

Article DOI: <https://doi.org/10.3201/eid2608.191042>

Appendix Table. Total human and parasite proteins identified in plasma-derived EVs from two healthy donors and a chronic Chagas disease patient before and after benznidazole treatment. Proteins were identified by at least one unique peptide. Exclusive unique peptides are shown in the table. Normalized total spectrum count values are also shown in parenthesis. Student's t-test was performed to compare healthy donors with chronic Chagas disease patient before treatment (significant proteins are shown in green). Normalized total spectrum count values were used for the Student's t-test analysis. Human proteins described as classical markers of plasma-derived EVs are shown in italics (reference 9 in main text). Parasite proteins associated to EVs, previously identified in other proteomic studies are shown in bold type (references 11–13 in main text). Appendix Table. Total human and parasite proteins identified in plasma-derived EVs from two healthy donors and a chronic Chagas disease patient before and after benznidazole treatment. Proteins were identified by at least one unique peptide. Exclusive unique peptides are shown in the table. Normalized total spectrum count values are also shown in parenthesis. Student's t-test was performed to compare healthy donors with chronic Chagas disease patient before treatment (significant proteins are shown in green). Normalized total spectrum count values were used for the Student's t-test analysis. Human proteins described as classical markers of plasma-derived EVs are shown in italics (reference 9 in main text). Parasite proteins associated to EVs, previously identified in other proteomic studies are shown in bold type (references 11–13 in main text).

	Accession Number	t test (Healthy / CD_04_pre)	Healthy 1	Healthy 2	Ch_04_pre	Ch_04_post
<i>T. cruzi</i> Protein Name						
ABC transporter OS=Trypanosoma cruzi Dm28c GN=TCDM_08331 PE=4 SV=1	V5BCE1_TRYCR	ND	0	0	1 (0.48)	0
Actin OS=Trypanosoma cruzi GN=Act PE=3 SV=1	I6LE98_TRYCR	ND	0	0	1 (0.48)	0
Dispersed gene family protein 1 (DGF-1). putative OS=Trypanosoma cruzi marinkellei GN=MOQ_004643 PE=4 SV=1	K2MWP1_TRYCR	ND	0	0	0	1 (0.62)
Group of Elongation factor 1-alpha (Fragment) OS=Trypanosoma cruzi GN=EF-1alpha PE=3 SV=1+16	I6LEB2_TRYCR (+16)	ND	0	0	1 (0.48)	1 (0.62)
Group of Histone H2B OS=Trypanosoma cruzi (strain CL Brener) GN=Tr00.1047053511635.10 PE=3 SV=1+1	Q4CTD8_TRYCC (+1)	ND	0	0	1 (0.48)	0
Pyruvate. phosphate dikinase OS=Trypanosoma cruzi marinkellei GN=MOQ_000480 PE=3 SV=1	K2MVM1_TRYCR	ND	0	0	2 (0.96)	0
Recombination initiation protein NBS1 OS=Trypanosoma cruzi Dm28c GN=TCDM_11142 PE=4 SV=1	V5B5K8_TRYCR	ND	0	0	0	1 (0.62)
Uncharacterized protein OS=Trypanosoma cruzi marinkellei GN=MOQ_002108 PE=4 SV=1	K2MQY8_TRYCR	ND	0	0	1 (0.48)	0
Uncharacterized protein OS=Trypanosoma cruzi marinkellei GN=MOQ_003577 PE=4 SV=1	K2MBN5_TRYCR	ND	0	0	1 (0.96)	0
Uncharacterized protein OS=Trypanosoma cruzi marinkellei GN=MOQ_003666 PE=4 SV=1	K2N3I6_TRYCR	ND	0	0	1 (0.48)	0
Uncharacterized protein OS=Trypanosoma cruzi marinkellei GN=MOQ_007485 PE=4 SV=1	K2NIK7_TRYCR	ND	0	0	1 (0.48)	1 (0.62)
Uncharacterized protein OS=Trypanosoma cruzi marinkellei GN=MOQ_010042 PE=4 SV=1	K2LU69_TRYCR	ND	0	0	1 (0.48)	0
Human Protein Name						
Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	C1S_HUMAN	0.013872895	0(6.03)	0(7.78)	22(76.39)	23(88.66)
HCG40889. isoform CRA_b OS=Homo sapiens GN=hCG_40889 PE=4 SV=1	tr A0A024R962 A0A024R962_HUMAN	0.015242509	0(6.03)	0(7.78)	3(70.15)	2(100.97)
FLJ00385 protein (Fragment) OS=Homo sapiens GN=FLJ00385 PE=1 SV=1	tr Q8NF17 Q8NF17_HUMAN	0.015292422	1(18.09)	1(15.56)	7(108.10)	7(84.35)
cDNA FLJ75416. highly similar to Homo sapiens complement factor H (CFH). mRNA OS=Homo sapiens PE=2 SV=1	tr A8KST0 A8KST0_HUMAN	0.01609827	0(6.03)	0(7.78)	1(66.78)	0(96.04)
Group of Apolipoprotein D (Fragment) OS=Homo sapiens GN=APOD PE=1 SV=1+1	C9JF17_HUMAN (+1)	0.050531134	1(6.03)	1(7.78)	9(25.94)	6(18.47)
C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	C4BPA_HUMAN	0.050765794	0(18.09)	0(31.11)	1(165.76)	1(180.39)
cDNA FLJ51597. highly similar to C4b-binding protein alpha chain OS=Homo sapiens PE=2 SV=1	tr B4E1D8 B4E1D8_HUMAN	0.050765794	0(18.09)	0(31.11)	1(165.76)	0(179.77)
Group of IgG L chain OS=Homo sapiens PE=2 SV=1+1	tr S6B2A1 S6B2A1_HUMAN (+1)	0.062258534	1(12.06)	1(15.56)	0(44.68)	0(40.02)
IGH@ protein OS=Homo sapiens GN=IGH@ PE=1 SV=1	tr Q6GMX6 Q6GMX6_HUMAN	0.06614987	0(12.06)	0(0)	3(106.18)	2(60.34)
Immunoglobulin gamma-1 heavy chain OS=Homo sapiens PE=1 SV=1	sp P0DOX5 IGG1_HUMAN	0.06911193	0(12.06)	0(0)	0(101.86)	1(57.87)
Apolipoprotein A-I. isoform CRA_a OS=Homo sapiens GN=APOA1 PE=3 SV=1	tr A0A024R3E3 A0A024R3E3_HUMAN	0.07005303	0(0)	0(7.78)	24(64.86)	18(55.41)
Putative uncharacterized protein DKFZp686O01196 OS=Homo sapiens GN=DKFZp686O01196 PE=2 SV=1	tr Q6N094 Q6N094_HUMAN	0.072729096	0(12.06)	0(0)	1(97.05)	1(57.87)
Putative uncharacterized protein DKFZp686N02209 OS=Homo sapiens GN=DKFZp686N02209 PE=2 SV=1	tr Q7Z351 Q7Z351_HUMAN	0.073498234	0(12.06)	0(0)	1(96.09)	0(56.03)
Uncharacterized protein OS=Homo sapiens GN=DKFZp686K03196 PE=1 SV=1	tr Q6N095 Q6N095_HUMAN	0.07428375	0(12.06)	0(0)	1(95.13)	1(56.64)
Apolipoprotein B (Including Ag(X) antigen) OS=Homo sapiens GN=APOB PE=4 SV=1	tr C0JYY2 C0JYY2_HUMAN	0.103158824	25(271.35)	23(256.70)	139(186.42)	83(106.51)
Immunoglobulin alpha-2 heavy chain OS=Homo sapiens PE=1 SV=1	sp P0DOX2 IGA2_HUMAN	0.10670707	0(6.03)	0(7.78)	3(15.86)	2(14.16)
Mannan-binding lectin serine protease 1 OS=Homo sapiens GN=MASP1 PE=1 SV=3	MASP1_HUMAN	0.11263748	0(6.03)	0(7.78)	10(15.37)	7(14.16)
Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	A2MG_HUMAN	0.1268302	9(132.66)	9(147.80)	58(205.16)	48(205.02)
cDNA FLJ14473 fis. clone MAMMA1001080. highly similar to Homo sapiens SNC73 protein (SNC73) mRNA OS=Homo sapiens	tr Q96K68 Q96K68_HUMAN	0.13510403	0(18.09)	0(23.34)	1(41.80)	1(37.56)
Group of Protein S isoform 1 (Fragment) OS=Homo sapiens GN=PROS1 PE=2 SV=1+1	tr A0A0S224K3 A0A0S224K3_HUMAN (+1)	0.1440487	0(0)	1(7.78)	20(33.15)	19(40.63)
Epididymis secretory sperm binding protein Li 62p OS=Homo sapiens GN=HEL-5-62p PE=2 SV=1	tr V9HWA9 V9HWA9_HUMAN	0.14834405	1(6.03)	2(23.34)	61(77.83)	49(79.42)
Fibronectin 1. isoform CRA_n OS=Homo sapiens GN=FN1 PE=4 SV=1	tr A0A024R462 A0A024R462_HUMAN	0.14999393	1(6.03)	4(31.11)	62(109.06)	53(107.74)

Anti-FactorVIII scFv (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2KBC6 A2KBC6_HUMAN	0.1685051	0(6.03)	0(7.78)	1(12.49)	2(9.85)
Group of Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1+3	tr Q53G76 Q53G76_HUMAN (+3)	0.18459478	5(60.30)	4(46.67)	10(13.93)	9(8.00)
Apolipoprotein M OS=Homo sapiens GN=APOM PE=1 SV=2	APOM_HUMAN	0.18785997	1(6.03)	1(7.78)	3(1.92)	2(2.46)
Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	ZA2G_HUMAN	0.18785997	1(6.03)	1(7.78)	3(1.92)	3(3.08)
Group of IGHV1-2 protein (Fragment) OS=Homo sapiens GN=IGHV1-2 PE=4 SV=1+2	tr A0A0F7T7M3 A0A0F7T7M3_HUMAN (+2)	0.18785997	0(6.03)	0(7.78)	1(1.92)	1(2.46)
IgG H chain OS=Homo sapiens PE=2 SV=1	tr S6BGF5 S6BGF5_HUMAN	0.20139302	0(0)	0(0)	1(12.01)	1(10.47)
Immunoglobulin heavy chain variant (Fragment) OS=Homo sapiens PE=2 SV=1	tr Q9NPP6 Q9NPP6_HUMAN	0.22295393	0(18.09)	0(23.34)	1(33.15)	1(23.40)
Lectin galactoside-binding soluble 3 binding protein isoform 1 (Fragment) OS=Homo sapiens GN=LGALS3BP PE=2 SV=1	tr A0A0S2Z3Y1 A0A0S2Z3Y1_HUMAN	0.23785137	1(6.03)	0(0)	12(16.34)	11(15.39)
Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	DCD_HUMAN	0.23827662	1(12.06)	1(7.78)	1(0.48)	2(1.23)
Group of Annexin OS=Homo sapiens GN=ANXA2 PE=3 SV=1+1	tr A0A024R5Z7 A0A024R5Z7_HUMAN (+1)	0.23827662	2(12.06)	1(7.78)	1(0.48)	2(1.23)
Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	TLN1_HUMAN	0.24942042	1(6.03)	1(7.78)	19(10.57)	2(1.23)
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	CLUS_HUMAN	0.25336882	2(12.06)	1(7.78)	14(18.74)	13(20.93)
NANUC-2 heavy chain (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2NKM7 A2NKM7_HUMAN	0.2572878	0(6.03)	0(7.78)	1(3.36)	0(3.69)
Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	APOE_HUMAN	0.25797376	12(132.66)	9(93.35)	20(33.63)	18(34.48)
IGH@ protein OS=Homo sapiens GN=IGH@ PE=2 SV=1	tr Q6P089 Q6P089_HUMAN	0.25961557	0(18.09)	0(23.34)	1(31.23)	1(22.78)
IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1	tr Q6PIL8 Q6PIL8_HUMAN	0.28625292	0(18.09)	0(38.89)	1(65.82)	0(55.41)
F5-20 (Fragment) OS=Homo sapiens GN=F5-20 PE=2 SV=1	tr A0N719 A0N719_HUMAN	0.29252774	1(6.03)	1(7.78)	2(3.84)	1(3.078)
Group of Epididymis luminal protein 114 OS=Homo sapiens GN=HEL114 PE=2 SV=1+2	tr V9HWK2 V9HWK2_HUMAN (+2)	0.3087208	2(12.06)	1(7.78)	6(2.88)	0(0)
Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	TPM4_HUMAN	0.3087208	2(12.06)	1(7.78)	5(2.88)	2(1.23)
Apolipoprotein L1 (Fragment) OS=Homo sapiens GN=APOL1 PE=4 SV=1	tr U5LJ1 U5LJ1_HUMAN	0.31792966	2(24.12)	2(15.56)	7(6.25)	3(4.31)
Immunoglobulin heavy variable 3-74 OS=Homo sapiens GN=IGHV3-74 PE=3 SV=1	sp A0A0B4J1X5 HV374_HUMAN	0.32494876	0(6.03)	0(7.78)	1(9.61)	2(9.23)
Group of IgGfC-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=1+1	A0A087WXI2_HUMAN (+1)	0.3299586	3(18.09)	0(0)	39(36.51)	36(43.10)
Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	GELS_HUMAN	0.33790725	1(6.03)	1(7.78)	7(4.32)	2(1.85)
Group of Integrin beta (Fragment) OS=Homo sapiens PE=3 SV=1+3	H3BM21_HUMAN (+3)	0.35286456	1(12.06)	3(23.34)	4(1.92)	1(0.62)
Lambda-chain (AA -20 to 215) OS=Homo sapiens PE=1 SV=1	tr A2NUT2 A2NUT2_HUMAN	0.35387355	0(36.18)	0(62.23)	2(85.52)	2(96.66)
Integrin alpha-IIb OS=Homo sapiens GN=ITGA2B PE=1 SV=3	ITA2B_HUMAN	0.37255552	2(12.06)	1(7.78)	9(4.32)	4(2.46)
Uncharacterized protein OS=Homo sapiens PE=2 SV=1	tr Q8NEJ1 Q8NEJ1_HUMAN	0.377889	0(36.18)	0(62.23)	2(82.64)	1(92.97)
Group of Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4+1	PZP_HUMAN (+1)	0.38502312	2(12.06)	0(0)	13(21.14)	8(24.63)
Anti-HER3 scFv (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2J422 A2J422_HUMAN	0.39780143	0(6.03)	0(7.78)	1(4.80)	0(4.93)
IGL@ protein OS=Homo sapiens GN=IGL@ PE=1 SV=1	tr Q5FWF9 Q5FWF9_HUMAN	0.40019	0(36.18)	0(62.23)	1(80.24)	1(90.50)
IgG L chain OS=Homo sapiens PE=1 SV=1	tr S6BGD6 S6BGD6_HUMAN	0.4049259	0(36.18)	0(62.23)	1(79.76)	0(89.89)
Uncharacterized protein OS=Homo sapiens PE=1 SV=1	B4E1Z4_HUMAN	0.4100639	0(18.09)	0(46.67)	12(65.34)	8(56.64)
IGL@ protein OS=Homo sapiens GN=IGL@ PE=2 SV=1	tr Q6IN99 Q6IN99_HUMAN	0.4103792	0(36.18)	0(62.23)	1(78.31)	1(88.66)
Truncated beta globin OS=Homo sapiens PE=3 SV=1	tr B3VL12 B3VL12_HUMAN	0.41267264	0(12.06)	0(23.34)	1(4.80)	1(8.62)
IGL@ protein OS=Homo sapiens GN=IGL@ PE=2 SV=1	tr Q6GMW4 Q6GMW4_HUMAN	0.41972768	0(24.12)	0(38.89)	0(48.53)	1(44.94)
SWISS-PROT:P02768-1 Tax_id=9606 Gene_Symbol=ALB Isoform 1 of Serum albumin precursor	P02768-1	0.42335185	3(78.39)	5(124.46)	30(152.30)	30(139.76)
Putative uncharacterized protein DKFZp686K18196 (Fragment) OS=Homo sapiens GN=DKFZp686K18196 PE=2 SV=1	tr Q6N092 Q6N092_HUMAN	0.44704914	0(0)	1(23.34)	1(35.55)	1(29.55)
Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1	APOC3_HUMAN	0.4477036	1(18.09)	1(7.78)	2(2.40)	1(2.46)
Rheumatoid factor RF-IP14 (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2J1N0 A2J1N0_HUMAN	0.45524907	0(6.03)	0(7.78)	1(8.65)	0(8.00)
cDNA FLJ41981 fis. clone SMINT2011888. highly similar to Protein Tro alpha1 H.myeloma OS=Homo sapiens PE=2 SV=1	tr Q6ZVX0 Q6ZVX0_HUMAN	0.45524907	0(24.12)	0(31.11)	1(34.59)	1(27.09)
Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	FIBA_HUMAN	0.47599223	15(223.11)	12(264.48)	42(205.16)	48(286.28)
Rheumatoid factor RF-ET6 (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2J1N5 A2J1N5_HUMAN	0.47872153	0(6.03)	0(7.78)	2(5.29)	0(4.93)
Apolipoprotein A-1 A175P variant (Fragment) OS=Homo sapiens PE=4 SV=1	tr Q8TDB0 Q8TDB0_HUMAN	0.48055565	0(0)	0(7.78)	1(11.05)	0(14.16)
Group of Serum amyloid A protein OS=Homo sapiens PE=2 SV=1+1	tr B2R5G8 B2R5G8_HUMAN (+1)	0.49431434	2(18.09)	1(7.78)	4(3.84)	4(6.16)
CD5 antigen-like OS=Homo sapiens GN=CD5L PE=1 SV=1	CD5L_HUMAN	0.5407139	1(6.03)	3(23.34)	14(27.87)	10(26.47)
Group of Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=1+1	A0A087WYJ9_HUMAN (+1)	0.5515356	1(223.11)	1(350.04)	2(193.14)	2(177.93)
Hemoglobin beta subunit variant (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	tr Q9UK54 Q9UK54_HUMAN	0.55184966	0(0)	1(7.78)	1(9.61)	1(11.08)

Group of Apolipoprotein A-II (Fragment) OS=Homo sapiens GN=APOA2 PE=1 SV=1+3	V9GYG9_HUMAN (+3)	0.597903	1(12.06)	1(7.78)	4(7.21)	4(6.77)
Putative uncharacterized protein DKFZp781M0386 OS=Homo sapiens GN=DKFZp781M0386 PE=2 SV=1	tr Q5CZ94 Q5CZ94_HUMAN	0.59881264	0(24.12)	0(38.89)	1(40.84)	0(35.71)
Putative uncharacterized protein DKFZp686C02220 (Fragment) OS=Homo sapiens GN=DKFZp686C02220 PE=2 SV=1	tr Q6N091 Q6N091_HUMAN	0.63477117	0(18.09)	0(23.34)	2(17.78)	1(16.00)
Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=4	H0Y300_HUMAN	0.63517284	0(36.18)	3(132.24)	9(137.89)	9(150.84)
Immunoglobulin mu heavy chain OS=Homo sapiens PE=1 SV=1	sp P0DOX6 IGM_HUMAN	0.6488087	0(144.72)	0(264.48)	0(140.77)	1(137.91)
Full-length cDNA clone CSDD006YL02 of Neuroblastoma of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1	tr Q86TT1 Q86TT1_HUMAN	0.66562855	0(180.90)	0(311.15)	2(180.65)	1(169.31)
cDNA FLJ52243, highly similar to Heat-shock protein beta-1 OS=Homo sapiens PE=2 SV=1	tr B4DL87 B4DL87_HUMAN	0.6666667	2(12.06)	0(0)	0(0)	0(0)
Group of Plakophilin 1 (Ectodermal dysplasia/skin fragility syndrome), isoform CRA_a OS=Homo sapiens GN=PKP1 PE=4 SV=1	tr A0A024R952 A0A024R952_HUMAN (+1)	0.6666667	3(24.12)	0(0)	0(0)	0(0)
Group of Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3+1	PLAK_HUMAN (+1)	0.68150413	2(18.09)	0(0)	1(0.48)	2(1.23)
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	DESP_HUMAN	0.68338615	8(48.24)	0(0)	3(1.44)	2(1.23)
Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D OS=Homo sapiens GN=SSC5D PE=1 SV=3	SRCRL_HUMAN	0.6913734	1(6.03)	0(0)	9(5.77)	8(6.16)
Lactoferrin OS=Homo sapiens PE=2 SV=1	tr Q2TUW9 Q2TUW9_HUMAN	0.7017695	0(0)	1(7.78)	1(0.48)	2(1.85)
Immunoglobulin kappa light chain OS=Homo sapiens PE=1 SV=1	sp P0DOX7 IGK_HUMAN	0.7055189	0(18.09)	0(38.89)	3(37.48)	3(28.32)
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	HORN_HUMAN	0.7364676	2(12.06)	0(0)	3(1.44)	4(2.46)
Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	DSG1_HUMAN	0.7614258	2(12.06)	0(0)	3(1.92)	4(3.08)
Desmocollin 1, isoform CRA_b OS=Homo sapiens GN=DSC1 PE=4 SV=1	tr Q9HB00 Q9HB00_HUMAN	0.7614258	1(6.03)	0(0)	2(0.96)	2(1.23)
Group of Catalase OS=Homo sapiens GN=CAT PE=1 SV=3+1	CATA_HUMAN (+1)	0.7614258	1(6.03)	0(0)	2(0.96)	2(1.23)
Group of 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2+1	1433G_HUMAN (+1)	0.7614258	1(6.03)	0(0)	1(0.96)	1(0.62)
Beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1	tr C8C504 C8C504_HUMAN	0.76575434	0(12.06)	0(23.34)	0(13.93)	1(18.47)
Testicular tissue protein Li 70 OS=Homo sapiens PE=2 SV=1	tr A0A140VJ6 A0A140VJ6_HUMAN	0.7736892	1(120.60)	1(155.57)	3(126.84)	3(170.54)
Group of Apolipoprotein C-IV OS=Homo sapiens GN=APOC4 PE=1 SV=1+1	APOC4_HUMAN (+1)	0.77810544	0(0)	1(7.78)	1(1.44)	1(0.62)
Group of Immunoglobulin kappa variable 2-29 OS=Homo sapiens GN=IGKV2-29 PE=3 SV=2+1	sp A2NJV5 KV229_HUMAN (+1)	0.77810544	0(0)	0(7.78)	1(1.44)	0(1.23)
Group of Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=1+1	QSHY54_HUMAN (+1)	0.82736206	4(24.12)	2(15.56)	30(17.78)	3(1.85)
Apolipoprotein E (Fragment) OS=Homo sapiens GN=APOE PE=4 SV=1	tr Q8TCZ8 Q8TCZ8_HUMAN	0.84085125	0(12.06)	0(0)	2(3.36)	2(3.69)
Serum albumin (Fragment) OS=Homo sapiens GN=ALB PE=1 SV=1	H7C013_HUMAN	0.8529773	0(42.21)	0(70.01)	1(50.45)	0(43.10)
sp HBB_HUMAN	sp HBB_HUMAN	0.8555339	0(12.06)	1(31.11)	1(17.78)	1(21.55)
Hemoglobin subunit delta (Fragment) OS=Homo sapiens GN=HBD PE=1 SV=1	E9PEW8_HUMAN	0.86168706	0(0)	1(7.78)	1(2.40)	1(3.69)
Lipoprotein, Lp(A) OS=Homo sapiens GN=LPA PE=3 SV=1	tr Q1HP67 Q1HP67_HUMAN	0.86502707	1(6.03)	2(38.89)	14(16.34)	17(24.01)
Complement C1q subcomponent subunit A OS=Homo sapiens GN=C1QA PE=1 SV=2	C1QA_HUMAN	0.86994517	0(0)	1(7.78)	5(5.29)	2(5.54)
GCT-A9 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A125QY5 A0A125QY5_HUMAN	0.86994517	0(0)	1(7.78)	2(5.29)	2(7.39)
APOA4 protein (Fragment) OS=Homo sapiens GN=APOA4 PE=2 SV=1	tr Q13784 Q13784_HUMAN	0.87447494	1(6.03)	1(7.78)	0(7.21)	0(7.39)
Protein APOC4-APOC2 OS=Homo sapiens GN=APOC4-APOC2 PE=1 SV=1	K7ER74_HUMAN	0.8969333	2(12.06)	0(0)	3(4.32)	3(5.54)
Epididymis secretory sperm binding protein Li 89n OS=Homo sapiens GN=HEL-S-89n PE=2 SV=1	tr V9HWB4 V9HWB4_HUMAN	0.9256494	0(6.03)	0(0)	4(2.40)	2(1.85)
Group of Apolipoprotein C-I (Fragment) OS=Homo sapiens GN=APOC1 PE=1 SV=1+1	K7ER19_HUMAN (+1)	0.9256494	1(6.03)	0(0)	3(2.40)	3(2.46)
von Willebrand factor OS=Homo sapiens GN=VWF PE=1 SV=4	VWF_HUMAN	0.9262151	1(277.38)	1(155.57)	5(204.19)	5(174.85)
cDNA FLJ53952, highly similar to Fibrinogen beta chain OS=Homo sapiens PE=2 SV=1	tr B4E1D3 B4E1D3_HUMAN	0.93794954	0(150.75)	0(210.03)	1(175.37)	0(189.01)
Haptoglobin (Fragment) OS=Homo sapiens GN=HP PE=4 SV=1	tr A0A0U4EXB4 A0A0U4EXB4_HUMAN	0.93948036	1(18.09)	2(62.23)	4(36.51)	4(36.94)
Group of IGHV3-72 protein (Fragment) OS=Homo sapiens GN=IGHV3-72 PE=4 SV=1+1	tr A0A0F7TAG7 A0A0F7TAG7_HUMAN (+1)	0.95760846	1(6.03)	0(0)	2(3.36)	2(3.08)
von Willebrand factor OS=Homo sapiens GN=VWF PE=4 SV=1	tr L8E853 L8E853_HUMAN	0.9694858	0(259.29)	0(147.80)	2(198.91)	2(169.31)
Fibrinogen gamma chain, isoform CRA_a OS=Homo sapiens GN=FGG PE=4 SV=1	tr D3DP16 D3DP16_HUMAN	0.98054105	0(90.45)	0(116.68)	1(104.26)	1(147.76)
Group of Immunoglobulin heavy variable 1-3 OS=Homo sapiens GN=IGHV1-3 PE=3 SV=1+1	sp A0A0C4DH29 HVH103_HUMAN (+1)	0.98388535	1(6.03)	0(0)	3(2.88)	1(2.46)
Cryocrycstalglobulin CC1 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr B1N7B6 B1N7B6_HUMAN	0.98388535	1(6.03)	0(0)	2(2.88)	2(4.31)
Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=2 SV=2	HPTR_HUMAN	0.98636234	0(36.18)	0(93.34)	5(65.82)	2(73.88)
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	MYH9_HUMAN	0.98683375	2(12.06)	0(0)	12(6.25)	10(6.62)
Immunoglobulin J chain OS=Homo sapiens GN=JCHAIN PE=1 SV=4	IGJ_HUMAN	0.9907701	1(6.03)	1(31.11)	5(18.26)	6(16.01)
Cold agglutinin FS-1 L-chain (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2NB45 A2NB45_HUMAN	0.99568194	0(0)	0(7.78)	2(3.84)	1(2.46)
Epididymis secretory sperm binding protein Li 78p OS=Homo sapiens GN=HEL-S-78p PE=2 SV=1	tr V9HVY1 V9HVY1_HUMAN	0.9973346	0(150.75)	0(210.03)	2(180.17)	3(195.78)

Group of Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2+1	SHRM3_HUMAN (+1)	0.2046276	1(53.44)	1(77.04)	1(3.84)	1(4.94)
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	ANXA1_HUMAN	0.6666667	1(5.94)	0(0)	0(0)	0(0)
C-type lectin domain family 7 member A OS=Homo sapiens GN=CLEC7A PE=1 SV=1	CLC7A_HUMAN	0.6666667	1(5.94)	0(0)	0(0)	0(0)
E3 ubiquitin-protein ligase HERC2 OS=Homo sapiens GN=HERC2 PE=1 SV=2	HERC2_HUMAN	0.6666667	1(5.94)	0(0)	0(0)	0(0)
Group of Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=1+1	I6L8B7_HUMAN (+1)	0.6666667	1(11.87)	0(0)	0(0)	0(0)
Galectin-7 OS=Homo sapiens GN=LGALS7 PE=1 SV=2	LEG7_HUMAN	0.6666667	1(5.94)	0(0)	0(0)	0(0)
Group of C-X-C motif chemokine (Fragment) OS=Homo sapiens PE=3 SV=1+1	tr D3JV42 D3JV42_HUMAN (+1)	0.7130525	1(5.94)	0(0)	1(0.48)	1(0.62)
Group of Complement component 9, isoform CRA_a OS=Homo sapiens GN=C9 PE=4 SV=1+1	tr A0A024R035 A0A024R035_HUMAN (+1)	ND	0(0)	0(0)	9(5.77)	6(4.93)
Group of Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3+2	APOH_HUMAN (+2)	ND	0(0)	0(0)	8(8.65)	6(6.77)
Group of Thrombospondin-4 OS=Homo sapiens GN=THBS4 PE=1 SV=1+1	E7ES19_HUMAN (+1)	ND	0(0)	0(0)	8(6.73)	3(3.08)
Group of Cartilage oligomeric matrix protein variant (Fragment) OS=Homo sapiens PE=2 SV=1+1	tr Q53FR6 Q53FR6_HUMAN (+1)	ND	0(0)	0(0)	8(6.25)	2(1.85)
Group of Serpin peptidase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 3, isoform CRA_c OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	tr A0A024R6P0 A0A024R6P0_HUMAN (+1)	ND	0(0)	0(0)	8(6.25)	5(5.54)
Group of Kininogen 1, isoform CRA_a OS=Homo sapiens GN=KNG1 PE=4 SV=1+1	tr D3DNU8 D3DNU8_HUMAN (+1)	ND	0(0)	0(0)	8(4.32)	8(6.77)
Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	CO6A3_HUMAN	ND	0(0)	0(0)	8(3.84)	1(0.62)
Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	E9PGN7_HUMAN	ND	0(0)	0(0)	8(12.49)	8(12.93)
Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	FBLN1_HUMAN	ND	0(0)	0(0)	7(6.73)	6(6.16)
Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	THR_B_HUMAN	ND	0(0)	0(0)	7(6.25)	8(8.62)
Group of Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITI1 PE=1 SV=3+1	ITI1_HUMAN (+1)	ND	0(0)	0(0)	7(5.77)	6(5.54)
C4b-binding protein beta chain OS=Homo sapiens GN=C4BPB PE=1 SV=1	C4BPB_HUMAN	ND	0(0)	0(0)	7(18.26)	6(19.09)
Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2	FCN3_HUMAN	ND	0(0)	0(0)	6(8.17)	4(5.54)
Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	HEMO_HUMAN	ND	0(0)	0(0)	6(4.80)	4(5.54)
Group of 14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=1 SV=1+1	E7EX29_HUMAN (+1)	ND	0(0)	0(0)	6(3.84)	1(0.62)
Group of Epididymis secretory protein Li 51 OS=Homo sapiens GN=HEL-S-51 PE=2 SV=1+1	tr V9HWI6 V9HWI6_HUMAN (+1)	ND	0(0)	0(0)	6(3.84)	7(6.16)
Chondroitin sulfate proteoglycan 2 (Versican), isoform CRA_c OS=Homo sapiens GN=CSPG2 PE=4 SV=1	tr A0A024RAL1 A0A024RAL1_HUMAN	ND	0(0)	0(0)	6(3.36)	2(1.85)
Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens GN=C1QB PE=1 SV=4	A0A0A0MSV6_HUMAN	ND	0(0)	0(0)	6(25.94)	5(28.32)
Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3	C1QC_HUMAN	ND	0(0)	0(0)	6(23.06)	7(25.86)
Serpin peptidase inhibitor, clade C (Antithrombin), member 1, isoform CRA_a OS=Homo sapiens GN=SERPINC1 PE=3 SV=1	tr A0A024R944 A0A024R944_HUMAN	ND	0(0)	0(0)	6(2.88)	5(3.08)
Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	IGHG2_HUMAN	ND	0(0)	0(0)	5(93.69)	3(49.25)
Group of Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITI3 PE=1 SV=1+1	A0A087VW43_HUMAN (+1)	ND	0(0)	0(0)	5(4.80)	2(1.23)
Vitronectin OS=Homo sapiens GN=VTN PE=4 SV=1	tr D9ZGG2 D9ZGG2_HUMAN	ND	0(0)	0(0)	5(4.80)	4(3.08)
Serum amyloid P-component OS=Homo sapiens GN=APCS PE=1 SV=2	SAMP_HUMAN	ND	0(0)	0(0)	5(3.84)	5(3.69)
Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	MMRN1_HUMAN	ND	0(0)	0(0)	5(3.36)	8(8.62)
Coagulation factor XIII B chain OS=Homo sapiens GN=F13B PE=1 SV=3	F13B_HUMAN	ND	0(0)	0(0)	5(2.88)	5(4.93)
Complement factor properdin isoform 1 (Fragment) OS=Homo sapiens GN=CFP PE=2 SV=1	tr A0A0S2Z4I5 A0A0S2Z4I5_HUMAN	ND	0(0)	0(0)	5(2.88)	6(6.77)
Group of Laminin subunit gamma-1 OS=Homo sapiens GN=LAMC1 PE=1 SV=3+1	LAMC1_HUMAN (+1)	ND	0(0)	0(0)	5(2.88)	2(1.23)
V5-6 protein (Fragment) OS=Homo sapiens GN=V5-6 PE=4 SV=1	tr Q5NV92 Q5NV92_HUMAN	ND	0(0)	0(0)	5(2.40)	3(2.46)
MS-D4 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A0X9UWK7 A0A0X9UWK7_HUMAN	ND	0(0)	0(0)	4(4.80)	3(4.31)
sp HBA_HUMAN	sp HBA_HUMAN	ND	0(0)	0(0)	4(3.36)	3(6.77)
Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3	CO8G_HUMAN	ND	0(0)	0(0)	4(2.88)	1(0.62)
Group of Angiotensinogen (Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1 antiproteinase, antitrypsin), member 8 OS=Homo sapiens GN=ANGPT1 PE=1 SV=1	tr Q53YY1 Q53YY1_HUMAN (+5)	ND	0(0)	0(0)	4(2.88)	1(0.62)
Group of Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3+1	CO6_HUMAN (+1)	ND	0(0)	0(0)	4(2.40)	5(3.08)
Group of Transferrin variant (Fragment) OS=Homo sapiens PE=2 SV=1+1	tr Q53H26 Q53H26_HUMAN (+1)	ND	0(0)	0(0)	37(43.24)	26(33.25)
Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	TSP1_HUMAN	ND	0(0)	0(0)	36(39.40)	31(43.71)
Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	APOA4_HUMAN	ND	0(0)	0(0)	3(9.13)	4(10.47)
Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	A1AG1_HUMAN	ND	0(0)	0(0)	3(6.25)	2(5.54)
Group of Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=1+1	tr A0A0U1RR20 A0A0U1RR20_HUMAN (+1)	ND	0(0)	0(0)	3(5.77)	2(4.31)
Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	IGHG4_HUMAN	ND	0(0)	0(0)	3(42.76)	3(35.71)

Group of HCG2043239 (Fragment) OS=Homo sapiens GN=IGLV3-9 PE=1 SV=1+1	A0A075B6K5_HUMAN (+1)	ND	0(0)	0(0)	3(4.80)	3(6.77)
Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	tr Q0ZCJ6 Q0ZCJ6_HUMAN	ND	0(0)	0(0)	3(4.80)	3(3.69)
Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	A1AG2_HUMAN	ND	0(0)	0(0)	3(4.32)	2(3.69)
Group of Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1+1	tr Q0ZCH6 Q0ZCH6_HUMAN (+1)	ND	0(0)	0(0)	3(3.36)	1(2.46)
Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	PON1_HUMAN	ND	0(0)	0(0)	3(2.88)	3(3.08)
Group of Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2+1	H4_HUMAN (+1)	ND	0(0)	0(0)	3(2.40)	1(0.62)
V2-7 protein (Fragment) OS=Homo sapiens GN=V2-7 PE=4 SV=1	tr A2MYD4 A2MYD4_HUMAN	ND	0(0)	0(0)	3(10.57)	3(8.62)
Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	A2AP_HUMAN	ND	0(0)	0(0)	3(1.44)	4(3.08)
Carboxypeptidase N catalytic chain OS=Homo sapiens GN=CPN1 PE=1 SV=1	CBPN_HUMAN	ND	0(0)	0(0)	3(1.44)	3(1.85)
Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	CO6A1_HUMAN	ND	0(0)	0(0)	3(1.44)	0(0)
Epididymis secretory sperm binding protein Li 163pA OS=Homo sapiens GN=HEL-S-163pA PE=2 SV=1	tr V9HWD8 V9HWD8_HUMAN	ND	0(0)	0(0)	3(1.44)	2(1.23)
Group of Angiotensin-related protein 6 OS=Homo sapiens GN=ANGPTL6 PE=1 SV=1+1	ANGL6_HUMAN (+1)	ND	0(0)	0(0)	3(1.44)	0(0)
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1	J3KND3_HUMAN	ND	0(0)	0(0)	3(1.44)	1(0.62)
Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens GN=LRP1 PE=1 SV=2	LRP1_HUMAN	ND	0(0)	0(0)	3(1.44)	2(1.23)
sp PPIA_HUMAN	sp PPIA_HUMAN	ND	0(0)	0(0)	3(1.44)	0(0)
Group of TNC variant protein (Fragment) OS=Homo sapiens GN=TNC variant protein PE=2 SV=1+1	tr Q4LE33 Q4LE33_HUMAN (+1)	ND	0(0)	0(0)	26(16.34)	4(2.46)
Group of Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=1+2	B4DPQ0_HUMAN (+2)	ND	0(0)	0(0)	24(44.68)	26(70.19)
Anti-streptococcal/anti-myosin immunoglobulin lambda light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr Q96SB0 Q96SB0_HUMAN	ND	0(0)	0(0)	2(6.25)	1(6.16)
V2-19 protein (Fragment) OS=Homo sapiens GN=V2-19 PE=4 SV=1	tr Q5NV91 Q5NV91_HUMAN	ND	0(0)	0(0)	2(5.29)	1(3.69)
IBM-B2 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A125QY9 A0A125QY9_HUMAN	ND	0(0)	0(0)	2(4.32)	1(3.69)
V1-22 protein (Fragment) OS=Homo sapiens GN=V1-22 PE=1 SV=1	tr Q5NV88 Q5NV88_HUMAN	ND	0(0)	0(0)	2(4.32)	2(2.46)
Immunoglobulin heavy variable 5-10-1 OS=Homo sapiens GN=IGHV5-10-1 PE=3 SV=1	sp A0A0J9YX1 HV5X1_HUMAN	ND	0(0)	0(0)	2(3.84)	1(1.85)
MS-D1 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A0X9TD47 A0A0X9TD47_HUMAN	ND	0(0)	0(0)	2(3.84)	2(3.69)
cDNA. FLJ93312. highly similar to Homo sapiens adipose most abundant gene transcript 1 (APM1). mRNA OS=Homo sapiens	tr B2R773 B2R773_HUMAN	ND	0(0)	0(0)	2(3.36)	2(5.54)
GCT-A4 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A0X9T7V9 A0A0X9T7V9_HUMAN	ND	0(0)	0(0)	2(2.88)	2(3.69)
V1-16 protein (Fragment) OS=Homo sapiens GN=V1-16 PE=4 SV=1	tr Q5NV81 Q5NV81_HUMAN	ND	0(0)	0(0)	2(2.88)	0(3.08)
Cryocystallglobulin CC2 lambda light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr B1N7B9 B1N7B9_HUMAN	ND	0(0)	0(0)	2(2.40)	2(2.46)
Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	CO4A_HUMAN	ND	0(0)	0(0)	2(119.15)	2(130.52)
Myosin-reactive immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr Q9UL72 Q9UL72_HUMAN	ND	0(0)	0(0)	2(10.57)	2(11.08)
Group of Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1+4	A0A087WT59_HUMAN (+4)	ND	0(0)	0(0)	2(1.92)	2(3.69)
Mannan-binding lectin serine protease 2 OS=Homo sapiens GN=MASP2 PE=1 SV=4	MASP2_HUMAN	ND	0(0)	0(0)	2(1.92)	0(0)
Myosin regulatory light chain 12B OS=Homo sapiens GN=MYL12B PE=1 SV=2	ML12B_HUMAN	ND	0(0)	0(0)	2(1.92)	0(0)
Rheumatoid factor RF-ET9 (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2J1N6 A2J1N6_HUMAN	ND	0(0)	0(0)	2(1.92)	1(1.85)
Carboxypeptidase N subunit 2 OS=Homo sapiens GN=CPN2 PE=1 SV=3	CPN2_HUMAN	ND	0(0)	0(0)	2(1.44)	3(1.85)
Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	CO6A2_HUMAN	ND	0(0)	0(0)	2(1.44)	0(0)
Collectin sub-family member 10 (C-type lectin). isoform CRA_a OS=Homo sapiens GN=COLEC10 PE=4 SV=1	tr A0A024R9J3 A0A024R9J3_HUMAN	ND	0(0)	0(0)	2(1.44)	0(0)
Complement C1r subcomponent-like protein OS=Homo sapiens GN=C1RL PE=1 SV=2	C1RL_HUMAN	ND	0(0)	0(0)	2(1.44)	2(2.46)
Group of Coagulation factor XIII A chain OS=Homo sapiens GN=F13A1 PE=1 SV=4+2	F13A_HUMAN (+2)	ND	0(0)	0(0)	2(1.44)	0(0)
Group of Immunoglobulin lambda variable 7-43 OS=Homo sapiens GN=IGLV7-43 PE=3 SV=2+2	sp P04211 LV743_HUMAN (+2)	ND	0(0)	0(0)	2(1.44)	1(1.23)
Group of Olfactomedin-4 OS=Homo sapiens GN=OLFM4 PE=1 SV=1+1	OLFM4_HUMAN (+1)	ND	0(0)	0(0)	2(1.44)	1(0.62)
Group of Proteoglycan 1. secretory granule. isoform CRA_a OS=Homo sapiens GN=PRG1 PE=4 SV=1+1	tr A0A024QZL1 A0A024QZL1_HUMAN (+1)	ND	0(0)	0(0)	2(1.44)	1(0.62)
Putative uncharacterized protein DKFZp686M0562 (Fragment) OS=Homo sapiens GN=DKFZp686M0562 PE=2 SV=1	tr Q6MZL2 Q6MZL2_HUMAN	ND	0(0)	0(0)	2(1.44)	2(1.85)
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein. eta polypeptide. isoform CRA_b OS=Homo sapiens	tr A0A024R1K7 A0A024R1K7_HUMAN	ND	0(0)	0(0)	2(1.44)	0(0)
cDNA FLJ58441. highly similar to Attractin OS=Homo sapiens PE=2 SV=1	tr B4DZ36 B4DZ36_HUMAN	ND	0(0)	0(0)	2(0.96)	1(0.62)
Fibrinogen-like protein 1 OS=Homo sapiens GN=FGL1 PE=1 SV=3	FGL1_HUMAN	ND	0(0)	0(0)	2(0.96)	0(0)
Group of Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=1+2	E9PG40_HUMAN (+2)	ND	0(0)	0(0)	2(0.96)	2(1.85)
Group of Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3+1	G3P_HUMAN (+1)	ND	0(0)	0(0)	2(0.96)	1(0.62)

Group of Laminin subunit alpha-2 OS=Homo sapiens GN=LAMA2 PE=1 SV=1+1	A0A087WX80_HUMAN (+1)	ND	0(0)	0(0)	2(0.96)	0(0)
Group of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2+1	LDHA_HUMAN (+1)	ND	0(0)	0(0)	2(0.96)	0(0)
Group of MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-A PE=3 SV=1+3	tr D2KZ27 D2KZ27_HUMAN (+3)	ND	0(0)	0(0)	2(0.96)	0(0)
Group of Serum amyloid A protein OS=Homo sapiens GN=SAA1 PE=1 SV=1+2	E9PQD6_HUMAN (+2)	ND	0(0)	0(0)	2(0.96)	0(0)
Group of Transforming growth factor beta-induced 68kDa isoform 2 (Fragment) OS=Homo sapiens GN=TGFB1 PE=2 SV=1+1	tr A0A052Z4K6 A0A052Z4K6_HUMAN (+1)	ND	0(0)	0(0)	2(0.96)	0(0)
Heavy chain of factor I (Fragment) OS=Homo sapiens PE=2 SV=1	tr Q6LAM1 Q6LAM1_HUMAN	ND	0(0)	0(0)	2(0.96)	3(3.69)
Heparan sulfate proteoglycan 2 (Perlecan). isoform CRA_b OS=Homo sapiens GN=HSPG2 PE=4 SV=1	tr A0A024RAB6 A0A024RAB6_HUMAN	ND	0(0)	0(0)	2(0.96)	0(0)
Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	HEP2_HUMAN	ND	0(0)	0(0)	2(0.96)	2(1.23)
Hepatocyte growth factor activator OS=Homo sapiens GN=HGFA PE=1 SV=1	D6RAR4_HUMAN	ND	0(0)	0(0)	2(0.96)	1(0.62)
IBM-A3 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A0X9UWM4 A0A0X9UWM4_HUMAN	ND	0(0)	0(0)	2(0.96)	1(0.62)
Immunoglobulin delta heavy chain OS=Homo sapiens PE=1 SV=1	sp P0DOX3 IGD_HUMAN	ND	0(0)	0(0)	2(0.96)	2(1.23)
MS-D1 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A109PS45 A0A109PS45_HUMAN	ND	0(0)	0(0)	2(0.96)	1(0.62)
Neurogenic locus notch homolog protein 3 OS=Homo sapiens GN=NOTCH3 PE=1 SV=2	NOTC3_HUMAN	ND	0(0)	0(0)	2(0.96)	0(0)
Nidogen-1 OS=Homo sapiens GN=NID1 PE=1 SV=3	NID1_HUMAN	ND	0(0)	0(0)	2(0.96)	1(0.62)
Protein disulfide-isomerase A3 (Fragment) OS=Homo sapiens GN=PDIA3 PE=1 SV=1	H7BZJ3_HUMAN	ND	0(0)	0(0)	2(0.96)	1(0.62)
Protein IGHV3-38 (Fragment) OS=Homo sapiens GN=IGHV3-38 PE=1 SV=1	A0A0C4DH36_HUMAN	ND	0(0)	0(0)	2(0.96)	1(0.62)
Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	E9PFZ2_HUMAN	ND	0(0)	0(0)	18(13.93)	12(14.78)
Group of Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4+1	C05_HUMAN (+1)	ND	0(0)	0(0)	15(9.13)	11(9.23)
cDNA FLJ51742. highly similar to Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens PE=2 SV=1	tr B7Z544 B7Z544_HUMAN	ND	0(0)	0(0)	13(9.61)	9(9.85)
Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	PLMN_HUMAN	ND	0(0)	0(0)	13(8.65)	11(9.23)
Group of Inter-alpha (Globulin) inhibitor H2 OS=Homo sapiens GN=ITIH2 PE=2 SV=1+1	tr A2RTY6 A2RTY6_HUMAN (+1)	ND	0(0)	0(0)	13(12.97)	13(16.62)
Group of Coagulation factor V OS=Homo sapiens GN=F5 PE=1 SV=1+1	A0A0A0MRJ7_HUMAN (+1)	ND	0(0)	0(0)	12(6.73)	10(6.77)
Epididymis secretory sperm binding protein Li 44a OS=Homo sapiens GN=SERPINA1 PE=2 SV=1	tr E9KL23 E9KL23_HUMAN	ND	0(0)	0(0)	12(12.01)	12(14.16)
Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	C07_HUMAN	ND	0(0)	0(0)	11(9.13)	11(9.23)
Group of Sushi. von Willebrand factor type A. EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=1	A0A0A0MSD0_HUMAN (+1)	ND	0(0)	0(0)	11(5.77)	8(4.93)
Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4	PIGR_HUMAN	ND	0(0)	0(0)	11(10.57)	12(12.93)
Coagulation factor VIII OS=Homo sapiens GN=F8 PE=1 SV=1	FA8_HUMAN	ND	0(0)	0(0)	10(6.73)	7(4.93)
Group of Complement component 8. beta polypeptide. isoform CRA_b OS=Homo sapiens GN=C8B PE=2 SV=1+4	tr B7Z550 B7Z550_HUMAN (+4)	ND	0(0)	0(0)	10(6.25)	8(4.93)
Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	AMBP_HUMAN	ND	0(0)	0(0)	10(11.05)	10(11.70)
Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2	CO8A_HUMAN	ND	0(0)	0(0)	10(10.09)	9(11.08)
10E8 heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A193CHR0 A0A193CHR0_HUMAN	ND	0(0)	0(0)	1(8.65)	1(6.77)
IgG H chain OS=Homo sapiens PE=2 SV=1	tr S6BGD4 S6BGD4_HUMAN	ND	0(0)	0(0)	1(8.65)	1(9.85)
IgG H chain OS=Homo sapiens PE=1 SV=1	tr S6C4S0 S6C4S0_HUMAN	ND	0(0)	0(0)	1(8.17)	0(8.00)
VH-3 family (VH26)D/J protein (Fragment) OS=Homo sapiens GN=VH-3 family (VH26)D/J PE=4 SV=1	tr A2NWW1 A2NWW1_HUMAN	ND	0(0)	0(0)	1(6.25)	1(4.31)
VH3 protein (Fragment) OS=Homo sapiens GN=VH3 PE=2 SV=1	tr Q9Y509 Q9Y509_HUMAN	ND	0(0)	0(0)	1(5.77)	1(4.93)
Immunoglobulin lambda constant 7 OS=Homo sapiens GN=IGLC7 PE=1 SV=3	sp A0M8Q6 IGLC7_HUMAN	ND	0(0)	0(0)	1(46.60)	3(49.25)
Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2	FHR1_HUMAN	ND	0(0)	0(0)	1(4.80)	3(9.23)
cDNA FLJ53364. highly similar to Proteoglycan-4 (Fragment) OS=Homo sapiens PE=2 SV=1	tr B7Z4R8 B7Z4R8_HUMAN	ND	0(0)	0(0)	1(4.32)	0(3.08)
Platelet factor 4 OS=Homo sapiens GN=PF4 PE=1 SV=2	PLF4_HUMAN	ND	0(0)	0(0)	1(4.32)	1(6.77)
Ig kappa chain V-IV region (Fragment) OS=Homo sapiens GN=IGKV4-1 PE=4 SV=1	KV401_HUMAN	ND	0(0)	0(0)	1(3.84)	1(1.85)
Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	tr Q0ZCJ1 Q0ZCJ1_HUMAN	ND	0(0)	0(0)	1(3.84)	0(4.31)
Myosin-reactive immunoglobulin light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr Q9UL82 Q9UL82_HUMAN	ND	0(0)	0(0)	1(3.84)	1(2.46)
Platelet factor 4 variant OS=Homo sapiens GN=PF4V1 PE=1 SV=1	PF4V_HUMAN	ND	0(0)	0(0)	1(3.84)	0(6.16)
Fibronectin (Fragment) OS=Homo sapiens GN=FN1 PE=1 SV=1	HOY4K8_HUMAN	ND	0(0)	0(0)	1(3.36)	1(4.31)
cDNA FLJ53025. highly similar to Complement C4-B OS=Homo sapiens PE=2 SV=1	tr B7Z1F8 B7Z1F8_HUMAN	ND	0(0)	0(0)	1(28.35)	1(29.55)
Complement protein C4B frameshift mutant (Fragment) OS=Homo sapiens GN=C4B PE=4 SV=1	tr Q9UNU2 Q9UNU2_HUMAN	ND	0(0)	0(0)	1(25.94)	1(32.63)
cDNA FLJ51564. highly similar to Pregnancy zone protein OS=Homo sapiens PE=2 SV=1	tr B7Z7M2 B7Z7M2_HUMAN	ND	0(0)	0(0)	1(2.88)	1(4.31)

GCT-A5 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A0X9UWL5 A0A0X9UWL5_HUMAN	ND	0(0)	0(0)	1(2.88)	1(1.85)
Complement C1s subcomponent (Fragment) OS=Homo sapiens GN=C1S PE=1 SV=1	F5H7T4_HUMAN	ND	0(0)	0(0)	1(16.34)	0(21.55)
Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	C04B_HUMAN	ND	0(0)	0(0)	1(122.04)	1(134.22)
IgG H chain OS=Homo sapiens PE=2 SV=1	tr S6B2A6 S6B2A6_HUMAN	ND	0(6.03)	0(7.78)	1(11.53)	1(12.93)
Group of Complement factor H-related protein 2 OS=Homo sapiens GN=CFHR2 PE=1 SV=1+1	FHR2_HUMAN (+1)	ND	0(0)	0(0)	1(1.92)	1(3.69)
Group of Immunoglobulin heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1+1	tr Q0ZCF9 Q0ZCF9_HUMAN (+1)	ND	0(0)	0(0)	1(1.92)	1(1.85)
Group of Tubulin alpha chain (Fragment) OS=Homo sapiens PE=2 SV=1+4	tr Q53GA7 Q53GA7_HUMAN (+4)	ND	0(0)	0(0)	1(1.92)	1(0.62)
Immunoglobulin heavy variable 3-73 OS=Homo sapiens GN=IGHV3-73 PE=3 SV=1	sp A0A0B4J1V6 HV373_HUMAN	ND	0(0)	0(0)	1(1.92)	0(1.85)
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	TBA4A_HUMAN	ND	0(0)	0(0)	1(1.92)	0(0)
Group of Immunoglobulin lambda variable 4-60 OS=Homo sapiens GN=IGLV4-60 PE=3 SV=1+1	sp A0A075B611 LV460_HUMAN (+1)	ND	0(0)	0(0)	1(1.44)	2(1.85)
Group of MYL9 protein OS=Homo sapiens GN=MYL9 PE=2 SV=1+2	tr Q6IBG1 Q6IBG1_HUMAN (+2)	ND	0(0)	0(0)	1(1.44)	0(0)
Imunoglobulin heavy chain (Fragment) OS=Homo sapiens GN=VH PE=4 SV=1	tr Q9ULB6 Q9ULB6_HUMAN	ND	0(0)	0(0)	1(1.44)	1(1.85)
Light chain Fab (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2NVY4 A2NVY4_HUMAN	ND	0(0)	0(0)	1(1.44)	0(0.62)
Rheumatoid factor RF-ET12 (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2J1N9 A2J1N9_HUMAN	ND	0(0)	0(0)	1(1.44)	1(1.85)
V1-3 protein (Fragment) OS=Homo sapiens GN=V1-3 PE=4 SV=1	tr Q5NV84 Q5NV84_HUMAN	ND	0(0)	0(0)	1(1.44)	1(1.85)
<i>14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1</i>	<i>1433T_HUMAN</i>	ND	0(0)	0(0)	1(0.96)	1(0.62)
<i>Group of 14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=2 SV=1+1</i>	<i>tr B5BU24 B5BU24_HUMAN (+1)</i>	ND	0(0)	0(0)	1(0.96)	0(0)
Rheumatoid factor RF-IP12 (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2J1M8 A2J1M8_HUMAN	ND	0(0)	0(0)	1(0.96)	2(2.46)
Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	AFAM_HUMAN	ND	0(0)	0(0)	1(0.48)	3(1.85)
Complement factor H-related protein 4 OS=Homo sapiens GN=CFHR4 PE=1 SV=3	FHR4_HUMAN	ND	0(0)	0(0)	1(0.48)	4(2.46)
Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2	ECM1_HUMAN	ND	0(0)	0(0)	1(0.48)	2(1.23)
Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	FILA2_HUMAN	ND	0(0)	0(0)	1(0.48)	2(1.85)
Group of Alanyl (Membrane) aminopeptidase (Aminopeptidase N. aminopeptidase M. microsomal aminopeptidase. CD13. p. tr A0A024RC61 A0A024RC61_HUMAN (+1)	A0A024RC61_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	1(0.62)
Group of EMILIN-1 OS=Homo sapiens GN=EMILIN1 PE=1 SV=1+1	A0A0C4DFX3_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	2(1.23)
Group of LTBP1 protein OS=Homo sapiens GN=LTBP1 PE=2 SV=1+2	tr B7ZLY3 B7ZLY3_HUMAN (+2)	ND	0(0)	0(0)	1(0.48)	3(2.46)
Group of Lumican OS=Homo sapiens GN=LUM PE=1 SV=2+1	LUM_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	1(0.62)
Immunoglobulin heavy variable 3-13 OS=Homo sapiens GN=IGHV3-13 PE=1 SV=2	sp P01766 HV313_HUMAN	ND	0(0)	0(0)	1(0.48)	1(1.23)
Oncoprotein-induced transcript 3 protein OS=Homo sapiens GN=OIT3 PE=1 SV=2	OIT3_HUMAN	ND	0(0)	0(0)	1(0.48)	5(3.08)
Phosphatidylinositol-glycan-specific phospholipase D OS=Homo sapiens GN=GPLD1 PE=1 SV=3	PHLD_HUMAN	ND	0(0)	0(0)	1(0.48)	2(1.23)
Protein IGHV3OR16-10 (Fragment) OS=Homo sapiens GN=IGHV3OR16-10 PE=1 SV=1	A0A075B7F0_HUMAN	ND	0(0)	0(0)	1(0.48)	1(1.23)
Uncharacterized protein OS=Homo sapiens PE=1 SV=1	tr Q8TCD0 Q8TCD0_HUMAN	ND	0(0)	0(0)	0(6.73)	1(6.77)
C4B1 (Fragment) OS=Homo sapiens GN=C4B PE=4 SV=1	tr Q6U2E7 Q6U2E7_HUMAN	ND	0(0)	0(0)	0(1.92)	1(4.31)
Cadherin-related family member 2 OS=Homo sapiens GN=CDHR2 PE=1 SV=2	CDHR2_HUMAN	ND	0(0)	0(0)	0(0)	3(1.85)
cDNA FLJ53342. highly similar to Granulins OS=Homo sapiens PE=2 SV=1	tr B4DJ12 B4DJ12_HUMAN	ND	0(0)	0(0)	0(0)	2(1.23)
Immunoglobulin heavy variable 3-20 OS=Homo sapiens GN=IGHV3-20 PE=3 SV=2	sp A0A0C4DH32 HV320_HUMAN	ND	0(0)	0(0)	0(0)	1(1.23)
Intellectin 1 OS=Homo sapiens GN=ITLN1 PE=2 SV=1	tr Q5IWS5 Q5IWS5_HUMAN	ND	0(0)	0(0)	0(0)	2(1.23)
Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	PERM_HUMAN	ND	0(0)	0(0)	0(0)	2(1.23)
Vitamin D binding protein (Fragment) OS=Homo sapiens GN=Gc PE=4 SV=1	tr A0A1B1CYC5 A0A1B1CYC5_HUMAN	ND	0(0)	0(0)	0(0)	2(1.23)
Apolipoprotein F OS=Homo sapiens GN=APOF PE=1 SV=2	APOF_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Group of Apoptosis-stimulating of p53 protein 2 OS=Homo sapiens GN=TP53BP2 PE=1 SV=2+3	ASPP2_HUMAN (+3)	ND	0(0)	0(0)	0(0)	1(0.62)
Charged multivesicular body protein 3 OS=Homo sapiens GN=CHMP3 PE=1 SV=3	CHMP3_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Target of Nesh-SH3 OS=Homo sapiens GN=ABI3BP PE=1 SV=1	D3YTG3_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Complement C1q subcomponent subunit B (Fragment) OS=Homo sapiens GN=C1QB PE=1 SV=1	D6RGJ1_HUMAN	ND	0(0)	0(0)	1(0.96)	0(0)
ATP-dependent RNA helicase DHX36 OS=Homo sapiens GN=DHX36 PE=1 SV=2	DHX36_HUMAN	ND	0(0)	0(0)	0(0)	1(0.62)
Group of E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens GN=UBR5 PE=1 SV=1+1	E7EMW7_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	0(0)
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	ENOA_HUMAN	ND	0(0)	0(0)	1(0.96)	0(0)
Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3	FBN1_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)

Group of Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=1+1	G3XAI2_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	0(0)
Group of Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2+1	GPX3_HUMAN (+1)	ND	0(0)	0(0)	1(0.96)	0(0)
Group of Adipocyte plasma membrane-associated protein (Fragment) OS=Homo sapiens GN=APMAP PE=1 SV=1+1	HOY512_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	0(0)
Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2	H2BFS_HUMAN	ND	0(0)	0(0)	1(0.96)	0(0)
Calreticulin (Fragment) OS=Homo sapiens GN=CALR PE=1 SV=1	K7EB9_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Group of Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1+1	KLKB1_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	0(0)
Low-density lipoprotein receptor-related protein 1B OS=Homo sapiens GN=LRP1B PE=1 SV=2	LRP1B_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Mannose-binding protein C OS=Homo sapiens GN=MBL2 PE=1 SV=2	MBL2_HUMAN	ND	0(0)	0(0)	0(0)	1(0.62)
Pentraxin-related protein PTX3 OS=Homo sapiens GN=PTX3 PE=1 SV=3	PTX3_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Group of Immunoglobulin lambda variable 8-61 OS=Homo sapiens GN=IGLV8-61 PE=3 SV=7+1	sp A0A075B6I0 LV861_HUMAN (+1)	ND	0(0)	0(0)	1(1.44)	1(0.62)
Group of Immunoglobulin kappa variable 2-24 OS=Homo sapiens GN=IGKV2-24 PE=3 SV=1+1	sp A0A0C4DH68 KV224_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	0(0)
Immunoglobulin kappa variable 1-6 OS=Homo sapiens GN=IGKV1-6 PE=3 SV=1	sp A0A0C4DH72 KV106_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Immunoglobulin epsilon heavy chain OS=Homo sapiens PE=1 SV=1	sp P0DOX4 IGE_HUMAN	ND	0(0)	0(0)	1(0.48)	1(0.62)
Transforming growth factor beta-1 OS=Homo sapiens GN=TGFBI PE=1 SV=2	TGFBI_HUMAN	ND	0(0)	0(0)	1(0.48)	1(0.62)
Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A068LKQ2 A0A068LKQ2_HUMAN	ND	0(0)	0(0)	1(0.48)	1(1.24)
Ig heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A068LN03 A0A068LN03_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
MS-F1 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A0X9V9B3 A0A0X9V9B3_HUMAN	ND	0(0)	0(0)	1(0.96)	1(1.24)
MS-C2 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A109PP82 A0A109PP82_HUMAN	ND	0(0)	0(0)	1(0.48)	1(2.47)
MS-A1 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A0A109PSY4 A0A109PSY4_HUMAN	ND	0(0)	0(0)	1(2.4)	1(1.85)
B cell receptor heavy chain variable region (Fragment) OS=Homo sapiens PE=4 SV=1	tr A0A1C9J6Z4 A0A1C9J6Z4_HUMAN	ND	0(0)	0(0)	1(1.92)	1(3.71)
Anti-mucin1 light chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2JA19 A2JA19_HUMAN	ND	0(0)	0(0)	1(0.96)	0(0)
VH6DJ protein (Fragment) OS=Homo sapiens GN=VH6DJ PE=2 SV=1	tr A2N0S6 A2N0S6_HUMAN	ND	0(0)	0(0)	1(1.44)	1(1.24)
Heavy chain Fab (Fragment) OS=Homo sapiens PE=2 SV=1	tr A2NYU9 A2NYU9_HUMAN	ND	0(0)	0(0)	1(0.96)	0(0)
Group of Histone H2A OS=Homo sapiens GN=HIST1H2AH PE=2 SV=1+7	tr A3KPC7 A3KPC7_HUMAN (+7)	ND	0(0)	0(0)	1(2.88)	0(0)
cDNA FLJ60461. highly similar to Peroxiredoxin-2 (EC 1.11.1.15) OS=Homo sapiens PE=2 SV=1	tr B4DF70 B4DF70_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
cDNA FLJ59033. highly similar to Protein disulfide-isomerase (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	tr B4DLN6 B4DLN6_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Anti-Influenza A hemagglutinin heavy chain variable region (Fragment) OS=Homo sapiens PE=2 SV=1	tr G1FM91 G1FM91_HUMAN	ND	0(0)	0(0)	1(0.96)	1(0.62)
Group of HSP90AA1 protein (Fragment) OS=Homo sapiens GN=HSP90AA1 PE=2 SV=1+2	tr Q2VPJ6 Q2VPJ6_HUMAN (+2)	ND	0(0)	0(0)	1(0.48)	0(0)
Group of Vascular cell adhesion molecule 1 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1+1	tr Q53FL7 Q53FL7_HUMAN (+1)	ND	0(0)	0(0)	1(0.48)	0(0)
Tumor rejection antigen (Gp96) 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	tr Q59FC6 Q59FC6_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Kinase/transmembrane domain fusion protein (Fragment) OS=Homo sapiens GN=STK4/SLC36AL fusion PE=2 SV=1	tr Q86YK3 Q86YK3_HUMAN	ND	0(0)	0(0)	0(0)	1(0.62)
Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1	URP2_HUMAN	ND	0(0)	0(0)	1(0.96)	0(0)
WASP homolog-associated protein with actin. membranes and microtubules OS=Homo sapiens GN=WHAMM PE=1 SV=2	WHAMM_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)
Zinc finger protein 787 OS=Homo sapiens GN=ZNF787 PE=1 SV=3	ZNF787_HUMAN	ND	0(0)	0(0)	1(0.48)	0(0)

"The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE (1) partner repository with the dataset identifier PXD014668 and 10.6019/PXD014668". (1) Perez-Riverol Y, Csordas A, Bai J, Bernal-Llinares M, Hewapathirana S, Kundu DJ, Inuganti A, Griss J, Mayer G, Eisenacher M, Pérez E, Uszkoreit J, Pfeuffer J, Sachsenberg T, Yilmaz S, Tiwary S, Cox J, Audain E, Walzer M, Jarnuczak AF,