Electronic Supplementary Material (ESI) for Soft Matter.

Unexpected behavior of irradiated spider silk links conformational freedom to mechanical performance

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Table S1. Proteins identified in MAS silk.

Band 1

GenInfo[1]	Protein name [organism]	Sequence	MH+[2]	z[3]	Xcorr	Sp Score
150416774	major ampullate spidroin 1 [Latrodectus hesperus]	G.QGGAAAAASAAAAGGAGQGGY.G	1634.7517	2	3.53941	885.3103
		Q.GGAGQGGAAAAASAAAAGGAGQGGY.G	1876.8532	3	3.864634	2691.021
89276817	major ampullate spidroin 1 [Latrodectus hesperus]	Y.GRGGAGQGGAAAAAAAAGAGQGGY.G	1874.8852	3	3.848947	1179.488
164709220	major ampullate spidroin 1 locus 1 [Latrodectus hesperus]	G.AGQGGAAAAAAAAAAGGAGQGGY.G	1746.8154	3	3.461282	1637.874
		R.GGAGQGGAAAAAAAAAAGAGQGGYGGQGAGQGGAGA.A	2601.1785	3	3.421322	1232.023
		A.AAAAAAAAGAGQGGY.G	1177.5596	2	3.386639	1715.67
164709213	major ampullate spidroin 1 locus 2 [Latrodectus hesperus]	P.GGAGAAAAGGAGQGGQGGY.G	1434.6356	2	3.419002	1011.745
164709204	major ampullate spidroin 1 locus 3 [Latrodectus hesperus]	G.GAGQGGEAAAAAAAAGAGQGGY.G	1733.7838	2	3.277022	1040.063
164709248	major ampullate spidroin 1 variant 2 locus 2 [Latrodectus hesperus]	A.SAASAAAAGGAGQGGY.G	1266.5709	2	3.373932	1082.675
70913022	major ampullate spidroin 1-like [Latrodectus geometricus]	G.YGQGGFGQGSSGAAAAGGAGQGGY.L	2032.8744	3	4.084091	1827.586
70913273	major ampullate spidroin 2 [Argiope trifasciata]	F.LRFIGQSGAF.S	1095.5946	2	3.643025	1121.253
		F.SPNQLDDM*SSIGDTL.K	1608.7057	2	3.180354	593.5849
		L.RFIGQSGAF.S	982.51049	2	3.19967	784.921
38197759	major ampullate spidroin-2 [Argiope amoena]	Y.GPGAAAAAAAAGGY.G	1075.5167	2	4.248923	1846.762
56475413	major ampullate spidroin-like protein [Latrodectus hesperus]	G.YGQGGYGQGGVGQGGAGAAAAAAAAAGGAGQGGYG.Q	2813.2622	3	3.876196	1061.552
170672095	minor ampullate spidroin 1-like protein [Latrodectus hesperus]	G.QGAGAGAGAGAGAGGYG.Q	1249.5556	1	3.566612	1129.897
		G.QGQGAGAGAGAGAGAGGY.G	1377.6142	2	4.494239	1981.964
		G.QGAGAGAGAGAGAGGYG.Q	1249.5556	2	4.715492	2232.941

		G.QGAGAGAGAGAGAGGYGQ.G	1377.6142	1	4.442932	1160.012

Band 2

GenInfo[1]	Protein name [organism]	Sequence	MH+[2]	z[3]	Xcorr	Sp Score
13561984	AF350266_1 major ampullate spidroin 1 [Argiope trifasciata]	G.AAAAAAAASGAGGAGRGSLGAGGAGQGY.G	2176.049	3	3.24419	1903.01
13561998	AF350273_1 major ampullate spidroin 1 [Latrodectus geometricus]	Y.GQGGAGQGGAGAAAAAAAAAGGAGQGGY.G	2031.9227	3	3.232408	3360.91
62638184	egg case silk protein-1 [Latrodectus hesperus]	G.SSAGAAAGAHAASGGRAG.A	1426.6782	3	3.528497	1786.926
150416774	major ampullate spidroin 1 [Latrodectus hesperus]	G.QGGAAAAASAAAAGGAGQGGY.G	1634.7517	2	3.105627	751.6983
89276817	major ampullate spidroin 1 [Latrodectus hesperus]	G.GAGQGGAGAASAAAAAAGGAGQGGY.G	1876.8532	3	3.142674	1913.448
		Y.GRGGAGQGGAAAAAAAAGAGQGGY.G	1874.8852	3	3.155184	1412.575
164709219	major ampullate spidroin 1 locus 1 [Latrodectus hesperus]	A.GAAAAAAAAAGGAGQGGY.G	1362.6397	2	3.245192	1673.33
164709199	major ampullate spidroin 1 locus 3 [Latrodectus hesperus]	G.GAGQGEAAAAAAAAAGAGQGGY.G	1747.7994	2	3.658028	1406.875
164709204	major ampullate spidroin 1 locus 3 [Latrodectus hesperus]	D.QGAGQGGAGAAAAAATASGGAGQGGY.G	2034.9224	3	3.86881	2175.009
164709205	major ampullate spidroin 1 locus 3 [Latrodectus hesperus]	A.GQGGAGAAAAAAAAGWAGQGGQGGY.G	2032.922	3	4.202515	2342.892
70913022	major ampullate spidroin 1-like [Latrodectus geometricus]	G.YGQGGFGQGSSGAAAAGGAGQGGY.L	2032.8744	3	4.111824	1567.28
70913273	major ampullate spidroin 2 [Argiope trifasciata]	F.LRFIGQSGAF.S	1095.5946	2	3.617733	946.7495
		L.RFIGQSGAF.S	982.51049	2	3.256252	797.3625
38197759	major ampullate spidroin-2 [Argiope amoena]	Y.GPGAAAAAAAAGGY.G	1075.5167	2	4.399806	1956.231
56475413	major ampullate spidroin-like protein [Latrodectus geometricus]	G.AGAAAAAAAAGGAGQGGY.G	1362.6397	2	3.499596	1658.536
		G.YGQGGYGQGGVGQGGAGAAAAAAAAAGGAGQGGYG.Q	2813.2622	3	3.743197	1412.078
170672095	minor ampullate spidroin 1-like protein [Latrodectus geometricus]	G.QGAGAGAGAGAGAGGYG.Q	2499.1112	3	8.099863	3122.8979
		G.QGAGAGAGAGAGAGGYGQ.G	2755.2284	3	8.009627	2886.931
		G.QGQGAGAGAGAGAGAGGY.G	1377.6142	2	4.446899	1836.646

[1] Sequence identification number by NBCI (http://www.ncbi.nlm.nih.gov/)

[2] Molecular mass of the MH+ ion (Da)

[3] Positive charge of the MH+ ion

[4] Parameters related to peptide identification obtained using the database searching algorithm SEQUEST