

Supplementary Table 1: Patient sample demographics

Sex: 1, female; 2, male

Eye: 1, right, 2, left

MH: Macular Hole

MH-PM: Macular Hole with Pathological Myopia

ERM: Epithelial Retinal Membrane

MRS-PM: Myopic retinoschisis with PM

RRD: Rhegmatogenous Retinal Detachment

RRD-PM: Rhegmatogenous Retinal Detachment with Pathological myopia

CF: Counting Fingers before Eye

HM: Hand Moving before Eye

Grade of myopic degeneration: 0, no macular lesions; 1, tessellated fundus; 2, diffuse chorioretinal atrophy; 3, patchy chorioretinal atrophy; 4, macular atrophy.

Posterior Staphyloma: 0,no; 1, have posterior staphyloma

Cataract Grade (Lens Opacities Classification System III): nuclear opalescence (NO:1~6)+nuclear color (NC:1~6)+cortical cataracts (C:1~5)+posterior sub-capsular cataracts (P:1~5).

Other systemic disease: 0, no; 1, hypertension; 2, diabetic nephropathy

Label	Sex	Age	Eye	Best corrected visual acuity	Spherical equivalent of surgical eye	Axial Length of surgical eye (mm)	Posterior staphyloma	Cataract grade	Grade of myopic degeneration	Other systemic disease
MH-PM Patient#1	1	59	2	C1	-12	31.45	1	16	1	1
MH-PM Patient#2	2	64	2	20/2000	-9	27.41	1	15.5	1	1
MH-PM Patient#3	1	61	1	20/1000	-16	32.25	1	15	1	0
MH-PM Patient#4	1	52	1	20/133	-10	29.14	1	11.5	1	0
MH-PM Patient#5	1	53	1	20/2000	-18	31.13	1	11.4	1	0
MH-PM Patient#6	1	50	1	20/80	-12	27.61	1	10	1	0
MH-PM Patient#7	2	43	1	20/100	-9	31.06	1	11.5	2	0
MH-PM Patient#8	1	43	1	C1	-10.00	28.37	1	12	2	0
MH-PM Patient#9	1	66	2	C1	-12	27.48	1	14.1	4	1
MH-PM Patient#10	1	65	1	20/100	-11	30.12	1	15	2	0
MH-PM Patient#11	1	58	1	C1	-20	30.51	1	11.5	4	0
MH-PM Patient#12	1	77	1	HM	-10	30.12	1	7.5	2	0
MH-PM Patient#13	1	53	1	C1	-20	32.14	1	5	3	0
MH-PM Patient#14	1	61	1	20/133	-14	30.46	1	11.5	3	0
MH-PM Patient#15	1	56	1	20/1000	-12	31.55	1	10	2	0
MH-PM Patient#16	2	51	2	C1	-20	31.31	1	13	1	0
MH-PM Patient#17	1	59	1	C1	-15	30.64	1	13	1	0
MH-PM Patient#18	1	69	2	20/400	-10	31.96	1	11.5	1	0
MH-PM Patient#19	2	54	1	C1	-10	31.94	1	15	3	0
MH-PM Patient#20	1	44	2	C1	-20	32.01	1	6	3	0
MH-PM Patient#21	1	73	1	HM	-21	28.1	1	11	3	0

MH-PM Patient#22	1	58	2	20/400	-18	32.69	1	12	2	0
MH Patient#1	2	66	1	20/100	0	24.85	0	11	0	0
MH Patient#2	1	58	1	20/400	0	23.32	0	11.5	0	0
MH Patient#3	2	69	1	C1	0	23.6	0	11.5	0	0
MH Patient#4	2	67	2	HM	0	23.31	0	11	0	0
MH Patient#5	1	57	2	20/25	0	23.37	0	6.5	0	0
MH Patient#6	2	65	1	20/1000	0	23.88	0	11	0	0
MH Patient#7	2	71	2	20/166	0	22.45	0	9	0	1
MH Patient#8	1	68	1	20/2000	0	23.3	0	12	0	0
MH Patient#9	1	63	1	20/400	-3	23.34	0	11	0	0
MH Patient#10	1	60	2	20/200	0	22.52	0	10.5	0	0
MH Patient#11	1	70	1	20/200	0	23.51	0	10.5	0	1
MH Patient#12	1	52	2	20/100	-3.25	24.43	0	10	0	0
MH Patient#13	1	61	2	20/80	0	22.57	0	11	0	0
MH Patient#14	1	67	1	20/1000	0	23.38	0	10	0	0
MH Patient#15	1	59	1	20/133	0	22.43	0	11	0	0
MH Patient#16	1	64	1	20/50	0	22.46	0	10.5	0	0
MH Patient#17	1	68	1	20/1000	0	22.86	0	10	0	0
MH Patient#18	1	69	2	20/80	0	23.05	0	11	0	0
MH Patient#19	2	67	1	20/33	0	22.18	0	10	0	0
MH Patient#20	2	62	1	20/133	0	23.53	0	11	0	1
MH Patient#21	1	56	1	20/400	0	22.1	0	10	0	0
MH Patient#22	1	63	1	20/100	0	23.49	0	11	0	0
MRS-PM Patient#1	2	62	2	C1	-10	30.52	1	9.5	1	0
MRS-PM Patient#2	1	50	2	20/400	-17	28.76	1	10	1	0
MRS-PM Patient#3	1	67	2	C1	-20	30.89	1	9.5	1	1
MRS-PM Patient#4	1	54	1	20/33	-16.00	28.42	1	8	1	0
MRS-PM Patient#5	1	71	2	20/80	-9	28.79	1	8	1	0
MRS-PM Patient#6	1	56	1	C1	-16	31.52	1	8	1	0
MRS-PM Patient#7	2	42	2	20/80	-8	30.34	1	6.5	2	0
MRS-PM Patient#8	2	44	1	20/40	-13	29.19	1	6.5	2	0
MRS-PM Patient#9	1	54	1	20/400	-20.5	32.39	1	6.5	4	0
MRS-PM Patient#10	1	57	1	20/100	-20	31.77	1	11	2	0
MRS-PM Patient#11	1	62	1	20/133	-20	31.49	1	11	4	0
MRS-PM Patient#12	2	72	2	20/50	-13	30.93	1	14.5	2	0
MRS-PM Patient#13	1	52	2	20/200	-12	29.85	1	11.5	3	0
MRS-PM Patient#14	1	57	1	20/166	-16	31.41	1	11	3	0
MRS-PM Patient#15	2	62	1	20/1000	-12	34.54	1	10.5	2	1+2
MRS-PM Patient#16	1	68	1	20/1000	-15	31.92	1	10.5	1	1
MRS-PM Patient#17	1	72	1	20/133	-10	29.82	1	10	1	0
MRS-PM Patient#18	1	67	1	20/80	-15	28.27	1	11	1	0

MRS-PM Patient#19	1	68	2	20/200	-8	26.6	1	11	3	0
MRS-PM Patient#20	2	54	1	20/100	-15	29.86	1	11	3	0
MRS-PM Patient#21	2	38	1	20/80	-8.75	26.55	1	4	3	0
MRS-PM Patient#22	2	60	2	20/100	-17.5	31.2	1	10.5	2	0
ERM Patient#1	1	66	2	20/400	0	26.26	0	15	0	0
ERM Patient#2	1	63	1	20/166	0	22.99	0	11	0	0
ERM Patient#3	1	74	1	20/40	0	21.58	0	7	0	0
ERM Patient#4	1	52	1	20/100	0	22.77	0	8.5	0	0
ERM Patient#5	1	66	2	20/133	0	22.85	0	12	0	1
ERM Patient#6	1	60	1	20/80	-5	23.51	0	10	0	0
ERM Patient#7	1	70	2	20/100	0	23.83	0	10	0	0
ERM Patient#8	1	76	2	20/80	-1	23.02	0	11	0	0
ERM Patient#9	1	67	2	20/80	0	22.92	0	10.5	0	1
ERM Patient#10	1	61	1	20/166	0	23.61	0	10.5	0	1
ERM Patient#11	2	54	2	20/25	0	23.22	0	7	0	1
ERM Patient#12	1	69	1	20/80	0	22.5	0	9	0	0
ERM Patient#13	1	69	2	20/50	0	22.69	0	9	0	1
ERM Patient#14	1	65	2	20/25	0	23.15	0	8.5	0	0
ERM Patient#15	1	64	2	20/40	0	22.37	0	8.5	0	2
ERM Patient#16	2	65	1	20/133	0	23.29	0	8	0	1
ERM Patient#17	1	61	2	20/40	0	23.54	0	8	0	0
ERM Patient#18	1	70	2	20/400	0	22.64	0	8	0	0
ERM Patient#19	1	71	2	0.03	0	22.8	0	15	0	1
ERM Patient#20	1	64	2	20/50	-2	24.2	0	8	0	1
ERM Patient#21	1	64	1	20/100	0	24.7	0	8.5	0	0
ERM Patient#22	1	52	1	20/200	0	24.23	0	8	0	0
RRD-PM Patient#1	2	39	2	20/400	-9.00	26.68	1	5	1	0
RRD-PM Patient#2	1	62	2	C1	-12.00	30.3	1	10.5	3	0
RRD-PM Patient#3	2	48	1	20/400	-8.00	27.85	1	6	2	0
RRD-PM Patient#4	1	43	1	20/200	-6.00	26.59	1	6	1	0
RRD-PM Patient#5	2	38	1	20/400	-7.00	27.65	1	6	1	0
RRD-PM Patient#6	2	42	1	20/100	-10.00	28.72	1	6	1	0
RRD-PM Patient#7	2	46	2	C1	-6.00	27.04	1	6	1	0
RRD-PM Patient#8	2	21	2	20/400	-9.50	28.26	1	4	1	0
RRD-PM Patient#9	2	49	2	HM	-6.25	30.19	1	7	2	0
RRD-PM Patient#10	2	29	2	HM	-30	28.77	1	15	1	0
RRD-PM Patient#11	2	39	1	20/33	-11.00	28.26	1	10	1	0
RRD-PM Patient#12	1	44	2	HM	-13	27.99	1	8	2	0
RRD-PM Patient#13	2	64	2	HM	-16.00	32.26	1	11	1	1
RRD-PM Patient#14	2	34	2	20/200	-8.00	27.02	1	9	1	0
RRD-PM Patient#15	1	54	1	C1	-13.00	28.11	1	9	1	0

RRD-PM Patient#16	2	48	1	C1	-12.00	30.26	1	11	2	0
RRD-PM Patient#17	2	49	1	C1	-13	33.55	1	4	1	0
RRD-PM Patient#18	1	65	2	20/33	-7.00	26.77	1	11	1	0
RRD-PM Patient#19	2	55	2	C1	-10.00	30.16	1	11	1	0
RRD-PM Patient#20	2	48	1	20/50	-6.00	26.8	1	7	1	0
RRD-PM Patient#21	1	34	2	C1	-8.50	27.67	1	4	1	0
RRD-PM Patient#22	2	54	1	20/1000	-17.00	30.6	1	7	2	0
RRD Patient#1	1	54	2	20/400	0	25.52	0	7	0	0
RRD Patient#2	1	39	2	20/33	0	23.59	0	4	0	0
RRD Patient#3	2	65	2	20/200	0	23.9	0	11	0	0
RRD Patient#4	1	61	1	20/100	0	23.66	0	9	0	0
RRD Patient#5	1	67	2	20/200	0	22.29	0	9.5	0	0
RRD Patient#6	1	75	1	HM	0	23.05	0	13	0	1
RRD Patient#7	2	47	1	HM	0	26.1	0	7.5	0	0
RRD Patient#8	1	57	1	20/400	0	23.69	0	10	0	0
RRD Patient#9	2	71	2	20/400	0	23.52	0	10.5	0	1
RRD Patient#10	2	56	1	C1	0	23.73	0	10	0	0
RRD Patient#11	1	57	2	C1	0	23.9	0	10	0	0
RRD Patient#12	2	58	2	20/2000	0	25.65	0	10.5	0	0
RRD Patient#13	1	57	2	20/100	-3	23.49	0	10.5	0	0
RRD Patient#14	1	52	2	C1	-1.5	24.95	0	9.5	0	0
RRD Patient#15	2	55	2	20/200	-3.5	24.5	0	10.5	0	1
RRD Patient#16	2	58	2	C1	-3	23.3	0	10	0	0
RRD Patient#17	2	66	1	20/166	0	24.5	0	10.5	0	1
RRD Patient#18	2	64	1	20/200	0	23.92	0	10.5	0	1
RRD Patient#19	1	57	2	20/200	0	23.83	0	10	0	0
RRD Patient#20	1	73	1	20/33	0	25.81	0	11	0	0
RRD Patient#21	1	74	2	HM	0	22.64	0	11	0	1
RRD Patient#22	1	47	1	C1	0	23.57	0	6.5	0	0

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	655.25	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 A N36C_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	9.295 2	162.5 9	64.54 1	0	333.1 1	406.3	283.5	121.0 1	174.0 5	97.51 6	0	91.11 9	80.66 2	0.036 883	
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	0	50.77 8	905.8 1	566.5 7	404.2 6	0	259.1 8	214.6 3	0	0	0	0.045 635
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	502.0 2	301.8 5	192.5	0	164.3 4	0	0	0	0	0	0.046 604
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	657.4 2	2784. 1	6956. 6	4766. 4	8398. 5	4911. 9	6616. 4	2275. 4	3199. 7	177.8 7	0.004 898	

	OS=Homo sapiens PE=1 SV=1;>sp P01776 H V315_HUMAN Ig heavy chain V-III region WAS OS=Homo sapiens PE=1 SV=1;>sp P01774 H V																				
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	0	13372	66164	59839	72616	60992	63683	32837	17442	28995	0.015 297
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	0.019 107	
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	30.63	1	0	128.15	94.795	41.115	77.449	98.988	51.439	48.943	68.106	97.239	0.019 87

	GN=FCGBP PE=1 SV=3																					
sp P01624 KV306_HUMAN;sp P01605 KV13_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 KV13_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	0	0	0	0	0	0	0	0	0
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	0	
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	375.1 1	324.7 5	775.1 9	45.09 2	556.7 3	1239. 7	2010. 4	1264	1524. 7	1023. 2	952.0 5	756.9 4	1309. 1	1116. 4	0.057 422
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	0.062 081
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	582.6 6	684.2 1	1404. 4	10593	13311	1904. 5	5714. 5	2815	4149. 7	2313. 5	4030. 1	522.7 3	0.063 693
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	989.2 5	276	295.0 9	0	8681. 3	4832. 1	1837. 4	1867. 6	3017. 9	2023. 5	0	339.5 4	344.2 7	0.064 995
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	0.065 428
sp P10745 RET3_HUMAN	>sp P10745 RET3_HUMAN Retinol-binding protein 3	38117	45237	25294	12139	10352	12773	26224	24483	18163	11713 0	64914	34000	21123	20966	15264	44261	46491	45598	0.066 54

	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	32395 0	19766 0	14592 0	12399 0	12511 0	10838 0	43983	47237	43315	0.066 749
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	70.87 6	84.28 5	0	23.37 6	0	714.8 4	368.0 3	0	203.5 2	294.3 4	224.3 3	0	18.51 4	23.03 2	0.066 976
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	607.5 3	0	45.09 8	473.7 2	0	259.5 8	135.9 1	0.067 764
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 KV313_HUMAN SV=1;>sp P01622 KV312_HUMAN	25750	22206	12737	9192.1	6141	10983	8029. 9	6011. 7	4403. 5	71012	42988	23995	22013	18793	19169	11362	9883. 1	10168	0.069 301
sp P01042 KNG1_HUMAN	>sp P01042 KNG1_HUMAN Kininogen-1 OS=Homo sapiens	588.92	567.5	290.43	126.71	0	392.2 9	0	124.0 2	0	5597. 9	2662. 5	1262	738.6 6	693.3 6	568.5 6	514.9	227.6 1	147.2 3	0.069 574

	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	32330 0	25323 0	12400 0	95480	87258	80945	69321	52778	52280	0.071 376	
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	68.63 1	0	0	1233. 1	971.3	763.6 8	0	0	0	0	0	0	0	0.075 77
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	83.94 2	288.4 7	0	0	0	2615. 1	1408. 4	578.6 9	329.0 3	509.3 6	220.1 5	100.0 1	201.7 4	241.6 4	0.080 055	
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	351.8 5	618.8 6	213.2 4	380.6 9	123.7 9	13812	6054. 8	2516. 2	1592. 5	2183. 3	603.7 1	0	811.8 3	771.3 7	0.080 803	
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	57.15 9	0	773.3 6	595.9 2	0	504.7 3	258.3 8	943.3	0	0	88.28 2	0.082 686	

	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	36097 0	22709 0	11919 0	11743 0	10403 0	10482 0	64954	57476	42216	0.082 86
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	426.3 6	227.8 4	932.0 4	561.9 7	1334. 8	0	77.18 1	0	468.0 4	0	184.1 1	1297. 3	351.2 6	0.085 49
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	89.11 5	938.8	0	498.4 3	0	9044. 8	4693	2220. 2	1649. 5	1176. 3	1164. 4	711.1 1	0	549.8 2	0.088 917
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	0.089 127
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	104.7 2	0	0.891 43	0	0	6760. 1	2783. 3	443.7 2	895.7 3	1252. 6	520.4 9	297.5 5	0	0	0.089 568
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	915.2 3	2114. 1	0	426.0 4	50.58 9	34082	26518	9172. 9	2325. 8	3940. 7	2641. 4	1671. 2	507.6	534.6 1	0.089 634
sp P53673 CRBA4_HUMAN	>sp P53673 CRBA4_HUMAN Beta-crystallin A4 OS=Homo sapiens	0	0	0	0	0	0	0	0	160.3 1	13992 0	71029	60627	0	0	0	203.1 8	0	0	0.089 656

	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	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	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	0	132.85	0	0.098018
sp P01023 A2MG_HUMAN;CON__ENSEMBL:ENSBTAP0000024146;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	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	18.112	115.52	25.048	3.6467	15.442	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	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	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	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	12915	14976	11772	12207	92128	45442	39337	29797	26598	30453	25161	70886	15919	11923	0	0.107991
sp Q6NSJ5 LRC8E_HUMAN	>sp Q6NSJ5 LRC8E_HUMAN Volume-regulated anion channel subunit LRR8E 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	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		

sp P27169 PON1_HUMAN	>sp P27169 PON1_HUMAN Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3	872.44	674.91	256.12	0	0	0	33.765	0	0	860.82	880.45	608.25	647.48	704.14	526.04	0	0	38.087	0.122099	
sp P00352 AL1A1_HUMAN;sp P05091 ALDH2_HUMAN;sp P47895 AL1A3_HUMAN;sp P30837 AL1B1_HUMAN;sp O94788 AL1A2_HUMAN	>sp P00352 AL1A1_HUMAN Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	0	94.767	0	0	85.082	55.581	23.476	0	16.185	19175	11962	2919.5	77.212	0	0	0	0	73.099	87.916	0.123275
sp P07320 CRGD_HUMAN	>sp P07320 CRGD_HUMAN Gamma-crystallin D OS=Homo sapiens GN=CRYGD PE=1 SV=3	0	0	0	0	0	0	0	0	0	31972	12846	6214.5	0	1067.5	0	0	0	0	231.24	0.123866
sp Q86WG5 MTMRRD_HUMAN	>sp Q86WG5 MTMRRD_HUMAN Myotubularin-related protein 13 OS=Homo sapiens GN=SBF2 PE=1 SV=1	0	755.93	13.926	293.57	197.95	254.9	0	0	0	2854.1	1279.7	1565.8	0	814.53	56.895	0	0	0	0	0.123899
sp P05813 CRBA1_HUMAN	>sp P05813 CRBA1_HUMAN Beta-crystallin A3 OS=Homo sapiens GN=CRYBA1 PE=1 SV=4	0	146.15	0	0	0	133.46	288.64	0	67.938	110030	54956	20589	0	132.62	0	0	0	173.97	0	0.126107
sp P02753 RET4_HUMAN	>sp P02753 RET4_HUMAN Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3	478.48	0	0	288.05	0	0	0	0	186.98	0	0	0	0	0	0	0	0	0	94.863	0.127665
sp P01024 CO3_HUMAN;CON_Q2UVX4	>sp P01024 CO3_HUMAN Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	8300.3	7912	3589.5	3008.4	1678.3	2409.8	565.45	1651.3	620.03	34287	19250	9095.2	5328.6	6019.2	4186.4	1630.8	1952.6	2060.6	0.127963	

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	0	17.09 9	2054. 7	1371	262.1 2	0	0	0	0	0	0	0.128 423
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	0	3960. 9	1629. 9	1122. 2	0	0	478.6 7	35.82	11.92 8	15.38 9	0.129 027
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	895.6 3	346.3 3	631.5 9	1248. 6	1185. 2	12380	9722. 7	5101. 7	2845. 1	2838. 2	3016. 3	1874	2254. 3	2891. 9	0.131 112	
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	186.5 3	159.0 8	149.3 6	4736. 5	1858. 1	1336. 7	286.6 9	969.3 7	282.0 4	43.81 4	244.2 9	0	0.131 303	
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	0.133 952
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	524.0 4	0	0	0	0	0	0	0	0	0	0	0	0.135 07
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	417.4 1	14465	11294	3393	5254. 2	4837. 7	4919	6040. 2	6759	5840. 9	0.135 922	

	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	0	496.7 2	254.3 1	0	0	0	0	19.63 4	0	0	0	0.162 148
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	290.3 4	0	120.9 9	18380	9598. 7	4002. 4	1141. 3	0	0	0	608.8 4	0	0	0	0.167 584
sp P60174 TPIS_HUMAN	>sp P60174 TPIS_HUMAN Triosephosphate isomerase OS=Homo sapiens GN=TP11 PE=1 SV=3	0	81.848	0	0	0	0	125.5 6	48.53 4	26.00 8	1889. 3	648.0 6	333.9 5	0	0	0	0	54.51 7	65.96 2	0	0	0.168 036
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	539.3 4	0	0	0	0	0	0	0	0	0.168 14
sp O43490 PROM1_HUMAN	>sp O43490 PROM1_HUMAN Prominin-1 OS=Homo sapiens GN=PROM1 PE=1 SV=1	0	0	0	0	0	40.52 4	0	0	0	62.13 1	0	0	56.05 1	0	0	0	72.69 6	0	0	0	0.169 303
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	14.35 9	25.89 3	0	0	0	392.3 4	697.1 4	0	0	0	0	0	0	14.99 2	16.9	0	0.172 224
sp P10645 CMGA_HUMAN	>sp P10645 CMGA_HUMAN Chromogranin-A	343.86	686.41	0	0	0	83.87 7	0	57.16 8	0	2565. 6	1117. 9	0	101.1 2	888.1 4	106.0 2	203.2 4	0	0	0	0	0.173 893

	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	45622 0	16044 0	90422	93946	87141	86984	78880	49639	57603	0.174 429		
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	155.2 1	291.4 9	0	70.85 5	0	1444. 1	982.2 4	460.5 4	0	476.6 7	41.66 6	0	13.29 8	0	0.177 159		
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	174.0 2	237.5	139.5 4	139.7 5	7682. 8	1559. 3	1137	150.2 8	590.7 9	494.6 4	365.9 1	320.3 5	391.6 7	0.177 958		
sp Q5T7N2 LITD1_HUMAN	>sp Q5T7N2 LITD1_HUMAN LINE-1 type transposase domain-containing protein 1 OS=Homo sapiens GN=LITD1 PE=1 SV=1	4806.3	59.436	166.57	345.31	583.9 5	394.2 1	354.9 5	283.9 8	298.5 5	851.0 1	726.3 4	449.2 5	406.2 8	245.7 3	7421. 3	5291. 5	224.5 6	5169. 8	0.178 349		
sp P63261 ACTG_HUMAN;sp P60709 ACTB_HUMAN;sp Q6S8J3 POTEE_HUMAN;sp A5A3E0 POTEF_HUMAN;sp POCG38 POTEI_HUMAN;sp Q9BYX7 ACTBM_HUMAN;sp POCG39 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	951.7 6	25493	12606	8052. 1	170.7 3	250.1	178.6 7	504.0 5	789.1 3	814.2 7	0.187 373		

	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	218.57	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	9	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	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	10.80	1	0	0	4176.5	1236	492.4	31.38	0	0	43.89	0	0	0.260	493			
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	246.7	25.89	4	6	0	0	214.3	0	0	1142.3	212.7	0	0	36.79	0	0.260	943		
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	0	12515	6599.3	4206	0	2098.6	1805.2	0	0	0	0	0.262	808		
sp P02760 AMB_P_HUMAN	>sp P02760 AMB_P_HUMAN Protein AMBP OS=Homo sapiens GN=AMB_P PE=1 SV=1	369.79	201.21	158.91	271.59	0	55.98	22.03	9	4	4	0	3283.5	965.1	329.8	5	0	0	0	141.3	0	159.1	0.262	918	
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	11449.0	67263	17028	17012	26186	18595	8433.2	5669.1	6528.7	0.263	249				
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	76.36	157.5	221.6	7	6	6	226.8	257.7	230.7	4	431.1	95.97	0	0	222.0	77.61	239.5	393.6	0.265	274
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	0	0	0	0	0	901.2	545.0	82.97	0	259.1	0	0	0	0.265	431
sp P23142 FBLN1_HUMAN	>sp P23142 FBLN1_HUMAN Fibulin-1	119.26	353.37	0	0	0	0	0	0	0	0	0	213.7	0	58.27	306.0	363.4	0	0	0	0	163.4	0.276	607	

	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	

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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1573.3	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	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	0	0	0	0	0	0	0	0	0	0	0	0	0	385.37	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	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	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	0	0	0	0	0	0	0	0	0	0	0	94.471	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	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	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_HUMAN Ig kappa chain V-I region WEA OS=Homo sapiens PE=1 SV=1	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	12758 0	59979	39575 0	21056 0	15662 0	11467 0	10961 0	84761	13722 0	11646 0	12487 0	0.361 95
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	33208 0	19689 0	10796 0	74865	85716	59984	64756	56881	62537	0.366 577
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	119.0 5	38129	563.4 6	0	14169	15795	9313. 8	8908. 1	6952. 4	6101. 7	0.372 586
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	820.3 2	2617. 1	2833. 6	4263	1909. 5	72950	32093	11645	5341. 7	8000. 6	6775. 3	6309. 8	3963. 1	4227. 6	0.374 179
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	57.41 9	0	0	70.50 8	193.0 2	262.4 5	289.8 7	0	79.39 3	246.7 6	26.05 5	0	41.46 9	0	0.381 61
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	0.394 406
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	579.4 9	0	481.6 7	483.6 7	0	0	0	0.395 872

	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:ENSBTAP0000016285	>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	36.55 5	742.4 6	308.5	431.5 2	0	95.42 2	0	0	0	0	0.429 596	
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	34.08 9	0	0	13.07 4	6.261 6	741.9 3	117.0 2	0	92.18 5	131.9 1	0	0	6.795 8	0	0.432 449	
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	66.85 3	0	0	0	0	0	0	0	0	0	0	246.1 7	0.442 232	
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	277.9 7	165.2 4	0	0	0	0	0	0	0	0.442 378	
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	167.0 4	3643. 3	5757. 5	4291	4590. 7	87338	35526	22906	12292	12316	5	18429	3703. 5	6753. 3	11091	0.444 204
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	993.1 7	4896. 4	10840	2427. 2	6483	7957. 6	2096. 9	784.2 3	730.0 5	919.1 1	0.451 543	
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	0	149.3	0.457 296

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	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:ENSBTAP0000007350	>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	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	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	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		

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	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	486.4 1	403.5 8	888.5 4	292.8 1	2514	1444. 1	425.9 2	365.0 7	509.5	903.6 2	1360. 4	625	1545. 6	0.707 09
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	672.7 2	803.0 6	0	266.0 2	254.1 4	0	379.6	0	0	0.744 376
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	12905 0	60885	41139	28914	27434	17329	25652	24447	27383	0.763 291
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	105.5 2	0	0	0	0	0	0	0	0	0.770 742
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	357.1 1	0	2122. 4	1451	199.8 5	0	0	382.1 8	560.7 9	0	0	0.775 492
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	11.44 4	0	0	0	0	0	0	0	411.7 8	307.2 9	0	0	0	46.14 4	0.777 366
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	100.9 7	115.7 1	216.0 2	224.4 8	113.1 9	0	10.06 3	0	0	140.9 8	143.1 4	0.782 404

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	0	105.87	23.164	0	16.548	0	0	0	0.789054
sp O60500 NPHN_HUMAN	>sp O60500 NPHN_HUMAN Nephhrin OS=Homo sapiens GN=NPHS1 PE=1 SV=1	0	31.002	0	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	216	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	103	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	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	662	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	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	695	0.865
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	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	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	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	398	0.897
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	0.926477

Supplementary Table 3

Label	Spherical equivalent of surgical eye	Axial Length of surgical Eye (mm)	PGDS (ng/mL)	GPX3 (ng/mL)	Nrf-2 (pg/mL)	Label	Spherical equivalent of surgical eye	Axial length of surgical eye (mm)	PGDS (ng/mL)	GPX3 (ng/mL)	Nrf-2 (pg/mL)	Label	Spherical equivalent of surgical eye	Axial length of surgical eye (mm)	PGDS (ng/mL)	GPX3 (ng/mL)	Nrf-2 (pg/mL)
MH-PM Patient#15	-12	31.55	2133.692	3541.278	53.83722	MH-PM Patient#6	-12	27.61	2437.017			RRD Patient#13	-3	23.49	2424.514		
MH-PM Patient#19	-10	31.94	2261.483	290.5485	48.4679	MH-PM Patient#8	-10	28.37	3122.885			RRD Patient#14	-1.5	24.95	1987.517		
MH-PM Patient#22	-18	32.69	2126.091	2709.696	43.8177	MH-PM Patient#9	-12	27.48	2091.411	3768.073	43.8177	RRD Patient#15	-3.5	24.5	1969.397		
MH-PM Patient#1	-12	31.45	2391.768	2671.897	47.88021	MH-PM Patient#21	-21	28.1	2442.362			RRD Patient#4	0	23.66	1865.574	7056.601	53.23362
MH-PM Patient#7	-9	31.06	1783.216	3919.269	42.6738	MH-PM Patient#2	-9	27.41	1532.44			RRD Patient#19	0	23.83	2009.142	2520.7	47.58727
MH-PM Patient#10	-11	30.12	2043.311			ERM Patient#1	0	26.26	2438.453	3276.683	29.05199	RRD Patient#20	0	25.81	1819.576	2709.696	63.72406
MRS-PM Patient#22	-17.5	31.2	1617.539	1197.729	26.99765	MRS-PM Patient#2	-17	28.76	2545.687			ERM Patient#2	0	22.99	2365.972	3881.47	31.14271
MRS-PM Patient#8	-13	29.19	2389.987	3390.081	35.97399	MRS-PM Patient#19	-8	26.6	2780.842			ERM Patient#6	-5	23.51	2432.877		
MRS-PM Patient#13	-12	29.85	2255.307	4108.265	30.09288	MRS-PM Patient#21	-8.75	26.55	3491.65	5506.835	27.83622	ERM Patient#18	0	22.64	2644.745	4221.663	80.65726
MRS-PM Patient#11	-20	31.49	1925.734	2104.909	21.54662	MRS-PM Patient#4	-16.00	28.42	1840.223	3805.872	30.61668	ERM Patient#21	0	24.7	2524.873		
MRS-PM Patient#20	-15	29.86	1658.513			MRS-PM Patient#5	-9	28.79	2998.182			ERM Patient#22	0	24.23	2335.307	7812.584	58.72744
MRS-PM Patient#14	-16	31.41	1330.721			RRD-PM Patient#4	-6	26.59	3226.211	7056.601	50.83662	ERM Patient#8	-1	23.02	1933.873	3163.286	63.72406
MRS-PM Patient#9	-20.5	32.39	1774.308			RRD-PM Patient#6	-10	28.72	4143.67			MH Patient#8	0	23.3	2416.151		
RRD-PM Patient#9	-6.25	30.19	2107.444			RRD-PM Patient#7	-6	27.04	3559.346	4146.064	46.71027	MH Patient#9	-3	23.34	2106.713		
RRD-PM Patient#17	-13	33.55	2522.528			RRD-PM Patient#8	-9.5	28.26	3429.299	5884.826	53.23362	MH Patient#12	-3.25	24.43	2526.864		
RRD-PM Patient#13	-16	32.26	2208.988			RRD-PM Patient#10	-30	28.77	2700.675			MH Patient#15	0	22.43	1989.27		
RRD-PM Patient#16	-12	30.26	2363.977			RRD-PM Patient#18	-7.00	26.77	2031.444	7812.584	49.0574	MH Patient#18	0	23.05	1933.873	2709.696	45.54767
RRD-PM Patient#19	-10	30.16	2394.262			RRD-PM Patient#1	-9.00	26.68	1830.727	7094.4	44.96915	MH Patient#21	0	22.1	1939.1	3805.872	38.73085