

Supplementary Table 1

Mass spectrometric output for the proteins identified in the study

Spot No.	Swiss-Prot Accession #	Sequence coverage	Mascot total ion score	# of matched peptide / searched peptides	peptide sequence	error (ppm)	Mascot peptide score
1	P05109	39	242	4	GADVWFK	24.8	51
					GNFHAVYR	28.7	47
					ALNSIIDVYHK	29.7	92
					LLETECPQYIR	30.5	51
2	P06702	24	177	2	LGHPDTLNQGEFK	29.5	51
					NIETIINTFHQYSVK	26.5	126
3	P06396	9	59	7/23	AGKEPGLQIWR	-24.7	
					EVQGFESATFLGYFK	18.5	
					HVVPNEVVVQR	8.6	
					EGGQTAPASTR	17.1	
					TPSAAYLWVG TGASEAEK	12.6	
					YIETDPANR	8.9	
					YIETDPANRDR	8.9	
4	Q16891	12	252	4	VVSQYHELVVQAR	10.9	43
					GIEQAVQSHAVAEER	10.6	59
					LSQEQVDNFTLDINTAYAR	12.3	42
					ANCSDNEFTQALTAAPPELTR	8.9	60
5	Q13228	13	108	3	EEIVYLPCIYR	14.3	35
					FLYFSNWLHGDLR	21.9	32
					HNVMISTEWAAPNVLR	19.1	38
6	Q13228	15	108	2	EEIVYLPCIYR	23.5	30
					HNVMISTEWAAPNVLR	22.4	50
7	P02787	18	192	2	DSGFQMNQLR	34.1	31
					NLNEKDYELLCLDGTR	25.1	32
8	P02787	20	342	7	EGYYGYTGAFR	36.6	46
					KPVEEYANCHLAR	31.3	31
					EDPQTFYYAVAVVK	25.4	44
					ADRDQYELLCLDNTR	25.0	38
					NLNEKDYELLCLDGTR	23.9	44
					SAGWNIPIGLLYCDLPEPR	22.9	53
					KPVDEYKDCHLAQVPSHTVVAR	16.2	31
9	P61160	22	319	5	HLWDYTFGPEK	53.0	77
					GYAFNHSADFETVR	45.9	90
					LCYVGYNIEQEQK	40.6	30
					SMLEVNYPMENGIVR	39.1	62
					LALETTVLVESYTLPDGR	38.4	45
10	Q01995	31	481	6	LGFQVWLK	15.2	62
					QMEQVAQFLK	17.9	79
					VPENPPSMVFK	15.4	81
					TDMFQTVDLFEGK	15.7	114
					TDMFQTVDLFEGKDMAAVQR	15.6	80
					LVNSLYPDGSKPVKVPENPPSM	14.2	64
11	P09327	14	348	7	EVQGNESAEFR	18.1	31
					LQEENLVITPR	9.8	30
					LIIQWNGPESTR	12.9	51
					MVDDGSGEVQVWR	14.2	65
					GSLNITTPGLQIWR	12.5	34
					LYHVSDSEGNLVVR	12.1	60
					FDATSMHVKPQVAAQK	6.5	42

12	P25325	34	66	6/36	ALVSAQWVAEALR	1.2	
					AGQPLQLLDASWYLPK	-5.7	
					HIPGAFFDIDQCSDR	0.4	
					TSPYDHMLPGAEHFAEYAGR	5.9	
					SQPAPAEFR	5.2	
					DGIEPGHIPGTVNIPFTDFLSQEC	-17.6	
	P06733			8/36	LAMQEFMILPVGAANFR	3.8	
					AGYTDKVVIGMDVAASEFFR	-5.3	
					VVIGMDVAASEFFR	0.1	
					YDLDFKSPDDPSR	1.8	
13	P23526	7	90	2	YPQLLPGIR	55.2	30
					ALDIAENEMPGLMR	20.2	31
14	P06733	33	548	8	YISPDQLADLYK	31.9	71
					VVIGMDVAASEFFR	25.7	79
					AAVPSGASTGIYEALR	27.4	94
					LAMQEFMILPVGAANFR	18.8	85
					DATNVGDEGGFAPNILENK	21.0	35
					FTASAGIQVVGDDLTVTNPK	22.8	71
					SGETEDTFIADLVVGLCTGQIK	20.1	70
					DYPVVSIEDPFDQDDWGAWQK	24.2	42
					LAQANGWGMVSHR	-11.9	
					SGETEDTFIADLVVGLCTGQIK	0.0	
15	P06734	23	342	6	YISPDQLADLYK	13.3	58
					VVIGMDVAASEFFR	15.7	44
					AAVPSGASTGIYEALR	15.4	86
					LAMQEFMILPVGAANFR	16.4	67
					FTASAGIQVVGDDLTVTNPK	15.7	44
					SGETEDTFIADLVVGLCTGQIK	20.1	44
16	Q16555	17	217	3	VFNLYPR	13.7	33
					IVLEDGTLHVTEGSGR	8.0	52
					DIGAIAQVHAENGDIIEEQQR	4.4	73
17	P13639	13	464	6	VFDAIMNFK	31.4	38
					TFCQLILDPIFK	31.0	58
					STASLFYELSENDLNFIK	35.9	47
					ALLELQLEPEELYQTFQR	32.2	86
					VTDGALVVDCVSGVCVQTETV	33.5	91
					DGAGFLINLIDSPGHVDFSSEVT	32.0	125
18	P30040	25	62	5/24	LDKESYPVFYLF	23.0	
					ESYPVFYLF	26.1	
					DGDFENVPYTGAVK	20.1	
					GQGVYLGMPGCLPVYDALAGEF	6.7	
					ILDQGEDFPASEMTR	13.8	
19	P04075	19	69	5/15	PYQYPALTPEQK	-4.0	
					QLLLTADDRVNPCIGGVILFHETI	-22.6	
					VNPCIGGVILFHETLYQK	-6.1	
					ADDGRFPQVIK	-10.6	
					IGEHTPSALAIMENANVLAR	1.9	
20	P04406	23	287	5	LVINGNPITIFQER	31.9	74
					IISNASCTTNCLAPLAK	30.1	36
					LVINGNPITIFQERDPSK	31.0	32
					VIIISAPSADAPMFVMGVNHEK	26.1	114
					WGDAGAEYVVESTGVFTTMEK	24.1	31
21	P04406	21	269	3	VPTANVSVDLTCR	14.3	44
					LISWYDNEFGYSNR	14.9	100
					VIHDNFGIVEGLMTTVHAITATQK	4.9	118
22	P41250	4	81	2	LPFAAAQIGNSFR	-33.2	33

23	P15531	31	172		TLYVEEVVPPNVIEPSFGLGR	-46.5	48
				3	DRPFFAGLVK	62.3	43
					TFIAIKPDGVQR	51.3	41
24	P25786	37	358		VMLGETNPADSKPGTIR	37.6	67
				4	FVFDRPLPVS	5.3	40
					IHQIEYAMEAVK	4.3	80
25	P30101	18	69		HMSEFMECNLNLVK	5.7	107
					DLEFTIYDDDDVSPFLEGLEERP	-0.4	72
				8/28	AASNLRDNYR	29.9	
26	P14618	13	309		TFSHELSDFGLESTAGEIPVVAIF	-5.0	
					FVMQEEFSR	-6.1	
					FLQDYFDGNLK	3.1	
27	P14618	13	177		FLQDYFDGNLKR	-4.8	
					MDATANDVSPPYEVR	12.5	
					GFPTIYFSPANK	-19.6	
28	P00352	7	117		ELSDFISYLQR	-2.7	
				5	RFDEILEASDGIMVAR	-1.4	45
					FGVEQDVMVFASFIR	2.5	115
29	P00352	21	326		EAEAAIYHLQLFEELR	1.3	65
					EAEAAIYHLQLFEELRR	-3.5	47
					TATESFASDPILYRPVAVALDTK	-5.2	38
30	Q9NVA2	16	209	2	RFDEILEASDGIMVAR	47.9	47
					FGVEQDVMVFASFIR	38.7	102
				3	QAFQIGSPWR	15.5	33
31	P60174	49	621		TIPIDGNFFTYTR	26.0	30
					IFVEESIYDEFVR	22.9	57
				5	TIPIDGNFFTYTR	22.9	77
32	P60174	15	235		ANNTFYGLSAGVFTK	33.5	51
					IFVEESIYDEFVR	22.3	65
					ELGEYGFHEYTEVK	30.9	56
33	Q01469	17	86		GYFVQPTVFSNVTDEMR	22.9	46
				3	FESDPATHNEPGVR	39.5	46
					AAAQLLSQAQQSGAQQTK	25.3	60
34	P68871	60	434		NLSLSGHVGFDSLPLDQLVNK	25.2	88
				7	HVFGESDELIGQK	10.3	91
					TATPQQAQEVHEK	15.2	41
35	P02768	8	160		DCGATWVVLGHSER	15.7	64
					VVLAYEPVWAIGTGK	7.8	119
					VAHALAEGLGVIACIGEK	13.1	128
36	P02768	15	356		VPADTEVVCAPPTAYIDFAR	14.8	126
					ELASQPDVDGFLVGGASLKPEF'	20.0	44
				2	VAHALAEGLGVIACIGEK	-12.8	110
37	P68871	60	434		VPADTEVVCAPPTAYIDFAR	-8.2	125
				2	ELGVGIALR	7.9	41
					LVVECVMMNVCTCTR	8.0	46
38	P02768	8	160	5	LLVVYPWTQR	30.4	40
					EFTPPVQAAYQK	30.1	65
					VLGAFSDGLAHLNLK	37.6	104
39	P02768	8	160		LLGNVLVCVLAHHFGK	33.2	95
					GTFATLSELHCDKLHVDPENFR	33.0	83
				3	YLYEIR	39.3	32
40	P02768	15	356		LVNEVTEFAK	44.0	81
					LVRPEVDVMCTAFHDNEETFLKI	27.8	31
				6	LVNEVTEFAK	70.8	53
41	P02768	15	356		HPYFYAPELLFFAK	44.3	83
					RHPYFYAPELLFFAK	36.9	37
					NECFLQHKDDNPNLPR	37.2	30
42	P02768	15	356		LVRPEVDVMCTAFHDNEETFLK	32.8	34

37	P02675	21	269		LVRPEVDVMCTAFHDNEETFLKI	32.6	64
				4	YYWGGQYTWDMAK	16.8	41
					HQLYIDETVNSNIPTNLR	5.1	62
					VYCDMNTENGWTVIQNR	11.0	63
38	Q969H8	13	142		KGGETSEMYLIQPDSSVKPYR	6.6	58
				2	SYLYFTQFK	28.1	73
					ESDVPLKTEEFVTK	23.4	69
39	Q8WVM8	24	85	9/37	MLNFNVPNIK	6.8	
					FGQDIISPLLSVK	0.7	
					NQLYESYYLNFISAIR	-4.4	
					NIDLATPLHHTWTYQALVHDL	10.8	
					GSPFPEVAESVQQELESYR	6.2	
					LIDLHTNVATAVLEHIK	-3.1	
					KLDVYFEYEEK	10.5	
					LFLIYYISTQQAPSEADLEQYKK	-22.2	
					HILYGCSELFNATQFIK	-3.0	
	P02768	18	60	8/37	LVNEVTEFAK	1.8	
					LVRPEVDVMCTAFHDNEETFLKI	-0.2	
					YLYEIAR	17.2	
					NYAEAKDVFLGMFLYEYAR	23.4	
					RHPDYSVLLLLR	2.9	
					VFDEFKPLVEEPQNLIK	-4.9	
					FQNALLVR	13.0	
					RPCFSALEVDETYVPK	3.1	