

Kinase	Reference	Description	Labeling Site	Si Sequence	10uM	1uM	0.1uM	Torin1 IC ₅₀	10uM	1uM
					Torin1	Torin1	Torin1	(mM)	Torin2	Torin2
ABL,ARG	UniRef100_	F Proto-oncogene	Lys1	YSLTVAVkTK	25.8	17.2	25.6	>10	-5.5	-5.6
ACK	UniRef100_	C Activated CDC	Lys1	TVSVAVkCLK	6.5	-4.0	-19.3	>10	9.2	-9.1
AKT2,AKT3	UniRef100_	F RAC-beta series	ATP Loop	GTFGkVILVR	38.8	30.9	29.7	>10	-36.2	-25.0
AMPKa1	UniRef100_	C 5'-AMP-activated	ATP Loop	IGHYILGDTLG	-8.9	-13.7	-22.3	>10	-15.9	-8.1
AMPKa1,AM	UniRef100_	C 5'-AMP-activated	Lys1	VAVKILNR	-16.9	-32.4	-21.4	>10	19.9	2.1
AMPKa1,AM	UniRef100_	C 5'-AMP-activated	Lys2	DLkPENVLLD	-2.6	-7.6	5.4	>10	25.6	5.6
ARAF	UniRef100_	F A-Raf proto-oncogene	Lys2	DLkSNNIFLHE	27.2	23.6	8.3	>10	23.4	5.3
ATM	UniRef100_	C Serine-protein	ATP	QLVkgRDDLRF	>95	79.1	42.8	0.15	>95	>95
ATR	UniRef100_	C Serine/threonine	ATP	FYIMMckPK	98.7	95.5	70.3	0.039	99.5	99.5
ATR	UniRef100_	C Serine/threonine	Protein Kinase	kAGHHQTAY	-0.9	0.0	2.0	>10	-12.2	-7.0
AurA	UniRef100_	C Serine/threonine	Lys2	VIHRDIkPENL	14.6	-21.3	-30.2	>10	1.0	-3.0
AurA	UniRef100_	C Serine/threonine	Lys1	FILALKVLFK	1.3	5.3	-4.5	>10	21.1	5.9
AurA	UniRef100_	C Serine/threonine	Lys2	DIkPENLLLGS	0.1	5.4	1.6	>10	25.3	3.5
AurA,AurB,	UniRef100_	C Serine/threonine	ATP Loop	GkFGNVYLAR	-7.5	-7.2	3.6	>10	22.6	4.6
AurB	UniRef100_	C Serine/threonine	Lys1	SHFIVALkVLF	3.4	5.3	0.2	>10	23.1	13.4
BARK1	UniRef100_	F Beta-adrenergic	Lys2	DLkPANILLDE	0.8	-21.0	-5.0	>10	2.3	-0.3
BARK1,BAI	UniRef100_	F Beta-adrenergic	Activation	kKPHASVGTH	-19.5	-31.8	-13.4	>10	-13.2	-32.7
BLK	UniRef100_	F Tyrosine-protein	Lys1	VAIKTLKEGTM	0.1	51.6	4.4	>10	17.4	-1.4
BLK	UniRef100_	F Tyrosine-protein	Activation	IIDSEYTAQEG	-0.5	27.5	26.9	>10	19.8	-4.5
BRAF	UniRef100_	F B-Raf proto-oncogene	Lys2	DLkSNNIFLHE	3.2	4.9	-15.1	>10	-16.9	15.2
BTK	UniRef100_	C Tyrosine-protein	Activation	YVLDDEYTSS	10.0	5.2	8.8	>10	35.1	-4.5
CaMK1d	UniRef100_	C Calcium/calmodulin	Lys1	LFAVkcIPK	-1.6	-0.7	-1.7	>10	10.6	-5.0
CaMK2a,Ca	UniRef100_	C Calcium/calmodulin	Lys2	DLkPENLLLAS	-2.5	-35.3	7.7	>10	36.1	5.5
CaMK2d	UniRef100_	C Calcium/calmodulin	Lys1	IPTGQEYAAK	-9.1	12.1	14.0	>10	30.4	-10.6
CaMK2g	UniRef100_	C Calcium/calmodulin	Lys1	TSTQEYAAKII	3.0	-12.2	-14.4	>10	27.6	-1.2
CaMK2g	UniRef100_	C Calcium/calmodulin	Lys1	KTSTQEYAAK	-0.7	-22.1	14.1	>10	27.8	-29.8
CaMK4	UniRef100_	C Calcium/calmodulin	Lys2	DLkPENLLYAT	-2.7	-11.2	-11.5	>10	-5.6	-28.2
CaMK4	UniRef100_	C Calcium/calmodulin	Lys2	DLkPENLLYAT	-7.7	-20.7	-9.6	>10	7.5	3.1

CaMKK2	UniRef100_C Calcium/calmodulin-dependent protein kinase	LAYNENDNTY	-3.1	-19.6	-29.3	>10	-11.9	-45.0
CASK	UniRef100_C Peripheral protein tyrosine kinase	ETGQQFAVKI	-2.9	2.5	-5.8	>10	42.0	12.2
CDC2	UniRef100_F Cell division cyclin dependent kinase	DLkPQNLLIDP	6.6	21.0	12.6	>10	5.7	-15.3
CDK10	UniRef100_C Cell division protein tyrosine kinase	DLkVSNLLMTD	-10.3	-1.4	2.0	>10	-0.1	-10.1
CDK11,CDK12	UniRef100_F Cell division protein tyrosine kinase	DLkPANILVMG	82.5	39.8	6.8	1.52	50.9	3.9
CDK2	UniRef100_F Cell division protein tyrosine kinase	NKLTGEVVAL	6.9	-10.5	-10.1	>10	-2.4	-1.0
CDK2	UniRef100_F Cell division protein tyrosine kinase	DLkPQNLLINT	-9.6	-4.6	2.7	>10	14.5	-9.0
CDK5	UniRef100_C Cell division protein tyrosine kinase	DLkPQNLLINF	-6.8	-10.0	-9.1	>10	-4.5	-12.0
CDK5	UniRef100_C Cell division protein tyrosine kinase	NRETHEIVAL	-15.0	5.5	4.9	>10	-2.2	5.8
CDK6	UniRef100_C Cell division protein tyrosine kinase	VVHRDLkPQN	-29.3	-36.0	-37.5	>10	-1.9	-8.5
CDK6	UniRef100_C Cell division protein tyrosine kinase	DLkPQNILVTS	13.7	9.3	-0.6	>10	5.3	-10.6
CDK7	UniRef100_F Cell division protein tyrosine kinase	DLkPNNLLLD	-4.6	-3.8	6.1	>10	33.3	-6.3
CDK9	UniRef100_F Cell division protein tyrosine kinase	DMkAANVLIT	-14.6	-7.1	-7.3	>10	-0.8	-14.2
CHED	UniRef100_C Cell division cyclin dependent kinase	DIkCSNILLNM	-5.3	-71.3	-6.8	>10	-23.3	18.2
CHK1	UniRef100_C Serine/threonine kinase	LSkGDGLEFK	-12.7	6.3	1.9	>10	1.1	6.8
CHK2	UniRef100_C Serine/threonine kinase	DLkPENVLLSS	-7.9	-17.2	-27.3	>10	-6.5	25.0
CHK2	UniRef100_C Serine/threonine kinase	VAIKIISK	-19.5	-7.7	1.3	>10	-6.1	-7.2
CHK2	UniRef100_C Serine/threonine kinase	DLkPENVLLSS	2.3	28.0	1.8	>10	-2.2	-3.2
CK1a	UniRef100_F Casein kinase	DIkPDNFLMG	-12.4	-6.6	-7.7	>10	-3.6	0.3
CK1d,CK1e	UniRef100_F Casein kinase	DVkPDNFLMG	8.2	-4.5	3.7	>10	11.7	-8.3
CLK3	UniRef100_F Dual specificity ATP dependent protein kinase	YEIVGNLGEQ	6.0	-3.0	-6.1	>10	32.9	10.4
CSK	UniRef100_F Tyrosine-protein kinase	VSDFGLTkEAS	-0.2	-4.3	-4.1	>10	0.1	-0.6
CSK	UniRef100_F Tyrosine-protein kinase	EASSTQDTGK	-10.5	-3.7	-2.6	>10	3.0	8.4
DGKA	UniRef100_F Diacylglycerol dependent protein kinase	VLWkFQYILN	10.0	-10.9	-12.1	>10	-59.9	-11.7
DGKA	UniRef100_F Diacylglycerol dependent protein kinase	IDPVPNTHPL	37.5	5.1	12.6	>10	-1.5	-9.2
DGKH	UniRef100_C Diacylglycerol dependent protein kinase	ATFSFCVSPLL	-21.6	3.6	3.9	>10	18.0	29.0
DMPK1	UniRef100_C Myotonic protein tyrosine kinase	MKQTGQVYA	15.0	22.6	5.6	>10	7.8	9.7
DMPK1	UniRef100_C Myotonic protein tyrosine kinase	DIkPDNILLDR	-5.4	22.9	20.0	>10	7.9	-9.6
DNAPK	UniRef100_F DNA-dependent protein kinase	EHPFLVkgGE	>98	96.6	83.1	0.018	99.6	99.6

DNAPK	UniRef100_F DNA-depende ATP	GHDEREHPFL	98.6	93.4	67.7	0.044	98.9	98.8
DNAPK	UniRef100_F DNA-depende ATP	KGGSWIQEIN	98.8	94.9	64.0	0.052	98.5	97.2
eEF2K	UniRef100_C Elongation fac Protein Kir	YIKYNSNSGFV	-3.1	3.2	-0.7	>10	2.9	-1.3
Erk1	UniRef100_F Mitogen-activ Lys2	DLKPSNLLINT	-3.6	-14.7	-26.4	>10	2.2	-10.7
Erk5	UniRef100_C Mitogen-activ Lys2	DLKPSNLLVN	13.4	14.6	17.1	>10	13.3	30.8
FAK	UniRef100_C Focal adhesioi Lys1	CIGEGQFGDV	13.9	-27.7	-16.5	>10	-15.8	-9.0
FER	UniRef100_F Proto-oncogei Lys1	TSVAVkTCKE	0.6	-36.2	-10.1	>10	-3.3	0.6
FER	UniRef100_F Proto-oncogei Activation	QEDGGVYSSS	-12.0	-26.1	-9.4	>10	10.7	20.4
FGR	UniRef100_F Proto-oncogei Activation	LIKDDEYNPC	-0.8	4.4	1.5	>10	7.2	6.6
FRAP	UniRef100_F FKBP12-rapan ATP	IQSIAPSLQVIT	99.1	98.8	98.3	<0.01	98.5	98.7
FYN	UniRef100_F Proto-oncogei Lys1	VAIKTLKPGTM	7.0	-8.0	-2.9	>10	-7.7	-13.8
FYN,SRC,Y	UniRef100_F Proto-oncogei Activation	QGAKFPIKWT	-27.6	-52.7	-26.0	>10	-16.0	-21.4
GCK	UniRef100_C Mitogen-activ Lys2	IHRDIkGANLL	15.5	-48.7	-48.8	>10	-11.3	-27.8
GCK	UniRef100_C Mitogen-activ Lys1	DTVtSELAAV	38.4	4.9	-13.4	>10	8.2	-5.7
GCK	UniRef100_C Mitogen-activ Lys2	DIkGANLLLT	40.6	8.3	0.2	>10	19.8	-4.4
GCN2 dom:	UniRef100_C Eukaryotic tra Lys1	VQNKLDGCC	4.1	5.3	10.1	>10	-0.4	-16.1
GSK3A	UniRef100_F Glycogen synt Lys2	DIkPQNLLVD	0.9	-3.0	0.0	>10	61.6	3.4
GSK3B	UniRef100_F Glycogen synt Lys2	DIkPQNLLDF	-0.4	-10.0	-11.9	>10	29.0	-0.7
HPK1	UniRef100_C Mitogen-activ Lys1	VSGDLVALkM	24.1	-6.4	-21.3	>10	-3.7	4.1
HPK1	UniRef100_C Mitogen-activ Lys1	DKVSGDLVAL	16.6	-5.1	-2.6	>10	-1.9	-7.1
HPK1	UniRef100_C Mitogen-activ Lys2	DIkGANILIND	23.2	4.5	4.0	>10	15.2	3.0
IKKa	UniRef100_C Inhibitor of nu Lys2	IIHRDLkPENIV	-16.4	-36.3	-22.2	>10	-2.6	-30.3
IKKa	UniRef100_C Inhibitor of nu Lys2	DLkPENIVLQD	-8.8	-2.4	1.0	>10	0.0	5.4
IKKb	UniRef100_C Inhibitor of nu Lys2	DLkPENIVLQC	-8.4	-7.8	-4.3	>10	2.4	-13.0
IKKe	UniRef100_C Inhibitor of nu Lys1	SGELVAVkVF	5.7	-1.2	5.6	>10	6.3	-4.9
IKKe	UniRef100_C Inhibitor of nu Activation	ELDDDEkFVS	8.5	-22.1	7.8	>10	9.8	-1.8
IKKe,TBK1	UniRef100_C Inhibitor of nu Lys2	DIkPGNIMR	-14.0	-36.5	-21.2	>10	-8.0	-13.3
ILK	UniRef100_C Integrin-linker Protein Kir	ISMADVkfSF	-13.4	-1.3	-6.6	>10	-13.6	-24.4
ILK	UniRef100_C Integrin-linker Lys1	WQGNDIVVk	-19.5	-1.2	2.1	>10	1.4	-12.8

INSR	UniRef100_F Insulin recepti	Lys1	VAVkTVNESAA	8.0	-3.6	9.4	>10	24.5	30.3
IRAK4	UniRef100_C Interleukin-1 r	Lys1	GYVNNTTVA	2.9	-5.1	-8.7	>10	17.1	-9.7
IRAK4	UniRef100_C Interleukin-1 r	Lys2	DIK SANILLDE	-0.3	-6.4	-8.5	>10	18.8	-1.7
IRE1	UniRef100_C Endoribonucle	Lys2	DLkPHNILISM	7.3	-0.1	3.9	>10	-12.4	-19.4
ITPK1	UniRef100_C Inositol-tetrak	ATP	ESIFFNSHNVS	2.8	4.0	23.2	>10	-13.3	10.4
JAK1	UniRef100_F Tyrosine-prot	Other	QLASALSYLE	5.9	6.7	-8.3	>10	88.3	50.0
JAK1 doma	UniRef100_F Tyrosine-prot	Lys1	YDPEGDNTG	3.0	-7.4	-7.3	>10	-26.9	-9.4
JAK1 doma	UniRef100_F Tyrosine-prot	Activation	IGDFGLTkaIE	10.2	9.1	6.0	>10	24.0	7.7
JAK1 doma	UniRef100_F Tyrosine-prot	Activation	IGDFGLTkaIE	26.1	3.7	18.5	>10	27.0	2.4
JAK3 doma	UniRef100_F Tyrosine-prot	Lys1	YDPLGDNTGA	3.0	13.2	6.3	>10	-7.9	-5.4
JNK1,JNK2	UniRef100_F Mitogen-activ	Lys2	DLkPSNIVVK	23.6	-2.4	0.0	>10	51.7	9.2
KHS1	UniRef100_C Mitogen-activ	Lys1	NVHTGELAAY	16.7	-19.8	-16.0	>10	7.3	-4.3
KHS1	UniRef100_C Mitogen-activ	Lys2	DIKGANILLTD	12.4	1.5	-2.3	>10	15.5	22.7
LATS1	UniRef100_C Serine/threon	Lys1	ALYATkTLR	-5.5	-16.6	-13.5	>10	-0.9	-4.8
LCK	UniRef100_F Proto-oncoge	Activation	EGAkFPIKWT	-13.3	-41.6	-21.9	>10	3.4	-18.7
LIMK1	UniRef100_F LIM domain ki	Lys1	ETGEVMVMK	-15.6	-15.8	4.0	>10	1.9	-31.1
LIMK1	UniRef100_F LIM domain ki	Lys1	ETGEVMVMK	15.4	-29.1	4.4	>10	44.4	2.4
LKB1	UniRef100_C Serine/threon	Lys2	FPVCQAHGYF	0.1	2.5	0.5	>10	-23.9	-11.0
LKB1	UniRef100_C Serine/threon	Lys2	DIkPGNLLLTT	-0.5	4.2	24.2	>10	2.3	-3.2
LOK	UniRef100_C Serine/threon	Lys1	ETGALAAAkV	-14.0	-1.1	5.5	>10	13.1	9.3
LOK	UniRef100_C Serine/threon	Lys1	NKETGALAA	1.4	-7.2	-10.3	>10	5.2	13.3
LOK	UniRef100_C Serine/threon	Lys2	IIHRDLkAGNV	-9.3	-51.3	-14.5	>10	-15.5	-30.1
LOK	UniRef100_C Serine/threon	Lys2	DLkAGNVLM	2.4	-21.2	0.2	>10	11.6	-6.7
LYN	UniRef100_F Tyrosine-prot	Activation	EGAkFPIKWT	-3.9	-20.4	-13.2	>10	7.8	-5.0
LYN	UniRef100_F Tyrosine-prot	Lys1	VAVkTLKPGT	4.1	-3.2	-1.4	>10	12.3	-0.1
MAP2K1,M	UniRef100_C Dual specificit	Lys2	DVkPSNILVNS	-15.6	-24.3	-16.1	>10	-2.3	14.9
MAP2K3	UniRef100_F Dual specificit	Activation	MCDFGISGYL	-5.7	-49.3	-26.3	>10	-2.6	6.9
MAP2K3	UniRef100_F Dual specificit	Lys2	DVkPSNVLIN	-10.7	-18.9	-11.2	>10	0.5	8.6
MAP2K4	UniRef100_F Dual specificit	Lys2	DIkPSNILLDR	-11.1	-2.4	-5.2	>10	-0.8	1.7

MAP2K4	UniRef100_F Dual specificit Activation	LCDFGISGQLV	-6.4	4.7	1.7	>10	7.3	-6.1
MAP2K6	UniRef100_F Dual specificit Activation	MCDFGISGYL	-5.7	-30.1	-23.8	>10	-13.6	3.3
MAP2K6	UniRef100_F Dual specificit Lys2	DVkPSNVLIN	-1.7	-15.1	-13.2	>10	3.0	10.6
MAP2K6	UniRef100_F Dual specificit Lys1	HVPSGQIMAY	2.8	3.0	0.4	>10	5.1	-6.8
MAP2K7	UniRef100_C Dual specificit Lys2	DVkPSNILLDE	-14.1	0.6	-2.1	>10	2.6	-17.5
MAP3K1	UniRef100_C Mitogen-activ Lys2	DVkgANLLID	-11.2	-1.8	-9.2	>10	58.0	-2.1
MAP3K2	UniRef100_C Mitogen-activ Lys1	ELAVkQVQFD	10.5	25.5	6.7	>10	-2.8	12.9
MAP3K2	UniRef100_C Mitogen-activ Lys1	VYLCYDVRTG	41.1	2.7	13.9	>10	9.5	10.5
MAP3K2,M	UniRef100_C Mitogen-activ Lys2	DIkGANILR	-15.8	-4.1	-7.2	>10	2.5	3.5
MAP3K3	UniRef100_C Mitogen-activ Lys1	ELASKVQVQFD	-15.5	14.9	-12.4	>10	2.7	12.6
MAP3K4	UniRef100_C Mitogen-activ Lys2	DIkGANIFLTS	-11.3	3.8	-10.7	>10	12.5	3.9
MAP3K5	UniRef100_C Mitogen-activ Lys2	DIkGDNVLIN	-14.2	-3.8	-8.0	>10	-6.1	-25.7
MAP3K5,M	UniRef100_C Mitogen-activ Lys1	IAIkEIPERDS	-14.5	-30.9	-28.1	>10	-5.7	3.9
MAP3K7,T	UniRef100_C Mitogen-activ Lys2	DLkPPNLLLVA	-2.2	0.4	-3.0	>10	41.9	32.5
MAPKAPK3	UniRef100_C MAP kinase-α ATP Loop	KYAVTDDYQL	26.5	-35.4	-24.0	>10	27.1	3.8
MARK2	UniRef100_C Serine/threon Lys1	HILTGKEVAV	1.6	-12.8	-5.9	>10	-21.9	-53.4
MARK2	UniRef100_C Serine/threon Lys1	EVAVkiIDKTC	-12.4	-24.7	9.0	>10	1.3	-10.1
MARK2,MA	UniRef100_F MAP/microtub Lys2	DLkAENLLLD	0.4	2.6	8.9	>10	2.6	-13.6
MARK3	UniRef100_F MAP/microtub Lys1	EVAIkIIDKTQ	-3.7	0.0	4.5	>10	-9.7	-0.5
MAST1,MA	UniRef100_C Microtubule-α Lys2	DLkPDNLLITS	-10.1	-15.7	-7.6	>10	3.5	1.6
MAST2,MA	UniRef100_C Microtubule-α Lys2	DLkPDNLLVTS	3.1	-28.0	-16.1	>10	5.7	-8.3
MAST3	UniRef100_C Microtubule-α Lys2	DLkPDNLLITS	-0.5	1.6	5.0	>10	2.4	-7.7
MASTL	UniRef100_C Microtubule-α ATP Loop	GAFGkVYLGC	-5.2	-11.3	-8.7	>10	17.6	7.6
MASTL	UniRef100_C Microtubule-α Lys1	LYAVkVVVK	0.5	2.3	0.2	>10	20.0	1.4
MLK3	UniRef100_C Mitogen-activ Lys2	DLkSNNILLLO	11.1	-8.7	-1.6	>10	49.9	0.3
MLKL	UniRef100_C CDNA FLJ3438 Lys1	APVAIkVFK	-7.7	20.6	2.5	>10	3.4	-11.6
MPSK1	UniRef100_C Serine/threon Lys2	DLkPTNILLGD	50.9	-7.0	-17.6	>10	86.0	31.8
MSK1 dom	UniRef100_C Ribosomal prc Lys2	DIkLENILLDS	7.1	4.8	-4.3	>10	16.8	14.0
MSK1,MSK	UniRef100_C Ribosomal prc ATP Loop	VLGTGAYGkV	-3.7	-3.2	7.2	>10	8.4	-14.8

MST1	UniRef100_C Serine/threon Lys1	AHKETGQIVA	25.7	3.3	4.1	>10	8.8	3.6
MST1	UniRef100_C Serine/threon Lys1	ETGQIVAikQY	33.2	21.1	9.0	>10	16.3	21.8
MST1,MST2	UniRef100_C Serine/threon Lys2	DIKAGNILLNT	5.4	-61.4	-30.6	>10	-15.2	5.1
MST1,MST2	UniRef100_C Serine/threon Lys2	IHRDIkAGNIL	14.5	1.6	-5.5	>10	1.2	-8.9
MST1,MST2	UniRef100_C Serine/threon Activation	LADFGVAGQ	41.6	20.1	18.8	>10	10.9	16.8
MST2	UniRef100_C Serine/threon Lys1	ESGQVVAikQ	-24.8	-15.4	-26.1	>10	-57.8	-11.3
MST2	UniRef100_C Serine/threon Lys1	ESGQVVAikQ	21.3	2.1	-7.0	>10	10.3	7.1
MST3	UniRef100_C Serine/threon Lys2	DIKAANVLLSE	-19.2	-17.2	-17.3	>10	7.2	-16.0
MST3,MST4	UniRef100_C Serine/threon Activation	LADFGVAGQ	0.4	-3.6	-2.8	>10	-5.0	6.2
MST4	UniRef100_C Serine/threon Lys1	TQQVVAikIID	12.3	-32.9	6.5	>10	30.3	5.4
MST4,YSK1	UniRef100_C Serine/threon Lys2	DIKAANVLLSE	-3.8	-85.8	-31.2	>10	-4.0	-25.7
MST4,YSK1	UniRef100_C Serine/threon Lys2	DIKAANVLLSE	-14.1	2.8	0.1	>10	12.0	-14.1
NDR1	UniRef100_C Serine/threon Lys2	DIKPDNLLLDS	-2.0	6.5	7.6	>10	-17.9	-12.1
NDR2	UniRef100_C Serine/threon Lys1	DTGHIYAMki	-16.8	-30.0	-8.5	>10	-19.4	-10.7
NEK1	UniRef100_C Serine/threon Lys2	DIKSQNIFLTK	-3.7	4.5	6.1	>10	1.2	-7.4
NEK3	UniRef100_F Serine/threon Activation	SkNIFLTQNG	-4.8	-11.9	-0.5	>10	-1.2	1.5
NEK4	UniRef100_F Serine/threon Lys2	DLKTQNVFLT	5.9	10.4	4.3	>10	3.4	-2.8
NEK6,NEK7	UniRef100_C Serine/threon Lys2	VMHRDIkPAN	-7.1	-3.2	-5.2	>10	-8.7	-32.9
NEK6,NEK7	UniRef100_C Serine/threon Lys2	DIkPANVFITA	-22.2	-40.1	-4.4	>10	-5.3	-4.7
NEK7	UniRef100_C Serine/threon Lys1	AACLLDGVPV	5.4	17.9	4.9	>10	-1.3	0.5
NEK9	UniRef100_C Serine/threon Lys1	RTEDDSLvvV	-14.0	-26.7	-18.3	>10	-3.2	-0.7
NEK9	UniRef100_C Serine/threon Lys1	TEDDSLvvV	7.1	-11.8	-8.5	>10	1.5	0.0
NEK9	UniRef100_C Serine/threon Activation	LGDYGLAKK	2.2	-14.4	-6.5	>10	8.3	-1.5
NEK9	UniRef100_C Serine/threon Lys2	DIkTLNIFLTK	3.8	-1.3	14.4	>10	8.6	3.5
NuaK2	UniRef100_C Hypothetical Ꞥ Lys1	LVAikSIR	-16.5	4.9	8.5	>10	25.3	7.6
p38a	UniRef100_C Mitogen-activ Lys2	DLkPSNLAVN	-0.9	8.2	11.1	>10	2.2	-15.5
p38a	UniRef100_C Mitogen-activ Other	QELNKTIWEV	33.9	38.1	11.2	>10	2.4	3.0
p38d,p38g	UniRef100_F Mitogen-activ Lys2	DLkPGNLAVN	2.1	-12.1	-14.9	>10	29.3	6.2
p70S6K	UniRef100_F Ribosomal prc Activation	LTDFGLckESI	21.9	22.3	-8.1	>10	-26.9	10.3

p70S6K	UniRef100_F Ribosomal prc Lys2	DLkPENIMLN	-16.4	-8.8	-2.2	>10	-4.4	7.4
p70S6Kb	UniRef100_C Ribosomal prc Lys2	DLkPENIMLS	0.6	-17.3	-13.3	>10	-1.5	-13.1
p70S6Kb	UniRef100_C Ribosomal prc Activation	LTDFGLcKESI	29.4	-19.0	8.0	>10	24.0	-7.5
PAN3	UniRef100_C PAB-depende	Other VMDPTkILITC	-5.4	-2.2	10.6	>10	-2.8	-1.2
PCTAIRE1,I	UniRef100_C Serine/threon Lys2	DLkPQNLLINE	8.1	5.4	12.4	>10	36.0	-8.3
PCTAIRE2	UniRef100_C Serine/threon Lys2	DLkPQNLLINE	24.6	9.0	20.1	>10	48.5	16.5
PCTAIRE2,I	UniRef100_C Serine/threon Lys1	SKLTENLVALK	-13.8	-41.8	-25.2	>10	39.9	-2.5
PEK	UniRef100_C Eukaryotic tra Lys2	DLkPSNIFFTM	-0.9	-3.5	3.1	>10	0.3	4.0
PFTAIRE1	UniRef100_C Serine/threon Lys1	VNGKLVALkV	12.3	-7.8	-7.3	>10	27.4	4.7
PFTAIRE1	UniRef100_C Serine/threon Lys2	DLkPQNLLISD	-3.1	0.1	-6.3	>10	31.1	0.8
PFTAIRE1	UniRef100_C Serine/threon Lys1	LVALkVIR	8.2	9.1	9.1	>10	31.9	2.6
PFTAIRE2	UniRef100_C Serine/threon Lys2	DLkPQNLLISH	1.0	27.2	-0.5	>10	13.9	8.5
PHKg1	UniRef100_C Phosphorylasε Lys2	DLkPENILLDD	-0.6	4.2	-6.3	>10	15.8	11.0
PHKg2	UniRef100_F Phosphorylasε Lys1	ATGHEFAVKI	6.9	-21.8	-21.3	>10	-11.4	-14.2
PI4K2B	UniRef100_C Phosphatidylii ATP	SEEPYGQLNP	-26.5	-22.1	-32.7	>10	-36.4	-7.1
PI4KA,PI4K	UniRef100_F Phosphatidylii ATP	SGTPMQSAA	6.9	-18.2	-2.1	>10	78.1	13.6
PI4KB	UniRef100_C Phosphatidylii ATP	VPHTQAVVLM	4.8	-22.2	-12.2	>10	96.4	95.0
PI4KB	UniRef100_C Phosphatidylii ATP	VPHTQAVVLM	4.9	-14.7	-7.7	>10	97.4	85.7
PIK3C3	UniRef100_C Phosphatidylii ATP	TEDGGKYPVI	90.1	62.8	33.6	0.35	>98	>98
PIK3C3	UniRef100_C Phosphatidylii ATP	TEDGGKYPVI	92.2	59.3	2.9	0.75	96.3	91.5
PIK3CA	UniRef100_F Phosphatidylii ATP	RPLWLNWEN	>80	>80	39.4	0.11	>85	>85
PIK3CB	UniRef100_F Phosphatidylii ATP	VFGEDSVGVI	60.1	-2.2	-9.7	8.0	94.5	86.2
PIK3CD	UniRef100_C Phosphatidylii ATP	TKVNWLAHN	81.0	51.7	8.0	1.0	91.2	94.6
PIK3CG	UniRef100_F Phosphatidylii ATP	KkPLWLEFK	9.7	-51.3	-32.5	>10	42.7	32.6
PIP4K2A	UniRef100_F Phosphatidylii ATP	AKELPTLkDN	-3.9	-23.2	-10.6	>10	8.0	-7.0
PIP4K2A,PI	UniRef100_F Phosphatidylii ATP	TVkHGAGAEI	-25.8	-17.7	-11.4	>10	8.6	-10.2
PIP4K2C	UniRef100_C Phosphatidylii ATP	TLVIkEVSSD	10.1	-0.1	9.0	>10	87.8	48.0
PIP4K2C	UniRef100_C Phosphatidylii ATP	VKELPTLkDM	-4.4	-28.7	-22.5	>10	85.1	44.2
PIP5K3	UniRef100_C FYVE finger-cc ATP	GGkSGAAFYA	18.9	2.3	0.9	>10	77.9	31.9

PITSLRE	UniRef100_F PITSLRE serine Lys2	DLkTSNLLLSH	-3.9	-13.8	-23.6	>10	12.1	-0.2
PKD1,PKD2	UniRef100_C Serine/threon Lys2	NIVHCDLkPE	-0.2	20.2	2.6	>10	18.7	5.4
PKD2	UniRef100_C Protein kinase Lys1	DVAVkVIDK	6.8	0.6	-9.4	>10	1.7	9.0
PKD3	UniRef100_C Protein kinase Lys1	DVAIkVIDK	-15.3	-6.9	1.7	>10	-14.1	3.1
PKD3	UniRef100_C Protein kinase Lys2	NIVHCDLkPE	-0.9	-2.1	4.5	>10	-4.3	0.8
PKR	UniRef100_F Interferon-ind Lys2	DLkPSNIFLVD	-0.5	-5.4	-0.5	>10	-4.6	-9.9
PKR	UniRef100_F Interferon-ind Activation	IGDFGLVTSLK	3.5	15.5	5.8	>10	-1.3	-7.0
PLK1	UniRef100_F Serine/threon Lys1	CFEISDADTKB	-16.1	-31.0	-15.8	>10	-7.0	-15.5
PLK1	UniRef100_F Serine/threon Lys2	VIHRDLkLGN	-2.2	-0.5	-6.3	>10	5.7	-3.1
PLK1	UniRef100_F Serine/threon Lys2	DLkLGNLFLN	-4.8	-29.6	-5.2	>10	11.4	19.5
PRKACB	UniRef100_F cAMP-depend Lys2	DLkPENLLIDH	-15.6	-23.4	-24.9	>10	24.0	-22.4
PRP4	UniRef100_C Serine/threon Other	AAGIGkDFKE	-8.2	-21.3	-28.1	>10	-17.2	-12.1
PRP4	UniRef100_C Serine/threon Lys2	CNILHADIkPD	-5.3	-13.5	2.3	>10	-6.5	6.4
PRPK	UniRef100_C TP53-regulatio ATP Loop	FLSGLELVkQC	-11.0	-4.0	-11.5	>10	-3.3	-22.9
PYK2	UniRef100_C Protein tyrosin Activation	YIEDEDYYkAS	-2.6	-11.2	2.4	>10	25.6	14.6
QSK	UniRef100_C Serine/threon Lys1	VAIkIIDKTQL	17.8	8.5	-17.4	>10	12.9	19.9
RIPK3	UniRef100_C Receptor-inte Lys2	DLkPSNVLLD	13.0	13.0	17.1	>10	16.5	-17.6
ROCK1	UniRef100_C Rho-associate Other	kLQLELNQER	10.5	4.9	-5.1	>10	-15.3	4.7
ROCK1,RO	UniRef100_C Rho-associate Lys2	DVkpDNMLL	-1.9	-9.0	4.6	>10	-17.3	-3.6
RSK1 dom	UniRef100_C Ribosomal prc Lys2	DLkPENILLDE	-8.5	-40.2	-32.7	>10	13.6	-13.4
RSK1 dom	UniRef100_C Ribosomal prc Lys2	DLkPSNILYVD	17.2	7.2	0.6	>10	55.9	12.4
RSK1 dom	UniRef100_C Ribosomal prc Lys2	TVEYLHSQGV	1.8	19.4	-10.4	>10	-38.1	-53.9
RSK1,RSK2	UniRef100_C Ribosomal prc Lys2	DLkPENILLDE	-11.5	-33.5	-24.6	>10	7.0	2.6
RSK1,RSK2	UniRef100_C Ribosomal prc Lys2	DLkPENILLDE	10.4	6.6	0.1	>10	14.0	-7.3
RSK1,RSK3	UniRef100_C Ribosomal prc Other	SkrRDPSEEIEIL	-6.0	-18.0	-43.2	>10	31.8	27.4
RSK2 dom	UniRef100_F Ribosomal prc ATP Loop	VLGQGSFGkV	-15.7	-14.0	-12.7	>10	15.3	-6.4
RSK2 dom	UniRef100_F Ribosomal prc Activation	LTDFGLSkESI	-16.1	5.0	4.8	>10	15.6	2.3
RSK2 dom	UniRef100_F Ribosomal prc Lys2	DLkPSNILYVD	1.5	0.3	-0.2	>10	25.3	4.5
RSK2 dom	UniRef100_F Ribosomal prc Protein Kir	SkrRDPTEEIEIL	5.7	10.5	0.7	>10	31.7	18.2

RSKL1	donr	UniRef100_(Ribosomal prc Protein Kir	VLGVIDkVLLV	3.1	-4.4	-8.7	>10	-8.6	-3.6
SGK3		UniRef100_(Serine/threon Lys1	FYAVkVLQK	-3.6	-1.7	-3.1	>10	5.5	2.6
SLK		UniRef100_(CTCL tumor ar Lys2	IHRDLkAGNI	-25.5	-76.5	-40.8	>10	-16.0	-29.2
SLK		UniRef100_(CTCL tumor ar Lys2	DLkAGNILFTL	-11.7	-4.7	-8.7	>10	-6.6	-33.7
SLK		UniRef100_(CTCL tumor ar Lys1	AQNKETSVAL	-10.4	-2.8	-8.7	>10	-5.9	-17.8
SLK		UniRef100_(CTCL tumor ar Lys2	DLkAGNILFTL	16.1	-44.7	-0.1	>10	17.3	-4.0
SMG1		UniRef100_(Serine/threon Other	DTVTIHSVGG	43.6	1.6	-2.5	>10	98.1	85.2
SNRK		UniRef100_(SNF-related sε Lys2	DLkPENVVFF	10.7	27.3	5.3	>10	15.7	-0.3
SRPK1		UniRef100_(Serine/threon Lys2	IIHTDikPENIL	-7.7	4.0	-9.0	>10	4.4	-11.0
SRPK1,SRF		UniRef100_(Serine/threon Lys1	FVAMkVVVK	-22.2	-20.0	-4.9	>10	-12.6	11.0
STLK5		UniRef100_(STE20-related Activation	YSVkVLPWLS	-1.2	-7.0	-11.4	>10	-3.0	8.9
SYK		UniRef100_(Tyrosine-protr Activation	ISDFGLSkALR	-9.9	-24.7	-14.5	>10	-12.8	-35.7
SYK		UniRef100_(Tyrosine-protr Lys1	TVAVkILKNEA	-7.6	-2.5	2.7	>10	-7.0	-33.8
SYK		UniRef100_(Tyrosine-protr Activation	ISDFGLSkALR	-2.7	-19.2	7.1	>10	7.8	3.7
TAO1,TAO3		UniRef100_(Serine/threon Lys2	DIkAGNILLTE	-13.2	5.9	3.0	>10	15.4	-9.5
TAO2		UniRef100_(Serine/threon Lys2	DVkAGNILLSB	4.4	17.5	5.6	>10	21.5	0.5
TAO3		UniRef100_(Serine/threon Lys2	KPLQEVEIAAM	-33.1	-16.9	-20.8	>10	11.3	1.1
TBK1		UniRef100_(Serine/threon Lys1	TGDLFAikVFN	1.8	7.3	3.7	>10	-8.6	-8.2
TEC		UniRef100_(Tyrosine-protr Activation	YVLDDQYTSS	10.1	24.2	30.9	>10	-32.1	-36.0
TLK1		UniRef100_(Serine/threon Lys1	YAAVkiHQLN	0.6	-16.6	-19.2	>10	-9.4	-12.0
TLK1		UniRef100_(Serine/threon Lys2	YLNEIkPPIIHY	-0.4	5.7	2.6	>10	5.5	-6.5
ULK3		UniRef100_(Unc-51-like kii Lys2	NISHLDLkPQF	18.4	-10.5	-13.5	>10	2.8	-3.4
ULK3		UniRef100_(Unc-51-like kii Lys1	EVVAIKCVAK	-3.7	-8.2	-6.5	>10	3.5	5.9
VRK2		UniRef100_(Serine/threon Lys2	MLDVLEIYHE	-3.5	-6.8	5.6	>10	10.0	18.7
Wee1		UniRef100_(Wee1-like pro Lys2	YIHMSMLVHM	5.1	2.7	6.9	>10	-12.2	-8.0
Wnk1,Wnk2		UniRef100_(Serine/threon Lys2	DLkCDNIFITG	-6.1	-8.4	-23.2	>10	0.7	5.0
Wnk1,Wnk2		UniRef100_(Serine/threon Activation	IGDLGLATLkR	-6.6	-0.4	4.8	>10	0.8	-1.3
YANK3		UniRef100_(PKE protein ki Lys2	DVkPDNILLD	3.4	-3.2	12.3	>10	-3.9	-8.4
ZAK		UniRef100_(Mitogen-activ Lys1	WISQDKEVAV	-4.6	-8.5	-12.3	>10	82.7	25.6

ZAP70	UniRef100_F Tyrosine-protein tyrosine kinase	ISDFGLSkALG	-7.5	-11.1	-36.5	>10	2.7	-6.2
ZC1/HGK	UniRef100_C Mitogen-activated protein kinase 1	TGQLAAIkVM	-18.1	-25.2	-14.4	>10	14.0	7.8
ZC1/HGK	UniRef100_C Mitogen-activated protein kinase 1	TGQLAAIkVM	33.5	9.8	25.5	>10	16.3	-5.5
ZC1/HGK,ZC1	UniRef100_C Mitogen-activated protein kinase 2	DIkGQNVLLT	-9.1	5.3	-4.6	>10	40.7	-0.7

0.1uM Torin2	Torin2 IC ₅₀ (mM)
-9.4	>10
6.2	>10
-43.8	>10
-3.1	>10
12.8	>10
4.0	>10
0.3	>10
>95	<0.01
98.8	<0.01
-2.1	>10
10.9	>10
16.1	>10
2.3	>10
6.5	>10
3.6	>10
12.1	>10
-1.7	>10
-11.3	>10
-17.4	>10
15.0	>10
1.7	>10
6.7	>10
7.3	>10
-5.5	>10
-0.9	>10
-23.0	>10
-7.1	>10
7.6	>10

-8.9	>10
7.5	>10
-25.7	>10
-10.4	>10
-6.0	10
4.0	>10
-3.5	>10
-3.9	>10
-5.7	>10
-1.7	>10
1.6	>10
-3.7	>10
2.7	>10
-25.4	>10
1.1	>10
6.8	>10
8.8	>10
2.6	>10
3.8	>10
0.4	>10
-9.7	>10
-7.2	>10
11.4	>10
11.3	>10
3.9	>10
14.1	>10
-1.5	>10
-12.5	>10
98.2	<0.01

97.2	<0.01
96.8	<0.01
3.0	>10
-0.9	>10
-0.8	>10
17.3	>10
11.9	>10
16.0	>10
5.9	>10
98.2	<0.01
7.2	>10
3.3	>10
-5.3	>10
-3.4	>10
-1.4	>10
4.4	>10
-0.3	7.3
-4.9	>10
5.3	>10
-3.7	>10
3.3	>10
0.4	>10
1.4	>10
-14.2	>10
2.6	>10
2.6	>10
2.3	>10
-11.6	>10
-6.6	>10

-5.9	>10
-4.3	>10
-0.8	>10
-1.2	>10
-4.0	>10
3.6	1.0
-18.9	>10
1.7	>10
-5.7	>10
-11.9	>10
4.1	9.7
-15.9	>10
23.1	>10
1.8	>10
-4.7	>10
-3.3	>10
-4.0	>10
13.9	>10
-4.8	>10
3.3	>10
2.8	>10
-4.2	>10
-5.6	>10
-1.0	>10
7.6	>10
0.7	>10
17.6	>10
8.3	>10
9.2	>10

-2.1	>10
12.1	>10
5.5	>10
3.0	>10
7.3	>10
3.1	8.7
3.9	>10
-8.3	>10
-2.5	>10
12.6	>10
-9.0	>10
-2.4	>10
6.2	>10
18.5	>10
21.9	>10
-25.4	>10
-5.2	>10
-9.0	>10
-2.6	>10
16.4	>10
4.3	>10
-3.2	>10
0.0	>10
6.2	>10
14.3	>10
-8.0	>10
17.6	2.2
6.1	>10
-8.5	>10

1.0	>10
10.1	>10
19.9	>10
13.9	>10
9.3	>10
36.3	>10
1.9	>10
1.2	>10
-0.7	>10
25.9	>10
-5.6	>10
0.7	>10
1.3	>10
9.7	>10
-9.1	>10
2.6	>10
-5.8	>10
-15.2	>10
3.0	>10
4.5	>10
3.6	>10
-0.9	>10
4.6	>10
-2.3	>10
1.4	>10
-13.4	>10
-1.9	>10
8.4	>10
-2.2	>10

0.7	>10
3.5	>10
-13.7	>10
-2.5	>10
-12.2	>10
2.5	>10
5.0	>10
-2.9	>10
16.4	>10
-2.5	>10
2.2	>10
5.0	>10
4.4	>10
-6.8	>10
2.4	>10
-3.9	3.9
50.8	0.093
43.4	0.13
92.5	<0.01
83.1	0.014
>85	<0.01
34.2	0.18
79.2	0.018
14.5	>10
8.9	>10
1.2	>10
15.6	0.99
16.8	1.1
10.5	2.0

5.3	>10
5.2	>10
7.2	>10
-2.2	>10
4.5	>10
-4.7	>10
-9.0	>10
-6.0	>10
0.2	>10
10.9	>10
-5.5	>10
-2.3	>10
3.4	>10
-10.1	>10
10.0	>10
-9.3	>10
-27.7	>10
-4.0	>10
7.1	>10
6.2	>10
-1.6	6.8
-43.4	>10
9.7	>10
-5.4	>10
0.8	>10
-4.2	>10
6.6	>10
4.7	>10
13.7	>10

-7.4	>10
-5.5	>10
-2.1	>10
-5.3	>10
0.1	>10
-10.5	>10
21.7	0.27
3.9	>10
0.6	>10
-0.3	>10
11.7	>10
-9.3	>10
-6.0	>10
3.5	>10
-3.1	>10
4.0	>10
40.0	>10
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-16.3	>10
-13.1	>10
2.3	>10
2.7	>10
4.9	>10
7.9	>10
-3.1	>10
-4.1	>10
4.1	>10
-18.2	>10
1.8	2.6

-1.2
6.3
-26.8
-4.2

>10
>10
>10
>10

