

Protein accession	Protein description	Gene name	MW [kDa]	Score	Coverage [%]	Peptides	B/A Ratio	P value
P80723	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1	BASP1	22.693	323.31	84.6	16	4.211	1.62448E-12
Q9UQN3	Charged multivesicular body protein 2b OS=Homo sapiens GN=CHMP2B	CHMP2B	23.906	32.712	30	10	2.234	1.62448E-12
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1	SOD1	15.936	35.253	35.7	7	9.093	6.5113E-07
O43895	Xaa-Pro aminopeptidase 2 OS=Homo sapiens GN=XPNPEP2	XPNPEP2	75.624	122.19	19.7	15	2.223	1E-32
Q9H008	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase OS=Homo sapiens GN=LHPP LHPP	LHPP	29.165	8.4514	11.1	3	3.144	1.8805E-09
P48637	Glutathione synthetase OS=Homo sapiens GN=GSS	GSS	52.384	22.307	19.2	9	2.265	8.4063E-05
P63208	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1	SKP1	18.658	32.911	13.5	2	2.239	0.0064199
P29373	Cellular retinoic acid-binding protein 2 OS=Homo sapiens GN=CRABP2	CRABP2	15.693	29.029	24.6	3	3.454	0.000444
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1	TPI1	30.791	149.74	35	10	3.004	4.23783E-12
P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2	TAGLN2	22.391	20.561	18.6	4	2.106	4.7708E-08
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH	HAGH	33.805	14.542	19.5	6	3.433	0.00181943
P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11	S100A11	11.74	7.202	26.7	3	4.784	5.6504E-05
Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1	ACY1	45.884	59.546	29.7	12	3.392	3.66374E-15
Q7LBR1	Charged multivesicular body protein 1b OS=Homo sapiens GN=CHMP1B	CHMP1B	22.109	11.963	30.2	8	3.535	1.62459E-12
P23588	Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B	EIF4B	69.15	30.308	3.6	2	2.736	0.029215
Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD	HGD	49.963	15.484	10.6	4	3.29	0.0102787
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2	PRDX2	21.892	8.5666	26.8	6	2.721	1.71874E-05
P09327	Villin-1 OS=Homo sapiens GN=VIL1	VIL1	92.694	25.174	7.5	6	2.442	0.00077926
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6	PSMA6	27.399	6.121	8.5	2	2.431	0.043237
P30626	Sorcin OS=Homo sapiens GN=SRI	SRI	21.676	28.132	29.8	6	2.872	3.6028E-05
Q99417	C-Myc-binding protein OS=Homo sapiens GN=MYCBP	MYCBP	11.967	4.8947	18.4	2	2.437	0.0093602
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1	ENO1	47.168	127.52	31.3	18	3.045	1E-32
P46952	3-hydroxyanthranilate 3,4-dioxygenase OS=Homo sapiens GN=HAAO	HAAO	32.556	7.132	13.6	4	4.428	0.00046066
P29966	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS	MARCKS	31.554	68.63	19	4	3.336	0.0042951
P62328	Thymosin beta-4 OS=Homo sapiens GN=TMSB4X	TMSB4X	5.0526	10.306	77.3	5	3.516	0.036279
P30046	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT	DDT	12.712	27.5	17.8	2	3.811	0.0055243
Q13938	Calcyphosin OS=Homo sapiens GN=CAPS	CAPS	20.967	30.292	32.8	6	3.119	6.4015E-05
P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB	FGB	55.928	20.297	5.5	3	3.113	0.00099757
P10599	Thioredoxin OS=Homo sapiens GN=TXN	TXN	11.737	19.514	40	5	7.004	5.9185E-05
Q9Y266	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC	NUDC	38.242	17.115	8.5	3	2.479	0.0180577
P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6	S100A6	10.18	6.0238	34.4	4	4.369	4.7521E-08
Q02383	Semenogelin-2 OS=Homo sapiens GN=SEMG2	SEMG2	65.444	323.31	64.3	41	2.255	1.62426E-12
P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4	TPM4	28.521	40.98	35.5	11	3.28	0.00031849
O75368	SH3 domain-binding glutamic acid-rich-like protein OS=Homo sapiens GN=SH3BGRL	SH3BGRL	12.774	32.364	22.8	3	4.353	0.00043952
Q9H0W9	Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54	C11orf54	35.117	38.586	14.3	4	3.579	0.0034968
Q99584	Protein S100-A13 OS=Homo sapiens GN=S100A13	S100A13	11.471	19.506	35.7	4	4.682	4.0517E-05
O75347	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA	TBCA	12.855	10.288	26.9	4	7.017	0.0060404
Q96LB4	V-type proton ATPase subunit G 3 OS=Homo sapiens GN=ATP6V1G3	ATP6V1G3	13.917	21.281	38.1	3	2.083	0.0034013
Q15907	Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B	RAB11B	24.488	36.125	28.4	7	2.046	2.3798E-06
P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1	AKR1B1	35.853	19.128	21.2	9	2.601	8.4436E-08
Q9BY43	Charged multivesicular body protein 4a OS=Homo sapiens GN=CHMP4A	CHMP4A	25.098	87.242	23.9	5	2.131	0.00028473
Q9NZZ3	Charged multivesicular body protein 5 OS=Homo sapiens GN=CHMP5	CHMP5	24.57	40.247	16.9	4	4.504	0.000162624
P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B	RAD23B	43.171	66.679	19.3	8	2.589	0.000181308

P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP	PNP	32.118	28.154	15.6	4	2.091	1.544E-05
O75348	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1	ATP6V1G1	13.757	45.317	43.2	5	3.824	0.027684
Q96FJ2	Dynein light chain 2, cytoplasmic OS=Homo sapiens GN=DYNLL2	DYNLL2	10.35	1.201	7.9	1	2.52	0.0163791
P07148	Fatty acid-binding protein, liver OS=Homo sapiens GN=FABP1	FABP1	14.208	29.419	24.4	3	5.375	0.00093876
P49006	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1	MARCKSL1	19.529	55.877	19.5	3	3.932	0.00193808
O75363	Breast carcinoma-amplified sequence 1 OS=Homo sapiens GN=BCAS1	BCAS1	61.708	28.571	16.4	10	2.302	1.50411E-05
Q9Y2Q5	Ragulator complex protein LAMTOR2 OS=Homo sapiens GN=LAMTOR2	LAMTOR2	13.507	6.8398	24.8	3	2.864	0.000197753
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1	PEBP1	21.057	52.404	29.4	6	5.399	7.7946E-08
Q04760	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1	GLO1	20.777	6.5737	17.4	5	2.888	1.53611E-05
P02788	Lactotransferrin OS=Homo sapiens GN=LTF	LTF	78.181	323.31	42.3	27	2.011	1E-32
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1	ALDH9A1	53.801	58.95	21.3	10	2.28	1.3641E-09
Q6P1N9	Putative deoxyribonuclease TATDN1 OS=Homo sapiens GN=TATDN1	TATDN1	33.601	8.2036	10.1	3	2.145	0.029663
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6	PSMB6	25.357	17.224	13.4	3	2.282	0.007717
Q15847	Adipogenesis regulatory factor OS=Homo sapiens GN=ADIRF	ADIRF	7.8547	45.77	38.2	3	5.131	0.007097
P12821	Angiotensin-converting enzyme OS=Homo sapiens GN=ACE	ACE	149.71	142.55	14.5	20	2.633	1E-32
P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH	FAH	46.374	16.297	9.8	4	2.675	0.00032189
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1	PRDX1	22.11	47.953	52.8	11	2.413	1.22125E-15
Q5T2W1	Na(+)/H(+) exchange regulatory cofactor NHE-RF3 OS=Homo sapiens GN=PDZK1	PDZK1	57.129	85.05	19.1	11	2.02	1.63014E-12
Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT	BHMT	44.998	98.046	28.6	12	3.641	4.6741E-06
P05937	Calbindin OS=Homo sapiens GN=CALB1	CALB1	30.025	55.551	36.4	12	3.494	8.00471E-13
Q9H7C9	Mth938 domain-containing protein OS=Homo sapiens GN=AAMDC	AAMDC	13.332	24.757	29.5	3	2.373	0.002096
O43633	Charged multivesicular body protein 2a OS=Homo sapiens GN=CHMP2A	CHMP2A	25.104	15.759	22.5	6	3.475	1.7087E-08
P29218	Inositol monophosphatase 1 OS=Homo sapiens GN=IMPA1	IMPA1	30.188	23.802	12.6	3	2.888	2.8213E-06
Q99497	Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7	PARK7	19.891	119.1	40.7	9	3.546	1.3771E-09
O00757	Fructose-1,6-bisphosphatase isozyme 2 OS=Homo sapiens GN=FBP2	FBP2	36.743	7.2214	8.3	3	3.909	0.00076104
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A	FKBP1A	11.951	62.383	25	2	2.934	0.0064967
P36543	V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1	ATP6V1E1	26.145	11.979	24.3	6	2.329	1.63175E-05
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA	RHOA	21.768	36.607	22.8	6	2.055	1.6559E-09
P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12	HRSP12	14.494	17.728	20.4	3	4.488	0.0036603
Q96HD9	N-acyl-aromatic-L-amino acid amidohydrolase (carboxylate-forming) OS=Homo sapiens GN=ACY3	ACY3	35.241	13.274	11.6	4	3.883	0.0038162
P04040	Catalase OS=Homo sapiens GN=CAT	CAT	59.755	61.825	20.3	10	2.778	0.00146262
P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR	QDPR	25.789	22.376	16.8	4	2.776	0.00083581
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH	APEH	81.224	15.147	8.2	8	2.126	5.9806E-05
Q8NFI4	Putative protein FAM10A5 OS=Homo sapiens GN=ST13P5	ST13P5	41.377	51.447	11.9	4	2.68	4.4887E-05
O75223	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT	GGCT	21.007	40.676	28.2	5	3.354	4.8116E-06
P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3	UBE2L3	17.861	6.546	16.2	3	2.32	2.0181E-05
Q9BQI0	Allograft inflammatory factor 1-like OS=Homo sapiens GN=AIF1L	AIF1L	17.068	4.8329	27.3	4	3.587	0.0197358
Q9H444	Charged multivesicular body protein 4b OS=Homo sapiens GN=CHMP4B	CHMP4B	24.95	108.16	29.5	9	3.535	2.7385E-10
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1	SLC9A3R1	38.868	155.55	40.2	15	2.973	2.2674E-11
P16083	Ribosylidihydroxynicotinamide dehydrogenase [quinone] OS=Homo sapiens GN=NQO2	NQO2	25.918	19.706	21.6	5	2.736	0.0124758
Q5VV67	Peroxisome proliferator-activated receptor gamma coactivator-related protein 1 OS=Homo sapiens GN=PPRC1	PPRC1	177.54	1.2258	0.4	1	2.111	0.00046446
P02679	Fibrinogen gamma chain OS=Homo sapiens GN=FGG	FGG	51.511	18.614	13.2	7	2.126	1.9822E-08
P46926	Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1	GNPDA1	32.668	12.111	14.2	4	2.314	0.004756
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1	STIP1	62.639	19.904	17.5	11	2.234	1.2409E-06
Q6UWP2	Dehydrogenase/reductase SDR family member 11 OS=Homo sapiens GN=DHRS11	DHRS11	28.308	18.492	15	4	2.562	7.5283E-05

Q9NUP9	Protein lin-7 homolog C OS=Homo sapiens GN=LIN7C	LIN7C	21.834	10.158	20.3	4	2.185	0.0140432
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C	NSFL1C	40.572	6.0811	6.5	3	2.003	0.0064403
Q9HD42	Charged multivesicular body protein 1a OS=Homo sapiens GN=CHMP1A	CHMP1A	21.703	8.636	19.9	5	2.721	6.0441E-08
O00244	Copper transport protein ATOX1 OS=Homo sapiens GN=ATOX1	ATOX1	7.4016	2.9949	13.2	2	2.471	0.038036
P12955	Xaa-Pro dipeptidase OS=Homo sapiens GN=PEPD	PEPD	54.548	23.812	13.8	7	4.634	0.0025396
P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP	ANPEP	109.54	323.31	21.7	24	2.474	1E-32
P62158	Calmodulin OS=Homo sapiens GN=CALM1	CALM1	16.837	47.685	32.9	7	4.905	1.7069E-11
P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1	FBP1	36.842	42.397	25.7	10	4.384	1.70039E-05
Q8IYE0	Coiled-coil domain-containing protein 146 OS=Homo sapiens GN=CCDC146	CCDC146	112.81	4.1252	0.9	1	4.048	0.0095977
Q96C23	Aldose 1-epimerase OS=Homo sapiens GN=GALM	GALM	37.765	49.133	8.5	2	2.812	0.00020438
Q9BRF8	Serine/threonine-protein phosphatase CPPED1 OS=Homo sapiens GN=CPPED1	CPPED1	35.548	14.676	15.6	5	2.291	0.023059
P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4	S100A4	11.728	6.4601	16.8	3	2.396	0.00071948
Q9BUT1	3-hydroxybutyrate dehydrogenase type 2 OS=Homo sapiens GN=BDH2	BDH2	26.724	39.326	33.5	7	2.429	3.4967E-08
P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1	GSTP1	23.356	18.355	21	4	2.509	0.0062045
Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2	NIT2	30.608	58.309	26.1	6	3.234	2.2196E-05
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3	PSMA3	28.433	10.159	15.3	4	2.06	2.3729E-05
P27487	Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4	DPP4	88.278	166.35	26.9	24	2.324	1E-32
Q9HC38	Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4	GLOD4	34.793	49.946	31	10	2.178	2.2668E-08
P05413	Fatty acid-binding protein, heart OS=Homo sapiens GN=FABP3	FABP3	14.858	10.591	41.4	6	5.416	2.8137E-07
Q9NRV9	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1	HEBP1	21.097	17.492	32.3	6	2.175	4.295E-05
Q9Y5Z4	Heme-binding protein 2 OS=Homo sapiens GN=HEBP2	HEBP2	22.875	18.933	24.9	5	2.934	0.00036188
Q5T601	Adhesion G-protein coupled receptor F1 OS=Homo sapiens GN=ADGRF1	ADGRF1	101.36	14.511	6.2	6	2.431	0.025377
P08236	Beta-glucuronidase OS=Homo sapiens GN=GUSB	GUSB	74.731	6.6001	5.8	5	2.454	6.0229E-05
P20810	Calpastatin OS=Homo sapiens GN=CAST	CAST	76.572	17.71	10.7	6	2.596	0.000135961
P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1	ALDH1A1	54.861	27.614	13.4	8	2.154	1.98121E-05
P07108	Acyl-CoA-binding protein OS=Homo sapiens GN=DBI	DBI	10.044	31.403	54	4	10.377	1.3946E-06
P21283	V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1	ATP6V1C1	43.941	19.171	19.1	9	2.111	4.248E-08
Q08257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ	CRYZ	35.206	31.714	23.7	8	2.351	9.4287E-08