Table S3

Data for spot 4 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.

HB1133-WILD_TYPE-LRWT (100%), 34,050.4 Da
Leader-Removed with tag
31 exclusive unique peptides, 39 exclusive unique spectra, 118 total spectra, 222/298 amino acids (74% coverage)

METSCIFGLE RPWQQQPLPP QQSFSQQPPF SQQQQQPLPQ QPSFSQQQPP
FSQQQPILSQ QPPFSQQQQP VLPQQSPFSQ QQQLVLPPQQ QQQQLVQQQI
PIVQPSVLQQ LNPCKVFLQQ QCSPVAMPQR LARSQMWQQS SCHVMQQQCC
QQLQQIPEQS RYEAIRAIIY SIILQEQQQG FVQPQQQQPQ QSGQGVSQSQ
QQSQQQLGQC SFQQPQQQLG QQPQQQQQQQ VLQGTFLQPH QIAHLEAVTS
IALRTLPTMC SVNVPLYSAT TSVPFGVGTG VGAYHHHHHH DYKDDDDK

Peptide	Amino Acid		Peptide	Mascot			X! Tandem	lumber 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) t	Start index
METSCIF	-	G	0,98	46,4	32,4	38		1				903,36	1
GLERPW	F	Q	1,00	40,9	32,1	20	1,42	1	2			757,40	8
GLERPWQQQPLPPQQSF	F	S	1,00				19,20			1		2036,04	8
QQQPLPPQQSF	W	S	1,00	63	30,3	46,4	5,68		16			1297,65	14
IVNGEEAVPGSWPWQVSLQDKTGF	R	H	1,00				7,74			1		2644,30	16
SQQPPFSQQQQQPLPQQPSF	F	S	1,00	57,2	27,8	57,2	5,02			1		2325,13	25
QVSLQDKTGF	W	H	1,00	73,5	32,1	49,5	3,70		4			1122,58	30
DQGSSSEKIQ	F	K	1,00				4,62		1			1078,50	72
DQGSSSEKIQKL	F	K	1,00	56,4	31,3	46,7	6,85		2			1319,68	72
KIAKVF	L	K	1,00	32,7	33,1	3,53	2,96	1	3			705,47	84
VLPPQQQQQ	L	Q	0,98				3,00		1			1065,57	85
VLPPQQQQQQL	L	V	1,00	31,7	31,4	15,8	5,57		4			1306,71	85
VLPPQQQQQQLVQQQIPIVQPSVL	L	Q	1,00	50,6	25,4	50,6	-1,97			4	1	2736,54	85
VQQQIPIVQPSVL	L	Q	1,00	51,8	31,2	38,4	3,96		11			1448,85	96
TINNDITLL	L	K	1,00	53,3	31,5	15,2	0,70	2	1			1016,56	98
KLSTAASF	L	S	1,00	53,4	31,7	16,6	1,96	3				824,45	107
QQLNPCKVF	L	L	1,00	39,2	33,9	20,9	4,72	2	7			1133,58	109
LQQQCSPVAMPQ	F	R	0,93				2,16		1			1386,65	118
QQSSCHVM	W	Q	1,00	60	33,8		2,77		1			976,40	138
ANTPDRLQQA	N	S	0,98				3,04		1			1113,56	149
ANTPDRLQQASLPL	N	L	0,98				3,35		1			1523,82	149
CCQQLQQIPEQSRY	Q	E	1,00				9,01		1			1837,83	149
QQIPEQSRY	L	E	1,00	59	31,7	47,8	6,48		4			1148,57	154
EAIRAIIY	Y	S	1,00	40,5	32,7	11,5	3,48	2	9			948,55	163
EAIRAIIYSIILQEQQQGF	Y	V	1,00				9,40			1		2220,20	163
SIILQEQQQGF	Y	V	1,00	84,6	32,3	74,8	-2,61		1			1290,67	171
GTKIKDAM	W	I	0,99	25,6	34	12,2	2,11		1			863,47	173
VQPQQQQPQQSGQ	F	G	0,99				4,10		1			1480,71	182
VQPQQQQPQQSGQGVSQSQQQSQQQL	F	G	0,97	19	25	7,97	1,92				1	2907,39	182
GDSGGPL	M	V	1,00	39,2	32,2	7,74	2,40	2				602,28	193
TLVGIVSW	W	G	1,00	42,5	32,7	31,6	2,37	2	1			874,50	208
VGIVSW	L	G	0,95	32,5	32,3	11,1	0,04	1				660,37	210
ARVTALVNWVQQTL	Y	A	0,98				3,41		4			1598,90	229
QGTFLQPHQIAHLEAVTSIAL	L	R	0,97				4,11			2		2257,20	233
LQPHQIAHL	F	E	1,00	40,9	32,4	15,1	2,00		4			1056,60	237
LQPHQIAHLEAVTS	F	I	1,00				8,64		1			1543,82	237
EAVTSIAL	L	R	0,99	50,3	32,5	18,4		2				803,45	246
RTLPTM	L	C	0,93	18,9	33,4		0,89	1				718,39	254
RTLPTMCSVNVPL	L	Y	1,00	61,7	32	48,8	-2,54		7			1487,77	254
RTLPTMCSVNVPLY	L	S	0,99				3,82		4			1650,83	254
SATTSVPF	Y	G	0,99	27,8	32,6		0,77	2				809,40	268