Supplemental Table 4: Peptides

Protein name	Protein accession numbers	Protein identification probability	Exclusive unique peptide count	Exclusive unique spectrum count	Exclusive spectrum count	Percentage of total spectra	Percentage sequence coverage	Peptide sequence	Best Peptide identification probability	Best SEQUEST XCorr score	Best SEQUEST DCn score	Best Mascot Ion score	Best Mascot Identity score	Best Mascot Delta Ion score	Number of identified +1H spectra	Number of identified +2H spectra	Number of identified +3H spectra	Number of identified +4H spectra	Number of enzymatic termini	Calculated +1H Peptide Mass (AMU)	Median Retention Time	Total TIC
Alpha-1-antitrypsin GN=SERPINA1	sp|P01009|A1	100.00%	6	6	8	0.03%	0.00%	LVDKFLEDVKK	99.70%	3.56	0.290	30.2	29.8	19.8	0	0	1	0	2	1333.77	4,880.93	206,534.00
Alpha-1-antitrypsin GN=SERPINA1	sp|P01009|A1	100.00%	6	6	8	0.03%	0.00%	LNQPDSQLQLTTGNG	99.70%	2.61	0.427	39.0	33.3	24.0	0	1	0	0	2	1585.78	4,977.88	160,958.00
Alpha-1-antitrypsin GN=SERPINA1	sp|P01009|A1	100.00%	6	6	8	0.03%	0.00%	LTHDIITKFLENEDR	99.70%	3.29	0.463	33.5	34.1	33.5	0	0	1	0	2	1843.96	6,875.47	314,076.00
Alpha-1-antitrypsin GN=SERPINA1	sp|P01009|A1	100.00%	6	6	8	0.03%	0.00%	LLRTLNQPDSQLQ	99.70%	3.86	0.524	58.4	32.0	43.6	0	2	0	0	2	1525.83	4,643.69	1,101,580.00
Alpha-1-antitrypsin GN=SERPINA1	sp|P01009|A1	100.00%	6	6	8	0.03%	0.00%	VLGQLGITKVFSNGADLSG	99.70%	3.34	0.576	29.6	33.0	29.6	0	1	0	0	2	1876.02	7,666.30	446,286.00
Alpha-1-antitrypsin GN=SERPINA1	sp|P01009|A1	100.00%	6	6	8	0.03%	0.00%	LLRTLNQPDSQLQLTTGNG	99.70%	3.87	0.588	79.3	33.9	79.3	0	2	0	0	2	2069.10	5,690.56	456,283.00
Alpha-1-antitrypsin GN=SERPINA1	sp|P01009|A1	100.00%	1	1	3	0.02%	0.00%	LLRTLNQPDSQLQ	99.70%	4.02	0.483	54.1	31.2	38.7	0	3	0	0	2	1525.83	3,887.19	1,436,800.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	LAKYNQLLRIEEELGSK	99.70%	2.29	0.280	30.1	32.0	16.0	0	0	0	1	2	2004.11	6,932.90	65,552.50
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	SGKYDLDFKSPDDPSRY	99.70%	3.08	0.369	27.7	32.0	13.6	0	0	0	2	2	1989.92	5,089.54	669,241.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	FAPNILENKEGLEL	99.70%	2.78	0.387	24.6	33.4	11.3	0	1	0	0	2	1586.84	7,570.14	225,040.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	AVPSGASTGIYEALE	99.70%	2.73	0.427	36.3	33.4	36.3	0	1	0	0	2	1464.72	6,618.71	426,736.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	ISPDQLADLYKSF	99.70%	2.63	0.446	58.3	33.5	58.3	0	3	0	0	2	1496.76	8,634.74	317,561.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	LLRIEEELGSK	99.70%	3.57	0.513	31.1	31.3	17.5	0	0	1	0	2	1286.73	5,282.63	504,381.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	VVSIEDPFDQDDWGA	99.70%	3.05	0.554	46.7	29.4	46.7	0	1	0	0	2	1692.74	8,569.66	125,911.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	VVSIEDPFDQDDWGAWQK	99.70%	4.30	0.582	67.7	31.8	67.7	0	3	1	0	2	2134.97	8,484.07	1,268,050.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	9	10	15	0.06%	0.00%	GNPTVEVDLFTSKG	99.70%	3.28	0.614	47.1	33.6	47.1	0	1	0	0	2	1463.74	6,443.75	684,183.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	3	3	5	0.03%	0.00%	AAVPSGASTGIYEALE	99.70%	2.38	0.402	35.9	33.9	24.2	0	1	0	0	2	1535.76	5,856.76	441,223.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	3	3	5	0.03%	0.00%	LLRIEEELGSK	99.70%	3.13	0.439	26.3	30.4	11.0	0	0	2	0	2	1286.73	4,233.41	468,368.00
Alpha-enolase GN=ENO1	sp|P06733|EN	100.00%	3	3	5	0.03%	0.00%	VVSIEDPFDQDDWGAWQK	99.70%	4.68	0.606	57.5	32.7	57.5	0	2	0	0	2	2134.97	7,346.33	414,427.00
Arginase-1 GN=ARG1	sp|P05089|AR	100.00%	1	1	1	0.01%	5.59%	FTPATGTPVVGGLTYREG	99.70%	3.51	0.470	59.1	33.8	59.1	0	1	0	0	2	1822.93	5,412.40	922,780.00
Asporin GN=ASPN	sp|Q9BXN1|AS	100.00%	2	2	3	0.01%	6.32%	LTSVPTNIPFDTR	99.70%	1.97	0.379	44.8	33.6	44.8	0	2	0	0	2	1460.77	6,106.10	1,560,260.00
Asporin GN=ASPN	sp|Q9BXN1|AS	100.00%	2	2	3	0.01%	6.32%	LSEIPLNLPKS	99.70%	2.83	0.484	30.6	29.5	30.6	0	1	0	0	2	1210.70	6,210.56	782,965.00
ATP-dependent RNA helicase A GN=DHX9	sp|Q08211|DH	100.00%	1	1	2	0.01%	0.00%	FATPEQISMDLKNE	99.70%	3.84	0.531	60.1	33.0	60.1	0	2	0	0	2	1622.77	6,801.37	353,213.00
Basement membrane-specific heparan sulfate proteoglycan core protein GN=HSPG2	sp|P98160|PG	100.00%	1	1	1	0.00%	0.23%	LADLDELLIR	99.70%	3.44	0.276	65.2	30.5	39.5	0	1	0	0	2	1170.67	7,850.43	231,771.00
Basement membrane-specific heparan sulfate proteoglycan core protein GN=HSPG2	sp|P98160|PG	100.00%	1	1	1	0.01%	0.23%	LAGIDTLLIR	99.70%	3.30	0.399	40.6	25.4	28.3	0	1	0	0	2	1084.67	6,673.22	89,207.40
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	IELEDLLR	99.70%	2.26	0.090	54.5	32.1	26.1	0	2	0	0	2	1000.57	7,584.44	216,577.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	LHLDHNKIQAIELEDLLR	99.70%	3.69	0.297	34.1	32.3	12.0	0	0	0	2	2	2170.20	7,177.34	314,931.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	LRISEAKLTGIPKDLPET	99.70%	3.38	0.304	33.2	30.1	21.9	0	0	1	0	2	1981.13	5,891.87	170,460.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	VPSGLPDLKL	99.70%	1.73	0.310	58.3	27.9	29.5	0	3	0	0	2	1038.62	7,061.66	201,013.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	IQAIELEDLLR	99.70%	2.88	0.374	56.0	30.6	43.1	0	2	0	0	2	1312.75	8,390.46	712,945.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	LTGIPKDLPETLNE	99.70%	2.49	0.385	25.5	32.5	25.5	0	1	0	0	2	1539.83	6,293.37	1,517,430.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	LFNNPVPYWEVQPAT	99.70%	3.39	0.397	24.1	33.9	14.0	0	1	0	0	2	1774.88	8,064.55	211,759.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	VPSGLPDLKLLQ	99.70%	3.12	0.411	51.1	27.6	33.6	0	3	0	0	2	1279.76	7,556.88	1,280,740.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	ISEAKLTGIPKDLPETLNE	99.70%	3.41	0.414	41.5	33.5	22.1	0	0	1	0	2	2068.12	6,344.33	572,200.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	LRISEAKLTGIPKDLPETLNE	99.70%	2.89	0.425	20.3	32.0	20.3	0	0	1	0	2	2337.30	6,551.40	227,561.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	ISPDTTLLDLQNNDISE	99.70%	3.36	0.450	60.0	33.6	48.3	0	3	0	0	2	1887.92	7,464.82	1,091,150.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	FDGLKLNY	99.70%	2.67	0.457	32.6	31.9	18.1	0	1	0	0	2	969.50	6,341.23	248,724.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	ISLFNNPVPYWEVQPAT	99.70%	4.21	0.489	32.4	34.5	32.4	0	1	0	0	2	1975.00	9,047.03	129,518.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	LENSGFEPGAFDGLKLNY	99.70%	3.71	0.517	44.3	33.8	44.3	0	1	0	0	2	1970.95	8,032.06	245,452.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	15	15	25	0.10%	0.00%	VPSGLPDLKLLQVVY	99.70%	2.68	0.633	26.2	28.5	26.2	0	2	0	0	2	1640.96	9,178.51	604,215.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	2	2	2	0.01%	0.00%	LTGIPKDLPETLNE	99.70%	2.85	0.301	29.1	31.9	16.6	0	1	0	0	2	1539.83	5,625.92	177,296.00
Biglycan GN=BGN	sp|P21810|PG	100.00%	2	2	2	0.01%	0.00%	VPSGLPDLKL	99.70%	2.62	0.343	33.4	26.3	14.8	0	1	0	0	2	1038.62	6,366.13	69,478.40
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	2	3	4	0.02%	4.37%	LMVGPVDEVRE	99.70%	2.16	0.318	37.4	32.6	15.7	0	1	0	0	2	1243.64	5,329.05	194,485.00
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	2	3	4	0.02%	4.37%	IVDTGTSLMVGPVDEVRE	99.70%	4.49	0.591	79.9	34.3	79.9	0	3	0	0	2	1932.96	6,496.07	896,552.00
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	6	7	8	0.05%	12.90%	LMVGPVDEVRE	99.70%	2.49	0.325	45.7	32.7	26.3	0	1	0	0	2	1243.64	4,560.37	548,999.00
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	6	7	8	0.05%	12.90%	IAAKFDGILG	99.70%	2.28	0.362	22.2	29.5	22.2	0	1	0	0	2	1004.58	5,429.11	114,689.00
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	6	7	8	0.05%	12.90%	ILGDVFIGR	99.70%	2.49	0.424	28.3	29.1	14.1	0	1	0	0	2	989.58	5,684.31	144,705.00
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	6	7	8	0.05%	12.90%	IVDTGTSLMVGPVDEVR	99.70%	3.05	0.505	63.7	34.1	63.7	0	1	0	0	2	1803.92	5,182.50	103,947.00
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	6	7	8	0.05%	12.90%	FYLSRDPDAQPGGELM	99.70%	2.90	0.533	45.7	32.6	45.7	0	1	0	0	2	1811.83	4,623.58	297,631.00
Cathepsin D GN=CTSD	sp|P07339|CA	100.00%	6	7	8	0.05%	12.90%	IVDTGTSLMVGPVDEVRE	99.70%	4.72	0.575	72.7	34.4	60.4	0	3	0	0	2	1932.96	5,238.24	2,582,960.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	FLPQPPQE	99.70%	2.02	0.138	34.1	31.6	4.6	0	1	0	0	2	955.49	4,980.29	348,213.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPSAGFDF	99.70%	1.49	0.172	49.9	30.4	31.6	0	1	0	0	2	894.40	6,697.48	45,750.80
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPSAGFDFSFLPQ	99.70%	2.39	0.310	40.3	32.8	26.3	0	2	0	0	2	1466.70	8,721.79	233,505.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	FDFSFLPQPPQ	99.70%	2.52	0.311	43.4	32.9	27.9	0	3	0	0	2	1322.64	8,406.93	977,449.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPSAGFDFSF	99.70%	2.99	0.355	21.7	29.9	21.7	0	1	0	0	2	1128.50	8,257.71	31,989.70
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	SAGFDFSFLPQPPQ	99.70%	2.29	0.363	43.5	32.7	26.4	0	2	0	0	2	1537.73	8,660.00	182,233.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPGPPSAGFDF	99.70%	2.91	0.391	24.2	30.1	24.2	0	1	0	0	2	1145.53	6,766.02	59,624.60
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	FDFSFLPQPPQE	99.70%	2.08	0.416	28.4	32.6	9.6	0	1	0	0	2	1451.68	8,421.88	175,067.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPGPPSAGFDFS	99.70%	2.49	0.448	78.4	30.6	60.2	0	6	0	0	2	1232.56	6,426.12	6,112,860.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GLDGAKGDAGPA	99.70%	3.22	0.476	70.0	31.3	51.3	0	1	0	0	2	1028.50	2,393.43	83,881.20
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPSAGFDFSFLPQPPQ	99.70%	3.55	0.494	57.2	33.5	46.3	0	19	0	0	2	1788.86	8,544.66	6,062,990.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPSAGFDFSFLPQPPQE	99.70%	3.71	0.523	36.6	32.9	20.3	0	7	0	0	2	1917.90	8,606.73	1,304,040.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GFSGLDGAKGDAGPA	99.70%	4.52	0.532	82.3	32.0	55.2	0	7	0	0	2	1319.62	4,333.52	12,900,000.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	FSGLDGAKGDAGPA	99.70%	4.68	0.534	84.9	32.4	67.1	0	11	0	0	2	1262.60	4,206.41	12,100,000.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPSAGFDFSFLPQPP	99.70%	3.54	0.560	21.9	33.3	21.9	0	2	0	0	2	1660.80	8,990.53	184,803.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	16	16	92	0.35%	2.46%	GPPSAGFDFS	99.70%	3.03	0.567	71.8	29.6	59.2	0	27	0	0	2	981.43	7,264.00	31,700,000.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	7	7	17	0.11%	3.55%	GLDGAKGDAGPA	99.70%	2.50	0.360	50.1	31.5	27.5	0	1	0	0	2	1028.50	1,765.47	50,022.90
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	7	7	17	0.11%	3.55%	GPAGARGNDGATGAA	99.70%	2.68	0.417	28.4	32.2	17.0	0	1	0	0	2	1242.58	1,378.06	70,721.80
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	7	7	17	0.11%	3.55%	GPQGIAGQR	99.70%	3.19	0.421	42.3	30.2	0.0	0	1	0	0	2	883.47	1,557.79	53,465.30
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	7	7	17	0.11%	3.55%	GPPGPPSAGFDFS	99.70%	2.36	0.483	57.1	31.1	44.4	0	3	0	0	2	1232.56	5,620.17	3,006,710.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	7	7	17	0.11%	3.55%	GFSGLDGAKGDAGPA	99.70%	4.16	0.520	71.4	32.9	56.1	0	4	0	0	2	1319.62	3,323.83	6,765,780.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	7	7	17	0.11%	3.55%	GPPSAGFDFS	99.70%	2.44	0.542	64.5	31.0	54.2	0	4	0	0	2	981.43	4,785.07	3,104,940.00
Collagen alpha-1(I) chain GN=COL1A1	sp|P02452|CO	100.00%	7	7	17	0.11%	3.55%	FSGLDGAKGDAGPA	99.70%	4.58	0.580	80.0	32.7	52.1	0	3	0	0	2	1262.60	3,111.37	5,013,940.00
Collagen alpha-1(II) chain GN=COL2A1	sp|P02458|CO	100.00%	0	0	0	0.00%	0.61%	GPQGLAGQR	99.70%	3.19	0.421	42.3	30.2	0.0	0	1	0	0	2	883.47	1,557.79	53,465.30
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	4	4	7	0.03%	1.02%	GIAGITGAR	99.70%	2.09	0.450	31.7	30.2	0.1	0	1	0	0	2	815.47	3,625.29	54,491.70
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	4	4	7	0.03%	1.02%	GPLGIAGITGARG	99.70%	2.77	0.462	32.1	29.8	32.1	0	1	0	0	2	1139.65	5,750.33	1,227,070.00
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	4	4	7	0.03%	1.02%	GPLGIAGITGARGLA	99.70%	3.42	0.522	62.2	28.8	43.4	0	2	0	0	2	1323.77	6,854.49	3,812,750.00
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	4	4	7	0.03%	1.02%	GPLGIAGITGAR	99.70%	3.82	0.572	65.5	29.2	65.5	0	3	0	0	2	1082.63	5,787.41	2,194,180.00
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	6	6	13	0.09%	1.91%	PGADGVPGKDGPR	99.70%	2.64	0.339	34.5	32.9	19.9	0	0	1	0	2	1222.62	1,639.06	10,885.40
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	6	6	13	0.09%	1.91%	IAGITGARGLA	99.70%	2.65	0.423	36.8	28.2	19.9	0	1	0	0	2	999.59	4,015.04	1,145,590.00
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	6	6	13	0.09%	1.91%	GPLGIAGITGARG	99.70%	3.11	0.452	52.1	28.4	52.1	0	2	0	0	2	1139.65	4,984.00	1,802,650.00
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	6	6	13	0.09%	1.91%	GPLGIAGITGARGLA	99.70%	3.48	0.507	65.9	27.4	49.9	0	5	0	0	2	1323.77	9,320.19	4,398,810.00
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	6	6	13	0.09%	1.91%	GPLGIAGITGAR	99.70%	3.55	0.516	57.6	28.3	57.6	0	2	0	0	2	1082.63	5,019.91	836,742.00
Collagen alpha-1(III) chain GN=COL3A1	sp|P02461|CO	100.00%	6	6	13	0.09%	1.91%	PLGIAGITGAR	99.70%	2.41	0.534	16.2	27.0	16.2	0	2	0	0	2	1025.61	4,818.66	152,590.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	6	8	11	0.04%	0.00%	GPPGTMLMLP	99.70%	2.19	0.424	28.4	32.2	11.5	0	1	0	0	2	1045.51	7,047.43	109,671.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	6	8	11	0.04%	0.00%	AQESQAQAILQQAR	99.70%	4.00	0.448	41.9	33.6	26.2	0	1	0	0	2	1541.80	5,053.70	262,942.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	6	8	11	0.04%	0.00%	GPPGEVIQPLPIQASRT	99.70%	3.73	0.459	71.5	32.8	71.5	0	3	0	0	2	1759.97	5,938.76	1,746,200.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	6	8	11	0.04%	0.00%	VSAQESQAQAILQQARLA	99.70%	3.77	0.478	81.6	33.5	51.6	0	1	1	0	2	1912.02	6,943.31	1,484,590.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	6	8	11	0.04%	0.00%	GPMVSAQESQAQAILQQAR	99.70%	4.62	0.479	60.2	34.4	50.0	0	1	0	0	2	2013.02	6,211.56	172,120.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	6	8	11	0.04%	0.00%	VSAQESQAQAILQQAR	99.70%	4.58	0.499	81.9	33.7	70.1	0	2	1	0	2	1727.90	5,466.24	4,227,270.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	3	3	4	0.03%	0.00%	VSAQESQAQAILQQAR	99.70%	5.09	0.482	85.5	33.4	67.7	0	1	0	0	2	1727.90	4,380.79	752,268.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	3	3	4	0.03%	0.00%	VSAQESQAQAILQQARLA	99.70%	4.29	0.548	73.6	32.7	73.6	0	2	0	0	2	1912.02	5,988.05	1,007,090.00
Collagen alpha-1(V) chain GN=COL5A1	sp|P20908|CO	100.00%	3	3	4	0.03%	0.00%	GPPGEVIQPLPIQASRT	99.70%	4.02	0.580	45.0	31.5	34.9	0	1	0	0	2	1759.97	5,685.67	373,513.00
Collagen alpha-1(VI) chain GN=COL6A1	sp|P12109|CO	100.00%	6	10	14	0.05%	6.23%	LHYSDEVEIIQG	99.70%	2.53	0.192	37.5	32.7	12.9	0	1	0	0	2	1402.69	5,746.76	984,944.00
Collagen alpha-1(VI) chain GN=COL6A1	sp|P12109|CO	100.00%	6	10	14	0.05%	6.23%	VAITPDHLEPRLS	99.70%	1.86	0.297	27.0	32.7	0.0	0	0	1	0	2	1447.79	5,175.77	671,031.00
Collagen alpha-1(VI) chain GN=COL6A1	sp|P12109|CO	100.00%	6	10	14	0.05%	6.23%	LQWMAGGTFTGEA	99.70%	2.02	0.464	34.9	31.3	34.9	0	1	0	0	2	1368.63	7,448.62	126,584.00
Collagen alpha-1(VI) chain GN=COL6A1	sp|P12109|CO	100.00%	6	10	14	0.05%	6.23%	FINDATDVNDALGYVTR	99.70%	2.64	0.488	59.4	33.5	59.4	0	1	0	0	2	1883.91	7,148.55	78,946.80
Collagen alpha-1(VI) chain GN=COL6A1	sp|P12109|CO	100.00%	6	10	14	0.05%	6.23%	LASAVDAMDFINDATDVNDALGYVTR	99.70%	3.98	0.545	74.1	33.5	74.1	0	2	3	0	2	2773.30	9,262.93	342,575.00
Collagen alpha-1(VI) chain GN=COL6A1	sp|P12109|CO	100.00%	6	10	14	0.05%	6.23%	AVDAMDFINDATDVNDALGYVTR	99.70%	5.31	0.590	114.0	32.3	114.0	0	3	2	0	2	2502.15	8,939.03	304,039.00
Collagen alpha-1(XII) chain GN=COL12A1	sp|Q99715|CO	100.00%	4	4	4	0.02%	2.12%	FNQMLNQIPNDYQSSR	99.70%	3.24	0.400	33.5	32.2	33.5	0	1	0	0	2	1954.91	5,743.26	260,861.00
Collagen alpha-1(XII) chain GN=COL12A1	sp|Q99715|CO	100.00%	4	4	4	0.02%	2.12%	FKTNWSPAGENVFS	99.70%	2.18	0.442	24.1	32.8	24.1	0	1	0	0	2	1583.75	6,656.10	92,846.90
Collagen alpha-1(XII) chain GN=COL12A1	sp|Q99715|CO	100.00%	4	4	4	0.02%	2.12%	FGSSDKMETILNGDENT	99.70%	3.89	0.518	42.1	29.9	42.1	0	1	0	0	2	1857.82	5,822.95	152,875.00

Collagen alpha-1(XII) chain GN=COL12A1	sp|Q99715|CO	100.00%	4	4	4	0.02%	2.12%	IATDPDDTHAYNVADFES	99.70%	2.99	0.523	40.9	28.4	40.9	0	1	0	0	2	1980.85	5,775.83	58,043.60
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	VRAPHPDQPEFTPVQDELEAMEL	99.70%	2.59	0.226	42.3	34.1	42.3	0	0	1	0	2	2648.27	8,339.64	121,081.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	ILNQIPSHSSSIRTVQ	99.70%	2.09	0.244	26.5	32.7	16.4	0	0	1	0	2	1779.97	4,304.79	426,436.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	FSTKDEVIEAVR	99.70%	3.31	0.350	28.9	33.2	17.8	0	0	1	0	2	1393.73	4,777.69	414,987.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	LALPMASDLL	99.70%	2.29	0.373	28.2	33.0	12.1	0	1	0	0	2	1059.58	8,109.46	22,179.20
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	LLAVLDDGSESEVVT	99.70%	2.33	0.377	35.4	33.8	25.4	0	1	0	0	2	1546.78	6,796.67	383,667.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	VYAMFGEEASDPVTGQETT	99.70%	2.91	0.412	22.5	28.3	22.5	0	1	0	0	2	2047.88	5,653.74	82,340.60
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	GERGDLQSQAMVR	99.70%	3.27	0.415	28.3	33.0	28.3	0	0	1	0	2	1446.71	3,179.70	49,980.10
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	VRAPHPDQPEFTPVQDELEAME	99.70%	3.18	0.491	64.4	33.0	64.4	0	0	7	0	2	2535.18	6,053.60	7,784,130.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	ISDSDVQQFRVTY	99.70%	2.93	0.497	19.1	32.8	19.1	0	1	0	0	2	1557.75	6,068.55	203,579.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	LVEKDFSSVEGVSMEPGTFN	99.70%	2.53	0.507	27.3	32.3	27.3	0	1	0	0	2	2188.01	5,947.66	39,889.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	APHPDQPEFTPVQDELEAMEL	99.70%	3.88	0.515	55.5	31.9	55.5	0	2	0	0	2	2409.09	8,095.33	111,392.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	MFGEEASDPVTGQETT	99.70%	2.68	0.527	55.1	27.8	55.1	0	2	0	0	2	1698.72	5,353.53	1,031,990.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	ITGPPTELITSEVTARS	99.70%	3.20	0.538	82.8	33.6	82.8	0	1	0	0	2	1771.94	6,753.50	473,618.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	LTGVFTTEEVPAQQYLEIDEVTTDSFR	99.70%	3.47	0.570	28.5	35.2	28.5	0	0	1	0	2	3088.50	8,970.11	253,867.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	ITGPPTELITSEVTAR	99.70%	3.72	0.587	78.7	33.2	78.7	0	1	0	0	2	1684.91	6,676.52	949,147.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	VFTTEEVPAQQYLEIDEVTTDSFR	99.70%	4.86	0.604	70.0	34.4	70.0	0	2	2	0	2	2817.35	8,478.99	1,982,370.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	MFGEEASDPVTGQETTLA	99.70%	3.58	0.621	40.2	30.8	40.2	0	2	0	0	2	1882.84	6,473.66	812,348.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	18	24	39	0.15%	10.40%	APHPDQPEFTPVQDELEAME	99.70%	4.85	0.632	52.5	29.7	52.5	0	8	2	0	2	2296.01	6,401.52	6,948,940.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	2	4	6	0.04%	1.22%	VRAPHPDQPEFTPVQDELEAME	99.70%	2.83	0.451	63.2	33.6	63.2	0	0	3	0	2	2551.18	5,155.03	1,269,530.00
Collagen alpha-1(XIV) chain GN=COL14A1	sp|Q05707|CO	100.00%	2	4	6	0.04%	1.22%	APHPDQPEFTPVQDELEAME	99.70%	3.77	0.554	32.1	31.4	32.1	0	3	0	0	2	2280.01	6,580.67	390,406.00
Collagen alpha-1(XVI) chain GN=COL16A1	sp|Q07092|CO	100.00%	1	2	2	0.01%	0.81%	FIRQEIIKMFDER	99.70%	3.42	0.337	15.9	33.5	1.5	0	0	1	1	2	1724.92	7,297.69	253,618.00
Collagen alpha-1(XVIII) chain GN=COL18A1	sp|P39060|CO	100.00%	1	1	1	0.00%	0.91%	LFVAQAGGADPDKFQG	99.70%	3.30	0.467	38.0	33.7	38.0	0	1	0	0	2	1620.80	5,466.48	370,160.00
Collagen alpha-1(XVIII) chain GN=COL18A1	sp|P39060|CO	100.00%	1	1	1	0.01%	0.91%	LFVAQAGGADPDKFQG	99.70%	2.61	0.399	25.0	34.0	25.0	0	1	0	0	2	1620.80	4,688.29	227,848.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GERGVVGPQ	99.70%	2.17	0.182	34.6	31.2	17.4	0	1	0	0	2	898.47	2,230.85	20,562.20
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GPKGEIGAVGNAGPA	99.70%	3.25	0.277	76.6	32.9	55.2	0	1	0	0	2	1294.68	3,529.85	76,215.20
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GADGRAGVM	99.70%	1.82	0.285	40.9	31.3	15.1	0	1	0	0	2	833.39	2,446.25	26,543.90
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GEIGAVGNAGPA	99.70%	3.08	0.294	57.6	31.6	39.8	0	2	0	0	2	1012.51	3,865.24	339,034.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GARGSDGSVGPV	99.70%	2.78	0.445	41.2	32.1	41.2	0	1	0	0	2	1058.52	2,685.25	128,478.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GVVGAVGTAGPS	99.70%	2.65	0.508	58.7	32.1	42.4	0	2	0	0	2	971.52	3,742.89	2,028,180.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	FGYDGDFYRA	99.70%	3.20	0.532	72.4	28.2	56.2	0	12	0	0	2	1210.52	6,024.07	11,500,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	YDGDFYRA	99.70%	1.96	0.573	34.8	27.9	34.8	0	1	0	0	2	1006.43	4,346.11	46,336.40
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	FGYDGDFYR	99.70%	3.15	0.605	57.2	28.1	57.2	0	4	0	0	2	1139.48	5,686.38	3,027,140.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GGGYDFGYDGDF	99.70%	2.22	0.619	48.0	25.0	48.0	0	4	0	0	2	1269.47	7,174.94	1,601,400.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GGGYDFGYDGDFY	99.70%	4.19	0.652	66.5	25.0	66.5	0	59	0	0	2	1432.53	9,543.64	81,100,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	VSGGGYDFGYDGDFYR	99.70%	4.73	0.711	85.8	26.1	85.8	0	16	0	0	2	1774.73	6,607.92	8,334,980.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	VSGGGYDFGYDGDFYRA	99.70%	4.82	0.716	89.8	27.4	89.8	0	16	0	0	2	1845.77	6,830.43	13,400,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GGGYDFGYDGDFYRA	99.70%	4.63	0.719	72.0	25.3	72.0	0	32	0	0	2	1659.67	6,980.32	82,600,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GVSGGGYDFGYDGDFYRA	99.70%	4.85	0.724	101.0	26.8	101.0	0	47	0	0	2	1902.79	7,483.65	87,500,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GVSGGGYDFGYDGDFY	99.70%	3.62	0.726	66.0	25.0	66.0	0	53	0	0	2	1675.65	9,516.96	74,700,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	VSGGGYDFGYDGDFY	99.70%	3.44	0.748	62.7	25.0	62.7	0	12	0	0	2	1618.63	7,580.47	11,900,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GVSGGGYDFGYDGDF	99.70%	3.87	0.751	72.1	25.0	72.1	0	10	0	0	2	1512.59	7,290.29	7,703,980.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GVSGGGYDFGYDGDFYR	99.70%	4.75	0.757	93.9	26.2	93.9	0	30	0	0	2	1831.76	6,809.31	44,300,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	20	20	326	1.25%	5.49%	GGGYDFGYDGDFYR	99.70%	3.65	0.774	68.8	25.0	68.8	0	22	0	0	2	1588.63	6,588.50	36,300,000.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GLRGEIGN	99.70%	1.65	0.198	43.5	31.6	27.2	0	1	0	0	2	815.44	1,935.28	19,960.40
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GPVGRTGEVGAV	99.70%	1.86	0.242	36.8	31.5	12.2	0	1	0	0	2	1098.59	2,653.30	367,114.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GPAGARGSDGSVGPV	99.70%	2.39	0.310	57.5	32.9	57.5	0	1	0	0	2	1283.63	2,351.49	76,981.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GPKGEIGAVGNAGPA	99.70%	3.94	0.349	70.2	32.7	48.6	0	1	0	0	2	1294.68	2,790.99	253,971.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	FGYDGDFYRA	99.70%	3.14	0.376	49.9	29.8	49.9	0	4	0	0	2	1210.52	4,668.67	1,068,970.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GPKGEIGAVGNA	99.70%	2.73	0.440	25.2	31.3	25.2	0	1	0	0	2	1069.56	2,333.63	78,831.40
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GPAGARGSDGSVGPVGPA	99.70%	2.84	0.469	35.3	33.8	23.2	0	1	0	0	2	1508.75	2,711.28	450,425.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GGGYDFGYDGDFYR	99.70%	2.62	0.534	53.6	25.9	53.6	0	2	0	0	2	1588.63	5,198.81	282,658.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GVVGAVGTAGPS	99.70%	3.33	0.537	59.6	31.4	45.8	0	2	0	0	2	971.52	3,205.33	2,640,830.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GGGYDFGYDGDFY	99.70%	3.22	0.603	50.3	25.0	50.3	0	6	0	0	2	1432.53	6,175.13	3,093,160.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GGGYDFGYDGDFYRA	99.70%	3.91	0.654	64.9	27.1	64.9	0	4	0	0	2	1659.67	5,524.27	1,884,890.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GVSGGGYDFGYDGDFY	99.70%	3.40	0.672	63.7	25.0	63.7	0	7	0	0	2	1675.65	6,259.36	6,623,990.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GVSGGGYDFGYDGDF	99.70%	3.49	0.676	57.2	25.2	57.2	0	7	0	0	2	1512.59	5,904.81	3,408,590.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GVSGGGYDFGYDGDFYRA	99.70%	4.84	0.680	77.7	28.2	77.7	0	11	0	0	2	1902.79	5,635.19	5,417,900.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	VSGGGYDFGYDGDFY	99.70%	2.87	0.715	46.6	25.0	46.6	0	6	0	0	2	1618.63	6,243.35	1,566,070.00
Collagen alpha-2(I) chain GN=COL1A2	sp|P08123|CO	100.00%	16	16	62	0.41%	6.08%	GVSGGGYDFGYDGDFYR	99.70%	3.92	0.727	74.6	27.8	74.6	0	7	0	0	2	1831.76	5,402.00	1,226,970.00
Collagen alpha-2(IV) chain GN=COL4A2	sp|P08572|CO	100.00%	2	3	7	0.03%	1.11%	GIAGIPQKIAVQPGTV	99.70%	2.34	0.191	37.9	27.9	26.8	0	2	0	0	2	1548.91	6,142.93	531,956.00
Collagen alpha-2(IV) chain GN=COL4A2	sp|P08572|CO	100.00%	2	3	7	0.03%	1.11%	GIAGIPQKIAVQPGTVGPQ	99.70%	4.04	0.558	68.8	30.2	68.8	0	3	2	0	2	1831.04	5,877.87	2,950,430.00
Collagen alpha-2(IV) chain GN=COL4A2	sp|P08572|CO	100.00%	2	3	5	0.03%	1.11%	GIAGIPQKIAVQPGTV	99.70%	2.59	0.310	32.5	26.6	32.5	0	1	0	0	2	1548.91	5,806.55	529,002.00
Collagen alpha-2(IV) chain GN=COL4A2	sp|P08572|CO	100.00%	2	3	5	0.03%	1.11%	GIAGIPQKIAVQPGTVGPQ	99.70%	4.77	0.624	75.8	28.7	75.8	0	3	1	0	2	1831.04	5,619.40	6,710,130.00
Collagen alpha-2(V) chain GN=COL5A2	sp|P05997|CO	100.00%	4	6	15	0.06%	2.27%	LGDIMGHYDESMPDPLPE	99.70%	2.41	0.446	21.6	29.1	21.6	0	1	0	0	2	2015.87	7,342.70	555,590.00
Collagen alpha-2(V) chain GN=COL5A2	sp|P05997|CO	100.00%	4	6	15	0.06%	2.27%	GEPGLVPVVTGIR	99.70%	2.39	0.556	43.4	29.2	43.4	0	1	0	0	2	1293.75	6,451.61	747,044.00
Collagen alpha-2(V) chain GN=COL5A2	sp|P05997|CO	100.00%	4	6	15	0.06%	2.27%	LVPVVTGIR	99.70%	1.86	0.564	39.6	25.0	39.6	0	1	0	0	2	953.61	5,289.24	1,291,090.00
Collagen alpha-2(V) chain GN=COL5A2	sp|P05997|CO	100.00%	4	6	15	0.06%	2.27%	LGDIMGHYDESMPDPLPEFTE	99.70%	3.18	0.594	55.4	27.9	55.4	0	11	1	0	2	2393.03	8,494.71	2,201,580.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	LGSDVDMDVLTT	99.70%	2.07	0.245	39.1	32.1	25.3	0	1	0	0	2	1265.59	6,607.07	510,481.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	VTMQSPTDILLFH	99.70%	2.18	0.278	37.3	33.7	19.2	0	1	0	0	2	1501.77	8,068.71	80,861.80
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	LGSDVDMDVLTTLSLGDRA	99.70%	2.92	0.357	39.0	34.2	39.0	0	1	0	0	2	1977.98	8,704.91	41,966.80
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	ISQLQNEFYLDQVA	99.70%	2.94	0.418	35.5	33.7	35.5	0	1	0	0	2	1667.83	7,608.95	244,067.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	LLQFGGPGEQQ	99.70%	2.70	0.422	32.0	32.8	20.6	0	2	0	0	2	1173.59	5,696.52	653,138.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	MLPDSTEIDQDTINR	99.70%	3.96	0.435	65.4	32.3	65.4	0	3	0	0	2	1747.82	5,262.63	802,016.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	IHEALETTQY	99.70%	2.43	0.445	23.5	32.8	23.5	0	1	0	0	2	1204.58	4,206.30	341,674.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	VGVVQYSHEGTFEA	99.70%	2.85	0.493	24.0	32.5	24.0	0	1	0	0	2	1522.72	5,264.00	318,862.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	LAQPGFFDRF	99.70%	2.69	0.494	54.8	32.5	39.3	0	2	0	0	2	1197.61	7,526.59	1,344,530.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	VALLQFGGPGEQQ	99.70%	2.95	0.542	60.1	33.2	43.4	0	2	0	0	2	1343.70	6,978.13	622,934.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	LGSDVDMDVLTTLSLGDRAA	99.70%	5.28	0.572	116.0	34.4	105.0	0	4	0	0	2	2049.02	8,392.91	941,932.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	IHEALETTQYLNS	99.70%	3.15	0.576	41.0	33.1	41.0	0	2	0	0	2	1518.74	5,104.68	1,504,920.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	13	14	23	0.09%	0.00%	LGSDVDMDVLTTLSLGDR	99.70%	3.84	0.576	56.7	34.0	45.3	0	2	0	0	2	1922.94	7,884.93	226,804.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	2	2	2	0.01%	0.00%	LAQPGFFDRF	99.70%	2.70	0.409	26.2	32.6	10.1	0	1	0	0	2	1197.61	6,345.32	417,271.00
Collagen alpha-2(VI) chain GN=COL6A2	sp|P12110|CO	100.00%	2	2	2	0.01%	0.00%	LGSDVDMDVLTTLSLGDRAA	99.70%	3.76	0.431	29.4	34.6	29.4	0	1	0	0	2	2065.01	7,171.49	55,217.40
Collagen alpha-2(VIII) chain GN=COL8A2	sp|P25067|CO	100.00%	1	1	1	0.00%	2.56%	LRPNDQVWVQMPSDQANG	99.70%	3.54	0.568	38.0	32.8	38.0	0	1	0	0	2	2054.97	5,988.10	164,669.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVFIPAEFR	99.70%	1.95	0.122	40.8	30.3	9.9	0	1	0	0	2	1091.62	7,586.93	648,769.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FRELPNIEER	99.70%	1.90	0.168	48.7	33.2	34.3	0	0	1	0	2	1302.68	4,723.93	48,358.50
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FAIGNKGADQAELEEIA	99.70%	2.99	0.248	55.3	34.1	31.3	0	1	0	0	2	1775.88	6,443.63	2,362,060.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FDFDEYQPEMLEKFR	99.70%	1.95	0.307	33.6	31.3	21.7	0	0	2	0	2	1993.90	7,874.72	410,594.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVDKSTELNEEPLMR	99.70%	3.54	0.311	37.2	34.2	23.0	0	0	1	0	2	1773.91	4,906.76	191,337.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	VAPFTIARNADQEELVKIS	99.70%	2.55	0.349	28.9	33.8	28.9	0	0	1	0	2	2101.13	6,666.08	2,211,960.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	VSTFRELPSLEQKL	99.70%	2.69	0.366	24.2	32.2	14.1	0	0	1	0	2	1646.91	6,559.80	173,393.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVLISSGKSDDEVDDPAVE	99.70%	3.32	0.413	28.5	34.0	28.5	0	1	0	0	2	1987.97	5,808.65	380,983.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	VAIPTFRQLGTVQQ	99.70%	2.85	0.413	27.6	31.8	16.4	0	1	0	0	2	1557.87	6,676.64	278,841.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	VREFRELPNIEER	99.70%	3.16	0.413	20.9	33.7	10.3	0	0	1	0	2	1686.89	4,855.72	249,412.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FAIGNKGADQAELEE	99.70%	3.32	0.416	75.0	32.8	60.3	0	1	0	0	2	1591.76	5,003.32	883,198.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	ITNDPRLVFT	99.70%	2.53	0.418	38.2	32.6	38.2	0	1	0	0	2	1175.64	5,830.86	204,680.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	IAFVITGGKSVEDAQDVS	99.70%	3.83	0.442	69.2	34.2	49.1	0	1	0	0	2	1835.94	6,141.54	1,186,800.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FRELPNIEERIMNS	99.70%	2.85	0.446	35.6	34.2	19.4	0	0	2	0	2	1747.88	6,603.55	865,620.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FTIARNADQEELVKIS	99.70%	3.64	0.451	36.8	33.9	36.8	0	0	1	0	2	1833.97	5,819.31	413,831.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	VREFRELPNIEERIMNS	99.70%	3.50	0.471	23.8	34.6	23.8	0	0	1	0	2	2132.09	6,596.91	618,735.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVFIPAEFRAAPLQG	99.70%	2.74	0.477	23.4	31.4	23.4	0	1	0	0	2	1628.92	8,155.43	270,303.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVQYNSDPTDEFF	99.70%	2.56	0.484	28.4	30.3	28.4	0	1	0	0	2	1574.70	7,670.16	354,549.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FRVGNVQELSELSEQVLET	99.70%	4.03	0.490	65.1	34.6	65.1	0	1	0	0	2	2177.11	8,713.66	256,056.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVLPAGRDLTDFLENV	99.70%	3.11	0.492	35.8	33.1	35.8	0	1	0	0	2	1771.96	9,808.32	111,312.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	ISFIPDFAVAIPT	99.70%	2.97	0.496	46.0	32.5	33.0	0	1	0	0	2	1390.76	10,070.90	73,442.70
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FSDDPKVEFL	99.70%	2.81	0.506	32.3	32.6	17.4	0	2	0	0	2	1196.58	6,800.15	577,297.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LIDGSQSAGPEFQYVRT	99.70%	3.33	0.508	62.6	34.2	50.0	0	1	0	0	2	1867.92	5,885.54	78,616.20

Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVNSLDIGNDNIRVG	99.70%	3.05	0.511	45.0	33.2	45.0	0	1	0	0	2	1598.85	6,304.80	290,805.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	IGNKGADQAELEEIAFDSS	99.70%	3.28	0.515	24.1	32.8	24.1	0	1	0	0	2	1993.94	6,668.29	296,701.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LYTGSALDFVR	99.70%	2.39	0.515	40.4	32.6	40.4	0	1	0	0	2	1241.65	6,675.77	305,999.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	VIQFSDDPKVEFL	99.70%	3.56	0.524	29.3	33.7	9.3	0	2	0	0	2	1536.79	7,827.45	470,320.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	QLGTVQQVISERVTQ	99.70%	3.52	0.548	51.7	32.8	51.7	0	1	0	0	2	1685.92	6,133.36	386,091.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	VGNVQELSELSEQVLET	99.70%	3.80	0.556	46.4	34.1	46.4	0	1	0	0	2	1873.94	8,589.05	185,219.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FAIGNKGADQAELEEIAFDSS	99.70%	4.31	0.575	38.7	33.2	28.4	0	4	0	0	2	2212.04	7,539.73	1,642,580.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	QINVGNALEYVSR	99.70%	3.10	0.577	62.0	33.6	62.0	0	2	0	0	2	1462.76	6,860.00	1,918,970.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	GGAVPIGIGIGNADITEMQT	99.70%	4.22	0.609	35.0	34.1	23.5	0	2	0	0	2	1929.96	6,910.36	694,692.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	ISFIPDFAVAIPTFR	99.70%	3.02	0.619	62.0	32.5	62.0	0	1	0	0	2	1693.93	10,055.70	43,744.20
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LDTSEGVNQDTFGR	99.70%	4.17	0.642	65.4	31.5	65.4	0	1	0	0	2	1538.71	4,315.53	200,398.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	FALDTSEGVNQDTFGR	99.70%	4.08	0.655	59.6	32.0	59.6	0	1	0	0	2	1756.81	5,978.86	401,332.00
Collagen alpha-3(VI) chain GN=COL6A3	sp|P12111|CO	100.00%	36	36	45	0.17%	0.00%	LVLISSGKSDDEVDDPAVELKQFG	99.70%	5.29	0.663	50.0	35.3	50.0	0	0	1	0	2	2561.30	7,318.20	472,544.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	LTELHLDGNKISR	99.70%	2.19	0.308	27.0	32.1	27.0	0	0	1	0	2	1495.82	4,235.05	128,876.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	LHLDGNKISRVDAAS	99.70%	2.19	0.362	23.4	32.9	23.4	0	0	1	0	2	1595.85	4,047.96	179,221.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	VSLFSNPVQYWE	99.70%	3.49	0.407	38.1	33.3	18.9	0	2	0	0	2	1468.71	9,174.32	310,468.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	LFSNPVQYWE	99.70%	2.54	0.505	55.7	32.4	38.5	0	3	0	0	2	1282.61	8,235.64	2,643,200.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	IGPEVPDDRDFEPS	99.70%	2.64	0.525	34.1	31.0	34.1	0	1	0	0	2	1572.72	5,443.09	615,425.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	VDAASLKGLNNLAKLGLS	99.70%	4.06	0.565	30.4	29.8	30.4	0	0	1	0	2	1784.03	7,355.10	324,979.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	VDAASLKGLNNLAKLG	99.70%	3.02	0.578	35.1	30.0	35.1	0	0	1	0	2	1583.91	6,543.91	337,344.00
Decorin GN=DCN	sp|P07585|PG	100.00%	8	8	13	0.05%	15.90%	LTELHLDGNKISRVDAAS	99.70%	3.83	0.589	48.8	33.8	48.8	0	0	3	0	2	1939.02	4,886.37	2,789,480.00
Dermatopontin GN=DPT	sp|Q07507|DE	100.00%	2	2	2	0.01%	0.00%	YFESVLDREWQ	99.70%	2.28	0.332	21.7	32.0	21.7	0	1	0	0	2	1471.69	7,181.84	250,674.00
Dermatopontin GN=DPT	sp|Q07507|DE	100.00%	2	2	2	0.01%	0.00%	ISYNYDYYIR	99.70%	2.49	0.518	51.4	32.0	51.4	0	1	0	0	2	1369.64	6,215.31	300,082.00
EMILIN-1 GN=EMILIN1	sp|Q9Y6C2|EM	100.00%	2	2	2	0.01%	0.00%	LAHSEEPLTIFSGAL	99.70%	2.34	0.297	45.3	33.3	30.7	0	1	0	0	2	1584.83	8,492.25	124,193.00
EMILIN-1 GN=EMILIN1	sp|Q9Y6C2|EM	100.00%	2	2	2	0.01%	0.00%	VARVDSGGYEPEGLENKPVAESQPSPGTLGVFS	99.70%	3.42	0.478	32.1	35.9	32.1	0	0	1	0	2	3373.65	6,543.29	83,269.70
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	FFSPMLGEF	99.70%	1.82	0.202	38.1	30.3	24.3	0	1	0	0	2	1090.49	8,397.73	26,751.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	FFDTASTGKTFPG	99.70%	2.52	0.480	53.1	32.1	53.1	0	4	0	0	2	1375.65	5,712.80	2,483,390.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	FRPDSPGSGNARPNNPDWGTFEE	99.70%	3.22	0.481	24.3	30.1	24.3	0	0	1	0	2	2547.13	5,594.35	458,574.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	FFDTASTGKTFPGF	99.70%	2.81	0.487	36.1	32.6	24.9	0	4	0	0	2	1522.72	7,557.40	951,911.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	LIDEVNQDFTNR	99.70%	4.02	0.543	67.3	33.2	67.3	0	1	0	0	2	1463.71	5,061.25	906,723.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	FFSPMLGEFVSETESRGSESG	99.70%	4.46	0.619	70.3	30.1	59.1	0	4	0	0	2	2280.01	8,297.09	689,216.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	FFSPMLGEFVSETESR	99.70%	3.24	0.636	57.1	31.2	57.1	0	4	0	0	2	1878.86	8,377.40	978,614.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	8	10	20	0.08%	0.00%	NPSSAGSWNSGSSGPGSTGNR	99.70%	3.69	0.708	108.0	28.8	108.0	0	1	0	0	2	1963.85	3,109.44	26,520.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	4	4	4	0.03%	0.00%	LIDEVNQDFTNR	99.70%	3.09	0.457	50.5	33.4	50.5	0	1	0	0	2	1463.71	4,050.07	189,342.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	4	4	4	0.03%	0.00%	FFDTASTGKTFPGF	99.70%	2.65	0.476	36.0	33.0	18.9	0	1	0	0	2	1522.72	6,607.18	210,032.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	4	4	4	0.03%	0.00%	FFDTASTGKTFPG	99.70%	2.56	0.513	29.7	32.7	29.7	0	1	0	0	2	1375.65	4,805.45	902,865.00
Fibrinogen alpha chain GN=FGA	sp|P02671|FIB	100.00%	4	4	4	0.03%	0.00%	NPSSAGSWNSGSSGPGSTGNR	99.70%	3.77	0.637	50.2	29.7	50.2	0	1	0	0	2	1963.85	2,100.41	13,919.40
Fibrinogen beta chain GN=FGB	sp|P02675|FIB	100.00%	1	1	2	0.01%	0.00%	LRPAPPPISGGGYR	99.70%	2.16	0.417	25.0	31.7	12.4	0	0	2	0	2	1437.80	4,028.32	373,568.00
Fibrinogen beta chain GN=FGB	sp|P02675|FIB	100.00%	1	1	1	0.01%	0.00%	LRPAPPPISGGGYR	99.70%	3.06	0.463	33.9	30.7	18.4	0	0	1	0	2	1437.80	3,478.36	379,078.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FWLGNEKIHL	99.70%	2.18	0.339	23.8	32.4	10.3	0	0	1	0	2	1256.68	7,270.59	546,013.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FWLGNEKIHL	99.70%	2.18	0.339	23.8	32.4	10.3	0	0	1	0	2	1256.68	7,270.59	546,013.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FDGFDFGDDPSDKF	99.70%	3.26	0.620	66.0	25.2	66.0	0	2	0	0	2	1608.65	7,631.11	396,776.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FDGFDFGDDPSDKF	99.70%	3.26	0.620	66.0	25.2	66.0	0	2	0	0	2	1608.65	7,631.11	396,776.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FAGGDAGDAFDGFDFGDDPSDKFFTSHNGMQ	99.70%	3.97	0.630	37.7	25.0	37.7	0	0	1	0	2	3272.32	8,251.58	33,564.20
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FAGGDAGDAFDGFDFGDDPSDKFFTSHNGMQ	99.70%	3.97	0.630	37.7	25.0	37.7	0	0	1	0	2	3272.32	8,251.58	33,564.20
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FAGGDAGDAFDGFDFGDDPSDKFF	99.70%	4.82	0.684	77.7	25.0	77.7	0	1	0	0	2	2517.02	9,250.93	44,706.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FAGGDAGDAFDGFDFGDDPSDKFF	99.70%	4.82	0.684	77.7	25.0	77.7	0	1	0	0	2	2517.02	9,250.93	44,706.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	YFAGGDAGDAFDGFDFGDDPSDKF	99.70%	4.52	0.737	66.4	25.0	66.4	0	1	0	0	2	2533.01	8,617.98	50,170.50
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	YFAGGDAGDAFDGFDFGDDPSDKF	99.70%	4.52	0.737	66.4	25.0	66.4	0	1	0	0	2	2533.01	8,617.98	50,170.50
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FAGGDAGDAFDGFDFGDDPSDKF	99.70%	5.47	0.738	67.7	25.0	67.7	0	8	1	0	2	2369.95	8,213.68	2,501,710.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	100.00%	6	7	15	0.06%	0.00%	FAGGDAGDAFDGFDFGDDPSDKF	99.70%	5.47	0.738	67.7	25.0	67.7	0	8	1	0	2	2369.95	8,213.68	2,501,710.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	99.90%	1	1	4	0.03%	0.00%	FAGGDAGDAFDGFDFGDDPSDKF	99.70%	5.90	0.743	74.3	25.7	74.3	0	4	0	0	2	2369.95	7,194.95	479,557.00
Fibrinogen gamma chain GN=FGG	sp|P02679-2|F	99.90%	1	1	4	0.03%	0.00%	FAGGDAGDAFDGFDFGDDPSDKF	99.70%	5.90	0.743	74.3	25.7	74.3	0	4	0	0	2	2369.95	7,194.95	479,557.00
Galectin-3 GN=LGALS3	sp|P17931|LE	100.00%	2	2	2	0.01%	0.00%	IALDFQRGNDVA	99.70%	2.10	0.397	23.2	33.5	0.0	0	1	0	0	2	1318.68	5,618.34	116,679.00
Galectin-3 GN=LGALS3	sp|P17931|LE	100.00%	2	2	2	0.01%	0.00%	LHDALSGSGNPNPQGWPG	99.70%	3.63	0.536	32.4	31.5	32.4	0	1	0	0	2	1803.84	5,406.20	823,199.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LSSHIANVERVP	99.70%	3.01	0.265	27.6	32.6	16.4	0	0	1	0	2	1321.72	4,246.27	33,427.30
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LGWDDDYWS	99.70%	1.65	0.346	31.8	25.0	31.8	0	1	0	0	2	1156.46	7,895.79	215,908.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LVADENPFAQGA	99.70%	3.04	0.383	48.9	32.4	25.2	0	3	0	0	2	1231.60	6,191.33	1,836,580.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LDTWDQVFVWVGKDSQEEEKTEA	99.70%	3.01	0.411	36.3	33.0	36.3	0	0	1	0	2	2739.28	8,723.12	207,389.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	VLPEGGETPLFKQF	99.70%	2.09	0.412	19.1	33.5	5.3	0	1	0	0	2	1561.83	7,423.76	187,865.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	AVEVLPKAGALNSNDAFVLKTPSAAY	99.70%	3.44	0.428	24.9	34.1	24.9	0	0	1	0	2	2646.41	7,118.62	173,746.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	AQSTQDEVAASAILTAQLDEELGGTPVQSR	99.70%	3.75	0.442	37.3	35.8	21.5	0	0	1	0	2	3085.53	8,513.84	277,904.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LSSHIANVERVPFDAAT	99.70%	2.50	0.487	40.5	34.0	40.5	0	1	0	0	2	1826.94	5,564.42	282,030.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	VAASAILTAQLDEELGGTPVQSR	99.70%	3.08	0.492	19.5	34.5	8.3	0	0	1	0	2	2326.23	7,931.49	385,298.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	VLPEGGETPLFKQ	99.70%	2.45	0.502	20.3	32.9	20.3	0	1	0	0	2	1414.76	5,688.81	317,966.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LMQEDLATDDVML	99.70%	2.82	0.532	57.6	31.6	57.6	0	1	0	0	2	1493.69	7,712.75	247,014.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LGWDDDYWSVDPLDRA	99.70%	4.26	0.533	53.5	30.4	53.5	0	1	0	0	2	1922.86	8,704.37	325,738.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	IEGSNKVPVDPATYGQ	99.70%	3.01	0.582	33.3	33.9	33.3	0	2	0	0	2	1674.83	4,578.84	223,724.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LGWDDDYWSVDPLDRAMAE	99.70%	2.99	0.591	22.1	28.6	22.1	0	1	0	0	2	2269.97	8,521.57	38,284.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	LWVGTGASEAEKTGAQE	99.70%	4.98	0.605	66.1	33.7	66.1	0	1	0	0	2	1733.83	4,794.23	147,874.00
Gelsolin GN=GSN	sp|P06396|GE	100.00%	16	16	19	0.07%	0.00%	ASAILTAQLDEELGGTPVQSR	99.70%	3.67	0.646	26.1	34.6	26.1	0	1	0	0	2	2156.12	6,996.94	77,999.70
Isoform 14 of Fibronectin GN=FN1	sp|P02751-14|	100.00%	2	2	3	0.01%	0.00%	VTWAPPPSIDLTNF	99.70%	3.79	0.400	54.0	33.8	40.4	0	2	0	0	2	1557.79	8,943.48	248,112.00
Isoform 14 of Fibronectin GN=FN1	sp|P02751-14|	100.00%	2	2	3	0.01%	0.00%	QKTGLDSPTGIDFSDITANS	99.70%	2.55	0.437	21.9	33.6	21.9	0	1	0	0	2	2066.99	6,797.29	166,173.00
Isoform 15 of Fibronectin GN=FN1	sp|P02751-15|	100.00%	2	2	2	0.01%	0.00%	MLRGPGPGL	99.70%	1.91	0.327	34.6	30.2	16.1	0	1	0	0	2	897.50	2,473.30	1,614,430.00
Isoform 15 of Fibronectin GN=FN1	sp|P02751-15|	100.00%	2	2	2	0.01%	0.00%	VTWAPPPSIDLTNF	99.70%	2.69	0.495	33.2	33.5	33.2	0	1	0	0	2	1557.79	8,406.59	178,692.00
Isoform 3 of Dystonin GN=DST	sp|Q03001-3|D	99.70%	1	1	2	0.01%	0.00%	FQPPGAPLE	99.70%	2.12	0.000	40.2	31.3	0.0	0	2	0	0	2	955.49	4,947.44	744,654.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	ITSDILEALGR	99.70%	2.73	0.192	56.0	31.8	17.2	0	1	0	0	2	1187.66	7,265.75	109,702.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	LQNIILYH	99.70%	2.70	0.266	41.8	30.8	28.6	0	1	0	0	2	1013.58	5,764.71	125,115.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	ITSDILEALGRDGHFT	99.70%	2.01	0.330	46.6	34.1	30.1	0	2	3	0	2	1744.89	7,400.40	7,840,240.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	VLTQIGTSIQDFIEAEDDLSS	99.70%	4.17	0.417	24.2	34.5	24.2	0	0	1	0	2	2281.11	10,338.00	22,338.60
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	LLTQPGDWTL	99.70%	2.70	0.488	61.3	32.8	61.3	0	3	0	0	2	1143.60	8,215.85	826,155.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	VLPIDHVYGTLG	99.70%	2.49	0.507	16.4	31.8	16.4	0	2	0	0	2	1283.70	6,600.24	2,536,140.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	FAPSNEAWDNLDSDIR	99.70%	3.15	0.522	75.1	30.9	75.1	0	5	0	0	2	1849.84	6,884.61	4,304,140.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	LASALRPDGEYTL	99.70%	2.74	0.533	40.5	33.7	40.5	0	2	0	0	2	1405.73	5,950.49	966,067.00
Isoform 3 of Periostin GN=POSTN	sp|Q15063-3|P	100.00%	9	11	25	0.10%	0.00%	ITSDILEALGRDGHFTL	99.70%	2.81	0.545	35.6	34.0	21.4	0	2	3	0	2	1857.97	8,565.85	4,051,450.00
Isoform 4 of Plectin GN=PLEC	sp|Q15149-4|P	100.00%	3	3	3	0.01%	1.06%	LREQLQLLEEQHRAA	99.70%	3.77	0.294	36.0	33.1	24.3	0	0	1	0	2	1833.99	4,861.27	125,352.00
Isoform 4 of Plectin GN=PLEC	sp|Q15149-4|P	100.00%	3	3	3	0.01%	1.06%	LQEAGILSAEELQR	99.70%	3.55	0.391	39.8	33.3	39.8	0	1	0	0	2	1556.83	5,988.47	300,647.00
Isoform 4 of Plectin GN=PLEC	sp|Q15149-4|P	100.00%	3	3	3	0.01%	1.06%	LFDEEMNEILTDPSDDTKG	99.70%	4.12	0.493	25.1	29.8	25.1	0	1	0	0	2	2168.95	7,468.91	133,384.00
Isoform 5 of Protein disulfide-isomerase A6 GN=PDIA6	sp|Q15084-5|P	100.00%	1	2	2	0.01%	0.00%	LTDDSFDKNVLDSEDVWMVE	99.70%	2.92	0.500	25.5	29.2	25.5	0	2	0	0	2	2373.04	8,229.30	143,853.00
Isoform B of Collagen alpha-1(XI) chain GN=COL11A1	sp|P12107-2|C	100.00%	1	2	2	0.01%	0.00%	GPPGTMLMLP	99.70%	2.19	0.424	28.4	32.2	11.5	0	1	0	0	2	1045.51	7,047.43	109,671.00
Isoform B of Collagen alpha-1(XI) chain GN=COL11A1	sp|P12107-2|C	100.00%	1	2	2	0.01%	0.00%	ISAQEAQAQAILQQAR	99.70%	3.62	0.440	93.1	33.2	68.5	0	1	1	0	2	1725.92	5,847.44	398,302.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LEVNQLEKFDIKS	99.70%	2.51	0.277	18.5	33.2	7.7	0	0	1	0	2	1562.84	6,167.57	213,235.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LEVNQLEKFD	99.70%	3.24	0.367	56.5	33.4	43.5	0	1	0	0	2	1234.63	5,995.52	499,383.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LPSGLPVSLLT	99.70%	1.65	0.370	32.6	26.7	21.1	0	1	0	0	2	1096.66	8,541.42	80,462.60
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LVELDLSYNK	99.70%	3.47	0.400	38.4	32.5	26.9	0	1	0	0	2	1193.64	5,945.41	586,227.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	VNENLENYY	99.70%	2.58	0.423	31.7	29.0	31.7	0	2	0	0	2	1157.51	5,633.86	2,028,770.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LVELDLSYNKLKNIPT	99.70%	2.43	0.427	23.6	31.3	13.2	0	0	1	0	2	1860.05	6,953.39	2,293,280.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LSFNQIAR	99.70%	2.48	0.433	54.0	31.6	36.4	0	1	0	0	2	948.53	5,217.74	337,407.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LVELDLSYNKLKNIPTVNENLENYY	99.70%	4.53	0.459	51.6	35.8	36.5	0	0	3	0	2	2998.54	8,094.24	2,633,280.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	KNIPTVNENLENYY	99.70%	2.72	0.468	24.0	33.6	24.0	0	1	0	0	2	1710.83	6,037.11	301,557.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	IARLPSGLPVSL	99.70%	2.62	0.493	30.1	25.0	12.6	0	2	0	0	2	1222.75	7,352.31	544,986.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LSFNQIARLPSGLPVS	99.70%	3.34	0.510	31.3	31.5	31.3	0	2	0	0	2	1698.95	8,000.37	662,378.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LSYNKLKNIPTVNENLENYY	99.70%	2.94	0.517	0.0	0.0	0.0	0	0	1	0	2	2429.23	6,709.31	413,431.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LSFNQIARLPSGLPVSLLT	99.70%	2.88	0.525	20.4	28.8	20.4	0	1	0	0	2	2026.17	9,592.51	104,744.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	LKNIPTVNENLENYY	99.70%	4.06	0.632	31.1	34.2	31.1	0	1	0	0	2	1823.92	6,524.24	1,186,610.00
Lumican GN=LUM	sp|P51884|LU	100.00%	15	15	23	0.09%	0.00%	IARLPSGLPVSLLT	99.70%	2.11	0.634	21.8	25.0	21.8	0	4	0	0	2	1436.88	8,134.75	815,984.00
Lumican GN=LUM	sp|P51884|LU	100.00%	1	1	1	0.01%	0.00%	IARLPSGLPVSL	99.70%	2.37	0.429	24.2	25.0	24.2	0	1	0	0	2	1222.75	6,948.88	149,582.00

Microfibril-associated glycoprotein 4 GN=MFAP4	sp|P55083-2|N	100.00%	2	2	3	0.01%	0.00%	LFVAGFEDGGAGDSLSYHSGQK	99.70%	2.93	0.374	33.8	32.7	33.8	0	0	1	0	2	2242.04	6,198.12	375,568.00
Microfibril-associated glycoprotein 4 GN=MFAP4	sp|P55083-2|N	100.00%	2	2	3	0.01%	0.00%	LFVAGFEDGGAGDSLSYHSGQK	99.70%	2.93	0.374	33.8	32.7	33.8	0	0	1	0	2	2242.04	6,198.12	375,568.00
Microfibril-associated glycoprotein 4 GN=MFAP4	sp|P55083-2|N	100.00%	2	2	3	0.01%	0.00%	LFVAGFEDGGAGDS	99.70%	4.15	0.593	79.2	30.5	68.9	0	2	0	0	2	1341.60	6,619.08	609,098.00
Microfibril-associated glycoprotein 4 GN=MFAP4	sp|P55083-2|N	100.00%	2	2	3	0.01%	0.00%	LFVAGFEDGGAGDS	99.70%	4.15	0.593	79.2	30.5	68.9	0	2	0	0	2	1341.60	6,619.08	609,098.00
Microfibril-associated glycoprotein 4 GN=MFAP4	sp|P55083|MF	99.80%	1	1	1	0.01%	0.00%	LFVAGFEDGGAGDSLSYHSGQK	99.70%	2.57	0.322	23.9	33.5	13.4	0	0	1	0	2	2242.04	5,360.63	267,825.00
Peroxiredoxin-5, mitochondrial GN=PRDX5	sp|P30044|PRI	100.00%	4	4	7	0.03%	15.00%	LAPNIISQL	99.70%	2.26	0.422	35.5	28.5	21.4	0	3	0	0	2	968.58	7,590.33	1,019,800.00
Peroxiredoxin-5, mitochondrial GN=PRDX5	sp|P30044|PRI	100.00%	4	4	7	0.03%	15.00%	LLADPTGAFGKETDLLLDDSLVS	99.70%	3.06	0.486	25.7	35.0	25.7	0	1	0	0	2	2390.23	9,282.96	76,024.90
Peroxiredoxin-5, mitochondrial GN=PRDX5	sp|P30044|PRI	100.00%	4	4	7	0.03%	15.00%	LADPTGAFGKETDLLLDDS	99.70%	4.15	0.557	30.7	34.0	30.7	0	2	0	0	2	1977.97	7,924.70	468,169.00
Peroxiredoxin-5, mitochondrial GN=PRDX5	sp|P30044|PRI	100.00%	4	4	7	0.03%	15.00%	LLADPTGAFGKETDLLLDDS	99.70%	3.70	0.564	45.9	34.4	45.9	0	1	0	0	2	2091.05	8,467.37	91,505.60
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	5	5	7	0.03%	0.00%	AAVDELGKVLTPTQVKNRPTS	99.70%	2.99	0.322	29.0	32.3	29.0	0	0	1	0	2	2224.23	5,388.49	444,578.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	5	5	7	0.03%	0.00%	LVLTDPDAPSR	99.70%	2.45	0.450	36.9	32.2	25.4	0	1	0	0	2	1183.63	4,453.22	154,488.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	5	5	7	0.03%	0.00%	PVDLSKWSGPLS	99.70%	2.62	0.460	37.4	32.5	25.5	0	2	0	0	2	1285.68	6,722.26	413,447.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	5	5	7	0.03%	0.00%	LQEVDEQPQHPLHVTYAG	99.70%	2.50	0.537	25.6	33.9	14.4	0	0	1	0	2	2061.00	4,617.40	1,080,630.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	5	5	7	0.03%	0.00%	ISWDGLDSGKLYT	99.70%	3.68	0.629	53.2	33.1	53.2	0	2	0	0	2	1454.72	6,985.83	1,445,120.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	4	4	7	0.05%	0.00%	LVLTDPDAPSR	99.70%	2.38	0.360	43.4	31.8	24.8	0	1	0	0	2	1183.63	3,706.85	703,483.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	4	4	7	0.05%	0.00%	AAVDELGKVLTPTQVKNRPTS	99.70%	3.73	0.411	15.6	31.1	15.6	0	0	1	0	2	2224.23	4,713.98	165,923.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	4	4	7	0.05%	0.00%	ISWDGLDSGKLYT	99.70%	3.21	0.464	46.3	33.3	46.3	0	3	0	0	2	1454.72	6,040.50	1,492,800.00
Phosphatidylethanolamine-binding protein 1 GN=PEBP1	sp|P30086|PEE	100.00%	4	4	7	0.05%	0.00%	PVDLSKWSGPLS	99.70%	2.81	0.587	41.1	32.3	26.2	0	2	0	0	2	1285.68	5,732.65	913,639.00
Plasminogen activator inhibitor 1 RNA-binding protein GN=SERBP1	sp|Q8NC51|PA	99.90%	1	1	1	0.01%	0.00%	RPDQQLQGEGKIIDR	99.70%	3.18	0.362	28.5	32.5	28.5	0	0	1	0	2	1752.94	2,638.89	82,709.00
Prelamin-A/C GN=LMNA	sp|P02545|LM	100.00%	2	2	4	0.02%	0.00%	SVGGSGGGSFGDNLVTRSY	99.70%	3.98	0.596	52.0	32.4	52.0	0	1	0	0	2	1816.85	5,868.20	353,998.00
Prelamin-A/C GN=LMNA	sp|P02545|LM	100.00%	2	2	4	0.02%	0.00%	SVGGSGGGSFGDNLVTR	99.70%	4.12	0.638	95.1	33.0	95.1	0	3	0	0	2	1566.75	4,947.09	795,898.00
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	6	7	8	0.03%	12.80%	LRWINLDNNR	99.70%	3.96	0.336	36.6	32.5	21.6	0	0	1	0	2	1313.71	5,646.57	469,848.00
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	6	7	8	0.03%	12.80%	KIDQRVLEKLPG	99.70%	2.92	0.381	29.0	27.4	29.0	0	0	1	0	2	1395.83	4,605.43	196,337.00
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	6	7	8	0.03%	12.80%	FHDFSSDLENVPH	99.70%	3.71	0.479	25.6	30.2	25.6	0	1	1	0	2	1543.68	5,757.96	926,757.00
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	6	7	8	0.03%	12.80%	IPPGVFSKLENLLL	99.70%	2.53	0.496	33.6	28.1	33.6	0	1	0	0	2	1539.91	10,187.50	13,159.50
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	6	7	8	0.03%	12.80%	FSSDLENVPH	99.70%	2.63	0.514	63.4	30.9	46.8	0	1	0	0	2	1144.53	4,822.40	222,058.00
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	6	7	8	0.03%	12.80%	IPPGVFSKLENLL	99.70%	3.22	0.549	27.3	29.5	27.3	0	2	0	0	2	1426.83	9,423.88	347,422.00
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	2	2	2	0.01%	6.02%	LRWINLDNNR	99.70%	3.16	0.244	27.5	32.0	15.7	0	0	1	0	2	1313.71	4,528.35	232,564.00
Prolargin GN=PRELP	sp|P51888|PRE	100.00%	2	2	2	0.01%	6.02%	IPPGVFSKLENLL	99.70%	2.91	0.463	32.1	28.5	32.1	0	1	0	0	2	1426.83	8,598.11	45,887.70
Protein disulfide-isomerase GN=P4HB	sp|P07237|PDI	100.00%	3	3	6	0.02%	0.00%	LVESSEVAVIGFFKDVESDSAKQF	99.70%	2.88	0.299	53.9	35.2	40.5	0	0	1	0	2	2631.32	9,740.84	207,656.00
Protein disulfide-isomerase GN=P4HB	sp|P07237|PDI	100.00%	3	3	6	0.02%	0.00%	LQAAEAIDDIPFG	99.70%	3.28	0.407	55.8	33.3	39.3	0	4	0	0	2	1359.68	8,010.65	1,752,420.00
Protein disulfide-isomerase GN=P4HB	sp|P07237|PDI	100.00%	3	3	6	0.02%	0.00%	VIGFFKDVESDSAKQF	99.70%	3.86	0.546	26.8	34.0	26.8	0	0	1	0	2	1816.91	7,144.06	428,076.00
Protein disulfide-isomerase GN=P4HB	sp|P07237|PDI	100.00%	4	4	4	0.03%	0.00%	LVESSEVAVIGFFKDVESDSAKQF	99.70%	3.17	0.371	20.0	35.2	20.0	0	0	1	0	2	2631.32	8,597.98	187,069.00
Protein disulfide-isomerase GN=P4HB	sp|P07237|PDI	100.00%	4	4	4	0.03%	0.00%	VIGFFKDVESDSAKQF	99.70%	2.68	0.430	18.6	34.1	18.6	0	0	1	0	2	1816.91	6,007.97	345,148.00
Protein disulfide-isomerase GN=P4HB	sp|P07237|PDI	100.00%	4	4	4	0.03%	0.00%	LAKVDATEESDLAQQYG	99.70%	2.87	0.478	27.5	34.1	27.5	0	1	0	0	2	1837.88	4,112.85	211,672.00
Protein disulfide-isomerase GN=P4HB	sp|P07237|PDI	100.00%	4	4	4	0.03%	0.00%	LQAAEAIDDIPFG	99.70%	3.17	0.540	55.0	33.7	37.3	0	1	0	0	2	1359.68	7,231.47	1,446,240.00
Scavenger receptor class A member 5 GN=SCARA5 PE=2 SV=1	sp|Q6ZMJ2|SC	100.00%	1	1	1	0.00%	0.00%	GEKGDRAGDASGVE	99.70%	2.54	0.277	49.5	31.0	38.1	0	1	0	0	2	1347.61	5,354.82	670,037.00
Talin-1 GN=TLN1	sp|Q9Y490|TLI	100.00%	2	2	2	0.01%	0.00%	IHSQVDAITAGTASVVN	99.70%	3.24	0.583	19.7	33.6	19.7	0	1	0	0	2	1682.87	5,117.05	140,939.00
Talin-1 GN=TLN1	sp|Q9Y490|TLI	100.00%	2	2	2	0.01%	0.00%	IVLDTASDVLDKASS	99.70%	3.06	0.584	35.7	33.7	25.5	0	1	0	0	2	1533.80	6,089.93	896,955.00
Talin-1 GN=TLN1	sp|Q9Y490|TLI	100.00%	1	1	1	0.01%	0.00%	IVLDTASDVLDKASS	99.70%	3.02	0.459	34.7	33.6	34.7	0	1	0	0	2	1533.80	5,339.03	543,436.00
Tenascin-R GN=TNR	sp|Q92752|TEI	100.00%	1	1	1	0.00%	0.00%	VISNILSLP	99.70%	2.37	0.242	40.2	27.8	23.2	0	1	0	0	2	955.58	5,636.36	457,403.00
Tenascin-X GN=TNXB	sp|P22105|TEN	100.00%	2	2	2	0.01%	0.00%	LLVDGDQSKILISGLEPSTPYRF	99.70%	2.78	0.295	27.3	33.5	27.3	0	0	1	0	2	2548.37	7,706.61	171,218.00
Tenascin-X GN=TNXB	sp|P22105|TEN	100.00%	2	2	2	0.01%	0.00%	LLTWTEPPVRPAGYLLS	99.70%	2.64	0.451	21.6	31.5	21.6	0	1	0	0	2	1913.05	7,914.32	93,748.40
Tensin-1 GN=TNS1	sp|Q9HBL0|TEI	100.00%	1	1	1	0.01%	0.00%	FLPTTHSPPGPQQPPASLPG	99.70%	2.97	0.473	24.4	34.2	24.4	0	1	0	0	2	2026.04	5,088.49	550,147.00
Transforming growth factor-beta-induced protein ig-h3 GN=TGFBI	sp|Q15582|BG	100.00%	3	3	3	0.01%	6.00%	LAAESDVSTAIDLFRQAGLGNH	99.70%	2.47	0.322	20.9	34.7	20.9	0	0	1	0	2	2285.15	8,806.48	130,594.00
Transforming growth factor-beta-induced protein ig-h3 GN=TGFBI	sp|Q15582|BG	100.00%	3	3	3	0.01%	6.00%	IFAPSNEAWASLPAEVLDS	99.70%	3.18	0.479	19.0	34.2	19.0	0	1	0	0	2	2016.99	9,645.67	145,741.00
Transforming growth factor-beta-induced protein ig-h3 GN=TGFBI	sp|Q15582|BG	100.00%	3	3	3	0.01%	6.00%	LAAESDVSTAIDLFR	99.70%	4.53	0.656	69.5	33.7	69.5	0	1	0	0	2	1607.83	8,136.45	342,109.00
Transforming growth factor-beta-induced protein ig-h3 GN=TGFBI	sp|Q15582|BG	100.00%	1	1	1	0.01%	2.64%	LAAESDVSTAIDLFRQAG	99.70%	3.04	0.508	46.2	34.1	46.2	0	1	0	0	2	1863.94	7,432.78	99,947.50
Tryptase alpha/beta-1 GN=TPSAB1	sp|Q15661|TR	99.60%	1	1	1	0.00%	0.00%	IIVHPQFY	99.70%	2.10	0.377	19.0	32.3	19.0	0	1	0	0	2	1016.56	5,877.38	66,535.00
Versican core protein GN=VCAN	sp|P13611|CSF	100.00%	1	1	1	0.00%	0.32%	LTVDGVVFHYR	99.70%	2.27	0.366	26.5	33.2	11.8	0	0	1	0	2	1305.70	6,223.95	262,180.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LQEEIAFLKK	99.70%	3.03	0.190	35.5	29.4	7.5	0	0	1	0	2	1218.71	5,364.92	330,540.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	FADLSEAANR	99.70%	2.38	0.227	41.1	32.5	22.6	0	1	0	0	2	1093.53	4,045.90	86,497.70
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LADAINTEFKNTR	99.70%	2.58	0.254	33.3	33.5	7.3	0	0	1	0	2	1492.78	4,422.55	699,415.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	FLEQQNKILLAELEQ	99.70%	2.76	0.255	43.5	32.9	21.1	0	1	0	0	2	1815.99	7,649.90	543,487.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	HLREYQDLLNVKMA	99.70%	2.85	0.255	29.4	33.9	17.0	0	0	1	0	2	1729.91	6,048.52	113,013.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	VAAKNLQEAEEWYKSKFAD	99.70%	3.27	0.324	26.4	34.6	15.2	0	0	1	0	2	2227.10	6,761.34	762,996.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LDIEIATYR	99.70%	2.86	0.350	56.3	32.2	38.2	0	1	0	0	2	1093.59	6,075.93	682,783.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	SLYASSPGGVYATRSSAVR	99.70%	2.61	0.364	27.8	34.2	16.7	0	0	1	0	2	1928.98	4,438.02	716,561.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	VEVERDNLAEDIMR	99.70%	3.08	0.383	27.3	33.4	14.2	0	0	1	0	2	1688.83	5,809.65	464,962.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LGDLYEEEMRE	99.70%	2.42	0.387	34.0	30.1	23.4	0	1	0	0	2	1383.61	5,379.78	738,519.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LQAQIQEQHVQIDVDVSKPDLTAA	99.70%	4.10	0.423	25.8	35.0	25.8	0	0	1	0	2	2646.37	6,219.81	375,561.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	FANYIDKVRFLEQQNKIL	99.70%	3.23	0.425	0.0	0.0	0.0	0	0	0	1	2	2239.22	7,396.90	504,918.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LYASSPGGVYATRS	99.70%	2.75	0.433	48.4	33.1	38.0	0	1	0	0	2	1428.71	4,096.90	98,845.30
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LDIEIATYRKLLEGEESR	99.70%	3.51	0.441	26.1	34.0	15.4	0	0	1	0	2	2135.13	7,235.65	305,900.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	ISLPLPNFSS	99.70%	2.81	0.453	71.7	32.9	51.1	0	4	0	0	2	1074.58	8,163.73	1,195,560.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	VAAKNLQEAEEWYKSK	99.70%	3.49	0.458	33.5	34.2	33.5	0	0	1	1	2	1893.97	5,186.44	2,188,990.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	NNDALRQAKQESTEYR	99.70%	3.39	0.461	23.4	33.9	13.2	0	0	1	0	2	1922.93	3,435.06	209,055.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LYASSPGGVYATR	99.70%	2.68	0.468	47.7	33.1	37.2	0	1	0	0	2	1341.68	4,161.32	606,734.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LREYQDLLNVKMA	99.70%	2.75	0.472	25.8	33.7	25.8	0	0	2	0	2	1608.84	6,027.48	125,266.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	VEAANYQDTIGRLQDEIQN	99.70%	3.86	0.472	20.0	33.9	20.0	0	1	0	0	2	2177.05	6,909.17	144,280.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	FAVEAANYQDTIGRLQDEIQN	99.70%	3.86	0.478	23.1	34.3	23.1	0	1	0	0	2	2395.15	7,715.21	90,477.40
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	SSVPGVRLLQDSVDFS	99.70%	2.87	0.481	25.8	34.1	25.8	0	5	0	0	2	1705.88	7,649.78	4,626,550.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LRSSVPGVRLLQDSVDFS	99.70%	2.49	0.483	32.1	33.6	19.9	0	0	3	0	2	1975.06	7,354.97	1,975,660.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	SLYASSPGGVYATR	99.70%	3.42	0.486	48.7	33.0	36.6	0	2	0	0	2	1428.71	4,591.25	1,651,430.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	VRLLQDSVDFS	99.70%	2.83	0.492	50.2	33.4	39.4	0	1	0	0	2	1278.67	6,308.66	810,801.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LNDRFANYIDKVR	99.70%	3.36	0.497	47.4	33.1	35.5	0	0	1	0	2	1623.86	5,447.60	91,585.20
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	FAVEAANYQDTIGR	99.70%	4.12	0.502	56.8	32.9	45.6	0	1	0	0	2	1554.75	5,462.49	378,324.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	LADAINTEFKNTRTNEKVELQE	99.70%	3.46	0.514	0.0	0.0	0.0	0	0	1	0	2	2563.30	5,199.23	725,681.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	KVESLQEEIAFLKK	99.70%	3.55	0.517	31.1	30.3	31.1	0	0	1	0	2	1661.95	6,277.66	500,512.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	VAAKNLQEAEEWYKSKFADLSEAANR	99.70%	4.36	0.525	18.5	35.6	8.1	0	0	0	1	2	2968.48	7,514.58	762,921.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	TLLIKTVETRDGQVINETSQHHDDLE	99.70%	4.92	0.528	32.4	35.8	18.7	0	0	2	0	2	2991.50	5,440.26	876,706.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	VQIDVDVSKPDLTAA	99.70%	3.80	0.561	66.8	33.1	66.8	0	1	0	0	2	1570.83	5,926.72	495,729.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	AVEAANYQDTIGRLQDEIQN	99.70%	3.69	0.565	20.9	34.1	20.9	0	1	0	0	2	2248.08	7,008.80	87,018.80
Vimentin GN=VIM	sp|P08670|VIN	100.00%	34	36	49	0.19%	60.70%	ISLPLPNFSSLN	99.70%	2.45	0.594	53.5	32.9	40.5	0	3	0	0	2	1301.71	8,882.28	265,494.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	5	5	6	0.04%	13.30%	LQEEIAFLKK	99.70%	2.71	0.307	31.1	28.2	16.2	0	0	2	0	2	1218.71	4,456.77	161,247.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	5	5	6	0.04%	13.30%	KVESLQEEIAFLKK	99.70%	3.35	0.424	37.3	29.3	37.3	0	0	1	0	2	1661.95	5,236.58	147,662.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	5	5	6	0.04%	13.30%	SSVPGVRLLQDSVDFS	99.70%	2.85	0.440	27.8	34.1	27.8	0	1	0	0	2	1705.88	6,812.96	588,964.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	5	5	6	0.04%	13.30%	VAAKNLQEAEEWYKSK	99.70%	3.11	0.441	17.5	33.9	17.5	0	0	1	0	2	1893.97	3,937.53	300,788.00
Vimentin GN=VIM	sp|P08670|VIN	100.00%	5	5	6	0.04%	13.30%	NNDALRQAKQESTEYR	99.70%	3.34	0.455	29.6	34.3	29.6	0	0	1	0	2	1922.93	2,245.66	54,087.60
X-ray repair cross-complementing protein 5 GN=XRCC5	sp|P13010|XRC	100.00%	3	4	7	0.03%	0.00%	VFEEGGDVDDLLDMI	99.70%	3.43	0.464	54.9	30.5	54.9	0	3	0	0	2	1682.75	9,037.12	505,013.00
X-ray repair cross-complementing protein 5 GN=XRCC5	sp|P13010|XRC	100.00%	3	4	7	0.03%	0.00%	LAEGSVTSVGSVNPAENFR	99.70%	4.08	0.523	63.1	34.2	63.1	0	2	0	0	2	1933.96	5,758.40	360,173.00
X-ray repair cross-complementing protein 5 GN=XRCC5	sp|P13010|XRC	100.00%	3	4	7	0.03%	0.00%	LAPKDKPSGDTAAVFEEGGDVDDLLDMI	99.70%	3.59	0.545	49.9	34.5	35.2	0	0	2	0	2	2918.40	9,046.27	160,774.00