Supplementary Table 2: Detailed differential proteins
MH: Macular Hole
MH-PM: Macular Hole with Pathological Myopia
ERM: Epithelial Retinal Membrane
MRS-PM: Myopic retinoschisis
RRD: Rhegmatogenous Retinal Detachment
RRD-PM: Rhegmatogenous Retinal Detachment with Pathological myopia

Protein IDs	Fasta headers	iBAQ MH-PM1	iBAQ MH-PM2	iBAQ MH-PM3	iBAQ MRS-PM 1	iBAQ MRS-PM 2	iBAQ MRS-PM 3	iBAQ RRD-PM1	iBAQ RRD-PM2	iBAQ RRD-PM3	iBAQ MH1	iBAQ MH2	iBAQ MH3	iBAQ ERM 1	iBAQ ERM 2	iBAQ ERM 3	iBAQ RRD1	iBAQ RRD2	iBAQ RRD3	T-T
sp|P41222|PTGDS_HUMAN	>sp|P41222|PTGDS_HUMAN Prostaglandin-H2 D-isomerase OS=Homo sapiens GN=PTGDS PE=1 SV=1	153310	139880	71388	153550	161910	175770	90107	59086	44489	729210	526530	313820	208940	220680	215580	110440	106370	112030	0.037049
sp|P22352|GPX3_HUMAN	>sp|P22352|GPX3_HUMAN Glutathione peroxidase 3 OS=Homo sapiens GN=GPX3 PE=1 SV=2	12727	13860	9515	8440.3	3469.3	7427.3	7307.8	4602.9	3722.1	55948	49025	21528	17438	20350	14323	12137	7033.7	8021.7	0.023764
sp|Q17R60|IMPG1_HUMAN	>sp|Q17R60|IMPG1_HUMAN Interphotoreceptor matrix proteoglycan 1 OS=Homo sapiens GN=IMPG1 PE=1 SV=2	641.85	316.3	73.053	359.09	232.02	88.262	319.27	298.86	334.31	3102.2	1782.6	1517.2	444.87	751.96	595.14	629.03	961.47	887.8	0.006742
sp|P13611|CSPG2_HUMAN	>sp|P13611|CSPG2_HUMAN Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3	50.141	32.306	0	0	11.609	0	0	0	0	655.2	715.35	334.52	90.796	0	140.73	0	0	0	0.049314
sp|Q8N2N9|AN36B_HUMAN;sp|Q5JPF3|AN36C_HUMAN;sp|A6QL64|AN36A_HUMAN	>sp|Q8N2N9|AN36B_HUMAN Ankyrin repeat domain-containing protein 36B OS=Homo	0	0	14.462	40.99	0	45.503	0	0	0	49.175	35.889	61.712	0	32.204	88.76	30.663	0	96.894	0.023203

	sapiens GN=ANKRRD36B PE=1 SV=4;>sp|Q5JPF3|AN36C_HUMAN Ankyrin repeat domain-containing protein 36C OS=Homo sapiens GN=ANKRRD36C PE=2 SV=3;>sp|A6QL64|AN36A_HUMAN Ankyrin repeat domain																			
sp|P13521|SCG2_HUMAN	>sp|P13521|SCG2_HUMAN Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	128.96	129.74	0	69.563	0	9.2952	162.59	64.541	0	333.11	406.3	283.5	121.01	174.05	97.516	0	91.119	80.662	0.036883
sp|Q9BY67|CADM1_HUMAN	>sp|Q9BY67|CADM1_HUMAN Cell adhesion molecule 1 OS=Homo sapiens GN=CADM1 PE=1 SV=2	177.69	25.144	0	0	0	0	0	0	50.778	905.81	566.57	404.26	0	259.18	214.63	0	0	0	0.045635
sp|Q16610|ECM1_HUMAN	>sp|Q16610|ECM1_HUMAN Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2	0	0	0	0	0	0	0	0	0	502.02	301.85	192.5	0	164.34	0	0	0	0	0.046604
sp|P01765|HV304_HUMAN;sp|P01779|HV318_HUMAN;sp|P01776|HV315_HUMAN;sp|P01774|HV313_HUMAN	>sp|P01765|HV304_HUMAN Ig heavy chain V-III region TIL OS=Homo sapiens PE=1 SV=1;>sp|P01779|HV318_HUMAN Ig heavy chain V-III region TUR	2465.8	1485.9	849.19	1575.3	1236.3	2596.6	2320.5	0	657.42	2784.1	6956.6	4766.4	8398.5	4911.9	6616.4	2275.4	3199.7	177.87	0.004898

	OS=Homo sapiens PE=1 SV=1;>sp|P01776|HV315_HUMAN Ig heavy chain V-III region WAS OS=Homo sapiens PE=1 SV=1;>sp|P01774|HV																			
sp|P0CG05|LAC2_HUMAN;sp|P0CG06|LAC3_HUMAN;sp|P0CF74|LAC6_HUMAN;sp|A0M8Q6|LAC7_HUMAN	>sp|P0CG05|LAC2_HUMAN Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1;>sp|P0CG06|LAC3_HUMAN Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1;>sp|P0CF74|LAC6_HUMAN Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 PE=4 SV=1;>s	42289	23601	16429	32919	40405	38373	21924	15565	14359	133720	66164	59839	72616	60992	63683	32837	17442	28995	0.015297
sp|P01777|HV316_HUMAN;sp|P01766|HV305_HUMAN	>sp|P01777|HV316_HUMAN Ig heavy chain V-III region TEI OS=Homo sapiens PE=1 SV=1;>sp|P01766|HV305_HUMAN Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	14385	6674.2	6106.7	6609.9	4257.7	9435.4	6984.6	5079.7	3194.6	23279	16668	14485	10950	7725.7	9449.2	9209.9	7447.1	11141	0.019107
sp|Q9Y6R7|FCGBP_HUMAN	>sp|Q9Y6R7|FCGBP_HUMAN IgGFc-binding protein OS=Homo sapiens	137.14	50.003	55.076	10.405	0	11.67	0	30.631	0	128.15	94.795	41.115	77.449	98.988	51.439	48.943	68.106	97.239	0.01987

	GN=FCGBP PE=1 SV=3																			
sp|P01624|KV306_HUMAN;sp|P01605|KV113_HUMAN;sp|P04434|KV310_HUMAN;sp|P04207|KV308_HUMAN	>sp|P01624|KV306_HUMAN Ig kappa chain V-III region POM OS=Homo sapiens PE=1 SV=1;>sp|P01605|KV113_HUMAN Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1;>sp|P04434|KV310_HUMAN Ig kappa chain V-III region VH (Fragment) OS=Homo sapiens PE=4 SV=1;>sp|P	0	0	0	0	0	0	0	0	0	0	0	0	2018.4	1923.9	0	1548.9	975.3	0	0.029203
sp|P14136|GFAP_HUMAN	>sp|P14136|GFAP_HUMAN Glial fibrillary acidic protein OS=Homo sapiens GN=GFAP PE=1 SV=1	529.8	394.94	496.58	0	0	72.218	0	142.09	31.83	112.03	103.81	0	0	0	0	0	0	0	0.050512
sp|P01859|IGHG2_HUMAN	>sp|P01859|IGHG2_HUMAN Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	10583	7321.9	4813.5	6488.7	6553.6	3541.1	3302.2	3096.3	2433.9	55609	42703	13501	14985	10907	10798	5514.1	4471.2	4769	0.054052
sp|P10451|OSTP_HUMAN;CON__P31096	>sp|P10451|OSTP_HUMAN Osteopontin OS=Homo sapiens GN=SPP1 PE=1 SV=1	63786	55155	34514	11883	10634	19812	20186	19166	14468	103560	58995	34778	52546	69608	40942	43364	33745	13120	0.054319
sp|P01717|LV403_HUMAN	>sp|P01717|LV403_HUMAN Ig lambda chain V-IV region Hil OS=Homo sapiens PE=1 SV=1	6585.1	5272.8	0	1940.5	0	2303.5	2942	3344.4	2732.5	10027	983.37	3876.9	6562.2	5912.2	4003.2	3970.8	4733.1	5316.8	0.055482

sp|O43505|B4GA1_HUMAN	>sp|O43505|B4GA1_HUMAN Beta-1,4-glucuronyltransferase 1 OS=Homo sapiens GN=B4GAT1 PE=1 SV=1	1871.9	1384.8	1001	725.28	375.11	324.75	775.19	45.092	556.73	1239.7	2010.4	1264	1524.7	1023.2	952.05	756.94	1309.1	1116.4	0.057422
sp|P05155|IC1_HUMAN	>sp|P05155|IC1_HUMAN Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	13604	10474	4612.6	6467.9	5137.7	7036.3	4075.1	2433.7	1524.7	36595	21699	13149	10193	12314	9024	7489.4	6121.5	3836.5	0.062081
sp|B9A064|IGLL5_HUMAN;sp|P0CG04|LAC1_HUMAN	>sp|B9A064|IGLL5_HUMAN Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2;>sp|P0CG04|LAC1_HUMAN Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1	5292.8	2960	193.72	2750.3	2217.8	2215.5	582.66	684.21	1404.4	10593	13311	1904.5	5714.5	2815	4149.7	2313.5	4030.1	522.73	0.063693
sp|Q06481|APLP2_HUMAN	>sp|Q06481|APLP2_HUMAN Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2	1271.9	1119.8	945.72	987.8	492.4	989.25	276	295.09	0	8681.3	4832.1	1837.4	1867.6	3017.9	2023.5	0	339.54	344.27	0.064995
sp|Q6P587|FAHD1_HUMAN	>sp|Q6P587|FAHD1_HUMAN Acylpyruvase FAHD1, mitochondrial OS=Homo sapiens GN=FAHD1 PE=1 SV=2	10985	14112	243.09	37339	28830	34458	9541.2	3672.3	3609	87652	74663	47894	52420	38634	40660	6343	0	0	0.065428
sp|P10745|RET3_HUMAN	>sp|P10745|RET3_HUMAN Retinol-binding protein 3	38117	45237	25294	12139	10352	12773	26224	24483	18163	117130	64914	34000	21123	20966	15264	44261	46491	45598	0.06654

	OS=Homo sapiens GN=RBP3 PE=1 SV=2																			
sp|P02787|TRFE_HUMAN	>sp|P02787|TRFE_HUMAN Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	128050	99993	46446	81055	78907	67643	29757	34821	22731	323950	197660	145920	123990	125110	108380	43983	47237	43315	0.066749
sp|Q14515|SPRL1_HUMAN	>sp|Q14515|SPRL1_HUMAN SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2	113.23	77.616	0	61.123	70.876	84.285	0	23.376	0	714.84	368.03	0	203.52	294.34	224.33	0	18.514	23.032	0.066976
sp|O14773|TPP1_HUMAN	>sp|O14773|TPP1_HUMAN Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2	0	366.97	105.6	0	0	0	0	0	264.9	1846.5	1864.2	607.53	0	45.098	473.72	0	259.58	135.91	0.067764
sp|P01623|KV305_HUMAN;sp|P01620|KV302_HUMAN;sp|P04206|KV307_HUMAN;sp|P01622|KV304_HUMAN;sp|P18136|KV313_HUMAN;sp|P18135|KV312_HUMAN	>sp|P01623|KV305_HUMAN Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1;>sp|P01620|KV302_HUMAN Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1;>sp|P04206|KV307_HUMAN Ig kappa chain V-III region GOL OS=Homo sapiens PE=1 SV=1;>sp|P01622|KV	25750	22206	12737	9192.1	6141	10983	8029.9	6011.7	4403.5	71012	42988	23995	22013	18793	19169	11362	9883.1	10168	0.069301
sp|P01042|KNG1_HUMAN	>sp|P01042|KNG1_HUMAN Kininogen-1 OS=Homo sapiens	588.92	567.5	290.43	126.71	0	392.29	0	124.02	0	5597.9	2662.5	1262	738.66	693.36	568.56	514.9	227.61	147.23	0.069574

	GN=KNG1 PE=1 SV=2																			
sp|P01857|IGHG1_HUMAN	>sp|P01857|IGHG1_HUMAN Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	128800	80565	67419	70430	39712	57525	40585	39610	31299	323300	253230	124000	95480	87258	80945	69321	52778	52280	0.071376
sp|Q8N0Y7|PGAM4_HUMAN;sp|P18669|PGAM1_HUMAN;sp|P15259|PGAM2_HUMAN	>sp|Q8N0Y7|PGAM4_HUMAN Probable phosphoglycerate mutase 4 OS=Homo sapiens GN=PGAM4 PE=3 SV=1;>sp|P18669|PGAM1_HUMAN Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2;>sp|P15259|PGAM2_HUMAN Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1	0	0	0	0	0	0	68.631	0	0	1233.1	971.3	763.68	0	0	0	0	0	0	0.07577
sp|P19022|CADH2_HUMAN	>sp|P19022|CADH2_HUMAN Cadherin-2 OS=Homo sapiens GN=CDH2 PE=1 SV=4	126.4	497.17	353.87	139.4	83.942	288.47	0	0	0	2615.1	1408.4	578.69	329.03	509.36	220.15	100.01	201.74	241.64	0.080055
sp|P16870|CBPE_HUMAN	>sp|P16870|CBPE_HUMAN Carboxypeptidase E OS=Homo sapiens GN=CPE PE=1 SV=1	537.24	687.06	213.27	703.72	351.85	618.86	213.24	380.69	123.79	13812	6054.8	2516.2	1592.5	2183.3	603.71	0	811.83	771.37	0.080803
sp|P51693|APLP1_HUMAN	>sp|P51693|APLP1_HUMAN Amyloid-like protein 1 OS=Homo sapiens	446.95	238.17	65.655	164.23	0	0	0	57.159	0	773.36	595.92	0	504.73	258.38	943.3	0	0	88.282	0.082686

	GN=APLP1 PE=1 SV=3																			
sp|P36955|PEDF_HUMAN	>sp|P36955|PEDF_HUMAN Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	126330	147730	57407	66298	47184	60226	25963	39462	16396	360970	227090	119190	117430	104030	104820	64954	57476	42216	0.08286
sp|P36222|CH3L1_HUMAN	>sp|P36222|CH3L1_HUMAN Chitinase-3-like protein 1 OS=Homo sapiens GN=CHI3L1 PE=1 SV=2	3950.9	4404.7	2185.4	598.99	0	426.36	227.84	932.04	561.97	1334.8	0	77.181	0	468.04	0	184.11	1297.3	351.26	0.08549
sp|O94985|CSTN1_HUMAN	>sp|O94985|CSTN1_HUMAN Calsyntenin-1 OS=Homo sapiens GN=CLSTN1 PE=1 SV=1	1665.7	715.41	814.16	719.78	89.115	938.8	0	498.43	0	9044.8	4693	2220.2	1649.5	1176.3	1164.4	711.11	0	549.82	0.088917
sp|P02790|HEMO_HUMAN	>sp|P02790|HEMO_HUMAN Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	16829	13850	9007.9	8724.2	5880	6709.3	6319.2	4819.4	4362.2	59593	34307	19839	11835	9401.1	10956	8671.8	10931	7629.8	0.089127
sp|P05067|A4_HUMAN	>sp|P05067|A4_HUMAN Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3	88.469	821	68.374	8.0642	104.72	0	0.89143	0	0	6760.1	2783.3	443.72	895.73	1252.6	520.49	297.55	0	0	0.089568
sp|P00738|HPT_HUMAN;sp|P00739|HPTR_HUMAN	>sp|P00738|HPT_HUMAN Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	4208.7	2059.1	1368.7	2265.3	915.23	2114.1	0	426.04	50.589	34082	26518	9172.9	2325.8	3940.7	2641.4	1671.2	507.6	534.61	0.089634
sp|P53673|CRBA4_HUMAN	>sp|P53673|CRBA4_HUMAN Beta-crystallin A4 OS=Homo sapiens	0	0	0	0	0	0	0	0	160.31	139920	71029	60627	0	0	0	203.18	0	0	0.089656

	GN=CRYBA4 PE=1 SV=3																			
sp|P14174|MIF_HUMAN	>sp|P14174|MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	0	0	0	0	0	0	0	0	0	15016	7944.6	6155.7	0	0	0	0	0	0	0.090561
sp|P53674|CRBB1_HUMAN	>sp|P53674|CRBB1_HUMAN Beta-crystallin B1 OS=Homo sapiens GN=CRYBB1 PE=1 SV=2	2567.1	468.41	109.09	405.44	699.35	364.89	0	0	0	184520	126230	61725	1253.9	1298.4	1129.4	722.76	0	139.92	0.090588
sp|P22914|CRBS_HUMAN	>sp|P22914|CRBS_HUMAN Beta-crystallin S OS=Homo sapiens GN=CRYGS PE=1 SV=4	1296.4	444.7	2395.7	573.38	0	1417.9	0	88.43	91.625	400740	275760	133680	1080.2	1548.4	3153.4	65.759	748.67	0	0.090901
sp|P43320|CRBB2_HUMAN	>sp|P43320|CRBB2_HUMAN Beta-crystallin B2 OS=Homo sapiens GN=CRYBB2 PE=1 SV=2	3134	2901.7	1554.7	264.89	32.111	377.14	7.2877	0	138.61	751190	479350	265060	143.42	428.18	0	141.58	0	0	0.092731
sp|P98160|PGBM_HUMAN	>sp|P98160|PGBM_HUMAN Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=4	0	20.06	2.8565	0	0	0	0	0	0	59.09	32.737	31.197	0	19.81	0	0	0	0	0.093329
sp|P02647|APOA1_HUMAN;CON__P15497	>sp|P02647|APOA1_HUMAN Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	119730	81343	57514	44127	45560	50556	41169	30143	22200	288570	191060	100090	81017	79452	70198	52392	46330	46862	0.093676
sp|P02511|CRYAB_HUMAN	>sp|P02511|CRYAB_HUMAN Alpha-	2282.1	588.91	10.271	1.7148	261.83	88.269	59.024	0	0	710760	432240	236410	89.657	0	0	0	0	0	0.095521

	crystallin B chain OS=Homo sapiens GN=CRYAB PE=1 SV=2																			
sp|Q8NBJ4|GOLM1_HUMAN	>sp|Q8NBJ4|GOLM1_HUMAN Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 PE=1 SV=1	193.65	0	202.35	58.636	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.096486
sp|Q9H2D1|MFTC_HUMAN	>sp|Q9H2D1|MFTC_HUMAN Mitochondrial folate transporter/carrier OS=Homo sapiens GN=SLC25A32 PE=1 SV=2	0	0	0	0	0	0	0	0	0	1168.9	716.73	362.87	0	0	0	0	0	0	0.097419
sp|P32119|PRRDX2_HUMAN	>sp|P32119|PRRDX2_HUMAN Peroxiredoxin-2 OS=Homo sapiens GN=PRRDX2 PE=1 SV=5	0	0	0	0	0	0	529.41	421.66	419.25	0	0	0	0	0	0	0	132.85	0	0.098018
sp|P01023|A2MG_HUMAN;CON__ENSEMBL:ENSBTAP00000024146;sp|P20742|PZP_HUMAN	>sp|P01023|A2MG_HUMAN Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	12594	8667	3799.4	2583.3	1534.1	3024.4	2797.4	3022.6	1254.4	26465	16230	9485.4	5582.5	8068.8	5820.2	4658.3	3351.5	3983.1	0.098572
sp|P10643|CO7_HUMAN	>sp|P10643|CO7_HUMAN Complement component C7 OS=Homo sapiens GN=C7 PE=1 SV=2	160.37	60.834	73.78	0	0	0	0	12.485	0	0	0	0	0	0	17.759	0	0	0	0.102026
sp|O75326|SEM7A_HUMAN	>sp|O75326|SEM7A_HUMAN Semaphorin-7A OS=Homo sapiens GN=SEMA7A PE=1 SV=1	64.558	0	34.395	27.111	18.11	115.52	25.048	3.6467	15.44	765.42	233.4	144.16	157.32	108.18	0	0	55.822	71.545	0.104025
sp|P02649|APOE_HUMAN	>sp|P02649|APOE_HUMAN	33874	30175	18406	11693	7153.1	11901	13203	10108	8521.3	91845	46411	24595	28625	31120	21947	17107	12636	9630	0.104583

	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1																			
sp|P04792|HSPB1_HUMAN	>sp|P04792|HSPB1_HUMAN Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	0	0	0	0	0	0	0	0	0	12628	6443.4	3809.8	0	0	0	0	0	0	0.104732
sp|P07315|CRGC_HUMAN;sp|P07316|CRGB_HUMAN;sp|P11844|CRGA_HUMAN	>sp|P07315|CRGC_HUMAN Gamma-crystallin C OS=Homo sapiens GN=CRYGC PE=1 SV=2;>sp|P07316|CRGB_HUMAN Gamma-crystallin B OS=Homo sapiens GN=CRYGB PE=1 SV=3;>sp|P11844|CRGA_HUMAN Gamma-crystallin A OS=Homo sapiens GN=CRYGA PE=2 SV=3	0	0	0	0	0	0	0	0	0	18762	9140.4	5487.5	0	38.599	0	0	0	0	0.107445
sp|P02748|CO9_HUMAN;CON__Q3MHN2	>sp|P02748|CO9_HUMAN Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	451.69	474.48	921.75	0	0	0	0	195.08	0	0	0	0	0	145.5	0	0	0	187.12	0.107975
sp|P01834|IGKC_HUMAN	>sp|P01834|IGKC_HUMAN Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	467390	119040	73374	166660	129150	149760	117720	122070	92128	454420	393370	297970	265980	304530	251610	70886	159190	119230	0.107991
sp|Q6NSJ5|LRC8E_HUMAN	>sp|Q6NSJ5|LRC8E_HUMAN Volume-regulated anion channel subunit LRRC8E OS=Homo	0	0	0	0	0	0	0	116.47	0	854.36	804.16	0	0	0	0	309.34	0	0	0.108457

	sapiens GN=LRRC8E PE=1 SV=2																			
sp|P02489|CRYAA_HUMAN	>sp|P02489|CRYAA_HUMAN Alpha-crystallin A chain OS=Homo sapiens GN=CRYAA PE=1 SV=2	5962.8	1484.9	573.18	707.38	651.34	233.26	82.239	365.99	207.59	1463400	897270	351770	375.24	883.06	1168.1	556.99	98.094	91.874	0.108478
sp|P69905|HBA_HUMAN;CON__P01966	>sp|P69905|HBA_HUMAN Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	7122.6	9408.8	4239.6	2514.6	1476.7	3529.8	154760	142370	82953	9846.4	5782.8	610.21	1861.9	1396.2	697.7	21728	16658	26186	0.115092
sp|P68871|HBB_HUMAN;CON__Q3SX09;CON__P02070;sp|P69892|HBG2_HUMAN;sp|P69891|HBG1_HUMAN;sp|P02100|HBE_HUMAN	>sp|P68871|HBB_HUMAN Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	8416.7	2667.9	2561.5	7216.6	724.69	1322.6	189000	137590	117560	14853	6668.4	2559.5	3058.7	3391.4	2452.3	20257	20579	19149	0.115518
sp|P02652|APOA2_HUMAN	>sp|P02652|APOA2_HUMAN Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	34959	28029	22210	14008	5937.7	11847	743.89	7484.8	0	138550	67089	36170	35796	24052	15574	10817	9429.7	5668.1	0.117815
sp|P00441|SODC_HUMAN	>sp|P00441|SODC_HUMAN Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	388.85	374.98	0	0	53.702	0.120164
sp|P08670|VIME_HUMAN;sp|P17661|DESM_HUMAN;sp|Q16352|AINX_HUMAN;sp|P07196|NFL_HUMAN;sp|P07197|NFM_HUMAN;sp|P12036|NFH_HUMAN	>sp|P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	866	379.07	381.2	26.145	0	0	11.128	226.52	0	331.19	0	0	13.705	0	0	0	0	0	0.120896

<table>
<tr><td>sp|P27169|PON1_HUMAN</td><td>>sp|P27169|PON1_HUMAN Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3</td><td>872.44</td><td>674.91</td><td>256.12</td><td>0</td><td>0</td><td>0</td><td>33.765</td><td>0</td><td>0</td><td>860.82</td><td>880.45</td><td>608.25</td><td>647.48</td><td>704.14</td><td>526.04</td><td>0</td><td>0</td><td>38.087</td><td>0.122099</td></tr>
<tr><td>sp|P00352|AL1A1_HUMAN;sp|P05091|ALDH2_HUMAN;sp|P47895|AL1A3_HUMAN;sp|P30837|AL1B1_HUMAN;sp|O94788|AL1A2_HUMAN</td><td>>sp|P00352|AL1A1_HUMAN Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2</td><td>0</td><td>94.767</td><td>0</td><td>0</td><td>85.082</td><td>55.581</td><td>23.476</td><td>0</td><td>16.185</td><td>19175</td><td>11962</td><td>2919.5</td><td>77.212</td><td>0</td><td>0</td><td>0</td><td>73.099</td><td>87.916</td><td>0.123275</td></tr>
<tr><td>sp|P07320|CRGD_HUMAN</td><td>>sp|P07320|CRGD_HUMAN Gamma-crystallin D OS=Homo sapiens GN=CRYGD PE=1 SV=3</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>31972</td><td>12846</td><td>6214.5</td><td>0</td><td>1067.5</td><td>0</td><td>0</td><td>0</td><td>231.24</td><td>0.123866</td></tr>
<tr><td>sp|Q86WG5|MTMRRD_HUMAN</td><td>>sp|Q86WG5|MTMRRD_HUMAN Myotubularin-related protein 13 OS=Homo sapiens GN=SBF2 PE=1 SV=1</td><td>0</td><td>755.93</td><td>13.926</td><td>293.57</td><td>197.95</td><td>254.9</td><td>0</td><td>0</td><td>0</td><td>2854.1</td><td>1279.7</td><td>1565.8</td><td>0</td><td>814.53</td><td>56.895</td><td>0</td><td>0</td><td>0</td><td>0.123899</td></tr>
<tr><td>sp|P05813|CRBA1_HUMAN</td><td>>sp|P05813|CRBA1_HUMAN Beta-crystallin A3 OS=Homo sapiens GN=CRYBA1 PE=1 SV=4</td><td>0</td><td>146.15</td><td>0</td><td>0</td><td>0</td><td>133.46</td><td>288.64</td><td>0</td><td>67.938</td><td>110030</td><td>54956</td><td>20589</td><td>0</td><td>132.62</td><td>0</td><td>0</td><td>173.97</td><td>0</td><td>0.126107</td></tr>
<tr><td>sp|P02753|RET4_HUMAN</td><td>>sp|P02753|RET4_HUMAN Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3</td><td>478.48</td><td>0</td><td>0</td><td>288.05</td><td>0</td><td>0</td><td>0</td><td>0</td><td>186.98</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>0</td><td>94.863</td><td>0</td><td>0.127665</td></tr>
<tr><td>sp|P01024|CO3_HUMAN;CON__Q2UVX4</td><td>>sp|P01024|CO3_HUMAN Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2</td><td>8300.3</td><td>7912</td><td>3589.5</td><td>3008.4</td><td>1678.3</td><td>2409.8</td><td>565.45</td><td>1651.3</td><td>620.03</td><td>34287</td><td>19250</td><td>9095.2</td><td>5328.6</td><td>6019.2</td><td>4186.4</td><td>1630.8</td><td>1952.6</td><td>2060.6</td><td>0.127963</td></tr>
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sp|P00558|PGK1_HUMAN;sp|P07205|PGK2_HUMAN	>sp|P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	0	0	0	0	0	0	0	0	17.099	2054.7	1371	262.12	0	0	0	0	0	0	0.128423
sp|O95602|RPA1_HUMAN	>sp|O95602|RPA1_HUMAN DNA-directed RNA polymerase I subunit RPA1 OS=Homo sapiens GN=POLR1A PE=1 SV=2	0	0	783.04	0	0	0	0	0	0	3960.9	1629.9	1122.2	0	0	478.67	35.82	11.928	15.389	0.129027
sp|P01019|ANGT_HUMAN	>sp|P01019|ANGT_HUMAN Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1	7717.2	5298.7	2116.9	2097.5	895.63	346.33	631.59	1248.6	1185.2	12380	9722.7	5101.7	2845.1	2838.2	3016.3	1874	2254.3	2891.9	0.131112
sp|P43251|BTD_HUMAN	>sp|P43251|BTD_HUMAN Biotinidase OS=Homo sapiens GN=BTD PE=1 SV=2	621.87	807.81	431.03	64.569	0	0	186.53	159.08	149.36	4736.5	1858.1	1336.7	286.69	969.37	282.04	43.814	244.29	0	0.131303
sp|P80723|BASP1_HUMAN	>sp|P80723|BASP1_HUMAN Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	0	0	0	0	0	0	0	0	0	7533.8	3859.4	1085.2	0	0	0	0	0	0	0.133952
sp|P08294|SODE_HUMAN	>sp|P08294|SODE_HUMAN Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2	897.72	0	101.84	0	0	0	0	524.04	0	0	0	0	0	0	0	0	0	0	0.13507
sp|Q9UBM4|OPT_HUMAN	>sp|Q9UBM4|OPT_HUMAN Opticin OS=Homo sapiens	12252	7397.3	5298.9	2378.9	3250.3	2817.2	1341.2	3714.6	417.41	14465	11294	3393	5254.2	4837.7	4919	6040.2	6759	5840.9	0.135922

	GN=OPTC PE=1 SV=1																			
sp|P05546|HEP2_HUMAN	>sp|P05546|HEP2_HUMAN Heparin cofactor 2 OS=Homo sapiens GN=SERPIND1 PE=1 SV=3	0	216.95	0	0	0	0	0	0	0	1398.5	704.3	0	149.72	165.04	0	0	0	40.061	0.142316
sp|P04075|ALDOA_HUMAN	>sp|P04075|ALDOA_HUMAN Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	0	0	0	0	0	0	0	0	0	5095.7	1728.8	963.57	0	0	0	0	0	0	0.146464
sp|P02675|FIBB_HUMAN	>sp|P02675|FIBB_HUMAN Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	82.399	57.821	0	0	0	0	0	118.73	90.824	1378.9	567.67	179.5	0	89.695	0	0	213.89	0	0.148967
sp|Q96NB1|FOPNL_HUMAN	>sp|Q96NB1|FOPNL_HUMAN LisH domain-containing protein FOPNL OS=Homo sapiens GN=FOPNL PE=1 SV=1	1052	501.57	385.73	1544.5	243.24	1300.8	0	0	0	3362.9	826.35	4002.4	1167.9	2180.3	649.83	110.86	0	0	0.150234
sp|Q9NQ79|CRAC1_HUMAN	>sp|Q9NQ79|CRAC1_HUMAN Cartilage acidic protein 1 OS=Homo sapiens GN=CRTAC1 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	142.32	0	0	0	122.45	0	0	0.151449
sp|Q8WXD2|SCG3_HUMAN	>sp|Q8WXD2|SCG3_HUMAN Secretogranin-3 OS=Homo sapiens GN=SCG3 PE=1 SV=3	234.09	244.87	0	92.164	0	0	0	0	0	1660.4	560.32	317.87	160.05	136.87	0	111.68	0	52.591	0.152132
sp|P01008|ANT3_HUMAN;CON__P41361	>sp|P01008|ANT3_HUMAN	5085.8	3727.8	1878	1239.1	785.27	920.16	927.41	562.53	670.26	8526.4	5479	2989.9	3518.7	3323.5	2254.1	1111.5	504.89	1394.1	0.152377

	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1																			
sp|P01033|TIMP1_HUMAN	>sp|P01033|TIMP1_HUMAN Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	682.1	551.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.152808
sp|P16152|CBR1_HUMAN;sp|O75828|CBR3_HUMAN	>sp|P16152|CBR1_HUMAN Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3;>sp|O75828|CBR3_HUMAN Carbonyl reductase [NADPH] 3 OS=Homo sapiens GN=CBR3 PE=1 SV=3	0	0	0	0	0	0	0	0	0	2925	2338.4	0	0	0	0	0	0	0	0.153106
sp|P10253|LYAG_HUMAN	>sp|P10253|LYAG_HUMAN Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4	127.84	0	29.935	0	193.77	157.09	0	0	0	0	0	0	0	67.129	0	0	63.558	0	0.156261
sp|Q15904|VAS1_HUMAN	>sp|Q15904|VAS1_HUMAN V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2	132.22	0	0	0	0	0	0	0	0	323.06	324.35	139	0	0	0	0	0	0	0.160585
sp|P61769|B2MG_HUMAN	>sp|P61769|B2MG_HUMAN Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	5.4494	3.8924	0	1887.1	2379.2	1878.4	0	285.08	6.2279	0	1335	0	115.38	0	0	0	0	130.47	0.161287

sp|P05060|SCG1_HUMAN	>sp|P05060|SCG1_HUMAN Secretogranin-1 OS=Homo sapiens GN=CHGB PE=1 SV=2	0	0	0	0	0	0	0	0	0	496.72	254.31	0	0	0	19.634	0	0	0	0.162148
sp|P01781|HV320_HUMAN;sp|P01782|HV321_HUMAN	>sp|P01781|HV320_HUMAN Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1;>sp|P01782|HV321_HUMAN Ig heavy chain V-III region DOB OS=Homo sapiens PE=1 SV=1	3000.5	1505.7	972.6	0	0	0	290.34	0	120.99	18380	9598.7	4002.4	1141.3	0	0	608.84	0	0	0.167584
sp|P60174|TPIS_HUMAN	>sp|P60174|TPIS_HUMAN Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	0	81.848	0	0	0	0	125.56	48.534	26.008	1889.3	648.06	333.95	0	0	0	0	54.517	65.962	0.168036
sp|P06733|ENOA_HUMAN;sp|P13929|ENOB_HUMAN	>sp|P06733|ENOA_HUMAN Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	471.82	0	63.891	42.923	0	0	0	0	9.948	2717.2	1622.7	539.34	0	0	0	0	0	0	0.16814
sp|O43490|PROM1_HUMAN	>sp|O43490|PROM1_HUMAN Prominin-1 OS=Homo sapiens GN=PROM1 PE=1 SV=1	0	0	0	0	0	40.524	0	0	0	62.131	0	0	56.051	0	0	72.696	0	0	0.169303
sp|P12109|CO6A1_HUMAN	>sp|P12109|CO6A1_HUMAN Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3	0	7.8287	0	0	14.359	25.893	0	0	0	392.34	697.14	0	0	0	0	0	14.992	16.9	0.172224
sp|P10645|CMGA_HUMAN	>sp|P10645|CMGA_HUMAN Chromogranin-A	343.86	686.41	0	0	0	83.877	0	57.168	0	2565.6	1117.9	0	101.12	888.14	106.02	203.24	0	0	0.173893

	OS=Homo sapiens GN=CHGA PE=1 SV=7																			
sp|P10909|CLUS_HUMAN	>sp|P10909|CLUS_HUMAN Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	178490	118280	55288	42423	34355	41282	33660	48422	27824	456220	160440	90422	93946	87141	86984	78880	49639	57603	0.174429
sp|Q99574|NEUS_HUMAN	>sp|Q99574|NEUS_HUMAN Neuroserpin OS=Homo sapiens GN=SERPINI1 PE=1 SV=1	0	238.25	153.36	239.32	155.21	291.49	0	70.855	0	1444.1	982.24	460.54	0	476.67	41.666	0	13.298	0	0.177159
sp|P00734|THRB_HUMAN	>sp|P00734|THRB_HUMAN Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2	480.19	910.11	400.34	19.381	0	174.02	237.5	139.54	139.75	7682.8	1559.3	1137	150.28	590.79	494.64	365.91	320.35	391.67	0.177958
sp|Q5T7N2|LITD1_HUMAN	>sp|Q5T7N2|LITD1_HUMAN LINE-1 type transposase domain-containing protein 1 OS=Homo sapiens GN=L1TD1 PE=1 SV=1	4806.3	59.436	166.57	345.31	583.95	394.21	354.95	283.98	298.55	851.01	726.34	449.25	406.28	245.73	7421.3	5291.5	224.56	5169.8	0.178349
sp|P63261|ACTG_HUMAN;sp|P60709|ACTB_HUMAN;sp|Q6S8J3|POTEE_HUMAN;sp|A5A3E0|POTEF_HUMAN;sp|P0CG38|POTEI_HUMAN;sp|Q9BYX7|ACTBM_HUMAN;sp|P0CG39|POTEJ_HUMAN;sp|Q562R1|ACTBL_HUMAN	>sp|P63261|ACTG_HUMAN Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1;>sp|P60709|ACTB_HUMAN Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1;>sp|Q6S8J3|POTEE_HUMAN POTE ankyrin domain family member E OS=Homo sapiens	5025	3014.7	1079.9	99.852	0	0	1411.7	536	951.76	25493	12606	8052.1	170.73	250.1	178.67	504.05	789.13	814.27	0.187373

	GN=POTEE PE=1 SV=3;>sp|A5A																			
sp|P19823|ITIH2_HUMAN;CON__Q9TRI1	>sp|P19823|ITIH2_HUMAN Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	1700.8	1192.9	569.92	446.08	396.95	257.3	788.72	48.728	429.85	4964.6	3143.2	1331.2	929.41	806.01	620.1	352.23	212.44	394.25	0.188224
sp|P01598|KV106_HUMAN;sp|P01602|KV110_HUMAN	>sp|P01598|KV106_HUMAN Ig kappa chain V-I region EU OS=Homo sapiens PE=1 SV=1;>sp|P01602|KV110_HUMAN Ig heavy chain V-I region 5 (Fragment) OS=Homo sapiens GN=IGKV1-5 PE=4 SV=2	1113.7	0	0	0	0	0	0	0	0	3756.4	2105.3	0	0	882.51	0	54.86	0	0	0.189368
sp|P01860|IGHG3_HUMAN	>sp|P01860|IGHG3_HUMAN Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	2435.7	3108.7	3054.1	89.351	0	217.42	0	468.11	0	902.1	0	311.84	351.52	587.15	0	758.51	616.62	0	0.192251
sp|P00915|CAH1_HUMAN	>sp|P00915|CAH1_HUMAN Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	0	0	0	0	0	0	1119.5	1261.4	1059.5	168.29	0	0	0	47.864	0	391.71	0	389.94	0.193419
sp|Q9BQT9|CSTN3_HUMAN	>sp|Q9BQT9|CSTN3_HUMAN Calsyntenin-3 OS=Homo sapiens GN=CLSTN3 PE=1 SV=1	0	0	0	0	0	0	0	0	0	227.93	83.358	0	0	0	0	0	0	0	0.199697
sp|P04406|G3P_HUMAN	>sp|P04406|G3P_HUMAN Glyceraldehyde-3-	738.19	589.05	447.17	0	0	0	0	0	0	8186.8	4284.8	901.64	0	0	0	0	0	0	0.20046

	phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3																			
sp|P01876|IGHA1_HUMAN	>sp|P01876|IGHA1_HUMAN Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	22353	16494	4261.8	2656.2	1802.3	2141.4	1101.2	4276.9	617.22	48168	25793	16076	6397.3	5634.2	3958.7	5540.3	5445.4	5469.8	0.201649
sp|P02671|FIBA_HUMAN	>sp|P02671|FIBA_HUMAN Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	0	0	0	0	0	0	0	0	0	975.35	296.28	17.97	0	7.0222	0	0	0	0	0.204146
sp|P09972|ALDOC_HUMAN	>sp|P09972|ALDOC_HUMAN Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	0	0	0	0	0	0	0	0	0	540.75	186.15	0	0	0	0	0	0	0	0.204447
sp|Q14118|DAG1_HUMAN	>sp|Q14118|DAG1_HUMAN Dystroglycan OS=Homo sapiens GN=DAG1 PE=1 SV=2	64.296	0	96.06	11.11	0	0	0	0	0	0	0	0	0	0	26.133	0	0	0	0.206407
sp|O15066|KIF3B_HUMAN	>sp|O15066|KIF3B_HUMAN Kinesin-like protein KIF3B OS=Homo sapiens GN=KIF3B PE=1 SV=1	1000.4	1201.1	0	0	0	0	0	0	0	0	0	0	0	0	130.63	138.36	0	0	0.208546
sp|P07339|CATD_HUMAN	>sp|P07339|CATD_HUMAN Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	19136	17248	9519.4	5678.3	3495.6	7247.4	6956.3	6118.9	3499.6	54261	27496	7660.6	7866.9	7192.2	7715.3	11589	10061	10446	0.209333

sp|P08185|CBG_HUMAN	>sp|P08185|CBG_HUMAN Corticosteroid-binding globulin OS=Homo sapiens GN=SERPINA6 PE=1 SV=1	1324.9	487.72	547.96	85.311	0	0	0	0	0	1397.4	2610.9	0	728.46	712.91	687.92	75.717	49.119	0	0.209369
sp|P25311|ZA2G_HUMAN	>sp|P25311|ZA2G_HUMAN Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	4743.8	3224.2	2155.6	1042.6	1844.5	1283.4	687.11	645.29	419.38	20648	9997.7	2514.4	2855	2158.5	2208.6	912.06	218.5	1055.7	0.210311
sp|Q99972|MYOC_HUMAN	>sp|Q99972|MYOC_HUMAN Myocilin OS=Homo sapiens GN=MYOC PE=1 SV=2	0	107.72	0	21.552	0	23.301	0	0	0	0	0	0	0	0	0	0	13.377	0	0.211861
sp|P18206|VINC_HUMAN	>sp|P18206|VINC_HUMAN Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	0	0	0	0	0	0	0	0	0	40569	0	11839	0	0	0	0	0	0	0.217421
sp|P02774|VTDB_HUMAN	>sp|P02774|VTDB_HUMAN Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1	9299.1	9689	5610	4070.4	509.63	2457.1	5075.2	3528.5	2166.4	42601	19671	7716.3	3962	5419.6	3194.5	3733.4	3110.9	4774.9	0.218894
sp|P01617|KV204_HUMAN;sp|P01614|KV201_HUMAN;sp|P06309|KV205_HUMAN;sp|P06310|KV206_HUMAN	>sp|P01617|KV204_HUMAN Ig kappa chain V-II region TEW OS=Homo sapiens PE=1 SV=1;>sp|P01614|KV201_HUMAN Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1;>sp|P06309|KV205_HUMAN Ig kappa chain V-II	11057	10452	5884.1	4964.7	0	0	5176.1	4339.2	4012.4	30651	16911	4437.5	6007.5	6630.1	4608.1	0	6540	7800.1	0.224779

	region GM607 (Fragment) OS=Homo sapiens PE=4 SV=1;>sp																			
sp|P26998|CRBB3_HUMAN	>sp|P26998|CRBB3_HUMAN Beta-crystallin B3 OS=Homo sapiens GN=CRYBB3 PE=1 SV=4	0	199.39	0	0	0	117.45	0	0	0	0	1631.4	739.26	0	0	0	0	93.628	0	0.225945
sp|P01714|LV301_HUMAN	>sp|P01714|LV301_HUMAN Ig lambda chain V-III region SH OS=Homo sapiens PE=1 SV=1	0	685.8	295.41	0	0	0	0	224.48	0	3414.7	0	1776	0	569.47	0	0	0	0	0.231113
sp|P19827|ITIH1_HUMAN;CON__Q0VCM5	>sp|P19827|ITIH1_HUMAN Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	1265.3	776.2	755.34	130.06	0	77.86	14.621	280.7	0	4876.5	1669.6	528.27	538.91	388.68	881.84	154.7	98.66	101.93	0.231765
sp|P02042|HBD_HUMAN	>sp|P02042|HBD_HUMAN Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	0	0	0	0	0	119.34	3879.9	318.31	502.43	0	0	102.04	0	0	0	0	0	0	0.232534
sp|Q92622|RUBIC_HUMAN	>sp|Q92622|RUBIC_HUMAN Run domain Beclin-1-interacting and cysteine-rich domain-containing protein OS=Homo sapiens GN=RUBCN PE=1 SV=4	0	0	23.668	186.64	0	47.236	0	55.649	0	0	133.47	0	69.936	0	0	85.359	151.54	352.8	0.239832
sp|Q75WM6|H1FNT_HUMAN	>sp|Q75WM6|H1FNT_HUMAN Testis-specific H1 histone OS=Homo sapiens	0	14070	0	0	0	0	0	0	0	15360	0	6083.9	0	0	4719.8	0	6668.2	6667.4	0.240473

	GN=H1FNT PE=2 SV=3																			
sp|P50897|PPT1_HUMAN	>sp|P50897|PPT1_HUMAN Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1	0	238.93	0	0	0	0	0	0	0	0	699.9	217.19	0	0	228.53	0	0	0	0.241613
sp|P01625|KV402_HUMAN;sp|P06312|KV401_HUMAN;sp|P06313|KV403_HUMAN;sp|P06314|KV404_HUMAN	>sp|P01625|KV402_HUMAN Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2;>sp|P06312|KV401_HUMAN Ig kappa chain V-IV region (Fragment) OS=Homo sapiens GN=IGKV4-1 PE=4 SV=1;>sp|P06313|KV403_HUMAN Ig kappa chain V-IV region JI OS=Homo sapiens PE=4 SV=1	1411.8	815.72	0	0	0	137.77	261.31	0	0	4328.9	6676.3	770.88	0	0	0	0	0	0	0.242309
sp|Q15846|CLUL1_HUMAN	>sp|Q15846|CLUL1_HUMAN Clusterin-like protein 1 OS=Homo sapiens GN=CLUL1 PE=2 SV=1	300.32	53.756	128.95	0	0	0	0	0	0	389.47	0	0	0	0	0	467.28	0	595.86	0.2453
sp|P14314|GLU2B_HUMAN	>sp|P14314|GLU2B_HUMAN Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	1401.1	436.86	0	0	0	0	0	0	0	0	0	0	126.96	0	0	0	0	0	0.245821
sp|P07602|SAP_HUMAN	>sp|P07602|SAP_HUMAN Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2	265.28	640.35	142.02	88.047	0	0	0	0	0	3301.1	1090.7	795.26	0	0	0	0	0	0	0.246779

sp|P00747|PLMN_HUMAN	>sp|P00747|PLMN_HUMAN Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	741.87	147.64	78.931	98.123	0	0	10.801	0	0	4176.5	1236	492.41	31.388	0	0	43.896	0	0	0.260493
sp|Q15424|SAFB1_HUMAN	>sp|Q15424|SAFB1_HUMAN Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4	0	0	0	0	0	246.74	25.896	0	0	214.38	0	0	1142.3	212.78	0	0	36.799	0	0.260943
sp|P04433|KV309_HUMAN	>sp|P04433|KV309_HUMAN Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	7589	416.12	2074.1	0	0	0	0	0	0	12515	6599.3	4206	0	2098.6	1805.2	0	0	0	0.262808
sp|P02760|AMBP_HUMAN	>sp|P02760|AMBP_HUMAN Protein AMBP OS=Homo sapiens GN=AMBP PE=1 SV=1	369.79	201.21	158.91	271.59	0	55.989	22.034	32.954	0	3283.5	965.14	329.85	0	0	0	141.38	0	159.12	0.262918
sp|P19652|A1AG2_HUMAN	>sp|P19652|A1AG2_HUMAN Alpha-1-acid glycoprotein 2 OS=Homo sapiens GN=ORM2 PE=1 SV=2	36002	49756	12827	11914	7884.8	10467	5589.1	3944.3	4484.7	114490	67263	17028	17012	26186	18595	8433.2	5669.1	6528.7	0.263249
sp|P08697|A2AP_HUMAN	>sp|P08697|A2AP_HUMAN Alpha-2-antiplasmin OS=Homo sapiens GN=SERPINF2 PE=1 SV=3	1183.2	802.5	137.61	63.825	76.367	157.56	221.66	226.8	257.72	230.74	431.1	95.97	0	0	222.08	77.618	239.51	393.69	0.265274
sp|P07711|CATL1_HUMAN	>sp|P07711|CATL1_HUMAN Cathepsin L1 OS=Homo sapiens GN=CTSL PE=1 SV=2	0	323.34	263.43	0	0	0	0	0	0	901.23	0	545.03	82.972	0	259.12	0	0	0	0.265431
sp|P23142|FBLN1_HUMAN	>sp|P23142|FBLN1_HUMAN Fibulin-1	119.26	353.37	0	0	0	0	0	0	0	213.79	0	58.279	306.06	363.47	0	0	0	163.44	0.276607

	OS=Homo sapiens GN=FBLN1 PE=1 SV=4																			
sp|P29622|KAIN_HUMAN	>sp|P29622|KAIN_HUMAN Kallistatin OS=Homo sapiens GN=SERPINA4 PE=1 SV=3	717.86	205.02	270.01	0	0	0	0	0	0	216.01	0	0	0	123.89	0	0	0	0	0.281811
sp|P10523|ARRS_HUMAN	>sp|P10523|ARRS_HUMAN S-arrestin OS=Homo sapiens GN=SAG PE=1 SV=3	0	0	0	0	0	0	40.409	45.392	38.729	0	0	0	0	0	0	347.16	90.375	66.68	0.292937
sp|P0CG12|CTF8A_HUMAN	>sp|P0CG12|CTF8A_HUMAN Chromosome transmission fidelity protein 8 homolog isoform 2 OS=Homo sapiens GN=CHTF8 PE=1 SV=1	0	452.38	168.44	135.22	218.58	355.33	0	127.8	0	1067.8	232.6	0	293.12	0	3275.7	0	0	128.4	0.293896
sp|P02656|APOC3_HUMAN	>sp|P02656|APOC3_HUMAN Apolipoprotein C-III OS=Homo sapiens GN=APOC3 PE=1 SV=1	2508	2228.9	1527.8	0	0	0	0	0	0	0	0	0	0	1112.3	0	0	1089.2	256.86	0.296331
sp|Q5HYK7|SH319_HUMAN	>sp|Q5HYK7|SH319_HUMAN SH3 domain-containing protein 19 OS=Homo sapiens GN=SH3D19 PE=1 SV=2	14381	3369.8	2049.1	3841.1	5118.4	4195.6	0	2599.2	0	23086	34834	7177.7	1214.8	2858.6	1415.2	3973.2	1229.2	1109.1	0.298939
sp|P04196|HRG_HUMAN	>sp|P04196|HRG_HUMAN Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	730.41	1757.1	1590.1	167.19	0	65.355	0	58.998	0	4811.8	2970.8	429.02	497.48	574.48	0	609.37	133.7	109.5	0.300213
sp|P30086|PEBP1_HUMAN	>sp|P30086|PEBP1_HUMAN	720.66	987.59	981.92	0	0	0	0	0	0	4470.8	1530.4	1581.9	0	0	0	141.57	0	0	0.302844

	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3																			
sp|P04217|A1BG_HUMAN;CON__Q2KJF1	>sp|P04217|A1BG_HUMAN Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4	24655	20790	8464.6	1336	540.45	1360.9	4027.4	4691.9	2074.9	47580	19457	9618	10643	4091	3985.8	8879	8014.4	7592.4	0.304671
sp|P35858|ALS_HUMAN	>sp|P35858|ALS_HUMAN Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	0	167.65	0	0	0	52.073	0	0	0	438.58	174.73	0	0	0	103.24	0	0	0	0.312747
sp|Q9UBP4|DKK3_HUMAN	>sp|Q9UBP4|DKK3_HUMAN Dickkopf-related protein 3 OS=Homo sapiens GN=DKK3 PE=1 SV=2	29201	39380	18392	5880.5	4782.2	6304.5	5698.6	5019.7	4216	64275	25925	17575	15510	18027	11126	13539	10956	8325.2	0.319141
sp|P01621|KV303_HUMAN	>sp|P01621|KV303_HUMAN Ig kappa chain V-III region NG9 (Fragment) OS=Homo sapiens PE=2 SV=1	1794.2	1383.8	650.2	0	0	0	0	862.61	0	0	449.85	0	0	0	1000.6	0	0	783.69	0.32121
sp|P02679|FIBG_HUMAN	>sp|P02679|FIBG_HUMAN Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	496.33	230.25	109.58	70.649	0	0	11.928	0	0	1693.1	447.7	141.5	0	264.65	0	113.15	0	0	0.324314
sp|A6NFN9|ANKUB_HUMAN	>sp|A6NFN9|ANKUB_HUMAN Protein ANKUB1 OS=Homo sapiens	0	0	0	679.36	405.27	711.56	213.27	95.752	90.689	303.63	0	578.93	0	247.8	0	0	0	0	0.33144

	GN=ANKUB1 PE=2 SV=2																			
sp|P04035|HMDH_HUMAN	>sp|P04035|HMDH_HUMAN 3-hydroxy-3-methylglutaryl-coenzyme A reductase OS=Homo sapiens GN=HMGCR PE=1 SV=1	0	0	9883.7	0	0	0	0	0	21.996	0	0	0	0	0	16.65	0	0	0	0.331813
sp|B5MCN3|S14L6_HUMAN	>sp|B5MCN3|S14L6_HUMAN Putative SEC14-like protein 6 OS=Homo sapiens GN=SEC14L6 PE=5 SV=1	0	68.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|O14983|AT2A1_HUMAN;sp|Q93084|AT2A3_HUMAN	>sp|O14983|AT2A1_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Homo sapiens GN=ATP2A1 PE=1 SV=1;>sp|Q93084|AT2A3_HUMAN Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 OS=Homo sapiens GN=ATP2A3 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	80.331	0	0	0	0	0	0	0	0.332195
sp|P00746|CFAD_HUMAN	>sp|P00746|CFAD_HUMAN Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5	0	288.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|P00748|FA12_HUMAN	>sp|P00748|FA12_HUMAN Coagulation factor XII OS=Homo sapiens GN=F12 PE=1 SV=3	0	0	0	0	0	0	0	0	0	469.13	0	0	0	0	0	0	0	0	0.332195

sp|P05090|APOD_HUMAN	>sp|P05090|APOD_HUMAN Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	0	0	0	0	0	0	1573.3	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|P07357|CO8A_HUMAN	>sp|P07357|CO8A_HUMAN Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2	197.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|P08238|HS90B_HUMAN;sp|P07900|HS90A_HUMAN	>sp|P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4;>sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	0	0	0	0	0	0	0	0	0	385.37	0	0	0	0	0	0	0	0	0.332195
sp|P48723|HSP13_HUMAN	>sp|P48723|HSP13_HUMAN Heat shock 70 kDa protein 13 OS=Homo sapiens GN=HSPA13 PE=1 SV=1	0	139.8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|Q12906|ILF3_HUMAN	>sp|Q12906|ILF3_HUMAN Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	2143.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|Q6NUN0|ACSM5_HUMAN	>sp|Q6NUN0|ACSM5_HUMAN Acyl-coenzyme A synthetase ACSM5,	0	0	0	0	0	0	0	0	0	0	0	94.471	0	0	0	0	0	0	0.332195

	mitochondrial OS=Homo sapiens GN=ACSM5 PE=1 SV=2																			
sp|Q6TCH4|PAQR6_HUMAN	>sp|Q6TCH4|PAQR6_HUMAN Progestin and adipoQ receptor family member 6 OS=Homo sapiens GN=PAQR6 PE=2 SV=2	0	0	0	0	0	0	0	0	0	3663.5	0	0	0	0	0	0	0	0	0.332195
sp|Q8NG57|ELOA3_HUMAN;sp|Q3SY89|EA3L1_HUMAN;sp|A6NLF2|EA3L2_HUMAN	>sp|Q8NG57|ELOA3_HUMAN RNA polymerase II transcription factor SIII subunit A3 OS=Homo sapiens GN=TCEB3C PE=1 SV=2;>sp|Q3SY89|EA3L1_HUMAN RNA polymerase II transcription factor SIII subunit A3-like-1 OS=Homo sapiens GN=TCEB3CL PE=2 SV=1;>sp|A6NLF2|EA3L2_HUM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.329	0	0	0	0.332195
sp|Q8TBA6|GOGA5_HUMAN	>sp|Q8TBA6|GOGA5_HUMAN Golgin subfamily A member 5 OS=Homo sapiens GN=GOLGA5 PE=1 SV=3	0	0	44.728	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|Q9NSK0|KLC4_HUMAN	>sp|Q9NSK0|KLC4_HUMAN Kinesin light chain 4 OS=Homo sapiens GN=KLC4 PE=1 SV=3	0	896.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195
sp|Q9UJA3|MCM8_HUMAN	>sp|Q9UJA3|MCM8_HUMAN DNA	56.505	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.332195

	helicase MCM8 OS=Homo sapiens GN=MCM8 PE=1 SV=2																			
sp|B1AK76|SNUFL_HUMAN	>sp|B1AK76|SNUFL_HUMAN Putative SNURF-like protein OS=Homo sapiens GN=SNURFL PE=5 SV=2	7836.7	0	5506.4	2842.6	6050.3	0	0	5269.1	0	0	0	0	8276.6	4657.3	0	1655.8	0	0	0.333984
sp|P68133|ACTS_HUMAN;sp|P68032|ACTC_HUMAN;sp|P63267|ACTH_HUMAN;sp|P62736|ACTA_HUMAN	>sp|P68133|ACTS_HUMAN Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1;>sp|P68032|ACTC_HUMAN Actin, alpha caRRDiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1;>sp|P63267|ACTH_HUMAN Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 P	647.97	356.57	184.41	0	0	0	0	12.004	18.236	3580.6	1305.1	0	0	0	0	0	28.239	0	0.334576
sp|Q9UP83|COG5_HUMAN	>sp|Q9UP83|COG5_HUMAN Conserved oligomeric Golgi complex subunit 5 OS=Homo sapiens GN=COG5 PE=1 SV=3	104.07	167.81	0	0	0	0	0	0	0	865.28	188.36	0	0	0	85.376	0	0	0	0.335585
sp|Q08380|LG3BP_HUMAN	>sp|Q08380|LG3BP_HUMAN Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	648.37	1176.1	60.48	56.232	0	26.675	855.47	398.96	21.425	889.09	1033.7	0	519.81	206.02	46.255	739.84	630.33	903.93	0.339171

sp|P55058|PLTP_HUMAN	>sp|P55058|PLTP_HUMAN Phospholipid transfer protein OS=Homo sapiens GN=PLTP PE=1 SV=1	265.05	356.33	263.64	0	0	0	0	0	0	601.55	339.64	205.63	0	0	101.56	278.91	85.913	0	0.34862
sp|P80362|KV125_HUMAN;sp|P01610|KV118_HUMAN;sp|P01609|KV117_HUMAN;sp|P01608|KV116_HUMAN;sp|P01607|KV115_HUMAN;sp|P01600|KV108_HUMAN;sp|P01599|KV107_HUMAN;sp|P01594|KV102_HUMAN;sp|P01593|KV101_HUMAN	>sp|P80362|KV125_HUMAN Ig kappa chain V-I region WAT OS=Homo sapiens PE=1 SV=1;>sp|P01610|KV118_HUMAN Ig kappa chain V-I region WEA OS=Homo sapiens PE=1 SV=1;>sp|P01609|KV117_HUMAN Ig kappa chain V-I region Scw OS=Homo sapiens PE=1 SV=1;>sp|P01608|KV116_HU	22277	28197	12492	19947	11439	18648	1346.6	14595	1070.5	15889	12086	60661	27426	21111	9616.2	4087.6	15296	18087	0.351123
sp|Q8WVR3|CG043_HUMAN	>sp|Q8WVR3|CG043_HUMAN Uncharacterized protein C7orf43 OS=Homo sapiens GN=C7orf43 PE=1 SV=2	0	263.34	170.81	234.88	256.25	593.91	0	0	85.93	0	236.96	0	576.53	0	0	0	0	0	0.352797
sp|Q9BZV3|IMPG2_HUMAN	>sp|Q9BZV3|IMPG2_HUMAN Interphotoreceptor matrix proteoglycan 2 OS=Homo sapiens GN=IMPG2 PE=1 SV=3	112.73	0	61.921	0	59.873	0	125.83	85.478	0	0	0	39.11	0	0	0	232.66	332.9	260.39	0.355183
sp|P01011|AACT_HUMAN	>sp|P01011|AACT_HUMAN Alpha-1-antichymotrypsin	39889	29834	17154	7911.4	7282.7	9031.7	12108	13088	6728.7	44856	24611	12229	14684	17645	12215	21182	18210	20855	0.355883

	OS=Homo sapiens GN=SERPINA3 PE=1 SV=2																			
sp|P01034|CYTC_HUMAN	>sp|P01034|CYTC_HUMAN Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	266750	226090	141260	83324	39380	65766	95184	127580	59979	395750	210560	156620	114670	109610	84761	137220	116460	124870	0.36195
sp|P01009|A1AT_HUMAN;sp|P20848|A1ATR_HUMAN	>sp|P01009|A1AT_HUMAN Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	205140	161770	100820	51054	32855	52435	50742	47189	29390	332080	196890	107960	74865	85716	59984	64756	56881	62537	0.366577
sp|Q9UBP8|KAAG1_HUMAN	>sp|Q9UBP8|KAAG1_HUMAN Kidney-associated antigen 1 OS=Homo sapiens GN=KAAG1 PE=2 SV=1	35884	1103	277.55	6381.1	3816.2	7654.7	0	0	119.05	38129	563.46	0	14169	15795	9313.8	8908.1	6952.4	6101.7	0.372586
sp|P06727|APOA4_HUMAN;CON__Q32PJ2	>sp|P06727|APOA4_HUMAN Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	32547	21264	12437	3204.3	820.32	2617.1	2833.6	4263	1909.5	72950	32093	11645	5341.7	8000.6	6775.3	6309.8	3963.1	4227.6	0.374179
sp|P05154|IPSP_HUMAN	>sp|P05154|IPSP_HUMAN Plasma serine protease inhibitor OS=Homo sapiens GN=SERPINA5 PE=1 SV=3	821.81	168.75	179.14	211.19	57.419	0	0	70.508	193.02	262.45	289.87	0	79.393	246.76	26.055	0	41.469	0	0.38161
sp|P0C0L5|CO4B_HUMAN	>sp|P0C0L5|CO4B_HUMAN Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=2	15279	12764	8888.1	3951	2623.5	4247.9	4199.3	4285.7	2604.1	22069	14578	7848.8	4656.4	5850.6	4423.5	7639.3	6102.9	5360.9	0.394406
sp|P04208|LV106_HUMAN;sp|P01700|LV102_HUMAN	>sp|P04208|LV106_HUMAN Ig lambda chain V-I region	0	1587.6	356.38	0	0	0	0	0	0	4274.1	0	579.49	0	481.67	483.67	0	0	0	0.395872

	WAH OS=Homo sapiens PE=1 SV=1;>sp|P01700|LV102_HUMAN Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1																			
sp|Q66K66|TM198_HUMAN	>sp|Q66K66|TM198_HUMAN Transmembrane protein 198 OS=Homo sapiens GN=TMEM198 PE=1 SV=1	0	0	0	0	0	121.4	0	0	0	0	227.79	0	0	131.04	0	0	0	0	0.402837
sp|P22061|PIMT_HUMAN	>sp|P22061|PIMT_HUMAN Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4	0	0	0	0	0	0	0	0	108.47	748.14	0	0	0	0	0	0	0	0	0.409937
sp|P07360|CO8G_HUMAN	>sp|P07360|CO8G_HUMAN Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3	475.09	70.165	0	0	76.985	0	0	64.489	0	349.44	698.76	0	111.89	246.68	0	0	0	0	0.412948
sp|Q9HCB6|SPON1_HUMAN	>sp|Q9HCB6|SPON1_HUMAN Spondin-1 OS=Homo sapiens GN=SPON1 PE=1 SV=2	1558.9	1188.6	284.73	239.04	46.753	412.5	54.283	99.443	18.931	5404.2	1018.1	474.27	710.31	256.32	444.83	0	69.876	0	0.419447
sp|Q96PD5|PGRP2_HUMAN;CON__ENSEMBL:ENSBTAP00000016285	>sp|Q96PD5|PGRP2_HUMAN N-acetylmuramoyl-L-alanine amidase OS=Homo sapiens	1022.1	433.78	332.75	0	0	0	148.83	232.36	266.85	527.2	458.56	0	0	44.201	0	0	230.16	233.49	0.425285

	GN=PGLYRP2 PE=1 SV=1																			
sp|P05543|THBG_HUMAN	>sp|P05543|THBG_HUMAN Thyroxine-binding globulin OS=Homo sapiens GN=SERPINA7 PE=1 SV=2	259.77	213.5	341.06	0	0	0	0	0	36.555	742.46	308.5	431.52	0	95.422	0	0	0	0	0.429596
sp|P02751|FINC_HUMAN	>sp|P02751|FINC_HUMAN Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	161.97	224.77	38.323	0	34.089	0	0	13.074	6.2616	741.93	117.02	0	92.185	131.91	0	0	6.7958	0	0.432449
sp|O60888|CUTA_HUMAN	>sp|O60888|CUTA_HUMAN Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2	268.01	0	233.81	0	0	0	66.853	0	0	0	0	0	0	0	0	0	0	246.17	0.442232
sp|P13671|CO6_HUMAN	>sp|P13671|CO6_HUMAN Complement component C6 OS=Homo sapiens GN=C6 PE=1 SV=3	131.11	0	49.532	0	0	0	0	0	0	277.97	165.24	0	0	0	0	0	0	0	0.442378
sp|P02765|FETUA_HUMAN	>sp|P02765|FETUA_HUMAN Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	53201	42815	18898	561.36	167.04	3643.3	5757.5	4291	4590.7	87338	35526	22906	12292	12316	3703.5	18429	6753.3	11091	0.444204
sp|E7ETH6|Z587B_HUMAN	>sp|E7ETH6|Z587B_HUMAN Zinc finger protein 587B OS=Homo sapiens GN=ZNF587B PE=1 SV=1	2787.6	2262.9	1133.1	4605.3	5032.3	5085.2	3721.7	2328.3	993.17	4896.4	10840	2427.2	6483	7957.6	2096.9	784.23	730.05	919.11	0.451543
sp|Q96S96|PEBP4_HUMAN	>sp|Q96S96|PEBP4_HUMAN Phosphatidylethanolamine-binding protein 4 OS=Homo sapiens GN=PEBP4 PE=1 SV=3	0	506.4	0	0	0	0	0	0	0	1697.9	0	0	0	0	0	0	0	149.3	0.457296

sp|P01764|HV303_HUMAN	>sp|P01764|HV303_HUMAN Ig heavy chain V-III region 23 OS=Homo sapiens GN=IGHV3-23 PE=1 SV=2	0	1626.9	591.67	0	0	0	0	0	0	0	0	0	0	0	856.49	0	0	0	0.476464
sp|P00751|CFAB_HUMAN	>sp|P00751|CFAB_HUMAN Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	7754.2	3586.4	3387.6	1114.4	458.78	477.44	1113	561.96	244.9	7105.5	3874.4	1568.9	3384.8	3523.9	1439.7	2001.5	1266.7	1287	0.481621
sp|Q9UPN3|MACF1_HUMAN	>sp|Q9UPN3|MACF1_HUMAN Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4	0	0	0	16.907	8.6744	12.808	0	0	0	0	0	0	11.048	10.228	0	0	0	0	0.496556
sp|Q7Z3B1|NEGR1_HUMAN	>sp|Q7Z3B1|NEGR1_HUMAN Neuronal growth regulator 1 OS=Homo sapiens GN=NEGR1 PE=1 SV=3	197.47	0	0	0	0	0	0	0	0	0	0	0	0	0	59.655	0	0	0	0.513603
sp|P0C0L4|CO4A_HUMAN;CON__ENSEMBL:ENSBTAP00000007350	>sp|P0C0L4|CO4A_HUMAN Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=2	113.86	59.207	96.022	6.8488	35.575	18.863	41.575	0	4.8884	122.29	101.33	25.626	0	55.918	18.19	6.294	122.29	51.241	0.515994
sp|Q12860|CNTN1_HUMAN	>sp|Q12860|CNTN1_HUMAN Contactin-1 OS=Homo sapiens GN=CNTN1 PE=1 SV=1	21.073	0	18.259	0	0	0	0	0	0	117.47	0	0	0	0	0	0	0	0	0.525332
sp|P01861|IGHG4_HUMAN	>sp|P01861|IGHG4_HUMAN Ig gamma-4 chain C region OS=Homo sapiens	695.12	1725.9	878.21	420.85	596.17	0	0	805.27	0	2005	0	1706.5	1137.2	1086.5	0	556.96	363.51	0	0.548823

	GN=IGHG4 PE=1 SV=1																			
sp|P06681|CO2_HUMAN	>sp|P06681|CO2_HUMAN Complement C2 OS=Homo sapiens GN=C2 PE=1 SV=2	0	258.84	148.62	0	0	0	0	0	0	195.56	112.69	195.4	87.352	0	0	0	0	39.84	0.559349
sp|P01031|CO5_HUMAN	>sp|P01031|CO5_HUMAN Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	95.228	0	28.498	0	0	0	0	18.765	0	115.58	49.385	0	0	19.529	0	0	25.2	20.214	0.561567
sp|A5PLL1|AN34B_HUMAN	>sp|A5PLL1|AN34B_HUMAN Ankyrin repeat domain-containing protein 34B OS=Homo sapiens GN=ANKRRD34B PE=2 SV=3	5410.5	302.08	182.52	0	0	0	0	593.95	0	635.42	3531.8	100.25	2011.2	1966.3	1850.9	0	132.72	95.782	0.563009
sp|O14791|APOL1_HUMAN	>sp|O14791|APOL1_HUMAN Apolipoprotein L1 OS=Homo sapiens GN=APOL1 PE=1 SV=5	0	333.47	0	0	0	0	0	0	0	471.76	0	0	79.106	113.41	0	0	0	0	0.571526
sp|P06396|GELS_HUMAN;CON__Q3SX14	>sp|P06396|GELS_HUMAN Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	15346	11824	4834.9	1871.3	1400.5	2188.7	1254.4	1887.6	560.51	19113	11190	4221.5	3903.8	2885.7	2231.8	3505.5	3085.4	3983.3	0.583118
sp|Q7Z7G0|TARSH_HUMAN	>sp|Q7Z7G0|TARSH_HUMAN Target of Nesh-SH3 OS=Homo sapiens GN=ABI3BP PE=1 SV=1	106.63	20.08	62.96	0	0	0	0	0	0	0	0	0	0	103.8	0	0	0	0	0.586906
sp|P24592|IBP6_HUMAN	>sp|P24592|IBP6_HUMAN Insulin-like growth factor-binding protein 6 OS=Homo sapiens	0	767.15	145.8	269.12	0	451.73	0	80.805	117.03	1366.6	572.97	0	160.08	95.863	0	0	229.08	205	0.609969

	GN=IGFBP6 PE=1 SV=1																			
sp|P01871|IGHM_HUMAN;sp|P04220|MUCB_HUMAN	>sp|P01871|IGHM_HUMAN Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	793.82	8710.7	203.38	0	0	0	0	0	0	0	75.598	0	1434.8	1950.2	1532.4	153.28	0	0	0.617653
sp|P00450|CERU_HUMAN;CON__ENSEMBL:ENSBTAP00000031900	>sp|P00450|CERU_HUMAN Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1	24800	25928	13009	4416	2402.1	4193	4417.9	5551.8	4150.5	42223	18548	9014.8	6543.7	8662.5	5836.3	8359.3	5412.1	6509.4	0.629669
sp|Q15582|BGH3_HUMAN	>sp|Q15582|BGH3_HUMAN Transforming growth factor-beta-induced protein ig-h3 OS=Homo sapiens GN=TGFBI PE=1 SV=1	0	39.191	91.955	115.4	0	0	94.703	65.206	0	0	0	0	0	0	0	100.86	145.68	54.613	0.636525
sp|P02766|TTHY_HUMAN	>sp|P02766|TTHY_HUMAN Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	104910	83863	46303	14217	10501	10080	49675	44613	26544	124060	87604	37172	31472	19931	17176	32209	53863	54484	0.64759
sp|Q96KN2|CNDP1_HUMAN	>sp|Q96KN2|CNDP1_HUMAN Beta-Ala-His dipeptidase OS=Homo sapiens GN=CNDP1 PE=1 SV=4	0	344.21	77.988	0	0	0	0	20.16	0	0	0	0	0	0	249.84	0	0	0	0.654794
sp|Q12805|FBLN3_HUMAN	>sp|Q12805|FBLN3_HUMAN EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2	0	1744.7	511.27	0	0	0	96.913	58.807	0	282.55	211.59	0	0	906.9	425.49	0	787.31	725.1	0.655887

sp|Q13613|MTMR1_HUMAN	>sp|Q13613|MTMR1_HUMAN Myotubularin-related protein 1 OS=Homo sapiens GN=MTMR1 PE=1 SV=4	197.38	0	0	0	0	0	0	81.705	0	196.73	0	0	0	0	92.53	124.01	0	0	0.661936
sp|Q13822|ENPP2_HUMAN	>sp|Q13822|ENPP2_HUMAN Ectonucleotide pyrophosphatase/phosphodiesterase family member 2 OS=Homo sapiens GN=ENPP2 PE=1 SV=3	1100.7	604.45	434.58	0	0	102.1	392.65	239.78	289.63	757.9	284.82	170.14	411.36	166.52	386.95	619.26	623.22	283.04	0.66387
sp|Q16270|IBP7_HUMAN	>sp|Q16270|IBP7_HUMAN Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	0	586.64	236.84	0	0	0	0	52.145	0	0	0	0	0	0	285.2	0	0	281.88	0.667851
sp|P05156|CFAI_HUMAN	>sp|P05156|CFAI_HUMAN Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	4116	2399.5	2109.8	216.32	88.737	222.86	0	66.399	0	2640	1570.4	102.34	946.94	1039.5	247.42	465.2	0	118.7	0.692241
sp|P02749|APOH_HUMAN	>sp|P02749|APOH_HUMAN Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	1577	0	3769.8	0	0	0	0	0	0	81.049	0	0	1033.5	1059.4	1051.9	479.52	14.83	0	0.702183
sp|P02750|A2GL_HUMAN	>sp|P02750|A2GL_HUMAN Leucine-rich alpha-2-glycoprotein OS=Homo sapiens GN=LRG1 PE=1 SV=2	1588.4	1574.3	700.45	149.73	0	180.18	281.41	231.9	113.36	1910.3	1144.1	810.52	617.18	698.73	172.96	0	195.34	276.36	0.703058

sp|P04004|VTNC_HUMAN;CON__Q3ZBS7	>sp|P04004|VTNC_HUMAN Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	4705.9	3326.9	1578.5	65.014	0	486.41	403.58	888.54	292.81	2514	1444.1	425.92	365.07	509.5	903.62	1360.4	625	1545.6	0.70709
sp|Q9UHG2|PCSK1_HUMAN	>sp|Q9UHG2|PCSK1_HUMAN ProSAAS OS=Homo sapiens GN=PCSK1N PE=1 SV=1	1808.7	520.25	266.3	225.34	0	207.4	0	0	0	672.72	803.06	0	266.02	254.14	0	379.6	0	0	0.744376
sp|P02763|A1AG1_HUMAN	>sp|P02763|A1AG1_HUMAN Alpha-1-acid glycoprotein 1 OS=Homo sapiens GN=ORM1 PE=1 SV=1	93510	119280	39945	17434	8570.3	12950	16776	14653	9720.8	129050	60885	41139	28914	27434	17329	25652	24447	27383	0.763291
sp|Q709C8|VP13C_HUMAN	>sp|Q709C8|VP13C_HUMAN Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1	35.591	28.023	0	0	0	0	8.276	0	0	105.52	0	0	0	0	0	0	0	0	0.770742
sp|P01877|IGHA2_HUMAN	>sp|P01877|IGHA2_HUMAN Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3	3288.5	1120	1027.4	77.162	0	0	0	357.11	0	2122.4	1451	199.85	0	0	382.18	560.79	0	0	0.775492
sp|Q92520|FAM3C_HUMAN	>sp|Q92520|FAM3C_HUMAN Protein FAM3C OS=Homo sapiens GN=FAM3C PE=1 SV=1	287.69	424.12	239.19	0	11.444	0	0	0	0	0	0	0	411.78	307.29	0	0	0	46.144	0.777366
sp|P43652|AFAM_HUMAN	>sp|P43652|AFAM_HUMAN Afamin OS=Homo sapiens GN=AFM PE=1 SV=1	230.78	182.92	109.29	0	0	0	0	100.97	115.71	216.02	224.48	113.19	0	10.063	0	0	140.98	143.14	0.782404

sp|Q8IZJ3|CPMD8_HUMAN	>sp|Q8IZJ3|CPMD8_HUMAN C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 OS=Homo sapiens GN=CPAMD8 PE=1 SV=2	0	59.773	0	51.084	0	0	0	0	0	0	0	105.87	23.164	0	16.548	0	0	0	0.789054
sp|O60500|NPHN_HUMAN	>sp|O60500|NPHN_HUMAN Nephrin OS=Homo sapiens GN=NPHS1 PE=1 SV=1	0	31.002	0	0	0	0	0	0	0	0	0	20.875	0	0	0	0	0	0	0.789889
sp|Q6EMK4|VASN_HUMAN	>sp|Q6EMK4|VASN_HUMAN Vasorin OS=Homo sapiens GN=VASN PE=1 SV=1	720.48	407.79	382.1	0	96.92	0	167.16	233.65	0	1010.6	203.71	38.688	0	155.66	182.18	0	226	504.5	0.799216
sp|Q96JP9|CDHR1_HUMAN	>sp|Q96JP9|CDHR1_HUMAN Cadherin-related family member 1 OS=Homo sapiens GN=CDHR1 PE=1 SV=2	388.02	410.89	249.64	0	0	0	0	180.18	0	311.75	0	68.621	0	0	0	265.23	307.57	108.19	0.806103
sp|Q86UD1|OAF_HUMAN	>sp|Q86UD1|OAF_HUMAN Out at first protein homolog OS=Homo sapiens GN=OAF PE=2 SV=1	0	0	0	170.78	162.34	429.45	184.46	124.11	0	0	529.59	0	324.4	0	0	0	0	365.24	0.848309
sp|P08571|CD14_HUMAN	>sp|P08571|CD14_HUMAN Monocyte differentiation antigen CD14 OS=Homo sapiens GN=CD14 PE=1 SV=2	945.98	742.31	255.15	0	0	0	623.63	633.25	126.17	749.94	0	0	0	0	209.2	624.61	913.17	1161	0.853662
sp|Q5S007|LRRK2_HUMAN	>sp|Q5S007|LRRK2_HUMAN Leucine-rich repeat serine/threonine-	0	247.47	154.73	0	0	0	0	0	0	122.75	0	0	200.37	17.682	0	0	0	0	0.863532

	protein kinase 2 OS=Homo sapiens GN=LRRK2 PE=1 SV=2																			
sp|Q9H8N7|ZN395_HUMAN	>sp|Q9H8N7|ZN395_HUMAN Zinc finger protein 395 OS=Homo sapiens GN=ZNF395 PE=1 SV=2	30106	34347	38757	7595.5	3192.1	8483.4	17000	20479	0	37175	26308	12836	19467	14438	8509.8	0	18163	13970	0.865695
sp|O94822|LTN1_HUMAN	>sp|O94822|LTN1_HUMAN E3 ubiquitin-protein ligase listerin OS=Homo sapiens GN=LTN1 PE=1 SV=6	0	0	0	0	38.059	0	0	0	0	0	29.915	0	0	0	0	0	0	0	0.868507
sp|Q8N3L3|TXLNB_HUMAN	>sp|Q8N3L3|TXLNB_HUMAN Beta-taxilin OS=Homo sapiens GN=TXLNB PE=1 SV=3	0	0	10.196	0	0	0	7.3101	0	0	0	0	0	0	0	0	21.546	0	0	0.871384
sp|P14618|KPYM_HUMAN	>sp|P14618|KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	225.93	0	0	0	0	0	0	0	0	111.52	0	73.89	0	0	0	0	0	0	0.877456
sp|Q14624|ITIH4_HUMAN	>sp|Q14624|ITIH4_HUMAN Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	1433	1308.8	1066.2	54.912	0	47.265	0	184.55	0	1536.8	743.79	468.77	128.66	365.02	349.48	316.77	226.24	255.95	0.897398
sp|O75150|BRE1B_HUMAN	>sp|O75150|BRE1B_HUMAN E3 ubiquitin-protein ligase BRE1B OS=Homo sapiens GN=RNF40 PE=1 SV=4	0	63.87	886.83	39.12	0	0	0	0	0	0	322.23	0	119.43	343.42	297.89	0	0	0	0.926477

sp|Q9ULI4|KI26A_HUMAN	>sp|Q9ULI4|KI26A_HUMAN Kinesin-like protein KIF26A OS=Homo sapiens GN=KIF26A PE=2 SV=3	0	0	0	28.786	0	0	57.213	47.639	0	0	0	0	0	3.9122	0	0	0	140.51	0.945987
sp|Q4L180|FIL1L_HUMAN	>sp|Q4L180|FIL1L_HUMAN Filamin A-interacting protein 1-like OS=Homo sapiens GN=FILIP1L PE=1 SV=2	538.4	161.53	80.061	117.56	176.88	159.75	0	29.926	0	237.64	448.15	0	0	0	148.97	164.75	217.25	90.174	0.949153
sp|P80748|LV302_HUMAN	>sp|P80748|LV302_HUMAN Ig lambda chain V-III region LOI OS=Homo sapiens PE=1 SV=1	11219	9149	5701.2	730.22	226.5	0	2203.8	2461.1	0	14354	7487.9	713.97	2499.8	0	562.61	1890	2452.6	2778.2	0.955887
sp|P08253|MMP2_HUMAN	>sp|P08253|MMP2_HUMAN 72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2	93.983	90.923	0	0	0	0	0	0	0	193.5	0	0	0	0	0	0	0	0	0.970518
sp|Q92823|NRCAM_HUMAN	>sp|Q92823|NRCAM_HUMAN Neuronal cell adhesion molecule OS=Homo sapiens GN=NRCAM PE=1 SV=3	219.53	306.98	149.47	0	0	0	0	36.514	0	272.48	0	54.781	0	163.86	198.66	34.835	0	0	0.979731
sp|Q6AI39|GSC1L_HUMAN	>sp|Q6AI39|GSC1L_HUMAN GLTSCR1-like protein OS=Homo sapiens GN=GLTSCR1L PE=1 SV=2	538.93	764.78	336.03	31.223	287.24	828.27	571.02	0	0	253.83	0	0	746.34	541.4	550.86	648.29	315.2	296.56	0.996871
sp|O75366|AVIL_HUMAN	>sp|O75366|AVIL_HUMAN Advillin OS=Homo sapiens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!

	GN=AVIL PE=1 SV=3																			
sp|P02458|CO2A1_HUMAN	>sp|P02458|CO2A1_HUMAN Collagen alpha-1(II) chain OS=Homo sapiens GN=COL2A1 PE=1 SV=3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P02654|APOC1_HUMAN	>sp|P02654|APOC1_HUMAN Apolipoprotein C-I OS=Homo sapiens GN=APOC1 PE=1 SV=1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P05538|DQB2_HUMAN	>sp|P05538|DQB2_HUMAN HLA class II histocompatibility antigen, DQ beta 2 chain OS=Homo sapiens GN=HLA-DQB2 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P07858|CATB_HUMAN	>sp|P07858|CATB_HUMAN Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P09104|ENOG_HUMAN	>sp|P09104|ENOG_HUMAN Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P19086|GNAZ_HUMAN	>sp|P19086|GNAZ_HUMAN Guanine nucleotide-binding protein G(z) subunit alpha OS=Homo sapiens GN=GNAZ PE=2 SV=3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P35542|SAA4_HUMAN	>sp|P35542|SAA4_HUMAN Serum amyloid A-4 protein OS=Homo sapiens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!

	GN=SAA4 PE=1 SV=2																			
sp|P38398|BRCA1_HUMAN	>sp|P38398|BRCA1_HUMAN Breast cancer type 1 susceptibility protein OS=Homo sapiens GN=BRCA1 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P39060|COIA1_HUMAN	>sp|P39060|COIA1_HUMAN Collagen alpha-1(XVIII) chain OS=Homo sapiens GN=COL18A1 PE=1 SV=5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P49916|DNLI3_HUMAN	>sp|P49916|DNLI3_HUMAN DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|P53672|CRBA2_HUMAN	>sp|P53672|CRBA2_HUMAN Beta-crystallin A2 OS=Homo sapiens GN=CRYBA2 PE=1 SV=3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q00796|DHSO_HUMAN	>sp|Q00796|DHSO_HUMAN Sorbitol dehydrogenase OS=Homo sapiens GN=SORRD PE=1 SV=4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q02790|FKBP4_HUMAN	>sp|Q02790|FKBP4_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q02818|NUCB1_HUMAN	>sp|Q02818|NUCB1_HUMAN Nucleobindin-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!

	OS=Homo sapiens GN=NUCB1 PE=1 SV=4																			
sp|Q06033|ITIH3_HUMAN	>sp|Q06033|ITIH3_HUMAN Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q15910|EZH2_HUMAN	>sp|Q15910|EZH2_HUMAN Histone-lysine N-methyltransferase EZH2 OS=Homo sapiens GN=EZH2 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q4KMG0|CDON_HUMAN	>sp|Q4KMG0|CDON_HUMAN Cell adhesion molecule-related/down-regulated by oncogenes OS=Homo sapiens GN=CDON PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q969R5|LMBL2_HUMAN	>sp|Q969R5|LMBL2_HUMAN Lethal(3)malignant brain tumor-like protein 2 OS=Homo sapiens GN=L3MBTL2 PE=1 SV=1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q9BQE3|TBA1C_HUMAN;sp|Q71U36|TBA1A_HUMAN;sp|P68363|TBA1B_HUMAN	>sp|Q9BQE3|TBA1C_HUMAN Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1;>sp|Q71U36|TBA1A_HUMAN Tubulin alpha-1A	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!

	chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1;>sp|P68363|TBA1B_HUMAN Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1																			
sp|Q9NR16|C163B_HUMAN	>sp|Q9NR16|C163B_HUMAN Scavenger receptor cysteine-rich type 1 protein M160 OS=Homo sapiens GN=CD163L1 PE=1 SV=2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!
sp|Q9NTI5|PDS5B_HUMAN	>sp|Q9NTI5|PDS5B_HUMAN Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens GN=PDS5B PE=1 SV=1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	#DIV/0!