

**Supplement to:** A. A. Belogurov, Jr., O. M. Ivanova, Y. A. Lomakin, R. H. Ziganshin, M. I. Vaskina, V. D. Knorre, E. A. Klimova, A. G. Gabibov, V. T. Ivanov, and V. M. Govorun, Mediators and Biomarkers of Inflammation in Meningitis: Cytokine and Peptidome Profiling of Cerebrospinal Fluid (ISSN 0006-2979, *Biochemistry (Moscow)*, 2016, Vol. 81, No. 11, pp. 1293-1302)

**Table S1.** List of protein precursors of endogenous peptides identified in CSF

Accession	Protein name	Number of identified peptides
P02671-2	Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	37
O15240	Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	29
Q5G689	Serum albumin OS=Homo sapiens PE=2 SV=1	26
A0A087WV47,A0A087WYE1,A0A087X010,V9HW68	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	23
ASK008	cDNA FLJ78387 OS=Homo sapiens PE=1 SV=1	23
Q6N089	Putative uncharacterized protein DKFZp686P15220 OS=Homo sapiens GN=DKFZp686P15220 PE=1 SV=1	20
P10645	Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	19
A0A024R617	Serpin peptidase inhibitor, clade A (Alpha-1 antiprotease, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	17
Q6MZQ6	Putative uncharacterized protein DKFZp686G11190 OS=Homo sapiens GN=DKFZp686G11190 PE=2 SV=1	17
Q6N093	Putative uncharacterized protein DKFZp686I04196 (Fragment) OS=Homo sapiens GN=DKFZp686I04196 PE=2 SV=1	17
P01024,V9HWA9	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	15
Q6MZL6	Putative uncharacterized protein DKFZp686C15213 OS=Homo sapiens GN=DKFZp686C15213 PE=2 SV=1	15
A6XGL1,E9K136,P02766	Transthyretin OS=Homo sapiens PE=2 SV=1	14
P01861	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	14
POCOL4,POCOL4-2	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	14
P10909,P10909-2,P10909-5	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	14
P05060	Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	13
ASK9P0	cDNA FLJ78413, highly similar to Homo sapiens albumin, mRNA OS=Homo sapiens PE=2 SV=1	12
B4DEA7	cDNA FLJ58131, highly similar to Secretogranin-1 OS=Homo sapiens PE=2 SV=1	12
A0A024R8G3,P41222	Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS=Homo sapiens GN=PTGDS PE=3 SV=1	11
A0A024RDE6,P10451-5	Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	11
P13521	Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	11
Q9UHG2	ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	11
B2RM59,Q14624	Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) OS=Homo sapiens GN=ITHH4 PE=2 SV=1	10
A2KBC5	Anti-HCS scFv (Fragment) OS=Homo sapiens PE=2 SV=1	8
B2R5S2,P51693,P51693-2	cDNA, FLJ92596, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1),mRNA OS=Homo sapiens PE=2 SV=1	8
A6XMV6	Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	7
B3VL17,Q4TWB7	Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	7
P08697	Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	7
A0A024R6P0,B3KS79,P01011	Serpin peptidase inhibitor, clade A (Alpha-1 antiprotease, antitrypsin), member 3, isoform CRA_c OS=Homo sapiens GN=SERPINA3 PE=3 SV=1	5
A0A024R911,P05408,P05408-2	Secretory granule, neuroendocrine protein 1 (7B2 protein), isoform CRA_a OS=Homo sapiens GN=SGNE1 PE=4 SV=1	5
B4E3Q1,O94985,O94985-2	cDNA FLJ61580, highly similar to Calsyntenin-1 OS=Homo sapiens PE=2 SV=1	5
P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	5
P02652,V9GYE3,V9GYM3	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	5
P61769	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	5
Q6PJF2	IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	5
Q8WDX2	Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	5
A0A024QZL1,P10124	Proteoglycan 1, secretory granule, isoform CRA_a OS=Homo sapiens GN=PRG1 PE=4 SV=1	4
A2VCK8,P62328,Q0P5N8,Q0P5P4,Q0P5Q0,Q0P5T0,Q0P5U7	Thymosin beta 4, X-linked OS=Homo sapiens GN=TMSB4X PE=2 SV=1	4
B4D169,B4D1D6	cDNA FLJ59893, highly similar to Dickkopf-related protein 3 OS=Homo sapiens PE=2 SV=1	4
BSZZE5,C9JRR0,Q9H1Z8	Angurin OS=Homo sapiens GN=C2orf40 PE=1 SV=1	4
P02675,V9HYV1	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	4
A0A024R1P8,O95502	Neuronal pentraxin receptor, isoform CRA_a OS=Homo sapiens GN=NPTXR PE=4 SV=1	3
B4DQ92	cDNA FLJ59379, highly similar to Hematopoietic lineage cell-specific protein OS=Homo sapiens PE=2 SV=1	3
B4E1Z4	Uncharacterized protein OS=Homo sapiens PE=1 SV=1	3
C9JC84,C9JEU5,P02679,P02679-2	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=1	3
D6W5K2,P63313	Thymosin, beta 10, isoform CRA_a (Fragment) OS=Homo sapiens GN=TMSB10 PE=4 SV=1	3
P01034	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	3
P04217,V9HWD8	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	3
P23471-2	Isoform 2 of Receptor-type tyrosine-protein phosphatase zeta OS=Homo sapiens GN=PTRZ1	3
P81172	Hepcidin OS=Homo sapiens GN=HAMP PE=1 SV=2	3
Q9CF0	Putative Polycomb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	3
V9HW34	Epididymis luminal protein 213 OS=Homo sapiens GN=HEL-213 PE=2 SV=1	3
A0A024R0A1	Colony stimulating factor 1 (Macrophage), isoform CRA_a OS=Homo sapiens GN=CSF1 PE=4 SV=1	2
A0A024R0T8,K7ER19,P02654	Apolipoprotein C-1, isoform CRA_a OS=Homo sapiens GN=APOC1 PE=4 SV=1	2
A0A024R1G8,A0A024R1Q4,ASPL32,B2R9E5,O14791,O14791-2,Q1WWL5,Q29RW7,Q2KH06	Apolipoprotein L, 1, isoform CRA_b OS=Homo sapiens GN=APOL1 PE=4 SV=1	2
A0A024R3E3,P02647	Apolipoprotein A-I, isoform CRA_a OS=Homo sapiens GN=APOA1 PE=4 SV=1	2
A0A024R7V4,P01210	Proenkephalin, isoform CRA_a OS=Homo sapiens GN=PENK PE=3 SV=1	2
A0A024RAB9,D6R934,P02746	Complement component 1, q subcomponent, B chain, isoform CRA_a OS=Homo sapiens GN=C1QB PE=4 SV=1	2
A0A075B6P5,A0A0A0MTQ6,A2NB45,P01617,P06309	Protein IGKV2-28 (Fragment) OS=Homo sapiens GN=IGKV2D-28 PE=1 SV=1	2
A0A087WWC9,A0A087WWT5,A0A087WWU7,A0A087WXC3,A0A087WYN7	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=1 SV=1	2
A0A0A0MQX7,Q08629	Testican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	2
A0A0C4DH69	Protein IGKV1-9 (Fragment) OS=Homo sapiens GN=IGKV1-9 PE=4 SV=1	2
A4D158,P01303	Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	2
ASK0R8,E7EVP0,Q13519,Q13519-2,Q9BYY3	cDNA FLJ75574, highly similar to Homo sapiens preproconceptrin (PNO), mRNA OS=Homo sapiens PE=2 SV=1	2
BOZBE2,B2R5S1,B4DE80,B4E1B3,P01019,Q53YY1,Q59EP2,Q86U78	Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) OS=Homo sapiens GN=AGT PE=3 SV=1	2
B4DPP8,D3DNUS,P01042-2,Q05CF8	cDNA FLJ53075, highly similar to Kininogen-1 OS=Homo sapiens PE=2 SV=1	2
CSCHS3,Q16610	Truncated extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=4 SV=1	2
D3DQ54,Q8N3X1,Q8N3X1-2	Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNB4 PE=4 SV=1	2
D9YZU5,P68871	Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	2
D9ZGG2,P04004	Vitronectin OS=Homo sapiens GN=VTN PE=4 SV=1	2
E7EM83,Q92932,Q92932-4	Protein-tyrosine-phosphatase OS=Homo sapiens GN=PTPRN2 PE=1 SV=1	2
E9K126,E9PGN7,H9K1V48,P05155,P05155-3	Epididymis tissue protein Li 173 OS=Homo sapiens PE=2 SV=1	2
P01606	Ig kappa chain V-1 region OU OS=Homo sapiens PE=1 SV=1	2

P06307,Q6FG82	Cholecystokinin OS=Homo sapiens GN=CCK PE=1 SV=1	2
P06396	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	2
P06727	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	2
P07998,W0UV93	Ribonuclease pancreatic OS=Homo sapiens GN=RNASE1 PE=1 SV=4	2
P61278	Somatostatin OS=Homo sapiens GN=SST PE=1 SV=1	2
P81605	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	2
Q6GMX0	Uncharacterized protein OS=Homo sapiens PE=1 SV=1	2
Q6ZP85	CDNA FLJ26301 fis, clone DMC07540 OS=Homo sapiens PE=2 SV=1	2
Q96FE7-4	Isoform 4 of Phosphoinositide-3-kinase-interacting protein 1 OS=Homo sapiens GN=PIK3IP1	2
S6C4R6	IgG L chain OS=Homo sapiens PE=2 SV=1	2
A0A024R035,P02748	Complement component 9, isoform CRA_a OS=Homo sapiens GN=C9 PE=4 SV=1	1
A0A024RS24,Q06710-3	Paired box gene 8, isoform CRA_d OS=Homo sapiens GN=PAX8 PE=4 SV=1	1
A0A024RAA7,P02747	Complement component 1, q subcomponent, C chain, isoform CRA_a OS=Homo sapiens GN=C1QC PE=4 SV=1	1
A0A024RAG6,P02745	Complement component 1, q subcomponent, A chain, isoform CRA_a OS=Homo sapiens GN=C1QA PE=4 SV=1	1
A0A024RD97,ASJ20,Q9Y6R1,Q9Y6R1-2,Q9Y6R1-5	Anion exchange protein OS=Homo sapiens GN=SLC4A4 PE=3 SV=1	1
A0A024RDE1,Q14515	SPARC-like 1 (Mast9, hevin), isoform CRA_a OS=Homo sapiens GN=SPARCL1 PE=4 SV=1	1
A0A059RS22	NADH-ubiquinone oxidoreductase chain 5 OS=Homo sapiens GN=ND5 PE=3 SV=1	1
A0A068LKQ0	Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	1
A0A087X054,B3KXH0,B7Z2N4,Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	1
A0A087X130	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	1
A0A087X118,Q7Z3E5	LisH domain-containing protein ARMC9 OS=Homo sapiens GN=ARMC9 PE=1 SV=1	1
A0A090N7U6,Q8N8U9	BMP-binding endothelial regulator protein OS=Homo sapiens GN=BMPER PE=4 SV=1	1
A0A0A0MSM0,Q92598-4	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	1
A0A0C4DFX2,Q5TBA9	Protein furry homolog OS=Homo sapiens GN=FRY PE=1 SV=1	1
A0NSG1,P01602	Rheumatoid factor C6 light chain (Fragment) OS=Homo sapiens GN=V $\kappa$ 1 PE=2 SV=1	1
A2A3C2,A2A3C3,A2A3C6,O60241,O60241-2,O60241-3,O60241-4	Protein ADGRB2 OS=Homo sapiens GN=ADGRB2 PE=1 SV=1	1
A2ACR1,B4DZW2,P28065,P28065-2	Proteasome subunit beta type OS=Homo sapiens GN=PSMB9 PE=1 SV=1	1
ASK144,Q96GW7	cDNA FLJ76746, highly similar to Homo sapiens brevican (BCAN), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	1
ASK2F4,Q96JM7,Q96JM7-2	cDNA FLJ75620 OS=Homo sapiens PE=2 SV=1	1
ASK2U2,E9PB90,P52789	Hexokinase OS=Homo sapiens PE=2 SV=1	1
ASK3L0,B4DRF2,Q6LAM1,Q8WW88	cDNA FLJ76262, highly similar to Homo sapiens I factor (complement) (IF), mRNA OS=Homo sapiens PE=2 SV=1	1
ASK444,B7Z8Q8,Q6NUS8	UDP glycosyltransferase 3 family, polypeptide A1, isoform CRA_a OS=Homo sapiens GN=UGT3A1 PE=2 SV=1	1
ASK4T8,B4DRG7,C9J470,E9PHA2,Q15003,Q15003-2	Condensin complex subunit 2 OS=Homo sapiens PE=2 SV=1	1
ASK7Q1,B4DZX0,Q02818,Q53GX6	cDNA FLJ77770, highly similar to Homo sapiens nucleobindin 1 (NUCB1), mRNA OS=Homo sapiens PE=2 SV=1	1
ASK832,P04085,P04085-2	cDNA FLJ75285, highly similar to Homo sapiens platelet-derived growth factor alpha polypeptide(PDGF $\alpha$ ), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	1
B3KWXX,Q53GR6,Q8TE82,Q9NXX4	SH3 domain and tetrapeptide repeats 1, isoform CRA_f OS=Homo sapiens GN=SH3TC1 PE=2 SV=1	1
B3VL05	Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	1
B4DDT3,E9PIT3,P00734	cDNA FLJ54622, highly similar to Prothrombin (EC 3.4.21.5) OS=Homo sapiens PE=2 SV=1	1
B4DI09,Q9H987	cDNA FLJ57015, highly similar to Synaptosidin 2-like protein OS=Homo sapiens PE=2 SV=1	1
B4DM35	cDNA FLJ57323, highly similar to Synaptotagmin-4 OS=Homo sapiens PE=2 SV=1	1
B4DS10,H3BSW6,Q2VPK5,Q2VPK5-5	Cytoplasmic tRNA 2-thiolation protein 2 OS=Homo sapiens GN=CTU2 PE=1 SV=1	1
B4DV48,P06681,P06681-3,Q53GZ8,Q5PJ69	cDNA FLJ55526, highly similar to Complement C2 (EC 3.4.21.43) OS=Homo sapiens PE=2 SV=1	1
B4DYQ3	cDNA FLJ60974, highly similar to Mediator of RNA polymerase II transcription subunit 12 OS=Homo sapiens PE=2 SV=1	1
B7Z1F8	cDNA FLJ53025, highly similar to Complement C4-B OS=Homo sapiens PE=2 SV=1	1
B7Z507,P14780	cDNA FLJ51036, highly similar to Matrix metalloproteinase-9 (EC3.4.24.35) OS=Homo sapiens PE=2 SV=1	1
B7Z549,P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITH1 PE=1 SV=3	1
B7ZLJ8,Q9BYH1,Q9BYH1-4,Q9BYH1-5,Q9BYH1-6,Q9BYH1-7	SEZL4 protein OS=Homo sapiens GN=SEZL4 PE=1 SV=1	1
B7ZMH4	ODZ1 protein OS=Homo sapiens GN=ODZ1 PE=2 SV=1	1
B9EG60,H0YVY3,Q9UMS6,Q9UMS6-2,Q9UMS6-3,Q9UMS6-4	Synaptosidin 2 OS=Homo sapiens GN=SYNPO2 PE=2 SV=1	1
C7E9P5,KTEQG4,O00168	FXD1 domain-containing ion transport regulator 1 transcript variant b (Fragment) OS=Homo sapiens GN=FXD1 PE=2 SV=1	1
C9JMN4,Q92520	Protein FAM3C (Fragment) OS=Homo sapiens GN=FAM3C PE=1 SV=1	1
C9JN77,P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	1
D3DV57	DNA segment on chromosome 4 (Unique) 234 expressed sequence, isoform CRA_a OS=Homo sapiens GN=DIS234E PE=4 SV=1	1
D6REX7,D6RHD2,D6RIE6,O43609	Protein sprouty homolog 1 (Fragment) OS=Homo sapiens GN=SPRY1 PE=1 SV=1	1
D6RFM1,P20396	Pro-thyrotropin-releasing hormone OS=Homo sapiens GN=TRH PE=1 SV=1	1
E7EM72,E7EWQ4,O75912	Diacylglycerol kinase OS=Homo sapiens GN=DGKI PE=1 SV=1	1
E9POX3	Tetrapeptide repeat protein 39A (Fragment) OS=Homo sapiens GN=TTC39A PE=1 SV=1	1
E9POZ2,Q11206,Q11206-2,Q11206-3,Q11206-4,Q11206-5,Q11206-6,Q11206-7,Q61BE6,Q8N6A7,Q8NFD3	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 4 (Fragment) OS=Homo sapiens GN=ST3GAL4 PE=1 SV=1	1
F6SYF8,Q9UBP4	Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=1 SV=1	1
H0Y300	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4	1
H0YLVS,H0YMB3	GMP reductase 2 OS=Homo sapiens GN=GMPR2 PE=1 SV=1	1
I3L2Z5,I3L411	Myc-associated zinc finger protein (Fragment) OS=Homo sapiens GN=MAZ PE=1 SV=1	1
I3L504	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=1	1
I6L9F7,Q99879	Histone H2B (Fragment) OS=Homo sapiens GN=HIST1H2BM PE=2 SV=1	1
J3KNL6	Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=1	1
J3QXK2	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1A PE=1 SV=1	1
O00519	Fatty-acid amide hydrolase 1 OS=Homo sapiens GN=FAAH PE=1 SV=2	1
O14772-3	Isoform 6 of Fucose-1-phosphate guanylyltransferase OS=Homo sapiens GN=FPGT	1
O43189	PHD finger protein 1 OS=Homo sapiens GN=PHF1 PE=1 SV=3	1
O95158	Neurexophilin-4 OS=Homo sapiens GN=NXPH4 PE=2 SV=3	1
O95628-7	Isoform 7 of CCR4-NOT transcription complex subunit 4 OS=Homo sapiens GN=CNOT4	1
P01344-3	Isoform 3 of Insulin-like growth factor II OS=Homo sapiens GN=IGF2	1
P01768	Ig heavy chain V-III region CAM OS=Homo sapiens PE=1 SV=1	1
P01780	Ig heavy chain V-III region JON OS=Homo sapiens PE=1 SV=1	1
P02774,P02774-3,V9HWI6	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	1
P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	1
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	1

P05546,Q81VC0	Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	1
P08670,Q53HUR,V9HWE1	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	1
P14543,P14543-2	Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	1
P19320-2	Isoform 2 of Vascular cell adhesion protein 1 OS=Homo sapiens GN=VCAM1	1
P25788,P25788-2,Q61B71	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	1
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	1
Q03692	Collagen alpha-1(X) chain OS=Homo sapiens GN=COL10A1 PE=1 SV=2	1
Q06033	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	1
Q08378,Q08378-2	Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	1
Q13444-4	Isoform 4 of Disintegrin and metalloproteinase domain-containing protein 15 OS=Homo sapiens GN=ADAM15	1
Q13790	Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=2	1
Q14126	Desmoglein-2 OS=Homo sapiens GN=DSG2 PE=1 SV=2	1
Q14191	Werner syndrome ATP-dependent helicase OS=Homo sapiens GN=WRN PE=1 SV=2	1
Q14847-2	Isoform 2 of LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1	1
Q2KHM9,Q2KHM9-2	Uncharacterized protein KIAA0753 OS=Homo sapiens GN=KIAA0753 PE=1 SV=3	1
Q53F10	UV excision repair protein RAD23 homolog B variant (Fragment) OS=Homo sapiens PE=2 SV=1	1
Q59G16	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant (Fragment) OS=Homo sapiens PE=2 SV=1	1
Q5SPY9,Q8NCE1,Q8WXX4,Q9NQX5	Neural proliferation differentiation and control protein 1 OS=Homo sapiens GN=NPDC1 PE=1 SV=1	1
Q5TSC7	Serine--rRNA ligase, cytoplasmic OS=Homo sapiens GN=SARS PE=1 SV=1	1
Q7Z528,Q9NXI2,Q9Y287	E3-16 OS=Homo sapiens PE=2 SV=1	1
Q8N1U0	cDNA FLJ37558 fis, clone BRCOC1000087 OS=Homo sapiens PE=2 SV=1	1
Q8NHH4	Hepatocellular carcinoma-associated antigen HCA25a OS=Homo sapiens PE=2 SV=1	1
Q8TCD0	Uncharacterized protein OS=Homo sapiens PE=1 SV=1	1
Q8TDY2,Q8TDY2-2	RB1-inducible coiled-coil protein 1 OS=Homo sapiens GN=RB1CC1 PE=1 SV=3	1
Q8WYP5,Q8WYP5-2,Q8WYP5-3	Protein ELYS OS=Homo sapiens GN=AHCTF1 PE=1 SV=3	1
Q99674,Q99674-4,Q99674-5	Cell growth regulator with EF hand domain protein 1 OS=Homo sapiens GN=CGREF1 PE=2 SV=2	1
Q99900	CD44 protein (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1	1
Q9C011,Q9C011-2,Q9C011-3	Myotubularin-related protein 12 OS=Homo sapiens GN=MTMR12 PE=1 SV=2	1
Q9HBM0	Yezatin OS=Homo sapiens GN=VEZT PE=1 SV=3	1
Q9HCJ3,Q9HCJ3-2	Ribonucleoprotein PTB-binding 2 OS=Homo sapiens GN=RAVER2 PE=1 SV=2	1
Q9HCK8	Chromodomain-helicase-DNA-binding protein 8 OS=Homo sapiens GN=CHD8 PE=1 SV=5	1
Q9NQC3	Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	1
Q9NRD8	Dual oxidase 2 OS=Homo sapiens GN=DUOX2 PE=1 SV=2	1
Q9NXX3	CDNA FLJ20006 fis, clone ADKA02694 OS=Homo sapiens PE=2 SV=1	1
Q9ULD5,Q9ULD5-2,Q9ULD5-3	Zinc finger protein 777 OS=Homo sapiens GN=ZNF777 PE=1 SV=2	1
Q9Y216,Q9Y216-2	Ninein-like protein OS=Homo sapiens GN=NINL PE=1 SV=2	1
Q9Y3R5	Protein dopey-2 OS=Homo sapiens GN=DOPEY2 PE=1 SV=5	1
Q9Y623	Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2	1
R4GMX1	Tensin-2 (Fragment) OS=Homo sapiens GN=TNS2 PE=1 SV=1	1

**Table S2.** List of endogenous peptides identified in CSF

Protein name	Protein accession numbers	Database sources	Protein molecular weight	Protein identity	Percentage seq. assigned	Peptide sequence	Peptide identity	Maxort Ion m/z	Observed m/z	Actual peptide	Calculated +1H1 Peq Spectra	Actual minus cal.	Actual minus	Peptide star	Peptide site	Exclusive	Other Protein		
ProSAAS OS-Homo sapiens GN~PCSKIN PE=1 SV=1	Q9LHG2	UniProtKB-HS_20150717_TaD.fasta	27 373.20	100.00%	12.70%	true	AADHDVGSLEPPGVGLGA	99.70%	91.6	867.4246	1 732.83	1 733.83	2	0.007578	4.371	221	238	true	
ProSAAS OS-Homo sapiens GN~PCSKIN PE=1 SV=1	Q9LHG2	UniProtKB-HS_20150717_TaD.fasta	27 373.20	100.00%	12.70%	true	AADHDVGSLEPPGVGLGALLRV	99.70%	47.4	1 108.09	2 214.17	2 215.17	2	0.006678	3.015	221	242	true	
Apolipoprotein E OS-Homo sapiens GN~APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	AATVGLAGQPLQER	99.70%	73.2	749.4074	1 496.80	1 497.80	2	0.005378	3.591	210	224	true	
Apolipoprotein E OS-Homo sapiens GN~APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	13.60%	true	AAVGTSAAPVPSDNH	99.70%	48	697.3403	1 392.67	1 393.67	2	0.002678	1.922	303	317	true	
Alpha-2 globin chain OS-Homo sapiens GN~HBA2 PE=3 SV=1	D1MGQ2.P09965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.10%	true	AAWGKGVAGHAGEYGAELERMLFSPTTK	98.70%	30	1 032.53	3 094.56	3 095.54	3	0.0285	9.207	13	41	true	
Hemoglobin, beta OS-Homo sapiens GN~HBB PE=3 SV=1	DHYZL5.P08871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	35.40%	true	AAVQVAVGANALAHKYH	99.70%	69	671.0379	2 010.09	2 011.09	3	0.012	5.968	129	147	true	
Delta globin OS-Homo sapiens GN~HBD PE=3 SV=1	A1N071.P02042	UniProtKB-HS_20150717_TaD.fasta	16 055.20	77.20%	21.10%	false	AAVQVAVGANALAHKYH	99.70%	69	671.0379	2 010.09	2 011.09	3	0.012	5.968	129	147	false	DHYZL5.P08871
Secretogranin-1 OS-Homo sapiens GN~CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	100.00%	18.20%	true	ADASEHSSRRGEAGAGEEDIQGPTKADTEKWAEGGHSRE	96.20%	30.3	879.5958	4 392.94	4 393.94	5	0.00705	1.604	90	132	true	
Isomorph 2 of Fibrinogen alpha chain OS-Homo sapiens GN~FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	17.70%	true	ADSGEGDFLAEGGVR	99.70%	138	768.856	1 535.70	1 536.69	2	0.0198	7.795	20	35	true	
cDNA FLJ54367, highly similar to Amyloid beta A4 protein (APP) (ABPP)(Alzheimer disease amyloid protein homolog) OS-Homo sapiens PE=2 SV=1	B4DM00.B4DM05.P05067.P05067-4.P05067-6.P05067-8	UniProtKB-HS_20150717_TaD.fasta	60 073.50	100.00%	3.79%	true	AEDVGSNGAHLVGGVV	99.70%	61.4	943.5167	1 885.02	1 886.01	2	0.02068	10.96	450	469	true	
Serum albumin OS-Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	AEEGKLVASQAALG	72.70%	30.5	514.955	1 541.84	1 542.85	3	0.001702	1.103	593	608	true	
Serum albumin OS-Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	AEEGKLVASQAALGL	99.70%	81.8	552.6486	1 654.92	1 655.93	3	-0.001598	-0.965	593	609	true	
Serum albumin OS-Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	7.22%	true	AFAEAVSK	99.00%	56.8	440.7246	879.434648	880.441046	2	0.0008781	0.9973	250	257	true	
Zinc finger protein 367 OS-Homo sapiens GN~ZNF367 PE=1 SV=1	Q7RTV3	UniProtKB-HS_20150717_TaD.fasta	38 411.30	68.10%	2.57%	true	AENPPPPPP	75.30%	45.9	458.2318	914.449048	915.457246	2	-0.0009219	-1.007	10	18	true	
Fibrinogen gamma chain OS-Homo sapiens GN~FGG PE=1 SV=1	C9C34.C9EUS.P02679.P02679-2	UniProtKB-HS_20150717_TaD.fasta	52 338.20	99.80%	4.99%	true	AQILTYNFDSSKPNMIDATLK	99.70%	79.9	840.7678	2 519.28	2 520.27	3	0.0235	9.325	89	111	true	
Transferrin OS-Homo sapiens PE=2 SV=1	A6NGL1.E9K136.P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	ALLSPVSYSTAVTVNPKI	98.90%	136	1 021.04	2 040.07	2 041.05	2	0.02388	11.7	166	184	true	
Apolipoprotein E OS-Homo sapiens GN~APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	ALMDETMKELK	69.70%	19.5	436.8893	1 307.65	1 308.65	3	-0.0006979	-0.5333	80	90	true	
Putative Polcomb group protein ASXL3 OS-Homo sapiens GN~ASXL3 PE=2 SV=1	Q9CF09	UniProtKB-HS_20150717_TaD.fasta	241 918.70	100.00%	1.02%	true	ALFPVPPPPPP	96.20%	56.2	538.8161	1 075.62	1 076.61	2	0.01068	9.918	2030	2040	true	
cDNA FLJ61580, highly similar to Calyculin-1 OS-Homo sapiens PE=2 SV=1	B4E3Q1.O94985.O94985-2	UniProtKB-HS_20150717_TaD.fasta	107 814.80	100.00%	3.64%	true	ANPHFVAVPSTAT	99.70%	43.3	704.8667	1 407.72	1 408.72	2	0.004178	2.966	829	842	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	14.20%	true	APEAQVSVQ	79.00%	52.7	464.7396	927.464648	928.473446	2	-0.001522	-1.639	23	31	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	17.40%	true	APEAQVSVQPN	99.70%	62.6	570.2896	1 138.56	1 139.57	2	0.002778	2.438	23	33	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	13.70%	true	APEAQVSVQPNF	97.10%	51	643.8253	1 285.64	1 286.64	2	0.005778	4.491	23	34	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	13.70%	true	APEAQVSVQPNFQ	99.70%	66.8	707.8558	1 413.70	1 414.70	2	0.008178	5.781	23	35	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	14.20%	true	APEAQVSVQPNFQQ	99.70%	90.8	771.8851	1 541.76	1 542.75	2	0.008178	5.301	23	36	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQD	99.70%	56.4	820.4027	1 636.79	1 637.78	2	0.01638	9.879	23	37	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	13.70%	true	APEAQVSVQPNFQQDK	92.90%	47.5	893.4483	1 784.88	1 785.88	2	0.01258	7.043	23	38	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKF	99.70%	67.4	966.9845	1 931.95	1 932.95	2	0.01658	8.577	23	39	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFL	99.70%	92	1 023.53	2 045.04	2 046.03	2	0.01948	9.52	23	40	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLG	99.70%	67.5	1 052.04	2 102.06	2 103.05	2	0.01798	8.548	23	41	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	17.40%	true	APEAQVSVQPNFQQDKFLGR	99.70%	92.9	751.7253	2 258.15	2 259.15	3	0.009502	4.206	23	42	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLGRW	99.10%	47	815.7605	2 444.26	2 445.23	3	0.0358	14.64	23	43	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLGRWF	99.70%	103	864.7792	2 591.32	2 592.30	3	0.0235	9.866	23	44	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	17.40%	true	APEAQVSVQPNFQQDKFLGRWFS	99.70%	44.8	893.7869	2 678.34	2 679.33	3	0.0146	5.45	23	45	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLGRWFSAG	99.70%	78.9	917.4751	2 749.40	2 750.37	3	0.0421	15.31	23	46	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLGRWFSAGL	99.70%	74.2	936.4717	2 806.39	2 807.39	3	0.0104	3.705	23	47	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLGRWFSAGLA	99.70%	69.2	974.1674	2 919.48	2 920.47	3	0.0134	4.589	23	48	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLGRWFSAGLAS	99.60%	50.7	1 026.86	3 077.57	3 078.54	3	0.0341	11.08	23	50	true	
Prostaglandin D2 synthase 21kDa (Brain), isoform CRA_a OS-Homo sapiens GN~PTGDS PE=3 SV=1	A0M24R8G3.P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	APEAQVSVQPNFQQDKFLGRWFSAGLASN	99.70%	62	1 064.87	3 191.59	3 192.59	3	0.0122	3.822	23	51	true	
Alpha-2-HS-glycoprotein OS-Homo sapiens GN~AHSG PE=1 SV=1	C9V77.P02765	UniProtKB-HS_20150717_TaD.fasta	39 410.50	96.70%	3.53%	true	APIHGGLYRQPN	96.40%	42.4	473.922	1 418.74	1 419.75	3	0.002102	1.481	19	31	true	
Pinopsin receptor GPR37L1 OS-Homo sapiens GN~GPR37L1 PE=1 SV=2	Q60883	UniProtKB-HS_20150717_TaD.fasta	52 770.60	99.90%	4.78%	true	APIHLGRHRAETEEQQRS	89.00%	34.5	551.0396	2 200.13	2 201.13	4	0.008226	3.737	26	44	true	
Neurosecretory protein VGF OS-Homo sapiens GN~VGF PE=1 SV=2	Q15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	22.80%	true	APPEVPPPP	67.90%	33.2	450.7444	899.474248	900.482746	2	-0.001222	-1.357	486	494	true	
Neurosecretory protein VGF OS-Homo sapiens GN~VGF PE=1 SV=2	Q15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	23.40%	true	APPEVPPPPR	99.70%	72.5	528.7954	1 055.58	1 056.58	2	-0.0003219	-0.3047	486	495	true	
Neurosecretory protein VGF OS-Homo sapiens GN~VGF PE=1 SV=2	Q15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	23.40%	true	APPEVPPPPRA	99.00%	47.2	564.3129	1 126.61	1 127.62	2	-0.002422	-2.148	486	496	true	
Neurosecretory protein VGF OS-Homo sapiens GN~VGF PE=1 SV=2	Q15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	19.50%	true	APPEVPPPPRAAAPT	99.70%	56.1	782.9308	1 563.85	1 564.85	2	0.005878	3.756	486	501	true	
Neurosecretory protein VGF OS-Homo sapiens GN~VGF PE=1 SV=2	Q15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	23.40%	true	APPEVPPPPRAAAPTIV	99.70%	51.2	600.9983	1 799.97	1 800.98	3	0.004602	2.555	486	503	true	
Neurosecretory protein VGF OS-Homo sapiens GN~VGF PE=1 SV=2	Q15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	19.50%	true	APPCGPEAGPPPLSSEIKPEKAVDAGVPGKDGSAPEVRG	81.70%	24	647.6722	3 879.99	3 880.96	6	0.03857	9.939	23	61	true	

Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15340	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	20.00%	true	APPGRPEAQPPPLSEHKEPVAGDAVPGKDGSAPEVRGA	99.70%	72.2	659.5007	3 951.01	3 952.00	6	0.02647	6.699	23	62	true	
cDNA FLJ76489, highly similar to Homo sapiens sortilin 1 (SORT1), mRNA OS=Homo sapiens PE=2 SV=1	AIKAO1.Q99523	UniProtKB-HS_20150717_TaD.fasta	92 038.60	100.00%	2.17%	true	APPPAAFLPR	99.70%	76.7	542.3184	1 082.62	1 083.63	2	-0.001622	-1.497	39	49	true	
cDNA FLJ76489, highly similar to Homo sapiens sortilin 1 (SORT1), mRNA OS=Homo sapiens PE=2 SV=1	AIKAO1.Q99523	UniProtKB-HS_20150717_TaD.fasta	92 038.60	100.00%	2.17%	true	APPPAAFLPWSGPG	80.80%	25.9	840.969	1 679.92	1 680.92	2	0.008378	4.984	39	55	true	
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDC1 PE=1 SV=2	Q9CID6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	2.01%	false	APPPPPPP	90.90%	45.4	433.7424	865.470248	866.477346	2	0.0001781	0.2055	33	41	false	C9K005
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0A0AMQW5.Q96Q04	UniProtKB-HS_20150717_TaD.fasta	157 098.90	94.20%	1.48%	false	APPPPPPP	90.50%	45.4	433.7424	865.470248	866.477346	2	0.0001781	0.2055	781	709	false	C9K005
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	3.29%	false	APPPPPPP	90.50%	45.4	433.7424	865.470248	866.477346	2	0.0001781	0.2055	217	225	false	C9K005
Nucleosome-remodeling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3	Q12830.Q12830.4	UniProtKB-HS_20150717_TaD.fasta	338 256.30	67.60%	0.62%	false	APPPPPPP	77.30%	41.6	433.7412	865.467848	866.477346	2	-0.002222	-2.564	23	31	false	C9K005
Isform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5.3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	56.90%	2.50%	false	APPPPPPP	77.30%	41.6	433.7412	865.467848	866.477346	2	-0.002222	-2.564	1038	1046	false	C9K005
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDC1 PE=1 SV=2	Q9CID6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	1.85%	true	APPPPPPP	99.70%	56.6	482.2697	962.524848	963.530146	2	0.001978	2.653	33	42	true	
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	1.73%	false	APPPPPPP	99.70%	56.6	482.2697	962.524848	963.530146	2	0.001978	2.653	217	226	false	Q9CID6
Isform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5.3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	67.90%	2.06%	false	APPPPPPP	86.40%	54.7	482.2686	962.522648	963.530146	2	-0.0002219	-0.2303	1038	1047	false	Q9CID6
Isform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5.3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	86.30%	2.60%	false	APPPPPPPPP	97.10%	60.9	579.3221	1 156.63	1 157.64	2	0.001178	1.018	1038	1049	false	Q9CID6
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	3.29%	false	APPPPPPPPP	97.10%	60.9	579.3221	1 156.63	1 157.64	2	0.001178	1.018	217	228	false	Q9CID6
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A6XMV6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	77.00%	11.50%	true	AQDLNAPSDWDSRGKDSYETSLEDDQSAETHSHKQS	93.20%	24.7	807.7692	4 033.81	4 034.75	5	0.06385	16.32	208	243	true	
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A6XMV6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	97.70%	16.20%	true	AQDLNAPSDWDSRGKDSYETSLKDDQSAETHSHKQS	95.00%	55.7	807.5636	4 032.78	4 033.80	5	-0.01455	-3.607	208	243	true	
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A6XMV6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	96.30%	23.60%	true	AQDLNAPSDWDSRGKDSYETSLKDDQSAETHSHKQSLY	98.50%	65.5	894.0142	4 465.03	4 466.05	5	-0.01095	-2.25	208	246	true	
Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	A0M24RDE6.P10451.5	UniProtKB-HS_20150717_TaD.fasta	33 843.10	100.00%	29.30%	true	AQDLNAPSDWDSRGKDSYETSLKDDQSAETHSHKQS	98.50%	66.4	807.5658	4 032.79	4 033.77	5	0.03285	8.144	194	229	true	
Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	A0M24RDE6.P10451.5	UniProtKB-HS_20150717_TaD.fasta	33 843.10	100.00%	13.00%	true	AQDLNAPSDWDSRGKDSYETSLKDDQSAETHSHKQSLY	99.40%	64.8	894.0146	4 465.04	4 466.02	5	0.02835	6.348	194	232	true	
cDNA FLJ61580, highly similar to Calyculin-1 OS=Homo sapiens PE=2 SV=1	B4E3QL.O494985.O49485.2	UniProtKB-HS_20150717_TaD.fasta	107 814.80	100.00%	3.64%	true	AQGFVPEHRSFVDSGHNLNMPHVAVPSTAT	87.70%	17	951.9854	3 803.91	3 804.90	4	0.02033	5.342	808	842	true	
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9LHG2	UniProtKB-HS_20150717_TaD.fasta	27 373.20	100.00%	17.70%	true	ARPKFERGLSASAPLAETGAPRF	91.20%	25.1	547.11	2 730.51	2 731.51	5	0.00925	3.386	34	59	true	
Isform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5.3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	83.70%	1.88%	true	ASAPPPPPPP	93.20%	61.1	528.2829	1 054.55	1 055.55	2	0.006278	5.948	296	306	true	
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909.2.P10909.5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	24.30%	true	ASHTSDDVPSGVTVE	96.10%	25.8	794.3622	1 586.71	1 587.71	2	0.003778	2.38	390	405	true	
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909.2.P10909.5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.80%	true	ASHTSDDVPSGTEVVVLFDSDDFTVYVPEV	99.70%	89.2	1 175.94	3 524.80	3 525.78	3	0.0175	4.964	390	423	true	
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909.2.P10909.5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	25.20%	true	ASSIDELFQDR	67.80%	17.5	697.3536	1 392.69	1 393.70	2	0.003978	2.854	183	194	true	
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	P06396	UniProtKB-HS_20150717_TaD.fasta	85 697.80	99.60%	2.94%	true	ATASRGASGAGAPQQRVPEAKPN	99.70%	51.4	563.0459	2 248.15	2 249.15	4	0.01233	5.48	28	50	true	
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	13.60%	true	AVGTSAPVPSDNH	99.70%	80.8	661.8204	1 321.63	1 322.63	2	-0.0002194	-0.01659	304	317	true	
Tetican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	A0M0AMQX7.Q08629	UniProtKB-HS_20150717_TaD.fasta	42 228.00	100.00%	5.57%	true	AVTEDEDEDDKDEIDE	99.70%	83.8	934.8364	1 867.66	1 868.67	2	-0.002522	-1.35	357	372	true	
Tetican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	A0M0AMQX7.Q08629	UniProtKB-HS_20150717_TaD.fasta	42 228.00	100.00%	5.57%	true	AVTEDEDEDDKDEIDVGY	99.70%	62.6	1 094.42	2 186.83	2 187.82	2	0.01948	8.903	357	375	true	
Tetican-1 OS=Homo sapiens GN=SPOCK1 PE=1 SV=1	A0M0AMQX7.Q08629	UniProtKB-HS_20150717_TaD.fasta	42 228.00	100.00%	5.57%	true	AVTEDEDEDDKDEIDVGTW	99.50%	85.5	1 244.01	2 486.00	2 486.98	2	0.02608	10.49	357	377	true	
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P09060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	100.00%	14.60%	true	AYTMSDFREE	92.60%	50.9	624.7662	1 247.52	1 248.52	2	0.004978	3.987	428	437	true	
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPYZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	35.40%	true	AYQKVAGVANALAHKYH	98.20%	32.1	647.3601	1 939.06	1 940.05	3	0.0157	8.094	130	147	true	
Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	A0N071.P02042	UniProtKB-HS_20150717_TaD.fasta	16 055.20	77.20%	21.10%	false	AYQKVAGVANALAHKYH	98.20%	32.1	647.3601	1 939.06	1 940.05	3	0.0157	8.094	130	147	false	DPYZUS.P68871
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G49	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	DAHKSEVAHBF	99.70%	49.2	432.8862	1 295.64	1 296.64	3	-0.0002979	-0.2298	25	35	true	
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G49	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	DAHKSEVAHFRKDLGEEEN	96.10%	34.5	521.2576	2 081.00	2 082.00	4	0.008526	4.095	25	42	true	
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G49	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	8.37%	true	DAHKSEVAHFRKDLGEEENFKALVIAFAQYQQ	80.70%	20	764.0104	3 815.02	3 815.99	5	0.03585	9.395	25	57	true	
cDNA FLJ76489, highly similar to Homo sapiens sortilin 1 (SORT1), mRNA OS=Homo sapiens PE=2 SV=1	AIKAO1.Q99523	UniProtKB-HS_20150717_TaD.fasta	92 038.60	100.00%	2.17%	true	DAPPPAAFLPR	99.70%	72.1	599.8331	1 197.65	1 198.66	2	0.0007781	0.6491	38	49	true	
cDNA FLJ76489, highly similar to Homo sapiens sortilin 1 (SORT1), mRNA OS=Homo sapiens PE=2 SV=1	AIKAO1.Q99523	UniProtKB-HS_20150717_TaD.fasta	92 038.60	100.00%	2.17%	true	DAPPPAAFLPWSGPG	99.70%	61.8	898.4832	1 794.95	1 795.95	2	0.009778	5.444	38	55	true	
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G49	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	9.69%	true	DDNPFLPR	98.80%	47	470.7281	939.441648	940.448446	2	0.0004781	0.5083	131	138	true	
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	PICOL4.PIC0L4.2	UniProtKB-HS_20150717_TaD.fasta	192 786.80	100.00%	1.20%	true	DDPDAFLQPVTPT	91.00%	24.8	632.8067	1 263.60	1 264.61	2	0.0001781	0.1408	1429	1440	true	
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	PICOL4.PIC0L4.2	UniProtKB-HS_20150717_TaD.fasta	192 786.80	100.00%	1.20%	true	DDPDAFLQPVTPLQ	89.90%	22.9	753.3784	1 504.74	1 505.75	2	0.0008781	0.5831	1429	1442	true	
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	PICOL4.PIC0L4.2	UniProtKB-HS_20150717_TaD.fasta	192 786.80	100.00%	2.12%	true	DDPDAFLQPVTPLQLFEGRRN	94.90%	26	793.4156	2 377.22	2 378.21	3	0.0219	9.209	1429	1449	true	
Isform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671.2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	12.30%	true	DEAGSEADHEGTHSRKRGHAKSRPV	99.70%	65.7	532.6569	2 658.25	2 659.26	5	-0.00155	-0.5828	605	629	true	
Proenkephalin, isoform CRA_a OS=Homo sapiens GN=PENK PE=3 SV=1	A0M24R7V4.P01210	UniProtKB-HS_20150717_TaD.fasta	30 788.30	100.00%	8.24%	true	DEEGSYSEKVEPME	99.70%	70	879.3633	1 756.71	1 757.71	2	0.01338	7.611	244	258	true	
cDNA FLJ92596, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	B2R3S2.P51693.P51693.2	UniProtKB-HS_20150717_TaD.fasta	72 103.90	100.00%	4.31%	true	DELAPAGTGVSR	99.30%	50.8	586.8001	1 171.59	1 172.59	2	0.002178	1.857	568	579	true	
cDNA FLJ92596, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	B2R3S2.P51693.P51693.2	UniProtKB-HS_20150717_TaD.fasta	72 103.90	100.00%	4.31%	true	DELAPAGTGVSRKE	99.70%	64.6	651.323	1 300.63	1 301.63	2	0.005378	4.132	568	580	true	
cDNA FLJ92596, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	B2R3S2.P51693.P51693.2	UniProtKB-HS_20150717_TaD.fasta	72 103.90	100.00%	4.31%	true	DELAPAGTGVSRREA	99.70%	74.7	686.8396	1 371.66	1 372.67	2	0.001478	1.077	568	581	true	
cDNA FLJ92596, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	B2R3S2.P51693.P51693.2	UniProtKB-HS_20150717_TaD.fasta	72 103.90	100.00%	4.31%	true	DELAPAGTGVSRREAVSG	99.70%	79.2	808.3998	1 614.79	1 615.79	2	-0.0002194	-0.01358	568	584	true	
cDNA FLJ92596, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	B2R3S2.P51693.P51693.2	UniProtKB-HS_20150717_TaD.fasta	72 103.90	100.00%	4.15%	true	DELAPAGT												

cDNA FLJ9296, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	BKRS2.P51693.P51693-2	UniProtKB-HS_20150717_TaD.fasta	72	103.90	100.00%	3.85%	true	DELAPAGTGVSRVAVSGLLIMGAGG	99.70%	108	1164.60	2327.18	2328.19	2	0.003978	1.709	568	592	true
cDNA FLJ9296, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	BKRS2.P51693.P51693-2	UniProtKB-HS_20150717_TaD.fasta	72	103.90	100.00%	4.31%	true	DELAPAGTGVSRVAVSGLLIMGAGGGS	99.70%	121	1236.63	2471.25	2472.24	2	0.01648	6.665	568	594	true
cDNA FLJ9296, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	BKRS2.P51693.P51693-2	UniProtKB-HS_20150717_TaD.fasta	72	103.90	100.00%	4.31%	true	DELAPAGTGVSRVAVSGLLIMGAGGGSLS	99.20%	39.9	862.453	2584.34	2585.32	3	0.0201	7.775	568	595	true
cDNA FLJ5889, highly similar to GTP-binding protein PTD004 OS=Homo sapiens PE=1 SV=1	B4DK14	UniProtKB-HS_20150717_TaD.fasta	38	683.50	56.50%	2.56%	true	DKGKPPP	77.10%	40.9	362.2041	722.393648	723.403846	2	-0.092922	-4.079	8	14	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	12.70%	true	DHWGSELPPGG	99.70%	79.3	626.2801	1250.55	1251.55	2	0.003878	3.699	223	234	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	12.70%	true	DHWGSELPPGGVL	99.70%	48	732.3567	1462.70	1463.70	2	0.004578	3.128	223	236	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	12.70%	true	DHWGSELPPGGVLG	99.70%	82.1	760.8677	1519.72	1520.72	2	0.005078	3.339	223	237	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	12.70%	true	DHWGSELPPGGVLGA	99.70%	100	796.3856	1590.76	1591.76	2	0.003778	2.374	223	238	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	13.10%	true	DHWGSELPPGGVLLGALL	98.90%	41	909.473	1816.93	1817.93	2	0.01038	5.709	223	240	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	11.90%	true	DHWGSELPPGGVLLGALLRV	99.70%	97.4	1037.06	2072.11	2073.10	2	0.02088	10.07	223	242	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	13.10%	true	DHWGSELPPGGVLLGALLRVK	96.30%	25.4	734.4078	2200.20	2201.19	3	0.016	7.27	223	243	true
Uncharacterized protein OS=Homo sapiens PE=1 SV=1	QGGMX0	UniProtKB-HS_20150717_TaD.fasta	25	807.40	99.90%	11.90%	true	DQMTQSPSSL	93.20%	43.3	603.7898	1205.57	1206.57	2	0.005078	4.209	23	33	true
Uncharacterized protein OS=Homo sapiens PE=1 SV=1	QGGMX0	UniProtKB-HS_20150717_TaD.fasta	25	807.40	99.90%	11.90%	true	DQMTQSPSSLSA	98.70%	75.3	682.8251	1363.64	1364.64	2	0.006578	4.82	23	35	true
Ig kappa chain V-1 region OU OS=Homo sapiens PE=1 SV=1	P01606	UniProtKB-HS_20150717_TaD.fasta	11	769.30	98.10%	20.40%	true	DQMTQSPSSLSAVGRRVITIT	99.70%	97.4	1146.58	2291.15	2292.15	2	0.01058	4.615	1	22	true
Ig L chain OS=Homo sapiens PE=2 SV=1	SEC4R6	UniProtKB-HS_20150717_TaD.fasta	20	315.20	99.20%	12.00%	true	DIVMTQSPDLAVLGERATIN	99.70%	102	1159.10	2316.19	2317.17	2	0.02408	10.39	21	42	true
Prostaglandin D2 synthase 218Ds (Brain), isoform CRA_a OS=Homo sapiens GN=PTGDS PE=1 SV=1	A0M24R8G3.P4122	UniProtKB-HS_20150717_TaD.fasta	21	028.10	100.00%	17.40%	true	DLQAAFGAIVSQVFN	80.10%	35.1	783.8958	1565.78	1566.78	2	0.008378	5.347	19	33	true
cDNA FLJ61580, highly similar to Calyculin-1 OS=Homo sapiens PE=2 SV=1	BHEJQ1.O94985.O94985-2	UniProtKB-HS_20150717_TaD.fasta	107	814.80	100.00%	2.39%	true	DLGHNLANPHFF	99.20%	41.7	709.847	1417.68	1418.68	2	0.005478	3.861	822	834	true
Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	A4D1S1.P01303	UniProtKB-HS_20150717_TaD.fasta	10	852.30	100.00%	20.60%	true	DNPGEDAPAEIDMARY	99.70%	64.1	825.8427	1649.67	1650.67	2	0.007978	4.773	34	48	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78	276.10	100.00%	17.40%	true	DPADASAEHSSSRGEGAGPEEDDQGPTKA	99.60%	41.1	767.3466	3065.36	3066.35	4	0.01253	4.02	88	118	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78	276.10	100.00%	11.20%	true	DPADASAEHSSSRGEGAGPEEDDQGPTKADTEKWAEGGGHSRE	99.70%	58.9	922.0245	4605.09	4606.02	5	0.07075	15.36	88	132	true
Synaptotagmin-7 (Fragment) OS=Homo sapiens GN=SYT7 PE=1 SV=1	F5HHG7.O43581	UniProtKB-HS_20150717_TaD.fasta	18	894.30	95.70%	8.57%	true	DPEAASFGAPSRDVL	99.10%	44.2	741.3707	1480.73	1481.72	2	0.01088	7.341	4	18	true
Synaptotagmin-7 (Fragment) OS=Homo sapiens GN=SYT7 PE=1 SV=1	F5HHG7.O43581	UniProtKB-HS_20150717_TaD.fasta	18	894.30	99.80%	10.90%	true	DPEAASFGAPSRDVLVSA	91.30%	24.1	926.4824	1850.95	1851.94	2	0.01268	6.846	4	22	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	20.00%	true	DPHTVTVPEV	99.70%	44.5	584.8282	1167.64	1168.65	2	0.002978	2.548	413	423	true
Trichoblytin OS=Homo sapiens GN=TCHH PE=1 SV=2	Q07283	UniProtKB-HS_20150717_TaD.fasta	253	921.70	74.20%	0.41%	true	DPKTYDLI	80.40%	45.1	450.7564	899.498248	900.503946	2	0.001578	1.752	50	57	true
Beta-1,3-N-acetylglucosaminyltransferase haptic fringe OS=Homo sapiens GN=LFNG PE=1 SV=2	QINES3.QINES3-3	UniProtKB-HS_20150717_TaD.fasta	41	774.20	99.90%	3.17%	true	DPPPPPLP	89.50%	45.9	415.2257	828.438648	829.445746	2	-0.001622	-1.955	27	34	true
Beta-1,3-N-acetylglucosaminyltransferase haptic fringe OS=Homo sapiens GN=LFNG PE=1 SV=2	QINES3.QINES3-3	UniProtKB-HS_20150717_TaD.fasta	41	774.20	89.80%	3.17%	true	DPPPPPLPAERG	95.20%	51	621.828	1241.64	1242.65	2	0.0006781	0.5457	27	38	true
cDNA FLJ78680, highly similar to Homo sapiens TSPY-like 2 (TSPYL2), mRNA OS=Homo sapiens PE=2 SV=1	AIKU7.B3K3VZ.QH12G4	UniProtKB-HS_20150717_TaD.fasta	79	418.10	92.80%	1.44%	true	DPPPPPPPPP	96.20%	55.8	504.2634	1006.51	1007.52	2	-0.0005219	-0.518	24	33	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	25.20%	true	DQTVSDNELQEM	97.30%	33.9	704.8018	1407.59	1408.59	2	0.006478	4.599	23	34	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	13.60%	true	DQTVSDNELQEMSN	99.70%	64.6	805.3435	1608.67	1609.66	2	0.01408	9.305	23	36	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	13.60%	true	DQTVSDNELQEMSNQ	99.70%	55.8	869.3704	1736.73	1737.72	2	0.01018	5.857	23	37	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	19.80%	true	DQTVSDNELQEMSNQG	99.70%	106	897.883	1793.75	1794.74	2	0.01388	7.753	23	38	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	22.00%	true	DQTVSDNELQEMSNQSKYVN	99.70%	99.3	1193.53	2385.05	2386.05	2	0.01228	5.146	23	43	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	22.00%	true	DQTVSDNELQEMSNQSKYVNSE	98.40%	34.5	881.7363	2642.19	2643.18	3	0.0103	3.898	23	45	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	19.80%	true	DQTVSDNELQEMSNQSKYVNSEIQN	99.10%	41.4	1000.14	2997.39	2998.37	3	0.0208	8.939	23	48	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	19.40%	true	DQTVSDNELQEMSNQSKYVNSEIQNA	92.80%	21.2	1023.81	3068.42	3069.41	3	0.0207	6.745	23	49	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52	495.00	100.00%	21.80%	true	DQTVSDNELQEMSNQSKYVNSEIQNAVN	99.70%	67.6	1094.87	3281.58	3282.52	3	0.0654	19.92	23	51	true
MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=4 SV=1	VSLDG7	UniProtKB-HS_20150717_TaD.fasta	8	705.50	39.40%	13.90%	true	DRENLETLGG	76.10%	30.6	580.3021	1158.59	1159.60	2	0.001378	1.188	56	65	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78	276.10	100.00%	18.20%	true	DRNLYNTEGEGAPGWQQGDLQDTENKEERAFQDKQYSSHTAE	99.70%	38.7	909.7559	5452.49	5453.48	6	0.01587	2.911	468	513	true
Xylosetransferase 1 OS=Homo sapiens GN=XYLT1 PE=1 SV=1	Q86Y38	UniProtKB-HS_20150717_TaD.fasta	107	571.00	97.20%	2.92%	true	DSGGERRRGAIVGGEGPPAPAPAPRE	96.60%	32.4	540.6748	2698.34	2699.34	5	0.00885	3.279	39	66	true
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02871-2	UniProtKB-HS_20150717_TaD.fasta	69	756.90	100.00%	17.70%	true	DSGEGDFLAEGGVR	99.70%	114	733.336	1484.66	1485.66	2	0.009078	6.194	21	35	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6NGL1.E9KL36.P02766	UniProtKB-HS_20150717_TaD.fasta	20	198.60	100.00%	27.70%	true	DSGPRRYTIAALLSPYSYITAVYTN	78.40%	21	935.1473	2802.42	2803.43	3	0.001202	0.4288	156	181	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6NGL1.E9KL36.P02766	UniProtKB-HS_20150717_TaD.fasta	20	198.60	100.00%	15.80%	true	DSGPRRYTIAALLSPYSYITAVYTNPKI	99.70%	88.9	790.1642	3156.63	3157.62	4	0.01843	5.835	156	184	true
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02871-2	UniProtKB-HS_20150717_TaD.fasta	69	756.90	100.00%	17.70%	true	DSHSLTINMEILR	99.70%	72.2	815.4277	1628.84	1629.83	2	0.02148	13.18	101	114	true
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02871-2	UniProtKB-HS_20150717_TaD.fasta	69	756.90	100.00%	18.90%	true	DSHSLTINMEILRQDFSSANN	99.70%	69.5	808.0517	2421.13	2422.13	3	0.0101	4.171	101	122	true
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02871-2	UniProtKB-HS_20150717_TaD.fasta	69	756.90	100.00%	14.90%	true	DSHSLTINMEILRQDFSSANNR	99.70%	72.1	645.3154	2577.23	2578.23	4	0.008226	3.191	101	123	true
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7	304.80	100.00%	69.40%	true	DSSEKFLR	99.70%	58.6	370.8507	1109.53	1110.54	3	-0.005098	-4.591	20	28	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27	373.20	100.00%	12.70%	true	DVSGELPPGGVLLGALLRV	99.70%	68.1	911.0155	1820.02	1821.01	2	0.01178	6.468	225	242	true
cDNA FLJ5487, highly similar to Amyloid beta A4 protein (APP) (BPP2A)(Alzheimer disease amyloid protein homolog) OS=Homo sapiens PE=2 SV=1	B4DM00.B4DM05.P05067.P05067-4.P05067-6.P05067-8	UniProtKB-HS_20150717_TaD.fasta	60	073.50	99.20%	3.41%	true	DVGSNKGAIIGMYGGV	99.70%	68.3	843.4731	1684.93	1685.93	2	0.01318	7.816	452	469	true

Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AA087WV47,AA087WYE1,AA087X010,VH0W68	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	EALINHHTQKSLSLSPG	69.40%	22.8	627.9891	1 880.95	1 881.95	3	0.007302	3.88	449	465	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	91.30%	13.60%	false	EALINHHTQKSLSLSPG	69.40%	22.8	627.9891	1 880.95	1 881.95	3	0.007302	3.88	455	471	false
Anguin OS=Homo sapiens GN=C2orf80 PE=1 SV=1	BZ2ZES,C9IR80,Q9H1Z8	UniProtKB-HS_20150717_TaD.fasta	13 614.30	100.00%	24.10%	true	EAPVPTKTKVAVDENKAKE	99.70%	69.8	514.2839	2 053.11	2 054.11	4	0.0007261	0.3555	6	24	true
Anguin OS=Homo sapiens GN=C2orf80 PE=1 SV=1	BZ2ZES,C9IR80,Q9H1Z8	UniProtKB-HS_20150717_TaD.fasta	13 614.30	100.00%	24.10%	true	EAPVPTKTKVAVDENKAKEFLGSLKIQ	99.70%	104	597.5423	2 982.68	2 983.66	5	0.02455	8.228	6	32	true
Prostaglandin D2 synthase 2(LDa) (Brain), isoform CRA_a OS=Homo sapiens GN=PTGDS PE=3 SV=1	AA024R8G3,P41222	UniProtKB-HS_20150717_TaD.fasta	21 029.10	100.00%	15.30%	true	EAQSVQPNFQQDKFLGRWFA	81.70%	24.2	861.4429	2 581.31	2 582.28	3	0.0354	13.71	25	46	true
Serpin peptidase inhibitor, clade A (Alpha-1 antitrypsin, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=1 SV=1	AA024R847	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	9.57%	true	EDPGDAAQKTD	99.70%	56.5	688.304	1 374.59	1 375.60	2	0.003178	2.31	25	37	true
Serpin peptidase inhibitor, clade A (Alpha-1 antitrypsin, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=1 SV=1	AA024R847	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	12.20%	true	EDPGDAAQKTDTSHHQDHPFTN	96.60%	40.8	673.5419	2 690.14	2 691.13	4	0.01513	5.621	25	48	true
cDNA FLJ54367, highly similar to Amyloid beta A4 protein (APP) (Alzheimer disease amyloid protein homolog) OS=Homo sapiens PE=2 SV=1	B4DM00,B4DM05,P05067,P05067-4,P05067-6,P05067-8	UniProtKB-HS_20150717_TaD.fasta	60 073.50	100.00%	3.79%	true	EDVGSNGEAGLVMVGGVV	99.70%	92	907.9952	1 813.98	1 814.97	2	0.01478	8.142	451	469	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q5G69	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	EEGKKLVASQAALGL	99.70%	69.7	792.9569	1 583.90	1 584.90	2	0.01078	6.8	594	609	true
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	12.00%	true	EGDFLAEGGGVR	99.70%	68.7	603.793	1 205.57	1 206.58	2	0.003578	2.965	24	35	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q5G69	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	2.96%	true	EGKKLVASQAALGL	79.90%	36.8	728.4341	1 454.85	1 455.85	2	0.007778	5.343	595	609	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	12.00%	true	EGQEEEDNRDSSMLSFRA	98.10%	31.9	786.3536	2 356.04	2 357.03	3	0.0151	6.407	359	378	true
Sortilin-related VPS10 domain containing receptor 3 OS=Homo sapiens GN=SORCS3 PE=2 SV=1	Q1788,Q9JUPJ3	UniProtKB-HS_20150717_TaD.fasta	135 787.60	99.90%	2.37%	true	ETWDAATGGPGRPAAPSRPALSPLSR	99.70%	32.5	732.1405	2 924.53	2 925.53	4	0.006826	2.333	34	62	true
IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	Q6P9F2	UniProtKB-HS_20150717_TaD.fasta	25 520.90	100.00%	15.30%	true	EIVLQSPATL	79.40%	27.8	586.3339	1 170.65	1 171.66	2	0.003478	2.968	21	31	true
IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	Q6P9F2	UniProtKB-HS_20150717_TaD.fasta	25 520.90	100.00%	15.30%	true	EIVLQSPATLSLSPGERATL	99.70%	86.8	1 092.11	2 182.21	2 183.19	2	0.02068	9.471	21	41	true
Anti-HCS scFv (Fragment) OS=Homo sapiens PE=2 SV=1	A2KBC5	UniProtKB-HS_20150717_TaD.fasta	25 223.30	95.00%	8.82%	true	EIVLQSPGTLSSPGERATL	97.00%	39.6	1 085.10	2 168.18	2 169.18	2	0.01028	4.738	131	151	true
Anti-HCS scFv (Fragment) OS=Homo sapiens PE=2 SV=1	A2KBC5	UniProtKB-HS_20150717_TaD.fasta	25 223.30	48.50%	9.24%	true	EIVLQSPGTLSSPGERATLS	65.00%	26.9	1 128.63	2 255.25	2 256.21	2	0.04428	19.62	131	152	true
Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	AA087X130	UniProtKB-HS_20150717_TaD.fasta	25 136.10	100.00%	15.60%	true	EIVMTSPATLSVSPGERA	98.10%	39.8	987.0175	1 972.02	1 973.00	2	0.02678	13.57	21	39	true
Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	AA087X130	UniProtKB-HS_20150717_TaD.fasta	25 136.10	100.00%	15.60%	true	EIVMTSPATLSVSPGERATL	99.70%	81.3	1 094.09	2 186.16	2 187.13	2	0.02998	13.71	21	41	true
cDNA FLJ92596, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1),mRNA OS=Homo sapiens PE=2 SV=1	B2R352,P51693,P51693-2	UniProtKB-HS_20150717_TaD.fasta	72 103.90	100.00%	8.62%	true	ELAPAGTGVSAEVSNG	99.70%	50.3	750.8888	1 499.76	1 500.77	2	0.004978	3.317	569	584	true
Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	Q9W0D2	UniProtKB-HS_20150717_TaD.fasta	53 008.20	99.90%	3.65%	true	ELSAERPLNEQIAEED	99.70%	86.4	1 021.99	2 041.96	2 042.95	2	0.01528	7.478	35	52	true
Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	Q9W0D2	UniProtKB-HS_20150717_TaD.fasta	53 008.20	100.00%	6.62%	true	ELSAERPLNEQIAEEDIKI	98.30%	33.2	1 142.58	2 283.14	2 284.13	2	0.01418	6.207	35	54	true
Galgi autoantigen, galgin subfamily a, 2, isoform CRA_a OS=Homo sapiens GN=GOLGA2 PE=1 SV=1	AA04CDG55,Q80379	UniProtKB-HS_20150717_TaD.fasta	111 658.30	49.10%	0.91%	true	EPFPPPEPA	65.50%	33.5	465.7357	929.456848	930.456946	2	0.007178	7.714	436	444	true
CD99 antigen-like 2, isoform CRA_d OS=Homo sapiens GN=CD99L2 PE=4 SV=1	AA024RC16,Q9TC22,Q9TC22-2,Q9TC22-3,Q9TC22-5	UniProtKB-HS_20150717_TaD.fasta	27 986.30	97.50%	6.11%	true	EPFPPPEFA	73.50%	35.9	465.7357	929.456848	930.456946	2	0.007178	7.714	252	260	true
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	D3DQ54,Q9N3X1,Q9N3X1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.15%	true	EPFPPPPPPPP	90.00%	38.7	511.272	1 020.53	1 021.54	2	0.001078	1.655	904	913	true
Sine oculis-binding protein homolog OS=Homo sapiens GN=SOBP PE=1 SV=2	A7X9Q1	UniProtKB-HS_20150717_TaD.fasta	92 658.90	74.10%	1.03%	true	EQPFPFPPPP	88.60%	44.3	478.2476	954.480648	955.488646	2	-0.0007219	-0.7556	743	751	true
FXVD domain-containing ion transport regulator 1 transcript variant b (Fragment) OS=Homo sapiens GN=FXVD1 PE=2 SV=1	C7E9P5,KEQG4,Q00168	UniProtKB-HS_20150717_TaD.fasta	7 098.90	92.90%	31.70%	true	ESPKEDHDFTYDQSLQGG	88.90%	21.9	771.0255	2 310.05	2 311.05	3	0.01083	4.458	15	34	true
FXVD domain-containing ion transport regulator 1 transcript variant b (Fragment) OS=Homo sapiens GN=FXVD1 PE=2 SV=1	C7E9P5,KEQG4,Q00168	UniProtKB-HS_20150717_TaD.fasta	7 098.90	88.90%	39.70%	true	ESPKEDHDFTYDQSLQGGVIAG	98.20%	29.3	922.1273	2 763.36	2 764.35	3	0.0205	7.417	15	39	true
GLTSCR1-like protein OS=Homo sapiens GN=GLTSCR1L PE=1 SV=2	Q6439	UniProtKB-HS_20150717_TaD.fasta	115 082.90	45.50%	1.39%	true	ETDSLEAAVNSLE	69.40%	25.4	802.4114	1 602.81	1 603.81	2	0.009278	5.785	1064	1078	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.80%	true	ETVAEKALQEVKKHREE	97.80%	24.6	561.8903	2 243.17	2 244.17	4	0.006126	2.73	432	449	true
CDNA FLJ26301, clone DMC07580 OS=Homo sapiens PE=2 SV=1	Q6Z9P5	UniProtKB-HS_20150717_TaD.fasta	25 803.50	97.90%	8.47%	true	EVQVESGGGLVPGESLRL	97.60%	40.4	1 034.07	2 066.13	2 067.14	2	-0.008022	-3.881	20	39	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	99.80%	7.84%	true	EVQVESGGGLVPGG	99.70%	61.1	763.4215	1 524.83	1 525.82	2	0.01338	8.768	20	35	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	100.00%	8.69%	true	EVQVESGGGLVPGGSLRL	87.30%	52.6	998.032	1 994.09	1 995.12	2	-0.02002	-13.49	20	39	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	91.30%	13.60%	true	EVQVESGGGLVPGGSLRLS	96.90%	65.9	1 041.58	2 081.14	2 082.16	2	-0.004922	-2.364	20	40	true
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AA087WV47,AA087WYE1,AA087X010,VH0W68	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	EVQVESGGGLVQPG	98.20%	65.3	734.8918	1 467.77	1 468.76	2	0.01188	8.087	20	34	true
Putative uncharacterized protein DKFZp688P15220 OS=Homo sapiens GN=DKFZp688P15220 PE=1 SV=1	Q6N089	UniProtKB-HS_20150717_TaD.fasta	51 723.90	99.60%	7.84%	false	EVQVESGGGLVQPG	84.90%	36.7	734.8888	1 467.76	1 468.76	2	0.005878	4.002	20	34	false
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AA087WV47,AA087WYE1,AA087X010,VH0W68	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	EVQVESGGGLVQPGG	98.60%	74.3	763.4034	1 524.79	1 525.79	2	0.01338	8.899	20	35	true
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AA087WV47,AA087WYE1,AA087X010,VH0W68	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	EVQVESGGGLVQPGGSLRL	98.30%	103	998.058	1 994.10	1 995.09	2	0.02148	10.77	20	39	true
Putative uncharacterized protein DKFZp688P15220 OS=Homo sapiens GN=DKFZp688P15220 PE=1 SV=1	Q6N089	UniProtKB-HS_20150717_TaD.fasta	51 723.90	99.60%	7.84%	true	EVQVESGGGLVQPGR	99.70%	64.9	812.9377	1 623.86	1 624.87	2	0.002578	1.587	20	35	true
cDNA FLJ54022, highly similar to Prothombin (EC 3.4.21.5) OS=Homo sapiens PE=2 SV=1	B4DDT3,E9PPT3,P00734	UniProtKB-HS_20150717_TaD.fasta	53 149.10	100.00%	2.76%	true	EYQTFNPR	90.80%	28.5	601.2893	1 200.56	1 201.56	2	0.007678	6.39	168	176	true
Proenkephalin, isoform CRA_a OS=Homo sapiens GN=PENK PE=3 SV=1	AA024R7N4,P01210	UniProtKB-HS_20150717_TaD.fasta	30 788.30	100.00%	8.24%	true	FAELPSDEEGESYSKEVPEME	99.70%	65.1	1 237.04	2 472.07	2 473.06	2	0.01868	7.553	237	258	true
cDNA FLJ54367, highly similar to Amyloid beta A4 protein (APP) (Alzheimer disease amyloid protein homolog) OS=Homo sapiens PE=2 SV=1	B4DM00,B4DM05,P05067,P05067-4,P05067-6,P05067-8	UniProtKB-HS_20150717_TaD.fasta	60 073.50	96.30%	2.08%	true	FAEDVGSNKGGA	90.70%	38.7	547.7601	1 093.51	1 094.51	2	0.001578	1.442	449	459	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q5G69	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	2.96%	true	FAEEGKKLVASQAALG	99.70%	79.5	845.4689	1 688.92	1 689.92	2	0.01338	7.916	592	608	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q5G69	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	FAEEGKKLVASQAALGL	99.70%	131	902.0993	1 802.60	1 803.60	2	0.01098	5.59	592	609	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	22.00%	true	FDSDPITVTVPIEY	95.40%	34.4	759.3939	1 516.77	1 517.77	2	0.006978	4.598	410	423	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	21.40%	true	FDSDPITVTVPIEYSRKNPK	99.70%	68.5	557.8066	2 227.20	2 228.19	4	0.01223	5.487	410	429	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	12.00%	true	FEDELSVLENNQSQAEKE	99.70%	48.6	1 162.56	2 323.10	2 324.08	2	0.03298	14.19	100	119	true
E3-16 OS=Homo sapiens PE=2 SV=1	Q7Z538,Q9NX12,Q9Y287	UniProtKB-HS_20150717_TaD.fasta	30 426.30	99.60%	3.38%	true	FENKFAVET	99.70%	58.2	542.7704	1 083.53	1 084.53	2</					



cDNA FLJ29296, highly similar to Homo sapiens amyloid beta (A4)-like protein 1 (APLP1), mRNA OS=Homo sapiens PE=2 SV=1	BDRS2.P51693.P51693-2	UniProtKB-HS_20150717_TaD.fasta	72 103.90	100.00%	5.54%	true	FHSSEQRDELAPAGTGVREANSGLLIMGAGGGSL	65.00%	16.8	893.2155	3 588.83	3 589.80	4	0.03813	10.88	560	595	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	DIMGQ2.P6995	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.10%	true	FLASVSTVLSKY	99.70%	79.5	708.3948	1 414.78	1 415.78	2	0.004278	3.022	129	141	true
Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	P02652.VG0YE3.VG0YM3	UniProtKB-HS_20150717_TaD.fasta	11 175.30	100.00%	15.00%	true	FLSYFVELGTQPAT	99.70%	57.6	786.907	1 571.80	1 572.79	2	0.01218	7.543	86	99	true
Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	P02652.VG0YE3.VG0YM3	UniProtKB-HS_20150717_TaD.fasta	11 175.30	99.50%	15.00%	true	FLSYFVELGTQPATQ	99.70%	88.3	850.9378	1 699.86	1 700.85	2	0.01518	8.824	86	100	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	25.20%	true	FMETVAEK	89.00%	34.7	477.7335	953.452468	954.460146	2	-0.0004219	-0.4421	430	437	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	25.20%	true	FMETVAEKALQEVK	99.60%	41.8	572.289	1 713.85	1 714.85	3	0.0005502	3.208	430	443	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	22.00%	true	FMETVAEKALQEVKHHREE	99.70%	65.7	505.2632	2 521.28	2 522.28	5	0.00475	1.883	430	449	true
Serpis peptidase inhibitor, clade A (Alpha-1 antiproteinae, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	A0M24R447	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	10.00%	true	FMGKVVNPQK	69.80%	24.2	624.8384	1 247.66	1 248.68	2	-0.007532	-6.024	408	418	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TaD.fasta	70 942.70	100.00%	18.60%	true	FPVGPKNDDTPNRQ	92.20%	31.6	561.2813	1 680.82	1 681.83	3	-0.0001979	-0.1177	569	583	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TaD.fasta	70 942.70	100.00%	18.60%	true	FPVGPKNDDTPNRQWDEDLMLKYLEYLNQEAKEGHEHA	99.70%	47.3	831.4276	4 982.52	4 983.47	6	0.05517	11.87	569	610	true
Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	A0M24RDE6.P10451-5	UniProtKB-HS_20150717_TaD.fasta	33 843.10	100.00%	18.00%	true	FRISHIELDSASSEVN	99.70%	49.6	564.2727	1 689.80	1 690.80	3	0.0005021	0.2969	286	300	true
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A0XMY6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	97.70%	16.20%	false	FRISHIELDSASSEVN	99.70%	49.6	564.2727	1 689.80	1 690.80	3	0.0005021	0.2969	300	314	false
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G49	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	7.39%	true	FSALVEDIYVPEFN	99.70%	56.7	944.4601	1 886.91	1 887.90	2	0.01178	6.239	512	527	true
Sodium/potassium/calcium exchanger 2 OS=Homo sapiens GN=SLC24A2 PE=1 SV=1	Q9UL40.Q9UL40-2	UniProtKB-HS_20150717_TaD.fasta	73 666.20	99.20%	4.24%	true	FSEITDQSTGEASVSGPRVAQGYHQRT	99.70%	64.2	749.615	2 994.43	2 995.41	4	0.02403	8.021	59	86	true
cDNA FLJ61580, highly similar to Calyptzin-1 OS=Homo sapiens PE=2 SV=1	B4E3Q1.O494985.O49485-2	UniProtKB-HS_20150717_TaD.fasta	107 814.80	100.00%	3.22%	true	FVDSLGHN	84.70%	33.5	444.7159	887.417248	888.421046	2	0.003478	3.915	820	827	true
cDNA FLJ61580, highly similar to Calyptzin-1 OS=Homo sapiens PE=2 SV=1	B4E3Q1.O494985.O49485-2	UniProtKB-HS_20150717_TaD.fasta	107 814.80	100.00%	2.39%	true	FVDSLGHNLANPHPF	99.70%	58.8	832.9173	1 663.82	1 664.82	2	0.009278	5.573	820	834	true
cDNA FLJ61580, highly similar to Calyptzin-1 OS=Homo sapiens PE=2 SV=1	B4E3Q1.O494985.O49485-2	UniProtKB-HS_20150717_TaD.fasta	107 814.80	100.00%	2.39%	true	FVDSLGHNLANPHPFAVVPSTAT	99.70%	66.5	1 196.12	2 390.23	2 391.21	2	0.03148	13.16	820	842	true
cDNA FLJ61580, highly similar to Calyptzin-1 OS=Homo sapiens PE=2 SV=1	B4E3Q1.O494985.O49485-2	UniProtKB-HS_20150717_TaD.fasta	107 814.80	100.00%	3.22%	true	FVHPHHSFVDSLGHNLANPHPFAVVPSTAT	97.60%	30	845.9379	3 379.72	3 380.69	4	0.03743	11.87	812	842	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	25.00%	true	GDFLAEGGGVR	75.00%	25.5	539.2716	1 076.53	1 077.53	2	0.003378	3.135	25	35	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	12.00%	true	GEGDFLAEGGGVR	99.70%	74.2	632.3044	1 262.59	1 263.60	2	0.004878	3.86	23	35	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	17.40%	true	GEVSSPKTHLGEALAPLSKAVGVAAPPFK	86.10%	28.6	1 036.57	3 106.69	3 107.65	3	0.0487	15.67	248	278	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	GENQALMGOSTEELR	90.90%	32	824.4114	1 646.81	1 647.80	2	0.01468	8.968	138	152	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	20.00%	true	GGEEVGEDEEAEEAEAEAEAEERARQNA	99.70%	48.8	808.6048	3 230.39	3 231.39	4	0.006626	2.112	373	402	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	23.40%	true	GGEEVGEDEEAEEAEAEAEERARQNALLFAEEDEGEAGA	99.70%	44.8	1 141.50	4 561.98	4 562.98	4	0.007326	1.606	373	415	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	20.00%	true	GGEEVGEDEEAEEAEAEAEERARQNALLFAEEDEGEAGAE	80.00%	25.5	1 173.37	4 691.03	4 692.02	4	0.02073	4.417	373	416	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	23.40%	true	GGEEVGEDEEAEEAEAEAEERARQNALLFAEEDEGEAGAE	99.10%	118	1 202.53	4 806.07	4 807.05	4	0.02973	6.184	373	417	true
Keratin, type I cytokeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	P35527	UniProtKB-HS_20150717_TaD.fasta	62 065.90	100.00%	3.37%	true	GGGGGGGLSGSGSIRSSY	98.20%	31.6	741.8509	1 481.69	1 482.69	2	0.001078	0.7271	15	32	true
Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	Q1W0D2	UniProtKB-HS_20150717_TaD.fasta	53 008.20	97.70%	6.62%	true	GGSDKSLHNKLSAERPLNQLQAEAEEDI	96.10%	34.1	693.5486	3 402.71	3 403.71	5	0.00875	2.526	24	54	true
Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	P02675.VH0Y1	UniProtKB-HS_20150717_TaD.fasta	55 928.60	100.00%	5.70%	true	GHRPLDKKREEAPSAPPPISGGGVR	98.60%	32	608.5336	3 037.64	3 038.64	5	0.00895	2.945	45	72	true
Apolipoprotein C-II, isoform CRA_a OS=Homo sapiens GN=APOC2 PE=4 SV=1	A0M24R079.KTER74.P02655.VG0Y38	UniProtKB-HS_20150717_TaD.fasta	11 284.10	99.60%	14.90%	true	GIFTDQVLSVKGEE	99.70%	63.2	817.94	1 633.87	1 634.86	2	0.008878	5.43	87	101	true
Transferrin OS=Homo sapiens PE=2 SV=1	A0XGL1.E9KL36.P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	27.70%	true	GISPFHAEVFTANDSGPRRYTHAALLSPYSYSTAVVNPKE	99.70%	41.3	979.5076	4 892.50	4 893.45	5	0.06655	12.37	140	184	true
ATP synthase subunit beta (Fragment) OS=Homo sapiens GN=ATP5B PE=1 SV=1	HYH181.P06576.Q0QEN7.VH0W1	UniProtKB-HS_20150717_TaD.fasta	38 250.20	99.60%	3.87%	true	GIVPVDPLDTSR	99.70%	41	745.8798	1 489.75	1 490.75	2	0.003578	2.4	330	343	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	D9YZU5.P08871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	35.40%	true	GKEFTPPQAVQKVVAGVANALAHKYH	99.70%	67.3	749.411	2 993.61	2 994.59	4	0.02723	9.892	120	147	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G49	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	7.39%	true	GKKLVAASQAALGL	99.70%	54.8	663.9094	1 325.80	1 326.81	2	0.0099781	0.7371	596	609	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	26.20%	true	GLOEAAEERESAREEEEA	94.10%	26.7	678.3087	2 031.90	2 032.91	3	0.006102	3.002	350	367	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	26.20%	true	GLOEAAEERESAREEEATQE	99.70%	41.3	807.023	2 418.05	2 419.05	3	0.005202	2.15	350	370	true
Uncharacterized protein OS=Homo sapiens PE=1 SV=1	Q6GM20	UniProtKB-HS_20150717_TaD.fasta	25 807.40	99.90%	11.90%	false	GLSSPVTKSFNRGEC	63.40%	19.7	527.929	1 580.77	1 581.77	3	0.003402	2.151	222	236	false
Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	A0M87X130	UniProtKB-HS_20150717_TaD.fasta	25 136.10	100.00%	15.60%	false	GLSSPVTKSFNRGEC	63.40%	19.7	527.929	1 580.77	1 581.77	3	0.003402	2.151	217	231	false
HGK0 protein OS=Homo sapiens GN=HGK0 PE=1 SV=1	Q6PF2	UniProtKB-HS_20150717_TaD.fasta	25 528.90	100.00%	15.30%	true	GLSSPVTKSFNRGEC	63.40%	19.7	527.929	1 580.77	1 581.77	3	0.003402	2.151	221	235	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	13.60%	true	GLVEKQVAVGTSAAPVPSDNI	99.10%	28.1	716.3751	2 146.10	2 147.11	3	0.001502	0.6996	296	317	true
Basic salivary proline-rich protein 1 OS=Homo sapiens GN=PRB1 PE=1 SV=2	GTV1M9.G5E9X6.P94280.Q80YA1	UniProtKB-HS_20150717_TaD.fasta	32 456.70	65.90%	3.03%	true	GPPPPPGKPKQ	83.10%	39.6	486.2691	970.523648	971.531246	2	-0.0002319	-0.3314	49	58	true
Proline-rich protein HaellI subfamily 1, isoform CRA_b OS=Homo sapiens GN=PRH1 PE=4 SV=1	A0M24R4Q4.A0M24R4B0.A0M87W42.A0M87WY5.A0M87WY70.A0M87WZ1.A0M87WZ1.P02810	UniProtKB-HS_20150717_TaD.fasta	25 791.70	100.00%	9.43%	true	GPPPPPGKPKQ	99.70%	67.2	534.7966	1 067.58	1 068.58	2	0.001878	1.758	215	225	true
Formin-1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYVM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	99.20%	1.59%	true	GPPPPPPPPP	98.20%	67.6	426.7321	851.449648	852.461746	2	-0.004822	-5.657	822	830	true
Formin-1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYVM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	99.90%	1.67%	true	GPPPPPPPPP	94.40%	52.5	475.2603	948.506048	949.514546	2	-0.001222	-1.287	822	831	true
Proline-rich protein HaellI subfamily 1, isoform CRA_b OS=Homo sapiens GN=PRH1 PE=4 SV=1	A0M24R4Q4.A0M24R4B0.A0M87W42.A0M87WY5.A0M87WY70.A0M87WZ1.A0M87WZ1.P02810	UniProtKB-HS_20150717_TaD.fasta	25 791.70	100.00%	9.43%	true	GPPQGGHFRPP	96.30%	37.4	408.8763	1 223.61	1 224.62	3	-0.003198	-2.611	188	199	true
Transferrin OS=Homo sapiens PE=2 SV=1	A0XGL1.E9KL36.P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	GIPRYTAAALLSPYSYSTAVVNPKE	99.70%	77.6	739.6485	2 954.56	2 955.56	4	0.01463	4.949	158	184	true
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	Q95466.Q95466-2.Q95466-3	UniProtKB-HS_20150717_TaD.fasta	121 858.20	88.30%	1.82%	true	GVPVPPPPP	79.00%	54.4	427.747	853.479448	854.477346	2	0.009378	10.98	599	607	true
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	Q95466.Q95466-2.Q95466-3	UniProtKB-HS_20150717_TaD.fasta	121 858.20	100.00%	1.91%	true	GVPVPPPPP	99.70%	77.6	476.2745</								

Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	20.00%	true	GRPEAQPPPLSSEHKPEPVAGDAPGPKDGSAPGV	99.70%	55.2	851.4293	3 401.69	3 402.69	4	0.002426	0.713	26	59	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	23.40%	true	GRPEAQPPPLSSEHKPEPVAGDAPGPKDGSAPVIRG	98.90%	24.2	603.4775	3 614.82	3 615.82	6	0.01307	3.616	26	61	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	20.00%	true	GRPEAQPPPLSSEHKPEPVAGDAPGPKDGSAPVIRGA	99.70%	92.3	738.1774	3 685.85	3 686.85	5	0.00525	1.424	26	62	true
Proline-rich protein HarIII subfamily 1, isoform CRA_b OS=Homo sapiens GN=PRH1 PE=4 SV=1	A0M2HRQAQ, A0M2HRAR0, A0M8T7WV42, A0M8T7WY5, A0M8T7WY0, A0M8T7WZY1, A0M8MT31, P02810	UniProtKB-HS_20150717_TaD.fasta	25 791.70	99.90%	18.00%	true	GRPGPQGGHQGGHQGGPPPPPGKPGQPPGGKPGQPPGGSPQ	99.70%	40.5	874.6457	4 368.19	4 369.18	5	0.01475	3.376	201	244	true
Hemerythrin OS=Homo sapiens GN=HNR PE=1 SV=2	Q8VZ23	UniProtKB-HS_20150717_TaD.fasta	282 372.70	31.50%	0.46%	true	GSGGWSSSRGVY	76.30%	21.6	642.7863	1 283.56	1 284.56	2	0.004978	3.875	1498	1510	true
cDNA FLJ93426, highly similar to Homo sapiens plasminogen (PLG), mRNA OS=Homo sapiens PE=2 SV=1	B2R7F8, P08747	UniProtKB-HS_20150717_TaD.fasta	90 537.40	33.30%	1.60%	true	GTMSKTKNGITCQ	69.90%	37.2	684.825	1 367.64	1 368.66	2	-0.01852	-13.53	113	125	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	D9YZU5, P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	29.30%	true	GVANALAHKYH	97.60%	54.7	394.2107	1 179.61	1 180.62	3	-0.004598	-3.895	137	147	true
Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	A1N071, P02842	UniProtKB-HS_20150717_TaD.fasta	16 055.20	77.20%	21.10%	false	GVANALAHKYH	84.70%	47.6	394.2106	1 179.61	1 180.62	3	-0.004898	-4.149	137	147	false
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	GYGVGPPQVPEQPLYPQVPPQVQVQY	85.30%	23.5	1 117.21	3 348.61	3 349.55	3	0.0644	19.23	34	61	true
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	GYGVGPPQVPEQPLYPQVPPQVQVQYTF	82.80%	20.3	1 166.23	3 495.68	3 496.62	3	0.068	19.45	34	62	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9LHG2	UniProtKB-HS_20150717_TaD.fasta	27 373.20	100.00%	11.90%	true	HDVGSLLPPEG	80.00%	43.8	568.7647	1 135.51	1 136.52	2	0.0000786	0.06868	224	234	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9LHG2	UniProtKB-HS_20150717_TaD.fasta	27 373.20	100.00%	13.10%	true	HDVGSLLPPEGLGA	99.70%	67	738.8759	1 475.74	1 476.73	2	0.01138	7.765	224	238	true
Proopiomelanocortin receptor GPR37L1 OS=Homo sapiens GN=GPR37L1 PE=1 SV=2	Q68883	UniProtKB-HS_20150717_TaD.fasta	52 778.60	99.90%	4.78%	true	HLGHHBAETQEQSRS	85.90%	28	480.7452	1 918.95	1 919.95	4	0.004626	2.409	29	44	true
Putative Polycomb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	Q9C0F9	UniProtKB-HS_20150717_TaD.fasta	241 918.70	100.00%	1.02%	true	HPFFFFFF	99.10%	61.5	466.7532	931.491848	932.499146	2	-0.00002194	-0.02353	2016	2024	true
cDNA FLJ50735, highly similar to Calyptin-3 OS=Homo sapiens PE=2 SV=1	B4DRB1, BTZ9U4, Q9BQ79	UniProtKB-HS_20150717_TaD.fasta	106 097.30	99.90%	2.30%	true	HRGHPPPMAGHSLASHRS	99.60%	45.7	478.8337	2 389.13	2 390.13	5	0.01145	4.791	821	842	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	25.00%	true	HRHPEAAFFDTASTGK	99.70%	62.9	472.4747	1 885.87	1 886.88	4	-0.001174	-0.6222	511	527	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	12.30%	true	HSGFEDELSEVLENG	99.60%	43.8	866.8908	1 731.77	1 732.77	2	0.008178	4.72	97	111	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	12.30%	true	HSGFEDELSEVLENGSQAEKAEVEPSSKDV	99.70%	101	912.4313	3 645.70	3 646.69	4	0.01533	4.263	97	129	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	7.66%	true	HSGFEDELSEVLENGSQAEKAEVEPSSKDVDM	99.70%	97.2	945.1998	3 776.77	3 777.73	4	0.04883	12.92	97	130	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	12.00%	true	HSGFEDELSEVLENGSQAEKAEVEPSSKDVME	99.70%	133	977.4596	3 905.81	3 906.77	4	0.04543	11.63	97	131	true
CD99 antigen-like 2, isoform CRA_d OS=Homo sapiens GN=CD99L2 PE=4 SV=1	A0M24RC16, Q8TCZ2, Q8TCZ2-2, Q8TCZ2-3, Q8TCZ2-5	UniProtKB-HS_20150717_TaD.fasta	27 998.30	97.50%	6.11%	true	HTQSALPPPPPEARI	98.50%	30.9	575.3042	1 722.89	1 723.88	3	0.0216	12.53	247	262	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909, P10909-2, P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	20.00%	true	HTSDSDVPSGVTE	99.70%	46	665.795	1 329.58	1 330.58	2	0.006878	5.169	392	404	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909, P10909-2, P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.80%	true	HTSDSDVPSGVTEV	99.70%	62.2	715.3288	1 428.64	1 429.64	2	0.006678	4.251	392	405	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909, P10909-2, P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.80%	true	HTSDSDVPSGVTEVV	88.80%	26.4	764.868	1 527.72	1 528.71	2	0.01608	10.52	392	406	true
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	P61769	UniProtKB-HS_20150717_TaD.fasta	13 714.90	100.00%	30.30%	true	HVYLSQPKVWDRDM	99.70%	105	651.6888	1 952.05	1 953.04	3	0.0171	8.757	104	119	true
Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	P01861	UniProtKB-HS_20150717_TaD.fasta	35 939.50	99.30%	3.67%	true	HYTQKSLSLSG	99.70%	63.5	667.3621	1 332.71	1 333.71	2	0.005778	4.332	315	326	true
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0M8T7WV47, A0M8T7WY1, A0M8T7X010, V9HW8	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	HYTQKSLSLSPG	99.70%	88.9	659.3465	1 316.68	1 317.68	2	0.005878	4.461	454	465	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	91.30%	13.60%	false	HYTQKSLSLSPG	99.70%	88.9	659.3465	1 316.68	1 317.68	2	0.005878	4.461	460	471	false
Putative uncharacterized protein DKFZp686G11190 OS=Homo sapiens GN=DKFZp686G11190 PE=2 SV=1	Q6M2Q6	UniProtKB-HS_20150717_TaD.fasta	52 042.10	98.40%	4.42%	false	HYTQKSLSLSPG	97.00%	36.8	439.8989	1 316.67	1 317.68	3	0.002302	1.747	463	474	false
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0M8T7WV47, A0M8T7WY1, A0M8T7X010, V9HW8	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	HYTQKSLSLSPGK	99.70%	62.6	482.5971	1 444.77	1 445.77	3	0.001902	1.316	454	466	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	91.30%	13.60%	false	HYTQKSLSLSPGK	99.70%	62.6	482.5971	1 444.77	1 445.77	3	0.001902	1.316	460	472	false
Transferrin OS=Homo sapiens PE=2 SV=1	A6NGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	LAALLSPYSSTAVTNPKE	99.70%	87.6	1 113.10	2 224.18	2 225.17	2	0.02068	9.293	164	184	true
Isiorm 2 of Neural cell adhesion molecule 1L1 like protein OS=Homo sapiens GN=CHL1	Q8833-2	UniProtKB-HS_20150717_TaD.fasta	136 708.50	99.50%	1.31%	true	IEEPSVQQVPTHQ	99.70%	52.4	890.5219	1 779.63	1 780.62	2	0.01478	8.302	25	40	true
S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	B4DEX1, P11153	UniProtKB-HS_20150717_TaD.fasta	43 660.90	99.60%	3.29%	true	IGGPGQDAGLGTGR	99.70%	56.8	599.8128	1 197.61	1 198.62	2	0.0004781	0.3988	252	264	true
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	IGRFYGVGPPVPEQP	99.70%	58.3	1 013.02	2 024.02	2 024.99	2	0.03798	18.75	30	47	true
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	IGRFYGVGPPVPEQPLYPQVPPQVQVQ	96.50%	34	1 186.93	3 537.77	3 538.71	3	0.0693	19.47	30	59	true
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	IGRFYGVGPPVPEQPLYPQVPPQVQVQVQ	89.40%	25.1	1 241.29	3 720.84	3 721.78	3	0.074	19.88	30	60	true
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	IGRFYGVGPPVPEQPLYPQVPPQVQVQYTF	97.80%	34.7	993.2457	3 968.95	3 969.89	4	0.06943	17.49	30	62	true
Chatterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909, P10909-2, P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	22.00%	true	HIDELFQDRF	97.90%	41.2	648.3347	1 294.65	1 295.66	2	-0.001122	-0.8659	186	195	true
Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=1	C9C84, C9EUS, P02679, P02679-2	UniProtKB-HS_20150717_TaD.fasta	52 339.20	99.90%	5.42%	true	IKAQLYNPDESSKPNMIDAATLK	79.10%	25.2	921.1455	2 760.41	2 761.44	3	-0.0225	-8.147	87	111	true
E3-16 OS=Homo sapiens PE=2 SV=1	Q7Z528, Q9NX12, Q9Y287	UniProtKB-HS_20150717_TaD.fasta	30 426.30	100.00%	12.40%	true	IKDDVILNEPSADAPAA	93.70%	32.5	869.9524	1 737.89	1 738.89	2	0.01148	6.601	94	110	true
Haploglobin OS=Homo sapiens GN=HP PE=1 SV=4	HHY300	UniProtKB-HS_20150717_TaD.fasta	49 105.50	100.00%	5.20%	true	ILGGHLDKRG	72.10%	36.2	490.7807	979.546848	980.552646	2	0.001478	1.507	198	207	true
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	HKV28, O60610, O60610-2, O60610-3, Q6URC4	UniProtKB-HS_20150717_TaD.fasta	136 857.50	96.00%	2.28%	false	IPPPPPP	63.10%	35.5	357.712	713.409448	714.418746	2	-0.002022	-2.83	643	649	false
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	P61769	UniProtKB-HS_20150717_TaD.fasta	13 714.90	100.00%	36.10%	true	IQRTPKIQVY	77.90%	20.2	623.369	1 244.72	1 245.73	2	-0.0008219	-0.6598	21	30	true
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	P61769	UniProtKB-HS_20150717_TaD.fasta	13 714.90	100.00%	30.30%	true	IQRTPKIQVYSRHPAEN	99.70%	52	510.0319	2 036.10	2 037.10	4	0.006826	3.351	21	37	true
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	P61769	UniProtKB-HS_20150717_TaD.fasta	13 714.90	100.00%	36.10%	true	IQRTPKIQVYSRHPAENGKSNFLN	85.90%	21.1	467.0891	2 796.49	2 797.49	6	0.01247	4.459	21	44	true
Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein L, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	A0M24RDE6, P10451-5	UniProtKB-HS_20150717_TaD.fasta	33 843.10	100.00%	17.30%	true	ISHELDSASSEVN	99.70%	100	694.3225	1 386.63	1 387.63	2	0.004178	3.011	288	300	true
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A6NMY6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	99.60%	17.20%	false	ISHELDSASSEVN	99.70%	100	694.3225	1 386.63	1 387.63	2	0.004178	3.011	302	314	false
cDNA FLJ37323, highly similar to Synaptotagmin-																		

Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	P01024,VHWNA9	UniProtKB-HS_20150717_TaD.fasta	187 149.10	100.00%	1.02%	true	KTHRHIVESASLLR	83.60%	25.3	462.5156	1 846.03	1 847.04	4	0.0006261	0.339	1306	1320	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	KKLVAASQAALG	96.30%	40.8	386.239	1 155.70	1 156.70	3	-0.002498	-2.16	597	608	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	5.91%	true	KKLVAASQAALG	99.70%	84.4	635.3971	1 268.78	1 269.79	2	-0.002122	-1.671	597	609	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	6.08%	true	KLVAASQAALG	96.90%	46.1	514.8102	1 027.61	1 028.61	2	0.003178	3.09	598	608	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	6.08%	true	KLVAASQAALGL	99.70%	87.2	571.3528	1 140.69	1 141.69	2	0.004278	3.747	598	609	true
Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) OS=Homo sapiens GN=AGT PE=3 SV=1	B0ZBE2,B2R5S1,B4DE80,B4E1B3,P01019,Q53YV1,Q9HEP2,Q86U78	UniProtKB-HS_20150717_TaD.fasta	53 154.80	100.00%	7.84%	true	KPEVLEVLNRPFLFAVYDQSATALHFLGRVANPLSTA	99.70%	72.2	1 047.08	4 184.27	4 185.25	4	0.03243	7.748	448	485	true
Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinasae, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	A0M24R847	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	9.57%	true	KPFVFLMIEQN	99.70%	40	683.3674	1 364.72	1 365.72	2	0.003878	2.84	392	402	true
Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinasae, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	A0M24R847	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	10.00%	true	KPFVFLMEQNTKSLPFLMGKVNPTQK	99.70%	147	1 041.24	3 120.69	3 121.69	3	0.005002	1.602	392	418	true
Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	Q9W0D2	UniProtKB-HS_20150717_TaD.fasta	53 008.20	79.80%	7.85%	true	KPGGSGQKSLHNRELSAERPLNEQAEAEEDKI	75.00%	16.7	738.5841	3 687.88	3 688.85	5	0.03845	10.42	22	54	true
cDNA FLJ4595 fs, clone BLADE2004849 OS=Homo sapiens PE=2 SV=1	Q6ZTJ3	UniProtKB-HS_20150717_TaD.fasta	32 450.70	99.80%	3.57%	true	KPPPPPPPP	95.50%	61.7	402.271	922.527448	923.535246	2	-0.0005219	-0.5652	165	173	true
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	PIC0L4,PIC0L4-2	UniProtKB-HS_20150717_TaD.fasta	192 786.80	100.00%	3.56%	true	KPRLLLSPSVVHLGVLPSVGLQDVPKGVKGVFLFN	99.70%	66.1	740.1073	4 434.60	4 435.58	6	0.02517	5.721	20	60	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	25.00%	true	KPVPDLVPGN	74.60%	29	518.2959	1 034.58	1 035.58	2	0.0009781	0.9455	227	236	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	18.90%	true	KPVPDLVPGNF	99.70%	56.3	591.8309	1 181.65	1 182.65	2	0.002578	2.18	227	237	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	14.90%	true	KPVPDLVPGNFK	99.70%	75.5	655.8784	1 309.74	1 310.75	2	0.002578	1.967	227	238	true
Fibrinogen beta chain OS=Homo sapiens GN=FBG PE=1 SV=2	P02675,VHWY1	UniProtKB-HS_20150717_TaD.fasta	55 928.60	100.00%	4.28%	true	KREEAPSLRPAPPPISGGGY	83.80%	25.2	693.7085	2 078.10	2 079.10	3	0.0125	6.013	52	71	true
Fibrinogen beta chain OS=Homo sapiens GN=FBG PE=1 SV=2	P02675,VHWY1	UniProtKB-HS_20150717_TaD.fasta	55 928.60	100.00%	5.70%	true	KREEAPSLRPAPPPISGGGYR	99.70%	71	559.5565	2 234.20	2 235.20	4	0.004026	2.07	52	72	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	6.62%	true	KVQAVETEPEPEL	99.70%	55	799.4056	1 596.80	1 597.80	2	0.008178	5.118	19	32	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	KVQAVETEPEPELR	99.70%	62.9	585.3056	1 752.89	1 753.90	3	0.005402	3.08	19	33	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	17.00%	true	KVQAVETEPEPELRQ	78.50%	33.8	627.9925	1 880.96	1 881.96	3	0.007502	3.886	19	34	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	6.62%	true	KVQAVETEPEPELRQQ	99.70%	55.5	670.6796	2 009.02	2 010.01	3	0.0102	5.076	19	35	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	13.60%	true	KVQAVETEPEPELRQTEWQ	99.70%	49.1	852.0884	2 553.24	2 554.24	3	0.008402	3.289	19	39	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	D9YZU5,P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	21.10%	true	KVLGAFSDGLAHLDNLK	99.70%	87.3	600.0026	1 796.99	1 797.99	3	0.007202	4.006	67	83	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	9.69%	true	KVQVSTPTLVEYSR	90.60%	29.1	547.3193	1 638.94	1 639.94	3	0.005502	3.355	438	452	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	D9YZU5,P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	38.80%	true	KVAGVANALAHKYH	86.50%	21.9	395.2283	1 576.88	1 577.89	4	0.0003261	0.2066	133	147	true
Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	A0N071,P02042	UniProtKB-HS_20150717_TaD.fasta	16 055.20	34.70%	21.10%	false	KVAGVANALAHKYH	86.50%	21.9	395.2283	1 576.88	1 577.89	4	0.0003261	0.2066	133	147	false
Ig lambda-7 chain C region (Fragment) OS=Homo sapiens GN=IGLC7 PE=1 SV=2	A0M7586L1	UniProtKB-HS_20150717_TaD.fasta	11 307.00	96.20%	40.60%	true	KYASSYLSLTPQWKSHRSYSCRVTHEGSTEKVTAPAEC	89.20%	22.4	935.6602	4 673.26	4 674.24	5	0.03675	7.862	65	106	true
cDNA FLJ61580, highly similar to Calyptin-1 OS=Homo sapiens PE=2 SV=1	BHE3QLQ494985,Q94985-2	UniProtKB-HS_20150717_TaD.fasta	107 814.80	100.00%	3.22%	true	LANPHFPAVVPSTAT	80.90%	32.3	761.4127	1 520.81	1 521.81	2	0.01208	7.937	828	842	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	LAVYQAGAREGAER	89.20%	31.1	497.5952	1 489.76	1 490.77	3	0.00002058	0.001381	177	190	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P09060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	100.00%	18.20%	true	LDRNVLNYGEEGAPKWKQQDGLQDTKFNREARFQDKQYSHHTAE	94.20%	31.8	928.6031	5 565.57	5 566.57	6	0.01407	2.69	407	513	true
Xylyltransferase 1 OS=Homo sapiens GN=XYLT1 PE=1 SV=1	Q86Y38	UniProtKB-HS_20150717_TaD.fasta	107 571.00	97.30%	3.02%	true	LDSGAGERGGGAAGGGEQPPAPARRI	83.10%	24.1	563.2894	2 811.41	2 812.42	5	-0.00225	-0.8	38	66	true
Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinasae, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	A0M24R847	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	10.00%	true	LEAPMSIPPEVFNKPFVFLMEQNTKSLPFLMGKVNPTQK	99.70%	52.4	798.7705	4 786.58	4 787.57	6	0.01197	2.501	377	418	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	12.30%	true	LEGQEEEDNRSSMKLSIF	88.00%	17.8	748.3336	2 241.98	2 242.98	3	0.009202	4.103	358	376	true
Chromogranin-A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	UniProtKB-HS_20150717_TaD.fasta	50 688.10	100.00%	12.30%	true	LEGQEEEDNRSSMKLSIFRA	99.20%	28.1	618.2834	2 469.11	2 470.12	4	0.004526	1.832	358	378	true
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	20.00%	true	LEMHIEAQQAMDHF	99.70%	43.2	604.9521	1 811.83	1 812.84	3	0.0008021	0.4424	248	262	true
cDNA FLJ75574, highly similar to Homo sapiens preproenkephalin (PNOCK), mRNA OS=Homo sapiens PE=2 SV=1	AK0RKL7EYV9,Q13519,Q13519-2,Q98YY3	UniProtKB-HS_20150717_TaD.fasta	20 279.40	98.60%	12.50%	true	LFQEQEPEPEMEAGEMEQQK	98.50%	35.6	865.0433	2 592.11	2 593.11	3	0.008102	3.124	104	125	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	LGPLVEQGR	96.80%	60.6	484.7801	967.545648	968.552546	2	0.0003781	0.3903	199	207	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	LGPLVEQGRV	83.30%	41.5	534.3153	1 066.62	1 067.62	2	0.002378	2.227	199	208	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1,E9K136,P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	LSPSYSTTAVVTPKE	99.70%	113	985.5165	1 969.02	1 970.01	2	0.01398	7.095	167	184	true
Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	A0M24RDE6,P10451-5	UniProtKB-HS_20150717_TaD.fasta	33 843.10	99.90%	13.00%	true	LNAPSDWDSRGKDSYETSQLDQQAETHSHKQS	96.00%	57.3	744.7403	3 718.67	3 719.64	5	0.02805	7.541	197	229	true
cDNA FLJ57844, highly similar to Serum paraoxonase/arylesterase 1 (EC 3.1.1.2) OS=Homo sapiens PE=2 SV=1	B4DX19,P27169	UniProtKB-HS_20150717_TaD.fasta	39 722.00	68.20%	2.54%	true	LNDVAVGP	78.40%	52.6	449.2598	896.505048	897.504146	2	0.008178	9.112	167	175	true
Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	Q9W0D2	UniProtKB-HS_20150717_TaD.fasta	53 008.20	85.60%	2.78%	true	LNQQAIAEEDKI	80.00%	45.9	751.3797	1 580.74	1 581.74	2	0.01388	9.241	42	54	true
Ras association (RaGDS/AF-6) and pleckstrin homology domains 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K005	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.08%	true	LPPPPPPP	63.20%	43.1	357.7106	713.406648	714.418746	2	-0.004822	-6.75	680	686	true
Formin 1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30,Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	74.60%	1.59%	false	LPPPPPPP	63.20%	43.1	357.7106	713.406648	714.418746	2	-0.004822	-6.75	805	811	false
Putative Polycarb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	Q9C0F0	UniProtKB-HS_20150717_TaD.fasta	241 918.70	91.30%	0.98%	false	LPPPPPPP	63.20%	43.1	357.7106	713.406648	714.418746	2	-0.004822	-6.75	2031	2037	false
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	2.39%	false	LPPPPPPP	63.20%	43.1	357.7106	713.406648	714.418746	2	-0.004822	-6.75	680	686	false
Espin OS=Homo sapiens GN=ESPN PE=1 SV=1	B1AK53	UniProtKB-HS_20150717_TaD.fasta	91 733.40	67.80%	2.34%	false	LPPPPPPP	66.00%	40.7	357.7121	713.409648	714.418746	2	-0.001822	-2.55	595	601	false
Isiorm 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	67.90%	2.06%	false	LPPPPPPP	66.00%	40.7	357.7121	713.409648	714.418746	2	-0.001822	-2.55	1501	1507	false
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	O95466,O95466-2,O95466-3	UniProtKB-HS_20150717_TaD.fasta	121 858.20	64.20%	1.91%	false	LPPPPPPP	66.00%	40.7	357.7121	713.409648	714.418746	2	-0.001822	-2.55	584	590	false
Putative Polycarb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	Q9C0F0	UniProtKB-HS_20150717_TaD.fasta	241 918.70	100.00%	1.02%	false												

Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	O95466.O95466-2.O95466-3	UniProtKB-HS_20150717_TnD.fasta	121 858.20	93.80%	2.80%	false	LPPPPPPPP	77.10%	41.8	454.7656	907.516648	908.524346	2	-0.0004219	-0.4644	584	592	false	C9K0J5
Epsin OS=Homo sapiens GN=ESPN PE=1 SV=1	BLAK53	UniProtKB-HS_20150717_TnD.fasta	91 733.40	100.00%	2.81%	false	LPPPPPPPP	77.10%	41.8	454.7656	907.516648	908.524346	2	-0.0004219	-0.4644	595	603	false	C9K0J5
Ras association (RaGDS/AF-6) and pleckstrin homology domains 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TnD.fasta	141 180.90	99.60%	1.00%	true	LPPPPPPPP	88.70%	55	503.2907	1 004.57	1 005.58	2	-0.003022	-3.005	680	689	true	C9K0J5
Formin-1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30.Q6IDA7	UniProtKB-HS_20150717_TnD.fasta	146 508.90	79.20%	1.51%	false	LPPPPPPPP	88.70%	55	503.2907	1 004.57	1 005.58	2	-0.003022	-3.005	805	814	false	C9K0J5
Epsin OS=Homo sapiens GN=ESPN PE=1 SV=1	BLAK53	UniProtKB-HS_20150717_TnD.fasta	91 733.40	78.50%	2.34%	false	LPPPPPPPP	88.70%	55	503.2907	1 004.57	1 005.58	2	-0.003022	-3.005	595	604	false	C9K0J5
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	O95466.O95466-2.O95466-3	UniProtKB-HS_20150717_TnD.fasta	121 858.20	92.80%	1.91%	false	LPPPPPPPP	92.60%	53.2	503.293	1 004.57	1 005.58	2	0.001578	1.569	584	593	false	C9K0J5
Putative Polycarb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	QC0IF0	UniProtKB-HS_20150717_TnD.fasta	241 918.70	99.40%	1.07%	false	LPPPPPPPP	92.60%	53.2	503.293	1 004.57	1 005.58	2	0.001578	1.569	2031	2040	false	C9K0J5
Ras association (RaGDS/AF-6) and pleckstrin homology domains 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TnD.fasta	141 180.90	100.00%	1.69%	true	LPPPPPPPP	85.70%	41.9	551.8211	1 101.63	1 102.63	2	0.004978	4.515	680	690	true	C9K0J5
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	O95466.O95466-2.O95466-3	UniProtKB-HS_20150717_TnD.fasta	121 858.20	92.80%	1.91%	false	LPPPPPPPP	85.70%	41.9	551.8211	1 101.63	1 102.63	2	0.004978	4.515	584	594	false	C9K0J5
Epsin OS=Homo sapiens GN=ESPN PE=1 SV=1	BLAK53	UniProtKB-HS_20150717_TnD.fasta	91 733.40	71.00%	2.34%	false	LPPPPPPPP	85.70%	41.9	551.8211	1 101.63	1 102.63	2	0.004978	4.515	595	605	false	C9K0J5
Tiamatin OS=Homo sapiens PE=2 SV=1	AMKGL1.E9KL36.P02766	UniProtKB-HS_20150717_TnD.fasta	20 198.60	100.00%	15.80%	true	LSPPSYSTAVVTPKE	99.70%	83	928.9738	1 855.93	1 856.93	2	0.01268	6.827	168	184	true	C9K0J5
cDNA FLJ35342, highly similar to Homo sapiens solute carrier family 12, (potassium-chloride transporter) member 5 (SLC12A5), mRNA OS=Homo sapiens PE=2 SV=1	AKK143.Q9H2X8.Q9H2X8-2	UniProtKB-HS_20150717_TnD.fasta	123 484.00	37.80%	1.88%	true	LTVTKDKVAEKNKGPSSS	65.10%	27.4	1 130.10	2 228.19	2 229.20	2	0.002578	1.141	1006	1026	true	C9K0J5
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TnD.fasta	69 084.60	100.00%	5.91%	true	LVASQAALGL	86.70%	36.8	507.3047	1 012.59	1 013.60	2	0.003078	3.037	599	609	true	C9K0J5
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TnD.fasta	69 084.60	100.00%	9.69%	true	LVNVEVFAK	99.70%	59.1	575.3128	1 148.61	1 149.62	2	0.003278	2.851	66	75	true	C9K0J5
Serum albumin OS=Homo sapiens PE=2 SV=1	Q56G89	UniProtKB-HS_20150717_TnD.fasta	69 084.60	100.00%	9.69%	true	LVIIDLK	90.00%	46.9	395.2376	788.400648	789.471846	2	-0.003922	-4.968	258	264	true	C9K0J5
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TnD.fasta	69 756.90	100.00%	17.70%	true	LVTSGDKELR	99.70%	64.7	415.9088	1 244.70	1 245.72	3	-0.004498	-3.611	433	443	true	C9K0J5
cDNA FLJ1580, highly similar to Calystegalin-1 OS=Homo sapiens PE=2 SV=1	BHE3Q1.O94985.O94985-2	UniProtKB-HS_20150717_TnD.fasta	107 814.80	100.00%	3.85%	true	MAQPQVHPEHRSFDLSGHNLANPHFVAVPSTAT	97.60%	29.8	1 002.51	4 006.00	4 006.98	4	0.03313	8.267	806	842	true	C9K0J5
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TnD.fasta	69 756.90	100.00%	14.90%	true	MADAEAGSEADHEGTHSTKRGHA	99.60%	36.2	459.6041	2 292.98	2 293.99	5	0.00615	2.681	603	624	true	C9K0J5
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TnD.fasta	69 756.90	100.00%	14.90%	true	MADAEAGSEADHEGTHSTKRGHAKSRPV	99.50%	27.8	573.0743	2 860.34	2 861.33	5	0.00785	2.743	603	629	true	C9K0J5
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	19.60%	true	METVAEKALQEVKKHREE	98.40%	35.8	594.5615	2 374.22	2 375.21	4	0.01043	4.39	431	449	true	C9K0J5
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TnD.fasta	69 756.90	100.00%	17.70%	true	MKPPDVLVPCNF	98.10%	42.8	657.3524	1 312.69	1 313.69	2	0.005078	3.865	226	237	true	C9K0J5
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TnD.fasta	69 756.90	100.00%	12.30%	true	MKPPDVLVPCNFK	99.70%	80.8	721.3987	1 440.78	1 441.79	2	0.002678	1.857	226	228	true	C9K0J5
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TnD.fasta	67 257.90	100.00%	17.40%	true	NAPPEVPPPR	98.30%	58.3	585.818	1 169.62	1 170.63	2	0.001978	1.69	485	495	true	C9K0J5
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TnD.fasta	67 257.90	100.00%	23.40%	true	NAPPEVPPRAAPATHV	99.70%	60.7	639.0122	1 914.01	1 915.02	3	0.003402	1.777	485	503	true	C9K0J5
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TnD.fasta	67 257.90	100.00%	23.40%	true	NAPPEVPPRAAPATHVRSQPMPAPARDELDP	98.30%	34.8	758.6129	3 788.03	3 789.00	5	0.02665	9.646	485	521	true	C9K0J5
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TnD.fasta	67 257.90	100.00%	23.40%	true	NAPPEVPPRAAPATHVRSQPMPAPARDELDPD	99.70%	43.1	781.6129	3 903.03	3 904.03	5	0.00955	2.446	485	522	true	C9K0J5
E3-18 OS=Homo sapiens PE=2 SV=1	Q72528.Q9N312.Q9Y287	UniProtKB-HS_20150717_TnD.fasta	30 426.30	100.00%	12.40%	true	NCFARIH	90.00%	35.3	430.7137	859.412848	860.419546	2	0.0005781	0.6718	247	253	true	C9K0J5
Fibrinogen beta chain OS=Homo sapiens GN=FBG PE=1 SV=2	P02675.W9HYV1	UniProtKB-HS_20150717_TnD.fasta	55 928.60	100.00%	8.55%	true	NDNEEGFFSAR	90.70%	33.7	643.2779	1 284.54	1 285.54	2	0.004178	3.25	34	44	true	C9K0J5
Ig lambda-7 chain C region (Fragment) OS=Homo sapiens GN=IGLC7 PE=1 SV=2	A0M07586L1	UniProtKB-HS_20150717_TnD.fasta	11 307.00	96.20%	40.60%	true	NKYAASYSLSLTPQWKSHSYSCRVTHEGTVKTVAPACIS	61.10%	19	958.4655	4 787.29	4 788.28	5	0.02015	4.25	64	106	true	C9K0J5
Secretory granule, neuroendocrine protein 1 (7B2 protein), isoform CRA_a OS=Homo sapiens GN=SGNE1 PE=4 SV=1	A0M24R0H1.P05408.P05408-2	UniProtKB-HS_20150717_TnD.fasta	23 729.90	100.00%	14.60%	true	NPYLQGGRLDNYVA	98.80%	35	793.9204	1 585.83	1 586.83	2	0.004878	3.074	184	197	true	C9K0J5
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TnD.fasta	67 257.90	100.00%	17.40%	true	NSEPDQEGELFGVDR	99.70%	59.3	958.9419	1 915.87	1 916.86	2	0.01418	7.396	64	80	true	C9K0J5
Cell adhesion molecule 3 OS=Homo sapiens GN=CADM3 PE=1 SV=1	Q9N126.Q9N126-2.Q9N126-3	UniProtKB-HS_20150717_TnD.fasta	43 308.70	100.00%	4.77%	true	NVNDSPVSPSSST	99.70%	48.1	684.3222	1 386.63	1 387.63	2	0.003578	2.579	315	328	true	C9K0J5
Cell adhesion molecule 3 OS=Homo sapiens GN=CADM3 PE=1 SV=1	Q9N126.Q9N126-2.Q9N126-3	UniProtKB-HS_20150717_TnD.fasta	43 308.70	100.00%	4.77%	true	NVNDSPVSPSSSTYHA	99.70%	59.4	586.9318	1 757.79	1 758.79	3	0.00002018	0.00117	315	331	true	C9K0J5
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	P0C0L4.P0C0L4-2	UniProtKB-HS_20150717_TnD.fasta	192 786.80	100.00%	2.12%	true	NVNFQKAINELGQYA	98.60%	40.3	918.9893	1 835.96	1 836.96	2	0.01098	5.976	680	695	true	C9K0J5
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05960	UniProtKB-HS_20150717_TnD.fasta	78 276.10	100.00%	14.60%	true	NYPSLELDKMAHG	90.90%	24.9	492.2396	1 473.70	1 474.70	3	0.004602	3.121	388	400	true	C9K0J5
Isoform 3 of Insulin-like growth factor II OS=Homo sapiens GN=IGF2	P01344-3	UniProtKB-HS_20150717_TnD.fasta	26 338.80	93.70%	5.51%	true	PAHGAPPHEMANS	96.70%	46.7	618.2812	1 234.55	1 235.55	2	0.007678	6.214	222	234	true	C9K0J5
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDC1 PE=1 SV=2	QC0ID6	UniProtKB-HS_20150717_TnD.fasta	124 764.70	100.00%	2.01%	false	PAPPPPPPP	90.50%	45.4	433.7424	865.470248	866.477346	2	0.0001781	0.2055	32	40	false	C9K0J5
Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1	Q9UMN6	UniProtKB-HS_20150717_TnD.fasta	293 512.20	96.60%	0.99%	false	PAPPPPPPP	90.50%	45.4	433.7424	865.470248	866.477346	2	0.0001781	0.2055	2251	2259	false	C9K0J5
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M10M0W5.Q96Q04	UniProtKB-HS_20150717_TnD.fasta	157 098.90	94.20%	1.48%	false	PAPPPPPPP	90.50%	45.4	433.7424	865.470248	866.477346	2	0.0001781	0.2055	780	788	false	C9K0J5
Ras association (RaGDS/AF-6) and pleckstrin homology domains 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TnD.fasta	141 180.90	100.00%	1.77%	true	PAPPPPPPP	90.50%	45.4	433.7424	865.470248	866.477346	2	0.0001781	0.2055	988	996	true	C9K0J5
Nucleosome-remodelling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3	Q12830.Q12830-4	UniProtKB-HS_20150717_TnD.fasta	338 256.30	67.60%	0.62%	false	PAPPPPPPP	77.30%	41.6	433.7412	865.467848	866.477346	2	-0.002222	-2.564	22	30	false	C9K0J5
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDC1 PE=1 SV=2	QC0ID6	UniProtKB-HS_20150717_TnD.fasta	124 764.70	100.00%	1.05%	true	PAPPPPPPP	99.70%	56.6	482.2697	962.524848	963.530146	2	0.001978	2.053	32	41	true	C9K0J5
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M10M0W5.Q96Q04	UniProtKB-HS_20150717_TnD.fasta	157 098.90	92.40%	1.48%	false	PAPPPPPPP	91.90%	52.9	482.2689	962.523248	963.530146	2	0.0003781	0.3924	780	789	false	QC0ID6
Nucleosome-remodelling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3	Q12830.Q12830-4	UniProtKB-HS_20150717_TnD.fasta	338 256.30	67.60%	0.62%	false	PAPPPPPPP	94.70%	43.9	482.2686	962.522648	963.530146	2	-0.0002219	-0.2303	22	31	false	QC0ID6
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDC1 PE=1 SV=2	QC0ID6	UniProtKB-HS_20150717_TnD.fasta	124 764.70	100.00%	2.01%	true	PAPPPPPPPPP	97.10%	60.9	579.3221	1 156.63	1 157.64	2	0.001178	1.018	32	43	true	C9K0J5
Isoform H7 of Myeloperoxidase OS=Homo sapiens GN=MPO	P05164-3	UniProtKB-HS_20150717_TnD.fasta	87 251.00	57.40%	1.54%	true	PAGLVNLSKSSG	72.70%	31.5	600.8221	1 199.63	1 200.66	2	-0.02142	-17.84	146	157	true	C9K0J5
Similar to Kruppel-like factor 2 (Lang) (Fragment) OS=Homo sapiens PE=2 SV=1	QHUNA.Q9Y5W3	UniProtKB-HS_20150717_TnD.fasta	22 707.90	75.40%	8.48%	false	PEPPPPPPPP	66.00%	37.5	511.271	1 020.53	1 02							

Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909.P10909-2.P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.20%	true	PKFMETVAEKALQEVKHKHREE	99.70%	92	550.2926	2 746.43	2 747.43	5	0.00395	1.438	428	449	true
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	P61769	UniProtKB-HS_20150717_TaD.fasta	13 714.90	100.00%	30.30%	true	PKIKWDRDMD	96.40%	31	429.9016	1 286.68	1 287.69	3	0.00202	1.71	110	119	true
cDNA FLJ4595 fs. clone BLADE2064849 OS=Homo sapiens PE=2 SV=1	QZGTJ3	UniProtKB-HS_20150717_TaD.fasta	32 458.70	99.80%	3.57%	true	PKVFPFPPPP	95.50%	61.7	462.271	922.527448	923.532346	2	-0.0005219	-0.5632	164	172	true
Serpine peptidase inhibitor, clade A (Alpha-1 antitrypsin, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	A0M2R847	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	12.20%	true	PLFMGKVVNPTQK	87.00%	30.9	486.9423	1 457.81	1 458.81	3	-0.001598	-1.095	406	418	true
Ras association (RaGDS/AF-6) and plectrolin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.08%	true	PLPFPFPP	63.20%	43.1	357.7106	713.406648	714.418746	2	-0.004822	-6.75	679	685	true
Formin 1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	74.60%	1.59%	false	PLPFPFPP	63.20%	43.1	357.7106	713.406648	714.418746	2	-0.004822	-6.75	804	810	false
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	2.39%	false	PLPFPFPP	63.20%	43.1	357.7106	713.406648	714.418746	2	-0.004822	-6.75	679	685	false
isoform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	67.90%	2.06%	false	PLPFPFPP	66.00%	40.7	357.7121	713.409648	714.418746	2	-0.001822	-2.55	1500	1506	false
Ras association (RaGDS/AF-6) and plectrolin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.69%	true	PLPFPFPPPP	90.80%	43	454.7657	907.516848	908.524346	2	-0.0002219	-0.2443	679	687	true
Formin 1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	99.20%	1.51%	false	PLPFPFPPPP	90.80%	43	454.7657	907.516848	908.524346	2	-0.0002219	-0.2443	804	812	false
Ras association (RaGDS/AF-6) and plectrolin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	99.60%	1.00%	true	PLPFPFPPPPPP	88.70%	55	503.2907	1 004.57	1 005.58	2	-0.003022	-3.005	679	688	true
Formin 1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	79.20%	1.51%	false	PLPFPFPPPPPP	88.70%	55	503.2907	1 004.57	1 005.58	2	-0.003022	-3.005	804	813	false
Ras association (RaGDS/AF-6) and plectrolin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.69%	true	PLPFPFPPPPPPPP	85.70%	41.9	551.8211	1 101.63	1 102.63	2	0.004978	4.515	679	689	true
Formin 1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	98.90%	1.67%	false	PLPFPFPPPPPPPP	85.70%	41.9	551.8211	1 101.63	1 102.63	2	0.004978	4.515	804	814	false
Thymosin beta 4_X linked OS=Homo sapiens GN=TMSB4X PE=2 SV=1	A7VCKK.P62328.Q0P5N1.Q0P5P4.Q0P5Q6.Q0P5T0.Q0P5U7	UniProtKB-HS_20150717_TaD.fasta	5 052.90	98.80%	38.60%	true	PLSKETIEQEKGAGES	99.60%	45.6	624.3204	1 869.94	1 870.94	3	0.007102	3.796	28	44	true
Statlerin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	PLYPQYQYQYQYQY	92.60%	30.1	957.4723	1 912.93	1 913.91	2	0.003028	15.82	47	61	true
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M6M0QW5.Q96Q04	UniProtKB-HS_20150717_TaD.fasta	157 098.90	90.80%	0.81%	true	PPAIPFPFPPPP	87.20%	51.3	482.2676	962.520648	963.530146	2	-0.002222	-2.306	779	788	true
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDCl PE=1 SV=2	Q9CID6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	2.01%	true	PPAIPFPFPPPP	87.20%	51.3	482.2676	962.520648	963.530146	2	-0.002222	-2.306	31	40	true
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDCl PE=1 SV=2	Q9CID6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	1.22%	true	PPAIPFPFPPPPPP	93.90%	53.3	579.3236	1 156.63	1 157.64	2	0.004178	3.609	31	42	true
Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1	Q9UMN6	UniProtKB-HS_20150717_TaD.fasta	293 512.20	96.60%	0.99%	true	PPAIPFPYK	78.40%	39.1	433.7423	865.470048	866.477246	2	0.0000706	0.99009	2289	2296	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	26.20%	true	PPFPVPPPK	98.00%	48.8	493.2764	984.530248	985.546746	2	-0.001222	-1.24	487	495	true
Neuroblastoma suppressor of tumorigenicity 1 OS=Homo sapiens GN=NBL1 PE=1 SV=1	A0M8W7YS.P41271.P41271-2	UniProtKB-HS_20150717_TaD.fasta	23 237.70	99.50%	6.51%	true	PPGAPHITEEEGAED	99.70%	76.8	718.3041	1 434.59	1 435.60	2	0.003478	2.423	202	215	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	20.00%	true	PPGKPEAQFPPLSEHKPEPAGDVGPKDGSAPVPGA	99.70%	57	647.6659	3 879.95	3 880.96	6	0.0007741	0.1995	24	62	true
cDNA FLJ94187, highly similar to Homo sapiens CD99 antigen (CD99), mRNA OS=Homo sapiens PE=2 SV=1	B2R932	UniProtKB-HS_20150717_TaD.fasta	18 947.30	99.80%	5.95%	true	PKKMPMPNPNFN	99.70%	56.4	601.8044	1 201.59	1 202.60	2	0.002678	2.227	72	82	true
ProSAAS OS=Homo sapiens GN=PCSKIN PE=1 SV=1	Q9UHG2	UniProtKB-HS_20150717_TaD.fasta	27 373.20	100.00%	11.90%	true	PPLAETGAPR	93.40%	46.1	504.7767	1 007.54	1 008.55	2	-0.001322	-1.311	48	57	true
Ras association (RaGDS/AF-6) and plectrolin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.69%	true	PPPLPFPFPP	66.00%	39.7	454.7662	907.517848	908.524346	2	0.0007781	0.8564	678	686	true
Formin 1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	98.90%	1.67%	false	PPPLPFPFPP	66.00%	39.7	454.7662	907.517848	908.524346	2	0.0007781	0.8564	803	811	false
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	2.55%	false	PPPLPFPFPP	66.00%	39.7	454.7662	907.517848	908.524346	2	0.0007781	0.8564	678	686	false
isoform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	97.50%	2.01%	false	PPPLPFPFPP	66.00%	39.7	454.7662	907.517848	908.524346	2	0.0007781	0.8564	1499	1507	false
Ras association (RaGDS/AF-6) and plectrolin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.08%	true	PPPLPFPFPPPP	86.20%	49.8	503.2926	1 004.57	1 005.58	2	0.0007781	0.7737	678	687	true
Formin 1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYM30.Q64DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	97.00%	1.59%	false	PPPLPFPFPPPP	86.20%	49.8	503.2926	1 004.57	1 005.58	2	0.0007781	0.7737	803	812	false
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDCl PE=1 SV=2	Q9CID6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	2.01%	true	PPPAFPFPPPP	93.50%	50.4	482.2685	962.522448	963.530146	2	-0.0004219	-0.4379	30	39	true
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M6M0QW5.Q96Q04	UniProtKB-HS_20150717_TaD.fasta	157 098.90	94.20%	1.48%	false	PPPAFPFPPPP	93.50%	50.4	482.2685	962.522448	963.530146	2	-0.0004219	-0.4379	778	787	false
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M6M0QW5.Q96Q04	UniProtKB-HS_20150717_TaD.fasta	157 098.90	93.80%	1.48%	false	PPPAFPFPPPPPP	92.20%	49.2	579.3213	1 156.63	1 157.64	2	-0.0004219	-0.3645	778	789	false
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDCl PE=1 SV=2	Q9CID6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	1.22%	true	PPPAFPFPPPPPP	92.20%	49.2	579.3213	1 156.63	1 157.64	2	-0.0004219	-0.3645	30	41	true
Similar to Kruppel-like factor 2 (Lang) (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UUNA.Q9Y5W3	UniProtKB-HS_20150717_TaD.fasta	22 707.90	83.90%	3.12%	true	PPPDITFP	90.00%	56.1	360.6871	719.359648	720.356546	2	0.01038	14.41	169	175	true
Adenyl cyclase-associated protein OS=Homo sapiens PE=2 SV=1	B2RDY9.B0D138.D1D1PU12	UniProtKB-HS_20150717_TaD.fasta	51 615.20	42.20%	1.89%	true	PPPGFPFPP	69.10%	38.6	426.7334	851.423248	852.461746	2	-0.002222	-2.607	233	241	true
Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1	Q9UMN6	UniProtKB-HS_20150717_TaD.fasta	293 512.20	95.50%	0.63%	true	PPPLCFPP	90.60%	49	409.2125	816.410448	817.427946	2	-0.01022	-12.51	425	432	true
isoform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	86.30%	2.60%	false	PPPLPFPFPPPP	86.20%	49.8	503.2926	1 004.57	1 005.58	2	0.0007781	0.7737	1498	1507	false
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	3.29%	true	PPPLPFPFPPPP	86.20%	49.8	503.2926	1 004.57	1 005.58	2	0.0007781	0.7737	677	686	true
cDNA FLJ76489, highly similar to Homo sapiens sortilin 1 (SORT1), mRNA OS=Homo sapiens PE=2 SV=1	AKKAQ3.Q99523	UniProtKB-HS_20150717_TaD.fasta	92 038.60	100.00%	1.44%	true	PPPPAAPLPR	99.70%	64.2	506.801	1 011.59	1 012.59	2	0.0006781	0.6696	40	49	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	26.20%	true	PPPPAPAPARDELFD	99.70%	47.9	770.3977	1 538.78	1 539.78	2	0.007578	4.921	508	522	true
Similar to Kruppel-like factor 2 (Lang) (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UUNA.Q9Y5W3	UniProtKB-HS_20150717_TaD.fasta	22 707.90	71.10%	7.59%	false	PPPPDITFP	91.70%	49.1	409.2137	816.412848	817.409346	2	0.01078	13.19	168	175	false
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	D1DQ54.QIN3X1.QIN3X1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.05%	true	PPPPESFP	91.70%	49.1	409.2137	816.412848	817.409346	2	0.01088	13.31	716	723	true
Histone-lysine N-methyltransferase 2B OS=Homo sapiens GN=KMT2B PE=1 SV=1	Q9UMN6	UniProtKB-HS_20150717_TaD.fasta	293 512.20	71.70%	0.37%	true	PPPLCFPPPP	75.00%	41.4	506.2694	1 010.52	1 011.53	2	-0.002022	-1.999	424	433	true
Proline rich 11, isoform CRA_a OS=Homo sapiens GN=PRR11 PE=2 SV=1	D2SNZA.Q96HE9	UniProtKB-HS_20150717_TaD.fasta	40 086.40	33.20%	5.28%	true	PPPLPFPFPP	67.10%	43.6	503.2923	1 004.57	1 005.58	2	0.0001781	0.1771	189	198	true
isoform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	90.20%	1.57%	true	PPPLPFPFPP	67.10%	43.6	503.2923	1 004.57	1 005.58	2	0.0001781	0.1771	1497	1506	true
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	99.00%	2.47%	true	PPPLPFPFPP	67.10%	43.6	503.2923	1 004.57	1 005.58	2	0.0001781	0.1771	676	685	true
Similar to Kruppel-like factor 2 (Lang) (Fragment) OS=Homo sapiens PE=2 SV=1	Q9UUNA.Q9Y5W3	UniProtKB-HS_																

Ras association (RaGDS/AF-6) and plectroin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C8K0I5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.69%	false	FFFFFFES	67.60%	37.7	360.6871	719.359648	720.356446	2	0.01048	14.55	969	975	false	DIDQ54.QINX1.QINX1-2
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.24%	true	FFFFFFES	67.60%	37.7	360.6871	719.359648	720.356446	2	0.01048	14.55	715	721	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.75%	true	FFFFFFESP	94.70%	54.9	409.2125	816.410448	817.409246	2	0.008478	10.37	715	722	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.24%	true	FFFFFFESP	97.70%	66.7	457.7408	913.467048	914.462046	2	0.01228	13.43	715	723	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.15%	true	FFFFFFESFP	81.50%	52.5	506.2688	1 010.52	1 011.51	2	0.01548	15.3	715	724	true	
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	H9KY2S.O60610.O60610-2.O60610-3.Q6URC4	UniProtKB-HS_20150717_TaD.fasta	136 857.50	96.00%	2.28%	true	FFFFFFGFGV	92.30%	36	506.2694	1 010.52	1 011.53	2	0.001478	1.461	704	713	true	
Zinc finger RNA-binding protein 2 OS=Homo sapiens GN=ZFR2 PE=2 SV=3	Q9UPR6	UniProtKB-HS_20150717_TaD.fasta	101 330.00	78.30%	1.06%	true	FFFFFFPPOQ	90.30%	40.8	506.2686	1 010.52	1 011.53	2	0.003778	3.735	223	232	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.65%	true	FFFFFFES	98.60%	68.9	409.2139	816.413248	817.409246	2	0.01128	13.8	714	721	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.95%	true	FFFFFFESP	98.00%	66.3	457.7403	913.466048	914.462046	2	0.01128	12.33	714	722	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.85%	true	FFFFFFESP	76.40%	50.5	506.2705	1 010.53	1 011.51	2	0.01888	18.66	714	723	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.15%	true	FFFFFFESFP	95.10%	50.9	554.7916	1 107.57	1 108.57	2	0.008278	7.467	714	724	true	
Epsin OS=Homo sapiens GN=ESPN PE=1 SV=1	BIAK53	UniProtKB-HS_20150717_TaD.fasta	91 733.40	100.00%	2.81%	true	FFFFFFLPEA	96.50%	52.6	506.2741	1 010.53	1 011.55	2	-0.01032	-10.2	600	609	true	
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.95%	true	FFFFFFPES	98.00%	66.3	457.7403	913.466048	914.462046	2	0.01128	12.33	713	721	true	
cDNA FLJ44595 fs, clone BLAD2004849 OS=Homo sapiens PE=2 SV=1	Q6ZTJ3	UniProtKB-HS_20150717_TaD.fasta	32 450.70	96.80%	3.37%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	166	173	false	DIDQ54.QINX1.QINX1-2
Ras association (RaGDS/AF-6) and plectroin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C8K0I5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.69%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	681	688	false	DIDQ54.QINX1.QINX1-2
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M0M0M0W5.Q96Q04	UniProtKB-HS_20150717_TaD.fasta	157 098.90	96.20%	1.48%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	448	455	false	DIDQ54.QINX1.QINX1-2
cDNA FLJ73640, highly similar to Homo sapiens TSPY-like 2 (TSPYL2), mRNA OS=Homo sapiens PE=2 SV=1	A8KU7.BUKY2.Q9H2G4	UniProtKB-HS_20150717_TaD.fasta	79 410.10	92.80%	1.44%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	25	32	false	DIDQ54.QINX1.QINX1-2
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	H1BLZS.Q92841.Q92841-1.Q92841-2.Q92841-3	UniProtKB-HS_20150717_TaD.fasta	80 441.30	90.00%	1.37%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	720	727	false	DIDQ54.QINX1.QINX1-2
Formin-1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYVM30.Q68DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	98.90%	1.67%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	806	813	false	DIDQ54.QINX1.QINX1-2
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.24%	true	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	712	719	true	
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	O95466.O95466-2.O95466-3	UniProtKB-HS_20150717_TaD.fasta	121 858.20	92.80%	1.91%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	585	592	false	DIDQ54.QINX1.QINX1-2
Putative Polycomb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	Q9C0F0	UniProtKB-HS_20150717_TaD.fasta	241 918.70	99.40%	1.07%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	2032	2039	false	DIDQ54.QINX1.QINX1-2
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHD1C1 PE=1 SV=2	Q9C0D6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	1.22%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	34	41	false	DIDQ54.QINX1.QINX1-2
Similar to Kruppel-like factor 2 (Lang) (Fragment) OS=Homo sapiens PE=2 SV=1	Q9HUNA.Q9Y5W3	UniProtKB-HS_20150717_TaD.fasta	22 707.90	75.40%	8.48%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	64	71	false	DIDQ54.QINX1.QINX1-2
Epsin OS=Homo sapiens GN=ESPN PE=1 SV=1	BIAK53	UniProtKB-HS_20150717_TaD.fasta	91 733.40	71.00%	2.34%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	596	603	false	DIDQ54.QINX1.QINX1-2
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	2.55%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	17	24	false	DIDQ54.QINX1.QINX1-2
Isoform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	97.50%	2.01%	false	FFFFFFFP	80.10%	40.9	398.2239	794.433248	795.440246	2	0.0002781	0.3496	835	842	false	DIDQ54.QINX1.QINX1-2
Nucleosome-remodelling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3	Q12X30.Q12X30-4	UniProtKB-HS_20150717_TaD.fasta	338 256.30	67.60%	0.62%	false	FFFFFFFP	73.20%	40.9	398.2226	794.430648	795.440246	2	-0.002322	-2.919	24	31	false	DIDQ54.QINX1.QINX1-2
cDNA, FLJ79373, highly similar to Protein diaphanous homolog 3 (Fragment) OS=Homo sapiens PE=2 SV=1	BTZB09.Q9NSV4.Q9NSV4-4.Q9NSV4-5.Q9NSV4-7	UniProtKB-HS_20150717_TaD.fasta	116 520.00	55.20%	1.57%	false	FFFFFFFP	73.20%	40.9	398.2226	794.430648	795.440246	2	-0.002322	-2.919	588	595	false	DIDQ54.QINX1.QINX1-2
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	H9KY2S.O60610.O60610-2.O60610-3.Q6URC4	UniProtKB-HS_20150717_TaD.fasta	136 857.50	96.00%	2.28%	false	FFFFFFFP	73.20%	40.9	398.2226	794.430648	795.440246	2	-0.002322	-2.919	564	571	false	DIDQ54.QINX1.QINX1-2
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	100.00%	1.65%	false	FFFFFFFP	99.70%	60.2	446.7492	891.483848	892.493046	2	-0.001922	-2.153	218	226	false	DIDQ54.QINX1.QINX1-2
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.85%	true	FFFFFFFP	99.70%	60.2	446.7492	891.483848	892.493046	2	-0.001922	-2.153	722	730	true	
cDNA FLJ44595 fs, clone BLAD2004849 OS=Homo sapiens PE=2 SV=1	Q6ZTJ3	UniProtKB-HS_20150717_TaD.fasta	32 450.70	99.80%	3.37%	false	FFFFFFFP	99.70%	60.2	446.7492	891.483848	892.493046	2	-0.001922	-2.153	166	174	false	DIDQ54.QINX1.QINX1-2
Formin-1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	HYVM30.Q68DA7	UniProtKB-HS_20150717_TaD.fasta	146 508.90	99.60%	1.36%	false	FFFFFFFP	99.70%	60.2	446.7492	891.483848	892.493046	2	-0.001922	-2.153	806	814	false	DIDQ54.QINX1.QINX1-2
Epsin OS=Homo sapiens GN=ESPN PE=1 SV=1	BIAK53	UniProtKB-HS_20150717_TaD.fasta	91 733.40	99.60%	2.22%	false	FFFFFFFP	99.70%	60.2	446.7492	891.483848	892.493046	2	-0.001922	-2.153	596	604	false	DIDQ54.QINX1.QINX1-2
Putative Polycomb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	Q9C0F0	UniProtKB-HS_20150717_TaD.fasta	241 918.70	99.80%	0.53%	false	FFFFFFFP	99.70%	60.2	446.7492	891.483848	892.493046	2	-0.001922	-2.153	2017	2025	false	DIDQ54.QINX1.QINX1-2
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	O95466.O95466-2.O95466-3	UniProtKB-HS_20150717_TaD.fasta	121 858.20	99.70%	1.82%	false	FFFFFFFP	99.70%	60.2	446.7492	891.483848	892.493046	2	-0.001922	-2.153	585	593	false	DIDQ54.QINX1.QINX1-2
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	H1BLZS.Q92841.Q92841-1.Q92841-2.Q92841-3	UniProtKB-HS_20150717_TaD.fasta	80 441.30	91.10%	1.37%	false	FFFFFFFP	94.10%	52.7	446.7498	891.485048	892.493046	2	-0.0007219	-0.8089	720	728	false	DIDQ54.QINX1.QINX1-2
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHD1C1 PE=1 SV=2	Q9C0D6	UniProtKB-HS_20150717_TaD.fasta	124 764.70	100.00%	2.01%	false	FFFFFFFP	94.10%	52.7	446.7498	891.485048	892.493046	2	-0.0007219	-0.8089	34	42	false	DIDQ54.QINX1.QINX1-2
Ras association (RaGDS/AF-6) and plectroin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C8K0I5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	99.90%	1.00%	false	FFFFFFFP	94.10%	52.7	446.7498	891.485048	892.493046	2	-0.0007219	-0.8089	681	689	false	DIDQ54.QINX1.QINX1-2
Isoform 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	83.70%	1.08%	false	FFFFFFFP	76.30%	52.6	446.7508	891.487048	892.493046	2	0.001278	1.432	835	843	false	DIDQ54.QINX1.QINX1-2
cDNA FLJ73640, highly similar to Homo sapiens TSPY-like 2 (TSPYL2), mRNA OS=Homo sapiens PE=2 SV=1	A8KU7.BUKY2.Q9H2G4	UniProtKB-HS_20150717_TaD.fasta	79 410.10	67.20%	1.44%	false	FFFFFFFP	76.30%	52.6	446.7508	891.487048	892.493046	2	0.001278	1.432	25	33	false	DIDQ54.QINX1.QINX1-2
cDNA, FLJ79373, highly similar to Protein diaphanous homolog 3 (Fragment) OS=Homo sapiens PE=2 SV=1	BTZB09.Q9NSV4.Q9NSV4-4.Q9NSV4-5.Q9NSV4-7	UniProtKB-HS_20150717_TaD.fasta	116 520.00	55.20%	1.57%	false	FFFFFFFP	95.30%	49.8	446.7497	891.484848	892.493046	2	-0.0009219	-1.033	588	596	false	DIDQ54.QINX1.QINX1-2
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	H9KY2S.O60610.O60610-2.O60610-3.Q6URC4	UniProtKB-HS_20150717_TaD.fasta	136 857.50	96.00%	2.28%	false	FFFFFFFP	95.30%	49.8	446.7497	891.484848	892.493046	2	-0.0009219	-1.033	564	572	false	DIDQ54.QINX1.QINX1-2
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1.QINX1-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.06%	true	FFFFFFFP	98.90%	64.3	495.2763	988.538048	989.545846	2	-0.0005219	-0.5275	722	731	true	
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHD1C1 PE=1 SV=2																			

Isomern 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	97.50%	2.01%	false	FFFFFFFF	99.70%	64	495.2778	988.541048	989.545846	2	0.002478	2.504	1039	1048	false	DIDQ54.QINX1X1.QINX1X-2
cDNA, FLJ79373, highly similar to Protein diaphanous homolog 3 (Fragment) OS=Homo sapiens PE=2 SV=1	BTZB09.Q9NSV4.Q9NSV4-4.Q9NSV4-5.Q9NSV4-7	UniProtKB-HS_20150717_TaD.fasta	116 520.00	55.20%	1.57%	false	FFFFFFFF	99.50%	58	495.2764	988.538248	989.545846	2	-0.0003219	-0.3253	588	597	false	DIDQ54.QINX1X1.QINX1X-2
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	HKVY25.O60610.O60610-2.O60610-3.Q6URC4	UniProtKB-HS_20150717_TaD.fasta	136 857.50	96.00%	2.28%	false	FFFFFFFF	99.50%	58	495.2764	988.538248	989.545846	2	-0.0003219	-0.3253	564	573	false	DIDQ54.QINX1X1.QINX1X-2
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1X1.QINX1X-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	2.95%	true	FFFFFFFF	99.70%	69.3	543.8043	1 085.59	1 086.60	2	0.002678	2.465	905	915	true	
Isomern 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	84.60%	1.67%	false	FFFFFFFF	99.70%	69.3	543.8043	1 085.59	1 086.60	2	0.002678	2.465	835	845	false	DIDQ54.QINX1X1.QINX1X-2
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	98.60%	1.73%	false	FFFFFFFF	99.70%	69.3	543.8043	1 085.59	1 086.60	2	0.002678	2.465	218	228	false	DIDQ54.QINX1X1.QINX1X-2
cDNA, FLJ79373, highly similar to Protein diaphanous homolog 3 (Fragment) OS=Homo sapiens PE=2 SV=1	BTZB09.Q9NSV4.Q9NSV4-4.Q9NSV4-5.Q9NSV4-7	UniProtKB-HS_20150717_TaD.fasta	116 520.00	55.20%	1.57%	false	FFFFFFFF	99.70%	64.5	543.8028	1 085.59	1 086.60	2	-0.0003219	-0.2963	588	598	false	DIDQ54.QINX1X1.QINX1X-2
Putative Polycomb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	Q9C9F9	UniProtKB-HS_20150717_TaD.fasta	241 918.70	100.00%	1.02%	false	FFFFFFFF	99.70%	64.5	543.8028	1 085.59	1 086.60	2	-0.0003219	-0.2963	2017	2027	false	DIDQ54.QINX1X1.QINX1X-2
Ras association (RaGDS/AF-6) and plectroin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.69%	false	FFFFFFFF	99.70%	64.5	543.8028	1 085.59	1 086.60	2	-0.0003219	-0.2963	681	691	false	DIDQ54.QINX1X1.QINX1X-2
Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	HKVY25.O60610.O60610-2.O60610-3.Q6URC4	UniProtKB-HS_20150717_TaD.fasta	136 857.50	96.00%	2.28%	false	FFFFFFFF	99.70%	64.5	543.8028	1 085.59	1 086.60	2	-0.0003219	-0.2963	564	574	false	DIDQ54.QINX1X1.QINX1X-2
Formin-like protein 1 OS=Homo sapiens GN=FMNL1 PE=1 SV=3	O95466.O95466-2.O95466-3	UniProtKB-HS_20150717_TaD.fasta	121 858.20	100.00%	1.91%	false	FFFFFFFF	99.70%	64.5	543.8043	1 085.59	1 086.60	2	0.002678	2.465	585	595	false	DIDQ54.QINX1X1.QINX1X-2
Ras association (RaGDS/AF-6) and plectroin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	C9K0J5	UniProtKB-HS_20150717_TaD.fasta	141 180.90	100.00%	1.69%	false	FFFFFFFF	98.90%	57.8	592.332	1 182.65	1 183.65	2	0.005278	4.459	681	692	false	DIDQ54.QINX1X1.QINX1X-2
Formin binding protein 4, isoform CRA_d OS=Homo sapiens GN=FNBP4 PE=4 SV=1	DIDQ54.QINX1X1.QINX1X-2	UniProtKB-HS_20150717_TaD.fasta	110 248.60	100.00%	3.24%	true	FFFFFFFF	98.90%	57.8	592.332	1 182.65	1 183.65	2	0.005278	4.459	905	916	true	
Putative Polycomb group protein ASXL3 OS=Homo sapiens GN=ASXL3 PE=2 SV=3	Q9C9F9	UniProtKB-HS_20150717_TaD.fasta	241 918.70	99.40%	1.07%	false	FFFFFFFF	98.90%	57.8	592.332	1 182.65	1 183.65	2	0.005278	4.459	2017	2028	false	DIDQ54.QINX1X1.QINX1X-2
Proline rich 11, isoform CRA_a OS=Homo sapiens GN=PRR11 PE=2 SV=1	D2SNZA.Q96HE9	UniProtKB-HS_20150717_TaD.fasta	40 086.40	33.20%	5.28%	false	PPPPPSPE	93.50%	60.7	457.7409	913.407248	914.402046	2	0.01248	13.65	34	42	false	DIDQ54.QINX1X1.QINX1X-2
Proline rich 11, isoform CRA_a OS=Homo sapiens GN=PRR11 PE=2 SV=1	D2SNZA.Q96HE9	UniProtKB-HS_20150717_TaD.fasta	40 086.40	75.10%	2.22%	true	PPPPPSPE	83.70%	53.6	409.2129	816.411248	817.409246	2	0.009278	11.35	35	42	true	
Nucleosome-remodelling factor subunit BPTF OS=Homo sapiens GN=BPTF PE=1 SV=3	Q12K30.Q12K30-4	UniProtKB-HS_20150717_TaD.fasta	338 256.30	67.60%	0.62%	true	PPPPSPPPP	77.10%	33.7	441.7395	881.464448	882.472246	2	-0.0005219	-0.5915	2809	2817	true	
Arginine glutamic acid dipeptide (RE) repeats, isoform CRA_a OS=Homo sapiens GN=REPE PE=4 SV=1	A0M24R4E9.Q9P2R6	UniProtKB-HS_20150717_TaD.fasta	172 425.10	65.90%	0.51%	true	PQAPAPAV	67.30%	32	390.7146	779.414648	780.425146	2	-0.003222	-4.128	788	795	true	
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M0M0QW5.Q96Q04	UniProtKB-HS_20150717_TaD.fasta	157 098.90	96.20%	1.48%	false	PPPPPPPP	94.40%	58.7	427.7478	853.481048	854.488546	2	-0.0002219	-0.2597	446	453	false	Q9ULL5
Serine/threonine-protein kinase LMTK3 OS=Homo sapiens GN=LMTK3 PE=1 SV=1	A0M0M0QW5.Q96Q04	UniProtKB-HS_20150717_TaD.fasta	157 098.90	96.90%	1.48%	false	PPPPPPPP	99.30%	65.5	476.2743	950.534048	951.541346	2	-0.0002194	-0.02306	446	454	false	Q9ULL5
Transferrin OS=Homo sapiens PE=2 SV=1	A6NGL1.E9K136.P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	PKRYTLAALLPSYSSTAVTNPK	99.70%	78.3	725.3943	2 897.55	2 898.54	4	0.01933	6.667	159	184	true	
Proline-rich protein 12 OS=Homo sapiens GN=PRR12 PE=1 SV=2	Q9ULL5	UniProtKB-HS_20150717_TaD.fasta	129 995.60	35.60%	2.55%	false	PSPPPPPP	85.00%	44	441.7394	881.464248	882.472246	2	-0.0007219	-0.8181	689	697	false	DIDQ54.QINX1X1.QINX1X-2
Isomern 3 of Proline-rich protein 12 OS=Homo sapiens GN=PRR12	Q9ULL5-3	UniProtKB-HS_20150717_TaD.fasta	211 049.50	75.10%	2.50%	false	PSPPPPPP	85.00%	44	441.7394	881.464248	882.472246	2	-0.0007219	-0.8181	1510	1518	false	DIDQ54.QINX1X1.QINX1X-2
Ray/Rap GTPase-activating protein SyGAP OS=Homo sapiens GN=SYNGAP1 PE=1 SV=4	Q96P90.Q96P90-3	UniProtKB-HS_20150717_TaD.fasta	148 288.40	86.90%	0.82%	true	PTKEKPPPPPP	85.70%	41.2	592.826	1 183.64	1 184.67	2	-0.02302	-19.43	789	799	true	
Transferrin OS=Homo sapiens PE=2 SV=1	A6NGL1.E9K136.P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	PSYSSTAVTNPK	99.70%	117	828.9182	1 655.82	1 656.81	2	0.01758	10.61	170	184	true	
Voltage-gated potassium channel subunit beta-2 (Fragment) OS=Homo sapiens GN=KCNAB2 PE=1 SV=1	KTEI85	UniProtKB-HS_20150717_TaD.fasta	17 754.80	64.20%	5.56%	true	QGEPPPPPPP	73.40%	40.4	458.2327	914.450848	915.457346	2	0.0007781	0.8499	136	144	true	
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TaD.fasta	70 942.70	100.00%	18.60%	true	QGSSQETDKLAPVS	92.50%	28.8	723.8583	1 445.70	1 446.71	2	0.002078	1.436	553	566	true	
Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	P02675.W9HVV1	UniProtKB-HS_20150717_TaD.fasta	55 928.60	100.00%	2.85%	true	QGVNDNEEGFFSAR	94.00%	37	785.3638	1 568.71	1 569.69	2	0.02748	17.51	31	44	true	
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	19.50%	true	QPPPPAPAPADELPPD	99.70%	54.9	834.4284	1 666.84	1 667.84	2	0.01038	6.222	507	522	true	
Ig heavy chain V-HH region CAM OS=Homo sapiens PE=1 SV=1	P01768	UniProtKB-HS_20150717_TaD.fasta	13 663.20	97.10%	16.40%	true	QVEVSEGGGVVEPGRSLRL	98.30%	46.3	1 041.08	2 080.14	2 081.14	2	0.01358	6.524	1	20	true	
Protein LBBP4 OS=Homo sapiens GN=LBBP4 PE=1 SV=1	J3QLP7.J3QRK5	UniProtKB-HS_20150717_TaD.fasta	25 154.90	78.70%	10.30%	true	REDGRSLSDVNIQESTLHLVLR	96.30%	33.9	910.476	2 728.41	2 729.43	3	-0.0197	-7.217	50	72	true	
Tumor suppressor OS=Homo sapiens GN=TSC1 PE=2 SV=1	Q59W9	UniProtKB-HS_20150717_TaD.fasta	50 251.70	42.30%	2.86%	true	RHSDSLASLTLRS	67.40%	16.9	721.8912	1 441.77	1 442.77	2	0.004078	2.827	433	445	true	
Isomern 2 of Receptor-type tyrosine-protein phosphatase zeta OS=Homo sapiens GN=PTPRZ1	P23471-2	UniProtKB-HS_20150717_TaD.fasta	253 673.30	100.00%	1.00%	true	RIGLAEGLESEKKAIVPLVVS	99.70%	87.4	774.4663	2 320.38	2 321.38	3	0.009982	4.222	1624	1645	true	
Isomern 2 of Receptor-type tyrosine-protein phosphatase zeta OS=Homo sapiens GN=PTPRZ1	P23471-2	UniProtKB-HS_20150717_TaD.fasta	253 673.30	100.00%	1.00%	true	RIGLAEGLESEKKAIVPLVISA	99.70%	67.4	798.1442	2 391.41	2 392.42	3	0.0004021	0.1681	1624	1646	true	
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	RIGRFYGYGYPVQPPVEQP	95.30%	31.2	727.7081	2 180.10	2 181.09	3	0.0219	10.04	29	47	true	
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	RIGRFYGYGYPVQPPVEQPLYPQVQVQ	94.00%	27.7	824.6753	3 294.67	3 295.63	4	0.00663	14.15	29	56	true	
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	RIGRFYGYGYPVQPPVEQPLYPQVQVQVQ	71.50%	22	1 153.59	3 457.76	3 458.70	3	0.0684	19.70	29	57	true	
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	RIGRFYGYGYPVQPPVEQPLYPQVQVQVQ	97.70%	34.7	1 196.28	3 585.81	3 586.75	3	0.0588	16.39	29	58	true	
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	RIGRFYGYGYPVQPPVEQPLYPQVQVQVQ	95.80%	32.6	1 238.97	3 713.87	3 714.81	3	0.0672	18.09	29	59	true	
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	RIGRFYGYGYPVQPPVEQPLYPQVQVQVQY	97.70%	34.6	995.5053	3 977.99	3 978.92	4	0.07513	18.88	29	61	true	
Statherin OS=Homo sapiens GN=STATH PE=1 SV=2	P02808	UniProtKB-HS_20150717_TaD.fasta	7 304.80	100.00%	69.40%	true	RIGRFYGYGYPVQPPVEQPLYPQVQVQVQYTF	85.90%	20.2	826.0171	4 125.65	4 125.99	5	0.06375	15.45	29	62	true	
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A6SMV6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	95.60%	16.20%	false	RISHELDSASSEVN	99.70%	84.5	515.2518	1 542.73	1 543.73	3	0.006202	4.018	301	314	false	A0M24R4E6.P10451-5
Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	A0M24R4E6.P10451-5	UniProtKB-HS_20150717_TaD.fasta	33 843.10	100.00%	4.67%	true	RISHELDSASSEVN	99.70%	84.5	515.2518	1 542.73	1 543.73	3	0.006202	4.018	287	300	true	
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	RLAVYQAGAREGAE	79.40%	23.4	412.4729	1 645.86	1 646.87	4	-0.002374	-1.441	176	190	true	
Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) OS=Homo sapiens GN=AGT PE=3 SV=1	B0ZBE2.B28551.B4DE30.B4E1B3.P01019.Q51YV1.Q9HFP2.Q8H478	UniProtKB-HS_20150717_TaD.fasta	53 154.80	100.00%	7.84%	true	RPFVAYDQSATALHFLGRVANPLSTA	99.50%	41.5	766.4144	3 061.63	3 062.62	4	0.01463	4.776	458	485	true	
Serpin peptidase inhibitor, clade A (Alpha-1 antitrypsinase, antitrypsin), member 3, isoform CRA_c OS=Homo sapiens GN=SERPINA3 PE=3 SV=1	A0M24R6P9.B3K579.P10111	UniProtKB-HS_20150717_TaD.fasta	47 653.00	30.60%	6.38%	true	RPFVLMHVPEDTQNFVMSKVTNPKQA	64.30%	16.1	1 046.24	3 135.70	3 136.67	3	0.0365	11.64	397	423		

Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=1 SV=1	FHSYFR,QIUBP4	UniProtKB-HS_20150717_TnD.fasta	39 949.40	86.80%	9.07%	true	RQELEDLEKSTTEEMALREPAAAAAALLGEEI	97.90%	28.4	896.2147	3 580.83	3 581.81	4	0.02503	6.987	332	364	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1,E9KL36,P02766	UniProtKB-HS_20150717_TnD.fasta	20 198.60	100.00%	27.70%	true	RKYTAAALLSPYSYSTAVVTPNKE	92.30%	29.1	701.1278	2 800.48	2 801.48	4	0.006126	2.187	160	184	true
Beta-2-microglobulin OS=Homo sapiens GN=β2M PE=1 SV=1	P61769	UniProtKB-HS_20150717_TnD.fasta	13 714.90	100.00%	36.10%	true	KVNIVLTSQPKVWDRDM	99.70%	37.8	465.255	2 321.24	2 322.25	5	-0.00425	-1.83	101	119	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1,E9KL36,P02766	UniProtKB-HS_20150717_TnD.fasta	20 198.60	100.00%	15.80%	true	KYTAALLSPYSYSTAVVTPNKE	99.70%	114	882.4729	2 644.40	2 645.38	3	0.022	8.317	161	184	true
FXFD domain containing ion transport regulator 6, isoform CRA_a OS=Homo sapiens GN=FXFD6 PE=4 SV=1	A0M24R3U,AA087W2K2,E0PHZ3,E0PHZ2,Q3QKN1,Q9H9Q3	UniProtKB-HS_20150717_TnD.fasta	10 542.50	92.30%	24.20%	true	SAEKEKEMDPHYDQTLRIGG	89.40%	42.9	672.076	2 684.27	2 685.26	4	0.0263	7.644	19	41	true
Angiotensinogen (Serpin peptidase inhibitor, clade A, member 8) OS=Homo sapiens GN=AGT PE=3 SV=1	B0ZBE2,B2RSS1,B4DEB0,B4E1B3,P01019,Q53YV1,Q9HEP2,Q86U78	UniProtKB-HS_20150717_TnD.fasta	53 154.80	100.00%	7.84%	true	SATALHFLGRVANPLSTA	99.70%	79.9	913.5047	1 824.99	1 825.99	2	0.01018	5.574	468	485	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TnD.fasta	36 153.50	100.00%	37.50%	true	SELEEQTVAEETR	99.70%	112	865.9326	1 729.85	1 730.84	2	0.01348	7.787	94	108	true
cDNA FLJ54622, highly similar to Prothombin (EC 3.4.21.5) OS=Homo sapiens PE=2 SV=1	B4DDT3,E0PHZ3,P00734	UniProtKB-HS_20150717_TnD.fasta	53 149.10	100.00%	2.76%	true	SEVQTFNFR	84.40%	35.4	644.8097	1 287.60	1 288.60	2	0.01648	12.79	167	176	true
Apolipoprotein A-I, isoform CRA_a OS=Homo sapiens GN=AP0AI PE=4 SV=1	A0M24R3E3,P02647	UniProtKB-HS_20150717_TnD.fasta	30 778.50	96.10%	7.49%	true	SFKNSFLSALEEYTKLNTQ	95.30%	31	778.4255	2 332.25	2 333.24	3	0.0231	9.901	248	267	true
Epsin OS=Homo sapiens GN=ESPN PE=1 SV=1	BIAK53	UniProtKB-HS_20150717_TnD.fasta	91 733.40	96.70%	2.22%	true	SFFPPPPPP	98.30%	68.5	466.7536	931.492648	932.487846	2	0.01208	12.95	436	444	true
Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	P01861	UniProtKB-HS_20150717_TnD.fasta	35 939.50	73.00%	11.30%	false	SGALTSGVHTFPVAVLQ	99.70%	65.8	792.9295	1 583.84	1 584.84	2	0.01358	8.567	43	58	false
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AA087WV47,AA087WYE1,AA087X010,VH0W8	UniProtKB-HS_20150717_TnD.fasta	51 152.80	100.00%	12.20%	true	SGALTSGVHTFPVAVLQ	99.70%	65.8	792.9295	1 583.84	1 584.84	2	0.01358	8.567	179	194	true
cDNA FLJ73387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TnD.fasta	51 595.70	91.10%	13.60%	false	SGALTSGVHTFPVAVLQ	94.20%	40.7	792.9291	1 583.84	1 584.84	2	0.01278	8.063	185	200	false
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AA087WV47,AA087WYE1,AA087X010,VH0W8	UniProtKB-HS_20150717_TnD.fasta	51 152.80	100.00%	9.01%	true	SGALTSGVHTFPVAVLQS	99.70%	61.2	836.4432	1 670.87	1 671.87	2	0.008978	5.37	179	195	true
cDNA FLJ73387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TnD.fasta	51 595.70	91.10%	13.60%	false	SGALTSGVHTFPVAVLQS	99.70%	50.2	836.4449	1 670.88	1 671.87	2	0.01238	7.404	185	201	false
Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	P01861	UniProtKB-HS_20150717_TnD.fasta	35 939.50	99.60%	10.10%	false	SGALTSGVHTFPVAVLQS	99.70%	48.1	836.443	1 670.87	1 671.87	2	0.008578	5.131	43	59	false
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AA087WV47,AA087WYE1,AA087X010,VH0W8	UniProtKB-HS_20150717_TnD.fasta	51 152.80	100.00%	9.01%	true	SGALTSGVHTFPVAVLQSSGLY	99.70%	66.7	1 046.55	2 091.08	2 092.07	2	0.01968	9.406	179	199	true
cDNA FLJ73387 OS=Homo sapiens PE=1 SV=1	A8K008	UniProtKB-HS_20150717_TnD.fasta	51 595.70	75.50%	12.30%	false	SGALTSGVHTFPVAVLQSSGLY	99.70%	66.7	1 046.55	2 091.08	2 092.07	2	0.01968	9.406	185	205	false
Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	P01861	UniProtKB-HS_20150717_TnD.fasta	35 939.50	99.60%	10.10%	false	SGALTSGVHTFPVAVLQSSGLY	99.70%	66.7	1 046.55	2 091.08	2 092.07	2	0.01968	9.406	43	63	false
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TnD.fasta	69 756.90	100.00%	4.50%	true	SGEGDFLAEGGGVR	99.70%	98.8	675.8234	1 349.63	1 350.63	2	0.01088	8.054	22	35	true
cDNA, FLJ79373, highly similar to Protein diaphanous homolog 3 (Fragment) OS=Homo sapiens PE=2 SV=1	B7ZB09,Q9NSV4,Q9NSV4_4,Q9NSV4_5,Q9NSV4_7	UniProtKB-HS_20150717_TnD.fasta	116 520.00	55.20%	1.57%	true	SGGGVPPPPPP	89.60%	35.8	528.282	1 054.55	1 055.55	2	0.004378	4.148	583	594	true
cDNA FLJ61580, highly similar to Calretinin-1 OS=Homo sapiens PE=2 SV=1	B4E3Q1,Q94985,Q94985-2	UniProtKB-HS_20150717_TnD.fasta	107 814.80	100.00%	3.64%	true	SGHNLANPFPFVAVPSTAT	97.90%	24.9	639.6599	1 915.96	1 916.96	3	0.003802	1.983	824	842	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1,E9KL36,P02766	UniProtKB-HS_20150717_TnD.fasta	20 198.60	100.00%	15.80%	true	SGPRKYTAAALLSPYSYSTAVVTPNKE	99.70%	79.6	761.4072	3 041.60	3 042.59	4	0.01743	5.727	157	184	true
Dialyglycerol kinase OS=Homo sapiens GN=DGKE PE=2 SV=1	A1LAQ0,L0L12,P52429,Q9WFU4	UniProtKB-HS_20150717_TnD.fasta	63 927.90	60.60%	2.47%	true	SGTNMGEGLLGEFR	80.70%	21.1	734.3363	1 466.66	1 467.69	2	-0.02452	-16.71	228	241	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	19.60%	true	SHTSDSDVPSGVTEV	99.70%	85.5	758.846	1 515.68	1 516.68	2	0.008478	5.59	391	405	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	19.80%	true	SHTSDSDVPSGVTEVVKLFSDPITVYVPEV	99.50%	38.9	1 152.27	3 453.78	3 454.75	3	0.0386	11.17	391	423	true
Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4	HHY300	UniProtKB-HS_20150717_TnD.fasta	49 105.50	100.00%	5.20%	true	SKQDWQKTAEN	99.70%	56.9	766.397	1 530.78	1 531.78	2	0.01148	7.493	430	442	true
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	P01024,VH0W89	UniProtKB-HS_20150717_TnD.fasta	187 149.10	100.00%	1.92%	true	SKTHRHWHESALLR	99.70%	80	645.3657	1 933.08	1 934.07	3	0.01096	5.482	1305	1320	true
Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	A4D15L,P01303	UniProtKB-HS_20150717_TnD.fasta	10 852.30	99.60%	16.50%	true	SKPDNPGEDAPAEADMA	99.70%	47.8	822.351	1 642.69	1 643.69	2	0.009078	5.523	31	46	true
Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	A4D15L,P01303	UniProtKB-HS_20150717_TnD.fasta	10 852.30	100.00%	20.60%	true	SKPDNPGEDAPAEADMARY	94.90%	29.5	654.9556	1 961.84	1 962.85	3	0.002202	1.122	31	48	true
cDNA, FLJ29296, highly similar to Homo sapiens amyloid beta (Aβ)-like protein 1 (APLP1),mRNA OS=Homo sapiens PE=2 SV=1	B2KSS2,P51693,P51693-2	UniProtKB-HS_20150717_TnD.fasta	72 103.90	100.00%	7.23%	true	SLAGGSPGAAEAPGSAQVAG	88.80%	38	827.9116	1 653.81	1 654.80	2	0.01268	7.661	39	58	true
Beta-1,3-N-acetylglucosaminyltransferase I isoform 5 OS=Homo sapiens GN=β1NGT5 PE=1 SV=2	QINES3,QINES3-3	UniProtKB-HS_20150717_TnD.fasta	41 774.20	82.30%	7.92%	true	SLAGPAGAAPAPGLGAAAAAGALVRDVHS	80.70%	23.4	865.1366	2 592.39	2 593.38	3	0.0195	4.05	44	73	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TnD.fasta	70 942.70	100.00%	18.60%	true	SIATLESVQELGKLTGPNNQ	99.70%	63.2	1 123.60	2 245.18	2 246.17	2	0.02018	8.983	194	214	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2,P69965	UniProtKB-HS_20150717_TnD.fasta	15 257.60	100.00%	36.60%	true	SLDKFLASVST	99.70%	41.8	584.3182	1 166.62	1 167.63	2	0.003478	2.979	125	135	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2,P69965	UniProtKB-HS_20150717_TnD.fasta	15 257.60	100.00%	48.60%	true	SLDKFLASVSTVLSKY	99.70%	100	930.0143	1 858.01	1 859.02	2	0.005178	2.785	125	141	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2,P69965	UniProtKB-HS_20150717_TnD.fasta	15 257.60	100.00%	52.80%	true	SLDKFLASVSTVLSKYR	99.70%	100	672.3818	2 014.12	2 015.12	3	0.0136	6.75	125	142	true
Isoform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TnD.fasta	69 756.90	100.00%	25.00%	true	SLFEYQKCNK	76.70%	29.1	424.2183	1 269.63	1 270.64	3	-0.002298	-1.808	91	108	true
UDP-GlcNAc6S-Gal beta-1,3-N-acetylglucosaminyltransferase 6, isoform CRA_a OS=Homo sapiens GN=β6GNT6 PE=4 SV=1	A0M24R3F9,B3KQO7,B4DENS,O43585	UniProtKB-HS_20150717_TnD.fasta	47 119.40	99.80%	5.78%	true	SLLSGLHGEEQDQYFEFFPPSPK	99.70%	43	936.7973	2 807.37	2 808.33	3	0.0507	18.05	31	54	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	24.30%	true	SLMPFSPEPLN	97.60%	36	697.8413	1 393.67	1 394.67	2	0.009178	6.581	228	239	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	24.30%	true	SLMPFSPEPLNF	97.70%	28.9	771.3752	1 540.74	1 541.73	2	0.008578	5.564	228	240	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	24.30%	true	SLMPFSPEPLNFHA	99.70%	40.7	875.4214	1 748.83	1 749.83	2	0.004978	2.845	228	242	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	24.30%	true	SLMPFSPEPLNFHAM	99.70%	63	940.9527	1 879.89	1 880.87	2	0.02708	14.4	228	243	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TnD.fasta	52 495.00	100.00%	20.00%	true	SLMPFSPEPLNFHAMQFP	99.70%	47.5	1 200.57	2 399.13	2 400.12	2	0.01948	8.115	228	247	true
Probable helicase senataxin OS=Homo sapiens GN=SETX PE=1 SV=4	Q7Z333,Q7Z333-3,Q7Z333-4	UniProtKB-HS_20150717_TnD.fasta	302 882.60	84.00%	0.34%	true	SLYHTPSDS	82.90%	34	503.7293	1 005.44	1 006.45	2	0.003678	3.654	2507	2515	true
Somatostatin OS=Homo sapiens GN=SST PE=1 SV=1	P61278	UniProtKB-HS_20150717_TnD.fasta	12 736.00	98.80%	7.76%	true	SNPAMAPRE	99.70%	44.8	486.7315	971.484488	972.456746	2	-0.001022	-1.051	92	108	true
Interleukin 15 receptor alpha isoform β3 OS=Homo sapiens GN=β3ra PE=1 SV=1	K9N2Q6	UniProtKB-HS_20150717_TnD.fasta	37 213.50	68.60%	3.47%	true	SPALVEGAGQMP	77.10%	40.2	578.7925	1 155.57	1 156.57	2	0.01088	9.405	307	318	true
Serpin peptidase inhibitor, clade A (Alpha-1 antitrypsinase, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	A0M24R647	UniProtKB-HS_20150717_TnD.fasta	46 709.90	100.00%	9.57%	true	SLPLMGKVNPTQK	99.70%	72.2	773.4304	1 544.85	1 545.85	2	0.007578	4.902	405	418	true
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	P01024,VH0W89	UniProtKB-HS_20150717_TnD.fasta	187 149.10	100.00%	1.92%	true	SPMYSHTPNLRLE	99.70%	47.8	873.9779	1 745.94	1 746.95	2	0.002478</				



Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O15240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	26.20%	true	SPQPPPPAPAPARDELFD	91.20%	22.8	617.9025	1 850.93	1 851.92	3	0.009002	4.861	505	522	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	SPVSYTAVVTPKE	99.70%	137	872.4307	1 742.85	1 743.84	2	0.01058	6.066	169	184	true
Ribonuclease pancreatic OS=Homo sapiens GN=RNASE1 PE=1 SV=4	P07996_WU0193	UniProtKB-HS_20150717_TaD.fasta	17 643.80	99.50%	10.30%	true	SPVYVHFDFASVEDT	99.70%	59.5	875.4098	1 748.81	1 749.80	2	0.01568	8.96	141	156	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TaD.fasta	70 942.70	100.00%	18.60%	true	SQETDKLAPVS	92.10%	30.6	587.804	1 173.59	1 174.60	2	0.005578	4.749	556	566	true
Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	Q16270	UniProtKB-HS_20150717_TaD.fasta	29 129.80	90.70%	10.60%	true	SQGGASAKITVDALHEIPVKKGEGAEI	98.60%	25	759.164	3 032.63	3 033.62	4	0.01233	4.063	253	282	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	25.00%	true	SQQLKVPPEWALTDMPQMKMELERPGGN	70.60%	14	842.4283	3 365.68	3 366.68	4	0.01533	4.552	239	267	true
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	P61769	UniProtKB-HS_20150717_TaD.fasta	13 714.90	100.00%	13.40%	true	SQPKVKWDRDM	72.00%	40.7	501.5975	1 501.77	1 502.78	3	-0.0006979	-0.4644	108	119	true
Isiorm 3 of Cartilage acidic protein 1 OS=Homo sapiens GN=CRTRC1	Q9NQ79-3	UniProtKB-HS_20150717_TaD.fasta	68 060.70	88.30%	2.07%	true	SQRAEPMFTAVTN	83.70%	32.3	726.3567	1 450.70	1 451.69	2	0.01138	7.838	28	40	true
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909_P10909-2_P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.20%	true	SKKNPKFMETVAEKALQEVYKHKHREE	99.70%	71.3	539.6225	3 231.69	3 232.70	6	-0.002326	-0.7195	424	449	true
Keratin, type I cytokeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	P35527	UniProtKB-HS_20150717_TaD.fasta	62 065.90	100.00%	3.37%	true	SRSGGGGGGGGLSGGGSIRSSY	99.70%	64	604.9586	1 811.85	1 812.86	3	0.002702	1.49	12	32	true
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	P01024_VH0WA9	UniProtKB-HS_20150717_TaD.fasta	187 149.10	100.00%	1.02%	true	SKKTHRHWEASLL	99.70%	71.7	622.3418	1 864.00	1 865.00	3	0.000802	4.291	1304	1319	true
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	P01024_VH0WA9	UniProtKB-HS_20150717_TaD.fasta	187 149.10	100.00%	1.02%	true	SKKTHRHWEASLLR	99.70%	86.5	674.3733	2 020.10	2 021.10	3	0.001402	0.6937	1304	1320	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	100.00%	11.50%	true	SSGGSLPSEKGGHPQEESEESVMSALG	89.80%	17.1	1 025.46	3 073.35	3 074.35	3	0.0102	3.318	293	322	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	100.00%	18.20%	true	SSGGSLPSEKGGHPQEESEESVMSALGE	99.70%	67.9	1 068.47	3 202.39	3 203.39	3	0.009602	2.997	293	323	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	17.00%	true	SSQVQLER	99.70%	59.2	524.2753	1 046.54	1 047.54	2	0.0003781	0.3609	71	79	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	17.00%	true	SSQVQLERLALMDETM	99.70%	65.2	919.9393	1 837.86	1 838.86	2	0.000878	4.828	71	86	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	17.70%	true	SSSYKQFTSSTSY	92.30%	25	780.3524	1 558.69	1 559.69	2	0.01168	7.487	576	589	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	17.70%	true	SSSYKQFTSSTSYNRGDDTFESK	99.70%	55.4	671.0581	2 080.20	2 081.20	4	0.01453	5.418	576	599	true
Isiorm 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	25.00%	true	SSSYKQFTSSTSYNRGDDTFESKSY	90.10%	25.8	733.5844	2 930.31	2 931.29	4	0.02443	8.333	576	601	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	STTAVVTPKE	99.70%	83.8	573.8045	1 145.59	1 146.60	2	0.001578	1.376	174	184	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TaD.fasta	70 942.70	100.00%	18.60%	true	SVFQELKLTGPNQ	99.70%	55.4	816.4288	1 630.84	1 631.84	2	0.01138	6.972	200	214	true
Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	P01861	UniProtKB-HS_20150717_TaD.fasta	35 939.50	87.70%	11.30%	true	SYMHEALJNHVYTKSLSLSLG	85.60%	17.9	784.7392	2 351.20	2 352.18	3	0.0265	11.27	306	326	true
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WV47, A0A087WYE1, A0A087X010, VH0W8	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	SYMHEALJNHVYTKSLSLSPG	99.70%	72.9	779.3925	2 335.16	2 336.15	3	0.0177	7.577	445	465	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A0K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	91.10%	13.60%	false	SYMHEALJNHVYTKSLSLSPG	99.70%	72.9	779.3925	2 335.16	2 336.15	3	0.0177	7.577	451	471	false
Putative uncharacterized protein DKFZp680P15220 OS=Homo sapiens GN=DKFZp680P15220 PE=1 SV=1	Q9N089	UniProtKB-HS_20150717_TaD.fasta	51 723.90	99.60%	7.84%	false	SYMHEALJNHVYTKSLSLSPG	84.60%	32	584.7954	2 335.15	2 336.15	4	0.01453	6.218	451	471	false
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0A087WV47, A0A087WYE1, A0A087X010, VH0W8	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	SYMHEALJNHVYTKSLSLSPGK	73.40%	17.8	616.8175	2 463.24	2 464.24	4	0.007926	3.216	445	466	true
cDNA FLJ7387 OS=Homo sapiens PE=1 SV=1	A0K008	UniProtKB-HS_20150717_TaD.fasta	51 595.70	91.10%	13.60%	false	SYMHEALJNHVYTKSLSLSPGK	73.40%	17.8	616.8175	2 463.24	2 464.24	4	0.007926	3.216	451	472	false
Putative uncharacterized protein DKFZp686G11190 OS=Homo sapiens GN=DKFZp686G11190 PE=2 SV=1	Q6MQZ6	UniProtKB-HS_20150717_TaD.fasta	52 042.10	98.40%	4.42%	true	SYMHEGLJNHVYTKSLSLSPG	99.40%	43.1	774.7205	2 321.14	2 322.13	3	0.0173	7.451	454	474	true
Secretory granule, neuroendocrine protein 1 (7B2 protein), isiorm CRA_a OS=Homo sapiens GN=SGNE1 PE=4 SV=1	A0M24R9H1, P05408, P05408-2	UniProtKB-HS_20150717_TaD.fasta	23 729.90	100.00%	14.60%	true	SVNPLYOGQRLDN	92.70%	25.4	752.3821	1 502.75	1 503.76	2	0.001778	1.182	182	194	true
Secretory granule, neuroendocrine protein 1 (7B2 protein), isiorm CRA_a OS=Homo sapiens GN=SGNE1 PE=4 SV=1	A0M24R9H1, P05408, P05408-2	UniProtKB-HS_20150717_TaD.fasta	23 729.90	100.00%	14.60%	true	SVNPLYOGQRLDNVVA	99.70%	62.8	886.9737	1 771.93	1 772.93	2	0.01108	6.248	182	197	true
Secretory granule, neuroendocrine protein 1 (7B2 protein), isiorm CRA_a OS=Homo sapiens GN=SGNE1 PE=4 SV=1	A0M24R9H1, P05408, P05408-2	UniProtKB-HS_20150717_TaD.fasta	23 729.90	100.00%	14.60%	true	SVNPLYOGQRLDNVAKKSPHFSDKDKD	90.10%	22.1	657.9433	3 284.68	3 285.65	5	0.03725	11.34	182	210	true
Secretory granule, neuroendocrine protein 1 (7B2 protein), isiorm CRA_a OS=Homo sapiens GN=SGNE1 PE=4 SV=1	A0M24R9H1, P05408, P05408-2	UniProtKB-HS_20150717_TaD.fasta	23 729.90	100.00%	14.60%	true	SVNPLYOGQRLDNVAKKSPHFSDKDKDPE	99.70%	49.6	878.702	3 510.78	3 511.75	4	0.04063	11.57	182	212	true
Secretory granule, neuroendocrine protein 1 (7B2 protein), isiorm CRA_a OS=Homo sapiens GN=SGNE1 PE=4 SV=1	A0M24R9H1, P05408, P05408-2	UniProtKB-HS_20150717_TaD.fasta	23 729.90	100.00%	14.60%	true	SVPHFSDKDKDPE	99.30%	44.3	501.2196	1 500.64	1 501.64	3	-0.00009794	-0.06522	200	212	true
DNA segment on chromosome 4 (Uniqe) 234 expressed sequence, isiorm CRA_a OS=Homo sapiens GN=D4S24E PE=4 SV=1	D1DVS7	UniProtKB-HS_20150717_TaD.fasta	24 741.50	100.00%	11.70%	true	SVSPWMSVLSSEKSEGETAAEKSA	99.70%	93.8	951.4586	2 851.35	2 852.35	3	0.0106	3.717	197	222	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2, P09965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	SVSTVLTSKYR	99.70%	67.9	414.233	1 239.68	1 240.69	3	-0.005098	-4.109	132	142	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	SYSTAVVTPKE	99.70%	107	698.8542	1 395.69	1 396.70	2	0.005678	4.065	172	184	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	27.70%	true	SYWKALGISPFHEHNVVTAANDSGPRRYTIAALLSPSYSTAVVTPKE	99.70%	61.8	941.1499	5 640.86	5 641.84	6	0.02367	4.232	134	184	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	27.70%	true	TANDSGPRRYTIAALLSPSYSTAVVTPKE	99.70%	44.1	861.7033	3 442.78	3 443.74	4	0.04713	13.68	153	184	true
Gelatin OS=Homo sapiens GN=GSN PE=1 SV=1	P06396	UniProtKB-HS_20150717_TaD.fasta	85 697.80	99.90%	2.94%	true	TASRGASQAGAPGRVPEARPN	89.50%	31.4	545.2852	2 177.11	2 178.11	4	0.006626	3.042	29	50	true
cDNA FLJ54022, highly similar to Prothombin (EC 3.4.21.5) OS=Homo sapiens PE=2 SV=1	B4DDT3, E9PPT3, P00734	UniProtKB-HS_20150717_TaD.fasta	53 149.10	100.00%	2.76%	true	TATSEYQTFNPR	99.70%	92.6	781.3716	1 560.73	1 561.73	2	0.007778	4.98	164	176	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	27.70%	true	TAVVTPKE	99.70%	71	479.7619	957.509248	958.52046	2	-0.003922	-4.092	176	184	true
SPARC-like 1 (Man9, hev9), isiorm CRA_a OS=Homo sapiens GN=SPARCL1 PE=4 SV=1	A0M24RDE1, Q14515	UniProtKB-HS_20150717_TaD.fasta	75 207.50	99.50%	3.16%	true	TDFLAPGVSSFTDSNQEIST	99.70%	64.6	1 122.53	2 243.05	2 244.03	2	0.02628	11.71	138	158	true
Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	P01024_VH0WA9	UniProtKB-HS_20150717_TaD.fasta	187 149.10	100.00%	1.02%	true	THRHWEASLLR	97.00%	35.8	535.9594	1 604.86	1 605.86	3	0.002802	1.745	1308	1320	true
Transferrin OS=Homo sapiens PE=2 SV=1	A6XGL1, E9K136, P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	15.80%	true	TIALLSPSYSTAVVTPKE	98.50%	145	1 163.63	2 325.24	2 326.22	2	0.02698	11.6	163	184	true
Serpins peptidase inhibitor, clade A (Alpha-1 antiprotease, antitrypsin), member 1, isiorm CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	A0M24R67	UniProtKB-HS_20150717_TaD.fasta	46 709.90	100.00%	6.46%	true	TKSPLFMGKVVNPTQK	99.70%	85.3	592.3371	1 773.99	1 774.99	3	0.008302	4.565	403	418	true
Cell adhesion molecule 3 OS=Homo sapiens GN=CADM3 PE=1 SV=1	Q9N126, Q9N126-2, Q9N126-3	UniProtKB-HS_20150717_TaD.fasta	43 300.70	100.00%	4.77%	true	TLNVNDPSPVSSSST	98.90%	41.7	801.3887	1 600.76	1 601.77	2	0.004778	2.983	313	328	true
Cell adhesion molecule 3 OS=Homo sapiens GN=CADM3 PE=1 SV=1	Q9N126, Q9N126-2, Q9N126-3	UniProtKB-HS_20150717_TaD.fasta	43 300.70	76.50%	4.27%	true	TLNVNDPSPVSSSSTY	63.00%	20.7	882.9244	1 763.83	1 764.83	2	0.01288	7.297	313	329	true
Cell adhesion molecule 3 OS=Homo sapiens GN=CADM3 PE=1 SV=1	Q9N126, Q9N126-2, Q9N126-3	UniProtKB-HS_20150717_TaD.fasta	43 300.70	100.00%	4.77%	true	TLNVNDPSPVSSSSTYHA	99.70%	66									

Apolipoprotein C-I, isoform CRA_a OS=Homo sapiens GN=APOC1 PE=4 SV=1	A0M24R0T8,KTERP1,P02654	UniProtKB-HS_20150717_TaD.fasta	9 332.40	35.60%	12.80%	true	TPDVSALDK	73.00%	44	516.7625	1 031.51	1 032.52	2	-0.00322	-3.12	27	36	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	38.80%	true	TPPQAAQKVVAGVANALAHKYH	97.60%	28.5	634.099	2 532.37	2 533.37	4	0.006726	2.655	124	147	true
Uncharacterized protein OS=Homo sapiens PE=1 SV=1	BHE1Z4	UniProtKB-HS_20150717_TaD.fasta	149 943.50	99.30%	0.79%	true	TPWSLARPOG	99.70%	56.4	556.7976	1 111.58	1 112.58	2	0.003078	2.767	528	537	true
Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	A0M87WV47,A0M87WYE1,A0M87X010,VHFW8	UniProtKB-HS_20150717_TaD.fasta	51 152.80	100.00%	13.50%	true	TQKSLSLSPG	95.20%	44.2	509.2831	1 016.55	1 017.56	2	0.001278	1.256	456	465	true
cDNA FLJ73387 OS=Homo sapiens PE=1 SV=1	A0K088	UniProtKB-HS_20150717_TaD.fasta	51 595.70	91.10%	13.60%	false	TQKSLSLSPG	95.20%	44.2	509.2831	1 016.55	1 017.56	2	0.001278	1.256	462	471	false
Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=1	C9C84,C9EUS,P02679,P02679-2	UniProtKB-HS_20150717_TaD.fasta	52 339.20	100.00%	6.94%	true	TSEVKQLIK	89.70%	28.7	523.3148	1 044.62	1 045.63	2	-0.003022	-2.89	80	88	true
cDNA FLJ54622, highly similar to Prothrombin (EC.14.2.1.5) OS=Homo sapiens PE=2 SV=1	B4DDT3,E9PT3,P0734	UniProtKB-HS_20150717_TaD.fasta	53 149.10	100.00%	2.76%	true	TSEYQTFNPR	88.50%	23	495.33	1 388.65	1 389.64	2	0.009378	6.748	166	176	true
Transferrin OS=Homo sapiens PE=2 SV=1	A0XGL1,E9KL36,P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	25.50%	true	TTAVTNPKE	99.70%	80.6	530.2871	1 058.56	1 059.57	2	-0.001222	-1.153	175	184	true
cDNA FLJ57323, highly similar to Synaptotagmin-4 OS=Homo sapiens PE=2 SV=1	B4DM35	UniProtKB-HS_20150717_TaD.fasta	15 375.00	92.60%	10.80%	true	TTSREEDFDEIPTVYG	97.30%	36	840.4162	1 678.82	1 679.81	2	0.01268	7.547	5	19	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.80%	true	TVAEKALQEVKKHREE	99.40%	45	423.8325	2 114.13	2 115.13	5	0.00275	1.3	433	449	true
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	C9V77,P02765	UniProtKB-HS_20150717_TaD.fasta	39 418.50	100.00%	6.79%	true	TVQPSVGAAG	96.80%	39.5	506.2775	998.540448	999.546946	2	0.000781	0.7784	342	352	true
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	C9V77,P02765	UniProtKB-HS_20150717_TaD.fasta	39 418.50	100.00%	6.79%	true	TVQPSVGAAG	85.30%	33.7	528.7886	1 055.56	1 056.57	2	0.001478	1.399	342	353	true
Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	C9V77,P02765	UniProtKB-HS_20150717_TaD.fasta	39 418.50	100.00%	7.64%	true	TVQPSVGAAGPVPVPCGRIHPEV	74.80%	27	685.6414	2 738.54	2 739.52	4	0.01963	7.164	342	368	true
Serum albumin OS=Homo sapiens PE=2 SV=1	Q96G89	UniProtKB-HS_20150717_TaD.fasta	69 084.60	100.00%	9.69%	true	TYETTLK	74.70%	28.5	492.7486	983.482648	984.488546	2	0.001378	1.4	376	383	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.10%	true	TYFFFDLSHGSQV	97.70%	31.9	853.4103	1 704.81	1 705.80	2	0.01638	9.601	42	56	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.10%	true	TYFFFDLSHGSQVQK	99.10%	30.2	459.2288	1 832.89	1 833.89	4	0.001426	0.7776	42	57	true
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A0XNV6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	95.60%	16.20%	true	VAQDLNAPSDWRBGRKDSYETSLLKDDQSAETHSHKQS	83.10%	51.8	827.3801	4 131.86	4 132.87	5	-0.000499	-0.1089	207	243	true
Secreted phosphoprotein 1 (Osteopontin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	A0M24RDE6,P10451-5	UniProtKB-HS_20150717_TaD.fasta	33 843.10	100.00%	17.30%	true	VAQDLNAPSDWRBGRKDSYETSLLKDDQSAETHSHKQS	83.90%	41	827.3801	4 131.86	4 132.84	5	0.0395	8.699	193	229	true
Angiogenin OS=Homo sapiens GN=C2orf80 PE=1 SV=1	BZZE3,C9R80,Q9H1Z8	UniProtKB-HS_20150717_TaD.fasta	13 614.30	100.00%	24.10%	true	VDEKAKEFLGSLKRQ	99.70%	47.7	466.2628	1 861.02	1 862.01	4	0.01613	8.66	17	32	true
IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	Q4PFI2	UniProtKB-HS_20150717_TaD.fasta	25 528.90	99.60%	8.51%	true	VDNALQSGNSQESVTEQDSK	99.70%	48.1	712.6652	2 134.97	2 135.97	3	0.0122	5.713	171	190	true
Plexin domain-containing protein 2 OS=Homo sapiens GN=PLXDC2 PE=1 SV=1	Q6UC71,Q6UC71-2	UniProtKB-HS_20150717_TaD.fasta	59 583.00	99.60%	3.02%	true	VDTNRASVGGQDFEPR	99.70%	62.7	576.6178	1 726.83	1 727.83	3	0.008802	4.631	75	90	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.10%	true	VGAIHAGEYGAEALER	99.70%	50	510.583	1 528.73	1 529.73	3	0.0001021	0.06672	18	32	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.10%	true	VGAIHAGEYGAEALERMFLSFPTTK	99.50%	40.6	861.4337	2 581.28	2 582.27	3	0.0156	6.042	18	41	true
Alpha-2 macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	P01023	UniProtKB-HS_20150717_TaD.fasta	163 289.90	99.80%	0.75%	true	VGVEYSDVMGR	99.70%	82.4	630.2925	1 258.57	1 259.57	2	0.005178	4.111	705	715	true
Xylosyltransferase 1 OS=Homo sapiens GN=XYLT1 PE=1 SV=1	Q8QV38	UniProtKB-HS_20150717_TaD.fasta	107 571.00	94.70%	1.67%	true	VGGGEQPPAPAPRKE	90.10%	38.6	538.9512	1 613.83	1 614.83	3	0.004102	2.54	51	66	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TaD.fasta	70 942.70	100.00%	18.60%	true	VGPKNDPTPNRQWDEEDLMKLVLEYQEKAEKGREH	97.60%	29.9	760.0468	4 554.24	4 555.23	6	0.01277	2.884	571	608	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13521	UniProtKB-HS_20150717_TaD.fasta	70 942.70	100.00%	18.60%	true	VGPKNDPTPNRQWDEEDLMKLVLEYQEKAEKGREHA	97.40%	29.3	796.7396	4 738.39	4 739.35	6	0.04837	10.21	571	610	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	13.60%	true	VGTSAPVPSDNH	99.70%	66.9	626.3029	1 250.59	1 251.60	2	0.002078	1.66	305	317	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	38.80%	true	VHLTPEEKSAVTA	92.10%	40.2	461.2492	1 380.73	1 381.73	3	0.0008021	0.5805	2	14	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	98.10%	54.30%	false	VHLTPEEKSAVTA	92.10%	40.2	461.2492	1 380.73	1 381.73	3	0.0008021	0.5805	2	14	false
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	35.40%	true	VHLTPEEKSAVTALW	98.50%	70.5	840.9591	1 679.90	1 680.90	2	0.01528	9.089	2	16	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	93.00%	54.30%	false	VHLTPEEKSAVTALW	98.50%	70.5	840.9591	1 679.90	1 680.90	2	0.01528	9.089	2	16	false
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	38.80%	true	VHLTPEEKSAVTALWG	99.10%	58.8	869.4663	1 736.92	1 737.92	2	0.008178	4.706	2	17	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	98.10%	54.30%	false	VHLTPEEKSAVTALWG	99.10%	58.8	869.4663	1 736.92	1 737.92	2	0.008178	4.706	2	17	false
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	35.40%	true	VHLTPEEKSAVTALWGKVN	99.20%	92.8	693.7178	2 078.13	2 079.12	3	0.0154	7.408	2	20	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	93.00%	54.30%	false	VHLTPEEKSAVTALWGKVN	99.20%	92.8	693.7178	2 078.13	2 079.12	3	0.0154	7.408	2	20	false
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	38.80%	true	VHLTPEEKSAVTALWGKVVN	69.80%	40.3	726.7423	2 177.21	2 178.19	3	0.0205	9.412	2	21	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	98.10%	54.30%	false	VHLTPEEKSAVTALWGKVVN	69.80%	40.3	726.7423	2 177.21	2 178.19	3	0.0205	9.412	2	21	false
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	35.40%	true	VHLTPEEKSAVTALWGKVVND	91.90%	49.3	765.0871	2 292.24	2 293.22	3	0.0279	12.17	2	22	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	93.00%	54.30%	false	VHLTPEEKSAVTALWGKVVND	91.90%	49.3	765.0871	2 292.24	2 293.22	3	0.0279	12.17	2	22	false
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	38.80%	true	VHLTPEEKSAVTALWGKVVNDVNG	98.30%	54.4	860.1258	2 577.36	2 578.35	3	0.0115	4.461	2	25	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	98.10%	54.30%	false	VHLTPEEKSAVTALWGKVVNDVNG	98.30%	54.4	860.1258	2 577.36	2 578.35	3	0.0115	4.461	2	25	false
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPVZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	38.80%	true	VHLTPEEKSAVTALWGKVVNDVNGGALGR	98.70%	52	791.1718	3 160.66	3 161.66	4	0.006126	1.938	2	31	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	98.10%	54.30%	false	VHLTPEEKSAVTALWGKVVNDVNGGALGR	98.70%	52	791.1718	3 160.66	3 161.66	4	0.006126	1.938	2	31	false
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	98.10%	54.30%	true	VHLTPEEKSAVTALWGKVVNDVNGGALGRLLVYVPTKRFESFGDLSTPDVNMGN	80.50%	20.2	891.3198	6 232.19	6 233.13	7	0.0616	9.882	2	58	true
Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	BVL17.Q4TWP87	UniProtKB-HS_20150717_TaD.fasta	11 483.80	93.00%	54.30%	true	VHLTPEEKSAVTALWGKVVNDVNGGALGRLLVYVPTKRFESFGDLSTPDVNMGN	98.80%	87.6	1 247.26	6 231.25	6 232.19	5	0.07015	11.26	2	58	true
Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	A0N071,P02642	UniProtKB-HS_20150717_TaD.fasta	16 055.20	77.30%	21.10%	true	VHLTPEEKTAVN	95.30%	43.1	446.5732	1 336.70	1 337.71	3	-0.0009979	-0.746	2	13	true
cDNA FLJ76290, highly similar to Homo sapiens TIA1 cytosolic granule-associated RNA binding protein-like 1 (TIAL1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	A0K5CA,Q01085,Q01085-2,Q01085-2	UniProtKB-HS_20150717_TaD.fasta	41 575.90	69.40%	2.40%	true	VIPPNQAG	77.80%	39.5	446.7496	891.484648	892.488846	2	0.003078	3.449	358	366	true
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909,P10909-2,P10909-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	18.80%	true	VKLFDSDDPTVTVPEV	81.80%	43.7	928.5141	1 837.61	1 838.62	2	-0.0001219	-0.06563			

Transferrin OS=Homo sapiens PE=2 SV=1	A6NGL1,ENK136,P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	25.50%	true	VLDVAVRGSFANVAWVWF	98.10%	32.3	932.5313	1 863.05	1 864.04	2	0.01138	6.104	36	53	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPYZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	21.10%	true	VLGAFSDGLAHLDLNL	97.60%	29.6	771.4037	1 540.79	1 541.80	2	0.004078	2.645	68	82	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPYZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	21.10%	true	VLGAFSDGLAHLDLNLK	99.70%	58.7	557.3024	1 668.89	1 669.89	3	0.001602	0.9594	68	83	true
DNA segment on chromosome 4 (Uniqseq) 234 expressed sequence, isoform CRA_a OS=Homo sapiens GN=D48236 PE=4 SV=1	D1DVS7	UniProtKB-HS_20150717_TaD.fasta	24 741.50	99.80%	8.56%	true	VLSSEKLSQEQTAEAKSA	99.70%	66.2	693.3465	2 077.02	2 078.01	3	0.0113	5.479	204	222	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	36.60%	true	VLSPADKTNVK	99.70%	69.1	391.227	1 170.66	1 171.67	3	-0.001798	-1.535	2	12	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVKA	86.10%	31	414.9063	1 241.70	1 242.71	3	-0.000979	-0.803	2	13	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVAAA	95.50%	38.6	657.3789	1 312.74	1 313.74	2	0.008078	6.149	2	14	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVKAAW	99.70%	61.6	500.6131	1 498.82	1 499.82	3	0.003002	2.002	2	15	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVKAAWG	94.80%	39.2	519.6205	1 555.84	1 556.84	3	0.007302	2.378	2	16	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	48.60%	true	VLSPADKTNVKAAGKVG	99.70%	38.5	614.349	1 840.03	1 841.03	3	0.004302	2.337	2	19	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	27.50%	true	VLSPADKTNVKAAGKVGGA	74.20%	19	638.0317	1 911.07	1 912.07	3	0.0153	8.003	2	20	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVKAAGKVGGAH	97.40%	38.8	513.038	2 048.12	2 049.12	4	0.006026	2.941	2	21	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVKAAGKVGGAHA	99.50%	146	707.3966	2 119.17	2 120.16	3	0.014	6.604	2	22	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	48.60%	true	VLSPADKTNVKAAGKVGGAHAG	99.20%	32.1	436.2427	2 176.18	2 177.18	5	0.00165	0.7579	2	23	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVKAAGKVGGAHAGEY	99.30%	41.1	618.0811	2 468.30	2 469.29	4	0.01393	5.64	2	25	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	52.80%	true	VLSPADKTNVKAAGKVGGAHAGEYGY	99.70%	44.8	632.3374	2 525.32	2 526.31	4	0.01763	6.977	2	26	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	48.60%	true	VLSPADKTNVKAAGKVGGAHAGEYGAELERMLF	99.70%	43.9	718.1772	3 585.85	3 586.85	5	0.00915	2.551	2	35	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	48.60%	true	VLSPADKTNVKAAGKVGGAHAGEYGAELERMLFSPT	87.00%	22	1 065.52	4 018.06	4 019.05	4	0.02153	5.356	2	39	true
Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1MGQ2.P69965	UniProtKB-HS_20150717_TaD.fasta	15 257.60	100.00%	48.60%	true	VLSPADKTNVKAAGKVGGAHAGEYGAELERMLFSPTTKTYPPHFDLSHG	95.10%	23.6	925.8073	5 548.80	5 549.77	6	0.03307	5.959	2	52	true
cDNA FLJ50735, highly similar to Calyculin-3 OS=Homo sapiens PE=2 SV=1	B4DRB1.B75U4.Q9BQ79	UniProtKB-HS_20150717_TaD.fasta	106 097.30	99.80%	3.03%	true	VLSQQFLHRGHOPPPMAGHLSASSHN	99.70%	38.4	641.9236	3 204.58	3 205.58	5	0.00175	0.5459	813	841	true
Radin OS=Homo sapiens GN=RDXX PE=2 SV=1	B0Y3H.P35241.P35241-5	UniProtKB-HS_20150717_TaD.fasta	68 565.50	87.50%	1.89%	true	VMSAPPPPPPP	92.20%	56.2	543.7883	1 085.56	1 086.57	2	0.003878	3.589	466	476	true
Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	P02675.V9HVVY1	UniProtKB-HS_20150717_TaD.fasta	59 928.60	100.00%	8.55%	true	VNDNEEGFFSAR	99.70%	81.3	692.8167	1 383.62	1 384.61	2	0.01338	9.662	33	44	true
Isform 2 of Fibrinogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	UniProtKB-HS_20150717_TaD.fasta	69 756.90	100.00%	12.00%	true	VPDVPGNFK	97.30%	47	543.3046	1 084.59	1 085.60	2	0.002778	2.559	229	238	true
Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13321	UniProtKB-HS_20150717_TaD.fasta	79 942.70	100.00%	18.60%	true	VPGQGSDDLQEEHQEQAKEHNLQGGSETDKLAPVS	99.70%	103	1 088.28	4 349.07	4 350.05	4	0.02843	6.535	527	566	true
Cholecystikinin OS=Homo sapiens GN=CCK PE=1 SV=1	P06307.Q6FG82	UniProtKB-HS_20150717_TaD.fasta	12 669.60	90.70%	16.50%	true	VPPADPAGSGLORAELEAPR	95.00%	30.7	640.0019	1 916.98	1 917.98	3	0.0132	6.883	23	41	true
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P02649	UniProtKB-HS_20150717_TaD.fasta	36 153.50	100.00%	37.50%	true	VQAAVGTSAPVPSDNH	99.70%	103	810.9066	1 619.80	1 620.80	2	0.008278	5.107	301	317	true
Proopiomelanocortin GPR37L1 OS=Homo sapiens GN=GPR37L1 PE=1 SV=2	O60883	UniProtKB-HS_20150717_TaD.fasta	52 770.60	99.40%	4.78%	true	VSGGAPLHLGRHRAETQEQSRSS	99.30%	43.8	626.0742	2 500.27	2 501.27	4	0.003226	1.29	22	44	true
Cystatin C OS=Homo sapiens GN=CST3 PE=1 SV=1	P01034	UniProtKB-HS_20150717_TaD.fasta	15 799.20	99.80%	9.59%	true	VSPAAGSSPGKPPR	99.70%	101	436.5738	1 306.70	1 307.71	3	0.0001021	0.07804	21	34	true
cDNA FLJ54802, highly similar to Integrin alpha-10 OS=Homo sapiens PE=2 SV=1	BHE2A1	UniProtKB-HS_20150717_TaD.fasta	119 352.30	55.20%	0.73%	true	VTFALDNT	77.00%	40.5	440.7234	879.43248	880.44146	2	-0.001622	-1.842	723	730	true
cDNA FLJ50362, highly similar to Hepatocyte nuclear factor 3-alpha OS=Homo sapiens PE=2 SV=1	BHE257.P53117.P53117-2	UniProtKB-HS_20150717_TaD.fasta	45 440.90	28.60%	2.05%	true	VYTRSPIEP	66.20%	24.2	500.279	998.543448	999.547066	2	0.003678	3.68	411	419	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPYZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	21.10%	true	VVAGVANALAHK	99.70%	64.7	383.8946	1 148.66	1 149.67	3	-0.004598	-3.999	134	145	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPYZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	21.10%	true	VVAGVANALAHKYH	99.70%	118	483.9369	1 448.79	1 449.80	3	0.0001021	0.07039	134	147	true
Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	A1N071.P02042	UniProtKB-HS_20150717_TaD.fasta	16 055.20	77.20%	21.10%	false	VVAGVANALAHKYH	78.70%	19.9	483.9362	1 448.79	1 449.80	3	-0.001998	-1.378	134	147	false
Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P19099.P19099-2.P19099-5	UniProtKB-HS_20150717_TaD.fasta	52 495.00	100.00%	19.80%	true	VKLFDSDDPTVTVYVEV	99.70%	82.9	979.0562	1 956.10	1 957.09	2	0.01568	8.011	406	423	true
Isform 3 of Apical endosomal glycoprotein OS=Homo sapiens GN=MAMDC4	Q6LXC1-3	UniProtKB-HS_20150717_TaD.fasta	104 432.80	64.90%	0.94%	true	WGAPPPPPP	87.60%	46.7	458.2312	914.447848	915.472546	2	-0.01742	-19.03	945	953	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	99.20%	1.48%	true	VFMSDTREE	93.00%	45	589.2469	1 176.48	1 177.48	2	0.003478	2.954	429	437	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	100.00%	8.86%	true	VGEEGAPGWQQGDLQDTKENREEA	99.70%	65.9	741.5942	2 962.35	2 963.34	4	0.01433	4.834	474	499	true
E3-16 OS=Homo sapiens PE=2 SV=1	Q7Z5X.Q9NX12.Q9Y287	UniProtKB-HS_20150717_TaD.fasta	30 426.30	100.00%	10.20%	true	YIKDDVILNEPSADAPAA	95.30%	39.5	951.4928	1 900.97	1 901.95	2	0.02998	15.24	93	110	true
Secreted phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	A6XMY6	UniProtKB-HS_20150717_TaD.fasta	35 405.50	68.30%	17.50%	true	YKAPVAQDNLNAPSOWDSRGSYETSLEKDDQSAETHSHKQS	89.20%	40.8	785.0402	4 704.20	4 705.20	6	0.006741	0.1433	202	243	true
Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P05060	UniProtKB-HS_20150717_TaD.fasta	78 276.10	100.00%	8.86%	true	VLYNGEAGPWQQGDLQDTKENREEA	99.70%	71.9	839.1421	3 352.54	3 353.53	4	0.01563	4.46	471	499	true
Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=1	H1BLZS.Q92841.Q92841-1.Q92841-2.Q92841-3	UniProtKB-HS_20150717_TaD.fasta	80 441.30	99.00%	1.37%	true	YPPPPPPPPP	99.60%	64.9	528.2825	1 054.55	1 055.56	2	0.001378	1.306	719	728	true
Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	A4D1SL.P01303	UniProtKB-HS_20150717_TaD.fasta	10 852.30	100.00%	20.60%	true	YPSKFDNPGEDAPAE	98.40%	38.3	793.8536	1 585.69	1 586.70	2	0.002778	1.751	29	43	true
Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	A4D1SL.P01303	UniProtKB-HS_20150717_TaD.fasta	10 852.30	100.00%	20.60%	true	YPSKFDNPGEDAPAEID	99.70%	65.8	851.3675	1 700.72	1 701.72	2	0.003578	2.103	29	44	true
Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	A4D1SL.P01303	UniProtKB-HS_20150717_TaD.fasta	10 852.30	100.00%	20.60%	true	YPSKFDNPGEDAPAEADMA	84.00%	23.8	952.4138	1 902.81	1 903.80	2	0.01858	9.758	29	46	true
Neuropeptide Y OS=Homo sapiens GN=NPY PE=2 SV=1	A4D1SL.P01303	UniProtKB-HS_20150717_TaD.fasta	10 852.30	100.00%	20.60%	true	YPSKFDNPGEDAPAEADMARY	86.80%	20.3	741.6647	2 221.97	2 222.97	3	0.0134	6.029	29	48	true
Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	O13240	UniProtKB-HS_20150717_TaD.fasta	67 257.90	100.00%	17.40%	true	YQCVAAFPFK	90.00%	35.5	539.291	1 076.57	1 077.57	2	0.001878	1.743	269	278	true
Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	DPYZUS.P68871	UniProtKB-HS_20150717_TaD.fasta	15 998.00	100.00%	35.40%	true	YQKVAGVANALAHKYH	99.40%	44.2	468.0087	1 868.01	1 869.01	4	0.00002066	0.01394	131	147	true
Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	A1N071.P02042	UniProtKB-HS_20150717_TaD.fasta	16 055.20	77.20%	21.10%	false	YQKVAGVANALAHKYH	99.40%	44.2	468.0087	1 868.01	1 869.01	4	0.00002066	0.01394	131	147	false
Transferrin OS=Homo sapiens PE=2 SV=1	A6NGL1,ENK136,P02766	UniProtKB-HS_20150717_TaD.fasta	20 198.60	100.00%	27.70%	true	YSTAVTNPKE	99.70%	99.2	655.3383	1 388.66	1 389.66	2	0.003878	4.488	173	184	true

**Table S3.** List of peptidogenic proteins identified in CSF

#	Protein names	Accession Number	Molecular Weight	Control (number of identified peptide fragments)																		Viral meningitis (number of identified peptide fragments)				Bacterial meningitis (number of identified peptide fragments)							
				Patient-1	Patient-2	Patient-3	Patient-4	Patient-5	Patient-6	Patient-7	Patient-8	Patient-9	Patient-10	Patient-11	Patient-12	Patient-13	Patient-14	Patient-15	Patient-16	Patient-17	Patient-18	Patient-19	Patient-20	Patient-1	Patient-2	Patient-3	Patient-4	Patient-1	Patient-2	Patient-3	Patient-4		
1	Serpine peptidase inhibitor, clade A (Alpha-1 antitrypsin, antitrypsin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	MM458B47	47 kDa	3	5	3	4	5	5	3	4	4	3	3	3	3	2	2	1	3	3	3	9	6	8	8	14	82	14	9			
2	Transferrin OS=Homo sapiens PE=2 SV=1	M0GL1(+2)	20 kDa	14	21	21	18	18	14	17	18	16	17	17	14	15	17	17	14	17	15	20	14	10	13	8	6	22	8	4			
3	Serum albumin OS=Homo sapiens PE=2 SV=1	Q5SG09	69 kDa	5	7	7	7	8	7	6	7	5	12	7	8	6	7	4	3	6	10	9	2	19	18	9	14	10	12	47	97		
4	Neurosecretory protein VGF OS=Homo sapiens GN=VGF PE=1 SV=2	Q15260	67 kDa	17	11	14	5	4	11	9	11	4	10	20	12	8	7	11	6	7	12	8	3	2	11	27	3	93	12	0	0		
5	Isoform 2 of Fibronogen alpha chain OS=Homo sapiens GN=FGA	P02671-2	70 kDa	15	2	1	5	3	3	8	9	21	17	4	16	16	7	7	2	2	4	5	11	4	22	17	14	13	83	59	0	0	
6	Prostaglandin D2 synthase 214Da (Brain), isoform CRA_a OS=Homo sapiens GN=PTGDS PE=3 SV=1	MM458B47(+1)	21 kDa	15	16	16	15	12	13	17	15	15	17	18	15	14	12	10	11	13	18	10	4	1	9	7	4	10	2	3	2		
7	Chaperin OS=Homo sapiens GN=CLU PE=1 SV=1	P10909(+2)	52 kDa	11	9	13	6	2	13	16	16	14	11	22	15	10	8	11	8	9	11	4	3	2	5	11	1	14	15	0	3		
8	Ferritin binding protein 4, isoform CRA_b OS=Homo sapiens GN=FNBP1 PE=4 SV=1	D1DQ54(+2)	110 kDa	4	6	9	2	4	8	11	5	5	1	10	3	7	7	7	6	1	10	5	4	0	2	1	0	0	0	0	0		
9	Complement C1 OS=Homo sapiens GN=C1 PE=1 SV=2	P01024(+1)	197 kDa	4	1	1	2	2	2	2	2	2	2	4	2	2	2	2	2	1	2	1	2	2	14	0	1	17	42	54	40		
10	Prokasin OS=Homo sapiens GN=PCSK1N PE=1 SV=1	Q9ULG2	27 kDa	4	9	7	3	2	4	9	4	4	1	10	3	6	7	7	3	4	8	5	4	2	9	9	3	9	1	1	0		
11	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	AM087W47(+3)	51 kDa	2	2	1	2	3	12	4	2	2	3	2	3	3	3	1	0	2	2	2	2	22	8	4	12	9	7	22	19		
12	Ras association (RapGDS/RAF-1) and pleckstrin homology domain 1, isoform CRA_b OS=Homo sapiens GN=RAPH1 PE=1 SV=1	CY8053	141 kDa	3	2	4	0	0	2	8	4	3	2	7	4	0	5	3	0	0	6	0	0	0	0	0	0	0	0	0	0	0	
13	Chaperonin A OS=Homo sapiens GN=CHGA PE=1 SV=7	P10645	51 kDa	3	3	3	1	1	1	3	5	3	2	3	2	4	3	3	2	3	2	3	2	2	7	17	1	1	99	11	1	0	
14	Secreted phosphoprotein 1 (Oncoferrin, bone sialoprotein 1, early T-lymphocyte activation 1), isoform CRA_c OS=Homo sapiens GN=SPPI PE=4 SV=1	MM458B47(+1)	34 kDa	2	2	2	1	0	3	5	1	2	0	5	4	1	1	1	1	2	2	0	7	1	5	2	105	19	0	0			
15	Complement C-4A OS=Homo sapiens GN=C4A PE=1 SV=2	P0C14(+1)	193 kDa	2	1	1	0	0	2	1	2	1	2	1	0	0	1	0	0	1	0	0	5	3	4	0	3	26	10	10	10		
16	Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	P10560	78 kDa	3	3	4	1	0	2	2	1	4	2	5	4	1	0	2	1	0	3	1	2	3	8	10	1	38	4	0	0		
17	FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDC1 PE=1 SV=2	Q9C9D6	125 kDa	3	0	7	0	0	7	7	5	2	2	7	4	4	2	6	0	2	5	2	0	0	0	0	0	0	0	0	0	0	
18	cDNA FLJ29296, highly similar to Homo sapiens amyloid beta (A4) like protein 1 (A4PL1), mRNA OS=Homo sapiens PE=2 SV=1	B2352(+2)	72 kDa	4	4	8	6	2	8	12	10	6	12	9	7	7	11	6	4	8	4	7	0	5	8	2	3	0	1	0	0		
19	Serpine peptidase inhibitor, clade A (Alpha-1 antitrypsin, antitrypsin), member 3, isoform CRA_c OS=Homo sapiens GN=SERPINA1 PE=3 SV=1	MM458B47(+2)	48 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3	3	0	13	11	5	3			
20	Beta-2-microglobulin OS=Homo sapiens GN=BM PE=1 SV=1	P19750	14 kDa	5	3	2	3	2	2	5	1	3	1	5	4	2	2	2	1	2	5	2	2	4	4	4	2	5	1	1	0	2	
21	Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	P13321	71 kDa	5	4	5	2	1	3	7	3	3	3	4	3	3	3	1	2	3	2	2	0	7	9	2	17	7	2	0	0		
22	Apolipoprotein A-I, isoform CRA_a OS=Homo sapiens GN=APOA1 PE=4 SV=1	MM458B47(+1)	31 kDa	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	
23	Ig kappa chain V-4 region OU OS=Homo sapiens PE=1 SV=1	P11666	12 kDa	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1		
24	Inter-alpha (Globulin) inhibitor IH (Plasma Kallikrein-sensitive glycoprotein) OS=Homo sapiens GN=IH1H4 PE=2 SV=1	B23M59(+1)	103 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	10	0	1	0	7	33	11	14			
25	Hemoglobin, beta OS=Homo sapiens GN=HBB PE=3 SV=1	D9Y2J5(+1)	16 kDa	0	0	0	0	0	4	0	2	12	3	14	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
26	Alpha-2 globulin chain OS=Homo sapiens GN=HBA2 PE=3 SV=1	D1M0G2(+1)	15 kDa	0	0	0	0	0	4	0	10	15	1	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
27	Uncharacterized protein OS=Homo sapiens PE=1 SV=1	B4E1Z4	141 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	1	0	2	0	2	0	3	20	2	10		
28	cDNA FLJ10380, highly similar to Calyculin-1 OS=Homo sapiens PE=2 SV=1	B4E2Q1(+2)	108 kDa	2	1	5	2	1	3	4	6	3	3	8	4	2	1	3	1	0	3	1	4	0	4	3	1	8	0	0	0	0	
29	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	P10549	36 kDa	3	1	3	3	1	1	5	11	4	2	9	4	3	1	4	2	7	4	0	2	1	5	3	1	2	2	0	0	0	
30	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	P10323	163 kDa	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	
31	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	P10727	45 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
32	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	P19291(+1)	42 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
33	Secretory granule, neuroendocrine protein 1 (TR2 protein), isoform CRA_b OS=Homo sapiens GN=SGNE1 PE=4 SV=1	MM458B47(+2)	24 kDa	1	1	2	1	1	1	3	1	3	2	1	5	1	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	
34	CP protein OS=Homo sapiens GN=CP PE=2 SV=1	A3PL27(+1)	122 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
35	IgG 1 chain OS=Homo sapiens PE=2 SV=1	S6C4B6	20 kDa	1	0	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	2	1	1	1	1	1	1	1	1	1	
36	cDNA FLJ78499, highly similar to Homo sapiens sortilin 1 (SORT1), mRNA OS=Homo sapiens PE=2 SV=1	A3K4Q1(+1)	92 kDa	2	3	2	2	1	4	4	4	3	2	4	3	2	3	2	2	2	2	2	3	0	0	0	0	0	0	0	0	0	
37	Globulin OS=Homo sapiens GN=G2N PE=1 SV=1	P10596	86 kDa	0	1	0	1	0	1	2	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	1	1	1	1	1	1	1	
38	Vibronectin OS=Homo sapiens GN=VTN PE=4 SV=1	D9DZG2(+1)	54 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
39	Angiogenin OS=Homo sapiens GN=C1orf40 PE=1 SV=1	B23Z51(+2)	14 kDa	1	2	2	2	1	2	2	2	1	2	2	1	2	2	0	2	0	2	2	1	1	1	3	2	3	2	0	0	0	
40	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	P10246	29 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
41	Hemoglobin OS=Homo sapiens GN=HP PE=1 SV=4	P10730	49 kDa	0	0	0	1	0	0	0	1	0	1	0	1	2	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	
42	Serum amyloid A protein OS=Homo sapiens GN=SAAI PE=3 SV=1	D1DQ57	14 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
43	Apolipoprotein C-I, isoform CRA_a OS=Homo sapiens GN=APOC1 PE=4 SV=1	MM458B47(+2)	9 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
44	Proline-rich protein 12 OS=Homo sapiens GN=PRK12 PE=1 SV=2	Q9UL13	130 kDa	2	2	3	1	2	1	3	1	0	1	3	2	1	2	3	1	2	3	1	2	0	0	0	0	0	0	0	0	0	0
45	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	P15109	11 kDa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
46	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHS2 PE=1 SV=1	C9VY7(+1)	39 kDa	0	1	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
47	Serpine peptidase inhibitor, clade A, member 3 OS=Homo sapiens GN=AGT PE=3 SV=1	B23BE2(+7)	53 kDa	2	1	3	2	1	1	3	2	2	1	3	1	3	2	1	0	1	2	1	0	2	0	1	0	1	0	1	1	1	
48	Ferritin-1 OS=Homo sapiens GN=FMN1 PE=1 SV=1	P10Y30(+1)	147 kDa	1	1	1	1	1	1	2	1	1	1	1	1	1	2	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0
49	E3-38 OS=Homo sapiens PE=2 SV=1	P23228(+2)	30 kDa	0	1	1	0	0	2	2	1	1	2	2	1	1	1	0	1	0	1	0											















