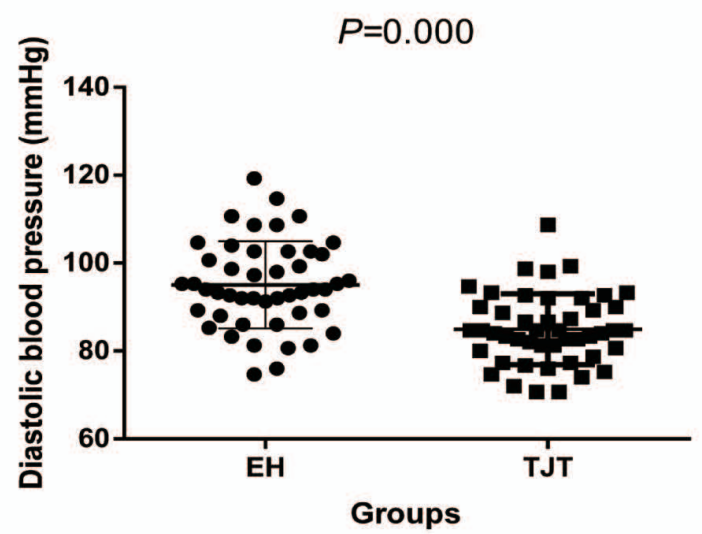


(a)



(b)

Supplementary Figure 1

Supplementary table 1. The clinical parameters of EH patients between discovery section (n=30) and verification section (n=30).

Clinical parameters	Discovery section (n=30)	Verification section (n=30)	<i>P</i> -value
Age(years)	57.1 ± 9.9	59.9 ± 9.2	0.946 ^a
Sex(♂ / ♀)	16/14	14/16	0.606 ^b
BMI	25.5 ± 3.0	23.7 ± 2.3	0.126 ^a
Smoker	14/30	12/30	0.602
Blood pressure of EH			
Systolic	150.3 ± 8.3	149.3 ± 7.1	0.618 ^a
Diastolic	95.0 ± 11.3	95.0 ± 8.3	1.000 ^a
Blood pressure of TJJT			
Systolic	133.1 ± 5.4	132.2 ± 5.1	0.512 ^a
Diastolic	84.6 ± 9.2	84.9 ± 6.5	0.889 ^a

Data were expressed as Mean±SD; a) *P*- value between two experiment sections with independent samples T-test; b) Chi-square Test, $P \leq 0.05$ was considered to be statistically significant. In additional, the blood pressures between EH and TJJT groups were also statistically analyzed by Spss16.0 with Paired-sample T-test, both of the systolic and diastolic blood pressure were significantly different before and after TJJT treatment ($P=0.000$).

*A total of 47 EH individuals were involved in our study. Firstly, 30 patients were selected in the discovery section randomly. Secondly, the remaining 17 patients and 13 patients involved in the first section were jointly analyzed in verification section.

*BMI=Weight (Kg)/Height²(m²)

supplementary table2. A list of identified and quantified proteins by iTRAQ proteomics

Hits	Accession	Description	Mass	Seq	Score	Cov	SameSets	Spectrum	Unique	Spei	Peptide	Unique	Pept	A-VS-B@R	A-VS-B@R
1	tr B0YJC6 B0YJC6_HUMAN	Vitamin K-dependent protein Z variant 1 OS=Hom	53450	MAGCVPL	31	2.9	1	1	1	1	1	1	1	---	---
2	tr Q7Z7Q0 Q7Z7Q0_HUMAN	Apob protein OS=Homo sapiens GN=Apob PE=	113702	MDPPRPA	5835	45.5	-	588	1	39	1	1	---	---	---
3	sp P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Hom	76630	MSCQISC	275	15.5	-	23	13	10	8	0.608	0.607		
4	tr B4DNG0 B4DNG0_HUMAN	Olfactomedin-like protein 3 OS=Homo sapiens GN	44167	MLPLLEF	40	5.8	1	4	4	2	2	---	---	---	---
5	sp P23412 FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 S'	86744	MERAAPS	851	28.3	-	87	60	17	8	1.115	1.048		
6	tr L0R4T3 L0R4T3_HUMAN	Histone H2B OS=Homo sapiens GN=ABCF2 PE=	8880	MSIMNSF	32	13.4	20	4	4	1	1	---	---	---	---
7	tr C9JF17 C9JF17_HUMAN	Apolipoprotein D (Fragment) OS=Homo sapiens G	28800	MFKQLSC	857	28.8	1	84	84	6	6	0.834	0.781		
8	sp P18428 LBP_HUMAN	Lipopolysaccharide-binding protein OS=Homo sap	60518	MGALARA	2335	20.2	-	145	145	9	9	0.794	0.784		
9	tr B2RMS9 B2RMS9_HUMAN	Inter-alpha (Globulin) inhibitor H4 (Plasma Kallik	116303	MKPPRPV	3903	25.2	1	263	263	21	21	1.114	1.097		
10	sp P03950 ANGI_HUMAN	Angiogenin OS=Homo sapiens GN=ANG PE=1 S'	19315	MYMGLG	40	26.5	-	9	9	4	4	0.78	0.697		
11	tr Q0PW96 Q0PW96_HUMAN	Intersectin 1 short form variant 7 OS=Homo sapien	157455	MAQFPPT	25	0.7	10	1	1	1	1	---	---	---	---
12	tr L0R8K6 L0R8K6_HUMAN	Alternative protein TRIM25 OS=Homo sapiens G	9186	MWSLEVI	21	13.6	-	3	3	1	1	---	---	---	---
13	tr B3KRN4 B3KRN4_HUMAN	cDNA FLJ34625 fis, clone KIDNE2015244, highl	57113	MGWAAR	45	5.6	2	3	3	2	2	0.831	0.903		
14	sp P01608 KV116_HUMAN	Ig kappa chain V-I region Roy OS=Homo sapiens I	14018	DIQMTQSI	137	24.1	-	11	6	2	1	---	---	---	---
15	tr B7Z7R8 B7Z7R8_HUMAN	cDNA FLJ55622, highly similar to Multimerin-1 C	133624	MQHKIVT	301	10.9	2	24	24	10	10	1.033	0.938		
16	sp P00739 HPTK_HUMAN	Haptoglobin-related protein OS=Homo sapiens GN	48340	MSDLGAV	677	36.2	-	72	22	11	4	0.676	0.704		
17	tr B4DEB9 B4DEB9_HUMAN	cDNA FLJ61099, highly similar to ADP-ribosylati	23649	MGNIFAN	29	5.8	7	1	1	1	1	---	---	---	---
18	sp Q13790 APOF_HUMAN	Apolipoprotein F OS=Homo sapiens GN=APOF P	39065	MTGLCGY	45	8.3	-	3	3	2	2	---	---	---	---
19	tr Q6IB71 Q6IB71_HUMAN	Proteasome subunit alpha type OS=Homo sapiens C	34405	MSSIGTG	81	25.5	1	2	2	1	1	1.029	1.096		
20	tr Q6ZNX5 Q6ZNX5_HUMAN	CDNA FLJ26936 fis, clone RCT06808 OS=Homo	18632	MAWALLI	41	4.8	-	2	2	1	1	---	---	---	---
21	tr Q5CZ94 Q5CZ94_HUMAN	Putative uncharacterized protein DKFZp781M038	29340	MAWTPLF	708	30.8	-	75	2	6	1	---	---	---	---
22	tr A0A087WTS5 A0A087WTS5_HUMAN	Ig kappa chain C region OS=Homo sapiens GN=IC	30209	MDMRVP	1394	44.1	-	155	1	7	1	---	---	---	---
23	tr A2MYC8 A2MYC8_HUMAN	V5-2 protein (Fragment) OS=Homo sapiens GN=V	12669	QPVLTQPI	50	28.8	1	6	6	3	3	---	---	---	---
24	tr G3V2W1 G3V2W1_HUMAN	Protein Z-dependent protease inhibitor OS=Homo	65592	MSRSTQE	346	15.1	1	33	3	8	1	1.054	0.935		
25	sp P19652 A1AG2_HUMAN	Alpha-1-acid glycoprotein 2 OS=Homo sapiens G	28132	MALSWVI	61	9.5	-	7	7	2	2	0.897	0.763		
26	tr D6RF35 D6RF35_HUMAN	Vitamin D-binding protein OS=Homo sapiens GN=	67663	MKRVLVL	55	18.5	1	17	17	9	9	1.692	1.092		
27	tr K7ER19 K7ER19_HUMAN	Truncated apolipoprotein C-I (Fragment) OS=Hom	11075	MRLFLSL	409	32.5	1	51	51	3	3	0.739	0.71		
28	sp O76076 WISP2_HUMAN	WNT1-inducible-signaling pathway protein 2 OS=	29677	MRGTPKT	35	4	-	2	2	1	1	---	---	---	---
29	tr Q1L857 Q1L857_HUMAN	Ceruloplasmin (Fragment) OS=Homo sapiens PE=	136274	MKILLIGI	862	16.7	3	82	82	13	13	1.059	1.013		
30	tr Q9UL89 Q9UL89_HUMAN	Myosin-reactive immunoglobulin heavy chain vari	14841	VQSGAEV	62	10.3	1	1	1	1	1	---	---	---	---
31	tr Q5SRP5 Q5SRP5_HUMAN	Apolipoprotein M OS=Homo sapiens GN=APOM	17751	MAAGSAP	61	17.8	1	11	11	3	3	0.669	0.73		
32	tr B3KRFP B3KRFP_HUMAN	cDNA FLJ34156 fis, clone FCBBF3013266, highl	35578	MPWPLLF	124	7.2	1	8	8	2	2	0.946	0.878		
33	tr H0Y7V6 H0Y7V6_HUMAN	Pulmonary surfactant-associated protein B (Fragm	46516	XHLQLWI	24	4.3	5	1	1	1	1	---	---	---	---
34	tr Q7Z351 Q7Z351_HUMAN	Putative uncharacterized protein DKFZp686N022	63846	MEFLQWT	3561	29.9	-	309	2	11	1	---	---	---	---
35	sp Q15113 PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 OS=Hom	55490	MLPAATA	347	28.1	-	40	40	11	11	1.08	1.092		
36	tr A0A068LKR7 A0A068LKR7_HUMAN	Ig heavy chain variable region (Fragment) OS=Hom	15875	QVQLVES	102	32.8	1	10	3	3	1	1.055	0.94		
37	tr F8VV32 F8VV32_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 S	13895	MKALIVL	163	23.1	1	12	12	2	2	1.512	1.505		
38	sp Q6U7Y4 ATL4_HUMAN	ADAMTS-like protein 4 OS=Homo sapiens GN=A	123181	MENWTLG	64	3.8	1	3	3	3	3	0.878	0.978		
39	tr Q8TAN2 Q8TAN2_HUMAN	Frizzled homolog 9 (Drosophila) OS=Homo sapien	71986	MAVAPTR	31	1.7	1	9	9	1	1	---	---	---	---
40	sp P34096 RNA54_HUMAN	Ribonuclease 4 OS=Homo sapiens GN=RNASE4	19111	MALQRTA	49	18.4	-	5	5	2	2	1.505	0.764		
41	tr B2R984 B2R984_HUMAN	cDNA, FLJ94268, highly similar to Homo sapiens	41045	MSETAPA	48	8.2	5	2	2	2	2	---	---	---	---
42	sp Q86UD1 Q86UD1_HUMAN	Out at first protein homolog OS=Homo sapiens GN	35194	MRLPGVP	90	3.3	-	11	11	1	1	1.119	1.026		
43	sp P02741 CRP_HUMAN	C-reactive protein OS=Homo sapiens GN=CRP PE	29757	MEKLLCF	309	23.7	-	59	59	6	6	1.125	1.098		
44	sp P80108 PHLD_HUMAN	Phosphatidylinositol-glycan-specific phospholipase	103248	MSAFLWF	206	11.1	-	18	18	8	8	1.146	1.04		
45	tr A0A075B7C3 A0A075B7C3_HUMAN	C-C motif chemokine 5 (Fragment) OS=Homo sapi	19150	XAALAVII	23	5.3	2	2	2	1	1	---	---	---	---
46	tr F1C4A7 F1C4A7_HUMAN	Monocyte differentiation antigen CD14 OS=Homo	43702	MERASCL	185	19.2	2	18	18	6	6	0.594	0.483		
47	tr S6C4Q9 S6C4Q9_HUMAN	IgG L chain OS=Homo sapiens PE=2 SV=1	26779	MAWALLI	1176	24	-	134	2	5	1	---	---	---	---
48	tr A5PLK9 A5PLK9_HUMAN	Metalloendopeptidase OS=Homo sapiens GN=BM	131159	MPGVARI	78	1.9	2	4	4	2	2	0.963	1.105		
49	tr B3KRVP B3KRVP_HUMAN	cDNA FLJ34967 fis, clone NTONG2004690, high	63225	MESKALL	89	10.8	4	8	8	5	5	1.056	1.014		
50	sp Q14520 HABP2_HUMAN	Hyaluronan-binding protein 2 OS=Homo sapiens C	76908	MFARMSE	160	10.2	-	34	34	6	6	1.19	1.1		
51	tr Q5VY30 Q5VY30_HUMAN	Retinol binding protein 4, plasma, isoform CRA_b	26952	MNYSKIP	63	15.1	1	7	7	3	3	2.028	1.684		
52	tr Q9NSD0 Q9NSD0_HUMAN	Protein S OS=Homo sapiens PE=2 SV=1	89278	MSKQQA	489	16.3	2	60	60	12	12	1.181	1.13		
53	sp P20160 CAP7_HUMAN	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 S	27933	MTRLTVL	123	8	-	8	8	2	2	1.254	1.791		
54	tr A0N8J8 A0N8J8_HUMAN	V lambda B (Fragment) OS=Homo sapiens PE=4 SV	13760	MAWTPLF	57	21.6	2	11	2	3	1	---	---	---	---
55	tr Q6PIK1 Q6PIK1_HUMAN	IGL @ protein OS=Homo sapiens GN=IGL @ PE=	29690	MAWALLI	816	34	-	95	4	7	1	---	---	---	---
56	tr B4E1T8 B4E1T8_HUMAN	cDNA FLJ151452, highly similar to Lysyl oxidase I	51776	MALARTS	28	4.6	1	1	1	1	1	---	---	---	---
57	sp P35579 MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 S'	290921	MAQQAAI	34	1.4	-	4	2	3	2	---	---	---	---
58	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens C	59172	MTTCSRC	50	4.4	1	2	1	2	1	---	---	---	---
59	sp Q15166 PON3_HUMAN	Serum paraoxonase/lactonase 3 OS=Homo sapiens	46199	MGLKVAI	183	14.7	-	39	39	5	5	1.026	0.971		
60	tr B3KML9 B3KML9_HUMAN	cDNA FLJ11352 fis, clone HEMBA1000020, high	49175	MRENVHL	52	10.1	16	4	4	3	3	---	---	---	---
61	tr H0Y512 H0Y512_HUMAN	Adipocyte plasma membrane-associated protein (F	50834	XVVTDD	169	8.6	1	14	14	3	3	0.922	0.865		
62	tr U3KPS2 U3KPS2_HUMAN	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=	25269	MASLQMF	42	5.6	2	2	2	1	1	---	---	---	---
63	tr B2RBW9 B2RBW9_HUMAN	cDNA, FLJ95746, highly similar to Homo sapiens	41072	MTSSLLT	90	5.1	1	13	13	2	2	0.832	0.786		
64	tr A0A068LL62 A0A068LL62_HUMAN	Ig heavy chain variable region (Fragment) OS=Hom	14698	QVQLQQV	40	12.7	-	6	2	2	1	---	---	---	---
65	tr H0YK48 H0YK48_HUMAN	Tropomyosin alpha-1 chain OS=Homo sapiens GN	36225	MAGSSSL	52	9.7	5	3	1	2	1	---	---	---	---
66	tr B7Z4X6 B7Z4X6_HUMAN	cDNA FLJ51012, highly similar to Plasminogen ac	43747	MLQLTTG	40	14.9	-	12	12	5	5	1.167	1.24		
67	sp P01009 A1AT_HUMAN	Alpha-1-antitrypsin OS=Homo sapiens GN=SERP	57525	MPSSWSC	610	29.2	-	47	47	11	11	0.877	0.901		
68	sp P08294 SODE_HUMAN	Extracellular superoxide dismutase [Cu-Zn] OS=H	28116	MLALLCS	390	25.8	-	19	19	4	4	1.044	1.053		
69	tr Q6U2E7 Q6U2E7_HUMAN	C4B1 (Fragment) OS=Homo sapiens GN=C4B PE	6651	VSAGSPHI	291	80.3	-	45	1	3	1	---	---	---	---
70	tr A2RRB2 A2RRB2_HUMAN	ZNF608 protein OS=Homo sapiens GN=ZNF608 I	57576	MSVNSTP	25	2	3	2	2	1	1	---	---	---	---
71	sp P04180 LCAT_HUMAN	Phosphatidylcholine-sterol acyltransferase OS=H	53843	MGPPGSP	341	14.8	-	35	35	6	6	0.988	1.027		
72	tr J3KRPO J3KRPO_HUMAN	Beta-Ala-His dipeptidase OS=Homo sapiens GN=A	59295	MDPKLGR	122	15.5	2	12	12	8	8	1.078	1.127		
73	tr J3KQ60 J3KQ60_HUMAN	Reelin OS=Homo sapiens GN=RELN PE=4 SV=1	428795	MERSGVR	39	0.7	1	4	4	3	3	---	---	---	---
74	tr Q9HCC1 Q9HCC1_HUMAN	Single chain Fv (Fragment) OS=Homo sapiens PE=	13566	EVQLVES	64	36.6	-	9	2	3	1	---	---	---	---
75	tr B7ZIF8 B7ZIF8_HUMAN	cDNA FLJ53025, highly similar to Complement C	36015	MCPEDES	8244	56.7	-	678	64	14	2	1.052	1.046		
76	sp P20851 C4BPA_HUMAN	C4b-binding protein beta chain OS=Homo sapiens	35088	MFFWCAC	477	21.8	-	43	43	5	5	0.841	0.783		
77	tr Q9UL70 Q9UL70_HUMAN	Myosin-reactive immunoglobulin light chain variat	13869	DIQMTQSI	123	23.1	-	6	1	2	1	---	---	---	---
78	sp Q02985 FHR3_HUMAN	Complement factor H-related protein 3 OS=Homo	44580	MLLLINVI	81	14.5	-	11	10	5	4	1.233	1.352		
79	tr A8K6C1 A8K6C1_HUMAN	cDNA FLJ76868, highly similar to Homo sapiens	63358	MLAATVL	447	10.8	1	41	41	6	6	0.721	0.829		
80	tr B3KS79 B3KS79_HUMAN	cDNA FLJ35730 fis, clone TESTI2003131, highl	59285	MKIHYSR	136	9.8	1	11	11	4	4	1.034	0.889		
81	sp P01137 TGFB1_HUMAN	Transforming growth factor beta-1 OS=Homo sapi	50777	MPPSGLR	52	8.7	-	7	7	4	4	0.822	0.9		
82	tr B5MCZ9 B5MCZ9_HUMAN	Glutaminyl-peptide cyclotransferase (Fragment) O	35244	MAGGRHI	31	4.9	1	2	2	1	1	---	---	---	---
83	tr D6REX5 D6REX5_HUMAN	Selenoprotein P (Fragment) OS=Homo sapiens GN	42698	MWRSLGI	165	12.6	1	9	9	4	4	0.731	0.894		
84	tr B2R7Z6 B2R7Z6_HUMAN	cDNA, FLJ93674 OS=Homo sapiens PE=2 SV=1	62079	MAGPWIT	99	10.7	1	7	7	5	5	0.703	0.649		
85	tr B2R6W1 B2R6W1_HUMAN	cDNA, FLJ93143, highly similar to Homo sapiens	111585	MKVISLFI	635	25.9	-	91	4	19	2	1.218	1.098		

106	spP02671 FIBA_HUMAN	Fibrinogen alpha chain OS=Homo sapiens GN=FG	109041	MFSMRIV	373	16.9	-		42	42	13	13	1.008	1.028
107	tr B7Z565 B7Z565_HUMAN	cDNA FLJ54739, highly similar to Alpha-actinin-1	111056	MLLLEVIS	38	2.4		2	4	4	2	2	---	---
108	tr A0A024RDT5 A0A024RDT5_HUMAN	Periostin, osteoblast specific factor, isoform CRA_a	106758	MIPFLPMF	55	2.1		3	1	1	1	1	---	---
109	tr A0A024R755 A0A024R755_HUMAN	Calumenin, isoform CRA_a OS=Homo sapiens GN=	45743	MDLRQFL	47	5.7		3	3	3	2	2	---	---
110	sp P10909 CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=	62157	MMKTLTL	3979	33.9	-		340	340	15	15	0.957	1
111	tr A2J1N0 A2J1N0_HUMAN	Rheumatoid factor RF-IP14 (Fragment) OS=Homo	11519	QLVEFSGL	99	30.2	-		15	4	3	1	---	---
112	sp P10645 CMGA_HUMAN	Chromogranin A OS=Homo sapiens GN=CHGA F	60563	MRSAAVL	118	6.1	-		7	7	3	3	1.061	1.172
113	tr Q9NPP6 Q9NPP6_HUMAN	Immunoglobulin heavy chain variant (Fragment) O	50481	PGKGLWE	578	22.1	-		72	2	8	1	---	---
114	sp T22692 IBP4_HUMAN	Insulin-like growth factor-binding protein 4 OS=H	33068	MLPLCLV	34	5.4	-		3	3	1	1	1.051	0.927
115	sp P16191 KV301_HUMAN	Ig kappa chain V-III region B6 OS=Homo sapiens	12959	ZVLZTSP	179	16.7	-		8	8	3	3	1.039	0.874
116	sp P16610 ECM1_HUMAN	Extracellular matrix protein 1 OS=Homo sapiens C	67099	MGTTARA	464	27	-		54	54	13	13	0.93	0.848
117	sp P06331 HV209_HUMAN	Ig heavy chain V-II region ARH-77 OS=Homo sap	18519	MKHLWFI	58	17.1	-		6	4	2	1	1.099	1.024
118	sp P14543 NID1_HUMAN	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV	148268	MLASSSRI	80	5.4	-		10	10	6	6	1.16	0.906
119	sp Q96PD5 PGRP2_HUMAN	N-acetyluramoyl-L-alanine amidase OS=Homo s	66703	MAQQVFL	186	8.7	-		13	13	4	4	0.813	0.694
120	tr Q6FGL0 Q6FGL0_HUMAN	Galectin (Fragment) OS=Homo sapiens GN=LGA1	28940	MADNFSL	38	4.4		3	1	1	1	1	---	---
121	tr Q1HP67 Q1HP67_HUMAN	Lipoprotein, Lp(A) OS=Homo sapiens GN=LPA P	240494	MEHKEV	211	10.1		1	17	17	10	10	0.451	0.452
122	tr B4D157 B4D157_HUMAN	cDNA FLJ54111, highly similar to Serotransferrin	80545	MNQLRG	134	6.2		4	11	11	6	6	1.114	0.93
123	tr C9JCS4 C9JCS4_HUMAN	Fibrinogen gamma chain OS=Homo sapiens GN=F	63883	MSWSLFP	299	25.8		2	32	32	11	11	0.977	1.13
124	sp P04197 GPV_HUMAN	Platelet glycoprotein V OS=Homo sapiens GN=GF	65693	MLRGTL	67	13.2	-		10	10	6	6	0.68	0.474
125	tr B2R773 B2R773_HUMAN	cDNA, FLJ93312, highly similar to Homo sapiens	30174	MLLLGAV	151	16		1	12	12	3	3	1.067	1.1
126	tr B4DUV1 B4DUV1_HUMAN	Fibulin-1 OS=Homo sapiens PE=2 SV=1	79879	MATHQKI	284	25.9	-		42	15	13	4	---	---
127	tr E7EV88 E7EV88_HUMAN	A disintegrin and metalloproteinase with thrombos	52259	MASDGA	75	8.8		1	6	6	4	4	1.187	0.911
128	sp P08697 A2AP_HUMAN	Alpha-2-antiplasmin OS=Homo sapiens GN=SER1	60957	MALLWGL	421	17.7	-		62	62	8	8	0.94	0.815
129	tr Q6MZM7 Q6MZM7_HUMAN	Putative uncharacterized protein DKFZp686O121c	262413	ARAGCAA	9056	32.7	-		750	1	54	1	---	---
130	tr K7ER74 K7ER74_HUMAN	Protein APOC4-APOC2 OS=Homo sapiens GN=A	23306	MSLLRNR	455	28.1		1	66	66	4	4	0.977	0.997
131	tr A2J1N5 A2J1N5_HUMAN	Rheumatoid factor RF-ET6 (Fragment) OS=Homo	12382	VESGGGV	49	23.4	-		6	1	2	1	---	---
132	tr A0A0A0MT96 A0A0A0MT9_HUMAN	Protein IGKJ3 (Fragment) OS=Homo sapiens GN=	2332	XFTFGPG	28	69.2	-		1	1	1	1	---	---
133	tr S6AWD3 S6AWD3_HUMAN	IgG L chain OS=Homo sapiens PE=2 SV=1	22895	MRLPAQL	907	23.5	-		130	1	4	1	---	---
134	sp P07357 C08A_HUMAN	Complement component C8 alpha chain OS=Homo	76870	MFAVVVF	244	15.2	-		28	28	8	8	1.216	1.033
135	tr D3DQX7 D3DQX7_HUMAN	Serum amyloid A protein OS=Homo sapiens GN=	15436	MKLLTGL	105	20.5	-		10	9	3	2	1.459	1.048
136	tr B2R6M6 B2R6M6_HUMAN	cDNA, FLJ93024, highly similar to Homo sapiens	60522	MLKALFL	224	9.7		6	22	22	4	4	1.206	1.336
137	tr Q96K68 Q96K68_HUMAN	cDNA FLJ14473 fis, clone MAMMA1001080, hi	59670	MELGLRW	1125	28.3	-		121	58	11	4	1.124	1.135
138	tr Q6ZRG8 Q6ZRG8_HUMAN	cDNA FLJ46365 fis, clone TEST14051054 OS=H	23673	MGPGLV	30	3.2		1	5	1	1	1	---	---
139	sp P67936 TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens GN	36528	MAGLNSL	106	21.8	-		11	6	5	3	1.325	1.22
140	tr A6YD2 A6YD2_HUMAN	Fibronectin splice variant A (Fragment) OS=Homo	74428	SQMQLP	2728	39.2		3	214	1	16	1	---	---
141	sp P27169 PONI_HUMAN	Serum paraoxonase/arylesterase 1 OS=Homo sapie	46266	MAKLIA	613	23.1	-		81	81	8	8	1.039	0.917
142	tr A0A024RCD0 A0A024RCD0_HUMAN	Protein convertase subtilisin/kexin type 6, isofo	109973	MDPQVK	25	2.1		7	2	2	2	2	---	---
143	tr B4DN21 B4DN21_HUMAN	cDNA FLJ53365, highly similar to Homo sapiens	38489	MIFEEHGI	2830	43.1		1	173	4	11	1	0.911	0.845
144	sp P02763 A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GP	28288	MALSWV	54	7.5	-		5	5	1	1	0.797	0.895
145	tr E1U340 E1U340_HUMAN	ZNF511/PRAP1 fusion protein OS=Homo sapiens	41096	MQVADV	30	5.5		2	4	4	2	2	---	---
146	tr D6RAR4 D6RAR4_HUMAN	Hepatocyte growth factor activator OS=Homo sapi	78528	MGRWAW	45	1.7		1	4	4	1	1	---	---
147	tr A0A087WYJ9 A0A087WYJ9_HUMAN	Ig mu chain C region OS=Homo sapiens GN=IGHI	74671	MSVSFLF	7728	35.4	-		611	4	21	2	---	---
148	tr B2RBZ5 B2RBZ5_HUMAN	cDNA, FLJ95778, highly similar to Homo sapiens	60491	MKVVPVL	328	16.4	-		31	1	8	1	---	---
149	tr D3DQHS D3DQHS_HUMAN	Coiled-coil domain containing 69, isoform CRA_a	41482	MGCRHSR	29	4.7	-		2	2	2	2	---	---
150	tr B7Z549 B7Z549_HUMAN	cDNA FLJ56821, highly similar to Inter-alpha-tryp	87971	MDMGAM	1649	28.1		1	119	119	15	15	1.098	1.03
151	tr F5H0G0 F5H0G0_HUMAN	ATP-binding cassette sub-family B member 9 OS=	33165	MRLWAK	33	2.6		3	5	5	1	1	---	---
152	tr A2IP14 A2IP14_HUMAN	HRV Fab 025-VL (Fragment) OS=Homo sapiens	14086	MAELQM	67	8.8	-		2	2	1	1	---	---
153	sp P00734 THR8_HUMAN	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=	80601	MAHVRI	5988	58.5	-		555	555	31	31	1.043	1.089
154	sp Q92954 PRG4_HUMAN	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1	202736	MAWKTLI	94	4.5	-		12	12	7	7	0.695	0.696
155	sp P01861 IGHG4_HUMAN	Ig gamma-4 chain C region OS=Homo sapiens GN	44036	ASTKGPS	603	25.1	-		38	3	6	2	---	---
156	tr Q8TCZ8 Q8TCZ8_HUMAN	Apolipoprotein E (Fragment) OS=Homo sapiens G	7933	RLGADME	953	54.4	-		49	1	3	1	---	---
157	sp P01708 V205_HUMAN	Ig lambda chain V-II region BUR OS=Homo sapie	13495	QSALTOP	36	10.1	-		1	1	1	1	---	---
158	sp P07996 TSP1_HUMAN	Thrombospondin-1 OS=Homo sapiens GN=THBS	150327	MGLAWPI	1599	25.5	-		210	4	27	1	1.534	0.833
159	sp Q4G0X9 CCD40_HUMAN	Coiled-coil domain-containing protein 40 OS=Hom	155929	MAEPGGA	21	0.7	-		4	4	1	1	---	---
160	sp O00187 MASP2_HUMAN	Mannan-binding lectin serine protease 2 OS=Homo	86928	MRLTLTL	241	12.5	-		30	30	9	9	1.078	1.235
161	tr B1AH77 B1AH77_HUMAN	Ras-related C3 botulinum toxin substrate 2 OS=Hc	21005	MVDSKPV	35	9.5		3	1	1	1	1	---	---
162	tr B4E1D8 B4E1D8_HUMAN	cDNA FLJ51597, highly similar to C4b-binding pr	71792	MDITLTI	1578	33.4	-		226	226	16	16	1.059	1.036
163	tr Q4LE64 Q4LE64_HUMAN	NUMA1 variant protein (Fragment) OS=Homo sap	286341	LSGTMFL	24	0.3		1	1	1	1	1	---	---
164	sp Q8617 SPA11_HUMAN	Serpin A11 OS=Homo sapiens GN=SERPINA11 I	53519	MGPAPWL	42	3.3	-		1	1	1	1	---	---
165	tr B7ZLY3 B7ZLY3_HUMAN	LTBP1 protein OS=Homo sapiens GN=LTBP1 PE	175722	MDTKLM	66	3		3	6	6	3	3	0.923	0.852
166	tr B4DDF8 B4DDF8_HUMAN	cDNA FLJ51786, highly similar to Retinal dehydr	56272	MDASERG	24	2.1		3	1	1	1	1	---	---
167	tr G3XAM2 G3XAM2_HUMAN	Complement factor 1 light chain OS=Homo sapiens	80796	MKLLHVF	64	5.7		4	5	5	3	3	1.123	1.084
168	sp P01024 C03_HUMAN	Complement C3 OS=Homo sapiens GN=C3 PE=1	223249	MGPTSGP	14077	52.2	-		1426	1426	79	79	0.879	0.874
169	tr B0Y1W2 B0Y1W2_HUMAN	Apolipoprotein C-III OS=Homo sapiens GN=APO	14994	MGTWGA	1654	29.1		1	130	130	3	3	0.871	0.87
170	tr A0A075B6J9 A0A075B6J9_HUMAN	HCG1782423 (Fragment) OS=Homo sapiens GN=	13724	MAWALLI	43	10.8		1	1	1	1	1	---	---
171	sp P0DJJ9 SAA2_HUMAN	Serum amyloid A-2 protein OS=Homo sapiens GN	15401	MKLLTGL	29	20.5	-		2	1	2	1	---	---
172	sp P01031 C05_HUMAN	Complement C5 OS=Homo sapiens GN=C5 PE=1	226401	MGLGLGL	1032	21.8	-		167	167	36	36	1.115	1.104
173	tr C1K3N3 C1K3N3_HUMAN	Insulin-like growth factor binding protein 1 (Fragm	31823	SEVPVAR	94	11.2		3	9	9	3	3	0.994	0.859
174	tr A0A068LRW6 A0A068LRW6_HUMAN	Ig heavy chain variable region (Fragment) OS=H	16657	QVTLRES	25	5.5	-		2	1	1	1	---	---
175	tr A0A024R035 A0A024R035_HUMAN	Phospholipase A2, group VII (Platelet-activating f	59600	MVPPKHL	38	1.8	-		2	2	1	1	---	---
176	tr A0A087X1J7 A0A087X1J7_HUMAN	Glutathione peroxidase OS=Homo sapiens GN=GP	30481	MARLLQA	713	34.7		1	101	101	7	7	1.097	1.038
177	sp P48740 MASP1_HUMAN	Mannan-binding lectin serine protease 1 OS=Homo	92409	MRWLLA	566	26	-		59	15	14	6	1.306	1.34
178	sp P04220 MUCB_HUMAN	Ig mu heavy chain disease protein OS=Homo sapie	49019	DSPLEQSC	2388	33.8	-		286	3	12	1	---	---
179	tr J3KPY9 J3KPY9_HUMAN	Anthrax toxin receptor 2 OS=Homo sapiens GN=A	54148	MRLSFVF	65	16.8		1	8	7	6	5	0.535	0.454
180	sp P02760 AMBP_HUMAN	Protein AMBP OS=Homo sapiens GN=AMBP PE=	45666	MRLSLGA	138	16.5	-		11	11	4	4	1.126	1.171
181	sp P58166 INHB_HUMAN	Inhibin beta E chain OS=Homo sapiens GN=INHE	41712	MRLPDVQ	64	2.3	-		5	5	1	1	0.859	0.921
182	sp Q07960 RHG01_HUMAN	Rho GTPase-activating protein 1 OS=Homo sapier	59892	MDPLSEL	31	2.3	-		1	1	1	1	---	---
183	tr H0YJ31 H0YJ31_HUMAN	Fibulin-5 (Fragment) OS=Homo sapiens GN=FB	19441	XFTGSCS	44	10.2		4	1	1	1	1	---	---
184	tr B4E0A4 B4E0A4_HUMAN	cDNA FLJ57023, highly similar to Homo sapiens	149266	MKRKHRI	124	4.3		4	12	12	5	5	0.562	0.549
185	sp P06312 KV401_HUMAN	Ig kappa chain V-IV region (Fragment) OS=Homo	15007	MVLQTVQ	177	17.4		1	19	2	2	1	---	---
186	sp P01591 IGJ_HUMAN	Immunoglobulin J chain OS=Homo sapiens GN=IC	21585	MKNHLLF	69	35.2	-		23	23	5	5	1.166	1.094
187	tr A0A087WZ88 A0A087WZ88_HUMAN	Protein IGKV3-11 OS=Homo sapiens GN=IGKV3	29520	MEAPAPL	1412	49.8	-		164	2	8	1	---	---
188	tr A0A0A0MRJ7 A0A0A0MRJ7_HUMAN	Coagulation factor V OS=Homo sapiens GN=F5 P	292156	MFPGCPRL	1409	16.3		1	166	164	33	32	0.961	0.975
189	tr B4DPQ0 B4DPQ0_HUMAN	Complement C1r subcomponent OS=Homo sapiens	94632	MSVRFVR	429	26.6		4	48	48	16	16	1.163	1.031
190	sp P0C0S8 H2A1_HUMAN	Histone H2A type 1 OS=Homo sapiens GN=HIST	18646	MSGRGKC	46	14.6		12	2	2	1	1	1.529	1.57
191	sp P05164 PERM_HUMAN	Myeloperoxidase OS=Homo sapiens GN=MPO PE=	91781	MGPVPFFS	129	8.5	-		15	8	6	4	1.748	1.988
192	tr L8E853 L8E853_HUMAN	von Willebrand factor OS=Homo sapiens GN=VW	341812	MIPARFAC	627	7.5	-		65	65	19	19	0.813	0.665
193	tr A0A024R035 A0A024R035_HUMAN	Complement component 9, isoform CRA_a OS=Hc	76205	MSACWQS	1009	28.3		1	111	111	18	18	1.023	1.05
194														

215	trQ96JD0 Q96JD0_HUMAN	Amyloid lambda 6 light chain variable region SAR	13922	NFMLTQP	149	20.7	-	39	1	2	1	---	---
216	trG3XAK1 G3XAK1_HUMAN	Hepatocyte growth factor-like protein alpha chain (91508	MGLWVV	56	4.1		2	3	3	2	---	---
217	trE7EUT5 E7EUT5_HUMAN	Glyceraldehyde-1-phosphate dehydrogenase OS=H	34412	MEEMRDI	175	18.5		1	11	11	3	1.515	1.089
218	tr A0A087X079 A0A087X079	Ig gamma-1 chain C region OS=Homo sapiens GN	62850	MEFGLSW	3604	35.1	-		315	1	13	1	---
219	tr A0A087WW89 A0A087WW	Protein IGHV3-72 OS=Homo sapiens GN=IGHV3	13100	EVQLVLSW	387	49.5	-		12	1	4	1	---
220	tr Q6NUL6 Q6NUL6_HUMAN	PITPNA protein (Fragment) OS=Homo sapiens GN	44984	PQRRPAP	25	5.1	-		1	1	1	1	---
221	spP01008 ANT3_HUMAN	Antithrombin-III OS=Homo sapiens GN=SERPIN	64585	MYSNVIG	7673	52.8	-		676	676	25	25	0.925
222	tr A0A024R9Q1 A0A024R9Q1	Thrombospondin 1, isoform CRA_a OS=Homo sap	150297	MGLAWG	1658	25.0	-		214	8	27	1	1.307
223	tr Q6PIQ7 Q6PIQ7_HUMAN	IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 S	29910	MAWALLI	1404	38.1	-		186	8	8	1	---
224	tr A0A087WU43 A0A087WU4	Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 S	79244	MGVPVSR	34	2.9		10	2	2	2	---	---
225	tr A0A075B6H6 A0A075B6H6	Ig kappa chain C region (Fragment) OS=Homo sap	14622	XTVAAPS	1005	80.4	-		74	45	6	2	0.791
226	tr A0A024R972 A0A024R972	Laminin, gamma 1 (Formerly LAMB2), isoform C1	204490	MDECTDE	53	1		1	1	1	1	---	---
227	tr S6BGE0 S6BGE0_HUMAN	IgG H chain OS=Homo sapiens PE=2 SV=1	37846	MEFGLSW	1429	22.7	-		130	2	5	1	---
228	spP35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens G	70468	MSCRQFS	62	10.4	-		7	7	5	0.63	0.618
229	tr B3KQ18 B3KQ18_HUMAN	cDNA FLJ32632 fis, clone SYN0V1000190, high	56595	MLKKQSA	53	2		4	2	2	1	1	---
230	spP02747 C1QC_HUMAN	Complement C1q subcomponent subunit C OS=Ho	29940	MDVGPSS	716	21.2	-		50	50	4	4	1.129
231	spP15169 CBPN_HUMAN	Carboxypeptidase N catalytic chain OS=Homo sap	58014	MSDLLSV	37	2	-		4	4	1	1	---
232	tr A0A068LKQ0 A0A068LKQ	Ig heavy chain variable region (Fragment) OS=Hoi	15284	EVQLVQS	181	10	-		8	8	1	1	0.98
233	spP23560 BDNF_HUMAN	Brain-derived neurotrophic factor OS=Homo sapie	33675	MTILFTLV	48	6.1	-		1	1	1	1	---
234	tr B2R7N9 B2R7N9_HUMAN	cDNA, FLJ93532, highly similar to Homo sapiens	57509	MGLSPY	41	2.4		1	1	1	1	1	---
235	spP13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens C	66321	MSVRYSS	504	13.5	-		23	22	7	6	0.468
236	tr B2RDL6 B2RDL6_HUMAN	cDNA, FLJ96669, highly similar to Homo sapiens	41811	MRAWIFF	160	7.9	-		4	15	3	3	1.205
237	sp PCOL4 C04A_HUMAN	Complement C4-A OS=Homo sapiens GN=C4A PI	217989	MRLLWGI	18599	42	-		1660	16	65	2	0.79
238	tr E7EQB2 E7EQB2_HUMAN	Lactotransferrin (Fragment) OS=Homo sapiens GN	92148	MGLCLAG	602	30.2		2	52	52	18	2.479	2.434
239	sp P07360 C08G_HUMAN	Complement component C8 gamma chain OS=Hon	24260	MLPPTGA	327	55	-		28	28	9	9	1.086
240	tr S6BAR0 S6BAR0_HUMAN	IgG L chain OS=Homo sapiens PE=2 SV=1	27347	MAWTPFL	1409	34.7	-		168	29	7	2	0.988
241	tr V9GYE7 V9GYE7_HUMAN	Complement factor H-related protein 2 OS=Homo	34920	MWLLVGS	444	24.8		1	37	7	6	2	1.319
242	tr B2R7D2 B2R7D2_HUMAN	cDNA, FLJ93389, highly similar to Homo sapiens	64534	MLRAPGC	36	2.1		2	2	2	1	1	---
243	tr C9I8S2 C9I8S2_HUMAN	Retinoic acid receptor responder protein 2 (Fragme	21794	MRLLLIPI	118	14.5		1	7	7	2	2	1.025
244	tr B4E1Z4 B4E1Z4_HUMAN	Uncharacterized protein OS=Homo sapiens PE=2 S	168440	MGLPMLV	349	10.3		1	40	40	13	13	0.965
245	sp PDJ18 SAA1_HUMAN	Serum amyloid A-1 protein OS=Homo sapiens GN	15406	MKLLTGL	125	20.5	-		8	7	2	1	1.061
246	tr Q5J875 Q5J875_HUMAN	GUGU gamma form OS=Homo sapiens GN=GUG	41888	MGLFLPL	47	8.5		3	7	7	3	0.264	
247	sp PCOL5 C04B_HUMAN	Complement C4-B OS=Homo sapiens GN=C4B PI	217898	MRLLWGI	19149	42	-		1692	38	65	2	0.844
248	tr A0A087X232 A0A087X232	Complement C1s subcomponent OS=Homo sapiens	89564	MYGELIS	364	16.1		3	53	53	11	11	1.125
249	sp P02743 SAMP_HUMAN	Serum amyloid P-component OS=Homo sapiens G1	29440	MNKLPLW	926	34.1	-		102	102	9	9	1.086
250	tr C8C504 C8C504_HUMAN	Beta-globin OS=Homo sapiens GN=HBB PE=3 S'	20056	MVHLTPE	157	35.4		1	14	14	5	5	1.11
251	sp O00391 QSOK1_HUMAN	Sulphydryl oxidase 1 OS=Homo sapiens GN=QSO	93667	MRRNCNG	373	21.3	-		61	61	16	16	0.816
252	sp P22792 CPN2_HUMAN	Carboxypeptidase N subunit 2 OS=Homo sapiens C	65328	MLPGAWI	167	15.2	-		26	26	8	8	1.162
253	tr B3BN62 B3BN62_HUMAN	Breast cancer anti-estrogen resistance protein 1 (Fr	28074	XPQFQSP	30	7.1	-		1	1	1	1	---
254	tr Q5NV90 Q5NV90_HUMAN	V2-17 protein (Fragment) OS=Homo sapiens GN=	11730	SYELTOPF	145	41.2	-		16	2	3	1	---
255	sp P02790 HEMO_HUMAN	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV	59077	MARVLG	33	6.5	-		3	3	3	3	---
256	sp P01768 HV307_HUMAN	Ig heavy chain V-III region CAM OS=Homo sapie	15294	QVELVES	87	21.3	-		12	12	3	3	1.168
257	sp Q5SNT2 TM201_HUMAN	Transmembrane protein 201 OS=Homo sapiens G2	79528	MEGVSAI	29	1.5	-		2	2	1	1	---
258	sp P68366 TBA4A_HUMAN	Tubulin alpha-4A chain OS=Homo sapiens GN=TI	56718	MRECSIVS	81	9.8	-		5	1	3	1	---
259	tr A2NYU7 A2NYU7_HUMAN	Heavy chain Fab (Fragment) OS=Homo sapiens PI	16036	QVKLLSES	26	7.1	-		1	1	1	1	---
260	sp P43251 BTD_HUMAN	Biotinidase OS=Homo sapiens GN=BTD PE=1 SV	68090	MAHAHIQ	145	5.7	-		12	12	3	3	0.999
261	tr A0A096LPE2 A0A096LPE2	Protein SAA2-SAA4 OS=Homo sapiens GN=SAA	26856	MKLLTGL	304	21.2	-		60	59	4	3	0.759
262	tr A0A024R498 A0A024R498	Serpin peptidase inhibitor, clade E (Nexin, plasmin	53326	MNWHPLI	36	9.1		2	3	3	3	3	1.064
263	tr B7Z8Q2 B7Z8Q2_HUMAN	cDNA FLJ55606, highly similar to Alpha-2-HS-gl	53042	MFAGCFF	264	13.4		2	24	24	5	5	0.99
264	tr B2R815 B2R815_HUMAN	cDNA, FLJ93695, highly similar to Homo sapiens	57184	MHLIDYL	167	17.1		1	25	25	7	7	0.774
265	sp P13671 C06_HUMAN	Complement component C6 OS=Homo sapiens GN	128749	MARRSRV	809	19.5	-		77	77	18	18	1.06
266	sp Q4L235 ACSF4_HUMAN	Acyl-CoA synthetase family member 4 OS=Homo	147330	MTLQELV	32	0.7		4	6	6	1	1	---
267	tr B3KP53 B3KP53_HUMAN	cDNA FLJ32131 fis, clone PEBLM2000267, high	52809	MPSDKTK	100	15.4		8	7	3	4	2	1.209
268	tr Q4ZFWS Q4ZFWS_HUMAN	Putative uncharacterized protein IHH OS=Homo si	34275	MNQWPHG	29	4.1		1	1	1	1	1	---
269	sp P00742 FA10_HUMAN	Coagulation factor X OS=Homo sapiens GN=F10	66408	MGRPLHL	37	11.7	-		6	5	6	5	---
270	sp P01023 A2MG_HUMAN	Alpha-2-macroglobulin OS=Homo sapiens GN=A2	191992	MGKNKLI	479	10.3	-		41	31	14	11	1.113
271	tr A8K7Q1 A8K7Q1_HUMAN	cDNA FLJ77770, highly similar to Homo sapiens i	62976	MPPSGPR	55	10.2		2	5	5	4	4	1.074
272	tr Q53GU8 Q53GU8_HUMAN	Transforming growth factor, beta-induced, 68kDa	85574	MALFVPL	69	9.2		1	6	6	6	6	1.021
273	sp Q03591 FHR1_HUMAN	Complement factor H-related protein 1 OS=Homo	43938	MWLLVSF	957	33	-		97	20	10	2	1.343
274	tr A2RTY6 A2RTY6_HUMAN	Inter-alpha (Globulin) inhibitor H2 OS=Homo sapi	126903	MKRLTCF	1439	27.7		3	145	145	24	24	1.103
275	sp P00451 FA8_HUMAN	Coagulation factor VIII OS=Homo sapiens GN=F8	316692	QMIJELST	129	3.1	-		10	10	7	7	1.019
276	tr Q6U2L6 Q6U2L6_HUMAN	C4B (Fragment) OS=Homo sapiens GN=C4B PE=	11768	RSMQGGC	306	15	-		53	52	4	3	0.744
277	tr B7Z3Y2 B7Z3Y2_HUMAN	cDNA FLJ51879, highly similar to Prenylcysteine	56786	MVQGOE	40	5.2		5	2	2	2	2	---
278	tr A0A024R1G8 A0A024R1G8	Apolipoprotein L, 1, isoform CRA_b OS=Homo sa	54476	MRFKSHT	561	20		11	63	63	9	9	0.359
279	tr A0A024RDB8 A0A024RDB8	Heparanase, isoform CRA_a OS=Homo sapiens G	73287	MLLRSKT	105	6.6		2	14	14	4	4	1.427
280	tr A0A087WSY6 A0A087WSY	Protein IGKV3-15 (Fragment) OS=Homo sapien	13346	MEAPAPL	49	25.9	-		3	1	2	1	---
281	tr A0A024R3W6 A0A024R3W	Neurophilin 2, isoform CRA_h OS=Homo sapiens C	115991	MDMFPLT	59	1.1		7	2	2	1	1	0.88
282	sp Q07954 LRP1_HUMAN	Protein tyrosine phosphatase-related protein	576082	MLTPPLLI	243	3.5	-		29	29	14	14	1.193
283	tr A0A024R592 A0A024R592	Glucosidase, alpha neutral AB, isoform CRA_b O	104019	MTTRFRDI	52	3.1		7	6	6	3	3	---
284	tr A2J1N7 A2J1N7_HUMAN	Rheumatoid factor RF-ET10 (Fragment) OS=Homo	13037	VESGGGL	24	7.3	-		4	4	1	1	---
285	tr A0A024R462 A0A024R462	Fibronectin 1, isoform CRA_n OS=Homo sapiens	286673	MLRGPGP	10599	36.3	-		863	66	64	9	1.11
286	tr A0A075B6I1 A0A075B6I1	Protein IGLV4-60 (Fragment) OS=Homo sapiens C	14671	MAWTPLL	19	7.5		1	1	1	1	1	---
287	tr Q5T9B7 Q5T9B7_HUMAN	Adenylate kinase isoenzyme 1 OS=Homo sapiens C	29708	MGCCSSS	40	5.7		2	1	1	1	1	---
288	tr Q53FV4 Q53FV4_HUMAN	Lumican variant (Fragment) OS=Homo sapiens PE	46640	MSLSAFTI	253	17.1	-		35	35	7	7	1.047
289	tr B2R892 B2R892_HUMAN	cDNA, FLJ93793, highly similar to Homo sapiens	54181	MPFGNTH	256	8.1		2	12	12	2	2	0.976
290	tr Q6N093 Q6N093_HUMAN	Putative uncharacterized protein DKFZp686I0419	55234	FFNYAMH	1173	28.1	-		132	1	9	1	---
291	tr Q86T71 Q86T71_HUMAN	Full-length cDNA clone CS0DD006YL02 of Neur	47597	MQGTDEF	6862	43.7	-		516	8	15	1	1.026
292	tr A8K5T0 A8K5T0_HUMAN	cDNA FLJ75416, highly similar to Homo sapiens	168175	MRLLAKII	2190	29.7	-		270	5	32	1	1.214
293	tr H0Y485 H0Y485_HUMAN	Insulin-like growth factor-binding protein 3 (Fragr	22968	XESPSVSS	48	20.3		14	6	6	3	3	1.494
294	sp P05546 HEP2_HUMAN	Heparin cofactor 2 OS=Homo sapiens GN=SERPI	67548	MKHSLSA	699	28.1	-		115	16	16	16	0.473
295	sp Q8NBP7 PCSK9_HUMAN	Proprotein convertase subtilisin/kexin type 9 OS=F	80589	MGTVSSR	198	7.1	-		14	14	4	4	1.034
296	sp P05154 IPSP_HUMAN	Plasma serine protease inhibitor OS=Homo sapiens	53365	MQLLQLL	1239	31.3	-		88	88	13	13	0.9
297	sp Q6P988 NOTUM_HUMAN	Protein notum homolog OS=Homo sapiens GN=N	61196	MGRGVRY	60	2.4		2	2	2	1	1	---
298	tr B2R8A1 B2R8A1_HUMAN	cDNA, FLJ93802, highly similar to Homo sapiens	42151	MVSGSSG	91	3		4	17	17	1	1	0.938
299	tr A0A024R0A9 A0A024R0A9	Stromal cell derived factor 4, isoform CRA_b OS=	46142	MVWPVVV	59	8.6		3	5	5	3	3	0.988
300	tr F2RM37 F2RM37_HUMAN	Coagulation factor IX OS=Homo sapiens GN=F9 I	61901	MQVRMNV	56	10		1	4	1	4	1	---
301	tr B0AZL7 B0AZL7_HUMAN	cDNA, FLJ79457, highly similar to Insulin-like gr	70047	MALRKGC	48	5.3		2	4	4	3	3	---
302	tr B2R8I2 B2R8I2_HUMAN	cDNA, FLJ93914, highly similar to Homo sapiens	67498	MKALLAA	211	22.1		1	29	29	11	11	1.28
303	tr Q5CAQ5 Q5CAQ5_HUMAN	Tumor rejection antigen (Gp96) 1 OS=Homo sapie	116600	MRALWVI	294	17.2		1	33	30	14	13	1.054
304	tr A0A024RDF8 A0A024RDF8	Alcohol dehydrogenase 4 (Class II), pi polypeptide	51465	MGTKGK	41	6.8		2	3	3	3	3	---
305	tr A0A087X0N5 A0A087X0N5	Protein IGKV1-17 OS=Homo sapiens GN=IGKV1	11818	DIQMTQSI	161	35.1		2	9	4	2	1	0.876
306	tr Q6N030 Q6N030_HUMAN	Putative uncharacterized protein DKFZp686I1521	68162	MDWTSWR	1925	18.1		6	173	49	9	3	1.197
307	tr F5GY80 F5GY80_HUMAN	Complement component C8 beta chain OS=Homo	70611	MDTCMTI	214	14		6	41				

324	tr A2N011 A2N011_HUMAN	Vhl1-D-J3-region (Fragment) OS=Homo sapiens	15986	QVHLVQS	125	9.4	-	8	8	1	1	0.981	0.909
325	tr B4DPQ3 B4DPQ3_HUMAN	cDNA FLJ51034, highly similar to Vitamin K-dep	66152	MAAGRR1	518	19	3	60	23	10	6	1.153	1.161
326	tr V9GYG9 V9GYG9_HUMAN	Apolipoprotein A-II (Fragment) OS=Homo sapiens	14103	MKLLAAT	186	38.9	2	60	60	3	3	0.603	0.615
327	sp P11021 GRP78_HUMAN	78 kDa glucose-regulated protein OS=Homo sapien	91263	MKLSLVA	59	5.7	-	4	4	3	3	1.068	0.99
328	tr B2R5S1 B2R5S1_HUMAN	cDNA, FLJ92595, highly similar to Homo sapiens	60156	MRKRAPQ	350	9.5	6	15	15	4	4	0.857	0.825
329	tr A0A087WU91 A0A087WU9	Protein IGHV3-49 OS=Homo sapiens GN=IGHV3	14625	AILKGVCQ	59	17.5	2	5	5	2	2	---	---
330	tr H0YAC1 H0YAC1_HUMAN	Plasma kallikrein heavy chain (Fragment) OS=Homo sapien	91778	XSEDECEV	95	8.6	1	9	9	6	6	0.965	0.982
331	sp Q06033 ITTH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 OS=H	118324	MAFAWW	320	9.2	-	33	33	7	7	0.962	1.004
332	sp Q8WZ8 OIT3_HUMAN	Oncoprotein-induced transcript 3 protein OS=Homo sapien	68290	MPPFLLLI	100	4	-	7	7	2	2	1.26	0.993
333	sp P15907 SIAT1_HUMAN	Beta-galactoside alpha-2,6-sialyltransferase 1 OS=	58648	MHTNLK1	46	3.7	-	1	1	1	1	---	---
334	tr H0YM48 H0YM48_HUMAN	ATP-dependent Clp protease ATP-binding subunit	37716	MPSCGAC	21	2.6	2	1	1	1	1	---	---
335	sp P05543 THBG_HUMAN	Thyroxine-binding globulin OS=Homo sapiens GN	55459	MSPLLY1	38	4.6	-	3	3	2	2	---	---
336	tr E7ESK7 E7ESK7_HUMAN	14-3-3 protein zeta/delta (Fragment) OS=Homo sapien	20060	MDKNELA	51	14.6	2	3	3	2	2	---	---
337	tr B3L145 B3L145_HUMAN	Sex hormone-binding globulin OS=Homo sapiens GN	41647	MTFDLTK	39	12.5	1	9	9	4	4	---	---
338	tr Q15430 Q15430_HUMAN	Coagulation factor V (Fragment) OS=Homo sapien	29475	PPESTVM	68	8.9	-	3	1	2	1	---	---
339	tr F5H1C6 F5H1C6_HUMAN	Ferritin family homolog 3 (Fragment) OS=Homo sapien	38768	MAGMKT	46	7.7	1	3	3	2	2	---	---
340	tr B2R608 B2R608_HUMAN	cDNA, FLJ92718, highly similar to Homo sapiens	64480	MGLQACL	24	3.7	5	3	3	2	2	---	---
341	tr Q8ZD7 Q8ZD7_HUMAN	Anti-thyroglobulin heavy chain variable region (Fr	15338	QVQLQGS	38	6.9	-	1	1	1	1	---	---
342	sp P33908 MA1A1_HUMAN	Mannosyl-oligosaccharide 1,2-alpha-mannosidase	86231	MPVGGLL	32	2.5	-	2	2	1	1	---	---
343	tr G5E9W0 G5E9W0_HUMAN	Phospholipase A1 member A OS=Homo sapiens GN	56514	MHKSSSIV	30	3	1	2	2	2	2	---	---
344	tr C0UY22 C0UY22_HUMAN	Apolipoprotein B (Including Ag(X) antigen) OS=H	625263	MDPPRPA	22843	45.3	-	2373	1080	198	94	0.397	0.395
345	tr E1B4S7 E1B4S7_HUMAN	Apolipoprotein B (Fragment) OS=Homo sapiens GN	30390	PTVSSSM	1108	50	-	65	1	9	1	---	---
346	tr Q6GMX6 Q6GMX6_HUMAN	IGH@ protein OS=Homo sapiens GN=IGH@ PE=	62325	MKHLWFI	3567	35.3	-	314	5	13	2	---	---
347	tr D3DNU8 D3DNU8_HUMAN	Kininogen 1, isoform CRA_a OS=Homo sapiens GN	59249	MKLITLFL	208	25.1	3	31	31	10	10	0.835	0.757
348	tr B4DVE1 B4DVE1_HUMAN	cDNA FLJ53478, highly similar to Galectin-3-bim	70995	MTPLRLFA	808	19.4	1	93	93	12	12	1.019	1.105
349	tr A0A5E4 A0A5E4_HUMAN	Uncharacterized protein OS=Homo sapiens PE=2	28363	MAWMMI	1459	35.3	-	173	14	7	1	1.594	1.193
350	sp Q13103 SP24_HUMAN	Secreted phosphoprotein 24 OS=Homo sapiens GN	27041	MISRMKEK	138	15.6	-	14	14	3	3	1.208	1.231
351	tr B4E335 B4E335_HUMAN	cDNA FLJ52842, highly similar to Actin, cytoplas	45627	MDDDIAA	366	33.6	7	42	42	9	9	1.33	1.27
352	tr X6RLJ0 X6RLJ0_HUMAN	Complement C1q subcomponent subunit A (Fragm	27065	MEGPRGV	58	11.8	1	8	8	3	3	1.178	1.254
353	tr Q5T4F6 Q5T4F6_HUMAN	Cartilage acidic protein 1 (Fragment) OS=Homo sapien	60780	YALRDRQ	74	4.2	1	1	1	1	1	---	---
354	tr B3KWZ6 B3KWZ6_HUMAN	cDNA FLJ44343 fis, clone TRACH3005479, high	150152	MAPEDKE	32	0.6	1	6	6	2	2	---	---
355	tr B4DNS6 B4DNS6_HUMAN	cDNA FLJ54278, highly similar to SPARC-like pr	71190	MKTGLFF	116	9.6	4	13	13	4	4	1.336	1.124
356	sp P13667 PDIA4_HUMAN	Protein disulfide-isomerase A4 OS=Homo sapiens	93307	MRPKAF	23	1.7	-	1	1	1	1	---	---
357	tr Q6N095 Q6N095_HUMAN	Putative uncharacterized protein DKFZp686K0315	63050	MDWTWR	3542	25.1	-	308	2	10	1	---	---
358	tr B3KU15 B3KU15_HUMAN	Hyaluronidase OS=Homo sapiens PE=2 SV=1	51312	MAAHLFP	196	11.5	2	14	14	4	4	1.042	0.988
359	tr A0A087WV47 A0A087WV4	Ig gamma-1 chain C region OS=Homo sapiens GN	62206	MELGLSV	4000	36.5	1	342	1	14	1	---	---
360	sp P10720 PF4V_HUMAN	Platelet factor 4 variant OS=Homo sapiens GN=PF	548	-	49	-	-	53	8	4	2	1.076	1.139
361	tr A0A087WT59 A0A087WT5	Transferrin OS=Homo sapiens GN=TTR PE=3	23099	MASHRLI	813	21.1	4	56	56	5	5	1.202	1.129
362	sp P55056 APOC4_HUMAN	Apolipoprotein C-IV OS=Homo sapiens GN=APO	17623	MSLLRNR	288	20.5	-	35	35	3	3	0.708	0.668
363	sp P1678 PERE_HUMAN	Eosinophil peroxidase OS=Homo sapiens GN=EP	88347	MHLPLP	43	3.9	-	8	1	3	1	---	---
364	sp P06888 V109_HUMAN	Ig lambda chain V-1 region EPS OS=Homo sapiens	13042	QSVLTQP	39	14.7	-	2	1	2	1	---	---
365	tr Q8ZZ5 Q8ZZ5_HUMAN	Coagulation factor XII-Mie OS=Homo sapiens PE	76113	MRALLLL	71	3.3	1	3	3	1	1	1.214	0.934
366	tr Q0VAS5 Q0VAS5_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1H4H	15015	MSGRGKC	41	23.3	1	2	2	2	2	---	---
367	tr D3DP13 D3DP13_HUMAN	Fibrinogen beta chain, isoform CRA_c OS=Homo	48076	MYLLKDL	199	24.4	3	19	19	8	8	1.334	0.857
368	sp P02649 APOE_HUMAN	Apolipoprotein E OS=Homo sapiens GN=APOE	40505	MKVLVA	3398	64	-	373	325	23	21	1.17	1.149
369	tr H0YJW9 H0YJW9_HUMAN	Uncharacterized protein (Fragment) OS=Homo sapien	18921	PGQVDAA	41	31.8	-	5	1	3	1	---	---
370	tr A0A024R962 A0A024R962	HCG40889, isoform CRA_b OS=Homo sapiens GN	168295	MRLLAKII	2249	30.5	1	277	12	33	2	1.072	1.227
371	sp Q4KW8 PLCH1_HUMAN	1-phosphatidylinositol 4,5-bisphosphate phosphodi	231978	MADLEVY	30	0.5	-	1	1	1	1	---	---
372	tr A0A024R5Z9 A0A024R5Z9	Pyruvate kinase OS=Homo sapiens GN=PKM2	70098	MSKPHSE	56	4.9	6	3	3	3	3	---	---
373	tr H0YDT2 H0YDT2_HUMAN	Cathepsin W (Fragment) OS=Homo sapiens GN=C	27350	ALTAHPS	29	6.2	2	1	1	1	1	---	---
374	tr Q9UL88 Q9UL88_HUMAN	Myosin-reactive immunoglobulin heavy chain vari	17289	EVQLVES	71	19.8	-	6	4	2	1	1.031	0.992
375	sp O43866 CD5L_HUMAN	CD5 antigen-like OS=Homo sapiens GN=CD5L	44774	MALLFSLI	484	43.8	-	37	37	12	12	1.081	1.02
376	tr Q9UL84 Q9UL84_HUMAN	Myosin-reactive immunoglobulin heavy chain vari	15510	EVQLVES	60	14.8	-	3	1	2	1	---	---
377	tr G3XAP6 G3XAP6_HUMAN	Cartilage oligomeric matrix protein OS=Homo sapi	88600	MLRELQE	51	1.4	8	5	5	1	1	---	---
378	tr A0A0A0MSV6 A0A0A0MSV	Complement C1q subcomponent subunit B (Fragm	29198	MKIPWGS	760	23.1	2	63	63	6	6	0.976	0.873
379	sp P06753 TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens GN	44851	MMEAIKK	40	8.4	-	3	1	2	1	---	---
380	tr Q5IWS5 Q5IWS5_HUMAN	Intelectin 1 OS=Homo sapiens GN=ITLN1	39480	MNQLSFL	96	6.4	1	12	12	2	2	1.203	1.042
381	tr Q59HB3 Q59HB3_HUMAN	Apolipoprotein B variant (Fragment) OS=Homo sa	222441	TIEGPLTSI	7264	45	-	713	7	67	1	0.468	0.416
382	tr A0A024QZL1 A0A024QZL1	Proteoglycan 1, secretory granule, isoform CRA_a	19609	MMQKLLI	60	8.2	1	3	3	1	1	---	---
383	tr A0A087WSY5 A0A087WSY	Carboxypeptidase B2 OS=Homo sapiens GN=CPE	51257	MKLCSLA	157	18.7	1	22	22	7	7	1.064	0.768
384	tr E1B2D1 E1B2D1_HUMAN	Hemoglobin alpha-1 globin chain variant (Fragme	13799	MVLSPAD	63	22	7	4	4	2	2	---	---
385	tr A0A075B6K6 A0A075B6K6	Protein IGLV4-3 OS=Homo sapiens GN=IGLV4-3	15013	MAWVSF	22	13.9	1	4	4	2	2	---	---
386	tr Q6MZL2 Q6MZL2_HUMAN	Putative uncharacterized protein DKFZp686M056	38922	NPGIYTC	103	12.8	-	10	9	4	3	1.362	1.527
387	tr Q6P528 Q6P528_HUMAN	ASPN protein OS=Homo sapiens GN=ASPN	54606	MKEYVLL	26	2.9	1	1	1	1	1	---	---
388	tr D6RHH7 D6RHH7_HUMAN	Corticotropin-releasing factor-binding protein OS=	30563	MSPNFKL	48	8	1	4	4	2	2	1.539	1.112
389	tr M0R009 M0R009_HUMAN	Alpha-1B-glycoprotein (Fragment) OS=Homo sapi	37179	LTCQAHL	103	14.7	1	11	11	5	5	0.994	0.965
390	tr A0A0A0MRQ5 A0A0A0MR	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1	14073	MSSGNAK	29	8.2	5	1	1	1	1	---	---
391	sp P02775 CXCL7_HUMAN	Platelet basic protein OS=Homo sapiens GN=PPB	18429	MSLRDLT	164	37.5	-	11	11	4	4	1.149	1.167

A-VS-B@C A-VS-B@C A-VS-B@S A-VS-B@S				KEGG(ko_j GO Biologi GO Molecu GO Cellular_Component
-	-	-	-	K01344 1 9: GO:000759 GO:000425 GO:0005788//endoplasmic reticulum lumen;GO:0005796//Golgi lumen;GO:0005576//extracellular region
-	-	-	-	K14462 1 0: GO:001088 GO:005075 GO:0030669//clathrin-coated endocytic vesicle membrane;GO:0034360//chylomicron remnant;GO:0005788//endoplasmic reticulum lumen
-	4	4 *	*	K07605 1 0: GO:003298 GO:000520 GO:0005794//Golgi apparatus;GO:0045095//keratin filament
-	-	-	-	K04593 1 1: GO:000727 - GO:0005576//extracellular region
33	33 *	-	-	K08023 1 8: GO:001095 GO:001650 GO:0005615//extracellular space;GO:0005604//basement membrane
-	-	-	-	K11252 1 1: GO:000633 GO:000367 GO:0000786//nucleosome;GO:0005634//nucleus
55	55 -	-	-	K03098 1 6: GO:004866 GO:003609 GO:0005783//endoplasmic reticulum;GO:0005615//extracellular space;GO:0022626//cytosolic ribosome;GO:0048471//perinuclear region
106	106 *	-	-	K05399 1 0: GO:003272 GO:000510 GO:0005615//extracellular space
174	174 -	-	-	K05316 1 8: GO:001095 GO:000486 GO:0005737//cytoplasm;GO:0005886//plasma membrane;GO:0005576//extracellular region
2	2 -	-	-	K01172 1 1: GO:004866 GO:000550 GO:0030426//growth cone;GO:0005615//extracellular space;GO:0005605//basal lamina;GO:0032311//angiogenin-PR1 complex;GO:0005
-	-	-	-	K12472 1 4: GO:004801 GO:000508 GO:0005829//cytosol;GO:0030054//cell junction;GO:0043005//neuron projection;GO:0045202//synapse;GO:0005905//coated pit;GO:003
-	-	-	-	-
2	2 -	-	-	K08784 1 0: GO:003051 GO:000425 GO:0005615//extracellular space;GO:0031012//extracellular matrix;GO:0005829//cytosol
1	1 -	-	-	K06554 1 5: -
15	14 -	*	*	K14611 1 7: GO:000257 - GO:0031093//platelet alpha granule lumen;GO:0005576//extracellular region
18	18 *	*	*	K14477 1 0: GO:000695 GO:003049 GO:0031838//haptoglobin-hemoglobin complex;GO:0034366//spherical high-density lipoprotein particle
-	-	-	-	K07937 1 9: GO:001603 GO:000505 GO:0000139//Golgi membrane;GO:0005829//cytosol;GO:0048471//perinuclear region of cytoplasm;GO:0005886//plasma membrane;GO:
1	1 -	-	-	- GO:000686 GO:000531 GO:0034362//low-density lipoprotein particle;GO:0034364//high-density lipoprotein particle
2	2 -	-	-	K02727 1 3: GO:000020 GO:000551 GO:0005654//nucleoplasm;GO:0005829//cytosol;GO:0019773//proteasome core complex, alpha-subunit complex
1	1 -	-	-	K06554 1 2: -
-	-	-	-	K06554 1 2: -
1	1 -	-	-	K06554 1 4: GO:004508 GO:000382 GO:0005886//plasma membrane;GO:0005576//extracellular region
1	1 -	-	-	K06553 1 5: -
3	3 -	-	-	K03984 1 5: GO:001095 GO:000486 GO:0005576//extracellular region
3	3 -	*	*	- GO:000268 GO:000551 GO:0005615//extracellular space
2	2 -	-	-	K12258 1 0: GO:005072 GO:000510 GO:0005829//cytosol;GO:0005615//extracellular space;GO:0030424//axon;GO:0043202//lysosomal lumen;GO:0048471//perinuclear regi
14	14 *	-	-	K04524 1 9: GO:001087 GO:003121 GO:0042627//chylomicron;GO:0034361//very-low-density lipoprotein particle;GO:0034364//high-density lipoprotein particle;GO:000578
1	1 -	-	-	K06827 1 5: GO:000155 GO:000552 GO:0005615//extracellular space;GO:0005886//plasma membrane
50	50 -	-	-	K13624 1 0: GO:000682 GO:005108 GO:0005615//extracellular space
1	1 -	-	-	K06856 1 9: -
2	2 -	*	*	- GO:003334 GO:000554 GO:0034362//low-density lipoprotein particle;GO:0034365//discoidal high-density lipoprotein particle;GO:0034361//very-low-density lip
5	4 -	*	*	K08130 1 3: - GO:0005576//extracellular region
-	-	-	-	K12382 1 3: GO:000166 - GO:0042599//lamellar body;GO:0005764//lysosome;GO:0005771//multivesicular body;GO:0005615//extracellular space
1	1 -	-	-	K06856 1 3: -
21	21 -	-	-	K05502 1 7: GO:001095 GO:000820 GO:0005615//extracellular space;GO:0031012//extracellular matrix
3	3 *	-	-	K06856 1 2: -
7	7 *	*	*	K13915 1 5: GO:004274 GO:000379 GO:0005615//extracellular space
2	2 *	-	-	K08632 1 1: GO:003019 GO:000202 GO:0005614//interstitial matrix
-	-	-	-	K02842 1 0: GO:000635 GO:000493 GO:0031527//filopodium membrane;GO:0016021//integral to membrane;GO:0009986//cell surface;GO:0048471//perinuclear region of cy
2	2 -	-	-	K01172 1 1: GO:000637 GO:000452 GO:0005576//extracellular region
1	1 -	-	-	K11275 1 1: GO:001658 GO:000367 GO:0005694//chromosome;GO:0005634//nucleus
6	6 -	-	-	-
23	23 *	*	*	K01672 1 7: GO:000166 GO:004687 GO:0005615//extracellular space
10	10 -	-	-	K01127 1 0: GO:004306 GO:000462 GO:0005615//extracellular space;GO:0043231//intracellular membrane-bounded organelle;GO:0005578//proteinaceous extracellular matri
-	-	-	-	K12499 1 1: GO:007144 GO:004362 GO:0005737//cytoplasm;GO:0005615//extracellular space
11	11 *	*	*	K04391 1 0: GO:000690 GO:007089 GO:0045121//membrane raft;GO:0005615//extracellular space;GO:0031225//anchored to membrane;GO:0009986//cell surface;GO:00058
-	-	-	-	K06554 1 6: -
2	2 -	-	-	K05502 1 0: GO:000662 GO:000827 GO:0031988//membrane-bounded vesicle;GO:0005581//collagen;GO:0005615//extracellular space
5	5 -	-	-	K01059 1 0: GO:003437 GO:000446 GO:0042627//chylomicron;GO:0009986//cell surface;GO:0031012//extracellular matrix;GO:0034361//very-low-density lipoprotein partic
8	8 *	-	-	K08648 1 0: GO:000715 GO:000553 GO:0005615//extracellular space
4	4 *	*	*	- GO:000609 GO:003463 GO:0005615//extracellular space
19	20 *	-	-	K03908 1 0: GO:003016 GO:000550 GO:0000139//Golgi membrane;GO:0031093//platelet alpha granule lumen;GO:0005789//endoplasmic reticulum membrane;GO:0005576//
4	4 -	-	-	K01327 1 2: GO:004211 GO:000425 GO:0042582//azurophil granule;GO:0005576//extracellular region
-	-	-	-	K06554 1 6: -
1	1 -	-	-	K06554 1 6: GO:004508 GO:000382 GO:0005886//plasma membrane;GO:0005576//extracellular region
-	-	-	-	K14678 1 0: GO:001827 - GO:0005576//extracellular region;GO:0031012//extracellular matrix
-	-	-	-	K10352 1 0: GO:003022 GO:004280 GO:0005826//actomyosin contractile ring;GO:0001772//immunological synapse;GO:0031594//neuromuscular junction;GO:0005829//cyto
1	1 -	-	-	K07604 1 0: GO:001021 GO:000551 GO:0005829//cytosol;GO:0005739//mitochondrion;GO:0005730//nucleolus;GO:0071944//cell periphery;GO:0045095//keratin filament
17	17 -	-	-	K01045 1 0: GO:004639 GO:004687 GO:0005615//extracellular space
1	1 -	-	-	K07375 1 0: GO:004226 GO:000552 GO:0045298//tubulin complex;GO:0005829//cytosol;GO:0005874//microtubule;GO:0005634//nucleus
9	9 -	*	*	K01774 1 1: GO:000905 GO:000406 GO:0016021//integral to membrane;GO:0009986//cell surface
1	1 -	-	-	K01350 1 8: GO:009702 GO:001989 GO:0005829//cytosol;GO:0031012//extracellular matrix;GO:0005886//plasma membrane
4	4 -	-	-	K04667 1 0: GO:004000 GO:000808 GO:0005576//extracellular region
-	-	-	-	K06856 1 1: -
-	-	-	-	K10373 1 1: GO:003461 GO:004280 GO:0032059//bleb;GO:0005862//muscle thin filament tropomyosin;GO:0005829//cytosol;GO:0031941//filamentous actin;GO:0001725//s
3	3 -	-	-	K03982 1 0: GO:000717 GO:000486 GO:0005615//extracellular space;GO:0005886//plasma membrane;GO:0031093//platelet alpha granule lumen;GO:0031012//extracellular
26	26 *	-	-	K03984 1 0: GO:003398 GO:000486 GO:0005615//extracellular space;GO:0031093//platelet alpha granule lumen;GO:0005578//proteinaceous extracellular matrix
15	15 -	-	-	K00518 1 6: GO:004668 GO:000820 GO:0005615//extracellular space;GO:0031012//extracellular matrix;GO:0005634//nucleus;GO:0005829//cytosol;GO:0005802//trans-Gol
-	-	-	-	K03989 1 1: GO:000695 GO:000486 GO:0005615//extracellular space;GO:0005886//plasma membrane
-	-	-	-	K10847 1 4: -
21	22 -	-	-	K00650 1 0: GO:004215 GO:000460 GO:0034364//high-density lipoprotein particle
2	2 -	-	-	K05604 1 0: GO:000650 GO:004687 GO:0005576//extracellular region
-	-	-	-	K06249 1 0: GO:002176 GO:007032 GO:0005615//extracellular space;GO:0005737//cytoplasm;GO:0005578//proteinaceous extracellular matrix;GO:0030425//dendrite
-	-	-	-	K06856 1 7: -
59	59 -	-	-	K03989 1 2: GO:000695 GO:000486 GO:0005615//extracellular space;GO:0005886//plasma membrane
25	25 *	-	-	K04003 1 2: GO:000695 - GO:0005576//extracellular region;GO:0005886//plasma membrane
-	-	-	-	K06554 1 7: -
4	4 -	*	*	K04004 1 8: GO:000686 GO:000531 GO:0005615//extracellular space
17	17 *	*	*	K05399 1 1: GO:004369 GO:001712 GO:0031982//vesicle;GO:0034364//high-density lipoprotein particle
3	3 -	-	-	K04525 1 0: GO:001095 GO:000486 GO:0005576//extracellular region;GO:0005634//nucleus
2	2 -	-	-	K13375 1 0: GO:000717 GO:000808 GO:0030424//axon;GO:0043025//neuronal cell body;GO:0005902//microvillus;GO:0005796//Golgi lumen;GO:0009986//cell surface;GO
1	1 -	-	-	K00683 1 7: GO:000650 GO:001660 GO:0005576//extracellular region
5	4 *	*	*	- GO:001026 GO:000843 GO:0005615//extracellular space
2	2 -	-	-	- GO:000828 GO:0005615//extracellular space
2	2 *	-	-	K03996 1 0: GO:000695 - GO:0005579//membrane attack complex;GO:0005576//extracellular region
1	1 -	-	-	K08767 1 4: GO:000663 GO:000517 GO:0005615//extracellular space
21	21 *	*	*	K04004 1 1: GO:000695 - GO:0005576//extracellular region
1	1 -	-	-	K06554 1 2: -
-	-	-	-	K06554 1 2: -
-	-	-	-	K06856 1 6: -
-	-	-	-	K10031 1 1: GO:007009 GO:004523 GO:0005615//extracellular space;GO:0009897//external side of plasma membrane
12	12 -	-	-	K15412 1 0: GO:004274 - GO:0005615//extracellular space;GO:0031012//extracellular matrix
1	1 -	-	-	K03386 1 1: GO:004274 GO:000837 GO:0005829//cytosol;GO:0005739//mitochondrion
1	1 -	-	-	K03906 1 0: GO:000759 - GO:0005576//extracellular region
5	1 -	-	-	K06554 1 1: -
-	-	-	-	K06856 1 2: -
50	51 *	*	*	K05407 1 2: GO:001652 GO:000820 GO:0031093//platelet alpha granule lumen;GO:0005615//extracellular space
9	9 *	*	*	K09025 1 0: GO:004572 GO:005075 GO:0042627//chylomicron;GO:0034361//very-low-density lipoprotein particle;GO:0034364//high-density lipoprotein particle;GO:003436
1	1 -	-	-	K01046 1 0: GO:000663 GO:000462 GO:0034364//high-density lipoprotein particle
197	197 -	-	-	K08760 1 0: GO:0009986//cell surface;GO:0034364//high-density lipoprotein particle;GO:0042627//chylomicron;GO:0005788//endoplasmic reticulum
5	3 -	*	*	K04001 1 2: GO:003016 GO:000551 GO:0031093//platelet alpha granule lumen;GO:0005615//extracellular space
1	1 -	-	-	K02731 1 8: GO:000020 GO:000429 GO:0005654//nucleoplasm;GO:0005829//cytosol;GO:0019773//proteasome core complex, alpha-subunit complex
9	9 -	-	-	K09580 1 0: GO:000666 GO:000375 GO:0005793//endoplasmic reticulum-Golgi intermediate compartment;GO:0009986//cell surface;GO:0042470//melanosome;GO:0005788
-	-	-	-	K15288 1 1: -
21	22 *	-	-	K07605 1 0: GO:000697 GO:000487 GO:0045095//keratin filament;GO:0005886//plasma membrane

19	19	-	-	K03903 1 0. GO:003016 GO:003067 GO:0009897//external side of plasma membrane;GO:0031093//platelet alpha granule lumen;GO:0005938//cell cortex;GO:0005577//fibrin
1	1	-	-	K05699 1 0. GO:003016 GO:000517 GO:0005925//focal adhesion;GO:0031143//pseudopodium;GO:0031093//platelet alpha granule lumen;GO:0005576//extracellular region;C
1	1	-	-	- GO:000859 GO:000820 GO:0005578//proteinaceous extracellular matrix
1	1	-	-	- GO:003016 GO:000550 GO:0033018//saroplasmic reticulum lumen;GO:0042470//melanosome;GO:0005576//extracellular region;GO:0005794//Golgi apparatus
191	191	-	-	- GO:006107 GO:003162 GO:0034366//spherical high-density lipoprotein particle;GO:0031093//platelet alpha granule lumen;GO:0031966//mitochondrial membran
-	-	-	-	K06856 1 2. -
5	5	-	-	- GO:005088 GO:000550 GO:0030658//transport vesicle membrane;GO:0030141//secretory granule;GO:0005576//extracellular region
-	-	-	-	K06856 1 1. -
3	3	-	-	K10138 1 2. GO:004434 GO:000552 GO:0005615//extracellular space
5	5	-	*	K06554 1 2. -
26	26	-	*	- GO:000196 GO:000487 GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix
2	2	-	-	K06856 1 8. -
3	3	-	-	K06826 1 0. GO:000716 GO:004323 GO:0005605//basal lamina;GO:0071944//cell periphery
7	7	-	-	K01446 1 0. GO:003282 GO:000827 GO:0005622//intracellular;GO:0005576//extracellular region;GO:0016020//membrane
1	1	-	-	K06831 1 7. GO:000838 GO:001986 GO:0005681//spliceosomal complex;GO:0005743//mitochondrial inner membrane;GO:0005578//proteinaceous extracellular matrix;GO:00
9	9	-	*	K09644 1 0. GO:003016 GO:000425 GO:0031093//platelet alpha granule lumen;GO:0034358//plasma lipoprotein particle;GO:0031232//extrinsic to external side of plasma me
8	8	-	*	K14736 1 0. GO:005508 GO:000819 GO:0030141//secretory granule;GO:0009925//basal plasma membrane;GO:0005739//mitochondrion;GO:0030139//endocytic vesicle;GO:(
15	14	-	*	K03905 1 0. GO:003016 GO:003067 GO:0009897//external side of plasma membrane;GO:0031093//platelet alpha granule lumen;GO:0005938//cell cortex;GO:0005577//fibrin
4	4	-	*	K06260 1 0. GO:000716 GO:000551 GO:0005887//integral to plasma membrane;GO:0009986//cell surface
9	8	-	*	K07296 1 4. GO:003303 GO:004349 GO:0005783//endoplasmic reticulum;GO:0005615//extracellular space;GO:0071944//cell periphery;GO:0048471//perinuclear region of cy
1	1	-	-	K08023 1 4. GO:001904 GO:000520 GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix
3	3	-	-	K08627 1 0. GO:003016 GO:000827 GO:0005615//extracellular space;GO:0009986//cell surface;GO:0005578//proteinaceous extracellular matrix
18	18	-	*	K03983 1 0. GO:000203 GO:004280 GO:0005577//fibrinogen complex;GO:0031093//platelet alpha granule lumen
1	1	-	-	K05717 1 0. GO:001095 GO:001650 GO:0016324//apical plasma membrane;GO:0005604//basement membrane
29	29	-	-	- GO:004295 GO:006023 GO:0042627//chylomicron;GO:0034366//spherical high-density lipoprotein particle;GO:0034361//very-low-density lipoprotein particle;G
1	1	-	-	K06856 1 4. -
-	-	-	-	-
-	-	-	-	K06554 1 5. GO:004508 GO:000382 GO:0005886//plasma membrane;GO:0005576//extracellular region
10	10	-	-	K03997 1 0. GO:000695 - GO:0005615//extracellular space;GO:0005579//membrane attack complex
7	7	-	*	- GO:003016 GO:000166 GO:0034364//high-density lipoprotein particle
7	6	-	*	K08023 1 1. GO:001810 GO:000550 GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix
39	39	-	-	K06856 1 1. -
1	1	-	-	-
2	2	-	-	K10375 1 2. GO:000697 GO:000830 GO:0005829//cytosol;GO:0030863//cortical cytoskeleton;GO:0002102//podosome;GO:0001725//stress fiber;GO:0005862//muscle thin fil
1	1	-	-	K05717 1 0. GO:000152 GO:001650 GO:0005604//basement membrane;GO:0005793//endoplasmic reticulum-Golgi intermediate compartment;GO:0031093//platelet alpha gra
35	35	-	*	K01045 1 0. GO:001087 GO:000406 GO:0034366//spherical high-density lipoprotein particle
-	-	-	-	K08672 1 0. GO:000735 GO:004349 GO:0005796//Golgi lumen;GO:0005615//extracellular space;GO:0009986//cell surface;GO:0012505//endomembrane system;GO:003101
2	2	-	-	K05717 1 8. GO:000152 GO:001650 GO:0005604//basement membrane;GO:0005793//endoplasmic reticulum-Golgi intermediate compartment;GO:0031093//platelet alpha gra
5	5	-	*	- GO:000268 GO:000551 GO:0005615//extracellular space
1	1	-	-	- GO:000635 GO:000367 GO:0005576//extracellular region;GO:0005634//nucleus
-	-	-	-	K09631 1 0. GO:000650 GO:000425 GO:0005615//extracellular space;GO:0005791//rough endoplasmic reticulum
-	-	-	-	K06856 1 1. GO:000695 GO:000382 GO:0005576//extracellular region;GO:0016021//integral to membrane;GO:0005886//plasma membrane
1	1	-	-	K03984 1 4. GO:001095 GO:000486 GO:0005576//extracellular region
-	-	-	-	-
85	85	-	-	K04861 1 2. GO:003021 GO:000486 GO:0005576//extracellular region
1	1	-	-	K05656 1 1. GO:000191 GO:004697 GO:0042825//TAP complex;GO:0005743//mitochondrial inner membrane;GO:0005765//lysosomal membrane;GO:0005769//early endoso
1	1	-	-	K06554 1 7. -
307	307	-	-	K01313 1 0. GO:000759 GO:000808 GO:0005788//endoplasmic reticulum lumen;GO:0005615//extracellular space;GO:0005886//plasma membrane;GO:0005796//Golgi lumen
3	4	-	*	K06251 1 3. GO:000695 GO:003024 GO:0005576//extracellular region;GO:00016021//integral to membrane
1	1	-	-	K06856 1 3. -
-	-	-	-	K04524 1 3. GO:000664 GO:005075 GO:0031232//extrinsic to external side of plasma membrane;GO:0034364//high-density lipoprotein particle;GO:0042627//chylomicron;G
1	1	-	-	K06554 1 4. -
2	2	-	-	K04659 1 0. GO:001652 GO:007005 GO:0005577//fibrinogen complex;GO:0009897//external side of plasma membrane;GO:0031093//platelet alpha granule lumen;GO:00310
-	-	-	-	- GO:006028 - GO:0005737//cytoplasm;GO:0005929//cilium
20	20	-	*	K03993 1 0. GO:000695 GO:000425 GO:0005576//extracellular region
1	1	-	-	K07860 1 4. GO:000741 GO:000552 GO:0005829//cytosol;GO:0005635//nuclear envelope;GO:0005886//plasma membrane
112	112	-	*	K04002 1 0. GO:004508 GO:000551 GO:0005737//cytoplasm;GO:0005886//plasma membrane;GO:0005576//extracellular region
-	-	-	-	- GO:006048 GO:000551 GO:0005730//nucleolus;GO:0000922//spindle pole;GO:0005876//spindle microtubule;GO:0005694//chromosome;G
1	1	-	-	K04525 1 2. GO:001095 GO:000486 GO:0005737//cytoplasm;GO:0005576//extracellular region;GO:0016020//membrane
2	2	-	-	K08023 1 0. GO:003558 GO:000502 GO:0005578//proteinaceous extracellular matrix
-	-	-	-	K07249 1 0. GO:003232 GO:000549 GO:0005829//cytosol
2	2	-	-	K01333 1 0. GO:000695 GO:000504 GO:0005615//extracellular space;GO:0016020//membrane
676	676	-	-	K03990 1 0. GO:000250 GO:003171 GO:0005615//extracellular space;GO:0005886//plasma membrane
87	87	-	-	K08759 1 6. GO:000718 GO:001548 GO:0042627//chylomicron;GO:0034366//spherical high-density lipoprotein particle;GO:0034361//very-low-density lipoprotein particle;G
1	1	-	-	K06554 1 6. -
-	-	-	-	- GO:003016 GO:000166 GO:0034364//high-density lipoprotein particle
55	56	-	*	K03994 1 0. GO:003360 GO:003171 GO:0005579//membrane attack complex;GO:0005615//extracellular space
3	3	-	-	K10138 1 7. GO:000698 GO:000552 GO:0005615//extracellular space
-	-	-	-	K06856 1 4. -
1	1	-	-	K10162 1 0. GO:003444 GO:000384 GO:0034362//low-density lipoprotein particle
43	43	-	*	K00432 1 1. GO:004274 GO:000460 GO:0005615//extracellular space
9	9	-	*	K03992 1 0. GO:000650 GO:000550 GO:0005615//extracellular space
-	-	-	-	K06856 1 2. GO:000695 GO:000382 GO:0005576//extracellular region;GO:0016021//integral to membrane;GO:0005886//plasma membrane
3	3	-	*	- GO:002241 GO:000487 GO:0005788//endoplasmic reticulum membrane;GO:0005886//plasma membrane;GO:0016021//integral to membrane;GO:0005576//extra
7	7	-	-	K03909 1 2. GO:004216 GO:000486 GO:0005576//extracellular region;GO:0005886//plasma membrane
2	2	-	-	K04667 1 0. GO:004000 GO:000808 GO:0005576//extracellular region
-	-	-	-	K10360 1 6. GO:003285 GO:000507 GO:0005829//cytosol;GO:0043231//intracellular membrane-bounded organelle;GO:0001726//ruffle;GO:0005886//plasma membrane
1	1	-	-	- GO:003439 GO:000550 GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix;GO:0005737//cytoplasm;GO:0016020//membrane;GO:
8	8	-	*	K06238 1 0. GO:000741 GO:000486 GO:0030133//transport vesicle;GO:0005615//extracellular space;GO:0005788//endoplasmic reticulum lumen;GO:0042383//sarcolemma;C
-	-	-	-	K06554 1 5. -
5	4	-	*	- GO:000695 GO:000382 GO:0005576//extracellular region
1	1	-	-	K06554 1 6. -
103	103	-	-	K03902 1 0. GO:003016 GO:000550 GO:0005615//extracellular space;GO:0031093//platelet alpha granule lumen;GO:0005886//plasma membrane
27	27	-	-	K01330 1 0. GO:004508 GO:000425 GO:0005576//extracellular region
2	2	-	-	K11251 1 9. GO:000633 GO:000367 GO:0000786//nucleosome;GO:0005634//nucleus
6	6	-	*	K10789 1 0. GO:000695 GO:004687 GO:0005764//lysosome;GO:0030141//secretory granule;GO:0005615//extracellular space;GO:0005634//nucleus
31	31	-	*	K03900 1 0. GO:003016 GO:004748 GO:0009897//external side of plasma membrane;GO:0033093//Weibel-Palade body;GO:0005578//proteinaceous extracellular matrix;GO:
70	70	-	-	K04000 1 0. GO:001983 - GO:0005579//membrane attack complex;GO:0005576//extracellular region
2	2	-	*	K06554 1 5. -
-	-	-	-	K01319 1 1. GO:007094 GO:000425 GO:0030141//secretory granule;GO:0005615//extracellular space;GO:0009986//cell surface;GO:0031012//extracellular matrix;GO:00058
1	1	-	-	K06238 1 2. GO:003444 GO:004687 GO:0031258//lamellipodium membrane;GO:0016021//integral to membrane;GO:0031527//filopodium membrane
19	18	-	*	K01883 1 5. GO:005118 GO:000843 GO:0005615//extracellular space
448	448	-	-	K06251 1 0. GO:003209 GO:000517 GO:0005615//extracellular space;GO:0071062//alphav-beta3 integrin-vitronectin complex;GO:0031012//extracellular matrix
7	7	-	-	K14477 1 6. GO:000695 GO:003049 GO:0005615//extracellular space;GO:0031838//haptoglobin-hemoglobin complex
2	2	-	-	K06271 1 0. GO:000741 GO:003027 GO:0005925//focal adhesion;GO:0005911//cell-cell junction;GO:0032587//ruffle membrane;GO:0043231//intracellular membrane-bound
-	-	-	-	K06856 1 5. -
-	-	-	-	K06825 1 0. GO:003558 GO:000550 GO:0005604//basement membrane;GO:0005615//extracellular space;GO:0001527//microfibril
-	-	-	-	K13073 1 0. - GO:0005576//extracellular region;GO:0005887//integral to plasma membrane;GO:0055038//recycling endosome membrane;GO:0030133/
-	-	-	-	K05901 1 8. GO:004428 GO:004260 GO:0005829//cytosol
7	7	-	*	K03989 1 3. GO:000695 GO:000486 GO:0005615//extracellular space;GO:0005886//plasma membrane
1	1	-	-	K06554 1 1. -
-	-	-	-	K03996 1 0. GO:000695 - GO:0005579//membrane attack complex;GO:0005576//extracellular region
-	-	-	-	K08288 1 0. GO:000724 GO:000508 GO:0005788//endoplasmic reticulum lumen
14	14	-	*	K10104 1 7. GO:000822 GO:000382 GO:0005615//extracellular space;GO:0005581//collagen
-	-	-	-	K01323 1 0. GO:000759 GO:000551 GO:0005615//extracellular space;GO:0005886//plasma membrane
48	48	-	*	K10104 1 2. GO:000716 GO:003024 GO:0005615//extracellular space;GO:0005581//collagen
-	-	-	-	K10414 1 0. GO:003090 GO:000377 GO:0035085//cilium axoneme;GO:0005829//cytosol;GO:0030286//microtubule;GO:0005874//microtubule;GO:0031512//motile prima
1	1	-	-	- GO:000693 - GO:0005737//cytoplasm;GO:0005615//extracellular space
603	603	-	-	K08757 1 1. GO:007050 GO:000554 GO:0030139//endocytic vesicle;GO:0005788//endoplasmic reticulum lumen;GO:0005886//plasma membrane;GO:0030141//secretory gran

1	1	-	-	K06553 1 9-	-
1	1	-	-	K05460 1 1:	GO:000156 GO:000425 GO:0005576/extracellular region;GO:0005829/cytosol;GO:0005634/nucleus
8	8	*	-	K00134 1 3:	GO:0005140 GO:0005128 GO:0005829/cytosol;GO:0015630/microtubule cytoskeleton;GO:0048471/perinuclear region of cytoplasm;GO:0005811/lipid particle;C
1	1	-	-	K06856 1 2-	-
-	-	-	-	K06856 1 3-	-
-	-	-	-	K01106 1 3:	GO:000741 GO:000852 GO:0016021/integral to membrane;GO:0005737/cytoplasm
347	347	-	-	K03911 1 0:	GO:0005511 GO:000486 GO:0005615/extracellular space;GO:0005971/ribonucleoside-diphosphate reductase complex;GO:0005886/plasma membrane
6	6	*	-	K04659 1 0:	GO:001652 GO:007005 GO:0005577/fibrinogen complex;GO:0009897/external side of plasma membrane;GO:0031093/platelet alpha granule lumen;GO:0031012/extracellular space
-	-	-	-	K06554 1 2-	-
1	1	-	-	K05689 1 0:	GO:007097 GO:003050 GO:0009986/cell surface;GO:0016235/aggresome;GO:0043296/apical junction complex;GO:0005925/focal adhesion;GO:0005802/tra
20	20	-	-	K06554 1 2:	GO:004508 GO:000382 GO:0005886/plasma membrane;GO:0005576/extracellular region
1	1	-	-	K05635 1 0:	GO:001647 GO:004320 GO:0043260/laminin-11 complex;GO:0005606/laminin-1 complex;GO:0005615/extracellular space;GO:0043259/laminin-10 complex
-	-	-	-	K06856 1 1-	-
3	3	*	-	K07604 1 1:	GO:000728 GO:000520 GO:0045095/keratin filament;GO:0048471/perinuclear region of cytoplasm
1	1	-	-	K00726 1 0:	GO:001827 GO:004687 GO:0016021/integral to membrane;GO:0000139/Golgi membrane
25	25	*	-	K03988 1 9:	GO:000695 - GO:0005581/collagen
-	-	-	-	K01292 1 0:	GO:000662 GO:000418 GO:0005615/extracellular space
7	7	*	-	K06856 1 8-	-
1	1	-	-	K04355 1 6:	GO:001404 GO:000808 GO:0016023/cytoplasmic membrane-bounded vesicle;GO:0005576/extracellular region
1	1	-	-	K08124 1 0:	GO:004234 - GO:0043202/lysosomal lumen;GO:0005796/Golgi lumen;GO:0005578/proteinaceous extracellular matrix
14	14	*	-	K07604 1 0:	GO:007127 GO:003028 GO:0005737/cytoplasm;GO:0045095/keratin filament
9	9	*	-	K08136 1 3:	GO:007136 GO:000550 GO:0005604/basement membrane;GO:0005615/extracellular space;GO:0031093/platelet alpha granule lumen;GO:0005634/nucleus
5	5	*	-	K03989 1 0:	GO:000695 GO:000486 GO:0005615/extracellular space;GO:0005886/plasma membrane
26	26	*	-	K14736 1 0:	GO:004274 GO:000819 GO:0030141/secretory granule;GO:0097013/phagocytic vesicle lumen;GO:0005576/extracellular region
13	13	-	-	K03999 1 2:	GO:000695 GO:001984 GO:0005615/extracellular space;GO:0005579/membrane attack complex
8	8	-	-	K06554 1 5-	-
2	2	-	-	K04004 1 3-	- GO:0005576/extracellular region
1	1	-	-	K03103 1 0:	GO:003028 GO:000399 GO:0005788/endoplasmic reticulum lumen
5	4	-	-	K10044 1 1:	GO:005087 GO:000510 GO:0031012/extracellular matrix;GO:0005576/extracellular region
21	21	-	-	K01335 1 0:	GO:000695 GO:000425 GO:0005886/plasma membrane;GO:0005576/extracellular region
7	7	-	-	-	GO:003016 GO:000166 GO:0034364/high-density lipoprotein particle
3	3	*	-	K03898 1 8-	- GO:0005576/extracellular region
29	29	*	-	K03989 1 0:	GO:000695 GO:000486 GO:0005615/extracellular space;GO:0005886/plasma membrane
26	26	*	-	K01331 1 0:	GO:004508 GO:000425 GO:0005576/extracellular region
56	56	-	-	K01672 1 2:	GO:000645 GO:004687 GO:0005615/extracellular space;GO:0043234/protein complex;GO:0031012/extracellular matrix
5	5	-	-	K13823 1 3:	GO:004274 GO:000460 GO:0031838/haptoglobin-hemoglobin complex;GO:0005833/hemoglobin complex
19	18	*	-	K10758 1 0:	GO:004545 GO:000905 GO:0005615/extracellular space;GO:0030173/integral to Golgi membrane
9	9	*	-	K13023 1 0:	GO:005082 GO:003023 GO:0005576/extracellular region
-	-	-	-	K05726 1 1:	GO:004801 GO:000487 GO:0005925/focal adhesion;GO:0030027/lamellipodium;GO:0005829/cytosol;GO:0001726/ruffle
-	-	-	-	K06554 1 6-	-
1	1	-	-	K01396 1 3:	GO:000687 GO:000551 GO:0005615/extracellular space
2	2	-	-	K06856 1 5-	-
-	-	-	-	-	GO:0016020/membrane
1	1	-	-	K07374 1 0:	GO:000022 GO:000551 GO:0005881/cytoplasmic microtubule;GO:0005576/extracellular region;GO:0005829/cytosol
-	-	-	-	K06856 1 1-	-
11	11	-	-	K01435 1 0:	GO:000741 GO:000407 GO:0005730/nucleolus;GO:0005615/extracellular space;GO:0045177/apical part of cell;GO:0043204/perikaryon
19	19	*	-	-	GO:000695 - GO:0034364/high-density lipoprotein particle
2	2	-	-	K03982 1 3:	GO:004587 GO:000820 GO:0031232/extrinsic to external side of plasma membrane;GO:0031594/neuromuscular junction;GO:0005829/cytosol;GO:0005615/ex
14	13	-	-	-	GO:000150 GO:003029 GO:0005615/extracellular space;GO:0043234/protein complex;GO:0031012/extracellular matrix
11	11	*	-	K04525 1 1:	GO:001095 GO:000486 GO:0005615/extracellular space
39	39	-	-	K03995 1 0:	GO:001983 GO:000551 GO:0005615/extracellular space;GO:0005579/membrane attack complex
-	-	-	-	K00142 1 0:	GO:000663 GO:000552 -
3	3	*	-	K07374 1 0:	GO:005108 GO:001990 GO:0030496/midbody;GO:0005881/cytoplasmic microtubule
-	-	-	-	K11989 1 2:	GO:000205 GO:000511 GO:0005615/extracellular space;GO:0005886/plasma membrane;GO:0031012/extracellular matrix
-	-	-	-	K01314 1 0:	GO:000759 GO:000550 GO:0005815/microtubule organizing center;GO:0005796/Golgi lumen;GO:0031233/intrinsic to external side of plasma membrane;GO:0
20	21	*	-	K03910 1 0:	GO:003016 GO:001996 GO:0031093/platelet alpha granule lumen;GO:0005615/extracellular space;GO:0005829/cytosol
2	2	-	-	K12385 1 9-	- GO:000367 GO:0015630/microtubule cytoskeleton;GO:0016020/membrane;GO:0005615/extracellular space;GO:0005793/endoplasmic reticulum-C
3	3	-	-	-	GO:000152 GO:000584 GO:0005615/extracellular space;GO:0005886/plasma membrane;GO:0005578/proteinaceous extracellular matrix
10	10	*	-	K04004 1 6:	GO:004508 - GO:0005615/extracellular space
55	55	*	-	K04861 1 3:	GO:003021 GO:000486 GO:0005576/extracellular region
5	5	*	-	K03899 1 0:	GO:003016 GO:000550 GO:0005615/extracellular space;GO:0031093/platelet alpha granule lumen;GO:0005886/plasma membrane
10	10	*	-	K03989 1 9:	GO:004508 - GO:0005576/extracellular region;GO:0005886/plasma membrane
1	1	-	-	K05906 1 0:	GO:003032 GO:000855 GO:0005764/lysosome;GO:0034361/very-low-density lipoprotein particle;GO:0005886/plasma membrane
32	32	*	-	K14480 1 0:	GO:001983 GO:000828 GO:0031224/intrinsic to membrane;GO:0034364/high-density lipoprotein particle;GO:0034361/very-low-density lipoprotein particle
4	4	*	-	K07964 1 0:	GO:003369 GO:000456 GO:0045121/membrane raft;GO:0005765/lysosomal membrane;GO:0005576/extracellular region;GO:0043202/lysosomal lumen;GO:0
-	-	-	-	K06554 1 2-	-
2	2	-	-	K06819 1 0:	GO:000741 GO:001983 GO:0016021/integral to membrane;GO:0005576/extracellular region;GO:0030424/axon;GO:0002116/semaphorin receptor complex;G
16	16	*	-	K04550 1 0:	GO:004295 GO:000504 GO:0005905/coated pit;GO:0030425/dendrite;GO:0043025/neuronal cell body;GO:0005768/endosome;GO:0048471/perinuclear regio
1	1	-	-	K05546 1 0:	GO:001827 GO:003391 GO:0042470/melanosome;GO:0005788/endoplasmic reticulum lumen;GO:0017177/glucosidase II complex;GO:0005794/Golgi apparat
-	-	-	-	K06856 1 1-	-
30	30	-	-	K05717 1 0:	GO:000152 GO:001650 GO:0005604/basement membrane;GO:0005793/endoplasmic reticulum-Golgi intermediate compartment;GO:0031093/platelet alpha gra
-	-	-	-	K06553 1 9-	-
1	1	-	-	K00939 1 2:	GO:000705 GO:000401 GO:0005737/cytoplasm;GO:0005886/plasma membrane
16	16	-	-	K08122 1 0:	GO:007084 GO:000520 GO:0005615/extracellular space;GO:0005796/Golgi lumen;GO:0043202/lysosomal lumen;GO:0005583/fibrillar collagen
12	12	-	-	K00933 1 0:	GO:000660 GO:000411 GO:0005829/cytosol
1	1	-	-	K06856 1 8-	-
7	7	-	-	K06856 1 8:	GO:000695 GO:000382 GO:0005576/extracellular region;GO:0016021/integral to membrane;GO:0005886/plasma membrane
2	2	-	-	K04004 1 0:	GO:000695 - GO:0005615/extracellular space
2	2	-	-	K10138 1 2:	GO:004356 GO:003199 GO:0042567/insulin-like growth factor ternary complex;GO:0042568/insulin-like growth factor binary complex;GO:0005634/nucleus
33	33	*	-	K03912 1 0:	GO:000693 GO:000486 GO:0005576/extracellular region
6	6	*	-	K13050 1 0:	GO:004308 GO:003419 GO:0005615/extracellular space;GO:0005764/lysosome;GO:0005794/Golgi apparatus;GO:0005770/late endosome;GO:0005769/early
56	56	-	-	K03913 1 0:	GO:001095 GO:000197 GO:0097183/protein C inhibitor-coagulation factor XI complex;GO:0036030/protein C inhibitor-plasma kallikrein complex;GO:0036024
1	1	-	-	-	GO:001678 GO:0005576/extracellular region
2	2	-	-	K01899 1 4:	GO:000610 GO:000387 GO:0045244/succinate-CoA ligase complex (GDP-forming);GO:0005743/mitochondrial inner membrane;GO:0005886/plasma membrar
2	2	-	-	-	GO:004547 GO:000550 GO:0005796/Golgi lumen;GO:0032059/bleb;GO:0005770/late endosome;GO:0005886/plasma membrane
-	-	-	-	K01321 1 0:	GO:000759 GO:000550 GO:0005796/Golgi lumen;GO:0005788/endoplasmic reticulum lumen;GO:0005576/extracellular region;GO:0005886/plasma membran
1	1	-	-	K13023 1 3:	GO:000715 GO:000802 GO:0005730/nucleolus;GO:0042567/insulin-like growth factor ternary complex
18	18	*	-	-	GO:004306 GO:000486 GO:0005886/plasma membrane;GO:0031093/platelet alpha granule lumen;GO:0005576/extracellular region
10	10	*	-	K09487 1 0:	GO:003043 GO:004679 GO:0005788/endoplasmic reticulum lumen;GO:0042470/melanosome;GO:0005789/endoplasmic reticulum membrane;GO:0005829/cyt
1	1	-	-	K13980 1 0:	GO:004257 GO:005128 GO:0005829/cytosol;GO:0015630/microtubule cytoskeleton
4	4	-	-	K06554 1 9-	-
47	47	-	-	K06856 1 4-	-
9	10	-	-	K03998 1 0:	GO:000695 - GO:0005615/extracellular space;GO:0005579/membrane attack complex
34	34	*	-	K05768 1 0:	GO:005159 GO:000550 GO:0030027/lamellipodium;GO:0015629/actin cytoskeleton;GO:0005615/extracellular space;GO:0005829/cytosol;GO:0001726/ruffl
4	5	*	-	K10104 1 0:	GO:000822 GO:000382 GO:0005615/extracellular space;GO:0005581/collagen
5	5	*	-	K06840 1 0:	GO:004884 GO:000487 GO:0005615/extracellular space;GO:0016020/membrane
1	1	-	-	K04079 1 0:	GO:000741 GO:003091 GO:0042470/melanosome;GO:0005829/cytosol;GO:0005886/plasma membrane
42	42	-	-	K03917 1 0:	GO:001814 GO:004687 GO:0031093/platelet alpha granule lumen;GO:0005576/extracellular region
6	5	*	-	K10066 1 2:	GO:000727 GO:000553 GO:0005581/collagen
54	55	*	-	K01315 1 0:	GO:003016 GO:003418 GO:0031232/extrinsic to external side of plasma membrane;GO:0005615/extracellular space;GO:0031093/platelet alpha granule lumen
21	21	*	-	K08761 1 0:	GO:001018 GO:000828 GO:0005576/extracellular region
6	6	*	-	K06554 1 4-	-
4	4	-	-	K06554 1 3:	GO:004508 GO:000382 GO:0005886/plasma membrane;GO:0005576/extracellular region
27	28	*	-	K03910 1 0:	GO:003016 GO:001996 GO:0031093/platelet alpha granule lumen;GO:0005615/extracellular space;GO:0005829/cytosol
5	5	-	-	K06554 1 4-	-
-	-	-	-	-	GO:003291 GO:000487 GO:0009897/external side of plasma membrane;GO:0016021/integral to membrane
1	1	-	-	K05465 1 0:	GO:003313 GO:003097 GO:0005615/extracellular space;GO:0045121/membrane raft;GO:0005886/plasma membrane;GO:0005902/microvillus
1	1	-	-	K06255 1 0:	GO:000602 GO:000802 GO:0005796/Golgi lumen;GO:0005604/basement membrane;GO:0043202/lysosomal lumen;GO:0005615/extracellular space;GO:0005
239	239	-	-	K01883 1 7:	GO:004668 GO:005108 GO:0005604/basement membrane;GO:0005814/centriole;GO:0031093/platelet alpha granule lumen;GO:0043296/apical junction comp

8	8	-	-	K068561 1 -	-
10	10	*	*	K01344 1 0. GO:001718 GO:000550 GO:0005796//Golgi lumen;GO:0005615//extracellular space;GO:0005788//endoplasmic reticulum lumen;GO:0005886//plasma membrane	
10	10	*	*	K08758 1 2. GO:0006069 GO:004280 GO:004262//chylomicron;GO:0005788//endoplasmic reticulum lumen;GO:0034361//very-low-density lipoprotein particle;GO:0034366//	
3	3	-	-	K09490 1 0. GO:003051 GO:005108 GO:0009986//cell surface;GO:0034663//endoplasmic reticulum chaperone complex;GO:0030496//midbody;GO:0005788//endoplasmic ret	
11	11	-	*	K09821 1 0. GO:004816 GO:000808 GO:0005615//extracellular space;GO:004444//cytoplasmic part	
1	1	-	-	K068561 1 -	-
4	4	-	-	K01324 1 0. GO:000759 GO:001670 GO:0005615//extracellular space;GO:0005886//plasma membrane	
21	21	-	-	K05316 1 4. GO:003021 GO:000486 GO:0005576//extracellular region	
4	4	*	-	K13912 1 2- GO:000550 GO:0005635//nuclear envelope	
1	1	-	-	K00778 1 0. GO:001827 GO:000383 GO:0032580//Golgi cisterna membrane;GO:0030173//integral to Golgi membrane;GO:0005576//extracellular region	
-	-	-	-	K03544 1 5. GO:000645 GO:004687 GO:0005730//nucleolus;GO:0005743//mitochondrial inner membrane;GO:0042645//mitochondrial nucleoid;GO:0009841//mitochondrial e	
1	1	-	-	K04525 1 2. GO:003469 GO:000486 GO:0005615//extracellular space	
1	1	-	-	K06630 1 6. GO:003016 GO:001630 GO:0005654//nucleoplasm;GO:0042470//melanosome;GO:0005829//cytosol;GO:0031252//cell leading edge;GO:0043234//protein compl	
1	1	-	-	K05464 1 5. GO:000991 GO:000549 GO:0005576//extracellular region	
-	-	-	-	K03902 1 3. GO:003016 GO:000550 GO:0005615//extracellular space;GO:0031093//platelet alpha granule lumen;GO:0005886//plasma membrane	
1	1	-	-	- GO:003362 GO:000517 GO:0002102//podosome;GO:0030054//cell junction;GO:0042995//cell projection	
-	-	-	-	K01279 1 0. GO:004236 GO:000843 GO:0005829//cytosol;GO:0005654//nucleoplasm;GO:0000783//nuclear telomere cap complex;GO:0043202//lysosomal lumen;GO:000572	
1	1	-	-	K068561 3 -	-
-	-	-	-	K01230 1 0. GO:001827 GO:000457 GO:0000139//Golgi membrane;GO:0005793//endoplasmic reticulum-Golgi intermediate compartment;GO:0016021//integral to membrane	
-	-	-	-	K13618 1 0. GO:000665 GO:000897 GO:0005576//extracellular region	
519	519	*	-	K14462 1 0. GO:001088 GO:005075 GO:0030669//clathrin-coated endocytic vesicle membrane;GO:0034360//chylomicron remnant;GO:0005788//endoplasmic reticulum lumen	
-	-	-	-	K14462 1 4. GO:001088 GO:005075 GO:0030669//clathrin-coated endocytic vesicle membrane;GO:0034360//chylomicron remnant;GO:0005788//endoplasmic reticulum lumen	
1	1	-	-	K068561 3 -	-
12	12	-	*	K03898 1 0. GO:003016 GO:000510 GO:0031093//platelet alpha granule lumen;GO:0005615//extracellular space;GO:0005886//plasma membrane	
35	35	-	*	K13912 1 2. GO:000696 GO:000504 GO:0016020//membrane;GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix	
3	3	*	-	K06554 1 1-	-
5	5	*	*	- GO:000646 GO:000486 GO:0043234//protein complex;GO:0005576//extracellular region	
22	22	*	*	K05692 1 0. GO:000741 GO:001990 GO:0030863//cortical cytoskeleton;GO:0031941//filamentous actin;GO:0005829//cytosol;GO:0030016//myofibril;GO:0030424//axon;GC	
2	2	-	*	K03986 1 3. GO:004508 GO:000551 GO:0005602//complement component C1 complex;GO:0005581//collagen	
1	1	-	-	- GO:000550 GO:0005578//proteinaceous extracellular matrix	
1	1	-	-	- GO:0005730//nucleolus;GO:0005929//cilium;GO:0005874//microtubule	
8	8	*	-	K08136 1 2. GO:000716 GO:000550 GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix	
-	-	-	-	K09582 1 0. GO:004545 GO:000905 GO:0005788//endoplasmic reticulum lumen;GO:0042470//melanosome	
-	-	-	-	K068561 3 -	-
10	10	-	-	K01197 1 0. GO:000961 GO:000441 GO:0005615//extracellular space;GO:0031410//cytoplasmic vesicle;GO:0043202//lysosomal lumen;GO:0036117//hyaluronan cable	
-	-	-	-	K068561 3 -	-
7	7	-	*	K05407 1 6. GO:001652 GO:000820 GO:0031093//platelet alpha granule lumen;GO:0005615//extracellular space	
45	45	*	-	K07127 1 1- GO:000551 GO:0005576//extracellular region	
15	14	*	*	- GO:000662 GO:000531 GO:0034364//high-density lipoprotein particle;GO:0034361//very-low-density lipoprotein particle	
-	-	-	-	K10788 1 0. GO:004274 GO:004687 -	
-	-	-	-	K06554 1 2- -	
3	3	-	-	K01328 1 0. GO:000759 GO:005178 GO:0005615//extracellular space;GO:0005886//plasma membrane	
1	1	-	-	K11254 1 2. GO:000633 GO:000367 GO:0000786//nucleosome;GO:0005634//nucleus	
12	11	*	*	K03904 1 0. GO:003016 GO:003067 GO:0009897//external side of plasma membrane;GO:0031093//platelet alpha granule lumen;GO:0005938//cell cortex;GO:0005577//fibrin	
138	138	-	-	K04524 1 5. GO:000664 GO:005075 GO:0031232//extrinsic to external side of plasma membrane;GO:0034364//high-density lipoprotein particle;GO:0042627//chylomicron;GC	
-	-	-	-	K06251 1 6. GO:003209 GO:000517 GO:0005615//extracellular space;GO:0071062//alphav-beta3 integrin-vitronectin complex;GO:0031012//extracellular matrix	
8	8	-	*	K04004 1 0. GO:000695 - GO:0005615//extracellular space	
-	-	-	-	K05857 1 4. GO:001604 GO:000487 GO:0031965//nuclear membrane;GO:0005829//cytosol	
1	1	-	-	K00873 1 0. GO:001631 GO:000474 GO:0005886//plasma membrane;GO:0005634//nucleus;GO:0005829//cytosol;GO:0005739//mitochondrion	
-	-	-	-	K08569 1 2. GO:000695 GO:000823 -	
3	3	-	-	K068561 2- -	
24	24	-	-	K13912 1 4. GO:000696 GO:000504 GO:0016020//membrane;GO:0005615//extracellular space	
-	-	-	-	K068561 3 -	-
1	1	-	-	K04659 1 0. GO:006017 GO:000820 GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix	
43	43	-	*	K03987 1 8. GO:000695 GO:000551 GO:0005576//extracellular region	
-	-	-	-	K09290 1 1. GO:003004 - GO:0005829//cytosol;GO:0030863//cortical cytoskeleton;GO:0002102//podosome;GO:0001725//stress fiber;GO:0005862//muscle thin fil	
4	4	-	-	- GO:004632 GO:000510 GO:0031526//brush border membrane;GO:0045121//membrane raft;GO:0005576//extracellular region;GO:0031225//anchored to membra	
7	7	*	*	K14462 1 0. GO:001088 GO:005075 GO:0030669//clathrin-coated endocytic vesicle membrane;GO:0034360//chylomicron remnant;GO:0005788//endoplasmic reticulum lumen	
1	1	-	-	K06849 1 1. GO:003338 GO:000551 GO:0000139//Golgi membrane;GO:0031093//platelet alpha granule lumen;GO:0005615//extracellular space;GO:0042588//zymogen gran	
4	5	-	-	K01300 1 0. GO:004249 GO:000418 GO:0005615//extracellular space	
1	1	-	-	K13822 1 2. GO:004274 GO:000460 GO:0022627//cytosolic small ribosomal subunit;GO:0031838//haptoglobin-hemoglobin complex;GO:0005833//hemoglobin complex	
-	-	-	-	K06553 1 2- -	
4	4	*	*	K03992 1 0. GO:000650 GO:000550 GO:0005615//extracellular space	
-	-	-	-	K08120 1 0. GO:007017 GO:001528 GO:0046930//pore complex;GO:0005578//proteinaceous extracellular matrix	
3	3	*	-	- GO:007127 GO:000551 GO:0031045//dense core granule;GO:0043196//varicosity;GO:0043679//axon terminus;GO:0005615//extracellular space;GO:0005794//G	
5	5	-	-	K06512 1 7- - GO:0005576//extracellular region	
-	-	-	-	K13279 1 8. GO:000150 GO:000837 GO:0042470//melanosome;GO:0005634//nucleus;GO:0005739//mitochondrion	
9	9	-	*	K10029 1 2. GO:003016 GO:000535 GO:0005615//extracellular space;GO:0031093//platelet alpha granule lumen	

supplementary table3. A list of dysregulated proteins between group A(EH) and group B(TJT)

Hits	Accession	Desription	Mass	Seq	Score	Cov	SameSets	Spectrum	Unique Spe	Peptide	Unique Pep
1	spP35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT7	76630	MSCQISC	275	15.5 -		23	13	10	8
2	tr B4E0A4 B4E0A4_HUMAN	cDNA FLJ57023, highly similar to Homo sapiens collagen, type VI, al	149266	MRKHRHL	124	4.3	4	12	12	5	5
3	sp P18428 LBP_HUMAN	Lipoplysaccharide-binding protein OS=Homo sapiens GN=LBP PE=	60518	MGALARL	2335	20.2 -		145	145	9	9
4	tr L8E853 L8E853_HUMAN	von Willebrand factor OS=Homo sapiens GN=VWF PE=4 SV=1	341812	MIPARFA	627	7.5 -		65	65	19	19
5	sp P00739 HPTTR_HUMAN	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2	48340	MSDLGAV	677	36.2 -		72	22	11	4
6	sp P19652 A1AG2_HUMAN	Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV	28132	MALSWVI	61	9.5 -		7	7	2	2
7	tr K7ER19 K7ER19_HUMAN	Truncated apolipoprotein C-I (Fragment) OS=Homo sapiens GN=APC	11075	MRLFLSLI	409	32.5	1	51	51	3	3
8	tr Q5SRP5 Q5SRP5_HUMAN	Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=1	17751	MAAGSAF	61	17.8	1	11	11	3	3
9	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV:	70468	MSCRFQS	62	10.4 -		7	7	5	5
10	tr F1C4A7 F1C4A7_HUMAN	Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14	185	19.2		2	18	18	6	6	6
11	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 S	66321	MSVRYSS	504	13.5 -		23	22	7	6
12	sp P0C0L4 C04A_HUMAN	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	217989	MRLWLGI	18599	42 -		1660	16	65	2
13	tr Q5J875 Q5J875_HUMAN	GUGU gamma form OS=Homo sapiens GN=GUGU PE=2 SV=1	41888	MGLFLPL	47	8.5	3	7	7	3	3
14	sp P0C0L5 C04B_HUMAN	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	217898	MRLWLGI	19149	42 -		1692	38	65	2
15	sp O00391 QSOX1_HUMAN	Sulfhydryl oxidase 1 OS=Homo sapiens GN=QSOX1 PE=1 SV=3	93667	MRRNCSC	373	21.3 -		61	61	16	16
16	tr A8K6C1 A8K6C1_HUMAN	cDNA FLJ76868, highly similar to Homo sapiens cholesterol ester tra	63358	MLAATVL	447	10.8	1	41	41	6	6
17	tr D6REX5 D6REX5_HUMAN	Selenoprotein P (Fragment) OS=Homo sapiens GN=SEPP1 PE=4 SV:	42698	MWRSLGI	165	12.6	1	9	9	4	4
18	tr A0A096LPE2 A0A096LPE2	Protein SAA2-SAA4 OS=Homo sapiens GN=SAA2-SAA4 PE=4 SV:	26856	MKLLTGL	304	21.2 -		60	59	4	3
19	tr B2R815 B2R815_HUMAN	cDNA, FLJ93695, highly similar to Homo sapiens serpin peptidase in	57184	MHLIDYLI	167	17.1	1	25	25	7	7
20	tr Q6U2L6 Q6U2L6_HUMAN	C4B (Fragment) OS=Homo sapiens GN=C4B PE=4 SV=1	11768	RSMQGGH	306	15 -		53	52	4	3
21	tr A0A024R1G8 A0A024R1G8	Apolipoprotein L1, isoform CRA_b OS=Homo sapiens GN=APOL1	54476	MRFKSGT	561	20	11	63	63	9	9
22	tr H6VRF8 H6VRF8_HUMAN	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	75006	MSRQFTS	670	24.8	4	46	36	13	11
23	sp P05546 HEP2_HUMAN	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	67548	MKHSLLA	699	28.1 -		115	115	16	16
24	tr A0A0A0MS51 A0A0A0MS51	Gelsolin OS=Homo sapiens GN=GSN PE=4 SV=1	96753	MAEEELA	655	18.4	6	64	64	12	12
25	tr C9JPG5 C9JPG5_HUMAN	Semaphorin-3F OS=Homo sapiens GN=SEMA3F PE=4 SV=1	86066	MYVGSKI	40	0.9	2	5	5	1	1
26	sp Q96PD5 PGRP2_HUMAN	N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens GN=PGLYR	66703	MAQGVLV	186	8.7 -		13	13	4	4
27	tr Q1HP67 Q1HP67_HUMAN	Lipoprotein, Lp(A) OS=Homo sapiens GN=LPA PE=1 SV=1	240494	MEHKEVV	211	6.1	1	17	17	10	10
28	tr B3KUE5 B3KUE5_HUMAN	Phospholipid transfer protein, isoform CRA_c OS=Homo sapiens GN	62359	MGLSGSD	390	18.3	2	33	33	9	9
29	sp P40197 GPV_HUMAN	Platelet glycoprotein V OS=Homo sapiens GN=GP5 PE=1 SV=1	65693	MLRGTLT	67	13.2 -		10	10	6	6
30	sp P08697 A2AP_HUMAN	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	60957	MALLWGI	421	17.7 -		62	62	8	8
31	tr V9GYG9 V9GYG9_HUMAN	Apolipoprotein A-II (Fragment) OS=Homo sapiens GN=APOA2 PE=	14103	MKLLAAT	186	38.9	2	60	60	3	3
32	tr B2R5S1 B2R5S1_HUMAN	cDNA, FLJ92595, highly similar to Homo sapiens angiotensinogen (se	60156	MRKRAPC	350	9.5	6	15	15	4	4
33	sp P02763 A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV	28288	MALSWVI	54	7.5 -		5	5	1	1
34	tr C0JY22 C0JY22_HUMAN	Apolipoprotein B (Including Ag(X) antigen) OS=Homo sapiens GN=A	625263	MDPPRPA	22843	45.3 -		2373	1080	198	94
35	tr D3DNU8 D3DNU8_HUMAN	Kininogen 1, isoform CRA_a OS=Homo sapiens GN=KNG1 PE=4 SV	59249	MKLTITLF	208	25.1	3	31	31	10	10
36	sp Q92954 PRG4_HUMAN	Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2 >tr A0A02	202736	MAWKTLI	94	4.5 -		12	12	7	7
37	sp P55056 APOC4_HUMAN	Apolipoprotein C-IV OS=Homo sapiens GN=APOC4 PE=1 SV=1	17623	MSLLRNR	288	20.5 -		35	35	3	3
38	tr Q9YHB3 Q9YHB3_HUMAN	Apolipoprotein B variant (Fragment) OS=Homo sapiens PE=2 SV=1	222441	TIEGPLTS	7264	45 -		713	7	67	1
39	tr J3KP79 J3KP79_HUMAN	Anthrax toxin receptor 2 OS=Homo sapiens GN=ANTXR2 PE=1 SV:	54148	MRLSFVF	65	16.3	1	8	7	6	5
1	sp P05164 PERM_HUMAN	Lactoperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	91781	MGVPPFS	129	8.5 -		15	8	6	4
2	tr Q9UMV1 Q9UMV1_HUMA	Complement C4B1a (Fragment) OS=Homo sapiens GN=C4B PE=4 S	5960	AAIESPGV	102	23.9	1	14	14	1	1
3	sp Q15485 FCN2_HUMAN	Ficolin-2 OS=Homo sapiens GN=FCN2 PE=1 SV=2	39607	MELDRVA	308	14.7 -		38	38	5	5
4	tr Q6UXM4 Q6UXM4_HUMA	Ficolin (Collagen/fibrinogen domain containing) 3 (Hakata antigen), is	34547	MDLLWIL	731	26.4	1	80	80	8	8
5	tr E7EUT5 E7EUT5_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=G	34412	MEEMRDF	175	18.5	1	11	11	3	3
6	tr F8VV32 F8VV32_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	13895	MKALIVLA	163	23.1	1	12	12	2	2
7	tr Q5VY30 Q5VY30_HUMAN	Retinol binding protein 4, plasma, isoform CRA_b OS=Homo sapiens	26952	MNYSKIP	63	15.1	1	7	7	3	3
8	tr E7EQB2 E7EQB2_HUMAN	Lactotransferrin (Fragment) OS=Homo sapiens GN=LTF PE=1 SV=1	92148	MGLCLAC	602	30.2	2	52	52	18	18
9	sp Q02985 FHR3_HUMAN	Complement factor H-related protein 3 OS=Homo sapiens GN=CFHR	44580	MLLLINVI	81	14.5 -		11	10	5	4
10	tr B3KPS3 B3KPS3_HUMAN	cDNA FLJ32131 fis, clone PEBLM2000267, highly similar to Tubulir	100	15.4		8	7	3	4	2	2
11	tr B2R6W1 B2R6W1_HUMAN	cDNA, FLJ93143, highly similar to Homo sapiens complement compo	111585	MKVISLFI	635	25.9 -		91	4	19	2
12	sp Q03591 FHR1_HUMAN	Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR	43938	MWLLVSV	957	33 -		97	20	10	2
13	tr B0YIW1 B0YIW1_HUMAN	Apolipoprotein A-V variant 3 OS=Homo sapiens GN=APOA5 PE=2 S	45822	MAAVLTV	228	19.8	2	22	22	7	7
14	tr A0A024RDB8 A0A024RDB8	Heparanase, isoform CRA_a OS=Homo sapiens GN=HPSE PE=4 SV:	73287	MLLRSKP	105	6.6	2	14	14	4	4
15	sp Q07954 LRP1_HUMAN	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapier	576082	MLTPPLLI	243	3.5 -		29	29	14	14
16	tr B2R812 B2R812_HUMAN	cDNA, FLJ93914, highly similar to Homo sapiens histidine-rich glyco	67498	MKALIAA	211	22.1	1	29	29	11	11
17	sp O00602 FCN1_HUMAN	Ficolin-1 OS=Homo sapiens GN=FCN1 PE=1 SV=2	42205	MELSGAT	99	8.9 -		9	9	3	3
18	tr A0A075B6R9 A0A075B6R9	Protein IGKV2D-24 (Fragment) OS=Homo sapiens GN=IGKV2D-24	14040	MRLLAQL	160	16.7 -		8	7	2	1
19	tr D3DQX7 D3DQX7_HUMA	Serum amyloid A protein OS=Homo sapiens GN=SAA1 PE=3 SV=1	15436	MKLLTGL	105	20.5 -		10	9	3	2
20	sp P07357 CO8A_HUMAN	Complement component C8 alpha chain OS=Homo sapiens GN=C8A	76870	MFAVVVF	244	15.2 -		28	28	8	8
21	tr B2R6M6 B2R6M6_HUMAN	cDNA, FLJ93024, highly similar to Homo sapiens EGF-containing fib	60522	MLKALFL	224	9.7	6	22	22	4	4
22	tr A0A5E4 A0A5E4_HUMAN	Uncharacterized protein OS=Homo sapiens PE=2 SV=1	28363	MAWMMI	1459	35.3 -		173	14	7	1
23	sp Q13103 SPP24_HUMAN	Secreted phosphoprotein 24 OS=Homo sapiens GN=SPP2 PE=1 SV=	27041	MISRMKE	138	15.6 -		14	14	3	3
24	tr B4E335 B4E335_HUMAN	cDNA FLJ52842, highly similar to Actin, cytoplasmic 1 OS=Homo sa	45627	MDDDDIA	366	33.6	7	42	42	9	9
25	tr X6RLJ0 X6RLJ0_HUMAN	Complement C1q subcomponent subunit A (Fragment) OS=Homo sap	27065	MEGPRGV	58	11.8	1	8	8	3	3
26	tr B4DNS6 B4DNS6_HUMAN	cDNA FLJ54278, highly similar to SPARC-like protein 1 OS=Homo s	71190	MKTGLFF	116	9.6	4	13	13	4	4
27	tr A0A087WT59 A0A087WT5	Transthyretin OS=Homo sapiens GN=TTR PE=3 SV=1	23099	MASHRLI	813	21.1	4	56	56	5	5
28	tr A0A024R962 A0A024R962	HCG40889, isoform CRA_b OS=Homo sapiens GN=hCG_40889 PE:	168295	MRLAKII	2249	30.5	1	277	12	33	2
29	tr Q6MZL2 Q6MZL2_HUMAN	Putative uncharacterized protein DKFZp686M0562 (Fragment) OS=H	38922	NPGIYTS	103	12.8 -		10	9	4	3
30	tr D6RHH7 D6RHH7_HUMAN	Corticotropin-releasing factor-binding protein OS=Homo sapiens GN=	30563	MSPNFKL	48	8	1	4	4	2	2
31	sp P48740 MASP1_HUMAN	Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MAS	92409	MRWLLLY	566	26 -		59	15	14	6

A-VS-B@R	A-VS-B@R	A-VS-B@C	A-VS-B@C	A-VS-B@S	A-VS-B@S	A-VS-B@A	A-VS-B@S	KEGG(ko_i	GO Biologi	GO Molecu	GO Cellular_Component
0.608	0.607	4	4	*	*	0.6075	0.000707	K07605 1 0	GO:003298	GO:000520	GO:0005794//Golgi apparatus;GO:0045095//keratin filament
0.562	0.549	8	8	-	*	0.5555	0.009192	K06238 1 0	GO:000741	GO:000486	GO:0030133//transport vesicle;GO:0005615//extracellular space;GO:0005788//endoplasmic reticulum
0.794	0.784	106	106	*	-	0.789	0.007071	K05399 1 0	GO:003272	GO:000510	GO:0005615//extracellular space
0.813	0.665	31	31	*	-	0.739	0.104652	K03900 1 0	GO:003016	GO:0004748	GO:0009897//external side of plasma membrane;GO:0033093//Weibel-Palade body;GO:0005788//endoplasmic reticulum
0.676	0.704	18	18	*	*	0.69	0.019799	K14477 1 0	GO:000695	GO:003049	GO:0031838//haptoglobin-hemoglobin complex;GO:0034366//spherical high-density lipoprotein particle
0.897	0.763	3	3	-	*	0.83	0.094752	-	GO:000268	GO:000551	GO:0005615//extracellular space
0.739	0.71	14	14	*	-	0.7245	0.020506	K04524 1 9	GO:001087	GO:003121	GO:0042627//chylomicron;GO:0034361//very-low-density lipoprotein particle;GO:0034362//low-density lipoprotein particle;GO:0034365//discoidal high-density lipoprotein particle
0.669	0.73	2	2	-	*	0.6995	0.043134	-	GO:003334	GO:000554	GO:0034362//low-density lipoprotein particle;GO:0034365//discoidal high-density lipoprotein particle
0.63	0.618	3	3	*	-	0.624	0.008485	K07604 1 1	GO:000728	GO:000520	GO:0045095//keratin filament;GO:0048471//perinuclear region of cytoplasm
0.594	0.483	11	11	*	*	0.5385	0.078489	K04391 1 0	GO:000690	GO:007089	GO:0045121//membrane raft;GO:0005615//extracellular space;GO:0031225//anchored protein
0.468	0.442	14	14	*	*	0.455	0.018385	K07604 1 0	GO:007127	GO:003028	GO:0005737//cytoplasm;GO:0045095//keratin filament
0.79	0.622	5	5	*	*	0.706	0.118794	K03989 1 0	GO:000695	GO:000486	GO:0005615//extracellular space;GO:0005886//plasma membrane
0.264	0.215	3	3	*	*	0.2395	0.034648	K03898 1 8	-	-	GO:0005576//extracellular region
0.844	0.653	29	29	-	*	0.7485	0.135057	K03989 1 0	GO:000695	GO:000486	GO:0005615//extracellular space;GO:0005886//plasma membrane
0.816	0.801	19	19	*	*	0.8085	0.010607	K10758 1 0	GO:004545	GO:000905	GO:0005615//extracellular space;GO:0030173//integral to Golgi membrane
0.721	0.829	17	17	*	*	0.775	0.076368	K05399 1 1	GO:004369	GO:001712	GO:0031982//vesicle;GO:0034364//high-density lipoprotein particle
0.731	0.894	5	4	*	*	0.8125	0.115258	-	GO:001026	GO:000843	GO:0005615//extracellular space
0.759	0.724	19	19	*	-	0.7415	0.024749	-	GO:000695	-	GO:0034364//high-density lipoprotein particle
0.774	0.751	11	11	*	*	0.7625	0.016263	K04525 1 1	GO:001095	GO:000486	GO:0005615//extracellular space
0.744	0.707	10	10	*	*	0.7255	0.026163	K03989 1 9	GO:0004508	-	GO:0005576//extracellular region;GO:0005886//plasma membrane
0.359	0.325	32	32	*	*	0.342	0.024042	K14480 1 0	GO:001983	GO:000828	GO:0031224//intrinsic to membrane;GO:0034364//high-density lipoprotein particle;GO:0034365//discoidal high-density lipoprotein particle
0.504	0.562	21	22	*	-	0.533	0.041012	K07605 1 0	GO:000697	GO:000487	GO:0045095//keratin filament;GO:0005886//plasma membrane
0.473	0.441	33	33	*	*	0.457	0.022627	K03912 1 0	GO:000693	GO:000486	GO:0005576//extracellular region
0.678	0.645	34	34	*	*	0.6615	0.023335	K05768 1 0	GO:005159	GO:000550	GO:0030027//lamellipodium;GO:0015629//actin cytoskeleton;GO:0005615//extracellular space
0.627	0.636	5	5	*	*	0.6315	0.006364	K06840 1 0	GO:004884	GO:000487	GO:0005615//extracellular space;GO:0016020//membrane
0.813	0.694	7	7	*	-	0.7535	0.084146	K01446 1 0	GO:000382	GO:000827	GO:0005622//intracellular;GO:0005576//extracellular region;GO:0016020//membrane
0.451	0.452	9	9	-	*	0.4515	0.000707	K09644 1 0	GO:003016	GO:000425	GO:0031093//platelet alpha granule lumen;GO:0034358//plasma lipoprotein particle;GO:0005576//extracellular region
0.438	0.444	21	21	*	*	0.441	0.004243	K08761 1 0	GO:001018	GO:000828	GO:0005576//extracellular space
0.68	0.474	4	4	*	*	0.577	0.145664	K06260 1 0	GO:000716	GO:000551	GO:0005887//integral to plasma membrane;GO:0009986//cell surface
0.94	0.815	18	18	-	*	0.8775	0.088388	K03983 1 0	GO:000203	GO:000428	GO:0005577//fibrinogen complex;GO:0031093//platelet alpha granule lumen
0.603	0.615	10	10	*	*	0.609	0.008485	K08758 1 2	GO:000609	GO:000486	GO:0042627//chylomicron;GO:0005788//endoplasmic reticulum lumen;GO:0034361//very-low-density lipoprotein particle
0.857	0.825	11	11	-	*	0.841	0.022627	K09821 1 0	GO:004816	GO:000808	GO:0005615//extracellular space;GO:0044444//cytoplasmic part
0.797	0.895	5	5	*	-	0.846	0.069296	-	GO:000268	GO:000551	GO:0005615//extracellular space
0.397	0.395	519	519	*	-	0.396	0.001414	K14462 1 0	GO:001088	GO:0005075	GO:0030669//clathrin-coated endocytic vesicle membrane;GO:0034360//chylomicron;GO:0034362//low-density lipoprotein particle
0.835	0.757	12	12	-	*	0.796	0.055154	K03989 1 1	GO:003016	GO:000510	GO:0031093//platelet alpha granule lumen;GO:0005615//extracellular space;GO:0005576//extracellular region
0.695	0.696	3	4	*	-	0.6955	0.000707	K06251 1 3	GO:000695	GO:003024	GO:0005576//extracellular region;GO:0016021//integral to membrane
0.708	0.668	15	14	*	*	0.688	0.028284	-	GO:000662	GO:000531	GO:0034364//high-density lipoprotein particle;GO:0034361//very-low-density lipoprotein particle
0.468	0.416	7	7	*	*	0.442	0.036777	K14462 1 0	GO:001088	GO:0005075	GO:0030669//clathrin-coated endocytic vesicle membrane;GO:0034360//chylomicron;GO:0034362//low-density lipoprotein particle
0.535	0.454	3	3	*	*	0.4945	0.057276	-	GO:002241	GO:000487	GO:0005789//endoplasmic reticulum membrane;GO:0005886//plasma membrane;GO:0005576//extracellular space
1.748	1.988	6	6	*	*	1.868	0.169706	K10789 1 0	GO:000695	GO:000487	GO:0005764//lysosome;GO:0030141//secretory granule;GO:0005615//extracellular space
2.168	1.75	7	7	*	*	1.959	0.295571	K03989 1 3	GO:000695	GO:000486	GO:0005615//extracellular space;GO:0005886//plasma membrane
2.859	2.981	14	14	*	*	2.92	0.086267	K10104 1 7	GO:000822	GO:000382	GO:0005615//extracellular space;GO:0005581//collagen
1.18	1.258	48	48	*	*	1.219	0.055154	K10104 1 2	GO:000716	GO:003024	GO:0005615//extracellular space;GO:0005581//collagen
1.515	1.089	8	8	*	-	1.302	0.301227	K00134 1 3	GO:005140	GO:005128	GO:0005829//cytosol;GO:0015630//microtubule cytoskeleton;GO:0048471//perinuclear region of cytoplasm
1.512	1.505	7	7	*	*	1.5085	0.00495	K13915 1 5	GO:004274	GO:000379	GO:0005615//extracellular space
2.028	1.684	4	4	*	*	1.856	0.243245	-	GO:000609	GO:003463	GO:0005615//extracellular space
2.479	2.434	26	26	*	*	2.4565	0.03182	K14736 1 0	GO:004274	GO:000819	GO:0030141//secretory granule;GO:0097013//phagocytic vesicle lumen;GO:0005576//extracellular space
1.233	1.352	4	4	-	*	1.2925	0.084146	K04004 1 8	GO:000686	GO:000531	GO:0005615//extracellular space
1.209	1.279	3	3	-	*	1.244	0.049497	K07374 1 0	GO:005108	GO:001990	GO:0030496//midbody;GO:0005881//cytoplasmic microtubule
1.218	1.098	2	2	*	-	1.158	0.084853	K03996 1 0	GO:000695	-	GO:0005579//membrane attack complex;GO:0005576//extracellular region
1.343	1.296	10	10	*	-	1.3195	0.033234	K04004 1 6	GO:004508	-	GO:0005615//extracellular space
1.378	1.211	9	9	*	*	1.2945	0.118087	K09025 1 0	GO:004572	GO:0005075	GO:0042627//chylomicron;GO:0034361//very-low-density lipoprotein particle;GO:0034362//low-density lipoprotein particle
1.427	1.471	4	4	*	*	1.449	0.031113	K07964 1 0	GO:003369	GO:000456	GO:0045121//membrane raft;GO:0005765//lysosomal membrane;GO:0005576//extracellular space
1.193	1.208	16	16	-	*	1.2005	0.010607	K04550 1 0	GO:004295	GO:000504	GO:0005905//coated pit;GO:0030425//dendrite;GO:0043025//neuronal cell body;GO:0005576//extracellular space
1.28	1.223	18	18	-	*	1.2515	0.040305	-	GO:004306	GO:000486	GO:0005886//plasma membrane;GO:0031093//platelet alpha granule lumen;GO:0005576//extracellular space
1.321	1.366	4	5	*	*	1.3435	0.03182	K10104 1 0	GO:000822	GO:000382	GO:0005615//extracellular space;GO:0005581//collagen
1.346	1.158	6	6	*	*	1.252	0.132936	K06554 1 4	-	-	-
1.459	1.048	7	7	*	-	1.2535	0.290621	-	GO:003016	GO:000166	GO:0034364//high-density lipoprotein particle
1.216	1.033	10	10	*	-	1.1245	0.129401	K03997 1 0	GO:000695	-	GO:0005615//extracellular space;GO:0005579//membrane attack complex
1.206	1.336	7	6	*	*	1.271	0.091924	K08023 1 1	GO:001810	GO:000550	GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix
1.594	1.193	3	3	*	-	1.3935	0.28355	K06554 1 1	-	-	-
1.208	1.231	5	5	*	*	1.2195	0.016263	-	GO:000646	GO:000486	GO:0043234//protein complex;GO:0005576//extracellular region
1.33	1.27	22	22	*	*	1.3	0.042426	K05692 1 0	GO:000741	GO:001990	GO:0030863//cortical cytoskeleton;GO:0031941//filamentous actin;GO:0005829//cytoskeleton
1.178	1.254	2	2	-	*	1.216	0.05374	K03986 1 3	GO:004508	GO:000551	GO:0005602//complement component C1 complex;GO:0005581//collagen
1.336	1.124	8	8	*	-	1.23	0.149907	K08136 1 2	GO:000716	GO:000550	GO:0005615//extracellular space;GO:0005578//proteinaceous extracellular matrix
1.202	1.129	45	45	*	-	1.1655	0.051619	K07127 1 1	-	GO:000551	GO:0005576//extracellular region
1.072	1.227	8	8	-	*	1.1495	0.109602	K04004 1 0	GO:000695	-	GO:0005615//extracellular space
1.362	1.527	4	4	*	*	1.4445	0.116673	K03992 1 0	GO:000650	GO:000550	GO:0005615//extracellular space
1.539	1.112	3	3	*	-	1.3255	0.301935	-	GO:007127	GO:000551	GO:0031045//dense core granule;GO:0043196//varicosity;GO:0043679//axon terminus
1.306	1.34	9	9	-	*	1.323	0.024042	K03992 1 0	GO:000650	GO:000550	GO:0005615//extracellular space