

Supplementary Information

Table S1. MS/MS data for mTORC1 interacting proteins identified by ESI Q-TOF MS/MS analysis.

Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
Raptor	14 (11)	1 MESEMLQSPL LGLGEEDEAD LTDWNLPLAF MKKRHCEKIE GSKSLAQSWR
		51 MKDRMKT VSV ALVLCLNVGV DPPDVVK TTP CARLECWIDP LSMGPQK ALE
		101 TIGANLQK QY ENWQPRARYK QSLDPTVDEV KKLCTSLRRN AKEERVLFHY
		151 NGHGVPRPTV NGEVWVFNKN YTQYIPLSIY DLQTMWGSPS IFVYDCSNAG
		201 LIVKSFKQFA LQREQELEVA AINPNHPLAQ MPLPPSMKNC IQLAACEATE
		251 LLPMIPDLPA DLFTSCLTTP IKIALRWFCM QKCVSLVPGV TLDLIEKIPG
		301 RLNDRRTPLG ELNWIFTAIT DTIAWNVLPR DLFQKLFR QD LLVASLFRNF
		351 LLAERIM RSY NCTPVSSPRL PPTYMHAMWQ AWDLAVDICL SQLPTIIIEG
		401 TAFRHSPFFA EQLTAFQVWL TMGVENRNPP EQLPIVLQVL LSQVHRLRAL
		451 DLLGRFLDLG PWAVSLALSV GIFPYVLKLL QSSARELRPL LVFIWAKILA
		501 VDSSCQADLV KDNHGKYFLS VLADPYMPAE HRTMTAFILA VIVNSYHTGQ
		551 EACLQGNLIA ICLEQLNDPH PLLRQWVAIC LGRI WQNFDS AR WCGVRDSA
		601 HEK LYSLLSD PIPEVR CAAV FALGTFVGNS AERTDHSTTI DHNVAMMLAQ
		651 LVSDGSPMVR KELVVALSHL VVQYESNFCT VALQFIEEEK NYALPSPATT
		701 EGGSLTPVRD SPCTPRL RSV SSYGNIR AVA TARSLNKSQ NLSLTEESGG
		751 AVAFSPGNLS TSSSASSTLG SPENEEHILS FETIDKMRA SSYSSLNSLI
		801 GVSFNSVYTQ IWRVLLHLAA DPYPEVSDVA MK VLNSIAYK ATVNARPQRV
		851 LDTSSLTQSA PASPTNKG VVH IHQAGGSPPA SSTSSSSLTN DVAKQPVSRD
		901 LPSGRPGTTG PAGAQYTPHS HQFPRTRKMF DK GPEQTADD ADDAAGH KSF
		951 ISATVQTGFC DWSARYFAQP VMKIPEEHDL ESQIRKEREW RFLNRSRVRR
		1001 QAQQVIQKGI TR LDDQIFLN RNP GVPSVVK FHPFTPCIAV ADKDSICFWD
		1051 WEKGEKLDYF HNGNPRYTRV TAMEYLNQGD CSLLLTATDD GAIRVWKNFA
		1101 DLEKNPEMVT AWQGLSDMLP TTRGAGMVVD WEQETGLLMS SGDVRIVRIW
		1151 DTDREMKVQD IPTGADSCVT SLSCDSHR SL IVAGLGDGSI RVYDRRMALS
		1201 ECRVMTYREH TAWVVKASLQ KRPDGHIVSV SVNGDVRIFD PRMPESVNVL
		1251 QIVKGLTALD IHPQADLIAC GSVNQFTAIY NSSGELINNI KYDGFMGQR
		1301 VGAISCLAFH PHWPHLAVGS NDYYISVYSV EKRVR
		Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence
		98 -108 579.3115 1156.60841156.6452 -0.0367 0 U K.ALETIGANLQK.Q
		98 -108 579.3149 1156.6152 1156.6452 -0.0299 0 U K.ALETIGANLQK.Q
		339 -348 581.3126 1160.6106 1160.6553 -0.0447 0 R.QDLLVASLFR.N
		349 -355 431.7291 861.4436 86 1.4708 -0.0272 0 R.NFLLAER.I
		584 -592 568.7628 1135.5110 1135.5410 -0.0300 0 U R.IWQNFDSAR.W
		604 -616 751.3935 1500.7724 1500.8188 -0.0463 0 U K.LYSLLSDPIPEVR.C
		604 -616 751.3962 1500.7778 1500.8188 -0.0409 0 U K.LYSLLSDPIPEVR.C
		719 -727 491.7391 981.4636 981.4879 -0.0243 0 U R.SVSSYGNIR.A
		833 -840 454.2522 906.4898 906.5174 -0.0276 0 U K.VLNSIAYK.A
		933 -948 533.2261 1596.6565 1596.6652 -0.0087 0 U K.GPEQTADDADDAAGHK.S
		1013 -1021 567.2834 1132.5522 1132.5877 -0.0354 0 U R.LDDQIFLN.R
		1013 -1021 567.2839 1132.5532 1132.5877 -0.0344 0 U R.LDDQIFLN.R
		1149 -1154 403.1828 804.3510 804.3766 -0.0256 0 U R.IWDTDR.E
		1179 -1191 629.3464 1256.6782 1256.7088 -0.0306 0 UR.SLIVAGLGDGSIR.V
		MS/MS Fragmentation of SLIVAGLGDGSIR

Table S1. Cont.

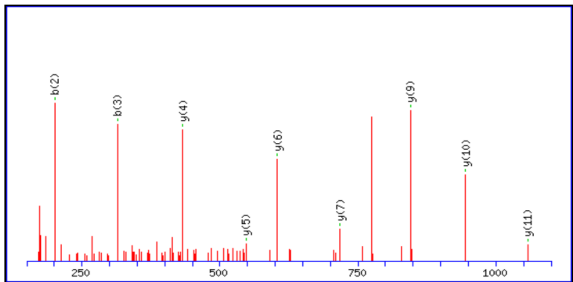
Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
Raptor	14 (11)	
mTOR	18 (11)	1 MLGTGPAAAT TAATTSSNVS VLQQFASGLK SRNEETRAKA AKELQHYVTM 51 ELREMSQEEES TRFYDQLNHH IFELVSSSDA NERKGGILAI ASLIGVEGGN 101 ATRIGRFANY LRNLLPSNDP VVMEMASKAI GRLAMAGDTF TAEYVEFEVK 151 RALEWLGADR NEGRRHAAVL VLRELAISVP TFFQVQVQPF FDNIFAVWD 201 PKQAIREGAV AALRACLILT TQREPKEQK PQWYRHTFEE AEKGFDETLA 251 KEKGMNRDDR IHGALLILNE LVRISMEGE RLREEMEEIT QQQLVHDKYC 301 KDLMGFGTKP RHITPFTSFQ AVQPQQSNAL VGLLGYSSHQ GLMGFGTSPS 351 PAKSTLVESR CCRDLMEEFK DQVCQWVLKC RNSKNSLIQM TILNLLPRLA 401 AFRPSAFTDT QYLQDTMNHV LSCVKKEKER TAAFQALGLL SVAVRSEFKV 451 YLPRVLDIIR AALPPKDFAH KRQKAMQVDA TVFTCISMLA RAMGPGIQQD 501 IKELLEPMLA VGLSPALTAV LYDLRQIPQ LKKDIQDGLL KMLSLVLMHK 551 PLRHGPMPKG LAHQLASPLG TTLPEASDVG SITLALRTLG SFEFEGHSLT 601 QFVRHCADHF LNSEHKEIRM EAARTCSRLL TPSIHLISGH AHVVSQTAVQ 651 VVADVLSKLL VVGITDPDPD IRYCVLASLD ERFDAHLAQA ENLQALFVAL 701 NDQVFEIREL AICTVGRLLS MNPAFVMPFL RKMLIQILTE LEHSGIGRIK 751 EQSARMLGHL VSNAPRLIRP YMEPILKALI LKLKDPDPDP NPGVINNVLA 801 TIGELAQVSG LEMRKWVDEL FIIIMDMLQD SLLAKRQVA LWTLGQLVAS 851 TGYVVEPYRK YPTLLEVLLN FLKTEQNQGT RREAIRVLGL LGALDPYKHK 901 VNIGMIDQSR DASAVLSSES KSSQDSSDYS TSEMLVNMGN LPLDEFYPAY 951 SMVALMRIFR DQSLSHHHTM VVQAITFIK SLGLKCVQFL PQVMPTFLNV 1001 IRVCDGAIRE FLFQQLGMLV SFVKSHIRPY MDEIVTLMRE FWVMNTSIQS 1051 TIILLIEQIV VALGGEFKLY LPQLIPHMLR VFMHDNSPGR IVSIKLLAAI 1101 QLFGANLDDY LLLLLPIVK LFDAPEAPLP SRKAALETVD RLTESLDFTD 1151 YASRIHPIV RTLDQSPELR STAMDTLSSL VFQLGKKYQI FIPMVNKLVL 1201 RHRINHQRVD VLICRIVKGY TLADEEEDPL IYQHRMLRSQ QGDALASGPV 1251 ETGPMKKLHV STINLQAWG AARRVSKDDW LEWLRRLSLE LLKDSSSPSL 1301 RSCWALAQAY NPMARDLFNA AFVSCWSELN EDQQDELIRS IELALTSQDI 1351 A EVTQTLLNL AEFMEHSDKG PLPLRDDNGI VLLGERAAKC RAYAKALHYK 1401 ELEFQKGPTP AILESLISIN NKLQQPEAAA GVLEYAMKHF GELEIQATWY 1451 EKLHEWEDAL VAYDKKMDTN KDDPELMLGR MRCLEALGEW GQLHQQCCEK 1501 WTLVNDETQA KMARMAAAAA WGLGQWDSME EYTCMIPRDT HDGAFYRAVL 1551 ALHQDLFSLA QQCIDKARDL LDAELTAMAG ESYSRAYGAM VSCHMLSELE 1601 EVIQYKLVPE RREIRQIWW ERLQGCQRIV EDWQKILMVR SLVSPHEDM 1651 RTWLKYASLC GKSGRLALAH KTLVLLLGVD PSRQLDHPLP TVHPQVYAY 1701 MKNMWKSARK IDAFQHMQH FVQTMQQQAQH AIATEDQQHK QELHKLMARC 1751 FLKLG EWQLN LQGINESTIP KVLQYYS AAT EHDRSWYKAW HAWAVMNFEA 1801 VLHYKHQNA RDEKKLRHA SGANITNATT AATTAATATT TASTEGSNSE 1851 SEAESTENSP TPSPLQKKVT EDLSKTLLMY TVPAVQGFFR SISLSRGNNL 1901 QDTLRVLTLW FDYGHWPVN EALVEGVKAI QIDTWLQVIP QLIARIDTPR

Table S1. Cont.

Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
mTOR	18 (11)	1951 PLVGRLIHLQ LTDIGRYHPQ ALIYPLTVAS KSTTTARHNA ANKILKNMCE
		2001 HSNTLVQQAM MVSEELIRVA ILWHEMWHEG LEEASRLYFG ERNVKGMFEV
		2051 LEPLHAMMER GPQTLK ETSF NQAYGR DLME AQEWCRKYMK SGNVKDLTQA
		2101 WDLYYHVFR ISKQLPQLTS LELQYVSPKL LMCRDLELAV PGTYDPNQPI
		2151 IRIQSIAPSL QVITSK QRPR KLTLMGSNGH EFVFLKLGHE DLRQDERVMQ
		2201 LFGLVNTLLA NDPTSLRKNL SIQRYAVIPL STNSGLIGWV PHCDTLHALI
		2251 RDYREKKKIL LNIHRIMLR MAPDYDHLTL MQK VEVFEHA VNNTAGDDLA
		2301 KLLWLKSPSS EVWFDRRTNY TRSLAVMSMV GYILGLGDRH PSNLMLDRLS
		2351 GKILHIDFGD CFEVAMTREK FPEKIPFRLT RMLTNAMEVT GLDGNYRITC
		2401 HTVMEVLREH KDSVMAVLEA FVYDPLLNR LMDTNTKGNK RSRTRTDSYS
		2451 AGQSVEILDG VELGEPAAHK TGTTVPESIH SFIGDGLVKP EALNKKAIQI
		2501 INRVDRKLTG RDFSHDDTLD VPTQVELLIK QATSHENLCQ CYIGWCPFW
		Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence
		588 – 604 652.3008 1953.8806 1953.9585 -0.0779 0 U R.TLGSFEFEGHSLTQFVR.H
		911 – 921 547.2456 1092.4766 1092.5299 -0.0532 0 U R.DASAVSLSESK.S
		911 – 921 547.2457 1092.4768 1092.5299 -0.0530 0 U R.DASAVSLSESK.S
		1121 – 1132 656.8223 1311.6300 1311.6823 -0.05220 U K.LFDAPEAPLPSR.K
		1121 – 1132 656.8223 1311.6300 1311.6823 -0.05220 U K.LFDAPEAPLPSR.K
		1162 – 1170 529.7536 1057.4926 1057.5404 -0.04770 U R.TLDQSPELR.S
		1162 – 1170 529.7536 1057.4926 1057.5404 -0.0477 0 U R.TLDQSPELR.S
		1219 – 1235 683.6269 2047.8589 2047.9487 -0.0898 0 U K.GYTLADEEEDPLIQHR.M
		1219 – 1235 683.6269 2047.8589 2047.9487 -0.0898 0 U K.GYTLADEEEDPLIQHR.M
		1407 – 1422 833.9456 1665.8766 1665.9301 -0.0535 0 U K.GPTPAILESISINNK.L
		1672 – 1683 641.8618 1281.7090 1281.7656 -0.0566 0 U K.TLVLLLGVDPSR.Q
		1897 – 1905 515.7442 1029.4738 1029.5203 -0.04650 U R.GNNLQDTLR.V
		1897 – 1905 515.7442 1029.4738 1029.5203 -0.0465 0 U R.GNNLQDTLR.V
		2067 – 2076 586.7448 1171.4750 1171.5258 -0.0507 0 U K.ETSFNQAYGR.D
		2153 – 2166 742.9078 1483.8010 1483.8610 -0.0599 0 U R.IQSIAPSLQVITSK.Q
		2153 – 2166 742.9078 1483.8010 1483.8610 -0.0599 0 U R.IQSIAPSLQVITSK.Q
		2153 – 2166 742.9268 1483.8390 1483.8610 -0.0219 0 U R.IQSIAPSLQVITSK.Q
		2284 – 2301 643.6200 1927.8382 1927.9276 -0.089 0 UK.VEVFEHAVNNTAGDDLAK.L
		MS/MS Fragmentation of LFDAPEAPLPSR

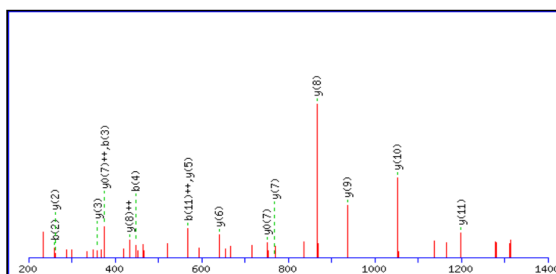


Table S1. Cont.

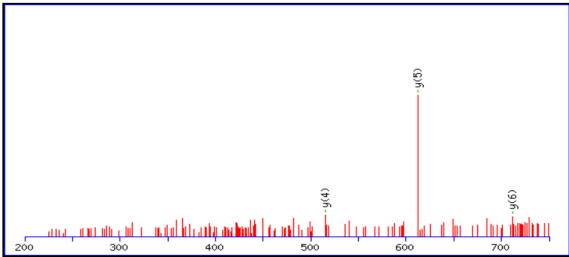
Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
Dynammin 2	5 (3)	1 MGNRGMEELI PLVNLQDAF SSIGQSCHLD LPQIAVVGQ SAGKSSVLEN
		51 FVGRDFLPRG SGIVTRRPLI LQLIFSKTEH AEFLHCKSKK FTDDEVVRQE
		101 IEAETDRVTG TNKGISPVPINLRVYSPHVL NLTLDLPKI TKVPVGDQPP
		151 DIEYQIKDMI LQFISRESSL ILAVTPANMD LANSALKLA KEVDPQGLRT
		201 IGVITKLDLM DEGTDARDVL ENKLLPLRRG YIGVVNRSQK DIEGKKDIRA
		251 ALAAERKFFL SHPAYRHMD RMGTPHLQKT LNQQLTNHIR ESLPALRSKL
		301 QSLLSLEKE VEEYKNFRPD DPTRKTKALL QMVQQFGVDF EKRIEGSGDQ
		351 VDTLELSGGA RINRIFHERF PFELVKMEFD EKDLRREISY AIKNIHGVRT
		401 GLFTPDFAE AIVKKQVVKL KEPCLKCVDL VIQELINTVR QCTSKLSSYP
		451 RLREETERIV TTYIREREGR TKDQILLID IEQSYINTNH EDFIGFANAQ
		501 QRSTQLNKKR AIPNQGEILV IRRGWLTIIN ISLMKGSKE YWVLTAEIS
		551 SWYKDEEKE KKYMLPLDNL KIRDVEKGF SNKHVFAFN TEQRNVYKDL
		601 RQIELACDSQ EDVDSWKASF LRAGVYPEKD QAENEDGAQE NTFSMDPQLE
		651 RQVETIRNLV DSYVAIINKS IRDLMPKTI HLMINNTKAF IHHELLAYLY
		701 SSADQSSLME ESADQAQRD DMLRMYHALK EALNIIGDIS TSTVSTPVPP
		751 PVDDTWLQSA SSHSPTPQRR PVSSIHPPGR PPAVRGPTPG PPLIPVPVGA
		801 AASFSAPIIP SRPGQSVFA NSDLFPAPPQ IPSRPVRIIP GIPPGVPSRR
		851 PPAAPSRPTI IRPAEPSLLD
		Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence
		114-123 533.3640 1064.7134 1064.6342 0.0792 0 K.GISPVPINLR.V
		114-123 533.3641 1064.7136 1064.6342 0.0794 0 K.GISPVPINLR.V
		230-237 439.2754 876.5362 876.4818 0.0545 0 R.GYIGVVNR.S
		838-849 593.8988 1185.7830 1185.6870 0.0961 0 R.IPPGIPPGVPSR.R
		838-849 593.8989 1185.7832 1185.6870 0.0963 0 R.IPPGIPPGVPSR.R
Glyceraldehyde -3-phosphate dehydrogenase	7 (4)	MS/MS Fragmentation of GISPVPINLR
		
		1 MGKVKGVNG FGRIGRLVTR AAFNSGKVDI VAINDPFIDL NYMVMFYQYD
		51 STHGKFHGTV KAENGKLVIN GNPITIFQER DPSKIKWGDA GAEEYVESTG
		101 VFTTMEKAGA HLQGGAKRVI ISAPSADAPM FVMGVNHEKY DNSLKIISNA
		151 SCTTNCLAPL AKVIHDNFGI VEGLMTTVHA ITATQKTVDG PSGKLWRDGR
		201 GALQNIIPAS TGAAKAVGKV IPELNGKLTG MAFRVPTANV SVVDLTCRLE
		251 KPAKYDDIKK VVKQASEGPL KGILGYTEHQ VVSSDFNSDT HSSTFDAGAG
		301 IALNDHFVKL ISWYDNEFGY SNRVVDLMAH MASKE
		Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence
		6-13 403.2117 804.4088 804.4243 -0.0154 0 K.VGVNGFGR.I
		85-107 840.0733 2517.1981 2517.2097 -0.01171 K.IKWGDAGAEEYVESTGVFTTMEK.A
		163-186 649.5874 2594.3205 2594.3527-0.0322 0 K.VIHDNFGIVEGLMTTVHAITATQK.T
		163-186 649.5874 2594.3205 2594.3527-0.0322 0 K.VIHDNFGIVEGLMTTVHAITATQK.T
		163-186 649.5876 2594.3213 2594.3527-0.0314 0 K.VIHDNFGIVEGLMTTVHAITATQK.T

Table S1. Cont.

Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
Glyceraldehyde- 3-phosphate dehydrogenase	7 (4)	201-215 706.3884 1410.7622 1410.7831 -0.0208 0 R.GALQNIIPASTGAAK.A 201-215 706.3887 1410.7628 1410.7831 -0.0202 0 R.GALQNIIPASTGAAK.A MS/MS Fragmentation of GALQNIIPASTGAAK
		1 MPREDRATWK SNYFLKIIQL LDDYPKCFIV GADNVGSKQM QQIRMSLRGK 51 AVVLMGKNTM MRKAIRGHLE NNPALKLLP HIRGNVGFVF TKEDLTEIRD 101 MLLANKVPAA ARAGAIAPCE VTTPAQNTGL GPEKTSFFQA LGITTKISRG 151 TIEILSDVQL IKTGDKVGAS EATLLNMLNI SPFSFGLVIQ QVFDNGSIYN 201 PEVLDATEET LHSRFLEGVR NVASVCLQIG YPTVASVPHS IINGYKRVLA 251 LSVETDYTFP LAEKVKAFLA DPSAFVAAAP VAAATTAAPA AAAAPAKVEA 301 KEESEESDED MGFGFLFD Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence 17-26 609.3789 1216.7432 1216.6703 0.0729 0 K.IIQLLDDYPK.C 135-146 657.3974 1312.7802 1312.7027 0.0775 0 K.TSFFQALGITTK.I 150-162 714.9611 1427.9076 1427.82350.0841 0 R.GTIEILSDVQLIK.T MS/MS Fragmentation of GTIEILSDVQLIK
60S acidic ribosomal protein P0	3 (3)	
Nucleolin	8 (5)	1 MVKLAKAGKN QGDPKMKAPP PKEVEEDED EEMSEDEEDD SSGEEVVIQ 51 KKGKAAATS AKKVVVSPTK KVAATPAKK AAVTPGKKAA ATPAKKTVTP 101 AKAVTTPGKK GATPGKALVA TPGKKGAAIP AKGAKNGKNA KKEDSDEEED 151 DDSEDEEEDD EDEDEDEDEI EPAAMKAAAA APASEDEDE DDEDEDDDD 201 DEEDDSEEEA METTPAKGKK AAKVVPVKAK NVAEDEDEEE DDEDEDDDD 251 EDEDDDDDED DEEEEEEEEEE EPVKEAPGKR KKEMAKQKAA PEAKKQKVEG 301 TEPTTAFNLF VGNLNFNLSA PELKTGISDV FAKNDLAVVD VRIGMTRKFG 351 YVDFESAEDL EKALELTGLK VFGNEIKLEK PKGKDSKKER DARTLLAKNL 401 PYKVTQDELK EVFEDAAEIR LVSKDGKSKG IAYIEFKTEA DAEKTFEEKQ 451 GTEIDGRSIS LYYTGEKGQN QDYRGGKNST WSGESKTLVL SNLSYSATEE 501 TLQEVFEKAT FIKVPQNNQNG KSKGYAFIEF ASFEDAKEAL NSCNKREIEG 551 RAIRLELQGP RGSPNARSQP SKTLFVKGLS EDTTEETLKE SFDGSVRARI 601 VTDRETGSSK GFGFVDFNSE EDAKAAKEAM EDGEIDGNKV TLDWAKPKGE 651 GGFGRGGGR GGFGRGGGR GGRGGFGGRG RGGFGGRGGF RGGRGGGGDH 701 KPQGKKTKFE

Table S1. Cont.

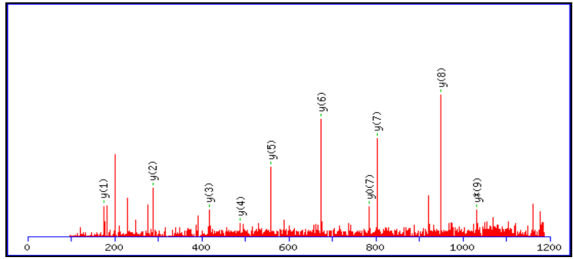
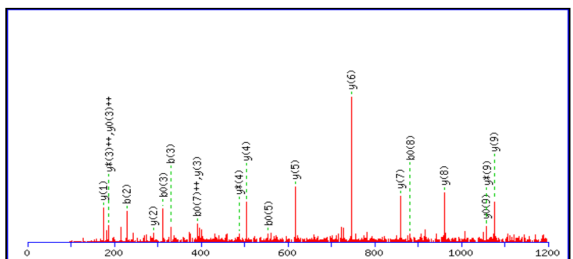
Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
Nucleolin	8 (5)	Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence 325-333 469.2511 936.4876 936.4917 -0.0040 0 K.TGISDVFAK.N 349-362 824.8773 1647.7400 1647.7304 0.0096 0 K.FGYVDFESAEDLEK.A 349-362 824.8777 1647.7408 1647.7304 0.0104 0 K.FGYVDFESAEDLEK.A 404-420 664.6686 1990.9840 1990.9847 -0.0008 1 K.VTQDELKEVFEDAAEIR.L 411-420 589.7883 1177.5620 1177.5615 0.0006 0 K.EVFEDAAEIR.L 411-420 589.7883 1177.5620 1177.5615 0.0006 0 K.EVFEDAAEIR.L 411-420 589.7886 1177.5626 1177.5615 0.0012 0 K.EVFEDAAEIR.L 487-508 834.4281 2500.2625 2500.2584 0.0040 0 K.TLVLSNLSYSATEETLQEVFEK.A MS/MS Fragmentation of EVFEDAAEIR
		
		1 MEKTLETVPL ERKKREKEQF RKLFIGGLSF ETTEESLRNY YEQWGKLTDC 51 VMRDPASKR SRGFGVTF S MAEVDAA MA ARPHSIDGRV VEPKRAVARE 101 ESGKPGAHT VKKLFVGGIK EDTEEHLLRD YFEEYGIKIDT IEIITDRQSG 151 KKRGFVTF DDHDPVDKIV LQKYHTINGH NAEVRKALSR QEMQEVQSSR 201SGRGGNFGFGDSRGGGGNFGPGPGSNFRGSDGYGSGRFGDGYNGYGGG 251PGGGNFGGSPGYGGGRGGYGGGGPGYGNQGGGYGGGYDNYGGGNYGSGNY 301 NDFGNYNQQP SNYGPMKSGN FGSRNMGGP YGGGNYGPGSGSGSGGYGGR 351 SRY Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence 100-112 446.8949 1337.66291 337.6939 -0.0311 0 R.EESGKPGAHTVTK.K 138-147 594.8220 1187.6294 1187.6398 -0.0103 0 K.IDTIEIITDR.Q 204-213 507.2202 1012.4258 1012.4363 -0.0104 0 R.GGNFGFGDSR.G MS/MS Fragmentation of IDTIEIITDR
		
		1 MFHLRTCAAK LRPLTASQTV KTF SQNRPA A ARTFQQIRCY SAPVAAEPFL 51 SGTSSNYVEE MYCAWLENPK SVHKSWDIFF RNTNAGAPPG TAYQSPLPLS 101 RGSAAVAHA QSLVEAQP NV DKLVEDHLAV QSLIRAYQIR GHVHAQLDPL 151 GILDADLDSS VPADIISST D KLG FYGLDES DL DKVFHLPT TFIGGQESA 201 LPLREIIRRL EMAYCQHIGV EFMFINDLEQ CQWIRQKFET PGIMQFTNEE 251 KRTLLARLVR STRFEEFLQR KWSSEKRFGL EGCEVLIPAL KTIIDKSEN 301 GVDYVIMGMP HRGRLNVLAN VIRKELEQIF CQFDSKLEAA DEGSGDVKYH 351 LGMYHRRINR VTDNRITLSL VANPSHLEAA DPVVMGKTKA EQFYCGDTEG
Heterogeneous nuclear ribonucleoprotei ns A2/B1	3 (3)	
2-oxoglutarate dehydrogenase mitochondrial	9 (5)	

Table S1. Cont.

Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
2-oxoglutarate dehydrogenase mitochondrial	9 (5)	401 KKVMSILLHG DAAFAGQGIV YETFHLSDLP SYTTHGTVHV VVNNQIGFTT 451 DPRMARSSPY PTDVARVVNA PIFHVNSDDP EAVMYVCKVA AEWRSTFHKD 501 VVVDLVCYRR NGHNMDEPM FTQPLMYKQI RKQKPVQLKY AELLVSQGVV 551 NQPEYEEEIS KYDKICEEAF ARSKDEKILH IKHWLDSPWP GFFTLDGQPR 601 SMSCPSTGLT EDILTHIGNV ASSVPVENFT IHGGLSRILK TRGEMVKNRT 651 VDWALAEYMA FGSLLEKGIH IRLSGQDVER GTFSHRHHVL HDQNVDKRTC 701 IPMNHLWPNQ APYTVCNSSL SEYGVLGFEF GFAMASPNAL VLWEAQFGDF 751 HNTAQCIIDQ FICPGQAKWV RQNGIVLLLP HGMEGMGPEH SSARPERFLQ 801 MCNDDPDVLP DLKEANFDIN QLYDCNWWVV NCSTPGNFFH VLRRQILLPF 851 RKPLIIFTPK SLLRHPEARS SFDEMLPGTH FQRVIPEDGP AAQNPENVKR 901 LLFCTGKVVY DLTRERKARD MVGQVAITRI EQLSPFPFDL LLKEVQKYPN 951 AELAWCQEEH KNQGYDYVK PRLRTTISRA KPVWYAGRDP AAAPATGNKK 1001 THLTELRLL DTAFLDVFV NFS Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence 845-851 443.7497 885.4848 885.5436 -0.0588 0 R.QILLPFR.K 845-851 443.7497 885.4848 885.5436 -0.0588 0 R.QILLPFR.K 852-860 528.8093 1055.6040 1055.6743 -0.0702 0 R.KPLIIFTPK.S 852-860 528.8093 1055.6040 1055.6743 -0.0702 0 R.KPLIIFTPK.S 884-899 839.3747 1676.7348 1676.8369 -0.1021 0 R.VIPEDGPAAQNPENVK.R 884-899 839.3747 1676.7348 1676.8369 -0.1021 0 R.VIPEDGPAAQNPENVK.R 908-914 465.2073 928.4000 928.4654 -0.0654 0 K.VYYDLTR.E 908-914 465.2073 928.4000 928.4654 -0.0654 0 K.VYYDLTR.E 920-929 545.2526 1088.4906 1088.5648 -0.0742 0 R.DMVGQVAITR.I MS/MS Fragmentation of KPLIIFTPK
Glycosyl transferase 25 domain1	6 (6)	1 MAAAPRAGR RGQPLLALL LLLAPLPPGA PPGADAYFPE ERWSPESPLQ 51 APRVLIALLA RNAAHALPTT LGALERLRHP RERTALWVAT DHNMDNTSTV 101 LREWLVA VKS LYHSVEWRPA EEPRSYDDEE GPKHWSDSRY EHVMLKRQAA 151 LKSARDMWAD YILFVDADNL ILNPDTLSLL IAENKTVVAP MLDSRAAYSN 201 FWCGMTSQGY YKRTPAYIPI RKRRDRGCFA VPMVHSTFLI DLRKAASRN 251 AFYPPHPDYT WSFDDIIVFA FSCKQAEVQM YVCNKEEYGF LPVPLRAHST 301 LQDEAESFMH VQLEVMVKHP PAEPSRFISA PTKTPDKMGF DEVFMINLRR 351 RQDRRERMLR ALQAQIEICR LVEAVDGKAM NTSQVEALGI QMLPGYRDPY 401 HGRPLTKGEL GCFLSHYNIW KEVVDRLQK SLVFEDDLRF EIFFKRRLMN 451 LMRDVEREGL DWDLIYVGRK RMQVEHPEKA VPRVRNLVEA DYSYWTLAYV 501 ISLQGARKLL AAELPSKMLP VDEFLPVMFD KHPVSEYKAH FSLRNLHAFS 551 VEPLLIYPH YTGDDGYVSD TETSVVWNNE HVKTDWDRAK SQKMREQQAL 601 SREAKNSDVL QSPPLSAARD EL Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence 54-61 434.7851 867.5556 867.5905 -0.0349 0 R.VLIALLAR.N 62-76 512.2635 1533.7687 1533.8263 -0.0576 0 R.NAAHALPTTLGALER.L

Table S1. Cont.

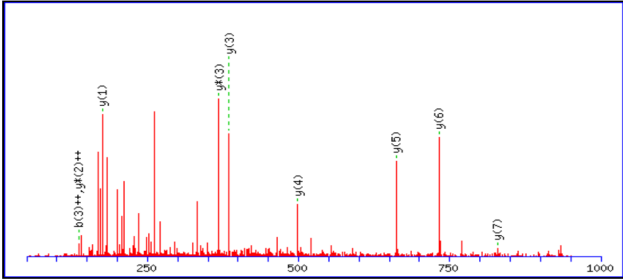
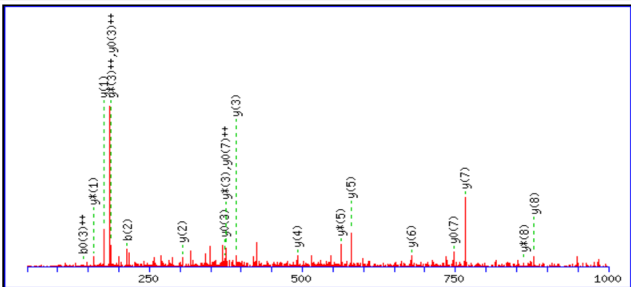
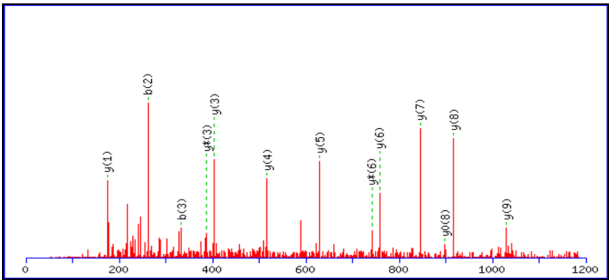
Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
Glycosyl transferase 25 domain1	6 (6)	214-221 465.7565 929.4984 929.5334 -0.0350 0 R.TPAYIPIR.K
		319-326 445.7151 889.4156 889.4406 -0.0249 0 K.HPPAEPSR.F
		458-469 718.3516 1434.6886 1434.7143 -0.0257 0 R.EGLDWDLIYVGR.K
		508-517 535.3163 1068.6180 1068.6543 -0.0362 1 R.KLLAAEPLSK.M
		MS/MS Fragmentation of TPAYIPIR
Enhancer of mRNA decapping protein 4	3 (3)	
		1 MASCASIDIE DATQHRLDIL KLDRPAGGPS AESPRSSAY NGDLNGLLVP
		51 DPLCSGDSTS ANKTGLRTMP PINLQEKQVI CLSGDDSSSTC IGILAKEVEI
		101 VASSDSSISS KARGSNKVKI QPVAKYDWEQ KYYYGNLIIV SNSFLAYAIR
		151 AANNGSAMVR VISVSTSER LLKGFTGSAV DLAFAHLNSP QLACLDEAGN
		201 LFWWRLALVN GKIQEEILVH IRQPEGTPLN HFRRIIWCPF IPEESEDCC
		251 ESSPTVALLH EDRAEVWLDL MLRSSHSTWP VDVSIKQGF IVVKGHSTCL
		301 SEGALSPDGT VLATASHDGY VKFWQIYIEG QDEPRCLHEW KPHDGRPLSC
		351 LLFCDNHKKQ DPDPVFWRFL ITGADQNREL KMWCTVSWTC LQTIRFSPDI
		401 FSSVSVPPSL KVCLDLSEAY LILSDVQRKV LYVMELLQNG EEGHACFSSI
		451 SEFLLTHPVL SFGIQVVSRC RLRHTEVLPA EEENDSLGAD GTHGAGAMES
		501 AAGVLIKLFC VHTKALQDVQ IRFQPQLNPD VVAPLPTHTA HEDFTFGESR
		551 PELGSEGLGS AAHGSQPDRL RIVELPAPAD FLSLSSETKP KLMTDPDAFMT
		601 PSASLQQITA SPSSSSSSGSS SSSSSSSSSL TAVSAMSSTS AVDPSLTRPP
		651 EELTLSPKLQ LDGSLTMSSS GSLQASPRGL LPGLLPAPAD KLTPKGPQGV
		701 PTATSALSLE LQEVEPLGLP QASPSRTRSP DVISSASTAL SQDIPEIASE
		751 ALSRFGGSSA PEGLEPDSMA SAASALHLLS PRPRGPPELG PQLGLDGGPG
		801 DGDRHNTPSL LEAALTQEAS TPDSQVWPTA PDITRETCST LAESPRNGLQ
		851 EKHKSIAFHR PPYHLLQQRD SQDASAEQSD HDDEVASLAS ASGGFGTKVP
		901 APRLPAKDWK TKGSPRTSPK LKRKSKKDDG DAAMGSRLTE HQVAEPPEDW
		951 PALIWQQQRE LAELRHSQEE LLQRL CTQLE GLQSTVTGHV ERALETRHEQ
		1001 EQRRLERALA EGQQRGGQLQ EQLTQQLSQA LSSAVAGRLE RSIRDEIKKT
		1051 VPPCVSRSL EPMAGQLNSV ATKLTAVEGS MKENISKLLK SKNLTDIAIR
		1101 AAADTLQGPM QAAYREAFQS VVLPAFEKSC QAMFQQINDS FRLGTQEYLQ
		1151 QLESHMKSRK AREQEAREPV LAQLR GLVST LQSATEQMAA TVAGSVRAEV
		1201 QHQLHVAVGS LQESILAQVQ RIVKGEVSA LKEQQAAVTS SIMQAMRSAA
		1251 GTPVPSAHL D CQAQQAHLQ LLQQGHLNQA FQQALTAADL NLVLYVCETV
		1301 DPAQVFGQPP CPLSQPVLLS LIQQLASDLG TRTDLKLSYL EEAVMHLDHS
		1351 DPITRDHMG S VMAQVRQKLF QFLQAEPHNS LGKAARRLSL MLHGLVTPSL
		1401 P
		Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence
		161-169 489.2541 976.4936 976.5189 -0.0253 0 R.VISVSTSER.T
		966-974 570.2798 1138.5450 1138.5731 -0.0280 0 R.HSQEELLQR.L
		1168-1175 463.2606 924.5066 924.5392 -0.0326 0 R.EPVLAQLR.G
		MS/MS Fragmentation of VISVSTSER

Table S1. Cont.

Protein Name	^a Peptides Matches (sequences)	^b MS/MS Analysis
Enhancer of mRNA decapping protein 4	3 (3)	
Prohibitin 2	3 (3)	1 MAQNKLKLAG RLPAGPRGMG TALKLLLKAG AVAYGVRESV FTVEGGHRAI 51 FFNRIGGVQQ DTILAEGLHF RIPWFQYPII YDIRARPRKI SSPTGSKDLQ 101 MVNISLRVLS RPNAQELPSM YQRLGLDYEE RVLPSIVNEV LKSVVAKFNA 151 SQKITQRAQV SLLIRRELTE RAKDFSLILD DVAITELSF S REYTAAVEAK 201 QVAQQEAQRA QFLVEKAKQE QRQKIVQAEG EAEAAKMLGE ALSKNPGYIK 251 LRKIRAAQNI SKTIATSQNR IYLTADNLVL NLQDESFTRG SDSLIKGKK Start-End Observed Mr(expt) Mr(calc) Delta Miss Sequence 124-131 497.7442 993.4738 993.4767 -0.0029 0 R.LGLDYEER.V 132-142 605.8679 1209.7212 1209.7333 -0.0120 0 R.VLPSIVNEVLK.S 148-157 589.3073 1176.6000 1176.6251 -0.0251 0 K.FNASQLITQR.A MS/MS Fragmentation of FNASQLITQR 

^a Peptide matches (sequences): the number of total peptides matched with protein in the MS/MS query (the number of unique peptide sequences); ^b MS/MS analysis: the protein sequence with MS/MS identified the peptides (bold) and one exemplary MS/MS spectra of the peptide with the highest ion score.