

Supplementary Table 3: LC-MS/MS analysis for a long and short form of dSTING

Range	Sequence	m/z (1) (measured)	z (2)	# spectra (3)	Mascot score (4)	Rt (5) [min]	Dm/z (6) [ppm]	m/z (1) (measured)	z (2)	# spectra (3)	Mascot score (4)	Rt (5) [min]	Dm/z (6) [ppm]
2-15	M.AIASNVVEAGNAVR.A	685.8729	2	11	92.0	19.10	-0.14	685.8730	2	2	66.3	18.75	0.07
2-15	M.*AIASNVVEAGNAVR.A	706.8773	2	4	128.7	24.17	-1.37						
2-18	M.AIASNVVEAGNAVRAEK.G	566.9755	3	2	83.5	18.98	-0.83						
28 - 38	K.MIGDYIDTSIR.I	642.3198	2	2	63.6	23.95	1.81	642.3180	2	4	68.5	24.03	-1.02
28 - 38	K.M*IGDYIDTSIR.I	650.3156	2	2	59.1	22.37	-0.76	650.3164	2	6	71.7	22.60	0.47
45 - 51	F.LADLLLR.L	407.2714	2	1	23.8	30.68	19.89						
55 - 64	R.C*VVEYGSNGR.Y	570.7626	2	2	50.7	13.42	6.75	570.7585	2	3	61.5	13.62	-0.43
65 - 71	R.YYLPEDRL.L	478.2429	2	2	31.3	17.23	27.67	478.2336	2	3	35.6	17.32	8.29
101 - 108	R.ISVTGNYSR.N	455.2423	2	4	48.8	14.80	-1.77	455.2428	2	6	46.1	14.83	-0.67
165 - 170	K.LSLPERK.K	357.7099	2	6	39.1	17.00	-2.71	357.7108	2	6	40.3	16.77	-0.11
165 - 171	K.LSLPERK.D	421.7596	2	1	31.1	14.53	2.96	421.7579	2	3	31.5	14.87	-1.17
179 - 185	R.LAMYEDK.N							435.2070	2	2	34.6	14.28	-0.70
179 - 193	R.LAMYEDKNNVTFGIK.R							581.6314	3	3	95.3	23.62	0.87
179 - 193	R.LAM*YEDKNNVTFGIK.R							586.9627	3	5	129.2	21.28	0.17
179 - 194	R.LAMYEDKNNVTFGIK.R.L							475.4996	4	2	54.8	23.53	-1.50
179 - 194	R.LAM*YEDKNNVTFGIK.R.L							479.4986	4	5	93.8	20.85	-0.88
186 - 193	K.NNVTFGIK.R							446.7535	2	1	38.9	18.98	12.35
186 - 194	K.NNVTFGIK.R.L							350.2017	3	2	33.5	16.97	0.59
217 - 227	K.AEPLTQFINR.A	659.3436	2	4	82.4	22.05	0.11	659.3445	2	7	67.0	22.03	1.43
228 - 235	R.AGYRPFK.H	469.2656	2	2	30.3	15.90	-1.63	469.2651	2	4	46.3	16.18	-2.67
294 - 303	K.ELITWPETR.D	623.3279	2	1	55.1	23.92	0.95	623.3277	2	4	44.0	24.22	0.60
304 - 317	R.DLVLIYNSHDSK.G	549.2874	3	4	80.5	31.77	2.71	549.2865	3	2	57.8	31.75	1.07
318 - 334	K.GNLVDVGGELLVAHM*QNK.T							618.3248	3	4	89.5	30.15	0.73

*: acetylation. **: oxidation. ***: carbamidomethylation.

N: putative N-glycosylation site.

(1) mass-over-charge value from the precursor peptide. (2) charge from the fragmented peptide. (3)

number of peptide-spectrum-matches sharing the same sequence.

(4) score returned by the Mascot search engine. (5) retention time from the sequenced peptide. (6) mass accuracy compared to the theoretical mass-over-charge value.