Supplementary information
Table S1. List of peptides identified by LC-MS/MS in the CM-P1 secretome

Search Engine: Mascot
Version: 2.2.0
Samples: All Samples
Fragment Tolerance: 0,60 Da (Monoisotopic)
Parent Tolerance: 25 PPM (Monoisotopic)
Fixed Modifications: +57 on C (Carbamidomethyl)
Variable Modifications: +16 on M (Oxidation)
Database: the uniprot_sprot_release_2011_09_of_21-Sep-2011 database (selected for Homo sapiens, unknown version, 20323 entries)
Digestion Enzyme: Trypsin
Max Missed Cleavages: 1
Scaffold: Version: Scaffold_4.0.1
Peptide Thresholds: 95,0% minimum
Protein Thresholds: 95,0% minimum and 2 peptides minimum

Protein name	Protein AC	Protein Mw (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage	Peptide sequence	Previous amino acid	Next amino acid	Best Peptide identification probability	Best Mascot Ion score	Best Mascot Identity 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)	Peptide start index	Peptide stop index
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	AFQVWSDVTPLR	R	F	99.70%	45.5	26.3	0	1	0	0	2	1418.7427	147	158
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	ELAVQYLNTFYGCPK	K	E	99.70%	55.6	25	0	1	0	0	2	1802.8783	48	62
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	IDAVYEAPQEEK	K	A	99.70%	49.3	25.5	0	2	0	0	2	1391.6690	520	531
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	IIGYTPDLDPETVDDAFAR	R	A	99.70%	86.3	25	0	1	0	0	2	2108.0186	128	146
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	LSQDDIK	R	G	99.70%	32	27.2	0	1	0	0	2	818.4256	433	439
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	QDIVFDGIAQIR	K	G	99.70%	61.6	25.3	0	1	0	0	2	1374.7378	471	482
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	SDGFLWCSTTYNFEK	R	D	99.70%	39	25	0	1	0	0	2	1854.8004	253	267
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	VDAAFNWSK	R	N	98.70%	25.5	25.6	0	1	0	0	2	1037.5050	568	576
72 kDa type IV collagenase	P08253	73885.1	100.00%	9	9	10	0.08%	16.70%	WDKNQITYR	K	I	99.20%	21.8	26.6	0	0	1	0	2	1223.6168	119	127
78 kDa glucose-regulated protein	P11021	72334.7	100.00%	4	4	4	0.03%	8.56%	ELEEIVQPIISK	K	L	99.70%	41.5	25	0	1	0	0	2	1397.7888	622	633
78 kDa glucose-regulated protein	P11021	72334.7	100.00%	4	4	4	0.03%	8.56%	NQLTSNPENTVFDAK	K	R	99.70%	64.9	25.1	0	1	0	0	2	1677.8079	82	96
78 kDa glucose-regulated protein	P11021	72334.7	100.00%	4	4	4	0.03%	8.56%	SQIFSTASDNQPTVTIK	K	V	99.70%	62.6	25.1	0	1	0	0	2	1836.9339	448	464
78 kDa glucose-regulated protein	P11021	72334.7	100.00%	4	4	4	0.03%	8.56%	TWNDPSVQQDIK	R	F	99.70%	56	25.4	0	1	0	0	2	1430.6912	102	113
Annexin A2	P07355	38606.1	100.00%	7	7	8	0.07%	23.30%	AEDGSVIDYELIDQDAR	R	D	99.70%	39	25	0	1	0	0	2	1908.8824	180	196
Annexin A2	P07355	38606.1	100.00%	7	7	8	0.07%	23.30%	DIISDTSGDFR	K	K	99.70%	53.5	25	0	1	0	0	2	1225.5697	158	168
Annexin A2	P07355	38606.1	100.00%	7	7	8	0.07%	23.30%	GLGTDEDSLIEIICSR	K	T	99.70%	59	25.3	0	1	0	0	2	1777.8640	120	135
Annexin A2	P07355	38606.1	100.00%	7	7	8	0.07%	23.30%	GVDEVTIVNILTNR	K	S	99.70%	59.2	25	0	1	0	0	2	1542.8487	50	63
Annexin A2	P07355	38606.1	100.00%	7	7	8	0.07%	23.30%	QDIAFAYQR	R	R	99.70%	36	25.3	0	2	0	0	2	1111.5531	69	77
Annexin A2	P07355	38606.1	100.00%	7	7	8	0.07%	23.30%	RAEDGSVIDYELIDQDAR	R	D	99.70%	61.5	25	0	0	1	0	2	2064.9835	179	196
Annexin A2	P07355	38606.1	100.00%	7	7	8	0.07%	23.30%	SLYYYIQQDTK	K	G	99.70%	48.5	25.7	0	1	0	0	2	1421.6948	314	324
Biglycan	P21810	41655.9	100.00%	6	6	6	0.05%	16.30%	EISPDTTLLDLQNNDISELR	K	K	99.10%	25.9	25	0	1	0	0	2	2286.1463	87	106
Biglycan	P21810	41655.9	100.00%	6	6	6	0.05%	16.30%	EISPDTTLLDLQNNDISELRK	K	D	96.80%	17	25	0	0	1	0	2	2414.2413	87	107
Biglycan	P21810	41655.9	100.00%	6	6	6	0.05%	16.30%	IQAIELEDLLR	K	Y	99.70%	57.3	25	0	1	0	0	2	1312.7473	241	251
Biglycan	P21810	41655.9	100.00%	6	6	6	0.05%	16.30%	LAIQFGNYK	R	-	99.70%	32.8	25	0	1	0	0	2	1053.5728	359	367
Biglycan	P21810	41655.9	100.00%	6	6	6	0.05%	16.30%	VPSGLPDLK	R	L	99.30%	26.6	25	0	1	0	0	2	925.5355	292	300
Biglycan	P21810	41655.9	100.00%	6	6	6	0.05%	16.30%	VVQCSDLGLK	R	S	99.70%	37	26.4	0	1	0	0	2	1118.5876	73	82
Bone morphogenetic protein 1	P13497	111249.3	99.80%	2	2	2	0.02%	2.74%	AAAFLGDIALDEEDLR	K	A	99.70%	31.5	25.4	0	1	0	0	2	1718.8598	49	64
Bone morphogenetic protein 1	P13497	111249.3	99.80%	2	2	2	0.02%	2.74%	AFQVQQAVDLR	R	R	99.70%	60.1	26.1	0	1	0	0	2	1274.6852	65	75
Calreticulin	P27797	48142.9	100.00%	3	3	3	0.03%	9.83%	EQFLDGDGWTSR	K	W	99.70%	35.9	25	0	1	0	0	2	1410.6286	25	36
Calreticulin	P27797	48142.9	100.00%	3	3	3	0.03%	9.83%	FYALSASFEPFSNK	R	G	99.70%	86.3	25	0	1	0	0	2	1607.7739	74	87
Calreticulin	P27797	48142.9	100.00%	3	3	3	0.03%	9.83%	IKDPDASKPEDWDER	K	A	97.50%	17.4	25	0	0	0	1	2	1800.8402	208	222
Calumenin	O43852	37107.7	100.00%	6	7	7	0.06%	18.70%	DWILPSDYDHAEAEAR	K	H	99.70%	59.2	25	0	1	0	0	2	1887.8509	256	271
Calumenin	O43852	37107.7	100.00%	6	7	7	0.06%	18.70%	EQFVEFR	R	D	99.70%	39	25	0	1	0	0	2	954.4679	235	241
Calumenin	O43852	37107.7	100.00%	6	7	7	0.06%	18.70%	IDGDKDGFVTVDELK	K	D	99.70%	67	25.5	0	1	1	0	2	1650.8225	80	94
Calumenin	O43852	37107.7	100.00%	6	7	7	0.06%	18.70%	TFDQLTPEESK	K	E	99.70%	41.9	25.6	0	1	0	0	2	1294.6163	60	70
Calumenin	O43852	37107.7	100.00%	6	7	7	0.06%	18.70%	TFDQLTPEESKER	K	L	99.70%	27	25	0	0	1	0	2	1579.7600	60	72
Calumenin	O43852	37107.7	100.00%	6	7	7	0.06%	18.70%	WIYEDVER	R	Q	99.70%	31.2	25	0	1	0	0	2	1109.5262	104	111
Coiled-coil domain-containing protein 80	Q76M96	108176.4	100.00%	5	5	5	0.04%	7.47%	ASGVEGQVVAEGNDGGGGAGRPSLGSEK	K	K	99.70%	39.4	25	0	0	1	0	2	2542.2131	283	310
Coiled-coil domain-containing protein 80	Q76M96	108176.4	100.00%	5	5	5	0.04%	7.47%	LLLITAPK	R	A	99.70%	29.9	25	0	1	0	0	2	868.5868	625	632
Coiled-coil domain-containing protein 80	Q76M96	108176.4	100.00%	5	5	5	0.04%	7.47%	SVADLLGSFEGK	K	R	99.70%	71	26.1	0	1	0	0	2	1222.6315	611	622
Coiled-coil domain-containing protein 80	Q76M96	108176.4	100.00%	5	5	5	0.04%	7.47%	SVFDLIDTFQSR	K	I	99.70%	48.7	25.6	0	1	0	0	2	1427.7166	735	746
Coiled-coil domain-containing protein 80	Q76M96	108176.4	100.00%	5	5	5	0.04%	7.47%	VVDDEDLVDQR	R	L	99.70%	46	25	0	1	0	0	2	1302.6174	686	696
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	ALLLQGSNEIEIR	K	A	99.70%	63.7	25	0	2	0	0	2	1455.8167	1387	1399
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	DGEAGAQGPPGPAGPAGER	K	G	99.70%	51.2	25	0	1	0	0	2	1690.7783	613	631
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	DGLNGLPGPIGPPGPR	K	G	97.40%	22.7	25	0	1	0	0	2	1513.8126	1153	1168
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	DLEVDTTLK	R	S	99.60%	29.4	26.8	0	1	0	0	2	1033.5414	1228	1236
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	DRDLEVDTTLK	R	S	99.70%	42.3	26.4	0	1	1	0	2	1304.6695	1226	1236
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	EGAPGAEGSPGR	R	D	99.40%	26.5	25	0	1	0	0	2	1084.5019	1015	1026
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	FTYSVTVDGCTSHTGAWGK	R	T	99.70%	27.1	25	0	0	1	0	2	2073.9336	1406	1424
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GANGAPGIAGAPGFPGAR	K	G	99.70%	34.5	25.4	0	1	0	0	2	1537.7872	398	415
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GAPGDRGEPGPPGPAGFAGPPGADGQPGAK	R	G	99.70%	26.8	25	0	0	1	0	2	2639.2604	797	826
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GDAGAPGAPGSQGAPGLQGMPGER	K	G	99.70%	51	25	0	1	0	0	2	2150.9889	710	733
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GDAGPPGPAGPAGPPGPIGNVGAPGAK	K	G	99.70%	60	25	0	1	1	0	2	2233.1366	836	862
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GDRGETGPAGPPGAPGAPGAPGPVGPAGK	K	S	99.70%	30.8	25	0	0	1	0	2	2449.2225	1034	1062
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GEPGPPGPAGAAGPAGNPGADGQPGAK	R	G	99.70%	58.7	25	0	1	1	0	2	2252.0696	371	397
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GEPGPPGPAGFAGPPGADGQPGAK	R	G	99.70%	63.1	25	0	1	1	0	2	2085.9994	803	826
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GEPGPTGLPGPPGER	R	G	99.70%	31	25.5	0	1	0	0	2	1417.7074	473	487
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GEPGPVGVQGPPGPAGEEGK	K	R	99.70%	52.5	25	0	1	0	0	2	1815.8876	449	468
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GEPGPVGVQGPPGPAGEEGKR	K	G	99.40%	22	25.1	0	0	1	0	2	1971.9887	449	469
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GEQGPAGSPGFQGLPGPAGPPGEAGKPGEQGVPGDLGAPGPSGAR	R	G	99.70%	34.2	25	0	0	3	0	2	4016.9495	632	676
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GETGPAGPPGAPGAPGAPGPVGPAGK	R	S	99.70%	85.7	25	0	2	1	0	2	2121.0729	1037	1062
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GETGPAGRPGEVGPPGPPGPAGEK	R	G	99.70%	35.6	25	0	0	1	0	2	2168.0736	911	934
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GFPGADGVAGPK	R	G	99.70%	35.2	25.2	0	1	0	0	2	1072.5424	494	505
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GFPGLPGPSGEPGK	R	Q	99.70%	32.9	25.6	0	1	0	0	2	1296.6586	971	984
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GFSGLQGPPGPPGSPGEQGPSGASGPAGPR	R	G	99.70%	79.9	25	0	1	2	0	2	2657.2708	1112	1141
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GLTGPIGPPGPAGAPGDK	R	G	99.70%	39.8	26	0	1	0	0	2	1558.8229	764	781
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GLTGPIGPPGPAGAPGDKGESGPSGPAGPTGAR	R	G	99.70%	35.1	25	0	0	2	0	2	2837.4184	764	796
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GLTGSPGSPGPDGK	K	T	99.70%	79.5	25.5	0	1	0	0	2	1226.6015	539	552
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GNDGATGAAGPPGPTGPAGPPGFPGAVGAK	R	G	99.70%	41.7	25	0	0	1	0	2	2500.2221	323	352
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GPPGPMGPPGLAGPPGESGR	R	E	99.70%	65	25	0	1	0	0	2	1800.8703	995	1014
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GQAGVMGFPGPK	R	G	99.70%	45.5	25.9	0	2	0	0	2	1161.5724	575	586
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GSAGPPGATGFPGAAGR	R	V	99.70%	117	25.4	0	2	0	0	2	1427.7028	866	882
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GSPGADGPAGAPGTPGPQGIAGQR	K	G	99.70%	59.4	25	0	1	2	0	2	2073.0113	935	958
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GVPGPPGAVGPAGK	R	D	99.70%	35.6	25.5	0	1	0	0	2	1160.6425	599	612
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	GVQGPPGPAGPR	R	G	99.70%	34	26.7	0	2	0	0	2	1089.5802	686	697
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	KALLLQGSNEIEIR	K	A	99.70%	31.3	25	0	0	1	0	2	1583.9117	1386	1399
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	NWYISK	K	N	99.60%	27.5	25	0	1	0	0	2	810.4144	1311	1316
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	SGEYWIDPNQGCNLDAIK	K	V	99.70%	53.2	25	0	1	0	0	2	2079.9443	1271	1288
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	SLSQQIENIR	K	S	99.70%	54.8	26	0	1	0	0	2	1187.6379	1237	1246
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	TGPPGPAGQDGRPGPPGPPGAR	K	G	96.50%	17.6	25	0	0	1	0	2	1993.0004	553	574
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	VGPPGPSGNAGPPGPPGPAGK	R	E	99.70%	47.8	25.3	0	1	2	0	2	1764.9032	883	903
Collagen alpha-1(I) chain	P02452	138941.4	100.00%	40	48	60	0.60%	45.90%	VLCDDVICDETK	K	N	99.70%	61.8	25	0	2	0	0	2	1466.6505	68	79
Collagen alpha-1(III) chain	P02461	138565.0	100.00%	6	6	7	0.06%	6.62%	DGPPGPAGNTGAPGSPGVSGPK	K	G	99.70%	61.1	25	0	2	0	0	2	1873.9043	902	923
Collagen alpha-1(III) chain	P02461	138565.0	100.00%	6	6	7	0.06%	6.62%	FTYTVLEDGCTK	K	H	99.70%	40.3	25	0	1	0	0	2	1433.6619	1408	1419
Collagen alpha-1(III) chain	P02461	138565.0	100.00%	6	6	7	0.06%	6.62%	GPPGLAGAPGLR	R	G	99.70%	52.8	25	0	1	0	0	2	1062.6057	684	695
Collagen alpha-1(III) chain	P02461	138565.0	100.00%	6	6	7	0.06%	6.62%	GPPGPQGLPGLAGTAGEPGR	R	D	99.70%	84	25.3	0	1	0	0	2	1785.9247	993	1012
Collagen alpha-1(III) chain	P02461	138565.0	100.00%	6	6	7	0.06%	6.62%	GSPGGPGAAGFPGAR	R	G	99.70%	64.8	25.1	0	1	0	0	2	1255.6180	864	878
Collagen alpha-1(III) chain	P02461	138565.0	100.00%	6	6	7	0.06%	6.62%	SVNGQIESLISPDGSR	K	K	99.70%	30.8	25	0	1	0	0	2	1658.8345	1240	1255
Collagen alpha-1(IV) chain	P02462	160617.5	100.00%	3	3	3	0.03%	3.83%	GEPGPPGLPGSVGSPGVPGIGPPGAR	R	G	99.70%	32.1	25	0	1	0	0	2	2263.1835	782	807
Collagen alpha-1(IV) chain	P02462	160617.5	100.00%	3	3	3	0.03%	3.83%	GPPGGVGFPGSR	R	G	99.70%	34.3	25.5	0	1	0	0	2	1084.5536	586	597
Collagen alpha-1(IV) chain	P02462	160617.5	100.00%	3	3	3	0.03%	3.83%	IVPLPGPPGAEGLPGSPGFPGPQGDR	K	G	99.70%	37.7	25	0	1	0	0	2	2466.2782	641	666
Collagen alpha-1(V) chain	P20908	183562.7	100.00%	3	3	3	0.03%	2.18%	LGVPGLPGYPGR	K	Q	96.80%	22.4	25	0	1	0	0	2	1182.6632	867	878
Collagen alpha-1(V) chain	P20908	183562.7	100.00%	3	3	3	0.03%	2.18%	TGPIGPQGAPGKPGPDGLR	K	G	99.70%	34	25	0	0	1	0	2	1771.9455	1422	1440
Collagen alpha-1(V) chain	P20908	183562.7	100.00%	3	3	3	0.03%	2.18%	TVLEIDTPK	K	V	99.70%	35.2	27.4	0	1	0	0	2	1015.5672	1798	1806
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	DTTPLNVLCSPGIQVVSVGIK	R	D	99.70%	74.5	25	0	1	0	0	2	2197.1900	737	757
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	ENYAELLEDAFLK	K	N	99.70%	60.9	25.7	0	1	0	0	2	1554.7687	791	803
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	GLEQLLVGGSHLK	K	E	99.70%	30.4	25	0	0	2	0	2	1350.7742	136	148
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	IALVITDGR	R	S	99.70%	52.3	25	0	1	0	0	2	957.5729	723	731
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	LLLFSDGNSQGATPAAIEK	R	A	99.70%	129	25.1	0	1	0	0	2	1932.0075	939	957
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	LSIIATDHTYR	R	R	99.70%	43.3	26.3	0	1	1	0	2	1289.6849	200	210
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	NNVEQVCCSFECQPAR	K	G	99.70%	72.9	25	0	1	0	0	2	1997.8262	241	256
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	TAEYDVAYGESHLFR	K	V	99.70%	60.5	25	0	1	1	0	2	1757.8129	991	1005
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	VAVVQYSGTGQQRPER	R	A	99.70%	57.8	25.1	0	0	1	0	2	1774.9195	873	888
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	VFSVAITPDHLEPR	K	L	99.70%	47.3	25	0	0	1	0	2	1580.8432	186	199
Collagen alpha-1(VI) chain	P12109	108531.0	100.00%	11	13	14	0.12%	15.20%	VPSYQALLR	R	G	99.70%	45.7	25	0	1	0	0	2	1046.5993	1006	1014
Collagen alpha-1(VIII) chain	P27658	73366.6	99.80%	2	2	2	0.02%	3.09%	EIPLASLR	K	G	99.40%	26.8	25	0	1	0	0	2	898.5357	110	117
Collagen alpha-1(VIII) chain	P27658	73366.6	99.80%	2	2	2	0.02%	3.09%	GVPGLPGVPGLLGPK	K	G	99.60%	28.4	25	0	1	0	0	2	1357.8206	468	482
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	ALALGALQNIR	K	Y	99.70%	74.2	25	0	1	0	0	2	1139.6896	2385	2395
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	DELLAAIK	R	K	99.70%	42.4	26.7	0	1	0	0	2	872.5089	201	208

Protein name	Protein AC	Protein Mw (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage	Peptide sequence	Previous amino acid	Next amino acid	Best Peptide identification probability	Best Mascot Ion score	Best Mascot Identity 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)	Peptide start index	Peptide stop index
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	DYKPQVGVIADPSSK	R	T	99.50%	27.2	25.3	0	1	1	0	2	1603.8328	2603	2617
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	GDTTNTVLQGLK	R	E	99.70%	64.6	26.5	0	1	0	0	2	1246.6640	863	874
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	GEVQTVTFDTEEVK	R	T	99.70%	42.4	25	0	1	0	0	2	1581.7644	2628	2641
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	GISGAIGPPGPR	R	G	99.70%	43.2	25	0	1	0	0	2	1078.6006	2768	2779
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	IEQELAAIK	R	K	99.70%	44.9	25.9	0	1	0	0	2	1014.5831	620	628
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	ITEVTSEGFR	K	G	99.70%	59.6	26.3	0	1	0	0	2	1138.5739	1663	1672
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	ITYQPSTGEGNEQTTTIGGR	R	Q	99.70%	34.3	25	0	1	0	0	2	2110.0050	1785	1804
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	IVEVFDIGPK	R	R	99.70%	50	25	0	1	0	0	2	1116.6301	1225	1234
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	IYIDCYEIIEK	K	D	99.70%	48.4	25.6	0	1	0	0	2	1458.7187	2662	2672
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	LGELVVGPYDNTVVLEELR	R	A	99.70%	51.9	25	0	1	0	0	2	2115.1334	1130	1148
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	LLPETPSDPFAIWQITDR	R	D	99.70%	36.5	25	0	1	0	0	2	2099.0811	2585	2602
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	LNWNPSPSPVTGYK	K	V	99.70%	47.9	25.9	0	1	0	0	2	1559.7853	352	365
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	LQPQTTYDITVLPIYK	R	M	99.70%	45.2	25	0	1	0	0	2	1893.0371	1055	1070
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	NNVILQPLQPDTPYK	R	I	99.70%	43.7	25	0	2	0	0	2	1739.9329	2078	2092
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	NQPGPPGPPGPPGSAGAR	R	G	99.70%	41.2	25.2	0	2	0	0	2	1610.8037	2939	2956
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	SLLQAVANLPYK	K	G	99.70%	64.3	25	0	1	0	0	2	1316.7573	1261	1272
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	SLYDDVDTGEK	K	N	99.70%	45.9	25	0	1	0	0	2	1241.5534	941	951
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	SQDEVEIPAR	K	E	99.70%	49.8	25	0	1	0	0	2	1143.5641	253	262
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	TEFNLNQYYQR	R	D	99.70%	67.2	25	0	1	0	0	2	1475.6913	190	200
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	TLENLIPDTK	R	Y	96.40%	23.4	26.6	0	1	0	0	2	1143.6258	778	787
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	TLSFFNK	K	D	94.90%	20.9	25	0	1	0	0	2	856.4563	2618	2624
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	VAIIITDGK	K	S	99.70%	46.3	25	0	1	0	0	2	929.5668	244	252
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	VEDIIEAINTFPYR	K	G	99.70%	66.2	25.4	0	1	1	0	2	1679.8640	500	513
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	VPPTVTSTVLK	K	R	95.10%	20.9	25	0	1	0	0	2	1141.6828	1043	1053
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	VSWDPSPSPVLGYK	R	I	99.70%	38.4	26.1	0	1	0	0	2	1531.7792	2134	2147
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	VVYSPVDGTRPSESIVVPGNTR	R	M	99.70%	25.3	25	0	0	1	0	2	2329.2147	1966	1987
Collagen alpha-1(XII) chain	Q99715	333145.3	100.00%	29	31	33	0.33%	12.20%	VYDPSTSTLNVR	R	W	99.70%	65.3	25.6	0	1	0	0	2	1351.6852	1852	1863
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	AVILQGSNDVELVAEGNSR	K	F	99.70%	62.6	25	0	3	5	0	2	1971.0142	1289	1307
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	EGPVGLPGIDGRPGPIGPAGAR	K	G	99.70%	30	25	0	1	0	0	2	2040.0990	465	486
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	FTYTVLVDGCSK	R	K	99.70%	81.8	25.6	0	1	0	0	2	1389.6720	1308	1319
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GAAGLPGVAGAPGLPGPR	K	G	99.70%	38.3	25	0	4	1	0	2	1514.8441	310	327
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GAPGAVGAPGPAGATGDRGEAGAAGPAGPAGPR	R	G	99.60%	23.7	25	0	0	0	1	2	2695.3300	676	708
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GDGGPPGMTGFPGAAGR	R	T	99.70%	51.9	25	0	1	0	0	2	1517.6806	778	794
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GEIGAVGNAGPAGPAGPR	K	G	99.70%	90.6	25.9	0	2	0	0	2	1547.7927	265	282
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GEIGNPGR	R	D	98.10%	23.5	25	0	1	0	0	2	799.4058	664	671
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GEPGNIGFPGPK	R	G	99.70%	48.7	25.4	0	2	0	0	2	1169.5952	487	498
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GEPGVVGAVGTAGPSGPSGLPGER	K	G	99.70%	63.1	25	0	1	1	0	2	2105.0625	622	645
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GETGPSGPVGPAGAVGPR	R	G	99.70%	56.6	26	0	2	0	0	2	1562.7924	979	996
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GFPGTPGLPGFK	R	G	99.70%	31.7	26.5	0	2	0	0	2	1174.6258	166	177
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GLHGEFGLPGPAGPR	R	G	98.90%	21.3	26.1	0	0	1	0	2	1461.7600	574	588
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GLPGSPGNIGPAGK	R	E	96.00%	22	25.5	0	1	0	0	2	1221.6589	451	464
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GLPGVAGAVGEPGPLGIAGPPGAR	R	G	99.70%	101	25	0	1	4	0	2	2067.1350	883	906
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GPNGEAGSAGPPGPPGLR	R	G	99.70%	35.6	25.9	0	1	0	0	2	1587.7877	382	399
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GPPGAAGAPGPQGFQGPAGEPGEPGQTGPAGAR	R	G	99.20%	21.1	25	0	0	1	0	2	2895.3775	100	132
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GPPGAVGSPGVNGAPGEAGR	R	D	99.70%	89	25.2	0	1	0	0	2	1703.8462	907	926
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GPPGESGAAGPTGPIGSR	R	G	99.70%	67.2	25.4	0	1	0	0	2	1564.7717	592	609
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GPSGPPGPDGNKGEPGVVGAVGTAGPSGPSGLPGER	R	G	99.70%	29.5	25	0	0	1	0	2	3165.5566	610	645
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GSDGSVGPVGPAGPIGSAGPPGFPGAPGPK	R	G	99.70%	94.1	25	0	2	1	0	2	2541.2738	235	264
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GVGLGPGPMGLMGPR	K	G	99.70%	34.8	25.6	0	1	0	0	2	1427.7138	85	99
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GVVGPQGAR	R	G	99.70%	40.8	25	0	1	0	0	2	840.4687	157	165
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	GYPGNIGPVGAAGAPGPHGPVGPAGK	R	H	99.60%	22.9	25	0	0	2	0	2	2252.1575	949	974
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	HGNRGETGPSGPVGPAGAVGPR	K	G	99.70%	24.4	25	0	0	0	1	2	2027.0168	975	996
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	NSIAYMDEETGNLKK	K	A	99.70%	23.2	25	0	0	1	0	2	1728.8111	1274	1288
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	SLNNQIETLLTPEGSR	K	K	99.70%	32.2	25.4	0	1	0	0	2	1771.9186	1141	1156
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	TGEVGAVGPPGFAGEK	R	G	99.70%	42.7	25	0	1	0	0	2	1472.7382	831	846
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	TGPPGPSGISGPPGPPGPAGK	R	E	99.70%	82.5	25	0	2	0	0	2	1781.9186	795	815
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	VGAPGPAGAR	R	G	99.70%	30.5	25	0	2	0	0	2	852.4687	225	234
Collagen alpha-2(I) chain	P08123	129314.7	100.00%	31	36	56	0.56%	39.70%	VYCDFSTGETCIR	K	A	99.70%	64	25	0	1	0	0	2	1607.6830	1193	1205
Collagen alpha-2(IV) chain	P08572	167557.6	100.00%	7	7	8	0.07%	5.55%	AGFPGLPGSPGAR	R	G	99.70%	31.7	25.1	0	1	0	0	2	1183.6220	459	471
Collagen alpha-2(IV) chain	P08572	167557.6	100.00%	7	7	8	0.07%	5.55%	EGFPGPPGFIGPR	R	G	99.70%	30	25.4	0	1	0	0	2	1327.6796	728	740
Collagen alpha-2(IV) chain	P08572	167557.6	100.00%	7	7	8	0.07%	5.55%	GDDGWPGAPGLPGFPGLR	K	G	99.70%	34.1	25.2	0	1	0	0	2	1765.8661	1176	1193
Collagen alpha-2(IV) chain	P08572	167557.6	100.00%	7	7	8	0.07%	5.55%	GGVSAVPGFR	R	G	99.70%	35.1	26.9	0	1	0	0	2	946.5105	1443	1452
Collagen alpha-2(IV) chain	P08572	167557.6	100.00%	7	7	8	0.07%	5.55%	GIPGFAGADGGPGPR	R	G	99.70%	33.2	25.6	0	1	0	0	2	1325.6600	705	719
Collagen alpha-2(IV) chain	P08572	167557.6	100.00%	7	7	8	0.07%	5.55%	GLDGYQGPDGPR	R	G	99.70%	39.1	25	0	1	0	0	2	1231.5705	323	334
Collagen alpha-2(IV) chain	P08572	167557.6	100.00%	7	7	8	0.07%	5.55%	GLPGEVLGAQPGPR	R	G	99.00%	25.7	25.2	0	2	0	0	2	1347.7382	771	784
Collagen alpha-2(V) chain	P05997	144909.7	100.00%	7	7	9	0.08%	7.40%	DGEVGPSGPVGPPGLAGER	K	G	99.70%	78.9	25.3	0	2	0	0	2	1747.8613	647	665
Collagen alpha-2(V) chain	P05997	144909.7	100.00%	7	7	9	0.08%	7.40%	EGNPGPLGPIGPPGVR	K	G	99.70%	39.4	25	0	2	0	0	2	1513.8125	1187	1202
Collagen alpha-2(V) chain	P05997	144909.7	100.00%	7	7	9	0.08%	7.40%	GEPGLVPVVTGIR	K	G	97.10%	22.7	25	0	1	0	0	2	1293.7527	116	128
Collagen alpha-2(V) chain	P05997	144909.7	100.00%	7	7	9	0.08%	7.40%	GLPGPLGPPGPAGPTGEK	R	G	99.70%	32.3	25	0	1	0	0	2	1598.8542	798	815
Collagen alpha-2(V) chain	P05997	144909.7	100.00%	7	7	9	0.08%	7.40%	GSQGDPGRPGEPGLPGAR	K	G	99.70%	34.8	25.4	0	0	1	0	2	1704.8416	555	572
Collagen alpha-2(V) chain	P05997	144909.7	100.00%	7	7	9	0.08%	7.40%	GTQGPPGATGFPGSAGR	R	V	96.40%	22	25	0	1	0	0	2	1514.7349	900	916
Collagen alpha-2(V) chain	P05997	144909.7	100.00%	7	7	9	0.08%	7.40%	YIVLQDTCSK	R	R	99.70%	37.5	25.7	0	1	0	0	2	1226.6087	1443	1452
Collagen alpha-2(VI) chain	P12110	108580.8	100.00%	6	6	7	0.06%	6.67%	DYDSLAQPGFFDR	K	F	99.70%	49.2	25	0	2	0	0	2	1530.6861	1001	1013
Collagen alpha-2(VI) chain	P12110	108580.8	100.00%	6	6	7	0.06%	6.67%	LFAVAPNQNLK	R	E	99.70%	34.2	25.4	0	1	0	0	2	1214.6892	187	197
Collagen alpha-2(VI) chain	P12110	108580.8	100.00%	6	6	7	0.06%	6.67%	NFVINVVNR	K	L	99.70%	34.3	25.7	0	1	0	0	2	1074.6053	636	644
Collagen alpha-2(VI) chain	P12110	108580.8	100.00%	6	6	7	0.06%	6.67%	NLEWIAGGTWTPSALK	K	F	99.70%	85.5	25.1	0	1	0	0	2	1743.9066	693	708
Collagen alpha-2(VI) chain	P12110	108580.8	100.00%	6	6	7	0.06%	6.67%	NLQGISSFR	K	R	99.70%	43	25.9	0	1	0	0	2	1021.5425	121	129
Collagen alpha-2(VI) chain	P12110	108580.8	100.00%	6	6	7	0.06%	6.67%	VFAVVITDGR	R	H	99.70%	54.5	25	0	1	0	0	2	1076.6099	725	734
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	ALILVGLER	R	V	99.70%	64.8	25	0	1	0	0	2	983.6249	1976	1984
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	ALNLGYALDYAQR	K	Y	99.70%	63.3	25.3	0	2	0	0	2	1467.7591	913	925
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	DVVFLLDGSEGVR	K	S	99.10%	25.8	25	0	1	0	0	2	1405.7323	1029	1041
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	LLTPITTLTSEQIQK	K	L	99.70%	39.8	25	0	1	0	0	2	1685.9687	1404	1418
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	LQPVLQPLPSPGVGGK	R	R	99.70%	31.2	25	0	1	0	0	2	1586.9268	1216	1231
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	LSDAGITPLFLTR	K	Q	99.10%	25.7	25	0	1	0	0	2	1403.7895	2533	2545
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	QINVGNALEYVSR	R	N	99.70%	57.9	25.7	0	1	0	0	2	1462.7648	1309	1321
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	QLGTVQQVISER	R	V	99.70%	48.7	25.4	0	1	0	0	2	1357.7435	1193	1204
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	SSGIVSLGVGDR	R	N	99.70%	42.8	26.6	0	1	0	0	2	1146.6114	1565	1576
Collagen alpha-3(VI) chain	P12111	343667.4	100.00%	10	10	11	0.09%	4.00%	VVESLDVGQDR	R	V	99.70%	99.1	26.3	0	1	0	0	2	1216.6169	1054	1064
Decorin	P07585	39748.2	100.00%	4	4	4	0.03%	14.80%	DFEPSLGPVCPFR	R	C	99.70%	39.3	25.2	0	1	0	0	2	1520.7204	45	57
Decorin	P07585	39748.2	100.00%	4	4	4	0.03%	14.80%	DLPPDTTLLDLQNNK	K	I	99.70%	64.8	25	0	1	0	0	2	1696.8756	78	92
Decorin	P07585	39748.2	100.00%	4	4	4	0.03%	14.80%	VSPGAFTPLVK	K	L	99.70%	31.6	25	0	1	0	0	2	1115.6460	120	130
Decorin	P07585	39748.2	100.00%	4	4	4	0.03%	14.80%	VVQCSDLGLDKVPK	R	D	99.70%	29	25.5	0	0	1	0	2	1557.8308	64	77
EGF-like repeat and discoidin I-like domain protein 3	O43854	53765.0	99.80%	2	2	2	0.02%	4.58%	DFGHVQFVGSYK	K	L	99.70%	30.7	25.3	0	0	1	0	2	1383.6692	398	409
EGF-like repeat and discoidin I-like domain protein 3	O43854	53765.0	99.80%	2	2	2	0.02%	4.58%	NVIDPPIYAR	K	H	99.10%	26.2	25.8	0	1	0	0	2	1157.6314	445	454
Endoplasmin	P14625	92471.7	99.80%	2	2	3	0.03%	4.61%	ELISNASDALDK	R	I	99.70%	48	25	0	1	0	0	2	1275.6428	103	114
Endoplasmin	P14625	92471.7	99.80%	2	2	3	0.03%	4.61%	GVVDSDDLPLNVSR	K	E	99.70%	57.3	25.5	0	2	0	0	2	1485.7545	435	448
Endoplasmin	P14625	92471.7	99.80%	2	2	3	0.03%	4.61%	SILFVPTSAPR	K	G	99.70%	33.2	25	0	1	0	0	2	1187.6783	385	395
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	GEGWGDPCELCPTEPDEAFR	K	Q	99.70%	32	25	0	1	0	0	2	2321.9442	2089	2108
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	GFIYKPDLK	K	T	98.90%	25.3	25	0	1	0	0	2	1080.6090	795	803
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	GFQLDLR	K	G	99.70%	31.5	27	0	1	0	0	2	848.4626	479	485
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	GQCIKPLFGAVTK	R	S	99.70%	32.8	25	0	0	1	0	2	1418.7827	668	680
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	GTCWQTVIDGR	K	C	99.70%	70.3	25	0	1	0	0	2	1292.6054	851	861
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	NTPEYEELCPR	R	G	99.70%	51.7	25	0	1	0	0	2	1407.6210	1000	1010
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	SGNCYLDIRPR	R	G	99.70%	29.8	25.6	0	0	1	0	2	1350.6584	1531	1541
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	TCVDINECLLEPR	R	K	99.70%	75.5	25	0	1	0	0	2	1618.7566	1970	1982
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	TGCTDINECEIGAHNCGK	K	H	99.70%	30.4	25	0	0	1	0	2	2035.8269	1318	1335
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	TLPGGNQCIVPICR	K	H	99.70%	30.9	25.1	0	1	0	0	2	1584.7988	73	86
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	YEDEECTLPIAGR	R	H	99.70%	72.5	25	0	1	0	0	2	1552.6950	962	974
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	YLIESGNEDGFFK	R	I	99.40%	27	25	0	1	0	0	2	1518.7112	2793	2805
Fibrillin-1	P35555	312226.0	100.00%	13	13	13	0.11%	5.68%	YNAYCCPGWK	R	T	99.10%	25.9	25	0	1	0	0	2	1318.5344	63	72
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	CDPVDQCQDSETGTFYQIGDSWEK	K	Y	99.70%	69.8	25	0	1	1	0	2	2865.1619	555	578
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	DDKESVPISDTIIPAVPPPTDLR	K	F	99.70%	24.9	25	0	0	2	0	2	2475.2982	1252	1274
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	DLQFVEVTDVK	R	V	99.70%	62.6	26.2	0	3	0	0	2	1292.6734	912	922
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	DSMIWDCTCIGAGR	K	G	99.70%	90.6	25	0	1	0	0	2	1657.6770	117	130
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	DTLTSRPAQGVVTTLENVSPPR	K	R	99.70%	34.6	25	0	1	0	0	2	2338.2363	1797	1818
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	EESPLLIGQQSTVSDVPR	R	D	99.70%	55.6	25	0	1	0	0	2	1955.0082	1435	1452
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	EINLAPDSSSVVVSGLMVATK	K	Y	99.70%	58.3	25	0	1	0	0	2	2133.1109	1767	1787
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	ESVPISDTIIPAVPPPTDLR	K	F	99.50%	21.1	25	0	0	1	0	2	2117.1492	1255	1274
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	EYLGAICSCTCFGGQR	K	G	99.70%	75	25	0	1	0	0	2	1878.7933	2311	2326
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	FLATTPNSLLVSWQPPR	R	A	99.70%	61	25	0	2	1	0	2	1927.0437	1911	1927
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	FTQVTPTSLSAQWTPPNVQLTGYR	K	V	99.70%	66.4	25	0	1	0	0	2	2692.3731	1730	1753
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	GDSPASSKPISINYR	R	T	99.70%	42	25.4	0	1	1	0	2	1591.8075	1525	1539
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	GEWTCIAYSQLR	R	D	99.70%	51.3	25	0	1	0	0	2	1483.6999	504	515
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	GFNCESKPEAEETCFDK	R	Y	99.70%	63.1	25	0	1	1	0	2	2047.8374	84	100
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	GFNCESKPEAEETCFDKYTGNTYR	R	V	99.70%	36.2	25	0	0	2	0	2	2903.2249	84	107

Protein name	Protein AC	Protein Mw (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage	Peptide sequence	Previous amino acid	Next amino acid	Best Peptide identification probability	Best Mascot Ion score	Best Mascot Identity 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)	Peptide start index	Peptide stop index
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	GLAFTDVDVDSIK	K	I	99.70%	82.1	26.3	0	1	0	0	2	1379.7055	1637	1649
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	GNLLQCICTGNGR	R	G	99.70%	55.8	25	0	2	0	0	2	1462.6892	253	265
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	HTSVQTTSSGSGPFTDVR	R	A	99.70%	86.4	25	0	2	2	0	2	1863.8832	273	290
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	HYQINQQWER	K	T	99.70%	38.5	25	0	4	1	0	2	1401.6658	58	67
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	IAWESPQGQVSR	K	Y	99.70%	52.6	25.7	0	4	0	0	2	1357.6859	1650	1661
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	ISCTIANR	R	C	99.70%	53.8	26.9	0	1	0	0	2	934.4775	133	140
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	ITGYIIK	R	Y	99.60%	28	25	0	1	0	0	2	807.4976	1930	1936
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	ITYGETGGNSPVQEFTVPGSK	R	S	99.70%	38.5	25	0	1	3	0	2	2168.0508	1480	1500
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	LGVRPSQGGEAPR	K	E	99.70%	53.3	25	0	1	2	0	2	1323.7129	1117	1129
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	LLCQCLGFGSGHFR	K	C	99.70%	44.8	25	0	1	1	0	2	1651.7834	2231	2244
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	NLQPASEYTVSLVAIK	R	G	99.70%	52.6	25	0	1	1	0	2	1732.9480	1055	1070
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	NTFAEVTGLSPGVTYYFK	R	V	99.70%	66.7	25	0	1	0	0	2	1993.9906	959	976
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	QDGHLWCSTTSNYEQDQK	R	Y	99.70%	48	25	0	1	2	0	2	2196.9253	380	397
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	QYNVGPSVSK	R	Y	99.70%	32.4	26.7	0	1	0	0	2	1078.5527	1041	1050
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	QYNVGPSVSKYPLR	R	N	99.70%	40.2	25	0	0	1	0	2	1607.8540	1041	1054
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	RPGGEPSPEGTTGQSYNQYSQR	R	Y	99.70%	55.3	25	0	1	2	0	2	2396.0863	2335	2356
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	SSPVVIDASTAIDAPSNLR	R	F	99.70%	75.7	25	0	1	1	0	2	1912.9975	1892	1910
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	STTPDITGYR	R	I	99.70%	37.2	25	0	2	0	0	2	1110.5427	1198	1207
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	SYTITGLQPGTDYK	R	I	99.70%	70.3	25	0	1	0	0	2	1543.7641	1867	1880
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	TEIDKPSQMQVTDVQDNSISVK	R	W	99.70%	36.1	25	0	0	1	0	2	2478.2032	1540	1561
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	TETITGFQVDAVPANGQTPIQR	K	T	99.70%	31.6	25	0	1	0	0	2	2343.1942	1838	1859
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	TKTETITGFQVDAVPANGQTPIQR	R	T	99.70%	25.4	25	0	0	1	0	2	2572.3369	1836	1859
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	TYLGNALVCTCYGGSR	R	G	99.70%	68.8	25	0	1	1	0	2	1791.8154	68	83
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	VDVIPVNLPGEHGQR	R	L	99.70%	38.1	25	0	1	1	0	2	1629.8709	939	953
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	VGDTYERPK	R	D	99.70%	31.2	26.5	0	1	0	0	2	1064.5372	108	116
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	VPGTSTSATLTGLTR	R	G	99.70%	73.7	25	0	1	0	0	2	1461.7909	2150	2164
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	VTIMWTPPESAVTGYR	K	V	99.70%	33.1	25.1	0	2	0	0	2	1823.8998	923	938
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	VTWAPPPSIDLTNFLVR	R	Y	99.70%	68.1	25	0	2	0	0	2	1926.0485	1285	1301
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	WLPSSSPVTGYR	K	V	99.70%	40	26.2	0	2	0	0	2	1349.6848	1562	1573
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	WSRPQAPITGYR	R	I	99.70%	32.5	26.3	0	1	1	0	2	1431.7492	831	842
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	YEVSVYALK	K	D	99.60%	28.8	25.6	0	1	0	0	2	1071.5720	1788	1796
Fibronectin	P02751	262616.9	100.00%	47	65	87	0.73%	28.60%	YSFCTDHTVLVQTR	K	G	99.70%	90.3	25	0	1	1	0	2	1726.8218	398	411
Fibulin-1	P23142	77211.6	100.00%	3	4	4	0.03%	2.84%	DSFDIIK	R	R	99.70%	42	25.8	0	1	0	0	2	837.4354	643	649
Fibulin-1	P23142	77211.6	100.00%	3	4	4	0.03%	2.84%	DSFDIIKR	R	Y	99.70%	49.1	25.7	0	1	0	0	2	993.5365	643	650
Fibulin-1	P23142	77211.6	100.00%	3	4	4	0.03%	2.84%	EFTRPEEIIFLR	R	A	99.70%	34	25	0	1	1	0	2	1549.8374	608	619
Filamin-A	P21333	280729.4	100.00%	3	3	3	0.03%	1.74%	IANLQTDLSDGLR	R	L	99.70%	62.6	25.1	0	1	0	0	2	1415.7491	64	76
Filamin-A	P21333	280729.4	100.00%	3	3	3	0.03%	1.74%	TGVAVNKPAEFTVDAK	K	H	99.50%	22	25	0	0	1	0	2	1646.8749	685	700
Filamin-A	P21333	280729.4	100.00%	3	3	3	0.03%	1.74%	VTAQGPGLEPSGNIANK	K	T	97.40%	22.8	25.2	0	1	0	0	2	1652.8604	384	400
Follistatin-related protein 1	Q12841	34985.3	100.00%	6	6	6	0.05%	20.10%	CLNPSFNPPEKK	K	C	99.70%	35.6	25.5	0	0	1	0	2	1430.7098	221	232
Follistatin-related protein 1	Q12841	34985.3	100.00%	6	6	6	0.05%	20.10%	ICANVFCGAGR	K	E	99.70%	49.2	25	0	1	0	0	2	1224.5613	30	40
Follistatin-related protein 1	Q12841	34985.3	100.00%	6	6	6	0.05%	20.10%	LDSSEFLK	R	F	99.70%	44	25.2	0	1	0	0	2	938.4830	163	170
Follistatin-related protein 1	Q12841	34985.3	100.00%	6	6	6	0.05%	20.10%	LSFQEFLK	K	C	99.70%	51.7	25	0	1	0	0	2	1011.5510	213	220
Follistatin-related protein 1	Q12841	34985.3	100.00%	6	6	6	0.05%	20.10%	SVSPSASPVVCYQSNR	K	D	99.70%	82.6	25	0	1	0	0	2	1737.8223	103	118
Follistatin-related protein 1	Q12841	34985.3	100.00%	6	6	6	0.05%	20.10%	YVQELQK	R	H	98.70%	26.1	26.4	0	1	0	0	2	907.4884	286	292
Galectin-1	P09382	14715.8	100.00%	4	5	5	0.05%	31.90%	DSNNLCLHFNPR	K	F	99.70%	43.3	25	0	1	1	0	2	1486.6856	38	49
Galectin-1	P09382	14715.8	100.00%	4	5	5	0.05%	31.90%	FNAHGDANTIVCNSK	R	D	99.70%	36.5	25	0	0	1	0	2	1647.7544	50	64
Galectin-1	P09382	14715.8	100.00%	4	5	5	0.05%	31.90%	LPDGYEFK	K	F	95.30%	21	25	0	1	0	0	2	968.4725	101	108
Galectin-1	P09382	14715.8	100.00%	4	5	5	0.05%	31.90%	SFVLNLGK	K	D	99.70%	38.9	25	0	1	0	0	2	877.5142	30	37
Glia-derived nexin	P07093	44003.2	100.00%	5	5	5	0.04%	11.10%	DIVTVANAVFVK	K	N	99.70%	67.3	25	0	1	0	0	2	1275.7307	106	117
Glia-derived nexin	P07093	44003.2	100.00%	5	5	5	0.04%	11.10%	DVFQCEVR	K	N	99.70%	33.2	25	0	1	0	0	2	1052.4830	132	139
Glia-derived nexin	P07093	44003.2	100.00%	5	5	5	0.04%	11.10%	FTAVAQTDLK	K	E	99.70%	37.3	25.6	0	1	0	0	2	1093.5889	296	305
Glia-derived nexin	P07093	44003.2	100.00%	5	5	5	0.04%	11.10%	FTAVAQTDLKEPLK	K	V	97.10%	17.3	25	0	0	1	0	2	1560.8634	296	309
Glia-derived nexin	P07093	44003.2	100.00%	5	5	5	0.04%	11.10%	LVLVNAVYFK	R	G	99.70%	49.8	25	0	1	0	0	2	1165.6979	181	190
Heat shock protein HSP 90-beta	P08238	83267.3	100.00%	4	4	4	0.03%	6.22%	ADLINNLGTIAK	K	S	99.70%	60.2	25	0	1	0	0	2	1242.7054	96	107
Heat shock protein HSP 90-beta	P08238	83267.3	100.00%	4	4	4	0.03%	6.22%	ALLFIPR	R	R	99.70%	29.8	25	0	1	0	0	2	829.5295	331	337
Heat shock protein HSP 90-beta	P08238	83267.3	100.00%	4	4	4	0.03%	6.22%	ELISNASDALDK	R	I	99.70%	48	25	0	1	0	0	2	1275.6428	42	53
Heat shock protein HSP 90-beta	P08238	83267.3	100.00%	4	4	4	0.03%	6.22%	GVVDSEDLPLNISR	R	E	99.70%	69.4	25.3	0	1	0	0	2	1513.7858	379	392
Insulin-like growth factor-binding protein 2	P18065	34813.6	100.00%	4	4	5	0.04%	17.50%	LAACGPPPVAPPAAVAAVAGGAR	R	M	99.70%	45.3	25	0	1	0	0	2	2041.1013	50	72
Insulin-like growth factor-binding protein 2	P18065	34813.6	100.00%	4	4	5	0.04%	17.50%	LEGEACGVYTPR	R	C	99.70%	52.2	25	0	2	0	0	2	1351.6312	93	104
Insulin-like growth factor-binding protein 2	P18065	34813.6	100.00%	4	4	5	0.04%	17.50%	LIQGAPTIR	K	G	99.70%	29.1	25	0	1	0	0	2	968.5889	293	301
Insulin-like growth factor-binding protein 2	P18065	34813.6	100.00%	4	4	5	0.04%	17.50%	TPCQQELDQVLER	R	I	99.70%	102	25	0	1	0	0	2	1615.7747	225	237
Insulin-like growth factor-binding protein 3	P17936	31674.1	100.00%	6	7	8	0.08%	27.10%	ALAQCAPPPAVCAELVR	R	E	99.70%	41.7	25	0	2	1	0	2	1822.9304	47	63
Insulin-like growth factor-binding protein 3	P17936	31674.1	100.00%	6	7	8	0.08%	27.10%	EPGCGCCLTCALSEGQPCGIYTER	R	C	99.70%	25.5	25	0	0	1	0	2	2775.1304	64	87
Insulin-like growth factor-binding protein 3	P17936	31674.1	100.00%	6	7	8	0.08%	27.10%	FLNVLSPR	K	G	99.70%	44.5	25.6	0	1	0	0	2	945.5516	226	233
Insulin-like growth factor-binding protein 3	P17936	31674.1	100.00%	6	7	8	0.08%	27.10%	GFCWCVDK	R	Y	95.80%	21.4	25	0	1	0	0	2	1071.4388	260	267
Insulin-like growth factor-binding protein 3	P17936	31674.1	100.00%	6	7	8	0.08%	27.10%	GLCVNASAVSR	R	L	99.70%	69.5	26.4	0	1	0	0	2	1133.5731	112	122
Insulin-like growth factor-binding protein 3	P17936	31674.1	100.00%	6	7	8	0.08%	27.10%	YGQPLPGYTTK	K	G	99.60%	28.4	25.6	0	1	0	0	2	1224.6261	268	278
Insulin-like growth factor-binding protein 4	P22692	27933.7	100.00%	3	3	3	0.03%	15.90%	CRPPVGCEELVR	R	E	99.70%	48.2	25.2	0	0	1	0	2	1471.7146	38	49
Insulin-like growth factor-binding protein 4	P22692	27933.7	100.00%	3	3	3	0.03%	15.90%	GELDCHQLADSFRE	K	-	99.70%	27.5	25	0	0	1	0	2	1676.7335	245	258
Insulin-like growth factor-binding protein 4	P22692	27933.7	100.00%	3	3	3	0.03%	15.90%	THEDLYIIPIPNCDR	R	N	99.70%	45.3	25	0	1	0	0	2	1855.9010	192	206
Insulin-like growth factor-binding protein 7	Q16270	29129.8	100.00%	4	4	4	0.03%	22.70%	AGAAAGGPGVSGVCVCK	K	S	99.70%	83.1	25	0	1	0	0	2	1517.7201	98	114
Insulin-like growth factor-binding protein 7	Q16270	29129.8	100.00%	4	4	4	0.03%	22.70%	GTCEQGPSIVTPPK	K	D	99.70%	48.6	25.3	0	1	0	0	2	1470.7260	154	167
Insulin-like growth factor-binding protein 7	Q16270	29129.8	100.00%	4	4	4	0.03%	22.70%	ITVVDALHEIPVK	K	K	99.70%	47.2	25	0	1	0	0	2	1433.8364	263	275
Insulin-like growth factor-binding protein 7	Q16270	29129.8	100.00%	4	4	4	0.03%	22.70%	SRYPVCGSDGTTYPSGCQLR	K	A	99.70%	27.6	25	0	0	1	0	2	2261.0076	115	134
Latent-transforming growth factor beta-binding protein 2	Q14767	195043.4	100.00%	6	6	10	0.10%	4.39%	ALLEAPLK	R	Q	95.00%	20.9	25	0	1	0	0	2	854.5347	447	454
Latent-transforming growth factor beta-binding protein 2	Q14767	195043.4	100.00%	6	6	10	0.10%	4.39%	EQDAPVAGLQPVER	R	A	99.70%	64.5	25.7	0	2	0	0	2	1508.7705	74	87
Latent-transforming growth factor beta-binding protein 2	Q14767	195043.4	100.00%	6	6	10	0.10%	4.39%	GQSGSCVDVNECLTPGVCAHGK	R	C	95.80%	17.2	25	0	0	1	0	2	2332.0117	1003	1024
Latent-transforming growth factor beta-binding protein 2	Q14767	195043.4	100.00%	6	6	10	0.10%	4.39%	IVFTPTICK	K	Q	99.70%	30.1	25.1	0	1	0	0	2	1078.5967	353	361
Latent-transforming growth factor beta-binding protein 2	Q14767	195043.4	100.00%	6	6	10	0.10%	4.39%	SLGPGTCTLPLAQR	R	I	99.70%	49.1	25.4	0	2	0	0	2	1470.7736	677	690
Latent-transforming growth factor beta-binding protein 2	Q14767	195043.4	100.00%	6	6	10	0.10%	4.39%	SSEVYAQLCNVAR	R	I	99.70%	70.1	25	0	3	0	0	2	1496.7161	1628	1640
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	FNALQYLR	R	L	99.70%	44.7	25	0	2	0	0	2	1024.5574	228	235
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	ILGPLSYSK	K	I	99.70%	34	25	0	1	0	0	2	977.5667	297	305
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	ISNIPDEYFK	K	R	97.10%	22.9	25.5	0	1	0	0	2	1225.6100	217	226
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	LKEDAVSAAFK	R	G	99.70%	49.9	25.7	0	1	0	0	2	1178.6416	171	181
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	LPSGLPVSLLTLYLDNNK	R	I	99.60%	28	25	0	1	0	0	2	1957.1007	199	216
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	NIPTVNENLENYYLEVNQLEK	K	F	99.70%	49.5	25	0	1	0	0	2	2536.2566	268	288
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	RFNALQYLR	K	L	99.70%	32	25	0	1	0	0	2	1180.6585	227	235
Lumican	P51884	38431.5	100.00%	8	8	9	0.09%	26.30%	SLEDLQLTHNK	K	I	99.70%	47.4	25.3	0	1	0	0	2	1297.6748	138	148
Metalloproteinase inhibitor 1	P01033	23171.1	100.00%	5	6	7	0.06%	34.30%	EPGLCTWQSLR	R	S	95.80%	22.3	25.7	0	1	0	0	2	1346.6523	193	203
Metalloproteinase inhibitor 1	P01033	23171.1	100.00%	5	6	7	0.06%	34.30%	GFQALGDAADIR	K	F	99.70%	66.3	26.2	0	1	0	0	2	1233.6224	71	82
Metalloproteinase inhibitor 1	P01033	23171.1	100.00%	5	6	7	0.06%	34.30%	LQSGTHCLWTDQLLQGSEK	K	G	99.70%	78.4	25	0	1	2	0	2	2201.0659	162	180
Metalloproteinase inhibitor 1	P01033	23171.1	100.00%	5	6	7	0.06%	34.30%	SEEFLIAGK	R	L	99.70%	43.1	26.6	0	1	0	0	2	993.5252	103	111
Metalloproteinase inhibitor 1	P01033	23171.1	100.00%	5	6	7	0.06%	34.30%	TYTVGCEECTVFPCLSIPCK	K	L	99.70%	52.8	25	0	1	0	0	2	2421.0596	142	161
Nucleobindin-1	Q02818	53879.6	100.00%	3	3	3	0.03%	7.38%	DLELLIQTATR	R	D	99.70%	69.9	25	0	1	0	0	2	1272.7160	153	163
Nucleobindin-1	Q02818	53879.6	100.00%	3	3	3	0.03%	7.38%	LVTLEEFLASTQR	R	K	99.70%	36.2	25	0	1	0	0	2	1506.8163	311	323
Nucleobindin-1	Q02818	53879.6	100.00%	3	3	3	0.03%	7.38%	YLESLGEEQR	R	K	99.70%	30.5	25	0	1	0	0	2	1223.5903	190	199
Pentraxin-related protein PTX3	P26022	41975.9	100.00%	6	6	6	0.06%	24.90%	ALAAVLEELR	R	Q	99.20%	25.7	25	0	1	0	0	2	1084.6361	148	157
Pentraxin-related protein PTX3	P26022	41975.9	100.00%	6	6	6	0.06%	24.90%	GNIVGWGVTEIQPHGGAQYVS	R	-	99.70%	46	25	0	1	0	0	2	2169.0725	361	381
Pentraxin-related protein PTX3	P26022	41975.9	100.00%	6	6	6	0.06%	24.90%	LAESLARPCAPGAPAEAR	R	L	99.70%	40.5	25	0	0	1	0	2	1836.9386	95	112
Pentraxin-related protein PTX3	P26022	41975.9	100.00%	6	6	6	0.06%	24.90%	LTGFNIWDSVLSNEEIR	R	E	99.70%	77.4	25	0	1	0	0	2	1993.0026	333	349
Pentraxin-related protein PTX3	P26022	41975.9	100.00%	6	6	6	0.06%	24.90%	LTSALDELLQATR	R	D	99.70%	80.3	25	0	1	0	0	2	1430.7851	113	125
Pentraxin-related protein PTX3	P26022	41975.9	100.00%	6	6	6	0.06%	24.90%	SWLPAGCETAILFPMR	R	S	99.70%	28.3	25	0	1	0	0	2	1864.9086	173	188
Peptidyl-prolyl cis-trans isomerase B	P23284	23743.2	99.80%	2	2	2	0.02%	9.72%	TVDNFVALATGEK	K	G	99.70%	81.6	26	0	1	0	0	2	1364.7057	72	84
Peptidyl-prolyl cis-trans isomerase B	P23284	23743.2	99.80%	2	2	2	0.02%	9.72%	VIFGLFGK	R	T	99.40%	27.2	25	0	1	0	0	2	880.5292	60	67
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	DGHFTLFAPTNEAFEK	R	L	99.70%	29.5	25	0	1	0	0	2	1823.8600	266	281
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	ELLTQPGDWTLFVPTNDAFK	K	G	99.70%	29.4	25	0	1	0	0	2	2292.1550	523	542
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	GCPAVLPIDHVYGTLGIVGATTTQR	K	Y	99.70%	39.2	25	0	0	1	0	2	2596.3556	91	115
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	GFEPGVTNILK	K	T	99.70%	32.6	25.9	0	1	0	0	2	1174.6468	576	586
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	GRDQGPNVCALQQILGTK	R	K	99.70%	42.4	25.1	0	0	1	0	2	1955.0131	36	53
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	IIDGVPVEITEK	K	E	99.60%	27.9	25	0	1	0	0	2	1312.7361	736	747
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	TTVLYECCPGYMR	K	M	99.70%	58	25	0	1	0	0	2	1665.7071	73	85
Periostin	Q15063	93318.0	100.00%	8	8	8	0.07%	15.00%	VKIEGEPEFR	K	L	99.60%	23.1	26.6	0	0	1	0	2	1203.6369	703	712
Perlecan	P98160	468810.6	100.00%	4	4	4	0.03%	1.43%	AVTLECVSAGEPR	K	S	99.70%	50.2	25.1	0	1	0	0	2	1388.6839	3129	3141
Perlecan	P98160	468810.6	100.00%	4	4	4	0.03%	1.43%	GSVYIGGAPDVATLTGGR	K	F	99.70%	35.3	25	0	1	0	0	2	1690.8761	4330	4347
Perlecan	P98160	468810.6	100.00%	4	4	4	0.03%	1.43%	LLQVTPADSGEYVCR	R	V	99.70%	39.3	25	0	1	0	0	2	1707.8372	2490	2504
Perlecan	P98160	468810.6	100.00%	4	4	4	0.03%	1.43%	LYIFQASPADAGQYVCR	R	A	99.70%	29.3	25	0	1	0	0	2	1958.9430	2296	2312
Plasminogen activator inhibitor 1	P05121	45060.3	100.00%	3	3	3	0.03%	9.95%	FIINDWVK	R	T	98.20%	24.4	25.9	0	1	0	0	2	1034.5670	157	164
Plasminogen activator inhibitor 1	P05121	45060.3	100.00%	3	3	3	0.03%	9.95%	QFQADFTSLSDQEPLHVAQALQK	R	V	99.70%	35.6	25	0	0	1	0	2	2601.2946	324	346
Plasminogen activator inhibitor 1	P05121	45060.3	100.00%	3	3	3	0.03%	9.95%	QVDFSEVER	K	A	99.70%	45	25	0	1	0	0	2	1108.5269	146	154
Protein disulfide-isomerase	P07237	57118.1	100.00%	4	4	4	0.04%	8.66%	EADDIVNWLK	R	K	99.70%	39.1	26.3	0	1	0	0	2	1202.6053	121	130
Protein disulfide-isomerase	P07237	57118.1	100.00%	4	4	4	0.04%	8.66%	ENLLDFIK	K	H	99.70%	29.5	25.9	0	1	0	0	2	991.5460	223	230
Protein disulfide-isomerase	P07237	57118.1	100.00%	4	4	4	0.04%	8.66%	NFEDVAFDEK	K	K	99.70%	32.3	25	0	1	0	0	2	1213.5372	376	385
Protein disulfide-isomerase	P07237	57118.1	100.00%	4	4	4	0.04%	8.66%	VDATEESDLAQQYGVR	K	G	99.70%	69.2	25	0	1	0	0	2	1780.8349	82	97
Protein-lysine 6-oxidase	P28300	46944.2	100.00%	3	3	3	0.03%	9.59%	NQGTSDFLPSRPR	K	Y	99.70%	30.6	25.8	0	0	1	0	2	1474.7398	271	283
Protein-lysine 6-oxidase	P28300	46944.2	100.00%	3	3	3	0.03%	9.59%	TPILLIR	R	D	99.70%	31.3	25	0	1	0	0	2	825.5558	89	95
Protein-lysine 6-oxidase	P28300	46944.2	100.00%	3	3	3	0.03%	9.59%	VSVNPSYLVPESDYTNNVVR	K	C	99.70%	31.4	25	0	1	0	0	2	2252.1192	378	397

Protein name	Protein AC	Protein Mw (Da)	Protein identification probability	Number of unique peptides	Number of unique spectra	Number of total spectra	Percentage of total spectra	Percentage sequence coverage	Peptide sequence	Previous amino acid	Next amino acid	Best Peptide identification probability	Best Mascot Ion score	Best Mascot Identity 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)	Peptide start index	Peptide stop index
Serpin H1	P50454	46442.0	100.00%	5	5	6	0.06%	14.40%	AVLSAEQLR	K	D	99.70%	39.5	26.2	0	1	0	0	2	986.5629	95	103
Serpin H1	P50454	46442.0	100.00%	5	5	6	0.06%	14.40%	DEEVHAGLGELLR	R	S	99.70%	54.3	25.3	0	1	0	0	2	1437.7334	104	116
Serpin H1	P50454	46442.0	100.00%	5	5	6	0.06%	14.40%	DTQSGSLLFIGR	R	L	99.70%	62	25.7	0	2	0	0	2	1293.6799	394	405
Serpin H1	P50454	46442.0	100.00%	5	5	6	0.06%	14.40%	GVVEVTHDLQK	K	H	99.70%	37.6	25	0	1	0	0	2	1224.6584	309	319
Serpin H1	P50454	46442.0	100.00%	5	5	6	0.06%	14.40%	LYGPSSVSFADDFVR	R	S	99.70%	48.5	25	0	1	0	0	2	1659.8013	134	148
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	FFETCDLDNDK	R	Y	99.70%	66.3	25	0	2	0	0	2	1403.5786	269	279
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	LEAGDHPVELLAR	R	D	99.50%	21.4	25.2	0	0	1	0	2	1419.7592	206	218
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	LHLDYIGPCK	K	Y	99.70%	34.9	26.1	0	1	1	0	2	1215.6193	141	150
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	NVLVTLYER	K	D	99.70%	40.4	25	0	1	0	0	2	1106.6204	173	181
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	NVLVTLYERDEDNNLLTEK	K	Q	99.70%	67.2	25	0	1	1	0	2	2278.1563	173	191
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	RLEAGDHPVELLAR	K	D	99.70%	22.8	25	0	0	1	0	2	1575.8603	205	218
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	TFDSSCHFFATK	K	C	99.70%	73.4	25	0	1	0	0	2	1447.6311	118	129
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	YIALDEWAGCFGIK	K	Q	99.70%	54.4	25	0	1	0	0	2	1642.7936	280	293
SPARC	P09486	34631.9	100.00%	9	12	14	0.12%	31.70%	YIPPCLDSELTEFPLR	K	M	99.70%	40.8	25	0	2	1	0	2	1949.9680	151	166
Testican-1	Q08629	49124.8	99.80%	2	2	2	0.02%	4.33%	FDTSILPICK	R	D	99.70%	32.5	26	0	1	0	0	2	1193.6237	237	246
Testican-1	Q08629	49124.8	99.80%	2	2	2	0.02%	4.33%	SLLGAFIPR	K	C	99.70%	37.6	25	0	1	0	0	2	973.5830	328	336
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	EGVYTVFAPTNEAFR	R	A	99.70%	30	25	0	1	0	0	2	1700.8278	534	548
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	ELANILK	K	Y	95.10%	22.4	26.2	0	1	0	0	2	800.4877	564	570
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	FSMLVAAIQSAGLTETLNR	R	E	99.70%	71.8	25	0	2	2	0	2	2038.0639	515	533
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	GDELADSALEIFK	R	Q	99.70%	78.4	25.6	0	1	0	0	2	1407.7004	643	655
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	NSLCIENSCIAAHDKR	R	G	99.70%	27.7	25	0	0	1	1	2	1887.8801	470	485
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	SLQGDKLEVSLK	K	N	99.70%	61.7	25	0	1	1	0	2	1316.7422	591	602
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	SPYQLVLQHSR	K	L	99.70%	38.7	25	0	0	1	0	2	1327.7117	28	38
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	STVISYECCPGYEK	K	V	99.70%	53.8	25	0	1	0	0	2	1692.7245	77	90
TGF-beta-induced protein ig-h3	Q15582	74682.9	100.00%	9	13	15	0.13%	17.70%	YLYHGQTLETLGGK	K	K	99.70%	49	25.5	0	1	1	0	2	1579.8117	448	461
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	DCVGDVTENQICNK	K	Q	99.70%	86.5	25	0	1	0	0	2	1651.7053	530	543
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	DDDYAGFVFGYQSSSR	R	F	99.70%	59.3	25	0	1	0	0	2	1813.7664	1019	1034
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	DNCQYVYNVDQR	R	D	99.70%	58.4	25	0	1	0	0	2	1573.6700	811	822
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	FQDLVDAVR	K	A	99.70%	59.3	26.8	0	1	0	0	2	1062.5579	75	83
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	FTGSQPFGQGVEHATANK	R	Q	99.70%	24.3	25	0	0	1	0	2	1875.8985	624	641
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	FVFGTTPEDILR	R	N	99.70%	52.1	25.2	0	1	0	0	2	1394.7316	217	228
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	GFLLLASLR	K	Q	99.70%	44.1	25	0	1	0	0	2	989.6143	87	95
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	GGVNDNFQGVLQNVR	K	F	99.70%	69.9	25.8	0	1	0	0	2	1616.8140	202	216
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	GTLLALER	R	K	99.70%	44.2	26.1	0	1	0	0	2	872.5201	102	109
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	GTSQNDPNWVVR	K	H	99.70%	47.3	25	0	1	0	0	2	1372.6604	969	980
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	IPESGGDNSVFDIFELTGAAR	R	K	99.70%	81.1	25	0	1	0	0	2	2195.0617	21	41
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	LCNNPTPQFGGK	R	D	99.70%	40.2	25.2	0	1	0	0	2	1332.6367	518	529
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	SITLFVQEDR	K	A	99.70%	49.8	25.9	0	1	0	0	2	1207.6318	155	164
Thrombospondin-1	P07996	129381.7	100.00%	14	14	14	0.14%	15.30%	TIVTTLQDSIR	R	K	99.70%	43.7	25	0	1	0	0	2	1246.7003	289	299
Versican core protein	P13611	372812.6	100.00%	5	5	7	0.06%	1.50%	AQCGGGLLGVR	R	T	99.70%	38.2	27.3	0	1	0	0	2	1087.5679	313	323
Versican core protein	P13611	372812.6	100.00%	5	5	7	0.06%	1.50%	LATVGELQAAWR	R	N	99.70%	88.4	25.5	0	1	0	0	2	1314.7165	277	288
Versican core protein	P13611	372812.6	100.00%	5	5	7	0.06%	1.50%	LLASDAGLYR	K	C	99.70%	65.7	25.7	0	2	0	0	2	1078.5892	120	129
Versican core protein	P13611	372812.6	100.00%	5	5	7	0.06%	1.50%	YEINSLIR	R	Y	99.70%	36.4	25.2	0	1	0	0	2	1007.5520	3315	3322
Versican core protein	P13611	372812.6	100.00%	5	5	7	0.06%	1.50%	YTLNFEAAQK	R	A	99.70%	35.2	25	0	2	0	0	2	1184.5946	161	170
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	DNLAEDIMR	R	L	96.10%	21.8	25	0	1	0	0	2	1092.4992	176	184
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	EEAENTLQSFR	R	Q	99.70%	43	25	0	1	0	0	2	1323.6175	197	207
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	EMEENFAVEAANYQDTIGR	R	L	99.70%	52.1	25	0	1	0	0	2	2202.9609	346	364
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	ETNLDSLPLVDTHSK	R	R	99.70%	34.6	25	0	1	1	0	2	1668.8441	425	439
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	FADLSEAANR	K	N	99.70%	46.8	25.8	0	1	0	0	2	1093.5272	295	304
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	ILLAELEQLK	K	G	99.70%	56.1	25	0	1	0	0	2	1169.7142	130	139
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	ILLAELEQLKGQGK	K	S	99.70%	45.5	25	0	2	0	0	2	1539.9108	130	143
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	KVESLQEEIAFLK	R	K	99.70%	42	25	0	1	1	0	2	1533.8524	223	235
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	LGDLYEEEMR	R	E	99.70%	51.6	25	0	1	0	0	2	1270.5622	146	155
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	NLQEAEEWYK	K	S	99.70%	46.2	25	0	1	0	0	2	1309.6059	283	292
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	QDVDNASLAR	R	L	99.70%	47.7	25.8	0	1	0	0	2	1088.5331	208	217
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	QQYESVAAK	R	N	98.90%	26	25.9	0	1	0	0	2	1023.5105	274	282
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	QVQSLTCEVDALK	R	G	99.70%	72.8	26.1	0	2	0	0	2	1490.7521	322	334
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	SLYASSPGGVYATR	R	S	99.70%	61.6	25.2	0	1	0	0	2	1428.7117	51	64
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	SYVTTSTR	R	T	94.70%	21	25	0	1	0	0	2	914.4577	29	36
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	TNEKVELQELNDR	R	F	99.70%	41.5	25.9	0	0	1	0	2	1587.7974	101	113
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	TYSLGSALRPSTSR	R	S	97.80%	17.9	25	0	0	1	0	2	1495.7863	37	50
Vimentin	P08670	53652.7	100.00%	18	20	22	0.18%	41.20%	VELQELNDR	K	F	99.70%	44.9	25.2	0	1	0	0	2	1115.5692	105	113