

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 cysteine 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.

HB113T23H_AR# (100%), 33,629.8 Da

ASN cleavage

19 exclusive unique peptides, 21 exclusive unique spectra, 40 total spectra, 159 295 amino acids (54% coverage)

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S C I S G L E R P W Q Q O P L P P Q S F F S D Q P P F S Q Q Q Q Q P L P Q Q P S F S Q Q Q P P F S Q
O Q P I L S Q Q P P F S Q Q Q P V L P Q Q S P F S Q Q Q Q L V L P P Q Q Q Q Q L V D Q Q I P T I Y
Q P S V L G D L N P E W F L D Q Q S F V A M P Q R L A P S Q M W Q S S C H Y M Q D Q D Q D L
Q Q I P E Q S R Y E A I R A I Y S I I L Q E Q Q G F V D P Q Q Q P Q Q S G Q C V S Q S Q Q S
Q Q L L G Q C S F Q Q P Q Q L G Q Q P Q Q Q Q Q V L Q G T F L O P H O I A H L E A V T S I A L
R T L P T M C S V N V P L Y S A T T S V P F Q V G T G V G A Y H N H H H H D Y K D D D K
    
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Peptide	Amino Acid	Peptide	Mascot	XI Tandem	Number of identified	*1H Peptide	Peptide						
Sequence	Prior	Next	Probability	Ion Score	Identify 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
SCISGLERPWQQQLPPQSF	-	S	0.997				9.3			2		2463.21	1
QQQLPPQSF	W	S	0.996	22.3	22.3	30.3	3.4		1		2	1297.65	11
VLPPQQQQQL	L	V	0.997	31.9	12.6	31.4	4		2			1306.71	82
VLPPQQQQQLVQQQIPVPSVL	L	Q	0.997	64.4	64.4	28.2	2.38				2	2736.54	82
VQQQIPVPSVL	L	Q	0.997	52.2	37.5	31.2	4.19		3			1448.85	93
VQQQIPVPSVLQQLNPKVF	L	L	0.997				7.37				2	2563.41	93
QIPVPSVLQQLNPKVF	Q	L	0.997				5.57				1	2208.22	96
QQLNPKVF	L	L	0.992				6.24					1116.55	106
LQQGCSFVAMPQ	F	R	0.914				2.85					1386.65	115
QQIPCSRY	L	E	0.997	57.9	47.4	31.7						1148.57	151
EAIRAIY	Y	S	0.985	49.7	13.2	32.7						948.55	160
EAIRAIYSILQEQGGF	Y	V	0.997				11.5				2	2220.20	160
SILQEQGGF	Y	V	0.997	80.6	69.1	32.3	5.6					1250.67	168
VPPQQQQPQSGGVSQSQQQ	F	S	0.983				4.33				1	2323.10	179
LQPHQAHLEAVTSIALRTLPTMCSV	F	N	0.856				3.31					2886.53	234
RTLPTMCSVWVPL	L	Y	0.997	55	44.2	32	1.99				1	1487.77	251
HNNHHHDK	Y	-	0.997				9.77				3	1707.66	282
HNNHHHDKDDDK	Y	-	0.997	56.9	56.9	29.1	6.24				2	1835.76	282