

Supplementary Table S1. LC-MS/MS analysis of nitrated BSA. BSA treated with TNM for 1 h was trypsin digested and analyzed by LC-MS/MS with the QSTAR Elite. 24 nitrated peptides were detected using the Mascot search algorithm.

Peptide Order	Observed m/z	Mr(calc) (Da)	Mass error (ppm)	Expect. Value	Peptide Score	Missed clvg. site	Peptide Sequence
1	486.7434	971.4712	1	0.00011	40	0	K.YLYE ^Y IA ^R .R + Nitro (Y)
2	509.2375	1016.4563	4	6e-006	52	0	K.YLYE ^Y IA ^R .R + 2 Nitro (Y)
3	376.8764	1127.5723	31	0.011	19	1	K.YLYE ^Y IA ^R .H + Nitro (Y)
4	391.8644	1172.5574	12	0.045	13	1	K.YLYE ^Y IA ^R .H + 2 Nitro (Y)
5	495.6155	1483.7895	24	6.4e-008	72	1	R.RHPE ^Y AVSVLLR.L + Nitro (Y)
6	744.8258	1487.6198	12	3e-009	85	0	K.YICD ^Y NQDTISSK.L + Nitro (Y)
7	762.2674	1522.5010	13	7e-007	62	0	R.ET ^Y GDMAD ^C CCEK.Q + Nitro (Y)
8	770.2659	1538.4960	14	8.7e-008	71	0	R.ET ^Y GDMAD ^C CCEK.Q + Nitro (Y) + Oxid (M)
9	726.9575	2177.7936	26	2.5e-006	56	1	R.ET ^Y GDMAD ^C CCEKQEPER.N + Nitro (Y) + Oxid (M)
10	689.2893	2064.8187	13	5.5e-006	53	1	K.VASLRE ^Y TGDMAD ^C CCEK.Q + Nitro (Y) + Oxid (M)
11	762.9055	1523.7732	15	2.7e-014	136	0	K.LGE ^Y GFQNALIVR.Y + Nitro (Y)
12	519.2316	2072.0803	394	0.049	13	2	K.LGE ^Y GFQNALIVR ^Y TRK.V + Nitro (Y)
13	774.3158	1546.5915	17	1.6e-009	88	0	K.E ^Y EATLEECCA ^K .D + Nitro (Y)
14	620.6228	1858.8077	21	4.4e-008	74	1	R.LAKE ^Y EATLEECCA ^K .D + Nitro (Y)
15	533.8935	1598.6308	18	2.7e-006	56	0	K.DDPHAC ^Y STVFDK.L + Nitro (Y)
16	614.2873	1839.8098	17	4.6e-007	63	1	K.DDPHAC ^Y STVFDK ^L .H + Nitro (Y)
17	806.8784	1611.7205	13	3.9e-007	64	0	K.DAFLGSFL ^Y E ^Y SR.R + Nitro (Y)
18	829.3727	1656.7056	15	0.00013	39	0	K.DAFLGSFL ^Y E ^Y SR.R + 2 Nitro (Y)
19	595.9574	1784.8073	24	2.4e-006	56	0	R.M ^P CTED ^Y LSLILNR.L + Nitro (Y) + Oxid (M)
20	896.8625	1791.6828	15	6.4e-010	92	0	K. ^Y NGVFQ ^E CCQAEDK.G + Nitro (Y)
21	844.7180	2531.0879	18	8.1e-006	51	1	K. ^Y NGVFQ ^E CCQAEDK ^G ACLLPK.I + Nitro (Y)
22	642.6492	1924.8989	14	3.7e-007	64	0	R.RPCFSALTPDET ^Y VPK.A + Nitro (Y)
23	523.3000	2089.0057	79	0.027	16	1	R.RHP ^Y F ^Y APPELLY ^Y ANK.Y + Nitro (Y)
24	712.3465	2133.9908	13	7.4e-005	41	1	R.RHP ^Y F ^Y APPELLY ^Y ANK.Y + 2 Nitro (Y)