

Supporting Information

Corona protein composition and cytotoxicity evaluation of ultra-small zeolites synthesized from template free precursor suspensions

S. Laurent¹•, E.-P. Ng²•, C. Thirifays¹, L. Lakiss³, G.-M. Goupil³, S. Mintova^{3*}, C. Burtea¹, E. Oveisi^{4,5}, C. Hébert^{4,5}, M. de Vries⁶, M. Motazacker⁷, F. Rezaee^{#6*}, and M. Mahmoudi^{#,8,9*}

¹Department of General, Organic, and Biomedical Chemistry, NMR and Molecular Imaging Laboratory, University of Mons, Avenue Maistriau, 19, B-7000 Mons, Belgium

²School of Chemical Sciences, University Sains Malaysia, 11800 USM, Penang, Malaysia.

³Laboratory of Catalysis and Spectroscopy, ENSICAEN, University of Caen, CNRS, 6 Boulevard du Maréchal Juin, 14050 Caen, France

⁴Interdisciplinary Centre for Electron Microscopy, École Polytechnique Fédérale de Lausanne (EPFL), CH-1015 Lausanne, Switzerland

⁵Electron Spectrometry and Microscopy Laboratory, École Polytechnique Fédérale de Lausanne (EPFL), CH-1015 Lausanne, Switzerland

⁶Department of Cell Biology, University Medical Center Groningen, University of Groningen, Groningen, The Netherlands

⁷Department of Experimental Vascular Medicine, Academic Medical Center, Amsterdam, The Netherlands

⁸Department of Nanotechnology, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran

⁹Nanotechnology Research Center, Faculty of Pharmacy, Tehran University of Medical Sciences, Tehran, Iran

• These authors contributed equally to this work as first author.

#These authors contributed equally to this work as last author.*Corresponding Authors: mintova@ensicaen.fr (S.M.); f.rezaee@med.umcg.nl (F.R.); Mahmoudi@illinois.edu (M.M.)

Table S1: The accession number, gene name, species (Human), identification score (-10lgP), molecular weight (Mw) in kDa, protein description, total spectra per protein of LTL zeolite particles incubated with 10% human plasma, together with their relative amount (NpSpCkt value).

Accession	-10lgP	Mw (D)	Description	NpSpCk				Spectra				Total Spectra	Average NpSpCk
				Sample1	Sample2	Sample3	Sample4	Sample1	Sample2	Sample3	Sample4		
P01834 IGKC_HUMAN	196.84	11608.85	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	6.034	4.512	5.652	13.914	6	4	5	5	20	7.528
P02679 FIBG_HUMAN	299.49	51511.68	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	4.080	3.813	4.331	6.898	18	15	17	11	61	4.781
P02671 FIBA_HUMAN	387.69	94973.1	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	4.303	5.101	4.698	3.742	35	37	34	11	117	4.461
P02647 APOA1_HUMAN	237.89	30777.82	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	4.931	5.956	5.116	1.050	13	14	12	1	40	4.263
P01857 IGHG1_HUMAN	239.11	36105.91	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	3.880	3.989	3.998	3.579	12	11	11	4	38	3.862
P02768 ALBU_HUMAN	283.01	69366.8	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	4.208	3.209	4.162	3.726	25	17	22	8	72	3.826
P0CG05 LAC2_HUMAN	149.33	11293.56	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	2.068	4.638	4.648	2.860	2	4	4	1	11	3.553
P02652 APOA2_HUMAN	115.32	11175.02	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	4.179	4.687	4.697	0.000	4	4	4	0	12	3.391
P02675 FIBB_HUMAN	249.19	55928.21	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	2.923	3.044	3.285	2.310	14	13	14	4	45	2.890
P01623 KV305_HUMAN	177.59	11746.11	Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1	3.976	3.344	3.352	0.000	4	3	3	0	10	2.668
P01620 KV302_HUMAN	177.59	11775.06	Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	3.966	3.336	3.343	0.000	4	3	3	0	10	2.661
P01024 CO3_HUMAN	407.55	187146.9	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	2.433	2.309	1.893	2.762	39	33	27	16	115	2.349
P01598 KV106_HUMAN	71.45	11788.23	Ig kappa chain V-I region EU OS=Homo sapiens PE=1 SV=1	1.981	2.222	2.226	2.740	2	2	2	1	7	2.292
P04208 LV106_HUMAN	105.35	11724.96	Ig lambda chain V-I region WAH OS=Homo sapiens PE=1 SV=1	2.987	3.350	2.238	0.000	3	3	2	0	8	2.144
P01871 IGHM_HUMAN	171.05	49306.63	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	1.658	1.593	2.129	2.621	7	6	8	4	25	2.000
P80748 LV302_HUMAN	86.55	11935.15	Ig lambda chain V-III region LOI OS=Homo sapiens PE=1 SV=1	2.935	2.194	0.000	2.707	3	2	0	1	6	1.959
P01860 IGHG3_HUMAN	162.25	41286.99	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	1.980	2.220	2.225	0.000	7	7	7	0	21	1.606
P02649 APOE_HUMAN	227.41	36154.09	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	1.615	2.173	2.541	0.000	5	6	7	0	18	1.582

P01600 KV108_HUMAN	119.06	11670.97	Ig kappa chain V-I region Hau OS=Homo sapiens PE=1 SV=1	1.000	1.122	1.124	2.768	1	1	1	1	4	1.504
P80362 KV125_HUMAN	119.06	11737.07	Ig kappa chain V-I region WAT OS=Homo sapiens PE=1 SV=1	0.995	1.116	1.118	2.752	1	1	1	1	4	1.495
P01609 KV117_HUMAN	119.06	11764.01	Ig kappa chain V-I region Scw OS=Homo sapiens PE=1 SV=1	0.992	1.113	1.116	2.746	1	1	1	1	4	1.492
P01608 KV116_HUMAN	119.06	11782.19	Ig kappa chain V-I region Roy OS=Homo sapiens PE=1 SV=1	0.991	1.111	1.114	2.742	1	1	1	1	4	1.489
P01599 KV107_HUMAN	119.06	11814.2	Ig kappa chain V-I region Gal OS=Homo sapiens PE=1 SV=1	0.988	1.108	1.111	2.734	1	1	1	1	4	1.485
P01610 KV118_HUMAN	119.06	11840.2	Ig kappa chain V-I region WEA OS=Homo sapiens PE=1 SV=1	0.986	1.106	1.108	2.728	1	1	1	1	4	1.482
P01607 KV115_HUMAN	119.06	11902.26	Ig kappa chain V-I region Rei OS=Homo sapiens PE=1 SV=1	0.981	1.100	1.103	2.714	1	1	1	1	4	1.474
P01594 KV102_HUMAN	119.06	11939.24	Ig kappa chain V-I region AU OS=Homo sapiens PE=1 SV=1	0.978	1.097	1.099	2.706	1	1	1	1	4	1.470
P01593 KV101_HUMAN	119.06	11992.34	Ig kappa chain V-I region AG OS=Homo sapiens PE=1 SV=1	0.974	1.092	1.094	2.694	1	1	1	1	4	1.463
P01766 HV305_HUMAN	85.54	13226.74	Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	0.883	0.990	0.992	2.442	1	1	1	1	4	1.327
P01859 IGHG2_HUMAN	125.21	35900.65	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2	1.626	1.824	1.828	0.000	5	5	5	0	15	1.319
P01700 LV102_HUMAN	85.38	11896.17	Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1	1.963	2.201	1.103	0.000	2	2	1	0	5	1.317
B9A064 IGLL5_HUMAN	128.78	23063.24	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	1.012	1.136	1.707	1.401	2	2	3	1	8	1.314
A0M8Q6 LAC7_HUMAN	124.95	11302.66	Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 PE=1 SV=2	0.000	0.000	2.322	2.858	0	0	2	1	3	1.295
P0CG06 LAC3_HUMAN	149.33	11237.5	Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1	2.078	0.000	0.000	2.875	2	0	0	1	3	1.238
P01876 IGHA1_HUMAN	148.03	37654.66	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	1.550	1.739	1.394	0.000	5	5	4	0	14	1.171
P02746 C1QB_HUMAN	73.96	26721.75	Complement C1q subcomponent subunit B OS=Homo sapiens GN=C1QB PE=1 SV=3	0.000	0.980	0.982	2.418	0	2	2	2	6	1.095
P06727 APOA4_HUMAN	130.17	45399.07	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	1.800	0.577	0.867	0.712	7	2	3	1	13	0.989
P04004 VTNC_HUMAN	182.35	54305.59	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	1.075	0.964	1.208	0.595	5	4	5	1	15	0.961
P00751 CFAB_HUMAN	198.24	85532.94	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	0.956	1.225	1.074	0.378	7	8	7	1	23	0.908
P06310 KV206_HUMAN	99.86	14706.7	Ig kappa chain V-II region RPMI 6410 OS=Homo sapiens PE=4 SV=1	0.794	1.781	0.892	0.000	1	2	1	0	4	0.867
P06396 GELS_HUMAN	118.08	85697.48	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	0.545	0.917	0.459	1.131	4	6	3	3	16	0.763
P06309 KV205_HUMAN	99.86	12664.16	Ig kappa chain V-II region GM607	0.922	1.034	1.036	0.000	1	1	1	0	3	0.748

			(Fragment) OS=Homo sapiens PE=4 SV=1										
P01614 KV201_HUMAN	99.86	12676.25	Ig kappa chain V-II region Cum OS=Homo sapiens PE=1 SV=1	0.921	1.033	1.035	0.000	1	1	1	0	3	0.747
P0CF74 LAC6_HUMAN	124.95	11276.54	Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 PE=4 SV=1	0.000	0.000	0.000	2.865	0	0	0	1	1	0.716
P0CG04 LAC1_HUMAN	98.05	11347.66	Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 SV=1	0.000	0.000	0.000	2.847	0	0	0	1	1	0.712
P01611 KV119_HUMAN	74.55	11607.91	Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1	0.000	0.000	0.000	2.783	0	0	0	1	1	0.696
P04003 C4BPA_HUMAN	130.15	67033.3	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	0.871	0.781	0.979	0.000	5	4	5	0	14	0.658
P0C0L5 CO4B_HUMAN	207.03	192792.2	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=1	0.727	0.611	0.545	0.503	12	9	8	3	32	0.596
P08603 CFAH_HUMAN	188.42	139096.3	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	0.588	0.659	0.849	0.000	7	7	9	0	23	0.524
P00747 PLMN_HUMAN	77.59	90569.05	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	0.387	0.723	0.580	0.357	3	5	4	1	13	0.511
P04433 KV309_HUMAN	39.58	12575.17	Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	0.928	1.041	0.000	0.000	1	1	0	0	2	0.492
P0C0L4 CO4A_HUMAN	207.03	192770.2	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	0.727	0.611	0.545	0.000	12	9	8	0	29	0.471
P02766 TTHY_HUMAN	59.02	15887.02	Transthyretin OS=Homo sapiens GN=TTR PE=1 SV=1	0.000	0.824	0.826	0.000	0	1	1	0	2	0.413
P01591 IGJ_HUMAN	53.46	18098.58	Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4	0.000	0.723	0.725	0.000	0	1	1	0	2	0.362
P04114 APOB_HUMAN	270.42	515610.8	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	0.430	0.279	0.255	0.439	19	11	10	7	47	0.351
P10909 CLUS_HUMAN	78.74	52494.64	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	0.000	0.000	0.750	0.615	0	0	3	1	4	0.341
P02654 APOC1_HUMAN	37.4	9331.92	Apolipoprotein C-I OS=Homo sapiens GN=APOC1 PE=1 SV=1	1.251	0.000	0.000	0.000	1	0	0	0	1	0.313
P19827 ITIH1_HUMAN	133.93	101389.1	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3	0.345	0.000	0.259	0.637	3	0	2	2	7	0.310
P01709 LV206_HUMAN	38.46	11557.57	Ig lambda chain V-II region MGC OS=Homo sapiens PE=1 SV=1	0.000	0.000	1.135	0.000	0	0	1	0	1	0.284
P01707 LV204_HUMAN	38.46	11560.83	Ig lambda chain V-II region TRO OS=Homo sapiens PE=1 SV=1	0.000	0.000	1.135	0.000	0	0	1	0	1	0.284
P01712 LV209_HUMAN	38.46	11693.92	Ig lambda chain V-II region WIN OS=Homo sapiens PE=1 SV=1	0.000	0.000	1.122	0.000	0	0	1	0	1	0.281
P04196 HRG_HUMAN	48.64	59578.32	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	0.392	0.440	0.220	0.000	2	2	1	0	5	0.263
P01625 KV402_HUMAN	93.02	12640.07	Ig kappa chain V-IV region Len OS=Homo sapiens PE=1 SV=2	0.000	1.036	0.000	0.000	0	1	0	0	1	0.259

P01715 LV401_HUMAN	32.19	11305.55	Ig lambda chain V-IV region Bau OS=Homo sapiens PE=1 SV=1	1.033	0.000	0.000	0.000	1	0	0	0	1	0.258
P02749 APOH_HUMAN	66.52	38298.18	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	0.305	0.342	0.343	0.000	1	1	1	0	3	0.247
P01605 KV113_HUMAN	50.62	11834.15	Ig kappa chain V-I region Lay OS=Homo sapiens PE=1 SV=1	0.987	0.000	0.000	0.000	1	0	0	0	1	0.247
P02748 CO9_HUMAN	94.04	63173.49	Complement component C9 OS=Homo sapiens GN=C9 PE=1 SV=2	0.554	0.207	0.208	0.000	3	1	1	0	5	0.242
P02787 TRFE_HUMAN	80.6	77063.97	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3	0.455	0.000	0.511	0.000	3	0	3	0	6	0.241
P04434 KV310_HUMAN	50.62	12757.46	Ig kappa chain V-III region VH (Fragment) OS=Homo sapiens PE=4 SV=1	0.915	0.000	0.000	0.000	1	0	0	0	1	0.229
P23083 HV103_HUMAN	60.93	13008.71	Ig heavy chain V-I region V35 OS=Homo sapiens PE=1 SV=1	0.898	0.000	0.000	0.000	1	0	0	0	1	0.224
P09871 C1S_HUMAN	120.33	76684.54	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	0.305	0.000	0.513	0.000	2	0	3	0	5	0.204
P04207 KV308_HUMAN	50.62	14275.17	Ig kappa chain V-III region CLL OS=Homo sapiens PE=1 SV=2	0.818	0.000	0.000	0.000	1	0	0	0	1	0.204
P01042 KNG1_HUMAN	41.23	71957.42	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	0.000	0.364	0.000	0.449	0	2	0	1	3	0.203
P02751 FINC_HUMAN	121.41	262622	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	0.267	0.150	0.250	0.123	6	3	5	1	15	0.197
P01008 ANT3_HUMAN	81.11	52602.49	Antithrombin-III OS=Homo sapiens GN=SERPINC1 PE=1 SV=1	0.666	0.000	0.000	0.000	3	0	0	0	3	0.166
O60682 MUSC_HUMAN	31.29	22067.64	Musculin OS=Homo sapiens GN=MSC PE=1 SV=2	0.000	0.593	0.000	0.000	0	1	0	0	1	0.148
P35858 ALS_HUMAN	52.14	66035.11	Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	0.177	0.198	0.199	0.000	1	1	1	0	3	0.143
P19823 ITIH2_HUMAN	62.52	106463.4	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	0.219	0.246	0.000	0.000	2	2	0	0	4	0.116
P07357 CO8A_HUMAN	38.86	65163.25	Complement component C8 alpha chain OS=Homo sapiens GN=C8A PE=1 SV=2	0.000	0.201	0.201	0.000	0	1	1	0	2	0.101
O75636 FCN3_HUMAN	51.36	32902.97	Ficolin-3 OS=Homo sapiens GN=FCN3 PE=1 SV=2	0.000	0.398	0.000	0.000	0	1	0	0	1	0.099
P00739 HPTR_HUMAN	43.51	39029.59	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2	0.000	0.335	0.000	0.000	0	1	0	0	1	0.084
P30460 1B08_HUMAN	29.85	40330.92	HLA class I histocompatibility antigen, B-8 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1	0.000	0.325	0.000	0.000	0	1	0	0	1	0.081
P30479 1B41_HUMAN	29.85	40539.21	HLA class I histocompatibility antigen, B-41 alpha chain OS=Homo sapiens GN=HLA-B PE=1 SV=1	0.000	0.323	0.000	0.000	0	1	0	0	1	0.081

P23142 FBLN1_HUMAN	63.21	77214.17	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	0.302	0.000	0.000	0.000	2	0	0	0	2	0.076
P00738 HPT_HUMAN	35.67	45205.34	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	0.000	0.000	0.290	0.000	0	0	1	0	1	0.073
P05156 CFAI_HUMAN	48.34	65750.36	Complement factor I OS=Homo sapiens GN=CFI PE=1 SV=2	0.000	0.199	0.000	0.000	0	1	0	0	1	0.050
P01023 A2MG_HUMAN	32.38	163290.2	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	0.000	0.080	0.080	0.000	0	1	1	0	2	0.040
P01031 CO5_HUMAN	42.3	188304.2	Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	0.000	0.139	0.000	0.000	0	2	0	0	2	0.035
Q08AE8 SPIR1_HUMAN	35.7	85553.76	Protein spire homolog 1 OS=Homo sapiens GN=SPIRE1 PE=1 SV=2	0.136	0.000	0.000	0.000	1	0	0	0	1	0.034
Q14624 ITIH4_HUMAN	42.4	103357.4	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	0.113	0.000	0.000	0.000	1	0	0	0	1	0.028
Q86UR5 RIMS1_HUMAN	29.97	189071.3	Regulating synaptic membrane exocytosis protein 1 OS=Homo sapiens GN=RIMS1 PE=1 SV=1	0.000	0.069	0.000	0.000	0	1	0	0	1	0.017
Q8IWN7 RP1L1_HUMAN	32.56	261203	Retinitis pigmentosa 1-like 1 protein OS=Homo sapiens GN=RP1L1 PE=1 SV=4	0.045	0.000	0.000	0.000	1	0	0	0	1	0.011
P01774 HV313_HUMAN	91.64	2012710	Ig heavy chain V-III region POM OS=Homo sapiens PE=1 SV=1	0.000	0.013	0.013	0.016	0	2	2	1	5	0.011
P01779 HV318_HUMAN	91.64	2012188	Ig heavy chain V-III region TUR OS=Homo sapiens PE=1 SV=1	0.000	0.007	0.013	0.016	0	1	2	1	4	0.009
P01776 HV315_HUMAN	91.64	2012847	Ig heavy chain V-III region WAS OS=Homo sapiens PE=1 SV=1	0.000	0.007	0.013	0.016	0	1	2	1	4	0.009
P01777 HV316_HUMAN	85.54	2012559	Ig heavy chain V-III region TEI OS=Homo sapiens PE=1 SV=1	0.006	0.007	0.007	0.016	1	1	1	1	4	0.009
P01617 KV204_HUMAN	99.86	2012059	Ig kappa chain V-II region TEW OS=Homo sapiens PE=1 SV=1	0.006	0.007	0.007	0.000	1	1	1	0	3	0.005
P01765 HV304_HUMAN	91.64	6011611	Ig heavy chain V-III region TIL OS=Homo sapiens PE=1 SV=1	0.000	0.002	0.004	0.005	0	1	2	1	4	0.003
P01596 KV104_HUMAN	107.19	3011346	Ig kappa chain V-I region CAR OS=Homo sapiens PE=1 SV=1	0.000	0.000	0.000	0.011	0	0	0	1	1	0.003
P01781 HV320_HUMAN	88.57	8011764	Ig heavy chain V-III region GAL OS=Homo sapiens PE=1 SV=1	0.003	0.003	0.002	0.000	2	2	1	0	5	0.002

Table S2: The accession number, gene name, species (Human), identification score (-10lgP), molecular weight (Mw) in kDa, protein description, total spectra per protein of EMTzeolite particles incubated with 10% human plasma, together with their relative amount (NpSpCkt value).

Accession	-10lgP	Mw (D)	Description	NpSpCk				Spectra				Total Spectra	AverageNpSpCk
				Sample 1	Sample 2	Sample 3	Sample 4	Sample 1	Sample 2	Sample 3	Sample 4		
P02675 FIBB_HUMAN	322.98	55928.21	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	6.663	5.085	4.621		14	15	13		42	4.092
P02679 FIBG_HUMAN	268.22	51511.68	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	7.751	4.417	3.087		15	12	8		35	3.814
P01623 KV305_HUMAN	145.74	11746.11	Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1	6.798	3.228	3.385		3	2	2		7	3.353
P01620 KV302_HUMAN	145.74	11775.06	Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	6.782	3.220	3.377		3	2	2		7	3.345
P02671 FIBA_HUMAN	388.65	94973.1	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	7.007	2.795	3.140		25	14	15		54	3.235
P01857 IGHG1_HUMAN	251.46	36105.91	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	8.109	3.151	1.652		11	6	3		20	3.228
P02768 ALBU_HUMAN	220.8	69366.8	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	7.291	2.733	2.006		19	10	7		36	3.008
P01834 IGKC_HUMAN	136.64	11608.85	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	0.000	4.900	6.850		0	3	4		7	2.937
P0CG06 LAC3_HUMAN	131.93	11237.5	Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1	0.000	3.375	5.307		0	2	3		5	2.170
P0CF74 LAC6_HUMAN	131.93	11276.54	Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 PE=4 SV=1	0.000	3.363	5.289		0	2	3		5	2.163
P0CG05 LAC2_HUMAN	131.93	11293.56	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	0.000	3.358	5.281		0	2	3		5	2.160
A0M8Q6 LAC7_HUMAN	131.93	11302.66	Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 PE=1 SV=2	0.000	3.355	5.277		0	2	3		5	2.158
P01876 IGHA1_HUMAN	86.65	37654.66	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	4.948	1.511	0.528		7	3	1		11	1.747
P01600 KV108_HUMAN	109.71	11670.97	Ig kappa chain V-I region Hau OS=Homo sapiens PE=1 SV=1	0.000	3.249	3.407		0	2	2		4	1.664
P80362 KV125_HUMAN	109.71	11737.07	Ig kappa chain V-I region WAT OS=Homo sapiens PE=1 SV=1	0.000	3.231	3.388		0	2	2		4	1.655
P01609 KV117_HUMAN	109.71	11764.01	Ig kappa chain V-I region Scw OS=Homo sapiens PE=1 SV=1	0.000	3.223	3.380		0	2	2		4	1.651
P01608 KV116_HUMAN	109.71	11782.19	Ig kappa chain V-I region Roy OS=Homo sapiens PE=1 SV=1	0.000	3.219	3.375		0	2	2		4	1.648
P01622 KV304_HUMAN	135.63	11788.15	Ig kappa chain V-III region Ti OS=Homo sapiens PE=1 SV=1	0.000	3.217	3.373		0	2	2		4	1.647

P01599 KV107_HUMAN	109.71	11814.2	Ig kappa chain V-I region Gal OS=Homo sapiens PE=1 SV=1	0.000	3.210	3.365		0	2	2		4	1.644
P04206 KV307_HUMAN	135.63	11830.29	Ig kappa chain V-III region GOL OS=Homo sapiens PE=1 SV=1	0.000	3.205	3.361		0	2	2		4	1.642
P01610 KV118_HUMAN	109.71	11840.2	Ig kappa chain V-I region WEA OS=Homo sapiens PE=1 SV=1	0.000	3.203	3.358		0	2	2		4	1.640
P01607 KV115_HUMAN	109.71	11902.26	Ig kappa chain V-I region Rei OS=Homo sapiens PE=1 SV=1	0.000	3.186	3.341		0	2	2		4	1.632
P01594 KV102_HUMAN	109.71	11939.24	Ig kappa chain V-I region AU OS=Homo sapiens PE=1 SV=1	0.000	3.176	3.330		0	2	2		4	1.627
P01593 KV101_HUMAN	109.71	11992.34	Ig kappa chain V-I region AG OS=Homo sapiens PE=1 SV=1	0.000	3.162	3.315		0	2	2		4	1.619
P02647 APOA1_HUMAN	94.54	30777.82	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	4.324	1.848	0.000		5	3	0		8	1.543
P01860 IGHG3_HUMAN	221.89	41286.99	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	5.802	0.000	0.000		9	0	0		9	1.451
B9A064 IGLL5_HUMAN	121.12	23063.24	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	5.771	0.000	0.000		5	0	0		5	1.443
P01871 IGHM_HUMAN	185.79	49306.63	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	2.699	1.538	1.210		5	4	3		12	1.362
P01024 CO3_HUMAN	153.36	187146.9	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	2.845	1.317	1.062		20	13	10		43	1.306
P01766 HV305_HUMAN	64.2	13226.74	Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	2.012	2.867	0.000		1	2	0		3	1.220
P01611 KV119_HUMAN	84.93	11607.91	Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1	0.000	1.633	1.713		0	1	1		2	0.837
P01598 KV106_HUMAN	122.79	11788.23	Ig kappa chain V-I region EU OS=Homo sapiens PE=1 SV=1	0.000	1.608	1.686		0	1	1		2	0.824
P04004 VTNC_HUMAN	63.3	54305.59	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	0.980	1.047	1.098		2	3	3		8	0.781
P08603 CFAH_HUMAN	209.16	139096.3	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	1.914	0.409	0.429		10	3	3		16	0.688
P04220 MUCB_HUMAN	108.03	43057.34	Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1	0.000	1.321	1.385		0	3	3		6	0.677
P07360 CO8G_HUMAN	91.73	22277.46	Complement component C8 gamma chain OS=Homo sapiens GN=C8G PE=1 SV=3	2.390	0.000	0.000		2	0	0		2	0.597
P04003 C4BPA_HUMAN	75.11	67033.3	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	1.191	0.000	1.186		3	0	4		7	0.594
Q03591 FHR1_HUMAN	51.47	37650.59	Complement factor H-related protein 1 OS=Homo sapiens GN=CFHR1 PE=1 SV=2	2.121	0.000	0.000		3	0	0		3	0.530
P04433 KV309_HUMAN	46.2	12575.17	Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	2.117	0.000	0.000		1	0	0		1	0.529

P02749 APOH_HUMAN	87.8	38298.18	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	2.085	0.000	0.000	3	0	0	3	0.521
P0C0L4 CO4A_HUMAN	139.87	192770.2	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	0.967	0.590	0.516	7	6	5	18	0.518
P0C0L5 CO4B_HUMAN	139.87	192792.2	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=1	0.966	0.590	0.516	7	6	5	18	0.518
P04208 LV106_HUMAN	53.51	11724.96	Ig lambda chain V-I region WAH OS=Homo sapiens PE=1 SV=1	0.000	1.617	0.000	0	1	0	1	0.404
P01700 LV102_HUMAN	53.51	11896.17	Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1	0.000	1.594	0.000	0	1	0	1	0.398
P07358 CO8B_HUMAN	91.8	67046.97	Complement component C8 beta chain OS=Homo sapiens GN=C8B PE=1 SV=3	0.794	0.283	0.297	2	1	1	4	0.343
P00738 HPT_HUMAN	71.4	45205.34	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	1.178	0.000	0.000	2	0	0	2	0.294
P04114 APOB_HUMAN	165.78	515610.8	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	0.619	0.294	0.193	12	8	5	25	0.277
P02747 C1QC_HUMAN	62.08	25773.65	Complement C1q subcomponent subunit C OS=Homo sapiens GN=C1QC PE=1 SV=3	1.033	0.000	0.000	1	0	0	1	0.258
P04196 HRG_HUMAN	37.95	59578.32	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	0.447	0.318	0.000	1	1	0	2	0.255
P02751 FINC_HUMAN	82.53	262622	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	0.709	0.217	0.076	7	3	1	11	0.250
P00751 CFAB_HUMAN	135.89	85532.94	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	0.934	0.000	0.000	3	0	0	3	0.233
P01042 KNG1_HUMAN	57.7	71957.42	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	0.740	0.000	0.000	2	0	0	2	0.185
P35858 ALS_HUMAN	55.07	66035.11	Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	0.000	0.287	0.301	0	1	1	2	0.147
P01877 IGHA2_HUMAN	53	36526.34	Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3	0.000	0.000	0.544	0	0	1	1	0.136
P00739 HPTR_HUMAN	31.28	39029.59	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2	0.000	0.000	0.509	0	0	1	1	0.127
P10909 CLUS_HUMAN	37.99	52494.64	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	0.000	0.361	0.000	0	1	0	1	0.120
P06396 GELS_HUMAN	34.64	85697.48	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	0.000	0.221	0.000	0	1	0	1	0.074
P03952 KLKB1_HUMAN	56.5	71369.8	Plasma kallikrein OS=Homo sapiens GN=KLKB1 PE=1 SV=1	0.000	0.000	0.279	0	0	1	1	0.070
P00747 PLMN_HUMAN	66.81	90569.05	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	0.000	0.209	0.000	0	1	0	1	0.052
P26006 ITA3_HUMAN	29.19	116612.1	Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	0.000	0.000	0.170	0	0	1	1	0.043
P01777 HV316_HUMAN	64.2	2012559	Ig heavy chain V-III region TEI OS=Homo sapiens PE=1 SV=1	0.013	0.019	0.000	1	2	0	3	0.008

P01779 HV318_HUMAN	67.52	2012188	Ig heavy chain V-III region TUR OS=Homo sapiens PE=1 SV=1	0.000	0.009	0.010		0	1	1		2	0.005
P01774 HV313_HUMAN	67.52	2012710	Ig heavy chain V-III region POM OS=Homo sapiens PE=1 SV=1	0.000	0.009	0.010		0	1	1		2	0.005
P01776 HV315_HUMAN	67.52	2012847	Ig heavy chain V-III region WAS OS=Homo sapiens PE=1 SV=1	0.000	0.009	0.010		0	1	1		2	0.005
P01596 KV104_HUMAN	122.79	3011346	Ig kappa chain V-I region CAR OS=Homo sapiens PE=1 SV=1	0.000	0.006	0.007		0	1	1		2	0.003
P01765 HV304_HUMAN	67.52	6011611	Ig heavy chain V-III region TIL OS=Homo sapiens PE=1 SV=1	0.000	0.003	0.003		0	1	1		2	0.002

Table S3: The accession number, gene name, species (Human), identification score (-10lgP), molecular weight (Mw) in kDa, protein description, total spectra per protein of LTL zeolite particles incubated with 100% human plasma, together with their relative amount (NpSpCkt value).

Accession	-10lgP	Mw (D)	Description	Sample 1	Sample 2	Sample 3	Sample 4	Sample 1	Sample 2	Sample 3	Sample 4	Total Spectra	Average NpSpCkt
P02675 FIBB_HUMAN	260.4	55928.21	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	22.357	30.243	27.477	26.909	15	16	14	16	61	26.747
P02679 FIBG_HUMAN	235.05	51511.68	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	24.274	24.627	25.571	20.086	15	12	12	11	50	23.640
P02671 FIBA_HUMAN	257.06	94973.1	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	17.554	14.470	13.869	13.865	20	13	12	14	59	14.940
P02649 APOE_HUMAN	169.53	36154.09	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	6.917	5.848	6.072	5.203	3	2	2	2	9	6.010
P06396 GELS_HUMAN	195.87	85697.48	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	5.836	4.934	5.124	3.293	6	4	4	3	17	4.797
P02652 APOA2_HUMAN	37.79	11175.02	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	0.000	0.000	9.823	8.417	0	0	1	1	2	4.560
P01024 CO3_HUMAN	177.03	187146.9	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	2.227	4.519	6.452	5.026	5	8	11	10	34	4.556
P02768 ALBU_HUMAN	147.94	69366.8	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	4.807	4.572	3.165	4.068	4	3	2	3	12	4.153
P04004 VTNC_HUMAN	133.51	54305.59	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	6.140	1.947	2.021	1.732	4	1	1	1	7	2.960
P35542 SAA4_HUMAN	35.46	14746.64	Serum amyloid A-4 protein OS=Homo sapiens GN=SAA4 PE=1 SV=2	5.653	0.000	0.000	0.000	1	0	0	0	1	1.413
P01861 IGHG4_HUMAN	66.97	35940.57	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	0.000	2.941	0.000	2.617	0	1	0	1	2	1.390
P01857 IGHG1_HUMAN	66.97	36105.91	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	0.000	2.928	0.000	2.605	0	1	0	1	2	1.383
P01860 IGHG3_HUMAN	66.97	41286.99	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	0.000	2.560	0.000	2.278	0	1	0	1	2	1.210
Q96PM5 ZN363_HUMAN	25.91	30110.39	RING finger and CHY zinc finger domain-containing protein 1 OS=Homo sapiens GN=RCHY1 PE=1 SV=1	0.000	0.000	0.000	3.124	0	0	0	1	1	0.781
P04220 MUCB_HUMAN	86.08	43057.34	Ig mu heavy chain disease protein OS=Homo sapiens PE=1 SV=1	1.936	0.000	0.000	0.000	1	0	0	0	1	0.484
P01871 IGHM_HUMAN	86.08	49306.63	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	1.691	0.000	0.000	0.000	1	0	0	0	1	0.423
P04114 APOB_HUMAN	80.01	515610.8	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	0.000	0.410	0.426	0.547	0	2	2	3	7	0.346
P08603 CFAH_HUMAN	35.22	139096.3	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	0.599	0.000	0.000	0.000	1	0	0	0	1	0.150
Q96Q15 SMG1_HUMAN	26.86	410501.4	Serine/threonine-protein kinase SMG1	0.000	0.000	0.000	0.229	0	0	0	1	1	0.057

			OS=Homo sapiens GN=SMG1 PE=1 SV=3										
P49908 SEPP1_HUMAN	65.8	10041670	Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3	0.008	0.000	0.000	0.000	1	0	0	0	1	0.002

Table S4: The accession number, gene name, species (Human), identification score (-10lgP), molecular weight (Mw) in kDa., protein description, total spectra per protein of EMTzeolite particles incubated with 100% human plasma, together with their relative amount (NpSpCkt value).

Accession	-10lgP	Mw (D)	Description	NpSpCk				Spectra				Total Spectra	AverageNpSpCk
				Sample 1	Sample 2	Sample 3	Sample 4	Sample 1	Sample 2	Sample 3	Sample 4		
P02671 FIBA_HUMAN	219.4	94973.1	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	40.541	37.217	21.430	22.545	7	9	9	8	33	30.43
P02679 FIBG_HUMAN	129.51	51511.68	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	42.712	30.497	8.780	10.392	4	4	2	2	12	23.10
P02675 FIBB_HUMAN	116.5	55928.21	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	0.000	28.089	16.174	19.142	0	4	4	4	12	15.85
P02652 APOA2_HUMAN	27.25	11175.02	Apolipoprotein A-II OS=Homo sapiens GN=APOA2 PE=1 SV=1	0.000	0.000	20.236	23.950	0	0	1	1	2	11.05
P02647 APOA1_HUMAN	60.62	30777.82	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	0.000	0.000	22.043	17.392	0	0	3	2	5	9.86
P01024 CO3_HUMAN	100.8	187146.9	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	8.817	4.197	2.417	2.860	3	2	2	2	9	4.57
P02768 ALBU_HUMAN	106.44	69366.8	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	7.929	0.000	0.000	0.000	1	0	0	0	1	1.98
P06727 APOA4_HUMAN	27.05	45399.07	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	0.000	0.000	4.981	0.000	0	0	1	0	1	1.25
Q06203 PUR1_HUMAN	29.92	57399.04	Amidophosphoribosyltransferase OS=Homo sapiens GN=PPAT PE=1 SV=1	0.000	0.000	3.940	0.000	0	0	1	0	1	0.98
P01042 KNG1_HUMAN	34.77	71957.42	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	0.000	0.000	0.000	3.719	0	0	0	1	1	0.93

Table S5: The shared identified proteins in the LTL-10 and EMT-10 samples. The accession number, gene name, species (Human), identification score (-10lgP), molecular weight (Mw) in kDa, protein description, total spectra per protein of LTL and EMT zeolite particles incubated with 10% human plasma, and the relative amount (NpSpCk value) are shown; the average of four measurements is used.

Accession	-10lgP	Mw (D)	Description	Total Spectra (13-10%)	Average NpSpCk (13-10%)	Total Spectra (14-10%)	Average NpSpCk (14-10%)
P02675 FIBB_HUMAN	249.19	55928.21	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	45	2.89	42	4.092292097
P02679 FIBG_HUMAN	299.49	51511.68	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	61	4.78	35	3.813866733
P01623 KV305_HUMAN	177.59	11746.11	Ig kappa chain V-III region WOL OS=Homo sapiens PE=1 SV=1	10	2.67	7	3.352913064
P01620 KV302_HUMAN	177.59	11775.06	Ig kappa chain V-III region SIE OS=Homo sapiens PE=1 SV=1	10	2.66	7	3.344669326
P02671 FIBA_HUMAN	387.69	94973.1	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	117	4.46	54	3.235376435
P01857 IGHG1_HUMAN	239.11	36105.91	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1	38	3.86	20	3.228004248
P02768 ALBU_HUMAN	283.01	69366.8	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	72	3.83	36	3.007582442
P01834 IGKC_HUMAN	196.84	11608.85	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1	20	7.53	7	2.937444782
P0CG06 LAC3_HUMAN	149.33	11237.5	Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 SV=1	3	1.24	5	2.170432825
P0CF74 LAC6_HUMAN	124.95	11276.54	Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 PE=4 SV=1	1	0.72	5	2.162918666
P0CG05 LAC2_HUMAN	149.33	11293.56	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 SV=1	11	3.55	5	2.159657807
A0M8Q6 LAC7_HUMAN	124.95	11302.66	Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 PE=1 SV=2	3	1.30	5	2.157918908
P01876 IGHA1_HUMAN	148.03	37654.66	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2	14	1.17	11	1.746709228
P01600 KV108_HUMAN	119.06	11670.97	Ig kappa chain V-I region Hau OS=Homo sapiens PE=1 SV=1	4	1.50	4	1.663978686
P80362 KV125_HUMAN	119.06	11737.07	Ig kappa chain V-I region WAT OS=Homo sapiens PE=1 SV=1	4	1.50	4	1.654607239
P01609 KV117_HUMAN	119.06	11764.01	Ig kappa chain V-I region Scw OS=Homo sapiens PE=1 SV=1	4	1.49	4	1.650817933
P01608 KV116_HUMAN	119.06	11782.19	Ig kappa chain V-I region Roy OS=Homo sapiens PE=1 SV=1	4	1.49	4	1.648270206
P01599 KV107_HUMAN	119.06	11814.2	Ig kappa chain V-I region Gal OS=Homo sapiens PE=1 SV=1	4	1.49	4	1.643804202
P01610 KV118_HUMAN	119.06	11840.2	Ig kappa chain V-I region WEA OS=Homo sapiens PE=1 SV=1	4	1.48	4	1.640195501
P01607 KV115_HUMAN	119.06	11902.26	Ig kappa chain V-I region Rei OS=Homo sapiens PE=1 SV=1	4	1.47	4	1.631643228
P01594 KV102_HUMAN	119.06	11939.24	Ig kappa chain V-I region AU OS=Homo sapiens PE=1 SV=1	4	1.47	4	1.626589785
P01593 KV101_HUMAN	119.06	11992.34	Ig kappa chain V-I region AG OS=Homo sapiens PE=1 SV=1	4	1.46	4	1.61938639
P02647 APOA1_HUMAN	237.89	30777.82	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	40	4.26	8	1.543084783
P01860 IGHG3_HUMAN	162.25	41286.99	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2	21	1.61	9	1.450586455
B9A064 IGLL5_HUMAN	128.78	23063.24	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens GN=IGLL5 PE=2 SV=2	8	1.31	5	1.44265989

P01871 IGHM_HUMAN	171.05	49306.63	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3	25	2.00	12	1.361741678
P01024 CO3_HUMAN	407.55	187146.9	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2	115	2.35	43	1.305985701
P01766 HV305_HUMAN	85.54	13226.74	Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	4	1.33	3	1.219856809
P01611 KV119_HUMAN	74.55	11607.91	Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1	1	0.70	2	0.836508531
P01598 KV106_HUMAN	71.45	11788.23	Ig kappa chain V-I region EU OS=Homo sapiens PE=1 SV=1	7	2.29	2	0.823712836
P04004 VTNC_HUMAN	182.35	54305.59	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	15	0.96	8	0.781490825
P08603 CFAH_HUMAN	188.42	139096.3	Complement factor H OS=Homo sapiens GN=CFH PE=1 SV=4	23	0.52	16	0.687834096
P04003 C4BPA_HUMAN	130.15	67033.3	C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	14	0.66	7	0.594382605
P04433 KV309_HUMAN	39.58	12575.17	Ig kappa chain V-III region VG (Fragment) OS=Homo sapiens PE=1 SV=1	2	0.49	1	0.529176254
P02749 APOH_HUMAN	66.52	38298.18	Beta-2-glycoprotein 1 OS=Homo sapiens GN=APOH PE=1 SV=3	3	0.25	3	0.52126359
POC0L4 CO4A_HUMAN	207.03	192770.2	Complement C4-A OS=Homo sapiens GN=C4A PE=1 SV=1	29	0.47	18	0.518088976
POC0L5 CO4B_HUMAN	207.03	192792.2	Complement C4-B OS=Homo sapiens GN=C4B PE=1 SV=1	32	0.60	18	0.518029772
P04208 LV106_HUMAN	105.35	11724.96	Ig lambda chain V-I region WAH OS=Homo sapiens PE=1 SV=1	8	2.14	1	0.404276496
P01700 LV102_HUMAN	85.38	11896.17	Ig lambda chain V-I region HA OS=Homo sapiens PE=1 SV=1	5	1.32	1	0.398458136
P00738 HPT_HUMAN	35.67	45205.34	Haptoglobin OS=Homo sapiens GN=HP PE=1 SV=1	1	0.07	2	0.294411365
P04114 APOB_HUMAN	270.42	515610.8	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	47	0.35	25	0.27661325
P04196 HRG_HUMAN	48.64	59578.32	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	5	0.26	2	0.255
P02751 FINC_HUMAN	121.41	262622	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	15	0.20	11	0.250442649
P00751 CFAB_HUMAN	198.24	85532.94	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2	23	0.91	3	0.233400714
P01042 KNG1_HUMAN	41.23	71957.42	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2	3	0.20	2	0.184956123
P35858 ALS_HUMAN	52.14	66035.11	Insulin-like growth factor-binding protein complex acid labile subunit OS=Homo sapiens GN=IGFALS PE=1 SV=1	3	0.14	2	0.147044796
P00739 HPTR_HUMAN	43.51	39029.59	Haptoglobin-related protein OS=Homo sapiens GN=HPR PE=1 SV=2	1	0.08	1	0.127339149
P10909 CLUS_HUMAN	78.74	52494.64	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	4	0.34	1	0.120
P06396 GELS_HUMAN	118.08	85697.48	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	16	0.76	1	0.074
P00747 PLMN_HUMAN	77.59	90569.05	Plasminogen OS=Homo sapiens GN=PLG PE=1 SV=2	13	0.51	1	0.052337136
P01777 HV316_HUMAN	85.54	2012559	Ig heavy chain V-III region TEI OS=Homo sapiens PE=1 SV=1	4	0.01	3	0.008017022
P01779 HV318_HUMAN	91.64	2012188	Ig heavy chain V-III region TUR OS=Homo sapiens PE=1 SV=1	4	0.01	2	0.004825652
P01774 HV313_HUMAN	91.64	2012710	Ig heavy chain V-III region POM OS=Homo sapiens PE=1 SV=1	5	0.01	2	0.004824401
P01776 HV315_HUMAN	91.64	2012847	Ig heavy chain V-III region WAS OS=Homo sapiens PE=1 SV=1	4	0.01	2	0.004824072
P01596 KV104_HUMAN	107.19	3011346	Ig kappa chain V-I region CAR OS=Homo sapiens PE=1 SV=1	1	0.00	2	0.003224511
P01765 HV304_HUMAN	91.64	6011611	Ig heavy chain V-III region TIL OS=Homo sapiens PE=1 SV=1	4	0.00	2	0.001615227