

Supplemental Table 1: Identification of m/z 4937, m/z 4964 and m/z 3153 by Top-down sequencing. Each protein feature is annotated with UniProt accession number, Protein name, amino acids position of the identified sequence, identified modification, SEQUEST identification score, sequence coverage percentage, m/z of the monoisotopic ion precursor measured using a nanoESI-LTQ-Orbitrap XL instrument and the corresponding monoisotopic MH⁺, theoretical monoisotopic MH⁺, average m/z measured by IMS and the theoretical average MH⁺.

UniProt accession number	Protein name	Position of the identified sequence	Modification	SEQUEST score	Sequence Coverage %	Threshold score	Measured m/z (LC-MS)	Measured monoisotopic MH ⁺ (LC-MS)	Theoretical monoisotopic MH ⁺	Measured average MH ⁺ (IMS)	Theoretical average MH ⁺
P63312	Thymosin β-10	2-44	1 acetylation (Lys3)	230.6	97.73	4.78	823.2621 ⁶⁺	4934.5365	4934.5302	4937	4937.53
P62329	Thymosin β-4	2-44	1 acetylation (Lys3)	164.43	97.73	4.31	1241.1309 ⁴⁺	4961.5021	4961.4935	4964	4964.51
Q924N5	Long-chain-fatty-acid-CoA ligase ACSBG1	19-48	none	43.28	5.69	4.305	1051.1334 ³⁺	3151.3857	3151.3828	3153	3153.23