Supplemental Table S1: Putative Peptide IDs of elastin peptides derived from Elastase (MMP12) imaging mass spectrometry experiments. Intensity values are normalized by TIC (Total Ion Current). Chond: Chondrotinase ABC treated. NG: PNGaseF treated.

Centroid [m/z]	± [Da]	Putative Peptide Identification	Modification	Maximum Intensity (TIC) Elastase Alone	Maximum Intensity (TIC) Elastase post-Chond-NG
822.4190	0.0295	(A)GGLVPGAPGFGPGV(G)	None	2.6E+05	1.4E+06
837.4090	0.0291	(A)GGFPGFGVGVGGV(P)	None	9.8E+04	1.8E+05
852.4045	0.0265	(V)FYPGAGLGA(L)	None	4.2E+05	5.7E+04
868.4242	0.0295	(A)GQFPLGGVA(A)	1Deamidated	5.1E+04	1.9E+05
873.4166	0.0282	(A)LGPGGKPPKPGV(G)	None	7.1E+05	2.4E+06
874.4179	0.0337	(V)FYPGAGLGA(L)	None	4.0E+05	1.0E+06
875.4199	0.0329	(V)PGGAGAIPGI(G)	None	6.1E+04	3.2E+05
886.4386	0.0307	(L)PAGVPGFGV(G)	None	2.2E+04	5.0E+05
910.4536	0.0354	(A)QFGLGPGIGV(A)	1Deamidated	3.0E+04	1.4E+05
925.4983	0.0164	(V)PGAPGFGPGV(G)	None	6.1E+03	6.6E+04
928.4002	0.0152	(V)GAGGFPGFGV(G)	None	1.0E+04	1.1E+05
939.4689	0.0160	(A)GQFPLGGVAA(R)	1Deamidated	1.4E+04	9.1E+04
943.4293	0.0169	(V)GVGGVGVPGGA(G)	None	1.5E+04	5.9E+04
944.4568	0.0101	(A)AKAQFQAA(A)	2Deamidated	1.1E+04	5.5E+04
955.4231	0.0321	(A)KFGAGAAGV(L)	None	8.5E+04	8.7E+04
969.4907	0.0206	(A)PKLPGGYGL(P)	None	7.5E+03	1.1E+05
994.4364	0.0392	(A)QFGLVPGVGV(A)	None	4.4E+04	1.9E+05
1029.5049	0.0412	(A)GKAGYPTGT(G)	1Xlink:DSS1	1.3E+04	1.1E+05
1063.5128	0.0495	(I)IHPSQPGGVPGA(V)	None	4.9E+04	4.8E+05
1079.5696	0.0299	(V)LPGTGARFPGV(G)	None	1.9E+04	2.9E+05
1136.5752	0.0436	(L)PGGYGLPYST(G)	None	5.5E+04	1.5E+05
1154.5792	0.0254	(L)PGVYPGGVLPGA(R)	None	1.0E+04	1.1E+05
1158.5788	0.0330	(A)GVPGFGAGADEGV(R)	None	8.9E+03	1.7E+05
1180.5562	0.0247	(V)PGVGVPGVGV(P)	None	1.2E+04	3.7E+05
1188.5690	0.0216	(L)PYGYGPGGVAGAA(G)	None	6.7E+03	8.2E+04
1203.5700	0.0268	(V)PGAPGFGPGVGV(P)	None	6.9E+03	1.2E+05
1241.6165	0.0081	(L)GKSCGRKRK(-)	None	3.6E+03	1.1E+05
1241.6308	0.0062	(T)YGVGAGGFPGFGV(G)	None	3.6E+03	1.0E+05
1326.6959	0.0196	(I)KAPKLPGGYGL(P)	None	2.3E+03	1.0E+05
1366.8156	0.0361	(I)PGGVPGGVFYPGAGL(G)	None	2.6E+03	4.7E+05
1369.6442	0.0350	(L)PYGFGPGGVAGAA(G)	None	1.2E+04	1.3E+05
1388.7253	0.0299	(A)LGALGYQGGA(C)	None	1.2E+03	5.3E+05
1390.6470	0.0227	(S)IIHPSQPGGV(P)	None	9.9E+03	1.9E+05
1395.6660	0.0639	(A)GGFPGFGVGVGGIPGV(A)	None	3.1E+03	1.0E+05
1397.6684	0.0247	(A)FPAGAFPGA(L)	None	4.0E+03	6.1E+04
1434.6566	0.0258	(V)PGFGVGAGVPGFGA(G)	None	1.4E+03	1.6E+05
1498.9105	0.0381	(T)GVKAKAPGGGA(F)	None	3.3E+03	1.3E+06
1525.8351	0.0340	(V)PGFGVGAGVPGFGV(G)	None	2.6E+03	2.9E+05
1605.7924	0.0752	(A)KYGAAGLGGV(L)	None	5.4E+03	4.1E+04
1773.8071	0.0834	(V)GPFGGPQPGVPLGYPIKA(P	None	7.2E+03	4.1E+04
1962.0014	0.1164	(I)PGVGPFGGQQPGVPL(G)	1Deamidated	2.6E+03	7.9E+04
1962.9823	0.0047	(I)PGVGPFGGQQPGVPL(G)	2Deamidated	2.6E+03	7.1E+04