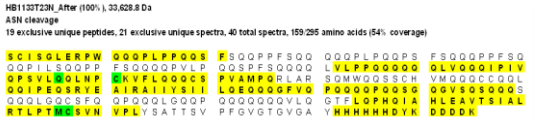
Table S4

Data for spot 5 showing identified sequence (highlighted in yellow) and a table showing identified peptides and associated ion statistics.

Modifications are shown in green: C, carbamidomethyl cysteine; M, oxidation; Q, deamidation. Note that not all cycteine residues are colored green although all have been converted to carboxymethyl amino cysteine. Modification of cysteine was defined in different Mascot searches as both a fixed and a variable modification in the database searching software. The result is that not all cysteine residues were color coded by the analysis software.



Peptide	Amino Acid		Peptide	Mascot			X! Tandem	Number of identified				'+1H Peptide	Peptide
Sequence	Prior	Next	Probability	Ion Score	Identity Score	Delta ion Score	-log(e) score	+1H spectra	+2H spectra	+3H spectra	+4H spectra	Mass (AMU)	Start index
SCISGLERPW	-	Q	0,997	59,2	42	31,6	4,28		2			1204,58	1
SCISGLERPWQQQPLPPQQSF	-	S	0,997				9,3			2		2483,21	1
QQQPLPPQQSF	W	S	0,996	22,3	22,3	30,3	3,4		1			1297,65	11
VLPPQQQQQQL	L	V	0,997	31,9	12,6	31,4	4		2			1306,71	82
VLPPQQQQQQLVQQQIPIVQPSVL	L	Q	0,997	64,4	64,4	28,2	2,38				2	2736,54	82
VQQQIPIVQPSVL	L	Q	0,997	52,2	37,5	31,2	4,19		3			1448,85	93
VQQQIPIVQPSVLQQLNPCKVF	L	L	0,997				7,37			2		2563,41	93
QPIVQPSVLQQLNPCKVF	Q	L	0,997				5,57			1		2208,22	96
QQLNPCKVF	L	L	0,992				6,24		4			1116,55	106
LQQQCSPVAMPQ	F	R	0,914				2,85		1			1386,65	115
QQIPEQSRY	L	E	0,997	57,9	47,4	31,7			1			1148,57	151
EAIRAIIY	Y	S	0,985	49,7	13,2	32,7			3			948,55	160
EAIRAIIYSIILQEQQQGF	Y	V	0,997				11,5			2		2220,20	160
SIILQEQQQGF	Y	V	0,997	80,6	69,1	32,3	5,6		4			1290,67	168
VQPQQQQPQQSGQGVSQSQQQ	F	S	0,983				4,33			1		2323,10	179
LQPHQIAHLEAVTSIALRTLPTMCSV	F	N	0,956				3,31				1	2886,53	234
RTLPTMCSVNVPL	L	Y	0,997	55	44,2	32	1,09		3			1487,77	251
HHHHHHDYKDDDD	Y	-	0,997				9,77			3		1707,66	282
HHHHHHDYKDDDDK	Y	-	0,997	56,9	56,9	29,1	6,24			2		1835,76	282