







## Profiling Alectinib in HeLa live cell

Kinase	Reference Sequence	Labeling Site	Alectinib 5µM
CLK3	UniRef100_FLHENQLTF	Lys2	ND
EphB2	UniRef100_FLEDDTSDP	Activation L	ND
STLK6	UniRef100_HTPTGTLVT	Lys1	ND
YSK1	UniRef100_EVVAIKIIDL	Lys1	ND
ZC3/MINK	UniRef100_TGQLAAIKV	Lys1	ND
CHK2	UniRef100_DLKPENVLL	Lys2	>99
CaMKK2	UniRef100_LAYNENDN	Lys1	>98
CHK2	UniRef100_VAIKIISK	Lys1	>98
SRPK1, SRP	UniRef100_FVAMKVVK	Lys1	>95
CaMKK2	UniRef100_DIKPSNLLV	Lys2	96.1
FER	UniRef100_TSVAVKTCK	Lys1	95.4
SRPK1	UniRef100_IHHTDIKPEN	Lys2	92.4
CaMK4	UniRef100_DLKPENLLY	Lys2	91.9
ACK	UniRef100_TVSVAVKCL	Lys1	90.4
CaMK2d	UniRef100_IPTGQEYAA	Lys1	85.1
RSK1 doma	UniRef100_DLKPENILLI	Lys2	84.7
RSK2 doma	UniRef100_LTDFGLSKE	Activation L	84.3
RSK2 doma	UniRef100_DLKPENILLI	Lys2	84.2
RSK1 doma	UniRef100_LTDFGLSKE	Activation L	83.6
RSK1 doma	UniRef100_KVTRPDSGF	Lys1	83.5
RSK1 doma	UniRef100_DLKPENILLI	Lys2	82.9
CaMK2g	UniRef100_TSTQEYAAK	Lys1	81.9
FER	UniRef100_QEDGGVYS	Activation L	80.9
RSK1 doma	UniRef100_DLKPSNILY	Lys2	78.5
MELK	UniRef100_DLKPENLLFI	Lys2	78.5
STLK5	UniRef100_YSVKVLPMI	Activation L	76.6
IRAK1	UniRef100_AIQFLHQDS	Lys2	76.5
CaMKK1	UniRef100_DIKPSNLLL	Lys2	74.3
EphB4	UniRef100_FLEENSSDP	Activation L	73.7
KHS2	UniRef100_NVNTGELA	Lys1	70.7
CaMK2a, C	UniRef100_DLKPENLLL	Lys2	68.0
RSK2 doma	UniRef100_DLKPSNILY	Lys2	66.9
STLK3	UniRef100_DLKAGNILL	Lys2	66.1
RSK2 doma	UniRef100_VLGQGSFGI	ATP Loop	65.9
LOK	UniRef100_DLKAGNVLI	Lys2	65.8
SLK	UniRef100_DLKAGNILF	Lys2	61.4
FAK	UniRef100_YMEDSTYYI	Activation L	57.0
FAK	UniRef100_CIGEGQFGI	Lys1	54.8
IRAK4	UniRef100_DIKSANILL	Lys2	53.2
SNRK	UniRef100_VAVKVIDK	Lys1	52.5
SNRK	UniRef100_DLKPENVVV	Lys2	51.6
PHKg2	UniRef100_ATGHEFAVI	Lys1	51.4
IRAK4	UniRef100_GYVNNTTV	Lys1	51.0
MAP3K2, N	UniRef100_DIKGANILR	Lys2	46.9
SGK3	UniRef100_FYAVKVLQK	Lys1	46.5

### Labeling Site Key

Lys1	Conserved Lysine 1
Lys2	Conserved Lysine 2
ATP Loop	ATP binding loop
Activation L	Activation loop
ATP	ATP site in non-canonic
Protein Kin	Other lysine within kina
Other	Labeling of residue outs

	>90% Inhibition
	75 - 90% Inhibition
	50 - 75% Inhibition
	35 - 50% Inhibition
	No change
	>100% increase in MS :
ND	Not determined

Data points inhibited >35% & not

MAP3K4	UniRef100_DIKGANIFL1 Lys2	46.5
PIP4K2C	UniRef100_VKELPTLKD ATP	44.3
OSR1	UniRef100_DVKAGNILL Lys2	43.9
KHS1	UniRef100_NVHTGELA Lys1	42.2
PIP4K2C	UniRef100_TLVIKEVSSE ATP	42.2
ILK	UniRef100_ISMADVKFS Protein Kin	41.9
ULK3	UniRef100_NISHLDLKPI Lys2	41.1
p70S6Kb	UniRef100_DLKPENIML Lys2	40.6
KSR1	UniRef100_SKNVFYDN( Activation	39.3
LOK	UniRef100_NKETGALA Lys1	38.5
BRAF	UniRef100_DLKSNIFLI Lys2	37.8
PIK3C2B	UniRef100_VIFKCGDDL ATP	37.7
GCK	UniRef100_DIKGANLLL Lys2	37.3
ULK3	UniRef100_EVVAIKCVA Lys1	34.1
RSKL1	UniRef100_VLGVIDKVL ATP	33.9
NEK3	UniRef100_SKNIFLTQN Activation	33.6
ARAF	UniRef100_DLKSNIFLI Lys2	33.4
STLK6	UniRef100_SIKASHILIS Lys2	33.1
LATS1	UniRef100_ALYATKTLR Lys1	32.6
SGK3	UniRef100_IVYRDLKPEI Lys2	31.7
PAN3	UniRef100_VMDPTKILI ATP	30.9
TAK1	UniRef100_DLKPPNLLL Lys2	30.4
LYN	UniRef100_EGAKFPIKM Activation	30.2
MAP2K7	UniRef100_DVKPSNILLI Lys2	29.9
PLK1	UniRef100_DLKLGNLFL Lys2	28.6
LATS2	UniRef100_VDTHALYAI Lys1	28.5
IKKe, TBK1	UniRef100_DIKPGNIMF Lys2	27.5
MAP2K5	UniRef100_DVKPSNML Lys2	27.4
TBK1	UniRef100_TGDLFAIKV Lys1	26.7
NEK8	UniRef100_DLKTQNILLI Lys2	26.6
PFTAIRE1	UniRef100_DLK PQNLLI Lys2	26.3
ZC1/HGK, Z	UniRef100_DIKGQNVLL Lys2	26.2
KSR1, KSR2	UniRef100_SKNVFYDN( Activation	25.6
Erk5	UniRef100_DLKPSNLLV Lys2	25.6
AMPKa1, A	UniRef100_DLKPENVLL Lys2	25.0
PFTAIRE1	UniRef100_LVALKVIR Lys1	24.5
LATS1	UniRef100_DIKPDNILID Lys2	24.4
Wnk1, Wnk	UniRef100_DLKCDNIFIT Lys2	24.4
ULK1	UniRef100_DLK PQNILL Lys2	24.2
MET	UniRef100_IHCAVKSLN Lys1	23.6
MAPKAPK3	UniRef100_QVLGLGVN ATP Loop	22.7
LYN	UniRef100_VAVKTLKPC Lys1	22.7
PKD3	UniRef100_DVAIKVIDK Lys1	21.7
Erk2	UniRef100_DLKPSNLLLI Lys2	20.2
GCK	UniRef100_DTVTSELAA Lys1	19.6
p38a	UniRef100_QELNKTIWI Protein Kin	18.6
PCTAIRE1, f	UniRef100_DLK PQNLLII Lys2	18.5
CHK1	UniRef100_DIKPENLLLI Lys2	18.4
p70S6K	UniRef100_DLKPENIML Lys2	17.7

Erk1	UniRef100_DLKPSNLLI	Lys2	17.7
MLK3	UniRef100_DLKSNILLI	Lys2	17.7
p38a	UniRef100_DLKPSNLAV	Lys2	17.4
MSK2 dom	UniRef100_DLKLENVLL	Lys2	17.2
p38d, p38g	UniRef100_DLKPGNLA	Lys2	16.9
FGFR1, FM	UniRef100_VAVKMLK	Lys1	16.6
PCTAIRE2, F	UniRef100_SKLTENLVA	Lys1	15.5
MAP2K3	UniRef100_HAQSGTIM	Lys1	15.4
NEK6, NEK7	UniRef100_DIKPANVFI	Lys2	15.1
AKT2, AKT3	UniRef100_GTFGKVILV	ATP Loop	13.8
MAP3K5	UniRef100_DIKGDNVLI	Lys2	13.5
JNK1, JNK2,	UniRef100_DLKPSNIVV	Lys2	13.4
MAP2K5	UniRef100_ILAVKVILLD	Lys1	12.8
CaMK1d	UniRef100_LFAVKCIPK	Lys1	12.3
HER2/ErbB	UniRef100_GIWIPDGEN	Lys1	11.6
AMPKa1, A	UniRef100_VAVKILNR	Lys1	11.4
CSK	UniRef100_VSDFGLTKE	Activation	10.7
PLK1	UniRef100_CFEISDADTI	Lys1	10.4
ZAK	UniRef100_WISQDKEV	Lys1	9.4
ILK	UniRef100_WQGNDIV	Lys1	8.6
PCTAIRE1	UniRef100_SKLTDNLVA	Lys1	7.7
MST1, MST	UniRef100_DIKAGNILLI	Lys2	7.2
AMPKa1	UniRef100_IGHYILGDTI	ATP Loop	7.0
AKT1	UniRef100_GTFGKVILV	ATP Loop	6.8
MLK4	UniRef100_DLKSSNILLI	Lys2	6.5
CaMK1a	UniRef100_LVAIKCIAK	Lys1	6.2
EGFR	UniRef100_LLGAEKEY	Activation	5.2
Wnk1, Wnk	UniRef100_IGDLGLATLI	Activation	5.1
PI4KB	UniRef100_VPHTQAVV	ATP	4.8
CaMK1d	UniRef100_DLKPENLLY	Lys2	4.2
Wnk1, Wnk	UniRef100_GSFKTVYK	ATP Loop	4.0
PI4KB	UniRef100_LLSVIVKCGI	ATP	3.9
SMG1	UniRef100_DTVTIHSVG	ATP	3.7
MAP2K1, N	UniRef100_KLIHLEIKPA	Lys1	3.4
PKN1	UniRef100_DLKLDNLLI	Lys2	3.0
NEK9	UniRef100_DIKTLNIFLT	Lys2	2.7
MAP2K3	UniRef100_DVKPSNVLI	Lys2	2.6
MAP2K6	UniRef100_HVPSGQIM	Lys1	2.2
CDK5	UniRef100_DLKPQNLLI	Lys2	1.8
CDK2	UniRef100_LTGEVVALK	Lys1	1.3
CCRK	UniRef100_DLKPANLLI	Lys2	1.1
MSK1 dom	UniRef100_DIKLENILLD	Lys2	0.8
MAP3K2	UniRef100_ELAVKQVQI	Lys1	0.4
CDC2	UniRef100_DLKPQNLLI	Lys2	-0.5
IKKa	UniRef100_DLKPENIVLI	Lys2	-1.6
p38b	UniRef100_QELNKTVM	Protein Kin	-1.9
NEK9	UniRef100_RTEDDSLVM	Lys1	-2.0
CDC2	UniRef100_DLKPQNLLI	Lys2	-2.7
CDK5	UniRef100_NRETHEIVA	Lys1	-3.4

LATS2	UniRef100_DIKPDNILID Lys2	-4.0
MAP3K3	UniRef100_ELASKQVQf Lys1	-4.1
MAP2K1, N	UniRef100_DVKPSNILV Lys2	-4.2
NEK1	UniRef100_DIKSQNIFL1 Lys2	-4.4
ITPK1	UniRef100_ESIFFNSHN' ATP	-4.6
NEK4	UniRef100_DLKTQNVFI Lys2	-5.8
PEK	UniRef100_DLKPSNIFF1 Lys2	-6.0
NDR1	UniRef100_DTGHVYAM Lys1	-7.1
NDR1	UniRef100_DIKPDNLLLI Lys2	-7.7
MAP2K4	UniRef100_DIKPSNILLD Lys2	-9.1
ABL, ARG	UniRef100_YSLTVAVKT Lys1	-9.3
NEK7	UniRef100_AACLLDGVF Lys1	-9.3
MAP2K1	UniRef100_IMHRDVKP' Lys2	-9.4
PIP5K3	UniRef100_GGKSGAAF' ATP	-9.6
AurA	UniRef100_FILALKVLFK Lys1	-9.6
SGK	UniRef100_HKAEEVFYA Lys1	-10.2
CDK7	UniRef100_DKNTNQIV' Lys1	-11.8
JAK1	UniRef100_QLASALSYL Protein Kin	-12.0
CK2a1	UniRef100_GGPNITLAI Protein Kin	-12.2
PKD2	UniRef100_DVAVKVIDf Lys1	-12.3
IKKe	UniRef100_SGELVAVKV Lys1	-12.7
MAP2K4	UniRef100_MVHKPSGC Lys1	-12.7
MAP3K6	UniRef100_DIKGDNVLI Lys2	-12.9
SLK	UniRef100_ETSVLAAAK Lys1	-13.4
IKKb	UniRef100_WHNQETGI Lys1	-13.7
MST1	UniRef100_ETGQIVAIK' Lys1	-13.8
PIK3C3	UniRef100_TEDGGKYP' ATP	-13.8
AurA	UniRef100_DIKPENLLLC Lys2	-14.5
MET	UniRef100_DMYDKEYY Activation	-15.1
CSK	UniRef100_VAVKCIK Lys1	-15.7
MAP3K1	UniRef100_DVKGANLLI Lys2	-16.6
BARK1	UniRef100_DLKPANILLI Lys2	-17.1
CDK2	UniRef100_DLKPQNLLII Lys2	-17.5
PKN1	UniRef100_VLLSEFRPSC Lys1	-17.8
ABL, ARG	UniRef100_LMTGDITYT Activation	-18.2
NuaK2	UniRef100_LVAIKSIR Lys1	-19.9
JAK1 domai	UniRef100_YDPEGDNT' Lys1	-20.6
CHK1	UniRef100_LSKGDGLEF Protein Kin	-21.2
NDR2	UniRef100_DIKPDNLLLI Lys2	-21.6
MAP2K6	UniRef100_DVKPSNVLI Lys2	-21.6
MASTL	UniRef100_GAFGKVYLC ATP Loop	-21.7
MAP3K15, I	UniRef100_IAIKEIPER Lys1	-21.9
SMG1	UniRef100_SYPYLFKGLI ATP	-22.0
IKKb	UniRef100_DLKPENIVLI Lys2	-22.2
NDR2	UniRef100_DTGHYIAM Lys1	-23.1
PKR	UniRef100_DLKPSNIFL\ Lys2	-24.4
EphA2	UniRef100_VLEDDPEAT Activation	-24.6
HER2/ErbB:	UniRef100_LLDIDETEYf Activation	-24.8
NLK	UniRef100_DIKPGNLLV Lys2	-24.8

CDK7	UniRef100_DLKPNLLLL	Lys2	-25.7
MST4, YSK1	UniRef100_DIKAANVLL	Lys2	-26.5
YANK3	UniRef100_DVKPDNILL	Lys2	-29.4
MARK3, M	UniRef100_EVAIKIIDK	Lys1	-31.4
PIK3C3	UniRef100_TEDGGKYP	ATP	-33.5
MARK1	UniRef100_EVAVKIIDK1	Lys1	-34.1
AurA, AurB	UniRef100_GKFGNVYL	ATP Loop	-34.2
MARK2	UniRef100_EVAVKIIDK1	Lys1	-35.0
MST2	UniRef100_ESGQVVAIK	Lys1	-36.1
MASTL	UniRef100_LYAVKVVK	Lys1	-38.1
MARK3	UniRef100_EVAIKIIDK1	Lys1	-39.4
ATM	UniRef100_QLVKGRDD	ATP	-39.7
AGK	UniRef100_ATVFLNPA	ATP	-40.0
TLK1	UniRef100_YLNEIKPPII	Lys2	-40.3
FYN, SRC, Y	UniRef100_QGAKFPIKV	Activation	-40.7
p70S6K, p70	UniRef100_GGYGKVFQ	ATP Loop	-41.1
CASK	UniRef100_ETGQQFAV	Lys1	-41.8
TLK2	UniRef100_YLNEIKPPII	Lys2	-42.0
MAST3	UniRef100_DLKPDNLLI	Lys2	-42.6
PKD1, PKD2	UniRef100_NIVHCDLKP	Lys2	-43.1
CHED	UniRef100_DIKCSNILLN	Lys2	-43.2
GCN2	UniRef100_DLKPVNIFLI	Lys2	-44.7
MARK1, M	UniRef100_EVAVKIIDK	Lys1	-45.0
ROCK1, RO	UniRef100_DVKPDNMI	Lys2	-45.5
PKR	UniRef100_IGDFGLVTS	Activation	-46.0
GPRK5	UniRef100_DLKPENILLI	Lys2	-46.7
MAST1, M	UniRef100_DLKPDNLLI	Lys2	-46.7
TLK1	UniRef100_YAAVKIHQL	Lys1	-46.7
MST3	UniRef100_DIKAANVLL	Lys2	-47.1
PIK3CB	UniRef100_VFGEDSVG	ATP	-47.5
NuaK1	UniRef100_VVAIKSIR	Lys1	-50.7
TLK2	UniRef100_YVAVKIHQL	Lys1	-52.2
GCN2	UniRef100_LDGCCYAVI	Lys1	-52.6
MST4	UniRef100_TQQVVAIKI	Lys1	-52.7
CDK11, CD	UniRef100_DLKPANILV	Lys2	-52.7
MST3	UniRef100_VVAIKIDLE	Lys1	-52.8
ANPa	UniRef100_GMLFLHNG	Lys2	-53.7
MARK2, M	UniRef100_DLKAENLLL	Lys2	-54.4
FRAP	UniRef100_IQSIAPSLQ	ATP	-54.7
PI4KA, PI4K	UniRef100_SGTPMQSA	ATP	-56.6
eEF2K	UniRef100_YIKYNSNSG	ATP	-56.8
ROCK1	UniRef100_KLQLELNQE	Protein Kin	-56.9
MPSK1	UniRef100_DLKPTNILL	Lys2	-60.2
MLKL	UniRef100_APVAIKVFK	Lys1	-64.5
PKCi	UniRef100_DLKLDNVLL	Lys2	-69.7
PKD3	UniRef100_NIVHCDLKP	Lys2	-72.1
JAK1 domai	UniRef100_IGDFGLTKA	Activation	-72.8
TAO1, TAO	UniRef100_DIKAGNILL1	Lys2	-75.6
CDK10	UniRef100_DLKVSNLLM	Lys2	-77.8

AurB	UniRef100_SHFIVALKVI Lys1	-79.5
CK1d, CK1e	UniRef100_DVKPDNFLI Lys2	-80.1
ATR	UniRef100_FYIMMCKPI ATP	-82.1
CK1a	UniRef100_DIKPDNFLM Lys2	-82.7
GSK3A	UniRef100_DIKPQNLLV Lys2	-85.7
IRE1	UniRef100_DLKPHNILIS Lys2	-89.0
PKN2	UniRef100_DLKLDNLLI Lys2	-90.1
VRK2	UniRef100_MLDVLEYIH Lys2	-94.4
PKCi	UniRef100_IYAMKVVK Lys1	-95.6
CK1g1	UniRef100_DVKPENFLI Lys2	-95.6
GSK3B	UniRef100_DIKPQNLLI Lys2	-102.4
CDK9	UniRef100_DMKAANVI Lys2	-113.0
DNAPK	UniRef100_KGGSWIQE ATP	-125.3
EGFR	UniRef100_IPVAIKELR Lys1	-133.8
PRP4	UniRef100_CNILHADIKI Lys2	-135.8
TAO2	UniRef100_DVKAGNILL Lys2	-139.7
CRK7	UniRef100_DIKCSNILLN Lys2	-140.8
CK1g2	UniRef100_DVKPENFLV Lys2	-143.8
PIP4K2A	UniRef100_AKELPTLKD ATP	-154.2
DNAPK	UniRef100_EHPFLVKGC ATP	-169.9
PRP4	UniRef100_AAGIGKDFK Protein Kin	-191.7
PRPK	UniRef100_FLSGLELVK( ATP Loop	-200.7
PITSLRE	UniRef100_DLKTSNLLI Lys2	-230.7
CLK3	UniRef100_YEIVGNLGE ATP Loop	-335.4

sal kinase (e.g. lipid kinase)

se domain, **possibly not in ATP binding site**

side of the protein kinase domain, **possibly not in ATP binding site**

signal (>2 fold increase)

: **considered significant are left uncolored**









