

Supplementary Materials:

Figure S1

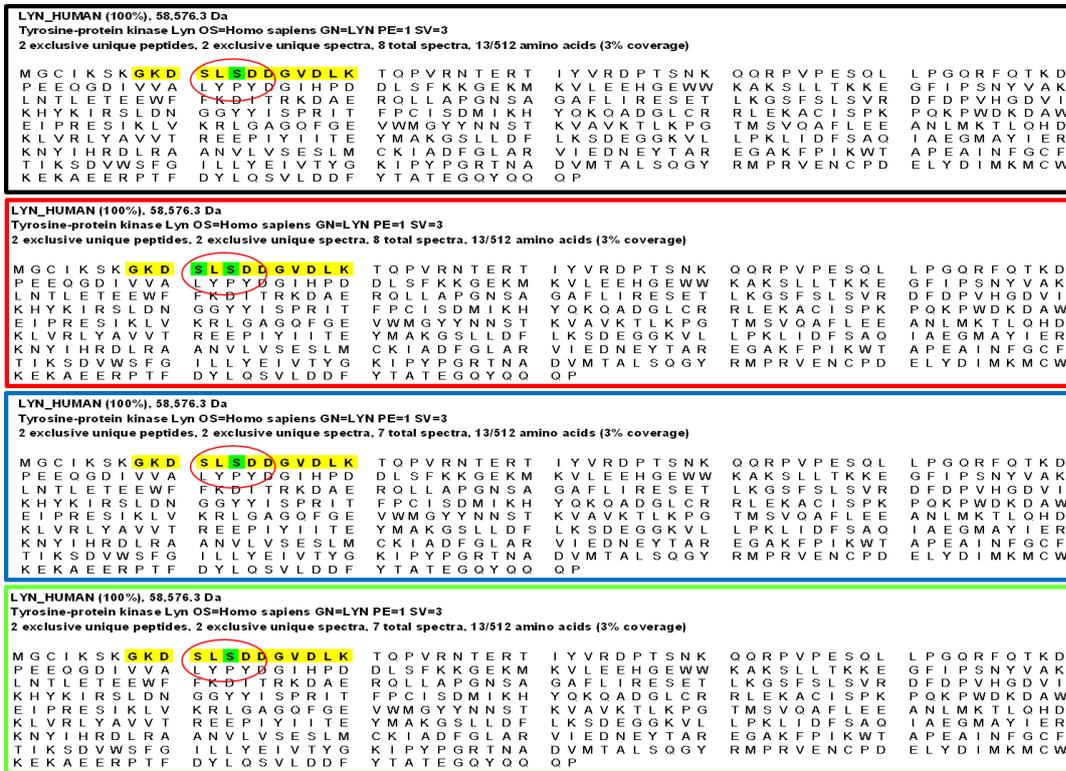


Figure S1: Comparative Analysis of Lyn Protein Sequence. The Lyn protein sequences are depicted under four different treatment conditions as provided by the Scaffold Viewer software. The protein sequence in stimulated cells is highlighted in the black box, while the sequence in cells infected with *M. bovis* BCG is shown in the red box. The blue box represents the sequence in cells previously treated with a PKC inhibitor, and the green box displays the protein sequence in cells treated with PMA/Ionomycin. Phosphorylated peptides identified in mass spectrometry are labeled in yellow, and phosphorylation sites are indicated in green, with 'S' and 'T' denoting serine and threonine residues, respectively.

Figure S2

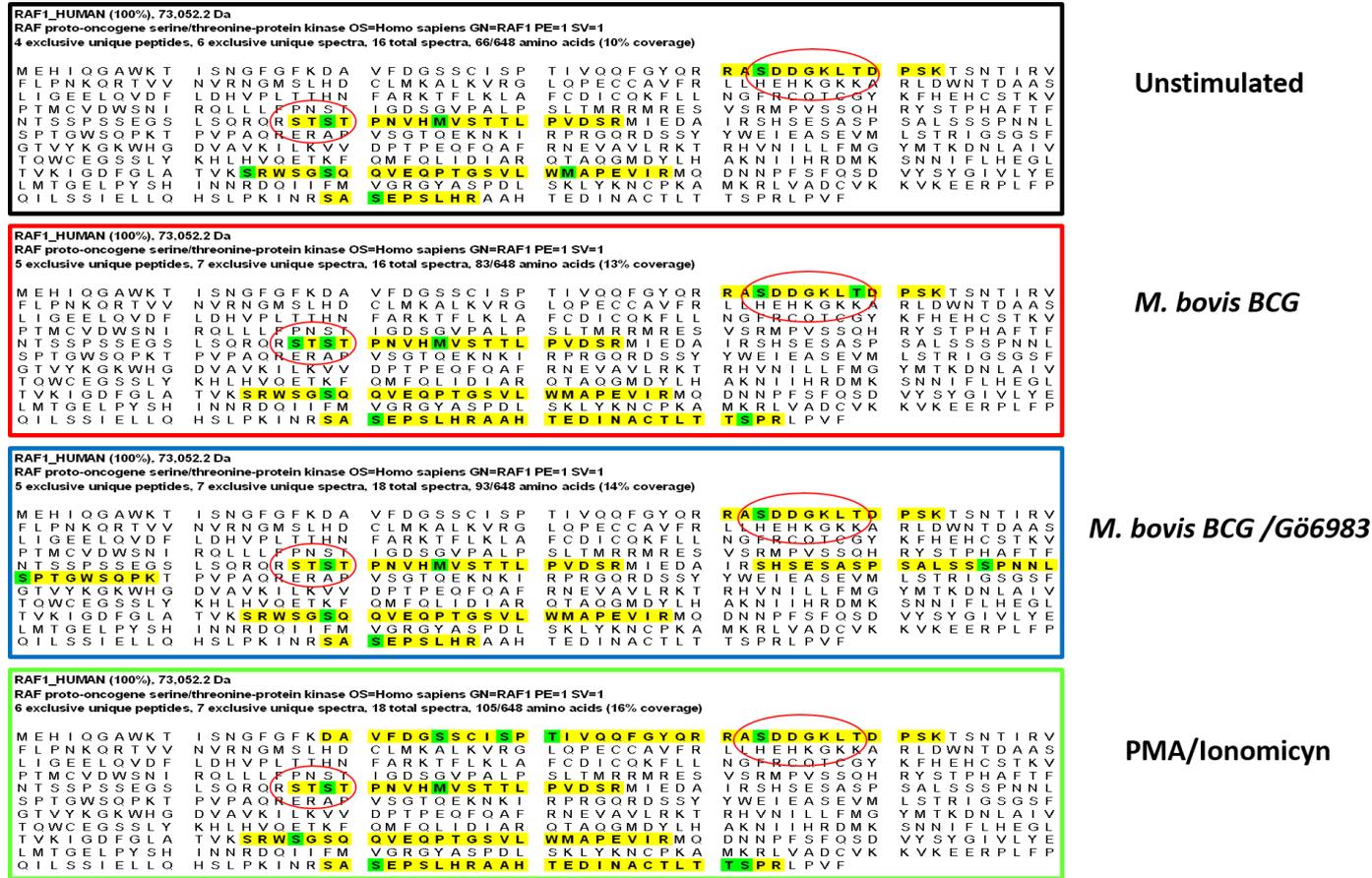
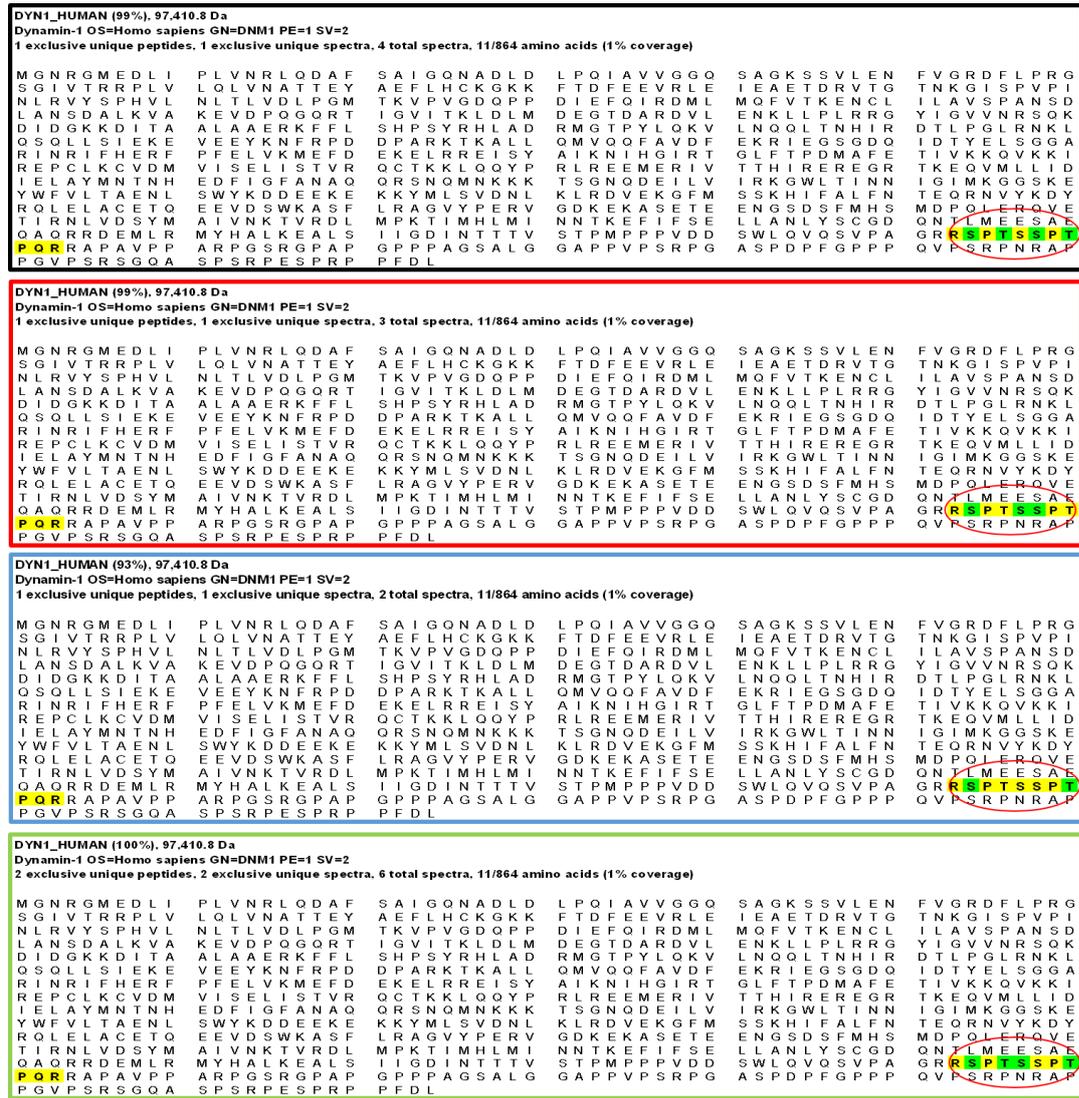


Figure S2: Comparative Analysis of Raf-1 Protein Sequence. The Raf-1 protein sequences are displayed under four distinct treatment conditions as provided by the Scaffold Viewer software. The protein sequence in stimulated cells is highlighted in the black box, while the sequence in cells infected with *M. bovis BCG* is depicted in the red box. The blue box represents the sequence in cells previously treated with a PKC inhibitor, and the green box displays the protein sequence in cells treated with PMA/Ionomycin. Phosphorylated peptides identified in mass spectrometry are denoted in yellow, and phosphorylation sites are indicated in green, with 'S' and 'T' signifying serine and threonine residues, respectively.

Figure S3



Unstimulated

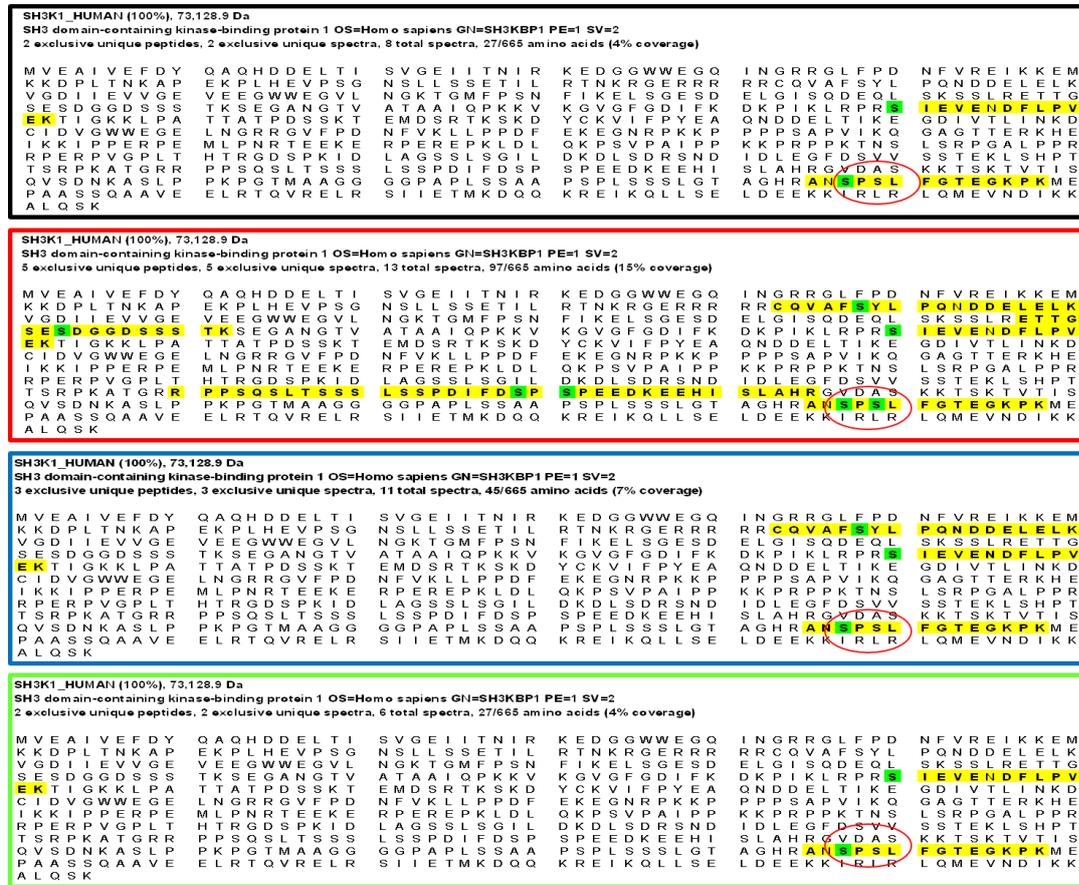
M. bovis BCG

M. bovis BCG /Gö6983

PMA/Ionomycin

Figure S3: Comparative Analysis of Dynamin-1 Protein Sequence. The Dynamin-1 protein sequences are displayed under four distinct treatment conditions as provided by the Scaffold Viewer software. The protein sequence in stimulated cells is highlighted in the black box, while the sequence in cells infected with *M. bovis BCG* is depicted in the red box. The blue box represents the sequence in cells previously treated with a PKC inhibitor, and the green box displays the protein sequence in cells treated with PMA/Ionomycin. Phosphorylated peptides identified in mass spectrometry are denoted in yellow, and phosphorylation sites are indicated in green, with 'S' and 'T' signifying serine and threonine residues, respectively.

Figure S4



Unstimulated

M. bovis BCG

M. bovis BCG /Gö6983

PMA/Ionicyn

Figure S4: Comparative Analysis of SH3K1 Protein Sequence. The sequence of the SH3K1 protein is presented under four distinct treatment conditions, as generated by the Scaffold Viewer software. The protein sequence observed in stimulated cells is enclosed within the black box, while the red box represents the sequence in cells infected with *M. bovis BCG*. Within the blue box is the sequence in cells previously treated with a PKC inhibitor, and the green box displays the protein sequence in cells treated with PMA/Ionicyn. Phosphorylated peptides, as identified by mass spectrometry, are highlighted in yellow, and phosphorylation events are denoted in green, with 'S' and 'T' indicating serine and threonine residues, respectively.

Figure S5

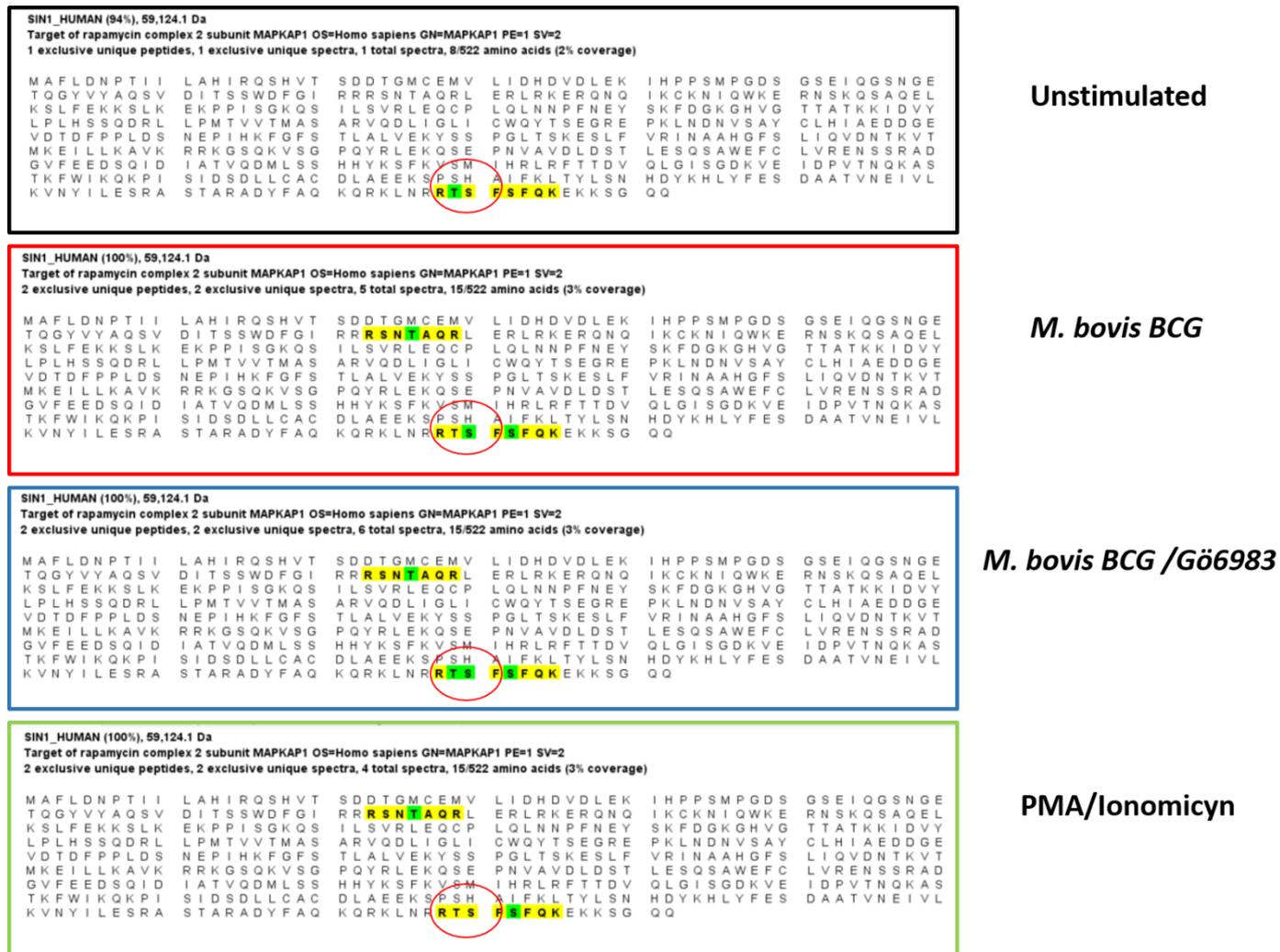


Figure S5: Comparative Analysis of Sin-1 Protein Sequence. The sequence of the Sin-1 protein is presented under four distinct treatment conditions, as generated by the Scaffold Viewer software. The protein sequence observed in stimulated cells is enclosed within the black box, while the red box represents the sequence in cells infected with *M. bovis BCG*. Within the blue box is the sequence in cells previously treated with a PKC inhibitor, and the green box displays the protein sequence in cells treated with PMA/Ionomycin. Phosphorylated peptides, as identified by mass spectrometry, are highlighted in yellow, and phosphorylation events are denoted in green, with 'S' and 'T' indicating serine and threonine residues, respectively.

Figure S6

TSC2_HUMAN (99%), 200,610.8 Da
Tuberin OS=Homo sapiens GN=TSC2 PE=1 SV=2
1 exclusive unique peptides, 1 exclusive unique spectra, 4 total spectra, 23/1807 amino acids (1% coverage)

MAKPTSKDSSG	LKEKFKILLG	LGTPRPNPRS	AEGKQTEFII	TAEILRELSM	ECGLNRRIRM	IGQICEVAKT
KKFEEHAVEA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEEL	ADFLVQWMDV	GLSSEFLLVV	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVQ	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSYEIVL	SITRLIKKYR
KELQVVAWDI	LLNIIERLLO	QLQTLDSPEL	RTIVHDLTT	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLIYSR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQLSHPIPEDK	DHQVRKLATQ	LLVDLAEAGCH	THHFNSLDDI	IEKVMARSL	PPPELEERDV	AAYSASLEDV
KTAVLGLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQHLYKH	SYTLPIASSI	RLQAFDFLLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYSLF	RVLQLCKLKE
SDWKVLLKLV	GRLPESLRYK	VLIIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DHLHVAVVPV
TALISYHNYL	DKTKQREMYV	CLEQGLIHR	ASOCVVALSI	CSVEMPDIII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AEEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWVIRC	RLPFRKDFVP
FITKGLRNSV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRTKTW	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
SRGARDRVRS	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAPKEKAS	AGTRVPVQEK	TNLAAYVPLL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSQVVM	EEGSPGEPV	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	RVYSSEGRP	SYDLSFDPSP	PLSK	SSSSSPE
PGDKADVGR	SPREKARSQS	GTLDGESAAW	SASGEDSRGG	PEPPLSSSSP	RSPSGLRPRG	YTI SDSAPSR
RGRKVERDAL	KSRATASNAE	KVPGINPSFY	FLQLYHSPFF	GDESINKPILL	PNESQSFRS	VQLLDQIPSY
DTHKI AVL VY	EGEQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMTKDV	DKHRCDDKRR	LGNDFVSIY	NDSGEDFKLG	TIKGOFNFVH	VIVTFLDYEC
NLVSLQCRKD	MEGLVDTVA	KIVSDRNLFF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQT	PAEPTPGYEV	GQRKRLISSV	EDFTEFV	

Unstimulated

TSC2_HUMAN (100%), 200,610.8 Da
Tuberin OS=Homo sapiens GN=TSC2 PE=1 SV=2
2 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 34/1807 amino acids (2% coverage)

MAKPTSKDSSG	LKEKFKILLG	LGTPRPNPRS	AEGKQTEFII	TAEILRELSM	ECGLNRRIRM	IGQICEVAKT
KKFEEHAVEA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEEL	ADFLVQWMDV	GLSSEFLLVV	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVQ	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSYEIVL	SITRLIKKYR
KELQVVAWDI	LLNIIERLLO	QLQTLDSPEL	RTIVHDLTT	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLIYSR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQLSHPIPEDK	DHQVRKLATQ	LLVDLAEAGCH	THHFNSLDDI	IEKVMARSL	PPPELEERDV	AAYSASLEDV
KTAVLGLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQHLYKH	SYTLPIASSI	RLQAFDFLLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYSLF	RVLQLCKLKE
SDWKVLLKLV	GRLPESLRYK	VLIIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DHLHVAVVPV
TALISYHNYL	DKTKQREMYV	CLEQGLIHR	ASOCVVALSI	CSVEMPDIII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AEEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWVIRC	RLPFRKDFVP
FITKGLRNSV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRTKTW	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
SRGARDRVRS	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAPKEKAS	AGTRVPVQEK	TNLAAYVPLL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSQVVM	EEGSPGEPV	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	RVYSSEGRP	SYDLSFDPSP	PLSK	SSSSSPE
PGDKADVGR	SPREKARSQS	GTLDGESAAW	SASGEDSRGG	PEPPLSSSSP	RSPSGLRPRG	YTI SDSAPSR
RGRKVERDAL	KSRATASNAE	KVPGINPSFY	FLQLYHSPFF	GDESINKPILL	PNESQSFRS	VQLLDQIPSY
DTHKI AVL VY	EGEQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMTKDV	DKHRCDDKRR	LGNDFVSIY	NDSGEDFKLG	TIKGOFNFVH	VIVTFLDYEC
NLVSLQCRKD	MEGLVDTVA	KIVSDRNLFF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQT	PAEPTPGYEV	GQRKRLISSV	EDFTEFV	

M. bovis BCG

TSC2_HUMAN (100%), 200,610.8 Da
Tuberin OS=Homo sapiens GN=TSC2 PE=1 SV=2
2 exclusive unique peptides, 2 exclusive unique spectra, 3 total spectra, 54/1807 amino acids (3% coverage)

MAKPTSKDSSG	LKEKFKILLG	LGTPRPNPRS	AEGKQTEFII	TAEILRELSM	ECGLNRRIRM	IGQICEVAKT
KKFEEHAVEA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEEL	ADFLVQWMDV	GLSSEFLLVV	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVQ	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSYEIVL	SITRLIKKYR
KELQVVAWDI	LLNIIERLLO	QLQTLDSPEL	RTIVHDLTT	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLIYSR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQLSHPIPEDK	DHQVRKLATQ	LLVDLAEAGCH	THHFNSLDDI	IEKVMARSL	PPPELEERDV	AAYSASLEDV
KTAVLGLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQHLYKH	SYTLPIASSI	RLQAFDFLLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYSLF	RVLQLCKLKE
SDWKVLLKLV	GRLPESLRYK	VLIIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DHLHVAVVPV
TALISYHNYL	DKTKQREMYV	CLEQGLIHR	ASOCVVALSI	CSVEMPDIII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AEEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWVIRC	RLPFRKDFVP
FITKGLRNSV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRTKTW	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
SRGARDRVRS	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAPKEKAS	AGTRVPVQEK	TNLAAYVPLL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSQVVM	EEGSPGEPV	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	RVYSSEGRP	SYDLSFDPSP	PLSK	SSSSSPE
PGDKADVGR	SPREKARSQS	GTLDGESAAW	SASGEDSRGG	PEPPLSSSSP	RSPSGLRPRG	YTI SDSAPSR
RGRKVERDAL	KSRATASNAE	KVPGINPSFY	FLQLYHSPFF	GDESINKPILL	PNESQSFRS	VQLLDQIPSY
DTHKI AVL VY	EGEQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMTKDV	DKHRCDDKRR	LGNDFVSIY	NDSGEDFKLG	TIKGOFNFVH	VIVTFLDYEC
NLVSLQCRKD	MEGLVDTVA	KIVSDRNLFF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQT	PAEPTPGYEV	GQRKRLISSV	EDFTEFV	

M. bovis BCG /Gö6983

TSC2_HUMAN (100%), 200,610.8 Da
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MAKPTSKDSSG	LKEKFKILLG	LGTPRPNPRS	AEGKQTEFII	TAEILRELSM	ECGLNRRIRM	IGQICEVAKT
KKFEEHAVEA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEEL	ADFLVQWMDV	GLSSEFLLVV	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVQ	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSYEIVL	SITRLIKKYR
KELQVVAWDI	LLNIIERLLO	QLQTLDSPEL	RTIVHDLTT	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLIYSR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQLSHPIPEDK	DHQVRKLATQ	LLVDLAEAGCH	THHFNSLDDI	IEKVMARSL	PPPELEERDV	AAYSASLEDV
KTAVLGLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQHLYKH	SYTLPIASSI	RLQAFDFLLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYSLF	RVLQLCKLKE
SDWKVLLKLV	GRLPESLRYK	VLIIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DHLHVAVVPV
TALISYHNYL	DKTKQREMYV	CLEQGLIHR	ASOCVVALSI	CSVEMPDIII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AEEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWVIRC	RLPFRKDFVP
FITKGLRNSV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRTKTW	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
SRGARDRVRS	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAPKEKAS	AGTRVPVQEK	TNLAAYVPLL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSQVVM	EEGSPGEPV	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	RVYSSEGRP	SYDLSFDPSP	PLSK	SSSSSPE
PGDKADVGR	SPREKARSQS	GTLDGESAAW	SASGEDSRGG	PEPPLSSSSP	RSPSGLRPRG	YTI SDSAPSR
RGRKVERDAL	KSRATASNAE	KVPGINPSFY	FLQLYHSPFF	GDESINKPILL	PNESQSFRS	VQLLDQIPSY
DTHKI AVL VY	EGEQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMTKDV	DKHRCDDKRR	LGNDFVSIY	NDSGEDFKLG	TIKGOFNFVH	VIVTFLDYEC
NLVSLQCRKD	MEGLVDTVA	KIVSDRNLFF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQT	PAEPTPGYEV	GQRKRLISSV	EDFTEFV	

PMA/Ionicin

Figure S6: Comparative Analysis of Tsc2 Protein Sequence. This figure illustrates the Tsc2 protein sequence under four distinct treatment conditions, which have been generated using the Scaffold Viewer software. The protein sequence from stimulated cells is enclosed within the black box, while the red box represents the sequence in cells infected with *M. bovis* BCG. Within the blue box, you can see the sequence from cells that were previously treated with a PKC inhibitor, and in the green box, you'll find the protein sequence from cells treated with PMA/Ionomycin. Notably, phosphorylated peptides identified through mass spectrometry are highlighted in yellow, and the specific phosphorylation events are indicated in green, with 'S' and 'T' denoting serine and threonine residues, respectively.

Figure S7

RPTOR_HUMAN (99%), 149.039.2 Da
Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1
1 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 18/1335 amino acids (1% coverage)

MESEMLQSP	LGLGEED	LTDWNLP	MKKRHCE	GSKSLAQ	MKDRMK
ALVLCN	DPPDVVK	CARLECW	LSMGPQK	TIGANLQ	ENWQPR
QSLDPT	KKLCSTL	AKEERVL	NGHGVPR	NGEVWVF	YTOYIP
DLQTMW	IFVYDCS	LIVKSFQ	LQREQEL	AINPNHP	MPLPPS
IQLAAC	LLPMIPD	DLFTSCL	IKIALRW	QKCVSL	TLDLIE
RLNDRR	ELNWI	DTIAWN	DLFQKLF	LLVASL	LLAERIM
NCTPVSS	PPTYMHAM	AWDLAVD	SQLP	TAFRHS	EQLTAF
TMGVEN	EQLPIV	LSQVHRL	DLLGRFL	PWAVSL	GIFPYV
QSSARE	LVIWAKI	VDSSCAD	KDNGHKY	VLADPY	HRMTAF
VIIVNS	EACLQGN	ICLEQLN	PLLRQWV	LGRWQNF	ARWCVR
HEKLYS	PIPEYRCA	FALGTFV	AERTDHS	DHNVAM	LVS
KELVVA	VVQYESN	VALQFIE	NYALPSP	EGGSLT	S
SSYGNIR	TARSLNK	NLSL	AVAFSPG	TSSASST	SPENEH
FETIDK	SSYSSLN	GVSFN	IWRVLL	DPYPEV	MKVLNS
ATVNA	LDTSSLT	PASPTNK	IHQAGGS	SSTSSSS	DVAKQ
LPSGR	PAGAQT	HQFPRT	DKGPEQ	ADDAAG	ISATVQ
DWSAR	VMKPIE	ESQIRK	RFLRNS	QAQQV	TRLDDQ
RNPGV	FHPFT	ADKDS	WEKGEK	HNGNPR	TAMEY
CSLL	GAI	DLEKN	AWQGL	TTRGAG	WEQET
SGDVR	GTDR	DLEKN	AWQGL	TTRGAG	WEQET
ECRVM	TAWVVK	KRPDGH	SVNGD	PRMPES	QIVKGL
IHPQ	GSVNF	NSSGEL	KYYD	VGAIS	PHWPH
NDYY	ISV	EKRVR			

Unstimulated

RPTOR_HUMAN (100%), 149.039.2 Da
Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1
2 exclusive unique peptides, 3 exclusive unique spectra, 13 total spectra, 45/1335 amino acids (3% coverage)

MESEMLQSP	LGLGEED	LTDWNLP	MKKRHCE	GSKSLAQ	MKDRMK
ALVLCN	DPPDVVK	CARLECW	LSMGPQK	TIGANLQ	ENWQPR
QSLDPT	KKLCSTL	AKEERVL	NGHGVPR	NGEVWVF	YTOYIP
DLQTMW	IFVYDCS	LIVKSFQ	LQREQEL	AINPNHP	MPLPPS
IQLAAC	LLPMIPD	DLFTSCL	IKIALRW	QKCVSL	TLDLIE
RLNDRR	ELNWI	DTIAWN	DLFQKLF	LLVASL	LLAERIM
NCTPVSS	PPTYMHAM	AWDLAVD	SQLP	TAFRHS	EQLTAF
TMGVEN	EQLPIV	LSQVHRL	DLLGRFL	PWAVSL	GIFPYV
QSSARE	LVIWAKI	VDSSCAD	KDNGHKY	VLADPY	HRMTAF
VIIVNS	EACLQGN	ICLEQLN	PLLRQWV	LGRWQNF	ARWCVR
HEKLYS	PIPEYRCA	FALGTFV	AERTDHS	DHNVAM	LVS
KELVVA	VVQYESN	VALQFIE	NYALPSP	EGGSLT	S
SSYGNIR	TARSLNK	NLSL	AVAFSPG	TSSASST	SPENEH
FETIDK	SSYSSLN	GVSFN	IWRVLL	DPYPEV	MKVLNS
ATVNA	LDTSSLT	PASPTNK	IHQAGGS	SSTSSSS	DVAKQ
LPSGR	PAGAQT	HQFPRT	DKGPEQ	ADDAAG	ISATVQ
DWSAR	VMKPIE	ESQIRK	RFLRNS	QAQQV	TRLDDQ
RNPGV	FHPFT	ADKDS	WEKGEK	HNGNPR	TAMEY
CSLL	GAI	DLEKN	AWQGL	TTRGAG	WEQET
SGDVR	GTDR	DLEKN	AWQGL	TTRGAG	WEQET
ECRVM	TAWVVK	KRPDGH	SVNGD	PRMPES	QIVKGL
IHPQ	GSVNF	NSSGEL	KYYD	VGAIS	PHWPH
NDYY	ISV	EKRVR			

M. bovis BCG

RPTOR_HUMAN (100%), 149.039.2 Da
Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1
2 exclusive unique peptides, 2 exclusive unique spectra, 6 total spectra, 45/1335 amino acids (3% coverage)

MESEMLQSP	LGLGEED	LTDWNLP	MKKRHCE	GSKSLAQ	MKDRMK
ALVLCN	DPPDVVK	CARLECW	LSMGPQK	TIGANLQ	ENWQPR
QSLDPT	KKLCSTL	AKEERVL	NGHGVPR	NGEVWVF	YTOYIP
DLQTMW	IFVYDCS	LIVKSFQ	LQREQEL	AINPNHP	MPLPPS
IQLAAC	LLPMIPD	DLFTSCL	IKIALRW	QKCVSL	TLDLIE
RLNDRR	ELNWI	DTIAWN	DLFQKLF	LLVASL	LLAERIM
NCTPVSS	PPTYMHAM	AWDLAVD	SQLP	TAFRHS	EQLTAF
TMGVEN	EQLPIV	LSQVHRL	DLLGRFL	PWAVSL	GIFPYV
QSSARE	LVIWAKI	VDSSCAD	KDNGHKY	VLADPY	HRMTAF
VIIVNS	EACLQGN	ICLEQLN	PLLRQWV	LGRWQNF	ARWCVR
HEKLYS	PIPEYRCA	FALGTFV	AERTDHS	DHNVAM	LVS
KELVVA	VVQYESN	VALQFIE	NYALPSP	EGGSLT	S
SSYGNIR	TARSLNK	NLSL	AVAFSPG	TSSASST	SPENEH
FETIDK	SSYSSLN	GVSFN	IWRVLL	DPYPEV	MKVLNS
ATVNA	LDTSSLT	PASPTNK	IHQAGGS	SSTSSSS	DVAKQ
LPSGR	PAGAQT	HQFPRT	DKGPEQ	ADDAAG	ISATVQ
DWSAR	VMKPIE	ESQIRK	RFLRNS	QAQQV	TRLDDQ
RNPGV	FHPFT	ADKDS	WEKGEK	HNGNPR	TAMEY
CSLL	GAI	DLEKN	AWQGL	TTRGAG	WEQET
SGDVR	GTDR	DLEKN	AWQGL	TTRGAG	WEQET
ECRVM	TAWVVK	KRPDGH	SVNGD	PRMPES	QIVKGL
IHPQ	GSVNF	NSSGEL	KYYD	VGAIS	PHWPH
NDYY	ISV	EKRVR			

M. bovis BCG /Gö6983

RPTOR_HUMAN (99%), 149.039.2 Da
Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1
1 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 18/1335 amino acids (1% coverage)

MESEMLQSP	LGLGEED	LTDWNLP	MKKRHCE	GSKSLAQ	MKDRMK
ALVLCN	DPPDVVK	CARLECW	LSMGPQK	TIGANLQ	ENWQPR
QSLDPT	KKLCSTL	AKEERVL	NGHGVPR	NGEVWVF	YTOYIP
DLQTMW	IFVYDCS	LIVKSFQ	LQREQEL	AINPNHP	MPLPPS
IQLAAC	LLPMIPD	DLFTSCL	IKIALRW	QKCVSL	TLDLIE
RLNDRR	ELNWI	DTIAWN	DLFQKLF	LLVASL	LLAERIM
NCTPVSS	PPTYMHAM	AWDLAVD	SQLP	TAFRHS	EQLTAF
TMGVEN	EQLPIV	LSQVHRL	DLLGRFL	PWAVSL	GIFPYV
QSSARE	LVIWAKI	VDSSCAD	KDNGHKY	VLADPY	HRMTAF
VIIVNS	EACLQGN	ICLEQLN	PLLRQWV	LGRWQNF	ARWCVR
HEKLYS	PIPEYRCA	FALGTFV	AERTDHS	DHNVAM	LVS
KELVVA	VVQYESN	VALQFIE	NYALPSP	EGGSLT	S
SSYGNIR	TARSLNK	NLSL	AVAFSPG	TSSASST	SPENEH
FETIDK	SSYSSLN	GVSFN	IWRVLL	DPYPEV	MKVLNS
ATVNA	LDTSSLT	PASPTNK	IHQAGGS	SSTSSSS	DVAKQ
LPSGR	PAGAQT	HQFPRT	DKGPEQ	ADDAAG	ISATVQ
DWSAR	VMKPIE	ESQIRK	RFLRNS	QAQQV	TRLDDQ
RNPGV	FHPFT	ADKDS	WEKGEK	HNGNPR	TAMEY
CSLL	GAI	DLEKN	AWQGL	TTRGAG	WEQET
SGDVR	GTDR	DLEKN	AWQGL	TTRGAG	WEQET
ECRVM	TAWVVK	KRPDGH	SVNGD	PRMPES	QIVKGL
IHPQ	GSVNF	NSSGEL	KYYD	VGAIS	PHWPH
NDYY	ISV	EKRVR			

PMA/Ionicin

Figure S7: Comparative Analysis of Raptor Protein Sequence. This figure presents the protein sequence of Raptor under four distinct treatment conditions, which have been visualized using the Scaffold Viewer software. Within the black box, you can observe the protein sequence from stimulated cells, while the red box corresponds to the sequence in cells infected with *M. bovis BCG*. The blue box encompasses the sequence in cells previously treated with a PKC inhibitor, and the green box represents the protein sequence in cells treated with PMA/Ionomycin. Notably, phosphorylated peptides identified through mass spectrometry are highlighted in yellow, and specific phosphorylation events are indicated in green, with 'S' denoting serine and 'T' representing threonine residues.

Figure S8

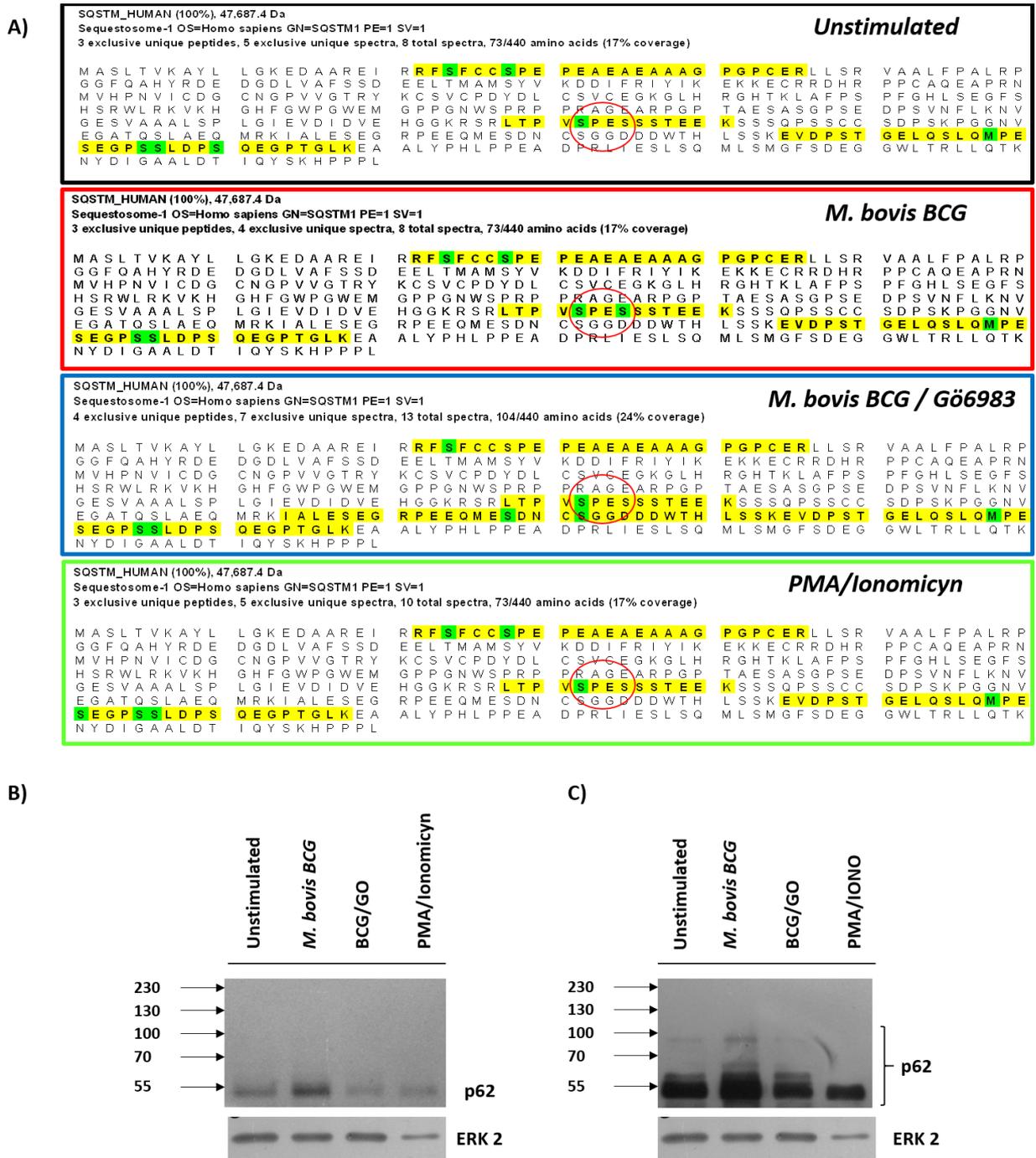


Figure S8: Phosphorylation of Sequestosome-1/p62 by PKC and Its Potential Regulation of Autophagy. Panel A) This panel figure provides insight into the Sequestosome-1/p62 protein sequence across four different treatment conditions, as visualized using the Scaffold Viewer software. The black box displays the protein sequence from stimulated cells, while the red box corresponds to cells infected with *M. bovis BCG*. The blue box encompasses the sequence from cells previously treated with a PKC inhibitor, and the green box represents the protein sequence from cells treated with PMA/Ionomycin. Notably, phosphorylated peptides identified through mass spectrometry are highlighted in yellow, with specific phosphorylation sites labeled in green ('S' for serine and 'T' for threonine residues). Panel B-C) To assess the presence of Sequestosome-1/p62 in response to mycobacterial infection, a Western blot assay was performed utilizing a specific antibody. Panel B) Displays p62 accumulation upon lower film exposure, whereas Panel C) shows p62 oligomerization upon film overexposure. This analysis sheds light on the phosphorylation of Sequestosome-1/p62 by PKC and its potential role in regulating autophagy.

Figure S9



Figure S9: Comparative Analysis of Map-1b Protein Sequence. This figure provides a comparative analysis of the Map-1b protein sequence under four distinct treatment conditions, as visualized using the Scaffold Viewer software. The black box represents the protein sequence observed in stimulated cells, while the red box illustrates the sequence in cells infected with *M. bovis* BCG. The blue box depicts the sequence from cells previously treated with a PKC inhibitor, and the green box showcases the protein sequence in cells treated with PMA/Ionomycin. Notably, phosphorylated peptides identified through mass spectrometry are highlighted in yellow, with specific phosphorylation sites labeled in green ('S' for serine and 'T' for threonine residues).

Table S1

Protein	Gene	ID
C2 domain-containing protein 2- like	C2C2L	Q14523
Small glutamine- rich tetratricopeptide repeat- containing protein alfa	SGTA	Q43765
trans- Golgi network integral membrane protein	TGON2	Q43493
Dynamin 2	DYN2	P50570
Osteopontin	OSTP	P10451
Death- associated protein 1	DAP1	P51397
SH3 domain-containing kinase-binding protein	SH3K1	Q96B97
Girdin	GRDN	Q3V6T2
Dynamin 1	DYN1	Q05193
Golgi-specific brefeldin A- Resistance guanine nucleotide exchange factor1	GBF1	Q92538
TBC9 Domain family member 9B	TBC9B	Q66K14
Sequestosome-1	SQSTM	Q13501
Syntaxin- 4	STX4	Q12846
Calcium homeostasis endoplasmic reticulum protein	CHERP	Q8IWX8
Tuberin	TSC2	P49815
Target of Myb protein 1	TOM1	Q60784
Gtpase- activating protein and VPS9 domain containing protein	GAPD1	Q14C86
Dedicator of citokinesis protein 8	DOCK8	Q8NF50
Poly (rC)- binding protein 2	PCB P2	Q15366
A-kinase anchor protein 13	AKP13	Q12802
Bcl2- associated transcription factor 1	BCLF1	Q9NYF8
Phosphatidylinositol 3,4,5- trisphosphate 5- phosphatase 1	SHIP1	Q92835
Prelamina- A/C	LMNA	P02545
ProteinNDRG1	NDRG1	Q92597
C-Jun - amino terminal kinase-interacting protein	JIP4	Q60271
Stromal membrane- asociated protein 2	SMAP2	Q8WU79
Microtubule associated protein 1B	MAP1B	P46821
Bridging interactor 2	BIN2	Q9UBW5
TBC1 domain family member 10 B	TB10B	Q4KMP7
Phosohatidylinositol 4- kinase type2- alpha	P4K2A	Q9BTU6
Glucocorticoid receptor	GCR	P04150
Niban like protein 1	NIBL1	Q96TA1
Wd repeat- containing protein 44	WDR44	Q5JSH3
Mitogen- activated protein kinase kinase kinase kinase 4	M4K4	Q95819
Plastin- 2	PLSL	P13796
RAF proto-oncogene serine/threonine- protein kinase RAF1	RAF1	P04049
Tyrosine-protein kinase Lyn	LYN	P07948
Regulatory- associated protein of mTOR	RPTOR	Q8N122
Protein- methionine sulfoxide oxidase MICAL 1	MICA1	Q8TDZ2
TNF AIP3	TNIP1	Q15025
Was/Wasl- interacting protein family member 2	WIPF2	Q8TF74
Brefeldin A-- inhibited guanine nucleotides-exchange protein	BIG2	Q9Y6D5
FK506-binding protein 15	FKB15	Q5T1M5
Amyloid beta A4 precursor protein-binding family member 1 interacting protein	AB1IP	Q7Z5R6

HLA class I histocompatibility antigen, A-2 alpha chain	HLA	P01892
Eukaryotic translation initiation factor 4E binding protein	4EBP1	Q13541
Zyxin	ZYX	Q15942
Serine threonine- protein Kinase Braf	BRAF	P15056
Eukaryotic translation initiation factor 4 gamma 2	IF4G2	P78344
Target of rapamycin complex 2 subunit MAPKAP1	SIN 1	Q9BPZ7
Protein EVI2B	EVI2B	P34910
Eukaryotic translation initiation factor 4E binding protein 2	4EBP2	Q13542
WD repeat- and domain- containing protein 4	WDFY4	Q6ZS81
WD repeat-containing protein 26	WDR26	Q9H7D7
Insulin receptor substrate 2	IRS2	Q9Y4H2

Table S1. Proteins involved in biological processes such as endocytosis, vesicular trafficking, autophagy and programmed cell death.

