

Master No.	Swiss-prot No.	Protein name	pI	MW	No. Match. Peptides	Cov. (%)	Score	Subcellular location	Functional ontology	Poor / Well Av.Ratio:	Poor / Well T-test	Matched peptides with top score
620	P02763	Alpha-1-acid glycoprotein 1	4.93	23725	9/49	29%	107/56	Secreted	Transport	1.94	0.017	K.WFYIASAFR.N K.TEDTIFLR.E
629	P02763	Alpha-1-acid glycoprotein 1	4.93	23725	13/59	51%	147/56	Secreted	Transport	1.86	0.00094	K.WFYIASAFR.N K.TEDTIFLR.E
652	P02763	Alpha-1-acid glycoprotein 1	4.93	23725	12/51	40%	148/56	Secreted	Transport	1.88	0.00066	K.WFYIASAFR.N K.TEDTIFLR.E
656	P02763	Alpha-1-acid glycoprotein 1	4.93	23725	13/52	48%	140/56	Secreted	Transport	1.94	0.0022	K.WFYIASAFR.N K.TEDTIFLR.E
674	P02763	Alpha-1-acid glycoprotein 1	4.93	23725	13/59	40%	130/56	Secreted	Transport	1.7	0.017	K.WFYIASAFR.N K.TEDTIFLR.E
681	P02763	Alpha-1-acid glycoprotein 1	4.93	23725	11/65	47%	127/56	Secreted	Transport	1.47	0.033	K.WFYIASAFR.N K.TEDTIFLR.E
668	P19652	Alpha-1-acid glycoprotein 2	5.03	23873	14/48	39%	141/56	Secreted	Transport	2.02	0.00071	K.WFYIASAFR.N K.TEDTIFLR.E
344	P01011	Alpha-1-antichymotrypsin	5.33	47792	17/56	32%	150/56	Secreted	Inflammatory response	1.72	0.0011	K.EQLSLLDR.F K.EQLSLLDR.F
296	P01011	Alpha-1-antichymotrypsin	5.33	47792	19/56	30%	150/56	Secreted	Inflammatory response	1.63	0.035	K.EQLSLLDR.F+Glu->pyro-Glu(N-termE) K.EQLSLLDR.F
334	P01011	Alpha-1-antichymotrypsin	5.33	47792	17/56	32%	150/56	Secreted	Inflammatory response	1.47	0.0096	K.EQLSLLDR.F+Glu->pyro-Glu(N-termE) K.EQLSLLDR.F
338	P01011	Alpha-1-antichymotrypsin	5.33	47792	19/68	39%	150/56	Secreted	Inflammatory response	1.75	0.00035	K.EQLSLLDR.F+Glu->pyro-Glu(N-termE) K.EQLSLLDR.F
350	P01011	Alpha-1-antichymotrypsin	5.33	47792	17/85	28%	127/56	Secreted	Inflammatory response	1.53	0.0019	K.EQLSLLDR.F+Glu->pyro-Glu(N-termE) K.EQLSLLDR.F
358	P01011	Alpha-1-antichymotrypsin	5.33	47792	19/50	37%	153/56	Secreted	Inflammatory response	1.65	0.00065	K.EQLSLLDR.F+Glu->pyro-Glu(N-termE) K.EQLSLLDR.F
378	P01011	Alpha-1-antichymotrypsin	5.33	47792	18/48	32%	152/56	Secreted	Inflammatory response	1.42	0.0018	K.EQLSLLDR.F+Glu->pyro-Glu(N-termE) K.EQLSLLDR.F
277	P01011	Alpha-1-antichymotrypsin	5.33	47792	26/89	40%	203/56	Secreted	Inflammatory response	1.47	0.0016	K.QLVLK.A K.EQLSLLDR.F+Glu->pyro-Glu(N-termE)
377	P01011	Alpha-1-antichymotrypsin	5.33	47792	20/50	33%	190/56	Secreted	Inflammatory response	1.38	0.0083	K.QLVLK.A K.EQLSLLDR.F+Glu->pyro-Glu(N-termE)
505	P01009	Alpha-1-antitrypsin	5.37	46878	17/60	27%	124/56	Secreted	Inflammatory response	1.32	0.049	K.FLEDVKK.L K.KQINDYVEK.G
459	P01009	Alpha-1-antitrypsin	5.37	46878	23/65	33%	180/56	Secreted	Inflammatory response	2.14	0.0011	K.ITPNLAEFASFSLYR.Q K.FLEDVKK.L
284	P01009	Alpha-1-antitrypsin	5.37	46878	17/39	22%	125/56	Secreted	Inflammatory response	1.42	0.0062	K.ITPNLAEFASFSLYR.Q K.KQINDYVEK.G
461	P01009	Alpha-1-antitrypsin	5.37	46878	28/100	47%	223/56	Secreted	Inflammatory response	2	0.0067	K.TDTSHHDQDHPFNF.K K.FLEDVK.K

509	P01009	Alpha-1-antitrypsin	5.37	46878	29/81	47%	202/56	Secreted	Inflammatory response	1.35	0.0069	K.TDTSHHDQDHPTFNK.I K.FLEDVKK.L
507	P01009	Alpha-1-antitrypsin	5.37	46878	14/35	30%	131/56	Secreted	Inflammatory response	1.86	0.016	K.TDTSHHDQDHPTFNK.I K.GKWERPFVEVK.D
416	P01009	Alpha-1-antitrypsin	5.37	46878	30/100	63%	284/56	Secreted	Inflammatory response	2.21	0.0015	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
423	P01009	Alpha-1-antitrypsin	5.37	46878	32/90	54%	270/56	Secreted	Inflammatory response	1.92	0.0014	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
431	P01009	Alpha-1-antitrypsin	5.37	46878	29/88	54%	238/56	Secreted	Inflammatory response	2.63	0.0000047	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
434	P01009	Alpha-1-antitrypsin	5.37	46878	29/88	54%	238/56	Secreted	Inflammatory response	2.48	0.000093	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
462	P01009	Alpha-1-antitrypsin	5.37	46878	20/68	39%	191/56	Secreted	Inflammatory response	2.24	0.00014	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
466	P01009	Alpha-1-antitrypsin	5.37	46878	27/83	48%	220/56	Secreted	Inflammatory response	2.02	0.000064	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
483	P01009	Alpha-1-antitrypsin	5.37	46878	35/100	59%	258/56	Secreted	Inflammatory response	1.94	0.00041	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
542	P01009	Alpha-1-antitrypsin	5.37	46878	29/85	55%	259/56	Secreted	Inflammatory response	2.5	0.013	K.TDTSHHDQDHPTFNK.I K.ITPNLAIEFAFSLYR.Q
174	P04217	Alpha-1B-glycoprotein	5.56	54790	12/44	22%	118/56	Secreted	Inflammatory response	1.88	0.0085	K.HQFLTGTQGR.Y R.SGLSTGWTQLSK.L
239	P04217	Alpha-1B-glycoprotein	5.56	54790	13/44	26%	135/56	Secreted	Inflammatory response	1.32	0.011	K.HQFLTGTQGR.Y R.SGLSTGWTQLSK.L
240	P04217	Alpha-1B-glycoprotein	5.56	54790	15/43	34%	187/56	Secreted	Inflammatory response	1.39	0.019	K.HQFLTGTQGR.Y R.SGLSTGWTQLSK.L
241	P04217	Alpha-1B-glycoprotein	5.56	54790	13/43	36%	165/56	Secreted	Inflammatory response	1.57	0.0076	K.NGVAQEPVHLDSPAIK.H K.HQFLTGTQGR.Y
400	P02765	Alpha-2-HS-glycoprotein	5.43	40098	5/27	11%	61/56	Secreted	Inflammatory response	2	0.019	K.HTLNQIDEVK.V K.EHAVEGDCDFQLLK.L
404	P02765	Alpha-2-HS-glycoprotein	5.43	40098	11/47	22%	74/56	Secreted	Inflammatory response	1.63	0.0037	K.HTLNQIDEVK.V K.EHAVEGDCDFQLLK.L+Glu->pyro-Glu(N-termE)
619	P06727	Apolipoprotein A-IV	5.28	45371	31/92	58%	237/56	Secreted	Transport	1.46	0.018	K.LGEVNTYAGDLQK.K K.KLVFPFATELHER.L
215	P04003	C4b-binding protein alpha chain	7.15	69042	13/43	19%	95/56	Secreted	Inflammatory response	-1.41	0.033	K.MAAWPFSR.L K.YTCLPGYVR.S
286	P04003	C4b-binding protein alpha chain	7.15	69042	20/39	25%	183/56	Secreted	Inflammatory response	-1.55	0.04	K.MAAWPFSR.L R.FKTGTTLK.Y
959	P00450	Ceruloplasmin	5.44	122983	14/24	9%	111/56	Secreted	Transport	-1.35	0.045	K.ALYLQYTDETR.T K.VYVHLK.N
762	P10909	Clusterin	5.89	53031	14/60	21%	61/56	Secreted	Apoptosis	1.31	0.013	K.EDALNETR.E+Glu->pyro-Glu(N-termE) R.ASSIIDELFQDR.F

744	P10909	Clusterin	5.89	53031	12/58	26%	76/56	Secreted	Apoptosis	1.43	0.025	K.QTCMKFYAR.V R.QQTHMLDVMQDHF.SR.A+Gln->pyro- Glu(N-termQ);2Oxidation(M)
299	P02746	Complement C1q subcomponent subunit B	8.83	26933	13/58	38%	120/56	Secreted	Inflammatory response	1.67	0.00031	K.GEKGLPGLAGDHGEFGEK.G K.IAFSATR.T
982	P02746	Complement C1q subcomponent subunit B	8.83	26933	12/32	38%	136/56	Secreted	Inflammatory response	-1.43	0.013	K.GEKGLPGLAGDHGEFGEK.G K.IAFSATR.T
131	P09871	Complement C1s subcomponent	4.86	78174	25/84	27%	170/56	Secreted	Inflammatory response	1.35	0.0086	R.LCGQR.S K.LQVIFK.S
257	P02748	Complement component C9	5.43	64615	13/53	18%	86/56	Secreted	Inflammatory response	1.47	0.0099	R.SIEVFGQFNGK.R R.VVEESELAR.T
86	P00751	Complement factor B	6.67	86847	33/74	28%	233/56	Secreted	Inflammatory response	1.61	0.0054	R.STGSWSTLK.T K.TQDQK.T
98	P00751	Complement factor B	6.67	86847	20/52	19%	152/56	Secreted	Inflammatory response	1.5	0.031	R.STGSWSTLK.T R.KVGSQYR.L
106	P00751	Complement factor B	6.67	86847	20/27	24%	221/56	Secreted	Inflammatory response	1.36	0.031	R.STGSWSTLK.T R.KVGSQYR.L
73	P00751	Complement factor B	6.67	86847	7/11	8%	74/56	Secreted	Inflammatory response	1.45	0.03	R.STGSWSTLK.T R.TCQVNGR.W
79	P00751	Complement factor B	6.67	86847	20/56	21%	131/56	Secreted	Inflammatory response	1.55	0.023	R.STGSWSTLK.T R.TCQVNGR.W
69	P00751	Complement factor B	6.67	86847	13/44	12%	78/56	Secreted	Inflammatory response	1.82	0.045	R.TCQVNGR.W R.KVGSQYR.L
76	P00751	Complement factor B	6.67	86847	15/24	18%	151/56	Secreted	Inflammatory response	1.74	0.011	R.TCQVNGR.W R.KVGSQYR.L
83	P00751	Complement factor B	6.67	86847	29/63	28%	232/56	Secreted	Inflammatory response	1.39	0.028	R.STGSWSTLK.T K.TQDQK.T
912	P36980	Complement factor H-related protein 2	6	31543	5/25	14%	58/56	Secreted	Inflammatory response	2.16	0.044	K.SFWTR.I R.ITCAEEGWSPTPK.C
984	Q7L5A8	Fatty acid 2-hydroxylase	8.76	42935	8/49	22%	63/56	Secreted	Lipid metabolism	-1.56	0.0019	MAPAPPPAASFSPSEVQR.R+Acetyl M.APAPPPAASFSPSEVQRR.L
256	P02671	Fibrinogen alpha chain	5.7	95656	31/94	29%	166/56	Secreted	Coagulation	1.64	0.0017	K.CPSGCR.M K.GLIDEVNQDFTNR.I
320	P02671	Fibrinogen alpha chain	5.7	95656	27/72	25%	155/56	Secreted	Coagulation	1.62	0.0086	K.CPSGCR.M K.GLIDEVNQDFTNR.I
321	P02671	Fibrinogen alpha chain	5.7	95656	46/100	33%	225/56	Secreted	Coagulation	1.58	0.0058	K.CPSGCR.M K.GLIDEVNQDFTNR.I
337	P02671	Fibrinogen alpha chain	5.7	95656	32/86	27%	169/56	Secreted	Coagulation	1.58	0.0054	K.CPSGCR.M K.GLIDEVNQDFTNR.I
272	P02671	Fibrinogen alpha chain	5.7	95656	29/58	25%	177/56	Secreted	Coagulation	1.43	0.034	K.GLIDEVNQDFTNR.I K.NSLFEYQK.N
308	P02671	Fibrinogen alpha chain	5.7	95656	33/82	28%	169/56	Secreted	Coagulation	1.47	0.036	K.GLIDEVNQDFTNR.I K.NSLFEYQK.N
322	P02671	Fibrinogen alpha chain	5.7	95656	12/53	12%	64/56	Secreted	Coagulation	1.48	0.013	K.NSLFEYQK.N R.GDFSSANNR.D

315	P02671	Fibrinogen alpha chain	5.7	95656	39/91	33%	218/56	Secreted	Coagulation	1.42	0.017	R.HQSACK.D K.CPSGCR.M
330	P02671	Fibrinogen alpha chain	5.7	95656	43/100	32%	229/56	Secreted	Coagulation	1.53	0.003	R.HQSACK.D K.CPSGCR.M
332	P02671	Fibrinogen alpha chain	5.7	95656	41/100	31%	208/56	Secreted	Coagulation	1.61	0.0015	R.HQSACK.D K.CPSGCR.M
335	P02671	Fibrinogen alpha chain	5.7	95656	40/99	29%	181/56	Secreted	Coagulation	1.52	0.0054	R.HQSACK.D K.CPSGCR.M
336	P02671	Fibrinogen alpha chain	5.7	95656	41/96	35%	217/56	Secreted	Coagulation	1.51	0.01	R.HQSACK.D K.CPSGCR.M
307	P02671	Fibrinogen alpha chain	5.7	95656	41/91	33%	210/56	Secreted	Coagulation	1.51	0.02	R.HQSACK.D K.DSDWPFCSDEDWNYK.C
726	P02671	Fibrinogen alpha chain	5.7	95656	43/100	33%	216/56	Secreted	Coagulation	1.45	0.026	R.HQSACK.D K.DSDWPFCSDEDWNYK.C
511	P02675	Fibrinogen beta chain	8.54	56577	20/59	25%	126/56	Secreted	Coagulation	-2.26	0.023	K.AAATQKK.V K.DLWQK.R
528	P02675	Fibrinogen beta chain	8.54	56577	10/30	14%	72/56	Secreted	Coagulation	-2.79	0.012	K.AAATQKK.V K.DLWQK.R
607	P02675	Fibrinogen beta chain	8.54	56577	27/77	45%	181/56	Secreted	Coagulation	-1.52	0.029	K.AAATQKK.V K.DLWQK.R
883	P02675	Fibrinogen beta chain	8.54	56577	27/77	41%	180/56	Secreted	Coagulation	1.36	0.029	K.DLWQK.R K.DNENVVNEYSSELEK.H
516	P02675	Fibrinogen beta chain	8.54	56577	24/59	36%	157/56	Secreted	Coagulation	-3.08	0.00011	K.DLWQKR.Q K.HQLYIDETVNSNIPTNLR.V
519	P02675	Fibrinogen beta chain	8.54	56577	14/31	25%	109/56	Secreted	Coagulation	-3.34	0.00011	R.EEAPSLRPAPPPISGGGYR.A K.DLWQK.R
520	P02675	Fibrinogen beta chain	8.54	56577	26/100	39%	151/56	Secreted	Coagulation	-3.36	0.00019	R.EEAPSLRPAPPPISGGGYR.A K.DLWQK.R
556	P02675	Fibrinogen beta chain	8.54	56577	24/64	36%	184/56	Secreted	Coagulation	-2.71	0.027	R.GHRPLDK.K K.AAATQKK.V
375	P02675	Fibrinogen beta chain	8.54	56577	21/52	34%	161/56	Secreted	Coagulation	-1.43	0.026	R.GHRPLDK.K K.DLWQK.R
522	P02675	Fibrinogen beta chain	8.54	56577	21/71	28%	151/56	Secreted	Coagulation	-2.35	0.0052	R.GHRPLDK.K K.DLWQK.R
539	P02675	Fibrinogen beta chain	8.54	56577	25/81	38%	177/56	Secreted	Coagulation	-2.95	0.00043	R.GHRPLDK.K K.DLWQK.R
515	P02675	Fibrinogen beta chain	8.54	56577	25/84	38%	174/56	Secreted	Coagulation	-3.27	0.018	R.GHRPLDK.K R.EEAPSLRPAPPPISGGGYR.A
524	P02675	Fibrinogen beta chain	8.54	56577	28/77	49%	183/56	Secreted	Coagulation	-3.08	0.002	R.GHRPLDK.K R.EEAPSLRPAPPPISGGGYR.A
536	P02675	Fibrinogen beta chain	8.54	56577	28/64	49%	230/56	Secreted	Coagulation	-3.17	0.00021	R.GHRPLDK.K R.EEAPSLRPAPPPISGGGYR.A
575	P02675	Fibrinogen beta chain	8.54	56577	20/61	35%	140/56	Secreted	Coagulation	-2.95	0.016	R.GHRPLDK.K R.EEAPSLRPAPPPISGGGYR.A

410	P02675	Fibrinogen beta chain	8.54	56577	28/83	47%	192/56	Secreted	Coagulation	1.39	0.019	R.EEAPSLRPAPPISGGGYR.A+Glu->pyro-Glu(N-termE) R.GHRPLDK.K
442	P02675	Fibrinogen beta chain	8.54	56577	37/86	51%	239/56	Secreted	Coagulation	1.33	0.0025	R.EEAPSLRPAPPISGGGYR.A+Glu->pyro-Glu(N-termE) R.GHRPLDK.K
447	P02675	Fibrinogen beta chain	8.54	56577	29/88	49%	206/56	Secreted	Coagulation	1.46	0.012	R.EEAPSLRPAPPISGGGYR.A+Glu->pyro-Glu(N-termE) R.GHRPLDK.K
1200	P02675	Fibrinogen beta chain	8.54	56577	14/28	20%	104/56	Secreted	Coagulation	1.48	0.0053	R.SILENLR.S K.ECEEIIR.K+Glu->pyro-Glu(N-termE)
506	P02679	Fibrinogen gamma chain	5.37	52106	10/43	13%	77/56	Secreted	Coagulation	2.91	0.048	M.SWSLHPR.N+Acetyl(ProteinN-term) R.DNCCILDER.F
1197	P02679	Fibrinogen gamma chain	5.37	52106	21/62	42%	124/56	Secreted	Coagulation	1.47	0.0023	R.DNCCILDER.F K.AIQLTYNPDESSKPNMIDAATLK.S
490	P02679	Fibrinogen gamma chain	5.37	52106	21/60	33%	174/56	Secreted	Coagulation	1.39	0.017	R.DNCCILDER.F K.YEASILTHDSSIR.Y
558	P02679	Fibrinogen gamma chain	5.37	52106	10/25	23%	110/56	Secreted	Coagulation	1.4	0.0018	R.DNCCILDER.F K.YEASILTHDSSIR.Y
491	P02679	Fibrinogen gamma chain	5.37	52106	14/49	35%	127/56	Secreted	Coagulation	1.53	0.024	R.DNCCILDER.F R.FGSYCPTTCGIADFLSTYQTK.V
644	P00738	Haptoglobin	6.13	45861	23/63	33%	193/56	Secreted	Inflammatory response	7.86	0.0000096	K.GSFPWQAK.M K.DIAPTLTLYVGK.K
735	P00738	Haptoglobin	6.13	45861	18/54	29%	166/56	Secreted	Inflammatory response	3.45	0.000097	K.GSFPWQAK.M K.DIAPTLTLYVGK.K
745	P00738	Haptoglobin	6.13	45861	14/56	29%	113/56	Secreted	Inflammatory response	1.93	0.0006	K.GSFPWQAK.M K.DIAPTLTLYVGK.K
753	P00738	Haptoglobin	6.13	45861	14/45	34%	128/56	Secreted	Inflammatory response	2.75	0.0036	K.GSFPWQAK.M K.DIAPTLTLYVGK.K
761	P00738	Haptoglobin	6.13	45861	15/39	31%	178/56	Secreted	Inflammatory response	1.33	0.0098	K.GSFPWQAK.M K.DIAPTLTLYVGK.K
635	P00738	Haptoglobin	6.13	45861	6/11	14%	78/56	Secreted	Inflammatory response	3.96	0.00013	K.GSFPWQAK.M K.DYAEVGR.V
677	P00738	Haptoglobin	6.13	45861	5/18	8%	60/56	Secreted	Inflammatory response	2.02	0.014	K.GSFPWQAK.M K.VSVNER.V
1122	P00738	Haptoglobin	6.13	45861	10/46	17%	90/56	Secreted	Inflammatory response	1.52	0.0093	K.LRTEGDGVYTLNDK.K R.TEGDGVYTLNDK.K
1134	P00738	Haptoglobin	6.13	45861	11/38	22%	103/56	Secreted	Inflammatory response	1.33	0.045	K.LRTEGDGVYTLNDK.K R.TEGDGVYTLNDK.K
1139	P00738	Haptoglobin	6.13	45861	6/19	12%	80/56	Secreted	Inflammatory response	1.3	0.04	K.LRTEGDGVYTLNDK.K R.TEGDGVYTLNDK.K
1130	P00738	Haptoglobin	6.13	45861	8/20	12%	80/56	Secreted	Inflammatory response	1.41	0.0055	K.LRTEGDGVYTLNDK.K R.YQCK.N
623	P00738	Haptoglobin	6.13	45861	12/26	24%	138/56	Secreted	Inflammatory response	9.99	0.000026	K.LRTEGDGVYTLNNEK.Q K.GSFPWQAK.M

694	P00738	Haptoglobin	6.13	45861	18/78	33%	163/56	Secreted	Inflammatory response	2.07	0.00047	K.LRTEGDGVYTLNNEK.Q R.ILGGHLDK.G
712	P00738	Haptoglobin	6.13	45861	24/78	41%	227/56	Secreted	Inflammatory response	3.01	0.00016	K.QWINKAVGDK.L+Gln->pyro-Glu(N-term) R.ILGGHLDK.G
306	P00738	Haptoglobin	6.13	45861	15/52	26%	136/56	Secreted	Inflammatory response	1.53	0.029	R.ILGGHLDK.G K.GSFPWQAK.M
606	P00738	Haptoglobin	6.13	45861	16/40	30%	139/56	Secreted	Inflammatory response	8.42	0.000043	R.ILGGHLDK.G K.GSFPWQAK.M
612	P00738	Haptoglobin	6.13	45861	19/62	32%	171/56	Secreted	Inflammatory response	1.92	0.0028	R.ILGGHLDK.G K.GSFPWQAK.M
648	P00738	Haptoglobin	6.13	45861	16/47	30%	155/56	Secreted	Inflammatory response	1.86	0.049	R.ILGGHLDK.G K.GSFPWQAK.M
670	P00738	Haptoglobin	6.13	45861	19/81	32%	149/56	Secreted	Inflammatory response	6.47	0.0000032	R.ILGGHLDK.G K.GSFPWQAK.M
682	P00738	Haptoglobin	6.13	45861	23/70	35%	217/56	Secreted	Inflammatory response	4.86	0.000014	R.ILGGHLDK.G K.GSFPWQAK.M
684	P00738	Haptoglobin	6.13	45861	21/60	35%	175/56	Secreted	Inflammatory response	2.48	0.012	R.ILGGHLDK.G K.GSFPWQAK.M
691	P00738	Haptoglobin	6.13	45861	18/85	34%	135/56	Secreted	Inflammatory response	3.3	0.000034	R.ILGGHLDK.G K.GSFPWQAK.M
698	P00738	Haptoglobin	6.13	45861	19/64	35%	142/56	Secreted	Inflammatory response	1.3	0.019	R.ILGGHLDK.G K.GSFPWQAK.M
719	P00738	Haptoglobin	6.13	45861	20/60	38%	180/56	Secreted	Inflammatory response	4.98	0.000049	R.ILGGHLDK.G K.GSFPWQAK.M
721	P00738	Haptoglobin	6.13	45861	18/64	30%	144/56	Secreted	Inflammatory response	2.18	0.00036	R.ILGGHLDK.G K.GSFPWQAK.M
724	P00738	Haptoglobin	6.13	45861	21/47	38%	213/56	Secreted	Inflammatory response	4.67	0.000054	R.ILGGHLDK.G K.GSFPWQAK.M
742	P00738	Haptoglobin	6.13	45861	13/44	29%	120/56	Secreted	Inflammatory response	1.87	0.0019	R.ILGGHLDK.G K.GSFPWQAK.M
1187	P00738	Haptoglobin	6.13	45861	7/35	11%	65/56	Secreted	Inflammatory response	31.94	0.000067	R.YQCK.N K.NYYK.L
739	P00739	Haptoglobin-related protein	6.63	39518	8/38	18%	73/56	Secreted	Inflammatory response	1.79	0.042	K.NYYR.L K.QWINKAVGDK.L
725	P00739	Haptoglobin-related protein	6.63	39518	11/33	23%	110/56	Secreted	Inflammatory response	2.81	0.001	K.NYYR.L R.ILGGHLDK.G
756	P00739	Haptoglobin-related protein	6.63	39518	10/33	24%	133/56	Secreted	Inflammatory response	2.19	0.02	K.NYYR.L R.ILGGHLDK.G
160	P02790	Hemopexin	6.55	52385	17/69	22%	138/56	Secreted	Transport	1.7	0.048	K.GEFVWK.S K.SHKWDR.E
183	P02790	Hemopexin	6.55	52385	19/52	25%	154/56	Secreted	Transport	1.89	0.0015	K.GEFVWK.S K.SHKWDR.E
206	P02790	Hemopexin	6.55	52385	24/78	40%	222/56	Secreted	Transport	1.62	0.012	K.GEFVWK.S K.SHKWDR.E

226	P02790	Hemopexin	6.55	52385	19/54	38%	161/56	Secreted	Transport	1.58	0.0028	K.NFPSPVDAAFR.Q R.QGHNSVFLIK.G+Gln->pyro-Glu(N-
237	P02790	Hemopexin	6.55	52385	15/41	38%	132/56	Secreted	Transport	1.36	0.014	K.SHKWDR.E K.NFPSPVDAAFR.Q
352	P01876	Ig alpha-1 chain C region	6.08	38486	11/45	32%	143/56	Secreted	Immune response	-1.31	0.04	K.SVTCHVK.H R.DASGVFTFTWPSSGK.S
360	P01876	Ig alpha-1 chain C region	6.08	38486	11/44	32%	124/56	Secreted	Immune response	-1.31	0.029	K.SVTCHVK.H R.DASGVFTFTWPSSGK.S
376	P01876	Ig alpha-1 chain C region	6.08	38486	11/61	28%	114/56	Secreted	Immune response	-1.35	0.048	K.SVTCHVK.H R.DASGVFTFTWPSSGK.S
384	P01876	Ig alpha-1 chain C region	6.08	38486	9/36	26%	83/56	Secreted	Immune response	1.41	0.016	K.SVTCHVK.H R.DASGVFTFTWPSSGK.S
526	P01857	Ig gamma-1 chain C region	8.46	36596	9/31	28%	104/56	Secreted	Immune response	-2.35	0.0016	K.GPSVFPLAPSSK.S K.STSGGTAALGCLVK.D
527	P01857	Ig gamma-1 chain C region	8.46	36596	9/31	28%	104/56	Secreted	Immune response	-2.14	0.003	K.GPSVFPLAPSSK.S K.STSGGTAALGCLVK.D
529	P01857	Ig gamma-1 chain C region	8.46	36596	9/21	22%	101/56	Secreted	Immune response	-2.07	0.0011	K.GPSVFPLAPSSK.S K.STSGGTAALGCLVK.D
1199	P01857	Ig gamma-1 chain C region	8.46	36596	11/66	30%	85/56	Secreted	Immune response	-2.82	0.00037	K.GPSVFPLAPSSK.S K.STSGGTAALGCLVK.D
534	P01859	Ig gamma-2 chain C region	7.66	36505	10/66	32%	90/56	Secreted	Immune response	-2.65	0.0012	K.GPSVFPLAPCSR.S R.STSESTAALGCLVK.D
512	P01860	Ig gamma-3 chain C region	8.23	42287	10/55	22%	79/56	Secreted	Immune response	-2.53	0.001	K.GPSVFPLAPCSR.S R.STSGGTAALGCLVK.D
1023	P01834	Ig kappa chain C region	5.58	11773	5/47	57%	69/56	Secreted	Immune response	-1.63	0.018	-TVAAPSVFIFPPSDEQLK.S K.DSTYSLSTLTLSK.A
939	P01834	Ig kappa chain C region	5.58	11773	7/98	91%	113/56	Secreted	Immune response	-1.44	0.031	-TVAAPSVFIFPPSDEQLK.S K.SGTASVVCLLNNFYPR.E
968	P01834	Ig kappa chain C region	5.58	11773	6/56	72%	108/56	Secreted	Immune response	-1.69	0.01	-TVAAPSVFIFPPSDEQLK.S K.SGTASVVCLLNNFYPR.E
1002	P01834	Ig kappa chain C region	5.58	11773	6/72	78%	100/56	Secreted	Immune response	-1.51	0.0088	-TVAAPSVFIFPPSDEQLK.S K.SGTASVVCLLNNFYPR.E
1005	P01834	Ig kappa chain C region	5.58	11773	6/36	72%	85/56	Secreted	Immune response	-1.56	0.043	-TVAAPSVFIFPPSDEQLK.S K.SGTASVVCLLNNFYPR.E
1012	P01834	Ig kappa chain C region	5.58	11773	6/42	72%	90/56	Secreted	Immune response	-1.73	0.01	-TVAAPSVFIFPPSDEQLK.S K.SGTASVVCLLNNFYPR.E
1027	P01834	Ig kappa chain C region	5.58	11773	7/57	84%	87/56	Secreted	Immune response	-1.88	0.037	-TVAAPSVFIFPPSDEQLK.S K.SGTASVVCLLNNFYPR.E
1201	P01834	Ig kappa chain C region	5.58	11773	6/48	72%	100/56	Secreted	Immune response	-1.64	0.0059	-TVAAPSVFIFPPSDEQLK.S K.SGTASVVCLLNNFYPR.E
996	P01834	Ig kappa chain C region	5.58	11773	6/73	76%	63/56	Secreted	Immune response	-1.66	0.001	-TVAAPSVFIFPPSDEQLK.S K.VDNALQSGNSQESVTEQDSK.D
1018	P01834	Ig kappa chain C region	5.58	11773	5/96	63%	58/56	Secreted	Immune response	-1.86	0.0065	-TVAAPSVFIFPPSDEQLK.S K.VDNALQSGNSQESVTEQDSK.D

928	P01834	Ig kappa chain C region	5.58	11773	5/16	50%	82/56	Secreted	Immune response	-1.67	0.0026	- .TVAAPSVFIFPPSDEQLK.S R.EAKVQWK.V+Glu->pyro-Glu(N-termE)
981	P01834	Ig kappa chain C region	5.58	11773	5/36	57%	59/56	Secreted	Immune response	-1.56	0.013	- .TVAAPSVFIFPPSDEQLK.S R.EAKVQWK.V+Glu->pyro-Glu(N-termE)
1010	P01834	Ig kappa chain C region	5.58	11773	7/55	83%	88/56	Secreted	Immune response	-1.63	0.0081	- .TVAAPSVFIFPPSDEQLK.S R.EAKVQWK.V+Glu->pyro-Glu(N-termE)
1016	P01834	Ig kappa chain C region	5.58	11773	5/43	48%	72/56	Secreted	Immune response	-2.21	0.042	- .TVAAPSVFIFPPSDEQLK.S R.EAKVQWK.V+Glu->pyro-Glu(N-termE)
931	P0CG05	Ig kappa chain C region	6.92	11458	5/42	55%	81/56	Secreted	Immune response	-2.6	0.027	K.AAPSVTLFPPSSEELQANK.A K.ADSSPVK.A
1021	P01834	Ig kappa chain C region	5.58	11773	6/27	64%	89/56	Secreted	Immune response	-1.5	0.014	- .TVAAPSVFIFPPSDEQLK.S R.EAKVQWK.V+Glu->pyro-Glu(N-termE)
993	P01623	Ig kappa chain V-III region WOL	9.07	11853	7/100	62%	72/56	Secreted	Immune response	-1.52	0.011	- .EIVLTQSPGTLSLSPGER.A R.ATLSCR.A
1011	P01623	Ig kappa chain V-III region WOL	9.07	11853	7/67	62%	71/56	Secreted	Immune response	-1.83	0.014	- .EIVLTQSPGTLSLSPGER.A+Glu->pyro- Glu(N-termE) R.ATLSCR.A
1004	P01623	Ig kappa chain V-III region WOL	9.07	11853	8/78	62%	92/56	Secreted	Immune response	-1.53	0.011	EIVLTQSPGTLSLSPGER.A+Glu->pyro- Glu(N-termE) - .EIVLTQSPGTLSLSPGER.A
983	P01623	Ig kappa chain V-III region WOL	9.07	11853	6/77	45%	82/56	Secreted	Immune response	-1.47	0.013	R.ATLSCR.A R.LLIYGASSR.A
1190	Q6ZVT0	Inactive polyglycylase TTLL10	9.36	75792	7/31	8%	71/56	Secreted	Unknown	24.72	0.000018	R.GKRPR.I R.VLRMEEFFPETYR.L
232	P01042	Kininogen-1	6.34	72996	18/57	25%	137/56	Secreted	Inflammatory response	1.37	0.0075	K.YNSQNSNNQFVLYR.I K.TVGSDTFYSFK.Y
613	P02750	Leucine-rich alpha-2- glycoprotein	6.45	38382	13/33	28%	138/56	Secreted	Inflammatory response	2.06	0.0091	- .MSSWSR.Q+Acetyl(ProteinN-term) K.DCQVFR.S
646	P02750	Leucine-rich alpha-2- glycoprotein	6.45	38382	13/55	31%	113/56	Secreted	Inflammatory response	2.07	0.0028	- .MSSWSR.Q+Acetyl(ProteinN-term) K.DCQVFR.S
580	P02750	Leucine-rich alpha-2- glycoprotein	6.45	38382	12/38	27%	134/56	Secreted	Inflammatory response	2.33	0.00076	K.DCQVFR.S R.VLDLTR.N
594	P02750	Leucine-rich alpha-2- glycoprotein	6.45	38382	12/53	29%	103/56	Secreted	Inflammatory response	4.12	0.0011	K.DCQVFR.S R.VLDLTR.N
630	P02750	Leucine-rich alpha-2- glycoprotein	6.45	38382	12/25	27%	147/56	Secreted	Inflammatory response	2	0.0055	K.DCQVFR.S R.VLDLTR.N
678	P02750	Leucine-rich alpha-2- glycoprotein	6.45	38382	12/40	25%	118/56	Secreted	Inflammatory response	2.46	0.0026	K.DCQVFR.S R.VLDLTR.N
364	Q14980	Nuclear mitotic apparatus protein 1	5.63	239199	23/51	10%	101/56	Nucleus matrix	Cell differentiation	-1.33	0.045	R.KHPSSPECLVSAQK.V K.HPSSPECLVSAQK.V
26	P05155	Plasma protease C1 inhibitor	6.09	55347	7/10	13%	91/56	Secreted	Coagulation	1.86	0.018	K.LYHAFSAMK.K+Oxidation(M) K.DFTCVHQALK.G
278	Q9HAH7	Probable fibrosin-1	9.96	48529	12/73	21%	92/56	Secreted	Fibroblast proliferation	1.59	0.0024	K.QLVLK.A K.EQLSLDDR.F+Glu->pyro-Glu(N-termE)
172	P02787	Serotransferrin	6.81	79294	25/58	31%	203/56	Secreted	Transport	1.35	0.031	R.WCAVSEHEATK.C K.CQSFR.D

275	P02768	Serum albumin	5.92	71317	42/100	49%	301/56	Secreted	Transport	-1.58	0.018	K.SEVAHR.F R.FKDLGEENFK.A
279	P02768	Serum albumin	5.92	71317	23/73	33%	157/56	Secreted	Transport	-1.87	0.023	K.SEVAHR.F R.FKDLGEENFK.A
290	P02768	Serum albumin	5.92	71317	28/83	35%	183/56	Secreted	Transport	-1.37	0.017	K.SEVAHR.F R.FKDLGEENFK.A
291	P02768	Serum albumin	5.92	71317	20/47	32%	170/56	Secreted	Transport	-1.77	0.0051	K.WVTFISLLFLFSSAYS.R.G R.FKDLGEENFK.A
255	P02768	Serum albumin	5.92	71317	20/96	23%	82/56	Secreted	Transport	1.7	0.034	R.DAHKSEVAHR.F K.SEVAHR.F
263	P02768	Serum albumin	5.92	71317	31/76	41%	233/56	Secreted	Transport	2.62	0.046	R.DAHKSEVAHR.F K.SEVAHR.F
300	P02768	Serum albumin	5.92	71317	31/95	34%	175/56	Secreted	Transport	-1.7	0.035	R.DAHKSEVAHR.F K.SEVAHR.F
313	P02768	Serum albumin	5.92	71317	24/91	27%	127/56	Secreted	Transport	-1.74	0.0022	R.DAHKSEVAHR.F K.SEVAHR.F
314	P02768	Serum albumin	5.92	71317	31/83	39%	224/56	Secreted	Transport	-1.82	0.0011	R.DAHKSEVAHR.F K.SEVAHR.F
247	P02768	Serum albumin	5.92	71317	19/57	28%	136/56	Secreted	Transport	-1.48	0.014	R.DAHKSEVAHR.F R.FKDLGEENFK.A
264	P02768	Serum albumin	5.92	71317	26/56	38%	222/56	Secreted	Transport	2.7	0.0058	R.DAHKSEVAHR.F R.FKDLGEENFK.A
271	P02768	Serum albumin	5.92	71317	17/62	22%	115/56	Secreted	Transport	1.85	0.0045	R.FKDLGEENFK.A K.LVNEVTEFAK.T
955	P02743	Serum amyloid P-component	6.1	25485	5/9	20%	75/56	Secreted	Transport	-1.41	0.021	K.VFVFPR.E R.AYSDLSR.A
1036	Q9P031	Thyroid transcription factor 1-associated protein 26	9.89	28880	15/93	34%	70/56	Nucleus	Transcription control	-1.53	0.0059	-.MAPVR.R+Acetyl(ProteinN-term) -.MAPVRR.S
1183	P02766	Transthyretin	5.52	15991	9/32	57%	119/56	Secreted	Transport	-1.58	0.0064	K.CPLMVK.V K.CPLMVK.V+Oxidation
1170	P02766	Transthyretin	5.52	15991	9/70	46%	98/56	Secreted	Transport	-1.39	0.02	K.CPLMVK.V K.CPLMVK.V+Oxidation(M)
1194	P28289	Tropomodulin-1	5.03	40658	7/53	19%	58/56	Cytoplasm	Cytoskeleton	16.99	0.00015	-.MSYRR.E+Acetyl K.DREDLVPYTGEK.R
496	P02774	Vitamin D-binding protein	5.4	54526	20/61	37%	166/56	Secreted	Transport	2.08	0.0017	K.EFSLGK.E K.EDFTSLSLVLYSR.K
444	P02774	Vitamin D-binding protein	5.4	54526	18/59	32%	127/56	Secreted	Transport	1.74	0.005	K.EFSLGK.E R.KFPSGTFEQVSQLVK.E
489	P02774	Vitamin D-binding protein	5.4	54526	24/71	35%	156/56	Secreted	Transport	1.46	0.033	R.GRDYEK.N K.EFSLGK.E+Glu->pyro-Glu(N-termE)
696	P25311	Zinc-alpha-2-glycoprotein	5.71	34465	22/56	54%	207/56	Secreted	Transcription control	1.33	0.0094	R.YSLTYIYTGLSK.H K.HVEDVPAFQALGSLNDLQFFR.Y
595	P25311	Zinc-alpha-2-glycoprotein	5.71	34465	23/72	47%	213/56	Secreted	Transcription control	2.45	0.00014	R.YSLTYIYTGLSK.H R.YNSKDR.K

687	P25311	Zinc-alpha-2-glycoprotein	5.71	34465	25/67	52%	238/56	Secreted	Transcription control	1.42	0.0081	R.YSLTYIYTGLSK.H R.YNSKDR.K
703	P25311	Zinc-alpha-2-glycoprotein	5.71	34465	23/53	47%	198/56	Secreted	Transcription control	1.57	0.0028	R.YSLTYIYTGLSK.H R.YNSKDR.K
