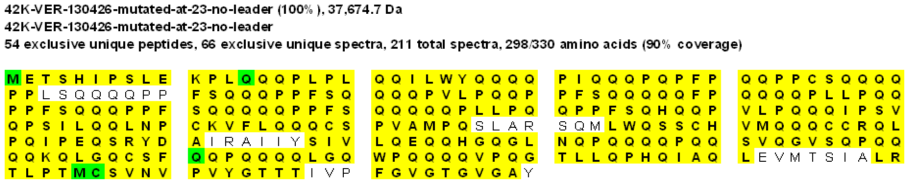
Table S1

Data for spot 1 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.



42K-VER-130426-mutated-at-23-no-leader (100%), 37,674.7 Da
42K-VER-130426-mutated-at-23-no-leader
54 exclusive unique peptides, 66 exclusive unique spectra, 211 total spectra, 298/330 amino acids (90% coverage)

METSHIPSLE KPLQQQPLPL QQILWYQQQQ PIQQQPQPFP QQPPCSQQQQ
PPLSQQQQPP FSQQQPPFSQ QQQPVLPQQP PFSQQQQQFP QQQQPLLPQQ
PPFSQQQPPF SQQQQQPPFS QQQQQPLLPQ QPPFSQHQQP VLPQQQIPSV
QPSILQQLNP CKVFLQQQCS PVAMPQSLAR SQMLWQSSCH VMQQQCCRQL
PQIPEQSRYD AIRAIIYSIV LQEQQHGQGL NQPQQQQPQQ SVQGVSQPQQ
QQKQLGQCSF QQPQQQQLGQ WPQQQQVPQG TLLQPHQIAQ LEVMTSIALR
TLPTMCSVNV PVYGTTTIVP FGVGTGVGAY

Peptide	Amino Acid		Peptide	Mascot			X! Tandem	Number of identified				'+1H Peptide pt	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 i	Start index
METSHIPSLEKPL	-	Q	1,00	42,7	34,4	29,5	4,03		3			1481,77	1
METSHIPSLEKPLQQQPLPL	-	Q	1,00	44,7	33	42,2			4			2302,21	1
LQQQPLP	P	L	0,99	42,8	38,4	14	0,05					823,47	13
LQQQPLPLQQ	P	I	1,00	43,7	36,3	17,5	3,40	1				1192,67	13
QQQPLPLQQILW	L	Y	1,00	53,5	34,9	39,2	2,34	2				1491,83	14
ILWYQQQQP	Q	I	1,00	50,2	36,1	35,2	0,72	4				1203,62	23
IQQQPQPFPQQPPCSQQQQPP	P	L	1,00	29,9	29,3	29,8	1,89		9			2486,19	32
FSQQQPPFSQQQQP	P	V	1,00	58,4	32,6	27,7	2,41	2				1674,79	61
VLPQQPP	P	F	0,99	41,2	38,7	12,4	1,24	1				778,45	75
FSQQQQQFPQQQQP	P	L	1,00	35,6	33,7	23,2	1,82	4				1746,82	82
LLPQQPP	P	F	0,98	30,3	38,5		0,21	4				792,46	96
LLPQQPPFSQQQPP	P	F	1,00	34,6	33,8	26,7	0,85	4				1604,84	96
FSQQQQQPP	P	F	1,00	43	37,6	22	1,92	6				1087,52	110
FSQQQQQP	P	L	0,99	32,3	38	13,2	0,29	3				990,46	119
LLPQQPPFSQHQQP	P	V	1,00	49,5	33,6		3,72	14	2			1644,85	127
LPQQPPFSQH	L	Q	1,00				2,82	2				1178,60	128
LPQQPPFSQHQQPVLPQQQIPSVQPSIL	L	Q	1,00	23,8	30,9	5,35	6,34		2	2		3159,70	128
PQQPPFSQHQQP	L	V	1,00				5,62	5				1418,68	129
FSQHQQP	P	V	0,97	34,7	37,4	2,92	1,10	1				871,41	134
SQHQQPVLPQQQIPSVQPSIL	F	Q	1,00	58	33	56	7,55		2			2352,27	135
QQPVLPQQQIPSVQPSIL	H	Q	1,00	39,4	33,9	36,7	3,89		2			2000,12	138
VLPQQQIPS	P	V	1,00	26	37,8	13,2	1,60	9				1009,57	141
VLPQQQIPSVQPS	P	I	0,98				2,09	2				1420,78	141
QQIPSVQPSIL	Q	Q	0,90				0,92	1				1209,68	145
QQLNPCKVF	L	L	1,00	45,9	35,4	26,1	3,04	3				1133,58	156
LNPCKVF	Q	L	0,99	43	38,5	19,1	0,51	5				877,46	158
LQQQCSP	F	V	0,95	35,7	38,9		-2,79	1				860,39	165
LQQQCSPVAMPQ	F	S	1,00				2,59	2				1386,65	165
LWQSSCH	M	V	0,99	25,1	38	5,68	0,75	4				917,39	184
QSSCHVM	W	Q	0,99	39,5	35,1	15,2	0,70	1				848,34	186
VMQQQCCRQLPQIPEQSRYDA	H	I	1,00				3,77		2			2635,22	191
MQQQCCRQLPQIPEQ	V	S	1,00				3,48		1			2057,93	192
CCRQLPQIPEQSRY	Q	D	1,00	0			3,10		2			1834,87	196
RQLPQIPEQSRY	C	D	1,00				4,66	1	1			1514,81	198
LPQIPEQSRYDA	Q	I	1,00	36,7	34,6	7,86	6,85	2				1416,71	200
SIVLQEQQHGQGL	Y	N	1,00	67,3	34,9	17,1	5,46	1	1			1436,75	218
IVLQEQQHGQG	S	L	1,00	48,7	35,6	18,8	5,09	19				1236,63	219
LNQPQQQQPQQS	G	V	1,00	46,9	35,3	39,8	6,77	13				1423,69	230
VQGVSQPQQQQKQ	S	L	1,00	55,2	33,5	48,4	7,22	1				1482,77	242
GVSQPQQQQKQL	Q	G	1,00				4,59	2				1368,72	244
VSQPQQQQKQ	G	L	1,00	74,2	36,5	61,7	5,18	12				1198,62	245
QQQKQLGQCSF	Q	Q	0,99				1,85	1				1351,64	250
LGQCSFQQPQQQQ	Q	L	1,00	60,2	33,7	56,5	5,18	1				1576,72	255
FQQPQQQQ	S	L	1,00	30,5	38	0,56	1,35	2				1031,49	260

QQPQQQQL	F	G	1,00	44,2	34,9	9,53	2,27	2	997,51	261
LGQWPQQQQVPQGT	Q	L	1,00	35,8	33,7		2,72	4	1594,80	268
LGQWPQQQQVPQGTL	Q	L	1,00	52	32,8		3,62	7	1707,88	268
LLQPHQ	T	I	0,90	31,6	38,9	1,34	2,54	1	735,41	282
LQPHQIAQL	L	E	1,00	32,4	34,8		1,01	2	1047,59	283
LRTLPTMCS	A	V	1,00	48,6	37,5	37,2		5	1094,53	299
RTLPTMCSVNVPVY	L	G	0,96	42,5	34,6	40,3		1	1652,81	300
VYGTTT	P	I	0,90	33,8	36,7	8,01	0,47		641,31	312
FGVGTGVG	P	A	1,00	32	38,2	17,1	3,92		693,36	321
GVGTGVGA	F	-	0,92				1,26		617,33	322