0616E+10
E9Q070	60S acidic ribosomal protein P0	Gm8730	4	4	4	14.2	14.2	14.2	34.216	317	3.9817E-10	2.3133	1.7933	107.44	3	222100000	46610000	175490000
E9Q3T0	60S acidic ribosomal protein P1	Gm10073	1	1	1	14	14	14	11.433	114	0.0019704	2.3366	2.7215	42.625	3	26936000	8346900	18589000
P99027	60S acidic ribosomal protein P2	Rplp2	4	4	4	40.9	40.9	40.9	11.651	115	5.0701E-19	1.907	2.123	133	3	980920000	437250000	543670000
P86048	60S ribosomal protein L10-like	Rpl10l	2	2	2	8.9	8.9	8.9	24.558	214	0.0053693	1.5877	2.0341	35.153	3	275270000	117820000	157450000
P35979	60S ribosomal protein L12	Rpl12	3	3	3	30.3	30.3	30.3	17.804	165	1.381E-63	2.893	2.5881	14.031	2	77335000	3205600	74129000
Q8BP67	60S ribosomal protein L24	Rpl24	2	2	2	14	14	14	17.779	157	0.00019918	5.0273	5.6466	8.1016	2	67306000	11853000	55454000
P62889	60S ribosomal protein L30	Rpl30	2	2	2	30.4	30.4	30.4	12.784	115	2.3036E-06	3.6729	5.3674	124.44	2	177580000	19404000	158170000
Q6ZWZ4	60S ribosomal protein L36	Rpl36	2	2	2	20	20	20	12.254	105	0.00044704	7.8286	8.4327	182.37	2	46803000	10024000	36779000
Q9D8E6	60S ribosomal protein L4	Rpl4	2	2	2	5.7	5.7	5.7	47.153	419	0.00042938	1.7424	2.0893	144.17	3	129380000	17710000	111670000
F6XI62	60S ribosomal protein L7	Rpl7	2	2	2	8.6	8.6	8.6	32.416	279	5.7187E-06	3.5897	3.3696	4.328	2	280610000	82911000	197700000
Q8C605	6-phosphofructokinase	Pfkp	6	5	5	7.3	6.1	6.1	85.546	784	2.2648E-12	1.7395	2.2341	60.015	3	233230000	94766000	138470000
P12382	6-phosphofructokinase, liver type	Pfkl	10	9	9	18.3	17.2	17.2	85.359	780	6.4248E-93	1.9999	2.0607	41.847	12	2423100000	885250000	1537900000
P47857	6-phosphofructokinase, muscle type	Pfkm	17	17	16	28.7	28.7	27.6	85.268	780	0	1.7713	1.9256	50.916	33	2.0111E+10	6863800000	1.3247E+10
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	Pgd	9	9	9	26.3	26.3	26.3	53.247	483	7.249E-132	1.1792	1.3209	70.334	11	1061700000	467810000	593930000
Q9CQ60	6-phosphogluconolactonase	Pgls	4	4	4	21.8	21.8	21.8	27.254	257	1.0879E-31	0.81355	0.97932	43.004	8	2153600000	1217400000	936240000
Q9R1Z7	6-pyruvoyl tetrahydrobiopterin synthase	Pts	1	1	1	9	9	9	16.188	144	4.8847E-06	0.79509	0.94585	15.339	2	34742000	18786000	15956000
P20029	78 kDa glucose-regulated protein	Hspa5	27	27	25	39.5	39.5	37.9	72.421	655	3.766E-268	0.80818	0.81733	68.705	39	7561600000	4647300000	2914200000
Q8K4F5	Abhydrolase domain-containing protein 11	Abhd11	3	3	3	21.8	21.8	21.8	33.56	307	2.987E-116	1.412	1.2578	29.798	3	63524000	33030000	30494000
E9QN99	Abhydrolase domain-containing protein 14B	Abhd14b	5	5	5	31.9	31.9	31.9	22.45	210	1.473E-116	0.75332	0.81719	27.204	10	814970000	428540000	386430000
Q80X81	Acetyl-CoA acetyltransferase, cytosolic	Acat3	3	3	3	14.4	14.4	14.4	41.47	397	1.4991E-19	0.74357	0.66177	89.195	3	196470000	71028000	125440000
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	Acat1	18	18	18	56.8	56.8	56.8	44.816	424	0	0.62547	0.90323	113.77	62	9.3509E+10	5.6527E+10	3.6982E+10
Q99NB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	Acss1	18	18	18	37.8	37.8	37.8	74.622	682	0	1.6972	1.8113	47.027	36	9138300000	3478400000	5659900000
Q9WV54	Acid ceramidase	Asah1	5	5	5	15.2	15.2	15.2	44.669	394	3.9514E-09	4.1031	3.6359	118.26	3	176320000	78185000	98132000
O35381	Acidic leucine-rich nuclear phosphoprotein 32 family member A	Anp32a	4	4	4	17.4	17.4	17.4	28.537	247	5.8582E-24	1.434	1.3309	52.354	6	1248400000	412790000	835650000
Q99KI0	Aconitate hydratase, mitochondrial	Aco2	45	45	45	57.9	57.9	57.9	85.462	780	0	1.4483	1.4267	91.148	288	1.9334E+11	8.4393E+10	1.0895E+11
P68134	Actin, alpha skeletal muscle	Acta1	12	1	1	54.4	5.8	5.8	42.051	377	3.421E-255	2.8322	3.1719	8.0313	2	527110000	152190000	374920000
P62737	Actin, aortic smooth muscle	Acta2	12	12	1	54.4	54.4	5.8	42.009	377	0	1.4842	1.4852	56.408	42	3.5283E+10	1.6259E+10	1.9024E+10
Q9Z2N8	Actin-like protein 6A	Actl6a	3	3	3	15.4	15.4	15.4	47.447	429	2.6509E-11	1.4664	1.4797	29.015	3	213860000	91400000	122460000
P61161	Actin-related protein 2	Actr2	5	5	5	19.8	19.8	19.8	44.76	394	2.7692E-23	1.862	1.853	34.641	4	540030000	164630000	375400000
Q9R0Q6	Actin-related protein 2/3 complex subunit 1A	Arpc1a	3	3	3	11.4	11.4	11.4	41.626	370	8.0724E-12	1.7764	2.1227	24.098	4	558030000	195180000	362850000
Q9WV32	Actin-related protein 2/3 complex subunit 1B	Arpc1b	5	5	5	15.1	15.1	15.1	41.063	372	7.406E-17	1.971	2.7185	147.03	5	714540000	264240000	450310000
Q9CVB6	Actin-related protein 2/3 complex subunit 2	Arpc2	8	8	8	24.3	24.3	24.3	34.357	300	7.2785E-45	0.9492	2.091	101.3	10	1323300000	659830000	663470000
Q9JM76	Actin-related protein 2/3 complex subunit 3	Arpc3	2	2	2	10.1	10.1	10.1	20.524	178	0.00010253	0.90225	0.89293	69.81	2	780480000	403920000	376560000
Q9CPW4	Actin-related protein 2/3 complex subunit 5	Arpc5	2	2	2	17.2	17.2	17.2	16.288	151	1.9297E-11	0.37776	0.82517	65.741	2	330720000	216090000	114630000
A3KGQ6	Actin-related protein 2/3 complex subunit 5	Arpc5l	2	2	2	20.3	20.3	20.3	17.109	153	7.7861E-27	0.62573	1.1178	40.108	3	477770000	284760000	193010000
Q99JY9	Actin-related protein 3	Actr3	11	11	11	44.7	44.7	44.7	47.357	418	2.001E-184	1.5723	2.0081	89.512	12	1351700000	505440000	846250000
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	Ahsa1	8	8	8	28.1	28.1	28.1	38.117	338	2.4649E-37	1.392	1.6795	99.553	6	554730000	193650000	361080000
Q9CR21	Acyl carrier protein, mitochondrial	Ndufab1	3	3	3	15.4	15.4	15.4	17.37	156	2.1782E-32	0.44638	0.44214	56.596	9	1993200000	1310600000	682510000
Q8R146	Acylamino-acid-releasing enzyme	Apeh	9	9	9	19.5	19.5	19.5	81.58	732	1.1957E-38	1.9531	2.1476	131.82	10	967450000	389270000	578180000
D3Z7X0	Acyl-CoA dehydrogenase family member 10	Acad12	12	12	12	27.4	27.4	27.4	61.389	555	9.767E-125	3.7539	4.2258	95.642	16	1800300000	675500000	1124800000
Q80XL6	Acyl-CoA dehydrogenase family member 11	Acad11	3	3	3	7.2	7.2	7.2	87.365	779	1.0353E-07	2.719	3.0429	63.1	3	113400000	21835000	91565000
Q8JZN5	Acyl-CoA dehydrogenase family member 9, mitochondrial	Acad9	9	9	9	21.6	21.6	21.6	68.721	625	4.257E-106	0.88498	1.0439	41.269	13	1209600000	676420000	533200000
Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial	Acsf2	6	6	6	14	14	14	67.95	615	6.1554E-75	2.4292	2.697	43.683	7	1440900000	407820000	1033000000
Q3URE1	Acyl-CoA synthetase family member 3, mitochondrial	Acsf3	6	6	6	18.4	18.4	18.4	65.076	583	6.042E-37	1.5975	1.5722	56.077	9	531850000	191080000	340770000
Q4VWZ5	Acyl-CoA-binding protein	Dbi	4	4	4	33.3	33.3	33.3	15.228	135	1.155E-208	0.58482	0.62913	61.629	19	2.2433E+10	1.4991E+10	7441500000
E9Q296	Acyl-coenzyme A oxidase	Acox3	2	2	2	4.7	4.7	4.7	81.21	728	5.5378E-07	1.4932	1.8125	103.29	2	98241000	37270000	60972000
O55137	Acyl-coenzyme A thioesterase 1	Acot1	9	2	2	29.1	6.2	6.2	46.135	419	5.898E-116	0.45891	0.69009	126.82	6	1142300000	813420000	328910000
Q9CQR4	Acyl-coenzyme A thioesterase 13	Acot13	6	6	6	48.6	48.6	48.6	15.183	140	1.9753E-45	0.75462	0.85632	52.402	10	1592700000	711480000	881220000
Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial	Acot2	12	12	5	41.3	41.3	20.1	49.656	453	1.472E-186	0.94233	0.96041	94.733	35	1.6394E+10	7508300000	8885700000
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial	Acot9	7	7	7	16.6	16.6	16.6	50.56	439	9.9161E-15	1.7598	1.9644	35.152	7	423930000	144740000	279190000
E9QJT5	Acylphosphatase	Acyp1	3	3	3	24.8	24.8	24.8	17.344	157	1.1761E-17	0.36852	0.44316	63.879	3	446130000	300150000	145980000
P56375	Acylphosphatase-2	Acyp2	6	6	6	59.4	59.4	59.4	11.877	106	1.112E-102	0.4446	0.85573	144.92	6	5599800000	3796000000	1803800000
P97823	Acyl-protein thioesterase 1	Lypla1	5	5	5	34.3	34.3	34.3	24.687	230	5.4594E-52	0.81894	1.0645	53.355	5	506400000	303810000	202580000
Q8R0F8	Acylpyruvase FAHD1, mitochondrial	Fahd1	2	2	2	17.2	17.2	17.2	25.172	227	8.8187E-38	2.3168	2.289	96.782	5	476230000	170300000	305930000
Q64010	Adapter molecule crk	Crk	4	4	4	18.8	18.8	18.8	33.814	304	2.673E-128	0.60856	0.62071	49.999	4	730610000	474380000	256240000
P55264	Adenosine kinase	Adk	9	9	9	29.4	29.4	29.4	40.148	361	5.63E-263	0.59454	0.73347	110.41	15	5005400000	3018500000	1986900000
P50247	Adenosylhomocysteinase	Ahcy	12	12	12	34	34	34	47.688	432	1.9171E-44	1.03	1.1512	84.568	15	3069000000	1586700000	1482300000
Q9WTP6	Adenylate kinase 2, mitochondrial	Ak2	6	6	6	38.1	38.1	38.1	26.468	239	0	0.75315	0.81566	38.969	12	6119200000	3467500000	2651700000
Q9R0Y5	Adenylate kinase isoenzyme 1	Ak1	12	12	12	60.8	60.8	60.8	21.539	194	0	0.4483	0.52155	100.39	42	5.3426E+10	3.8472E+10	1.4954E+10
Q9WUR9	Adenylate kinase isoenzyme 4, mitochondrial	Ak4	4	4	4	21.1	21.1	21.1	25.061	223	4.578E-111	2.8046	3.312	35.76	4	596620000	168470000	428160000
P54822	Adenylosuccinate lyase	Adsl	8	8	8	25.4	25.4	25.4	54.866	484	3.0726E-85	1.7288	1.8762	56.155	8	663550000	268340000	395210000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P28650	Adenylosuccinate synthetase isozyme 1	Adssl1	11	11	10	33	33	29.5	50.254	457	7.4549E-39	1.5782	1.8644	116.61	13	3090500000	1299200000	1791300000
P46664	Adenylosuccinate synthetase isozyme 2	Adss	3	2	2	10.1	6.6	6.6	50.02	456	1.9583E-08	1.0436	1.0045	5.1398	2	84083000	37926000	46157000
P40124	Adenylyl cyclase-associated protein 1	Cap1	3	3	3	9.9	9.9	9.9	51.564	474	3.0606E-15	1.7246	1.934	63.507	3	775500000	301060000	474430000
Q9CYT6	Adenylyl cyclase-associated protein 2	Cap2	5	5	5	16.8	16.8	16.8	52.861	476	1.092E-20	1.4885	1.5428	46.745	6	430190000	226790000	203410000
Q60994	Adiponectin	Adipoq	4	4	4	21.1	21.1	21.1	26.809	247	1.108E-137	0.49488	0.85123	138.46	6	1707100000	1330100000	376960000
P48962	ADP/ATP translocase 1	Slc25a4	15	15	10	43.6	43.6	29.5	32.904	298	3.5368E-95	1.5484	1.7403	103.56	54	4.4732E+10	2.0434E+10	2.4299E+10
Q3V132	ADP/ATP translocase 4	Slc25a31	3	1	1	7.8	2.8	2.8	35.257	320	2.6531E-16	1.392	1.5306	48.26	4	130910000	59890000	71017000
Q8BVU5	ADP-ribose pyrophosphatase, mitochondrial	Nudt9	2	2	2	6	6	6	38.604	350	1.2308E-18	0.33216	0.72306	41.095	3	152410000	97479000	54931000
P61205	ADP-ribosylation factor 3	Arf3	7	7	4	41.4	41.4	24.3	20.601	181	5.726E-92	1.2861	1.4444	53.16	10	1773300000	764150000	1009100000
Q8R0H9	ADP-ribosylation factor-binding protein GGA1	Gga1	2	2	2	6.5	6.5	6.5	69.971	635	0.000121	1.4953	1.2629	4.0937	2	6485700	2966400	3519300
Q9WUL7	ADP-ribosylation factor-like protein 3	Arl3	3	3	3	29.1	29.1	29.1	20.486	182	1.7923E-55	1.0806	1.1205	24.589	5	414480000	201360000	213120000
Q9JKX6	ADP-sugar pyrophosphatase	Nudt5	2	2	2	12.8	12.8	12.8	23.984	218	2.678E-09	0.92662	0.97195	94.749	3	253190000	126040000	127150000
P46656	Adrenodoxin, mitochondrial	Fdx1	2	2	2	9	9	9	20.123	188	7.2593E-06	0.46537	0.52777	119.69	3	621960000	411940000	210020000
E9Q9C3	Afadin	Mllt4	3	3	3	2.8	2.8	2.8	207.31	1827	3.5708E-11	1.1531	1.1721	68.186	2	15300000	6367200	8933000
O89020	Afamin	Afm	10	10	10	22.5	22.5	22.5	69.378	608	4.0631E-38	0.56135	0.67447	36.259	11	596190000	406020000	190170000
Q8JZQ2	AFG3-like protein 2	Afg3l2	4	3	3	5.2	4.2	4.2	89.518	802	1.0891E-07	0.63834	0.75229	43.398	3	108580000	66005000	42573000
Q8CG76	Aflatoxin B1 aldehyde reductase member 2	Akr7a2	5	5	5	18.3	18.3	18.3	40.612	367	4.2364E-37	1.5064	2.0428	66.776	9	3041600000	1005800000	2035700000
M0QWP1	Agrin	Agrn	3	3	3	2	2	2	216.65	2034	3.2857E-17	1.2132	1.2314	3.8816	2	78420000	33035000	45385000
O08715	A-kinase anchor protein 1, mitochondrial	Akap1	3	3	3	5.1	5.1	5.1	92.194	857	1.2464E-08	1.5903	1.5555	90.637	3	124210000	44962000	79251000
Q9WTQ5	A-kinase anchor protein 12	Akap12	11	11	11	8.8	8.8	8.8	180.69	1684	2.073E-107	0.59891	0.60758	40.347	11	477550000	290260000	187300000
F7AA26	A-kinase anchor protein 2	Gm20459	8	8	7	11.5	11.5	10.4	125.98	1137	9.4526E-54	0.53676	0.53193	87.979	10	862310000	551800000	310510000
Q8QZR5	Alanine aminotransferase 1	Gpt	9	9	9	24.4	24.4	24.4	55.142	496	1.651E-150	1.0104	1.0326	58.623	12	1588200000	834280000	753910000
Q8BGQ7	Alanine--tRNA ligase, cytoplasmic	Aars	7	7	7	9.8	9.8	9.8	106.91	968	5.3201E-26	0.66609	0.81699	80.291	4	252230000	154460000	97763000
Q9JII6	Alcohol dehydrogenase [NADP(+)]	Akr1a1	5	5	5	24	24	24	36.586	325	1.2342E-88	1.8144	1.8053	68.223	10	1489300000	541720000	947550000
P00329	Alcohol dehydrogenase 1	Adh1	4	4	4	18.1	18.1	18.1	39.771	375	1.4449E-25	1.4218	1.5679	11.238	6	351160000	147330000	203840000
P28474	Alcohol dehydrogenase class-3	Adh5	11	11	11	45.2	45.2	45.2	39.547	374	1.484E-196	0.8574	0.91581	102.91	15	3407600000	1870900000	1536700000
Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	Aldh1b1	12	11	11	32.4	30.8	30.8	57.552	519	4.004E-132	0.84347	0.83362	67.94	16	2578200000	1183700000	1394500000
P47738	Aldehyde dehydrogenase, mitochondrial	Aldh2	24	24	22	49.3	49.3	46.2	56.537	519	0	0.86563	0.8596	61.442	76	7693500000	4274300000	3419100000
Q8K157	Aldose 1-epimerase	Galm	2	2	2	7.3	7.3	7.3	37.798	342	2.0183E-07	0.66206	0.78449	4.6629	2	143530000	89396000	54134000
P45376	Aldose reductase	Akr1b1	12	12	12	42.1	42.1	42.1	35.732	316	0	0.70152	1.0161	116.29	28	2.7892E+10	1.6787E+10	1.1105E+10
G5E895	Aldose reductase-related protein 1	Akr1b10	10	10	10	39.9	39.9	39.9	35.848	316	0	1.1229	1.2294	130.41	18	1.0174E+10	5311500000	4862400000
Q60590	Alpha-1-acid glycoprotein 1	Orm1	3	3	3	18.4	18.4	18.4	23.895	207	1.0626E-32	0.41161	0.43647	26.157	3	231330000	169840000	61492000
P07758	Alpha-1-antitrypsin 1-1	Serpina1a	13	5	4	42.9	17.4	12.1	46.002	413	0	0.41406	0.52996	95.596	28	2.9656E+10	2.0547E+10	9109500000
P22599	Alpha-1-antitrypsin 1-2	Serpina1b	12	3	3	35.1	7.7	7.7	45.974	413	2.502E-282	0.44803	0.47376	142.28	4	1487700000	1020200000	467550000
Q00897	Alpha-1-antitrypsin 1-4	Serpina1d	15	15	6	41.4	41.4	15.3	45.998	413	0	0.4692	0.57271	85.387	27	1.2839E+10	8721200000	4117300000
Q00898	Alpha-1-antitrypsin 1-5	Serpina1e	9	4	4	25.9	13.8	13.8	45.891	413	9.49E-286	0.53459	0.60053	135.93	13	1.4263E+10	9399300000	4863700000
Q61234	Alpha-1-syntrophin	Snta1	2	2	2	6.6	6.6	6.6	53.664	503	2.55E-155	3.2045	3.2144	21.3	3	676030000	142130000	533900000
Q61247	Alpha-2-antiplasmin	Serpinf2	5	5	5	14.5	14.5	14.5	54.971	491	2.1844E-90	0.58134	0.54611	39.226	12	1086300000	676170000	410130000
P29699	Alpha-2-HS-glycoprotein	Ahsg	6	6	6	24.9	24.9	24.9	37.325	345	0	0.46976	0.63664	67.973	17	4207300000	2574700000	1632600000
D3YW52	Alpha-2-macroglobulin	Pzp	37	37	37	37.1	37.1	37.1	167.28	1507	0	0.62595	0.65061	53.771	74	2.8211E+10	1.7744E+10	1.0466E+10
P55302	Alpha-2-macroglobulin receptor-associated protein	Lrpap1	3	3	3	9.2	9.2	9.2	42.215	360	9.927E-06	0.53293	0.68939	65.503	3	179840000	123770000	56073000
Q9JI91	Alpha-actinin-2	Actn2	18	18	14	27.1	27.1	22.4	103.83	894	4.399E-245	8.5728	9.7653	112.17	21	3682600000	317650000	3365000000
P57780	Alpha-actinin-4	Actn4	12	10	6	16.9	14.7	8.9	104.98	912	4.3463E-56	5.3849	5.6069	100.69	9	605720000	129250000	476470000
Q9QYC0	Alpha-adducin	Add1	5	5	5	9.5	9.5	9.5	80.646	735	1.0375E-10	1.0146	1.6946	135	5	143250000	58360000	84888000
Q9DBF1	Alpha-aminoadipic semialdehyde dehydrogenase	Aldh7a1	2	2	2	4.8	4.8	4.8	58.861	539	0.0014161	1.4632	1.357	27.336	2	11488000	4572400	6915600
P61164	Alpha-centractin	Actr1a	1	1	1	5.9	5.9	5.9	42.613	376	9.7098E-31	5.9074	6.0235	2.0603	2	136840000	17445000	119390000
P23927	Alpha-crystallin B chain	Cryab	4	4	4	30.9	30.9	30.9	20.069	175	2.0148E-30	2.1799	2.4718	77.702	18	7088900000	2401900000	4687000000
P17182	Alpha-enolase	Eno1	13	11	5	41	37.8	14.5	47.14	434	1.798E-197	0.70563	1.0496	109.31	29	7742000000	4566600000	3175500000
Q91W89	Alpha-mannosidase 2C1	Man2c1	2	2	2	2.9	2.9	2.9	115.69	1039	5.6484E-05	0.90294	0.90141	113.49	2	15837000	8896100	6940600
O09174	Alpha-methylacyl-CoA racemase	Amacr	6	6	6	16.3	16.3	16.3	41.704	381	1.7372E-13	1.3194	1.318	45.203	4	355210000	147990000	207220000
P82350	Alpha-sarcoglycan	Sgca	6	6	6	20.9	20.9	20.9	43.286	387	4.3468E-29	1.9808	1.9912	71.566	7	519280000	226420000	292860000
Q9DB05	Alpha-soluble NSF attachment protein	Napa	3	3	3	16.3	16.3	16.3	33.189	295	3.4831E-34	0.87416	0.94438	33.547	2	115650000	59027000	56625000
O55042	Alpha-synuclein	Snca	4	4	4	37.9	37.9	37.9	14.485	140	2.4196E-15	0.5678	1.0229	84.757	4	149370000	87233000	62137000
Q8BW75	Amine oxidase [flavin-containing] B	Maob	4	4	4	10.6	10.6	10.6	58.557	520	5.0011E-13	1.0676	1.076	139.63	3	169280000	60397000	108880000
Q3UZG4	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	Aimp1	7	7	7	38.2	38.2	38.2	35.166	319	2.1498E-88	0.94833	1.0931	14.196	10	2155900000	1144300000	1011600000
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	Aimp2	2	2	2	11.6	11.6	11.6	35.377	320	4.4194E-20	1.5217	1.9122	3.337	3	102220000	42054000	60170000
Q99JW2	Aminoacylase-1	Acy1	3	3	3	9.1	9.1	9.1	45.78	408	1.123E-08	0.79846	1.077	59.486	3	370690000	222340000	148350000
Q8VCT3	Aminopeptidase B	Rnpep	8	8	8	16.2	16.2	16.2	72.415	650	2.665E-23	1.0465	1.9972	46.323	8	643890000	310100000	333780000
P97449	Aminopeptidase N	Anpep	6	6	6	8.1	8.1	8.1	109.65	966	4.6591E-46	1.1851	1.2316	57.243	7	713330000	300570000	412760000
Q9DCH6	AN1-type zinc finger protein 6	Zfand6	2	2	2	10.8	10.8	10.8	24.001	223	4.5673E-05	0.40743	0.35838	41.986	2	57957000	44153000	13804000
Q8WTY4	Anamorsin	Ciapin1	7	7	7	33	33	33	33.429	309	5.379E-227	0.45592	0.58556	89.099	7	1036000000	742550000	293490000
P09470	Angiotensin-converting enzyme	Ace	7	7	7	6.2	6.2	6.2	150.92	1312	6.1642E-15	1.0593	1.2688	18.354	5	231750000	113480000	118270000
S4R291	Ankyrin-2	Ank2	18	18	13	7.3	7.3	5.9	432.25	3954	3.4117E-60	2.3337	2.8999	81.506	12	554290000	175380000	378910000
P10107	Annexin A1	Anxa1	14	14	14	48.3	48.3	48.3	38.734	346	3.423E-146	0.83811	1.0751	68.2	13	1614700000	937980000	676770000
P97384	Annexin A11	Anxa11	13	13	13	25	25	25	54.079	503	7.314E-104	1.1458	1.3796	139.35	14	2354400000	1203000000	1151500000
P07356	Annexin A2	Anxa2	20	20	20	57.8	57.8	57.8	38.676	339	3.814E-298	1.0015	1.0005	86.162	20	2056300000	1006900000	1049400000
O35639	Annexin A3	Anxa3	10	10	10	34.7	34.7	34.7	36.384	323	1.3071E-60	0.79988	0.94787	62.16	12	1272600000	678580000	594010000
P97429	Annexin A4	Anxa4	12	11	11	37.6	35.4	35.4	35.915	319	7.096E-75	1.1099	1.3173	70.89	10	1324000000	608240000	715760000
P48036	Annexin A5	Anxa5	12	12	12	39.5	39.5	39.5	35.752	319	0	0.72614	0.78378	54.146	20	2359800000	1339300000	1020500000
P14824	Annexin A6	Anxa6	33	33	1	52.6	52.6	4.5	75.884	673	0	0.73106	0.87034	97.798	69	2.8604E+10	1.691E+10	1.1694E+10
Q07076	Annexin A7	Anxa7	9	9	9	21.4	21.4	21.4	49.925	463	4.2969E-24	1.3269	1.3258	28.267	11	1022500000	415980000	606510000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q14AT5	Anoctamin-7	Ano7	1	1	1	1.9	1.9	1.9	97.127	859	0.036338	1.2593	1.1381	39.248	2	652570000	291040000	361530000
P32261	Antithrombin-III	Serpinc1	16	16	16	37	37	37	52.003	465	2.7357E-58	0.40717	0.56967	91.478	20	4111500000	2965600000	1145900000
O35643	AP-1 complex subunit beta-1	Ap1b1	8	8	5	12.1	12.1	8.6	103.93	943	1.6019E-25	1.0188	1.1682	62.385	8	378720000	195700000	183020000
P35585	AP-1 complex subunit mu-1	Ap1m1	1	1	1	4.5	4.5	4.5	48.542	423	0.0013638	1.1855	1.3957	188.45	2	209900000	145880000	64028000
P17426	AP-2 complex subunit alpha-1	Ap2a1	5	3	3	6.3	3.8	3.8	107.66	977	4.3757E-10	1.0673	1.0063	215.63	2	77751000	50211000	27540000
P17427	AP-2 complex subunit alpha-2	Ap2a2	8	8	6	11.9	11.9	9.3	104.02	938	1.4014E-17	2.4138	2.2669	57.662	8	330650000	83417000	247240000
P84091	AP-2 complex subunit mu	Ap2m1	2	2	2	4.1	4.1	4.1	49.654	435	2.4126E-06	3.8849	7.2882	93.761	2	119400000	28069000	91328000
Q3UHJ0	AP2-associated protein kinase 1	Aak1	5	5	5	8.1	8.1	8.1	103.35	959	2.6461E-13	1.0349	1.0502	40.21	6	79718000	38058000	41660000
Q9Z1T1	AP-3 complex subunit beta-1	Ap3b1	2	2	2	2.9	2.9	2.9	122.74	1105	4.0822E-07	1.1839	1.2089	49.476	2	98605000	47954000	50651000
Q00623	Apolipoprotein A-I	Apoa1	9	9	9	31.4	31.4	31.4	30.615	264	1.7879E-40	1.3546	1.8506	116.54	10	1559400000	667100000	892340000
P06728	Apolipoprotein A-IV	Apoa4	10	10	10	31.4	31.4	31.4	45.029	395	9.3298E-92	0.63566	1.325	101.97	11	980450000	518290000	462160000
Q9DCZ4	Apolipoprotein O	Apoo	3	3	3	13.2	13.2	13.2	24.136	212	6.1172E-13	2.9245	3.6714	123.09	3	1142700000	277700000	865000000
Q78IK4	Apolipoprotein O-like	Apool	3	3	3	16.2	16.2	16.2	29.26	265	2.3775E-25	0.61365	0.58307	22.878	3	160770000	100500000	60273000
Q9EPB4	Apoptosis-associated speck-like protein containing a CARD	Pycard	2	2	2	18.7	18.7	18.7	21.458	193	2.4141E-44	0.80692	0.94237	27.053	3	281010000	154260000	126750000
Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial	Aifm1	11	11	11	24	24	24	66.765	612	5.8248E-63	0.88907	0.95504	117.62	14	5277100000	3205100000	2072000000
Q9D0I9	Arginine--tRNA ligase, cytoplasmic	Rars	8	8	8	15.9	15.9	15.9	75.673	660	3.6278E-27	1.9664	2.1649	53.281	11	884400000	301480000	582920000
Q91WU5	Arsenite methyltransferase	As3mt	10	10	10	32.2	32.2	32.2	41.793	376	8.4431E-58	0.52988	1.1677	83.93	12	963450000	604080000	359360000
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	Nars	5	5	5	11.6	11.6	11.6	64.279	559	1.562E-11	2.2883	2.9618	58.277	6	346580000	110590000	235990000
P05201	Aspartate aminotransferase, cytoplasmic	Got1	24	24	24	69.5	69.5	69.5	46.247	413	0	0.97681	1.0797	62.739	90	8.6178E+10	4.4158E+10	4.2019E+10
P05202	Aspartate aminotransferase, mitochondrial	Got2	22	22	22	62.8	62.8	62.8	47.411	430	0	1.4862	1.8533	102.98	59	5.6359E+10	2.1181E+10	3.5178E+10
Q922B2	Aspartate--tRNA ligase, cytoplasmic	Dars	7	7	7	18.6	18.6	18.6	57.147	501	3.1796E-16	1.6328	1.863	47.974	7	905920000	414740000	491180000
Q8BIP0	Aspartate--tRNA ligase, mitochondrial	Dars2	4	4	4	8.4	8.4	8.4	74.101	653	1.998E-11	0.97929	1.2565	259.4	4	1374800000	63248000	1311500000
Q91XE4	Aspartoacylase-2	Acy3	5	5	5	31.8	31.8	31.8	35.286	318	3.184E-224	0.9588	0.97935	49.769	8	2015000000	876960000	1138000000
Q9Z2W0	Aspartyl aminopeptidase	Dnpep	7	7	7	24.1	24.1	24.1	52.206	473	5.634E-22	2.3263	2.2084	44.924	8	599590000	176430000	423160000
Q8BSY0	Aspartyl/asparaginyl beta-hydroxylase	Asph	3	3	3	4.5	4.5	4.5	83.041	741	1.0864E-09	0.8338	1.103	111.99	2	132740000	55688000	77050000
Q62048	Astrocytic phosphoprotein PEA-15	Pea15	4	4	4	36.9	36.9	36.9	15.054	130	8.9123E-13	0.48553	0.54157	35.769	4	268380000	166140000	102240000
P28658	Ataxin-10	Atxn10	4	4	4	12.4	12.4	12.4	53.706	475	4.2804E-26	1.3093	1.52	46.003	3	139140000	65865000	73272000
E9QM77	Ataxin-2	Atxn2	4	4	4	4.1	4.1	4.1	136.46	1286	8.7046E-10	0.51278	1.6363	27.354	3	179470000	126540000	52935000
Q7TQH0	Ataxin-2-like protein	Atxn2l	3	3	3	3.1	3.1	3.1	110.65	1049	2.3459E-09	0.50125	0.50762	15.666	3	175690000	117920000	57768000
H3BLL2	ATP synthase mitochondrial F1 complex assembly factor 1	Atpaf1	8	8	8	23	23	23	38.796	348	7.529E-41	0.49837	0.54371	39.653	12	1890900000	1220600000	670330000
Q91YY4	ATP synthase mitochondrial F1 complex assembly factor 2	Atpaf2	4	4	4	20.1	20.1	20.1	33.289	289	7.1012E-74	1.4569	1.508	39.118	5	1370000000	997440000	372560000
P03930	ATP synthase protein 8	Mtatp8	2	2	2	31.3	31.3	31.3	7.7662	67	4.0092E-05	0.78861	0.81951	39.116	2	299350000	168480000	130870000
Q03265	ATP synthase subunit alpha, mitochondrial	Atp5a1	25	25	25	47.6	47.6	47.6	59.752	553	0	1.9474	1.9771	76.237	69	2.1213E+10	7192300000	1.4021E+10
Q9CQQ7	ATP synthase subunit b, mitochondrial	Atp5f1	6	6	6	25.4	25.4	25.4	28.948	256	1.0282E-96	1.096	1.476	36.373	7	534710000	252260000	282450000
P56480	ATP synthase subunit beta, mitochondrial	Atp5b	28	28	28	69.6	69.6	69.6	56.3	529	0	0.89831	0.97678	60.164	275	2.3073E+11	1.2211E+11	1.0862E+11
Q9DCX2	ATP synthase subunit d, mitochondrial	Atp5h	9	9	9	64	64	64	18.749	161	1.547E-300	0.52924	0.4968	36.792	17	1.8392E+10	1.2527E+10	5864900000
Q9D3D9	ATP synthase subunit delta, mitochondrial	Atp5d	3	3	3	28.6	28.6	28.6	17.6	168	3.9555E-57	0.68603	0.70569	54.515	6	998670000	593520000	405150000
Q06185	ATP synthase subunit e, mitochondrial	Atp5i	2	2	2	16.9	16.9	16.9	8.2355	71	0.0052953	0.95358	3.3354	24.727	5	100260000	51596000	48659000
P56382	ATP synthase subunit epsilon, mitochondrial	Atp5e	4	4	4	53.8	53.8	53.8	5.8378	52	4.6673E-06	0.4519	0.37843	159.63	4	337600000	152470000	185140000
P56135	ATP synthase subunit f, mitochondrial	Atp5j2	2	2	2	26.1	26.1	26.1	10.344	88	1.3557E-11	1.8031	1.7706	85.087	4	1893100000	678860000	1214300000
Q9CPQ8	ATP synthase subunit g, mitochondrial	Atp5l	3	3	3	42.7	42.7	42.7	11.424	103	9.9054E-11	0.69234	0.6287	124.6	3	245730000	139480000	106250000
Q91VR2	ATP synthase subunit gamma, mitochondrial	Atp5c1	8	8	8	23.8	23.8	23.8	32.886	298	1.4201E-39	1.9877	2.5344	106.48	11	6436900000	2259200000	4177700000
Q9DB20	ATP synthase subunit O, mitochondrial	Atp5o	7	7	3	49.8	49.8	26.8	23.363	213	7.227E-88	2.0494	2.1158	55.605	27	5786000000	1832900000	3953100000
P97450	ATP synthase-coupling factor 6, mitochondrial	Atp5j	6	6	6	46.3	46.3	46.3	12.496	108	4.903E-269	0.63876	0.55829	65.675	8	3858800000	2214200000	1644600000
O54984	ATPase Asna1	Asna1	4	4	4	18.7	18.7	18.7	38.822	348	1.7278E-12	1.1827	1.1605	37.352	7	331790000	129190000	202600000
Q9D5T0	ATPase family AAA domain-containing protein 1	Atad1	2	2	2	12.7	12.7	12.7	40.744	361	4.2151E-57	0.88095	0.91692	21.039	2	149350000	82848000	66499000
Q9CXJ4	ATP-binding cassette sub-family B member 8, mitochondrial	Abcb8	2	2	2	5.4	5.4	5.4	77.999	717	3.4161E-07	1.3861	1.5574	4.0178	2	131370000	44869000	86499000
P61222	ATP-binding cassette sub-family E member 1	Abce1	5	5	5	11	11	11	67.314	599	6.7701E-50	1.1847	1.4216	43.973	4	372510000	166100000	206410000
Q6P542	ATP-binding cassette sub-family F member 1	Abcf1	4	4	4	8.4	8.4	8.4	94.944	837	1.1523E-11	2.4445	2.3031	121.71	2	59437000	17596000	41841000
Q3V117	ATP-citrate synthase	Acly	5	5	5	5	5	5	120.79	1101	2.4226E-11	1.1733	1.2505	38.091	4	186090000	89885000	96201000
K3W4M4	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	Carkd	9	9	9	30.1	30.1	30.1	38.911	365	3.3878E-47	1.5108	1.3801	82.892	8	630730000	269900000	360830000
Q9JHS4	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	Clpx	3	3	3	5.7	5.7	5.7	69.228	634	5.6032E-07	0.61481	0.63702	17.401	2	137120000	90702000	46414000
Q91VR5	ATP-dependent RNA helicase DDX1	Ddx1	3	3	3	5.1	5.1	5.1	82.499	740	2.894E-07	7.0171	6.9562	34.92	2	209090000	42476000	166610000
Q61655	ATP-dependent RNA helicase DDX19A	Ddx19a	3	3	3	7.1	7.1	7.1	53.932	478	1.0233E-12	0.3469	0.32656	71.698	3	102150000	77216000	24931000
Q62167	ATP-dependent RNA helicase DDX3X	Ddx3x	4	3	2	8.2	6.5	5.1	73.101	662	2.2455E-14	5.9483	5.9748	65.629	3	255830000	29603000	226230000
Q80YD1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	Supv3l1	5	5	5	8.6	8.6	8.6	87.004	779	2.5994E-08	0.69179	0.61941	100.98	4	108720000	64382000	44335000
Q91YN9	BAG family molecular chaperone regulator 2	Bag2	5	5	5	31.9	31.9	31.9	23.473	210	7.2877E-13	0.92432	0.90331	15.501	6	287950000	154430000	133510000
Q9JLV1	BAG family molecular chaperone regulator 3	Bag3	15	15	15	41.9	41.9	41.9	61.859	577	1.041E-255	0.7747	0.78204	73.823	22	2426100000	1436800000	989270000
Q8CI32	BAG family molecular chaperone regulator 5	Bag5	2	2	2	9.6	9.6	9.6	50.942	447	1.996E-23	2.0747	2.5354	35.442	2	76880000	30962000	45919000
O70318	Band 4.1-like protein 2	Epb41l2	10	10	10	14.8	14.8	14.8	109.94	988	1.6917E-37	1.0061	0.87469	39.984	9	420590000	244240000	176350000
Q9R069	Basal cell adhesion molecule	Bcam	4	4	4	9.5	9.5	9.5	67.669	622	2.345E-125	1.0443	1.5651	105.59	5	639350000	296090000	343260000
E9PZ16	Basement membrane-specific heparan sulfate proteoglycan core protein	Hspg2	49	49	49	21.3	21.3	21.3	469.78	4383	0	2.5367	2.8517	51.237	60	7028100000	2012100000	5016000000
Q91VK1	Basic leucine zipper and W2 domain-containing protein 2	Bzw2	3	3	2	6.9	6.9	5.3	48.063	419	5.3652E-06	1.0119	2.5906	11.27	2	243740000	115190000	128560000
P18572	Basigin	Bsg	5	5	5	15.9	15.9	15.9	42.444	389	4.1173E-73	0.82491	1.1825	56.541	6	343970000	193590000	150380000
Q921K9	B-cell CLL/lymphoma 7 protein family member B	Bcl7b	1	1	1	11.9	11.9	11.9	22.238	202	1.2236E-48	0.6664	0.48875	5.2768	2	27995000	17579000	10417000
P59017	Bcl-2-like protein 13	Bcl2l13	6	6	6	20.7	20.7	20.7	46.719	434	1.5072E-28	1.2225	1.3462	38.056	12	512760000	223400000	289350000
Q01339	Beta-2-glycoprotein 1	Apoh	6	6	6	23.5	23.5	23.5	38.618	345	8.0907E-18	0.66932	0.78381	31.27	7	410600000	302890000	107710000
P21550	Beta-enolase	Eno3	19	19	15	51.2	51.2	40.8	47.024	434	0	0.54241	0.54641	94.645	47	7833600000	4518200000	3315400000
P23780	Beta-galactosidase	Glb1	3	3	3	7	7	7	73.12	647	5.5999E-06	3.3812	5.1285	37.397	2	107910000	25228000	82684000
P12265	Beta-glucuronidase	Gusb	3	3	3	7.7	7.7	7.7	74.194	648	1.9756E-06	7.7937	7.9299	31.547	4	215150000	30385000	184760000
Q99KR3	Beta-lactamase-like protein 2	Lactb2	3	3	3	12.8	12.8	12.8	32.754	288	3.091E-12	0.70612	0.68473	35.109	5	232910000	136200000	96713000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9ES46	Beta-parvin	Parvb	3	3	3	14	14	14	41.669	365	1.6646E-30	1.4288	1.5257	13.597	4	137570000	62895000	74680000
P82349	Beta-sarcoglycan	Sgcb	4	4	4	21.9	21.9	21.9	34.872	320	1.1531E-16	1.4721	1.6152	16.335	5	206950000	84148000	122800000
Q8VBT1	Beta-taxilin	Txlnb	12	12	12	32.1	32.1	32.1	77.206	685	1.438E-263	0.80462	0.98052	46.168	12	1763300000	1031300000	732020000
Q9DBL7	Bifunctional coenzyme A synthase	Coasy	2	2	2	6.7	6.7	6.7	62.022	563	1.5928E-19	2.2293	1.6229	70.199	2	87235000	27830000	59405000
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	Eprs	19	19	19	19.2	19.2	19.2	170.08	1512	0	2.6138	2.5469	72.428	22	1352900000	389660000	963240000
Q9EQQ9	Bifunctional protein NCOAT	Mgea5	5	5	5	7.6	7.6	7.6	103.16	916	4.3254E-14	1.7125	1.4006	78.624	5	279040000	73754000	205290000
Q9CWJ9	Bifunctional purine biosynthesis protein PURH	Atic	12	12	12	32.4	32.4	32.4	64.217	592	1.085E-180	0.9796	1.1062	63.431	15	1275500000	630230000	645310000
P28653	Biglycan	Bgn	2	2	2	9.5	9.5	9.5	41.639	369	7.3598E-46	3.51	3.0554	49.064	2	54466000	11781000	42685000
Q9CY64	Biliverdin reductase A	Blvra	6	6	6	26.8	26.8	26.8	33.524	295	3.6576E-79	1.0285	1.2242	83.863	7	868190000	386470000	481720000
Q5SQY2	Biorientation of chromosomes in cell division protein 1	Bod1	1	1	1	4	4	4	18.363	173	0.0037835	0.43872	0.46121	113.57	2	73553000	36053000	37500000
P56380	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	Nudt2	7	7	7	63.3	63.3	63.3	16.989	147	1.4756E-47	0.83946	0.79499	30.376	7	578730000	323300000	255430000
P15327	Bisphosphoglycerate mutase	Bpgm	7	7	7	30.1	30.1	30.1	29.978	259	1.978E-118	1.386	1.6274	59.924	14	2082700000	802470000	1280300000
Q8R016	Bleomycin hydrolase	Blmh	3	3	3	9.9	9.9	9.9	52.511	455	4.0419E-08	0.95651	1.0157	87.808	6	269710000	144630000	125080000
Q9ES83	Blood vessel epicardial substance	Bves	2	2	2	11.2	11.2	11.2	41.015	358	8.4244E-08	0.29268	0.33992	140.31	2	130430000	79265000	51163000
Q9D8S9	BolA-like protein 1	Bola1	4	4	4	39.4	39.4	39.4	14.379	137	7.4114E-22	0.80791	0.76463	12.406	3	452090000	276130000	175960000
Q8BGS2	BolA-like protein 2	Bola2	5	5	5	51.2	51.2	51.2	10.214	86	7.575E-18	0.64848	0.94724	47.175	6	411060000	240350000	170710000
E9PX89	BolA-like protein 3	Bola3	3	3	3	17.6	17.6	17.6	15.231	136	3.8753E-80	0.44983	0.76199	123.46	6	1222600000	841430000	381130000
Q9D023	Brain protein 44	Brp44	5	5	5	28.3	28.3	28.3	14.286	127	2.6171E-08	1.2174	1.5349	42.702	6	1438900000	638920000	800020000
O35855	Branched-chain-amino-acid aminotransferase, mitochondrial	Bcat2	16	16	16	40.5	40.5	40.5	44.127	393	0	2.2506	2.2205	69.458	22	1.0519E+10	3148000000	7370800000
Q3UI43	BRISC and BRCA1-A complex member 1	Babam1	1	1	1	11.1	11.1	11.1	36.793	333	1.5357E-60	1.1414	1.0664	17.116	3	44783000	21069000	23714000
Q6WVG3	BTB/POZ domain-containing protein KCTD12	Kctd12	5	5	4	19	19	15.6	35.892	327	7.2798E-28	0.72473	0.69308	15.492	5	253230000	142600000	110630000
Q8C7J6	BTB/POZ domain-containing protein KCTD8	Kctd12b	3	2	2	11	7.2	7.2	33.285	292	9.3003E-07	1.3777	1.595	44.152	2	26414000	9777600	16636000
Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	Mthfd1	4	4	4	8.1	8.1	8.1	101.2	935	1.1506E-24	1.5676	2.0944	49.801	4	272270000	129390000	142870000
P08607	C4b-binding protein	C4bpa	2	2	2	8.1	8.1	8.1	51.523	469	1.3747E-15	0.71626	0.7565	5.0551	2	84684000	48310000	36374000
Q80W54	CAAX prenyl protease 1 homolog	Zmpste24	1	1	1	3.4	3.4	3.4	54.734	475	0.00028979	0.71307	0.58377	103.09	2	49410000	27926000	21483000
Q9WTR5	Cadherin-13	Cdh13	6	6	6	12.7	12.7	12.7	78.185	714	1.2403E-63	0.56068	0.53656	23.502	7	716120000	465000000	251120000
P15116	Cadherin-2	Cdh2	5	5	5	11	11	11	99.795	906	3.9191E-16	0.35484	0.2959	91.016	4	735920000	576330000	159590000
Q8BFS6	Calcineurin-like phosphoesterase domain-containing protein 1	Cpped1	5	5	5	20.8	20.8	20.8	35.247	312	7.054E-234	0.56191	0.65172	88.769	6	721500000	476450000	245050000
Q91YS8	Calcium/calmodulin-dependent protein kinase type 1	Camk1	6	6	6	27.5	27.5	27.5	41.624	374	7.5799E-57	0.61099	0.64333	103.84	9	1592500000	949040000	643410000
E9Q1T1	Calcium/calmodulin-dependent protein kinase type II subunit delta	Camk2d	5	5	3	15.4	15.4	9.6	60.004	533	1.3551E-20	2.7139	3.3281	29.237	6	885920000	273800000	612120000
Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1	Slc25a12	14	14	11	29.4	29.4	25.7	74.569	677	3.056E-190	1.2856	1.5271	30.806	15	1922600000	729360000	1193200000
Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	Slc25a13	14	11	11	25.4	21.7	21.7	74.466	676	5.3552E-49	1.0744	1.3835	29.646	18	1722400000	848870000	873490000
Q06138	Calcium-binding protein 39	Cab39	4	4	4	11.7	11.7	11.7	39.842	341	7.2522E-08	1.0373	0.78528	70.953	4	397730000	192990000	204740000
J3QPI4	Calcium-regulated heat stable protein 1	Carhsp1	3	3	3	25.7	25.7	25.7	16.048	148	2.1154E-12	0.38167	0.39306	74.516	4	886340000	686150000	200200000
Q9CXW3	Calcyclin-binding protein	Cacybp	3	3	3	27.9	27.9	27.9	26.51	229	5.5525E-12	1.0971	1.1099	40.992	5	349220000	183570000	165650000
Q3UKW2	Calmodulin	Calm1	3	3	3	16.8	16.8	16.8	21.56	197	4.817E-115	0.67675	0.81342	21.615	4	623020000	392650000	230370000
P35564	Calnexin	Canx	7	7	7	16.2	16.2	16.2	67.277	591	3.6129E-68	1.3795	1.5279	65.298	6	445280000	196370000	248910000
O88456	Calpain small subunit 1	Capns1	4	4	4	32.7	32.7	32.7	28.463	269	1.7067E-69	1.1395	1.4575	25.78	6	513060000	251340000	261710000
O35350	Calpain-1 catalytic subunit	Capn1	10	10	10	17.1	17.1	17.1	82.105	713	3.9847E-26	1.9448	2.1193	48.319	10	298820000	103870000	194950000
O08529	Calpain-2 catalytic subunit	Capn2	12	12	12	23.3	23.3	23.3	79.871	700	3.5194E-77	2.0022	2.2166	70.606	15	1318700000	423100000	895560000
P51125	Calpastatin	Cast	14	14	14	32	32	32	84.921	788	0	0.54817	0.56483	97.397	19	829970000	519440000	310530000
Q08091	Calponin-1	Cnn1	5	5	5	18.5	18.5	18.5	33.355	297	8.3191E-84	0.55527	0.6454	68.445	5	848840000	515640000	333200000
Q9DAW9	Calponin-3	Cnn3	3	3	3	9.7	9.7	9.7	36.428	330	1.4257E-26	0.5695	0.54708	48.765	4	244450000	164030000	80418000
P14211	Calreticulin	Calr	15	15	15	49	49	49	47.994	416	0	0.8627	0.77684	109.99	25	9373900000	4447100000	4926900000
F6QYE1	Calsequestrin-2	Casq2	4	4	4	8.4	8.4	8.4	48.435	418	1.26E-67	5.243	5.5988	48.61	3	840870000	150160000	690710000
O35887	Calumenin	Calu	2	2	2	6.7	6.7	6.7	37.063	315	4.0079E-06	0.75259	1.5318	5.6487	2	104630000	68151000	36477000
Q3UHL1	CaM kinase-like vesicle-associated protein	Camkv	1	1	1	2	2	2	54.819	512	0.019773	0.03288	0.24435	64.91	2	3321800000	3293800000	27984000
P05132	cAMP-dependent protein kinase catalytic subunit alpha	Prkaca	5	5	3	15.1	15.1	12.3	40.57	351	3.704E-15	1.4413	3.224	150.69	6	470050000	192200000	277850000
P63248	cAMP-dependent protein kinase inhibitor alpha	Pkia	2	2	2	50	50	50	7.9604	76	2.5596E-66	0.31367	0.31786	20.55	5	1432500000	1132900000	299600000
Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit	Prkar1a	10	10	10	30.7	30.7	30.7	43.185	381	1.51E-48	0.99446	1.2447	124.26	12	3935300000	1046700000	2888700000
Q8K1M3	cAMP-dependent protein kinase type II-alpha regulatory subunit	Prkar2a	4	4	4	14.7	14.7	14.7	45.589	402	1.651E-213	1.031	1.1651	34.907	8	1066200000	556650000	509580000
F8WIA1	CAP-Gly domain-containing linker protein 1	Clip1	30	30	30	26.1	26.1	26.1	161.23	1437	0	0.57996	0.71431	85.392	37	5214700000	2176900000	3037800000
Q60865	Caprin-1	Caprin1	4	4	4	8.2	8.2	8.2	78.168	707	1.1447E-11	1.2131	1.1474	38.965	5	537860000	254430000	283430000
P13634	Carbonic anhydrase 1	Ca1	4	4	4	33.3	33.3	33.3	28.33	261	8.163E-178	1.3707	1.8808	63.331	6	1401400000	622070000	779360000
P00920	Carbonic anhydrase 2	Ca2	6	6	6	42.3	42.3	42.3	29.032	260	4.282E-233	1.163	1.0804	60.341	11	3024100000	1437900000	1586300000
P16015	Carbonic anhydrase 3	Ca3	8	8	8	38.8	38.8	38.8	29.366	260	2.6475E-72	0.36187	0.33761	78.756	17	1993500000	1444500000	548990000
P48758	Carbonyl reductase [NADPH] 1	Cbr1	5	5	5	24.5	24.5	24.5	30.641	277	1.2033E-98	1.1706	1.3551	88.364	8	764320000	298920000	465410000
Q91VT4	Carbonyl reductase family member 4	Cbr4	5	5	5	27.5	27.5	27.5	25.414	236	2.4604E-38	3.4152	3.7705	39.976	7	795680000	206470000	589210000
P23953	Carboxylesterase 1C	Ces1c	10	10	6	22.9	22.9	15.3	61.055	554	2.5185E-67	0.94193	0.88235	48.975	12	6389200000	4163400000	2225800000
Q8VCT4	Carboxylesterase 1D	Ces1d	7	6	6	17.2	15.9	15.9	61.787	565	7.333E-253	0.74439	0.72841	67.557	17	1256000000	696080000	559910000
Q8R1G2	Carboxymethylenebutenolidase homolog	Cmbl	5	5	5	18.4	18.4	18.4	27.902	245	4.811E-12	1.1468	1.3364	68.844	4	358720000	170440000	188280000
Q9DBB9	Carboxypeptidase N subunit 2	Cpn2	4	4	4	8.8	8.8	8.8	60.478	547	4.3049E-12	0.37063	0.46857	12.672	5	341940000	228430000	113510000
Q9WVJ3	Carboxypeptidase Q	Cpq	3	3	3	12.6	12.6	12.6	51.813	470	1.5841E-31	0.39793	0.35039	27.587	10	371130000	265760000	105370000
Q70KF4	Cardiomyopathy-associated protein 5	Cmya5	25	25	3	12.1	12.1	1.8	413.04	3739	9.763E-222	0.58086	0.63855	85.853	24	2837400000	1581300000	1256100000
P47934	Carnitine O-acetyltransferase	Crat	14	14	14	25.9	25.9	25.9	70.839	626	5.788E-187	1.8443	2.0902	95.711	18	5544800000	1887600000	3657200000
Q924X2	Carnitine O-palmitoyltransferase 1, muscle isoform	Cpt1b	8	8	8	11.4	11.4	11.4	88.216	772	3.248E-25	1.5777	1.5597	101.4	10	1522700000	582930000	939740000
P52825	Carnitine O-palmitoyltransferase 2, mitochondrial	Cpt2	11	11	11	22.8	22.8	22.8	73.98	658	4.985E-145	2.4454	2.2817	85.191	20	4986800000	1530900000	3455900000
Q60737	Casein kinase II subunit alpha	Csnk2a1	4	4	4	16.9	16.9	16.9	45.133	391	3.2549E-07	3.1737	3.3667	23.125	3	682680000	277670000	405010000
E9PY58	Caseinolytic peptidase B protein homolog	Clpb	4	4	4	8.1	8.1	8.1	79.509	707	5.9053E-17	2.2563	2.3016	34.007	4	323190000	89795000	233390000
P24270	Catalase	Cat	17	17	17	45	45	45	59.795	527	1.363E-217	1.4081	1.5482	83.858	28	6482200000	1969500000	4512700000
P26231	Catenin alpha-1	Ctnna1	6	6	6	9.5	9.5	9.5	100.11	906	1.463E-298	0.92442	1.0539	47.118	6	364690000	207880000	156810000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P10605	Cathepsin B	Ctsb	5	5	5	15.6	15.6	15.6	37.279	339	1.998E-223	1.6939	2.729	109.86	6	808510000	269630000	538870000
P18242	Cathepsin D	Ctsd	7	7	7	20.7	20.7	20.7	44.953	410	3.3639E-46	2.3128	2.1689	130.23	9	2485900000	548670000	1937200000
F6WR04	Cathepsin S	Ctss	1	1	1	3.8	3.8	3.8	38.63	341	0.0048682	0.89208	1.5199	44.14	2	27335000	15841000	11494000
Q9WUU7	Cathepsin Z	Ctsz	4	4	4	17.3	17.3	17.3	33.996	306	2.4092E-46	2.9574	2.8469	93.982	5	612280000	158790000	453490000
Q07113	Cation-independent mannose-6-phosphate receptor	Igf2r	2	2	2	0.8	0.8	0.8	273.81	2483	0.00064932	1.3276	1.6014	51.566	2	89668000	38399000	51269000
P49817	Caveolin-1	Cav1	2	2	2	19.7	19.7	19.7	20.538	178	1.4442E-80	1.305	1.5145	25.104	6	516310000	213600000	302710000
Q8K1J6	CCA tRNA nucleotidyltransferase 1, mitochondrial	Trnt1	3	3	3	9.9	9.9	9.9	49.895	434	5.9961E-05	0.55892	0.47635	89.552	3	354150000	179160000	174990000
Q9JLQ0	CD2-associated protein	Cd2ap	3	3	3	6.3	6.3	6.3	70.449	637	8.9506E-07	0.37205	0.44452	40.887	3	280460000	194040000	86418000
P35762	CD81 antigen	Cd81	2	2	2	19.1	19.1	19.1	25.814	236	1.0284E-27	1.6546	1.7208	5.4274	3	362240000	135640000	226610000
Q8CJ53	Cdc42-interacting protein 4	Trip10	4	4	4	7	7	7	68.489	603	2.8697E-09	1.4279	1.4115	70	4	177260000	77324000	99932000
Q91WS0	CDGSH iron-sulfur domain-containing protein 1	Cisd1	3	3	3	23.1	23.1	23.1	12.097	108	1.317E-82	0.96959	3.6515	132.78	4	1341400000	786320000	555040000
P53996	Cellular nucleic acid-binding protein	Cnbp	2	2	2	15.2	15.2	15.2	19.592	178	2.0927E-34	0.75155	0.68751	4.6035	2	45958000	29480000	16478000
E9PZD8	Ceruloplasmin	Cp	18	18	18	25.6	25.6	25.6	124.21	1086	0	0.69531	0.86139	62.706	22	2135800000	1239700000	896060000
P0C605	cGMP-dependent protein kinase 1	Prkg1	5	5	5	7	7	7	76.35	671	3.5602E-09	1.4247	2.4624	91.934	5	124310000	59978000	64336000
Q60936	Chaperone activity of bc1 complex-like, mitochondrial	Adck3	6	6	6	12.6	12.6	12.6	71.742	645	1.5858E-85	3.5288	3.1169	91.809	7	599670000	167900000	431770000
Q99LU0	Charged multivesicular body protein 1b-1	Chmp1b1	2	2	1	8.5	8.5	4	22.124	199	0.00025364	0.41369	0.48718	87.067	3	239890000	167790000	72097000
Q9D8B3	Charged multivesicular body protein 4b	Chmp4b	2	2	2	17	17	17	24.936	224	6.4099E-09	1.8408	2.863	268.41	2	545150000	60939000	484210000
Q9D7S9	Charged multivesicular body protein 5	Chmp5	3	3	3	18.7	18.7	18.7	24.575	219	0.00011222	1.1168	1.3083	38.548	2	45337000	22225000	23112000
Q9Z1Q5	Chloride intracellular channel protein 1	Clic1	3	3	3	13.7	13.7	13.7	27.013	241	3.8268E-25	0.73003	1.7533	150.58	2	190890000	109920000	80967000
Q9QYB1	Chloride intracellular channel protein 4	Clic4	11	11	11	50.2	50.2	50.2	28.729	253	8.944E-256	0.7921	0.99859	70.105	19	2007300000	1079100000	928160000
Q8BXK9	Chloride intracellular channel protein 5	Clic5	2	2	2	11.6	11.6	11.6	28.287	251	1.3057E-08	0.98904	0.99658	44.398	2	167060000	99680000	67381000
O55229	Choline/ethanolamine kinase	Chkb	2	2	2	7.4	7.4	7.4	45.126	394	0.00001703	1.3052	1.5134	51.358	2	78157000	32933000	45224000
Q8VHY0	Chondroitin sulfate proteoglycan 4	Cspg4	4	4	4	2.8	2.8	2.8	252.31	2327	2.961E-11	0.75445	0.72599	33.043	3	246920000	147670000	99254000
Q8R4N0	Citrate lyase subunit beta-like protein, mitochondrial	Clybl	14	14	14	40.2	40.2	40.2	37.548	338	1.404E-103	0.87671	1.0028	125.56	19	2574600000	1339500000	1235100000
Q9CZU6	Citrate synthase, mitochondrial	Cs	15	15	8	30	30	17	51.736	464	4.601E-190	1.5265	1.7546	87.471	60	2.1657E+10	8594300000	1.3062E+10
Q58A65	C-Jun-amino-terminal kinase-interacting protein 4	Spag9	10	10	9	11.3	11.3	10.7	146.22	1321	1.0926E-42	0.91766	1.0331	15.187	8	532290000	277420000	254870000
Q5SXR6	Clathrin heavy chain 1	Cltc	22	22	22	15.8	15.8	15.8	191.98	1679	0	3.9093	4.4459	102.57	30	6978600000	1827400000	5151200000
Q5SUH6	Clathrin interactor 1	Clint1	2	2	2	4.2	4.2	4.2	69.758	641	7.6558E-16	0.44146	0.48057	79.92	2	186360000	113040000	73315000
Q6IRU5	Clathrin light chain B	Cltb	4	4	4	17.9	17.9	17.9	25.171	229	6.1884E-15	0.94877	1.1405	106.84	5	533530000	204570000	328960000
E9QKH0	CLIP-associating protein 1	Clasp1	3	3	3	3.5	3.5	3.5	169.31	1536	7.1167E-30	1.3086	1.338	70.684	3	251420000	96873000	154540000
Q06890	Clusterin	Clu	5	5	5	16.5	16.5	16.5	51.655	448	2.651E-153	0.71457	0.74616	39.55	13	2456900000	1436800000	1020100000
Q1ERP8	CMRF35-like molecule 9	Cd300lg	2	2	2	6.6	6.6	6.6	36.756	331	1.813E-50	8.0598	7.8505	341.77	2	1008400000	83349000	925000000
Q9CQI6	Coactosin-like protein	Cotl1	4	4	4	30.3	30.3	30.3	15.944	142	6.7194E-28	1.0129	1.1034	34.365	4	944390000	647950000	296440000
Q9JIF7	Coatomer subunit beta	Copb1	2	2	2	5	5	5	107.06	953	4.1619E-24	2.8186	2.7184	10.441	2	59641000	9545800	50096000
Q5XJY5	Coatomer subunit delta	Arcn1	4	4	4	8.6	8.6	8.6	57.229	511	5.5261E-10	1.6811	1.7695	138.18	4	449130000	71729000	377400000
O89079	Coatomer subunit epsilon	Cope	3	3	3	13.6	13.6	13.6	34.567	308	8.4864E-09	1.8688	2.0873	2.402	2	138010000	49233000	88778000
Q9D273	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	Mmab	5	5	5	29.1	29.1	29.1	26.273	237	9.4706E-78	0.71909	0.6964	19.58	7	432950000	252980000	179970000
F8WGL3	Cofilin-1	Cfl1	6	6	6	36.6	36.6	36.6	24.576	227	3.247E-115	0.65504	0.69961	53.273	17	7087200000	4218700000	2868500000
P45591	Cofilin-2	Cfl2	4	4	4	34.3	34.3	34.3	18.709	166	8.6858E-33	0.94549	0.98533	30.512	8	1790400000	969430000	821010000
Q78PG9	Coiled-coil domain-containing protein 25	Ccdc25	3	3	3	15.9	15.9	15.9	24.48	208	1.5308E-05	0.40539	0.41892	69.862	2	196370000	128830000	67546000
Q8R3Q6	Coiled-coil domain-containing protein 58	Ccdc58	3	3	3	27.8	27.8	27.8	16.665	144	3.7292E-18	0.51185	0.77266	74.525	4	1105200000	746640000	358540000
Q8C3X2	Coiled-coil domain-containing protein 90B, mitochondrial	Ccdc90b	2	2	2	7	7	7	29.596	256	0.0017898	0.52302	0.68031	16.748	3	180310000	119320000	60994000
B2RPU8	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	2410018M08Rik	3	3	3	6.2	6.2	6.2	84.266	756	4.4362E-28	0.39633	0.4357	43.985	8	4624700000	3367900000	1256800000
Q9CRB9	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	Chchd3	3	3	3	22.9	22.9	22.9	26.334	227	2.333E-49	0.98373	5.8617	117.78	3	536870000	165720000	371150000
Q8BT51	Coiled-coil-helix-coiled-coil-helix domain-containing protein 8	Chchd8	1	1	1	11.5	11.5	11.5	10.135	87	5.1947E-05	0.95677	0.98335	57.055	2	33285000	17985000	15300000
Q91YQ3	Cold shock domain-containing protein C2	Csdc2	1	1	1	7.1	7.1	7.1	16.853	154	0.0032072	0.30452	0.30945	2.4206	2	76971000	58476000	18496000
Q91W50	Cold shock domain-containing protein E1	Csde1	9	9	9	13	13	13	88.79	798	7.9171E-22	0.63857	0.66439	60.628	9	406370000	244890000	161490000
P02463	Collagen alpha-1(IV) chain	Col4a1	2	2	2	1.7	1.7	1.7	160.68	1669	2.5975E-07	0.91782	0.95205	56.933	2	31144000	16645000	14499000
Q04857	Collagen alpha-1(VI) chain	Col6a1	3	3	3	3.7	3.7	3.7	108.49	1025	6.9234E-10	1.001	0.98073	57.419	3	321800000	169100000	152700000
O35206	Collagen alpha-1(XV) chain	Col15a1	7	7	7	6.4	6.4	6.4	140.47	1367	6.3197E-78	1.0742	1.0302	30.638	11	966370000	461700000	504680000
P08122	Collagen alpha-2(IV) chain	Col4a2	1	1	1	0.9	0.9	0.9	167.32	1707	6.0745E-05	0.85832	1.1342	7.4238	2	213830000	119280000	94558000
E9Q6A6	Collagen alpha-6(VI) chain	Col6a6	4	4	4	2.2	2.2	2.2	246.42	2265	4.6353E-17	0.88616	1.0197	69.954	6	158560000	71194000	87365000
E9Q6C2	Complement C1s-A subcomponent	C1s	2	2	2	3.2	3.2	3.2	77.499	694	1.3149E-11	0.96713	0.91699	22.486	2	22201000	11599000	10602000
P01027	Complement C3	C3	32	32	32	23.4	23.4	23.4	186.48	1663	1.673E-139	1.4624	2.1081	79.66	36	5340200000	2187100000	3153100000
P01029	Complement C4-B	C4b	8	8	8	8.1	8.1	8.1	192.91	1738	1.1901E-22	0.7338	0.78004	74.974	9	449130000	272270000	176860000
P06684	Complement C5	C5	1	1	1	0.8	0.8	0.8	188.88	1680	0.0022659	2.3953	5.0331	7.4029	2	20793000	6385500	14408000
Q8R5L1	Complement component 1 Q subcomponent-binding protein, mitochondrial	C1qbp	5	5	5	22.6	22.6	22.6	31.025	279	7.505E-136	0.58654	0.63269	69.815	12	1138000000	689950000	448040000
O89103	Complement component C1q receptor	Cd93	6	6	6	12.6	12.6	12.6	69.354	644	3.5302E-15	0.72591	0.63205	48.007	5	426490000	232100000	194400000
Q8K182	Complement component C8 alpha chain	C8a	2	2	2	5.1	5.1	5.1	66.08	587	6.1056E-07	1.3386	1.4197	58.707	2	112300000	49643000	62659000
Q8BH35	Complement component C8 beta chain	C8b	3	3	3	7.6	7.6	7.6	66.229	589	3.8407E-21	0.74667	0.82735	14.385	2	289950000	156850000	133100000
Q8VCG4	Complement component C8 gamma chain	C8g	2	2	2	17.3	17.3	17.3	22.508	202	1.8667E-07	0.95639	0.94423	7.8702	2	122850000	63314000	59541000
P06683	Complement component C9	C9	4	4	4	9.9	9.9	9.9	62.002	548	2.2168E-11	1.0942	1.0205	17.812	3	155360000	67866000	87494000
B8JJN0	Complement factor B	Gm20547	10	10	9	9.6	9.6	8.5	142.32	1276	8.18E-130	0.6831	0.7626	81.225	11	742300000	460310000	281990000
P03953	Complement factor D	Cfd	1	1	1	8.1	8.1	8.1	28.057	259	4.9175E-05	0.74204	0.76176	15.605	2	204460000	123390000	81072000
E9Q8I0	Complement factor H	Cfh	7	7	7	7.3	7.3	7.3	141.27	1252	1.291E-103	1.066	1.2441	102.75	7	1090900000	574890000	516010000
Q61129	Complement factor I	Cfi	5	5	5	9.6	9.6	9.6	67.26	603	5.1487E-08	0.63397	1.1387	95.536	4	191170000	112650000	78527000
G3UXW9	COP9 signalosome complex subunit 1	Gps1	3	3	3	7.6	7.6	7.6	58.86	526	1.2088E-10	1.0102	0.95757	67.497	2	22800000	10209000	12591000
P61202	COP9 signalosome complex subunit 2	Cops2	9	9	9	21.7	21.7	21.7	51.596	443	3.9366E-30	0.90776	1.0206	55.806	10	1173500000	591890000	581580000
O88543	COP9 signalosome complex subunit 3	Cops3	4	4	4	18.7	18.7	18.7	47.832	423	1.2698E-74	1.6361	1.404	10.128	5	244550000	98951000	145600000
O88544	COP9 signalosome complex subunit 4	Cops4	10	10	10	33.5	33.5	33.5	46.284	406	1.3214E-43	0.70689	1.1801	101.34	9	996290000	556490000	439810000
O35864	COP9 signalosome complex subunit 5	Cops5	3	3	3	12.3	12.3	12.3	37.548	334	2.2637E-57	0.89808	1.1125	27.929	3	391180000	231700000	159480000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O88545	COP9 signalosome complex subunit 6	Cops6	4	4	4	16.4	16.4	16.4	35.88	324	2.4268E-40	0.8903	1.3484	73.055	7	407030000	200180000	206850000
Q9CZ04	COP9 signalosome complex subunit 7a	Cops7a	5	5	5	24	24	24	30.224	275	6.135E-173	0.52749	0.64299	68.208	6	522200000	333490000	188710000
Q8VBV7	COP9 signalosome complex subunit 8	Cops8	4	4	4	30.1	30.1	30.1	23.255	209	1.123E-61	0.84601	0.88027	26.74	5	329400000	190960000	138440000
Q8C166	Copine-1	Cpne1	2	2	2	4.5	4.5	4.5	58.886	536	9.3361E-05	0.98276	0.98341	18.48	2	123800000	62191000	61610000
Q8BT60	Copine-3	Cpne3	5	5	5	11.6	11.6	11.6	59.584	533	5.0581E-79	0.8909	1.2746	76.784	4	344870000	178570000	166300000
Q9D8X1	Copper homeostasis protein cutC homolog	Cutc	2	2	2	12.1	12.1	12.1	29.003	272	2.9792E-09	0.92947	1.0123	58.644	2	122750000	72353000	50401000
O08997	Copper transport protein ATOX1	Atox1	3	3	3	47.1	47.1	47.1	7.3384	68	9.105E-144	0.5514	0.61	43.609	8	1264300000	822950000	441320000
P36552	Coproporphyrinogen-III oxidase, mitochondrial	Cpox	8	8	8	24.2	24.2	24.2	49.714	443	3.5742E-46	1.4601	2.2288	117.4	9	1342600000	820690000	521940000
Q3UMF0	Cordon-bleu protein-like 1	Cobll1	13	13	10	18.3	18.3	14.4	137.38	1273	1.572E-153	0.54946	0.66392	78.581	8	453140000	290960000	162180000
O89053	Coronin-1A	Coro1a	2	2	2	5	5	5	50.989	461	2.2685E-05	1.2276	1.2398	2.8465	2	21989000	9751800	12237000
Q9WUM3	Coronin-1B	Coro1b	3	3	3	14.3	14.3	14.3	53.912	484	5.4337E-41	2.1013	1.7516	42.395	5	130690000	43302000	87392000
Q9WUM4	Coronin-1C	Coro1c	3	3	3	8.9	8.9	8.9	53.12	474	3.1801E-27	3.1789	3.4207	5.5366	2	190960000	46959000	144000000
E9QMV2	Costars family protein ABRACL	3110003A17Rik	2	2	2	27.2	27.2	27.2	9.0583	81	2.6961E-06	0.51289	0.85702	144.23	3	398140000	126060000	272080000
Q04447	Creatine kinase B-type	Ckb	8	8	8	39.6	39.6	39.6	42.713	381	3.9155E-88	0.65538	1.1664	77.605	8	2441100000	1083600000	1357400000
P07310	Creatine kinase M-type	Ckm	28	28	28	63.8	63.8	63.8	43.044	381	0	0.63242	0.64469	100.43	126	1.6523E+11	1.0119E+11	6.4046E+10
Q6P8J7	Creatine kinase S-type, mitochondrial	Ckmt2	20	20	17	49.6	49.6	42	47.473	419	0	2.0554	2.1584	76.583	136	7.1103E+10	2.5823E+10	4.5279E+10
P47941	Crk-like protein	Crkl	5	5	5	22.1	22.1	22.1	33.83	303	3.4867E-16	0.76704	0.98421	68.783	8	1828900000	472840000	1356100000
O88712	C-terminal-binding protein 1	Ctbp1	4	4	4	15.2	15.2	15.2	47.744	441	2.262E-213	0.9328	1.0309	24.33	4	857510000	445590000	411920000
Q9Z0H4	CUGBP Elav-like family member 2	Celf2	3	3	2	8.3	8.3	6.3	54.27	508	1.2402E-14	1.1759	1.1568	25.766	6	578490000	310770000	267720000
Q9WTX6	Cullin-1	Cul1	3	3	3	4.8	4.8	4.8	89.69	776	3.2453E-08	2.7596	2.8198	7.8698	2	30066000	6436600	23629000
Q9JLV5	Cullin-3	Cul3	3	3	3	6.5	6.5	6.5	88.947	768	6.7057E-06	1.1707	1.5233	51.596	2	29214000	12706000	16509000
Q3TCH7	Cullin-4A	Cul4a	4	4	4	6.5	6.5	6.5	87.752	759	1.9133E-34	0.89107	1.0158	123.85	3	105270000	50704000	54565000
G3X914	Cullin-5	Cul5	2	2	2	2.7	2.7	2.7	99.04	855	6.985E-06	1.9742	2.0213	13.996	2	149210000	68666000	80547000
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	Cand1	11	11	11	11.5	11.5	11.5	136.33	1230	2.529E-106	2.0097	2.2131	56.466	8	974560000	290730000	683830000
Q6ZQ73	Cullin-associated NEDD8-dissociated protein 2	Cand2	4	4	4	4.4	4.4	4.4	135.63	1235	1.5221E-14	1.538	2.0569	41.634	2	63409000	19663000	43746000
Q64261	Cyclin-dependent kinase 6	Cdk6	2	2	2	7.4	7.4	7.4	37.028	326	0.00046041	0.80723	1.0357	81.71	2	42409000	21438000	20971000
Q62426	Cystatin-B	Cstb	2	2	2	30.6	30.6	30.6	11.045	98	4.6874E-46	0.77371	0.80402	19.406	4	2213000000	1307500000	905480000
P97315	Cysteine and glycine-rich protein 1	Csrp1	2	2	2	20.2	20.2	20.2	20.583	193	2.407E-123	1.2577	1.4515	23.901	4	1176600000	528360000	648190000
P50462	Cysteine and glycine-rich protein 3	Csrp3	12	12	12	60.3	60.3	60.3	20.895	194	0	1.2931	1.4578	65.505	28	4777600000	1743400000	3034200000
Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	Chordc1	2	2	2	9.4	9.4	9.4	37.35	331	3.6954E-39	1.1453	1.1794	7.2872	2	100910000	50247000	50667000
Q9Z1J3	Cysteine desulfurase, mitochondrial	Nfs1	8	8	8	26.8	26.8	26.8	50.569	459	2.1115E-32	2.5823	2.4638	86.19	7	1516100000	551140000	964970000
Q9DCT8	Cysteine-rich protein 2	Crip2	3	3	3	33.7	33.7	33.7	22.727	208	3.63E-144	0.66096	0.22808	48.263	4	1407500000	690120000	717390000
Q9ER72	Cysteine--tRNA ligase, cytoplasmic	Cars	3	3	3	3.7	3.7	3.7	94.859	831	0.0001098	0.77258	0.6882	81.923	3	226700000	152620000	74083000
P56395	Cytochrome b5	Cyb5a	3	3	3	32.1	32.1	32.1	15.241	134	7.762E-203	1.0884	1.1932	56.227	6	917150000	483350000	433800000
Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	Uqcrc1	12	12	12	34	34	34	52.851	480	0	0.97895	1.082	75.21	29	2.0302E+10	1.0351E+10	9950900000
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	Uqcrc2	17	17	17	40.4	40.4	40.4	48.234	453	0	1.1148	1.2748	103.15	29	9632800000	4286300000	5346500000
P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	Uqcrh	5	5	5	61.8	61.8	61.8	10.435	89	0	0.53931	0.61306	33.2	24	2831700000	1831000000	1000800000
Q9CQB4	Cytochrome b-c1 complex subunit 7	Uqcrb	8	8	8	51.4	51.4	51.4	13.561	111	8.5488E-87	0.7648	0.76442	55.724	12	1.2479E+10	7506100000	4973300000
Q9CQ69	Cytochrome b-c1 complex subunit 8	Uqcrq	3	3	3	36.6	36.6	36.6	9.7681	82	1.0593E-06	2.9572	12.411	107.78	2	1177100000	365910000	811180000
Q8R1I1	Cytochrome b-c1 complex subunit 9	Uqcr10	1	1	1	26.6	26.6	26.6	7.4454	64	2.897E-129	1.5377	1.6997	20.736	3	4198000000	1522500000	2675500000
Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochondrial	Uqcrfs1	10	10	10	40.1	40.1	40.1	29.367	274	8.069E-191	0.61152	0.61387	88.987	24	5142500000	3051200000	2091300000
P00397	Cytochrome c oxidase subunit 1	Mtco1	1	1	1	6.2	6.2	6.2	56.861	514	2.933E-137	1.5791	1.6776	10.981	3	409830000	155960000	253870000
P00405	Cytochrome c oxidase subunit 2	Mtco2	5	5	5	40.5	40.5	40.5	25.976	227	0	1.1715	1.3535	77.344	18	6664200000	3594500000	3069700000
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	Cox4i1	7	7	7	47.9	47.9	47.9	19.53	169	2.132E-103	0.88962	0.84764	70.309	25	1.2273E+10	6576300000	5696600000
P12787	Cytochrome c oxidase subunit 5A, mitochondrial	Cox5a	6	6	6	32.2	32.2	32.2	16.101	146	1.968E-150	0.47544	0.49159	32.295	27	1.5055E+10	9616900000	5437700000
Q9D881	Cytochrome c oxidase subunit 5B, mitochondrial	Cox5b	5	5	5	38.8	38.8	38.8	13.847	129	5.634E-205	0.44471	0.7265	68.375	7	843090000	580870000	262220000
P56391	Cytochrome c oxidase subunit 6B1	Cox6b1	5	5	5	54.7	54.7	54.7	10.071	86	2.667E-124	0.54779	0.59338	68.962	54	1.516E+10	1.0568E+10	4591200000
Q9CPQ1	Cytochrome c oxidase subunit 6C	Cox6c	2	2	2	19.7	19.7	19.7	8.4689	76	1.5678E-11	1.8374	1.7919	76.325	6	5013500000	1860200000	3153300000
P56392	Cytochrome c oxidase subunit 7A1, mitochondrial	Cox7a1	2	2	2	28.8	28.8	28.8	8.9863	80	2.5508E-05	0.60734	0.68182	12.903	3	521800000	299820000	221980000
P48771	Cytochrome c oxidase subunit 7A2, mitochondrial	Cox7a2	2	2	2	27.7	27.7	27.7	9.2908	83	6.1302E-10	0.75305	2.4424	299.05	3	1070600000	656730000	413840000
P62897	Cytochrome c, somatic	Cycs	11	11	8	76.2	76.2	45.7	11.605	105	0	0.56267	0.71359	80.191	65	4.2722E+10	2.674E+10	1.5982E+10
Q9D0M3	Cytochrome c1, heme protein, mitochondrial	Cyc1	6	6	6	25.8	25.8	25.8	35.327	325	0	1.236	1.5213	48.495	9	2635100000	1218400000	1416700000
Q9CX80	Cytoglobin	Cygb	4	4	4	26.8	26.8	26.8	21.465	190	1.3176E-10	1.0758	1.7076	47.965	3	404780000	229170000	175600000
A2A517	Cytohesin-1	Cyth1	3	3	3	5	5	5	52.492	460	4.7484E-06	0.60159	0.72468	10.535	2	101820000	57459000	44360000
P28271	Cytoplasmic aconitate hydratase	Aco1	13	13	13	18.6	18.6	18.6	98.124	889	1.1964E-40	1.5887	1.91	80.541	14	2031900000	891800000	1140100000
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	Dync1h1	21	21	21	7.3	7.3	7.3	532.04	4644	3.425E-236	2.9477	3.0395	83.145	18	1414300000	436660000	977600000
A2BFF9	Cytoplasmic dynein 1 intermediate chain 2	Dync1i2	7	7	7	17.2	17.2	17.2	71.424	638	2.222E-75	1.0356	1.1912	28.405	7	683620000	383300000	300320000
Q8R1Q8	Cytoplasmic dynein 1 light intermediate chain 1	Dync1li1	5	5	4	12.4	12.4	9.9	56.614	523	2.6209E-42	0.84973	0.90754	12.508	3	304160000	170090000	134070000
Q99M51	Cytoplasmic protein NCK1	Nck1	5	5	5	15.9	15.9	15.9	42.89	377	1.326E-07	0.89021	0.89524	65.053	5	269880000	137000000	132880000
A2AGT5	Cytoskeleton-associated protein 5	Ckap5	4	4	4	2.4	2.4	2.4	225.63	2032	1.2012E-08	1.3656	1.67	43.735	3	98795000	54664000	44132000
Q9CPY7	Cytosol aminopeptidase	Lap3	13	13	13	31.6	31.6	31.6	56.141	519	1.203E-209	1.4619	1.5152	76.801	17	704010000	332520000	371490000
A3KFX0	Cytosolic 5-nucleotidase 1A	Nt5c1a	4	4	4	12.3	12.3	12.3	40.678	365	2.0793E-06	1.2145	1.2472	33.281	2	95661000	41539000	54122000
Q9D020	Cytosolic 5-nucleotidase 3	Nt5c3	11	11	11	35.3	35.3	35.3	37.252	331	3.8322E-89	0.5365	1.024	117.34	16	1731600000	1147600000	584020000
E9PYH2	Cytosolic acyl coenzyme A thioester hydrolase	Acot7	3	3	3	11.5	11.5	11.5	42.826	384	8.8173E-08	0.72318	0.64224	25.398	3	170960000	97579000	73376000
Q9D1A2	Cytosolic non-specific dipeptidase	Cndp2	12	12	12	32.8	32.8	32.8	52.767	475	2.072E-159	1.1945	1.2668	53.691	12	1535000000	729130000	805870000
E9Q9M1	Cytosolic purine 5-nucleotidase	Nt5c2	4	4	4	10.1	10.1	10.1	67.703	586	8.7601E-14	1.3962	1.3918	87.407	7	287520000	126490000	161040000
Q3UGB5	DAZ-associated protein 1	Dazap1	2	2	2	7.6	7.6	7.6	43.157	406	1.446E-12	0.61708	0.66504	80.485	4	69912000	38142000	31770000
Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	Bdh1	6	6	6	23.6	23.6	23.6	38.299	343	8.2339E-86	1.3644	1.3447	59.118	7	622040000	248000000	374040000
Q8BZJ7	DCN1-like protein 2	Dcun1d2	2	2	2	10	10	10	30.068	259	2.5364E-08	1.1378	1.4044	26.525	3	283800000	141840000	141960000
Q9QY93	dCTP pyrophosphatase 1	Dctpp1	2	2	2	12.4	12.4	12.4	18.795	170	4.9091E-06	0.44298	0.4763	26.57	2	127700000	88995000	38702000
O35215	D-dopachrome decarboxylase	Ddt	6	6	6	71.2	71.2	71.2	13.077	118	3.449E-192	0.61595	0.60988	51.469	22	3502000000	1954700000	1547300000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P28654	Decorin	Dcn	4	4	4	12.1	12.1	12.1	39.809	354	9.4899E-17	2.3819	5.0564	56.666	2	803300000	207380000	595920000
Q3U0B3	Dehydrogenase/reductase SDR family member 11	Dhrs11	4	4	4	21.2	21.2	21.2	28.274	260	8.8568E-09	1.6641	3.5729	61.29	3	422340000	159820000	262530000
Q99LB2	Dehydrogenase/reductase SDR family member 4	Dhrs4	5	5	5	20.8	20.8	20.8	29.884	279	1.184E-285	1.4268	1.5572	147.78	12	5906100000	3272200000	2633900000
O35459	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Ech1	16	16	16	51.7	51.7	51.7	36.118	327	0	0.62628	0.66165	75.057	67	1.2588E+10	7444200000	5143300000
Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	Aldh4a1	11	11	11	26	26	26	61.84	562	5.967E-292	1.5237	1.473	83.078	25	4545700000	1816700000	2729000000
P10518	Delta-aminolevulinic acid dehydratase	Alad	6	6	6	27	27	27	36.023	330	1.2369E-75	1.3608	1.2293	39.809	8	587570000	263190000	324380000
P82347	Delta-sarcoglycan	Sgcd	3	3	3	12.1	12.1	12.1	32.133	289	5.2702E-09	1.4572	1.7621	111.95	3	187770000	76609000	111160000
Q9CQJ6	Density-regulated protein	Denr	4	4	4	18.2	18.2	18.2	22.166	198	2.4198E-26	0.5981	0.76053	81.896	4	396000000	244290000	151710000
Q9QX60	Deoxyguanosine kinase, mitochondrial	Dguok	3	3	3	15.9	15.9	15.9	32.281	277	3.6194E-95	1.7663	1.5939	32.34	5	478630000	188300000	290330000
Q99LN9	Deoxyhypusine hydroxylase	Dohh	4	4	4	30.1	30.1	30.1	32.905	302	1.5267E-39	0.5376	0.51333	28.052	5	255860000	177250000	78606000
O55111	Desmoglein-2	Dsg2	3	3	3	4.1	4.1	4.1	122.38	1122	6.65E-11	1.112	1.065	9.4417	3	132640000	60435000	72206000
Q7TMD7	Desmoglein-4	Dsg4	1	1	1	1.2	1.2	1.2	114.45	1041	0.025851	0.33226	0.27696	11.011	2	25184000	19904000	5280000
Q9R0P5	Destrin	Dstn	5	5	5	46.7	46.7	46.7	18.521	165	1.5104E-23	0.69415	0.69637	22.941	6	160850000	95327000	65522000
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	Dld	14	14	14	36.1	36.1	36.1	54.272	509	0	0.8513	1.0139	74.986	86	1.4154E+10	7282900000	6871500000
Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	Dlat	19	19	19	38.9	38.9	38.9	67.941	642	4.22E-279	0.53902	0.56806	61.614	78	1.786E+10	1.1038E+10	6821400000
Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	Dlst	9	9	9	21.1	21.1	21.1	48.994	454	1.793E-121	0.72401	0.71948	137.03	22	4.5333E+10	2.5157E+10	2.0176E+10
Q8BVI4	Dihydropteridine reductase	Qdpr	3	3	3	17	17	17	25.57	241	5.226E-97	0.95056	0.89183	108.13	4	187020000	95003000	92016000
O08553	Dihydropyrimidinase-related protein 2	Dpysl2	15	13	13	41.1	37.1	37.1	62.277	572	1.448E-239	0.87494	0.98356	71.649	19	3440300000	1797200000	1643100000
E9PWE8	Dihydropyrimidinase-related protein 3	Dpysl3	18	18	16	36.3	36.3	32.9	73.884	683	6.737E-236	0.76035	0.79472	96.117	21	2487400000	1410200000	1077200000
P31428	Dipeptidase 1	Dpep1	4	4	4	14.9	14.9	14.9	45.722	410	2.5753E-18	1.1233	1.3238	59.047	6	1363200000	549250000	813950000
Q99KK7	Dipeptidyl peptidase 3	Dpp3	3	3	3	7.5	7.5	7.5	82.897	738	1.0262E-98	1.4438	1.9772	16.26	4	415560000	181940000	233620000
Q9JI46	Diphosphoinositol polyphosphate phosphohydrolase 1	Nudt3	3	3	3	30.4	30.4	30.4	19.029	168	8.9591E-29	0.62365	0.75073	56.031	3	263500000	161280000	102220000
P98078	Disabled homolog 2	Dab2	6	6	6	13.1	13.1	13.1	82.311	766	1.0612E-32	0.91911	1.0191	56.538	5	603170000	223400000	379770000
E9Q9H0	Disks large homolog 1	Dlg1	1	1	1	2	2	2	100.82	912	2.9704E-17	1.1466	0.94297	31.522	2	70672000	31952000	38720000
Q3U1J4	DNA damage-binding protein 1	Ddb1	9	9	9	12	12	12	126.85	1140	1.4208E-67	1.9405	1.7451	39.509	12	771140000	299040000	472090000
O54786	DNA fragmentation factor subunit alpha	Dffa	3	3	3	11.8	11.8	11.8	36.572	331	3.3474E-28	0.45507	0.53092	15.24	2	86994000	54114000	32880000
Q9JKB3	DNA-binding protein A	Csda	5	2	2	14.4	8.9	8.9	38.813	361	5.7821E-23	0.29752	0.30534	119.92	2	40992000	29632000	11361000
Q91WD1	DNA-directed RNA polymerase III subunit RPC4	Polr3d	1	1	1	1.8	1.8	1.8	44.356	398	0.019374	0.8014	1.6091	158.28	2	639630000	410590000	229040000
P63037	DnaJ homolog subfamily A member 1	Dnaja1	2	2	2	8.1	8.1	8.1	44.868	397	2.5675E-07	2.5899	2.4909	7.1445	3	152570000	41863000	110710000
Q9QYJ0	DnaJ homolog subfamily A member 2	Dnaja2	4	4	4	11.9	11.9	11.9	45.745	412	6.2781E-11	1.6449	1.6845	146.4	5	1009000000	353100000	655930000
Q9JMC3	DnaJ homolog subfamily A member 4	Dnaja4	5	5	5	20.9	20.9	20.9	44.901	397	2.6843E-21	2.2816	1.9614	35.559	4	102860000	27885000	74980000
Q9D832	DnaJ homolog subfamily B member 4	Dnajb4	6	6	6	18.7	18.7	18.7	37.781	337	2.4079E-22	0.56391	0.68606	66.413	6	397610000	212430000	185180000
Q91YW3	DnaJ homolog subfamily C member 3	Dnajc3	2	2	2	5.8	5.8	5.8	57.463	504	7.3588E-06	2.2675	2.2219	44.563	2	108780000	38433000	70345000
Q9D113	DNL-type zinc finger protein	Dnlz	1	1	1	5.1	5.1	5.1	19.403	177	0.0033583	0.9922	0.93728	108.87	2	210440000	96359000	114080000
Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Rpn1	2	2	2	5.8	5.8	5.8	68.527	608	1.7741E-06	1.801	1.6818	61.002	2	112770000	33064000	79711000
Q62418	Drebrin-like protein	Dbnl	5	5	5	16.1	16.1	16.1	48.699	436	3.5105E-15	0.663	0.6368	7.0347	5	140340000	86874000	53465000
Q63932	Dual specificity mitogen-activated protein kinase kinase 2	Map2k2	3	3	3	11	11	11	44.402	401	2.5458E-06	1.5896	2.7429	45.422	3	266100000	91830000	174270000
B1AQF4	Dual specificity protein phosphatase 3	Dusp3	2	2	2	16.7	16.7	16.7	23.223	210	5.4705E-71	1.2096	2.6367	117.75	2	43642000	19435000	24207000
O08788	Dynactin subunit 1	Dctn1	5	5	5	6.9	6.9	6.9	141.67	1281	5.9345E-62	2.34	2.4954	26.861	4	149120000	38764000	110350000
Q99KJ8	Dynactin subunit 2	Dctn2	9	9	9	31.8	31.8	31.8	44.116	402	3.091E-38	1.073	1.2003	40.652	12	1325600000	601940000	723630000
Q9Z0Y1	Dynactin subunit 3	Dctn3	3	3	3	19.4	19.4	19.4	20.978	186	8.1236E-18	1.7416	1.8051	109.61	3	158730000	65351000	93376000
F8WIV5	Dynamin-2	Dnm2	3	3	2	5.6	5.6	3.4	98.096	870	3.3449E-09	1.4341	1.4477	56.005	4	192600000	86940000	105660000
H7BX01	Dynamin-like 120 kDa protein, mitochondrial	Opa1	12	12	12	14.4	14.4	14.4	113.23	978	1.8361E-45	0.70547	0.90932	65.848	13	989340000	569980000	419360000
Q9D0M5	Dynein light chain 2, cytoplasmic	Dynll2	3	3	3	14.6	14.6	14.6	10.35	89	2.7449E-06	0.59673	0.60805	89.174	3	102260000	65341000	36916000
E9Q423	Dysferlin	Dysf	2	2	2	1.2	1.2	1.2	239.13	2099	0.0015675	0.50036	0.4799	110.91	2	3805700000	2099300000	1706500000
S4R1P5	Dystonin	Dst	4	4	3	0.9	0.9	0.7	870.52	7717	7.9657E-11	1.242	1.0309	38.323	4	62447000	26128000	36319000
Q9D2N4	Dystrobrevin alpha	Dtna	3	3	3	7.5	7.5	7.5	84.066	746	3.7575E-06	3.4254	3.6393	56.312	4	126860000	24576000	102280000
Q62165	Dystroglycan	Dag1	8	8	8	12.5	12.5	12.5	96.904	893	1.963E-86	0.55559	0.72539	43.483	11	1124700000	713640000	411020000
P11531	Dystrophin	Dmd	8	8	8	2.9	2.9	2.9	425.83	3678	1.5019E-26	2.3321	1.9469	56.279	7	221550000	76863000	144690000
Q69ZR2	E3 ubiquitin-protein ligase HECTD1	Hectd1	2	2	2	1.1	1.1	1.1	290.08	2618	0.00066218	0.60747	0.5373	5.4078	2	90402000	52614000	37788000
A2AFQ0	E3 ubiquitin-protein ligase HUWE1	Huwe1	12	12	12	3.6	3.6	3.6	482.69	4378	3.639E-134	1.3993	1.473	42.338	12	262110000	105830000	156280000
Q80U04	E3 ubiquitin-protein ligase Praja-2	Pja2	1	1	1	3.3	3.3	3.3	77.957	707	0.00067531	0.8497	0.85678	4.9744	2	15222000	9155300	6066700
A2AN08	E3 ubiquitin-protein ligase UBR4	Ubr4	6	6	6	1.5	1.5	1.5	572.28	5180	3.3878E-32	1.0993	0.91591	259.09	4	474880000	299820000	175060000
Q8BL66	Early endosome antigen 1	Eea1	14	14	14	12.6	12.6	12.6	160.91	1411	1.777E-100	0.8052	1.0041	47.48	17	824520000	457020000	367510000
Q05BC3	Echinoderm microtubule-associated protein-like 1	Eml1	10	10	10	13.6	13.6	13.6	89.679	814	6.8107E-34	0.98649	1.0225	159.38	10	1741900000	1183600000	558250000
E9QK48	Echinoderm microtubule-associated protein-like 2	Eml2	10	10	10	15.6	15.6	15.6	90.791	841	6.6825E-83	1.4554	1.6202	46.875	17	1681300000	613180000	1068100000
Q8R2G4	Ecto-ADP-ribosyltransferase 3	Art3	8	8	8	27.5	27.5	27.5	42.014	371	6.3528E-44	1.38	1.4305	74.14	12	1442100000	563450000	878640000
Q8CDV7	Ectonucleoside triphosphate diphosphohydrolase 1	Entpd1	1	1	1	3.9	3.9	3.9	60.589	539	3.5692E-26	1.2755	1.0504	61.317	3	75963000	29794000	46169000
Q91YE3	Egl nine homolog 1	Egln1	4	4	4	9.8	9.8	9.8	43.11	400	1.0421E-06	1.3455	1.2862	26.889	3	22846000	10096000	12750000
E9QP49	EH domain-binding protein 1-like protein 1	Ehbp1l1	6	6	6	5.9	5.9	5.9	184.8	1718	1.1E-75	1.2673	2.0856	56.077	5	178920000	77448000	101470000
Q9WVK4	EH domain-containing protein 1	Ehd1	11	10	7	28.3	26.6	17.6	60.602	534	3E-160	1.7294	2.0652	47.597	15	1613100000	556480000	1056600000
Q8BH64	EH domain-containing protein 2	Ehd2	14	14	13	33.7	33.7	32	61.174	543	5.453E-104	3.0259	3.4429	85.485	13	777470000	173720000	603760000
Q9EQP2	EH domain-containing protein 4	Ehd4	12	12	11	29.6	29.6	27.5	61.48	541	2.2948E-52	3.3392	4.1238	79.228	16	3650500000	895130000	2755400000
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	Etfa	23	23	23	68.2	68.2	68.2	35.009	333	0	0.51552	0.58084	91.637	111	5.1542E+10	3.3918E+10	1.7624E+10
Q9DCW4	Electron transfer flavoprotein subunit beta	Etfb	16	16	16	59.2	59.2	59.2	27.623	255	0	0.55115	0.62736	88.812	128	1.4927E+11	9.1405E+10	5.7861E+10
Q921G7	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	Etfdh	11	11	11	21.9	21.9	21.9	68.09	616	1.375E-154	0.96807	1.6088	106.68	20	9632700000	4769300000	4863400000
P10126	Elongation factor 1-alpha 1	Eef1a1	15	8	8	39.6	23.6	23.6	50.113	462	2.57E-189	0.84775	0.75822	97.176	16	3468000000	1956000000	1512000000
P62631	Elongation factor 1-alpha 2	Eef1a2	19	19	12	55.9	55.9	41.7	50.454	463	5.212E-234	1.0731	0.97595	98.076	61	3.3496E+10	1.221E+10	2.1286E+10
O70251	Elongation factor 1-beta	Eef1b	8	8	7	55.1	55.1	49.8	24.693	225	1.517E-104	0.61994	0.66813	60.282	11	674240000	407310000	266940000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q80T06	Elongation factor 1-delta	Eef1d	7	6	2	34.5	30.2	12.1	31.292	281	0	0.85105	1.0931	77.379	14	2631800000	1130200000	1501600000
Q9D8N0	Elongation factor 1-gamma	Eef1g	18	18	18	41.6	41.6	41.6	50.06	437	1.131E-99	1.0607	1.0194	71.486	28	6365500000	3086000000	3279600000
P58252	Elongation factor 2	Eef2	17	17	17	24.7	24.7	24.7	95.313	858	9.784E-224	1.813	2.1028	102.81	24	3053500000	1228500000	1825000000
Q8K0D5	Elongation factor G, mitochondrial	Gfm1	13	13	13	22.6	22.6	22.6	83.549	751	6.2066E-48	1.1424	1.4667	71.722	15	2893800000	1345200000	1548700000
Q9CZR8	Elongation factor Ts, mitochondrial	Tsfm	5	5	5	31.8	31.8	31.8	35.334	324	1.48E-148	1.3586	1.312	55.813	12	1160500000	398170000	762310000
D3YVN7	Elongation factor Tu	Gm9755	13	13	13	35.4	35.4	35.4	49.538	452	0	2.1331	2.3121	85.278	35	1.4108E+10	4596100000	9511700000
O08600	Endonuclease G, mitochondrial	Endog	2	2	2	10.2	10.2	10.2	32.19	294	2.849E-17	2.4023	2.5586	59.551	2	29795000	7767500	22027000
Q9JK48	Endophilin-B1	Sh3glb1	2	2	2	5.2	5.2	5.2	40.855	365	2.8115E-06	1.1153	1.2343	68.474	2	133580000	67360000	66217000
A2AWI7	Endophilin-B2	Sh3glb2	3	3	3	8.4	8.4	8.4	44.907	404	2.8751E-08	0.9484	0.94753	7.5231	4	194610000	83352000	111260000
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	Erap1	7	7	7	8.9	8.9	8.9	106.6	930	4.1699E-15	0.56309	0.50169	178.02	5	435290000	228660000	206640000
Q9D1Q6	Endoplasmic reticulum resident protein 44	Erp44	4	4	4	13.5	13.5	13.5	46.852	406	1.4682E-47	0.64415	0.69729	92.237	9	535650000	308770000	226880000
P08113	Endoplasmin	Hsp90b1	25	23	23	33.7	31.9	31.9	92.475	802	0	0.86486	0.89106	118.85	34	6139100000	2571000000	3568100000
Q9JMG1	Endothelial differentiation-related factor 1	Edf1	2	2	2	16.9	16.9	16.9	16.369	148	1.1722E-08	0.42273	0.61044	106.03	3	348690000	259620000	89070000
B0QZL1	Enolase	Eno1	8	1	1	52	6.3	6.3	23.935	221	1.47E-122	0.93259	1.4754	112.55	3	125830000	65886000	59941000
P42125	Enoyl-CoA delta isomerase 1, mitochondrial	Eci1	11	11	11	37.4	37.4	37.4	32.25	289	6.192E-103	1.5569	1.6974	83.888	27	1.0641E+10	4992700000	5648600000
Q9WUR2	Enoyl-CoA delta isomerase 2, mitochondrial	Eci2	12	12	12	36.3	36.3	36.3	43.267	391	0	1.0412	1.0696	51.471	23	3775600000	1604500000	2171100000
Q3TLP5	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	Echdc2	9	9	9	40.9	40.9	40.9	31.852	296	1.144E-238	2.1051	2.1526	48.943	13	2801700000	997310000	1804400000
Q9D7J9	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	Echdc3	3	3	3	14.7	14.7	14.7	32.402	300	1.4119E-14	5.3196	5.0792	153.35	4	3433000000	345270000	3087700000
Q8BH95	Enoyl-CoA hydratase, mitochondrial	Echs1	16	16	16	51.4	51.4	51.4	31.474	290	0	0.55813	0.71196	99.665	49	3.0316E+10	1.9486E+10	1.083E+10
Q01279	Epidermal growth factor receptor	Egfr	9	9	9	8.3	8.3	8.3	134.85	1210	7.7201E-58	0.47848	0.89083	141.16	10	929000000	554690000	374310000
H3BK65	Epidermal growth factor receptor substrate 15	Eps15	3	3	3	5	5	5	102.23	933	9.9668E-12	0.84113	0.74078	57.539	4	225820000	167090000	58729000
Q60902	Epidermal growth factor receptor substrate 15-like 1	Eps15l1	5	5	5	8.6	8.6	8.6	99.307	907	8.0333E-26	0.56219	0.57863	84.606	4	74777000	44411000	30366000
Q9Z0J0	Epididymal secretory protein E1	Npc2	1	1	1	10.7	10.7	10.7	16.442	149	1.5974E-07	1.1522	0.98717	35.531	2	54941000	26363000	28578000
Q5M8N4	Epimerase family protein SDR39U1	Sdr39u1	2	2	2	7.5	7.5	7.5	32.994	308	1.4707E-07	2.0348	2.127	82.429	3	146080000	56771000	89313000
Q8VEH5	EPM2A-interacting protein 1	Epm2aip1	2	2	2	5	5	5	70.095	606	3.4288E-05	2.8798	2.9104	21.667	2	57766000	20914000	36852000
Q9D379	Epoxide hydrolase 1	Ephx1	2	2	2	7	7	7	52.576	455	3.2466E-06	0.92492	0.87522	46.995	2	113470000	45703000	67765000
P34914	Epoxide hydrolase 2	Ephx2	17	17	17	35.7	35.7	35.7	62.515	554	0	1.3322	1.6307	70.65	35	5605500000	2454900000	3150600000
Q80VP1	Epsin-1	Epn1	4	4	4	9	9	9	60.211	575	5.3449E-23	1.1556	1.0613	30.235	4	548710000	227280000	321430000
J3QNT7	Epsin-2	Epn2	2	2	2	5.3	5.3	5.3	68.39	640	4.4956E-87	0.56092	0.49943	30.379	4	159670000	105890000	53779000
Q8R180	ERO1-like protein alpha	Ero1l	2	2	2	8.8	8.8	8.8	54.084	464	2.3157E-13	0.72854	0.81783	32.211	3	411300000	257840000	153460000
P54116	Erythrocyte band 7 integral membrane protein	Stom	5	5	5	25.7	25.7	25.7	31.375	284	9.4785E-27	2.1531	2.5472	22.043	4	122840000	33428000	89414000
Q9D172	ES1 protein homolog, mitochondrial	D10Jhu81e	11	11	11	54.5	54.5	54.5	28.09	266	0	0.67546	0.68028	66.834	35	3.2468E+10	2.042E+10	1.2047E+10
P50171	Estradiol 17-beta-dehydrogenase 8	Hsd17b8	8	8	8	42.5	42.5	42.5	26.588	259	8.7628E-94	1.702	2.0993	66.601	10	1463900000	647190000	816760000
Q9D9V3	Ethylmalonyl-CoA decarboxylase	Echdc1	3	3	3	11.5	11.5	11.5	35.467	322	0.00068352	0.62053	1.1284	47.414	2	75422000	49391000	26030000
P60843	Eukaryotic initiation factor 4A-I	Eif4a1	11	11	7	33.3	33.3	20.9	46.153	406	4.079E-192	1.6977	1.731	54.689	12	1434500000	547530000	886960000
P10630	Eukaryotic initiation factor 4A-II	Eif4a2	9	5	5	25.1	12.8	12.8	46.402	407	1.098E-166	1.1215	1.4542	61.337	6	2552300000	1626400000	925880000
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	Gspt1	7	7	7	13.8	13.8	13.8	68.625	636	1.8853E-53	0.61603	0.61318	80.472	5	452400000	267420000	184980000
Q9D1M4	Eukaryotic translation elongation factor 1 epsilon-1	Eef1e1	1	1	1	14.4	14.4	14.4	19.859	174	0.00016332	1.6246	1.7266	3.2197	2	17562000	6926100	10636000
P48024	Eukaryotic translation initiation factor 1	Eif1	4	4	4	48.7	48.7	48.7	12.746	113	2.0461E-58	0.63801	0.90858	64.161	5	198190000	108840000	89346000
Q60872	Eukaryotic translation initiation factor 1A	Eif1a	2	2	2	14.6	14.6	14.6	16.502	144	0.00013021	2.1031	6.205	132.39	2	187470000	62998000	124470000
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	Eif2s1	5	5	5	22.5	22.5	22.5	36.108	315	1.15E-158	1.7159	2.0481	83.944	6	795220000	438280000	356940000
Q99L45	Eukaryotic translation initiation factor 2 subunit 2	Eif2s2	6	6	6	17.8	17.8	17.8	38.092	331	3.8594E-27	1.4048	1.8437	54.7	7	620190000	263800000	356390000
Q9Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	Eif2s3x	4	4	4	12.1	12.1	12.1	51.065	472	1.2136E-24	2.0986	2.1319	226.65	5	564980000	361290000	203690000
P23116	Eukaryotic translation initiation factor 3 subunit A	Eif3a	5	5	5	4.8	4.8	4.8	161.93	1344	1.5303E-11	7.0047	7.7922	71.75	5	531260000	65434000	465830000
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B	Eif3b	10	10	10	18.4	18.4	18.4	91.369	803	4.68E-117	2.9055	3.1404	84.277	13	1501500000	525030000	976480000
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	Eif3c	5	5	5	6	6	6	105.53	911	2.0765E-11	5.2508	6.1148	80.417	4	301420000	86985000	214440000
P60229	Eukaryotic translation initiation factor 3 subunit E	Eif3e	3	3	3	9	9	9	52.22	445	5.8225E-12	0.43426	0.41086	193.18	2	294480000	205800000	88673000
Q9DCH4	Eukaryotic translation initiation factor 3 subunit F	Eif3f	4	4	4	16.1	16.1	16.1	37.984	361	1.3545E-12	2.9388	2.5918	73.102	4	415570000	77834000	337730000
Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G	Eif3g	4	4	4	15.3	15.3	15.3	35.638	320	4.7368E-29	1.3063	1.519	87.491	6	412460000	126730000	285730000
Q91WK2	Eukaryotic translation initiation factor 3 subunit H	Eif3h	2	2	2	7.4	7.4	7.4	39.832	352	3.1623E-06	2.2224	4.4488	157.93	2	83507000	22921000	60586000
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L	Eif3l	3	3	3	5.3	5.3	5.3	66.612	564	1.3917E-07	2.7031	3.4007	117.41	2	72613000	9665100	62948000
Q99JX4	Eukaryotic translation initiation factor 3 subunit M	Eif3m	3	3	3	11	11	11	42.516	374	3.0345E-12	2.7524	2.9565	61.261	2	154020000	51363000	102650000
G3XA17	Eukaryotic translation initiation factor 4 gamma 2	Eif4g2	2	2	2	2.6	2.6	2.6	102.1	906	7.6443E-06	1.3382	1.4292	17.757	2	177660000	81831000	95831000
P63073	Eukaryotic translation initiation factor 4E	Eif4e	4	4	4	20.3	20.3	20.3	25.053	217	5.931E-07	0.91981	1.5094	26.606	4	316610000	147300000	169310000
Q9DBB5	Eukaryotic translation initiation factor 4E type 3	Eif4e3	3	3	3	24.6	24.6	24.6	22.836	207	6.7289E-19	1.1186	1.2034	16.957	5	363500000	173050000	190460000
Q9WUK2	Eukaryotic translation initiation factor 4H	Eif4h	3	3	3	12.1	12.1	12.1	27.341	248	4.903E-134	0.2952	0.33447	29.324	4	597450000	505130000	92321000
P59325	Eukaryotic translation initiation factor 5	Eif5	5	5	5	15.9	15.9	15.9	48.968	429	8.9387E-53	0.73212	1.1752	71.164	2	112050000	61125000	50927000
P63242	Eukaryotic translation initiation factor 5A-1	Eif5a	5	5	5	24.7	24.7	24.7	16.832	154	6.9666E-21	0.72634	0.89729	126.32	13	4853400000	2948700000	1904700000
Q05D44	Eukaryotic translation initiation factor 5B	Eif5b	8	8	8	11.3	11.3	11.3	137.61	1216	1.5357E-29	1.4894	1.4069	22.346	4	229120000	84321000	144800000
O55135	Eukaryotic translation initiation factor 6	Eif6	2	2	2	17.6	17.6	17.6	26.511	245	7.4235E-15	0.75244	0.74611	18.702	2	220240000	126130000	94108000
E9PUW7	Exportin-7	Xpo7	2	2	2	3.1	3.1	3.1	123.9	1088	1.0554E-05	1.4956	1.5326	126.69	2	65251000	25298000	39953000
P26040	Ezrin	Ezr	8	4	4	15.5	10.4	10.4	69.406	586	3.3914E-30	0.64569	0.5654	46.61	2	230850000	164050000	66792000
P47754	F-actin-capping protein subunit alpha-2	Capza2	3	3	3	19.2	19.2	19.2	32.967	286	5.0611E-22	0.66196	0.58488	80.879	3	69603000	41982000	27621000
P47757	F-actin-capping protein subunit beta	Capzb	2	2	2	6.9	6.9	6.9	31.345	277	0.00011173	0.77209	1.4753	102.99	2	117660000	64187000	53469000
Q8R123	FAD synthase	Flad1	6	6	6	23.2	23.2	23.2	54.766	492	9.0953E-70	1.3219	1.408	15.797	6	372620000	151790000	220830000
P56213	FAD-linked sulfhydryl oxidase ALR	Gfer	6	6	6	35.4	35.4	35.4	22.876	198	5.3761E-18	0.51747	0.56044	63.698	7	733550000	429490000	304070000
Q91WJ8	Far upstream element-binding protein 1	Fubp1	6	4	4	10.9	9.7	9.7	68.539	651	1.5315E-66	0.61985	0.80859	33.308	5	170360000	108170000	62195000
Q3U0V1	Far upstream element-binding protein 2	Khsrp	7	7	5	9.8	9.8	7.8	76.775	748	9.623E-18	0.69672	0.7471	80.38	7	442280000	218200000	224080000
Q61553	Fascin	Fscn1	4	4	4	12	12	12	54.507	493	8.9727E-22	1.1719	1.1901	17.327	6	827280000	400950000	426340000
P19096	Fatty acid synthase	Fasn	16	16	16	8.7	8.7	8.7	272.43	2504	6.9335E-80	0.8763	0.86658	92.876	12	758780000	247880000	510900000
P04117	Fatty acid-binding protein, adipocyte	Fabp4	11	11	11	68.9	68.9	68.9	14.65	132	2.0569E-68	0.50834	0.54828	113.67	34	2.3279E+10	1.5323E+10	7956800000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
E9Q0H6	Fatty acid-binding protein, brain	Fabp7	1	1	1	9.6	9.6	9.6	20.615	188	1.0042E-08	0.49849	0.59916	8.064	2	28020000	20444000	7576400
Q05816	Fatty acid-binding protein, epidermal	Fabp5	7	7	7	64.4	64.4	64.4	15.137	135	0	0.68806	0.87758	69.414	17	2988100000	1740300000	1247700000
P11404	Fatty acid-binding protein, heart	Fabp3	13	13	13	61.7	61.7	61.7	14.819	133	6.76E-303	0.36476	0.35286	87.03	73	2.1162E+11	1.5337E+11	5.8247E+10
Q3UQN2	FCH domain only protein 2	Fcho2	3	3	3	5.8	5.8	5.8	88.733	809	3.2238E-28	1.0247	1.5273	19.798	5	253080000	135090000	118000000
Q8CIB5	Fermitin family homolog 2	Fermt2	10	10	10	16.3	16.3	16.3	77.8	680	2.3262E-31	1.7547	1.9056	104.77	11	1165100000	457630000	707480000
Q8K1B8	Fermitin family homolog 3	Fermt3	3	3	3	7.7	7.7	7.7	75.634	665	5.5471E-13	0.82651	0.91226	102.6	3	238240000	132800000	105440000
Q9CPX4	Ferritin	Ftl1	6	6	6	53	53	53	20.772	183	3.388E-130	0.55467	0.65866	77.566	15	1606000000	922390000	683610000
P09528	Ferritin heavy chain	Fth1	9	9	9	59.3	59.3	59.3	21.066	182	6.045E-157	0.61875	0.71968	152.42	20	9257600000	5428200000	3829400000
Q544X6	Ferrochelatase	Fech	5	5	5	16.1	16.1	16.1	47.421	422	1.5472E-13	3.2595	3.8797	72.517	4	669980000	185720000	484260000
Q9QXC1	Fetuin-B	Fetub	4	4	4	21.6	21.6	21.6	42.712	388	1.835E-149	0.63817	0.64248	29.932	8	355900000	232850000	123050000
Q76LL6	FH1/FH2 domain-containing protein 3	Fhod3	5	5	5	5.4	5.4	5.4	175.65	1578	2.1857E-27	2.7838	2.661	19.921	2	102910000	25901000	77011000
A2AQ53	Fibrillin-1	Fbn1	9	9	9	3.3	3.3	3.3	312.3	2873	2.83E-16	0.32476	0.68285	91.839	6	574860000	289140000	285720000
Q8K0E8	Fibrinogen beta chain	Fgb	13	13	13	38.5	38.5	38.5	54.752	481	5.307E-124	1.9535	2.3323	73.285	15	1541300000	528350000	1012900000
Q8VCM7	Fibrinogen gamma chain	Fgg	11	11	11	31.2	31.2	31.2	49.391	436	3.831E-235	2.081	2.4614	104.09	14	1343900000	543790000	800080000
P61148	Fibroblast growth factor 1	Fgf1	5	5	5	25.8	25.8	25.8	17.417	155	1.2389E-13	0.60419	0.51627	51.901	7	467940000	301830000	166110000
Q08879	Fibulin-1	Fbln1	5	5	5	6.8	6.8	6.8	78.032	705	7.6991E-19	0.95376	1.1052	40.581	8	538690000	233940000	304740000
Q8BTM8	Filamin-A	Flna	37	34	34	21.3	20.2	20.2	281.22	2647	0	0.80868	0.85943	59.499	36	3534700000	2061200000	1473400000
Q80X90	Filamin-B	Flnb	18	13	13	8.8	7	7	277.82	2602	1.4773E-43	0.97458	1.0089	93.966	10	695160000	250460000	444700000
Q71FD7	Filamin-binding LIM protein 1	Fblim1	5	5	5	23.7	23.7	23.7	41.026	375	8.6148E-43	1.2444	1.0815	28.518	9	559440000	253110000	306330000
Q8VHX6	Filamin-C	Flnc	38	38	33	19.7	19.7	18	291.12	2726	2.51E-226	0.64752	0.82284	72.603	45	5019700000	3148300000	1871400000
Q923D2	Flavin reductase (NADPH)	Blvrb	7	7	7	50.5	50.5	50.5	22.197	206	3.6672E-64	1.1703	1.2469	51.275	11	3279100000	1602900000	1676200000
Q5SS83	Flotillin-2	Flot2	2	2	2	5.4	5.4	5.4	47.116	428	1.4029E-07	1.3499	1.3562	16.629	2	71988000	28747000	43241000
Q9JL04	Formin-2	Fmn2	1	1	1	0.8	0.8	0.8	167.38	1578	0.0079393	3.4396	3.4522	77.308	2	174230000	32995000	141240000
O70433	Four and a half LIM domains protein 2	Fhl2	8	8	8	39.4	39.4	39.4	32.072	279	1.648E-132	1.4577	1.8077	121.84	11	1463800000	624870000	838880000
Q61584	Fragile X mental retardation syndrome-related protein 1	Fxr1	2	2	2	4.7	4.7	4.7	76.221	677	5.2841E-18	0.75737	0.79326	70.201	3	308490000	165140000	143350000
P70695	Fructose-1,6-bisphosphatase isozyme 2	Fbp2	5	5	5	18	18	18	36.947	339	3.0076E-43	0.70022	0.67691	32.579	6	390930000	216590000	174340000
A6ZI44	Fructose-bisphosphate aldolase	Aldoa	25	25	21	66.5	66.5	56.5	45.12	418	0	1.0215	0.98789	103.2	106	7.651E+10	3.7221E+10	3.9289E+10
P97807	Fumarate hydratase, mitochondrial	Fh	19	19	19	51.9	51.9	51.9	54.356	507	0	0.72611	0.79722	71.297	80	2.5376E+10	1.5027E+10	1.0349E+10
P35505	Fumarylacetoacetase	Fah	4	4	4	15.8	15.8	15.8	46.175	419	1.2136E-38	1.4266	1.8627	53.145	4	554910000	240950000	313960000
Q3TC72	Fumarylacetoacetate hydrolase domain-containing protein 2A	Fahd2	11	11	11	49.5	49.5	49.5	34.69	313	3.36E-179	0.99545	1.1246	76.953	15	2049100000	1182900000	866220000
Q8VDC1	FYVE and coiled-coil domain-containing protein 1	Fyco1	4	4	4	4	4	4	162.33	1437	2.1733E-15	2.5841	2.5039	86.246	3	195980000	62952000	133030000
Q9R0N0	Galactokinase	Galk1	4	4	4	11.5	11.5	11.5	42.295	392	6.8747E-08	1.0585	1.5204	95.631	4	226550000	153880000	72674000
Q03249	Galactose-1-phosphate uridylyltransferase	Galt	2	2	2	11.6	11.6	11.6	43.232	379	7.3484E-12	1.845	1.8352	11.828	3	116160000	39211000	76952000
P16045	Galectin-1	Lgals1	6	6	6	49.6	49.6	49.6	14.866	135	1.5816E-64	0.53319	0.61761	129.36	13	8055200000	5170700000	2884500000
P17183	Gamma-enolase	Eno2	5	2	2	16.1	9	9	47.296	434	2.9747E-30	0.69445	0.75646	238.89	3	2936500000	2135600000	800940000
Q9D7X8	Gamma-glutamylcyclotransferase	Ggct	3	3	3	16.5	16.5	16.5	21.166	188	6.9229E-07	0.81613	2.3835	97.591	2	297880000	179180000	118700000
P82348	Gamma-sarcoglycan	Sgcg	2	2	2	11.3	11.3	11.3	32.081	291	6.7333E-12	1.4065	1.9109	37.683	3	463090000	183110000	279990000
Q9Z0F7	Gamma-synuclein	Sncg	4	4	4	42.3	42.3	42.3	13.159	123	2.6309E-54	0.41961	0.74433	154.97	5	364920000	299160000	65757000
P23242	Gap junction alpha-1 protein	Gja1	3	3	3	16	16	16	43.004	382	1.9043E-49	0.88977	1.1337	39.459	5	577380000	283620000	293760000
A2A7A7	GDH/6PGL endoplasmic bifunctional protein	H6pd	3	3	3	4.5	4.5	4.5	89.909	797	0.00032434	1.1318	1.2365	101.96	2	16121000	6426000	9694700
P23591	GDP-L-fucose synthase	Tsta3	3	3	3	10.3	10.3	10.3	35.877	321	3.4387E-10	1.2354	1.3505	79.195	2	92473000	47197000	45276000
Q9Z1Z0	General vesicular transport factor p115	Uso1	5	5	5	7.5	7.5	7.5	106.98	959	7.19E-36	2.9165	3.0632	58.321	4	422760000	128720000	294040000
A0JNY3	Gephyrin	Gphn	4	4	4	11	11	11	83.665	772	1.6922E-13	0.73955	0.60529	61.341	2	109570000	70956000	38610000
Q9WTN0	Geranylgeranyl pyrophosphate synthase	Ggps1	2	2	2	7	7	7	34.706	300	0.00041742	0.67281	0.636	3.5687	2	221140000	131420000	89717000
Q9JHK4	Geranylgeranyl transferase type-2 subunit alpha	Rabggta	3	3	3	6.5	6.5	6.5	64.989	567	1.5906E-06	1.0322	1.0184	65.234	2	112810000	54880000	57934000
Q9CQI3	Glia maturation factor beta	Gmfb	2	2	1	26.1	26.1	7	16.723	142	4.0759E-18	1.0299	0.84809	13.131	3	56231000	29178000	27053000
O88958	Glucosamine-6-phosphate isomerase 1	Gnpda1	3	3	3	15.6	15.6	15.6	32.549	289	2.8238E-28	1.4763	1.6598	14.183	4	252250000	103040000	149210000
Q00612	Glucose-6-phosphate 1-dehydrogenase X	G6pdx	5	5	5	10.5	10.5	10.5	59.262	515	4.0905E-76	1.2395	2.1354	24.836	3	139740000	65600000	74140000
P06745	Glucose-6-phosphate isomerase	Gpi	21	21	21	42.5	42.5	42.5	62.766	558	0	0.8001	0.92675	113.62	37	2.9374E+10	1.7148E+10	1.2226E+10
O08795	Glucosidase 2 subunit beta	Prkcsh	2	2	2	4.4	4.4	4.4	58.792	521	2.8544E-13	0.82366	0.73577	35.6	3	79611000	46976000	32634000
P17439	Glucosylceramidase	Gba	2	2	2	4.9	4.9	4.9	57.621	515	0.0024635	0.93014	0.79947	31.773	3	191320000	104080000	87241000
P26443	Glutamate dehydrogenase 1, mitochondrial	Glud1	12	12	12	29.7	29.7	29.7	61.336	558	5.5137E-74	4.4394	4.8312	184.33	13	5889100000	800930000	5088200000
P97494	Glutamate--cysteine ligase catalytic subunit	Gclc	5	5	5	11.8	11.8	11.8	72.571	637	5.0172E-12	1.0896	1.2696	47.019	7	359760000	178360000	181390000
O09172	Glutamate--cysteine ligase regulatory subunit	Gclm	2	2	2	10.6	10.6	10.6	30.534	274	1.0015E-08	1.6043	1.6749	10.243	3	186710000	73690000	113020000
P15105	Glutamine synthetase	Glul	5	5	5	16.4	16.4	16.4	42.119	373	3.425E-295	2.1598	2.4638	59.731	6	592310000	182220000	410090000
P16406	Glutamyl aminopeptidase	Enpep	2	2	2	2	2	2	107.96	945	0.00010666	0.88309	1.0154	2.2062	2	30726000	16543000	14183000
Q9CQM9	Glutaredoxin-3	Glrx3	8	8	8	30.3	30.3	30.3	37.778	337	2.0025E-57	0.59249	0.77558	70.155	11	857260000	576750000	280510000
Q9CWB7	Glutaredoxin-like protein C5orf63 homolog		2	2	2	17.4	17.4	17.4	13.43	115	0.0013604	0.4805	0.63668	16.036	2	33699000	23395000	10304000
Q80Y14	Glutaredoxin-related protein 5, mitochondrial	Glrx5	2	2	2	17.8	17.8	17.8	16.292	152	9.5687E-27	0.7372	0.76197	71.906	6	346170000	220620000	125550000
Q60759	Glutaryl-CoA dehydrogenase, mitochondrial	Gcdh	5	5	5	21	21	21	48.605	438	1.006E-105	2.5174	2.7136	23.586	9	1473700000	449270000	1024500000
Q76LV0	Glutathione peroxidase	Gpx4	2	2	2	9.9	9.9	9.9	29.211	253	9.3386E-05	0.45175	0.45422	183.96	2	336510000	201930000	134580000
P11352	Glutathione peroxidase 1	Gpx1	6	6	6	42.3	42.3	42.3	22.347	201	1.0844E-59	1.5044	3.3461	101.11	5	371240000	158380000	212860000
P46412	Glutathione peroxidase 3	Gpx3	4	4	4	23	23	23	25.442	226	1.925E-08	2.4835	2.2165	5.4559	2	89443000	29116000	60327000
P47791	Glutathione reductase, mitochondrial	Gsr	4	4	4	12.2	12.2	12.2	53.662	500	2.2956E-97	0.81808	0.94093	26.876	3	363740000	226780000	136960000
P30115	Glutathione S-transferase A3	Gsta3	2	2	2	7.2	7.2	7.2	25.36	221	4.9779E-08	0.34068	0.31783	38.637	2	69567000	48095000	21472000
P24472	Glutathione S-transferase A4	Gsta4	8	8	8	30.2	30.2	30.2	25.564	222	6.6065E-18	0.3433	0.38488	106.54	11	5013700000	3728600000	1285100000
Q9DCM2	Glutathione S-transferase kappa 1	Gstk1	9	9	9	45.1	45.1	45.1	25.704	226	9.585E-199	1.1225	1.3104	126.9	8	1287100000	517490000	769630000
P10649	Glutathione S-transferase Mu 1	Gstm1	14	14	7	58.3	58.3	25.2	25.97	218	5.657E-146	0.86225	0.98565	133.63	41	4.0576E+10	1.9311E+10	2.1265E+10
P15626	Glutathione S-transferase Mu 2	Gstm2	12	9	7	56	40.4	33	25.716	218	1.707E-240	0.86628	0.87592	90.355	21	3343200000	1811300000	1531900000
P48774	Glutathione S-transferase Mu 5	Gstm5	4	3	3	17.4	13.4	13.4	26.635	224	1.4588E-09	1.03	1.1436	107.16	3	421890000	190390000	231500000
Q80W21	Glutathione S-transferase Mu 7	Gstm7	10	5	5	45.9	22.5	22.5	25.709	218	1.9504E-81	0.8479	1.5695	90.028	8	791870000	406400000	385470000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O09131	Glutathione S-transferase omega-1	Gsto1	11	11	11	36.7	36.7	36.7	27.497	240	2.6491E-65	1.0551	1.0965	90.807	18	5237600000	2411000000	2826500000
P19157	Glutathione S-transferase P 1	Gstp1	8	8	8	51.9	51.9	51.9	23.609	210	1.235E-245	0.77545	0.88048	97.619	14	2319600000	1269900000	1049700000
P16858	Glyceraldehyde-3-phosphate dehydrogenase	Gapdh	20	20	8	61.9	61.9	25.2	35.81	333	0	0.6407	0.68145	46.341	175	2.5076E+10	1.4744E+10	1.0332E+10
Q64516	Glycerol kinase	Gk	5	5	5	10.9	10.9	10.9	61.227	559	1.4175E-25	0.85177	0.86001	28.298	7	278000000	148150000	129850000
P13707	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	Gpd1	11	11	11	30.9	30.9	30.9	37.572	349	0	0.50902	0.67614	53.056	12	1508900000	972130000	536790000
Q3ULJ0	Glycerol-3-phosphate dehydrogenase 1-like protein	Gpd1l	10	10	10	28.2	28.2	28.2	38.225	351	4.636E-58	0.60058	0.73848	94.07	10	1945000000	1188400000	756650000
Q8C0L9	Glycerophosphocholine phosphodiesterase GPCPD1	Gpcpd1	3	3	3	7.1	7.1	7.1	76.578	675	2.9656E-07	1.185	1.2496	43.317	4	208910000	125290000	83616000
Q9CZD3	Glycine--tRNA ligase	Gars	11	11	11	18.2	18.2	18.2	81.877	729	6.9871E-94	0.64387	0.7865	39.551	22	2037800000	1279300000	758470000
Q9Z1E4	Glycogen [starch] synthase, muscle	Gys1	11	11	11	22.1	22.1	22.1	83.926	738	5.2336E-85	2.2318	2.651	43.254	10	1258800000	363420000	895420000
Q8CI94	Glycogen phosphorylase, brain form	Pygb	38	38	30	49.3	49.3	38.6	96.729	843	0	2.0463	2.4328	86.649	70	4.1714E+10	1.3233E+10	2.8481E+10
Q9ET01	Glycogen phosphorylase, liver form	Pygl	6	2	2	7.3	2.7	2.7	97.462	850	4.0829E-13	1.4078	1.476	24.123	2	84272000	34064000	50208000
Q9WUB3	Glycogen phosphorylase, muscle form	Pygm	37	29	28	43.9	33.1	31.8	97.285	842	0	1.9013	1.9425	86.72	66	3.9494E+10	1.2127E+10	2.7368E+10
Q2NL51	Glycogen synthase kinase-3 alpha	Gsk3a	4	3	3	13.9	12	12	51.66	490	5.5281E-07	1.8017	2.6042	7.2725	2	53339000	15729000	37609000
E9QAQ5	Glycogen synthase kinase-3 beta	Gsk3b	4	4	3	15.7	15.7	13.6	47.989	433	7.449E-06	7.1694	8.4459	86.332	2	116430000	4439000	111990000
K3W4S6	Glycogenin-1	Gyg1	4	4	4	11.4	11.4	11.4	41.926	377	2.6057E-89	0.81263	0.85437	136.12	8	1861600000	1001600000	859990000
Q9CPV4	Glyoxalase domain-containing protein 4	Glod4	8	8	8	33.6	33.6	33.6	33.316	298	1.9301E-72	0.71567	0.70994	149.95	8	2064800000	1489700000	575040000
Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	Grhpr	8	8	8	27.4	27.4	27.4	35.328	328	1.7427E-79	1.4796	1.439	76.43	14	5044900000	2259600000	2785400000
Q9QZF2	Glypican-1	Gpc1	5	5	5	14.5	14.5	14.5	61.359	557	1.1321E-20	1.9752	1.9053	22.702	3	823460000	260170000	563290000
Q9DCZ1	GMP reductase 1	Gmpr	5	5	5	23.5	23.5	23.5	37.482	345	2.1285E-47	0.82582	1.0452	100.23	6	974940000	565550000	409390000
Q3THK7	GMP synthase [glutamine-hydrolyzing]	Gmps	8	8	8	16.3	16.3	16.3	76.723	693	3.8235E-51	0.85263	0.84791	55.227	6	381550000	183720000	197830000
Q91VW5	Golgin subfamily A member 4	Golga4	5	5	5	3.1	3.1	3.1	257.56	2238	6.8745E-10	1.229	1.4237	142.07	4	235310000	133470000	101840000
Q9QYY0	GRB2-associated-binding protein 1	Gab1	2	2	2	4.6	4.6	4.6	76.812	695	0.0035466	0.57044	0.60712	57.043	2	39500000	22342000	17158000
Q8C5Q4	G-rich sequence factor 1	Grsf1	2	2	2	8.6	8.6	8.6	53.076	479	7.227E-116	1.0244	0.93917	24.668	4	290660000	146900000	143760000
A2AEW8	GRIP1-associated protein 1	Gripap1	5	5	5	9.9	9.9	9.9	95.912	837	1.1718E-17	0.91031	0.8173	35.888	3	267050000	164280000	102770000
Q9JLM9	Growth factor receptor-bound protein 14	Grb14	1	1	1	4.5	4.5	4.5	60.572	538	6.5191E-32	0.74778	0.96137	8.3588	2	114560000	68982000	45582000
Q60631	Growth factor receptor-bound protein 2	Grb2	5	5	5	28.1	28.1	28.1	25.238	217	3.9966E-14	0.82191	0.82907	120.13	8	711470000	383860000	327610000
Q99LP6	GrpE protein homolog 1, mitochondrial	Grpel1	7	7	7	39.6	39.6	39.6	24.307	217	3.1192E-78	0.55709	0.91116	146.13	8	3525400000	2345600000	1179800000
Q9WTP7	GTP:AMP phosphotransferase, mitochondrial	Ak3	4	4	4	22.5	22.5	22.5	25.426	227	3.7123E-13	1.3402	1.5132	85.836	9	712820000	342310000	370510000
D3YTN4	GTPase IMAP family member 4	Gimap4	4	4	4	14	14	14	38.044	328	3.1381E-06	1.0329	1.14	19.235	4	449140000	260300000	188840000
P62827	GTP-binding nuclear protein Ran	Ran	5	5	5	28.7	28.7	28.7	24.423	216	1.0021E-29	1.5116	1.4877	47.334	10	1755800000	692030000	1063800000
Q9CQC9	GTP-binding protein SAR1b	Sar1b	4	4	2	23.7	23.7	15.7	22.382	198	1.9542E-10	2.1286	3.2414	82.976	4	242880000	90360000	152520000
Q9R111	Guanine deaminase	Gda	7	7	7	20	20	20	51.012	454	9.804E-26	1.4828	1.7253	87.7	9	892050000	297520000	594530000
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	Gnai2	7	7	5	25.1	25.1	18.6	40.489	355	1.001E-46	1.2087	1.921	117.45	7	761840000	293640000	468190000
P62874	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	Gnb1	3	3	2	10.6	10.6	7.4	37.377	340	8.985E-68	2.6521	3.1564	16.347	3	107050000	26375000	80679000
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	Gnb2l1	9	9	9	42.9	42.9	42.9	35.076	317	6.0952E-87	3.1408	3.5899	93.378	12	1052300000	258230000	794020000
Q9ERL9	Guanylate cyclase soluble subunit alpha-3	Gucy1a3	3	3	3	6.1	6.1	6.1	77.587	691	0.00016262	1.6096	1.4752	52.577	3	58604000	30236000	28368000
O54865	Guanylate cyclase soluble subunit beta-1	Gucy1b3	1	1	1	1.6	1.6	1.6	70.597	620	0.0075715	2.0185	2.4187	19.476	2	41240000	15664000	25576000
Q564G0	Guanylate kinase	Guk1	7	7	7	56.2	56.2	56.2	24.032	219	2.6149E-59	0.73296	0.79821	42.176	10	753540000	427770000	325770000
P01899	H-2 class I histocompatibility antigen, D-B alpha chain	H2-D1	3	1	0	10.2	2.8	0	40.836	362	3.2716E-08	1.097	1.2106	10.39	2	64824000	30173000	34651000
P01901	H-2 class I histocompatibility antigen, K-B alpha chain	H2-K1	3	3	2	11.1	11.1	7.9	41.301	369	8.5862E-07	1.2123	1.5511	15.201	3	53648000	37751000	15897000
P01898	H-2 class I histocompatibility antigen, Q10 alpha chain	H2-Q10	7	7	4	22.5	22.5	14.5	37.251	325	1.3481E-27	0.53062	0.57157	22.201	7	379130000	261880000	117250000
Q3UGR5	Haloacid dehalogenase-like hydrolase domain-containing protein 2	Hdhd2	2	2	2	12.7	12.7	12.7	28.73	259	0.00054313	0.94491	0.92932	4.6606	2	244940000	128880000	116060000
Q9CYW4	Haloacid dehalogenase-like hydrolase domain-containing protein 3	Hdhd3	3	3	3	11.6	11.6	11.6	28.027	251	0.00014155	0.93524	0.88434	10.625	3	93897000	51748000	42149000
Q61646	Haptoglobin	Hp	5	5	5	17.3	17.3	17.3	38.752	347	4.8396E-35	0.42328	0.46991	103.45	6	880840000	523880000	356960000
P17879	Heat shock 70 kDa protein 1B	Hspa1b	13	10	6	25.9	22.1	15.7	70.175	642	1.6931E-76	0.55945	0.52014	84.33	11	1445100000	1288300000	156770000
Q3U2G2	Heat shock 70 kDa protein 4	Hspa4	31	31	29	44.2	44.2	40.6	94.208	842	1.916E-291	0.73091	0.88687	74.263	41	5958000000	3539400000	2418500000
P48722	Heat shock 70 kDa protein 4L	Hspa4l	10	8	8	19.5	15.9	15.9	94.381	838	2.9068E-51	0.73718	0.78877	53.75	9	525580000	308910000	216670000
P63017	Heat shock cognate 71 kDa protein	Hspa8	25	23	16	38.9	38.9	28.2	70.87	646	0	0.70745	0.84861	46.903	72	6.6548E+10	3.8062E+10	2.8486E+10
Q61699	Heat shock protein 105 kDa	Hsph1	12	11	11	18.5	16.9	16.9	96.406	858	3.0823E-57	0.44605	0.49046	82.314	12	1102600000	746660000	355960000
Q9CQN1	Heat shock protein 75 kDa, mitochondrial	Trap1	11	11	11	22.4	22.4	22.4	80.208	706	2.591E-115	1.656	1.8429	67.484	21	1458300000	601480000	856850000
P14602	Heat shock protein beta-1	Hspb1	5	5	5	31.1	31.1	31.1	23.014	209	1.214E-33	1.0119	1.2499	71.733	7	5253300000	2498400000	2754900000
Q99PR8	Heat shock protein beta-2	Hspb2	4	4	4	41.8	41.8	41.8	20.374	182	8.0222E-65	0.88689	0.99603	28.775	7	978140000	543470000	434670000
Q9QZ57	Heat shock protein beta-3	Hspb3	1	1	1	14.9	14.9	14.9	17.229	154	1.429E-17	0.99449	1.3452	23.063	3	65262000	33816000	31446000
Q5EBG6	Heat shock protein beta-6	Hspb6	3	3	3	34.6	34.6	34.6	17.521	162	2.8029E-42	0.63473	0.56421	27.739	5	636450000	404360000	232090000
P35385	Heat shock protein beta-7	Hspb7	7	7	7	60.4	60.4	60.4	18.634	169	2.479E-135	0.95629	1.132	35.11	14	1167900000	596120000	571830000
P07901	Heat shock protein HSP 90-alpha	Hsp90aa1	27	15	15	39.6	24	24	84.787	733	0	0.72666	0.72871	60.856	17	2841300000	1676800000	1164500000
P11499	Heat shock protein HSP 90-beta	Hsp90ab1	34	34	20	43.2	43.2	25.6	83.28	724	0	0.71539	0.77342	87.944	78	2.5994E+10	1.4997E+10	1.0997E+10
P97825	Hematological and neurological expressed 1 protein	Hn1	3	3	3	27.9	27.9	27.9	16.08	154	5.3813E-44	0.39646	0.4795	106.26	6	520460000	473540000	46917000
Q91VB8	Hemoglobin subunit alpha	Hba-a1	12	12	10	92.3	92.3	85.9	15.112	142	0	0.8887	1.0504	136.06	133	2.0078E+11	1.2235E+11	7.8432E+10
P04444	Hemoglobin subunit beta-H1	Hbb-bh1	2	1	1	12.9	6.8	6.8	16.494	147	0.00010276	0.86325	0.77054	79.628	5	439430000	230110000	209320000
Q91X72	Hemopexin	Hpx	16	16	16	38.9	38.9	38.9	51.317	460	0	0.42912	0.53098	80.015	40	1.5817E+10	1.108E+10	4736800000
P49182	Heparin cofactor 2	Serpind1	2	2	2	3.8	3.8	3.8	54.496	478	5.2776E-06	0.56223	0.59704	18.782	2	291690000	182240000	109450000
G3UW70	Hepatitis B virus X-interacting protein homolog	Hbxip	1	1	1	13.8	13.8	13.8	15.354	145	8.229E-116	1.4617	1.6166	27.89	2	654430000	247750000	406670000
P51859	Hepatoma-derived growth factor	Hdgf	12	12	12	71.7	71.7	71.7	26.268	237	5.909E-299	0.48516	0.47443	82.693	19	2608300000	1751700000	856650000
Q9JMG7	Hepatoma-derived growth factor-related protein 3	Hdgfrp3	3	3	2	23.8	23.8	15.3	22.43	202	2.0342E-07	0.57097	0.71325	45.283	2	64584000	42297000	22287000
Q20BD0	Heterogeneous nuclear ribonucleoprotein A/B	Hnrnpab	5	5	5	12.7	12.7	12.7	36.21	332	2.8934E-52	0.67	3.9898	143.89	3	1097400000	703000000	394370000
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0	Hnrnpa0	3	3	3	9.2	9.2	9.2	30.53	305	9.0809E-47	1.6671	1.6773	104.51	9	2126200000	808280000	1317900000
Q5EBP8	Heterogeneous nuclear ribonucleoprotein A1	Hnrnpa1	5	5	5	23.1	23.1	23.1	38.833	373	2.9572E-74	1.1879	1.2982	46.753	7	819210000	484250000	334960000
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	Hnrnpa3	7	7	7	23.2	23.2	23.2	39.652	379	1.3781E-62	1.5622	1.7672	43.804	8	1612200000	618540000	993610000
Q60668	Heterogeneous nuclear ribonucleoprotein D0	Hnrnpd	7	7	6	18.6	18.6	16.3	38.354	355	1.6405E-43	0.63847	0.7887	77.658	9	1601900000	949600000	652300000
D3YTQ3	Heterogeneous nuclear ribonucleoprotein D-like	Hnrpdl	2	1	1	5	3.1	3.1	46.27	420	1.0804E-08	1.9594	2.1806	27.971	2	238770000	77989000	160780000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
J3QMQ5	Heterogeneous nuclear ribonucleoprotein F	Hnrnpf	2	1	1	6.3	3.9	3.9	45.847	415	5.3052E-07	1.4273	1.8581	9.8982	3	95655000	38651000	57005000
P61979	Heterogeneous nuclear ribonucleoprotein K	Hnrnpk	9	9	9	25.1	25.1	25.1	50.976	463	4.1484E-91	1.3893	1.6469	49.724	14	1153300000	491500000	661780000
G5E924	Heterogeneous nuclear ribonucleoprotein L	Hnrnpl	3	3	3	7	7	7	66.821	615	1.504E-25	2.6755	6.6195	83.779	2	255940000	78063000	177880000
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	Hnrnpm	1	1	1	2.1	2.1	2.1	77.648	729	1.9703E-05	1.6772	2.0658	31.981	2	472020000	131610000	340410000
Q7TMK9	Heterogeneous nuclear ribonucleoprotein Q	Syncrip	12	12	12	26	26	26	69.632	623	9.7034E-41	0.85911	0.97114	71.853	11	1607900000	1053500000	554400000
Q8VEK3	Heterogeneous nuclear ribonucleoprotein U	Hnrnpu	7	7	7	13.2	13.2	13.2	87.917	800	4.471E-176	2.2902	2.0284	56.917	7	838010000	238170000	599840000
Q8VDM6	Heterogeneous nuclear ribonucleoprotein U-like protein 1	Hnrnpul1	3	3	3	4.9	4.9	4.9	96.001	859	3.7724E-06	3.2691	3.1628	92.095	3	86908000	29655000	57253000
Q00PI9	Heterogeneous nuclear ribonucleoprotein U-like protein 2	Hnrnpul2	3	3	3	6.4	6.4	6.4	84.939	745	1.7907E-14	1.4893	1.4612	28.923	3	57232000	21833000	35399000
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	Hnrnpa2b1	7	7	7	23.2	23.2	23.2	37.402	353	4.4347E-33	1.1025	0.87928	115.08	9	2269500000	1296200000	973210000
Q9Z204	Heterogeneous nuclear ribonucleoproteins C1/C2	Hnrnpc	2	2	2	7	7	7	34.384	313	1.597E-07	1.2212	1.139	57.26	3	668100000	332090000	336010000
Q8BMS4	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	Coq3	3	3	3	16.8	16.8	16.8	40.956	370	9.72E-160	1.6488	1.7759	53.324	4	344450000	155330000	189120000
P17710	Hexokinase-1	Hk1	23	19	18	27	23.9	23	108.3	974	5.942E-219	1.7768	2.3528	62.335	20	4463300000	1750900000	2712300000
O08528	Hexokinase-2	Hk2	32	32	27	38.2	38.2	33.7	102.53	917	0	1.1966	1.6232	83.853	52	1.4044E+10	6206000000	7837900000
Q9JL35	High mobility group nucleosome-binding domain-containing protein 5	Hmgn5	4	4	4	12.6	12.6	12.6	45.343	406	3.7809E-07	0.38404	0.40593	29.661	4	636950000	511790000	125160000
P63158	High mobility group protein B1	Hmgb1	8	8	7	32.6	32.6	27	24.893	215	1.6089E-63	0.56634	0.71822	79.125	11	7093600000	4572400000	2521200000
P30681	High mobility group protein B2	Hmgb2	4	3	3	16.7	11	11	24.162	210	8.5216E-12	0.39452	0.54781	40.825	3	296910000	182990000	113920000
P62748	Hippocalcin-like protein 1	Hpcal1	4	4	4	22.3	22.3	22.3	22.338	193	6.2459E-11	0.65573	0.73414	49.38	4	444010000	268010000	175990000
P70349	Histidine triad nucleotide-binding protein 1	Hint1	6	6	6	58.7	58.7	58.7	13.777	126	9.212E-94	0.56155	0.52113	65.946	18	3021000000	2046300000	974760000
Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochondrial	Hint2	3	3	3	29.4	29.4	29.4	17.32	163	4.96E-221	0.69566	0.73269	35.133	35	3.3974E+10	2.0386E+10	1.3588E+10
Q9ESB3	Histidine-rich glycoprotein	Hrg	6	6	6	12.2	12.2	12.2	59.162	525	2.2729E-18	0.8668	0.7557	74.994	5	668360000	344840000	323520000
Q61035	Histidine--tRNA ligase, cytoplasmic	Hars	9	9	8	23.4	23.4	21.6	57.432	509	7.6411E-45	0.65881	0.79602	112.94	11	570400000	359060000	211330000
P43274	Histone H1.4	Hist1h1e	3	3	2	18.7	18.7	13.2	21.977	219	1.2565E-05	3.4104	3.7853	72.899	2	128610000	28834000	99777000
Q8CBB6	Histone H2B	Gm13646	2	2	2	17.9	17.9	17.9	14.888	134	7.2953E-11	8.8097	9.6858	9.1126	2	430930000	56730000	374200000
D3YUP1	Histone-arginine methyltransferase CARM1	Carm1	3	3	3	5.7	5.7	5.7	70.322	651	3.9404E-07	1.7673	2.99	57.986	2	92651000	35347000	57304000
Q60973	Histone-binding protein RBBP7	Rbbp7	3	3	3	15.5	15.5	15.5	47.789	425	2.3509E-22	0.97947	1.114	74.879	4	288870000	136760000	152110000
Q91WC0	Histone-lysine N-methyltransferase setd3	Setd3	2	2	2	4.4	4.4	4.4	67.175	594	0.00010293	1.5404	1.4539	18.916	3	120520000	57289000	63229000
Q8R1H0	Homeodomain-only protein	Hopx	3	3	3	47.9	47.9	47.9	8.2821	73	1.5484E-68	0.72261	0.75812	87.49	7	1402100000	871520000	530570000
Q9Z2Y3	Homer protein homolog 1	Homer1	5	5	4	17.8	17.8	15.6	41.412	366	1.1451E-52	0.7473	0.82814	47.973	4	183030000	105300000	77731000
Q9QWW1	Homer protein homolog 2	Homer2	4	3	3	10.2	7.9	7.9	40.57	354	3.4951E-07	0.43626	0.5209	29.739	3	157120000	105980000	51147000
B1AUX2	Host cell factor 1	Hcfc1	2	2	2	1.9	1.9	1.9	215.05	2090	8.2913E-17	0.96504	0.85455	16.86	2	70400000	41384000	29016000
Q99L47	Hsc70-interacting protein	St13	6	6	6	16.2	16.2	16.2	41.655	371	6.329E-167	0.61505	0.84756	135.05	12	2098100000	1286100000	811930000
Q61081	Hsp90 co-chaperone Cdc37	Cdc37	3	3	3	9.2	9.2	9.2	44.593	379	1.2213E-07	0.82763	2.9712	118.63	4	195250000	109500000	85750000
Q9CZP7	Hsp90 co-chaperone Cdc37-like 1	Cdc37l1	4	4	4	17	17	17	38.439	335	9.5589E-09	0.54885	0.57189	36.712	4	274490000	183840000	90656000
Q8R0N6	Hydroxyacid-oxoacid transhydrogenase, mitochondrial	Adhfe1	6	6	6	25.6	25.6	25.6	49.937	465	2.5196E-91	1.1944	1.3794	31.011	7	1563100000	662570000	900530000
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Hadh	12	12	12	43	43	43	34.463	314	0	1.1506	1.1986	101.94	50	2.0226E+10	1.3599E+10	6626600000
G5E8T9	Hydroxyacylglutathione hydrolase, mitochondrial	Hagh	4	4	4	16.8	16.8	16.8	34.103	309	2.009E-108	0.71965	0.83333	31.904	7	1285900000	742200000	543680000
P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	Hmgcl	6	6	6	22.2	22.2	22.2	34.238	325	1.1116E-67	0.87198	0.89278	94.624	12	1491800000	788110000	703660000
Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2	Hsdl2	18	18	18	54.1	54.1	54.1	54.208	490	0	1.2507	1.2203	44.61	29	4150200000	1832600000	2317600000
P00493	Hypoxanthine-guanine phosphoribosyltransferase	Hprt1	5	5	5	27.1	27.1	27.1	24.57	218	1.2401E-28	1.0045	1.1984	49.295	5	314140000	164320000	149820000
Q9JKR6	Hypoxia up-regulated protein 1	Hyou1	10	10	10	12.9	12.9	12.9	111.18	999	1.2947E-39	0.76008	0.83905	56.358	8	489270000	260470000	228810000
P01878	Ig alpha chain C region		2	2	2	6.7	6.7	6.7	36.875	344	0.0060801	0.4304	0.44728	17.58	2	85419000	53363000	32056000
P01869	Ig gamma-1 chain C region, membrane-bound form	Ighg1	3	3	3	8.1	8.1	8.1	43.386	393	1.0282E-32	1.0085	2.4638	51.074	4	315100000	161300000	153800000
F6TQW2	Ig gamma-2A chain C region secreted form	Ighg2c	4	4	4	12.4	12.4	12.4	44.095	403	2.2111E-48	0.34128	0.42864	99.864	6	919900000	800020000	119890000
P01867	Ig gamma-2B chain C region	Igh-3	5	5	5	15.3	15.3	15.3	44.259	404	3.291E-12	0.44178	0.50346	74.201	5	290370000	203890000	86486000
P18528	Ig heavy chain V region 6.96		1	1	1	19.4	19.4	19.4	11.007	98	3.6663E-13	0.25597	0.34623	4.8424	2	395890000	324490000	71404000
P06330	Ig heavy chain V region AC38 205.12		4	4	4	49.2	49.2	49.2	12.934	118	2.445E-152	0.26856	0.30802	95.739	5	1737500000	1415200000	322250000
P01783	Ig heavy chain V region MOPC 21		1	1	1	8.1	8.1	8.1	15.071	136	0.002962	0.435	0.4839	9.046	2	39942000	26765000	13177000
P01786	Ig heavy chain V region MOPC 47A		1	1	1	7.7	7.7	7.7	12.374	117	2.0173E-16	0.32836	0.30673	65.238	2	97976000	70921000	27055000
P01837	Ig kappa chain C region		4	4	4	50	50	50	11.778	106	7.287E-143	0.51944	0.5758	53.167	10	1240000000	813800000	426250000
P01660	Ig kappa chain V-III region PC 3741/TEPC 111		2	2	2	32.4	32.4	32.4	12.099	111	0.0026361	0.16178	0.17171	95.847	2	96095000	86759000	9335500
P01655	Ig kappa chain V-III region PC 7132		2	2	2	36.6	36.6	36.6	12.054	112	2.9603E-15	0.57619	0.49533	8.2067	2	29501000	20856000	8645300
P01644	Ig kappa chain V-V region HP R16.7		2	2	2	26.9	26.9	26.9	11.91	108	3.2533E-05	0.97161	1.5852	175.91	2	408250000	147310000	260940000
P01844	Ig lambda-2 chain C region	Iglc2	2	2	2	33.7	33.7	33.7	11.254	104	6.09E-23	0.32	0.25565	37.805	3	80493000	63072000	17421000
P01872	Ig mu chain C region secreted form	Igh-6	12	12	12	28.9	28.9	28.9	49.971	454	0	0.2292	0.25983	79.299	14	1911000000	1341200000	569780000
Q61249	Immunoglobulin-binding protein 1	Igbp1	6	6	6	23.5	23.5	23.5	38.97	340	1.5582E-51	0.49954	0.49469	61.31	7	285640000	186370000	99274000
P70168	Importin subunit beta-1	Kpnb1	9	9	9	14.4	14.4	14.4	97.183	876	6.083E-48	2.1595	2.1624	19.899	12	637740000	205500000	432240000
Q8BKC5	Importin-5	Ipo5	11	11	11	16.2	16.2	16.2	123.59	1097	1.773E-140	3.1991	2.8495	41.058	8	422410000	105150000	317260000
Q9EPL8	Importin-7	Ipo7	5	5	5	6.9	6.9	6.9	119.49	1038	4.2786E-17	1.9075	1.6885	57.734	7	568330000	193150000	375180000
P40936	Indolethylamine N-methyltransferase	Inmt	9	9	9	44.3	44.3	44.3	29.459	264	2.964E-246	1.3542	1.475	50.039	10	1080200000	548100000	532110000
Q920Q8	Influenza virus NS1A-binding protein homolog	Ivns1abp	5	5	5	11.7	11.7	11.7	71.58	642	1.1487E-20	1.7444	1.6701	9.3394	3	110500000	30855000	79644000
Q9DBD0	Inhibitor of carbonic anhydrase	Ica	13	13	13	23.4	23.4	23.4	76.765	700	2.1958E-47	0.67151	0.78123	55.109	14	786940000	442810000	344130000
Q9D819	Inorganic pyrophosphatase	Ppa1	17	17	17	73	73	73	32.667	289	0	0.56269	0.64763	140.95	24	4691900000	2306800000	2385100000
Q91VM9	Inorganic pyrophosphatase 2, mitochondrial	Ppa2	13	13	13	47.3	47.3	47.3	38.114	330	6.048E-178	0.81656	0.86562	78.045	16	3553500000	1849900000	1703500000
Q9D892	Inosine triphosphate pyrophosphatase	Itpa	4	4	4	31.8	31.8	31.8	21.897	198	1.1607E-24	0.99042	1.1609	48.558	6	508800000	249020000	259780000
P24547	Inosine-5-monophosphate dehydrogenase 2	Impdh2	3	3	3	9.7	9.7	9.7	55.814	514	2.3493E-13	2.0566	2.3854	53.806	2	261810000	99190000	162620000
E9Q9J4	Inositol hexakisphosphate and diphosphoinositol-pentakisphosphate kinase 2	Ppip5k2	2	2	2	2.5	2.5	2.5	140.37	1242	3.6209E-06	1.6634	4.1531	80.214	2	205990000	99938000	106060000
Q924B0	Inositol monophosphatase 1	Impa1	3	3	3	18.8	18.8	18.8	30.429	277	8.1877E-56	0.56274	0.64639	26.96	6	1096800000	682420000	414330000
Q91UZ5	Inositol monophosphatase 2	Impa2	3	3	3	15.9	15.9	15.9	31.716	290	4.0629E-73	0.85192	0.98717	16.249	4	485050000	257040000	228010000
P49442	Inositol polyphosphate 1-phosphatase	Inpp1	2	2	2	9.3	9.3	9.3	43.346	396	2.8225E-12	1.1995	1.4282	8.9639	2	194720000	81976000	112750000
Q9JHU9	Inositol-3-phosphate synthase 1	Isyna1	2	2	2	3.8	3.8	3.8	60.931	557	1.4605E-12	0.88324	0.79505	39.983	4	396980000	191080000	205910000
F8WH23	Insulin-like growth factor-binding protein 7	Igfbp7	3	3	3	17.4	17.4	17.4	29.1	282	1.0422E-35	0.62322	0.50252	32.134	2	66183000	41572000	24611000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
P70389	Insulin-like growth factor-binding protein complex acid labile subunit	Igfals	2	2	2	3.2	3.2	3.2	66.959	603	0.0004855	1.4222	1.7805	49.876	2	70854000	30476000	40378000
Q3V3R4	Integrin alpha-1	Itga1	5	5	5	4.8	4.8	4.8	130.81	1179	8.1471E-30	0.30057	0.34345	61.34	3	46191000	30605000	15586000
Q61739	Integrin alpha-6	Itga6	2	2	2	3.1	3.1	3.1	122.16	1091	2.9852E-09	1.0264	1.3697	31.11	2	35460000	17610000	17850000
Q61738	Integrin alpha-7	Itga7	3	3	3	3.9	3.9	3.9	129.33	1179	7.9959E-20	1.164	1.7505	44.704	3	218360000	108850000	109510000
P09055	Integrin beta-1	Itgb1	4	4	4	8	8	8	88.231	798	1.2875E-39	1.1282	1.2003	19.274	6	724200000	353720000	370480000
O55222	Integrin-linked protein kinase	Ilk	4	4	4	14.2	14.2	14.2	51.373	452	5.5E-25	3.5185	3.6393	40.266	5	173050000	24096000	148960000
F8WJ05	Inter-alpha-trypsin inhibitor heavy chain H1	Itih1	8	8	8	13.4	13.4	13.4	101.63	911	8.944E-55	1.1356	1.1977	63.961	8	608270000	293420000	314850000
G3X977	Inter-alpha-trypsin inhibitor heavy chain H2	Itih2	7	7	7	9.7	9.7	9.7	106.36	950	2.808E-179	0.68045	0.59213	84.126	7	985080000	624350000	360730000
Q8CGE8	Interferon-activable protein 205-A	Ifi205a	4	4	2	16.6	16.6	6.7	45.176	404	1.8353E-09	2.036	1.7785	111.03	4	102820000	34051000	68770000
Q3UVZ1	Interleukin-1 receptor accessory protein	Il1rap	7	7	7	12.8	12.8	12.8	78.639	685	7.7069E-17	0.31757	0.42955	46.878	5	609660000	478180000	131480000
Q9DCB8	Iron-sulfur cluster assembly 2 homolog, mitochondrial	Isca2	5	5	5	40.3	40.3	40.3	16.718	154	4.7131E-82	0.42159	0.61513	35.485	4	384790000	254500000	130290000
Q9D7P6	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	Iscu	3	3	3	19	19	19	18.098	168	1.5095E-14	0.40462	1.5065	172.19	3	195070000	140890000	54176000
Q8K3A0	Iron-sulfur cluster co-chaperone protein HscB, mitochondrial	Hscb	4	4	4	23.5	23.5	23.5	26.645	234	6.136E-132	0.56849	0.71078	55.784	2	308560000	179850000	128710000
Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	Acad8	7	7	7	24.5	24.5	24.5	45.019	413	1.0399E-24	2.8933	3.1185	55.779	6	1615000000	540330000	1074700000
Q91V64	Isochorismatase domain-containing protein 1	Isoc1	3	3	3	8.4	8.4	8.4	32.032	297	5.5806E-16	0.73446	0.64976	51.583	4	279510000	152520000	126990000
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	Isoc2a	3	3	3	29.6	29.6	29.6	22.417	206	1.3714E-24	1.607	1.491	32.482	11	1284500000	481730000	802720000
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	Idh3a	17	17	17	40.7	40.7	40.7	39.638	366	0	0.71948	0.7733	71.481	105	5.8609E+10	3.4072E+10	2.4537E+10
P70404	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	Idh3g	9	9	9	38.2	38.2	38.2	42.785	393	0	1.9262	2.1846	43.722	24	7432500000	2570200000	4862300000
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	Idh1	13	11	11	32.4	28.5	28.5	46.674	414	3.029E-260	1.0529	1.1257	95.117	18	3328500000	1827600000	1500900000
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	Idh2	29	29	27	53.8	53.8	52.2	50.906	452	0	1.9953	2.039	124.01	176	7.8118E+10	2.3546E+10	5.4571E+10
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic	Iars	4	4	4	3.4	3.4	3.4	144.27	1262	3.9471E-09	3.0834	2.6629	10.212	3	169850000	41719000	128130000
Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	Iars2	10	10	10	12.5	12.5	12.5	112.8	1012	2.092E-124	2.3674	3.1117	102.03	15	3630200000	1146600000	2483700000
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	Ivd	12	12	12	30.9	30.9	30.9	46.325	424	9.524E-283	0.62478	0.6672	118.05	26	8825300000	5620400000	3204900000
Q9CX00	IST1 homolog	Ist1	2	2	2	4.7	4.7	4.7	39.468	362	0.0030759	0.93527	1.0854	21.421	2	48015000	24738000	23277000
Q9ET78	Junctophilin-2	Jph2	5	5	5	9.6	9.6	9.6	74.691	696	4.8437E-28	1.7969	2.6685	21.253	7	541320000	185590000	355720000
E9Q1Q9	Ketohexokinase	Khk	3	3	3	17.8	17.8	17.8	37.724	343	9.9512E-17	0.51968	0.57636	19.329	6	338920000	214880000	124040000
Q60749	KH domain-containing, RNA-binding, signal transduction-associated protein 1	Khdrbs1	1	1	1	3.2	3.2	3.2	48.37	443	0.0024146	1.6096	1.9825	2.9814	2	211400000	89289000	122110000
F8VQC7	Kinectin	Ktn1	11	11	11	13.4	13.4	13.4	152.54	1327	4.662E-143	1.1543	1.5104	227.15	10	1054700000	521210000	533510000
Q61768	Kinesin-1 heavy chain	Kif5b	22	22	22	26.3	26.3	26.3	109.55	963	0	0.78687	0.73771	51.421	20	1961700000	1503900000	457790000
F8VQ75	Kinesin-like protein KIF13A	Kif13a	2	2	2	1.1	1.1	1.1	195.7	1749	0.00059188	1.1651	1.3011	32.543	2	9165100	4056600	5108500
Q60575	Kinesin-like protein KIF1B	Kif1b	2	2	2	1.1	1.1	1.1	204.08	1816	0.0005762	2.248	2.6061	3.3118	2	31107000	9901800	21205000
O08677	Kininogen-1	Kng1	10	10	9	22.8	22.8	19.8	73.101	661	0	0.60396	0.59912	92.474	19	5033600000	3082800000	1950800000
Q8BTY1	Kynurenine--oxoglutarate transaminase 1	Ccbl1	6	6	6	18.9	18.9	18.9	47.563	424	9.3891E-38	1.3226	1.6947	80.91	9	864020000	336480000	527540000
Q71RI9	Kynurenine--oxoglutarate transaminase 3	Ccbl2	6	6	6	19.1	19.1	19.1	51.126	455	8.1921E-20	2.0015	2.2676	72.246	9	821590000	263810000	557780000
Q91YP0	L-2-hydroxyglutarate dehydrogenase, mitochondrial	L2hgdh	4	4	4	9.5	9.5	9.5	50.898	464	2.7822E-08	2.1246	1.9988	69.151	3	102040000	36499000	65537000
P21956	Lactadherin	Mfge8	2	2	2	4.8	4.8	4.8	51.24	463	2.0097E-05	1.7606	2.1116	36.426	3	82519000	28389000	54130000
Q3V384	Lactation elevated protein 1	Lace1	1	1	1	3.5	3.5	3.5	54.313	480	0.010079	3.9707	3.3853	7.0335	2	74439000	17062000	57376000
Q9CPU0	Lactoylglutathione lyase	Glo1	8	8	8	30.4	30.4	30.4	20.809	184	1.798E-33	0.81087	1.0833	147.23	12	4049200000	2670400000	1378800000
Q61029	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma	Tmpo	7	7	7	27.4	27.4	27.4	50.372	452	1.127E-104	0.8624	1.0842	48.745	9	489320000	243140000	246180000
Q60675	Laminin subunit alpha-2	Lama2	71	71	71	30.6	30.6	30.6	343.81	3118	0	0.7169	0.81757	65.717	105	1.4734E+10	8613500000	6120600000
P97927	Laminin subunit alpha-4	Lama4	14	14	14	9.7	9.7	9.7	201.82	1816	1.0177E-37	1.0203	1.2395	109.55	13	1367400000	917710000	449730000
Q61001	Laminin subunit alpha-5	Lama5	7	7	7	2.4	2.4	2.4	404.05	3718	6.1358E-11	1.3022	1.3874	29.977	7	192470000	89250000	103220000
E9QN70	Laminin subunit beta-1	Lamb1	26	26	26	18	18	18	202.44	1834	2.168E-153	0.63313	0.74923	63.942	28	2959000000	1847700000	1111400000
Q61292	Laminin subunit beta-2	Lamb2	22	22	22	17	17	17	196.58	1799	2.975E-220	0.9754	0.97595	70.294	28	1601300000	734510000	866760000
F8VQJ3	Laminin subunit gamma-1	Lamc1	33	33	33	28.9	28.9	28.9	177.19	1607	0	0.70163	0.68289	59.794	43	4088900000	2432500000	1656400000
O89112	LanC-like protein 1	Lancl1	2	2	2	8.5	8.5	8.5	45.341	399	1.0741E-19	2.1584	2.3634	15.879	2	109500000	31325000	78171000
Q9Z1R2	Large proline-rich protein BAG6	Bag6	3	3	3	4.2	4.2	4.2	121.04	1154	9.5957E-24	0.99419	1.0541	23.019	2	103500000	52715000	50784000
Q8C0M9	L-asparaginase	Asrgl1	5	5	5	23	23	23	33.95	326	9.527E-224	0.56534	0.71757	135.77	6	887510000	577720000	309790000
Q8K4G1	Latent-transforming growth factor beta-binding protein 4	Ltbp4	6	6	6	6.1	6.1	6.1	178.64	1666	1.0183E-49	0.70986	0.80375	95.98	5	108730000	68604000	40128000
Q3UHZ5	Leiomodin-2	Lmod2	2	2	2	6.2	6.2	6.2	62.018	550	3.3993E-05	1.6776	1.907	31.125	2	205720000	79193000	126520000
Q9Z2I0	LETM1 and EF-hand domain-containing protein 1, mitochondrial	Letm1	9	9	9	18.7	18.7	18.7	82.988	738	1.6551E-48	0.79835	0.92493	35.834	8	333140000	188920000	144220000
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	Lrpprc	39	39	39	33.1	33.1	33.1	156.61	1392	1.662E-285	1.4655	1.8166	85.511	59	1.4797E+10	5447700000	9349600000
Q5S006	Leucine-rich repeat serine/threonine-protein kinase 2	Lrrk2	2	2	2	0.6	0.6	0.6	284.73	2527	0.0054867	0.80854	1.2687	152.97	4	2443100000	1126200000	1316900000
E9PV22	Leucine-rich repeat-containing protein 47	Lrrc47	4	4	4	10.4	10.4	10.4	65.903	603	1.9278E-16	2.0611	2.3122	49.868	4	178580000	56325000	122260000
Q8BMJ2	Leucine--tRNA ligase, cytoplasmic	Lars	2	2	2	3.6	3.6	3.6	134.19	1178	1.0051E-17	2.9865	3.3478	107.94	2	144960000	65358000	79598000
Q8C129	Leucyl-cystinyl aminopeptidase	Lnpep	6	6	6	7.1	7.1	7.1	117.3	1025	3.7644E-17	0.77977	0.80744	46.285	4	255850000	153040000	102800000
P42703	Leukemia inhibitory factor receptor	Lifr	3	3	3	4.9	4.9	4.9	122.57	1092	3.863E-15	0.92597	0.77613	115.9	2	56829000	20762000	36068000
P24527	Leukotriene A-4 hydrolase	Lta4h	16	16	16	30.4	30.4	30.4	69.05	611	6.906E-241	0.90467	1.1405	86.626	18	2098700000	1141600000	957070000
D3YU59	LIM and calponin homology domains-containing protein 1	Limch1	5	5	5	4.7	4.7	4.7	120.99	1083	1.561E-11	1.1406	1.4368	60.561	7	281000000	121110000	159890000
Q8VEE1	LIM and cysteine-rich domains protein 1	Lmcd1	4	4	4	14	14	14	40.996	365	2.2862E-98	0.4046	0.44567	126.61	2	115030000	79339000	35689000
Q9D7B2	LIM and senescent cell antigen-like-containing domain protein 1	Lims1	2	2	2	5.6	5.6	5.6	45.593	396	8.1455E-05	4.1765	4.8863	103.98	2	120180000	19278000	100900000
Q9JKS4	LIM domain-binding protein 3	Ldb3	19	19	5	36.7	36.7	9	76.431	723	0	0.69529	0.77371	111.07	36	1.3557E+10	7197100000	6360100000
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	Dbt	11	11	11	21	21	21	53.246	482	8.3221E-96	0.87718	1.229	76.699	10	3287700000	1638000000	1649700000
Q8BFW7	Lipoma-preferred partner homolog	Lpp	3	3	3	10.4	10.4	10.4	65.89	613	5.1607E-23	1.5582	1.5211	68.026	2	79642000	30220000	49423000
P11152	Lipoprotein lipase	Lpl	2	2	2	6.3	6.3	6.3	53.109	474	1.1234E-17	2.1628	4.1502	59.865	2	307900000	90763000	217140000
G3X9J4	LisH domain and HEAT repeat-containing protein KIAA1468	2310035C23Rik	2	2	2	2.6	2.6	2.6	134.57	1216	0.00034884	0.15955	0.14458	272.67	2	17400000	10533000	6866400
G5E8N5	L-lactate dehydrogenase	Ldha	14	12	12	39.3	32.4	32.4	39.758	361	1.625E-283	0.87851	1.111	73.369	26	1.6688E+10	8816600000	7871800000
P16125	L-lactate dehydrogenase B chain	Ldhb	17	17	15	44.6	44.6	37.1	36.572	334	0	0.67584	0.80695	85.959	53	8.3717E+10	5.0197E+10	3.352E+10
Q8CGK3	Lon protease homolog, mitochondrial	Lonp1	18	18	17	20	20	19.3	105.84	949	0	1.2408	1.3204	83.837	26	4849000000	2064300000	2784700000
P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadl	17	17	17	39.3	39.3	39.3	47.907	430	0	1.452	1.5374	66.826	113	1.5055E+10	5633500000	9421600000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
D3Z041	Long-chain-fatty-acid--CoA ligase 1	Acsl1	23	23	23	40.2	40.2	40.2	78.034	699	0	1.3279	1.4701	62.017	37	6234500000	2622700000	3611800000
P51885	Lumican	Lum	10	10	10	30.5	30.5	30.5	38.265	338	2.3331E-72	0.56603	0.58574	34.861	8	464460000	292940000	171520000
P32067	Lupus La protein homolog	Ssb	4	4	4	9.6	9.6	9.6	47.756	415	7.9052E-07	1.2863	1.2399	44.503	3	59020000	29919000	29101000
Q8K215	LYR motif-containing protein 4	Lyrm4	3	3	3	37.4	37.4	37.4	10.854	91	5.6488E-22	1.2906	1.4104	0.92275	2	60577000	28343000	32234000
Q91V16	LYR motif-containing protein 5	Lyrm5	1	1	1	10.5	10.5	10.5	10.391	86	0.029274	3.0017	4.7272	24.346	2	212370000	57583000	154790000
Q9DA03	LYR motif-containing protein 7	Lyrm7	1	1	1	18.3	18.3	18.3	12.047	104	1.2263E-16	0.9628	1.2422	3.3436	2	515710000	251240000	264460000
Q8BP40	Lysophosphatidic acid phosphatase type 6	Acp6	9	9	9	32.1	32.1	32.1	47.624	418	1.24E-159	0.57234	0.61746	54.717	12	2110800000	1420400000	690360000
Q9Z0M5	Lysosomal acid lipase/cholesteryl ester hydrolase	Lipa	1	1	1	5.5	5.5	5.5	45.325	397	7.0743E-05	2.2859	2.2393	55.703	2	155660000	43980000	111680000
P70699	Lysosomal alpha-glucosidase	Gaa	3	3	3	4.6	4.6	4.6	106.25	953	2.9187E-16	1.4055	1.6982	52.008	5	128280000	47265000	81018000
P10619	Lysosomal protective protein	CTSA	12	12	11	27.7	27.7	27.7	54.465	480	0	4.9081	5.2674	252.74	37	5.9352E+10	359740000	5.8992E+10
Q8R2P8	Lysyl-tRNA synthetase	Kars	9	9	9	15.1	15.1	15.1	71.29	624	8.3902E-98	1.1036	1.2678	81.478	13	1185300000	589410000	595880000
Q9DAR7	m7GpppX diphosphatase	Dcps	6	6	6	23.1	23.1	23.1	38.988	338	1.0821E-16	0.91166	1.1403	43.971	6	734510000	347610000	386900000
P09581	Macrophage colony-stimulating factor 1 receptor	Csf1r	1	1	1	1.6	1.6	1.6	109.18	977	1.2386E-14	0.65585	0.70047	14.641	2	130990000	73352000	57635000
Q61830	Macrophage mannose receptor 1	Mrc1	4	4	4	3	3	3	164.98	1456	5.1849E-06	1.262	1.0967	35.876	5	219230000	108720000	110510000
P24452	Macrophage-capping protein	Capg	3	3	3	15.6	15.6	15.6	39.24	352	1.5553E-12	1.145	0.94287	26.956	3	103070000	44310000	58758000
Q9D967	Magnesium-dependent phosphatase 1	Mdp1	3	3	3	25	25	25	18.582	164	2.6577E-11	1.7081	1.8072	71.177	4	36689000	9368800	27320000
A2CEL1	Major urinary protein 1	Mup1	8	2	2	62.2	12.8	12.8	20.634	180	2.736E-103	0.42802	0.89168	48.918	2	148380000	106690000	41690000
P11589	Major urinary protein 2	Mup2	8	8	2	60.6	60.6	11.1	20.663	180	3.646E-104	0.78064	0.79843	47.737	15	1571100000	937310000	633790000
E9Q3X0	Major vault protein	Mvp	4	4	4	6.6	6.6	6.6	96.856	870	3.5511E-10	4.822	4.8256	5.6796	2	242720000	40202000	202520000
P14152	Malate dehydrogenase, cytoplasmic	Mdh1	16	16	16	33.5	33.5	33.5	36.511	334	0	0.63317	0.71216	74.744	103	1.235E+11	7.2476E+10	5.1019E+10
P08249	Malate dehydrogenase, mitochondrial	Mdh2	24	24	24	64.2	64.2	64.2	35.611	338	0	0.63199	0.6898	82.598	257	1.5695E+11	9.5647E+10	6.13E+10
Q9WVL0	Maleylacetoacetate isomerase	Gstz1	3	3	3	17.6	17.6	17.6	24.275	216	1.5198E-34	1.3146	1.5816	87.84	4	522600000	223550000	299050000
Q99J39	Malonyl-CoA decarboxylase, mitochondrial	Mlycd	8	8	8	29.5	29.5	29.5	54.735	492	0	1.61	1.7981	58.399	9	1704900000	610790000	1094100000
Q922H4	Mannose-1-phosphate guanyltransferase alpha	Gmppa	2	2	2	7.1	7.1	7.1	46.244	420	0.00024687	1.4345	1.3045	45.954	3	38179000	20438000	17741000
Q8BTZ7	Mannose-1-phosphate guanyltransferase beta	Gmppb	4	4	4	16.7	16.7	16.7	39.916	360	4.0573E-10	1.0557	1.4284	111.77	5	735420000	476440000	258990000
Q924M7	Mannose-6-phosphate isomerase	Mpi	10	10	10	33.8	33.8	33.8	46.575	423	8.609E-243	0.53414	0.62718	83.798	13	995750000	750630000	245120000
P49138	MAP kinase-activated protein kinase 2	Mapkapk2	5	5	4	16.1	16.1	13	44.049	386	7.6513E-17	1.117	1.1105	28.54	7	821060000	429760000	391300000
P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadm	23	23	23	45.1	45.1	45.1	46.481	421	0	1.1422	1.2504	73.634	74	2.7845E+10	1.2384E+10	1.5461E+10
Q8BJ34	Meiosis arrest female protein 1	Marf1	1	1	1	0.4	0.4	0.4	192.06	1730	0.028995	1.5795	2.4328	14.46	2	241590000	98019000	143570000
O70423	Membrane primary amine oxidase	Aoc3	4	4	4	6.8	6.8	6.8	84.533	765	4.6965E-12	1.0488	1.0949	41.665	4	83397000	38022000	45375000
Q3UI33	Methionine aminopeptidase	Metap2	3	3	3	11.3	11.3	11.3	54.117	488	1.4951E-39	1.1789	1.22	5.7703	4	82713000	38287000	44427000
Q78J03	Methionine-R-sulfoxide reductase B2, mitochondrial	Msrb2	8	8	8	37.7	37.7	37.7	19.157	175	1.212E-237	0.46131	0.58433	102.84	13	3699000000	2506200000	1192800000
Q8BU85	Methionine-R-sulfoxide reductase B3, mitochondrial	Msrb3	4	4	4	19	19	19	26.832	253	3.3339E-08	0.50862	0.71322	109.77	4	464310000	309500000	154810000
E9QB02	Methionine--tRNA ligase, cytoplasmic	Mars	5	5	5	9	9	9	102.37	910	2.4114E-20	2.5332	2.3956	23.431	3	75782000	18548000	57234000
Q499X9	Methionine--tRNA ligase, mitochondrial	Mars2	3	3	3	9.2	9.2	9.2	65.804	586	1.8184E-07	2.6372	2.2975	50.466	3	145530000	45561000	99967000
Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	Mccc2	8	8	8	18.5	18.5	18.5	61.378	563	1.8152E-22	5.538	9.4324	51.919	4	343700000	52927000	290780000
Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	Mccc1	11	11	11	24.3	24.3	24.3	79.343	717	6.562E-118	3.5833	4.2905	45.132	11	1547500000	364490000	1183000000
Q9JLZ3	Methylglutaconyl-CoA hydratase, mitochondrial	Auh	7	7	7	25.5	25.5	25.5	33.395	314	0	1.708	2.2594	80.449	13	3576600000	1228000000	2348600000
Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Aldh6a1	23	23	23	59.6	59.6	59.6	57.915	535	0	1.3495	1.5675	68.729	53	1.536E+10	6255900000	9104000000
Q9D1I5	Methylmalonyl-CoA epimerase, mitochondrial	Mcee	2	2	2	18	18	18	19.017	178	9.616E-249	0.51328	0.5183	26.712	6	3174300000	2209300000	964990000
P16332	Methylmalonyl-CoA mutase, mitochondrial	Mut	15	15	15	27.4	27.4	27.4	82.843	748	1.188E-142	1.6166	2.2105	87.15	17	3296800000	1260800000	2035900000
Q99J09	Methylosome protein 50	Wdr77	4	4	4	19.6	19.6	19.6	36.942	342	3.8255E-15	1.3982	1.3263	32.236	2	99127000	45862000	53265000
Q9CQT1	Methylthioribose-1-phosphate isomerase	Mri1	2	2	2	8.7	8.7	8.7	39.41	369	1.712E-17	2.8472	3.0553	33.468	2	80692000	25359000	55332000
E9PVY8	Microtubule-actin cross-linking factor 1	Macf1	3	3	3	0.6	0.6	0.6	831.87	7355	2.3421E-05	3.0841	4.2719	0.65281	2	344520000	124290000	220230000
A2A5Y6	Microtubule-associated protein	Mapt	8	8	8	18.2	18.2	18.2	78.085	749	3.465E-154	0.6094	0.55598	68.968	12	713620000	491500000	222120000
F7CK47	Microtubule-associated protein	Mtap4	24	24	21	26.8	26.8	22.9	152.67	1441	5.713E-293	0.54026	0.57944	82.47	29	3015200000	1898800000	1116400000
A2ARP8	Microtubule-associated protein 1A	Mtap1a	2	2	2	0.8	0.8	0.8	325.88	3014	0.0011651	0.47552	0.51822	2.8953	2	38168000	24334000	13834000
P14873	Microtubule-associated protein 1B	Map1b	5	5	5	3.2	3.2	3.2	270.25	2464	5.9026E-16	1.9914	2.1299	160.75	4	117290000	40890000	76398000
P27546	Microtubule-associated protein 4	Map4	16	13	13	24.4	19.4	19.4	117.43	1125	0	0.5416	0.61257	93.356	16	1959200000	1246300000	712980000
Q61166	Microtubule-associated protein RP/EB family member 1	Mapre1	2	2	2	11.2	11.2	11.2	30.016	268	1.9956E-09	1.2592	1.3645	33.544	2	95341000	40500000	54841000
Q8R001	Microtubule-associated protein RP/EB family member 2	Mapre2	3	3	3	10.7	10.7	10.7	36.946	326	8.8743E-07	1.3338	4.0907	64.751	3	363480000	154030000	209460000
Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	Aldh1l2	7	7	7	10.6	10.6	10.6	101.59	923	2.6327E-20	0.80547	0.79792	47.483	6	340900000	187380000	153520000
Q9CR62	Mitochondrial 2-oxoglutarate/malate carrier protein	Slc25a11	8	8	8	27.1	27.1	27.1	34.155	314	3.485E-55	0.84394	1.0128	77.068	9	1285300000	689290000	596040000
Q8VCF0	Mitochondrial antiviral-signaling protein	Mavs	6	6	6	23.3	23.3	23.3	53.398	503	6.1471E-28	0.94281	0.93988	24.041	5	67311000	34481000	32830000
Q9Z2Z6	Mitochondrial carnitine/acylcarnitine carrier protein	Slc25a20	5	5	5	16.6	16.6	16.6	33.026	301	9.4237E-39	1.2383	1.095	88.337	6	780670000	384460000	396210000
Q791V5	Mitochondrial carrier homolog 2	Mtch2	6	6	6	29	29	29	33.499	303	1.0267E-32	1.1838	1.4363	30.931	7	912360000	465000000	447360000
Q9CQ92	Mitochondrial fission 1 protein	Fis1	2	2	2	15.8	15.8	15.8	17.008	152	8.9879E-06	0.535	0.57817	56.676	2	29326000	18254000	11072000
Q9CRB8	Mitochondrial fission process protein 1	Mtfp1	4	4	4	33.7	33.7	33.7	18.314	166	9.4881E-16	0.9931	0.93861	55.068	4	561750000	292110000	269630000
P62073	Mitochondrial import inner membrane translocase subunit Tim10	Timm10	3	3	3	23.3	23.3	23.3	10.333	90	2.6105E-09	0.76734	0.70883	10.705	2	337610000	184230000	153380000
P62075	Mitochondrial import inner membrane translocase subunit Tim13	Timm13	4	4	4	52.6	52.6	52.6	10.458	95	1.3887E-61	1.0766	1.0497	18.291	8	1412200000	715370000	696850000
O35857	Mitochondrial import inner membrane translocase subunit TIM44	Timm44	6	6	6	16.2	16.2	16.2	51.091	452	6.8053E-18	1.4327	1.4108	11.797	4	32937000	13636000	19301000
Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	Timm8a1	3	3	3	38.1	38.1	38.1	11.042	97	3.3593E-24	0.64634	1.2565	71.21	4	2107400000	1305100000	802320000
P62077	Mitochondrial import inner membrane translocase subunit Tim8 B	Timm8b	2	2	2	21.7	21.7	21.7	9.2864	83	4.5994E-22	0.79871	1.0788	54.069	4	415930000	257170000	158750000
Q9WV98	Mitochondrial import inner membrane translocase subunit Tim9	Timm9	3	3	3	52.8	52.8	52.8	10.344	89	6.964E-112	0.84572	1.2363	75.703	7	1346000000	681450000	664600000
Q9QYA2	Mitochondrial import receptor subunit TOM40 homolog	Tomm40	1	1	1	3	3	3	37.895	361	0.00019378	1.0616	1.0806	4.1732	2	91080000	46680000	44400000
Q9CZW5	Mitochondrial import receptor subunit TOM70	Tomm70a	3	3	3	5.4	5.4	5.4	67.589	611	1.5412E-05	0.99212	1.0405	102.61	2	62816000	29946000	32870000
Q8CAQ8	Mitochondrial inner membrane protein	Immt	13	13	13	23.2	23.2	23.2	83.899	757	8.788E-104	0.92361	1.1526	60.734	19	1560400000	793470000	766880000
Q8VEA4	Mitochondrial intermembrane space import and assembly protein 40	Chchd4	2	2	2	26.6	26.6	26.6	15.525	139	3.0738E-77	0.2965	0.25256	42.872	3	255880000	204120000	51754000
Q9D6Y7	Mitochondrial peptide methionine sulfoxide reductase	Msra	9	9	9	54.5	54.5	54.5	25.988	233	5.186E-118	0.7387	0.88913	42.292	16	2829300000	1543800000	1285500000
Q9DAT5	Mitochondrial tRNA-specific 2-thiouridylase 1	Trmu	2	2	2	7	7	7	47.24	417	0.00010453	2.0473	2.0114	2.2612	2	123020000	36257000	86765000
Q9DC61	Mitochondrial-processing peptidase subunit alpha	Pmpca	12	12	12	26.7	26.7	26.7	58.278	524	2.429E-84	1.2182	1.3645	17.114	15	3008800000	1206300000	1802500000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q9CXT8	Mitochondrial-processing peptidase subunit beta	Pmpcb	2	2	2	6.3	6.3	6.3	54.614	489	3.7132E-05	1.3626	1.3817	70.353	3	468830000	220510000	248310000
Q811U4	Mitofusin-1	Mfn1	3	3	3	6.3	6.3	6.3	83.725	741	0.00012117	1.5884	1.8905	43.556	3	77091000	39429000	37661000
P63085	Mitogen-activated protein kinase 1	Mapk1	3	3	3	13.1	13.1	13.1	41.275	358	3.4465E-11	2.2415	3.0319	80.481	3	238610000	96574000	142040000
P47811	Mitogen-activated protein kinase 14	Mapk14	5	5	5	18.1	18.1	18.1	41.287	360	2.6082E-14	3.156	3.4906	228.55	4	453570000	74377000	379190000
D3Z3G6	Mitogen-activated protein kinase 3	Mapk3	2	2	2	9.5	9.5	9.5	42.401	380	0.0054598	2.1257	5.2825	86.139	2	86786000	30829000	55957000
P26041	Moesin	Msn	13	9	9	22.2	17	17	67.766	577	2.6801E-75	1.3132	2.1931	75.405	12	1869900000	812030000	1057900000
D3YYS6	Monoglyceride lipase	Mgll	4	4	4	18.1	18.1	18.1	36.654	331	9.9577E-08	1.2806	1.5234	66.508	3	104980000	48165000	56811000
Q8BKY8	mTERF domain-containing protein 3, mitochondrial	Mterfd3	2	2	2	5.2	5.2	5.2	43.452	385	8.7149E-10	1.1383	1.115	6.1706	3	221160000	117460000	103700000
Q9DCL9	Multifunctional protein ADE2	Paics	12	12	12	36	36	36	47.006	425	2.433E-89	0.99143	1.0365	57.3	15	2770100000	1294400000	1475800000
A6H6E2	Multimerin-2	Mmrn2	2	2	2	3.2	3.2	3.2	105.21	943	3.3532E-13	0.80471	1.1993	22.395	2	148120000	91965000	56157000
Q9Z2L6	Multiple inositol polyphosphate phosphatase 1	Minpp1	4	4	4	12.5	12.5	12.5	54.537	481	3.7541E-11	0.85124	0.82976	14.595	3	152340000	79465000	72879000
P28665	Murinoglobulin-1	Mug1	29	29	29	24.6	24.6	24.6	165.3	1476	0	0.52016	0.60089	182.13	34	3.4935E+10	5296800000	2.9639E+10
A2AMM0	Muscle-related coiled-coil protein	Murc	3	3	3	12.7	12.7	12.7	41.008	362	3.9664E-21	1.9031	5.7471	85.124	4	123410000	31036000	92378000
V9GX62	Muscular LMNA-interacting protein	Mlip	7	1	1	35.6	3.7	3.7	29.564	270	1.762E-177	0.48059	0.63171	10.626	2	227620000	154250000	73375000
Q99JI1	Musculoskeletal embryonic nuclear protein 1	Mustn1	1	1	1	13.4	13.4	13.4	8.941	82	5.7583E-10	0.62012	0.62378	63.902	2	83320000	46667000	36653000
O08539	Myc box-dependent-interacting protein 1	Bin1	1	1	1	3.2	3.2	3.2	64.469	588	0.00029286	0.78635	0.78206	46.101	2	93784000	59016000	34768000
Q8CD15	Myc-induced nuclear antigen	Mina	2	2	2	5.6	5.6	5.6	53.516	465	0.0022222	8.274	7.6971	179.34	2	152620000	13541000	139080000
E9PZ54	Myocardial zonula adherens protein	Gcom1	5	5	5	9.5	9.5	9.5	63.506	550	2.0503E-10	0.95373	0.90442	13.513	4	126390000	65801000	60591000
P04247	Myoglobin	Mb	13	13	13	82.5	82.5	82.5	17.069	154	0	0.15988	0.16613	109.66	137	1.083E+11	9.2743E+10	1.5556E+10
Q62234	Myomesin-1	Myom1	39	39	39	27.5	27.5	27.5	185.46	1667	0	1.3036	1.5484	80.643	48	5756100000	2401800000	3354300000
P09542	Myosin light chain 3	Myl3	12	12	8	64.2	64.2	51	22.421	204	4.584E-196	0.65106	0.67894	87.872	82	5.5026E+10	3.2022E+10	2.3004E+10
P09541	Myosin light chain 4	Myl4	5	4	4	32.6	26.9	26.9	21.159	193	2.6158E-54	0.62495	0.77685	87.159	5	1129800000	680780000	449020000
B1B1A8	Myosin light chain kinase, smooth muscle	Mylk	9	9	9	7.8	7.8	7.8	213.61	1950	1.0892E-26	0.56814	0.63458	62.332	8	446500000	297440000	149060000
Q60605	Myosin light polypeptide 6	Myl6	4	4	4	36.4	36.4	36.4	16.93	151	9.4288E-09	1.1927	1.1628	92.343	4	460460000	190160000	270300000
Q9QVP4	Myosin regulatory light chain 2, atrial isoform	Myl7	7	7	7	55.4	55.4	55.4	19.45	175	6.3597E-33	0.57186	0.7404	84.814	9	2418200000	1568600000	849570000
P51667	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	Myl2	8	8	2	49.4	49.4	21.1	18.864	166	1.7348E-82	1.1444	1.3251	133.97	12	7829800000	4014500000	3815300000
Q02566	Myosin-6	Myh6	47	47	16	30.9	30.9	12.6	223.56	1938	0	2.3518	2.6214	72.452	55	9633400000	3197200000	6436200000
Q3UIK0	Myosin-binding protein C, cardiac-type	Mybpc3	58	58	58	55.9	55.9	55.9	141.39	1278	0	1.9412	2.1251	61.21	136	5.8763E+10	1.7117E+10	4.1647E+10
Q9JJW5	Myozenin-2	Myoz2	3	3	3	13.3	13.3	13.3	29.761	264	7.0973E-30	1.469	1.4763	44.279	5	508040000	226890000	281150000
P26645	Myristoylated alanine-rich C-kinase substrate	Marcks	2	2	2	11.7	11.7	11.7	29.661	309	1.0533E-43	0.41706	0.37341	46.229	5	136370000	96063000	40311000
Q64191	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	Aga	4	4	4	11.6	11.6	11.6	37.022	346	6.824E-29	0.87939	0.82829	97.02	3	72092000	35166000	36925000
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	Ddah1	2	2	2	9.1	9.1	9.1	31.381	285	1.1974E-06	0.38388	0.376	27.755	2	142380000	103050000	39327000
Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	Ddah2	4	4	4	17.9	17.9	17.9	29.645	285	1.4956E-46	0.66946	0.88177	84.717	3	425880000	322000000	103880000
P70441	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	Slc9a3r1	3	3	3	14.1	14.1	14.1	38.6	355	5.6319E-59	0.61511	0.5651	16.939	5	109190000	73529000	35661000
Q9JHL1	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	Slc9a3r2	7	7	7	25.2	25.2	25.2	37.402	337	8.2669E-39	0.8788	1.6063	72.255	10	1773600000	940420000	833190000
Q9D997	N-acetyl-D-glucosamine kinase	Nagk	3	3	3	11.4	11.4	11.4	39.346	361	4.7703E-08	1.8457	1.6861	21.28	4	578750000	209770000	368980000
Q8C5H8	NAD kinase domain-containing protein 1	Nadkd1	6	6	6	17.5	17.5	17.5	50.858	452	6.562E-13	2.1562	2.1295	49.705	7	555200000	240990000	314210000
Q61941	NAD(P) transhydrogenase, mitochondrial	Nnt	22	22	22	26.7	26.7	26.7	113.84	1086	2.048E-159	0.82608	0.95277	71.978	29	5889000000	3295800000	2593300000
Q64669	NAD(P)H dehydrogenase [quinone] 1	Nqo1	4	4	4	19.7	19.7	19.7	30.959	274	5.5477E-39	1.8437	2.5784	71.615	8	1306600000	451220000	855430000
Q8K4Z3	NAD(P)H-hydrate epimerase	Apoa1bp	7	7	7	33.3	33.3	33.3	30.972	282	2.3992E-78	1.5041	2.3425	73.725	12	736340000	299010000	437330000
Q8VDQ8	NAD-dependent protein deacetylase sirtuin-2	Sirt2	3	3	3	16.2	16.2	16.2	43.256	389	1.6102E-18	1.8279	2.2962	44.167	3	99060000	30954000	68106000
Q8R104	NAD-dependent protein deacetylase sirtuin-3	Sirt3	3	3	3	14.1	14.1	14.1	36.614	334	1.308E-16	1.7429	1.7789	53.111	4	465380000	165490000	299890000
Q8K2C6	NAD-dependent protein deacylase sirtuin-5, mitochondrial	Sirt5	11	11	11	44.8	44.8	44.8	34.134	310	8.306E-164	1.3413	1.4329	68.624	13	2471200000	1063000000	1408200000
O35683	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	Ndufa1	1	1	1	14.3	14.3	14.3	8.1384	70	0.00036386	1.5004	1.2477	0.65878	2	659150000	268130000	391020000
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	Ndufa10	10	10	10	31.3	31.3	31.3	40.603	355	0	1.7526	2.0064	94.675	24	9838100000	2429400000	7408700000
G5E814	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	Ndufa11	4	4	4	36.4	36.4	36.4	15.115	143	2.8709E-45	0.84616	0.84844	24.849	8	3180600000	1670400000	1510300000
Q7TMF3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	Ndufa12	4	4	4	32.4	32.4	32.4	17.086	145	5.7764E-17	1.1812	1.5191	49	5	365880000	156970000	208910000
Q9ERS2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	Ndufa13	2	2	2	18.1	18.1	18.1	16.859	144	8.6532E-07	1.0276	1.363	19.908	2	404460000	182550000	221910000
Q9CQ75	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	Ndufa2	3	3	3	33.3	33.3	33.3	10.916	99	1.5348E-74	0.65466	0.6681	170.49	3	643090000	432330000	210760000
Q9CQ91	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	Ndufa3	2	2	2	41.7	41.7	41.7	9.3308	84	5.6086E-25	1.3757	1.4473	82.569	3	392760000	169240000	223520000
Q62425	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	Ndufa4	3	3	3	28	28	28	9.3267	82	7.5977E-10	0.81445	0.87433	102.39	19	1432100000	691900000	740160000
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Ndufa5	6	6	6	63.8	63.8	63.8	13.36	116	4.462E-296	0.4685	0.52623	66.32	17	6329900000	4488700000	1841200000
Q9CQZ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	Ndufa6	3	3	3	31.3	31.3	31.3	15.283	131	2.437E-222	1.1869	1.4365	11.919	5	1079700000	467430000	612260000
Q9Z1P6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	Ndufa7	4	4	4	38.9	38.9	38.9	12.575	113	1.3611E-34	0.40095	0.38386	23.701	3	398530000	292400000	106140000
Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	Ndufa8	4	4	4	30.2	30.2	30.2	19.992	172	3.0965E-24	0.9108	0.88427	85.759	4	1079400000	555180000	524250000
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	Ndufa9	8	8	8	31.6	31.6	31.6	42.525	377	1.1366E-80	1.1078	1.0938	134.67	11	1200300000	352130000	848160000
Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Ndufb10	3	3	3	25.6	25.6	25.6	21.024	176	1.2799E-11	0.85122	2.101	56.457	3	404770000	221450000	183320000
O09111	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	Ndufb11	5	5	5	44.4	44.4	44.4	17.444	151	3.7982E-12	0.72787	1.1672	73.36	7	1149500000	692730000	456730000
Q9CPU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial	Ndufb2	1	1	1	8.6	8.6	8.6	11.967	105	0.0035792	1.4364	1.4117	13.285	2	102100000	43502000	58599000
Q9CQZ6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	Ndufb3	3	3	3	26	26	26	11.692	104	2.2474E-48	1.051	1.0063	49.98	3	1314500000	669830000	644700000
Q9CQC7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	Ndufb4	3	3	3	35.7	35.7	35.7	15.081	129	2.6363E-27	1.1809	1.2768	13.334	3	731410000	349500000	381910000
Q3UIU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	Ndufb6	3	3	3	18.8	18.8	18.8	15.515	128	2.2955E-06	1.4444	1.3557	14.41	3	846900000	396620000	450280000
Q9CR61	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	Ndufb7	2	2	2	25.5	25.5	25.5	16.331	137	8.4754E-06	1.2967	1.2329	40.817	3	178400000	87060000	91340000
Q9D6J5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	Ndufb8	5	5	5	34.9	34.9	34.9	21.876	186	1.9913E-10	0.76621	0.74143	49.98	6	695290000	389920000	305370000
Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	Ndufb9	5	5	5	42.5	42.5	42.5	21.984	179	2.3733E-51	2.0272	2.6089	33.656	5	475870000	171200000	304670000
Q9CQ54	NADH dehydrogenase [ubiquinone] 1 subunit C2	Ndufc2	4	4	4	28.3	28.3	28.3	14.164	120	1.8424E-35	0.90318	1.0881	38.729	10	2137100000	1157300000	979850000
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	Ndufv1	12	12	12	40.5	40.5	40.5	50.834	464	0	1.2623	1.2504	67.522	30	1.5726E+10	7103100000	8623000000
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	Ndufv2	7	7	7	44.8	44.8	44.8	27.285	248	0	0.44297	0.47067	57.296	15	3374500000	2281200000	1093400000
Q8BK30	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	Ndufv3	1	1	1	16.3	16.3	16.3	11.813	104	4.5322E-22	0.32815	0.44386	15.221	3	1087900000	808830000	279070000
Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	Ndufs2	11	11	11	32.4	32.4	32.4	52.625	463	4.3792E-82	1.6088	1.7925	63.883	15	1758700000	688450000	1070200000
Q9DCT2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	Ndufs3	8	8	8	30.8	30.8	30.8	30.149	263	4.253E-56	0.62249	0.73738	39.187	11	708780000	418710000	290080000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
E9QPX3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	Ndufs4	6	6	6	30.3	30.3	30.3	19.803	175	6.1118E-24	0.32049	0.30476	70.832	11	1.4168E+10	1.0762E+10	3406400000
Q99LY9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	Ndufs5	3	3	3	34.9	34.9	34.9	12.648	106	1.3E-121	0.76348	0.79237	28.396	4	352970000	225000000	127970000
P52503	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	Ndufs6	7	7	7	64.7	64.7	64.7	13.02	116	0	0.4254	0.77693	114.15	32	2.0397E+10	1.523E+10	5166800000
Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	Ndufs7	2	2	2	10.3	10.3	10.3	24.683	224	2.1881E-06	1.1774	3.5944	17.351	2	649650000	288850000	360800000
Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	Ndufs8	5	5	5	26.4	26.4	26.4	24.038	212	3.1714E-62	0.96857	1.1024	168.44	5	1598600000	363180000	1235400000
F2Z456	NADH-cytochrome b5 reductase 3	Cyb5r3	2	2	2	8	8	8	34.929	313	0.00033243	1.0131	1.1582	41.097	2	99470000	46843000	52627000
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	Ndufs1	22	22	22	36.7	36.7	36.7	79.776	727	0	0.76094	0.90156	90.166	35	1.0399E+10	6097100000	4301700000
P03899	NADH-ubiquinone oxidoreductase chain 3	Mtnd3	1	1	1	13	13	13	13.219	115	2.5452E-09	0.88506	0.78801	60.66	3	164100000	100130000	63970000
P03921	NADH-ubiquinone oxidoreductase chain 5	Mtnd5	2	2	2	4.4	4.4	4.4	68.44	607	2.3577E-09	0.86535	0.89264	59.355	5	340060000	182140000	157930000
P06801	NADP-dependent malic enzyme	Me1	6	6	6	15.9	15.9	15.9	63.953	572	5.04E-61	1.3789	1.7384	80.136	8	549980000	261590000	288390000
Q8BMF3	NADP-dependent malic enzyme, mitochondrial	Me3	15	15	15	36.6	36.6	36.6	67.098	604	4.313E-163	1.9263	2.2936	84.282	19	3434500000	1086600000	2347900000
Q61578	NADPH:adrenodoxin oxidoreductase, mitochondrial	Fdxr	3	3	3	11.3	11.3	11.3	54.201	494	2.8633E-23	1.8961	2.0113	3.8064	3	281070000	115240000	165830000
G3X8Y3	N-alpha-acetyltransferase 15, NatA auxiliary subunit	Naa15	2	2	2	4.9	4.9	4.9	101.09	865	2.0693E-36	1.5691	1.3368	29.303	2	84066000	22109000	61957000
Q6ZWM4	N-alpha-acetyltransferase 38, NatC auxiliary subunit	Naa38	2	2	2	26	26	26	10.403	96	1.6093E-07	0.39459	0.38218	87.033	2	491130000	299310000	191820000
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	Naca	62	62	62	46.5	46.5	46.5	220.5	2187	0	0.42318	0.48989	63.941	108	1.2294E+10	8596600000	3697200000
P05125	Natriuretic peptides A	Nppa	3	3	3	19.1	19.1	19.1	16.572	152	3.4919E-09	0.79251	3.9048	243.26	4	4346000000	2527800000	1818200000
Q80XB4	Nebulin-related-anchoring protein	Nrap	3	3	3	2.5	2.5	2.5	195.75	1728	2.424E-13	2.7052	3.3084	12.227	2	237920000	65013000	172910000
Q6A037	NEDD4-binding protein 1	N4bp1	2	2	2	1.9	1.9	1.9	99.146	893	0.0039101	0.80178	0.82288	105.65	2	400690000	218110000	182580000
P29595	NEDD8	Nedd8	2	2	2	34.6	34.6	34.6	8.9723	81	5.2571E-14	0.30251	0.33414	71.077	2	151150000	110940000	40213000
Q8C878	NEDD8-activating enzyme E1 catalytic subunit	Uba3	6	6	6	21.2	21.2	21.2	51.737	462	1.4664E-46	0.74267	0.72916	15.51	7	663850000	360380000	303470000
Q8VBW6	NEDD8-activating enzyme E1 regulatory subunit	Nae1	5	5	5	15.9	15.9	15.9	60.273	534	2.1021E-33	0.67764	0.64952	27.333	7	518700000	317760000	200940000
P61082	NEDD8-conjugating enzyme Ubc12	Ube2m	3	3	3	17.5	17.5	17.5	20.9	183	1.9643E-46	0.65679	0.66757	169.32	3	381210000	287260000	93947000
Q6P5H2	Nestin	Nes	4	4	4	3.3	3.3	3.3	207.12	1864	3.158E-105	1.9973	1.8514	141.46	4	135520000	62576000	72947000
Q9CQ45	Neudesin	Nenf	2	2	2	19.3	19.3	19.3	18.904	171	6.743E-13	0.59564	1.3866	113.92	2	245780000	173790000	71987000
Q91YP2	Neurolysin, mitochondrial	Nln	3	3	3	5.4	5.4	5.4	80.428	704	9.9352E-07	0.84139	1.3361	30.671	2	671690000	426330000	245360000
P97300	Neuroplastin	Nptn	1	1	1	4.5	4.5	4.5	44.373	397	0.00018552	0.88786	1.8548	7.7226	2	423040000	206090000	216950000
Q9QZ23	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	Nfu1	5	5	2	26.3	26.3	12.2	28.567	255	3.3014E-34	0.56397	0.53423	8.2308	5	1154400000	758420000	396010000
Q9EPA7	Nicotinamide mononucleotide adenylyltransferase 1	Nmnat1	2	2	2	15.8	15.8	15.8	32.355	285	2.6441E-11	1.8374	1.7003	126.51	2	421120000	272560000	148560000
Q99JR6	Nicotinamide mononucleotide adenylyltransferase 3	Nmnat3	2	2	2	13.1	13.1	13.1	27.702	245	2.3765E-06	3.2929	3.1137	63.774	4	107750000	31108000	76642000
Q99KQ4	Nicotinamide phosphoribosyltransferase	Nampt	15	15	15	39.1	39.1	39.1	55.446	491	4.069E-259	1.9304	2.4257	43.613	19	6116900000	2178900000	3938000000
Q8CC86	Nicotinate phosphoribosyltransferase	Naprt1	4	4	4	10.4	10.4	10.4	58.265	538	2.6378E-18	1.2496	1.8862	35.487	4	321590000	138120000	183470000
P10493	Nidogen-1	Nid1	25	25	24	26.1	26.1	25.3	136.54	1245	0	1.1991	1.3294	65.493	32	4906700000	2184400000	2722400000
O88322	Nidogen-2	Nid2	4	3	3	4.8	4.1	4.1	153.91	1403	2.5313E-43	1.1933	1.4363	10.733	3	20192000	9496300	10696000
Q9EQ80	NIF3-like protein 1	Nif3l1	2	2	2	9.6	9.6	9.6	41.745	376	1.6493E-18	1.2631	1.1573	98.577	3	593460000	502890000	90569000
Q8VDK1	Nitrilase homolog 1	Nit1	4	4	4	16.4	16.4	16.4	35.705	323	4.326E-14	1.8686	1.8203	41.601	3	175740000	70048000	105690000
Q99K48	Non-POU domain-containing octamer-binding protein	Nono	2	2	2	5.3	5.3	5.3	54.54	473	1.2977E-05	9.8095	10.812	52.6	2	305940000	42459000	263480000
P32020	Non-specific lipid-transfer protein	Scp2	6	6	6	10.8	10.8	10.8	59.125	547	3.806E-130	0.48034	0.46984	174.63	7	3384100000	2114400000	1269700000
Q9CZ44	NSFL1 cofactor p47	Nsfl1c	9	9	9	34.6	34.6	34.6	40.709	370	2.175E-170	0.57314	0.59918	64.242	16	2104100000	1213800000	890340000
B1AU75	Nuclear autoantigenic sperm protein	Nasp	4	4	4	7.6	7.6	7.6	84.012	773	1.1348E-60	0.55409	0.57595	35.278	5	250140000	172230000	77907000
Q8R3G1	Nuclear inhibitor of protein phosphatase 1	Ppp1r8	3	3	3	6.6	6.6	6.6	38.527	351	0.00048081	0.48956	0.55034	4.8148	2	57109000	40389000	16720000
O35685	Nuclear migration protein nudC	Nudc	2	2	2	6.9	6.9	6.9	38.358	332	1.8817E-05	0.7852	2.9383	206.7	2	401390000	236080000	165310000
Q63850	Nuclear pore glycoprotein p62	Nup62	2	2	2	4.6	4.6	4.6	53.254	526	4.1747E-11	0.53422	0.70015	36.251	3	110870000	68447000	42421000
P60670	Nuclear protein localization protein 4 homolog	Nploc4	5	5	5	10.2	10.2	10.2	68.016	608	1.2341E-09	1.627	2.0635	78.838	4	87585000	26381000	61203000
P61971	Nuclear transport factor 2	Nutf2	1	1	1	21.3	21.3	21.3	14.478	127	6.2088E-12	1.3177	1.2948	120.34	3	203130000	54610000	148520000
P62960	Nuclease-sensitive element-binding protein 1	Ybx1	7	7	4	37.6	37.6	31.4	35.73	322	0	0.38149	0.42862	48.454	12	546710000	417990000	128730000
Q02819	Nucleobindin-1	Nucb1	7	7	7	19	19	19	53.408	459	2.9233E-30	1.1317	1.0919	76.685	5	53839000	24988000	28851000
P81117	Nucleobindin-2	Nucb2	1	1	1	2.6	2.6	2.6	50.304	420	0.011598	0.84668	0.80576	47.03	2	60284000	30499000	29785000
Q9D1X0	Nucleolar protein 3	Nol3	5	5	5	36.8	36.8	36.8	24.567	220	3.269E-187	0.72615	0.76742	25.341	8	957170000	546580000	410590000
P09405	Nucleolin	Ncl	7	7	7	11.2	11.2	11.2	76.722	707	1.8513E-10	2.9605	4.0876	117.06	6	413680000	121340000	292340000
Q61937	Nucleophosmin	Npm1	3	3	3	12.3	12.3	12.3	32.56	292	1.3014E-17	1.3544	1.3218	21.191	2	301520000	123770000	177740000
E9PZF0	Nucleoside diphosphate kinase	Gm20390	14	14	14	76.8	76.8	76.8	30.2	267	5.312E-102	0.54508	0.65492	140.66	45	9.0547E+10	5.6294E+10	3.4253E+10
Q9WV85	Nucleoside diphosphate kinase 3	Nme3	1	1	1	13	13	13	19.099	169	1.3172E-09	0.87803	0.8806	7.1072	2	113760000	55847000	57915000
Q8JZU0	Nucleoside diphosphate-linked moiety X motif 13	Nudt13	2	2	2	11.1	11.1	11.1	39.136	352	1.9288E-05	1.2583	1.597	36.261	3	129850000	62283000	67569000
P11930	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	Nudt19	3	3	3	12.6	12.6	12.6	40.32	357	5.0062E-08	0.71748	1.5132	60.319	3	169040000	95900000	73138000
Q9CR24	Nucleoside diphosphate-linked moiety X motif 8, mitochondrial	Nudt8	4	4	4	23.8	23.8	23.8	23.252	210	1.1413E-09	2.4684	2.2179	9.8025	5	308590000	103140000	205450000
E9PW66	Nucleosome assembly protein 1-like 1	Nap1l1	4	3	3	13.4	11	11	48.542	418	1.2021E-40	1.4555	2.7767	59.264	2	38089000	15633000	22456000
Q78ZA7	Nucleosome assembly protein 1-like 4	Nap1l4	8	8	7	29.3	29.3	26.7	42.679	375	1.7601E-84	0.82029	0.99176	37.028	10	1391900000	780120000	611740000
Q922B1	O-acetyl-ADP-ribose deacetylase MACROD1	Macrod1	6	6	6	30.7	30.7	30.7	35.294	323	5.575E-284	1.047	1.1045	18.483	15	3664200000	1742100000	1922100000
Q9CZ30	Obg-like ATPase 1	Ola1	9	9	9	27.3	27.3	27.3	44.729	396	8.3359E-57	0.58639	0.78255	52.034	7	965540000	612750000	352800000
A2AAJ9	Obscurin	Obscn	25	25	2	4.6	4.6	0.2	966.36	8891	1.1045E-69	2.2998	2.5082	88.362	21	1546600000	489200000	1057400000
Q9CRD0	OCIA domain-containing protein 1	Ociad1	2	2	2	7.7	7.7	7.7	27.61	247	1.2009E-05	0.56084	0.52934	3.5807	2	168190000	108700000	59495000
Q9D8S4	Oligoribonuclease, mitochondrial	Rexo2	3	3	3	13.5	13.5	13.5	26.738	237	1.4122E-31	0.61556	0.5039	181.6	5	618180000	285880000	332300000
Q9JHW2	Omega-amidase NIT2	Nit2	8	8	8	44.2	44.2	44.2	30.501	276	8.962E-275	1.0827	1.193	79.528	17	1054200000	496850000	557330000
Q99PG2	Opioid growth factor receptor	Ogfr	2	2	2	4.7	4.7	4.7	70.678	633	0.00012461	2.5555	4.8036	211.28	2	53667000	13244000	40422000
P29758	Ornithine aminotransferase, mitochondrial	Oat	15	15	15	36.2	36.2	36.2	48.354	439	6.422E-155	1.1444	1.348	120.81	24	5344800000	2333100000	3011700000
Q62422	Osteoclast-stimulating factor 1	Ostf1	5	5	5	29.8	29.8	29.8	23.782	215	2.4102E-14	0.87005	0.81732	109.64	7	548110000	297270000	250840000
Q4KMM3	Oxidation resistance protein 1	Oxr1	3	3	3	4.6	4.6	4.6	95.911	866	7.8257E-27	0.51514	0.8105	96.243	2	362980000	280790000	82193000
Q8VE38	Oxidoreductase NAD-binding domain-containing protein 1	Oxnad1	6	6	6	20.3	20.3	20.3	34.727	311	2.5316E-18	1.4934	1.6124	44.081	9	934140000	407580000	526560000
Q3B7Z2	Oxysterol-binding protein 1	Osbp	4	4	4	8.2	8.2	8.2	88.796	805	6.1438E-18	1.4528	2.2054	65.085	5	162070000	66926000	95148000
Q9ET54	Palladin	Palld	4	4	4	3.3	3.3	3.3	152.13	1408	2.661E-08	0.76858	0.86049	45.656	4	304340000	235150000	69186000
Q3UVT7	Palmdelphin	Palmd	4	4	4	10.5	10.5	10.5	62.616	551	2.6136E-58	0.43917	0.61033	35.919	6	780150000	515460000	264690000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O88531	Palmitoyl-protein thioesterase 1	Ppt1	4	4	4	24.2	24.2	24.2	34.49	306	1.7273E-63	1.3391	1.4082	39.904	5	412500000	172060000	240450000
Q80YV4	Pantothenate kinase 4	Pank4	7	7	7	10.5	10.5	10.5	91.521	820	1.4653E-13	2.1043	2.2094	99.227	7	323720000	127590000	196130000
Q9Z0P4	Paralemmin-1	Palm	2	2	2	6.3	6.3	6.3	41.614	383	3.305E-52	0.5255	1.6282	39.547	3	69141000	42949000	26192000
F8VQ28	Paxillin	Pxn	1	1	1	3	3	3	64.506	591	0.00068012	0.96912	1.0581	15.628	2	150350000	73057000	77295000
Q99JF8	PC4 and SFRS1-interacting protein	Psip1	3	3	3	10	10	10	59.696	528	2.244E-09	1.3527	1.4748	27.595	2	12683000	5883700	6799700
O70400	PDZ and LIM domain protein 1	Pdlim1	11	11	11	49.8	49.8	49.8	35.774	327	3.3448E-80	0.75984	0.93363	71.896	11	1246500000	718340000	528110000
O70209	PDZ and LIM domain protein 3	Pdlim3	2	2	2	11.7	11.7	11.7	34.299	316	7.3425E-08	1.2393	1.6377	5.7895	2	240160000	113270000	126890000
Q8CI51	PDZ and LIM domain protein 5	Pdlim5	9	2	2	20.6	6.3	6.3	63.299	591	1.943E-214	2.9004	3.2997	273.02	2	61975000	36277000	25698000
Q9Z0G0	PDZ domain-containing protein GIPC1	Gipc1	3	3	3	18.6	18.6	18.6	36.129	333	1.5823E-06	0.96217	0.9663	68.756	3	448690000	153700000	294990000
Q8BFY6	Peflin	Pef1	2	2	2	6.9	6.9	6.9	29.227	275	5.3954E-06	0.8474	1.0463	15.088	2	95926000	52937000	42988000
Q14C51	Pentatricopeptide repeat-containing protein 3, mitochondrial	Ptcd3	5	5	5	8.6	8.6	8.6	77.795	685	1.1821E-22	2.4244	2.6049	57.006	4	96673000	24396000	72277000
A3KG59	Peptidase M20 domain-containing protein 2	Pm20d2	7	7	7	29.2	29.2	29.2	46.481	431	7.7057E-76	0.6802	0.71642	75.346	7	639780000	357450000	282330000
P97467	Peptidyl-glycine alpha-amidating monooxygenase	Pam	4	4	4	4.7	4.7	4.7	108.96	979	5.7416E-08	0.89053	1.4582	8.5805	3	136750000	66453000	70294000
P17742	Peptidyl-prolyl cis-trans isomerase A	Ppia	6	6	6	49.4	49.4	49.4	17.971	164	0	0.96321	1.0976	50.469	34	7708700000	4098500000	3610300000
P24369	Peptidyl-prolyl cis-trans isomerase B	Ppib	6	6	6	26.9	26.9	26.9	23.713	216	2.1275E-15	0.98259	0.96461	99.886	7	1774400000	917460000	856940000
Q9CR16	Peptidyl-prolyl cis-trans isomerase D	Ppid	8	8	8	24.9	24.9	24.9	40.742	370	1.2603E-23	0.49019	0.58799	81.677	10	1450200000	1035900000	414220000
Q99KR7	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	Ppif	4	4	4	30.6	30.6	30.6	21.737	206	0	0.76791	0.85781	111.71	11	6057900000	3461200000	2596800000
P26883	Peptidyl-prolyl cis-trans isomerase FKBP1A	Fkbp1a	3	3	3	28.7	28.7	28.7	11.922	108	4.9972E-80	0.81346	1.1219	38.075	4	866630000	490280000	376360000
P45878	Peptidyl-prolyl cis-trans isomerase FKBP2	Fkbp2	2	2	2	10.7	10.7	10.7	15.344	140	1.3167E-14	1.0565	3.9078	10.84	2	148710000	74221000	74489000
Q62446	Peptidyl-prolyl cis-trans isomerase FKBP3	Fkbp3	9	9	9	39.7	39.7	39.7	25.147	224	0	0.49481	0.81707	57.443	9	1077000000	704800000	372240000
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4	Fkbp4	20	20	20	51.7	51.7	51.7	51.572	458	1.317E-197	0.56966	0.67589	78.849	25	4238200000	2071700000	2166500000
O54998	Peptidyl-prolyl cis-trans isomerase FKBP7	Fkbp7	4	4	4	15.1	15.1	15.1	24.913	218	6.8484E-28	0.23394	0.26965	36.279	2	33713000	25268000	8444600
Q9CWW6	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	Pin4	3	3	3	25.2	25.2	25.2	13.815	131	1.2764E-16	0.48198	0.74469	37.068	3	84020000	55423000	28596000
Q8R2Y8	Peptidyl-tRNA hydrolase 2, mitochondrial	Ptrh2	2	2	2	19.3	19.3	19.3	19.526	181	0.00037831	1.3182	1.1721	52.446	2	76367000	31137000	45229000
Q8CGN5	Perilipin-1	Plin1	3	3	3	8.9	8.9	8.9	55.595	517	6.0275E-13	0.68745	0.66652	121.23	3	144820000	76576000	68242000
P43883	Perilipin-2	Plin2	3	3	3	12.7	12.7	12.7	46.646	425	1.516E-10	0.65827	0.64795	14.86	2	118220000	72911000	45310000
Q9DBG5	Perilipin-3	Plin3	6	6	6	21.1	21.1	21.1	47.262	437	1.9357E-50	0.99882	0.9669	37.283	9	2326300000	1325700000	1000600000
O88492	Perilipin-4	Plin4	9	9	9	11.9	11.9	11.9	139.41	1403	2.757E-152	0.61698	0.81409	82.413	9	584720000	348850000	235870000
Q62009	Periostin	Postn	3	3	3	4.5	4.5	4.5	93.142	838	1.0677E-08	0.80425	0.92107	20.689	3	111510000	50913000	60601000
P35700	Peroxiredoxin-1	Prdx1	12	12	10	61.8	61.8	52.8	22.176	199	2.031E-148	0.56864	0.56532	111.69	28	1.7843E+10	1.1418E+10	6424900000
Q61171	Peroxiredoxin-2	Prdx2	13	13	13	69.2	69.2	69.2	21.778	198	2.487E-213	0.52268	0.56584	83.357	42	1.2821E+10	8403000000	4417600000
O08807	Peroxiredoxin-4	Prdx4	7	5	5	32.5	29.6	29.6	31.052	274	2.6818E-23	0.60171	0.75418	37.738	9	709220000	451010000	258210000
P99029	Peroxiredoxin-5, mitochondrial	Prdx5	13	13	13	53.3	53.3	53.3	21.897	210	1.438E-149	0.49049	0.68923	119.03	79	4.535E+10	3.3545E+10	1.1805E+10
O08709	Peroxiredoxin-6	Prdx6	14	14	1	71	71	10.7	24.87	224	2.913E-274	0.53858	0.59943	60.257	25	2.3551E+10	1.561E+10	7941000000
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	Acox1	4	4	4	12.3	12.3	12.3	74.648	661	3.5411E-38	2.2265	2.0119	52.818	4	181820000	47985000	133830000
Q8VCI5	Peroxisomal biogenesis factor 19	Pex19	5	5	5	26.4	26.4	26.4	32.733	299	1.7353E-51	0.69479	0.52873	24.883	3	68379000	41104000	27275000
P51660	Peroxisomal multifunctional enzyme type 2	Hsd17b4	5	5	5	9	9	9	79.481	735	1.0771E-16	1.5613	1.6381	35.822	7	615200000	254830000	360370000
Q6P8I4	PEST proteolytic signal-containing nuclear protein	Pcnp	3	3	3	22.5	22.5	22.5	18.963	178	7.6302E-08	0.40495	0.47855	29.551	3	65302000	46578000	18724000
Q8C0C7	Phenylalanine--tRNA ligase alpha subunit	Farsa	2	2	2	6.3	6.3	6.3	57.598	508	2.6058E-08	1.7387	1.7039	14.063	2	101030000	43352000	57680000
Q9WUA2	Phenylalanine--tRNA ligase beta subunit	Farsb	4	4	4	9.5	9.5	9.5	65.696	589	2.0993E-08	1.2772	1.2134	46.116	2	88001000	34457000	53545000
Q8BVF2	Phosducin-like protein 3	Pdcl3	3	3	3	17.1	17.1	17.1	27.581	240	1.0895E-09	0.94895	1.5837	70.586	3	84330000	41347000	42983000
Q501J7	Phosphatase and actin regulator 4	Phactr4	3	3	3	7.2	7.2	7.2	76.631	694	2.9367E-07	0.84014	0.58097	58.616	3	46859000	26164000	20695000
G5E902	Phosphate carrier protein, mitochondrial	Slc25a3	6	6	6	19	19	19	39.736	358	2.025E-113	1.2397	1.2088	203.28	8	2652700000	1576700000	1076000000
P70296	Phosphatidylethanolamine-binding protein 1	Pebp1	11	11	11	63.1	63.1	63.1	20.83	187	0	0.45175	0.55527	69.184	33	2.9075E+10	1.935E+10	9725400000
Q9EP69	Phosphatidylinositide phosphatase SAC1	Sacm1l	2	2	2	3.2	3.2	3.2	66.943	587	0.0057368	0.77482	0.89697	173.35	2	344850000	78016000	266830000
Q80XI4	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta	Pip4k2b	2	2	2	5.8	5.8	5.8	47.318	416	0.00063593	1.0261	1.2928	13.646	2	17927000	6371600	11556000
J3QPW1	Phosphatidylinositol transfer protein alpha isoform	Pitpna	3	3	3	8.8	8.8	8.8	32.021	272	0.00005932	0.52099	0.44459	44.465	3	107710000	74823000	32888000
Q7M6Y3	Phosphatidylinositol-binding clathrin assembly protein	Picalm	4	4	4	7	7	7	71.543	660	7.1307E-22	1.3656	1.134	93.036	7	189990000	99839000	90152000
Q9CYR6	Phosphoacetylglucosamine mutase	Pgm3	3	3	3	7.6	7.6	7.6	59.452	542	1.2184E-17	0.7726	1.8349	54.114	3	255680000	128890000	126790000
Q8K212	Phosphofurin acidic cluster sorting protein 1	Pacs1	3	3	3	4.4	4.4	4.4	104.83	961	0.00054523	1.2731	1.0989	30.003	2	91241000	42724000	48517000
Q9D0F9	Phosphoglucomutase-1	Pgm1	20	20	2	44.1	44.1	4.8	61.417	562	0	0.72306	0.93919	88.42	49	1.6249E+10	9278200000	6971200000
Q7TSV4	Phosphoglucomutase-2	Pgm2	3	3	3	6.8	6.8	6.8	68.747	620	1.1326E-26	1.0228	0.98966	54.994	8	484370000	228300000	256060000
Q8BZF8	Phosphoglucomutase-like protein 5	Pgm5	9	9	9	23.1	23.1	23.1	62.219	567	5.34E-113	1.5526	1.3887	47.642	9	507790000	137750000	370040000
P09411	Phosphoglycerate kinase 1	Pgk1	23	23	23	62.1	62.1	62.1	44.55	417	0	0.59353	0.74937	94.228	58	6.9929E+10	4.4515E+10	2.5414E+10
Q9DBJ1	Phosphoglycerate mutase 1	Pgam1	9	7	7	44.1	35.8	35.8	28.832	254	0	1.1094	1.1851	53.316	18	9003700000	4614600000	4389100000
O70250	Phosphoglycerate mutase 2	Pgam2	10	10	8	38.3	38.3	30	28.827	253	6.514E-172	0.99572	1.1891	102.11	20	2.1049E+10	1.0292E+10	1.0757E+10
Q8CHP8	Phosphoglycolate phosphatase	Pgp	5	5	5	20.2	20.2	20.2	34.54	321	1.2297E-40	1.3225	1.4882	51.805	9	615160000	297340000	317820000
P27612	Phospholipase A-2-activating protein	Plaa	6	6	6	11.6	11.6	11.6	87.22	794	6.0066E-20	1.3254	1.7506	47.852	7	274330000	124150000	150180000
O35405	Phospholipase D3	Pld3	2	2	2	4.5	4.5	4.5	54.388	488	0.0015166	1.9791	1.8675	83.852	2	103510000	37380000	66127000
Q9Z2M7	Phosphomannomutase 2	Pmm2	6	6	6	22.7	22.7	22.7	27.656	242	2.7719E-20	0.95009	0.84092	48.25	7	711180000	378450000	332730000
Q8VDG5	Phosphopantothenate--cysteine ligase	Ppcs	4	4	4	10.9	10.9	10.9	33.794	311	6.3775E-06	1.1327	1.3036	40.505	3	312510000	165170000	147340000
B1AT82	Phosphoribosyl pyrophosphate synthase-associated protein 1	Prpsap1	2	2	2	9.9	9.9	9.9	42.467	385	8.1288E-10	2.2461	1.5772	85.667	2	133750000	39414000	94336000
Q8R574	Phosphoribosyl pyrophosphate synthase-associated protein 2	Prpsap2	1	1	1	6	6	6	40.88	369	5.5256E-40	1.6972	1.4329	5.973	2	58006000	20696000	37310000
Q5SUR0	Phosphoribosylformylglycinamidine synthase	Pfas	2	2	2	2.2	2.2	2.2	144.63	1337	0.003354	1.8353	2.2726	57.063	2	87315000	17983000	69331000
Q9DB26	Phytanoyl-CoA dioxygenase domain-containing protein 1	Phyhd1	3	3	3	14.1	14.1	14.1	32.517	291	6.252E-130	0.51421	1.5989	45.769	3	161470000	106630000	54848000
P26262	Plasma kallikrein	Klkb1	7	7	7	15.8	15.8	15.8	71.382	638	3.0995E-18	0.88169	0.90727	24.693	6	113030000	51762000	61269000
P97290	Plasma protease C1 inhibitor	Serping1	4	4	4	15.3	15.3	15.3	55.584	504	2.2611E-58	0.58376	0.59394	9.6457	5	661470000	413250000	248220000
P20918	Plasminogen	Plg	8	8	8	15.9	15.9	15.9	90.807	812	1.0588E-24	3.5007	3.4694	38.453	6	234800000	56028000	178770000
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein	Serbp1	6	6	6	15.5	15.5	15.5	44.714	407	2.5825E-20	0.62775	0.79924	141.97	5	517940000	294050000	223890000
Q61233	Plastin-2	Lcp1	12	9	9	25.5	20.6	20.6	70.148	627	0	1.5657	1.5945	55.953	13	1061100000	425410000	635680000
B1AX58	Plastin-3	Pls3	15	15	12	31.9	31.9	27.1	71.745	639	1.5285E-64	0.59352	0.60621	74.775	16	2706100000	1634300000	1071900000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
B1ARB3	Platelet endothelial cell adhesion molecule	Pecam1	3	3	3	7.9	7.9	7.9	81.917	732	4.4279E-35	0.87266	0.82009	13.264	4	189420000	92873000	96551000
Q08857	Platelet glycoprotein 4	Cd36	5	5	5	14.8	14.8	14.8	52.697	472	7.7436E-25	0.90692	0.99443	51.179	9	2180200000	903770000	1276400000
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	Pafah1b1	7	7	7	19.3	19.3	19.3	46.67	410	1.8431E-81	1.8731	1.9414	39.48	9	991390000	358340000	633050000
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	Pafah1b2	2	2	2	12.2	12.2	12.2	25.581	229	6.3639E-35	0.56536	0.66304	30.053	4	420060000	273170000	146890000
Q9JHK5	Pleckstrin	Plek	1	1	1	6.9	6.9	6.9	39.9	350	3.5954E-11	2.7722	3.4252	9.2747	2	168790000	36541000	132250000
Q80TI1	Pleckstrin homology domain-containing family H member 1	Plekhh1	1	1	1	0.9	0.9	0.9	150.91	1356	0.00243	0.67995	1.8574	54.219	2	580940000	321180000	259760000
Q9QXS1	Plectin	Plec	5	5	5	1.5	1.5	1.5	534.18	4691	1.5775E-13	0.76053	0.81711	164.89	4	680500000	606730000	73775000
B2RXS4	Plexin-B2	Plxnb2	2	2	2	2.9	2.9	2.9	206.23	1842	1.036E-06	0.080568	0.08573	65.07	2	187530000	183250000	4277900
P60335	Poly(rC)-binding protein 1	Pcbp1	3	3	3	18	18	18	37.497	356	1.6026E-33	0.96199	1.3138	54.955	4	156850000	84212000	72641000
Q61990	Poly(rC)-binding protein 2	Pcbp2	3	3	3	14.4	14.4	14.4	38.221	362	4.7602E-15	0.97231	1.0005	26.586	3	293590000	152200000	141390000
Q3UEB3	Poly(U)-binding-splicing factor PUF60	Puf60	2	2	2	6.7	6.7	6.7	60.248	564	6.0229E-21	0.99083	1.6576	28.391	3	94461000	44374000	50087000
P29341	Polyadenylate-binding protein 1	Pabpc1	5	3	1	10.2	6	2.4	70.67	636	1.0758E-93	0.78204	0.79054	25.593	5	355530000	200960000	154580000
O54724	Polymerase I and transcript release factor	Ptrf	11	11	11	28.3	28.3	28.3	43.953	392	5.498E-278	1.8298	3.2036	125.95	15	2571200000	846330000	1724800000
Q91Z31	Polypyrimidine tract-binding protein 2	Ptbp2	1	1	1	3.8	3.8	3.8	57.488	531	2.1536E-12	1.1333	1.2105	24.794	2	120780000	58571000	62212000
Q8K1R3	Polyribonucleotide nucleotidyltransferase 1, mitochondrial	Pnpt1	4	4	4	6.4	6.4	6.4	85.682	783	1.6304E-10	1.8758	1.897	45.776	3	315450000	123280000	192170000
P0CG50	Polyubiquitin-C	Ubc	2	2	2	22.1	22.1	22.1	82.549	734	2.0568E-05	0.82236	0.94697	108.83	3	1245800000	698490000	547320000
Q3TVI8	Pre-B-cell leukemia transcription factor-interacting protein 1	Pbxip1	3	3	3	5.4	5.4	5.4	81.163	727	3.6494E-09	1.5673	1.8682	59.984	2	49163000	18879000	30284000
Q9CQF7	Prefoldin subunit 1	Pfdn1	2	2	2	17.2	17.2	17.2	14.255	122	0.00001251	0.6114	0.56086	26.383	2	66276000	40178000	26098000
O70591	Prefoldin subunit 2	Pfdn2	3	3	3	23.4	23.4	23.4	16.534	154	3.0405E-36	0.37665	0.44237	38.696	4	324780000	224860000	99924000
P61759	Prefoldin subunit 3	Vbp1	2	2	2	15.8	15.8	15.8	22.435	196	5.0636E-13	0.61999	0.56823	4.0892	2	47966000	30574000	17392000
Q9WU28	Prefoldin subunit 5	Pfdn5	4	4	4	29.2	29.2	29.2	17.356	154	5.9861E-07	0.0751	0.11797	42.556	2	49145000	42778000	6367200
P48678	Prelamin-A/C	Lmna	3	3	3	5.1	5.1	5.1	74.237	665	4.7543E-09	1.5778	1.8322	44.339	4	126420000	54762000	71654000
Q99KP6	Pre-mRNA-processing factor 19	Prpf19	4	4	4	13.7	13.7	13.7	55.238	504	2.5281E-14	2.2401	2.3532	14.741	4	146300000	49148000	97148000
Q8K411	Presequence protease, mitochondrial	Pitrm1	17	17	17	19.9	19.9	19.9	117.37	1036	1.128E-131	1.4271	1.7172	122.13	22	3688700000	1418100000	2270600000
Q6NSR8	Probable aminopeptidase NPEPL1	Npepl1	4	4	4	13.7	13.7	13.7	55.939	524	1.3013E-22	1.4914	2.0413	44.798	6	447560000	165470000	282090000
B1AQL0	Probable arylformamidase	Afmid	2	2	2	7.4	7.4	7.4	40.769	363	0.0043022	29.236	29.295	160.42	3	5430800000	29335000	5401500000
Q8BGV0	Probable asparagine--tRNA ligase, mitochondrial	Nars2	2	2	2	7.1	7.1	7.1	53.961	477	0.00023029	3.2613	3.011	108.37	2	63711000	10449000	53262000
Q8BTS0	Probable ATP-dependent RNA helicase DDX5	Ddx5	5	5	3	11.7	11.7	7.8	69.265	615	1.8715E-14	3.255	3.9846	113.88	5	272070000	74551000	197520000
Q9WV35	Probable C->U-editing enzyme APOBEC-2	Apobec2	5	5	5	46.4	46.4	46.4	25.66	224	1.0192E-48	0.84138	0.80432	20.058	9	413070000	259390000	153680000
G3X975	Probable cysteine--tRNA ligase, mitochondrial	Cars2	6	6	6	15.8	15.8	15.8	61.342	552	4.6614E-28	1.5331	1.8626	30.028	8	627790000	235460000	392320000
Q7TNG8	Probable D-lactate dehydrogenase, mitochondrial	Ldhd	2	2	2	7	7	7	51.847	484	4.4657E-08	1.287	1.2364	37.334	2	105130000	44522000	60604000
Q8BZA9	Probable fructose-2,6-bisphosphatase TIGAR	Tigar	4	4	4	21.9	21.9	21.9	29.19	269	4.7316E-63	1.0234	1.1096	15.049	4	328960000	159160000	169800000
Q9CXJ1	Probable glutamate--tRNA ligase, mitochondrial	Ears2	4	4	4	11.9	11.9	11.9	58.326	523	7.1812E-15	2.1665	2.5166	152.26	4	662380000	502870000	159510000
Q99KK9	Probable histidine--tRNA ligase, mitochondrial	Hars2	4	3	3	8.1	6.3	6.3	56.985	505	5.4545E-08	1.1339	1.0103	68.063	3	131680000	66200000	65479000
Q8VDC0	Probable leucine--tRNA ligase, mitochondrial	Lars2	3	3	3	3.9	3.9	3.9	101.48	902	0.00000202	2.0931	2.1895	34.582	2	65154000	21547000	43607000
Q9WVQ5	Probable methylthioribulose-1-phosphate dehydratase	Apip	5	5	5	32.8	32.8	32.8	26.949	241	2.2677E-54	0.62931	0.8484	47.87	7	372110000	205880000	166220000
A2APY7	Probable methyltransferase C20orf7 homolog, mitochondrial	Ndufaf5	6	6	6	23.9	23.9	23.9	38.404	343	4.1471E-20	1.134	1.3967	32.6	5	529650000	221730000	307920000
P86049	Probable RNA-binding protein 46	Rbm46	1	1	1	2.3	2.3	2.3	60.077	533	0.011285	2.2765	2.5753	67.819	2	422990000	109010000	313980000
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	Usp9x	5	5	3	2.3	2.3	1.7	290.71	2559	1.5676E-23	3.4998	3.3056	50.937	4	174480000	49204000	125280000
P49935	Pro-cathepsin H	Ctsh	1	1	1	6.6	6.6	6.6	37.17	333	5.6192E-13	2.8214	2.808	13.997	2	157470000	44695000	112770000
Q9WU78	Programmed cell death 6-interacting protein	Pdcd6ip	8	8	8	12.9	12.9	12.9	96.023	869	5.1289E-77	1.1556	1.5729	87.724	10	1315900000	596630000	719270000
D3Z7Q5	Programmed cell death protein 5	Pdcd5	4	4	4	22.9	22.9	22.9	21.985	205	1.0968E-11	0.56128	0.93278	62.734	2	433190000	238080000	195110000
P12815	Programmed cell death protein 6	Pdcd6	2	2	2	9.9	9.9	9.9	21.867	191	0.002978	0.81426	1.04	68.341	3	308890000	159430000	149450000
P67778	Prohibitin	Phb	4	4	4	21.3	21.3	21.3	29.82	272	1.1602E-07	1.1284	1.8047	35.503	3	292920000	128100000	164820000
O35129	Prohibitin-2	Phb2	5	5	5	23.1	23.1	23.1	33.296	299	8.5491E-31	1.3043	1.3743	18.869	6	768250000	309710000	458540000
Q9JK53	Prolargin	Prelp	4	4	4	11.1	11.1	11.1	43.292	378	2.4228E-09	1.1409	1.1906	44.686	4	269310000	114840000	154470000
P50580	Proliferation-associated protein 2G4	Pa2g4	11	11	11	32	32	32	43.698	394	0	1.0842	1.2812	73.932	11	1328700000	703970000	624690000
Q9Z2Y8	Proline synthase co-transcribed bacterial homolog protein	Prosc	8	8	8	37.6	37.6	37.6	30.048	274	6.06E-108	0.82855	0.82335	65.923	8	577630000	323480000	254150000
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	Lrp1	7	7	7	1.5	1.5	1.5	504.74	4545	8.9496E-10	0.84493	0.87117	50.411	4	185230000	100050000	85183000
Q9QUR6	Prolyl endopeptidase	Prep	14	14	14	27.9	27.9	27.9	80.751	710	1.3618E-76	1.2623	1.8779	64.318	17	1252100000	531920000	720210000
Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondrial	Pcca	16	16	16	26.8	26.8	26.8	79.921	724	3.794E-191	0.84498	0.94726	82.135	37	7566700000	4923200000	2643600000
Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial	Pccb	12	12	12	35.5	35.5	35.5	58.408	541	0	1.1311	1.3367	69.044	21	2896300000	1443600000	1452700000
Q8BWM0	Prostaglandin E synthase 2	Ptges2	3	3	3	14.1	14.1	14.1	43.323	384	2.7203E-28	1.2769	1.6215	71.442	4	342730000	79399000	263330000
Q9R0Q7	Prostaglandin E synthase 3	Ptges3	3	3	3	17.5	17.5	17.5	18.721	160	1.0303E-13	1.5112	1.5076	34.545	4	812270000	336880000	475390000
Q8VDQ1	Prostaglandin reductase 2	Ptgr2	7	7	7	28.8	28.8	28.8	38.015	351	1.4945E-39	0.83924	0.7123	35.274	7	484920000	262390000	222530000
Q9DB60	Prostamide/prostaglandin F synthase	Fam213b	5	5	5	25.4	25.4	25.4	21.67	201	6.7242E-19	1.6229	1.7893	124.64	6	1550400000	663500000	886920000
P97371	Proteasome activator complex subunit 1	Psme1	6	6	6	28.5	28.5	28.5	28.673	249	2.6599E-20	0.55792	1.2804	126.43	8	1862400000	1069300000	793060000
P97372	Proteasome activator complex subunit 2	Psme2	5	5	5	25.1	25.1	25.1	27.057	239	1.3637E-11	0.74341	0.90397	76.514	6	502320000	296820000	205490000
Q5SSW2	Proteasome activator complex subunit 4	Psme4	4	4	4	2.9	2.9	2.9	211.19	1843	8.6618E-13	1.2216	1.3508	63.462	4	118570000	71178000	47388000
Q9R1P4	Proteasome subunit alpha type-1	Psma1	5	5	5	23.2	23.2	23.2	29.546	263	8.0107E-59	1.6709	2.9549	81.021	5	499070000	222660000	276410000
P49722	Proteasome subunit alpha type-2	Psma2	2	2	2	13.2	13.2	13.2	25.926	234	6.1005E-59	1.8836	1.7689	70.617	4	697110000	279000000	418120000
O70435	Proteasome subunit alpha type-3	Psma3	5	5	5	18.8	18.8	18.8	28.405	255	5.3846E-52	1.1366	1.2715	47.61	7	693660000	298200000	395460000
Q9R1P0	Proteasome subunit alpha type-4	Psma4	6	6	6	21.1	21.1	21.1	29.47	261	2.4536E-41	0.78696	1.0115	100.82	9	1955100000	1169700000	785340000
Q9Z2U1	Proteasome subunit alpha type-5	Psma5	5	5	5	32.8	32.8	32.8	26.411	241	7.554E-213	0.64862	0.60099	59.517	7	832270000	459630000	372640000
Q9QUM9	Proteasome subunit alpha type-6	Psma6	8	8	8	37.8	37.8	37.8	27.372	246	3.1269E-22	0.91641	1.109	66.008	9	1289000000	641880000	647170000
Q9Z2U0	Proteasome subunit alpha type-7	Psma7	9	9	9	40.3	40.3	40.3	27.855	248	0	0.67566	0.71557	80.09	18	3746800000	2322600000	1424300000
O09061	Proteasome subunit beta type-1	Psmb1	6	6	6	35.4	35.4	35.4	26.372	240	5.5718E-57	1.3813	1.399	21.021	7	1809000000	799000000	1010000000
Q9R1P3	Proteasome subunit beta type-2	Psmb2	5	5	5	30.3	30.3	30.3	22.906	201	1.0633E-32	1.6899	2.139	26.601	6	466730000	191700000	275020000
D3YVS3	Proteasome subunit beta type-3	Gm5356	2	2	2	11.7	11.7	11.7	22.985	205	2.569E-06	1.299	1.4265	49.728	3	481790000	230500000	251290000
P99026	Proteasome subunit beta type-4	Psmb4	1	1	1	8.3	8.3	8.3	29.116	264	3.5407E-59	2.18	2.5384	1.6869	2	477770000	171140000	306620000
O55234	Proteasome subunit beta type-5	Psmb5	5	5	5	23.1	23.1	23.1	28.532	264	2.7482E-56	2.3367	2.3689	34.411	6	643050000	187140000	455910000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q60692	Proteasome subunit beta type-6	Psmb6	2	2	2	13.4	13.4	13.4	25.378	238	4.6259E-42	1.0943	1.2021	15.751	2	295220000	146360000	148860000
P70195	Proteasome subunit beta type-7	Psmb7	6	6	6	17.7	17.7	17.7	29.891	277	6.4523E-63	0.9942	1.1409	25.879	6	1025900000	556530000	469400000
Q6PDI5	Proteasome-associated protein ECM29 homolog	Ecm29	4	4	4	3.5	3.5	3.5	203.7	1840	6.3291E-14	1.5181	1.7412	88.334	4	295170000	133770000	161400000
A2A841	Protein 4.1	Epb4.1	2	2	2	2.8	2.8	2.8	97.239	869	4.685E-06	0.92783	1.594	70.596	2	173310000	87792000	85518000
Q07456	Protein AMBP	Ambp	4	4	4	14.9	14.9	14.9	39.029	349	8.7924E-21	0.55128	0.47687	65.046	5	664190000	417220000	246980000
O35127	Protein C10	Grcc10	1	1	1	11.9	11.9	11.9	13.194	126	0.011606	0.38024	0.39905	1.6159	2	17799000	14020000	3778300
Q9QXT0	Protein canopy homolog 2	Cnpy2	3	3	3	22.5	22.5	22.5	20.767	182	3.9724E-08	0.846	0.77445	20.217	4	184460000	112280000	72175000
Q4VAA2	Protein CDV3	Cdv3	7	7	7	45.6	45.6	45.6	29.729	281	4.845E-135	0.58892	0.6443	71.862	9	698600000	408530000	290070000
A2ADY9	Protein DDI1 homolog 2	Ddi2	3	3	3	11.8	11.8	11.8	44.59	399	3.281E-08	0.56299	0.5062	53.486	3	144330000	89650000	54683000
P09103	Protein disulfide-isomerase	P4hb	20	20	20	33	33	33	57.058	509	2.531E-113	0.81152	0.88447	93.051	26	6364200000	3185100000	3179100000
P27773	Protein disulfide-isomerase A3	Pdia3	18	18	18	41.4	41.4	41.4	56.678	505	3.423E-238	1.1048	1.3891	93.938	23	4009300000	1922300000	2087000000
P08003	Protein disulfide-isomerase A4	Pdia4	10	10	10	19.9	19.9	19.9	71.982	638	1.7441E-60	0.67348	0.78371	76.222	11	989940000	661460000	328480000
Q3TML0	Protein disulfide-isomerase A6	Pdia6	4	4	4	13.7	13.7	13.7	48.689	445	3.4599E-29	2.0415	2.6736	57.503	5	550510000	178880000	371630000
Q99LX0	Protein DJ-1	Park7	10	10	10	62.4	62.4	62.4	20.021	189	0	0.56442	0.66834	93.785	24	1.3124E+10	9173100000	3950800000
E9QLZ9	Protein enabled homolog	Enah	4	4	4	4.9	4.9	4.9	86.052	804	1.3663E-12	1.8737	2.0471	36.492	2	94552000	41452000	53100000
Q9DCM0	Protein ETHE1, mitochondrial	Ethe1	6	6	6	33.9	33.9	33.9	27.738	254	1.6285E-40	0.82868	0.8106	20.366	10	2625200000	1658300000	966850000
Q61160	Protein FADD	Fadd	1	1	1	4.4	4.4	4.4	22.96	205	0.0053965	0.67226	0.72089	20.993	2	73709000	42306000	31404000
Q8VE88	Protein FAM114A2	Fam114a2	3	3	3	7.6	7.6	7.6	54.044	497	5.607E-09	0.54366	0.51818	15.05	2	27356000	19567000	7789000
Q9CR98	Protein FAM136A	Fam136a	5	5	5	52.2	52.2	52.2	15.674	138	3.406E-224	0.60536	0.93224	51.815	6	728200000	470060000	258140000
Q9D6U8	Protein FAM162A	Fam162a	3	3	3	22.6	22.6	22.6	17.725	155	1.9263E-12	0.79809	1.0254	94.436	4	1656200000	519750000	1136500000
Q9CQB2	Protein FAM195A	Fam195a	3	3	3	38.1	38.1	38.1	17.871	160	1.6163E-48	0.54191	0.61011	7.4054	3	194930000	135610000	59322000
Q9CWE0	Protein FAM54B	Fam54b	2	2	2	11.4	11.4	11.4	31.726	289	8.3436E-12	0.33067	0.38008	69.216	2	62120000	49951000	12169000
Q76LS9	Protein FAM63A	Fam63a	3	3	3	10.7	10.7	10.7	51.225	468	1.2164E-09	1.0568	0.90293	74.554	2	82185000	36481000	45704000
Q61239	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	Fnta	6	6	6	13.8	13.8	13.8	44.013	377	4.3684E-27	0.7058	0.64487	39.701	7	379760000	223160000	156600000
O55091	Protein IMPACT	Impact	1	1	1	3.8	3.8	3.8	36.276	318	0.0010749	0.81849	1.055	21.053	2	108870000	57753000	51119000
Q5SW19	Protein KIAA0664	Kiaa0664	14	14	14	15.1	15.1	15.1	148.07	1315	4.131E-152	1.6726	1.824	65.959	14	905750000	336880000	568870000
Q9WVE8	Protein kinase C and casein kinase substrate in neurons protein 2	Pacsin2	9	9	9	22	22	22	55.832	486	4.2325E-80	0.76361	1.2072	74.488	11	1708900000	915810000	793110000
Q8K3C3	Protein LZIC	Lzic	5	5	5	31.6	31.6	31.6	21.536	190	4.356E-122	0.45702	0.51824	73.214	9	1965000000	780540000	1184500000
Q91VH6	Protein MEMO1	Memo1	5	5	5	33.7	33.7	33.7	33.692	297	1.4967E-14	1.5278	1.6867	35.906	5	240780000	81804000	158980000
Q9CWG8	Protein midA homolog, mitochondrial	Ndufaf7	3	3	3	10.6	10.6	10.6	48.384	436	3.0269E-16	1.3077	1.3826	39.598	3	474680000	203870000	270810000
Q9QYG0	Protein NDRG2	Ndrg2	10	10	10	40.7	40.7	40.7	40.789	371	0	0.73727	0.81955	53.066	40	1.1249E+10	6362100000	4887200000
O55126	Protein NipSnap homolog 2	Gbas	6	6	6	32.4	32.4	32.4	32.932	281	3.395E-220	3.1254	2.8752	83.93	8	794280000	228780000	565500000
A5A4Y9	Protein phosphatase 1 regulatory subunit 11	Ppp1r11	1	1	1	12.2	12.2	12.2	14.532	131	9.1387E-29	0.49615	0.77691	2.1176	2	169080000	104120000	64960000
A6H644	Protein phosphatase 1 regulatory subunit 12B	Ppp1r12b	10	10	9	11.7	11.7	10.2	110.97	992	3.0972E-95	1.507	1.6047	59.532	9	607820000	255150000	352680000
Q8R4S0	Protein phosphatase 1 regulatory subunit 14C	Ppp1r14c	2	2	2	22.6	22.6	22.6	17.754	164	4.134E-121	0.39156	0.39636	9.881	7	1085400000	786320000	299080000
Q99MR9	Protein phosphatase 1 regulatory subunit 3A	Ppp1r3a	13	13	13	17.5	17.5	17.5	121.43	1089	0	0.64902	0.67062	33.925	14	1138900000	646400000	492490000
Q3UM45	Protein phosphatase 1 regulatory subunit 7	Ppp1r7	6	6	6	14.1	14.1	14.1	41.291	361	1.2302E-13	0.90606	0.92731	50.955	8	760390000	379930000	380450000
P49443	Protein phosphatase 1A	Ppm1a	5	5	3	18.8	18.8	13.1	42.432	382	5.505E-181	0.82079	0.98043	22.693	6	1027300000	597790000	429560000
Q8CGA0	Protein phosphatase 1F	Ppm1f	2	2	2	3.8	3.8	3.8	49.61	452	2.6615E-05	1.6875	1.6765	136.48	2	250360000	48262000	202100000
Q61074	Protein phosphatase 1G	Ppm1g	3	3	3	6.6	6.6	6.6	58.727	542	3.3883E-07	1.3868	1.0913	6.8276	2	91346000	30030000	61316000
Q9DCL8	Protein phosphatase inhibitor 2	Ppp1r2	5	5	5	31.1	31.1	31.1	23.119	206	7.3416E-37	0.57741	0.56478	40.752	5	524770000	363360000	161410000
Q6NVE9	Protein phosphatase PTC7 homolog	Pptc7	3	3	3	11.9	11.9	11.9	33.048	310	2.5096E-10	1.0524	1.6321	35.076	3	219320000	108340000	110980000
Q7TSC1	Protein PRRC2A	Prrc2a	8	8	7	6	6	5.7	229.2	2158	3.5927E-51	1.0084	0.95655	124.48	5	664750000	202640000	462120000
Q3TLH4	Protein PRRC2C	Prrc2c	6	5	5	2.9	2.6	2.6	310.89	2846	1.6053E-45	0.41392	0.49512	29.188	5	163080000	118390000	44691000
Q8BIW1	Protein prune homolog	Prune	6	6	6	21.8	21.8	21.8	50.239	454	4.1998E-73	1.0108	0.96056	44.88	10	712020000	331290000	380730000
Q52KR3	Protein prune homolog 2	Prune2	2	2	2	1.3	1.3	1.3	339.51	3084	6.6846E-09	1.1435	1.1943	36.633	3	117100000	50945000	66155000
Q9QYS9	Protein quaking	Qki	5	5	5	23.2	23.2	23.2	37.67	341	6.864E-17	0.89768	0.95235	13.965	6	922990000	504890000	418110000
Q91V77	Protein S100-A1	S100a1	5	5	5	62.8	62.8	62.8	10.505	94	2.6414E-45	0.97969	0.95864	34.204	7	1114000000	471020000	642940000
P08207	Protein S100-A10	S100a10	1	1	1	17.5	17.5	17.5	11.186	97	0.00024605	0.95929	1.2976	63.57	3	515000000	266340000	248660000
P50543	Protein S100-A11	S100a11	2	2	2	18.4	18.4	18.4	11.083	98	1.1885E-29	0.50847	0.85618	63.361	3	174690000	114510000	60174000
P31725	Protein S100-A9	S100a9	2	2	2	19.5	19.5	19.5	13.049	113	3.4621E-40	1.2561	1.4453	144.49	4	239240000	116970000	122270000
Q9D1M0	Protein SEC13 homolog	Sec13	3	3	3	10.9	10.9	10.9	35.565	322	1.1399E-55	0.74412	2.1476	132.06	2	299760000	172370000	127390000
Q9EQU5	Protein SET	Set	1	1	1	2.8	2.8	2.8	33.377	289	8.4409E-06	1.0579	0.87293	14.156	2	502060000	241010000	261060000
Q91YM4	Protein TBRG4	Tbrg4	4	4	4	9.8	9.8	9.8	71.513	630	1.4608E-09	1.4632	1.4747	125.3	5	275750000	121460000	154280000
Q01405	Protein transport protein Sec23A	Sec23a	6	6	6	10.7	10.7	10.7	86.161	765	1.7213E-22	2.3175	2.2111	137.05	4	886780000	602160000	284620000
Q3UPL0	Protein transport protein Sec31A	Sec31a	12	12	12	12.3	12.3	12.3	133.57	1230	3.1668E-37	1.5985	1.7073	74.177	11	1049200000	442640000	606600000
Q3TZ89	Protein transport protein Sec31B	Sec31b	2	2	2	1.3	1.3	1.3	125.63	1158	0.0010385	2.0123	1.5706	107.86	13	1570100000	514570000	1055500000
P21981	Protein-glutamine gamma-glutamyltransferase 2	Tgm2	9	9	9	19.7	19.7	19.7	77.06	686	0	1.7572	2.5054	92.509	7	826600000	334350000	492240000
E0CYV0	Protein-L-isoaspartate O-methyltransferase	Pcmt1	4	4	4	29.7	29.7	29.7	30.441	286	1.4412E-77	0.85781	0.98751	69.708	6	473700000	254440000	219260000
P19221	Prothrombin	F2	10	10	10	20.2	20.2	20.2	70.268	618	1.3147E-95	0.71926	0.85177	97.956	11	1649600000	847820000	801760000
Q9CZL5	Pterin-4-alpha-carbinolamine dehydratase 2	Pcbd2	5	5	5	33.1	33.1	33.1	14.83	136	1.9276E-11	0.65328	0.80402	41.556	5	487270000	315930000	171340000
Q80U58	Pumilio homolog 2	Pum2	2	2	2	1.9	1.9	1.9	114.31	1066	0.0038834	2.0221	2.0993	36.989	2	23016000	7899900	15116000
P23492	Purine nucleoside phosphorylase	Pnp	6	6	6	37.7	37.7	37.7	32.277	289	3.0329E-40	1.1466	1.1436	32.672	7	249260000	98347000	150910000
Q6W8Q3	Purkinje cell protein 4-like protein 1	Pcp4l1	3	3	3	60.3	60.3	60.3	7.5023	68	7.964E-139	0.35456	1.0632	133.61	2	411380000	301990000	109390000
Q11011	Puromycin-sensitive aminopeptidase	Npepps	17	17	17	21.6	21.6	21.6	103.32	920	2.6359E-90	0.9096	1.0721	87.127	18	3407800000	1940200000	1467600000
Q80SW1	Putative adenosylhomocysteinase 2	Ahcyl1	4	4	4	8.7	8.7	8.7	58.951	530	1.05E-08	1.6963	1.9451	96.195	5	337750000	185250000	152490000
O88696	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	Clpp	2	2	2	12.9	12.9	12.9	29.8	272	8.1886E-75	1.2654	1.321	32.99	6	568860000	251420000	317440000
Q6P8M1	Putative deoxyribonuclease TATDN1	Tatdn1	1	1	1	3.7	3.7	3.7	33.365	295	7.9669E-09	1.7493	2.1524	17.309	2	57534000	18578000	38956000
O88851	Putative hydrolase RBBP9	Rbbp9	4	4	4	29	29	29	20.911	186	5.6849E-14	0.70354	0.62165	40.629	6	422750000	262770000	159980000
Q8R1F5	Putative hydroxypyruvate isomerase	Hyi	1	1	1	7.6	7.6	7.6	30.448	277	4.7029E-17	1.5365	1.4831	6.2141	2	275140000	102650000	172490000
Q9D009	Putative lipoyltransferase 2, mitochondrial	Lipt2	4	4	4	28.6	28.6	28.6	24.955	231	9.1921E-10	1.3444	1.7256	51.676	3	138520000	68632000	69892000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q3UIZ8	Putative myosin light chain kinase 3	Mylk3	8	8	8	19.2	19.2	19.2	86.371	795	1.1494E-44	1.4284	1.2223	88.503	7	707810000	333570000	374230000
Q3TCN2	Putative phospholipase B-like 2	Plbd2	6	6	6	16.5	16.5	16.5	66.289	594	1.6689E-46	2.2783	2.5951	115.99	6	276650000	58244000	218400000
Q8CAK1	Putative transferase CAF17 homolog, mitochondrial	Iba57	5	5	5	16.2	16.2	16.2	38.399	358	2.7227E-26	1.3658	1.8476	68.117	7	770480000	339880000	430600000
Q8K183	Pyridoxal kinase	Pdxk	6	6	6	27.6	27.6	27.6	35.015	312	1.796E-53	1.276	1.2095	30.242	11	1572400000	695720000	876710000
Q99K01	Pyridoxal-dependent decarboxylase domain-containing protein 1	Pdxdc1	4	4	4	8	8	8	87.334	787	3.4419E-05	0.22405	0.32461	338.5	2	5705600000	5476000000	229570000
Q9ESW8	Pyroglutamyl-peptidase 1	Pgpep1	2	2	2	13.4	13.4	13.4	22.934	209	0.00015863	0.77595	1.3136	40.746	2	188020000	106820000	81201000
E9QPD7	Pyruvate carboxylase	Pcx	9	9	9	11.6	11.6	11.6	129.83	1179	6.3304E-72	2.4751	3.061	33.58	9	601360000	172020000	429340000
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	Pdha1	16	16	16	52.6	52.6	52.6	43.231	390	0	1.7304	1.9375	56.18	43	4.6693E+10	1.6076E+10	3.0617E+10
Q9D051	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	Pdhb	15	15	15	47.9	47.9	47.9	38.937	359	0	0.97046	1.4045	74.268	61	3.2262E+10	1.6245E+10	1.6018E+10
Q7TSQ8	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	Pdpr	5	5	5	8.3	8.3	8.3	99.229	878	5.58E-21	4.4144	4.5044	46.059	5	150180000	29317000	120860000
Q8BKZ9	Pyruvate dehydrogenase protein X component, mitochondrial	Pdhx	12	12	12	35.5	35.5	35.5	53.998	501	3.99E-207	0.62459	0.85793	77.442	19	9067200000	5633600000	3433600000
P52480	Pyruvate kinase isozymes M1/M2	Pkm2	24	24	24	47.6	47.6	47.6	57.844	531	0	0.83097	0.80961	74.701	68	2.1527E+10	1.1443E+10	1.0084E+10
P47199	Quinone oxidoreductase	Cryz	5	5	5	25.1	25.1	25.1	35.268	331	1.4635E-37	1.1305	1.3133	47.04	6	516680000	259460000	257220000
Q3UNZ8	Quinone oxidoreductase-like protein 2		2	2	2	11.7	11.7	11.7	37.808	350	2.4308E-25	0.63032	0.83956	117.15	3	69312000	22199000	47113000
P50396	Rab GDP dissociation inhibitor alpha	Gdi1	15	10	10	46.1	33.3	33.3	50.521	447	1.841E-248	0.84892	0.95302	67.904	18	1671800000	922410000	749350000
Q61598	Rab GDP dissociation inhibitor beta	Gdi2	24	24	19	64.5	64.5	51.7	50.537	445	0	1.1451	1.3175	49.534	33	3293100000	1617900000	1675300000
Q80UJ7	Rab3 GTPase-activating protein catalytic subunit	Rab3gap1	4	4	4	5.4	5.4	5.4	110.2	981	0.00002268	2.0497	1.634	24.205	2	25486000	16444000	9041900
E9QKE4	Rab3 GTPase-activating protein non-catalytic subunit	Rab3gap2	2	2	2	1.2	1.2	1.2	154.64	1387	5.4729E-05	4.8338	5.7406	0.97622	2	21777000	4592400	17184000
P31750	RAC-alpha serine/threonine-protein kinase	Akt1	5	5	3	11.2	11.2	6.5	55.707	480	6.5719E-10	1.0633	1.451	53.556	6	505640000	233680000	271960000
P26043	Radixin	Rdx	13	13	9	20.8	20.8	15.6	68.542	583	3.331E-108	0.68689	0.76305	64.956	13	5654000000	3428200000	2225800000
Q9CQ22	Ragulator complex protein LAMTOR1	Lamtor1	2	2	2	27.3	27.3	27.3	17.749	161	2.9524E-10	2.1051	3.0636	102.6	2	32497000	9973800	22523000
Q9JHS3	Ragulator complex protein LAMTOR2	Lamtor2	2	2	2	15.2	15.2	15.2	13.48	125	9.7538E-05	1.9118	2.3892	37.929	3	146330000	60511000	85822000
O88653	Ragulator complex protein LAMTOR3	Lamtor3	2	2	2	28.2	28.2	28.2	13.553	124	1.2369E-08	1.0387	1.0125	41.141	2	149940000	83803000	66138000
Q9CT10	Ran-binding protein 3	Ranbp3	4	4	4	13	13	13	52.572	491	1.5118E-13	0.45753	0.56107	49.632	2	104760000	72450000	32308000
P34022	Ran-specific GTPase-activating protein	Ranbp1	2	2	2	16.7	16.7	16.7	23.596	203	1.0573E-41	0.58577	0.47882	47.937	4	462670000	222190000	240480000
P97855	Ras GTPase-activating protein-binding protein 1	G3bp1	6	6	6	17.8	17.8	17.8	51.828	465	2.275E-21	1.1818	1.4187	76.439	9	455780000	164220000	291560000
P97379	Ras GTPase-activating protein-binding protein 2	G3bp2	4	4	4	11.6	11.6	11.6	54.087	482	9.6003E-14	1.08	1.3395	47.814	4	938230000	453950000	484270000
Q9JKF1	Ras GTPase-activating-like protein IQGAP1	Iqgap1	8	8	8	7.5	7.5	7.5	188.74	1657	2.307E-191	1.4749	1.2257	26.073	3	66803000	42726000	24077000
Q01730	Ras suppressor protein 1	Rsu1	2	2	2	5.8	5.8	5.8	31.55	277	8.8812E-05	3.0449	8.2404	88.826	2	168330000	47590000	120740000
Q3TLP8	Ras-related C3 botulinum toxin substrate 3	Rac1	3	3	3	14.2	14.2	14.2	23.432	211	8.9596E-12	1.2046	1.3597	265.43	3	337950000	170800000	167150000
Q99K70	Ras-related GTP-binding protein C	Rragc	2	2	2	11.8	11.8	11.8	44.12	398	7.0181E-06	1.8621	2.1092	22.516	2	77753000	26735000	51018000
P61027	Ras-related protein Rab-10	Rab10	3	2	2	17	11.5	11.5	22.541	200	4.5925E-18	1.1215	1.3481	29.788	2	89606000	37587000	52019000
P46638	Ras-related protein Rab-11B	Rab11b	7	7	7	29.4	29.4	29.4	24.489	218	2.6743E-71	0.95351	0.83043	39.103	7	1609100000	843810000	765280000
A2CG35	Ras-related protein Rab-12	Rab12	2	2	2	7.6	7.6	7.6	32.238	291	9.0541E-07	2.1808	2.1276	57.426	2	43859000	19244000	24614000
Q91V41	Ras-related protein Rab-14	Rab14	5	5	5	34.9	34.9	34.9	23.897	215	1.018E-154	1.5007	2.0485	55.055	7	531020000	226740000	304280000
P35293	Ras-related protein Rab-18	Rab18	2	2	2	12.1	12.1	12.1	23.035	206	0.00025191	1.0072	1.1282	26.027	3	51801000	25903000	25898000
Q9D1G1	Ras-related protein Rab-1B	Rab1b	4	4	2	24.9	24.9	15.4	22.187	201	6.6135E-10	0.91256	1.5732	211.68	5	473010000	333420000	139590000
P35282	Ras-related protein Rab-21	Rab21	7	7	7	33.8	33.8	33.8	24.106	222	7.1039E-50	1.0865	1.0488	30.251	6	136540000	63850000	72688000
P53994	Ras-related protein Rab-2A	Rab2a	5	5	5	33	33	33	23.547	212	1.9502E-24	1.4677	1.6799	35.532	5	129750000	46593000	83157000
P63011	Ras-related protein Rab-3A	Rab3a	2	2	2	14.1	14.1	14.1	24.97	220	6.4674E-06	0.57869	0.92219	91.593	2	16823000	10036000	6787000
Q8C266	Ras-related protein Rab-5C	Rab5c	3	3	3	14.1	14.1	14.1	25.352	234	2.7736E-09	1.6471	1.854	29.073	3	208920000	97468000	111450000
P51150	Ras-related protein Rab-7a	Rab7a	4	4	4	24.6	24.6	24.6	23.489	207	3.1375E-08	2.3563	2.3825	53.674	4	344790000	109840000	234960000
P63321	Ras-related protein Ral-A	Rala	2	2	2	10.2	10.2	10.2	23.553	206	4.0744E-05	2.2418	2.3124	43.499	2	79972000	29482000	50490000
P62835	Ras-related protein Rap-1A	Rap1a	2	2	2	13.6	13.6	13.6	20.987	184	4.0988E-07	1.6015	1.7754	51.042	4	70565000	24149000	46415000
P10833	Ras-related protein R-Ras	Rras	4	4	3	25.7	25.7	20.6	23.764	218	2.3842E-12	1.2814	1.5115	35.336	4	213410000	84401000	129010000
P62071	Ras-related protein R-Ras2	Rras2	3	2	2	17.2	11.8	11.8	23.399	204	1.6151E-19	0.95395	0.86563	7.197	2	132680000	70411000	62272000
G3X8R0	Receptor expression-enhancing protein 5	Reep5	2	2	2	9	9	9	21.447	189	0.00047591	2.0599	10.921	19.287	2	236850000	87337000	149520000
P28828	Receptor-type tyrosine-protein phosphatase mu	Ptprm	2	2	2	1.4	1.4	1.4	163.65	1452	0.0068059	0.45737	0.46748	17.857	2	41366000	28478000	12888000
Q9DCV4	Regulator of microtubule dynamics protein 1	Fam82b	7	7	7	21.3	21.3	21.3	35	305	3.0529E-30	0.58421	0.55338	113.4	9	1463000000	845900000	617090000
Q9EPU0	Regulator of nonsense transcripts 1	Upf1	3	3	3	3.6	3.6	3.6	123.97	1124	4.687E-07	2.6076	2.3831	4.7075	2	123150000	49166000	73987000
A2ACM0	Regulatory-associated protein of mTOR	Rptor	2	2	2	4.5	4.5	4.5	149.5	1335	1.6398E-08	1.559	1.5725	70.118	3	431610000	234870000	196740000
A7RDN6	Renalase	Rnls	2	2	2	9.1	9.1	9.1	37.597	342	0.00012394	0.3176	0.34119	3.0408	2	125820000	103360000	22466000
Q3TE40	Replication protein A 32 kDa subunit	Rpa2	1	1	1	8.1	8.1	8.1	29.44	270	0.0070449	1.3656	1.0795	11.149	2	69366000	31765000	37601000
Q05186	Reticulocalbin-1	Rcn1	2	2	2	8	8	8	38.113	325	0.00045322	1.6583	1.6502	6.366	2	63638000	23681000	39957000
Q99P72	Reticulon-4	Rtn4	5	5	5	8.1	8.1	8.1	126.61	1162	1.832E-28	1.0269	0.96359	67.44	6	201420000	111560000	89866000
Q924D0	Reticulon-4-interacting protein 1, mitochondrial	Rtn4ip1	8	8	8	29.5	29.5	29.5	43.371	396	8.0992E-35	2.0351	1.9883	63.013	7	991080000	392420000	598670000
P24549	Retinal dehydrogenase 1	Aldh1a1	8	7	7	28.3	26.7	26.7	54.467	501	1.489E-148	1.2111	1.2555	37.192	11	928160000	487590000	440570000
Q62148	Retinal dehydrogenase 2	Aldh1a2	4	2	2	11.8	8.7	8.7	56.625	518	3.9597E-08	2.15	2.2691	112.82	2	90500000	21798000	68702000
Q00915	Retinol-binding protein 1	Rbp1	3	3	3	25.9	25.9	25.9	15.846	135	1.336E-11	0.49547	0.7103	49.429	4	280410000	187030000	93376000
Q99PT1	Rho GDP-dissociation inhibitor 1	Arhgdia	6	6	6	39.2	39.2	39.2	23.407	204	2.0855E-61	1.0091	1.1332	93.246	11	1141100000	549750000	591390000
Q61599	Rho GDP-dissociation inhibitor 2	Arhgdib	2	2	2	20	20	20	22.851	200	5.1891E-08	0.90218	0.70006	20.452	2	264320000	165170000	99154000
F8VPK5	Rho-associated protein kinase 2	Rock2	5	5	3	4.6	4.6	3.1	160.61	1388	3.068E-27	0.80566	0.86048	68.121	5	333040000	196800000	136240000
Q62159	Rho-related GTP-binding protein RhoC	Rhoc	5	5	5	23.8	23.8	23.8	22.006	193	9.5592E-87	1.6761	2.8316	83.038	7	994720000	429500000	565220000
Q91VI7	Ribonuclease inhibitor	Rnh1	13	13	13	42.3	42.3	42.3	49.816	456	0	0.88285	1.0052	81.012	19	1522400000	818890000	703470000
P52760	Ribonuclease UK114	Hrsp12	3	3	3	24.4	24.4	24.4	14.255	135	1.3374E-05	0.2947	0.47584	114.23	4	297370000	242830000	54543000
Q8C5R8	Ribose-phosphate pyrophosphokinase	Prps1l1	3	3	1	10.7	10.7	4.1	34.82	318	1.1843E-11	1.1461	1.3553	112.72	5	492260000	234830000	257420000
Q9CS42	Ribose-phosphate pyrophosphokinase 2	Prps2	3	2	1	12.3	9.7	3.1	34.786	318	2.1073E-12	0.98851	0.97133	59.381	2	168760000	82038000	86726000
E9QAZ2	Ribosomal protein L15	Gm10020	1	1	1	5.9	5.9	5.9	24.077	204	0.0010311	10.073	8.6933	121.58	2	180910000	8961800	171950000
P18654	Ribosomal protein S6 kinase alpha-3	Rps6ka3	2	2	2	4.5	4.5	4.5	83.693	740	1.1048E-07	1.6934	1.3495	34.067	2	70858000	29283000	41575000
Q8BSK8	Ribosomal protein S6 kinase beta-1	Rps6kb1	2	2	2	3.6	3.6	3.6	59.145	525	0.00013338	0.89955	0.9804	19.237	3	55467000	29737000	25730000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q99PL5	Ribosome-binding protein 1	Rrbp1	12	12	12	9.2	9.2	9.2	172.88	1605	0	0.83477	0.83569	81.8	15	1135400000	657300000	478140000
Q9D6S7	Ribosome-recycling factor, mitochondrial	Mrrf	3	3	3	20.2	20.2	20.2	29.05	262	0	0.55764	0.57336	20.947	5	1410800000	980590000	430180000
Q9JI75	Ribosyldihydronicotinamide dehydrogenase [quinone]	Nqo2	8	8	8	40.3	40.3	40.3	26.248	231	5.044E-115	1.1508	1.2208	102.17	7	2399300000	609750000	1789600000
P56959	RNA-binding protein FUS	Fus	3	3	3	4.8	4.8	4.8	52.673	518	1.6465E-11	1.8204	2.9464	119.75	3	377000000	125810000	251190000
Q920Q6	RNA-binding protein Musashi homolog 2	Msi2	2	2	2	9	9	9	36.938	346	1.0024E-12	1.5046	3.443	128.03	2	38895000	15926000	22969000
Q9WVB0	RNA-binding protein with multiple splicing	Rbpms	6	6	6	32	32	32	21.816	197	7.4712E-88	0.81355	0.72589	26.515	5	532690000	305050000	227640000
E9Q401	Ryanodine receptor 2	Ryr2	13	13	13	3	3	3	564.81	4966	2.4195E-23	3.2615	3.4331	38.007	11	190430000	42618000	147820000
Q3THS6	S-adenosylmethionine synthase isoform type-2	Mat2a	4	4	4	17	17	17	43.688	395	3.6213E-27	0.85693	0.81785	21.647	5	1092000000	568620000	523420000
F8WJE0	SAM domain and HD domain-containing protein 1	Samhd1	4	4	4	6.4	6.4	6.4	75.892	658	1.9042E-07	2.188	2.1061	19.035	5	932620000	233330000	699290000
Q9D1J3	SAP domain-containing ribonucleoprotein	Sarnp	2	2	2	15.7	15.7	15.7	23.532	210	1.8104E-83	0.23729	0.94207	68.469	4	142750000	113370000	29381000
Q7TQ48	Sarcalumenin	Srl	26	26	26	41.8	41.8	41.8	99.183	910	0	1.5613	1.6182	98.656	51	1.7535E+10	7174300000	1.0361E+10
Q3URD3	Sarcolemmal membrane-associated protein	Slmap	2	2	2	2.4	2.4	2.4	96.932	845	3.1232E-10	0.79571	0.93836	19.716	2	253090000	134220000	118870000
O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	Atp2a2	33	33	33	33.9	33.9	33.9	114.86	1044	0	1.3002	1.5116	95.969	51	1.1934E+10	5043600000	6890300000
S4R1M2	Scaffold attachment factor B1	Safb	2	2	2	3.7	3.7	3.7	105.32	939	3.5952E-56	0.83338	0.74645	20.156	2	54419000	33656000	20762000
Q8BRF7	Sec1 family domain-containing protein 1	Scfd1	2	2	2	5.6	5.6	5.6	72.322	639	0.0013764	2.6232	2.0549	12.088	2	95002000	23069000	71933000
Q8VCA8	Secernin-2	Scrn2	5	5	5	24	24	24	46.6	425	3.4335E-62	1.6372	1.9684	27.162	6	751270000	266160000	485100000
Q3TMH2	Secernin-3	Scrn3	6	6	6	21.1	21.1	21.1	47.661	418	1.1256E-67	0.80875	0.91549	65.255	8	1416500000	684340000	732150000
Q921H9	Sel1 repeat-containing protein 1	Selrc1	3	3	3	21.6	21.6	21.6	25.617	231	2.2857E-47	1.1095	0.9575	5.9928	4	269520000	148670000	120850000
Q8BH69	Selenide, water dikinase 1	Sephs1	3	3	3	15.3	15.3	15.3	42.906	392	1.7282E-08	1.0255	1.1433	86.563	3	149540000	40321000	109220000
P97364	Selenide, water dikinase 2	Sephs2	2	2	2	11.3	11.3	11.3	47.851	452	2.0429E-16	0.78661	0.67181	13.636	2	55431000	30506000	24925000
P17563	Selenium-binding protein 1	Selenbp1	24	24	24	70.1	70.1	70.1	52.513	472	0	1.1801	1.288	44.75	45	1.6079E+10	6852500000	9226800000
Q9DBC0	Selenoprotein O	Selo	2	2	2	4.6	4.6	4.6	74.238	667	3.3437E-22	0.97891	1.1149	18.247	2	138130000	65484000	72643000
Q91XH5	Sepiapterin reductase	Spr	11	11	11	46.9	46.9	46.9	27.928	262	1.244E-262	0.78799	1.3428	48.176	21	1005200000	553780000	451430000
Q8C1B7	Septin-11	Sept11	8	8	4	22.7	22.7	10	49.694	431	3.932E-112	0.67597	0.7077	35.021	8	630940000	381180000	249760000
P42208	Septin-2	Sept2	7	7	7	31.3	31.3	31.3	41.525	361	5.7394E-88	1.0631	1.583	75.316	7	684600000	350900000	333700000
Q9R1T4	Septin-6	Sept6	4	1	1	12.9	4.6	4.6	49.619	434	1.2916E-30	0.5498	0.5366	12.568	2	184730000	112440000	72291000
E9Q1G8	Septin-7	Sept7	5	5	5	14.6	14.6	14.6	50.648	437	1.19E-121	1.7962	1.9185	30.242	5	820500000	330110000	490390000
B1AQZ0	Septin-8	Sept8	6	4	4	20	14.5	14.5	55.874	484	3.6216E-81	0.74694	1.0878	22.089	5	603530000	365540000	237990000
Q80UG5	Septin-9	Sept9	3	3	3	11.1	11.1	11.1	65.574	583	6.5871E-15	1.4251	1.3716	40.961	2	87029000	32162000	54868000
Q64337	Sequestosome-1	Sqstm1	1	1	1	5.9	5.9	5.9	48.162	442	0.00011843	1.2843	0.94488	5.5758	2	38289000	16466000	21823000
P54797	Ser/Thr-rich protein T10 in DGCR region	T10	6	6	6	30.1	30.1	30.1	30.947	276	1.9153E-43	1.2905	1.315	144.18	10	389530000	216070000	173460000
Q3U3G8	Serine hydrolase-like protein	Serhl	6	6	6	24	24	24	36.353	321	3.767E-16	1.9833	2.3636	118.17	6	677280000	214990000	462290000
G3UZ26	Serine hydroxymethyltransferase	Shmt1	4	4	4	9.8	9.8	9.8	48.334	439	2.4447E-17	1.7485	1.7597	11.179	2	128950000	76262000	52689000
Q9CZN7	Serine hydroxymethyltransferase	Shmt2	5	5	5	13.9	13.9	13.9	55.758	504	1.1608E-09	3.2734	3.1675	149.21	4	1942300000	1656300000	285980000
Q9JIY5	Serine protease HTRA2, mitochondrial	Htra2	6	6	6	20.3	20.3	20.3	49.348	458	8.2163E-17	2.0551	2.1694	101.2	8	1157800000	689830000	467930000
P07759	Serine protease inhibitor A3K	Serpina3k	9	9	5	26.3	26.3	15.6	46.879	418	2.859E-262	0.71192	0.70367	85.876	25	4552600000	2936200000	1616500000
Q03734	Serine protease inhibitor A3M	Serpina3m	7	3	2	18.2	7.4	4.5	47.064	418	3.86E-219	0.52867	0.37882	72.246	3	128800000	91005000	37795000
G3X8T9	Serine protease inhibitor A3N	Serpina3n	7	4	4	16	9.6	9.6	46.766	418	1.3595E-56	0.37671	0.75183	86.383	3	165210000	110290000	54918000
H7BX95	Serine/arginine-rich splicing factor 1	Srsf1	2	2	2	8.7	8.7	8.7	28.329	253	4.9656E-06	4.3914	4.6183	11.198	2	61504000	11107000	50397000
P84104	Serine/arginine-rich splicing factor 3	Srsf3	3	3	3	18.9	18.9	18.9	19.329	164	1.3867E-06	2.8187	3.46	109.68	4	108750000	37854000	70900000
Q99KH8	Serine/threonine-protein kinase 24	Stk24	4	4	4	11.6	11.6	11.6	47.953	431	3.0592E-26	0.94788	0.88465	25.201	4	151090000	80337000	70753000
Q9JI11	Serine/threonine-protein kinase 4	Stk4	1	1	1	3.3	3.3	3.3	55.541	487	0.056067	0.51907	0.50058	32.839	4	8457300000	5473500000	2983800000
Q3TYD6	Serine/threonine-protein kinase LMTK2	Lmtk2	2	2	2	2.7	2.7	2.7	160.51	1471	8.6798E-18	0.87706	0.8574	4.664	2	31439000	17557000	13882000
Q6P9R2	Serine/threonine-protein kinase OSR1	Oxsr1	4	4	4	11	11	11	58.213	527	5.6877E-24	0.86328	1.0231	115.96	5	758600000	521190000	237400000
Q8CIN4	Serine/threonine-protein kinase PAK 2	Pak2	6	6	6	16	16	16	57.93	524	1.4173E-75	0.71686	0.77157	49.442	10	1419500000	822420000	597090000
P83741	Serine/threonine-protein kinase WNK1	Wnk1	3	3	3	1.6	1.6	1.6	250.93	2377	2.0629E-09	0.93616	2.2388	124.13	2	265930000	118430000	147500000
Q6P1F6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	Ppp2r2a	5	5	5	13.9	13.9	13.9	51.691	447	3.5597E-44	1.2694	1.2761	157.8	5	1770800000	537160000	1233600000
Q6PD03	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	Ppp2r5a	3	3	3	8.2	8.2	8.2	56.346	486	8.3165E-11	1.0132	1.6852	61.431	4	283440000	124330000	159110000
Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	Ppp2r1a	18	18	18	38.2	38.2	38.2	65.322	589	1.2363E-76	1.0068	1.145	84.215	28	2887800000	1451400000	1436400000
P63330	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	Ppp2ca	8	8	8	39.2	39.2	39.2	35.608	309	1.758E-108	1.8561	1.6752	43.792	11	1108300000	375190000	733080000
P63328	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	Ppp3ca	4	4	4	8.8	8.8	8.8	58.643	521	3.4345E-09	0.81406	1.2568	41.064	2	104830000	55676000	49152000
Q60676	Serine/threonine-protein phosphatase 5	Ppp5c	6	6	6	15.6	15.6	15.6	56.876	499	1.1345E-32	0.7124	0.68435	57.668	8	502270000	347390000	154880000
Q9CQR6	Serine/threonine-protein phosphatase 6 catalytic subunit	Ppp6c	2	2	2	6.9	6.9	6.9	35.159	305	1.0811E-20	2.2708	2.1881	6.0998	2	74512000	22454000	52058000
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	Ppp1ca	10	10	4	29.7	29.7	12.1	37.54	330	2.4185E-40	2.317	2.7546	132.71	8	1605500000	493590000	1111900000
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	Ppp1cb	8	3	2	26	12.5	9.2	37.186	327	8.4306E-40	1.6348	1.4989	176.22	3	494230000	185860000	308370000
Q9Z1Z2	Serine-threonine kinase receptor-associated protein	Strap	8	8	8	29.1	29.1	29.1	38.442	350	4.8439E-90	0.59901	0.87821	76.659	12	885080000	557470000	327610000
Q8C483	Serine--tRNA ligase, cytoplasmic	Sars	10	10	10	21.8	21.8	21.8	61.166	536	1.2086E-30	1.793	1.8427	94.315	9	618330000	291680000	326660000
Q9JJL8	Serine--tRNA ligase, mitochondrial	Sars2	3	3	3	9.1	9.1	9.1	58.316	518	1.8956E-15	1.3508	1.2233	26.133	5	279490000	122030000	157460000
Q921I1	Serotransferrin	Tf	47	47	47	61.8	61.8	61.8	76.723	697	0	0.68818	0.73539	92.041	87	2.9099E+10	1.7148E+10	1.1951E+10
F8WIV2	Serpin B6	Serpinb6a	11	11	10	30.8	30.8	29.1	44.774	399	1.772E-150	0.94734	1.1924	61.922	15	4307100000	2337500000	1969500000
P19324	Serpin H1	Serpinh1	8	8	8	24	24	24	46.533	417	1.3804E-70	0.85766	1.2187	77.89	11	1239400000	588770000	650650000
Q99MR6	Serrate RNA effector molecule homolog	Srrt	4	4	4	4.9	4.9	4.9	100.45	875	5.2826E-07	1.8713	2.1851	21.817	4	72865000	24152000	48712000
P07724	Serum albumin	Alb	61	61	56	79.3	79.3	77.1	68.692	608	0	0.51161	0.58962	93.563	282	3.0458E+11	2.0683E+11	9.7753E+10
Q63918	Serum deprivation-response protein	Sdpr	3	3	3	10.5	10.5	10.5	46.763	418	6.6356E-43	1.2508	1.3628	39.402	7	1497900000	657280000	840580000
P97443	SET and MYND domain-containing protein 1	Smyd1	6	6	6	19.2	19.2	19.2	56.495	490	6.2383E-40	1.7244	1.4466	46.152	5	328560000	119530000	209040000
H3BKH6	S-formylglutathione hydrolase	Esd	7	7	7	31.5	31.5	31.5	32.829	295	1.086E-122	1.6608	2.0356	113.06	10	2898300000	1116500000	1781900000
Q9WUZ7	SH3 domain-binding glutamic acid-rich protein	Sh3bgr	5	5	5	31.3	31.3	31.3	23.102	214	1.785E-212	0.25377	0.3008	49.821	7	482970000	374810000	108160000
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	Sh3bgrl	5	5	5	58.8	58.8	58.8	12.811	114	5.8244E-46	0.67777	0.57377	114.52	5	298820000	164030000	134790000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q91VW3	SH3 domain-binding glutamic acid-rich-like protein 3	Sh3bgrl3	2	2	2	31.2	31.2	31.2	10.477	93	2.4564E-05	1.0595	1.1831	33.897	4	689610000	334860000	354750000
Q8R550	SH3 domain-containing kinase-binding protein 1	Sh3kbp1	3	3	3	6.3	6.3	6.3	78.169	709	2.154E-09	0.6367	1.6868	87.857	3	128350000	71230000	57116000
E9Q5L3	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	Acadsb	9	9	9	23	23	23	51.853	465	0	1.2208	1.4135	38.001	26	4537500000	1993400000	2544100000
Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	Acads	14	14	14	46.8	46.8	46.8	44.889	412	0	1.4478	1.6222	67.789	32	6878600000	2836000000	4042600000
Q9D104	Signal recognition particle 19 kDa protein	Srp19	2	2	2	15.3	15.3	15.3	16.094	144	0.00019124	1.8328	2.1949	72.462	2	123380000	56386000	66989000
P42232	Signal transducer and activator of transcription 5B	Stat5b	3	3	3	4.1	4.1	4.1	90.001	786	0.00051457	2.4849	3.048	55.85	2	16310000	5063600	11246000
Q9CYR0	Single-stranded DNA-binding protein, mitochondrial	Ssbp1	6	6	6	38.8	38.8	38.8	17.319	152	1.74E-139	0.77781	0.85048	80.113	6	558990000	298440000	260550000
Q8BJU0	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	Sgta	4	4	4	16.2	16.2	16.2	34.322	315	4.8969E-19	0.70917	0.66296	27.387	6	442970000	267780000	175190000
Q9DC77	Small muscular protein	Smpx	4	4	4	48.2	48.2	48.2	9.2525	85	8.9297E-80	0.50324	0.65849	63.756	5	338120000	221530000	116590000
P62307	Small nuclear ribonucleoprotein F	Snrpf	2	2	2	24.4	24.4	24.4	9.7251	86	3.9296E-09	1.5602	1.5619	42.625	2	20535000	7581100	12954000
Q9CQ65	S-methyl-5-thioadenosine phosphorylase	Mtap	5	5	5	27.2	27.2	27.2	31.062	283	2.0964E-38	1.2362	1.4648	18.487	5	355550000	171120000	184430000
D3Z3Q3	Smoothelin	Smtn	2	2	2	3.3	3.3	3.3	103.04	946	1.7892E-17	0.92134	0.78805	33.121	2	74458000	35301000	39157000
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	Atp1a1	20	20	11	23.1	23.1	11.4	112.98	1023	1.658E-157	1.4026	1.7687	72.823	26	6081500000	2455400000	3626100000
Q6PIE5	Sodium/potassium-transporting ATPase subunit alpha-2	Atp1a2	11	2	2	14	2.4	2.4	112.22	1020	1.222E-136	2.3243	2.4243	12.349	2	53511000	14427000	39084000
P14094	Sodium/potassium-transporting ATPase subunit beta-1	Atp1b1	6	6	6	19.1	19.1	19.1	35.194	304	6.6584E-32	0.94528	1.2786	99.418	7	1538400000	797500000	740930000
Q9WVL3	Solute carrier family 12 member 7	Slc12a7	4	4	4	5.1	5.1	5.1	119.48	1083	1.5214E-14	2.1154	2.1076	18.683	5	235680000	76630000	159050000
P14142	Solute carrier family 2, facilitated glucose transporter member 4	Slc2a4	2	2	2	6.1	6.1	6.1	54.755	509	2.1887E-06	2.6782	3.1747	8.9773	2	400030000	123510000	276520000
B9EKP8	Sorbin and SH3 domain-containing protein 2	Sorbs2	7	7	6	9.9	9.9	9	136.2	1214	1.7924E-69	1.4811	1.5827	101.35	9	1304100000	455700000	848430000
Q64442	Sorbitol dehydrogenase	Sord	8	8	8	30.3	30.3	30.3	38.249	357	1.0815E-58	0.86707	1.2478	67.92	12	1734000000	689780000	1044200000
Q6P069	Sorcin	Sri	4	4	4	24.2	24.2	24.2	21.627	198	2.002E-289	0.84236	0.80668	15.803	6	1361800000	688550000	673240000
Q8BGH2	Sorting and assembly machinery component 50 homolog	Samm50	2	2	2	5.5	5.5	5.5	51.863	469	9.3863E-07	1.0364	1.1891	31.937	3	87262000	35899000	51364000
Q9WV80	Sorting nexin-1	Snx1	4	3	3	9.4	7.3	7.3	58.951	522	3.4823E-13	0.5788	0.58484	16.164	2	84524000	48770000	35753000
Q8C080	Sorting nexin-16	Snx16	3	3	3	10.5	10.5	10.5	38.817	344	0.0001171	1.4608	1.344	96.86	3	40907000	24696000	16211000
Q9CWK8	Sorting nexin-2	Snx2	7	7	6	14.5	14.5	12.3	58.47	519	2.1325E-35	0.52304	0.62305	47.571	8	727150000	435690000	291450000
O70492	Sorting nexin-3	Snx3	2	2	2	10.5	10.5	10.5	18.757	162	5.5462E-05	0.83888	1.0525	13.844	2	294690000	159950000	134740000
Q9D8U8	Sorting nexin-5	Snx5	5	5	5	19.3	19.3	19.3	46.797	404	3.7118E-28	0.72037	1.0827	102.49	4	383240000	239170000	144070000
Q6P8X1	Sorting nexin-6	Snx6	2	2	2	6.2	6.2	6.2	46.648	406	6.8186E-05	0.87204	0.9178	47.455	2	168560000	91836000	76721000
Q8R1X6	Spartin	Spg20	4	4	4	8.6	8.6	8.6	72.654	671	3.5822E-08	1.3424	1.463	59.097	3	218740000	83391000	135340000
Q62261	Spectrin beta chain, brain 1	Sptbn1	31	31	28	20.7	20.7	19.4	274.22	2363	0	2.3359	2.3423	51.106	32	3053100000	949650000	2103500000
Q7TNE3	Sperm-associated antigen 7	Spag7	2	2	2	10.1	10.1	10.1	25.921	227	8.3543E-05	0.4445	0.4486	63.827	2	47479000	35967000	11512000
Q9WTX5	S-phase kinase-associated protein 1	Skp1	5	5	5	25.8	25.8	25.8	18.672	163	6.1057E-84	0.81597	0.80826	129.78	5	484920000	206520000	278390000
Q9Z1N5	Spliceosome RNA helicase Ddx39b	Ddx39b	6	6	6	23.8	23.8	23.8	49.035	428	2.7889E-55	1.6437	2.0946	123.95	11	1211700000	435500000	776210000
Q64213	Splicing factor 1	Sf1	4	4	4	9.6	9.6	9.6	70.402	653	2.6422E-16	0.55862	0.69235	27.372	4	218020000	155860000	62164000
Q8K4Z5	Splicing factor 3A subunit 1	Sf3a1	6	6	6	9.2	9.2	9.2	88.544	791	2.0773E-18	0.92299	0.88753	196.34	5	370800000	82717000	288080000
Q9D554	Splicing factor 3A subunit 3	Sf3a3	2	2	2	7.8	7.8	7.8	58.841	501	1.8416E-20	1.336	1.3409	9.6108	3	80028000	34072000	45956000
P26369	Splicing factor U2AF 65 kDa subunit	U2af2	3	3	3	10.7	10.7	10.7	53.516	475	3.8319E-05	1.6788	1.8691	40.978	3	66332000	24821000	41512000
Q91WK1	SPRY domain-containing protein 4	Spryd4	3	3	3	21.7	21.7	21.7	23.275	207	2.8148E-20	1.1783	1.0453	62.5	5	280240000	110200000	170040000
Q9D8T7	SRA stem-loop-interacting RNA-binding protein, mitochondrial	Slirp	2	2	2	22.3	22.3	22.3	12.605	112	0.00054165	1.1713	1.1991	49.711	4	358990000	163660000	195330000
Q60598	Src substrate cortactin	Cttn	2	2	2	5.5	5.5	5.5	61.249	546	3.8021E-07	0.74312	1.3285	113.07	2	67943000	35138000	32805000
Q78PY7	Staphylococcal nuclease domain-containing protein 1	Snd1	6	6	6	11.1	11.1	11.1	102.09	910	2.885E-37	7.9133	6.446	43.191	6	546720000	64102000	482620000
P54227	Stathmin	Stmn1	3	3	3	24.8	24.8	24.8	17.274	149	4.9547E-09	0.49921	0.58003	8.0335	3	109030000	72419000	36606000
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	Stk39	2	2	2	6.5	6.5	6.5	60.319	556	2.5725E-26	1.0748	1.006	41.499	5	622590000	381460000	241130000
O54988	STE20-like serine/threonine-protein kinase	Slk	3	3	3	3.7	3.7	3.7	141.46	1233	7.4743E-98	0.71697	0.83852	38.896	2	40853000	23602000	17251000
P38647	Stress-70 protein, mitochondrial	Hspa9	34	34	34	51.7	51.7	51.7	73.46	679	0	0.69581	0.83977	85.007	77	2.0845E+10	1.2087E+10	8758400000
Q60864	Stress-induced-phosphoprotein 1	Stip1	17	17	17	37.6	37.6	37.6	62.581	543	0	0.66886	0.87237	127.58	30	9527000000	5194800000	4332200000
E9QQ25	Striated muscle-specific serine/threonine-protein kinase	Speg	6	6	6	3.4	3.4	3.4	354.31	3262	1.497E-22	4.3714	4.4231	71.591	6	139170000	27555000	111620000
Q9ERG2	Striatin-3	Strn3	3	3	3	5.2	5.2	5.2	87.149	796	3.9786E-07	1.8003	1.7057	9.5813	2	228420000	88676000	139750000
Q9CXV1	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial	Sdhd	2	2	2	10.7	10.7	10.7	17.014	159	4.0928E-08	0.73093	0.83766	174.33	4	1175500000	588510000	587010000
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Sdha	20	20	20	46.5	46.5	46.5	72.585	664	0	1.41	1.5425	91.241	39	1.5303E+10	6011500000	9291200000
Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	Sdhb	6	6	6	21.3	21.3	21.3	31.814	282	3.467E-40	1.3107	1.0991	172.58	7	2137500000	1035400000	1102000000
Q9CZB0	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	Sdhc	5	5	5	38.5	38.5	38.5	18.382	169	5.2379E-22	1.0369	0.87723	48.997	5	1102000000	579290000	522670000
Q8BWF0	Succinate-semialdehyde dehydrogenase, mitochondrial	Aldh5a1	12	12	12	27.7	27.7	27.7	55.968	523	1.7935E-63	1.0166	1.1679	95.547	15	5575900000	2799800000	2776100000
Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	Suclg1	9	9	9	32.4	32.4	32.4	36.154	346	1.16E-180	1.5221	2.1141	109.42	27	1.1058E+10	4948900000	6108800000
Q9Z2I9	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	Sucla2	24	24	24	52.5	52.5	52.5	50.113	463	0	0.55279	0.63347	120.55	69	5.7007E+10	2.9538E+10	2.7469E+10
Q9Z2I8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	Suclg2	16	16	16	37	37	37	46.839	433	0	0.78753	0.97806	104.78	27	7122600000	4167700000	2954900000
Q9D0K2	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	Oxct1	17	17	17	33.5	33.5	33.5	55.988	520	3.334E-263	1.1908	1.4132	104	37	1.2576E+10	5459100000	7116400000
Q8BFQ1	Sulfated glycoprotein 1	Psap	6	6	6	10.6	10.6	10.6	61.05	554	3.226E-16	1.3758	1.6354	118.19	6	845210000	371510000	473700000
Q8BND5	Sulfhydryl oxidase 1	Qsox1	4	4	4	6.6	6.6	6.6	82.784	748	2.5971E-08	0.58504	0.5935	13.398	3	106630000	68589000	38038000
Q8R086	Sulfite oxidase, mitochondrial	Suox	12	12	12	37.9	37.9	37.9	60.755	546	2.173E-166	0.55405	0.67292	49.996	13	1508200000	993100000	515130000
Q3UW66	Sulfurtransferase	Mpst	5	5	5	22.2	22.2	22.2	33.097	297	1.0461E-28	1.2904	1.7123	52.816	8	503440000	224790000	278650000
Q9R1T2	SUMO-activating enzyme subunit 1	Sae1	5	5	5	13.7	13.7	13.7	38.62	350	1.8412E-10	0.866	0.79961	113.27	5	252650000	125680000	126970000
Q9Z1F9	SUMO-activating enzyme subunit 2	Uba2	2	2	2	4.1	4.1	4.1	70.568	638	1.6856E-10	0.99473	1.4172	32.7	2	68860000	35087000	33773000
P63280	SUMO-conjugating enzyme UBC9	Ube2i	4	4	4	20.3	20.3	20.3	18.007	158	1.5883E-07	0.91811	1.2638	35.855	3	172900000	81542000	91363000
P08228	Superoxide dismutase [Cu-Zn]	Sod1	6	6	6	47.4	47.4	47.4	15.942	154	3.079E-255	0.54325	0.67738	113.33	14	4.1619E+10	2.2414E+10	1.9205E+10
P09671	Superoxide dismutase [Mn], mitochondrial	Sod2	7	7	7	29.3	29.3	29.3	24.603	222	1.971E-104	0.64502	0.69062	61.547	93	2.6716E+10	1.6548E+10	1.0168E+10
Q8K4L3	Supervillin	Svil	4	4	4	2.5	2.5	2.5	243.16	2170	2.476E-15	1.74	2.9646	157.11	2	103880000	40456000	63425000
Q9CX34	Suppressor of G2 allele of SKP1 homolog	Sugt1	5	5	5	17.3	17.3	17.3	38.158	336	3.526E-208	0.92702	0.96074	27.61	6	271400000	132390000	139020000
Q6P9Z1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3	Smarcd3	1	1	1	1.9	1.9	1.9	54.985	483	0.012325	0.024566	0.75999	255.67	3	1813200000	1789300000	23886000
Q9D5V6	Synapse-associated protein 1	Syap1	2	2	2	13.7	13.7	13.7	41.349	365	5.901E-184	0.75481	0.89072	12.673	4	399450000	189740000	209710000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
O88935	Synapsin-1	Syn1	2	2	2	3.4	3.4	3.4	74.096	706	9.8765E-08	0.79349	0.66366	52.648	2	60717000	33324000	27394000
Q64332	Synapsin-2	Syn2	2	2	2	7.8	7.8	7.8	63.372	586	0.00012088	1.0672	1.3001	6.641	3	35206000	13920000	21286000
Q62465	Synaptic vesicle membrane protein VAT-1 homolog	Vat1	4	4	4	12.8	12.8	12.8	43.096	406	1.9631E-15	2.1598	4.3396	73.082	6	148250000	53395000	94857000
Q9CQW1	Synaptobrevin homolog YKT6	Ykt6	3	3	3	22.2	22.2	22.2	22.314	198	1.7337E-24	2.285	2.2586	42.012	4	386380000	94162000	292220000
B2RQK7	Synaptopodin 2-like protein	Synpo2l	3	3	3	4.9	4.9	4.9	103.27	978	4.0461E-11	0.92666	1.1402	15.288	3	270320000	135590000	134730000
E9Q1U2	Synaptopodin-2	Synpo2	3	3	3	3.3	3.3	3.3	135.76	1257	2.1621E-13	0.69691	0.80324	21.114	5	476140000	276300000	199850000
P26039	Talin-1	Tln1	37	37	34	20.6	20.6	19.3	269.82	2541	0	1.2888	1.427	49.013	42	3197700000	1443400000	1754300000
E9PUM4	Talin-2	Tln2	10	7	7	5.9	4.6	4.6	271.66	2542	2.5158E-29	1.8814	2.0514	51.118	6	265510000	86387000	179120000
Q921F2	TAR DNA-binding protein 43	Tardbp	2	2	2	8.7	8.7	8.7	44.547	414	4.0092E-19	2.3388	2.1087	46.218	3	105050000	30947000	74101000
Q3UDC3	Target of Myb protein 1	Tom1	11	11	11	34.3	34.3	34.3	57.145	516	7.912E-130	1.347	1.3178	71.199	18	1027400000	372670000	654720000
P11983	T-complex protein 1 subunit alpha	Tcp1	6	6	6	13.1	13.1	13.1	60.448	556	1.5023E-58	1.6752	1.8363	34.901	6	1365500000	478290000	887180000
P80314	T-complex protein 1 subunit beta	Cct2	12	12	12	24.5	24.5	24.5	57.477	535	1.507E-188	1.7518	2.2781	41.013	14	1475200000	486970000	988230000
P80315	T-complex protein 1 subunit delta	Cct4	9	9	9	19.7	19.7	19.7	58.066	539	1.9205E-61	2.4434	2.6288	34.612	7	1272400000	405870000	866520000
P80316	T-complex protein 1 subunit epsilon	Cct5	8	8	8	21.6	21.6	21.6	59.623	541	5.6745E-20	1.604	2.4094	99.81	8	1093500000	450370000	643100000
P80313	T-complex protein 1 subunit eta	Cct7	6	6	6	16.5	16.5	16.5	59.652	544	1.4869E-82	2.688	1.9572	80.556	6	317600000	99612000	217990000
P80318	T-complex protein 1 subunit gamma	Cct3	7	7	7	16.7	16.7	16.7	60.629	545	1.1108E-26	2.9623	2.7909	97.914	9	1247900000	280820000	967030000
P42932	T-complex protein 1 subunit theta	Cct8	10	10	10	25.9	25.9	25.9	59.555	548	2.0044E-76	1.3465	1.5106	67.085	12	944640000	401380000	543260000
E9QPA6	T-complex protein 1 subunit zeta	Cct6a	4	4	3	10.5	10.5	8.1	58.57	532	2.1829E-26	1.9705	4.7265	155.2	5	393900000	152260000	241640000
A3KMP2	Tetratricopeptide repeat protein 38	Ttc38	3	3	3	9.9	9.9	9.9	52.223	465	9.9874E-06	1.8704	2.1247	67.307	3	44742000	14550000	30191000
Q8C1A5	Thimet oligopeptidase	Thop1	9	9	9	14.1	14.1	14.1	78.025	687	3.3496E-31	0.96192	0.94014	93.736	9	586160000	373930000	212230000
O55060	Thiopurine S-methyltransferase	Tpmt	4	4	4	15.4	15.4	15.4	27.585	240	1.4306E-08	0.42872	0.45932	75.315	3	156450000	115000000	41455000
P10639	Thioredoxin	Txn	2	2	2	23.8	23.8	23.8	11.675	105	0.00019985	0.61369	1.3791	72.932	2	6432300000	3986000000	2446300000
Q9CQU0	Thioredoxin domain-containing protein 12	Txndc12	2	2	2	17.6	17.6	17.6	19.048	170	1.3491E-33	0.94213	0.80269	14.184	3	91868000	48496000	43371000
Q9CQM5	Thioredoxin domain-containing protein 17	Txndc17	2	2	2	27.6	27.6	27.6	14.015	123	3.0655E-93	0.49632	0.49075	18.087	5	504120000	340930000	163190000
Q91W90	Thioredoxin domain-containing protein 5	Txndc5	4	4	4	12.7	12.7	12.7	46.415	417	8.5552E-47	0.94994	0.96322	54.665	5	309610000	171990000	137620000
Q9JMH6	Thioredoxin reductase 1, cytoplasmic	Txnrd1	5	4	4	12.4	10	10	67.101	613	2.6688E-37	0.81296	0.8519	63.818	7	773650000	426190000	347460000
Q9JLT4	Thioredoxin reductase 2, mitochondrial	Txnrd2	10	10	9	24.8	24.8	21.9	56.62	524	9.099E-156	1.1667	1.2856	84.535	12	3725900000	1884800000	1841000000
P97493	Thioredoxin, mitochondrial	Txn2	3	3	3	22.3	22.3	22.3	18.255	166	4.23E-178	0.52878	0.61956	33.292	4	1915000000	1183700000	731330000
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	Prdx3	8	8	8	37	37	37	28.127	257	1.727E-114	1.0225	1.2053	87.894	30	1.1843E+10	4943000000	6900400000
Q8CDN6	Thioredoxin-like protein 1	Txnl1	10	10	10	47.8	47.8	47.8	32.237	289	0	0.63256	0.69369	53.269	15	2868500000	1755900000	1112700000
P52196	Thiosulfate sulfurtransferase	Tst	6	6	6	23.6	23.6	23.6	33.466	297	3.0995E-14	1.3894	1.8004	63.335	6	578640000	243160000	335480000
Q8BH55	Threonine synthase-like 1	Thnsl1	2	2	2	5.5	5.5	5.5	83.099	747	1.3797E-05	1.4798	1.755	12.538	2	69564000	26785000	42779000
Q9D0R2	Threonine--tRNA ligase, cytoplasmic	Tars	4	4	4	6.8	6.8	6.8	83.355	722	2.3546E-11	1.7645	1.9505	33.178	4	120940000	43582000	77362000
Q3UQ84	Threonine--tRNA ligase, mitochondrial	Tars2	3	3	3	5.7	5.7	5.7	81.699	723	1.0694E-06	2.831	2.4803	55.506	3	142160000	34656000	107500000
Q80YQ1	Thrombospondin-1	Thbs1	3	3	3	2.6	2.6	2.6	129.69	1171	4.2663E-35	2.5897	4.8601	17.008	2	82589000	27222000	55367000
Q99J36	THUMP domain-containing protein 1	Thumpd1	1	1	1	3.1	3.1	3.1	38.884	350	0.004399	0.93146	1.0859	6.5944	2	29031000	16610000	12422000
B9EHJ3	Tight junction protein ZO-1	Tjp1	6	6	6	4.6	4.6	4.6	188.85	1685	4.4494E-25	1.2996	1.6006	69.925	5	286750000	159900000	126850000
Q8BH58	TIP41-like protein	Tiprl	4	4	4	17.7	17.7	17.7	31.253	271	2.5721E-12	0.96423	0.84102	28.279	5	460830000	241410000	219420000
A2ASS6	Titin	Ttn	253	253	253	11.3	11.3	11.3	3906.4	35213	0	2.8796	3.6523	103.15	217	2.4722E+10	7515900000	1.7206E+10
Q9QZ06	Toll-interacting protein	Tollip	4	4	4	18.6	18.6	18.6	30.345	274	2.0802E-68	1.4486	1.5515	18.853	3	211980000	88932000	123040000
Q5SRX1	TOM1-like protein 2	Tom1l2	5	5	5	18.3	18.3	18.3	55.662	507	1.4167E-27	0.98496	0.99362	36.851	6	163280000	85115000	78162000
Q9D8Z2	TP53-regulated inhibitor of apoptosis 1	Triap1	2	2	2	28.9	28.9	28.9	8.7558	76	3.5386E-08	0.59315	0.68975	22.06	3	146020000	84399000	61618000
O55013	Trafficking protein particle complex subunit 3	Trappc3	2	2	2	10.6	10.6	10.6	20.302	180	5.0032E-06	1.1121	1.3209	57.996	2	48661000	22005000	26656000
Q9DBB8	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	Dhdh	4	4	4	16.8	16.8	16.8	36.3	333	1.7824E-17	1.2884	1.1751	38.627	6	894970000	409310000	485670000
Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial	Mecr	5	5	5	21.2	21.2	21.2	40.342	373	1.068E-104	1.6003	1.393	17.024	4	117700000	63564000	54140000
Q93092	Transaldolase	Taldo1	11	11	11	31.2	31.2	31.2	37.387	337	3.6615E-74	0.48067	0.60513	154.6	15	6563900000	4400200000	2163700000
E9PYD5	Transcription elongation factor A protein 1	Tcea1	4	4	4	14.1	14.1	14.1	35.031	312	6.1964E-19	0.4603	0.54146	56.886	2	37479000	25570000	11908000
P83940	Transcription elongation factor B polypeptide 1	Tceb1	4	4	4	38.4	38.4	38.4	12.473	112	1.7578E-19	0.79175	1.9058	88.421	5	667740000	408710000	259020000
P62869	Transcription elongation factor B polypeptide 2	Tceb2	2	2	2	28.8	28.8	28.8	13.17	118	2.6644E-45	0.79705	1.0159	43.763	3	628780000	376280000	252500000
Q5SSK3	Transcription elongation factor, mitochondrial	Tefm	2	2	2	7.7	7.7	7.7	41.873	364	0.00023706	2.2732	1.9558	65.81	3	110780000	23793000	86991000
Q8CGF7	Transcription elongation regulator 1	Tcerg1	2	2	2	2.4	2.4	2.4	123.79	1100	0.00033568	0.28169	0.36382	121.97	2	843550000	790050000	53491000
Q64152	Transcription factor BTF3	Btf3	4	4	4	37.7	37.7	37.7	22.031	204	5.261E-137	0.74112	0.67371	32.678	5	259730000	152120000	107610000
Q9CQH7	Transcription factor BTF3 homolog 4	Btf3l4	2	2	2	37.3	37.3	37.3	17.27	158	4.169E-112	0.62353	0.53722	28.736	2	118060000	80103000	37955000
P42669	Transcriptional activator protein Pur-alpha	Pura	3	3	3	18.1	18.1	18.1	34.883	321	1.1448E-70	2.7795	2.6217	74.136	5	658180000	175190000	482990000
P37804	Transgelin	Tagln	10	10	10	53.7	53.7	53.7	22.576	201	4.727E-89	0.64843	0.8692	129.28	13	3082100000	1754900000	1327200000
Q9WVA4	Transgelin-2	Tagln2	9	9	9	48.7	48.7	48.7	22.395	199	5.165E-133	0.62683	0.6331	97.831	10	897960000	575430000	322540000
Q01853	Transitional endoplasmic reticulum ATPase	Vcp	23	23	23	36.2	36.2	36.2	89.321	806	1.865E-243	1.1245	1.3182	57.776	40	1.1264E+10	4969500000	6294400000
P40142	Transketolase	Tkt	12	12	12	25.2	25.2	25.2	67.63	623	1.233E-107	0.96032	1.0634	75.175	19	2236800000	1219700000	1017100000
P63028	Translationally-controlled tumor protein	Tpt1	5	5	5	54.1	54.1	54.1	19.462	172	1.598E-188	0.50482	0.4988	52.648	16	798320000	502270000	296060000
Q62348	Translin	Tsn	3	3	3	20.6	20.6	20.6	26.201	228	3.2364E-23	0.77833	0.76316	39.177	2	161300000	75562000	85733000
Q8BQX5	Transmembrane and coiled-coil domain-containing protein 6	Tmco6	2	2	2	1.6	1.6	1.6	54.914	494	0.00065307	1.4392	1.2319	19.938	2	1313200000	605970000	707250000
G3X9F4	Transmembrane protein 143	Tmem143	2	2	2	8.3	8.3	8.3	51.579	458	1.5051E-08	1.5683	1.6005	4.2857	2	104150000	33951000	70197000
Q9CZX7	Transmembrane protein 55A	Tmem55a	2	2	2	14.4	14.4	14.4	28.038	257	5.7655E-07	1.1225	1.3208	56.795	2	39673000	17233000	22440000
Q6P2B1	Transportin-3	Tnpo3	3	3	3	4.1	4.1	4.1	104.17	923	7.8664E-06	3.0337	3.2363	17.83	2	119160000	33097000	86065000
P07309	Transthyretin	Ttr	6	6	6	63.3	63.3	63.3	15.776	147	3.3373E-78	0.48787	0.57244	58.024	28	1.2919E+10	8677100000	4241600000
H3BL37	Treacle protein	Tcof1	2	2	2	2.2	2.2	2.2	138.55	1356	3.437E-12	0.20359	0.21908	15.026	2	123430000	99728000	23704000
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	Hadha	28	28	28	45.2	45.2	45.2	82.669	763	0	2.9354	3.3039	109.2	63	1.0679E+10	3634400000	7044800000
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	Hadhb	19	19	19	48.4	48.4	48.4	51.386	475	5.107E-251	3.2777	3.2916	101.32	49	1.5066E+10	3424600000	1.1642E+10
Q64737	Trifunctional purine biosynthetic protein adenosine-3	Gart	13	13	13	18.1	18.1	18.1	107.5	1010	2.9324E-82	1.0788	1.1421	74.266	14	1933000000	796560000	1136400000
Q91ZE0	Trimethyllysine dioxygenase, mitochondrial	Tmlhe	5	5	5	11.2	11.2	11.2	49.609	421	4.8552E-07	2.3334	2.9039	36.4	6	473720000	142700000	331010000
P17751	Triosephosphate isomerase	Tpi1	14	14	14	54.8	54.8	54.8	32.191	299	0	0.55074	0.59234	90.333	83	6.8984E+10	4.3556E+10	2.5427E+10

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
Q1XH17	Tripartite motif-containing protein 72	Trim72	13	13	13	48	48	48	52.816	477	3.881E-156	1.7478	1.8629	41.709	23	4429900000	1510200000	2919600000
Q64514	Tripeptidyl-peptidase 2	Tpp2	9	9	9	9.4	9.4	9.4	139.88	1262	8.3333E-35	1.3631	3.5125	112.66	8	575900000	240530000	335360000
Q0KL02	Triple functional domain protein	Trio	1	1	1	0.3	0.3	0.3	347.86	3102	0.0040326	1.1268	1.6102	80.452	2	442150000	219500000	222650000
Q99LF4	tRNA-splicing ligase RtcB homolog	D10Wsu52e	4	4	4	9.9	9.9	9.9	55.249	505	6.1952E-23	1.9859	2.1496	76.44	4	265280000	92067000	173210000
P49813	Tropomodulin-1	Tmod1	7	7	7	23.7	23.7	23.7	40.466	359	7.2518E-24	1.7266	1.8212	62.818	7	143250000	48952000	94293000
P58771	Tropomyosin alpha-1 chain	Tpm1	19	19	4	51.4	51.4	8.1	32.68	284	0	1.0284	0.98673	89.162	30	2.6012E+10	1.1808E+10	1.4204E+10
E9Q5J9	Tropomyosin alpha-3 chain	Tpm3	11	2	0	28.1	4.6	0	33.28	285	0	1.0646	4.0066	172.99	2	833240000	428350000	404890000
Q6IRU2	Tropomyosin alpha-4 chain	Tpm4	8	8	8	32.3	32.3	32.3	28.467	248	1.9498E-58	0.85034	0.83245	81.762	9	812960000	428610000	384350000
P19123	Troponin C, slow skeletal and cardiac muscles	Tnnc1	4	4	4	23.6	23.6	23.6	18.42	161	4.553E-172	1.467	1.7392	86.25	11	1166200000	451980000	714200000
P48787	Troponin I, cardiac muscle	Tnni3	5	5	5	24.2	24.2	24.2	24.258	211	2.029E-60	1.4915	1.7689	42.843	8	1.6178E+10	5220800000	1.0957E+10
J3QQ13	Troponin T, cardiac muscle	Tnnt2	13	13	13	32.8	32.8	32.8	35.943	302	7.878E-244	1.1521	1.5352	92.411	48	2.547E+10	1.395E+10	1.152E+10
P32921	Tryptophan--tRNA ligase, cytoplasmic	Wars	2	2	2	6.2	6.2	6.2	54.357	481	3.5662E-09	1.3609	1.3289	53.22	3	270700000	114940000	155760000
P68369	Tubulin alpha-1A chain	Tuba1a	8	8	0	27.5	27.5	0	50.135	451	1.1352E-45	2.0948	2.092	43.099	10	1178000000	408880000	769130000
P68368	Tubulin alpha-4A chain	Tuba4a	6	2	1	20.3	5.4	2.2	49.924	448	2.7852E-38	2.4778	5.8309	129.7	2	99725000	35032000	64693000
P68372	Tubulin beta-4B chain	Tubb4b	12	12	12	45.2	45.2	45.2	49.83	445	1.564E-196	3.4174	4.9437	67.169	16	919770000	206480000	713290000
Q9CRB6	Tubulin polymerization-promoting protein family member 3	Tppp3	7	7	7	32.4	32.4	32.4	18.965	176	4.1209E-88	0.39463	0.59873	114.58	9	1198000000	831290000	366720000
Q9D1E6	Tubulin-folding cofactor B	Tbcb	4	4	4	13.9	13.9	13.9	27.385	244	3.1117E-07	0.44868	0.68207	113.64	4	411820000	267440000	144380000
P48428	Tubulin-specific chaperone A	Tbca	3	3	3	18.5	18.5	18.5	12.758	108	1.6367E-05	0.35894	0.35109	124.96	3	188620000	130320000	58299000
Q8C5W3	Tubulin-specific chaperone cofactor E-like protein	Tbcel	2	2	2	6.1	6.1	6.1	48.031	424	4.5638E-05	0.6078	0.60818	23.059	2	76694000	47904000	28790000
Q3UDE2	Tubulin--tyrosine ligase-like protein 12	Ttll12	2	2	2	4.1	4.1	4.1	74.042	639	0.00077018	2.5932	3.24	17.628	2	58585000	23757000	34827000
Q61187	Tumor susceptibility gene 101 protein	Tsg101	3	3	3	8.2	8.2	8.2	44.123	391	1.4034E-08	2.4433	2.5678	35.694	2	28804000	8656600	20148000
Q9Z0P5	Twinfilin-2	Twf2	4	4	4	21.2	21.2	21.2	39.47	349	1.8203E-30	1.9637	2.3219	42.92	3	255590000	88938000	166650000
P35235	Tyrosine-protein phosphatase non-receptor type 11	Ptpn11	13	13	13	30	30	30	68.46	597	2.2024E-59	0.87205	0.9532	64.914	11	588760000	316190000	272570000
Q6PB44	Tyrosine-protein phosphatase non-receptor type 23	Ptpn23	2	2	2	1.7	1.7	1.7	185.21	1692	1.7951E-05	0.3317	0.94838	71.815	2	172550000	161640000	10914000
A2A7S7	Tyrosine--tRNA ligase, cytoplasmic	Yars	12	12	12	17.6	17.6	17.6	63.001	564	5.3993E-23	0.6906	0.79762	89.234	10	724870000	417590000	307270000
Q62376	U1 small nuclear ribonucleoprotein 70 kDa	Snrnp70	1	1	1	2.5	2.5	2.5	51.991	448	0.057296	1.0711	1.3501	6.0299	2	322710000	146560000	176160000
O35900	U6 snRNA-associated Sm-like protein LSm2	Lsm2	4	4	4	55.8	55.8	55.8	10.834	95	8.0179E-07	0.941	1.2571	52.137	4	187460000	75800000	111660000
Q8R317	Ubiquilin-1	Ubqln1	4	2	2	9.1	4.8	4.8	61.976	582	5.0334E-16	0.99201	0.96991	2.1583	2	38885000	18612000	20273000
Q9QZM0	Ubiquilin-2	Ubqln2	4	4	2	8.8	8.8	4.9	67.35	638	3.4123E-22	0.83131	0.67622	95.844	4	27574000	20348000	7226500
Q8R1S0	Ubiquinone biosynthesis monooxygenase COQ6	Coq6	4	4	4	14.3	14.3	14.3	51.392	476	2.5168E-31	2.623	2.7904	39.518	6	594480000	126290000	468190000
P97478	Ubiquinone biosynthesis protein COQ7 homolog	Coq7	2	2	2	22.1	22.1	22.1	24.041	217	3.4044E-73	1.9147	2.9014	121.43	2	249190000	57149000	192040000
Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondrial	Coq9	7	7	7	24.9	24.9	24.9	35.082	313	1.632E-186	1.0291	1.1391	112.22	20	8441700000	4408000000	4033600000
E9PXY8	Ubiquitin carboxyl-terminal hydrolase	Usp7	3	3	3	3.8	3.8	3.8	132.85	1143	0.00061045	0.75163	0.98287	63.605	3	234690000	138650000	96035000
Q9JMA1	Ubiquitin carboxyl-terminal hydrolase 14	Usp14	8	8	8	22.3	22.3	22.3	56.001	493	0	0.72497	0.79705	66.503	9	1198800000	608570000	590220000
Q3UJD6	Ubiquitin carboxyl-terminal hydrolase 19	Usp19	1	1	1	1.3	1.3	1.3	150.55	1360	2.934E-09	1.0137	1.125	16.51	2	7168800	3301400	3867400
P35123	Ubiquitin carboxyl-terminal hydrolase 4	Usp4	6	6	6	8.3	8.3	8.3	108.34	962	2.0232E-11	1.4204	1.1167	47.971	5	152150000	67927000	84224000
P56399	Ubiquitin carboxyl-terminal hydrolase 5	Usp5	12	12	12	19.8	19.8	19.8	95.832	858	1.2005E-67	0.97146	0.92535	17.393	17	942180000	509760000	432420000
Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	Uchl1	5	5	5	41.3	41.3	41.3	24.838	223	0	0.56375	0.54465	205.66	6	1640700000	440780000	1199900000
Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3	Uchl3	8	8	8	49.6	49.6	49.6	26.151	230	0	0.71979	0.83611	40.882	15	1920400000	1055000000	865440000
Q9WUP7	Ubiquitin carboxyl-terminal hydrolase isozyme L5	Uchl5	3	3	3	15.2	15.2	15.2	37.616	329	5.1445E-17	0.77798	0.85289	25.001	2	267150000	151880000	115270000
P70362	Ubiquitin fusion degradation protein 1 homolog	Ufd1l	3	3	3	14	14	14	34.481	307	3.1021E-06	0.80065	0.7792	44.461	2	136680000	85495000	51182000
Q7TQI3	Ubiquitin thioesterase OTUB1	Otub1	6	6	6	30.3	30.3	30.3	31.27	271	4.8013E-50	0.71085	0.84283	35.596	6	260280000	169920000	90362000
Q8VDI7	Ubiquitin-associated domain-containing protein 1	Ubac1	3	3	3	12	12	12	45.53	409	1.161E-169	0.88703	1.5448	29.599	2	34539000	18444000	16095000
Q80X50	Ubiquitin-associated protein 2-like	Ubap2l	5	5	5	7	7	7	116.8	1107	1.5857E-69	0.61892	0.52217	71.845	5	242890000	110940000	131950000
P61087	Ubiquitin-conjugating enzyme E2 K	Ube2k	5	5	5	27.5	27.5	27.5	22.406	200	6.4762E-20	0.83503	0.94426	43.509	4	352340000	178440000	173890000
P68037	Ubiquitin-conjugating enzyme E2 L3	Ube2l3	5	5	5	42.9	42.9	42.9	17.861	154	5.7016E-89	0.54892	0.66341	60.919	19	8046400000	5238300000	2808100000
P61089	Ubiquitin-conjugating enzyme E2 N	Ube2n	4	4	4	29.6	29.6	29.6	17.138	152	2.158E-117	0.7281	1.2428	105.32	4	1786300000	1053500000	732770000
Q6ZPJ3	Ubiquitin-conjugating enzyme E2 O	Ube2o	5	5	5	7.5	7.5	7.5	140.83	1288	1.0842E-25	1.1119	1.3222	15.983	5	246580000	121320000	125260000
E9PY39	Ubiquitin-conjugating enzyme E2 variant 1	Gm20431	2	1	1	7	4.3	4.3	42.096	371	8.4563E-09	0.96627	0.88886	21.019	2	57076000	28432000	28643000
Q9D2M8	Ubiquitin-conjugating enzyme E2 variant 2	Ube2v2	3	3	2	22.8	22.8	15.9	16.367	145	3.2284E-07	0.40926	0.90423	55.578	3	102650000	70140000	32510000
Q9CR09	Ubiquitin-fold modifier-conjugating enzyme 1	Ufc1	3	3	3	15.6	15.6	15.6	19.481	167	3.7671E-06	1.5903	1.6638	25.484	4	183530000	76152000	107370000
Q02053	Ubiquitin-like modifier-activating enzyme 1	Uba1	21	21	21	27.9	27.9	27.9	117.81	1058	0	1.3135	1.4894	65.4	32	4830900000	2173600000	2657300000
Q64339	Ubiquitin-like protein ISG15	Isg15	2	2	2	21.7	21.7	21.7	17.897	161	2.9116E-21	0.86621	0.99349	21.956	2	282350000	171340000	111010000
E9QKT1	Ubiquitin-protein ligase E3A	Ube3a	2	2	2	3.2	3.2	3.2	99.818	870	4.0678E-07	1.0112	1.9848	95.851	4	230750000	111530000	119220000
Q922Y1	UBX domain-containing protein 1	Ubxn1	3	3	3	19.9	19.9	19.9	33.572	297	1.3527E-23	0.52696	0.3666	39.142	5	735460000	518660000	216800000
Q99PL6	UBX domain-containing protein 6	Ubxn6	4	4	4	13.1	13.1	13.1	49.795	442	3.7642E-11	1.2378	1.7641	33.141	4	214490000	104700000	109780000
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	Uggt1	2	2	2	2.3	2.3	2.3	176.43	1551	0.0025621	1.4446	1.4381	44.697	3	55478000	16250000	39229000
Q3UHZ7	UDP-N-acetylhexosamine pyrophosphorylase	Uap1	3	3	2	8.6	8.6	6.1	58.582	522	1.129E-51	0.54625	0.52805	28.006	2	147370000	96043000	51324000
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	Uap1l1	3	2	2	9.3	6.7	6.7	56.613	507	2.6214E-08	0.17102	0.19377	65.586	2	196490000	166290000	30197000
Q9DBP5	UMP-CMP kinase	Cmpk1	7	7	7	46.4	46.4	46.4	22.165	196	2.104E-46	0.46158	0.48613	59.074	6	840480000	620730000	219750000
Q3U5Q7	UMP-CMP kinase 2, mitochondrial	Cmpk2	5	5	5	20.6	20.6	20.6	50.036	447	4.0144E-16	0.88337	1.074	118.07	2	50656000	21670000	28986000
Q9CR10	Uncharacterized protein C17orf90 homolog	Oxld1	1	1	1	7.5	7.5	7.5	22.178	201	6.788E-50	0.56805	0.55764	19.849	2	667660000	413870000	253790000
Q0VAW6	Uncharacterized protein C18orf25 homolog	8030462N17Rik	2	2	2	8.5	8.5	8.5	42.78	399	6.4032E-35	0.4751	0.77141	6.4048	2	18320000	13487000	4833000
Q149B8	Uncharacterized protein C1orf170 homolog	Perm1	9	9	9	22.6	22.6	22.6	85.156	807	5.5314E-88	0.71021	0.67273	32.312	10	889780000	546820000	342960000
Q9CQF4	Uncharacterized protein C6orf203 homolog	1700021F05Rik	4	4	4	18.3	18.3	18.3	27.847	240	5.8322E-27	0.50356	0.59458	1.1792	2	94418000	63859000	30559000
Q9D727	Uncharacterized protein C6orf226 homolog		1	1	1	27.2	27.2	27.2	12.013	114	2.5125E-07	0.62062	0.65751	2.1966	2	18215000	11563000	6652100
Q6PIU9	Uncharacterized protein FLJ45252 homolog		4	4	4	15	15	15	37.704	354	2.3709E-15	0.70799	0.6683	129.93	3	44181000	26858000	17323000
Q8CC88	Uncharacterized protein KIAA0564 homolog	Kiaa0564	10	10	10	6.6	6.6	6.6	213.42	1905	1.2997E-34	4.8201	5.0885	70.838	8	710230000	133360000	576870000
Q9WTI7	Unconventional myosin-Ic	Myo1c	3	3	3	3.6	3.6	3.6	121.94	1063	0.00065391	3.1405	3.3244	64.926	4	178650000	23376000	155270000
Q9JK81	UPF0160 protein MYG1, mitochondrial	Myg1	2	2	2	6.8	6.8	6.8	42.722	380	3.1972E-06	1.336	1.3578	28.619	2	114470000	49107000	65368000
E9QMK9	UPF0317 protein C14orf159 homolog, mitochondrial	9030617O03Rik	10	10	10	23	23	23	69.921	647	3.6335E-74	0.70195	0.39025	99.219	9	904690000	488940000	415750000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
A6H630	UPF0364 protein C6orf211 homolog	Armt1	3	3	3	11.2	11.2	11.2	50.548	439	1.8938E-34	1.1179	1.1011	5.602	2	144450000	63989000	80457000
D3YZD8	UPF0366 protein C11orf67 homolog	1810020D17Rik	4	4	4	27.3	27.3	27.3	16.358	150	2.8774E-72	0.41427	0.47848	42.603	5	610820000	428370000	182460000
Q9D0B6	UPF0368 protein Cxorf26 homolog	Pbdc1	2	2	2	8.6	8.6	8.6	22.223	198	0.0017487	0.66793	0.66962	1.743	2	72299000	42615000	29684000
Q8BTE0	UPF0369 protein C6orf57 homolog	Sdhaf4	3	3	3	25	25	25	11.888	104	7.8533E-14	0.30476	0.2801	56.056	4	261330000	212430000	48897000
Q5F285	UPF0451 protein C17orf61 homolog	Tmem256	1	1	1	24.8	24.8	24.8	11.655	113	1.9757E-35	2.0008	1.2479	32.38	4	223340000	74060000	149280000
Q9CQE8	UPF0568 protein C14orf166 homolog		2	2	2	11.9	11.9	11.9	28.152	244	1.9222E-12	2.623	2.1096	10.054	2	196890000	64869000	132020000
Q80UY1	UPF0586 protein C9orf41 homolog	Carnmt1	3	3	3	7	7	7	46.338	400	7.7207E-05	0.73928	0.87642	5.247	2	116990000	66262000	50725000
Q8BHG2	UPF0587 protein C1orf123 homolog	0610037L13Rik	4	4	4	33.1	33.1	33.1	18.02	160	2.767E-134	0.53216	0.6793	22.235	3	184890000	110300000	74594000
Q8VE95	UPF0598 protein C8orf82 homolog		5	5	5	34.4	34.4	34.4	24.33	218	1.088E-116	1.4711	1.4372	76.044	5	2032500000	746340000	1286100000
Q9CWU4	UPF0690 protein C1orf52 homolog	2410004B18Rik	2	2	2	13.3	13.3	13.3	20.101	180	0.00018008	0.45025	0.39361	31.315	2	5191100	4003400	1187700
E9QNR6	UPF0696 protein C11orf68 homolog	AI837181	2	2	2	7.4	7.4	7.4	31.845	298	3.9317E-06	0.68616	2.0581	36.01	3	276930000	150680000	126250000
Q78IK2	Up-regulated during skeletal muscle growth protein 5	Usmg5	4	4	4	44.8	44.8	44.8	6.3814	58	3.235E-227	1.0226	1.164	71.961	10	2866400000	1528500000	1337900000
Q9D142	Uridine diphosphate glucose pyrophosphatase	Nudt14	1	1	1	6.3	6.3	6.3	24.443	222	0.043549	1.0491	1.1632	7.9127	2	167560000	80879000	86677000
P70697	Uroporphyrinogen decarboxylase	Urod	2	2	2	10.6	10.6	10.6	40.691	367	2.3637E-32	1.4679	1.5271	59.068	2	206750000	82446000	124310000
P51163	Uroporphyrinogen-III synthase	Uros	2	2	2	14.7	14.7	14.7	28.504	265	3.8084E-17	0.67424	0.58155	4.686	2	224660000	124730000	99928000
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	Ugp2	13	13	13	34.8	34.8	34.8	56.979	508	0	1.7163	2.4602	73.733	22	4525400000	1739600000	2785700000
P54726	UV excision repair protein RAD23 homolog A	Rad23a	5	4	4	23.7	21.5	21.5	39.706	363	1.1797E-18	0.52466	0.50549	20.831	3	71295000	46529000	24766000
P54728	UV excision repair protein RAD23 homolog B	Rad23b	6	6	5	16.8	16.8	14.9	43.512	416	1.056E-18	0.55149	0.59494	20.966	7	445560000	289820000	155740000
P40336	Vacuolar protein sorting-associated protein 26A	Vps26a	2	2	2	8	8	8	38.113	327	1.7254E-08	1.5869	3.0914	147.29	2	176610000	78522000	98091000
Q9D1C8	Vacuolar protein sorting-associated protein 28 homolog	Vps28	3	3	3	15.8	15.8	15.8	25.452	221	2.1775E-06	1.0009	1.2347	25.005	3	157530000	74943000	82583000
Q9QZ88	Vacuolar protein sorting-associated protein 29	Vps29	4	4	4	26.4	26.4	26.4	20.495	182	1.4402E-42	1.7689	2.5689	121.02	6	1076800000	383780000	692990000
Q9EQH3	Vacuolar protein sorting-associated protein 35	Vps35	9	9	9	14.4	14.4	14.4	91.712	796	1.101E-177	2.3411	2.6175	79.23	11	1792100000	778250000	1013900000
P97390	Vacuolar protein sorting-associated protein 45	Vps45	2	2	2	4.4	4.4	4.4	65.052	570	3.4885E-06	6.0054	5.9757	38.151	2	29259000	5642500	23616000
Q9CR26	Vacuolar protein sorting-associated protein VTA1 homolog	Vta1	2	2	2	10.7	10.7	10.7	33.913	309	9.18E-13	1.1205	0.98129	32.725	2	160060000	81103000	78956000
A2A4J8	Vacuolar protein-sorting-associated protein 25	Vps25	3	3	3	20.1	20.1	20.1	21.594	184	0.00010216	1.5046	1.3727	28.405	3	69990000	34006000	35984000
Q91XD6	Vacuolar protein-sorting-associated protein 36	Vps36	2	2	2	5.2	5.2	5.2	43.735	386	0.0061503	1.3747	1.4505	26.429	2	64461000	26419000	38042000
Q8R164	Valacyclovir hydrolase	Bphl	6	6	6	30.9	30.9	30.9	32.851	291	8.3875E-64	1.6285	1.8751	51.582	7	719310000	273430000	445880000
G3UY93	Valine--tRNA ligase	Vars	11	11	11	13.1	13.1	13.1	141.41	1278	3.9521E-43	2.6042	2.5673	55.238	14	791700000	243110000	548590000
P70460	Vasodilator-stimulated phosphoprotein	Vasp	2	2	2	9.9	9.9	9.9	39.666	375	2.0677E-35	0.87928	0.9376	12.865	4	73412000	39155000	34257000
Q62059	Versican core protein	Vcan	4	4	4	1.6	1.6	1.6	366.78	3357	1.9494E-08	0.60549	0.65337	85.36	3	344480000	213360000	131110000
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	Acadvl	27	27	27	40.7	40.7	40.7	70.875	656	0	1.3339	1.5671	84.451	51	2.6725E+10	1.082E+10	1.5905E+10
Q8BH80	Vesicle-associated membrane protein-associated protein B	Vapb	4	4	4	21.4	21.4	21.4	26.918	243	1.6186E-47	1.2076	1.2637	30.807	4	635100000	288680000	346420000
P46460	Vesicle-fusing ATPase	Nsf	4	4	4	5.6	5.6	5.6	82.613	744	6.3404E-07	1.8265	1.7147	101.61	3	109070000	57684000	51384000
Q8VDJ3	Vigilin	Hdlbp	5	5	5	4.6	4.6	4.6	141.74	1268	2.4792E-06	1.8723	2.1592	33.16	4	166490000	50099000	116390000
P20152	Vimentin	Vim	5	5	5	15.2	15.2	15.2	53.687	466	1.6969E-90	0.67269	0.71107	102.36	9	416560000	206820000	209740000
Q64727	Vinculin	Vcl	26	26	26	31.1	31.1	31.1	116.72	1066	4.972E-248	0.81774	0.87143	53.985	39	4507500000	2679000000	1828500000
P21614	Vitamin D-binding protein	Gc	12	12	12	35.7	35.7	35.7	53.6	476	1.246E-264	0.78185	0.95194	112.17	16	3304400000	1489500000	1814900000
P29788	Vitronectin	Vtn	3	3	3	14.2	14.2	14.2	54.848	478	1.9807E-16	2.273	2.4296	17.012	2	199420000	64744000	134670000
Q60932	Voltage-dependent anion-selective channel protein 1	Vdac1	8	8	8	38.2	38.2	38.2	32.351	296	0	0.928	1.1113	85.356	16	2611900000	1318300000	1293600000
Q60930	Voltage-dependent anion-selective channel protein 2	Vdac2	8	8	8	38	38	38	31.732	295	1.032E-302	0.93613	1.1153	105.65	11	1978500000	1013700000	964790000
J3QMG3	Voltage-dependent anion-selective channel protein 3	Vdac3	5	5	5	26.4	26.4	26.4	30.851	284	3.8199E-78	0.99739	1.1144	70.734	7	1650600000	610490000	1040100000
O08532	Voltage-dependent calcium channel subunit alpha-2/delta-1	Cacna2d1	5	5	5	5.6	5.6	5.6	124.63	1103	1.6959E-10	0.57067	0.54069	98.892	6	171940000	81531000	90405000
Q99KC8	von Willebrand factor A domain-containing protein 5A	Vwa5a	12	12	12	22.4	22.4	22.4	87.142	793	2.61E-135	0.9883	0.95711	103.03	16	952380000	587780000	364600000
P50516	V-type proton ATPase catalytic subunit A	Atp6v1a	9	9	9	20.6	20.6	20.6	68.325	617	1.3211E-76	2.0992	2.5645	67.317	11	499140000	178800000	320340000
P62814	V-type proton ATPase subunit B, brain isoform	Atp6v1b2	8	8	8	18.6	18.6	18.6	56.55	511	4.6565E-22	1.7209	1.7163	37.313	8	444140000	193740000	250400000
Q9Z1G3	V-type proton ATPase subunit C 1	Atp6v1c1	2	2	2	3.9	3.9	3.9	43.887	382	0.0021181	1.6265	2.1629	62.292	2	126100000	53623000	72478000
Q9CR51	V-type proton ATPase subunit G 1	Atp6v1g1	1	1	1	14.4	14.4	14.4	13.724	118	9.859E-65	0.99133	0.73329	14.502	3	53087000	27246000	25841000
Q8BVE3	V-type proton ATPase subunit H	Atp6v1h	2	2	2	5.4	5.4	5.4	55.854	483	1.1534E-05	0.86383	0.86794	60.014	2	6085100	3279500	2805700
Q8VDD8	WAS protein family homolog 1	Wash1	1	1	1	4	4	4	51.658	475	0.0014436	1.8331	1.2909	14.002	2	17618000	6117100	11501000
Q6PGL7	WASH complex subunit FAM21	Fam21	2	2	2	3.6	3.6	3.6	145.31	1334	0.00057573	1.1284	0.92925	5.7068	2	71300000	33428000	37872000
O88342	WD repeat-containing protein 1	Wdr1	14	14	14	36.6	36.6	36.6	66.406	606	0	1.0045	1.1266	67.171	23	6316000000	3292700000	3023300000
Q3UE92	Xaa-Pro aminopeptidase 1	Xpnpep1	6	6	6	12.3	12.3	12.3	74.559	666	1.2302E-17	0.95195	1.6548	51.748	7	308880000	141610000	167270000
Q00519	Xanthine dehydrogenase/oxidase	Xdh	6	6	6	5.7	5.7	5.7	146.56	1335	3.2513E-21	1.5165	1.4267	65.688	5	587060000	296810000	290240000
O70373	Xin actin-binding repeat-containing protein 1	Xirp1	13	13	13	17	17	17	123.43	1129	1.591E-115	0.44207	0.46792	154.2	15	3315000000	1924900000	1390100000
Q9Z2C8	Y-box-binding protein 2	Ybx2	3	1	1	10.8	5.6	5.6	38.27	360	1.5635E-16	0.52062	0.4485	25.962	3	61054000	41827000	19227000
P46938	Yorkie homolog	Yap1	4	4	4	16.8	16.8	16.8	52.383	488	4.425E-37	0.64823	0.70261	74.563	5	198640000	107540000	91097000
Q8CDC7	Zinc finger and BTB domain-containing protein 9	Zbtb9	1	1	1	2.8	2.8	2.8	49.536	459	0.0076076	0.8306	1.3034	40.004	2	69017000	35200000	33817000
Q3TIV5	Zinc finger CCCH domain-containing protein 15	Zc3h15	3	3	3	12.7	12.7	12.7	48.327	426	1.4812E-19	1.3196	1.7033	24.633	2	99481000	50371000	49110000
Q64726	Zinc-alpha-2-glycoprotein	Azgp1	5	5	5	19.5	19.5	19.5	35.332	307	5.251E-19	0.45127	1.2984	115.06	7	655640000	286530000	369100000
Q8BGC4	Zinc-binding alcohol dehydrogenase domain-containing protein 2	Zadh2	4	4	4	14.9	14.9	14.9	40.528	377	3.461E-283	1.6312	1.7214	58.323	8	1902600000	708500000	1194100000
Q62523	Zyxin	Zyx	3	3	3	7.3	7.3	7.3	60.545	564	5.9196E-22	0.51777	0.62876	35.161	4	151770000	98239000	53529000
Q8BGD8	Cytochrome c oxidase assembly factor 6 homolog	1810063B05Rik	2	2	2	30.4	30.4	30.4	9.2983	79	2.1656E-81	0.51482	0.65068	64.733	3	96771000	58357000	38414000
G3X8U3	MCG6895	2210016F16Rik	8	8	8	22.5	22.5	22.5	38.615	338	2.2596E-26	1.289	1.2112	20.787	8	414970000	185220000	229750000
V9GXP3	Muscular LMNA-interacting protein	2310046A06Rik	9	9	3	33.9	33.9	15.2	50.902	460	8.306E-188	0.50582	0.52015	176.71	10	5372800000	778740000	4594100000
D3Z1D3	Protein 3425401B19Rik	3425401B19Rik	2	2	2	2.3	2.3	2.3	154.48	1412	1.2979E-12	1.5618	1.2698	8.8435	2	74015000	30807000	43208000
E9Q4Z2	Acetyl-CoA carboxylase 2	Acacb	5	5	5	2.7	2.7	2.7	275.75	2448	1.6359E-28	1.3197	1.3951	122.81	4	403820000	321530000	82287000
F8VPN4	Protein Agl	Agl	30	30	30	28.7	28.7	28.7	174.29	1532	6.61E-304	2.8474	3.0437	56.103	53	1.0469E+10	2659800000	7809500000
E9Q616	Protein Ahnak	Ahnak	118	118	118	49.7	49.7	49.7	604.25	5656	0	0.68665	0.78885	82.931	168	3.78E+10	2.2203E+10	1.5598E+10
E9PYB0	Protein Ahnak2	Ahnak2	3	3	1	14.8	14.8	2.8	182.7	1739	8.5739E-10	1.1459	1.0474	18.539	5	1981300000	928410000	1052900000
S4R2S8	Ankyrin-3	Ank3	8	4	4	6.1	3.7	3.7	216.91	1985	1.204E-22	1.3997	1.4772	28.797	2	259260000	137690000	121570000
F6QRE9	Protein Erich3	BC007180	1	1	1	2.4	2.4	2.4	95.392	889	0.019158	0.10831	0.088929	198.12	2	323210000	296520000	26682000

Protein IDs	Protein names	Gene names	Peptides	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Unique + razor sequence	Unique sequence coverage	Mol. weight [kDa]	Sequence length	PEP	Ratio H/L	Ratio H/L normalized	Ratio H/L variability [%]	Ratio H/L count	Intensity	Intensity L	Intensity H
E9Q6A7	Protein Bptf	Bptf	2	2	2	1	1	1	321.59	2921	0.0034234	0.12913	0.35198	375.02	2	587160000	499800000	87361000
E9QA16	Protein Cald1	Cald1	7	7	0	19.2	19.2	0	61.836	536	7.0309E-92	0.86196	0.88167	62.328	8	305830000	153260000	152570000
D3Z5G7	Carboxylic ester hydrolase	Ces1b	7	3	3	16.6	9.2	9.2	62.196	567	5.9189E-40	0.55961	0.59251	59.211	2	62290000	48692000	13598000
E9QLJ0	Cardiomyopathy-associated protein 5	Cmya5	24	2	2	11.5	1.4	1.4	405.57	3676	1.373E-210	1.1385	3.1882	71.26	3	264240000	93319000	170920000
E9PWQ3	Protein Col6a3	Col6a3	6	6	6	2.7	2.7	2.7	353.93	3284	2.7141E-33	1.5936	1.9795	110.49	4	260660000	161100000	99566000
E9Q3H6	Protein Coq10a	Coq10a	4	4	4	18.5	18.5	18.5	28.927	259	4.2046E-15	4.4937	4.9422	15.896	5	450660000	81039000	369620000
E9Q9R9	Protein Dlg5	Dlg5	2	2	2	1.2	1.2	1.2	214.38	1921	0.0016771	0.19575	0.20649	88.168	3	434540000	337590000	96949000
D3YYQ8	Protein Dnah10	Dnahc10	3	3	3	0.7	0.7	0.7	529.56	4591	0.00050065	0.97489	1.072	125.73	3	1.5358E+10	7769800000	7587900000
E9PUD2	Dynamin-1-like protein	Dnm1l	14	14	1	26.3	26.3	3.2	79.532	712	1.0361E-56	1.815	1.9991	100.74	14	1452000000	570490000	881520000
E9PV24	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A	Fga	10	10	10	18	18	18	87.428	789	9.211E-204	1.3384	1.8559	102.49	11	1351200000	539730000	811460000
Q6DFZ1	Golgi-specific brefeldin A-resistance factor 1	Gbf1	2	2	2	1	1	1	206.78	1861	0.00010682	1.891	1.9232	124.58	2	384070000	191790000	192280000
L7N1X8	Protein Gbp6	Gbp10	6	6	2	9	9	3.3	70.451	611	6.2904E-17	0.66761	0.74207	48.696	5	300610000	202850000	97756000
Q3UKG2	Protein Prob1	Gm1614	8	8	8	14.3	14.3	14.3	106.42	1006	1.6565E-34	0.7694	0.81632	80.26	7	326910000	178960000	147950000
E9PVZ8	Protein Golgb1	Golgb1	3	3	3	1	1	1	370.15	3238	0.0007149	0.43017	1.5226	139.66	2	1790900000	1272300000	518560000
E9PY61	Protein Gpr179	Gpr179	2	2	2	0.7	0.7	0.7	248.71	2293	0.0058553	2.7563	3.3322	231.39	2	1.2284E+10	7353800000	4929800000
A8DUK4	Beta-globin	Hbb-b1	16	16	7	95.2	95.2	43.5	15.748	147	0	1.0052	1.1375	89.272	271	4.1328E+11	1.9143E+11	2.2185E+11
G5E8J6	Histidine rich calcium binding protein, isoform CRA_a	Hrc	4	4	4	9.3	9.3	9.3	85.171	738	1.223E-138	0.64509	0.82317	35.265	6	824520000	551260000	273250000
A2AFQ2	3-hydroxyacyl-CoA dehydrogenase type-2	Hsd17b10	12	12	2	43.9	43.9	8.9	28.374	271	1.664E-195	2.0649	2.2124	73.347	17	3744000000	1350500000	2393500000
Q91VA7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	Idh3b	8	8	8	27.3	27.3	27.3	42.194	384	1.892E-220	1.979	2.0065	108.85	28	8922100000	1794300000	7127800000
A6X935	Inter alpha-trypsin inhibitor, heavy chain 4	Itih4	10	10	10	14	14	14	104.66	942	4.2866E-46	0.60106	0.62211	57.376	11	671030000	398790000	272240000
A2AUC9	Kelch-like protein 41	Kbtbd10	11	11	11	19	19	19	68.189	606	3.2282E-28	0.68152	0.89287	72.699	11	1118300000	731470000	386830000
Q6S9I3	HMW kininogen-II	Kng2	4	3	3	9.5	6.4	6.4	71.272	644	6.508E-154	1.2428	1.1127	51.207	2	183310000	91464000	91844000
E9PYJ9	LIM domain-binding protein 3	Ldb3	16	2	2	33.4	4	4	72.312	679	0	0.34043	0.39697	35.408	2	53775000	44632000	9143600
E9PYF4	Protein Lmo7	Lmo7	9	9	9	8.9	8.9	8.9	192.55	1699	1.7351E-87	1.6554	1.7128	34.671	10	813760000	319320000	494440000
Q91XL1	Leucine-rich HEV glycoprotein	Lrg1	2	2	2	7.9	7.9	7.9	37.431	342	5.968E-07	0.11745	0.10393	182.05	2	430730000	403230000	27499000
Q3TMX5	Arginine-rich, mutated in early stage tumors, isoform CRA_b	Manf	2	2	2	6.1	6.1	6.1	20.388	179	2.6371E-05	0.89573	1.084	40.04	3	301110000	127850000	173260000
B5THE2	Maltase-glucoamylase	Mgam	1	1	1	0.5	0.5	0.5	208.55	1827	0.00011605	0.6927	0.71292	5.8053	2	30715000	17253000	13461000
Q9D6T9	28S ribosomal protein S36, mitochondrial	Mrps36	4	1	1	69	22	22	10.942	100	0	0.24331	0.20442	2.3446	2	751730000	620210000	131520000
Q14BI5	Myomesin 2	Myom2	28	28	28	27.5	27.5	27.5	164.74	1463	0	1.9346	1.9843	92.081	41	6450600000	2289000000	4161600000
Q3U422	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	Ndufv3	6	6	6	19.9	19.9	19.9	50.498	468	3.846E-147	0.64201	0.60558	27.745	6	318980000	230870000	88113000
B7ZCI2	Nebulette	Nebl	19	19	1	23.5	23.5	2.3	116.01	1014	0	1.4589	1.6701	74.124	25	3349300000	1478500000	1870800000
D3Z285	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	Nfu1	4	1	1	25.6	7.5	7.5	22.028	199	1.349E-132	0.58642	1.1131	50.659	2	60305000	38335000	21970000
E9Q7L0	Protein Ogdhl	Ogdhl	26	21	21	35.7	31	31	116.6	1029	0	1.8554	1.8642	65.069	40	7233700000	2720800000	4512900000
Q6PHQ9	Polyadenylate-binding protein	Pabpc4	12	12	10	22.6	22.6	18.5	72.242	660	3.35E-151	0.97502	1.1359	113.69	17	1662600000	801780000	860820000
E9Q8P5	PDZ and LIM domain protein 5	Pdlim5	11	11	4	51.9	51.9	16.3	26.355	239	0	0.79318	0.7337	83.493	28	9463200000	6056500000	3406700000
G3X9E8	MCG15724, isoform CRA_a	Ppp2r3a	2	2	2	4.3	4.3	4.3	61.105	530	5.156E-08	1.0958	1.3405	27.821	2	120350000	64809000	55543000
F7AI87	26S proteasome non-ATPase regulatory subunit 4	Psmd4	3	2	2	19.6	14.4	14.4	21.316	194	7.954E-183	0.94205	0.63048	32.496	4	186800000	96258000	90544000
Q8BML9	Glutaminyl-tRNA synthetase	Qars	5	5	5	9.8	9.8	9.8	87.676	775	1.7961E-37	2.0159	1.7559	80.803	3	155360000	47799000	107570000
E9Q912	Protein Rap1gds1	Rap1gds1	4	4	4	8.7	8.7	8.7	66.076	607	3.3516E-44	0.9095	0.94985	18.15	6	344500000	164340000	180150000
G5E867	MCG116540, isoform CRA_b	Raph1	3	3	3	7.7	7.7	7.7	76.269	679	2.2632E-07	0.64102	0.79366	46.417	4	161260000	76392000	84868000
E9PWZ3	Protein Rpl3l	Rpl3l	2	2	2	7.1	7.1	7.1	46.512	407	1.3141E-05	0.25985	0.14194	388.29	2	295700000	246120000	49581000
A2AIX1	Protein Sec16a	Sec16a	1	1	1	0.5	0.5	0.5	256.47	2377	0.00093838	0.5041	0.56206	20.971	2	8692700	5718100	2974600
G3X972	Protein Sec24c	Sec24c	8	8	8	9.7	9.7	9.7	118.58	1096	8.7095E-24	1.8205	2.1808	64.068	5	350720000	99924000	250800000
O08804	NK13	Serpinb6b	5	5	5	14.1	14.1	14.1	42.535	377	1.018E-120	0.73476	0.79409	33.61	3	605470000	336310000	269150000
Q3UWK8	MCG20280	Serpinb6d	2	1	1	4.5	2.7	2.7	43.315	375	0.00022603	18.945	10.26	324.55	3	2206100000	24152000	2181900000
O08797	Protein Serpinb9	Serpinb9	4	4	4	12.6	12.6	12.6	42.259	374	1.3159E-10	0.96711	0.93025	112.26	4	345570000	97220000	248350000
D3Z5J3	Sorbin and SH3 domain-containing protein 1	Sorbs1	7	6	2	13.1	11.9	5.8	103.98	938	3.5209E-21	0.93629	1.3981	53.858	5	179140000	92651000	86491000
E9Q447	Spectrin alpha chain, non-erythrocytic 1	Spna2	47	47	1	24.5	24.5	0.8	285.34	2478	0	0.9838	1.1196	90.341	67	9028900000	3626600000	5402300000
F8VQC1	Signal recognition particle subunit SRP72	Srp72	2	2	2	5.5	5.5	5.5	74.656	671	3.4825E-21	4.3674	4.0584	29.475	2	85293000	12718000	72575000
E9Q8T1	Transforming acidic coiled-coil-containing protein 2	Tacc2	34	34	34	23.5	23.5	23.5	305.23	2879	0	0.64647	0.60985	37.293	37	2326200000	1491400000	834800000
Q9Z1A1	Protein Tfg	Tfg	3	3	3	15.1	15.1	15.1	43.02	397	1.2454E-93	0.49552	0.51497	62.495	3	441820000	337330000	104500000
Q6XPS7	L-threonine aldolase	Tha1	5	5	5	16.5	16.5	16.5	43.496	400	5.0044E-07	1.1251	1.1217	79.801	3	142560000	79145000	63411000
E9Q0S6	Protein Tns1	Tns1	16	16	16	14.5	14.5	14.5	201.38	1888	6.491E-99	1.7595	1.5563	77.213	13	1166000000	460280000	705700000
O35452	Protein Tnxb	Tnxb	7	7	7	5	5	5	435.47	4006	3.1991E-14	1.3413	1.3965	186.47	7	574870000	289890000	284980000
F6ZDS4	Nucleoprotein TPR	Tpr	6	6	6	3.2	3.2	3.2	273.99	2431	1.1815E-41	0.76025	1.2627	37.664	2	88238000	43857000	44381000
E9Q6R7	Protein Utrn	Utrn	4	4	4	1.3	1.3	1.3	392.7	3430	2.5298E-12	2.426	2.8454	26.02	3	38810000	9167300	29642000

Table S-4. Proteins identified in all three replicates statistically analysed by limma. (NA is given to Fc < 0.01 by limma)

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8BGK2	[Protein ADP-ribosylarginine] hydrolase-like protein 1	0.17	-0.29	0.68	0.186666667	-0.40272308	0.776056415	0.47529917
A2AJQ0	[Pyruvate dehydrogenase [acetyl-transferring]]-phosphatase 1, mitochondrial	0.14	NA	1.2	0.67	-0.17310259	1.513102589	0.09885768
Q8BFP9	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial	0.86	0.95	0.77	0.86	0.39314282	1.326857175	0.00354086
Q9JK42	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial	0.48	0.34	0.29	0.37	-0.09783173	0.837831731	0.10290702
O70571	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial	1.43	0.89	1.08	1.133333333	0.62730776	1.639358909	0.00124214
F6ZHD8	1,4-alpha-glucan-branching enzyme	0.93	0.81	1.23	0.99	0.50011412	1.479885881	0.00217645
Q9DCT1	1,5-anhydro-D-fructose reductase	-1.27	0.1	0.62	-0.183333333	-1.05283651	0.686169843	0.63079205
Q64433	10 kDa heat shock protein, mitochondrial	-0.85	-0.74	-1.13	-0.906666667	-1.39283899	-0.420494344	0.00332283
Q9DAK9	14 kDa phosphohistidine phosphatase	-0.51	-1.47	-0.22	-0.733333333	-1.40937376	-0.057292902	0.03743505
Q9CQV8	14-3-3 protein beta/alpha	-0.25	-1.03	0.21	-0.356666667	-1.01776246	0.304429128	0.24047063
P62259	14-3-3 protein epsilon	-0.51	-0.53	-0.32	-0.453333333	-0.92343117	0.016764505	0.05652276
P68510	14-3-3 protein eta	-0.06	-0.66	-1.22	-0.646666667	-1.28301421	-0.010319128	0.04729519
P61982	14-3-3 protein gamma	-0.24	0.41	-0.13	0.013333333	-0.51793915	0.544605815	0.95396461
F6VW30	14-3-3 protein theta	-0.57	-1.25	-0.68	-0.833333333	-1.37110291	-0.295563761	0.008323
P63101	14-3-3 protein zeta/delta	-0.72	-1.02	-0.16	-0.633333333	-1.20062335	-0.066043321	0.03362748
P58871	182 kDa tankyrase-1-binding protein	0.34	-0.58	-0.76	-0.333333333	-0.97484893	0.308182265	0.25649761
Q8R3B1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-1	0.78	NA	1.09	0.935	0.27748505	1.592514949	0.01358442
Q9CQ62	2,4-dienoyl-CoA reductase, mitochondrial	0.29	-0.47	-0.28	-0.153333333	-0.70324629	0.396579623	0.5278331
P62334	26S protease regulatory subunit 10B	0.76	0.43	0.79	0.66	0.17414005	1.145859951	0.01513917
P62192	26S protease regulatory subunit 4	0.69	0.67	1.92	1.093333333	0.38256273	1.804103939	0.00861709
B7ZCF1	26S protease regulatory subunit 6A	0.13	0.04	-0.03	0.046666667	-0.41917318	0.512506511	0.81810964
P54775	26S protease regulatory subunit 6B	0.32	0.34	0.25	0.303333333	-0.15993293	0.766599597	0.16394601
Q8BVQ9	26S protease regulatory subunit 7	0.52	0.2	0.41	0.376666667	-0.10123823	0.854571567	0.10387724
P62196	26S protease regulatory subunit 8	1.03	0.87	0.51	0.803333333	0.29961944	1.307047226	0.00725795
Q3TXS7	26S proteasome non-ATPase regulatory subunit 1	0.27	0.25	0.25	0.256666667	-0.20530743	0.718640763	0.2281679
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	0.11	-0.16	-0.12	-0.056666667	-0.53146415	0.418130814	0.78427789
Q9D8W5	26S proteasome non-ATPase regulatory subunit 12	0.66	0.06	0.28	0.333333333	-0.1822219	0.848888567	0.16856009
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	0.09	-0.17	0.13	0.016666667	-0.46129779	0.494631127	0.93607867
O35593	26S proteasome non-ATPase regulatory subunit 14	0.35	0.79	-0.04	0.366666667	-0.19146712	0.924800456	0.16274191
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	0.43	0.05	0.52	0.333333333	-0.16543979	0.832106459	0.15660253
P14685	26S proteasome non-ATPase regulatory subunit 3	0.48	0.83	0.74	0.683333333	0.20151326	1.165153408	0.0125138
O35226	26S proteasome non-ATPase regulatory subunit 4	-0.55	-0.53	-0.72	-0.6	-1.06856132	-0.131438682	0.01948382
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5	0.61	0.04	0.51	0.386666667	-0.12916456	0.902497896	0.11862929
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	0.54	1.42	1.04	1	0.43057306	1.569426942	0.00451717
P26516	26S proteasome non-ATPase regulatory subunit 7	0.11	0.15	0.47	0.243333333	-0.24195993	0.728626598	0.2719346
Q9CX56	26S proteasome non-ATPase regulatory subunit 8	-0.32	-1.1	-0.56	-0.66	-1.21154972	-0.108450278	0.02569586
Q3UHX2	28 kDa heat- and acid-stable phosphoprotein	-1.1	-1.2	-0.01	-0.77	-1.44926094	-0.090739059	0.03173563
Q8BK72	28S ribosomal protein S27, mitochondrial	-0.41	0.41	0.98	0.326666667	-0.37426381	1.027597139	0.30420003
Q9D0G0	28S ribosomal protein S30, mitochondrial	1	1.16	1.67	1.276666667	0.74464459	1.808688746	0.00084317
Q9CQX8	28S ribosomal protein S36, mitochondrial	-0.84	-1.27	-1.4	-1.17	-1.682102	-0.657898	0.00111174

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q9CXI0	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	0.24	0.08	1.15	0.49	-0.14480984	1.124809843	0.10987249
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	1.15	0.76	0.91	0.94	0.45484362	1.425156379	0.00272194
Q3U3J1	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	0.22	0.32	0.43	0.323333333	-0.14530898	0.791975646	0.14550386
Q6P3A8	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	0.48	0.09	0.72	0.43	-0.09048254	0.950482537	0.09110455
Q9Z0S1	3(2),5-bisphosphate nucleotidase 1	-0.34	0.15	0.2	0.003333333	-0.51050742	0.517174084	0.98809308
Q921S7	39S ribosomal protein L37, mitochondrial	1.11	0.98	1.38	1.156666667	0.66979224	1.643541093	0.00089249
Q99L13	3-hydroxyisobutyrate dehydrogenase, mitochondrial	0.31	-0.09	-0.22	-3.20E-17	-0.50673762	0.506737623	1
Q8QZS1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	0.25	-0.16	-0.28	-0.063333333	-0.57059498	0.443928316	0.77465351
Q921H8	3-ketoacyl-CoA thiolase A, peroxisomal	0.43	NA	0.05	0.24	-0.42739588	0.907395877	0.4085127
Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial	0.08	0.02	1.01	0.37	-0.25349869	0.993498693	0.20138353
Q9D404	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial	0.82	0.24	0.46	0.506666667	-0.00534268	1.018676014	0.05182433
Q6ZWZ6	40S ribosomal protein S12	-0.56	-0.9	-0.31	-0.59	-1.10310158	-0.076898423	0.0300442
P62264	40S ribosomal protein S14	1.85	1.22	3.06	2.043333333	1.20002223	2.886644439	0.00079804
D3Z722	40S ribosomal protein S19	2.27	2.26	1.57	2.033333333	1.48104435	2.585622312	6.55E-05
D3Z6C3	40S ribosomal protein S3a	0.43	1.69	3.2	1.773333333	0.62948597	2.917180699	0.00830494
Q91V55	40S ribosomal protein S5	2.25	2.92	1.96	2.376666667	1.78390576	2.969427573	3.85E-05
P14206	40S ribosomal protein SA	1.38	1.17	0.87	1.14	0.6392523	1.640747703	0.00113404
P61922	4-aminobutyrate aminotransferase, mitochondrial	0.39	-0.79	0.21	-0.063333333	-0.72923422	0.602567557	0.82712753
Q3U367	4-trimethylaminobutyraldehyde dehydrogenase	-1.22	0.53	0.85	0.053333333	-0.90595114	1.012617805	0.89829162
Q8BRK8	5-AMP-activated protein kinase catalytic subunit alpha-2	-1.69	0.27	0.71	-0.236666667	-1.30567208	0.83233875	0.61414083
Q3UHB1	5-nucleotidase domain-containing protein 3	0.97	0.56	-0.01	0.506666667	-0.08599819	1.099331521	0.08248696
Q8K010	5-oxoprolinase	0.78	0.77	0.45	0.666666667	0.18354859	1.149784748	0.01413237
P63038	60 kDa heat shock protein, mitochondrial	-0.8	-1.02	-0.96	-0.926666667	-1.39646164	-0.456871691	0.00247645
P62889	60S ribosomal protein L30	1.81	3.14	2.14	2.363333333	1.66590419	3.060762472	0.00010924
F6XI62	60S ribosomal protein L7	2.22	1.13	1.47	1.606666667	0.9818302	2.231503138	0.00056744
P12382	6-phosphofructokinase, liver type	1	1.29	0.76	1.016666667	0.51323541	1.52009792	0.00218457
P47857	6-phosphofructokinase, muscle type	1.1	0.42	0.66	0.726666667	0.19652057	1.256812765	0.01455545
Q8C605	6-phosphofructokinase	0.77	1.06	0.88	0.903333333	0.42841596	1.378250706	0.00299858
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	0.46	0.43	0.12	0.336666667	-0.14656924	0.819902576	0.14219209
Q9CQ60	6-phosphogluconolactonase	0.18	-0.6	-0.31	-0.243333333	-0.7927284	0.306061737	0.32696407
Q9R1Z7	6-pyruvoyl tetrahydrobiopterin synthase	-2.91	-0.98	-0.36	-1.416666667	-2.52131891	-0.312014424	0.01936072
P20029	78 kDa glucose-regulated protein	-0.12	-0.13	-0.57	-0.273333333	-0.77427049	0.227603822	0.23570902
Q8K4F5	Abhydrolase domain-containing protein 11	-0.18	0.03	0.05	-0.033333333	-0.50512361	0.438456942	0.87101531
E9QN99	Abhydrolase domain-containing protein 14B	-0.14	-0.21	-0.57	-0.306666667	-0.80027661	0.186943281	0.1835139
Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial	-0.31	-0.93	-0.43	-0.556666667	-1.08098171	-0.032351623	0.04048717
Q99NB1	Acetyl-coenzyme A synthetase 2-like, mitochondrial	0.82	0.34	0.58	0.58	0.08387824	1.076121756	0.02817149
O35381	Acidic leucine-rich nuclear phosphoprotein 32 family member A	-0.76	-0.58	0.13	-0.403333333	-0.98592225	0.179255581	0.14433101
Q99KI0	Aconitate hydratase, mitochondrial	0.64	0.23	0.23	0.366666667	-0.12855537	0.861888705	0.12243404
P62737	Actin, aortic smooth muscle	-0.03	0.2	0.29	0.153333333	-0.32504784	0.631714507	0.47021165
Q9Z2N8	Actin-like protein 6A	0.64	0.47	0.28	0.463333333	-0.01813213	0.944798798	0.05691316
P61161	Actin-related protein 2	0.15	1	0.61	0.586666667	0.02416382	1.149169511	0.04316049
Q9WV32	Actin-related protein 2/3 complex subunit 1B	-0.92	0.78	1.16	0.34	-0.61487268	1.29487268	0.42460299

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q9CVB6	Actin-related protein 2/3 complex subunit 2	0.38	0.19	0.78	0.45	-0.06476323	0.964763225	0.07716291
Q9JM76	Actin-related protein 2/3 complex subunit 3	0.05	0.04	-0.45	-0.12	-0.62976203	0.389762031	0.59238033
A3KGQ6	Actin-related protein 2/3 complex subunit 5	-0.15	-0.79	-0.12	-0.353333333	-0.89637042	0.189703756	0.16623824
Q99JY9	Actin-related protein 3	1.21	0.46	0.72	0.796666667	0.25268684	1.340646492	0.01082115
Q8BK64	Activator of 90 kDa heat shock protein ATPase homolog 1	-0.9	0.23	0.47	-0.066666667	-0.7864315	0.653098163	0.83156201
Q9CR21	Acyl carrier protein, mitochondrial	-0.71	-1.21	-1.46	-1.126666667	-1.67106496	-0.582268372	0.00191491
Q8R146	Acylamino-acid-releasing enzyme	0.24	1.08	0.82	0.713333333	0.14886032	1.277806348	0.02058581
D3Z7X0	Acyl-CoA dehydrogenase family member 10	1.28	1.11	1.8	1.396666667	0.8610186	1.932314729	0.0005234
Q8JZN5	Acyl-CoA dehydrogenase family member 9, mitochondrial	0.16	-0.38	-0.22	-0.146666667	-0.65375994	0.360426604	0.51305396
Q8VCW8	Acyl-CoA synthetase family member 2, mitochondrial	0.14	0.14	1.15	0.476666667	-0.16124461	1.114577945	0.11959889
Q3URE1	Acyl-CoA synthetase family member 3, mitochondrial	0.47	0.66	0.37	0.5	0.02492282	0.975077182	0.04178303
Q4VWZ5	Acyl-CoA-binding protein	-0.57	-1.08	-0.95	-0.866666667	-1.36998482	-0.363348513	0.00498617
O55137	Acyl-coenzyme A thioesterase 1	-0.34	-1.41	-0.82	-0.856666667	-1.47056477	-0.242768565	0.01345048
Q9CQR4	Acyl-coenzyme A thioesterase 13	0.08	-0.37	-0.51	-0.266666667	-0.78382063	0.250487292	0.25979351
Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial	0.83	-0.19	-0.34	0.1	-0.56639943	0.766399429	0.73114859
Q9R0X4	Acyl-coenzyme A thioesterase 9, mitochondrial	0.2	-0.36	0.69	0.176666667	-0.43201595	0.785349287	0.51162689
E9QJT5	Acylphosphatase	-0.99	-1.95	-1.46	-1.466666667	-2.05363659	-0.879696742	0.00066932
P56375	Acylphosphatase-2	-0.55	-1.13	-0.51	-0.73	-1.26093303	-0.19906697	0.01435919
P97823	Acyl-protein thioesterase 1	-0.46	-0.44	-0.19	-0.363333333	-0.83896942	0.112302757	0.11293947
Q8R0F8	Acylpyruvase FAHD1, mitochondrial	1.95	-0.42	0.91	0.813333333	-0.19502315	1.82168982	0.09747518
Q64010	Adapter molecule crk	-0.67	-0.98	-0.97	-0.873333333	-1.35397036	-0.392696307	0.00379905
P55264	Adenosine kinase	-0.29	-0.72	-0.73	-0.58	-1.0792675	-0.080732498	0.02887501
P50247	Adenosylhomocysteinase	0.03	-0.04	-0.08	-0.03	-0.49379849	0.433798489	0.88180985
Q9WTP6	Adenylate kinase 2, mitochondrial	0.27	-0.74	-0.58	-0.35	-0.96735061	0.267350611	0.21981816
Q9R0Y5	Adenylate kinase isoenzyme 1	-1.1	-1.3	-1.22	-1.206666667	-1.67476199	-0.738571342	0.00055923
Q9WUR9	Adenylate kinase isoenzyme 4, mitochondrial	0.31	0.78	1.45	0.846666667	0.21404287	1.479290458	0.01614885
P54822	Adenylosuccinate lyase	0.5	0.47	0.63	0.533333333	0.06700489	0.999661774	0.03067501
P40124	Adenylyl cyclase-associated protein 1	-0.65	-0.31	0.67	-0.096666667	-0.79004331	0.596709976	0.74940329
Q60994	Adiponectin	-0.68	-0.95	-0.51	-0.713333333	-1.20463112	-0.222035548	0.01125511
P48962	ADP/ATP translocase 1	1.57	1.53	0.52	1.206666667	0.56253839	1.850794939	0.00324607
Q3V132	ADP/ATP translocase 4	1.65	1.61	0.33	1.196666667	0.46571733	1.927616005	0.00639507
P61205	ADP-ribosylation factor 3	-0.02	-0.23	0.25	6.01E-18	-0.49629386	0.496293856	1
Q8R0H9	ADP-ribosylation factor-binding protein GGA1	0.11	-0.14	0.05	0.006666667	-0.46560605	0.478939382	0.97409459
Q9WUL7	ADP-ribosylation factor-like protein 3	-1.2	-0.5	-0.12	-0.606666667	-1.22651751	0.013184173	0.0537912
E9Q9C3	Afadin	-0.37	NA	-0.05	-0.21	-0.86881217	0.44881217	0.46078874
O89020	Afamin	-1.02	-0.85	-0.85	-0.906666667	-1.37445783	-0.438875501	0.00271701
Q8CG76	Aflatoxin B1 aldehyde reductase member 2	0.99	0.47	0.75	0.736666667	0.23476441	1.23856892	0.01071253
M0QWP1	Agrin	0.38	-0.34	0.02	0.02	-0.51584288	0.555842884	0.93159289
O08715	A-kinase anchor protein 1, mitochondrial	-0.27	0.22	0.36	0.103333333	-0.42168703	0.628353692	0.65331909
Q9WTQ5	A-kinase anchor protein 12	-0.23	-1.27	-1	-0.833333333	-1.4490834	-0.217583266	0.01538676
F7AA26	A-kinase anchor protein 2	-0.93	-1.19	-1.19	-1.103333333	-1.57890957	-0.627757094	0.00102023
Q8QZR5	Alanine aminotransferase 1	0.51	-0.19	-0.24	0.026666667	-0.5331985	0.586531832	0.91278734

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8BGQ7	Alanine--tRNA ligase, cytoplasmic	-0.17	0.14	-0.57	-0.2	-0.73430008	0.334300082	0.4024575
Q9JII6	Alcohol dehydrogenase [NADP(+)]	0.8	0.87	0.57	0.746666667	0.26983512	1.223498214	0.00792094
P00329	Alcohol dehydrogenase 1	0.16	-0.07	0.37	0.153333333	-0.33750071	0.644167379	0.48110487
P28474	Alcohol dehydrogenase class-3	0.17	-0.57	-0.41	-0.27	-0.8174053	0.2774053	0.27912923
Q9CZS1	Aldehyde dehydrogenase X, mitochondrial	-0.02	-0.45	-0.54	-0.336666667	-0.84392832	0.170594982	0.15906964
P47738	Aldehyde dehydrogenase, mitochondrial	-0.04	-0.49	-0.5	-0.343333333	-0.84597235	0.159305686	0.14894864
Q8K157	Aldose 1-epimerase	0.12	-0.29	-0.63	-0.266666667	-0.8085493	0.275215962	0.28013082
P45376	Aldose reductase	-0.03	-0.34	-0.26	-0.21	-0.68758712	0.267587121	0.33021921
G5E895	Aldose reductase-related protein 1	0.21	0.28	0.02	0.17	-0.3029152	0.642915202	0.42040712
P07758	Alpha-1-antitrypsin 1-1	-0.79	-1.13	-1.2	-1.04	-1.53064069	-0.549359308	0.00168177
P22599	Alpha-1-antitrypsin 1-2	-1.12	-0.79	-1.36	-1.09	-1.5998737	-0.580126299	0.00160547
Q00897	Alpha-1-antitrypsin 1-4	-0.2	-0.96	-1.09	-0.75	-1.33729314	-0.162706856	0.01970616
Q00898	Alpha-1-antitrypsin 1-5	-1.19	-0.69	-1.02	-0.966666667	-1.46680764	-0.466525696	0.00275718
Q61234	Alpha-1-syntrophin	-0.27	0.99	1.4	0.706666667	-0.0961805	1.509513833	0.07557512
Q61247	Alpha-2-antiplasmin	-1.23	-0.5	-1.15	-0.96	-1.51191088	-0.408089122	0.00474005
P29699	Alpha-2-HS-glycoprotein	-1.64	-0.49	-0.93	-1.02	-1.65642209	-0.38357791	0.00708787
P55302	Alpha-2-macroglobulin receptor-associated protein	-0.52	-0.67	-0.82	-0.67	-1.14555629	-0.194443713	0.01288973
D3YW52	Alpha-2-macroglobulin	-1.01	-0.63	-0.9	-0.846666667	-1.33154916	-0.361784175	0.00464921
Q9JI91	Alpha-actinin-2	2.51	2.36	3.01	2.626666667	2.09818771	3.155145619	9.84E-06
P57780	Alpha-actinin-4	1.02	0.96	2.21	1.396666667	0.69217145	2.101161886	0.00241076
Q9QYC0	Alpha-adducin	-0.25	-0.09	0.48	0.046666667	-0.49846318	0.59179651	0.84411091
Q9DBF1	Alpha-aminoadipic semialdehyde dehydrogenase	0.38	0.48	0.16	0.34	-0.13812325	0.818123251	0.13536006
P61164	Alpha-centractin	1.31	0.23	2.31	1.283333333	0.37260797	2.194058699	0.01287925
P23927	Alpha-crystallin B chain	0.03	0.53	1.02	0.526666667	-0.06734151	1.120674845	0.07391302
P17182	Alpha-enolase	-0.34	-0.61	-0.21	-0.386666667	-0.87354109	0.10020776	0.10174234
O09174	Alpha-methylacyl-CoA racemase	0.87	-0.23	0.12	0.253333333	-0.37368607	0.880352739	0.36827153
P82350	Alpha-sarcoglycan	0.62	0.89	0.71	0.74	0.2666035	1.213396495	0.00798661
Q9DB05	Alpha-soluble NSF attachment protein	-0.31	-0.01	-0.36	-0.226666667	-0.71013815	0.256804812	0.30154991
O55042	Alpha-synuclein	-1.28	-1.23	-0.25	-0.92	-1.5566904	-0.283309599	0.01150349
Q8BW75	Amine oxidase [flavin-containing] B	0.5	0.65	-0.18	0.323333333	-0.24651004	0.893176709	0.21947938
Q3UZG4	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	0.56	0.08	-0.15	0.163333333	-0.37337653	0.700043199	0.49208201
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	0.85	0.74	0.65	0.746666667	0.27863216	1.214701175	0.00724697
Q99JW2	Aminoacylase-1	-0.03	-0.32	-0.17	-0.173333333	-0.64801089	0.301344225	0.41346386
Q8VCT3	Aminopeptidase B	0.06	0.19	0.72	0.323333333	-0.20858173	0.855248392	0.1919289
P97449	Aminopeptidase N	-0.35	-0.15	0.02	-0.16	-0.64256784	0.322567838	0.45570252
Q8WTY4	Anamorsin	-0.76	-0.93	-1.05	-0.913333333	-1.38813081	-0.438535853	0.00282687
P09470	Angiotensin-converting enzyme	-0.08	0.06	0.06	0.013333333	-0.45256761	0.479234281	0.94751613
P10107	Annexin A1	0.21	-0.62	-0.18	-0.196666667	-0.75480046	0.361467122	0.42920246
P97384	Annexin A11	0.23	0.07	0.18	0.16	-0.30600277	0.626002767	0.44055237
P07356	Annexin A2	0.36	-0.4	-0.28	-0.106666667	-0.66198827	0.448654938	0.66101534
O35639	Annexin A3	0.01	-0.55	-0.36	-0.3	-0.80942687	0.209426872	0.20443364
P97429	Annexin A4	0.25	0.17	0.12	0.18	-0.28453441	0.644534411	0.38702622

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
P48036	Annexin A5	-0.34	-0.75	-0.63	-0.573333333	-1.06184208	-0.084824588	0.02774394
Q07076	Annexin A7	0.25	0.33	0.13	0.236666667	-0.23142866	0.704761991	0.26831862
P32261	Antithrombin-III	-0.75	-0.74	-1.09	-0.86	-1.34574276	-0.37425724	0.00433552
O35643	AP-1 complex subunit beta-1	0.46	0.59	-0.06	0.33	-0.19980592	0.859805925	0.1825347
P35585	AP-1 complex subunit mu-1	-0.15	0.69	0.2	0.246666667	-0.31431595	0.807649286	0.33022503
P17427	AP-2 complex subunit alpha-2	1.07	0.8	0.9	0.923333333	0.45009721	1.396569452	0.0026235
P84091	AP-2 complex subunit mu	0.74	1.4	2.58	1.573333333	0.73188079	2.414785875	0.00327818
Q3UHJ0	AP2-associated protein kinase 1	-0.06	-0.79	-0.21	-0.353333333	-0.89919375	0.192527079	0.1681375
Q9Z1T1	AP-3 complex subunit beta-1	0.2	0.61	-0.01	0.266666667	-0.25290355	0.786236883	0.26180684
Q00623	Apolipoprotein A-I	-0.8	0.26	0.61	0.023333333	-0.69793279	0.744599452	0.94068642
P06728	Apolipoprotein A-IV	-0.82	-1.23	0.12	-0.643333333	-1.34051754	0.05385087	0.06523809
Q9EPB4	Apoptosis-associated speck-like protein containing a CARD	-1.26	-1.3	-0.37	-0.976666667	-1.58553632	-0.36779701	0.0070591
Q9Z0X1	Apoptosis-inducing factor 1, mitochondrial	0.71	0.45	-0.35	0.27	-0.35217329	0.892173289	0.33612901
Q9D0I9	Arginine--tRNA ligase, cytoplasmic	1	1.1	0.83	0.976666667	0.50343055	1.449902785	0.00194394
Q91WU5	Arsenite methyltransferase	-0.91	-1.04	-0.06	-0.67	-1.28207154	-0.057928463	0.03619914
Q8BP47	Asparagine--tRNA ligase, cytoplasmic	0.76	0.52	1.28	0.853333333	0.30627482	1.400391848	0.00806742
P05201	Aspartate aminotransferase, cytoplasmic	0.33	0.01	-0.17	0.056666667	-0.44318964	0.556522978	0.79478626
P05202	Aspartate aminotransferase, mitochondrial	0.74	0.4	0.61	0.583333333	0.10364485	1.06302182	0.02408911
Q922B2	Aspartate--tRNA ligase, cytoplasmic	0.55	0.47	0.62	0.546666667	0.08131593	1.012017403	0.02764198
Q8BIP0	Aspartate--tRNA ligase, mitochondrial	-1.26	-0.11	0.05	-0.44	-1.1499959	0.269995898	0.18447014
Q91XE4	Aspartoacylase-2	0.3	0.1	-0.31	0.03	-0.48807053	0.548070534	0.89409563
Q9Z2W0	Aspartyl aminopeptidase	0.44	0.77	0.86	0.69	0.19889539	1.181104614	0.0130492
Q62048	Astrocytic phosphoprotein PEA-15	-1.09	-0.98	-1.17	-1.08	-1.54746651	-0.612533489	0.00104443
P28658	Ataxin-10	-1.49	0.21	0.32	-0.32	-1.21418651	0.574186514	0.42238207
Q7TQH0	Ataxin-2-like protein	-0.47	-1.29	-1.26	-1.006666667	-1.58670925	-0.426624085	0.00479379
H3BLL2	ATP synthase mitochondrial F1 complex assembly factor 1	-0.6	-0.51	-1.16	-0.756666667	-1.28954414	-0.223789195	0.0124456
Q91YY4	ATP synthase mitochondrial F1 complex assembly factor 2	0.81	-0.15	0.31	0.323333333	-0.26368509	0.910351752	0.23176693
Q03265	ATP synthase subunit alpha, mitochondrial	0.43	0.37	0.7	0.5	0.01944195	0.980558053	0.04353074
Q9CQQ7	ATP synthase subunit b, mitochondrial	0.88	0.93	0.28	0.696666667	0.16016899	1.23316434	0.018371
P56480	ATP synthase subunit beta, mitochondrial	-0.44	-0.54	-0.32	-0.433333333	-0.90264332	0.035976656	0.06510713
Q9DCX2	ATP synthase subunit d, mitochondrial	NA	-0.39	-1.29	-0.84	-1.6310898	-0.048910196	0.04091919
Q9D3D9	ATP synthase subunit delta, mitochondrial	-0.58	-0.8	-0.78	-0.72	-1.19092467	-0.249075331	0.0088668
Q06185	ATP synthase subunit e, mitochondrial	-0.29	-1.37	1.46	-0.066666667	-1.23907504	1.105741706	0.89599171
P56135	ATP synthase subunit f, mitochondrial	1.2	0.94	0.54	0.893333333	0.36771691	1.418949757	0.00532056
Q9CPQ8	ATP synthase subunit g, mitochondrial	1.37	1.9	-0.95	0.773333333	-0.46012728	2.006793949	0.18004599
Q91VR2	ATP synthase subunit gamma, mitochondrial	0.85	1.11	1.06	1.006666667	0.53319	1.48014333	0.00165418
Q9DB20	ATP synthase subunit O, mitochondrial	0.88	1.28	0.8	0.986666667	0.48567269	1.487660644	0.00249701
P97450	ATP synthase-coupling factor 6, mitochondrial	-0.22	-0.81	-1.12	-0.716666667	-1.29316499	-0.140168344	0.02202713
O54984	ATPase Asna1	0.7	0.66	-0.07	0.43	-0.1359671	0.995967099	0.11455529
P61222	ATP-binding cassette sub-family E member 1	-0.22	1.61	0.23	0.54	-0.3149993	1.394999295	0.17727577
Q6P542	ATP-binding cassette sub-family F member 1	0.61	0.29	0.92	0.606666667	0.08720604	1.126127297	0.02828389
Q3V117	ATP-citrate synthase	0.95	1.34	0.04	0.776666667	0.0935056	1.459827737	0.03138632

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
K3W4M4	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	0.74	0.27	0.18	0.396666667	-0.11794907	0.911282407	0.11028314
Q91VR5	ATP-dependent RNA helicase DDX1	1.36	1.32	2.52	1.733333333	1.04209479	2.424571876	0.00065584
Q80YD1	ATP-dependent RNA helicase SUPV3L1, mitochondrial	-0.58	-0.08	-0.97	-0.543333333	-1.11487261	0.028205947	0.0592527
Q9JLV1	BAG family molecular chaperone regulator 3	-0.08	-0.68	-0.64	-0.466666667	-0.99336512	0.060031784	0.07406896
O70318	Band 4.1-like protein 2	-0.4	-0.67	-0.47	-0.513333333	-0.98717058	-0.039496082	0.03761268
Q9R069	Basal cell adhesion molecule	0.24	-1	0.36	-0.133333333	-0.86552781	0.598861141	0.67737536
E9PZ16	Basement membrane-specific heparan sulfate proteoglycan core protein	1.73	1.15	1.23	1.37	0.85077689	1.889223115	0.0004885
P18572	Basigin	-0.28	-0.69	-0.04	-0.336666667	-0.86092742	0.187594083	0.17106674
P59017	Bcl-2-like protein 13	0.11	0.11	0.15	0.123333333	-0.33888717	0.585553835	0.54522507
Q01339	Beta-2-glycoprotein 1	-0.11	-1.09	-0.63	-0.61	-1.20178364	-0.018216355	0.04499454
P21550	Beta-enolase	-0.28	-0.63	-1.15	-0.686666667	-1.25450838	-0.118824958	0.0246395
P23780	Beta-galactosidase	2.2	2.77	2.08	2.35	1.81082072	2.889179275	2.27E-05
P12265	Beta-glucuronidase	1.41	0.9	2.71	1.673333333	0.83117067	2.515495992	0.00238226
Q9ES46	Beta-parvin	-1.12	-0.71	0.33	-0.5	-1.22898654	0.228986539	0.14752528
P82349	Beta-sarcoglycan	0.69	0.61	0.41	0.57	0.09546239	1.04453761	0.0253106
Q8VBT1	Beta-taxilin	-0.4	-1.26	-0.31	-0.656666667	-1.26488144	-0.048451889	0.03808726
Q9DBL7	Bifunctional coenzyme A synthase	-0.14	-0.11	0.42	0.056666667	-0.46279396	0.576127297	0.80232898
Q8CGC7	Bifunctional glutamate/proline--tRNA ligase	1.43	0.74	1.07	1.08	0.54976442	1.610235581	0.00208661
Q9EQQ9	Bifunctional protein NCOAT	-0.03	0.62	0.2	0.263333333	-0.2612531	0.787919764	0.27144108
Q9CWJ9	Bifunctional purine biosynthesis protein PURH	0.07	-0.21	-0.14	-0.093333333	-0.56813081	0.381464147	0.65371236
Q9CY64	Biliverdin reductase A	0.29	0.06	0.01	0.12	-0.35543656	0.595436556	0.56658879
P56380	Bis(5-nucleosyl)-tetraphosphatase [asymmetrical]	0.83	-0.59	-0.61	-0.123333333	-0.89887592	0.652209251	0.71591473
P15327	Bisphosphoglycerate mutase	-0.29	0.12	0.42	0.083333333	-0.45114431	0.617810976	0.72118713
Q8R016	Bleomycin hydrolase	-0.05	0.02	-0.26	-0.096666667	-0.57146415	0.378130814	0.64238597
Q9D8S9	BolA-like protein 1	-0.25	-0.97	-0.67	-0.63	-1.16647999	-0.093520013	0.02768079
E9PX89	BolA-like protein 3	-0.61	-1.26	-0.67	-0.846666667	-1.38220843	-0.3111249	0.00756785
Q9D023	Brain protein 44	NA	0.76	0.34	0.55	-0.12386246	1.223862458	0.09197196
O35855	Branched-chain-amino-acid aminotransferase, mitochondrial	0.33	0.16	0.87	0.453333333	-0.08665485	0.993321521	0.0869901
Q6WVG3	BTB/POZ domain-containing protein KCTD12	-0.17	-0.1	-0.81	-0.36	-0.90818477	0.188184766	0.16287313
Q922D8	C-1-tetrahydrofolate synthase, cytoplasmic	0.37	-0.34	0.78	0.27	-0.35940586	0.89940586	0.34132432
Q9WTR5	Cadherin-13	-0.76	-1.06	-1.18	-1	-1.48988588	-0.510114119	0.00206223
P15116	Cadherin-2	0.48	-0.42	-2.04	-0.66	-1.72854376	0.408543759	0.18574618
Q8BFS6	Calcineurin-like phosphoesterase domain-containing protein 1	-1.05	-1.19	-0.9	-1.046666667	-1.52134422	-0.571989109	0.00135427
Q91YS8	Calcium/calmodulin-dependent protein kinase type 1	-0.11	-0.25	-0.92	-0.426666667	-0.992399	0.13906567	0.11677392
E9Q1T1	Calcium/calmodulin-dependent protein kinase type II subunit delta	0.94	0.03	1.45	0.806666667	0.09397629	1.519357044	0.03192043
Q8BH59	Calcium-binding mitochondrial carrier protein Aralar1	1.42	0.97	0.33	0.906666667	0.28686175	1.526471581	0.01087836
Q9QXX4	Calcium-binding mitochondrial carrier protein Aralar2	1.64	0.6	0.19	0.81	0.08101346	1.538986539	0.03423377
Q06138	Calcium-binding protein 39	-0.49	-0.55	-0.63	-0.556666667	-1.02158901	-0.091744323	0.02563571
Q9CXW3	Calcyclin-binding protein	0.06	-0.34	-0.13	-0.136666667	-0.62260473	0.349271396	0.52438252
Q3UKW2	Calmodulin	-0.79	-1.04	-0.58	-0.803333333	-1.29682793	-0.309838736	0.00657446
P35564	Calnexin	0.93	0.66	0.33	0.64	0.12545802	1.154541982	0.0219773
O88456	Calpain small subunit 1	-0.26	-0.42	0.26	-0.14	-0.67414023	0.394140228	0.55216577

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
O35350	Calpain-1 catalytic subunit	0.9	0.85	0.8	0.85	0.38656991	1.31343009	0.00362062
O08529	Calpain-2 catalytic subunit	0.52	0.59	0.87	0.66	0.17743216	1.142567838	0.0146962
P51125	Calpastatin	-0.68	-0.76	-1.11	-0.85	-1.34307141	-0.356928587	0.00495761
Q08091	Calponin-1	-1.07	-1.71	-0.91	-1.23	-1.79157431	-0.668425693	0.00140532
Q9DAW9	Calponin-3	-0.29	-0.93	-1.15	-0.79	-1.36182144	-0.218178557	0.01405929
P14211	Calreticulin	-0.23	-0.57	-0.65	-0.483333333	-0.97492073	0.008254067	0.05296896
F6QYE1	Calsequestrin-2	0.63	1.17	2.2	1.333333333	0.57467505	2.091991618	0.00449988
O35887	Calumenin	-1.01	-0.36	0.33	-0.346666667	-1.03149242	0.338159088	0.2677888
P05132	cAMP-dependent protein kinase catalytic subunit alpha	0.99	1.33	1.41	1.243333333	0.75174593	1.734920734	0.0006242
Q9DBC7	cAMP-dependent protein kinase type I-alpha regulatory subunit	0.56	-0.09	0.03	0.166666667	-0.36385516	0.697188492	0.47872933
Q8K1M3	cAMP-dependent protein kinase type II-alpha regulatory subunit	0.24	0.16	-0.06	0.113333333	-0.36319963	0.589866297	0.5886597
F8WIA1	CAP-Gly domain-containing linker protein 1	-1.07	-1.41	-0.77	-1.083333333	-1.60459919	-0.562067478	0.00187192
Q60865	Caprin-1	-0.3	-0.02	-0.08	-0.133333333	-0.60843049	0.341763821	0.52523793
P13634	Carbonic anhydrase 1	-1.07	-0.93	0.63	-0.456666667	-1.3053949	0.39206157	0.24160678
P00920	Carbonic anhydrase 2	-0.56	-0.04	-0.17	-0.256666667	-0.76167866	0.248345327	0.26605274
P16015	Carbonic anhydrase 3	-0.07	0.77	-1.85	-0.383333333	-1.49340953	0.726742862	0.43804758
P48758	Carbonyl reductase [NADPH] 1	0.7	0.03	0.16	0.296666667	-0.23738473	0.830718066	0.22823118
Q91VT4	Carbonyl reductase family member 4	0.6	0.38	1.63	0.87	0.18672782	1.553272175	0.01995019
P23953	Carboxylesterase 1C	-0.8	-1.56	-0.46	-0.94	-1.56763955	-0.312360453	0.00976189
Q8VCT4	Carboxylesterase 1D	0.1	-0.56	-0.74	-0.4	-0.96982672	0.169826724	0.13965571
Q8R1G2	Carboxymethylenebutenolidase homolog	0.26	0.02	0.14	0.14	-0.33068282	0.61068282	0.50157503
Q9DBB9	Carboxypeptidase N subunit 2	-1.14	-0.78	-1.38	-1.1	-1.61503965	-0.584960355	0.00161382
Q9WVJ3	Carboxypeptidase Q	-0.69	-1.28	-1.79	-1.253333333	-1.87451453	-0.632152134	0.00219509
P47934	Carnitine O-acetyltransferase	1.08	0.35	0.78	0.736666667	0.19815654	1.275176793	0.01468264
Q924X2	Carnitine O-palmitoyltransferase 1, muscle isoform	1.48	1.06	0.36	0.966666667	0.33769815	1.595635185	0.00865218
P52825	Carnitine O-palmitoyltransferase 2, mitochondrial	1.46	0.95	0.91	1.106666667	0.59006343	1.6232699	0.00158747
E9PY58	Caseinolytic peptidase B protein homolog	0.7	0.87	0.92	0.83	0.35998291	1.300017094	0.00439282
P24270	Catalase	0.35	0.31	0.35	0.336666667	-0.12555384	0.798887169	0.12759674
P26231	Catenin alpha-1	-0.77	-0.46	-0.21	-0.48	-0.98808403	0.028084027	0.06047538
P10605	Cathepsin B	1.15	0.56	1.17	0.96	0.42922784	1.490772162	0.00388959
P18242	Cathepsin D	0.94	1.05	0.84	0.943333333	0.47469102	1.411975646	0.00222296
Q9WUU7	Cathepsin Z	2.78	1.67	1.23	1.893333333	1.13399997	2.652666701	0.00067752
P49817	Caveolin-1	-0.09	0.51	0.32	0.246666667	-0.26993657	0.7632699	0.29344127
Q8K1J6	CCA tRNA nucleotidyltransferase 1, mitochondrial	-0.43	0.06	-1.35	-0.573333333	-1.28402384	0.137357169	0.09743005
Q9JLQ0	CD2-associated protein	-1.29	-1.09	-1.45	-1.276666667	-1.75819125	-0.795142082	0.00047497
Q8CJ53	Cdc42-interacting protein 4	0.4	-0.69	0.22	-0.023333333	-0.66186903	0.615202368	0.93302269
P53996	Cellular nucleic acid-binding protein	-0.02	-1.82	-0.82	-0.886666667	-1.70909501	-0.064238327	0.03828898
E9PZD8	Ceruloplasmin	-0.47	-0.73	-0.5	-0.566666667	-1.04086423	-0.092469102	0.02583542
Q60936	Chaperone activity of bc1 complex-like, mitochondrial	0.46	0.7	1.36	0.84	0.25948322	1.420516783	0.01143105
Q9D8B3	Charged multivesicular body protein 4b	-1.02	-1.43	1.24	-0.403333333	-1.58247217	0.775805503	0.44219055
Q9Z1Q5	Chloride intracellular channel protein 1	0.28	-0.29	0.53	0.173333333	-0.38693844	0.733605103	0.48519302
Q9QYB1	Chloride intracellular channel protein 4	-0.3	-0.91	-0.28	-0.496666667	-1.03178304	0.038449704	0.06403577

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8BXK9	Chloride intracellular channel protein 5	0.42	-0.12	-0.29	0.003333333	-0.53665485	0.543321521	0.98866959
Q8VHY0	Chondroitin sulfate proteoglycan 4	-0.37	-0.86	-0.74	-0.656666667	-1.15714901	-0.156184319	0.01758118
Q8R4N0	Citrate lyase subunit beta-like protein, mitochondrial	-0.15	-0.49	-0.28	-0.306666667	-0.78635515	0.17302182	0.17272878
Q9CZU6	Citrate synthase, mitochondrial	0.8	0.2	0.53	0.51	-0.00454198	1.024541982	0.05153888
Q58A65	C-Jun-amino-terminal kinase-interacting protein 4	-0.07	-0.53	-0.23	-0.276666667	-0.77102574	0.217692405	0.22514971
Q5SXR6	Clathrin heavy chain 1	1.73	1.92	1.87	1.84	1.37216827	2.307831731	4.34E-05
Q5SUH6	Clathrin interactor 1	-0.27	-0.55	-1.34	-0.72	-1.34340738	-0.096592624	0.02953688
Q6IRU5	Clathrin light chain B	-0.16	-0.16	-0.09	-0.136666667	-0.59956411	0.326230774	0.50463221
Q06890	Clusterin	-0.91	-0.68	-0.7	-0.763333333	-1.23512361	-0.291543058	0.00677154
Q9CQI6	Coactosin-like protein	-0.35	0.82	-0.14	0.11	-0.54944315	0.769443151	0.7028133
Q9D273	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	-0.18	-1.14	-0.8	-0.706666667	-1.29678043	-0.116552906	0.02562064
F8WGL3	Cofilin-1	-0.89	-1.28	-0.8	-0.99	-1.49040651	-0.489593494	0.00243752
P45591	Cofilin-2	-0.34	-1.2	-0.3	-0.613333333	-1.21377608	-0.012890588	0.0464519
B2RPU8	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial	-0.04	-0.78	-1.48	-0.766666667	-1.47979626	-0.05353707	0.03868602
Q9CRB9	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	0.8	1.25	2.27	1.44	0.70766299	2.172337011	0.002518
Q91W50	Cold shock domain-containing protein E1	-0.07	-0.17	-0.87	-0.37	-0.93702233	0.19702233	0.16519146
Q04857	Collagen alpha-1(VI) chain	-0.28	-0.55	-0.31	-0.38	-0.855197	0.095197003	0.09983377
O35206	Collagen alpha-1(XV) chain	0.71	0.15	-0.24	0.206666667	-0.37913819	0.792471525	0.42867132
E9Q6A6	Collagen alpha-6(VI) chain	0.21	-0.37	-0.25	-0.136666667	-0.65310457	0.379771234	0.5484425
P01027	Complement C3	0.18	0.39	0.79	0.453333333	-0.06437077	0.971037432	0.0767709
P01029	Complement C4-B	-0.7	-0.24	-0.64	-0.526666667	-1.02561098	-0.027722356	0.04134342
P06684	Complement C5	0.36	0.51	2.05	0.973333333	0.12981972	1.816846944	0.02964009
Q8R5L1	Complement component 1 Q subcomponent-binding protein, mitochondrial	-0.54	-1	-0.94	-0.826666667	-1.32561098	-0.327722356	0.00603251
Q8K182	Complement component C8 alpha chain	-1.26	0.2	0.22	-0.28	-1.06960742	0.50960742	0.42641411
Q8BH35	Complement component C8 beta chain	-0.48	0.25	-0.56	-0.263333333	-0.83497222	0.30830555	0.30937809
Q8VCG4	Complement component C8 gamma chain	-0.32	0.68	-0.36	3.20E-17	-0.64110132	0.641101319	1
P06683	Complement component C9	0.36	0.26	-0.25	0.123333333	-0.40038416	0.64705083	0.59223899
B8JJN0	Complement factor B	-0.25	-0.47	-0.67	-0.463333333	-0.95166723	0.025000568	0.05963076
E9Q8I0	Complement factor H	-0.34	-0.11	0.03	-0.14	-0.62292164	0.342921638	0.51210814
Q61129	Complement factor I	-0.88	-0.48	-0.09	-0.483333333	-1.03303919	0.066372527	0.07582187
G3UXW9	COP9 signalosome complex subunit 1	0.48	0.62	-0.34	0.253333333	-0.35201977	0.85868644	0.35245746
P61202	COP9 signalosome complex subunit 2	-0.57	-0.38	-0.25	-0.4	-0.87758712	0.077587121	0.08758798
O88543	COP9 signalosome complex subunit 3	0.55	-0.25	0.21	0.17	-0.38237487	0.722374875	0.48738439
O88544	COP9 signalosome complex subunit 4	-0.55	-0.5	-0.04	-0.363333333	-0.87160408	0.144937412	0.13364525
O35864	COP9 signalosome complex subunit 5	-0.01	-0.32	-0.13	-0.153333333	-0.63004547	0.323378803	0.46872172
O88545	COP9 signalosome complex subunit 6	0.16	-0.24	0.15	0.023333333	-0.4695841	0.516250771	0.91332177
Q9CZ04	COP9 signalosome complex subunit 7a	-1.13	-1.14	-0.92	-1.063333333	-1.53464068	-0.592025991	0.00119258
Q8VBV7	COP9 signalosome complex subunit 8	0.02	-0.62	-0.47	-0.356666667	-0.88309482	0.169761486	0.15177999
Q9D8X1	Copper homeostasis protein cutC homolog	-0.59	-0.01	-0.26	-0.286666667	-0.79806409	0.224730756	0.22447935
O08997	Copper transport protein ATOX1	-0.67	-1.36	-0.99	-1.006666667	-1.53697382	-0.47635951	0.00303017
P36552	Coproporphyrinogen-III oxidase, mitochondrial	0.6	0.34	0.87	0.603333333	0.10001518	1.106651487	0.02551834
Q3UMF0	Cordon-bleu protein-like 1	-0.52	-1.88	-0.87	-1.09	-1.79516833	-0.384831669	0.00842208

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
O89053	Coronin-1A	0.49	0.69	0.03	0.403333333	-0.12444493	0.931111593	0.11281495
Q9WUM3	Coronin-1B	-1.3	0.61	0.53	-0.053333333	-0.99028026	0.883613591	0.89588371
Q9WUM4	Coronin-1C	1.88	0.6	1.49	1.323333333	0.6462831	2.000383571	0.00259912
E9QMV2	Costars family protein ABRACL	-0.98	-2.37	-0.5	-1.283333333	-2.14955652	-0.417110148	0.01026289
Q04447	Creatine kinase B-type	-0.21	-0.31	-0.06	-0.193333333	-0.6648822	0.278215537	0.36167912
P07310	Creatine kinase M-type	-0.34	-0.74	-0.92	-0.666666667	-1.18000859	-0.153324742	0.01836299
Q6P8J7	Creatine kinase S-type, mitochondrial	0.63	0.07	0.83	0.51	-0.03927416	1.05927416	0.06395821
P47941	Crk-like protein	-0.52	-0.98	-0.3	-0.6	-1.13093303	-0.06906697	0.03211196
O88712	C-terminal-binding protein 1	0.1	-0.35	-0.24	-0.163333333	-0.65798023	0.331313561	0.45747089
Q9JLV5	Cullin-3	-0.33	0.42	0.33	0.14	-0.41571446	0.69571446	0.56729551
G3X914	Cullin-5	0.74	0.42	0.73	0.63	0.14814054	1.111859459	0.01784758
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	0.18	0.66	0.86	0.566666667	0.03480513	1.098528207	0.03997506
Q6ZQ73	Cullin-associated NEDD8-dissociated protein 2	-0.11	0.55	0.76	0.4	-0.1750481	0.975048103	0.14272552
P97315	Cysteine and glycine-rich protein 1	-0.69	-0.35	0.26	-0.26	-0.84758389	0.327583889	0.32739109
P50462	Cysteine and glycine-rich protein 3	-0.85	-0.72	0.26	-0.436666667	-1.08704004	0.213706709	0.15496307
Q9D1P4	Cysteine and histidine-rich domain-containing protein 1	0.13	-0.26	-0.04	-0.056666667	-0.54154916	0.428215825	0.78863186
Q9Z1J3	Cysteine desulfurase, mitochondrial	1.05	0.86	1.02	0.976666667	0.50838894	1.444944391	0.00183632
Q9DCT8	Cysteine-rich protein 2	-0.2	-1.16	-2.41	-1.256666667	-2.21190695	-0.301426387	0.01738371
Q9ER72	Cysteine--tRNA ligase, cytoplasmic	-1.49	1.56	-0.82	-0.25	-1.54463873	1.044638733	0.65934913
P56395	Cytochrome b5	0.34	-0.17	-0.03	0.046666667	-0.45619883	0.549532166	0.83124318
Q9CZ13	Cytochrome b-c1 complex subunit 1, mitochondrial	0.88	0.59	-0.17	0.433333333	-0.1837098	1.05037647	0.13950982
Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial	0.99	0.58	0.07	0.546666667	-0.03150804	1.124841374	0.06031319
P99028	Cytochrome b-c1 complex subunit 6, mitochondrial	-0.21	-0.74	-0.99	-0.646666667	-1.19771726	-0.095616073	0.02775544
Q9CQB4	Cytochrome b-c1 complex subunit 7	0.3	0.07	-0.67	-0.1	-0.69966791	0.499667914	0.70289455
Q9CQ69	Cytochrome b-c1 complex subunit 8	1.84	1.41	3.35	2.2	1.30314339	3.096856611	0.00074394
Q9CR68	Cytochrome b-c1 complex subunit Rieske, mitochondrial	0.33	-0.23	-0.99	-0.296666667	-0.97728125	0.38394792	0.33414774
P00405	Cytochrome c oxidase subunit 2	1.22	0.85	0.15	0.74	0.12237279	1.357627207	0.02556745
P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.85	0.4	-0.52	0.243333333	-0.45735343	0.944020095	0.4355773
P12787	Cytochrome c oxidase subunit 5A, mitochondrial	-0.47	-0.18	-1.31	-0.653333333	-1.29320503	-0.013461634	0.04652042
Q9D881	Cytochrome c oxidase subunit 5B, mitochondrial	-0.99	-0.88	-0.74	-0.87	-1.34146837	-0.398531625	0.00350939
P56391	Cytochrome c oxidase subunit 6B1	-0.4	-0.83	-1.03	-0.753333333	-1.27519954	-0.231467124	0.0115554
Q9CPQ1	Cytochrome c oxidase subunit 6C	1.23	1.06	0.56	0.95	0.41858466	1.481415344	0.00412817
P62897	Cytochrome c, somatic	0.33	-0.78	-0.77	-0.406666667	-1.07380609	0.26047276	0.19084197
Q9D0M3	Cytochrome c1, heme protein, mitochondrial	1.36	0.88	0.32	0.853333333	0.24704049	1.459626181	0.01294767
P28271	Cytoplasmic aconitate hydratase	0.97	0.87	0.65	0.83	0.35187675	1.308123251	0.00478758
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	0.79	0.8	1.32	0.97	0.45457362	1.485426385	0.00316971
A2BFF9	Cytoplasmic dynein 1 intermediate chain 2	0.09	-0.13	-0.03	-0.023333333	-0.49264332	0.445976656	0.90898456
Q8R1Q8	Cytoplasmic dynein 1 light intermediate chain 1	-0.36	-0.85	-0.42	-0.543333333	-1.04732971	-0.039336961	0.03829653
Q99M51	Cytoplasmic protein NCK1	-0.18	-1.13	-0.44	-0.583333333	-1.17542154	0.008754877	0.05260525
A2AGT5	Cytoskeleton-associated protein 5	0.21	0.46	0.46	0.376666667	-0.09789094	0.851224272	0.1019039
Q9CPY7	Cytosol aminopeptidase	0.47	0.11	0.32	0.3	-0.1816231	0.781623101	0.18251995
Q9D020	Cytosolic 5-nucleotidase 3	-0.76	-1.3	-0.25	-0.77	-1.37852671	-0.161473287	0.02047565

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q9D1A2	Cytosolic non-specific dipeptidase	0.51	0.36	0.06	0.31	-0.18318686	0.803186863	0.17907994
E9Q9M1	Cytosolic purine 5-nucleotidase	0.33	1.82	0.2	0.783333333	-0.03802134	1.604688002	0.05863103
Q80XN0	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	1.43	0.25	0.15	0.61	-0.09843055	1.318430547	0.08074755
Q8BZJ7	DCN1-like protein 2	-0.21	-0.44	0.21	-0.146666667	-0.6712531	0.377919764	0.52675342
O35215	D-dopachrome decarboxylase	-0.28	-0.49	-1	-0.59	-1.12981244	-0.050187559	0.03640481
P28654	Decorin	-0.12	0.82	2.06	0.92	-0.02552586	1.865525861	0.05486152
Q3U0B3	Dehydrogenase/reductase SDR family member 11	0.79	0.11	1.56	0.82	0.10377691	1.53622309	0.03055063
Q99LB2	Dehydrogenase/reductase SDR family member 4	0.75	0.36	0.36	0.49	-0.00214684	0.98214684	0.05075447
O35459	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	0.25	-0.46	-0.88	-0.363333333	-0.99505655	0.268389888	0.21395095
Q8CHT0	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	1.15	0.28	0.28	0.57	-0.02748033	1.167480335	0.05857098
P10518	Delta-aminolevulinic acid dehydratase	0.21	-0.02	0.02	0.07	-0.40110597	0.541105974	0.73366459
Q99LN9	Deoxyhypusine hydroxylase	-0.38	-1.4	-1.24	-1.006666667	-1.62688479	-0.386448546	0.00666849
Q9R0P5	Destrin	-0.64	-1.41	-0.8	-0.95	-1.50438104	-0.39561896	0.00510752
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	0.03	0.11	-0.26	-0.04	-0.52468676	0.444686763	0.84963353
Q8BMF4	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	-0.18	-0.7	-1.1	-0.66	-1.2383552	-0.081644796	0.03093595
Q9D2G2	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	0.26	-0.44	-0.76	-0.313333333	-0.92018933	0.29352266	0.25922527
Q8BVI4	Dihydropteridine reductase	0.3	0.14	-0.45	-0.003333333	-0.55303919	0.546372527	0.98886987
O08553	Dihydropyrimidinase-related protein 2	0.09	-0.37	-0.31	-0.196666667	-0.69561098	0.302277644	0.37936681
E9PWE8	Dihydropyrimidinase-related protein 3	-0.11	-0.55	-0.61	-0.423333333	-0.92907756	0.082410896	0.08773748
P31428	Dipeptidase 1	-0.59	-0.34	0.12	-0.27	-0.805896	0.265896005	0.26984126
Q99KK7	Dipeptidyl peptidase 3	1.3	0.18	0.7	0.726666667	0.10041951	1.35291382	0.02900601
Q9JI46	Diphosphoinositol polyphosphate phosphohydrolase 1	-0.28	-0.49	-0.7	-0.49	-0.97831447	-0.00168553	0.04941119
Q3U1J4	DNA damage-binding protein 1	0.43	0.92	0.52	0.623333333	0.12126096	1.125405706	0.02214483
P63037	DnaJ homolog subfamily A member 1	1.53	0.05	1.03	0.87	0.13785736	1.602142636	0.02641932
Q9QYJ0	DnaJ homolog subfamily A member 2	1.05	0.51	0.47	0.676666667	0.15409184	1.199241496	0.01859218
Q9JMC3	DnaJ homolog subfamily A member 4	0.31	0.36	0.69	0.453333333	-0.03412541	0.940792074	0.06362895
Q9D832	DnaJ homolog subfamily B member 4	0.25	0.43	-0.83	-0.05	-0.74118363	0.641183632	0.86797041
Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	1.22	2.64	0.47	1.443333333	0.49209459	2.394572078	0.00918799
Q62418	Drebrin-like protein	-0.55	-0.72	-0.93	-0.733333333	-1.21704027	-0.2496264	0.00922339
B1AQF4	Dual specificity protein phosphatase 3	-0.05	0.11	1.12	0.393333333	-0.27184045	1.058507114	0.20279374
O08788	Dynactin subunit 1	0.61	0.28	1.04	0.643333333	0.09924886	1.187417806	0.02694251
Q99KJ8	Dynactin subunit 2	-0.66	-0.3	-0.02	-0.326666667	-0.84815091	0.194817579	0.18037571
Q9Z0Y1	Dynactin subunit 3	-1.21	-0.11	0.57	-0.25	-1.07016391	0.570163909	0.4914056
F8WIV5	Dynamin-2	0.05	0.26	0.25	0.186666667	-0.28379435	0.657127683	0.37640783
E9Q423	Dysferlin	0.64	1.47	-1.34	0.256666667	-0.92652094	1.439854274	0.62115908
S4R1P5	Dystonin	0.08	-0.32	-0.24	-0.16	-0.64872236	0.328722358	0.4611559
Q9D2N4	Dystrobrevin alpha	0.79	1.34	1.58	1.236666667	0.6828336	1.790499734	0.00126314
Q62165	Dystroglycan	-1.21	-0.88	-0.74	-0.943333333	-1.43981834	-0.446848325	0.00301561
P11531	Dystrophin	0.2	0.87	0.68	0.583333333	0.05302618	1.11364049	0.03554901
A2AFQ0	E3 ubiquitin-protein ligase HUWE1	0.29	0.02	0.28	0.196666667	-0.27944797	0.6727813	0.35832463

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
A2AN08	E3 ubiquitin-protein ligase UBR4	0.32	0.9	-0.41	0.27	-0.40724641	0.947246414	0.37426437
Q8BL66	Early endosome antigen 1	-0.57	-0.56	-0.28	-0.47	-0.94830183	0.008301828	0.05307219
E9QK48	Echinoderm microtubule-associated protein-like 2	0.69	0.16	0.41	0.42	-0.08335586	0.923355856	0.08854516
Q8R2G4	Ecto-ADP-ribosyltransferase 3	-0.37	-0.07	0.23	-0.07	-0.58437599	0.444375987	0.755145
Q91YE3	Egl nine homolog 1	0.31	-0.69	0.08	-0.1	-0.70787146	0.507871464	0.7066741
E9QP49	EH domain-binding protein 1-like protein 1	0.58	-0.14	0.78	0.406666667	-0.18209488	0.995428218	0.14511825
Q9WVK4	EH domain-containing protein 1	0.05	0.19	0.76	0.333333333	-0.20875938	0.875426047	0.18747074
Q8BH64	EH domain-containing protein 2	0.34	0.83	1.5	0.89	0.25250534	1.527494656	0.01342333
Q9EQP2	EH domain-containing protein 4	0.27	0.59	1.76	0.873333333	0.12259587	1.624070799	0.02872076
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	-0.55	-1.05	-1.07	-0.89	-1.40260203	-0.377397968	0.00478363
Q9DCW4	Electron transfer flavoprotein subunit beta	-0.58	-0.97	-0.95	-0.833333333	-1.32405138	-0.342615291	0.00534235
Q921G7	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	0.61	0.27	0.4	0.426666667	-0.05302182	0.906355153	0.07319229
P10126	Elongation factor 1-alpha 1	-0.31	-0.72	-0.68	-0.57	-1.06237815	-0.077621854	0.02927021
P62631	Elongation factor 1-alpha 2	0.01	-0.59	-0.32	-0.3	-0.81454198	0.214541982	0.20843827
O70251	Elongation factor 1-beta	-1.31	-0.81	-0.86	-0.993333333	-1.49980874	-0.486857927	0.00255245
Q9D8N0	Elongation factor 1-gamma	0.67	0.49	-0.25	0.303333333	-0.2871662	0.893832871	0.26143251
P58252	Elongation factor 2	0.64	0.28	0.79	0.57	0.06754979	1.072450208	0.03164429
Q8K0D5	Elongation factor G, mitochondrial	0.68	0.35	0.27	0.433333333	-0.05680428	0.923470947	0.07456156
Q9CZR8	Elongation factor Ts, mitochondrial	0.65	-0.01	0.11	0.25	-0.28264594	0.782645939	0.30105385
O08600	Endonuclease G, mitochondrial	0.75	1.29	1.07	1.036666667	0.53137292	1.541960415	0.00200704
Q9JK48	Endophilin-B1	-0.36	-0.73	0.02	-0.356666667	-0.89833913	0.185005796	0.16191645
A2AWI7	Endophilin-B2	-0.57	-1.51	-0.36	-0.813333333	-1.46667618	-0.159990482	0.02190102
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	-0.08	-1.4	-1.28	-0.92	-1.63880183	-0.201198168	0.01952256
P08113	Endoplasmin	-0.22	-0.04	-0.45	-0.236666667	-0.72389177	0.250558433	0.28585927
B0QZL1	Enolase	-1.6	-0.55	0.28	-0.623333333	-1.47108837	0.224421703	0.12461005
P42125	Enoyl-CoA delta isomerase 1, mitochondrial	0.78	0.15	0.48	0.47	-0.04949716	0.989497162	0.06943277
Q9WUR2	Enoyl-CoA delta isomerase 2, mitochondrial	0.3	-0.2	-0.18	-0.026666667	-0.5355531	0.482219763	0.90410049
Q3TLP5	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial	0.41	0.1	0.82	0.443333333	-0.09295206	0.97961873	0.09094164
Q9D7J9	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	1.88	1.09	2.06	1.676666667	1.07258453	2.280748804	0.0003631
Q8BH95	Enoyl-CoA hydratase, mitochondrial	-0.45	-1.3	-0.77	-0.84	-1.40415354	-0.275846459	0.010029
Q01279	Epidermal growth factor receptor	-1.53	-0.03	-0.45	-0.67	-1.41448034	0.074480337	0.07058554
Q60902	Epidermal growth factor receptor substrate 15-like 1	-0.34	0.11	-1.07	-0.433333333	-1.07772671	0.211060042	0.15440776
Q5M8N4	Epimerase family protein SDR39U1	0.58	0.95	0.81	0.78	0.29707836	1.262921638	0.0068281
Q9D379	Epoxide hydrolase 1	0.84	1.43	-0.47	0.6	-0.2670334	1.467033403	0.14447724
P34914	Epoxide hydrolase 2	0.62	0.15	0.42	0.396666667	-0.09832539	0.891658728	0.09925257
Q80VP1	Epsin-1	0.08	-0.34	-0.2	-0.153333333	-0.64259901	0.335932347	0.47975432
P54116	Erythrocyte band 7 integral membrane protein	2.27	1.89	1.07	1.743333333	1.08951139	2.397155274	0.00045952
Q9D172	ES1 protein homolog, mitochondrial	-0.8	-1	-0.84	-0.88	-1.34874354	-0.411256463	0.00321009
P50171	Estradiol 17-beta-dehydrogenase 8	0.27	0.32	0.79	0.46	-0.05009697	0.970096969	0.07013984
P60843	Eukaryotic initiation factor 4A-I	-0.37	0.29	0.51	0.143333333	-0.43351053	0.720177192	0.57247973
P10630	Eukaryotic initiation factor 4A-II	-0.47	-0.25	0.26	-0.153333333	-0.69479555	0.388128881	0.52161521
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	-2.33	-2.74	-0.99	-2.02	-2.85081931	-1.189180692	0.00078257

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
P48024	Eukaryotic translation initiation factor 1	-0.85	-1.54	-0.42	-0.936666667	-1.56522773	-0.308105602	0.00999116
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	0.3	0.57	0.75	0.54	0.04750624	1.032493758	0.03597684
Q99L45	Eukaryotic translation initiation factor 2 subunit 2	0.43	-0.37	0.6	0.22	-0.38505522	0.825055218	0.41535616
Q9Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	0.76	0.68	0.81	0.75	0.28546559	1.214534411	0.00684138
P23116	Eukaryotic translation initiation factor 3 subunit A	0.8	1.46	2.68	1.646666667	0.79152311	2.501810221	0.00281167
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B	0.75	0.62	1.37	0.913333333	0.36125056	1.465416108	0.00607709
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	1.09	1.37	2.33	1.596666667	0.9227771	2.270556234	0.00090614
Q9DCH4	Eukaryotic translation initiation factor 3 subunit F	-0.06	0.16	1.09	0.396666667	-0.25562968	1.048963012	0.19177421
Q9Z1D1	Eukaryotic translation initiation factor 3 subunit G	-0.64	-0.57	0.32	-0.296666667	-0.9101937	0.316860371	0.28786207
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L	0.45	1.21	1.48	1.046666667	0.43369665	1.659636687	0.0051988
Q99JX4	Eukaryotic translation initiation factor 3 subunit M	-0.43	-0.23	1.28	0.206666667	-0.63650941	1.049842742	0.57757686
G3XA17	Eukaryotic translation initiation factor 4 gamma 2	-0.87	-0.29	0.23	-0.31	-0.93107426	0.311074264	0.27392416
P63073	Eukaryotic translation initiation factor 4E	-0.4	-0.48	0.31	-0.19	-0.75657033	0.376570329	0.45078948
Q9WUK2	Eukaryotic translation initiation factor 4H	-0.82	-2.52	-1.86	-1.733333333	-2.52801957	-0.938647093	0.00143799
P59325	Eukaryotic translation initiation factor 5	-0.94	-1.03	-0.05	-0.673333333	-1.29009961	-0.056567055	0.03656029
P63242	Eukaryotic translation initiation factor 5A-1	-0.9	-0.4	-0.44	-0.58	-1.08724294	-0.072757057	0.03070078
Q05D44	Eukaryotic translation initiation factor 5B	-0.24	-0.12	0.21	-0.05	-0.5442247	0.444224698	0.81634967
P26040	Ezrin	-0.44	-0.31	-1.1	-0.616666667	-1.17835924	-0.054974097	0.03580515
P47754	F-actin-capping protein subunit alpha-2	-0.09	-0.56	-1.06	-0.57	-1.15932535	0.019325349	0.05596703
Q8R123	FAD synthase	0.65	0.08	0.21	0.313333333	-0.2006182	0.827284868	0.19078611
P56213	FAD-linked sulfhydryl oxidase ALR	-0.23	-0.97	-1.12	-0.773333333	-1.35865206	-0.188014603	0.01706746
Q91WJ8	Far upstream element-binding protein 1	-0.47	-0.73	-0.59	-0.596666667	-1.0688791	-0.124454229	0.02059662
Q3U0V1	Far upstream element-binding protein 2	-0.63	-1.57	-0.7	-0.966666667	-1.57450691	-0.358826423	0.00735676
P19096	Fatty acid synthase	1.5	1.51	-0.49	0.84	-0.14420352	1.82420352	0.08289124
P04117	Fatty acid-binding protein, adipocyte	-1.2	-0.93	-1.15	-1.093333333	-1.56777096	-0.618895711	0.00105936
Q05816	Fatty acid-binding protein, epidermal	-0.75	-0.57	-0.47	-0.596666667	-1.0708042	-0.122529135	0.02094647
P11404	Fatty acid-binding protein, heart	-0.77	-1.84	-1.78	-1.463333333	-2.11072361	-0.815943053	0.00118023
Q8CIB5	Fermitin family homolog 2	0.6	0.56	0.65	0.603333333	0.14018998	1.066476689	0.01812481
P09528	Ferritin heavy chain	-1.01	-1.85	-0.76	-1.206666667	-1.83829976	-0.575033573	0.00293103
Q544X6	Ferrochelatase	1.43	0.96	1.67	1.353333333	0.81704794	1.88961873	0.00063235
Q9QXC1	Fetuin-B	-1.31	-1.1	-0.92	-1.11	-1.59480421	-0.62519579	0.00109855
Q76LL6	FH1/FH2 domain-containing protein 3	1.33	-0.05	1.13	0.803333333	0.07534973	1.531316938	0.0351286
Q8K0E8	Fibrinogen beta chain	0.45	0.69	0.94	0.693333333	0.19581737	1.190849297	0.01353042
Q8VCM7	Fibrinogen gamma chain	0.4	0.61	1.02	0.676666667	0.15709645	1.196236883	0.0181445
P61148	Fibroblast growth factor 1	-1.2	-0.92	-1.24	-1.12	-1.60026179	-0.639738214	0.0009909
Q8BTM8	Filamin-A	NA	-0.56	-0.5	-0.53	-1.16816494	0.108164936	0.08766199
Q80X90	Filamin-B	0.04	-0.78	-0.27	-0.336666667	-0.8942902	0.220956871	0.1945805
Q71FD7	Filamin-binding LIM protein 1	-0.24	-0.63	-0.17	-0.346666667	-0.84498301	0.151649676	0.14268567
Q923D2	Flavin reductase (NADPH)	-0.26	-0.3	0.04	-0.173333333	-0.65603879	0.309372125	0.42088055
O70433	Four and a half LIM domains protein 2	-1.28	-0.53	0.57	-0.413333333	-1.25373651	0.427069842	0.2803843
Q61584	Fragile X mental retardation syndrome-related protein 1	0.13	-0.16	-0.62	-0.216666667	-0.75959891	0.326265573	0.37382044
P70695	Fructose-1,6-bisphosphatase isozyme 2	0.36	-0.43	-0.84	-0.303333333	-0.95536779	0.348701122	0.30500002

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
A6ZI44	Fructose-bisphosphate aldolase	0.39	-0.01	-0.3	0.026666667	-0.50406974	0.557403073	0.90802642
P97807	Fumarate hydratase, mitochondrial	-0.16	-0.87	-0.61	-0.546666667	-1.08220843	-0.0111249	0.04656263
P35505	Fumarylacetoacetase	1.4	-0.3	0.62	0.573333333	-0.21761883	1.364285498	0.12913773
Q3TC72	Fumarylacetoacetate hydrolase domain-containing protein 2A	0.45	0.23	-0.11	0.19	-0.31858801	0.698588009	0.40333622
Q8VDC1	FYVE and coiled-coil domain-containing protein 1	-0.34	0.27	1.04	0.323333333	-0.37352416	1.020190823	0.30617247
Q9R0N0	Galactokinase	-0.22	0.12	0.32	0.073333333	-0.4324109	0.579077563	0.73980139
P16045	Galectin-1	-0.37	-1.04	-0.98	-0.796666667	-1.33665485	-0.256678479	0.01046219
P82348	Gamma-sarcoglycan	0.78	-0.1	0.65	0.443333333	-0.14130414	1.027970804	0.11513088
Q9Z0F7	Gamma-synuclein	-0.59	-1.31	-0.71	-0.87	-1.41594732	-0.32405268	0.00728554
P23242	Gap junction alpha-1 protein	-1.25	-1.59	-0.1	-0.98	-1.72863644	-0.231363557	0.01775442
P23591	GDP-L-fucose synthase	0.91	0.35	0.15	0.47	-0.07927416	1.01927416	0.08226505
Q9Z1Z0	General vesicular transport factor p115	1.05	1.09	1.33	1.156666667	0.68085107	1.632482267	0.00078334
Q9JHK4	Geranylgeranyl transferase type-2 subunit alpha	0.67	1.31	-0.26	0.573333333	-0.1804314	1.327098069	0.11421489
Q9CQI3	Glia maturation factor beta	-0.13	-1.01	-0.52	-0.553333333	-1.12257695	0.015910281	0.05504182
O88958	Glucosamine-6-phosphate isomerase 1	0.42	0.3	0.45	0.39	-0.07575836	0.855758362	0.0876484
Q00612	Glucose-6-phosphate 1-dehydrogenase X	0.64	1.14	0.81	0.863333333	0.36319236	1.363474304	0.00492481
P06745	Glucose-6-phosphate isomerase	0.05	0.13	-0.39	-0.07	-0.57791592	0.437915921	0.7521559
P26443	Glutamate dehydrogenase 1, mitochondrial	2.13	1.19	1.99	1.77	1.1701897	2.369810305	0.0002524
O09172	Glutamate--cysteine ligase regulatory subunit	-0.43	NA	0.46	0.015	-0.7730174	0.803017398	0.96395003
P15105	Glutamine synthetase	1.74	0.96	1.02	1.24	0.67378148	1.806218523	0.0014064
Q9CQM9	Glutaredoxin-3	-0.94	-0.77	-0.65	-0.786666667	-1.26146415	-0.311869186	0.00603224
Q80Y14	Glutaredoxin-related protein 5, mitochondrial	-0.32	-1.11	-0.67	-0.7	-1.25005098	-0.149949023	0.01999435
Q60759	Glutaryl-CoA dehydrogenase, mitochondrial	1.24	0.61	1.16	1.003333333	0.47388572	1.532780945	0.00305708
P11352	Glutathione peroxidase 1	0.11	0.77	1.46	0.78	0.09240873	1.467591273	0.03164918
P46412	Glutathione peroxidase 3	0.21	0.4	0.87	0.493333333	-0.03493012	1.021596787	0.06278161
P47791	Glutathione reductase, mitochondrial	0.55	0.01	-0.37	0.063333333	-0.51548106	0.642147729	0.80174362
P30115	Glutathione S-transferase A3	-0.07	-0.49	-1.94	-0.833333333	-1.70590846	0.039241793	0.05836518
P24472	Glutathione S-transferase A4	-1.58	-1.59	-1.66	-1.61	-2.0730614	-1.146938602	9.33E-05
Q9DCM2	Glutathione S-transferase kappa 1	-0.11	-0.19	0.11	-0.063333333	-0.5398663	0.413199631	0.76065336
P10649	Glutathione S-transferase Mu 1	-0.42	-0.67	-0.3	-0.463333333	-0.94668704	0.020020375	0.05765503
P15626	Glutathione S-transferase Mu 2	-0.31	-1.25	-0.47	-0.676666667	-1.27444866	-0.078884668	0.03190958
P48774	Glutathione S-transferase Mu 5	0.11	-0.07	-0.09	-0.016666667	-0.48597666	0.452643322	0.93490313
Q80W21	Glutathione S-transferase Mu 7	-0.5	-1.62	0.37	-0.583333333	-1.46647946	0.299812789	0.16079007
O09131	Glutathione S-transferase omega-1	0.29	0.21	-0.15	0.116666667	-0.37792268	0.61125601	0.59163979
P19157	Glutathione S-transferase P 1	-0.34	-0.92	-0.47	-0.576666667	-1.0924979	-0.060835438	0.03345553
P16858	Glyceraldehyde-3-phosphate dehydrogenase	-0.03	-0.62	-0.84	-0.496666667	-1.05632842	0.062995085	0.07370662
Q64516	Glycerol kinase	-0.97	-0.26	-0.5	-0.576666667	-1.11295206	-0.04038127	0.03865647
P13707	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	-0.56	-0.5	-0.85	-0.636666667	-1.11966689	-0.153666442	0.01723787
Q3ULJ0	Glycerol-3-phosphate dehydrogenase 1-like protein	-0.7	-0.71	-0.72	-0.71	-1.17195356	-0.248046443	0.00865104
Q8C0L9	Glycerophosphocholine phosphodiesterase GPCPD1	0.76	0.14	0.04	0.313333333	-0.23434924	0.861015904	0.21610684
Q9CZD3	Glycine--tRNA ligase	-0.35	-0.86	-0.63	-0.613333333	-1.11381568	-0.112850986	0.02334939
Q9Z1E4	Glycogen [starch] synthase, muscle	0.86	0.84	1.12	0.94	0.46330777	1.416692231	0.00248024

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8CI94	Glycogen phosphorylase, brain form	1.19	1.26	1	1.15	0.6770848	1.622915202	0.00078185
Q9WUB3	Glycogen phosphorylase, muscle form	1.45	1.51	0.68	1.213333333	0.63427309	1.792393574	0.00179073
Q2NL51	Glycogen synthase kinase-3 alpha	-0.15	0.13	1.1	0.36	-0.31699418	1.036994177	0.24660127
E9QAQ5	Glycogen synthase kinase-3 beta	1.06	0.64	2.8	1.5	0.52017354	2.479826458	0.00881325
K3W4S6	Glycogenin-1	-0.25	-0.34	-0.51	-0.366666667	-0.83918042	0.105847084	0.1083288
Q9CPV4	Glyoxalase domain-containing protein 4	-0.34	-0.02	-0.78	-0.38	-0.92427627	0.164276274	0.14147488
Q91Z53	Glyoxylate reductase/hydroxypyruvate reductase	1.14	0.44	0.24	0.606666667	0.02315013	1.1901832	0.04364743
Q9QZF2	Glypican-1	1.27	1.68	0.65	1.2	0.59466257	1.805337432	0.00241168
Q9DCZ1	GMP reductase 1	-0.34	-0.44	-0.22	-0.333333333	-0.80264332	0.135976656	0.13575444
Q3THK7	GMP synthase [glutamine-hydrolyzing]	-0.17	-0.41	-0.52	-0.366666667	-0.84789558	0.114562247	0.11370047
Q91VW5	Golgin subfamily A member 4	-0.14	-0.26	0.23	-0.056666667	-0.55714901	0.443815681	0.79503588
Q9QYY0	GRB2-associated-binding protein 1	-1.45	0.72	-1	-0.576666667	-1.55650281	0.403169475	0.20468014
Q8C5Q4	G-rich sequence factor 1	-0.79	-0.57	-0.37	-0.576666667	-1.06500057	-0.088332766	0.02708033
Q9JLM9	Growth factor receptor-bound protein 14	0.52	0.05	-0.34	0.076666667	-0.48805844	0.64139177	0.75571187
Q60631	Growth factor receptor-bound protein 2	-1.08	-1.71	-0.55	-1.113333333	-1.74999393	-0.476672739	0.00461482
Q99LP6	GrpE protein homolog 1, mitochondrial	-1.4	-1.09	-0.42	-0.97	-1.56681296	-0.373187042	0.00662456
Q9WTP7	GTP:AMP phosphotransferase, mitochondrial	0.54	0.39	0.32	0.416666667	-0.0529465	0.886279831	0.07375396
D3YTN4	GTPase IMAP family member 4	0.39	-0.86	-0.09	-0.186666667	-0.84978313	0.476449792	0.52401684
P62827	GTP-binding nuclear protein Ran	0.23	0.1	0.29	0.206666667	-0.26100278	0.674336113	0.32798208
Q9CQC9	GTP-binding protein SAR1b	-0.17	2.19	1.41	1.143333333	0.12528411	2.16138256	0.03288157
Q9R111	Guanine deaminase	NA	-0.97	0.51	-0.23	-1.22998501	0.769985005	0.59009495
P08752	Guanine nucleotide-binding protein G(i) subunit alpha-2	0.52	0.41	0.66	0.53	0.05853163	1.001468375	0.03276146
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	1.48	1.67	1.56	1.57	1.10253349	2.037466511	0.00011537
Q3UGR5	Haloacid dehalogenase-like hydrolase domain-containing protein 2	-0.2	0.05	-0.39	-0.18	-0.67098867	0.310988674	0.41171079
Q9CYW4	Haloacid dehalogenase-like hydrolase domain-containing protein 3	0.04	0.38	-0.46	-0.013333333	-0.57456961	0.547902943	0.95641928
Q3U2G2	Heat shock 70 kDa protein 4	-0.44	-0.66	-0.45	-0.516666667	-0.98797401	-0.045359324	0.03600356
P48722	Heat shock 70 kDa protein 4L	-0.02	0.01	-0.62	-0.21	-0.74408693	0.324086932	0.38047301
P63017	Heat shock cognate 71 kDa protein	-0.1	-0.38	-0.52	-0.333333333	-0.82259901	0.155932347	0.14984704
Q61699	Heat shock protein 105 kDa	-0.45	0.11	-1.31	-0.55	-1.26035664	0.160356643	0.10897745
Q9CQN1	Heat shock protein 75 kDa, mitochondrial	-0.3	0.05	0.6	0.116666667	-0.45824942	0.69158275	0.64345836
P14602	Heat shock protein beta-1	-0.9	-0.18	0.04	-0.346666667	-0.93909132	0.245757987	0.20697795
P35385	Heat shock protein beta-7	0.51	-0.36	-0.1	0.016666667	-0.5550718	0.588405135	0.94654141
P07901	Heat shock protein HSP 90-alpha	-0.98	0.09	-0.74	-0.543333333	-1.17008029	0.083413621	0.07912977
P11499	Heat shock protein HSP 90-beta	-0.43	-0.46	-0.65	-0.513333333	-0.98391535	-0.04275132	0.03666806
P97825	Hematological and neurological expressed 1 protein	-1.07	-1.77	-1.34	-1.393333333	-1.92653122	-0.860135443	0.00051676
Q91VB8	Hemoglobin subunit alpha	-1.39	-0.53	-0.21	-0.71	-1.36219451	-0.057805488	0.03694471
Q91X72	Hemopexin	-1.61	-0.86	-1.2	-1.223333333	-1.76521596	-0.681450705	0.00118839
P49182	Heparin cofactor 2	-0.6	-0.27	-1.03	-0.633333333	-1.17741781	-0.089248861	0.02865019
P51859	Hepatoma-derived growth factor	-0.64	-1.28	-1.36	-1.093333333	-1.64288382	-0.543782846	0.00236602
Q20BD0	Heterogeneous nuclear ribonucleoprotein A/B	-1.45	-0.82	1.71	-0.186666667	-1.53048797	1.157154636	0.75027714
Q9CX86	Heterogeneous nuclear ribonucleoprotein A0	-0.15	0.39	0.46	0.233333333	-0.29277028	0.759436945	0.32635605
Q5EBP8	Heterogeneous nuclear ribonucleoprotein A1	-0.05	-0.36	0.09	-0.106666667	-0.60016126	0.38682793	0.62239456

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	-0.07	0.4	0.54	0.29	-0.23102916	0.811029162	0.22741831
Q60668	Heterogeneous nuclear ribonucleoprotein D0	-0.77	-1.12	-0.62	-0.836666667	-1.33749016	-0.335843174	0.00579275
D3YTQ3	Heterogeneous nuclear ribonucleoprotein D-like	-0.35	-1.58	0.84	-0.363333333	-1.3865423	0.659875632	0.42581208
P61979	Heterogeneous nuclear ribonucleoprotein K	-0.47	-0.73	0.44	-0.253333333	-0.90772102	0.401054351	0.38743578
Q9D0E1	Heterogeneous nuclear ribonucleoprotein M	-0.86	-0.09	0.76	-0.063333333	-0.82960773	0.702941064	0.84941191
Q7TMK9	Heterogeneous nuclear ribonucleoprotein Q	-0.12	-0.91	-0.32	-0.45	-1.00622646	0.106226462	0.0966606
Q8VEK3	Heterogeneous nuclear ribonucleoprotein U	0.61	0.38	0.74	0.576666667	0.09472845	1.058604886	0.02570194
Q8VDM6	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.31	0.99	1.38	1.226666667	0.73885767	1.71447566	0.00064531
Q00PI9	Heterogeneous nuclear ribonucleoprotein U-like protein 2	0.92	0.38	0.27	0.523333333	-0.00793915	1.054605815	0.05263368
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	0.01	-0.07	-0.47	-0.176666667	-0.67766064	0.324327311	0.42886897
Q9Z204	Heterogeneous nuclear ribonucleoproteins C1/C2	0.53	-0.68	-0.09	-0.08	-0.72943898	0.569438978	0.77756937
Q8BMS4	Hexaprenyldihydroxybenzoate methyltransferase, mitochondrial	0.07	0.23	0.55	0.283333333	-0.21401095	0.780677619	0.2178339
P17710	Hexokinase-1	0.44	0.68	0.95	0.69	0.18959349	1.190406506	0.01417962
P63158	High mobility group protein B1	-0.65	-1.15	-0.76	-0.853333333	-1.35597235	-0.350694314	0.00534993
P30681	High mobility group protein B2	-1.26	-1.41	-1.15	-1.273333333	-1.74560605	-0.801060618	0.0004306
P70349	Histidine triad nucleotide-binding protein 1	-0.21	-1.1	-1.22	-0.843333333	-1.46515576	-0.221510911	0.01524582
Q9D0S9	Histidine triad nucleotide-binding protein 2, mitochondrial	-0.03	-0.68	-0.73	-0.48	-1.02787311	0.067873113	0.07665042
Q9ESB3	Histidine-rich glycoprotein	-0.99	0.16	-0.69	-0.506666667	-1.15158992	0.138256586	0.10479095
Q61035	Histidine--tRNA ligase, cytoplasmic	-0.48	-0.71	-0.61	-0.6	-1.07001709	-0.129982906	0.01973816
Q8CBB6	Histone H2B	0.97	2	2.99	1.986666667	1.0954989	2.877834434	0.00127462
D3YUP1	Histone-arginine methyltransferase CARM1	-0.19	0.17	1.3	0.426666667	-0.31996452	1.173297849	0.21657177
Q8R1H0	Homeodomain-only protein	-0.51	-1.17	-0.68	-0.786666667	-1.31600674	-0.257326596	0.01011738
B1AUX2	Host cell factor 1	-0.23	-0.44	-0.51	-0.393333333	-0.86813081	0.081464147	0.09039349
Q99L47	Hsc70-interacting protein	-0.99	-1.01	-0.52	-0.84	-1.34707456	-0.332925441	0.00603734
Q61081	Hsp90 co-chaperone Cdc37	-0.2	-0.53	1.29	0.186666667	-0.6785701	1.05190343	0.62303447
Q8R0N6	Hydroxyacid-oxoacid transhydrogenase, mitochondrial	-0.49	-0.05	0.18	-0.12	-0.64851486	0.408514861	0.60529712
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0.37	-0.13	-0.02	0.073333333	-0.42930569	0.575972353	0.73826633
G5E8T9	Hydroxyacylglutathione hydrolase, mitochondrial	-0.05	0.12	-0.54	-0.156666667	-0.68600674	0.372673404	0.50362376
P38060	Hydroxymethylglutaryl-CoA lyase, mitochondrial	0.2	-0.61	-0.45	-0.286666667	-0.85068564	0.277352304	0.26603705
Q2TPA8	Hydroxysteroid dehydrogenase-like protein 2	0.41	-0.04	0.01	0.126666667	-0.37130681	0.624640147	0.56365065
P00493	Hypoxanthine-guanine phosphoribosyltransferase	-1.44	-0.88	-0.02	-0.78	-1.49035664	-0.069643357	0.03578481
Q9JKR6	Hypoxia up-regulated protein 1	0.39	0.27	-0.53	0.043333333	-0.55311384	0.639780507	0.86740612
P01869	Ig gamma-1 chain C region, membrane-bound form	-2.04	0.16	1.02	-0.286666667	-1.56386919	0.990535852	0.60935342
F6TQW2	Ig gamma-2A chain C region secreted form	0.14	-0.44	-1.5	-0.6	-1.37915567	0.17915567	0.11056357
P01867	Ig gamma-2B chain C region	-0.88	0.99	-1.27	-0.386666667	-1.40853939	0.635206059	0.39763951
P06330	Ig heavy chain V region AC38 205.12	-1.46	-1.18	-1.98	-1.54	-2.09422698	-0.985773023	0.00036073
P01872	Ig mu chain C region secreted form	-1.94	-3.02	-2.23	-2.396666667	-3.02214061	-1.771192719	5.11E-05
Q61249	Immunoglobulin-binding protein 1	-1.02	-0.24	-1.3	-0.853333333	-1.47391852	-0.23274815	0.01435423
P70168	Importin subunit beta-1	0.64	0.57	0.83	0.68	0.2070848	1.152915202	0.01176219
Q8BKC5	Importin-5	0.76	0.54	1.23	0.843333333	0.31034903	1.376317633	0.00753746
Q9EPL8	Importin-7	0.33	0.49	0.47	0.43	-0.03655221	0.896552209	0.06548747
P40936	Indolethylamine N-methyltransferase	-1.31	0.25	0.28	-0.26	-1.08717952	0.567179525	0.47850733

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q920Q8	Influenza virus NS1A-binding protein homolog	1.66	1.26	0.46	1.126666667	0.47406492	1.779268416	0.00492134
Q9DBD0	Inhibitor of carbonic anhydrase	0.04	-0.72	-0.64	-0.44	-0.99913592	0.119135925	0.10432026
Q9D819	Inorganic pyrophosphatase	-0.84	-1.1	-0.91	-0.95	-1.4229152	-0.477084798	0.00224725
Q91VM9	Inorganic pyrophosphatase 2, mitochondrial	NA	-0.91	-0.49	-0.7	-1.37386246	-0.026137542	0.04407778
Q924B0	Inositol monophosphatase 1	-0.16	-0.51	-0.91	-0.526666667	-1.06844422	0.015110889	0.05503073
Q91UZ5	Inositol monophosphatase 2	-0.02	-0.53	-0.3	-0.283333333	-0.78381568	0.217149014	0.22041084
P49442	Inositol polyphosphate 1-phosphatase	-0.3	-0.68	0.23	-0.25	-0.82643248	0.326432483	0.33639891
Q61739	Integrin alpha-6	-0.28	-0.4	0.17	-0.17	-0.68454198	0.344541982	0.45722438
P09055	Integrin beta-1	-0.55	-0.03	-0.02	-0.2	-0.71542638	0.315426385	0.38639877
O55222	Integrin-linked protein kinase	-0.17	0.91	1.58	0.773333333	-0.03734688	1.584013543	0.05858609
G3X977	Inter-alpha-trypsin inhibitor heavy chain H2	-0.77	-0.28	-1.04	-0.696666667	-1.24242277	-0.150910561	0.01974028
Q3UVZ1	Interleukin-1 receptor accessory protein	-1.31	0.08	-1.5	-0.91	-1.70810568	-0.111894316	0.03103678
Q9DCB8	Iron-sulfur cluster assembly 2 homolog, mitochondrial	-0.72	-1.38	-0.98	-1.026666667	-1.55228309	-0.501050243	0.00260823
Q8K3A0	Iron-sulfur cluster co-chaperone protein HscB, mitochondrial	-0.4	-1.02	-0.77	-0.73	-1.2484001	-0.211599896	0.01291825
Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	1.75	1.38	1.36	1.496666667	1.00594862	1.987384709	0.00020708
Q91V64	Isochorismatase domain-containing protein 1	0.08	-0.87	-0.9	-0.563333333	-1.18798755	0.061320882	0.07012943
P85094	Isochorismatase domain-containing protein 2A, mitochondrial	0.71	0.06	0.29	0.353333333	-0.1712531	0.877919764	0.1538431
Q9D6R2	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	-0.18	-0.47	-0.65	-0.433333333	-0.92867032	0.062003654	0.07699312
P70404	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial	0.67	0.38	0.85	0.633333333	0.13799635	1.12867032	0.0196068
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	0.45	-0.16	-0.11	0.06	-0.46786814	0.587868144	0.79426029
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	0.96	0.6	0.75	0.77	0.2883769	1.251623101	0.00717246
Q8BU30	Isoleucine--tRNA ligase, cytoplasmic	1.05	0.87	1.13	1.016666667	0.54397222	1.489361113	0.00155306
Q8BIJ6	Isoleucine--tRNA ligase, mitochondrial	0.45	0.75	1.36	0.853333333	0.27387996	1.43278671	0.01055011
Q9JHI5	Isovaleryl-CoA dehydrogenase, mitochondrial	0.49	-0.47	-0.87	-0.283333333	-0.98438563	0.417718963	0.36813091
Q9ET78	Junctophilin-2	0.99	-0.63	1.13	0.496666667	-0.37404697	1.367380308	0.21731716
E9Q1Q9	Ketohexokinase	-0.93	-0.91	-1.08	-0.973333333	-1.44051559	-0.50615108	0.00184706
F8VQC7	Kinectin	0.39	0.59	0.31	0.43	-0.04453761	0.90453761	0.06909188
Q61768	Kinesin-1 heavy chain	-0.63	-0.9	-0.72	-0.75	-1.2233965	-0.276603505	0.00749186
F8VQ75	Kinesin-like protein KIF13A	-0.43	-0.39	0.1	-0.24	-0.7527686	0.272768601	0.30229432
O08677	Kininogen-1	-1.23	-0.77	-1.02	-1.006666667	-1.50016126	-0.51317207	0.00206994
Q8BTY1	Kynurenine--oxoglutarate transaminase 1	0.28	0.19	0.48	0.316666667	-0.1586102	0.791943534	0.157683
Q71RI9	Kynurenine--oxoglutarate transaminase 3	1.01	0.59	0.9	0.833333333	0.34307958	1.323587088	0.00531733
Q91YP0	L-2-hydroxyglutarate dehydrogenase, mitochondrial	1.07	1.68	0.72	1.156666667	0.56698721	1.746346127	0.00255072
Q3V384	Lactation elevated protein 1	-0.5	0.58	1.48	0.52	-0.35912944	1.399129439	0.20267927
Q9CPU0	Lactoylglutathione lyase	-0.31	-1.53	-0.17	-0.67	-1.39933789	0.059337891	0.06617252
Q60675	Laminin subunit alpha-2	0.01	-0.69	-0.57	-0.416666667	-0.95807631	0.124742973	0.11074207
P97927	Laminin subunit alpha-4	-0.07	-0.27	0.03	-0.103333333	-0.57938818	0.372721509	0.62094813
Q61001	Laminin subunit alpha-5	0.84	0.12	0.19	0.383333333	-0.16720044	0.93386711	0.1423853
E9QN70	Laminin subunit beta-1	0.12	-0.34	-0.7	-0.306666667	-0.86301253	0.249679195	0.23145651
Q61292	Laminin subunit beta-2	0.84	-0.11	-0.32	0.136666667	-0.51971897	0.793052299	0.63499535
F8VQJ3	Laminin subunit gamma-1	0.11	-0.59	-0.83	-0.436666667	-1.02755173	0.154218396	0.12302562
Q9Z1R2	Large proline-rich protein BAG6	0.51	-0.19	-0.21	0.036666667	-0.51926972	0.592603052	0.87950824

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8C0M9	L-asparaginase	-0.75	-1.07	-0.76	-0.86	-1.34185946	-0.378140541	0.00416267
Q8K4G1	Latent-transforming growth factor beta-binding protein 4	0.21	-1.02	-0.6	-0.47	-1.13021969	0.19021969	0.13500395
Q9Z2I0	LETM1 and EF-hand domain-containing protein 1, mitochondrial	0.14	-0.4	-0.39	-0.216666667	-0.73404075	0.300707418	0.35214269
Q6PB66	Leucine-rich PPR motif-containing protein, mitochondrial	0.45	0.17	0.58	0.4	-0.08819787	0.888197868	0.09327618
Q8BMJ2	Leucine--tRNA ligase, cytoplasmic	-0.12	1.06	1.46	0.8	0.02700644	1.572993557	0.04435969
Q8C129	Leucyl-cystinyl aminopeptidase	0.29	-0.82	-0.59	-0.373333333	-1.01267097	0.266004302	0.20782161
P42703	Leukemia inhibitory factor receptor	-1.2	-0.88	-0.65	-0.91	-1.41673762	-0.403262377	0.00403406
P24527	Leukotriene A-4 hydrolase	-0.06	-0.48	-0.09	-0.21	-0.70457016	0.284570158	0.34592374
D3YU59	LIM and calponin homology domains-containing protein 1	0.34	-0.65	0.24	-0.023333333	-0.6417589	0.595092234	0.93085136
Q8VEE1	LIM and cysteine-rich domains protein 1	-0.16	-0.31	-1.45	-0.64	-1.34476454	0.064764541	0.06862564
Q9JKS4	LIM domain-binding protein 3	0.01	-0.85	-0.65	-0.496666667	-1.06994649	0.076613158	0.07928051
P53395	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	-0.15	0.27	0.02	0.046666667	-0.44195861	0.53529194	0.82642047
Q8BFW7	Lipoma-preferred partner homolog	-0.13	-0.92	0.32	-0.243333333	-0.9049026	0.418235936	0.41025505
P11152	Lipoprotein lipase	0.53	0.9	1.77	1.066666667	0.40029572	1.733037618	0.00713057
G3X9J4	LisH domain and HEAT repeat-containing protein KIAA1468	0.33	0.21	-3.07	-0.843333333	-2.37055849	0.683891821	0.23071264
P16125	L-lactate dehydrogenase B chain	-0.45	-0.61	-0.59	-0.55	-1.01655221	-0.083447791	0.02726411
G5E8N5	L-lactate dehydrogenase	-0.03	0.13	-0.13	-0.01	-0.48237316	0.462373161	0.9611607
Q8CGK3	Lon protease homolog, mitochondrial	-0.48	-0.45	0.12	-0.27	-0.7976524	0.257652396	0.26311038
P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	0.7	0.38	0.34	0.473333333	-0.01195993	0.958626598	0.05441936
D3Z041	Long-chain-fatty-acid--CoA ligase 1	1.09	0.86	0.27	0.74	0.17857778	1.301422218	0.01724171
P51885	Lumican	-1.66	-1.76	-1.05	-1.49	-2.03537348	-0.944626525	0.00039847
P32067	Lupus La protein homolog	0.46	-0.21	0.03	0.093333333	-0.43482234	0.621489005	0.68628332
Q8BP40	Lysophosphatidic acid phosphatase type 6	-0.71	-1.44	-0.98	-1.043333333	-1.58268856	-0.503978104	0.00274505
P70699	Lysosomal alpha-glucosidase	1.88	0.39	0.48	0.916666667	0.13516416	1.69816917	0.02780762
P10619	Lysosomal protective protein	2.62	3.63	2.12	2.79	2.04823938	3.531760625	5.73E-05
Q8R2P8	Lysyl-tRNA synthetase	0.56	0.24	0.06	0.286666667	-0.21318964	0.786522978	0.2151179
Q9DAR7	m7GpppX diphosphatase	0.04	0.03	-0.09	-0.006666667	-0.47177266	0.458439322	0.97369559
Q61830	Macrophage mannose receptor 1	-0.37	-0.57	-0.15	-0.363333333	-0.85166723	0.125000568	0.12092248
Q9D967	Magnesium-dependent phosphatase 1	0.99	0.26	0.57	0.606666667	0.06836802	1.14496531	0.03244694
E9Q3X0	Major vault protein	0.61	1.11	1.99	1.236666667	0.53577681	1.937556527	0.00441133
P14152	Malate dehydrogenase, cytoplasmic	-0.39	-0.76	-0.77	-0.64	-1.12994398	-0.150056015	0.01791516
P08249	Malate dehydrogenase, mitochondrial	-0.17	-0.65	-0.82	-0.546666667	-1.07395929	-0.019374047	0.04408682
Q9WVL0	Maleylacetoacetate isomerase	0.52	0.26	0.38	0.386666667	-0.08554577	0.858879104	0.09343729
Q99J39	Malonyl-CoA decarboxylase, mitochondrial	1.18	0.36	0.56	0.7	0.13660383	1.263396168	0.02207601
Q922H4	Mannose-1-phosphate guanyltransferase alpha	0.45	0.59	0.1	0.38	-0.11960948	0.879609476	0.11422759
Q8BTZ7	Mannose-1-phosphate guanyltransferase beta	0.16	-0.81	0.23	-0.14	-0.7769586	0.496958598	0.61664506
Q924M7	Mannose-6-phosphate isomerase	-0.44	-0.92	-0.95	-0.77	-1.2798737	-0.260126299	0.00939226
P49138	MAP kinase-activated protein kinase 2	-0.19	-0.65	-0.13	-0.323333333	-0.83266707	0.1860004	0.17535716
P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	0.4	0.14	0.04	0.193333333	-0.28937212	0.676038791	0.37218876
Q8BJ34	Meiosis arrest female protein 1	0.93	NA	1	0.965	0.32655905	1.603440946	0.01052634
Q3UI33	Methionine aminopeptidase	0.31	-0.1	0.01	0.073333333	-0.41552491	0.562191579	0.73123518

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q78J03	Methionine-R-sulfoxide reductase B2, mitochondrial	-1.13	-0.89	-1.06	-1.026666667	-1.4978532	-0.555480135	0.00144621
Q8BU85	Methionine-R-sulfoxide reductase B3, mitochondrial	-0.07	-1.13	-0.77	-0.656666667	-1.27209304	-0.041240291	0.03976186
E9QB02	Methionine--tRNA ligase, cytoplasmic	0.67	1.23	0.98	0.96	0.45191597	1.468084027	0.00310465
Q499X9	Methionine--tRNA ligase, mitochondrial	0.84	0.85	0.92	0.87	0.4069386	1.333061398	0.00319732
Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	0.85	1.09	2.96	1.633333333	0.64689566	2.619771007	0.00605112
Q99MR8	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	-0.14	0.57	1.82	0.75	-0.12974444	1.629744435	0.08316738
Q9JLZ3	Methylglutaconyl-CoA hydratase, mitochondrial	0.43	0.16	0.89	0.493333333	-0.0460219	1.032688563	0.06708598
Q9EQ20	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	0.31	0.21	0.37	0.296666667	-0.16923428	0.762567614	0.17421473
Q9D1I5	Methylmalonyl-CoA epimerase, mitochondrial	-0.76	-1.13	-1.23	-1.04	-1.53824017	-0.541759829	0.00182828
P16332	Methylmalonyl-CoA mutase, mitochondrial	0.3	-0.3	0.86	0.286666667	-0.34968087	0.923014205	0.31936254
Q9CQT1	Methylthioribose-1-phosphate isomerase	-0.13	0.39	1.33	0.53	-0.19463919	1.254639193	0.12627803
E9PVY8	Microtubule-actin cross-linking factor 1	0.34	-0.14	1.81	0.67	-0.22501382	1.565013824	0.1190407
F7CK47	Microtubule-associated protein	-0.33	-1.13	-1.07	-0.843333333	-1.41462353	-0.272043135	0.01043456
P27546	Microtubule-associated protein 4	-0.18	-0.93	-0.99	-0.7	-1.27385883	-0.126141167	0.02379199
Q61166	Microtubule-associated protein RP/EB family member 1	0.24	-0.53	0.17	-0.04	-0.60263778	0.522637776	0.87021932
Q8R001	Microtubule-associated protein RP/EB family member 2	0.02	-0.44	1.75	0.443333333	-0.54281573	1.429482393	0.32028533
A2A5Y6	Microtubule-associated protein	-0.73	-0.72	-1.13	-0.86	-1.35445503	-0.365544968	0.00474173
Q8K009	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	-0.16	-1.59	-0.61	-0.786666667	-1.50619416	-0.067139169	0.03636313
Q9CR62	Mitochondrial 2-oxoglutarate/malate carrier protein	1.26	1.26	-0.26	0.753333333	-0.0540042	1.560670867	0.06294849
Q8VCF0	Mitochondrial antiviral-signaling protein	-0.09	-0.57	-0.37	-0.343333333	-0.839761	0.153094337	0.14467767
Q9Z2Z6	Mitochondrial carnitine/acylcarnitine carrier protein	0.65	0.4	-0.15	0.3	-0.255612	0.855612003	0.24012887
Q791V5	Mitochondrial carrier homolog 2	1.64	0.84	0.24	0.906666667	0.20366806	1.609665274	0.01890737
Q9CRB8	Mitochondrial fission process protein 1	0.96	-0.18	-0.37	0.136666667	-0.57602371	0.849357044	0.66153567
P62075	Mitochondrial import inner membrane translocase subunit Tim13	-0.12	-0.71	-0.21	-0.346666667	-0.86711274	0.173779408	0.15778085
O35857	Mitochondrial import inner membrane translocase subunit TIM44	-0.26	0.37	0.21	0.106666667	-0.41715953	0.630492859	0.64233086
Q9WVA2	Mitochondrial import inner membrane translocase subunit Tim8 A	-0.41	-1.24	0.05	-0.533333333	-1.20912108	0.14245441	0.10350523
Q8CAQ8	Mitochondrial inner membrane protein	0.97	1.21	-0.08	0.7	0.00622662	1.393773384	0.04848384
Q9D6Y7	Mitochondrial peptide methionine sulfoxide reductase	0.05	-0.74	-0.45	-0.38	-0.93160133	0.17160133	0.1460166
Q9DC61	Mitochondrial-processing peptidase subunit alpha	0.46	0.52	0.17	0.383333333	-0.09966689	0.866333558	0.10192897
Q9CXT8	Mitochondrial-processing peptidase subunit beta	1.16	0.64	0.18	0.66	0.06821636	1.251783645	0.03375798
Q811U4	Mitofusin-1	2.33	0.35	0.64	1.106666667	0.17697865	2.03635468	0.02623762
P63085	Mitogen-activated protein kinase 1	0.84	0.4	1.32	0.853333333	0.27550337	1.431163301	0.01041514
P47811	Mitogen-activated protein kinase 14	0.61	0.52	1.52	0.883333333	0.26077889	1.505887774	0.01248806
D3Z3G6	Mitogen-activated protein kinase 3	0.79	0.69	2.12	1.2	0.44094159	1.959058406	0.00756894
P26041	Moesin	-0.19	-0.49	0.85	0.056666667	-0.64681768	0.760151011	0.8531828
Q8BKY8	mTERF domain-containing protein 3, mitochondrial	0.04	0.2	-0.12	0.04	-0.43740828	0.517408278	0.84737563
Q9DCL9	Multifunctional protein ADE2	0.25	-0.78	-0.23	-0.253333333	-0.85713267	0.350466003	0.35130128
A6H6E2	Multimerin-2	-0.87	-0.87	-0.02	-0.586666667	-1.17865872	0.005325382	0.05156872
Q9Z2L6	Multiple inositol polyphosphate phosphatase 1	-0.61	-0.3	-0.55	-0.486666667	-0.96492882	-0.008404517	0.04707584
P28665	Murinoglobulin-1	-1.42	-0.93	-1.02	-1.123333333	-1.62540571	-0.621260961	0.00124919
A2AMM0	Muscle-related coiled-coil protein	0.09	-0.76	2.24	0.523333333	-0.73145167	1.778118336	0.35398482
E9PZ54	Myocardial zonula adherens protein	-1.6	-0.71	-0.43	-0.913333333	-1.56589146	-0.260775205	0.01327368

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
P04247	Myoglobin	-0.49	-1.38	-2.87	-1.58	-2.59815175	-0.561848254	0.00826686
Q62234	Myomesin-1	0.46	-0.14	0.35	0.223333333	-0.29765941	0.744326072	0.34164642
P09542	Myosin light chain 3	-0.36	-0.72	-0.84	-0.64	-1.13886824	-0.141131764	0.01933234
B1B1A8	Myosin light chain kinase, smooth muscle	-0.59	-1.32	-0.94	-0.95	-1.48780486	-0.41219514	0.00438595
Q9QVP4	Myosin regulatory light chain 2, atrial isoform	-0.52	-0.78	-0.72	-0.673333333	-1.1465093	-0.20015737	0.01232655
Q02566	Myosin-6	0.41	0.86	1.11	0.793333333	0.25949518	1.327171483	0.01011844
Q3UIK0	Myosin-binding protein C, cardiac-type	0.67	-0.11	0.81	0.456666667	-0.13767687	1.051010202	0.11121645
Q9JJW5	Myozenin-2	0.83	-0.93	0.28	0.06	-0.76151639	0.881516386	0.86671475
Q64191	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	0.57	-0.62	-0.55	-0.2	-0.8835221	0.483522096	0.50831904
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	-1.96	-2.15	-1.69	-1.933333333	-2.42705861	-1.439608062	4.46E-05
Q99LD8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	-0.44	-1.02	-0.46	-0.64	-1.1644598	-0.115540199	0.02375332
Q9JHL1	Na(+)/H(+) exchange regulatory cofactor NHE-RF2	-0.29	-0.24	0.4	-0.043333333	-0.58888076	0.502214098	0.85519698
Q9D997	N-acetyl-D-glucosamine kinase	0.35	0.6	0.47	0.473333333	0.00190521	0.944761455	0.04931133
Q8C5H8	NAD kinase domain-containing protein 1	0.45	0.53	0.81	0.596666667	0.11325407	1.080079264	0.02268029
Q61941	NAD(P) transhydrogenase, mitochondrial	1.14	0.29	-0.35	0.36	-0.36898654	1.088986539	0.2785958
Q64669	NAD(P)H dehydrogenase [quinone] 1	0.39	0.82	1.08	0.763333333	0.23184657	1.294820094	0.011824
Q8K4Z3	NAD(P)H-hydrate epimerase	1.21	0.46	0.95	0.873333333	0.32935351	1.417313158	0.00702979
Q8VDQ8	NAD-dependent protein deacetylase sirtuin-2	-0.02	0.69	0.92	0.53	-0.06163932	1.121639322	0.07160305
Q8K2C6	NAD-dependent protein deacylase sirtuin-5, mitochondrial	0.88	-0.12	0.24	0.333333333	-0.2661605	0.932827168	0.22784069
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	0.87	1.58	0.72	1.056666667	0.47918165	1.634151688	0.00366534
G5E814	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	1.13	0.66	-0.52	0.423333333	-0.36707881	1.213745474	0.24355858
Q7TMF3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	0.41	0.57	0.32	0.433333333	-0.03833626	0.905002922	0.06615406
Q9ERS2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	0.65	1.2	0.16	0.67	0.06381671	1.276183286	0.03491859
Q62425	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	0.78	0.62	-0.48	0.306666667	-0.38703833	1.000371663	0.32781644
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	-0.63	-1.05	-1.21	-0.963333333	-1.47756172	-0.449104942	0.00324586
Q9Z1P6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	0.51	-0.01	-1.66	-0.386666667	-1.3583343	0.585000971	0.37508929
Q9DCJ5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	0.92	0.74	-0.46	0.4	-0.33058577	1.130585774	0.23428046
Q9DC69	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	0.7	1.06	-0.15	0.536666667	-0.12145138	1.194784714	0.09453616
Q9DCS9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	0.59	0.58	0.79	0.653333333	0.18287232	1.123794349	0.0137422
O09111	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	0.36	0.2	-0.06	0.166666667	-0.32213335	0.655466679	0.4435757
Q9CPU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial	0.73	1.5	0.22	0.816666667	0.14603755	1.487295783	0.02395415
Q9CQZ6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	0.39	-0.07	-0.27	0.016666667	-0.51111159	0.544444927	0.94209801
Q9CQC7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	0.74	0.82	0.07	0.543333333	-0.01337057	1.10003724	0.05430202
Q3UIU2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	1.11	0.9	0.16	0.723333333	0.12741137	1.319255293	0.02427043
Q9D6J5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	0.27	0.71	-0.71	0.09	-0.62705724	0.807057236	0.77350299
Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	0.54	0.9	1.1	0.846666667	0.33755654	1.355776798	0.00592306
Q9CQ54	NADH dehydrogenase [ubiquinone] 1 subunit C2	0.34	0.73	-0.16	0.303333333	-0.26820595	0.874872614	0.24742805
Q91YT0	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	0.63	0.66	0.04	0.443333333	-0.08858173	0.975248392	0.08883133
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	-0.45	-0.63	-1.37	-0.816666667	-1.4071662	-0.226167129	0.013994
Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	1.03	1.21	0.56	0.933333333	0.40658084	1.460085828	0.00431848
Q9DCT2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	0.39	0.29	-0.72	-0.013333333	-0.66754699	0.640880328	0.96260692
E9QPX3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	-1.1	-0.62	-2	-1.24	-1.94197206	-0.53802794	0.0043858

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q99LY9	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	0.29	0.15	-0.62	-0.06	-0.65163932	0.531639322	0.81591551
P52503	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	-0.95	-0.73	-0.65	-0.776666667	-1.25319963	-0.300133703	0.00653575
Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	0.68	0.83	1.56	1.023333333	0.44064671	1.606019961	0.00451612
Q8K3J1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	0.6	0.4	-0.14	0.286666667	-0.25809753	0.831430859	0.25106917
F2Z456	NADH-cytochrome b5 reductase 3	0.68	0.79	-0.07	0.466666667	-0.1147484	1.048081736	0.098815
Q91VD9	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	0.58	0.54	-0.43	0.23	-0.40211363	0.862113626	0.41504526
P06801	NADP-dependent malic enzyme	1.23	0.95	0.52	0.9	0.36506098	1.434939022	0.00559447
Q8BMF3	NADP-dependent malic enzyme, mitochondrial	1	0.6	0.92	0.84	0.35127764	1.328722358	0.00503178
Q61578	NADPH:adrenodoxin oxidoreductase, mitochondrial	0.56	0.25	0.73	0.513333333	0.01627531	1.010391359	0.04469375
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	-0.74	-1.29	-1.31	-1.113333333	-1.63574472	-0.590921947	0.001633
P05125	Natriuretic peptides A	-2.12	-0.8	1.68	-0.413333333	-1.94055849	1.113891821	0.5396591
Q8C878	NEDD8-activating enzyme E1 catalytic subunit	-0.12	-0.4	-0.74	-0.42	-0.93790567	0.09790567	0.09601657
Q8VBW6	NEDD8-activating enzyme E1 regulatory subunit	-0.04	-0.36	-0.9	-0.433333333	-0.99981992	0.133153252	0.11252827
Q9CQ45	Neudesin	-1.34	-1.52	0.19	-0.89	-1.73616419	-0.043835811	0.04187652
Q9QZ23	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	-1	-1.55	-1.19	-1.246666667	-1.75437705	-0.738956283	0.00073969
Q99KQ4	Nicotinamide phosphoribosyltransferase	0.64	0.55	1	0.73	0.2343949	1.225605096	0.01054044
Q8CC86	Nicotinate phosphoribosyltransferase	0.35	-1.15	0.63	-0.056666667	-0.91393799	0.800604659	0.8792433
P10493	Nidogen-1	0.56	0.09	0.13	0.26	-0.24199677	0.761996771	0.25788413
O88322	Nidogen-2	0.9	0.22	0.24	0.453333333	-0.09310041	0.999767079	0.09001982
Q9EQ80	NIF3-like protein 1	-0.52	0.5	-0.07	-0.03	-0.63175294	0.571752939	0.908737
P32020	Non-specific lipid-transfer protein	-0.64	-1.18	-1.37	-1.063333333	-1.60647525	-0.520191415	0.00257683
Q9CZ44	NSFL1 cofactor p47	-0.5	-1.12	-1.02	-0.88	-1.40576082	-0.354239177	0.00573875
P60670	Nuclear protein localization protein 4 homolog	0.72	0.55	0.76	0.676666667	0.20717475	1.146158584	0.01163778
P61971	Nuclear transport factor 2	0.54	0.08	0.09	0.236666667	-0.26597235	0.739305686	0.29964235
P62960	Nuclease-sensitive element-binding protein 1	-1.03	-1.63	-1.5	-1.386666667	-1.90634645	-0.866986887	0.00045757
Q02819	Nucleobindin-1	-0.09	-0.22	-0.15	-0.153333333	-0.61782689	0.311160223	0.45759251
Q9D1X0	Nucleolar protein 3	-0.22	-1.21	-0.66	-0.696666667	-1.29115387	-0.102179465	0.02790785
P09405	Nucleolin	-0.37	0.2	1.75	0.526666667	-0.42127461	1.474607944	0.22816546
Q61937	Nucleophosmin	0.15	-0.27	0.12	-1.60E-17	-0.49457016	0.494570158	1
Q9WV85	Nucleoside diphosphate kinase 3	-2.28	-0.2	-0.47	-0.983333333	-1.9537111	-0.012955569	0.04776187
E9PZF0	Nucleoside diphosphate kinase	-0.7	-0.57	-0.89	-0.72	-1.19758712	-0.242412879	0.00946783
P11930	Nucleoside diphosphate-linked moiety X motif 19, mitochondrial	0.74	0.59	0.32	0.55	0.0609865	1.039013499	0.03269899
Q9CR24	Nucleoside diphosphate-linked moiety X motif 8, mitochondrial	1.16	0.53	0.87	0.853333333	0.33376312	1.37290355	0.00629626
E9PW66	Nucleosome assembly protein 1-like 1	0.43	0.4	1.19	0.673333333	0.1010972	1.245569467	0.02746433
Q78ZA7	Nucleosome assembly protein 1-like 4	-0.24	-0.47	-0.29	-0.333333333	-0.80415725	0.13749058	0.13681812
Q922B1	O-acetyl-ADP-ribose deacetylase MACROD1	0.33	-0.64	-0.14	-0.15	-0.73932535	0.439325349	0.56340572
Q9CZ30	Obg-like ATPase 1	-0.28	-0.71	-0.64	-0.543333333	-1.03694328	-0.049723386	0.0354597
Q9CRD0	OCIA domain-containing protein 1	-0.83	-0.24	-1.2	-0.756666667	-1.34557325	-0.167760087	0.01920878
Q9D8S4	Oligoribonuclease, mitochondrial	-0.21	-1.04	-1.27	-0.84	-1.46477572	-0.215224275	0.01583249
Q9JHW2	Omega-amidase NIT2	0.51	0.12	-0.03	0.2	-0.30752346	0.707523459	0.37947504
Q99PG2	Opioid growth factor receptor	-0.3	-1.09	1.98	0.196666667	-1.09178614	1.485119471	0.72675618
P29758	Ornithine aminotransferase, mitochondrial	0.19	-0.01	0.15	0.11	-0.35874354	0.578743537	0.59350921

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q62422	Osteoclast-stimulating factor 1	NA	-0.33	-0.57	-0.45	-1.0995312	0.199531197	0.13924769
Q4KMM3	Oxidation resistance protein 1	0.26	-0.66	-0.58	-0.326666667	-0.92767804	0.274344706	0.23734154
Q8VE38	Oxidoreductase NAD-binding domain-containing protein 1	0.37	-0.11	0.41	0.223333333	-0.28756288	0.734229545	0.3328514
Q3B7Z2	Oxysterol-binding protein 1	0.38	-0.28	0.86	0.32	-0.31233875	0.95233875	0.26792075
Q3UVT7	Palmdelphin	-0.29	-0.81	-0.99	-0.696666667	-1.23385366	-0.159479674	0.01847093
O88531	Palmitoyl-protein thioesterase 1	-0.32	0.19	0.21	0.026666667	-0.48783843	0.541171766	0.90514161
Q80YV4	Pantothenate kinase 4	-0.4	0.08	0.86	0.18	-0.48601488	0.846014875	0.54021058
Q9Z0P4	Paralemmin-1	-0.89	-1.19	0.42	-0.553333333	-1.34748209	0.240815422	0.14215783
Q99JF8	PC4 and SFRS1-interacting protein	0.43	-1	0.28	-0.096666667	-0.84831359	0.65498026	0.76811547
O70400	PDZ and LIM domain protein 1	-0.34	-0.87	-0.38	-0.53	-1.0427686	-0.017231399	0.0445623
Q8CI51	PDZ and LIM domain protein 5	-0.86	-0.73	1.44	-0.05	-1.12875134	1.028751341	0.91512108
A3KG59	Peptidase M20 domain-containing protein 2	-0.33	-0.37	-0.76	-0.486666667	-0.98211858	0.008785242	0.05314064
P97467	Peptidyl-glycine alpha-amidating monooxygenase	-0.2	-0.34	0.26	-0.093333333	-0.61241023	0.425743564	0.68116414
P17742	Peptidyl-prolyl cis-trans isomerase A	-0.4	-0.94	-0.15	-0.496666667	-1.04998552	0.056652183	0.07115945
P24369	Peptidyl-prolyl cis-trans isomerase B	-0.38	-0.55	-0.33	-0.42	-0.89001709	0.050017094	0.07215755
Q9CR16	Peptidyl-prolyl cis-trans isomerase D	-0.84	-0.65	-1.05	-0.846666667	-1.33260473	-0.360728604	0.00470027
Q99KR7	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	-0.55	-1.7	-0.5	-0.916666667	-1.60637983	-0.226953501	0.01664023
Q62446	Peptidyl-prolyl cis-trans isomerase FKBP3	-1.15	-1.81	-0.57	-1.176666667	-1.83430876	-0.519024578	0.00411012
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4	-0.64	-1.38	-0.85	-0.956666667	-1.50085577	-0.412477567	0.0044937
Q9CWW6	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	-1.6	-2.13	-0.71	-1.48	-2.19167781	-0.76832219	0.00186551
Q9DBG5	Perilipin-3	0.57	0.02	-0.33	0.086666667	-0.48824942	0.66158275	0.72997774
O88492	Perilipin-4	0.16	-0.51	-0.58	-0.31	-0.86530452	0.245304518	0.22618258
Q62009	Periostin	-0.4	-0.4	-0.4	-0.4	-0.86189193	0.061891932	0.07937831
P35700	Peroxiredoxin-1	-0.85	-0.98	-1.1	-0.976666667	-1.44809479	-0.505238545	0.00190417
Q61171	Peroxiredoxin-2	-0.8	-1.29	-1.1	-1.063333333	-1.56142113	-0.565245539	0.00161765
O08807	Peroxiredoxin-4	-0.51	-0.71	-0.69	-0.636666667	-1.10597666	-0.167356678	0.01522758
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	1.02	0.89	0.73	0.88	0.40528246	1.354717536	0.00342775
Q8VCI5	Peroxisomal biogenesis factor 19	-0.45	-1.54	-1.2	-1.063333333	-1.6881698	-0.438496862	0.00528672
P51660	Peroxisomal multifunctional enzyme type 2	0.6	0.18	0.43	0.403333333	-0.08529194	0.891958606	0.09132882
Q8C0C7	Phenylalanine--tRNA ligase alpha subunit	0.28	0.03	0.49	0.266666667	-0.22682793	0.760161264	0.23980164
Q9WUA2	Phenylalanine--tRNA ligase beta subunit	0.83	1.26	NA	1.045	0.36943026	1.72056974	0.00953747
Q8BVF2	Phosducin-like protein 3	3.16	-1.15	0.38	0.796666667	-0.91546497	2.5087983	0.30490783
G5E902	Phosphate carrier protein, mitochondrial	1.16	1.11	-0.01	0.753333333	0.07326267	1.433403995	0.03463011
P70296	Phosphatidylethanolamine-binding protein 1	-0.67	-1.51	-1.13	-1.103333333	-1.6637575	-0.542909162	0.00250152
Q7M6Y3	Phosphatidylinositol-binding clathrin assembly protein	0.18	-0.89	-0.1	-0.27	-0.89340738	0.353407376	0.3370195
Q9CYR6	Phosphoacetylglucosamine mutase	-2.47	-0.08	0.59	-0.653333333	-1.95195301	0.645286341	0.27047353
Q8K212	Phosphofurin acidic cluster sorting protein 1	0.06	-0.16	-0.15	-0.083333333	-0.55464068	0.387974009	0.68612145
Q9D0F9	Phosphoglucomutase-1	NA	-0.13	-0.37	-0.25	-0.8995312	0.399531197	0.37848752
Q7TSV4	Phosphoglucomutase-2	0.35	-0.39	-0.3	-0.113333333	-0.66665218	0.439985517	0.64041352
Q8BZF8	Phosphoglucomutase-like protein 5	0.53	0.15	0.19	0.29	-0.19802291	0.778022913	0.200843
P09411	Phosphoglycerate kinase 1	-0.47	-0.89	-0.7	-0.686666667	-1.17505886	-0.198274477	0.01300881
Q9DBJ1	Phosphoglycerate mutase 1	0.66	-0.58	-0.04	0.013333333	-0.64500095	0.671667612	0.96284076

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
O70250	Phosphoglycerate mutase 2	0.48	0.51	-0.03	0.32	-0.19553683	0.835536828	0.18385921
Q8CHP8	Phosphoglycolate phosphatase	0.8	0.18	0.29	0.423333333	-0.10168703	0.948353692	0.09756783
P27612	Phospholipase A-2-activating protein	0.05	-0.14	0.53	0.146666667	-0.38364049	0.676973823	0.53108452
Q9Z2M7	Phosphomannomutase 2	0.22	-0.18	-0.53	-0.163333333	-0.70511089	0.378444222	0.49599344
Q8VDG5	Phosphopantothenate--cysteine ligase	-0.61	0.36	0.1	-0.05	-0.64738504	0.547385041	0.84753281
B1AT82	Phosphoribosyl pyrophosphate synthase-associated protein 1	1	0.61	0.38	0.663333333	0.14442098	1.182245686	0.01962451
Q9DB26	Phytanoyl-CoA dioxygenase domain-containing protein 1	-0.5	-1.06	0.4	-0.386666667	-1.10931279	0.335979458	0.24396654
P26262	Plasma kallikrein	-0.45	-1.06	-0.42	-0.643333333	-1.17961873	-0.107047937	0.02544219
P97290	Plasma protease C1 inhibitor	-0.73	-0.59	-1.03	-0.783333333	-1.27538376	-0.291282903	0.00732034
Q9CY58	Plasminogen activator inhibitor 1 RNA-binding protein	-0.16	-1.1	-0.61	-0.623333333	-1.20572677	-0.040939896	0.03931979
P20918	Plasminogen	0.49	0.81	1.51	0.936666667	0.32981067	1.54352266	0.00848027
Q61233	Plastin-2	0.6	0.75	0.39	0.58	0.0983769	1.061623101	0.02505178
B1AX58	Plastin-3	-0.75	-0.86	-1	-0.87	-1.34146837	-0.398531625	0.00350939
B1ARB3	Platelet endothelial cell adhesion molecule	-0.79	-0.32	-0.57	-0.56	-1.05480033	-0.065199668	0.03193029
Q08857	Platelet glycoprotein 4	-0.07	-0.84	-0.29	-0.4	-0.9503614	0.150361397	0.12828642
P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	0.61	0.53	0.68	0.606666667	0.14131593	1.072017403	0.01806693
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	-0.72	-0.93	-0.87	-0.84	-1.30904708	-0.370952921	0.00409097
Q9JHK5	Pleckstrin	-0.1	-0.31	1.49	0.36	-0.514552	1.234552002	0.35988056
Q80TI1	Pleckstrin homology domain-containing family H member 1	-1.78	-0.59	0.61	-0.586666667	-1.59975468	0.426421347	0.21118346
Q9QXS1	Plectin	0.37	0.93	-0.57	0.243333333	-0.49180989	0.978476554	0.45642915
P60335	Poly(rC)-binding protein 1	-0.62	-0.43	0.11	-0.313333333	-0.85647525	0.229808585	0.21272238
Q61990	Poly(rC)-binding protein 2	-0.34	-0.36	-0.28	-0.326666667	-0.7896256	0.136292265	0.13793155
O54724	Polymerase I and transcript release factor	-0.36	0.12	1.4	0.386666667	-0.44073078	1.214064112	0.30297781
P61759	Prefoldin subunit 3	-1.5	-1.83	-1.1	-1.476666667	-2.01464793	-0.938685403	0.00038771
Q9WU28	Prefoldin subunit 5	-0.35	-1.07	-3.37	-1.596666667	-2.87333417	-0.319999163	0.0214887
P48678	Prelamin-A/C	-1.03	-0.1	0.59	-0.18	-0.94785776	0.587857758	0.59389624
Q8K411	Presequence protease, mitochondrial	0.63	0.31	0.5	0.48	0.00241288	0.957587121	0.0491406
Q6NSR8	Probable aminopeptidase NPEPL1	0.6	0.24	0.75	0.53	0.02754979	1.032450208	0.04144662
Q9WV35	Probable C->U-editing enzyme APOBEC-2	-0.13	-0.85	-0.6	-0.526666667	-1.06464793	0.011314597	0.05374713
Q7TNG8	Probable D-lactate dehydrogenase, mitochondrial	-0.6	-1	0.02	-0.526666667	-1.12975842	0.076425088	0.07740625
Q8BZA9	Probable fructose-2,6-bisphosphatase TIGAR	0.58	0.13	-0.13	0.193333333	-0.34220843	0.7288751	0.41852781
Q9CXJ1	Probable glutamate--tRNA ligase, mitochondrial	NA	0.38	1.05	0.715	-0.01160145	1.44160145	0.05267929
Q8VDC0	Probable leucine--tRNA ligase, mitochondrial	0.24	0.86	0.85	0.65	0.11601967	1.183980325	0.02399298
Q9WVQ5	Probable methylthioribulose-1-phosphate dehydratase	-0.49	-0.1	-0.52	-0.37	-0.86457016	0.124570158	0.11923205
A2APY7	Probable methyltransferase C20orf7 homolog, mitochondrial	0.6	-0.13	0.2	0.223333333	-0.31464793	0.761314597	0.35607997
P86049	Probable RNA-binding protein 46	0.56	0.96	1.08	0.866666667	0.36114763	1.372185706	0.00509585
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	0.69	1.22	1.44	1.116666667	0.57080625	1.662527079	0.00203845
Q9WU78	Programmed cell death 6-interacting protein	-0.44	-0.55	0.37	-0.206666667	-0.80421052	0.390877189	0.43736661
P12815	Programmed cell death protein 6	0.59	-0.28	-0.23	0.026666667	-0.56426657	0.617599902	0.9173516
P67778	Prohibitin	1.52	0.62	0.57	0.903333333	0.29008474	1.516581925	0.01053773
O35129	Prohibitin-2	1.03	0.99	0.18	0.733333333	0.14655743	1.320109241	0.02155135
Q9JK53	Prolargin	-0.03	0.22	-0.03	0.053333333	-0.42122427	0.527890939	0.79651286

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
P50580	Proliferation-associated protein 2G4	-0.4	-0.55	0.08	-0.29	-0.81440552	0.234405522	0.23010376
Q9Z2Y8	Proline synthase co-transcribed bacterial homolog protein	-0.5	-0.68	-0.56	-0.58	-1.04704006	-0.112959941	0.02211983
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	-0.58	0.24	-0.48	-0.273333333	-0.84542021	0.298753546	0.29315864
Q9QUR6	Prolyl endopeptidase	0.77	0.63	0.63	0.676666667	0.21076572	1.142567614	0.01123939
Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondrial	0.22	-0.28	-0.36	-0.14	-0.65922311	0.379223115	0.54112869
Q99MN9	Propionyl-CoA carboxylase beta chain, mitochondrial	0.37	0.07	0.14	0.193333333	-0.28349821	0.67016488	0.36668781
Q8BWM0	Prostaglandin E synthase 2	0.2	0.65	0.42	0.423333333	-0.06877494	0.915441611	0.08097519
Q9R0Q7	Prostaglandin E synthase 3	-0.66	0.17	0.31	-0.06	-0.66815237	0.548152371	0.82080756
Q8VDQ1	Prostaglandin reductase 2	0.07	-0.97	-0.77	-0.556666667	-1.17853487	0.065201532	0.07176756
Q9DB60	Prostamide/prostaglandin F synthase	1.15	1.07	0.56	0.926666667	0.40545542	1.44787791	0.0042446
P97371	Proteasome activator complex subunit 1	-0.61	-1.34	0.07	-0.626666667	-1.33124269	0.07790936	0.07320301
P97372	Proteasome activator complex subunit 2	-0.36	-1.18	-0.43	-0.656666667	-1.23197872	-0.081354616	0.03091074
Q9R1P4	Proteasome subunit alpha type-1	0.38	0.69	1.28	0.783333333	0.20683501	1.359831656	0.0151216
P49722	Proteasome subunit alpha type-2	1.21	0.33	0.54	0.693333333	0.11574974	1.270916931	0.02537514
O70435	Proteasome subunit alpha type-3	0.15	0.57	0.06	0.26	-0.24550027	0.765500269	0.26088395
Q9R1P0	Proteasome subunit alpha type-4	-0.06	-0.64	-0.27	-0.323333333	-0.83562059	0.18895392	0.17752802
Q9Z2U1	Proteasome subunit alpha type-5	-0.23	-0.36	-1.02	-0.536666667	-1.09835924	0.025025903	0.05828117
Q9QUM9	Proteasome subunit alpha type-6	0.42	-0.44	-0.13	-0.05	-0.6168717	0.516871703	0.83946041
Q9Z2U0	Proteasome subunit alpha type-7	-0.11	-0.4	-0.76	-0.423333333	-0.94650701	0.099840347	0.09661352
O09061	Proteasome subunit beta type-1	0.37	0.3	0.2	0.29	-0.17636913	0.756369134	0.18317491
P99026	Proteasome subunit beta type-4	1.23	0.81	1.06	1.033333333	0.54470806	1.521958606	0.00170311
O55234	Proteasome subunit beta type-5	0.89	0.86	0.96	0.903333333	0.43982135	1.366845315	0.00263928
Q6PDI5	Proteasome-associated protein ECM29 homolog	-0.38	0.26	0.52	0.133333333	-0.44587436	0.712541032	0.6004103
A2A841	Protein 4.1	-0.45	-0.35	0.39	-0.136666667	-0.71390517	0.440571838	0.59029898
Q07456	Protein AMBP	-1.48	-0.37	-1.35	-1.066666667	-1.71704004	-0.416293291	0.00633939
Q4VAA2	Protein CDV3	-1.12	-0.77	-0.92	-0.936666667	-1.41718523	-0.456148106	0.00263646
A2ADY9	Protein DDI1 homolog 2	-1.34	-0.66	-1.26	-1.086666667	-1.62702374	-0.546309595	0.00223416
P09103	Protein disulfide-isomerase	-0.3	-0.3	-0.46	-0.353333333	-0.82045465	0.113787985	0.11588529
P27773	Protein disulfide-isomerase A3	0.37	0.21	0.19	0.256666667	-0.21118535	0.724518679	0.23343954
P08003	Protein disulfide-isomerase A4	-0.37	-0.13	-0.63	-0.376666667	-0.87561098	0.122277644	0.11647611
Q99LX0	Protein DJ-1	-0.69	-1.02	-0.86	-0.856666667	-1.33504784	-0.378285493	0.00409217
Q9DCM0	Protein ETHE1, mitochondrial	0.62	-0.44	-0.58	-0.133333333	-0.81042561	0.543758947	0.65315271
Q61160	Protein FADD	-0.59	0.47	-0.75	-0.29	-0.97089335	0.390893355	0.34454889
Q8VE88	Protein FAM114A2	-0.82	0.31	-1.23	-0.58	-1.33860825	0.178608255	0.11267982
Q9CR98	Protein FAM136A	-0.78	-1.04	-0.38	-0.733333333	-1.25894976	-0.207716909	0.0134619
Q9D6U8	Protein FAM162A	-0.12	-0.38	-0.25	-0.25	-0.72219234	0.222192343	0.24846125
Q61239	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	-0.69	-1.28	-0.91	-0.96	-1.47376688	-0.446233119	0.00328939
O55091	Protein IMPACT	-0.61	-0.14	-0.2	-0.316666667	-0.81726276	0.183929422	0.17668113
Q5SW19	Protein KIAA0664	0.65	-0.08	0.59	0.386666667	-0.16726919	0.94060252	0.14154233
Q9WVE8	Protein kinase C and casein kinase substrate in neurons protein 2	-0.31	-0.79	-0.01	-0.37	-0.91906682	0.179066823	0.1536739
Q8K3C3	Protein LZIC	-0.71	-1.62	-1.23	-1.186666667	-1.76286865	-0.610464683	0.00196615
Q91VH6	Protein MEMO1	1.34	0.61	0.47	0.806666667	0.22564341	1.387689927	0.01375768

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q9CWG8	Protein midA homolog, mitochondrial	-0.28	0.49	0.19	0.133333333	-0.41356906	0.680235722	0.57955973
Q9QYG0	Protein NDRG2	-0.27	-0.93	-0.57	-0.59	-1.11489383	-0.065106167	0.0327737
O55126	Protein NipSnap homolog 2	0.43	0.73	1.24	0.8	0.24428554	1.35571446	0.01169958
A6H644	Protein phosphatase 1 regulatory subunit 12B	0.47	0.32	0.4	0.396666667	-0.06868407	0.862017403	0.08320094
Q8R4S0	Protein phosphatase 1 regulatory subunit 14C	-0.76	-1.21	-1.62	-1.196666667	-1.76119011	-0.632143225	0.00168132
Q99MR9	Protein phosphatase 1 regulatory subunit 3A	NA	-0.87	-0.86	-0.865	-1.50242124	-0.22757876	0.01642801
Q3UM45	Protein phosphatase 1 regulatory subunit 7	0.23	NA	-0.39	-0.08	-0.79447004	0.634470036	0.79100248
P49443	Protein phosphatase 1A	-0.2	-0.56	-0.31	-0.356666667	-0.83907718	0.125743844	0.12288287
Q8CGA0	Protein phosphatase 1F	0.3	-0.03	0.46	0.243333333	-0.25555392	0.742220589	0.28404216
Q9DCL8	Protein phosphatase inhibitor 2	-0.88	-1.63	-1.11	-1.206666667	-1.75200534	-0.661327989	0.00132846
Q6NVE9	Protein phosphatase PTC7 homolog	0.1	-0.76	0.42	-0.08	-0.73219451	0.572194512	0.77847881
Q7TSC1	Protein PRRC2A	-0.53	-1	-0.35	-0.626666667	-1.15341916	-0.099914172	0.0262975
Q3TLH4	Protein PRRC2C	-0.19	-1.19	-1.3	-0.893333333	-1.54624034	-0.240426322	0.01467006
Q8BIW1	Protein prune homolog	-0.1	-0.84	-0.34	-0.426666667	-0.96933669	0.11600336	0.10456975
Q52KR3	Protein prune homolog 2	0.63	0.42	-0.03	0.34	-0.18732861	0.867328608	0.16958246
Q9QYS9	Protein quaking	-0.83	-1.29	-0.35	-0.823333333	-1.40567789	-0.240988775	0.01268941
P08207	Protein S100-A10	-0.42	-1.03	0.09	-0.453333333	-1.07971684	0.173050169	0.1296401
P50543	Protein S100-A11	-1.33	-1.26	-0.51	-1.033333333	-1.60864538	-0.458021282	0.00403033
P31725	Protein S100-A9	-1.93	-0.04	0.25	-0.573333333	-1.57891948	0.432252814	0.21750696
Q9D1M0	Protein SEC13 homolog	-0.4	-1.01	0.82	-0.196666667	-1.03788237	0.644549036	0.5948661
Q9EQU5	Protein SET	-1.77	-0.55	-0.48	-0.933333333	-1.64952993	-0.21713674	0.01809608
Q91YM4	Protein TBRG4	0.94	0.28	0.28	0.5	-0.04406703	1.044067033	0.06608962
Q01405	Protein transport protein Sec23A	0.94	0.86	0.86	0.886666667	0.42346185	1.34987148	0.00290063
Q3UPL0	Protein transport protein Sec31A	0.67	1.03	0.49	0.73	0.22365575	1.236344247	0.01162199
Q3TZ89	Protein transport protein Sec31B	0.54	0.65	0.37	0.52	0.04600258	0.993997425	0.03590476
P21981	Protein-glutamine gamma-glutamyltransferase 2	-0.01	0.59	1.04	0.54	-0.06936814	1.14936814	0.07403277
E0CYV0	Protein-L-isoaspartate O-methyltransferase	-0.2	-0.26	-0.3	-0.253333333	-0.7167839	0.210117231	0.23495591
P19221	Prothrombin	-0.48	-0.36	-0.51	-0.45	-0.91575836	0.015758362	0.05616808
Q9CZL5	Pterin-4-alpha-carbinolamine dehydratase 2	-0.2	-0.64	-0.6	-0.48	-0.97703894	0.017038935	0.05625462
P23492	Purine nucleoside phosphorylase	0.07	0.28	-0.09	0.086666667	-0.39597982	0.569313149	0.68156241
Q6W8Q3	Purkinje cell protein 4-like protein 1	0.93	-2.2	-0.19	-0.486666667	-1.76936242	0.796029087	0.39643958
Q11011	Puromycin-sensitive aminopeptidase	0.09	-0.04	-0.18	-0.043333333	-0.51632879	0.429662119	0.83336195
O88696	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial	0.26	-0.17	0.12	0.07	-0.42064069	0.560640692	0.74380056
Q6P8M1	Putative deoxyribonuclease TATDN1	-0.06	0.08	0.82	0.28	-0.30364661	0.863646607	0.29134783
O88851	Putative hydrolase RBBP9	-0.46	-0.96	-0.97	-0.796666667	-1.30828669	-0.285046641	0.00813423
Q3UIZ8	Putative myosin light chain kinase 3	-0.22	-0.28	0.01	-0.163333333	-0.63944797	0.3127813	0.44092205
Q3TCN2	Putative phospholipase B-like 2	1.3	1.88	1.09	1.423333333	0.86775549	1.978911179	0.00057964
Q8CAK1	Putative transferase CAF17 homolog, mitochondrial	1.03	0.83	0.6	0.82	0.33040474	1.30959526	0.00572042
Q8K183	Pyridoxal kinase	0.77	-0.03	-0.01	0.243333333	-0.33272042	0.81938709	0.34825707
E9QPD7	Pyruvate carboxylase	0.73	0.74	1.33	0.933333333	0.4036707	1.462995962	0.00444043
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	0.58	0.88	0.67	0.71	0.23372596	1.186274041	0.00997376
Q9D051	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	0.34	0.12	0.21	0.223333333	-0.24603731	0.692703973	0.29498715

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q7TSQ8	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	1.07	1.48	1.89	1.48	0.92408068	2.035919317	0.00046368
Q8BKZ9	Pyruvate dehydrogenase protein X component, mitochondrial	-0.32	-0.67	-0.5	-0.496666667	-0.97706673	-0.0162666	0.04452333
P52480	Pyruvate kinase isozymes M1/M2	0.29	0.04	-0.59	-0.086666667	-0.66148372	0.488150382	0.72993346
P47199	Quinone oxidoreductase	0.37	-0.43	0.11	0.016666667	-0.53844986	0.571783193	0.9449438
P50396	Rab GDP dissociation inhibitor alpha	-0.34	-0.47	-0.35	-0.386666667	-0.85177266	0.078439322	0.0894831
Q61598	Rab GDP dissociation inhibitor beta	0.32	0.05	0.12	0.163333333	-0.31050392	0.637170585	0.4388301
P31750	RAC-alpha serine/threonine-protein kinase	-0.94	0.29	0.26	-0.13	-0.83258007	0.572580065	0.67254996
P26043	Radixin	-0.27	-1.29	-0.67	-0.743333333	-1.34642509	-0.140241579	0.02281121
Q9CQ22	Ragulator complex protein LAMTOR1	1.09	1.22	1.33	1.213333333	0.74263035	1.684036312	0.00055938
P34022	Ran-specific GTPase-activating protein	-1.37	-1.18	-1.34	-1.296666667	-1.76494439	-0.828388942	0.00036819
P97855	Ras GTPase-activating protein-binding protein 1	0.2	-0.26	0.22	0.053333333	-0.45196041	0.558627082	0.80858432
P97379	Ras GTPase-activating protein-binding protein 2	-0.02	-0.1	0.14	0.006666667	-0.46433859	0.477671924	0.97402491
Q9JKF1	Ras GTPase-activating-like protein IQGAP1	0.84	0.77	0.01	0.54	-0.03791207	1.117912067	0.06266889
Q01730	Ras suppressor protein 1	0.61	0.78	2.76	1.383333333	0.37007675	2.396589922	0.01481186
Q3TLP8	Ras-related C3 botulinum toxin substrate 3	-0.28	0.46	0.16	0.113333333	-0.42723442	0.653901083	0.63269035
Q99K70	Ras-related GTP-binding protein C	1.2	1.23	0.79	1.073333333	0.57558856	1.571078108	0.00153107
P61027	Ras-related protein Rab-10	1.33	0.63	0.15	0.703333333	0.06004527	1.346621395	0.0363593
P46638	Ras-related protein Rab-11B	0.45	-0.41	-0.55	-0.17	-0.78665858	0.446658578	0.53236682
Q91V41	Ras-related protein Rab-14	0.18	0.76	0.75	0.563333333	0.03787941	1.088787261	0.03908068
Q9D1G1	Ras-related protein Rab-1B	-0.14	0.02	0.37	0.083333333	-0.41873904	0.585405706	0.70420388
P35282	Ras-related protein Rab-21	0.25	-0.3	-0.21	-0.086666667	-0.59939826	0.426064924	0.69909087
P53994	Ras-related protein Rab-2A	0.55	1.16	0.47	0.726666667	0.1840491	1.269284236	0.01610486
Q8C266	Ras-related protein Rab-5C	0.76	0.55	0.61	0.64	0.17095292	1.109047079	0.01484827
P51150	Ras-related protein Rab-7a	0.55	1.48	0.97	1	0.41963034	1.580369658	0.00496981
P63321	Ras-related protein Ral-A	-0.35	0.48	0.93	0.353333333	-0.32000688	1.026673543	0.25226983
P62071	Ras-related protein R-Ras2	0.14	0.35	-0.49	-3.20E-17	-0.56757429	0.567574286	1
G3X8R0	Receptor expression-enhancing protein 5	1.23	1.25	3.17	1.883333333	0.92401919	2.842647479	0.00253912
Q9DCV4	Regulator of microtubule dynamics protein 1	-0.66	-1.07	-1.14	-0.956666667	-1.45828526	-0.455048073	0.00295711
Q9EPU0	Regulator of nonsense transcripts 1	0.14	1.36	0.97	0.823333333	0.1642644	1.482402269	0.021589
Q99P72	Reticulon-4	-0.15	0.37	-0.34	-0.04	-0.57875675	0.498756752	0.86453396
Q924D0	Reticulon-4-interacting protein 1, mitochondrial	0.34	0.4	0.71	0.483333333	-0.00225313	0.968919794	0.05080292
P24549	Retinal dehydrogenase 1	0.01	0.02	0.05	0.026666667	-0.43549225	0.48882558	0.89447139
Q00915	Retinol-binding protein 1	-1.21	-2.08	-0.78	-1.356666667	-2.03715577	-0.676177562	0.00233986
Q99PT1	Rho GDP-dissociation inhibitor 1	-0.44	NA	-0.1	-0.27	-0.93152191	0.391521908	0.35243348
Q61599	Rho GDP-dissociation inhibitor 2	-0.23	-0.51	-0.8	-0.513333333	-1.0228347	-0.003831962	0.04872621
F8VPK5	Rho-associated protein kinase 2	0.03	-0.3	-0.5	-0.256666667	-0.76077599	0.247442654	0.26527652
Q91VI7	Ribonuclease inhibitor	0.18	-0.32	-0.27	-0.136666667	-0.64314207	0.36980874	0.54082999
P52760	Ribonuclease UK114	-0.57	-0.58	-1.35	-0.833333333	-1.40546997	-0.261196698	0.01109454
Q99PL5	Ribosome-binding protein 1	0.19	-0.58	-0.54	-0.31	-0.8759671	0.255967099	0.23410516
Q9D6S7	Ribosome-recycling factor, mitochondrial	-0.79	-1.26	-1.08	-1.043333333	-1.53867032	-0.547996346	0.00174069
Q9JI75	Ribosyldihydronicotinamide dehydrogenase [quinone]	0.36	-0.43	0.01	-0.02	-0.57005098	0.530050977	0.93335472
P56959	RNA-binding protein FUS	1.14	-0.39	1.28	0.676666667	-0.16115831	1.514491643	0.09712111

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q920Q6	RNA-binding protein Musashi homolog 2	0.44	-0.33	1.5	0.536666667	-0.29638811	1.369721442	0.16989376
Q9WVB0	RNA-binding protein with multiple splicing	0.28	-0.43	-0.74	-0.296666667	-0.90413215	0.310798813	0.2834869
E9Q401	Ryanodine receptor 2	1.26	1.69	1.5	1.483333333	0.99366056	1.973006109	0.00021574
Q3THS6	S-adenosylmethionine synthase isoform type-2	-0.04	-0.08	-0.57	-0.23	-0.7427686	0.282768601	0.32129749
Q7TQ48	Sarcalumenin	-0.6	-0.69	0.41	-0.293333333	-0.94580421	0.359137546	0.32027248
O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	0.91	0.98	0.31	0.733333333	0.19429486	1.272371804	0.01504087
S4R1M2	Scaffold attachment factor B1	-0.22	-0.71	-0.7	-0.543333333	-1.05126794	-0.035398731	0.03940075
Q8VCA8	Secernin-2	1.01	0.47	0.7	0.726666667	0.22154195	1.231791381	0.01173639
Q3TMH2	Secernin-3	0.25	-0.12	-0.41	-0.093333333	-0.61835369	0.431687025	0.68453343
Q921H9	Sel1 repeat-containing protein 1	-1.67	-0.84	-0.34	-0.95	-1.63576728	-0.264232718	0.01389179
Q8BH69	Selenide, water dikinase 1	-1.02	-0.35	-0.09	-0.486666667	-1.07353959	0.100206258	0.09013436
P17563	Selenium-binding protein 1	0.19	0.05	0.08	0.106666667	-0.35856171	0.571895045	0.60183834
Q91XH5	Sepiapterin reductase	0.31	-0.1	0.14	0.116666667	-0.37067527	0.604008601	0.58626579
Q8C1B7	Septin-11	-0.25	-0.76	-0.78	-0.596666667	-1.11117177	-0.082161568	0.02907033
P42208	Septin-2	0.15	-0.03	0.38	0.166666667	-0.32055843	0.653891766	0.44217057
E9Q1G8	Septin-7	0.51	-0.11	0.66	0.353333333	-0.20183447	0.908501137	0.17439942
B1AQZ0	Septin-8	0.37	-1.04	-0.16	-0.276666667	-0.98527131	0.431937979	0.38362529
Q80UG5	Septin-9	0.19	-0.24	0.17	0.04	-0.45686709	0.536867093	0.85326726
P54797	Ser/Thr-rich protein T10 in DGCR region	0.26	0.01	0.11	0.126666667	-0.3448822	0.598215537	0.54260883
Q3U3G8	Serine hydrolase-like protein	1.64	0.71	0.96	1.103333333	0.51578174	1.690884925	0.00320574
Q9CZN7	Serine hydroxymethyltransferase	0.09	0.17	1.38	0.546666667	-0.16801799	1.261351322	0.11254487
Q9JIY5	Serine protease HTRA2, mitochondrial	1.19	-0.08	0.84	0.65	-0.02699418	1.326994177	0.05734873
P07759	Serine protease inhibitor A3K	-0.77	-0.24	-0.79	-0.6	-1.1184001	-0.081599896	0.02929374
P84104	Serine/arginine-rich splicing factor 3	0.04	-0.24	1.51	0.436666667	-0.40974419	1.283077521	0.25957501
Q6P9R2	Serine/threonine-protein kinase OSR1	-0.53	-0.85	-0.25	-0.543333333	-1.0577831	-0.028883564	0.04126138
Q8CIN4	Serine/threonine-protein kinase PAK 2	-0.79	-1.06	-0.66	-0.836666667	-1.32354109	-0.34979224	0.00503649
P83741	Serine/threonine-protein kinase WNK1	0.05	-0.34	0.88	0.196666667	-0.46240227	0.855735602	0.50024311
Q6P1F6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	-0.02	0.18	0.07	0.076666667	-0.39136784	0.544701175	0.70785638
Q6PD03	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform	0.33	-0.45	0.47	0.116666667	-0.47767687	0.711010202	0.65416623
Q76MZ3	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	0.26	-0.38	-0.09	-0.07	-0.59135686	0.451356862	0.75829671
P63328	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	0.48	0.59	0.05	0.373333333	-0.13627977	0.882946432	0.12576661
Q60676	Serine/threonine-protein phosphatase 5	0.44	-0.17	-0.83	-0.186666667	-0.85226826	0.478934922	0.52551864
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	1.08	0.52	0.3	0.633333333	0.08068368	1.185982986	0.03043793
Q9Z1Z2	Serine-threonine kinase receptor-associated protein	-0.79	-0.62	-0.47	-0.626666667	-1.10409482	-0.149238514	0.0175515
Q8C483	Serine--tRNA ligase, cytoplasmic	-0.04	0.3	0.6	0.286666667	-0.23459919	0.807932522	0.23242177
Q9JJL8	Serine--tRNA ligase, mitochondrial	-0.06	-0.06	0.01	-0.036666667	-0.49956411	0.426230774	0.85559205
Q921I1	Serotransferrin	-0.61	-0.42	-0.73	-0.586666667	-1.0633788	-0.10995453	0.0229538
F8WIV2	Serpin B6	0.21	-0.39	-0.03	-0.07	-0.58503965	0.445039645	0.75544808
P19324	Serpin H1	-0.38	-0.15	NA	-0.265	-0.91354983	0.383549826	0.35193943
P07724	Serum albumin	-1.16	-1.39	-1.04	-1.196666667	-1.67765891	-0.715674421	0.00068616
Q63918	Serum deprivation-response protein	-0.25	-0.14	0.16	-0.076666667	-0.56552491	0.412191579	0.71963986
P97443	SET and MYND domain-containing protein 1	-0.62	0.14	0.25	-0.076666667	-0.66071957	0.507386236	0.76349366

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
H3BKH6	S-formylglutathione hydrolase	1.23	0.7	0.74	0.89	0.3772314	1.402768601	0.00479143
Q9WUZ7	SH3 domain-binding glutamic acid-rich protein	-0.85	-1.74	-2.01	-1.533333333	-2.18379424	-0.882872426	0.00093257
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	-0.96	-1.22	-1.08	-1.086666667	-1.5588791	-0.614454229	0.0010678
Q8R550	SH3 domain-containing kinase-binding protein 1	-0.83	-1.17	0.47	-0.51	-1.30992262	0.28992262	0.17374481
Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	1	0.32	0.42	0.58	0.04140178	1.11859822	0.03845051
Q9CYR0	Single-stranded DNA-binding protein, mitochondrial	-0.84	-1.01	-0.52	-0.79	-1.28858285	-0.29141715	0.00748744
Q8BJU0	Small glutamine-rich tetratricopeptide repeat-containing protein alpha	-0.29	-0.98	-0.87	-0.713333333	-1.25332152	-0.173345145	0.01707856
Q9DC77	Small muscular protein	-0.89	-2.48	-0.88	-1.416666667	-2.25101891	-0.582314426	0.00534652
Q9CQ65	S-methyl-5-thioadenosine phosphorylase	0.35	0.06	0.27	0.226666667	-0.24884971	0.702183046	0.29418683
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	0.55	0.57	0.54	0.553333333	0.09129762	1.015369044	0.02561302
P14094	Sodium/potassium-transporting ATPase subunit beta-1	-0.47	-0.19	0.07	-0.196666667	-0.70150953	0.308176199	0.38463439
B9EKP8	Sorbin and SH3 domain-containing protein 2	0.14	-0.48	0.38	0.013333333	-0.55715907	0.583825739	0.95712551
Q64442	Sorbitol dehydrogenase	0.05	-0.37	0.04	-0.093333333	-0.58935945	0.402692785	0.66741612
Q6P069	Sorcin	-0.35	-0.42	-0.59	-0.453333333	-0.92451986	0.017853198	0.05695819
Q8BGH2	Sorting and assembly machinery component 50 homolog	1.25	0.93	-0.03	0.716666667	0.03404749	1.39928584	0.04215283
Q9WV80	Sorting nexin-1	-1.09	-0.76	-1.06	-0.97	-1.45197759	-0.488022405	0.00222512
Q9CWK8	Sorting nexin-2	-0.17	-1.28	-0.96	-0.803333333	-1.43514667	-0.171519997	0.02006892
O70492	Sorting nexin-3	-0.78	-0.66	-0.21	-0.55	-1.06454198	-0.035458018	0.03950543
Q9D8U8	Sorting nexin-5	-0.88	0.4	-0.17	-0.216666667	-0.88559577	0.452262436	0.46574001
Q6P8X1	Sorting nexin-6	1.01	-0.26	-0.41	0.113333333	-0.63489742	0.861564082	0.72874752
Q62261	Spectrin beta chain, brain 1	0.81	0.34	0.95	0.7	0.17897084	1.221029162	0.01588292
Q9WTX5	S-phase kinase-associated protein 1	-0.08	-0.99	-0.59	-0.553333333	-1.12933767	0.022671006	0.05724718
Q9Z1N5	Spliceosome RNA helicase Ddx39b	0.43	0.13	0.78	0.446666667	-0.07639818	0.969731516	0.08275969
Q64213	Splicing factor 1	-1.02	-1.41	-0.81	-1.08	-1.59586802	-0.564131983	0.00179906
Q8K4Z5	Splicing factor 3A subunit 1	-0.97	-1.1	-0.45	-0.84	-1.36980592	-0.310194075	0.00746499
Q9D554	Splicing factor 3A subunit 3	-0.64	-0.47	0.14	-0.323333333	-0.87932092	0.232654253	0.20947215
Q91WK1	SPRY domain-containing protein 4	0.08	0.05	-0.22	-0.03	-0.50842084	0.448420842	0.88539083
Q60598	Src substrate cortactin	-0.79	-1.07	0.13	-0.576666667	-1.23827896	0.084945629	0.07785451
Q78PY7	Staphylococcal nuclease domain-containing protein 1	2.02	1.62	2.41	2.016666667	1.46696081	2.566372527	6.69E-05
Q9Z1W9	STE20/SPS1-related proline-alanine-rich protein kinase	-0.44	-0.54	-0.27	-0.416666667	-0.88990279	0.056569452	0.07550674
O54988	STE20-like serine/threonine-protein kinase	-0.11	-0.89	-0.54	-0.513333333	-1.06127572	0.034609051	0.06214345
P38647	Stress-70 protein, mitochondrial	-0.36	-0.83	-0.53	-0.573333333	-1.06890014	-0.077766529	0.02934121
Q60864	Stress-induced-phosphoprotein 1	-0.72	-0.86	-0.48	-0.686666667	-1.17078537	-0.202547963	0.01250781
E9QQ25	Striated muscle-specific serine/threonine-protein kinase	1.32	0.22	1.86	1.133333333	0.35164873	1.915017938	0.01132856
Q9CXV1	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial	0.26	0.05	-0.54	-0.076666667	-0.63459641	0.481263078	0.75285546
Q8K2B3	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0.93	0.52	0.34	0.596666667	0.08149808	1.111835257	0.02921627
Q9CQA3	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1.36	0.84	-0.15	0.683333333	-0.05717261	1.42383928	0.06523065
Q9CZB0	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	0.64	1.05	-0.47	0.406666667	-0.34528317	1.158616503	0.23944864
Q8BWF0	Succinate-semialdehyde dehydrogenase, mitochondrial	0.36	-0.04	-0.06	0.086666667	-0.40861285	0.581946183	0.68915684
Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial	0.61	0.18	0.8	0.53	0.00962686	1.050373143	0.04692659
Q9Z2I9	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	-0.26	-0.95	-0.94	-0.716666667	-1.26657962	-0.16675371	0.01809277
Q9Z2I8	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	-0.98	-0.5	-0.31	-0.596666667	-1.12697382	-0.06635951	0.03265261

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q9D0K2	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	0.6	-0.27	0.22	0.183333333	-0.38380612	0.75047279	0.46658706
Q8R086	Sulfite oxidase, mitochondrial	-0.17	-0.47	-0.85	-0.496666667	-1.02530719	0.031973852	0.06157176
Q3UW66	Sulfurtransferase	-0.01	0.96	0.49	0.48	-0.10932535	1.069325349	0.09485214
Q9Z1F9	SUMO-activating enzyme subunit 2	-0.58	-0.1	0.22	-0.153333333	-0.70618898	0.399522312	0.52996431
P08228	Superoxide dismutase [Cu-Zn]	0.36	-0.69	-0.84	-0.39	-1.06581582	0.285815825	0.21258894
P09671	Superoxide dismutase [Mn], mitochondrial	-0.5	-0.68	-0.82	-0.666666667	-1.14415444	-0.189178895	0.0134188
Q8K4L3	Supervillin	0.34	0.01	1.29	0.546666667	-0.13507623	1.228409559	0.09907911
Q9CX34	Suppressor of G2 allele of SKP1 homolog	-0.56	-0.46	-0.34	-0.453333333	-0.92264332	0.015976656	0.05620853
Q9D5V6	Synapse-associated protein 1	0.56	-1.62	-0.45	-0.503333333	-1.44724213	0.440575466	0.24541852
Q64332	Synapsin-2	0.11	-0.58	0.1	-0.123333333	-0.67324629	0.426579623	0.6096204
Q62465	Synaptic vesicle membrane protein VAT-1 homolog	0.89	0.78	1.84	1.17	0.53223748	1.807762516	0.00361667
Q9CQW1	Synaptobrevin homolog YKT6	-0.36	0.66	0.89	0.396666667	-0.28549364	1.078826976	0.20951496
B2RQK7	Synaptopodin 2-like protein	1.4	-0.46	-0.09	0.283333333	-0.59145733	1.158123996	0.4657582
E9Q1U2	Synaptopodin-2	-0.27	-0.1	-0.6	-0.323333333	-0.8234743	0.176807637	0.16859861
P26039	Talin-1	-0.2	-0.51	0.23	-0.16	-0.70033951	0.380339512	0.50342323
E9PUM4	Talin-2	-0.02	0.3	0.75	0.343333333	-0.20304832	0.889714982	0.17919337
Q3UDC3	Target of Myb protein 1	-0.29	-0.11	0.12	-0.093333333	-0.58055843	0.393891766	0.66186274
P11983	T-complex protein 1 subunit alpha	-0.13	0.45	0.6	0.306666667	-0.23919375	0.852527079	0.22356075
P80314	T-complex protein 1 subunit beta	0.2	0.35	0.91	0.486666667	-0.05469039	1.028023727	0.07082535
P80315	T-complex protein 1 subunit delta	0.57	0.84	1.11	0.84	0.33517593	1.34482407	0.00590712
P80316	T-complex protein 1 subunit epsilon	0.11	0.38	0.99	0.493333333	-0.08029397	1.066960633	0.08103687
P80313	T-complex protein 1 subunit eta	0.79	0.85	0.69	0.776666667	0.31076572	1.242567614	0.00585382
P80318	T-complex protein 1 subunit gamma	0.93	1.07	1.2	1.066666667	0.59367121	1.539662119	0.00119554
P42932	T-complex protein 1 subunit theta	-0.21	-0.12	0.31	-0.006666667	-0.51392832	0.500594982	0.97588074
Q8C1A5	Thimet oligopeptidase	0.05	-0.26	-0.37	-0.193333333	-0.68358709	0.296920421	0.37915291
P10639	Thioredoxin	-0.81	-1.58	0.18	-0.736666667	-1.5469254	0.073592071	0.06837241
Q9CQU0	Thioredoxin domain-containing protein 12	0.77	-1.18	-0.6	-0.336666667	-1.22219477	0.548861434	0.39552509
Q9CQM5	Thioredoxin domain-containing protein 17	0.06	-1.26	-1.31	-0.836666667	-1.58299278	-0.090340552	0.03310604
Q91W90	Thioredoxin domain-containing protein 5	-0.21	-0.66	-0.34	-0.403333333	-0.8971739	0.090507235	0.09412185
Q9JMH6	Thioredoxin reductase 1, cytoplasmic	0.1	-0.15	-0.51	-0.186666667	-0.7032699	0.329936566	0.41812454
Q9JLT4	Thioredoxin reductase 2, mitochondrial	0.58	0.04	0.08	0.233333333	-0.28133772	0.748004386	0.31651416
P97493	Thioredoxin, mitochondrial	-0.09	-1.66	-0.97	-0.906666667	-1.65891929	-0.154414043	0.02496804
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	-0.71	-1.08	-0.01	-0.6	-1.21762721	0.017627207	0.05515377
Q8CDN6	Thioredoxin-like protein 1	-0.75	-1.11	-0.81	-0.89	-1.37427548	-0.405724524	0.0035838
P52196	Thiosulfate sulfurtransferase	0.23	-0.61	0.57	0.063333333	-0.58734635	0.714013016	0.82316526
Q9D0R2	Threonine--tRNA ligase, cytoplasmic	0.65	0.84	0.68	0.723333333	0.25505561	1.191611058	0.00844944
Q3UQ84	Threonine--tRNA ligase, mitochondrial	1.41	0.92	1.03	1.12	0.61902496	1.620975038	0.00125464
Q80YQ1	Thrombospondin-1	-0.87	-1.43	2	-0.1	-1.56321339	1.363213393	0.87518922
Q8BH58	TIP41-like protein	-1.09	-0.33	-0.53	-0.65	-1.19927416	-0.10072584	0.02685584
A2ASS6	Titin	1.52	0.78	1.59	1.296666667	0.7239333	1.869400033	0.00116969
Q9QZ06	Toll-interacting protein	0.25	-0.08	0.35	0.173333333	-0.31877494	0.665441611	0.42937545
Q5SRX1	TOM1-like protein 2	-0.55	-0.39	-0.29	-0.41	-0.88237316	0.062373161	0.07884358

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q9DBB8	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	0.62	0.14	-0.05	0.236666667	-0.29364049	0.766973823	0.32356415
Q9DCS3	Trans-2-enoyl-CoA reductase, mitochondrial	0.66	0.09	0.2	0.316666667	-0.19850192	0.831835257	0.18760588
Q93092	Transaldolase	-0.87	-1.75	-1.01	-1.21	-1.79364661	-0.626353393	0.00189697
P83940	Transcription elongation factor B polypeptide 1	-0.78	-0.72	0.65	-0.283333333	-1.04871565	0.482048985	0.40739951
P62869	Transcription elongation factor B polypeptide 2	-0.33	-0.47	-0.26	-0.353333333	-0.82221855	0.115551881	0.11702485
Q64152	Transcription factor BTF3	-0.47	-0.87	-0.85	-0.73	-1.22220468	-0.237795324	0.01021216
Q9CQH7	Transcription factor BTF3 homolog 4	-0.16	-1.05	-1.18	-0.796666667	-1.42022623	-0.173107104	0.01966972
P42669	Transcriptional activator protein Pur-alpha	1.15	1.04	1.11	1.1	0.63620151	1.563798489	0.00090099
P37804	Transgelin	-0.67	-1.11	-0.48	-0.753333333	-1.27563573	-0.231030937	0.01159921
Q9WVA4	Transgelin-2	-0.57	-1.46	-0.94	-0.99	-1.56197077	-0.418029234	0.0048586
Q01853	Transitional endoplasmic reticulum ATPase	0.08	0.1	0.12	0.1	-0.36213838	0.562138382	0.62201576
P40142	Transketolase	0.75	-0.06	-0.19	0.166666667	-0.4342026	0.767535933	0.52992397
P63028	Translationally-controlled tumor protein	-0.29	-1.39	-1.29	-0.99	-1.64114616	-0.338853841	0.0091015
Q62348	Translin	-0.27	-0.86	-0.67	-0.6	-1.11476323	-0.085236775	0.0285019
Q6P2B1	Transportin-3	0.48	0.96	1.41	0.95	0.3699247	1.530075297	0.0063841
P07309	Transthyretin	-0.52	-0.97	-1.09	-0.86	-1.37454198	-0.345458018	0.005779
H3BL37	Treacle protein	-1.97	-1.19	-2.47	-1.876666667	-2.54767769	-1.205655641	0.00034715
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	1.04	0.96	1.44	1.146666667	0.64567269	1.647660644	0.0011007
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	0.71	0.66	1.44	0.936666667	0.36932648	1.504006855	0.00613786
Q64737	Trifunctional purine biosynthetic protein adenosine-3	-0.1	-0.37	-0.09	-0.186666667	-0.66385627	0.290522933	0.38277623
P17751	Triosephosphate isomerase	-0.75	-1.19	-1.04	-0.993333333	-1.48509442	-0.501572246	0.00218181
Q1XH17	Tripartite motif-containing protein 72	-0.72	0.02	0.62	-0.026666667	-0.71211564	0.658782302	0.92870727
Q64514	Tripeptidyl-peptidase 2	1.23	0.58	1.53	1.113333333	0.52375043	1.702916239	0.00311417
Q99LF4	tRNA-splicing ligase RtcB homolog	0.86	0.99	0.82	0.89	0.42326479	1.356735213	0.00295952
P49813	Tropomodulin-1	0.55	0.05	0.58	0.393333333	-0.12028578	0.906952443	0.1121962
P58771	Tropomyosin alpha-1 chain	-0.44	-1.11	-0.3	-0.616666667	-1.182399	-0.05093433	0.0367696
E9Q5J9	Tropomyosin alpha-3 chain	-3.04	-1.8	1.72	-1.04	-2.95958574	0.879585741	0.23869521
P19123	Troponin C, slow skeletal and cardiac muscles	-0.05	-0.62	0.52	-0.05	-0.68112213	0.581122127	0.85556911
P48787	Troponin I, cardiac muscle	0.08	-0.58	0.54	0.013333333	-0.61418526	0.640851926	0.96101773
J3QQ13	Troponin T, cardiac muscle	-0.58	-0.99	0.34	-0.41	-1.10097768	0.280977681	0.20142589
P32921	Tryptophan--tRNA ligase, cytoplasmic	0.84	0.14	0.13	0.37	-0.18468904	0.924689037	0.1572762
P68368	Tubulin alpha-4A chain	0.14	1.21	2.26	1.203333333	0.27972772	2.126938949	0.01811465
P68372	Tubulin beta-4B chain	0.2	1.57	2.02	1.263333333	0.41189274	2.114773927	0.01019199
Q9CRB6	Tubulin polymerization-promoting protein family member 3	-1.15	-1.03	-1.02	-1.066666667	-1.53177266	-0.601560678	0.0010884
Q9D1E6	Tubulin-folding cofactor B	-0.59	-1.09	-0.83	-0.836666667	-1.33561098	-0.337722356	0.00568655
Q3UDE2	Tubulin--tyrosine ligase-like protein 12	0.91	0.84	1.41	1.053333333	0.53529943	1.571367235	0.00210597
Q9Z0P5	Twinfilin-2	-0.07	-0.21	0.93	0.216666667	-0.44166761	0.875000946	0.45889195
P35235	Tyrosine-protein phosphatase non-receptor type 11	-0.64	-0.22	-0.35	-0.403333333	-0.89288983	0.086223164	0.09182577
Q6PB44	Tyrosine-protein phosphatase non-receptor type 23	-0.36	3.36	-0.36	0.88	-0.80507805	2.565078052	0.25433013
A2A7S7	Tyrosine--tRNA ligase, cytoplasmic	-0.04	-0.24	-0.61	-0.296666667	-0.80750716	0.214173824	0.21003108
Q8R317	Ubiquilin-1	-0.49	-0.34	-0.33	-0.386666667	-0.85348319	0.080149858	0.09043035
Q9QZM0	Ubiquilin-2	-0.59	-0.76	-0.85	-0.733333333	-1.20584708	-0.260819583	0.00826305

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8R1S0	Ubiquinone biosynthesis monooxygenase COQ6	0.63	1.05	1.2	0.96	0.44712038	1.472879617	0.00326003
P97478	Ubiquinone biosynthesis protein COQ7 homolog	0.17	0.74	1.25	0.72	0.10394181	1.336058187	0.02820423
Q8K1Z0	Ubiquinone biosynthesis protein COQ9, mitochondrial	-0.3	-0.56	-0.09	-0.316666667	-0.8115437	0.178210366	0.17238836
Q9JMA1	Ubiquitin carboxyl-terminal hydrolase 14	-0.23	-0.98	-0.61	-0.606666667	-1.14833913	-0.064994204	0.0332246
P35123	Ubiquitin carboxyl-terminal hydrolase 4	-0.02	0.26	-0.12	0.04	-0.44521505	0.525215049	0.84979483
P56399	Ubiquitin carboxyl-terminal hydrolase 5	-0.21	-0.14	-0.39	-0.246666667	-0.71869822	0.22536489	0.25405669
Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	-1.27	-1.59	-1.16	-1.34	-1.8316839	-0.848316099	0.00040429
Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3	-0.41	-0.95	-0.54	-0.633333333	-1.14182805	-0.124838617	0.02185587
P70362	Ubiquitin fusion degradation protein 1 homolog	0.52	-0.06	-0.64	-0.06	-0.69628789	0.576287892	0.82857554
Q7TQI3	Ubiquitin thioesterase OTUB1	-0.27	-0.43	-0.53	-0.41	-0.88237316	0.062373161	0.07884358
Q80X50	Ubiquitin-associated protein 2-like	-0.06	-1.37	-1.22	-0.883333333	-1.59466441	-0.172002259	0.02212422
P61087	Ubiquitin-conjugating enzyme E2 K	-0.73	-0.4	-0.36	-0.496666667	-0.98330717	-0.010026162	0.04658981
P68037	Ubiquitin-conjugating enzyme E2 L3	-0.43	-0.9	-0.87	-0.733333333	-1.23608561	-0.230581061	0.01102162
P61089	Ubiquitin-conjugating enzyme E2 N	-0.52	-0.47	0.03	-0.32	-0.83575764	0.195757645	0.18402297
Q6ZPJ3	Ubiquitin-conjugating enzyme E2 O	-0.13	-0.18	0.12	-0.063333333	-0.54088072	0.414214051	0.76114269
Q02053	Ubiquitin-like modifier-activating enzyme 1	0.44	0.41	0.29	0.38	-0.08575836	0.845758362	0.09440001
Q64339	Ubiquitin-like protein ISG15	-0.37	-0.03	-0.29	-0.23	-0.71097252	0.250972518	0.29277444
Q922Y1	UBX domain-containing protein 1	-0.43	-1.45	-1.73	-1.203333333	-1.8960528	-0.510613865	0.00477156
Q99PL6	UBX domain-containing protein 6	-1.13	-0.56	0.54	-0.383333333	-1.17302487	0.406358201	0.28615189
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	-0.22	0.31	0.24	0.11	-0.40043169	0.620431688	0.62340863
Q3UHZ7	UDP-N-acetylhexosamine pyrophosphorylase	-0.22	-0.68	-1.2	-0.7	-1.29178364	-0.108216355	0.02690205
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	0.92	0.6	-2.65	-0.376666667	-1.93699003	1.183656701	0.5832006
Q9DBP5	UMP-CMP kinase	-1.11	-1.41	-1.32	-1.28	-1.75627404	-0.803725959	0.00043878
Q3U5Q7	UMP-CMP kinase 2, mitochondrial	0.59	-0.58	-0.18	-0.056666667	-0.70061814	0.587284811	0.83982733
Q149B8	Uncharacterized protein C1orf170 homolog	0.01	-0.87	-0.85	-0.57	-1.16752798	0.027527976	0.05858634
Q9CQF4	Uncharacterized protein C6orf203 homolog	-1.15	-1.79	-1.03	-1.323333333	-1.87865494	-0.768011729	0.00087711
Q6PIU9	Uncharacterized protein FLJ45252 homolog	-0.82	-0.8	-0.86	-0.826666667	-1.28913344	-0.36419989	0.00413009
Q8CC88	Uncharacterized protein KIAA0564 homolog	1.19	0.96	2.07	1.406666667	0.76732903	2.046004302	0.00137071
E9QMK9	UPF0317 protein C14orf159 homolog, mitochondrial	0.28	-0.29	-1.64	-0.55	-1.42572298	0.325722984	0.17938835
D3YZD8	UPF0366 protein C11orf67 homolog	-0.99	-1.15	-1.35	-1.163333333	-1.64485792	-0.681808749	0.00081139
Q5F285	UPF0451 protein C17orf61 homolog	1.54	1.78	0.04	1.12	0.27171907	1.968280927	0.01711727
Q9CQE8	UPF0568 protein C14orf166 homolog	-0.48	0.21	0.8	0.176666667	-0.49192191	0.845255248	0.54902293
Q8BHG2	UPF0587 protein C1orf123 homolog	-1.49	0.01	-0.84	-0.773333333	-1.50510003	-0.041566636	0.04116885
Q8VE95	UPF0598 protein C8orf82 homolog	0.89	0.1	0.24	0.41	-0.15081345	0.970813452	0.12641562
Q78IK2	Up-regulated during skeletal muscle growth protein 5	-1.08	0.11	-0.06	-0.343333333	-1.01353785	0.326871184	0.26261935
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	1.26	1.47	1.02	1.25	0.75785316	1.74214684	0.00060924
P54726	UV excision repair protein RAD23 homolog A	-0.98	-1.71	-1.27	-1.32	-1.85875675	-0.781243248	0.00074902
P54728	UV excision repair protein RAD23 homolog B	-0.6	-1.11	-1.03	-0.913333333	-1.4194714	-0.407195262	0.00393572
Q9D1C8	Vacuolar protein sorting-associated protein 28 homolog	-0.8	-1.21	0.02	-0.663333333	-1.32412765	-0.002539017	0.04934501
Q9QZ88	Vacuolar protein sorting-associated protein 29	0.91	0.35	1.08	0.78	0.23556685	1.324433153	0.01195641
Q9EQH3	Vacuolar protein sorting-associated protein 35	0.94	1.11	1.11	1.053333333	0.58554217	1.521124499	0.00120566
Q9CR26	Vacuolar protein sorting-associated protein VTA1 homolog	-0.38	-1.01	-0.31	-0.566666667	-1.11252708	-0.020806254	0.04388028

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q8R164	Valacyclovir hydrolase	0.59	0.43	0.63	0.55	0.08125646	1.018743537	0.02777089
P50544	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	0.57	-0.01	0.37	0.31	-0.20260203	0.822602032	0.19392966
Q8BH80	Vesicle-associated membrane protein-associated protein B	-0.27	0.02	0.06	-0.063333333	-0.5447988	0.418132132	0.7630144
P46460	Vesicle-fusing ATPase	-0.29	-0.36	0.5	-0.05	-0.63583725	0.535837253	0.84457435
Q8VDJ3	Vigilin	0.9	0.54	0.83	0.756666667	0.27284205	1.240491284	0.0079683
P20152	Vimentin	-0.81	-0.84	-0.77	-0.806666667	-1.26931806	-0.344015271	0.00468353
Q64727	Vinculin	-0.43	-0.64	-0.48	-0.516666667	-0.985916	-0.047417336	0.03542187
P21614	Vitamin D-binding protein	-0.35	-0.97	-0.35	-0.556666667	-1.09172984	-0.021603494	0.04354285
P29788	Vitronectin	0.05	0.59	1	0.546666667	-0.03865206	1.131985397	0.06276285
Q60932	Voltage-dependent anion-selective channel protein 1	0.99	0.55	-0.13	0.47	-0.15818356	1.098183557	0.1192056
Q60930	Voltage-dependent anion-selective channel protein 2	1.19	0.73	-0.12	0.6	-0.08177073	1.281770728	0.07561158
J3QMG3	Voltage-dependent anion-selective channel protein 3	0.68	1.09	-0.13	0.546666667	-0.11119181	1.204525143	0.08959843
O08532	Voltage-dependent calcium channel subunit alpha-2/delta-1	-1.34	-0.9	-1.17	-1.136666667	-1.62796445	-0.645368881	0.00103616
Q99KC8	von Willebrand factor A domain-containing protein 5A	0.08	-0.05	-0.35	-0.106666667	-0.59761669	0.384283355	0.62062632
P50516	V-type proton ATPase catalytic subunit A	1.04	0.89	1.08	1.003333333	0.53529883	1.471367842	0.00158133
P62814	V-type proton ATPase subunit B, brain isoform	1.01	0.81	0.5	0.773333333	0.27239618	1.274270489	0.00847254
Q9Z1G3	V-type proton ATPase subunit C 1	-0.16	0.2	0.83	0.29	-0.30690834	0.886908343	0.28577514
Q8BVE3	V-type proton ATPase subunit H	1.46	1.17	-0.49	0.713333333	-0.20514186	1.631808524	0.10808344
O88342	WD repeat-containing protein 1	-0.23	-0.33	-0.11	-0.223333333	-0.69264332	0.245976656	0.29492989
Q3UE92	Xaa-Pro aminopeptidase 1	0.15	0.03	0.44	0.206666667	-0.28184208	0.695175412	0.34757397
Q00519	Xanthine dehydrogenase/oxidase	0.97	0.59	0.23	0.596666667	0.05694212	1.136391212	0.0348919
P46938	Yorkie homolog	-0.67	-1.28	-0.79	-0.913333333	-1.43563573	-0.391030937	0.00461535
Q64726	Zinc-alpha-2-glycoprotein	-0.7	-0.54	0.09	-0.383333333	-0.94248623	0.175819561	0.14768746
Q8BGC4	Zinc-binding alcohol dehydrogenase domain-containing protein 2	-0.08	0.45	0.5	0.29	-0.23168436	0.811684357	0.22793997
Q62523	Zyxin	-0.99	-1.1	-0.95	-1.013333333	-1.47892869	-0.547737979	0.00145527
E9Q3H6	Protein Coq10a	2.11	0.72	2.02	1.616666667	0.86980676	2.363526569	0.00149942
F8VPN4	Protein Agl	1.58	1.43	1.32	1.443333333	0.97106062	1.915606049	0.00020457
Q8BML9	Glutaminyl-tRNA synthetase	0.9	1.4	0.53	0.943333333	0.37599314	1.510673522	0.00592836
E9Q4Z2	Acetyl-CoA carboxylase 2	0.94	1.24	0.2	0.793333333	0.1797599	1.406906766	0.01870754
E9Q7L0	Protein Ogdhl	1.66	-0.34	0.62	0.646666667	-0.23818612	1.531519452	0.12652946
Q14BI5	Myomesin 2	0.61	0.37	0.71	0.563333333	0.08299252	1.043674142	0.02782397
G3X972	Protein Sec24c	0.84	-0.03	0.84	0.55	-0.04748033	1.147480335	0.06574177
E9PWQ3	Protein Col6a3	0.05	0.89	0.7	0.546666667	-0.02237689	1.115710221	0.0572402
A2AFQ2	3-hydroxyacyl-CoA dehydrogenase type-2	0.78	-0.07	0.86	0.523333333	-0.080466	1.12713267	0.07917804
Q91VA7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial	0.23	0.59	0.72	0.513333333	0.01330621	1.01336046	0.04564128
E9Q0S6	Protein Tns1	0.73	0.29	0.36	0.46	-0.03514539	0.955145391	0.06384307
E9PV24	Fibrinogen alpha chain	0.41	0.26	0.61	0.426666667	-0.05385189	0.907185228	0.07358215
B7ZCI2	Nebulette	0.71	-0.01	0.46	0.386666667	-0.1513146	0.92464793	0.13187632
E9QLJ0	Cardiomyopathy-associated protein 5	0.25	-0.74	1.39	0.3	-0.62743992	1.227439924	0.46630765
O35452	Protein Tnxb	-0.02	0.47	0.2	0.216666667	-0.28096372	0.714297049	0.33464663
G3X8U3	MCG6895	0.29	0.35	-0.01	0.21	-0.27427548	0.694275476	0.3364659
E9PYF4	Protein Lmo7	0.72	-0.6	0.49	0.203333333	-0.50124269	0.90790936	0.51395661

ID	Protein name	exp1	exp2	exp3	Average logFc	CI.95 %L	CI.95 %R	p-value
Q6PHQ9	Polyadenylate-binding protein	0.63	0.01	-0.1	0.18	-0.36911866	0.729118664	0.46061349
Q3UKG2	Protein Prob1	0.53	0.42	-0.57	0.126666667	-0.52318128	0.776514609	0.65640131
A2AUC9	Kelch-like protein 41	0.06	0.3	-0.45	-0.03	-0.57485127	0.514851274	0.89926585
L7N1X8	Protein Gbp6	-0.01	-0.35	-0.71	-0.356666667	-0.88874225	0.175408915	0.15553105
F6ZDS4	Nucleoprotein TPR	-0.38	-0.74	0.05	-0.356666667	-0.90657962	0.19324629	0.16740635
E9Q912	Protein Rap1gds1	-0.42	-0.52	-0.36	-0.433333333	-0.89923428	0.032567614	0.06360605
O08804	NK13	-0.29	-0.63	-0.61	-0.51	-0.99380501	-0.026194994	0.04154386
G5E8J6	Histidine rich calcium binding protein, isoform CRA_a	-0.33	-0.77	-0.56	-0.553333333	-1.04416738	-0.062499287	0.03241138
O08797	Protein Serpinb9	-0.5	-0.8	-0.39	-0.563333333	-1.05219158	-0.074475088	0.02979555
E9Q8P5	PDZ and LIM domain protein 5	-0.2	-0.76	-0.73	-0.563333333	-1.08279396	-0.043872703	0.03747188
E9Q616	Protein Ahnak	-0.61	-0.7	-0.62	-0.643333333	-1.10672247	-0.179944194	0.01375914
A8DUK4	Beta-globin	-1.28	-0.59	-0.1	-0.656666667	-1.2996449	-0.013688434	0.04648044
F7AI87	26S proteasome non-ATPase regulatory subunit 4	-0.39	-0.7	-0.95	-0.68	-1.18808403	-0.171915973	0.01614782
Q3U422	NADH dehydrogenase [ubiquinone] flavoprotein 3,	-0.61	-0.61	-1.01	-0.743333333	-1.23700095	-0.24966572	0.00952178
E9Q8T1	Transforming acidic coiled-coil-containing protein 2	-0.26	-1.01	-1	-0.756666667	-1.32119011	-0.192143225	0.01604393
Q9Z1A1	Protein Tfg	-0.1	-1.43	-1.24	-0.923333333	-1.63602371	-0.210642956	0.01855044
Q8BGD8	Cytochrome c oxidase assembly factor 6 homolog	-0.31	-1.59	-0.9	-0.933333333	-1.60192191	-0.264744752	0.01342822
A6X935	Inter alpha-trypsin inhibitor, heavy chain 4	-1.27	-1.35	-0.97	-1.196666667	-1.6826633	-0.710670028	0.00072805
E9PYJ9	LIM domain-binding protein 3	-0.39	-1.68	-1.61	-1.226666667	-1.94286326	-0.510470073	0.00512047
E9PVZ8	Protein Golgb1	-3.41	-2.34	0.32	-1.81	-3.33101821	-0.288981795	0.0262701

Table S-5. List of significantly affected proteins in hCTSA-tg mice.

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
P10619	Cathepsin A	2.79	2.05	3.53	0.0001
Q9JI91	Alpha-actinin-2	2.63	2.10	3.16	0.0000
Q91V55	40S ribosomal protein S5	2.38	1.78	2.97	0.0000
P62889	60S ribosomal protein L30	2.36	1.67	3.06	0.0001
P23780	Beta-galactosidase	2.35	1.81	2.89	0.0000
Q9CQ69	Cytochrome b-c1 complex subunit 8	2.20	1.30	3.10	0.0007
P62264	40S ribosomal protein S14	2.04	1.20	2.89	0.0008
D3Z722	40S ribosomal protein S19	2.03	1.48	2.59	0.0001
Q78PY7	Staphylococcal nuclease domain-containing protein 1	2.02	1.47	2.57	0.0001
Q8CBB6	Histone H2B	1.99	1.10	2.88	0.0013
Q9WUU7	Cathepsin Z	1.89	1.13	2.65	0.0007
G3X8R0	Receptor expression-enhancing protein 5	1.88	0.92	2.84	0.0025
Q5SXR6	Clathrin heavy chain 1	1.84	1.37	2.31	0.0000
D3Z6C3	40S ribosomal protein S3a	1.77	0.63	2.92	0.0083
P26443	Glutamate dehydrogenase 1, mitochondrial	1.77	1.17	2.37	0.0003
P54116	Erythrocyte band 7 integral membrane protein	1.74	1.09	2.40	0.0005
Q91VR5	ATP-dependent RNA helicase DDX1	1.73	1.04	2.42	0.0007
Q9D7J9	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	1.68	1.07	2.28	0.0004
P12265	Beta-glucuronidase	1.67	0.83	2.52	0.0024
P23116	Eukaryotic translation initiation factor 3 subunit A	1.65	0.79	2.50	0.0028
Q3ULD5	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	1.63	0.65	2.62	0.0061
E9Q3H6	Protein Coq10a	1.62	0.87	2.36	0.0015
F6XI62	60S ribosomal protein L7	1.61	0.98	2.23	0.0006
Q8R1B4	Eukaryotic translation initiation factor 3 subunit C	1.60	0.92	2.27	0.0009
P84091	AP-2 complex subunit mu	1.57	0.73	2.41	0.0033
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	1.57	1.10	2.04	0.0001
E9QAQ5	Glycogen synthase kinase-3 beta	1.50	0.52	2.48	0.0088
Q9D7B6	Isobutyryl-CoA dehydrogenase, mitochondrial	1.50	1.01	1.99	0.0002
E9Q401	Ryanodine receptor 2	1.48	0.99	1.97	0.0002

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
Q7TSQ8	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial	1.48	0.92	2.04	0.0005
F8VPN4	Protein Agl	1.44	0.97	1.92	0.0002
Q91YQ5	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 1	1.44	0.49	2.39	0.0092
Q9CRB9	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	1.44	0.71	2.17	0.0025
Q3TCN2	Putative phospholipase B-like 2	1.42	0.87	1.98	0.0006
Q8CC88	Uncharacterized protein KIAA0564 homolog	1.41	0.77	2.05	0.0014
D3Z7X0	Acyl-CoA dehydrogenase family member 10	1.40	0.86	1.93	0.0005
P57780	Alpha-actinin-4	1.40	0.69	2.10	0.0024
E9PZ16	Basement membrane-specific heparan sulfate proteoglycan core protein	1.37	0.85	1.89	0.0005
Q544X6	Ferrochelatase	1.35	0.82	1.89	0.0006
F6QYE1	Calsequestrin-2	1.33	0.57	2.09	0.0045
Q9WUM4	Coronin-1C	1.32	0.65	2.00	0.0026
A2ASS6	Titin	1.30	0.72	1.87	0.0012
Q9D0G0	28S ribosomal protein S30, mitochondrial	1.28	0.74	1.81	0.0008
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	1.25	0.76	1.74	0.0006
P05132	cAMP-dependent protein kinase catalytic subunit alpha	1.24	0.75	1.73	0.0006
P15105	Glutamine synthetase	1.24	0.67	1.81	0.0014
Q9D2N4	Dystrobrevin alpha	1.24	0.68	1.79	0.0013
E9Q3X0	Major vault protein	1.24	0.54	1.94	0.0044
Q8VDM6	Heterogeneous nuclear ribonucleoprotein U-like protein 1	1.23	0.74	1.71	0.0006
Q9CQ22	Ragulator complex protein LAMTOR1	1.21	0.74	1.68	0.0006
Q9WUB3	Glycogen phosphorylase, muscle form	1.21	0.63	1.79	0.0018
P48962	ADP/ATP translocase 1	1.21	0.56	1.85	0.0032
Q9QZF2	Glypican-1	1.20	0.59	1.81	0.0024
D3Z3G6	Mitogen-activated protein kinase 3	1.20	0.44	1.96	0.0076
Q3V132	ADP/ATP translocase 4	1.20	0.47	1.93	0.0064
Q62465	Synaptic vesicle membrane protein VAT-1 homolog	1.17	0.53	1.81	0.0036
Q9Z1Z0	General vesicular transport factor p115	1.16	0.68	1.63	0.0008
Q921S7	39S ribosomal protein L37, mitochondrial	1.16	0.67	1.64	0.0009
Q91YP0	L-2-hydroxyglutarate dehydrogenase, mitochondrial	1.16	0.57	1.75	0.0026
Q8CI94	Glycogen phosphorylase, brain form	1.15	0.68	1.62	0.0008

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
Q8BMS1	Trifunctional enzyme subunit alpha, mitochondrial	1.15	0.65	1.65	0.0011
P14206	40S ribosomal protein SA	1.14	0.64	1.64	0.0011
O70571	Pyruvate dehydrogenase kinase isozyme 4, mitochondrial	1.13	0.63	1.64	0.0012
Q920Q8	Influenza virus NS1A-binding protein homolog	1.13	0.47	1.78	0.0049
Q3UQ84	Threonine-tRNA ligase, mitochondrial	1.12	0.62	1.62	0.0013
P70398	Probable ubiquitin carboxyl-terminal hydrolase FAF-X	1.12	0.57	1.66	0.0020
Q64514	Tripeptidyl-peptidase 2	1.11	0.52	1.70	0.0031
P52825	Carnitine O-palmitoyltransferase 2, mitochondrial	1.11	0.59	1.62	0.0016
Q3U3G8	Serine hydrolase-like protein	1.10	0.52	1.69	0.0032
P42669	Transcriptional activator protein Pur-alpha	1.10	0.64	1.56	0.0009
P62192	26S protease regulatory subunit 4	1.09	0.38	1.80	0.0086
Q8CGC7	Bifunctional glutamate/proline-tRNA ligase	1.08	0.55	1.61	0.0021
Q99K70	Ras-related GTP-binding protein C	1.07	0.58	1.57	0.0015
P80318	T-complex protein 1 subunit gamma	1.07	0.59	1.54	0.0012
P11152	Lipoprotein lipase	1.07	0.40	1.73	0.0071
Q99LC3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	1.06	0.48	1.63	0.0037
Q9EQH3	Vacuolar protein sorting-associated protein 35	1.05	0.59	1.52	0.0012
Q3UDE2	Tubulin-tyrosine ligase-like protein 12	1.05	0.54	1.57	0.0021
Q8QZY1	Eukaryotic translation initiation factor 3 subunit L	1.05	0.43	1.66	0.0052
Q9WUA2	Phenylalanine-tRNA ligase beta subunit	1.05	0.37	1.72	0.0095
O08600	Endonuclease G, mitochondrial	1.04	0.53	1.54	0.0020
P99026	Proteasome subunit beta type-4	1.03	0.54	1.52	0.0017
Q9DC70	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	1.02	0.44	1.61	0.0045
Q8BU30	Isoleucine-tRNA ligase, cytoplasmic	1.02	0.54	1.49	0.0016
P12382	6-phosphofructokinase, liver type	1.02	0.51	1.52	0.0022
Q91VR2	ATP synthase subunit gamma, mitochondrial	1.01	0.53	1.48	0.0017
P50516	V-type proton ATPase catalytic subunit A	1.00	0.54	1.47	0.0016
Q60759	Glutaryl-CoA dehydrogenase, mitochondrial	1.00	0.47	1.53	0.0031
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	1.00	0.43	1.57	0.0045
P51150	Ras-related protein Rab-7a	1.00	0.42	1.58	0.0050
F6ZHD8	1,4-alpha-glucan-branching enzyme	0.99	0.50	1.48	0.0022

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
Q9DB20	ATP synthase subunit O, mitochondrial	0.99	0.49	1.49	0.0025
Q9Z1J3	Cysteine desulfurase, mitochondrial	0.98	0.51	1.44	0.0018
Q9D0I9	Arginine-tRNA ligase, cytoplasmic	0.98	0.50	1.45	0.0019
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	0.97	0.45	1.49	0.0032
Q924X2	Carnitine O-palmitoyltransferase 1, muscle isoform	0.97	0.34	1.60	0.0087
E9QB02	Methionine--tRNA ligase, cytoplasmic	0.96	0.45	1.47	0.0031
Q8R1S0	Ubiquinone biosynthesis monooxygenase COQ6	0.96	0.45	1.47	0.0033
P10605	Cathepsin B	0.96	0.43	1.49	0.0039
Q9CPQ1	Cytochrome c oxidase subunit 6C	0.95	0.42	1.48	0.0041
Q6P2B1	Transportin-3	0.95	0.37	1.53	0.0064
Q8BML9	Glutaminyl-tRNA synthetase	0.94	0.38	1.51	0.0059
P18242	Cathepsin D	0.94	0.47	1.41	0.0022
Q9Z1E4	Glycogen synthase, muscle	0.94	0.46	1.42	0.0025
Q60597	2-oxoglutarate dehydrogenase, mitochondrial	0.94	0.45	1.43	0.0027
Q99JY0	Trifunctional enzyme subunit beta, mitochondrial	0.94	0.37	1.50	0.0061
P20918	Plasminogen	0.94	0.33	1.54	0.0085
Q91WD5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	0.93	0.41	1.46	0.0043
E9QPD7	Pyruvate carboxylase	0.93	0.40	1.46	0.0044
Q9DB60	Prostamide/prostaglandin F synthase	0.93	0.41	1.45	0.0042
P17427	AP-2 complex subunit alpha-2	0.92	0.45	1.40	0.0026
Q8JZQ9	Eukaryotic translation initiation factor 3 subunit B	0.91	0.36	1.47	0.0061
O55234	Proteasome subunit beta type-5	0.90	0.44	1.37	0.0026
Q8C605	6-phosphofructokinase	0.90	0.43	1.38	0.0030
P06801	NADP-dependent malic enzyme	0.90	0.37	1.43	0.0056
P56135	ATP synthase subunit f, mitochondrial	0.89	0.37	1.42	0.0053
Q99LF4	tRNA-splicing ligase RtcB homolog	0.89	0.42	1.36	0.0030
H3BKH6	S-formylglutathione hydrolase	0.89	0.38	1.40	0.0048
Q01405	Protein transport protein Sec23A	0.89	0.42	1.35	0.0029
Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1	0.88	0.41	1.35	0.0034
Q8K4Z3	NAD(P)H-hydrate epimerase	0.87	0.33	1.42	0.0070
Q499X9	Methionine-tRNA ligase, mitochondrial	0.87	0.41	1.33	0.0032

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
P86049	Probable RNA-binding protein 46	0.87	0.36	1.37	0.0051
Q00612	Glucose-6-phosphate 1-dehydrogenase X	0.86	0.36	1.36	0.0049
Q8BFP9	Pyruvate dehydrogenase [lipoamide] kinase isozyme 1, mitochondrial	0.86	0.39	1.33	0.0035
Q9CR24	Nucleoside diphosphate-linked moiety X motif 8, mitochondrial	0.85	0.33	1.37	0.0063
Q8BP47	Asparagine-tRNA ligase, cytoplasmic	0.85	0.31	1.40	0.0081
O35350	Calpain-1 catalytic subunit	0.85	0.39	1.31	0.0036
Q9CQJ8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	0.85	0.34	1.36	0.0059
Q8BKC5	Importin-5	0.84	0.31	1.38	0.0075
Q8BMF3	NADP-dependent malic enzyme, mitochondrial	0.84	0.35	1.33	0.0050
P80315	T-complex protein 1 subunit delta	0.84	0.34	1.34	0.0059
Q71RI9	Kynurenine-oxoglutarate transaminase 3	0.83	0.34	1.32	0.0053
E9PY58	Caseinolytic peptidase B protein homolog	0.83	0.36	1.30	0.0044
P28271	Cytoplasmic aconitate hydratase	0.83	0.35	1.31	0.0048
Q8CAK1	Putative transferase CAF17 homolog, mitochondrial	0.82	0.33	1.31	0.0057
P62196	26S protease regulatory subunit 8	0.80	0.30	1.31	0.0073
Q5M8N4	Epimerase family protein SDR39U1	0.78	0.30	1.26	0.0068
P80313	T-complex protein 1 subunit eta	0.78	0.31	1.24	0.0059
P62814	V-type proton ATPase subunit B, brain isoform	0.77	0.27	1.27	0.0085
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	0.77	0.29	1.25	0.0072
Q8VDJ3	Vigilin	0.76	0.27	1.24	0.0080
Q9Z0N1	Eukaryotic translation initiation factor 2 subunit 3, X-linked	0.75	0.29	1.21	0.0068
Q8R010	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	0.75	0.28	1.21	0.0072
Q9JII6	Alcohol dehydrogenase [NADP(+)]	0.75	0.27	1.22	0.0079
P82350	Alpha-sarcoglycan	0.74	0.27	1.21	0.0080
Q9D0R2	Threonine-tRNA ligase, cytoplasmic	0.72	0.26	1.19	0.0084
P35486	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial	0.71	0.23	1.19	0.0100
Q3ULJ0	Glycerol-3-phosphate dehydrogenase 1-like protein	-0.71	-1.17	-0.25	0.0087
Q9D3D9	ATP synthase subunit delta, mitochondrial	-0.72	-1.19	-0.25	0.0089
E9PZF0	Nucleoside diphosphate kinase	-0.72	-1.20	-0.24	0.0095
Q9QZM0	Ubiquilin-2	-0.73	-1.21	-0.26	0.0083
Q62418	Drebrin-like protein	-0.73	-1.22	-0.25	0.0092

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
Q3U422	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	-0.74	-1.24	-0.25	0.0095
Q61768	Kinesin-1 heavy chain	-0.75	-1.22	-0.28	0.0075
Q06890	Clusterin	-0.76	-1.24	-0.29	0.0068
Q924M7	Mannose-6-phosphate isomerase	-0.77	-1.28	-0.26	0.0094
P52503	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	-0.78	-1.25	-0.30	0.0065
P97290	Plasma protease C1 inhibitor	-0.78	-1.28	-0.29	0.0073
Q9CQM9	Glutaredoxin-3	-0.79	-1.26	-0.31	0.0060
Q9CYR0	Single-stranded DNA-binding protein, mitochondrial	-0.79	-1.29	-0.29	0.0075
O88851	Putative hydrolase RBBP9	-0.80	-1.31	-0.29	0.0081
Q3UKW2	Calmodulin	-0.80	-1.30	-0.31	0.0066
P20152	Vimentin	-0.81	-1.27	-0.34	0.0047
Q6PIU9	Uncharacterized protein FLJ45252 homolog	-0.83	-1.29	-0.36	0.0041
Q8R5L1	Complement component 1 Q subcomponent-binding protein, mitochondrial	-0.83	-1.33	-0.33	0.0060
Q9DCW4	Electron transfer flavoprotein subunit beta	-0.83	-1.32	-0.34	0.0053
F6VW30	14-3-3 protein theta	-0.83	-1.37	-0.30	0.0083
Q8CIN4	Serine/threonine-protein kinase PAK 2	-0.84	-1.32	-0.35	0.0050
Q9D1E6	Tubulin-folding cofactor B	-0.84	-1.34	-0.34	0.0057
Q60668	Heterogeneous nuclear ribonucleoprotein D0	-0.84	-1.34	-0.34	0.0058
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	-0.84	-1.31	-0.37	0.0041
Q99L47	Hsc70-interacting protein	-0.84	-1.35	-0.33	0.0060
Q8K4Z5	Splicing factor 3A subunit 1	-0.84	-1.37	-0.31	0.0075
D3YW52	Alpha-2-macroglobulin	-0.85	-1.33	-0.36	0.0046
Q9CR16	Peptidyl-prolyl cis-trans isomerase D	-0.85	-1.33	-0.36	0.0047
E9PX89	BolA-like protein 3	-0.85	-1.38	-0.31	0.0076
P51125	Calpastatin	-0.85	-1.34	-0.36	0.0050
P63158	High mobility group protein B1	-0.85	-1.36	-0.35	0.0053
Q99LX0	Protein DJ-1	-0.86	-1.34	-0.38	0.0041
Q8C0M9	L-asparaginase	-0.86	-1.34	-0.38	0.0042
P32261	Antithrombin-III	-0.86	-1.35	-0.37	0.0043
A2A5Y6	Microtubule-associated protein tau	-0.86	-1.35	-0.37	0.0047
P07309	Transthyretin	-0.86	-1.37	-0.35	0.0058

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
Q4VWZ5	Acyl-CoA-binding protein	-0.87	-1.37	-0.36	0.0050
B1AX58	Plastin-3	-0.87	-1.34	-0.40	0.0035
Q9D881	Cytochrome c oxidase subunit 5B, mitochondrial	-0.87	-1.34	-0.40	0.0035
Q9Z0F7	Gamma-synuclein	-0.87	-1.42	-0.32	0.0073
Q64010	Adapter molecule crk	-0.87	-1.35	-0.39	0.0038
Q9D172	ES1 protein homolog, mitochondrial	-0.88	-1.35	-0.41	0.0032
Q9CZ44	NSFL1 cofactor p47	-0.88	-1.41	-0.35	0.0057
Q8CDN6	Thioredoxin-like protein 1	-0.89	-1.37	-0.41	0.0036
Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial	-0.89	-1.40	-0.38	0.0048
O89020	Afamin	-0.91	-1.37	-0.44	0.0027
Q64433	10 kDa heat shock protein, mitochondrial	-0.91	-1.39	-0.42	0.0033
P42703	Leukemia inhibitory factor receptor	-0.91	-1.42	-0.40	0.0040
Q8WTY4	Anamorsin	-0.91	-1.39	-0.44	0.0028
P54728	UV excision repair protein RAD23 homolog B	-0.91	-1.42	-0.41	0.0039
P46938	Yorkie homolog	-0.91	-1.44	-0.39	0.0046
P63038	60 kDa heat shock protein, mitochondrial	-0.93	-1.40	-0.46	0.0025
P48024	Eukaryotic translation initiation factor 1	-0.94	-1.57	-0.31	0.0100
Q4VAA2	Protein CDV3	-0.94	-1.42	-0.46	0.0026
P23953	Carboxylesterase 1C	-0.94	-1.57	-0.31	0.0098
Q62165	Dystroglycan	-0.94	-1.44	-0.45	0.0030
Q9D819	Inorganic pyrophosphatase	-0.95	-1.42	-0.48	0.0022
B1B1A8	Myosin light chain kinase, smooth muscle	-0.95	-1.49	-0.41	0.0044
Q9R0P5	Destrin	-0.95	-1.50	-0.40	0.0051
Q9DCV4	Regulator of microtubule dynamics protein 1	-0.96	-1.46	-0.46	0.0030
P30416	Peptidyl-prolyl cis-trans isomerase FKBP4	-0.96	-1.50	-0.41	0.0045
Q61239	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha	-0.96	-1.47	-0.45	0.0033
Q61247	Alpha-2-antiplasmin	-0.96	-1.51	-0.41	0.0047
Q9CPP6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	-0.96	-1.48	-0.45	0.0032
Q00898	Alpha-1-antitrypsin 1-5	-0.97	-1.47	-0.47	0.0028
Q3U0V1	Far upstream element-binding protein 2	-0.97	-1.57	-0.36	0.0074
Q9WV80	Sorting nexin-1	-0.97	-1.45	-0.49	0.0022

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
Q99LP6	GrpE protein homolog 1, mitochondrial	-0.97	-1.57	-0.37	0.0066
E9Q1Q9	Ketohexokinase	-0.97	-1.44	-0.51	0.0018
P35700	Peroxiredoxin-1	-0.98	-1.45	-0.51	0.0019
Q9EPB4	Apoptosis-associated speck-like protein containing a CARD	-0.98	-1.59	-0.37	0.0071
F8WGL3	Cofilin-1	-0.99	-1.49	-0.49	0.0024
Q9WVA4	Transgelin-2	-0.99	-1.56	-0.42	0.0049
P63028	Translationally-controlled tumor protein	-0.99	-1.64	-0.34	0.0091
P17751	Triosephosphate isomerase	-0.99	-1.49	-0.50	0.0022
O70251	Elongation factor 1-beta	-0.99	-1.50	-0.49	0.0026
Q9WTR5	Cadherin-13	-1.00	-1.49	-0.51	0.0021
O08677	Kininogen-1	-1.01	-1.50	-0.51	0.0021
O08997	Copper transport protein ATOX1	-1.01	-1.54	-0.48	0.0030
Q7TQH0	Ataxin-2-like protein	-1.01	-1.59	-0.43	0.0048
Q99LN9	Deoxyhypusine hydroxylase	-1.01	-1.63	-0.39	0.0067
Q62523	Zyxin	-1.01	-1.48	-0.55	0.0015
P29699	Alpha-2-HS-glycoprotein	-1.02	-1.66	-0.38	0.0071
Q78J03	Methionine-R-sulfoxide reductase B2, mitochondrial	-1.03	-1.50	-0.56	0.0014
Q9DCB8	Iron-sulfur cluster assembly 2 homolog, mitochondrial	-1.03	-1.55	-0.50	0.0026
P50543	Protein S100-A11	-1.03	-1.61	-0.46	0.0040
P07758	Alpha-1-antitrypsin 1-1	-1.04	-1.53	-0.55	0.0017
Q9D1I5	Methylmalonyl-CoA epimerase, mitochondrial	-1.04	-1.54	-0.54	0.0018
Q9D6S7	Ribosome-recycling factor, mitochondrial	-1.04	-1.54	-0.55	0.0017
Q8BP40	Lysophosphatidic acid phosphatase type 6	-1.04	-1.58	-0.50	0.0027
Q8BFS6	Calcineurin-like phosphoesterase domain-containing protein 1	-1.05	-1.52	-0.57	0.0014
Q9CZ04	COP9 signalosome complex subunit 7a	-1.06	-1.53	-0.59	0.0012
Q61171	Peroxiredoxin-2	-1.06	-1.56	-0.57	0.0016
P32020	Non-specific lipid-transfer protein	-1.06	-1.61	-0.52	0.0026
Q8VCI5	Peroxisomal biogenesis factor 19	-1.06	-1.69	-0.44	0.0053
Q9CRB6	Tubulin polymerization-promoting protein family member 3	-1.07	-1.53	-0.60	0.0011
Q07456	Protein AMBP (Trypstatin)	-1.07	-1.72	-0.42	0.0063
Q62048	Astrocytic phosphoprotein PEA-15	-1.08	-1.55	-0.61	0.0010

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
Q64213	Splicing factor 1	-1.08	-1.60	-0.56	0.0018
F8WIA1	CAP-Gly domain-containing linker protein 1	-1.08	-1.60	-0.56	0.0019
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	-1.09	-1.56	-0.61	0.0011
A2ADY9	Protein DDI1 homolog 2	-1.09	-1.63	-0.55	0.0022
P22599	Alpha-1-antitrypsin 1-2	-1.09	-1.60	-0.58	0.0016
Q3UMF0	Cordon-bleu protein-like 1	-1.09	-1.80	-0.38	0.0084
P04117	Fatty acid-binding protein, adipocyte	-1.09	-1.57	-0.62	0.0011
P51859	Hepatoma-derived growth factor	-1.09	-1.64	-0.54	0.0024
Q9DBB9	Carboxypeptidase N subunit 2	-1.10	-1.62	-0.58	0.0016
F7AA26	A-kinase anchor protein 2	-1.10	-1.58	-0.63	0.0010
P70296	Phosphatidylethanolamine-binding protein 1	-1.10	-1.66	-0.54	0.0025
Q9QXC1	Fetuin-B	-1.11	-1.59	-0.63	0.0011
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	-1.11	-1.64	-0.59	0.0016
Q60631	Growth factor receptor-bound protein 2	-1.11	-1.75	-0.48	0.0046
P61148	Fibroblast growth factor 1	-1.12	-1.60	-0.64	0.0010
P28665	Murinoglobulin-1	-1.12	-1.63	-0.62	0.0012
Q9CR21	Acyl carrier protein, mitochondrial	-1.13	-1.67	-0.58	0.0019
O08532	Voltage-dependent calcium channel subunit alpha-2/delta-1	-1.14	-1.63	-0.65	0.0010
D3YZD8	UPF0366 protein C11orf67 homolog	-1.16	-1.64	-0.68	0.0008
Q9CQX8	28S ribosomal protein S36, mitochondrial	-1.17	-1.68	-0.66	0.0011
Q62446	Peptidyl-prolyl cis-trans isomerase FKBP3	-1.18	-1.83	-0.52	0.0041
Q8K3C3	Protein LZIC	-1.19	-1.76	-0.61	0.0020
P07724	Serum albumin	-1.20	-1.68	-0.72	0.0007
A6X935	Inter alpha-trypsin inhibitor, heavy chain 4	-1.20	-1.68	-0.71	0.0007
Q8R4S0	Protein phosphatase 1 regulatory subunit 14C	-1.20	-1.76	-0.63	0.0017
Q922Y1	UBX domain-containing protein 1	-1.20	-1.90	-0.51	0.0048
Q9R0Y5	Adenylate kinase isoenzyme 1	-1.21	-1.67	-0.74	0.0006
Q9DCL8	Protein phosphatase inhibitor 2	-1.21	-1.75	-0.66	0.0013
P09528	Ferritin heavy chain	-1.21	-1.84	-0.58	0.0029
Q93092	Transaldolase	-1.21	-1.79	-0.63	0.0019
Q91X72	Hemopexin	-1.22	-1.77	-0.68	0.0012

Protein IDs	Protein name	Mean (Fc CTSA/WT)	CI 95 % L	CI 95 % R	p-value
E9PYJ9	LIM domain-binding protein 3	-1.23	-1.94	-0.51	0.0051
Q08091	Calponin-1	-1.23	-1.79	-0.67	0.0014
E9QPX3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	-1.24	-1.94	-0.54	0.0044
Q9QZ23	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial	-1.25	-1.75	-0.74	0.0007
Q9WVJ3	Carboxypeptidase Q	-1.25	-1.87	-0.63	0.0022
P30681	High mobility group protein B2	-1.27	-1.75	-0.80	0.0004
Q9JLQ0	CD2-associated protein	-1.28	-1.76	-0.80	0.0005
Q9DBP5	UMP-CMP kinase	-1.28	-1.76	-0.80	0.0004
P34022	Ran-specific GTPase-activating protein	-1.30	-1.76	-0.83	0.0004
P54726	UV excision repair protein RAD23 homolog A	-1.32	-1.86	-0.78	0.0007
Q9CQF4	Uncharacterized protein C6orf203 homolog	-1.32	-1.88	-0.77	0.0009
Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	-1.34	-1.83	-0.85	0.0004
Q00915	Retinol-binding protein 1	-1.36	-2.04	-0.68	0.0023
P62960	Nuclease-sensitive element-binding protein 1	-1.39	-1.91	-0.87	0.0005
P97825	Hematological and neurological expressed 1 protein	-1.39	-1.93	-0.86	0.0005
Q9DC77	Small muscular protein	-1.42	-2.25	-0.58	0.0053
P11404	Fatty acid-binding protein, heart	-1.46	-2.11	-0.82	0.0012
E9QJT5	Acylphosphatase;Acylphosphatase-1	-1.47	-2.05	-0.88	0.0007
P61759	Prefoldin subunit 3	-1.48	-2.01	-0.94	0.0004
Q9CWW6	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	-1.48	-2.19	-0.77	0.0019
P51885	Lumican	-1.49	-2.04	-0.94	0.0004
Q9WUZ7	SH3 domain-binding glutamic acid-rich protein	-1.53	-2.18	-0.88	0.0009
P06330	Ig heavy chain V region AC38 205.12	-1.54	-2.09	-0.99	0.0004
P04247	Myoglobin	-1.58	-2.60	-0.56	0.0083
P24472	Glutathione S-transferase A4	-1.61	-2.07	-1.15	0.0001
Q9WUK2	Eukaryotic translation initiation factor 4H	-1.73	-2.53	-0.94	0.0014
H3BL37	Treacle protein	-1.88	-2.55	-1.21	0.0003
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	-1.93	-2.43	-1.44	0.0000
Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	-2.02	-2.85	-1.19	0.0008
P01872	Ig mu chain C region secreted form	-2.40	-3.02	-1.77	0.0001