Elucidating the Molecular Composition of Cartilage by Proteomics

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Supporting information

Figure S1

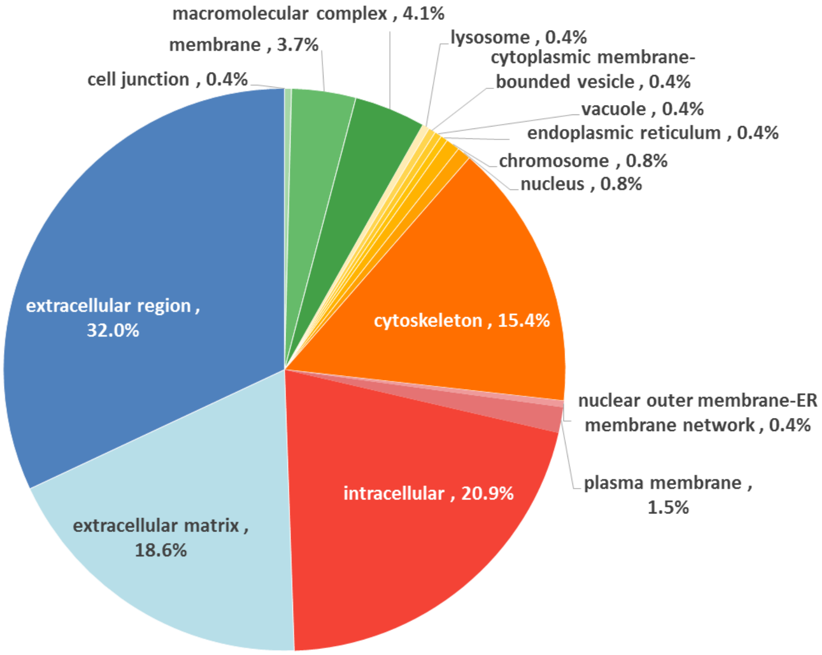

Figure S1. Gene ontology based classification of total proteins from cartilage by guanidine-HCl extraction. The pie chart depicts the putative protein type based on gene ontology IDs. This demonstrates that cartilage decellularization prior to extraction yields a majority (50.6%) of extracellular proteins representing a great enrichment.

Table S1. Peptide sequence, transitions, and collision energy for MRM

Table S2: Quantification results of MRM experiments

Table S3: Less abundant proteins identified from guanidine-HCl extraction

Table S4: Proteins identified in discovery assay

Table S5: MS 1 precursor ions for clusterin protein

(Provided in Excel Format file)

Table S1. Peptide sequence, transitions, and collision energy for MRM

Accesion	ID	Collision energy	Peptide sequence	Preursor m/z	Product m/z
O15232	MATN3	26.2	AQASGIELYAVGVDR	774.9	1021.53 (y9)892.49 (y8)779.4 (y7)616.34 (y6)446.24 (y4)
O15232	MATN3	23.9	IIDTLDIGPADTR	700.38	957.5 (y9)844.42 (y8)729.39 (y7)616.3 (y6)559.28 (y5)
O15232	MATN3	20.2	VAVVNYASTVK	575.83	980.54 (y9)881.47 (y8)782.4 (y7)668.36 (y6)
O15335	CHAD	23.3	FSDGAFLGVTTLK	678.36	738.35 (b7)878.53 (y8)731.47 (y7)618.38 (y6)
O15335	CHAD	23.4	NQLSSYPSAALSK	683.35	1123.6 (y11)1010.52 (y10)923.48 (y9)836.45 (y8)673.39 (y7)
O15335	CHAD	23	SIPDNAFQSFGR	669.83	1138.53 (y10)1041.47 (y9)926.45 (y8)741.37 (y6)
O15335	CHAD	29.2	YLETLWLDNTNLEK	876.45	1132.56 (y9)946.48 (y8)833.4 (y7)
O75339	CILP1	18	ASVTFLDPR	503.27	847.47 (y7)748.4 (y6)647.35 (y5)
O75339	CILP1	19.7	FAPIVLTMPK	558.83	898.54 (y8)801.49 (y7)688.41 (y6)589.34 (y5)
O75339	CILP1	28	FNPNAIGVPQPYLNK	836.45	813.43 (b8)1015.56 (y9)859.47 (y7)634.36 (y5)
O75339	CILP1	18.3	FYQIEGDR	514.25	717.35 (y6)589.29 (y5)476.21 (y4)
O75339	CILP1	21.3	GTFTLHVPQDTER	500.92	520.28 (b5)844.42 (y7)745.35 (y6)520.24 (y4)
O75339	CILP1	19.4	IVGPLEVNVR	548.33	883.5 (y8)826.48 (y7)729.43 (y6)616.34 (y5)
O75339	CILP1	17.4	LVLTFVDR	481.79	750.41 (y6)637.33 (y5)536.28 (y4)
O75339	CILP1	20.3	TFLVGNLEIR	581.33	913.55 (y8)800.46 (y7)701.39 (y6)
O75339	CILP1	16.3	TGFLSNPR	446.24	733.4 (y6)586.33 (y5)473.25 (y4)
P02458	CO2A1	20.7	DVWKPEPCR	593.79	786.39 (y6)658.3 (y5)432.2 (y3)658.3 (y5)432.2 (y3)
P02458	CO2A1	23.9	GPPGPQGPAGEQGPR	701.35	1247.61 (y13)1150.56 (y12)1093.54 (y11)868.43 (y9)811.41 (y8)
P02458	CO2A1	34	SGDYWIDPNQGCTLDAMK	1035.95	837.34 (b7)1349.58 (y12)1234.56 (y11)895.4 (y8)
P02458	CO2A1	20.5	SLNNQIESIR	587.31	973.51 (y8)859.46 (y7)617.36 (y5)504.28 (y4)
P02751	FINC	26.1	SYTITGLQPGTDYK	772.39	1079.54 (y10)978.49 (y9)680.32 (y6)
P02751	FINC	23.2	WLPSSSPVTGYR	675.35	1050.52 (y10)953.47 (y9)866.44 (y8)692.37 (y6)
P02751	FINC	19	YEVSVYALK	536.29	908.51 (y8)779.47 (y7)680.4 (y6)494.3 (y4)
P07585	PGS2	18.1	NLHALILVNNK	416.92	436.23 (b4)549.31 (b5)587.35 (y5)474.27 (y4)
P07585	PGS2	19.7	VSPGAFTPLVK	558.33	929.55 (y9)832.49 (y8)775.47 (y7)704.43 (y6)
P07585	PGS2	21.4	VVQCSDLGLDK	617.31	1035.48 (y9)907.42 (y8)747.39 (y7)
P07996	TSP1	23.8	FVFGTTPEDILR	697.87	1148.59 (y10)1001.53 (y9)843.46 (y7)742.41 (y6)
P07996	TSP1	18.4	GPDPSSPAFR	515.75	761.39 (y7)664.34 (y6)577.31 (y5)490.28 (y4)
P07996	TSP1	21	SITLFVQEDR	604.32	1007.52 (y8)793.38 (y6)646.32 (y5)547.25 (y4)
P08493	MGP	22.1	NANTFISPQQR	638.33	875.47 (y7)728.4 (y6)615.32 (y5)528.29 (y4)
P08493	MGP	26.3	YAMVYGYNAAYNR	778.35	1091.49 (y9)928.43 (y8)871.41 (y7)708.34 (y6)
P09486	SPRC	20.4	APLIPMEHCTTR	475.9	1031.44 (y8)803.35 (y6)674.3 (y5)537.24 (y4)516.22 (y8)
P09486	SPRC	20.3	LEAGDHPVELLAR	473.92	797.49 (y7)700.44 (y6)601.37 (y5)589.32 (y11)
P09486	SPRC	19.5	NVLVTLYER	553.81	893.51 (y7)780.43 (y6)681.36 (y5)
P10451	OSTP	25.7	AIPVAQDLNAPSDWDSR	927.95	1474.66 (y13)1275.56 (y11)1160.53 (y10)1047.45 (y9)933.41 (y8)862.37 (y7)993.54 (b10)
P10451	OSTP	17.4	GDSVVYGLR	483.26	793.46 (y7)706.42 (y6)607.36 (y5)508.29 (y4)345.22 (y3)
P10451	OSTP	29.9	YPDAVATWLNPDPSQK	901.44	1256.63 (y11)1185.59 (y10)671.34 (y6)459.26 (y4)
P10915	HPLN1	16.6	DPTAFGSGIHK	377.19	745.4 (y7)598.33 (y6)541.31 (y5)454.28 (y4)
P10915	HPLN1	17.3	FYYLIHPTK	394.55	708.44 (y6)595.36 (y5)482.27 (y4)345.21 (y3)
P10915	HPLN1	18.2	VGQIFAAWK	510.29	920.5 (y8)735.42 (y6)622.33 (y5)475.27 (y4)
P12109	CO6A1	23.2	GLEQLLVGGSHLK	675.89	923.57 (y9)810.48 (y8)697.4 (y7)598.33 (y6)
P12109	CO6A1	18.6	LSIIATDHTYR	430.57	976.48 (y8)863.4 (y7)792.36 (y6)576.29 (y4)
P12109	CO6A1	24.6	TAEYDVAYGESHLFR	586.61	1079.53 (y9)1008.49 (y8)845.43 (y7)659.36 (y5)
P12111	CO6A3	24	LSDAGITPLFLTR	702.4	1017.61 (y9)960.59 (y8)847.5 (y7)746.46 (y6)
P12111	CO6A3	24.4	SDDEVDDPAVELK	716.33	985.52 (y9)886.45 (y8)771.42 (y7)656.4 (y6)
P12111	CO6A3	24.8	SLDEISQPAQELK	729.38	1257.63 (y11)1013.56 (y9)900.48 (y8)813.45 (y7)685.39 (y6)
P13611	CSPG2	17.1	FTFEEAAK	471.73	795.39 (y7)694.34 (y6)547.27 (y5)
P13611	CSPG2	22.6	LATVGELQAAWR	657.86	1029.55 (y9)930.48 (y8)873.46 (y7)744.42 (y6)631.33 (y5)

P13611	CSPG2	19.1	LLASDAGLYR	539.8	852.42 (y8)781.38 (y7)694.35 (y6)579.32 (y5)
Accesion	**ID**	**Collision energy**	**Peptide sequence**	**Preursor m/z**	**Product m/z**
P13942	COBA2	18.7	DFSLLTVVR	525.3	787.5 (y7)700.47 (y6)587.39 (y5)474.3 (y4)
P13942	COBA2	19.1	ELECEGGQR	539.24	835.34 (y7)706.29 (y6)546.26 (y5)
P13942	COBA2	31	FLYEDQTGRPQPPSQPVFR	754.71	1152.62 (y10)927.5 (y8)830.45 (y7)1001.49 (y17)919.96 (y16)
P13942	COBA2	16.8	SPQQQPSR	464.24	743.38 (y6)615.32 (y5)487.26 (y4)359.2 (y3)
P16112	PGCA	18	ETWVDAER	503.24	775.37 (y6)589.29 (y5)490.23 (y4)
P16112	PGCA	16.3	GIVFHYR	446.25	721.38 (y5)622.31 (y4)475.24 (y3)
P16112	PGCA	20.4	LEGEVFFATR	584.8	1055.52 (y9)926.47 (y8)740.41 (y6)641.34 (y5)
P16112	PGCA	15.5	TIEGDFR	419.21	736.36 (y6)623.28 (y5)494.24 (y4)
P16112	PGCA	31.1	VSLPNYPAIPSDATLEVQSLR	757.41	1315.69 (y12)945.54 (y8)844.49 (y7)731.4 (y6)
P16112	PGCA	17.8	YEINSLVR	497.27	830.47 (y7)701.43 (y6)588.35 (y5)
P16112	PGCA	15.4	YPIVSPR	416.24	668.41 (y6)571.36 (y5)458.27 (y4)359.2 (y3)
P16112	PGCA	16.9	YTLDFDR	465.22	766.37 (y6)665.33 (y5)552.24 (y4)
P20774	MIME	17.5	ESAYLYAR	486.74	756.4 (y6)685.37 (y5)522.3 (y4)409.22 (y3)
P20774	MIME	18.5	LEGNPIVLGK	520.31	926.53 (y9)797.49 (y8)626.42 (y6)317.22 (y3)
P20774	MIME	30.1	LSLLEELSLAENQLLK	907.02	1128.66 (y10)1015.58 (y9)928.55 (y8)815.46 (y7)
P21810	PGS1	22.6	IQAIELEDLLR	656.88	1071.6 (y9)1000.57 (y8)887.48 (y7)758.44 (y6)
P21810	PGS1	18	LGLGHNQIR	504.29	724.38 (y6)667.36 (y5)530.3 (y4)
P21810	PGS1	16.8	VPSGLPDLK	463.27	666.35 (b7)826.47 (y8)729.41 (y7)642.38 (y6)472.28 (y4)
P21810	PGS1	19.7	VVQCSDLGLK	559.8	920.45 (y8)792.39 (y7)632.36 (y6)
P24821	TENA	16.8	AYAAGFGDR	464.22	693.33 (y7)622.29 (y6)551.26 (y5)494.24 (y4)
P24821	TENA	25.1	EEFWLGLDNLNK	739.37	1072.58 (y9)886.5 (y8)773.42 (y7)603.31 (y5)
P24821	TENA	29.3	GLEPGQEYNVLLTAEK	880.96	1461.76 (y13)1179.63 (y10)1050.58 (y9)887.52 (y8)674.41 (y6)
P24821	TENA	20.6	ITAQGQYELR	589.81	964.48 (y8)893.45 (y7)765.39 (y6)708.37 (y5)
P35443	TSP4	23.1	AFAGPSQKPETIELR	548.63	985.57 (y8)857.47 (y7)631.38 (y5)713.39 (y13)
P35443	TSP4	32.6	DVDIDSYPDEELPCSAR	990.93	808.34 (b7)1336.58 (y11)1173.52 (y10)703.36 (y6)590.27 (y5)
P35443	TSP4	28.1	SSATIFGLYSSTDNSK	839.4	1218.56 (y11)1071.5 (y10)901.39 (y8)738.33 (y7)
P35443	TSP4	23.2	YVPNSGQEDADR	675.8	1088.46 (y10)991.41 (y9)877.36 (y8)790.33 (y7)
P49747	COMP	21.7	DTDLDGFPDEK	626.27	920.44 (y8)807.35 (y7)692.32 (y6)488.24 (y4)
P49747	COMP	25.2	ELQETNAALQDVR	743.88	987.52 (y9)886.47 (y8)772.43 (y7)701.39 (y6)630.36 (y5)
P49747	COMP	22.6	LVPNPGQEDADR	655.82	1098.48 (y10)887.39 (y8)790.33 (y7)605.25 (y5)
P49747	COMP	18.4	SSTGPGEQLR	516.26	857.4 (b9)857.45 (y8)756.4 (y7)699.38 (y6)602.33 (y5)
P51884	LUM	18.3	FNALQYLR	512.78	877.49 (y7)763.45 (y6)692.41 (y5)579.32 (y4)
P51884	LUM	21.3	ISNIPDEYFK	613.31	1112.53 (y9)1025.49 (y8)798.37 (y6)
P51884	LUM	18.7	SLEDLQLTHNK	433.23	740.4 (y6)612.35 (y5)499.26 (y4)398.21 (y3)
P51888	PRELP	22.5	LENLLLLDLQHNR	530.97	1008.56 (y8)895.47 (y7)782.39 (y6)667.36 (y5)
P51888	PRELP	23.2	NQLEEVPSALPR	676.86	1110.62 (y10)997.53 (y9)868.49 (y8)739.45 (y7)640.38 (y6)
P51888	PRELP	22.6	VPTAIHQLYLDSNK	533.62	852.45 (y7)739.36 (y6)576.3 (y5)463.21 (y4)348.19 (y3)
P98160	PGBM	30.1	EVSEAVVDTLESEYLK	905.95	516.23 (b5)1196.6 (y10)1097.54 (y9)
P98160	PGBM	20.6	IAHVELADAGQYR	481.58	550.3 (b5)663.38 (b6)709.33 (y6)594.3 (y5)523.26 (y4)
P98160	PGBM	19.8	LEGDTLIIPR	563.83	884.52 (y8)827.5 (y7)712.47 (y6)611.42 (y5)
Q06828	FMOD	23.3	ELHLDHNQISR	681.35	982.51 (y8)869.42 (y7)754.4 (y6)617.34 (y5)
Q06828	FMOD	27.1	IPPVNTNLENLYLQGNR	652.35	736.4 (b7)750.39 (y6)587.33 (y5)474.24 (y4)
Q06828	FMOD	22.4	SAMPADAPLCLR	651.32	1012.52 (y9)844.43 (y7)729.41 (y6)658.37 (y5)
Q06828	FMOD	17.6	YLPFVPSR	489.77	702.39 (y6)605.34 (y5)458.27 (y4)359.2 (y3)
Q07507	DERM	20	GATTTFSAVER	570.29	910.46 (y8)809.42 (y7)708.37 (y6)
Q07507	DERM	18.3	YFESVLDR	514.76	527.21 (b4)718.37 (y6)589.33 (y5)
Q8IUL8	CILP2	22.5	DLTSAASAPSDLR	652.33	974.49 (y10)816.42 (y8)745.38 (y7)658.35 (y6)587.31 (y5)
Q8IUL8	CILP2	20.8	EMSEAAQAQAR	596.27	931.46 (y9)715.38 (y7)644.35 (y6)573.31 (y5)445.25 (y4)
Q8IUL8	CILP2	22.7	FVDSDGELAPLR	659.84	1072.53 (y10)957.5 (y9)755.44 (y7)456.29 (y4)385.26 (y3)

Accesion	ID	Collision energy	Peptide sequence	Preursor m/z	Product m/z
Q8IUL8	CILP2	21.2	IQGPQEYMVR	610.81	979.47 (y8)922.45 (y7)697.33 (y5)568.29 (y4)
Q8IUL8	CILP2	23.3	LLESPATALGDIR	678.38	1129.58 (y11)1000.54 (y10)913.51 (y9)745.42 (y7)
Q8IUL8	CILP2	24	TTDWALPSAVGER	701.85	899.49 (y9)828.46 (y8)715.37 (y7)
Q8IUL8	CILP2	20.1	VFLVGNVEIR	573.34	899.53 (y8)786.45 (y7)687.38 (y6)
Q8IUL8	CILP2	19.6	VVAADSGEPLR	557.3	915.45 (y9)844.42 (y8)773.38 (y7)658.35 (y6)
Q92743	HTRA1	16.1	LPVLLLGR	440.8	767.51 (y7)670.46 (y6)571.39 (y5)458.31 (y4)
Q92743	HTRA1	22.5	VTAGISFAIPSDK	653.36	1105.59 (y11)864.45 (y8)777.41 (y7)446.22 (y4)
Q92743	HTRA1	20.9	YNFIADVVEK	599.31	920.51 (y8)773.44 (y7)660.36 (y6)
Q92954	PRG4	20	DAGYPKPIFK	568.31	949.55 (y8)729.47 (y6)632.41 (y5)504.32 (y4)
Q92954	PRG4	23.5	DQYYNIDVPSR	685.32	1126.55 (y9)963.49 (y8)800.43 (y7)359.2 (y3)
Q92954	PRG4	27.7	GLPNVVTSAISLPNIR	825.98	1170.68 (y11)1071.62 (y10)812.5 (y7)699.41 (y6)
Q92954	PRG4	20.7	KPDGYDYYAFSK	485.23	676.29 (b6)839.36 (b7)615.31 (y5)452.25 (y4)
Q92954	PRG4	25.9	RPALNYPVYGETTQVR	622	911.51 (b8)953.47 (y8)790.41 (y7)733.38 (y6)
Q99983	OMD	16.6	IDYGVFAK	456.74	799.4 (y7)684.37 (y6)521.31 (y5)
Q99983	OMD	20.2	LLLGYNEISK	575.33	923.48 (y8)810.4 (y7)753.38 (y6)590.31 (y5)
Q9BXN1	ASPN	20.6	ISTVELEDFK	590.81	980.49 (y8)879.45 (y7)780.38 (y6)651.33 (y5)
Q9BXN1	ASPN	27.4	LYLSHNQLSEIPLNLPK	660.37	856.43 (b7)1185.59 (b10)1010.59 (y9)794.51 (y7)681.43 (y6)
Q9BXN1	ASPN	26.2	SLYSAISLFNNPVK	776.92	1031.59 (y9)918.5 (y8)831.47 (y7)718.39 (y6)343.23 (y3)
Q9BXN1	ASPN	22.8	YWEMQPATFR	664.81	979.47 (y8)850.42 (y7)719.38 (y6)591.32 (y5)

Table S2. Quantification results of MRM experiments

Accession	Protein Name	Peptide Sequence	Gu-HCl	Gu-HCl + Surfactant	In Situ digestion + Ultrafiltration	In Situ digestion
Q9H1Z8	AUGN	HYDEDSAIGPR	NA	NA	NA	NA
Q9H1Z8	AUGN	FEDDITYWLNR	NA	NA	NA	NA
Q9BXN1	ASPN	YWEMQPATFR	NA	NA	NA	NA
Q9BXN1	ASPN	SLYSAISLFNNPVK	NA	NA	NA	NA
Q9BXN1	ASPN	LYLSHNQLSEIPLNLPK	NA	NA	NA	NA
Q9BXN1	ASPN	ISTVELEDFK	2.7E+04	1.2E+05	8.4E+03	2.4E+03
Q99983	OMD	LLLGYNEISK	2.5E+04	9.2E+04	1.5E+05	1.1E+05
Q99983	OMD	IDYGVFAK	2.4E+04	8.5E+04	1.1E+05	1.0E+05
Q92954	PRG4	RPALNYPVYGETTQVR	2.6E+04	5.0E+04	4.9E+04	NA
Q92954	PRG4	KPDGYDYYAFSK	NA	NA	NA	NA
Q92954	PRG4	GLPNVVTSAISLPNIR	NA	NA	NA	NA
Q92954	PRG4	DQYYNIDVPSR	9.4E+04	1.5E+05	2.2E+05	2.2E+05
Q92954	PRG4	DAGYPKPIFK	2.7E+04	9.4E+04	1.5E+05	1.0E+05
Q92743	HTRA1	YNFIADVVEK	3.2E+04	1.5E+05	3.2E+04	NA
Q92743	HTRA1	VTAGISFAIPSDK	1.9E+04	1.2E+05	3.1E+05	NA
Q92743	HTRA1	LPVLLLGR	6.0E+04	3.9E+05	2.6E+05	NA
Q8IUL8	CILP2	VVAADSGEPLR	3.3E+04	6.3E+04	1.4E+05	8.8E+04
Q8IUL8	CILP2	VFLVGNVEIR	NA	NA	7.2E+06	NA
Q8IUL8	CILP2	TTDWALPSAVGER	1.7E+04	3.0E+04	8.9E+04	3.8E+04
Q8IUL8	CILP2	LLESPATALGDIR	3.4E+05	6.7E+05	5.2E+06	NA
Q8IUL8	CILP2	IQGPQEYMVR	5.0E+03	3.3E+04	2.0E+05	1.0E+05
Q8IUL8	CILP2	FVDSDGELAPLR	2.0E+04	4.8E+04	4.2E+04	3.9E+04
Q8IUL8	CILP2	EMSEAAQAQAR	9.2E+03	2.8E+04	1.1E+05	6.5E+04
Q8IUL8	CILP2	DLTSAASAPSDLR	2.6E+04	5.9E+04	3.7E+04	3.0E+04
Q6NUI6	CHADL	ITEVSLGALGPAR	NA	NA	NA	NA
Q6NUI6	CHADL	FLQVPGAALR	1.3E+04	2.0E+04	3.7E+04	NA
Q6NUI6	CHADL	ELLLDGGALQALGPR	NA	NA	NA	NA
Q6NUI6	CHADL	AAAAVFEDCPGWAAR	NA	NA	NA	NA
Q07507	DERM	YFESVLDR	4.3E+04	2.7E+05	7.5E+04	5.4E+04
Q07507	DERM	GATTTFSAVER	2.2E+04	1.3E+05	2.1E+05	1.5E+05
Q06828	FMOD	YLPFVPSR	5.9E+06	2.7E+07	2.2E+07	9.3E+06
Q06828	FMOD	SAMPADAPLCLR	6.6E+04	1.2E+06	2.0E+05	1.4E+05
Q06828	FMOD	IPPVNTNLENLYLQGNR	1.6E+06	8.6E+06	5.2E+06	NA
Q06828	FMOD	ELHLDHNQISR	NA	2.4E+05	8.3E+05	7.1E+05
P98160	PGBM	LEGDTLIIPR	2.3E+04	5.3E+04	1.0E+05	6.9E+04
P98160	PGBM	IAHVELADAGQYR	2.0E+04	4.9E+04	7.2E+04	NA
P98160	PGBM	EVSEAVVDTLESEYLK	NA	NA	NA	NA
P51888	PRELP	VPTAIHQLYLDSNK	8.5E+05	3.4E+06	NA	NA
P51888	PRELP	NQLEEVPSALPR	1.8E+07	6.1E+07	2.9E+07	2.7E+07
P51888	PRELP	LENLLLLDLQHNR	NA	NA	1.3E+05	NA
P51884	LUM	SLEDLQLTHNK	2.4E+05	1.4E+06	3.9E+05	2.0E+05
P51884	LUM	ISNIPDEYFK	1.5E+06	9.2E+06	2.7E+05	2.3E+05
P51884	LUM	FNALQYLR	1.7E+06	5.9E+06	9.2E+05	NA
P49747	COMP	SSTGPGEQLR	3.9E+06	8.0E+06	4.3E+06	3.5E+06
P49747	COMP	LVPNPGQEDADR	1.3E+06	1.5E+06	2.2E+05	1.5E+05
P49747	COMP	ELQETNAALQDVR	2.6E+06	5.0E+06	4.5E+06	3.6E+06
P49747	COMP	DTDLDGFPDEK	3.5E+06	5.5E+06	4.4E+06	3.0E+06
P35443	TSP4	YVPNSGQEDADR	1.0E+04	1.4E+04	NA	NA
P35443	TSP4	SSATIFGLYSSTDNSK	NA	2.2E+04	7.1E+04	NA
P35443	TSP4	DVDIDSYPDEELPCSAR	4.3E+04	1.3E+05	1.7E+05	1.2E+05
P35443	TSP4	AFAGPSQKPETIELR	1.9E+04	6.0E+04	8.7E+04	4.3E+04
P24821	TENA	ITAQGQYELR	3.7E+04	1.3E+05	3.5E+05	1.9E+05
P24821	TENA	GLEPGQEYNVLLTAEK	1.9E+04	4.7E+04	1.5E+05	NA
P24821	TENA	EEFWLGLDNLNK	NA	NA	NA	NA
P24821	TENA	AYAAGFGDR	2.1E+05	5.3E+05	5.2E+05	4.1E+05
P22105	TENX	LGPISADSTTAPLEK	3.4E+04	7.2E+04	2.1E+05	1.3E+05
P22105	TENX	ILISGLEPSTPYR	2.2E+04	7.6E+04	2.8E+05	NA
P22105	TENX	GLAPGQEYQVTVR	NA	1.4E+04	8.4E+04	4.8E+04
P21941	MATN1	VGIVFTDGR	NA	NA	NA	NA
P21941	MATN1	LAQVGLVQYSSSVR	NA	NA	NA	NA
P21815	SIAL	HAYFYPHLK	NA	NA	NA	NA
P21815	SIAL	AYEDEYSYFK	NA	NA	NA	NA
P21810	PGS1	VVQCSDLGLK	7.3E+06	2.8E+07	1.4E+07	9.7E+06
P21810	PGS1	VPSGLPDLK	1.6E+07	4.4E+07	1.9E+07	1.6E+07
P21810	PGS1	LGLGHNQIR	8.1E+05	3.3E+06	1.0E+06	1.0E+06
P21810	PGS1	IQAIELEDLLR	7.9E+06	2.9E+07	5.2E+06	NA

P20849	CO9A1	VIQEHFAEMAASLK	NA	NA	NA	NA
P20849	CO9A1	VIQEHFAEMAASLK	NA	NA	NA	NA
P20849	CO9A1	ETCHELPAR	NA	NA	6.7E+04	5.8E+04
P20774	MIME	LSLLEELSLAENQLLK	3.0E+04	1.4E+05	3.3E+05	1.5E+05
P20774	MIME	LEGNPIVLGK	1.5E+06	8.3E+06	1.5E+06	1.0E+06
P20774	MIME	ESAYLYAR	2.2E+06	1.3E+07	7.0E+06	5.7E+06
P16112	PGCA	YTLDFDR	4.0E+07	7.5E+07	1.6E+07	1.4E+07
P16112	PGCA	YPIVSPR	6.3E+07	1.0E+08	3.8E+07	3.6E+07
P16112	PGCA	YEINSLVR	1.8E+06	3.0E+06	1.2E+06	7.7E+05
P16112	PGCA	VSLPNYPAIPSDATLEVQSLR	1.3E+06	3.1E+06	1.6E+06	NA
P16112	PGCA	TIEGDFR	6.2E+06	9.5E+06	4.7E+06	3.5E+06
P16112	PGCA	LEGEVFFATR	NA	NA	NA	NA
P16112	PGCA	GIVFHYR	5.8E+06	1.7E+07	5.0E+06	1.2E+06
P16112	PGCA	ETWVDAER	2.6E+06	4.0E+06	3.6E+05	2.0E+05
P13942	COBA2	SPQQQPSR	NA	NA	NA	NA
P13942	COBA2	FLYEDQTGRPQPPSQPVFR	7.3E+04	1.2E+05	4.4E+04	NA
P13942	COBA2	ELECEGGQR	NA	2.2E+04	NA	NA
P13942	COBA2	DFSLLTVVR	1.2E+04	1.2E+05	1.4E+04	NA
P13611	CSPG2	LLASDAGLYR	1.7E+04	3.6E+04	2.8E+04	1.9E+04
P13611	CSPG2	LATVGELQAAWR	NA	NA	NA	NA
P13611	CSPG2	FTFEEAAK	NA	NA	NA	NA
P12111	CO6A3	SLDEISQPAQELK	1.2E+05	3.6E+05	6.2E+05	4.0E+05
P12111	CO6A3	SDDEVDDPAVELK	8.6E+04	2.2E+05	1.3E+06	9.1E+05
P12111	CO6A3	LSDAGITPLFLTR	4.6E+04	1.5E+05	3.0E+06	NA
P12109	CO6A1	TAEYDVAYGESHLFR	2.6E+04	8.9E+04	1.2E+06	NA
P12109	CO6A1	LSIIATDHTYR	6.1E+04	1.5E+05	1.0E+06	2.5E+05
P12109	CO6A1	GLEQLLVGGSHLK	NA	NA	2.9E+05	NA
P10915	HPLN1	VGQIFAAWK	NA	2.7E+06	4.1E+06	NA
P10915	HPLN1	FYYLIHPTK	NA	1.0E+05	6.1E+05	NA
P10915	HPLN1	DPTAFGSGIHK	2.7E+05	1.4E+06	1.4E+05	1.1E+05
P10451	OSTP	YPDAVATWLNPDPSQK	NA	NA	NA	NA
P10451	OSTP	GDSVVYGLR	NA	NA	NA	NA
P10451	OSTP	AIPVAQDLNAPSDWDSR	NA	NA	NA	NA
P09486	SPRC	NVLVTLYER	NA	NA	NA	NA
P09486	SPRC	LEAGDHPVELLAR	NA	NA	NA	NA
P09486	SPRC	APLIPMEHCTTR	NA	NA	NA	NA
P08493	MGP	YAMVYGYNAAYNR	NA	NA	NA	NA
P08493	MGP	NANTFISPQQR	1.6E+05	1.6E+05	5.1E+05	5.2E+05
P07996	TSP1	SITLFVQEDR	2.0E+05	3.9E+05	3.8E+05	NA
P07996	TSP1	GPDPSSPAFR	2.8E+05	5.7E+05	3.4E+05	3.0E+05
P07996	TSP1	FVFGTTPEDILR	1.2E+05	2.4E+05	1.5E+05	NA
P07585	PGS2	VVQCSDLGLDK	3.6E+06	1.3E+07	1.9E+06	1.4E+06
P07585	PGS2	VSPGAFTPLVK	5.1E+06	1.6E+07	1.0E+07	8.1E+06
P07585	PGS2	NLHALILVNNK	1.6E+06	4.0E+06	1.6E+06	NA
P02751	FINC	YEVSVYALK	3.5E+05	1.1E+06	2.7E+06	5.9E+05
P02751	FINC	WLPSSSPVTGYR	2.0E+05	4.6E+05	3.3E+06	2.4E+06
P02751	FINC	SYTITGLQPGTDYK	1.2E+06	2.4E+06	4.9E+06	4.1E+06
P02461	CO3A1	QQEAVEGGCSHLGQSYADR	NA	9.5E+03	7.4E+04	4.7E+04
P02461	CO3A1	QQEAVEGGCSHLGQSYADR	2.6E+03	1.0E+04	1.1E+05	6.0E+04
P02461	CO3A1	GPVGPSGPPGK	7.0E+05	1.7E+06	5.5E+07	5.2E+07
P02461	CO3A1	GPVGPSGPPGK	1.1E+06	2.3E+06	8.8E+07	8.0E+07
P02458	CO2A1	SLNNQIESIR	7.2E+04	1.7E+05	7.3E+04	4.1E+04
P02458	CO2A1	SGDYWIDPNQGCTLDAMK	NA	NA	NA	NA
P02458	CO2A1	GPPGPQGPAGEQGPR	NA	NA	NA	NA
P02458	CO2A1	DVWKPEPCR	NA	NA	NA	NA
P02458	CO2A1	DVWKPEPCR	NA	NA	NA	NA
O75339	CILP1	TGFLSNPR	1.2E+06	2.5E+06	1.7E+07	1.5E+07
O75339	CILP1	TFLVGNLEIR	5.2E+05	1.2E+06	7.9E+06	NA
O75339	CILP1	LVLTFVDR	1.5E+05	5.1E+05	2.3E+04	NA
O75339	CILP1	IVGPLEVNVR	7.4E+05	2.1E+06	1.4E+07	1.1E+07
O75339	CILP1	GTFTLHVPQDTER	3.9E+04	1.3E+05	NA	NA
O75339	CILP1	FYQIEGDR	7.3E+05	1.3E+06	1.1E+06	9.5E+05
O75339	CILP1	FNPNAIGVPQPYLNK	5.1E+04	1.1E+05	3.0E+06	1.8E+06
O75339	CILP1	FAPIVLTMPK	NA	NA	NA	NA
O75339	CILP1	ASVTFLDPR	5.7E+04	1.5E+05	8.2E+04	6.8E+04
O15335	CHAD	YLETLWLDNTNLEK	NA	9.7E+04	4.9E+04	NA
O15335	CHAD	SIPDNAFQSFGR	1.7E+05	9.1E+05	5.8E+05	3.9E+05
O15335	CHAD	NQLSSYPSAALSK	6.0E+05	2.6E+06	9.4E+05	7.9E+05
O15335	CHAD	FSDGAFLGVTTLK	1.8E+05	9.1E+05	4.8E+05	NA

O15232	MATN3	VAVVNYASTVK	5.0E+04	2.7E+05	4.3E+05	3.3E+05
O15232	MATN3	IIDTLDIGPADTR	1.2E+05	3.7E+05	2.5E+05	2.1E+05
O15232	MATN3	AQASGIELYAVGVDR	4.3E+04	8.7E+04	1.5E+05	NA

Table S3. Less abundant proteins identified from guanidine-HCl extraction

Accession	Gene ID	Description	MW [kDa]	Peptides #	Coverage (%)
P02768	ALB	Serum albumin	69.3	34	56.3
P01024	C3	Complement C3	187.0	26	19.2
P04264	KRT1	Keratin, type II cytoskeletal 1	66.0	26	38.5
P08670	VIM	Vimentin	53.6	22	50.0
P35908	KRT2	Keratin, type II cytoskeletal 2 epidermal	65.4	21	39.4
P13645	KRT10	Keratin, type I cytoskeletal 10	58.8	20	37.0
P35527	KRT9	Keratin, type I cytoskeletal 9	62.0	19	34.5
O75339	CILP	Cartilage intermediate layer protein 1	132.5	18	18.2
P07996	THBS1	Thrombospondin-1	129.3	18	20.4
P02787	TF	Serotransferrin	77.0	17	30.9
P13647	KRT5	Keratin, type II cytoskeletal 5	62.3	16	25.9
P51888	PRELP	Prolargin	43.8	14	41.6
P21810	BGN	Biglycan	41.6	12	38.9
P08254	MMP3	Stromelysin-1	53.9	12	24.3
P00558	PGK1	Phosphoglycerate kinase 1	44.6	12	37.9
P24821	TNC	Tenascin	240.7	12	7.6
P06733	ENO1	Alpha-enolase	47.1	11	32.3
P02533	KRT14	Keratin, type I cytoskeletal 14	51.5	11	26.3
P14618	PKM	Pyruvate kinase PKM	57.9	11	27.9
P07355	ANXA2	Annexin A2	38.6	9	31.3
P06396	GSN	Gelsolin	85.6	9	17.4
P10915	HAPLN1	Hyaluronan and proteoglycan link protein 1	40.1	9	32.2
P02545	LMNA	Prelamin-A/C	74.1	9	15.2
P51884	LUM	Lumican	38.4	9	32.2
P10909	CLU	Clusterin	52.5	8	19.8
P07585	DCN	Decorin	39.7	8	22.8
P02675	FGB	Fibrinogen beta chain	55.9	8	17.9
P02538	KRT6A	Keratin, type II cytoskeletal 6A	60.0	8	12.9
P04259	KRT6B	Keratin, type II cytoskeletal 6B	60.0	8	11.7
P60709	ACTB	Actin, cytoplasmic 1	41.7	7	22.9
P02647	APOA1	Apolipoprotein A-I	30.8	7	30.0
O15335	CHAD	Chondroadherin	40.5	7	21.7
Q06828	FMOD	Fibromodulin	43.2	7	21.0
P01857	IGHG1	Ig gamma-1 chain C region	36.1	7	26.4
P08779	KRT16	Keratin, type I cytoskeletal 16	51.2	7	14.6
P20774	OGN	Mimecan	33.9	7	25.2
P01009	SERPINA1	Alpha-1-antitrypsin	46.7	7	14.6
O60687	SRPX2	Sushi repeat-containing protein SRPX2	52.9	7	20.6
P35443	THBS4	Thrombospondin-4	105.8	7	11.4
P0C0L4	C4A	Complement C4-A	192.7	6	4.4
P00751	CFB	Complement factor B	85.5	6	11.0
P08603	CFH	Complement factor H	139.0	6	6.6
P00738	HP	Haptoglobin	45.2	6	18.0
P00338	LDHA	L-lactate dehydrogenase A chain	36.7	6	19.3
Q08431	MFGE8	Lactadherin	43.1	6	19.9
P22105	TNXB	Tenascin-X	464.0	6	3.3
P04083	ANXA1	Annexin A1	38.7	5	18.8
P02743	APCS	Serum amyloid P-component	25.4	5	23.8
Q8IUL8	CILP2	Cartilage intermediate layer protein 2	126.2	5	5.4
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	36.0	5	23.3
P68871	HBB	Hemoglobin subunit beta	16.0	5	46.9
P01859	IGHG2	Ig gamma-2 chain C region	35.9	5	16.6
P01860	IGHG3	Ig gamma-3 chain C region	41.3	5	14.3
Q15113	PCOLCE	Procollagen C-endopeptidase enhancer 1	47.9	5	16.5
P36955	SERPINF1	Pigment epithelium-derived factor	46.3	5	13.6
P08294	SOD3	Extracellular superoxide dismutase [Cu-Zn]	25.8	5	30.0
P02760	AMBP	Protein AMBP	39.0	4	15.9
P02649	APOE	Apolipoprotein E	36.1	4	13.2
Q9BXN1	ASPN	Asporin	43.4	4	11.1
P05452	CLEC3B	Tetranectin	22.5	4	24.3

Q60814	HIST1H2BK	Histone H2B type 1-K	13.9	4	34.9

Accession	Gene ID	Description	MW [kDa]	Peptides #	Coverage (%)
P01876	IGHA1	Ig alpha-1 chain C region	37.6	4	13.0
Q5XKE5	KRT79	Keratin, type II cytoskeletal 79	57.8	4	6.9
P61626	LYZ	Lysozyme C	16.5	4	26.4
O15232	MATN3	Matrilin-3	52.8	4	11.9
P04004	VTN	Vitronectin	54.3	4	11.1
Q562R1	ACTBL2	Beta-actin-like protein 2	42.0	3	11.2
P36222	CHI3L1	Chitinase-3-like protein 1	42.6	3	11.5
P02679	FGG	Fibrinogen gamma chain	51.5	3	7.7
P69905	HBA2	Hemoglobin subunit alpha	15.2	3	25.4
P16402	HIST1H1D	Histone H1.3	22.3	3	14.5
P02790	HPX	Hemopexin	51.6	3	9.3
P08107	HSPA1B	Heat shock 70 kDa protein 1A/1B	70.0	3	6.1
P11021	HSPA5	78 kDa glucose-regulated protein	72.3	3	6.3
P11142	HSPA8	Heat shock cognate 71 kDa protein	70.9	3	6.2
P01834	IGKC	Ig kappa chain C region	11.6	3	51.9
P13646	KRT13	Keratin, type I cytoskeletal 13	49.6	3	6.6
Q86Y46	KRT73	Keratin, type II cytoskeletal 73	58.9	3	5.0
Q06830	PRDX1	Peroxiredoxin-1	22.1	3	15.6
P34096	RNASE4	Ribonuclease 4	16.8	3	19.7
P01011	SERPINA3	Alpha-1-antichymotrypsin	47.6	3	10.9
P01008	SERPINC1	Antithrombin-III	52.6	3	8.8
Q15582	TGFBI	Transforming growth factor-beta-induced protein ig-h3	74.6	3	5.3
Q7Z7G0	ABI3BP	Target of Nesh-SH3	118.6	2	2.1
P03950	ANG	Angiogenin	16.5	2	10.9
P08758	ANXA5	Annexin A5	35.9	2	5.3
P81605	DCD	Dermcidin	11.3	2	12.7
Q05639	EEF1A2	Elongation factor 1-alpha 2	50.4	2	4.1
P02671	FGA	Fibrinogen alpha chain	94.9	2	3.3
P02794	FTH1	Ferritin heavy chain	21.2	2	12.0
P02792	FTL	Ferritin light chain	20.0	2	12.6
P16104	H2AFX	Histone H2AX	15.1	2	11.2
P02042	HBD	Hemoglobin subunit delta	16.0	2	17.0
P68431	HIST1H3F	Histone H3.1	15.4	2	11.8
P62805	HIST1H4A	Histone H4	11.4	2	21.4
P08238	HSP90AB1	Heat shock protein HSP 90-beta	83.2	2	3.6
P14625	HSP90B1	Endoplasmin	92.4	2	3.2
Q92743	HTRA1	Serine protease HTRA1	51.3	2	4.6
P0CF74	IGLC6	Ig lambda-6 chain C region	11.3	2	32.1
P12036	NEFH	Neurofilament heavy polypeptide	112.4	2	1.7
Q9UKZ9	PCOLCE2	Procollagen C-endopeptidase enhancer 2	45.7	2	6.0
P14555	PLA2G2A	Phospholipase A2, membrane associated	16.1	2	19.4
P62937	PPIA	Peptidyl-prolyl cis-trans isomerase A	18.0	2	10.9
P07998	RNASE1	Ribonuclease pancreatic	17.6	2	17.9
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	18.0	2	16.0
P05155	SERPING1	Plasma protease C1 inhibitor	55.1	2	4.2
P01620		Ig kappa chain V-III region SIE	11.8	2	24.8
Q8IUX7	AEBP1	Adipocyte enhancer-binding protein 1	130.8	1	0.9
P00568	AK1	Adenylate kinase isoenzyme 1	21.6	1	5.2
P04075	ALDOA	Fructose-bisphosphate aldolase A	39.4	1	3.8
P09972	ALDOC	Fructose-bisphosphate aldolase C	39.4	1	6.3
P09525	ANXA4	Annexin A4	35.9	1	3.8
P06727	APOA4	Apolipoprotein A-IV	45.4	1	2.8
P02746	C1QB	Complement C1q subcomponent subunit B	26.7	1	5.5
P00746	CFD	Complement factor D	27.0	1	8.7
Q9Y240	CLEC11A	C-type lectin domain family 11 member A	35.7	1	2.8
P13942	COL11A2	Collagen alpha-2(XI) chain	171.7	1	0.6
P05997	COL5A2	Collagen alpha-2(V) chain	144.8	1	1.0
Q14050	COL9A3	Collagen alpha-3(IX) chain	63.6	1	1.8
Q8IWT3	CUL9	Cullin-9	281.0	1	1.7
Q07507	DPT	Dermatopontin	24.0	1	4.0

P23142	FBLN1	Fibulin-1	77.2	1	1.7
Accession	**Gene ID**	**Description**	**MW [kDa]**	**Peptides #**	**Coverage (%)**
Q9BYJ0	FGFBP2	Fibroblast growth factor-binding protein 2	24.6	1	9.0
P21802	FGFR2	Fibroblast growth factor receptor 2	92.0	1	3.7
Q13642	FHL1	Four and a half LIM domains protein 1	36.2	1	3.7
Q5D862	FLG2	Filaggrin-2	247.9	1	0.5
Q92765	FRZB	Secreted frizzled-related protein 3	36.2	1	3.4
P06744	GPI	Glucose-6-phosphate isomerase	63.1	1	1.6
P04196	HRG	Histidine-rich glycoprotein	59.5	1	2.7
Q86YZ3	HRNR	Hornerin	282.2	1	2.8
P98160	HSPG2	Basement membrane-specific heparan sulfate proteoglycan core protein	468.5	1	0.3
P19827	ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1	101.3	1	1.3
P19823	ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2	106.4	1	1.6
Q14624	ITIH4	Inter-alpha-trypsin inhibitor heavy chain H4	103.3	1	1.3
Q5TB80	KIAA1009	Centrosomal protein of 162 kDa	161.8	1	0.4
P01042	KNG1	Kininogen-1	71.9	1	2.2
P07195	LDHB	L-lactate dehydrogenase B chain	36.6	1	4.8
P01593		Ig kappa chain V-I region AG	12.0	1	16.7
P08493	MGP	Matrix Gla protein	12.3	1	10.7
P03956	MMP1	Interstitial collagenase	54.0	1	3.0
P30101	PDIA3	Protein disulfide-isomerase A3	56.7	1	2.2
P07737	PFN1	Profilin-1	15.0	1	10.0
P36871	PGM1	Phosphoglucomutase-1	61.4	1	2.7
P12273	PIP	Prolactin-inducible protein	16.6	1	7.5
Q92954	PRG4	Proteoglycan 4	151.0	1	0.8
P35030	PRSS3	Trypsin-3	32.5	1	4.3
P05387	RPLP2	60S acidic ribosomal protein P2	11.7	1	28.7
P05109	S100A8	Protein S100-A8	10.8	1	22.6
Q9Y3Z3	SAMHD1	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	72.2	1	1.6
A6NMB1	SIGLEC16	Sialic acid-binding Ig-like lectin 16	53.0	1	1.5
Q9H3U7	SMOC2	SPARC-related modular calcium-binding protein 2	49.6	1	4.0
P78539	SRPX	Sushi repeat-containing protein SRPX	51.5	1	2.6
P01033	TIMP1	Metalloproteinase inhibitor 1	23.2	1	5.8
P29401	TKT	Transketolase	67.8	1	2.9
P06753	TPM3	Tropomyosin alpha-3 chain	32.9	1	3.5
Q9Y4K3	TRAF6	TNF receptor-associated factor 6	59.5	1	4.8
P68363	TUBA1B	Tubulin alpha-1B chain	50.1	1	3.3
Q13509	TUBB3	Tubulin beta-3 chain	50.4	1	3.3
Q6UXI7	VIT	Vitrin	73.9	1	1.6
P63104	YWHAZ	14-3-3 protein zeta/delta	27.7	1	5.7
P01597		Ig kappa chain V-I region DEE	11.7	1	16.7
P01772		Ig heavy chain V-III region KOL	13.7	1	12.7
P01766		Ig heavy chain V-III region BRO	13.2	1	15.8
P06326		Ig heavy chain V-I region Mot	13.6	1	9.6
P06310		Ig kappa chain V-II region RPMI 6410	14.7	1	9.8
P01699		Ig lambda chain V-I region VOR	11.5	1	15.3

Table S4. Proteins identified in discovery assay

Accession	Gene ID	Description	MW [kDa]	# Peptides	Coverage (%)
P22105	TNXB	Tenascin-X	464.0	86	30.6
P02751	FN1	Fibronectin	262.5	83	54.9
P12111	COL6A3	Collagen alpha-3(VI) chain	343.5	82	34.8
Q99715	COL12A1	Collagen alpha-1(XII) chain	332.9	65	31.9
P02458	COL2A1	Collagen alpha-1(II) chain	141.7	61	63.0
P24821	TNC	Tenascin	240.7	60	41.9
P01024	C3	Complement C3	187.0	56	42.5
P07996	THBS1	Thrombospondin-1	129.3	50	56.0
P49747	COMP	Cartilage oligomeric matrix protein	82.8	49	77.1
P02461	COL3A1	Collagen alpha-1(III) chain	138.5	49	55.1
P98160	HSPG2	Basement membrane-specific heparan sulfate proteoglycan core protein	468.5	45	16.4
P02768	ALB	Serum albumin	69.3	44	70.1
P16112	ACAN	Aggrecan core protein	250.0	40	19.3
O75339	CILP	Cartilage intermediate layer protein 1	132.5	40	38.9
Q8IUL8	CILP2	Cartilage intermediate layer protein 2	126.2	37	43.5
P02452	COL1A1	Collagen alpha-1(I) chain	138.9	36	43.4
P08603	CFH	Complement factor H	139.0	35	39.6
P08123	COL1A2	Collagen alpha-2(I) chain	129.2	34	47.8
P35555	FBN1	Fibrillin-1	312.0	31	16.3
P02787	TF	Serotransferrin	77.0	30	51.7
P0C0L5	C4B	Complement C4-B	192.6	30	23.3
P0C0L4	C4A	Complement C4-A	192.7	29	22.5
P08670	VIM	Vimentin	53.6	26	57.1
P35443	THBS4	Thrombospondin-4	105.8	25	44.0
P04264	KRT1	Keratin, type II cytoskeletal 1	66.0	24	51.6
P02675	FGB	Fibrinogen beta chain	55.9	24	66.4
P10915	HAPLN1	Hyaluronan and proteoglycan link protein 1	40.1	23	77.7
P12110	COL6A2	Collagen alpha-2(VI) chain	108.5	22	30.7
P02788	LTF	Lactotransferrin	78.1	22	39.3
P12109	COL6A1	Collagen alpha-1(VI) chain	108.5	21	31.3
P14618	PKM	Pyruvate kinase PKM	57.9	21	54.0
O15232	MATN3	Matrilin-3	52.8	21	61.1
P13645	KRT10	Keratin, type I cytoskeletal 10	58.8	21	40.6
P02545	LMNA	Prelamin-A/C	74.1	21	34.3
P02679	FGG	Fibrinogen gamma chain	51.5	20	62.3
Q15582	TGFBI	Transforming growth factor-beta-induced protein ig-h3	74.6	20	41.7
P21810	BGN	Biglycan	41.6	19	60.6
P51888	PRELP	Prolargin	43.8	19	56.3
P10909	CLU	Clusterin	52.5	19	35.6
P02671	FGA	Fibrinogen alpha chain	94.9	19	28.6
Q08431	MFGE8	Lactadherin	43.1	18	58.4
P35527	KRT9	Keratin, type I cytoskeletal 9	62.0	18	53.6
P00747	PLG	Plasminogen	90.5	17	34.1
P04083	ANXA1	Annexin A1	38.7	16	53.8
P08254	MMP3	Stromelysin-1	53.9	16	31.4
P07355	ANXA2	Annexin A2	38.6	16	51.9
Q7Z7G0	ABI3BP	Target of Nesh-SH3	118.6	16	20.1
P13942	COL11A2	Collagen alpha-2(XI) chain	171.7	16	14.7
P23352	KAL1	Anosmin-1	76.1	16	35.3
P07585	DCN	Decorin	39.7	15	54.3
O60687	SRPX2	Sushi repeat-containing protein SRPX2	52.9	15	44.7
P06396	GSN	Gelsolin	85.6	15	33.9
P08253	MMP2	72 kDa type IV collagenase	73.8	15	30.0
Q6UWX4	HHIPL2	HHIP-like protein 2	80.7	15	26.0
P00751	CFB	Complement factor B	85.5	15	25.0
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	36.0	14	57.9
P01857	IGHG1	Ig gamma-1 chain C region	36.1	14	59.4
P06733	ENO1	Alpha-enolase	47.1	14	45.6

Q6UXI7	VIT	Vitrin	73.9	14	26.5
Q8IUX7	AEBP1	Adipocyte enhancer-binding protein 1	130.8	14	15.8

Accession	Gene ID	Description	MW [kDa]	# Peptides	Coverage (%)
P20774	OGN	Mimecan	33.9	13	47.3
P00558	PGK1	Phosphoglycerate kinase 1	44.6	13	46.3
Q9BXN1	ASPN	Asporin	43.4	13	40.3
P11021	HSPA5	78 kDa glucose-regulated protein	72.3	13	26.8
Q09666	AHNAK	Neuroblast differentiation-associated protein AHNAK	628.7	13	11.0
Q06828	FMOD	Fibromodulin	43.2	12	38.6
P51884	LUM	Lumican	38.4	12	37.3
Q15113	PCOLCE	Procollagen C-endopeptidase enhancer 1	47.9	12	36.5
P35908	KRT2	Keratin, type II cytoskeletal 2 epidermal	65.4	12	23.0
P00738	HP	Haptoglobin	45.2	12	36.2
P23142	FBLN1	Fibulin-1	77.2	12	28.3
Q92954	PRG4	Proteoglycan 4	151.0	12	11.7
Q15063	POSTN	Periostin	93.3	12	22.0
O15335	CHAD	Chondroadherin	40.5	11	46.8
P02042	HBD	Hemoglobin subunit delta	16.0	11	85.7
P36955	SERPINF1	Pigment epithelium-derived factor	46.3	11	33.0
Q92743	HTRA1	Serine protease HTRA1	51.3	11	30.8
P04075	ALDOA	Fructose-bisphosphate aldolase A	39.4	11	46.2
Q9H3U7	SMOC2	SPARC-related modular calcium-binding protein 2	49.6	11	31.4
P00734	F2	Prothrombin	70.0	11	23.3
P02538	KRT6A	Keratin, type II cytoskeletal 6A	60.0	11	20.9
P06732	CKM	Creatine kinase M-type	43.1	11	39.6
P08779	KRT16	Keratin, type I cytoskeletal 16	51.2	11	28.1
P05997	COL5A2	Collagen alpha-2(V) chain	144.8	11	14.2
P68871	HBB	Hemoglobin subunit beta	16.0	10	77.6
P01859	IGHG2	Ig gamma-2 chain C region	35.9	10	48.5
Q9UKZ9	PCOLCE2	Procollagen C-endopeptidase enhancer 2	45.7	10	32.0
P01876	IGHA1	Ig alpha-1 chain C region	37.6	10	40.8
P13611	VCAN	Versican core protein	372.6	10	4.4
P02790	HPX	Hemopexin	51.6	10	29.4
P01023	A2M	Alpha-2-macroglobulin	163.2	10	9.2
P01860	IGHG3	Ig gamma-3 chain C region	41.3	9	32.6
O75596	CLEC3A	C-type lectin domain family 3 member A	22.2	9	48.7
P00338	LDHA	L-lactate dehydrogenase A chain	36.7	9	32.5
P60709	ACTB	Actin, cytoplasmic 1	41.7	9	29.1
P07093	SERPINE2	Glia-derived nexin	44.0	9	24.6
P13647	KRT5	Keratin, type II cytoskeletal 5	62.3	9	15.8
P02533	KRT14	Keratin, type I cytoskeletal 14	51.5	9	22.2
P02649	APOE	Apolipoprotein E	36.1	9	34.7
P02748	C9	Complement component C9	63.1	9	21.3
P14625	HSP90B1	Endoplasmin	92.4	9	13.4
P30101	PDIA3	Protein disulfide-isomerase A3	56.7	9	23.4
P61626	LYZ	Lysozyme C	16.5	8	55.4
P01861	IGHG4	Ig gamma-4 chain C region	35.9	8	38.2
Q9BYJ0	FGFBP2	Fibroblast growth factor-binding protein 2	24.6	8	48.9
P04004	VTN	Vitronectin	54.3	8	22.2
P05452	CLEC3B	Tetranectin	22.5	8	42.6
P01009	SERPINA1	Alpha-1-antitrypsin	46.7	8	26.8
P04259	KRT6B	Keratin, type II cytoskeletal 6B	60.0	8	14.5
P68032	ACTC1	Actin, alpha cardiac muscle 1	42.0	8	27.3
P11142	HSPA8	Heat shock cognate 71 kDa protein	70.9	8	16.6
P36222	CHI3L1	Chitinase-3-like protein 1	42.6	8	26.4
P19827	ITIH1	Inter-alpha-trypsin inhibitor heavy chain H1	101.3	8	13.7
Q76M96	CCDC80	Coiled-coil domain-containing protein 80	108.1	8	11.7
P17213	BPI	Bactericidal permeability-increasing protein	53.9	8	24.4
Q9UKU9	ANGPTL2	Angiopoietin-related protein 2	57.1	8	19.9
P55107	GDF10	Bone morphogenetic protein 3B	53.1	8	23.0
P00450	CP	Ceruloplasmin	122.1	8	10.0
Q12805	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	54.6	8	19.7

P06727	APOA4	Apolipoprotein A-IV	45.4	8	26.0
P19823	ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2	106.4	8	12.2

Accession	**Gene ID**	**Description**	**MW [kDa]**	**# Peptides**	**Coverage (%)**
P08294	SOD3	Extracellular superoxide dismutase [Cu-Zn]	25.8	7	37.1
P03950	ANG	Angiogenin	16.5	7	53.1
P14555	PLA2G2A	Phospholipase A2, membrane associated	16.1	7	47.2
Q13642	FHL1	Four and a half LIM domains protein 1	36.2	7	31.0
P08107	HSPA1B	Heat shock 70 kDa protein 1A/1B	70.0	7	17.8
Q06830	PRDX1	Peroxiredoxin-1	22.1	7	40.2
P07451	CA3	Carbonic anhydrase 3	29.5	7	41.2
P02647	APOA1	Apolipoprotein A-I	30.8	7	22.5
P01011	SERPINA3	Alpha-1-antichymotrypsin	47.6	7	22.5
P26038	MSN	Moesin	67.8	7	10.9
P13671	C6	Complement component C6	104.7	7	10.8
P14780	MMP9	Matrix metalloproteinase-9	78.4	7	11.0
P00736	C1R	Complement C1r subcomponent	80.1	7	12.6
O43854	EDIL3	EGF-like repeat and discoidin I-like domain-containing protein 3	53.7	7	22.3
P01834	IGKC	Ig kappa chain C region	11.6	6	80.2
P69905	HBA2	Hemoglobin subunit alpha	15.2	6	57.7
P02743	APCS	Serum amyloid P-component	25.4	6	28.7
P62937	PPIA	Peptidyl-prolyl cis-trans isomerase A	18.0	6	49.1
P23284	PPIB	Peptidyl-prolyl cis-trans isomerase B	23.7	6	30.1
P68104	EEF1A1	Elongation factor 1-alpha 1	50.1	6	16.5
P01619		Ig kappa chain V-III region B6	11.6	6	16.7
P01877	IGHA2	Ig alpha-2 chain C region	36.5	6	20.6
P12107	COL11A1	Collagen alpha-1(XI) chain	181.0	6	6.4
P20908	COL5A1	Collagen alpha-1(V) chain	183.4	6	5.9
P09525	ANXA4	Annexin A4	35.9	6	18.8
Q6UXX5	ITIH6	Inter-alpha-trypsin inhibitor heavy chain H6	143.1	6	5.6
P07358	C8B	Complement component C8 beta chain	67.0	6	15.1
P34096	RNASE4	Ribonuclease 4	16.8	5	34.0
P30086	PEBP1	Phosphatidylethanolamine-binding protein 1	21.0	5	52.9
P02746	C1QB	Complement C1q subcomponent subunit B	26.7	5	27.3
P02775	PPBP	Platelet basic protein	13.9	5	38.3
P02760	AMBP	Protein AMBP	39.0	5	19.0
P00568	AK1	Adenylate kinase isoenzyme 1	21.6	5	30.4
P34931	HSPA1L	Heat shock 70 kDa protein 1-like	70.3	5	10.6
O60814	HIST1H2BK	Histone H2B type 1-K	13.9	5	35.7
P06899	HIST1H2BJ	Histone H2B type 1-J	13.9	5	35.7
P13646	KRT13	Keratin, type I cytoskeletal 13	49.6	5	8.7
P07737	PFN1	Profilin-1	15.0	5	45.7
P08758	ANXA5	Annexin A5	35.9	5	14.4
P07360	C8G	Complement component C8 gamma chain	22.3	5	39.6
Q92765	FRZB	Secreted frizzled-related protein 3	36.2	5	16.9
P30043	BLVRB	Flavin reductase (NADPH)	22.1	5	47.1
P00746	CFD	Complement factor D	27.0	5	40.3
P68363	TUBA1B	Tubulin alpha-1B chain	50.1	5	16.6
P41218	MNDA	Myeloid cell nuclear differentiation antigen	45.8	5	15.2
P00918	CA2	Carbonic anhydrase 2	29.2	5	26.2
P20849	COL9A1	Collagen alpha-1(IX) chain	91.8	5	9.9
Q00688	FKBP3	Peptidyl-prolyl cis-trans isomerase FKBP3	25.2	5	26.3
P50454	SERPINH1	Serpin H1	46.4	5	19.6
P02774	GC	Vitamin D-binding protein	52.9	5	19.8
P01871	IGHM	Ig mu chain C region	49.3	5	14.6
P07357	C8A	Complement component C8 alpha chain	65.1	5	13.2
P29401	TKT	Transketolase	67.8	5	14.3
Q07092	COL16A1	Collagen alpha-1(XVI) chain	157.7	5	7.1
P08582	MFI2	Melanotransferrin	80.2	5	10.0
P32119	PRDX2	Peroxiredoxin-2	21.9	5	28.3
Q7Z304	MAMDC2	MAM domain-containing protein 2	77.5	5	9.5
P0CG05	IGLC2	Ig lambda-2 chain C regions	11.3	4	65.1

B9A064	IGLL5	Immunoglobulin lambda-like polypeptide 5	23.0	4	32.2
P13929	ENO3	Beta-enolase	47.0	4	12.0
Accession	**Gene ID**	**Description**	**MW [kDa]**	**# Peptides**	**Coverage (%)**
P16402	HIST1H1D	Histone H1.3	22.3	4	14.9
P62805	HIST1H4A	Histone H4	11.4	4	40.8
P07998	RNASE1	Ribonuclease pancreatic	17.6	4	48.1
P04179	SOD2	Superoxide dismutase [Mn], mitochondrial	24.7	4	23.0
P02747	C1QC	Complement C1q subcomponent subunit C	25.8	4	21.2
P03973	SLPI	Antileukoproteinase	14.3	4	38.6
P02749	APOH	Beta-2-glycoprotein 1	38.3	4	20.6
P02776	PF4	Platelet factor 4	10.8	4	35.6
Q9Y240	CLEC11A	C-type lectin domain family 11 member A	35.7	4	14.2
P16401	HIST1H1B	Histone H1.5	22.6	4	15.5
P00915	CA1	Carbonic anhydrase 1	28.9	4	21.1
P49746	THBS3	Thrombospondin-3	104.1	4	4.5
P23528	CFL1	Cofilin-1	18.5	4	35.5
P01033	TIMP1	Metalloproteinase inhibitor 1	23.2	4	24.6
P60174	TPI1	Triosephosphate isomerase	30.8	4	19.9
P35442	THBS2	Thrombospondin-2	129.9	4	3.7
P05090	APOD	Apolipoprotein D	21.3	4	24.9
Q07507	DPT	Dermatopontin	24.0	4	25.4
P35625	TIMP3	Metalloproteinase inhibitor 3	24.1	4	20.4
P05155	SERPING1	Plasma protease C1 inhibitor	55.1	4	10.2
Q9Y6C2	EMILIN1	EMILIN-1	106.6	4	6.3
P07437	TUBB	Tubulin beta chain	49.6	4	12.2
P24752	ACAT1	Acetyl-CoA acetyltransferase, mitochondrial	45.2	4	18.3
P21333	FLNA	Filamin-A	280.6	4	1.7
Q14767	LTBP2	Latent-transforming growth factor beta-binding protein 2	194.9	4	3.0
Q9H336	CRISPLD1	Cysteine-rich secretory protein LCCL domain-containing 1	56.9	4	9.6
Q9NQ79	CRTAC1	Cartilage acidic protein 1	71.4	4	10.0
P04003	C4BPA	C4b-binding protein alpha chain	67.0	4	7.4
P01042	KNG1	Kininogen-1	71.9	4	6.5
Q9NRN5	OLFML3	Olfactomedin-like protein 3	46.0	4	11.3
P01620		Ig kappa chain V-III region SIE	11.8	3	39.4
P09238	MMP10	Stromelysin-2	54.1	3	6.1
P04908	HIST1H2AB	Histone H2A type 1-B/E	14.1	3	26.9
P05787	KRT8	Keratin, type II cytoskeletal 8	53.7	3	6.2
Q562R1	ACTBL2	Beta-actin-like protein 2	42.0	3	11.2
P01597		Ig kappa chain V-I region DEE	11.7	3	16.7
Q96HC4	PDLIM5	PDZ and LIM domain protein 5	63.9	3	8.1
P12830	CDH1	Cadherin-1	97.4	3	3.2
Q99969	RARRES2	Retinoic acid receptor responder protein 2	18.6	3	21.5
P16035	TIMP2	Metalloproteinase inhibitor 2	24.4	3	14.5
P02794	FTH1	Ferritin heavy chain	21.2	3	19.1
Q14050	COL9A3	Collagen alpha-3(IX) chain	63.6	3	9.4
P02792	FTL	Ferritin light chain	20.0	3	21.1
P21246	PTN	Pleiotrophin	18.9	3	23.8
P12724	RNASE3	Eosinophil cationic protein	18.4	3	15.0
P01625		Ig kappa chain V-IV region Len	12.6	3	36.8
P01768		Ig heavy chain V-III region CAM	13.7	3	18.0
P18428	LBP	Lipopolysaccharide-binding protein	53.4	3	7.1
Q96PD5	PGLYRP2	N-acetylmuramoyl-L-alanine amidase	62.2	3	11.3
P08238	HSP90AB1	Heat shock protein HSP 90-beta	83.2	3	5.0
P84243	H3F3A	Histone H3.3	15.3	3	35.3
P78539	SRPX	Sushi repeat-containing protein SRPX	51.5	3	7.5
P03956	MMP1	Interstitial collagenase	54.0	3	7.2
Q16851	UGP2	UTP--glucose-1-phosphate uridylyltransferase	56.9	3	6.9
P06702	S100A9	Protein S100-A9	13.2	3	37.7
Q14055	COL9A2	Collagen alpha-2(IX) chain	65.1	3	11.5
P04792	HSPB1	Heat shock protein beta-1	22.8	3	21.0
P18669	PGAM1	Phosphoglycerate mutase 1	28.8	3	18.9

Q96CG8	CTHRC1	Collagen triple helix repeat-containing protein 1	26.2	3	13.2
Q99983	OMD	Osteomodulin	49.5	3	7.6

Accession	Gene ID	Description	MW [kDa]	# Peptides	Coverage (%)
Q16674	MIA	Melanoma-derived growth regulatory protein	14.5	3	21.4
P27918	CFP	Properdin	51.2	3	9.4
Q16627	CCL14	C-C motif chemokine 14	10.7	3	47.3
P12883	MYH7	Myosin-7	223.0	3	2.2
P09871	C1S	Complement C1s subcomponent	76.6	3	6.1
Q16610	ECM1	Extracellular matrix protein 1	60.6	3	6.5
P01008	SERPINC1	Antithrombin-III	52.6	3	7.8
P27797	CALR	Calreticulin	48.1	3	12.2
Q7Z794	KRT77	Keratin, type II cytoskeletal 1b	61.9	2	3.8
Q86UW8	HAPLN4	Hyaluronan and proteoglycan link protein 4	42.8	2	4.0
P19013	KRT4	Keratin, type II cytoskeletal 4	57.3	2	3.7
P01609		Ig kappa chain V-I region Scw	11.8	2	27.8
P01593	LOC100128009	Ig kappa chain V-I region AG	12.0	2	31.5
P01766		Ig heavy chain V-III region BRO	13.2	2	25.0
P01608		Ig kappa chain V-I region Roy	11.8	2	24.1
P09972	ALDOC	Fructose-bisphosphate aldolase C	39.4	2	13.7
O14960	LECT2	Leukocyte cell-derived chemotaxin-2	16.4	2	11.3
P01616		Ig kappa chain V-II region MIL	12.0	2	11.6
P62979	RPS27A	Ubiquitin-40S ribosomal protein S27a	18.0	2	16.0
O00300	TNFRSF11B	Tumor necrosis factor receptor superfamily member 11B	46.0	2	5.7
P02766	TTR	Transthyretin	15.9	2	23.8
Q03591	CFHR1	Complement factor H-related protein 1	37.6	2	7.3
P59665	DEFA1	Neutrophil defensin 1	10.2	2	19.1
P80748		Ig lambda chain V-III region LOI	11.9	2	21.6
Q92522	H1FX	Histone H1x	22.5	2	10.3
O75829	LECT1	Leukocyte cell-derived chemotaxin 1	37.1	2	9.3
P01765		Ig heavy chain V-III region TIL	12.3	2	26.1
Q9H1Z8	C2orf40	Augurin	17.2	2	14.9
P04208		Ig lambda chain V-I region WAH	11.7	2	27.5
P02144	MB	Myoglobin	17.2	2	18.8
P02745	C1QA	Complement C1q subcomponent subunit A	26.0	2	9.4
P06331		Ig heavy chain V-II region ARH-77	16.2	2	17.1
Q14315	FLNC	Filamin-C	290.8	2	0.9
P05387	RPLP2	60S acidic ribosomal protein P2	11.7	2	39.1
P07195	LDHB	L-lactate dehydrogenase B chain	36.6	2	6.3
P01701		Ig lambda chain V-I region NEW	11.4	2	27.0
Q15323	KRT31	Keratin, type I cuticular Ha1	47.2	2	5.3
P01598		Ig kappa chain V-I region EU	11.8	2	26.9
P09211	GSTP1	Glutathione S-transferase P	23.3	2	14.8
P62424	RPL7A	60S ribosomal protein L7a	30.0	2	9.0
P45378	TNNT3	Troponin T, fast skeletal muscle	31.8	2	8.2
P02763	ORM1	Alpha-1-acid glycoprotein 1	23.5	2	8.5
P08493	MGP	Matrix Gla protein	12.3	2	11.7
P24593	IGFBP5	Insulin-like growth factor-binding protein 5	30.6	2	7.0
P04040	CAT	Catalase	59.7	2	5.3
P67936	TPM4	Tropomyosin alpha-4 chain	28.5	2	9.7
P28300	LOX	Protein-lysine 6-oxidase	46.9	2	7.9
P39059	COL15A1	Collagen alpha-1(XV) chain	141.6	2	2.2
P09429	HMGB1	High mobility group protein B1	24.9	2	15.3
P05109	S100A8	Protein S100-A8	10.8	2	23.7
Q14624	ITIH4	Inter-alpha-trypsin inhibitor heavy chain H4	103.3	2	2.3
P21741	MDK	Midkine	15.6	2	16.8
P45452	MMP13	Collagenase 3	53.8	2	8.3
Q8WZ42	TTN	Titin	3813.7	2	0.1
P62258	YWHAE	14-3-3 protein epsilon	29.2	2	7.5
Q9BXR6	CFHR5	Complement factor H-related protein 5	64.4	2	4.0
P04196	HRG	Histidine-rich glycoprotein	59.5	2	4.0
Q15198	PDGFRL	Platelet-derived growth factor receptor-like protein	41.8	2	6.1
P20160	AZU1	Azurocidin	26.9	2	8.4

O75888	TNFSF13	Tumor necrosis factor ligand superfamily member 13	27.4	2	9.6
P09651	HNRNPA1	Heterogeneous nuclear ribonucleoprotein A1	38.7	2	4.8
Accession	**Gene ID**	**Description**	**MW [kDa]**	**# Peptides**	**Coverage (%)**
P36871	PGM1	Phosphoglucomutase-1	61.4	2	4.8
P26583	HMGB2	High mobility group protein B2	24.0	2	11.5
P02741	CRP	C-reactive protein	25.0	2	11.2
P00488	F13A1	Coagulation factor XIII A chain	83.2	2	3.8
P06744	GPI	Glucose-6-phosphate isomerase	63.1	2	4.1
P10643	C7	Complement component C7	93.5	2	4.9
P22626	HNRNPA2B1	Heterogeneous nuclear ribonucleoproteins A2/B1	37.4	2	8.5
P62269	RPS18	40S ribosomal protein S18	17.7	2	12.5
P05546	SERPIND1	Heparin cofactor 2	57.0	2	3.2
P07305	H1F0	Histone H1.0	20.9	1	6.7
P06326		Ig heavy chain V-I region Mot	13.6	1	9.6
P01762		Ig heavy chain V-III region TRO	13.5	1	15.6
Q14103	HNRNPD	Heterogeneous nuclear ribonucleoprotein D0	38.4	1	3.9
P01772		Ig heavy chain V-III region KOL	13.7	1	12.7
P01714		Ig lambda chain V-III region SH	11.4	1	16.7
P01743	LOC652102	Ig heavy chain V-I region HG3	12.9	1	9.4
P01781		Ig heavy chain V-III region GAL	12.7	1	7.8
Q5JSP0	FGD3	FYVE, RhoGEF and PH domain-containing protein 3	79.4	1	1.2
P48061	CXCL12	Stromal cell-derived factor 1	10.7	1	15.1
P35268	RPL22	60S ribosomal protein L22	14.8	1	8.6
P04433	IGKV3D-11	Ig kappa chain V-III region VG (Fragment)	12.6	1	7.8
P01034	CST3	Cystatin-C	15.8	1	7.5
Q6NZI2	PTRF	Polymerase I and transcript release factor	43.5	1	4.6
P23083	IGHV1OR15-1	Ig heavy chain V-I region V35	13.0	1	10.3
P05976	MYL1	Myosin light chain 1/3, skeletal muscle isoform	21.1	1	5.7
Q01523	DEFA5	Defensin-5	10.1	1	12.8
O00339	MATN2	Matrilin-2	106.8	1	1.2
P81605	DCD	Dermcidin	11.3	1	10.0
P05019	IGF1	Insulin-like growth factor I	21.8	1	5.1
P62753	RPS6	40S ribosomal protein S6	28.7	1	6.0
O95965	ITGBL1	Integrin beta-like protein 1	53.9	1	2.8
Q93091	RNASE6	Ribonuclease K6	17.2	1	7.3
Q9UGM3	DMBT1	Deleted in malignant brain tumors 1 protein	260.6	1	7.0
P07477	PRSS1	Trypsin-1	26.5	1	4.0
P62826	RAN	GTP-binding nuclear protein Ran	24.4	1	5.1
P04207		Ig kappa chain V-III region CLL	14.3	1	7.0
P61158	ACTR3	Actin-related protein 3	47.3	1	2.6
O14950	MYL12B	Myosin regulatory light chain 12B	19.8	1	6.4
P01621		Ig kappa chain V-III region NG9 (Fragment)	10.7	1	9.0
Q6YHK3	CD109	CD109 antigen	161.6	1	1.2
P05156	CFI	Complement factor I	65.7	1	1.7
P20962	PTMS	Parathymosin	11.5	1	10.8
Q14766	LTBP1	Latent-transforming growth factor beta-binding protein 1	186.7	1	0.7
P83731	RPL24	60S ribosomal protein L24	17.8	1	8.3
Q6UWY5	OLFML1	Olfactomedin-like protein 1	45.9	1	2.7
Q53RD9	FBLN7	Fibulin-7	47.3	1	1.6
P40121	CAPG	Macrophage-capping protein	38.5	1	3.4
P09913	IFIT2	Interferon-induced protein with tetratricopeptide repeats 2	54.6	1	2.5
Q16658	FSCN1	Fascin	54.5	1	3.2
P01703		Ig lambda chain V-I region NEWM	10.9	1	16.5
P55774	CCL18	C-C motif chemokine 18	9.8	1	24.7
Q9NT22	EMILIN3	EMILIN-3	82.6	1	2.5
O60701	UGDH	UDP-glucose 6-dehydrogenase	55.0	1	2.0
P19338	NCL	Nucleolin	76.6	1	1.7
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	32.9	1	3.5
P23297	S100A1	Protein S100-A1	10.5	1	16.0
P05164	MPO	Myeloperoxidase	83.8	1	1.6
P0DJI8	SAA1	Serum amyloid A-1 protein	13.5	1	16.4

P62314	SNRPD1	Small nuclear ribonucleoprotein Sm D1	13.3	1	16.8
Q15782	CHI3L2	Chitinase-3-like protein 2	43.5	1	2.8

Accession	Gene ID	Description	MW [kDa]	# Peptides	Coverage (%)
P01771		Ig heavy chain V-III region HIL	13.6	1	9.1
P06703	S100A6	Protein S100-A6	10.2	1	7.8
Q6IQ22	RAB12	Ras-related protein Rab-12	27.2	1	4.5
O75792	RNASEH2A	Ribonuclease H2 subunit A	33.4	1	2.7
Q13103	SPP2	Secreted phosphoprotein 24	24.3	1	6.2
P26927	MST1	Hepatocyte growth factor-like protein	80.3	1	2.0
Q05707	COL14A1	Collagen alpha-1(XIV) chain	193.4	1	1.2
P07237	P4HB	Protein disulfide-isomerase	57.1	1	5.9
Q7Z5L7	PODN	Podocan	68.9	1	2.6
Q15084	PDIA6	Protein disulfide-isomerase A6	48.1	1	5.5
P30041	PRDX6	Peroxiredoxin-6	25.0	1	5.4
P14649	MYL6B	Myosin light chain 6B	22.8	1	6.3
P14174	MIF	Macrophage migration inhibitory factor	12.5	1	9.6
Q9BQB4	SOST	Sclerostin	24.0	1	8.5
Q14533	KRT81	Keratin, type II cuticular Hb1	54.9	1	2.2
P01031	C5	Complement C5	188.2	1	0.6
P62750	RPL23A	60S ribosomal protein L23a	17.7	1	8.3
P02511	CRYAB	Alpha-crystallin B chain	20.1	1	4.6
P45877	PPIC	Peptidyl-prolyl cis-trans isomerase C	22.7	1	3.8
P83110	HTRA3	Serine protease HTRA3	48.6	1	3.1
P55058	PLTP	Phospholipid transfer protein	54.7	1	2.2
P08311	CTSG	Cathepsin G	28.8	1	7.1
P27105	STOM	Erythrocyte band 7 integral membrane protein	31.7	1	4.2
P61353	RPL27	60S ribosomal protein L27	15.8	1	6.6
Q6NUN7	C11orf63	Uncharacterized protein C11orf63	88.5	1	1.4
P40925	MDH1	Malate dehydrogenase, cytoplasmic	36.4	1	3.6
P07910	HNRNPC	Heterogeneous nuclear ribonucleoproteins C1/C2	33.7	1	3.9
P15531	NME1	Nucleoside diphosphate kinase A	17.1	1	11.2
P35637	FUS	RNA-binding protein FUS	53.4	1	3.0
Q9Y2Q0	ATP8A1	Probable phospholipid-transporting ATPase IA	131.3	1	0.6
O15230	LAMA5	Laminin subunit alpha-5	399.5	1	0.3
P46093	GPR4	G-protein coupled receptor 4	41.0	1	1.9
Q9UKB5	AJAP1	Adherens junction-associated protein 1	44.5	1	6.1
P26373	RPL13	60S ribosomal protein L13	24.2	1	6.2
Q86VQ1	GLCCI1	Glucocorticoid-induced transcript 1 protein	58.0	1	2.4
P17936	IGFBP3	Insulin-like growth factor-binding protein 3	31.7	1	2.7
Q8N976	LOC4687	Putative uncharacterized protein FLJ38264	14.9	1	10.6
P00966	ASS1	Argininosuccinate synthase	46.5	1	3.2
P17931	LGALS3	Galectin-3	26.1	1	4.4
Q9NSB4	KRT82	Keratin, type II cuticular Hb2	56.6	1	1.9
Q03692	COL10A1	Collagen alpha-1(X) chain	66.1	1	2.8
P48634	PRRC2A	Protein PRRC2A	228.7	1	0.8
P08133	ANXA6	Annexin A6	75.8	1	2.2
Q6ZWJ8	KCP	Kielin/chordin-like protein	159.8	1	0.8
O75594	PGLYRP1	Peptidoglycan recognition protein 1	21.7	1	11.7
Q7Z2Z2	EFTUD1	Elongation factor Tu GTP-binding domain-containing protein 1	125.4	1	0.7
P40227	CCT6A	T-complex protein 1 subunit zeta	58.0	1	4.0
P36578	RPL4	60S ribosomal protein L4	47.7	1	2.8
Q8IZC6	COL27A1	Collagen alpha-1(XXVII) chain	186.8	1	2.4
P62861	FAU	40S ribosomal protein S30	6.6	1	16.9
P06316		Ig lambda chain V-I region BL2	13.6	1	6.2
Q8NBJ5	COLGALT1	Procollagen galactosyltransferase 1	71.6	1	1.4
P62917	RPL8	60S ribosomal protein L8	28.0	1	6.2
O60840	CACNA1F	Voltage-dependent L-type calcium channel subunit alpha-1F	220.5	1	1.0
P62158	CALM3	Calmodulin	16.8	1	11.4
P56696	KCNQ4	Potassium voltage-gated channel subfamily KQT member 4	77.1	1	1.7

P41229	KDM5C	Lysine-specific demethylase 5C	175.6	1	1.3

Accession	Gene ID	Description	MW [kDa]	# Peptides	Coverage (%)
P03952	KLKB1	Plasma kallikrein	71.3	1	1.6
Q8ND61	C3orf20	Uncharacterized protein C3orf20	101.2	1	1.2
O60844	ZG16	Zymogen granule membrane protein 16	18.2	1	5.4
P35613	BSG	Basigin	42.2	1	4.7
Q8N655	C10orf12	Uncharacterized protein C10orf12	137.1	1	2.9
Q8N474	SFRP1	Secreted frizzled-related protein 1	35.4	1	5.1

Table S5. MS1 precursor ions for clusterin protein

Protein	Peptide selected	Charge	Precursor m/z	[M+1] m/z	[M+2] m/z	Xcorr	Percolator PEP
P10909	TLLSNLEEAK	2	559.31	559.81	560.31	2.95	5.47E-04
Clusterin	ASSIIDELFQDR	2	697.35	697.85	698.35	3.91	1.04E-05
	LANLTQGEDQYYLR	2	842.42	842.92	843.42	4.88	7.57E-07
	VTTVASHTSDSDVPSGVTEVVVK	3	1157.59	1158.09	1158.60	3.79	6.07E-07
	LFDSDPITVTVPVEVSR	2	937.50	938.00	938.50	3.63	8.75E-09