

Supplementary Table 1-3. List of proteins included in the EVs secreted from YafuSS cell line

Accession	Description	Sum (Coverage)	Sum (# Peptides)	Sum (# Unique Peptides)	Sum (# Peptides)	Sum (# PSMs)	Area	# Peptides A10	# Peptides A10	# PSM A10	# PSM A10	Coverage A10	Score A10	Score A10	F.AAs	MW [kDa]	calc pI
P07477	Trypsin I OS-Homo sapiens GN-PRES1 PE-1 SV-1 [TRY1_HUMAN]	4.05%	1	1	1	103	2,801.09	1	1	51	52	4.05%	4.05%	12.21	930.98	247	6.51
P07223	Brain acid soluble protein 1 OS-Homo sapiens GN-BASPI1 PE-1 SV-2 [BASPI_HUMAN]	73.13%	14	14	14	46	1,511.08	14	13	23	23	73.13%	69.60%	62.84	476.79	227	22.7
Q06K65	Histone H2A type 1-H OS-Homo sapiens GN-HIST2AH1 PE-1 SV-2 [HIST2AH_HUMAN]	27.34%	15	3	3	10	1,005.08	3	3	5	5	27.34%	27.34%	15.98	141.73	128	13.9
P02605	Histone H4 OS-Homo sapiens GN-HIST4HA PE-1 SV-2 [HIST4_HUMAN]	51.16%	1	6	6	1,103.08	6	6	8	8	51.16%	51.16%	28.58	27.07	103	11.4	
P07478	Cytochrome c OS-Homo sapiens GN-CYTC PE-1 SV-1 [CYTC_HUMAN]	31.46%	11	11	11	7,401.07	11	11	11	11	11	31.46%	31.46%	27.54	409	67.8	5.7
P12109	Collagen alpha 1(VI) chain OS-Homo sapiens GN-COLA1A1 PE-1 SV-3 [COLA1_HUMAN]	31.46%	1	21	21	55	5,971.07	21	20	28	27	31.46%	27.82%	83.55	708.86	1028	108.5
Q8N272	Histone H3.L3C OS-Homo sapiens GN-H3F3C PE-1 SV-3 [H3C_HUMAN]	11.85%	5	3	3	5,831.07	1	2	1	2	6.67%	11.85%	27.77	15.43	135	15.2	
P02606	Serum albumin OS-Homo sapiens GN-SALU1 PE-1 SV-2 [ALBU_HUMAN]	21.82%	7	7	7	4,531.07	7	7	7	7	21.82%	21.82%	25.49	473	609	62.8	
P16401	Histone H1.5 OS-Homo sapiens GN-HIST1H5 PE-1 SV-3 [H1C_HUMAN]	11.85%	1	4	4	5	4,251.07	4	4	5	5	11.85%	11.85%	10.78	95.9	226	22.6
P04264	Keratin, type II cytokeletal 1 OS-Homo sapiens GN-KRT11 PE-1 SV-6 [KCT1_HUMAN]	43.32%	1	17	22	54	3,861.07	21	22	26	28	42.08%	43.32%	80.71	989.96	644	66
P11142	Heat shock cognate 7 kDa protein OS-Homo sapiens GN-HSPA7 PE-1 SV-1 [HSP7C_HUMAN]	43.32%	1	17	22	54	3,861.07	19	19	27	26	40.09%	40.09%	78.2	817.67	646	70.9
P04265	Polyubiquitin OS-Homo sapiens GN-UB1 PE-1 SV-3 [UB1_HUMAN]	44.67%	3	3	3	3,621.07	3	3	3	3	44.67%	44.67%	8.96	108.65	685	77	
P00333	CD81 antigen OS-Homo sapiens GN-CD81 PE-1 SV-1 [CD81_HUMAN]	28.39%	1	4	4	10	3,361.07	4	4	5	5	28.39%	28.39%	35.36	172.37	236	25.8
P10124	Ras-related protein Rap-1b OS-Homo sapiens GN-RAP1B1 PE-1 SV-1 [RAP1B_HUMAN]	45.31%	1	3	3	20	3,331.07	8	8	10	10	45.31%	45.31%	19.43	284.02	184	20.8
P02627	Phosphoglycolytic-tinase isomerase OS-Homo sapiens GN-PPIA PE-1 SV-2 [PPIA_HUMAN]	45.31%	7	7	7	15	2,771.07	5	5	6	6	28.08%	41.21%	14.06	237.59	165	18
P25527	Keratin, type I cytokeletal 9 OS-Homo sapiens GN-KRT9 PE-1 SV-3 [K9C_HUMAN]	44.14%	2	18	19	41	2,541.07	16	19	23	40.29%	44.14%	57.4	870.27	623	62	
P03104	14-3-3 protein zeta/delta OS-Homo sapiens GN-VWHAZ PE-1 SV-1 [143Z2_HUMAN]	45.31%	1	7	9	3	2,561.07	8	9	15	16	42.04%	45.31%	41.07	45.62	245	27.7
P11047	Laminin subunit gamma 1 OS-Homo sapiens GN-LAMC1 PE-1 SV-3 [LAMC1_HUMAN]	31.20%	1	35	35	90	2,461.07	35	34	46	44	31.20%	30.76%	140.13	170.65	1609	177.5
P04606	Cytochrome b5 reductase OS-Homo sapiens GN-CYB1 PE-1 SV-2 [CYB_HUMAN]	29.55%	6	6	6	13	2,401.07	6	6	7	6	29.55%	29.55%	20.93	292.93	335	36
Q15113	Procollagen C-propeptidase enhancer 1 OS-Homo sapiens GN-PCOLCE1 PE-1 SV-2 [PCOC1_HUMAN]	31.20%	1	10	10	20	2,341.07	9	10	10	10	29.18%	31.61%	32.03	365.98	449	47.9
P08253	72 kDa type IV collagenase OS-Homo sapiens GN-MMP2 PE-1 SV-2 [MMP2_HUMAN]	34.49%	1	17	17	48	2,231.07	17	17	24	24	34.49%	34.09%	66.78	533.97	660	73.8
P55613	Basigin OS-Homo sapiens GN-BSG PE-1 SV-2 [BSG_HUMAN]	18.44%	1	6	6	26	1,941.07	6	6	13	13	18.44%	18.44%	45.75	450.05	385	42.2
P07842	Laminin subunit beta 1 OS-Homo sapiens GN-LAMB1 PE-1 SV-2 [LAMB1_HUMAN]	20.72%	27	27	27	1,811.07	27	26	27	30	30	19.65%	19.65%	40.14	819.63	1786	197.9
P29966	Methylated alanine-rich Calnexin substrate OS-Homo sapiens GN-MARCKS PE-1 SV-4 [MARCKS_HUMAN]	40.06%	1	6	6	18	1,791.07	6	6	6	6	40.06%	40.06%	31.57	318.32	332	31
Q06H18	GTP-binding protein Ras-2 OS-Homo sapiens GN-RAS2 PE-1 SV-1 [RAS2_HUMAN]	5.53%	1	1	1	2	1,781.07	1	1	1	1	5.53%	5.53%	3.25	39.88	199	22.5
Q03810	Guanine nucleotide exchange factor 1 OS-Homo sapiens GN-GEF1 PE-1 SV-1 [GEF1_HUMAN]	36.99%	1	10	17	30	1,721.07	10	10	12	12	36.99%	36.99%	14.83	121.4	627	61.9
P12141	Mdk1a OS-Homo sapiens GN-MDK1 PE-1 SV-1 [MDK_HUMAN]	30.77%	1	3	3	6	1,751.07	3	3	3	3	30.77%	30.77%	10.78	120.77	143	15.6
P08107	Heat shock 70 kDa protein 1A1B OS-Homo sapiens GN-HSPA1A PE-1 SV-2 [HSP70_HUMAN]	30.72%	2	13	14	47	1,671.07	14	14	23	24	30.72%	30.72%	69.73	541.31	641	70
Q06060	Systemin OS-Homo sapiens GN-SDCIP1 PE-1 SV-1 [SDCIP1_HUMAN]	16.78%	1	3	3	7	1,581.07	3	3	3	3	16.78%	16.78%	5.01	97.33	298	32.4
P02628	Heat shock cognate 90 kDa beta OS-Homo sapiens GN-HSP90B1 PE-1 SV-1 [HSP90B_HUMAN]	24.86%	8	7	15	37	1,361.07	15	14	19	18	24.86%	23.90%	58.13	635.02	724	83.2
P23528	Codf1in OS-Homo sapiens GN-COFL1 PE-1 SV-3 [COFL_HUMAN]	27.11%	2	3	3	7	1,361.07	3	3	3	4	27.11%	27.11%	11.15	161.91	166	18.5
P02630	Keratin, type II cytokeletal 2 OS-Homo sapiens GN-KRT2 PE-1 SV-2 [K2C_HUMAN]	6.55%	1	6	6	1	1,321.07	6	6	6	6	6.55%	6.55%	47.52	63.49	639	65.6
P02158	Calmodulin OS-Homo sapiens GN-CALM1 PE-1 SV-2 [CALM_HUMAN]	44.30%	2	3	3	6	2,124.07	6	6	13	13	44.30%	44.30%	28.77	227.84	149	16.8
P02649	Apolipoprotein E OS-Homo sapiens GN-APOE PE-1 SV-1 [APOE_HUMAN]	35.02%	1	10	10	12	1,201.07	10	12	12	12	35.02%	35.02%	38.02	538.42	317	36.1
P13946	14-3-3 protein beta OS-Homo sapiens GN-VWHAZ PE-1 SV-1 [143B2_HUMAN]	40.24%	2	4	8	27	1,151.07	8	8	14	13	40.24%	40.24%	39.26	379.44	246	28.1
P08862	CD81 antigen OS-Homo sapiens GN-CD81 PE-1 SV-2 [CD81_HUMAN]	21.29%	2	1	1	11	1,121.07	1	1	1	1	21.29%	21.29%	19.43	238	824	83.8
Q04075	Fructose-bisphosphate aldolase OS-Homo sapiens GN-ALDOA PE-1 SV-2 [ALDOA_HUMAN]	32.69%	1	10	10	11	1,121.07	8	9	10	11	32.69%	32.69%	20.01	373.03	364	39.4
P02628	Heat shock cognate 90 kDa beta OS-Homo sapiens GN-HSP90B1 PE-1 SV-1 [HSP90B_HUMAN]	39.22%	1	7	8	29	1,091.07	8	8	15	14	39.22%	39.22%	36.86	339.9	255	29.2
Q04076	Fructokinase 1 OS-Homo sapiens GN-CKFB1 PE-1 SV-1 [CKFB_HUMAN]	47.20%	1	1	1	2	8,821.07	1	1	1	1	47.20%	47.20%	19.32	119	212	21.9
P15531	Nucleoside diphosphate kinase A OS-Homo sapiens GN-NME1 PE-1 SV-1 [NDKA_HUMAN]	40.79%	3	5	5	8	1,101.07	5	5	9	9	40.79%	40.79%	27.81	286.13	152	17.1
P01981	14-3-3 protein gamma OS-Homo sapiens GN-VWHAZ PE-1 SV-2 [143G2_HUMAN]	30.77%	2	4	7	7	1,071.07	7	7	13	14	30.77%	30.77%	28.88	292.82	247	28.3
P07900	Heat shock protein HSP 90 alpha OS-Homo sapiens GN-HSP90A1 PE-1 SV-3 [HSP90A_HUMAN]	19.54%	7	4	12	29	1,061.07	12	12	14	14	19.54%	19.54%	45.89	515.23	732	84.6
P13957	CY59 glycoprotein OS-Homo sapiens GN-CY59 PE-1 SV-1 [CY59_HUMAN]	20.72%	1	1	1	1	1,041.07	1	1	1	1	20.72%	20.72%	11.84	127.5	129	14.2
Q06048	Agrin OS-Homo sapiens GN-AGRN PE-1 SV-1 [AGRN_HUMAN]	20.13%	1	26	26	71	9,941.07	26	26	35	35	20.13%	20.13%	113.94	931.28	2067	217.1
P27348	14-3-3 protein zeta/delta OS-Homo sapiens GN-VWHAZ PE-1 SV-1 [143Z2_HUMAN]	43.67%	2	6	9	27	9,831.07	9	9	14	13	43.67%	43.67%	38.85	463.92	245	27.7
Q05311	Eukaryotic translation initiation factor 4E OS-Homo sapiens GN-EIF4E PE-1 SV-1 [EIF4E_HUMAN]	2.17%	1	1	1	9,841.07	1	1	1	1	2.17%	2.17%	57.81	38.41	283	38.1	
P13645	Keratin, type I cytokeletal 10 OS-Homo sapiens GN-KRT10 PE-1 SV-1 [K10C_HUMAN]	33.90%	15	12	15	32	9,741.07	15	15	16	16	33.90%	33.90%	51.47	739.02	584	58.8
P0174	Triosephosphate isomerase OS-Homo sapiens GN-TPI1 PE-1 SV-3 [TPIS_HUMAN]	38.81%	1	8	8	20	9,721.07	8	8	10	10	38.81%	38.81%	32.67	331.33	286	30.8
Q02029	Cholesterol intracellular chaperon protein 1 OS-Homo sapiens GN-CLIC1 PE-1 SV-4 [CLIC1_HUMAN]	43.57%	1	6	6	14	9,651.07	6	6	6	6	43.57%	43.57%	32.16	214.44	241	26.9
P02630	Keratin, type II cytokeletal 2 OS-Homo sapiens GN-KRT2 PE-1 SV-2 [K2C_HUMAN]	6.55%	1	6	6	9	9,451.07	6	6	6	6	6.55%	6.55%	47.52	63.49	639	65.6
Q08431	Lactoferrin OS-Homo sapiens GN-MFG8 PE-1 SV-2 [MFG8_HUMAN]	30.23%	1	8	8	21	9,341.07	8	7	11	10	30.23%	25.58%	31	230.37	387	43.1
Q07540	Programmed cell death protein 1 OS-Homo sapiens GN-PCDCD1 PE-1 SV-1 [PDCD1_HUMAN]	23.04%	1	4	4	10	9,271.07	4	4	5	5	23.04%	23.04%	15.74	168.72	191	21.9
Q02982	Prostaglandin H2 receptor negative regulator OS-Homo sapiens GN-PTGER4 PE-1 SV-2 [PTGER_HUMAN]	18.54%	13	13	13	9,041.07	14	14	14	14	18.54%	18.54%	41.14	879	98.5	6.61	
Q04214	Tyrosine phosphatase SH-PTPase OS-Homo sapiens GN-SHP2 PE-1 SV-2 [SH2_HUMAN]	3.32%	1	1	1	2	8,951.07	1	1	1	1	3.32%	3.32%	3.97	9.91	161	17.9
P08758	Ancxin A5 OS-Homo sapiens GN-ANXA5 PE-1 SV-2 [ANXA5_HUMAN]	36.88%	1	8	10	12	8,821.07	9	10	12	14	35.00%	36.88%	32.97	331.68	320	35.9
P07377	Profilin 1 OS-Homo sapiens GN-PFN1 PE-1 SV-2 [PROF1_HUMAN]	50.71%	1	6	6	14	8,551.07	6	6	7	7	50.71%	50.71%	19.44	202.27	140	15
P02630	MARCKS-related protein OS-Homo sapiens GN-MARCKS PE-1 SV-1 [MARCKS_HUMAN]	37.76%	1	6	6	7	8,271.07	6	6	6	6	37.76%	37.76%	35.47	402.61	339	38.6
P07355	Ancxin A2 OS-Homo sapiens GN-ANXA2 PE-1 SV-2 [ANXA2_HUMAN]	37.46%	1	11	11	24	8,151.07	11	11	12	12	37.46%	37.46%	36.47	402.61	339	38.6
Q04917	14-3-3 protein zeta/delta OS-Homo sapiens GN-VWHAZ PE-1 SV-1 [143Z2_HUMAN]	24.80%	2	4	6	15	8,001.07	5	6	7	8	24.80%	24.80%	16.41	232.67	246	28.2
P55058	Phospholipid transfer protein OS-Homo sapiens GN-PLTP PE-1 SV-1 [PLTP_HUMAN]	19.27%	1	7	7	16	7,941.07	7	7	8	8	19.27%	19.27%	22.42	275.24	493	54.7
Q04076	Fructokinase 1 OS-Homo sapiens GN-CKFB1 PE-1 SV-1 [CKFB_HUMAN]	47.20%	1	1	1	2	7,941.07	1	1	1							

Q15365	Poly(C)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	7.02%	3	2	2	4	1.44E+06	2	2	2	2	7.02%	7.02%	5.61	67.15	356	37.5	7.09
P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	10.44%	1	2	2	3	1.41E+06	2	1	2	1	10.44%	6.32%	2.48	17.33	364	39.4	6.87
P23990	EST1 homolog OS=Homo sapiens GN=EST1 PE=1 SV=1 - [EST1_HUMAN]	10.44%	1	3	3	6	1.48E+06	3	3	3	3	10.44%	10.44%	6.47	42.63	364	39.7	5.35
O75695	Protein XRP2 OS=Homo sapiens GN=XRP2 PE=1 SV=4 - [XRP2_HUMAN]	6.29%	1	2	2	4	1.27E+06	2	2	2	2	6.29%	6.29%	2.89	66	350	39.6	5.12
Q53E24	Centromeres protein of 55 kDa OS=Homo sapiens GN=CEP55 PE=1 SV=3 - [CEP55_HUMAN]	10.56%	1	5	5	11	1.24E+06	4	5	5	6	10.34%	10.56%	17.42	220.6	464	54.1	7.01
Q15599	Naf-1(H)/c exchange regulatory cofactor NHE-R2 OS=Homo sapiens GN=SLC3A2 PE=1 SV=2 - [NHE-R2_HUMAN]	12.46%	1	3	3	5	1.22E+06	3	2	3	2	12.46%	6.5%	8.81	110.57	337	37.4	7.93
O14964	Hepatitis growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1 - [HGS_HUMAN]	2.70%	1	2	2	4	1.22E+06	2	2	2	2	2.70%	2.70%	4.91	34.91	777	86.1	6.16
O14791	Apolipoprotein L1 OS=Homo sapiens GN=APOLI1 PE=1 SV=5 - [APOLI1_HUMAN]	3.77%	1	1	1	2	1.22E+06	1	1	1	1	3.77%	3.77%	3.83	63.3	398	43.9	5.81
Q02783	Signal transducing adaptor molecule 1 OS=Homo sapiens GN=STAM PE=1 SV=3 - [STAM1_HUMAN]	4.67%	1	2	2	4	1.21E+06	2	2	2	2	4.67%	4.67%	7.47	104.99	540	59.1	4.82
P07996	Thrombospondin-1 OS=Homo sapiens GN=THSD1 PE=1 SV=2 - [THSD1_HUMAN]	1.03%	1	1	1	2	1.19E+06	1	1	1	1	1.03%	1.03%	3.57	41.13	1170	129.3	4.94
Q9H9H4	Vacuolar protein sorting-associated protein 37B OS=Homo sapiens GN=VPS37B PE=1 SV=1 - [VPS37B_HUMAN]	9.82%	1	2	2	4	1.18E+06	2	2	2	2	9.82%	9.82%	5.81	81.89	285	31.3	7.34
Q9Y696	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4 - [CLIC4_HUMAN]	17.00%	1	3	3	11	1.13E+06	3	3	5	6	17.00%	17.00%	12.53	72.96	253	28.8	5.59
P23985	Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 - [MOT1_HUMAN]	6.49%	1	3	3	7	1.12E+06	3	2	4	3	6.49%	5.80%	7.67	51.01	560	53.9	8.66
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1 - [UBE2N_HUMAN]	17.11%	2	2	2	6	1.11E+06	2	2	3	3	17.11%	17.11%	8.89	58.37	152	17.1	6.57
P05386	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 - [RPLA1_HUMAN]	28.95%	1	1	2	6	1.11E+06	2	2	3	3	28.95%	28.95%	8.31	49.51	114	11.5	4.32
Q02818	Nucleobindin-3 OS=Homo sapiens GN=NUCB3 PE=1 SV=4 - [NUCB3_HUMAN]	4.56%	1	2	2	4	1.07E+06	2	2	2	2	4.56%	4.56%	6.03	135	461	53.8	5.25
Q98Z77	Charged multivesicular body protein 6 OS=Homo sapiens GN=CIMBP6 PE=1 SV=2 - [CIMBP6_HUMAN]	6.47%	1	1	1	2	9.61E+05	1	1	1	1	6.47%	6.47%	3.51	85.7	201	23.5	5.31
Q9HAM9	EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2 - [EHD1_HUMAN]	4.49%	1	2	2	4	9.48E+05	2	2	2	2	4.49%	4.49%	5.33	49.52	534	60.6	6.83
P31948	Stress-induced phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1 - [STIP1_HUMAN]	5.34%	1	2	2	4	8.77E+05	2	2	2	2	5.34%	5.34%	5.69	61.12	543	62.6	6.8
Q15443	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1 - [CDC37_HUMAN]	10.05%	1	2	2	4	7.76E+05	2	2	2	2	10.05%	10.05%	6.36	31.94	378	44.4	5.25
Q14108	Lysozyme membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2 - [SCARB2_HUMAN]	2.72%	1	1	1	2	6.93E+05	1	1	1	1	2.72%	2.72%	3.15	24.97	478	54.3	5.14
A6NDB9	Paralemmn-3 OS=Homo sapiens GN=PALM3 PE=1 SV=2 - [PALM3_HUMAN]	2.23%	1	1	1	2	6.54E+05	1	1	1	1	2.23%	2.23%	2.83	62.26	673	71.7	4.53
O60716	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	1.03%	1	1	1	2	6.49E+05	1	1	1	1	1.03%	1.03%	2.61	22.72	968	108.1	6.23
O15347	Tubulin-specific chaperone A OS=Homo sapiens GN=TRCA PE=1 SV=3 - [TRCA_HUMAN]	17.99%	1	2	2	3	6.08E+05	1	2	1	2	8.26%	17.99%	2.6	49.43	108	12.8	5.29
A5DSV6	Vacuolar protein sorting-associated protein 37C OS=Homo sapiens GN=VPS37C PE=1 SV=2 - [VPS37C_HUMAN]	3.10%	1	1	1	2	4.91E+05	1	1	1	1	3.10%	3.10%	3.58	69.69	355	38.6	5.21
P63218	Guanine nucleotide-binding protein G(i)(G12)(G13) subunit gamma5 OS=Homo sapiens GN=GNCG5 PE=1 SV=3 - [GBG5_HUMAN]	13.24%	1	1	1	2	3.63E+05	1	1	1	1	13.24%	13.24%	2.18	37.98	68	7.3	9.85
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 - [GRP75_HUMAN]	1.33%	1	1	1	2	3.54E+05	1	1	1	1	1.33%	1.33%	2.72	44.86	679	73.6	6.16
P14550	Alcohol dehydrogenase [NAD(P)+] OS=Homo sapiens GN=AKH1A1 PE=1 SV=3 - [AKH1A1_HUMAN]	5.85%	1	1	1	4	3.33E+05	1	1	2	2	5.85%	5.85%	5.76	47.87	325	36.5	6.79
Q9BX67	Junctional adhesion molecule C OS=Homo sapiens GN=JAM3 PE=1 SV=1 - [JAM3_HUMAN]	2.58%	1	1	1	2	3.21E+05	1	1	1	1	2.58%	2.58%	1.74	31.54	310	35	7.59
P05067	Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3 - [A4_HUMAN]	4.29%	1	3	3	4	2.71E+05	1	3	1	3	4.69%	4.29%	1.93	49.27	770	86.9	4.82
Q9C8E2	Protein trexy homolog 3 OS=Homo sapiens GN=TTXB3 PE=1 SV=3 - [TTXB3_HUMAN]	5.93%	1	2	2	5	2.68E+05	2	2	3	3	5.93%	5.93%	4.85	53.22	523	57.5	5.39
P60981	Dextrin OS=Homo sapiens GN=DSTN PE=1 SV=3 - [DSTN_HUMAN]	7.88%	1	1	1	2	1.01E+05	1	1	1	1	7.88%	7.88%	2.18	25.8	165	18.5	7.85
P27105	Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3 - [STOM_HUMAN]	7.64%	1	2	2	3	7.24E+04	1	2	1	2	4.17%	7.64%	3.16	53.24	288	31.7	7.88