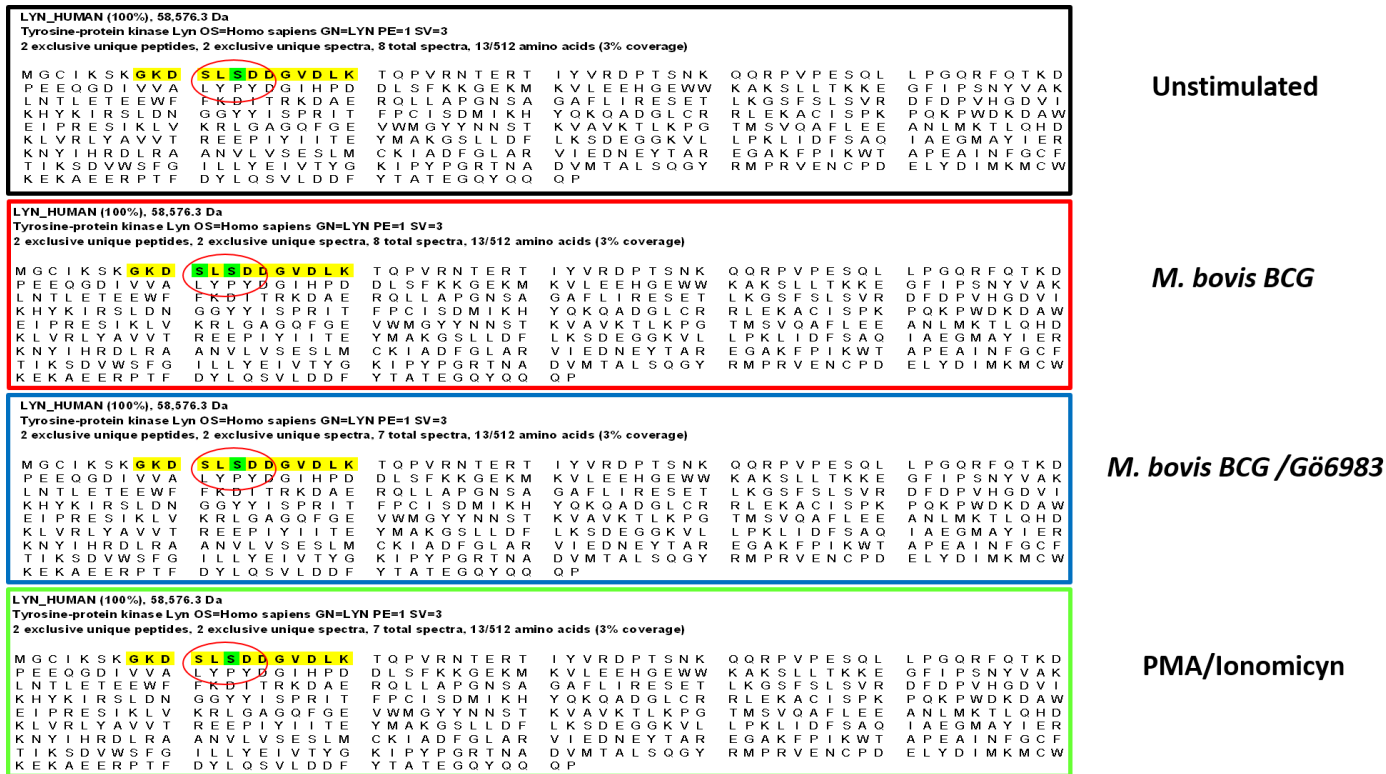


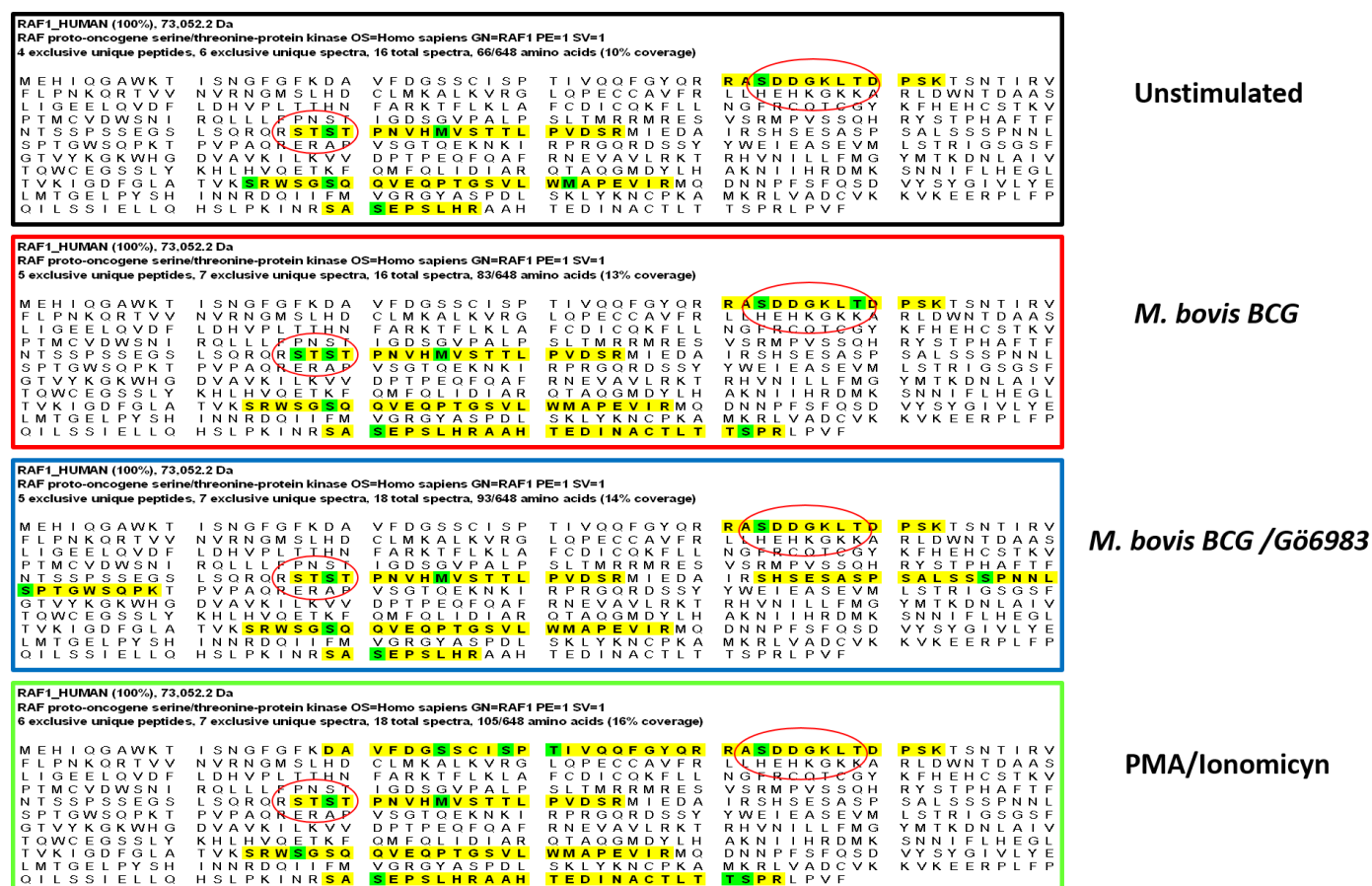
# Supplementary Materials:

Figure S1



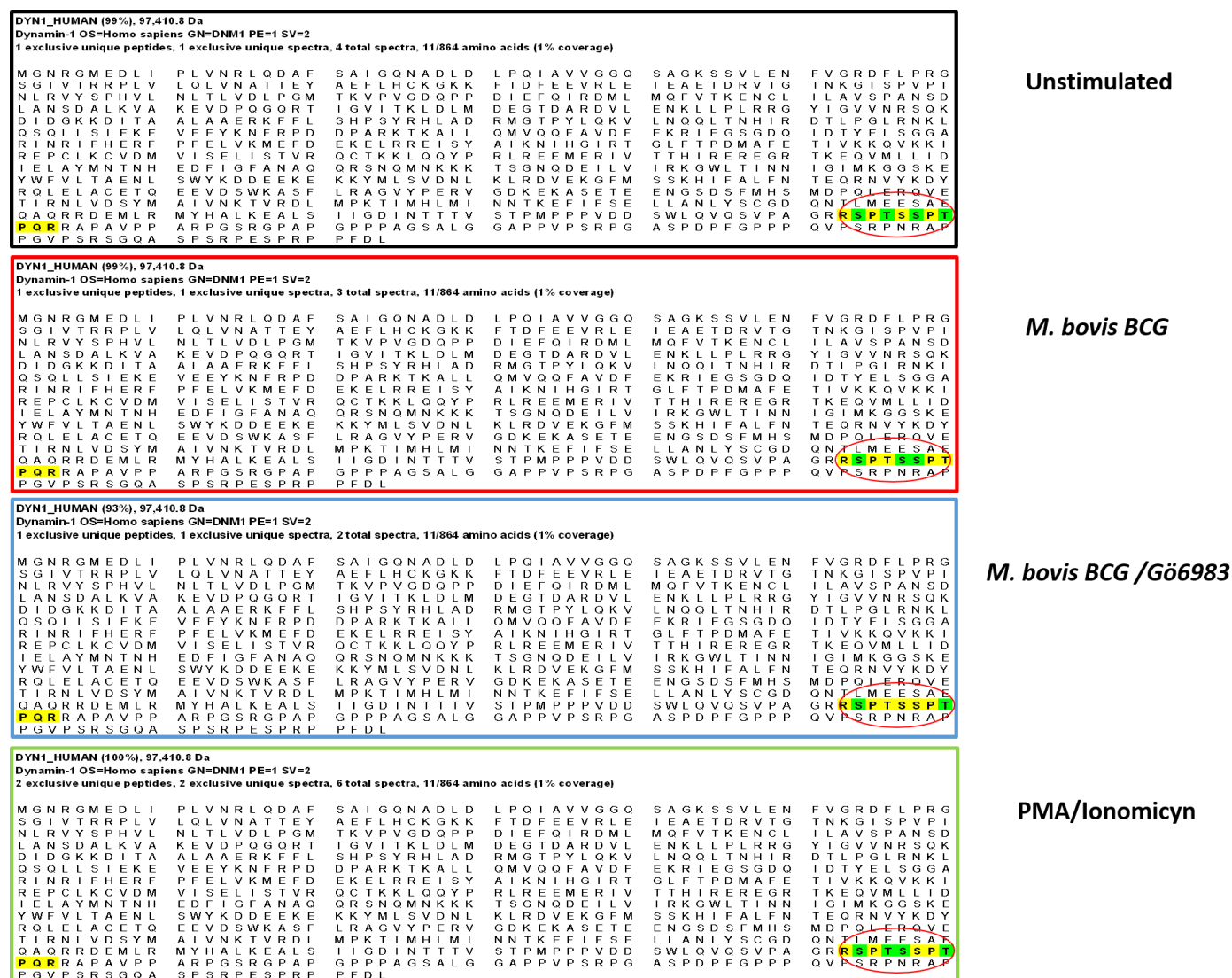
**Figure S1: Comparative Analysis of Lyn Protein Sequence.** The Lyn protein sequences are depicted under four different treatment conditions as provided by the Scaffold Viewer software. The protein sequence in stimulated cells is highlighted in the black box, while the sequence in cells infected with *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



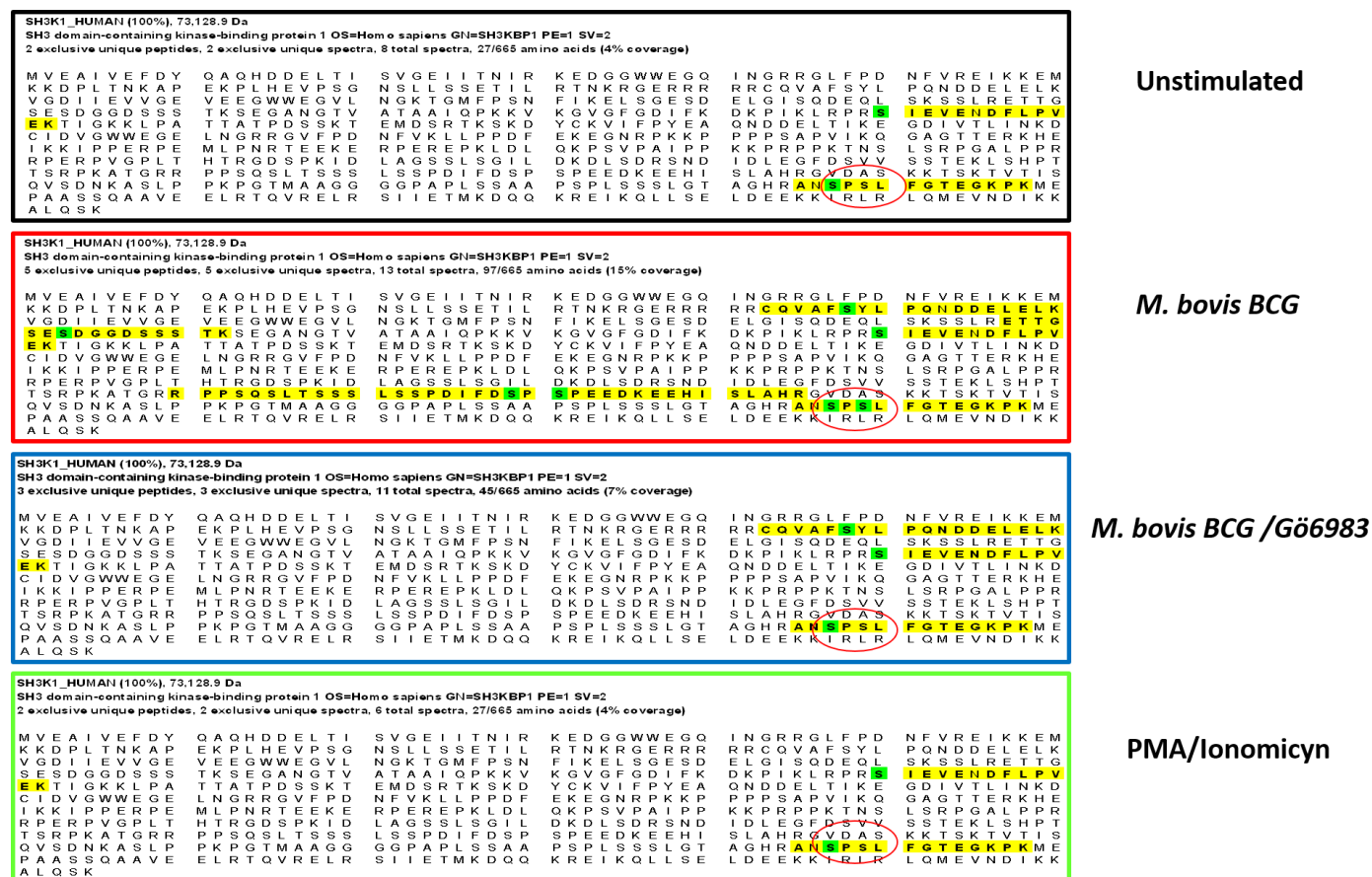
**Figure S2: Comparative Analysis of Raf-1 Protein Sequence.** The Raf-1 protein sequences are displayed under four distinct treatment conditions as provided by the Scaffold Viewer software. The protein sequence in stimulated cells is highlighted in the black box, while the sequence in cells infected 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



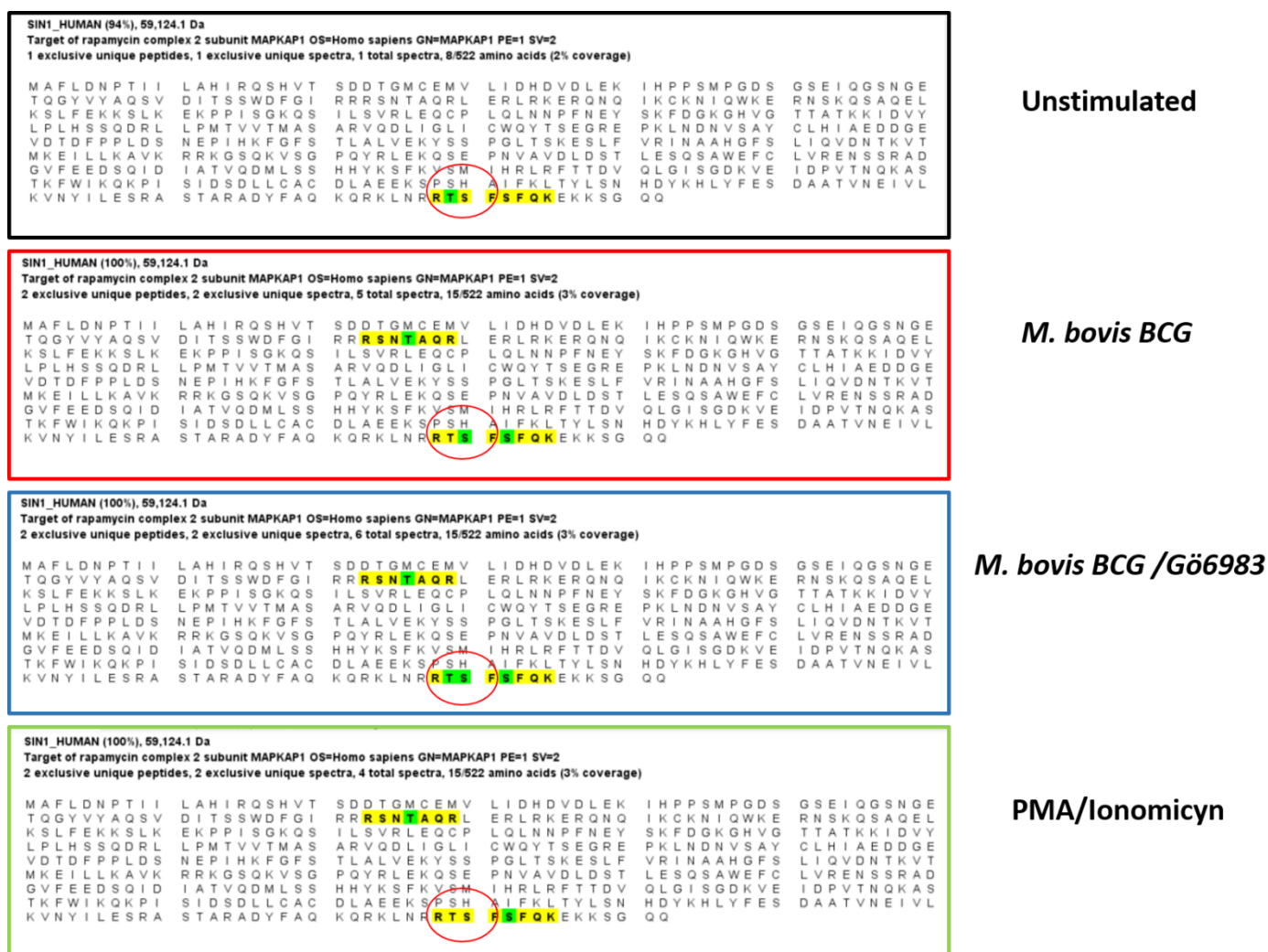
**Figure S3: Comparative Analysis of Dynamin-1 Protein Sequence.** The Dynamin-1 protein sequences are displayed under four distinct treatment conditions as provided by the Scaffold Viewer software. The protein sequence in stimulated cells is highlighted in the black box, while the sequence in cells 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



**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/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 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	TAEILRELISM	ECGLNNRIRM	IGQICEVAKT
KKFEEHAEVA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEL	ADFLVQWMDV	GLSSEFLLVL	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVG	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSVEIVL	SITRLIKKYR
KELQVVAWDI	LLNI IERLLQ	QLQTLDSPEL	RTIVHDLTTL	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLISYR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQSLSHIPEDK	DHQVRKCLATQ	LLVDLAEGCH	THHFNLSLLDI	IEKVMARSL	PPPELEERDV	AAYASLEEDV
KTAVLGLLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQLHYKH	SYTLPIASSI	RLQAFDFLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYLLF	RVLQCLCKQE
SDWKVLKLV	GRLPESLRYK	VLIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DLHLAVVPVL
TALISYHNYL	DKTKQREMYV	CLEQGLIHRC	ASQCVALSI	CSVEMPDII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AAEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWFI	RCPFRKDFVP
FITKGLRSNV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRKTW	LVGNKLVTVT	TSVGTGTRSL	LGLDSGELQS	GPSSSSSPGV	HVRQTKAEP	KLESQAGQV
SRGARDVR	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAKPEKAS	AGTRVPVQEK	TNLAAVPL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSLVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSDVVM	EEGSPGEVVP	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	<b>RYVSEEGGRP</b>	<b>SVDLSPSPSQ</b>	<b>PLSK</b>	<b>SSSSPE</b>
PGDKADVGR	SPVEKARSQS	GTLDGESAIF	<b>SASSED</b>	<b>RGQ</b>	<b>PEPLSSSP</b>	<b>RGPRG</b>
RGRKVERDAL	KSRATASNAE	KVPGINPSFV	FLQLYHSPFF	GDESNKPI	LL	<b>PSY</b>
DTHKIAYLVY	GEGQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMPTKDV	DKHRCDDKRRH	LGNDFVSI	NDSGEDFKLG	TIKGQFNFMV	VIVTPLYDEC
NLVSLQCRKD	MEGLVDTSSA	KIVSDRNLPF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQ	PAEPTPGYEV	GQRKRLISSV	EDTFEFV	

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	TAEILRELISM	ECGLNNRIRM	IGQICEVAKT
KKFEEHAEVA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEL	ADFLVQWMDV	GLSSEFLLVL	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVG	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSVEIVL	SITRLIKKYR
KELQVVAWDI	LLNI IERLLQ	QLQTLDSPEL	RTIVHDLTTL	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLISYR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQSLSHIPEDK	DHQVRKCLATQ	LLVDLAEGCH	THHFNLSLLDI	IEKVMARSL	PPPELEERDV	AAYASLEEDV
KTAVLGLLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQLHYKH	SYTLPIASSI	RLQAFDFLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYLLF	RVLQCLCKQE
SDWKVLKLV	GRLPESLRYK	VLIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DLHLAVVPVL
TALISYHNYL	DKTKQREMYV	CLEQGLIHRC	ASQCVALSI	CSVEMPDII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AAEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWFI	RCPFRKDFVP
FITKGLRSNV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRKTW	LVGNKLVTVT	TSVGTGTRSL	LGLDSGELQS	GPSSSSSPGV	HVRQTKAEP	KLESQAGQV
SRGARDVR	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAKPEKAS	AGTRVPVQEK	TNLAAVPL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSLVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSDVVM	EEGSPGEVVP	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	<b>RYVSEEGGRP</b>	<b>SVDLSPSPSQ</b>	<b>PLSK</b>	<b>SSSSPE</b>
PGDKADVGR	SPVEKARSQS	GTLDGESAIF	<b>SASSED</b>	<b>RGQ</b>	<b>PEPLSSSP</b>	<b>RGPRG</b>
RGRKVERDAL	KSRATASNAE	KVPGINPSFV	FLQLYHSPFF	GDESNKPI	LL	<b>PSY</b>
DTHKIAYLVY	GEGQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMPTKDV	DKHRCDDKRRH	LGNDFVSI	NDSGEDFKLG	TIKGQFNFMV	VIVTPLYDEC
NLVSLQCRKD	MEGLVDTSSA	KIVSDRNLPF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQ	PAEPTPGYEV	GQRKRLISSV	EDTFEFV	

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	TAEILRELISM	ECGLNNRIRM	IGQICEVAKT
KKFEEHAEVA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEL	ADFLVQWMDV	GLSSEFLLVL	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVG	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSVEIVL	SITRLIKKYR
KELQVVAWDI	LLNI IERLLQ	QLQTLDSPEL	RTIVHDLTTL	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLISYR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQSLSHIPEDK	DHQVRKCLATQ	LLVDLAEGCH	THHFNLSLLDI	IEKVMARSL	PPPELEERDV	AAYASLEEDV
KTAVLGLLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQLHYKH	SYTLPIASSI	RLQAFDFLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYLLF	RVLQCLCKQE
SDWKVLKLV	GRLPESLRYK	VLIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DLHLAVVPVL
TALISYHNYL	DKTKQREMYV	CLEQGLIHRC	ASQCVALSI	CSVEMPDII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AAEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWFI	RCPFRKDFVP
FITKGLRSNV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRKTW	LVGNKLVTVT	TSVGTGTRSL	LGLDSGELQS	GPSSSSSPGV	HVRQTKAEP	KLESQAGQV
SRGARDVR	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAKPEKAS	AGTRVPVQEK	TNLAAVPL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSLVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSDVVM	EEGSPGEVVP	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	<b>RYVSEEGGRP</b>	<b>SVDLSPSPSQ</b>	<b>PLSK</b>	<b>SSSSPE</b>
PGDKADVGR	SPVEKARSQS	GTLDGESAIF	<b>SASSED</b>	<b>RGQ</b>	<b>PEPLSSSP</b>	<b>RGPRG</b>
RGRKVERDAL	KSRATASNAE	KVPGINPSFV	FLQLYHSPFF	GDESNKPI	LL	<b>PSY</b>
DTHKIAYLVY	GEGQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMPTKDV	DKHRCDDKRRH	LGNDFVSI	NDSGEDFKLG	TIKGQFNFMV	VIVTPLYDEC
NLVSLQCRKD	MEGLVDTSSA	KIVSDRNLPF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQ	PAEPTPGYEV	GQRKRLISSV	EDTFEFV	

M. bovis BCG /Gö6983

**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, 32/1807 amino acids (2% coverage)**

MAKPTSKDSSG	LKEKFKILLG	LGTPRPNPRS	AEGKQTEFII	TAEILRELISM	ECGLNNRIRM	IGQICEVAKT
KKFEEHAEVA	LWKAVADLLQ	PERPLEARHA	VLALLKAIIVQ	GQGERLGVLR	ALFFKVIKDY	PSNEDLHERL
EVFKALTDNG	RHITYLEEL	ADFLVQWMDV	GLSSEFLLVL	VNLVKFNCSY	LDEYIARMVQ	MICLLCVRTA
SSVDIEVSLQ	VLDADVVCYNC	PAESLPLFI	VTLCRTINVK	ELCEPCWKLM	RNLLGTHLGH	SAIYNMCHLM
EDRAYMEDAP	LLRGAVFFVG	MALWGAHRLY	SLRNSPTSVL	PSFYQAMACP	NEVVSVEIVL	SITRLIKKYR
KELQVVAWDI	LLNI IERLLQ	QLQTLDSPEL	RTIVHDLTTL	VEELCDQNEF	HGSQERYFEL	VERCADORPE
SSLLNLISYR	AQSIHPAKDG	WIQNLQALME	RFRFRSESRGA	VRIKVLVDVLS	FVLLINRQFY	EEELINSVVI
SQSLSHIPEDK	DHQVRKCLATQ	LLVDLAEGCH	THHFNLSLLDI	IEKVMARSL	PPPELEERDV	AAYASLEEDV
KTAVLGLLLVI	LQTKLYTLPA	SHATRVYEML	VSHIQLHYKH	SYTLPIASSI	RLQAFDFLL	LRADSLHRLG
LPNKDGVVRF	SPYCVCDYME	PERGSEKKT	GPLSPPTGPP	GPAPAGPAVR	LGSVPYLLF	RVLQCLCKQE
SDWKVLKLV	GRLPESLRYK	VLIFTSPCSV	DQLCSALCSM	LSGPKTLERL	RGAPGEGFSR	DLHLAVVPVL
TALISYHNYL	DKTKQREMYV	CLEQGLIHRC	ASQCVALSI	CSVEMPDII	KALPVLVVKL	THISATASMA
VPLLEFLSTL	ARLPHLYRNF	AAEQYASVFA	ISLPTYNPSK	FNQYIVCLAH	HVIAMWFI	RCPFRKDFVP
FITKGLRSNV	LLSFDDTPEK	DSFRARSTSL	NERPKSLRIA	RPPKQGLNNS	PPVKEFKESS	AAEAFCRCSI
SVSEHVVRSR	IQTSLTSASL	GSADENSVAQ	ADDSLKNLHL	ELTETCLDMM	ARYVFSNFTA	VPKRSPVGEF
LLAGGRKTW	LVGNKLVTVT	TSVGTGTRSL	LGLDSGELQS	GPSSSSSPGV	HVRQTKAEP	KLESQAGQV
SRGARDVR	MSGGHGLRVG	ALDVPASQFL	GSATSPGPR	APAAKPEKAS	AGTRVPVQEK	TNLAAVPL
TQGWAEILVR	RPTGNTSWLM	SLENPLSPFS	SDINNMPLQE	LSNALMAAER	FKEHRDTALY	KLSLVPAAST
AKPPPLPRSN	TVASFSSLYQ	SSCQGLHRS	VSWDSDVVM	EEGSPGEVVP	LVEPPGLEDD	EALGMDDRR
DAYSRSSSVS	SQEEKSLHAE	ELVGRGPIE	<b>RYVSEEGGRP</b>	<b>SVDLSPSPSQ</b>	<b>PLSK</b>	<b>SSSSPE</b>
PGDKADVGR	SPVEKARSQS	GTLDGESAIF	<b>SASSED</b>	<b>RGQ</b>	<b>PEPLSSSP</b>	<b>RGPRG</b>
RGRKVERDAL	KSRATASNAE	KVPGINPSFV	FLQLYHSPFF	GDESNKPI	LL	<b>PSY</b>
DTHKIAYLVY	GEGQSNSELA	ILSNEHGSYR	YTEFLTGLGR	LIELKDCQPD	KVYLGGLDVC	GEDGQFTYCW
HDDIMQAVFH	IATLMPTKDV	DKHRCDDKRRH	LGNDFVSI	NDSGEDFKLG	TIKGQFNFMV	VIVTPLYDEC
NLVSLQCRKD	MEGLVDTSSA	KIVSDRNLPF	VARQMALHAN	MASQVHHSRS	NPTDIYPSKW	IARLRHIKRL
RQRICEEAA	SNPSLPLVHP	PSHSHKAPAQ	PAEPTPGYEV	GQRKRLISSV	EDTFEFV	

PMA/Ionomycin

**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)

[illegible]

Unstimulated

RPTOR HUMAN (100%), 149.039.2 Da

Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1

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)

M	A	E	S	E	M	L	C	S	L	Q	S	P	L	L	G	L	D	D	E	E	A	D	L	T	D	N	L	L	P	L	A	F	M	K	K	R	H	C	E	K	I	E	G	S	K	S	L	A	Q	S	W	R	M	K	D	R	M	K	T	S	V	S										
N	A	L	V	E	L	C	L	N	V	G	V				L	P	P	D	V	V	K	T	T	P		C	A	R	L	E	C	W	I	D	P	L	S	M	G	P	Q	K	A	L	E	T	I	G	A	N	L	Q	K	Q		E	N	W	P	R	A	R	K									
Q	S	L	D	P	T	V	D	E	V						K	K	L	C	T	S	L	R	N		A	A	K	E	R	V	L	F	H		L	N	G	H	V	P	R	P	T		N	G	E	V	W	F	N	K	N		Y	T	Q	Y	I	P	L	S	I	Y								
D	L	Q	L	A	T	W	M	G	S	P	S				I	F	V	M	T	D	C	S	N		A	G	L	I	V	K	S	F	K	Q	F	A		L	R	Q	E	V	E	L	V	A		A	I	N	P	N	H	L	A	Q		M	P	L	P	S	M	K	N							
I	Q	L	A	E	A	C	E	A	T						L	L	P	M	I	P	D	L	A		I	D	L	F	T	S	C	L	T				I	K	I	A	L	R	W	F	C	M		Q	K	C	S	V	L	P	V	G		T	L	D	L	I	E	K	I	P	G					
R	L	N	D	R	R	T	P	L	G						E	L	N	W	I	F	T	A		I	A	D	T	I	A	W	N	V	L	P	R				D	L	F	Q	K	L	R	F	Q	M		L	L	V	A	S	L	R	F	N	F		L	A	E	R	I	M	R	S	Y			
N	C	T	P	V	S	S	P	R	L						P	P	T	Y	W	H	A		M	W	Q	A	A	W	D	L	A	I	C	L				S	Q	L	P	T	I	E	E		T	A	F	R	H	S	P	F	F	A		E	Q	L	T	A	F	Q	W	V	L					
O	S	S	A	R	E	L	R	L	P						L	V	I	W	I	A	K		L	A	L	A	V	D	S	S	C	O	A	D					K	D	N	G	H	K	Y	F	L	S		V	L	A	D	P	Y	M	P	A	E		H	R	T	M	T	A						
V	I	V	I	N	S	T	H	T	G						E	A	C	L	Q	G	N	L		A	I	A	I	C	L	E	Q	L	N	D	P				P	L	L	R	O	W	V	A	I	C		L	G	R	I	W	O	N	F	D	S		A	R	W	C	G	V	R	D	S	A		
H	E	K	L	Y	S	L	L	S							P	P	E	V	E	R	C	A		A	I	A	I	F	A	L	G	T	F	V	G	N	S			A	E	R	T	D	H	S	T		A	I		D	H	N	V	A	M	M	L	A	Q		L	V	S	D	G	P	M	V	R	
K	E	L	V	A	L	S	H	L							V	V	Q	Y	E	S	N		F	N	C	T		V	A	L	Q	I	E	E	E	K				N	Y	A	L	P	S	P	A	T		E	G	G	S	L	T	P	V	R	D		S	P	C	T	P	R	L	R	S			
S	S	Y	G	N	I	R	A	V	A						T	A	R	S	L	N		K	S	L	O			N	L	S	L	T	E	E	S	G				A	V	A	F	S	P	G	N	L	S		T	S	S	A	S	S	T	L	G		S	P	E									

*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)

[illegible]

*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)

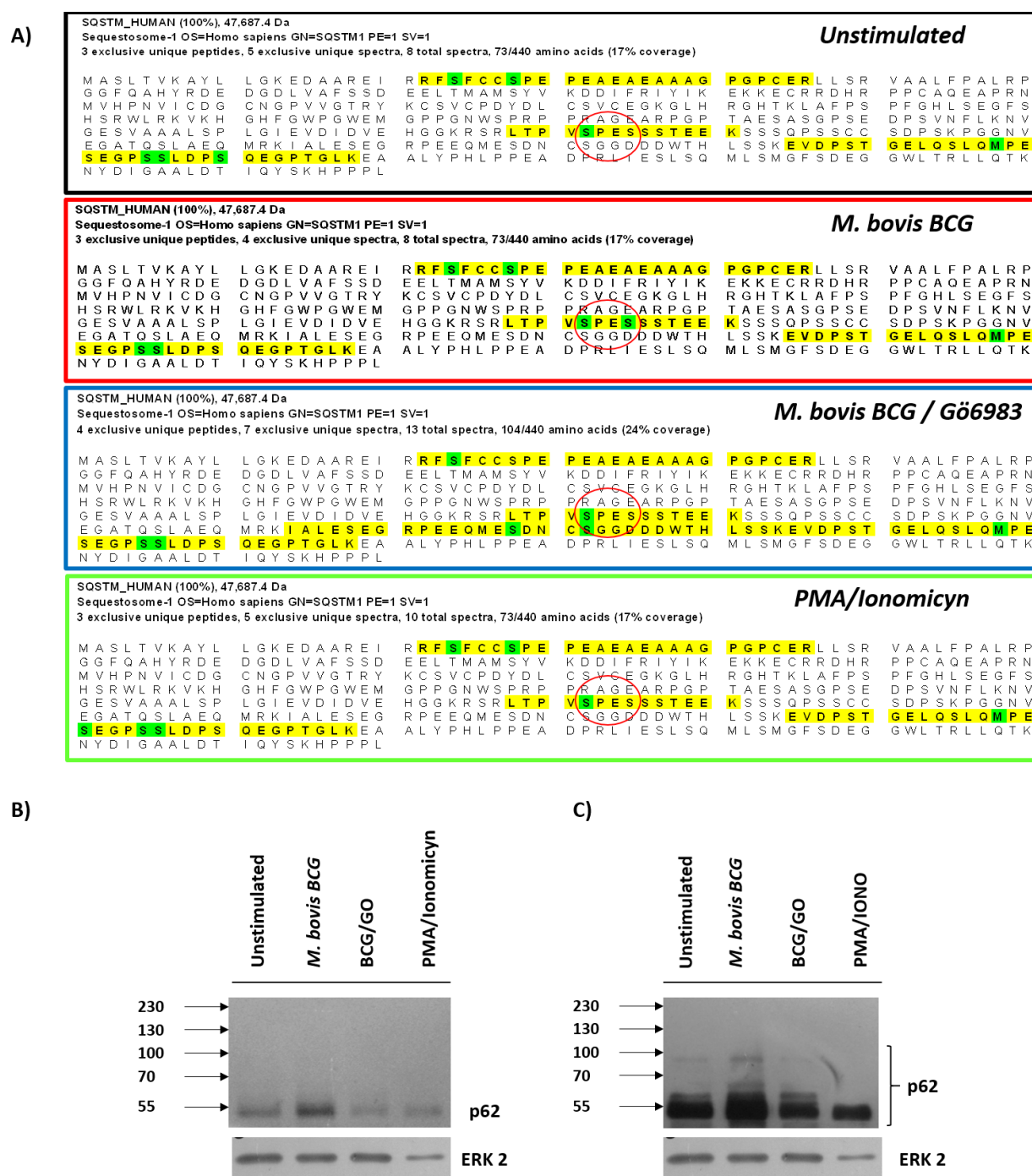
[illegible]

### PMA/Ionomycin



**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/Ionomicyn. 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	<a href="#">Q14523</a>
Small glutamine- rich tetratricopeptide repeat- containing protein alfa	SGTA	<a href="#">Q43765</a>
trans- Golgi network integral membrane protein	TGON2	<a href="#">Q43493</a>
Dynamin 2	DYN2	<a href="#">P50570</a>
Osteopontin	OSTP	<a href="#">P10451</a>
Death- associated protein 1	DAP1	<a href="#">P51397</a>
SH3 domain-containing kinase-binding protein	SH3K1	<a href="#">Q96B97</a>
Girdin	GRDN	<a href="#">Q3V6T2</a>
Dynamin 1	DYN1	<a href="#">Q05193</a>
Golgi-specific brefeldin A- Resistance guanine nucleotide exchange factor1	GBF1	<a href="#">Q92538</a>
TBC9 Domain family member 9B	TBC9B	<a href="#">Q66K14</a>
Sequestosome-1	SQSTM	<a href="#">Q13501</a>
Syntaxin- 4	STX4	<a href="#">Q12846</a>
Calcium homeostasis endoplasmic reticulum protein	CHERP	<a href="#">Q81WX8</a>
Tuberin	TSC2	<a href="#">P49815</a>
Target of Myb protein 1	TOM1	<a href="#">Q60784</a>
Gtpase- activating protein and VPS9 domain containing protein	GAPD1	<a href="#">Q14C86</a>
Dedicator of citokinesis protein 8	DOCK8	<a href="#">Q8NF50</a>
Poly (rC)- binding protein 2	PCB P2	<a href="#">Q15366</a>
A-kinase anchor protein 13	AKP13	<a href="#">Q12802</a>
Bcl2- associated transcription factor 1	BCLF1	<a href="#">Q9NYF8</a>
Phosphatidylinositol 3,4,5- trisphosphate 5- phosphatase 1	SHIP1	<a href="#">Q92835</a>
Prelamina- A/C	LMNA	<a href="#">P02545</a>
ProteinNDRG1	NDRG1	<a href="#">Q92597</a>
C-Jun - amino terminal kinase-interacting protein	JIP4	<a href="#">Q60271</a>
Stromal membrane- asociated protein 2	SMAP2	<a href="#">Q8WU79</a>
Microtubule associated protein 1B	MAP1B	<a href="#">P46821</a>
Bridging interactor 2	BIN2	<a href="#">Q9UBW5</a>
TBC1 domain family member 10 B	TB10B	<a href="#">Q4KMP7</a>
Phosohatidylinositol 4- kinase type2- alpha	P4K2A	<a href="#">Q9BTU6</a>
Glucocorticoid receptor	GCR	<a href="#">P04150</a>
Niban like protein 1	NIBL1	<a href="#">Q96TA1</a>
Wd repeat- containing protein 44	WDR44	<a href="#">Q5JSH3</a>
Mitogen- activated protein kinase kinase kinase kinase 4	M4K4	<a href="#">Q95819</a>
Plastin- 2	PLSL	<a href="#">P13796</a>
RAF proto-oncogene serine/threonine- protein kinase RAF1	RAF1	<a href="#">P04049</a>
Tyrosine-protein kinase Lyn	LYN	<a href="#">P07948</a>
Regulatory- associated protein of mTOR	RPTOR	<a href="#">Q8N122</a>
Protein- methionine sulfoxide oxidase MICAL 1	MICA1	<a href="#">Q8TDZ2</a>
TNF AIP3	TNIP1	<a href="#">Q15025</a>
Was/Wasl- interacting protein family member 2	WIPF2	<a href="#">Q8TF74</a>
Brefeldin A-- inhibited guanine nucleotides-exchange protein	BIG2	<a href="#">Q9Y6D5</a>
FK506-binding protein 15	FKB15	<a href="#">Q5T1M5</a>
Amyloid beta A4 precursor protein-binding family member 1 interacting protein	AB1IP	<a href="#">Q7Z5R6</a>

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

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



