

Kinase ID	TAE684	WZ-4-49-8	HG-7-92-01	HG-7-27-01
<i>Screening concentration (μ M)</i>	10	10	10	10
AAK1	2.8	69		84
ABL1	7.3		0.1	
ABL1(E255K)	19		1.2	
ABL1(F317I)	0.45		0.05	
ABL1(F317L)	0.7		0.1	
ABL1(H396P)	6.4		0.7	
ABL1(M351T)	5		0.35	
ABL1(Q252H)	2.2		0.4	
ABL1(T315I)	0.1		0	
ABL1(Y253F)	4.2		1.1	
ABL1(E255K)-phosphorylated		67		0.3
ABL1(F317I)-nonphosphorylated		16		0
ABL1(F317I)-phosphorylated		12		6.3
ABL1(F317L)-nonphosphorylated		31		0
ABL1(F317L)-phosphorylated		5.2		3.6
ABL1(H396P)-nonphosphorylated		25		0
ABL1(H396P)-phosphorylated		75		0
ABL1(M351T)-phosphorylated		53		3.8
ABL1(Q252H)-nonphosphorylated		35		0
ABL1(Q252H)-phosphorylated		42		0.1
ABL1(T315I)-nonphosphorylated		45		0
ABL1(T315I)-phosphorylated		16		1.5
ABL1(Y253F)-phosphorylated		61		0.1
ABL1-nonphosphorylated		72		0
ABL1-phosphorylated		72		0
ABL2	1.4	97	0.6	0.7
ACVR1	0	60		100
ACVR1B	0.05	100		96
ACVR2A	12	100		100
ACVR2B	22	100		92
ACVRL1	1.7	100		79
ADCK3	9.2	84		100
ADCK4	0	29		93
AKT1	40	100		100
AKT2	40	100		46
AKT3	40	100		81
ALK	0.25	34	0.55	100
AMPK-alpha1	0.1	51	33	18

AMPK-alpha2	0.15	100		14
ANKK1	40	100	23	9.6
ARK5	0.75	100		98
ASK1		100		100
ASK2		99		93
AURKA	0	100		78
AURKB	1	100		100
AURKC	0.1	100		45
AXL	0.1	100		26
BIKE	2.8	47		100
BLK	0.1	100	0.45	0.1
BMPR1A	0	100		100
BMPR1B	1.2	49		77
BMPR2	40	85		100
BMX	12	100	2.4	12
BRAF	40	100	9.1	0.8
BRAF(V600E)	40	98	4	0
BRK		10	28	91
BRSK1	1.2	100		91
BRSK2	0.5	94		100
BTK	0	32		0.2
CAMK1	1.4	4.6	0	90
CAMK1D	0.1	1	6.2	100
CAMK1G	31	26	20	99
CAMK2A	1.2	34		100
CAMK2B	5.8	65		92
CAMK2D	4.1	34		100
CAMK2G	2	71		100
CAMK4	0.5	1		100
CAMKK1	0.2	46		98
CAMKK2	0.1	46	28	95
CASK		100		72
CDC2L1	40	100	0.35	78
CDC2L2	40	100	0.05	69
CDC2L5		100		46
CDK11	40	100	0.1	3.5
CDK2	24	100	11	100
CDK3	40	85	10	100
CDK4-cyclinD1		82		100
CDK4-cyclinD3		100		64
CDK5	5.2	96	19	96

CDK7	0.15	42	2.4	3
CDK8	40	100	3.9	3.6
CDK9	40	100	5.8	99
CDKL1		100		61
CDKL2	40	91	0.9	0.15
CDKL3		100		0.55
CDKL5		100		13
CHEK1	0	100		82
CHEK2	0	23		83
CIT	40	100	0.1	0.2
CLK1	0.4	0.4		29
CLK2	0	2.2		86
CLK3	3	50		100
CLK4	1.2	5.2		31
CSF1R	0	99	0	1.1
CSK	2	100	0.45	0.55
CSNK1A1		55		14
CSNK1A1L	40	78		99
CSNK1D	40	92		95
CSNK1E	40	74		100
CSNK1G1	40	71		100
CSNK1G2	40	46		96
CSNK1G3	40	50		100
CSNK2A1	27	100		89
CSNK2A2	40	94		72
CTK		100		100
DAPK1	6.4	60		85
DAPK2	12	64		66
DAPK3	4.5	83		91
DCAMKL1	0	5.2		97
DCAMKL2	0	19		100
DCAMKL3	0	100		87
DDR1	0.05	100	0.05	0
DDR2	14	93	5.1	0
DLK	0	100		18
DMPK	1.8	70		100
DMPK2	23	100		100
DRAK1	5.9	100		11
DRAK2	40	100		2
DYRK1A		63		44
DYRK1B	40	42		76

DYRK2		90		74
EGFR	0.1	4.1	5.6	12
EGFR(E746-A750del)	0	20	8.4	17
EGFR(G719C)	9.9	81	12	1.8
EGFR(G719S)	9.6	100	14	5.4
EGFR(L747-E749del, A750P)	0	10	1.5	2.9
EGFR(L747-S752del, P753S)	0.95	40	1.2	0.2
EGFR(L747-T751del,Sins)	0.6	19	1.1	4.6
EGFR(L858R)	0.1	6.6	14	3.4
EGFR(L858R,T790M)		25		65
EGFR(L861Q)	0.15	7.7	15	0.85
EGFR(S752-I759del)	1.4	49	4.6	6.2
EGFR(T790M)		0.25		9.4
EIF2AK1		100		100
EPHA1	0.15	100		10
EPHA2	27	100	3.1	5.4
EPHA3	40	100	3.4	4.4
EPHA4	30	100	5.8	16
EPHA5	21	100	11	20
EPHA6	3.1	100		51
EPHA7	0.4	100		76
EPHA8	40	100	0.1	0.35
EPHB1	0.1	100		16
EPHB2	33	100	11	5.7
EPHB3	18	100		100
EPHB4	17	99		23
EPHB6		71		1.6
ERBB2	8	37		0
ERBB3		55		100
ERBB4	1.2	7.8	28	7
ERK1	0.1	0.75		94
ERK2	0.3	0.7		100
ERK3	40	94		100
ERK4	40	100		100
ERK5	0	0.9		100
ERK8	0.25	100		100
ERN1		92		71
FAK		0.2	23	100
FER	0.05	9.1	0.5	78
FES	0.3	3.6	2.2	9.4
FGFR1	0	100	1.7	1.6

FGFR2	0.95	100	1.4	10
FGFR3	2.6	94	9.4	12
FGFR3(G697C)	0.25	97	16	23
FGFR4	0	100	0.45	34
FGR	2.8	82	1.2	4.5
FLT1	2.8	100	1.6	27
FLT3	0.05	100	0.15	3.8
FLT3(D835H)	0.05	74	1.2	2.4
FLT3(D835Y)	0.05	59	14	3.2
FLT3(ITD)	0	100	0.7	5.6
FLT3(K663Q)	0.3	100	0	0.15
FLT3(N841I)	0.45	100	0	0
FLT3(R834Q)		100		8.6
FLT4	0.05	100	0.2	26
FRK	0.2	18	0.7	7
FYN	5.6	100	1.6	4.6
GAK	0.1	6	31	51
GCN2(Kin.Dom.2,S808G)	4.5	100		0.8
GRK1		98		100
GRK4		92		80
GRK7		100		73
GSK3A	40	100		81
GSK3B	40	84		100
HCK	0.35	100	0.4	0.4
HIPK1	40	82	6.2	34
HIPK2		89		49
HIPK3		79		48
HIPK4		44		15
HPK1		54	1.6	0
HUNK		100		93
ICK		89		71
IGF1R	0	0.25		87
IKK-alpha	40	100	0.95	0
IKK-beta	40	100	24	0.95
IKK-epsilon	25	100		90
INSR	0	0.3	30	65
INSRR	0.35	0.4	23	44
IRAK1		93		50
IRAK3	0.15	100		87
IRAK4		87		77
ITK	0.1	40		86

JAK1(Kin.Dom.1)	4.2		11	
JAK1(Kin.Dom.2)	4.7			
JAK2(Kin.Dom.2)	2		11	
JAK3(Kin.Dom.2)	0		2.4	
JAK1(JH1domain-catalytic)		100		80
JAK1(JH2domain-pseudokinase)		1.3		94
JAK2(JH1domain-catalytic)		50		29
JAK3(JH1domain-catalytic)		84		3.2
JNK1	5.2	4.3	0	24
JNK2	12	22	0	0.7
JNK3	2.6	7.2	12	54
KIT	0.1	87	0	0.15
KIT(A829P)		100		33
KIT(D816H)		73		20
KIT(D816V)	3.1	74	10	25
KIT(L576P)		67		0.2
KIT(V559D)	0.1	86	0	0.05
KIT(V559D,T670I)	0.95	100	0.05	14
KIT(V559D,V654A)	7.4	100	2.7	3.7
LATS1	32	100		55
LATS2	17	88	13	36
LCK	0.1	84	0.8	0.45
LIMK1	2.2	100		15
LIMK2	6.5	51		9.6
LKB1	40	100		76
LOK	0	100	0	0
LRRK2		0.65		63
LRRK2(G2019S)		4.8		75
LTK	0	1.7	1.2	100
LYN	5	100	0.75	1
LZK		100		6.6
MAK		100		49
MAP3K1		82		75
MAP3K15		77		100
MAP3K2		28		0.4
MAP3K3	2.8	69	12	0.3
MAP3K4	13	100		2.5
MAP3K5	40			
MAP4K1	3.2			
MAP4K2	9.4	97	0.3	0.1

MAP4K3	2.5	10	18	0.9
MAP4K4	5.4	100	0	0.1
MAP4K5	0.3	58	11	0.55
MAPKAPK2	40	100		100
MAPKAPK5	40	100		80
MARK1	0	100		100
MARK2	4.6	86		100
MARK3	3.2	100		58
MARK4	0	71		100
MAST1		46		87
MEK1	3.6	100		35
MEK2	1.8	94		11
MEK3	0.8	7		100
MEK4	1.6	8.2		100
MEK5		55		0.1
MEK6	40	100		100
MELK	0.95	92		25
MERTK	0	100		31
MET	0	100		78
MET(M1250T)		100		89
MET(Y1235D)		100		93
MINK	40	71		4.3
MKK7		78		30
MKNK1	40	53		89
MKNK2	1.4	100	4.2	18
MLCK	40	100		59
MLK1	0.35	94		21
MLK2	4.6	100		30
MLK3	20	100	25	10
MRCKA	40	100		100
MRCKB	25	100		100
MST1	4.1	100		22
MST1R	3	100		85
MST2	0.25	100		100
MST3	24	82	31	30
MST4	27	100		4.6
MTOR		86		100
MUSK	0.35	100	0.2	5.2
MYLK	0.5	0.9		67
MYLK2	40	100	8.4	3.8
MYLK4		100		100

MYO3A	0.25	38	6.4	60
MYO3B	0.6	18	4.8	67
NDR1		98		79
NDR2	7.3	100	6.8	84
NEK1	40	100		91
NEK11		100		40
NEK2	2.5	100		100
NEK3		76		59
NEK4		74		28
NEK5	40	100		49
NEK6	1.8	100		100
NEK7	3.8	100		100
NEK9	3.3	100		27
NIM1		100		100
NLK	40	97	14	65
OSR1		0.05		76
p38-alpha	40	98	0	4.6
p38-beta	40	100	0	3.2
p38-delta	40	100	0.55	83
p38-gamma	40	100	0	39
PAK1	4.8	90		87
PAK2	30	82		69
PAK3	0.85	59		14
PAK4	9.6	85		100
PAK6	13	100		91
PAK7		80		100
PAK7/PAK5	2.7			
PCK1	2.2	98	11	60
PCK2	9.9	100	0.1	60
PCK3	40	100	1.8	81
PDGFRA	0.85	100	0.6	2.8
PDGFRB	0.25	69	0	0
PDPK1	28	100		100
PFCDPK1(P.falciparum)		44		0.2
PFPK5(P.falciparum)		100		55
PFTAIRE2	16	100	6	53
PFTK1	40	100	0.4	88
PHKG1	0.1	24		100
PHKG2	0	21		100
PIK3C2B	40	100		79
PIK3C2G		100		87

PIK3CA	40	99		92
PIK3CA(C420R)		100		80
PIK3CA(E542K)		100		94
PIK3CA(E545A)		100		100
PIK3CA(E545K)	40	100		100
PIK3CA(H1047L)		100		97
PIK3CA(H1047Y)		100		68
PIK3CA(I800L)		100		94
PIK3CA(M1043I)		100		73
PIK3CA(Q546K)		100		100
PIK3CB	40	17		85
PIK3CD	40	100		50
PIK3CG	40	100		100
PIK4CB		58		63
PIM1	40	100		76
PIM2	40	100		50
PIM3	40	100		55
PIP5K1A	1.3	39		86
PIP5K1C		82		65
PIP5K2B	11	100		83
PIP5K2C		100		61
PKAC-alpha	11	100	25	26
PKAC-beta	9.9	100	14	90
PKMYT1	40	69		100
PKN1	0.5	100		100
PKN2	3.2	100		100
PKNB(M.tuberculosis)		75		100
PLK1	0.1	47		100
PLK2		100		69
PLK3	0	98		83
PLK4	0	74		92
PRKCD	28	100		100
PRKCE	16	62	20	68
PRKCH	40	100	26	100
PRKCI		100		74
PRKCQ	13	100		81
PRKD1	1	73		90
PRKD2	0.05	96	29	76
PRKD3	0	36		71
PRKG1	1.3	100		100

PRKG2	7.6	100		88
PRKR	40	100		80
PRKX	28	100		100
PRP4		100		85
PTK2	0			
PTK2B	0			
PTK6	0.15			
PYK2		5	2.1	36
QSK		100		100
RAF1	40	100	7	43
RET	0	100	0	0.15
RET(M918T)	0.05	100	0	0.2
RET(V804L)	0.25	82	0.8	1.2
RET(V804M)	0.5	100	1	0.15
RIOK1	2.6	100		100
RIOK2	5.3	76		85
RIOK3	3.2	88		78
RIPK1	18	100	0	2.7
RIPK2	40	100	9.8	5.4
RIPK4	40	76		17
RIPK5		2.8		69
ROCK1		4.8		100
ROCK2	0.95	25		51
ROS1	0.45	5.8		100
RPS6KA1(Kin.Dom.1)	0.25			
RPS6KA1(Kin.Dom.2)	10			
RPS6KA2(Kin.Dom.1)	0.05			
RPS6KA2(Kin.Dom.2)	6.2			
RPS6KA3(Kin.Dom.1)	0.55			
RPS6KA4(Kin.Dom.1)	4.4	100	3.3	100
RPS6KA4(Kin.Dom.2)	40	97		43
RPS6KA5(Kin.Dom.1)	40	100	4.7	100
RPS6KA5(Kin.Dom.2)	40	100		73
RPS6KA6(Kin.Dom.1)	1.1			
RPS6KA6(Kin.Dom.2)	1.8			
RSK1(Kin.Dom.1-N-terminal)		1.8		100
RSK1(Kin.Dom.2-C-terminal)		14		13
RSK2(Kin.Dom.1-N-terminal)		2		43
RSK3(Kin.Dom.1-N-terminal)		77		69
RSK3(Kin.Dom.2-C-terminal)		7.4		43

RSK4(Kin.Dom.1-N-terminal)		23		100
RSK4(Kin.Dom.2-C-terminal)		2.1		11
S6K1		100		6.2
SBK1		57		82
SgK085	40			
SgK110	0	100		100
SGK3		92		80
SIK		100	5.3	3.6
SIK2		85		61
SLK	0.1	14	2	2.4
SNARK	0	27		81
SNF1LK	0			
SNF1LK2	7.5			
SNRK		40		84
SRC	0.2	69	0.2	0.25
SRMS	0	27	4.6	8.2
SRPK1	2.2	100		77
SRPK2	12	100		100
SRPK3	1.7	100		82
STK16	2.8	76		100
STK33	0.1	15		90
STK35	16	100	3	57
STK36	5.8	100	0.2	0.1
STK39		37		100
SYK	3.4	100	6.2	15
TAK1	2.2	59	0.15	0.75
TAOK1	0.1	33	3	7
TAOK2		66		5.7
TAOK3	0.1	36	0.15	0
TBK1		100		96
TEC	0.7	98		24
TESK1	40	100		23
TGFBR1	0.2	95		99
TGFBR2	2.7	100		54
TIE1	0	76	0.95	2.8
TIE2	0	100	0	0
TLK1	40	75		100
TLK2	40	100		100
TNIK	12	87	8.2	1.9
TNK1	0.45	2.4	0.35	13

TNK2	0	3.4		32
TNNI3K	15	100	4.8	12
TRKA	12	72	27	0.45
TRKB	8.4	59	9.6	1
TRKC	40	54	3.8	1
TRPM6		100		67
TSSK1B		92		100
TSSK1	0			
TTK	0	6.5	24	85
TXK	6.9	100	12	4
TYK2(JH1domain-catalytic)		87		29
TYK2(JH2domain-pseudokinase)		63		100
TYK2(Kin.Dom.1)	11		0	
TYK2(Kin.Dom.2)	0.45			
TYRO3	24	100		37
ULK1	0.1	1.8		83
ULK2	1.1	3.4		32
ULK3	0	100	0.1	1.6
VEGFR2	2.2	100	1.5	37
VRK2		68		62
WEE1	17	100		100
WEE2	40	100		83
YANK1		32		100
YANK2	0.2	64		100
YANK3	3.1	88		96
YES	0.1	84	1.6	1.4
YSK1	40	95		35
YSK4		100		0
ZAK	40	100	0.35	1.2
ZAP70	10	32	9.8	15

