Supporting Information

Structure-guided Inhibitor Design Expands the Scope of Analog-Sensitive Kinase Technology

Chao Zhang^{1, 4,} ¶, Michael S. Lopez^{1,} ¶, Arvin C. Dar^{1, 5}, Eva LaDow², Steven Finkbeiner², Cai-Hong Yun³, Michael J. Eck³ and Kevan M. Shokat^{1, 6}*

¹Howard Hughes Medical Institute and Department of Cellular & Molecular Pharmacology, University of California, San Francisco, California 94143, USA

²Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School, Boston, Massachusetts 02115, USA

³Gladstone Institute of Neurological Disease, San Francisco, CA 94158

⁴Current Address

Department of Chemistry, University of Southern California, California 90089, USA

⁵Current Address

Departments of Oncological Sciences and Structural and Chemical Biology, Mount Sinai School of Medicine, NY, NY 10029, USA.

⁶Department of Chemistry, University of California, Berkeley, California 94720, USA

Supplementary Figure and Tables



Supplementary Figure S1. HEK 293T cells were transfected with Venus-Pkd1-WT or Venus-Pkd1-AS2 and the cells were then treated with DMSO, 10nM PMA or 1 μ M 1NA-PP1. The cells were lysed and probed for total Pkd1 and p-S916-Pkd1.

S. Cerevisiae Kinases										
	26									
Kinase	Ref	GK	Inhib.							
Pho85	1,2	F82G	5uM 1NA-PP1							
Elm1	3	T200G	25uM1NM-PP1							
Kin28	4	L83G	6μM 1NA-PP1							
Srb10	4	Y236G	24µM 1NA-PP1							
Cla4	5	M640A & T710A	1NM-PP1							
Cdc15	6	L99G	10μM 1NM-PP1							
Cdc28	7	F88G	5μM 1NM-PP1							
Mps1	8	M516G	10µM1NM-PP1							
Ipl1	9	M181G & T244A	1NA-PP1							
Ime2	10	M146G	20µM 1NA-PP1							
Mek1	11,12	Q247G	1µM 1NA-PP1							
Ire1	13	L745G	20µM 1NM-PP1							
Prk1	14	M108G & C175A	40µM 1NA-PP1							
Apg1	15	M102A	20µM 1NA-PP1							
Cbk1	16,17	M429A	20μ 1NA-PP1							
Hog1	18,19	T100G	12μM 1NM-PP1							
Fus3	7	Q93G	5μM 1NM-PP1							
Tpk1	20-25	M164G	1µM 1NM-PP1							
Tpk2	23-25	M147G	1µM 1NM-PP1							
Tpk3	23-25	M165G	1µM 1NM-PP1							
Sch9	24,25	T492G	0.1 1NM-PP1							
Tos3	26	L135G	2.5µM 2,3-dMB-PP1							
Cdc7	27	L120A & V181A	15µM PP1							
Cdc5	28,29	L158G, <mark>C96V</mark>	СМК							
Snf1	30,31	I132G	10 μM 2NM-PP1							
Bur1	32	L149G	6µM 3MB-PP1							

	S. Pombe Kinases									
	15									
Kinase	Ref	GK	Inhib.							
Hhp1	33	M84G	1NM-PP1							
Cdc2	33	F84G	0.5µM 1NM-PP1							
Cdk9	33	T120G	10µM1NM-PP1							
Ckal	33	F117G	5µM 9Ch-ANPUR							
Crk1	33	L87G	30µM 3BrB-PP1							
Ksgl	33	L177G	5μM 1NM-PP1							
Nak1	33	M77G	40µM 3BrB-PP1							
Orb6	33	M170G	5μM 3BrB-PP1							
Pat1	33	L95A	10µM 1NM-PP1							
Plo1	33	L117G	10µM 3BrB-PP1							
Ppk37	33	M537G	30µM 1NM-PP1							
Prp4	33	F238A	30µM 3BrB-PP1							
Shk1	33	M460A	20µM 3BrB-PP1							
Sid2	33	M285G	40µM 3BrB-PP1							
Ark1	33,34	L166A S229A	5μM 1NM-PP1							

Mammalian Tyr Kinases									
18									
Kinase	Ref	GK	Conc. Used µM	Inhib.					
v-Src	35	I338G	0.25	1NA-PP1					
CSK	36	T266G	10	3IB-PP1					
Fyn	7	T339G	0.005 (in vitro)	1NA-PP1					
Lck	37	T316G	10	1NA-PP1					
TrkA	38	F592A	0.1	1NM-PP1					
TrkB	38	F616A	0.1	1NM-PP1					
TrkC	38	F617A	0.1	1NM-PP1					
Bcr-Abl	39	T316A	2	1NA-PP1					
v-ErbB	40	T210A	2	1NA-PP1					
Jak1	41	M956G	40	1NM-PP1					
Jak3	41	M902G	40	1NM-PP1					
Zap70	42	M414A C405V	10	3MB-PP1					
Syk	43	M442A M429L R428Q	6	2,3DMB-PP1					
EphB1	44	T697G	0.25	1NA-PP1					
EphB2	44	T699A	0.25	1NA-PP1					
EphB3	44	T706A	0.25	1NA-PP1					
Ret	45	V805A	0.1	1NA-PP1					
Yes	46	T346G	10	1NM-PP1					

Mammalian Ser/Thr Kinases										
21										
Kinase	Ref	GK	Conc. used in cells (µM)	Inhib.						
Cdk1	47	F80G	0.6	1NM-PP1						
Cdk2	48	F80G	10	3MB-PP1						
Cdk7	49	F91G	5	3MB-PP1						
ΡΚΑα	50	M120A	10	1NM-PP1						
ΡΚΑβ	50	M120G & K46I	10	1NM-PP1						
РКСє	51	M486A	1	1NA-PP1						
GRK2	28,52	L271G & C221V	2.5	1NA-PP1						
JNK1	53	M108G & L168A	1	1NM-PP1						
JNK2	54	M108G	10	1NM-PP1						
CaMIIKα	55,56	F89G	5	1NM-PP1						
Ire1a	57	I642G	5	1NM-PP1						
Plk1	58,59	C67V & L130G	10	3MB-PP1						
Mps1	60,61	M602A	5	3MB-PP1						
Lkb	62	M129G	10	1NM-PP1						
Akt1	63,64	M227G	2.5	3IB-PP1, PrIDZ						
Akt2	63,64	M225G	2.5	PrIDZ						
Akt3	63,64	M229G	2.5	PrIDZ						
Pdk1	65	L159G	2	Cpac-BX						
Mekk1	28	I1304G, C1238V	N.D.	N.D.						
Pkd1	This Publication	M665A	1	1NA-PP1						
Aurora B	66	L154G, H250Y	2	1NA-PP1						
NDR	67	M166A, M152L, S229A	1	1NA-PP1						

	Plant Kinases									
	3									
Kinase	Ref	GK	Inhib.							
MPK4	68	Y124G	100μM 1NA-PP1							
			10μM 1NM-PP1							
Pto	28,69	Y114A, <mark>L681I</mark>	10 µM 3MB-PP1							
LeMPK3	70	T123A	1µM Bn-PP1(in vitro)							

C. Elegans									
	1								
Kinase	Ref	GK	Inhib.						
Sad1	71	L123A	33µM 1NA-PP1						

Supplementary Table S1. Analog-sensitive kinases reported in peer-reviewed publications. Information listed includes the kinase, associated references (Ref), gatekeeper mutation (GK), suppressor mutations in red, inhibitor sensitizing mutations in green, and the concentration and identity of inhibitor used in publication (Inhib).

Legend



Conc (nM)	1000	1000	1000	1000	1000
Compound	1NAPP1	1NMPP1	3MBP1	3IB-PP1 (17)	3MSB-PP1 (18)

ABL1	Activity	Km app	26	14	16	-6	-10
ABL1 E255K	Activity	Km app	24	14	17	8	8
ABL1 G250E	Activity	Km app	18	9	13	24	19
ABL1 T315I	Activity	Km app	8	5	8	-2	-2
ABL1 Y253F	Activity	Km app	29	14	18	19	13
ABL2 (Arg)	Activity	Km app	19	16	13	5	3
ACVR1 (ALK2)	Binding					20	13
ACVR1B (ALK4)	Activity	Km app	65	-3	5	25	9

ACVR2B	Binding						
ADRBK1 (GRK2)	Activity	Km app	3	3	-1	12	9
ADRBK2 (GRK3)	Activity	Km app	6	-3	-6	3	3
AKT1 (PKB alpha)	Activity	Km app	0	2	-1	-6	-6
AKT2 (PKB beta)	Activity	Km app	-1	-2	0	6	6
AKT3 (PKB gamma)	Activity	Km app	9	1	1	2	1
ALK	Activity	Km app	1	3	-1	5	8
AMPK A1/B1/G1	Activity	Km app	2	1	-2	-18	-1
AMPK A2/B1/G1	Activity	Km app	9	4	8	10	12
AURKA (Aurora A)	Activity	Km app	6	0	4	0	-2
AURKB (Aurora B)	Activity	Km app	5	7	3	5	8
AURKC (Aurora C)	Activity	Km app	6	2	6	-10	-12
AXL	Activity	Km app	4	2	3	2	-1
BLK	Activity	Km app	38	16	15	12	11
BMPR1A (ALK3)	Binding						
ВМХ	Activity	Km app	26	52	25	41	47
BRAF	Binding					14	12
BRAF	Activity	100	29	19	26	8	11
BRAF V599E	Binding					9	2
BRAF V599E	Activity	100	17	9	32	12	11
BRSK1 (SAD1)	Activity	Km app	9	8	7	2	1
ВТК	Activity	Km app	49	61	39	19	20
CAMK1 (CaMK1)	Activity	10	-16	-20	12	-17	-21
CAMK1 (CaMK1)	Activity	100					
CAMK1D (CaMKI delta)	Activity	Km app	-2	-5	-5	-1	3

CAMK2A (CaMKII alpha)	Activity	Km app	2	1	-3	12	14
CAMK2B (CaMKII beta)	Activity	Km app	14	15	9	19	21
CAMK2D (CaMKII delta)	Activity	Km app	4	0	-2	15	15
CAMK4 (CaMKIV)	Activity	Km app	-6	10	-5	-2	-1
CAMKK1 (CAMKKA)	Binding		7/////			9	6
CAMKK2 (CaMKK beta)	Binding					1	1
CDC42 BPA (MRCKA)	Activity	Km app	-2	-2	5	6	4
CDC42 BPB (MRCKB)	Activity	Km app	9	2	3	2	2
CDK1/cyclin B	Activity	Km app	2	2	3	8	10
CDK2/cyclin A	Activity	Km app	8	9	11	2	1
CDK5/p25	Activity	Km app	2	2	3	6	7
CDK5/p35	Activity	Km app	0	-2	2	10	16
CDK7/cyclin H/MNAT1	Activity	Km app	-5	14	-15	12	8
CDK8/cyclin C	Binding					12	16
CDK9/cyclin K	Binding					4	3
CDK9/cyclin T1	Activity	Km app	3	-2	-4	4	8
CHEK1 (CHK1)	Activity	Km app	3	6	4	-6	-6
CHEK2 (CHK2)	Activity	Km app	12	7	9	-3	-3
CHUK (IKK alpha)	Activity	10	4	-20	-12		
CHUK (IKK alpha)	Activity	Km app				3	-1
CLK1	Activity	Km app	7	7	7	13	12
CLK2	Activity	Km app	10	10	14	32	38
CLK3	Activity	Km app	4	7	6	1	5
CLK4	Binding		7/////				
CSF1R (FMS)	Activity	Km	40	28	20	30	19

		app					
СЅК	Activity	Km app	28	29	17	28	27
CSNK1A1 (CK1 alpha 1)	Activity	Km app	12	1	13	18	17
CSNK1D (CK1 delta)	Activity	Km app	38	14	70	90	89
CSNK1E (CK1 epsilon)	Activity	Km app	91	96	85	100	100
CSNK1G1 (CK1 gamma 1)	Activity	Km app	0	2	-2	6	3
CSNK1G2 (CK1 gamma 2)	Activity	Km app	-2	-1	-2	14	11
CSNK1G3 (CK1 gamma 3)	Activity	Km app	0	2	2	6	4
CSNK2A1 (CK2 alpha 1)	Activity	Km app	6	7	3	5	5
CSNK2A2 (CK2 alpha 2)	Activity	Km app	4	3	1	4	3
DAPK1	Activity	Km app	-3	12	3	2	-1
DAPK3 (ZIPK)	Activity	Km app	0	2	-1	2	-3
DCAMKL2 (DCK2)	Activity	Km app	2	1	-1	7	9
DDR1	Binding						
DDR2	Binding					6	4
DMPK	Binding					6	7
DNA-PK	Activity	Km app					
DYRK1A	Activity	Km app	4	2	3	-3	-4
DYRK1B	Activity	Km app	12	11	10	-10	-9
DYRK3	Activity	Km app	0	2	0	3	3
DYRK4	Activity	Km app	2	2	1	1	2
EEF2K	Activity	Km app	2	3	1	20	18
EGFR (ErbB1)	Activity	Km app	28	24	36	56	65
EGFR (ErbB1) L858R	Activity	Km app	40	29	34	48	27

EGFR (ErbB1) L861Q	Activity	Km app	34	17	30	34	20
EGFR (ErbB1) T790M	Activity	Km app	48	38	44	66	81
EGFR (ErbB1) T790M L858R	Activity	Km app	65	53	56	66	55
EPHA1	Activity	Km app	93	83	71	48	47
EPHA2	Activity	Km app	75	43	44	22	13
EPHA3	Binding						
EPHA3	Activity	Km app	45	18	21	12	4
EPHA4	Activity	Km app	83	43	46	36	25
EPHA5	Activity	Km app	86	56	61	40	21
EPHA7	Binding					6	8
EPHA8	Activity	Km app	67	51	40	39	24
EPHB1	Activity	Km app	63	44	43	34	27
EPHB2	Activity	Km app	78	58	58	38	25
EPHB3	Activity	Km app	48	35	52	31	14
EPHB4	Activity	Km app	73	62	63	45	25
ERBB2 (HER2)	Activity	Km app	9	19	25	21	32
ERBB4 (HER4)	Activity	Km app	10	38	35	63	85
FER	Activity	Km app	29	24	15	12	15
FES (FPS)	Activity	Km app	20	13	4	15	15
FGFR1	Activity	Km app	13	8	17	7	7
FGFR2	Activity	Km app	16	10	12	11	9
FGFR3	Activity	Km app	1	4	-3	14	15
FGFR3 K650E	Activity	Km app	5	2	4	25	22

FGFR4	Activity	Km app	14	-2	5	20	15
FGR	Activity	Km app	71	42	55	52	33
FLT1 (VEGFR1)	Activity	Km app	5	5	4	10	9
FLT3	Activity	Km app	13	12	20	28	35
FLT3 D835Y	Activity	Km app	16	14	-2	1	13
FLT4 (VEGFR3)	Activity	Km app	9	8	20	21	17
FRAP1 (mTOR)	Activity	Km app	0	0	-3	6	-5
FRK (PTK5)	Activity	Km app	89	47	74	60	33
FYN	Activity	Km app	45	37	32	37	39
GRK4	Activity	Km app	-10	-9	-12	-3	-5
GRK5	Activity	Km app	-4	1	-5	4	3
GRK6	Activity	Km app	-5	-4	-6	1	-1
GRK7	Activity	Km app	-4	-6	-6	-2	-3
GSG2 (Haspin)	Activity	Km app				28	49
GSK3A (GSK3 alpha)	Activity	Km app	5	6	2	9	11
GSK3B (GSK3 beta)	Activity	Km app	4	5	7	-3	-3
нск	Activity	Km app	59	31	31	17	11
HIPK1 (Myak)	Activity	Km app	1	0	-1	5	5
HIPK2	Activity	Km app				4	5
HIPK3 (YAK1)	Activity	Km app					
HIPK4	Activity	Km app	9	9	8	12	10
IGF1R	Activity	Km app	4	7	2	11	10
IKBKB (IKK beta)	Activity	Km	4	5	4	5	6

		арр					
IKBKE (IKK epsilon)	Activity	Km app	1	-2	-4	-1	-6
INSR	Activity	Km app	7	6	4	4	4
INSRR (IRR)	Activity	Km app	-6	-5	-6	24	21
IRAK1	Activity	Km app				7	11
IRAK4	Activity	Km app	5	2	4	-3	-2
ітк	Activity	Km app	6	4	3	6	4
JAK1	Activity	Km app	0	-6	-3	5	3
JAK2	Activity	Km app	-2	-1	4	-8	-10
JAK2 JH1 JH2	Activity	Km app	3	4	4	-3	-2
JAK2 JH1 JH2 V617F	Activity	Km app	-6	-5	-7	7	6
JAK3	Activity	Km app	-6	-6	-5	3	8
KDR (VEGFR2)	Activity	Km app	24	21	41	25	21
кіт	Activity	Km app	38	24	21	-4	-5
KIT T670I	Activity	Km app	7	5	10	-2	-1
KIT V654A	Binding					3	6
LCK	Activity	Km app	52	35	36	24	20
LIMK1	Binding					0	-5
LIMK2	Binding					-3	1
LRRK2	Activity	Km app	13	-7	5	-13	3
LRRK2 G2019S	Activity	Km app	19	10	1	4	8
LTK (TYK1)	Activity	Km app	-2	1	-2	0	1
LYN A	Activity	Km app	82	55	59	49	39
LYN B	Activity	Km app	81	55	55	43	33

MAP2K1 (MEK1)	Binding					22	38
MAP2K1 (MEK1)	Activity	100	5	15	9	1	4
MAP2K1 (MEK1) S218D S222D	Binding					18	28
MAP2K2 (MEK2)	Binding					12	21
MAP2K2 (MEK2)	Activity	100	14	8	8	-4	0
MAP2K3 (MEK3)	Binding					16	14
MAP2K6 (MKK6)	Binding					7	10
MAP2K6 (MKK6)	Activity	100	4	4	3	-11	-16
MAP2K6 (MKK6) S207E T211E	Binding					17	9
MAP3K10 (MLK2)	Binding					11	13
MAP3K11 (MLK3)	Binding					0	1
MAP3K14 (NIK)	Binding					-1	-2
MAP3K2 (MEKK2)	Binding					31	15
MAP3K3 (MEKK3)	Binding					62	35
MAP3K5 (ASK1)	Binding					6	5
MAP3K7/MAP3K7IP1 (TAK1-TAB1)	Binding					2	4
MAP3K8 (COT)	Activity	100	14	10	12	26	22
MAP3K9 (MLK1)	Activity	Km app	1	3	0	-6	0
MAP4K2 (GCK)	Activity	Km app	7	2	4	4	6
MAP4K4 (HGK)	Activity	Km app	92	56	28	8	1
MAP4K5 (KHS1)	Activity	Km app	69	31	38	26	30
MAPK1 (ERK2)	Activity	Km app	4	6	3	2	0
MAPK10 (JNK3)	Binding					21	18
MAPK10 (JNK3)	Activity	100	4	5	6	-6	-7
MAPK11 (p38 beta)	Activity	Km app	12	15	16	14	15
MAPK12 (p38 gamma)	Activity	Km app	1	2	2	6	8
MAPK13 (p38 delta)	Activity	Km app	2	3	4	11	11
MAPK14 (p38 alpha)	Activity	100	15	26	24	7	12

MAPK14 (p38 alpha) Direct	Activity	Km app				-1	-1
MAPK3 (ERK1)	Activity	Km app	6	4	5	9	7
MAPK8 (JNK1)	Binding		77777			1	3
MAPK8 (JNK1)	Activity	100	-7	-11	-5	-7	3
MAPK9 (JNK2)	Binding					15	18
MAPK9 (JNK2)	Activity	100	0	6	4	9	3
МАРКАРК2	Activity	Km app	-2	0	-1	-6	-6
МАРКАРК3	Activity	Km app	2	-1	3	-1	-1
MAPKAPK5 (PRAK)	Activity	Km app	-2	0	0	1	1
MARK1 (MARK)	Activity	Km app	6	4	3	10	10
MARK2	Activity	Km app	11	8	7	14	13
MARK3	Activity	Km app				1	-12
MARK4	Activity	Km app				-2	-1
MATK (HYL)	Activity	Km app	-2	0	-3	13	10
MELK	Activity	Km app	21	17	16	16	16
MERTK (cMER)	Activity	Km app	5	5	7	21	19
MET (cMet)	Activity	Km app	-2	-1	0	3	3
MET M1250T	Activity	Km app	-2	-5	-4	3	3
MINK1	Activity	Km app	89	52	37	40	28
MKNK1 (MNK1)	Activity	Km app					
MKNK2 (MNK2)	Binding						
MLCK (MLCK2)	Binding					6	4
MST1R (RON)	Activity	Km app	2	2	3	-2	-2
MST4	Activity	Km app	25	13	13	1	3
MUSK	Activity	Km	-3	2	-2	28	29

		app					
MYLK (MLCK)	Binding					2	1
MYLK2 (skMLCK)	Activity	Km app	0	5	-2	-3	3
NEK1	Activity	Km app	9	8	10	-8	1
NEK2	Activity	Km app	8	6	9	5	3
NEK4	Activity	Km app	3	3	3	8	5
NEK6	Activity	Km app	8	3	0	3	3
NEK7	Activity	Km app	3	4	-1	24	25
NEK9	Activity	Km app	-6	-5	-8	2	2
NLK	Binding		7/////			34	20
NTRK1 (TRKA)	Activity	Km app	4	10	16	40	33
NTRK2 (TRKB)	Activity	Km app	6	10	46	63	62
NTRK3 (TRKC)	Activity	Km app	20	12	34	66	66
NUAK1 (ARK5)	Activity	Km app				3	10
PAK1	Activity	Km app				20	26
PAK2 (PAK65)	Activity	Km app	-3	11	9	6	5
PAK3	Activity	Km app	7	7	3	11	3
PAK4	Activity	Km app	16	1	17	2	9
PAK6	Activity	Km app	14	10	11	14	14
PAK7 (KIAA1264)	Activity	Km app	8	8	4	10	13
PASK	Activity	Km app	2	3	3	-2	2
PDGFRA (PDGFR alpha)	Activity	Km app	7	3	10	11	9
PDGFRA D842V	Activity	Km app	0	-4	3	3	3
PDGFRA T674I	Activity	Km	-1	5	-2	20	21

		app					
PDGFRA V561D	Activity	Km app	20	15	29	22	15
PDGFRB (PDGFR beta)	Activity	Km app	12	-4	9	-2	-2
PDK1	Activity	100	3	0	2	18	18
PDK1 Direct	Activity	Km app				-1	1
PHKG1	Activity	Km app	6	7	5	5	5
PHKG2	Activity	Km app	-1	0	2	-9	-5
PI4KA (PI4K alpha)	Activity	10				1	-7
PI4KB (PI4K beta)	Activity	Km app				17	14
PIK3C2A (PI3K-C2 alpha)	Activity	Km app				-1	4
PIK3C2B (PI3K-C2 beta)	Activity	10				11	-1
PIK3C2B (PI3K-C2 beta)	Activity	100					
PIK3C3 (hVPS34)	Activity	Km app				-13	-9
		••					
PIK3CA/PIK3R1 (p110 alpha/p85 alpha)	Activity	Km app	0	-35	-29	-14	-4
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha)	Activity Activity	Km app Km app	0	-35	-29	-14 13	-4 8
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha) PIK3CG (p110 gamma)	Activity Activity Activity	Km app Km app Km app	0 12	-35	-29 10	-14 13 10	-4 8 -9
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha) PIK3CG (p110 gamma) PIM1	Activity Activity Activity Activity	Km app Km app Km app Km app	0 12 -4	-35 4 -2	-29 10 0	-14 13 10 1	-4 8 -9 6
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha) PIK3CG (p110 gamma) PIM1 PIM2	Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km	0 12 -4 1	-35 4 -2 0	-29 10 0 2	-14 13 10 1 -8	-4 8 -9 6 -7
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha) PIK3CG (p110 gamma) PIM1 PIM2 PKN1 (PRK1)	Activity Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km app	0 12 -4 1 8	-35 4 -2 0 12	-29 10 0 2 5	-14 13 10 1 -8 -7	-4 8 -9 6 -7 5
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha) PIK3CG (p110 gamma) PIM1 PIM2 PKN1 (PRK1) PLK1	Activity Activity Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km app Km app	0 12 -4 1 8 5	-35 4 -2 0 12 4	-29 10 0 2 5 6	-14 13 10 1 -8 -7 1	-4 8 -9 6 -7 5 -6
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha) PIK3CG (p110 gamma) PIM1 PIM2 PKN1 (PRK1) PLK1 PLK2	Activity Activity Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km app Km app Km	0 12 -4 1 8 5 7	-35 4 -2 0 12 4 13	-29 10 0 2 5 6 9	-14 13 10 1 -8 -7 1 -3	-4 8 -9 6 -7 5 -6 4
PIK3CA/PIK3R1 (p110 alpha/p85 alpha) PIK3CD/PIK3R1 (p110 delta/p85 alpha) PIK3CG (p110 gamma) PIM1 PIM2 PKN1 (PRK1) PLK1 PLK2 PLK3	Activity Activity Activity Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km app Km app Km app Km	0 12 -4 1 8 5 7 16	-35 4 -2 0 12 4 13 5	-29 10 0 2 5 6 9 8	-14 13 10 1 -8 -7 1 -3 -3	-4 8 -9 6 -7 5 -6 4 -7
PiK3CA/PiK3R1 (p110 alpha/p85 alpha) PiK3CD/PiK3R1 (p110 delta/p85 alpha) PiK3CG (p110 gamma) PiM1 PiM2 PKN1 (PRK1) PLK1 PLK2 PLK3 PRKACA (PKA)	Activity Activity Activity Activity Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km app Km app Km app Km app Km app	0 12 -4 1 8 5 7 16 12	-35 4 -2 0 12 4 13 5 41	-29 10 0 2 5 6 9 8 8 38	-14 13 10 1 -8 -7 1 -3 -6 56	-4 8 -9 6 -7 5 -6 4 -7 53

PRKCB1 (PKC beta I)	Activity	Km app	5	6	0	7	7
PRKCB2 (PKC beta II)	Activity	Km app	-4	1	-5	9	7
PRKCD (PKC delta)	Activity	Km app	4	6	9	-1	3
PRKCE (PKC epsilon)	Activity	Km app	-2	2	1	26	30
PRKCG (PKC gamma)	Activity	Km app	4	-2	2	3	6
PRKCH (PKC eta)	Activity	Km app	2	3	4	8	15
PRKCI (PKC iota)	Activity	Km app	11	7	7	13	15
PRKCN (PKD3)	Activity	Km app	69	65	72	77	100
PRKCQ (PKC theta)	Activity	Km app	22	15	17	5	12
PRKCZ (PKC zeta)	Activity	Km app	1	5	-4	1	3
PRKD1 (PKC mu)	Activity	Km app	59	56	65	79	102
PRKD2 (PKD2)	Activity	Km app	75	83	83	85	101
PRKD2 (PKD2) PRKG1	Activity Activity	Km app Km app	75 -1	83 0	83 0	85 7	101 6
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2)	Activity Activity Activity	Km app Km app Km app	75 -1 4	83 0 6	83 0 4	85 7 -4	101 6 0
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2) PRKX	Activity Activity Activity Activity	Km app Km app Km app Km app	75 -1 4 4	83 0 6 4	83 0 4 5	85 7 -4 1	101 6 0 2
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2) PRKX PTK2 (FAK)	Activity Activity Activity Activity Activity	Km app Km app Km app Km app	75 -1 4 4 20	83 0 6 4 11	83 0 4 5 10	85 7 -4 1 12	101 6 0 2 10
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2) PRKX PTK2 (FAK) PTK2B (FAK2)	Activity Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km	75 -1 4 4 20 5	83 0 6 4 11	83 0 4 5 10 -2	85 7 -4 1 12 4	101 6 0 2 10 1
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2) PRKX PTK2 (FAK) PTK2B (FAK2) PTK6 (Brk)	Activity Activity Activity Activity Activity Activity	Km app Km app Km app Km app Km app Km	75 -1 4 4 20 5	83 0 6 4 11 1 1 55	83 0 4 5 10 -2 87	85 7 -4 1 12 4 9	101 6 0 2 10 1 1
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2) PRKX PTK2 (FAK) PTK2B (FAK2) PTK6 (Brk) RAF1 (cRAF) Y340D Y341D	Activity Activity Activity Activity Activity Activity Activity Binding	Km app Km app Km app Km app Km app	75 -1 4 4 20 5 98	83 0 6 4 11 1 55	83 0 4 5 10 -2 87	85 7 -4 1 12 4 9 28	101 6 0 2 10 1 11 22
PRKD2 (PKD2)PRKG1PRKG2 (PKG2)PRKXPTK2 (FAK)PTK2B (FAK2)PTK6 (Brk)RAF1 (cRAF) Y340D Y341DRAF1 (cRAF) Y340D Y341D	Activity Activity Activity Activity Activity Activity Binding Activity	Km app Km app Km app Km app Km app	75 -1 4 4 20 5 98	83 0 6 4 11 1 55	 83 0 4 5 10 -2 87 10 	85 7 -4 1 12 4 9 28 38	101 6 0 2 10 1 1 11 22 22
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2) PRKX PRKX PTK2 (FAK) PTK2 (FAK) PTK6 (Brk) RAF1 (cRAF) Y340D Y341D RAF1 (cRAF) Y340D Y341D	Activity Activity Activity Activity Activity Activity Binding Activity	Km app Km app Km app Km app Km app 100 Km app	75 -1 4 20 5 98 14	83 0 6 4 11 1 55 1 65	 83 0 4 5 10 -2 87 87 10 67 	85 7 -4 1 12 4 9 28 38 38	 101 6 0 2 10 1 11 22 22 46
PRKD2 (PKD2) PRKG1 PRKG2 (PKG2) PRKG2 (PKG2) PRKX PTK2 (FAK) PTK2 (FAK2) PTK6 (Brk) RAF1 (cRAF) Y340D Y341D RAF1 (cRAF) Y340D Y341D RET	Activity Activity Activity Activity Activity Activity Binding Activity Activity	Km app Km app Km app Km app 100 Km app Km app	75 -1 4 20 5 98 14 79 11	83 0 6 4 11 55 1 65 15	 83 0 4 5 10 -2 87 40 67 10 	85 7 -4 1 12 4 9 28 38 38 38 47	 101 6 0 2 10 1 11 22 22 46 2

RIPK2	Binding					75	57
ROCK1	Activity	Km app	-1	6	0	5	3
ROCK2	Activity	Km app	3	3	-2	-13	-9
ROS1	Activity	Km app	6	5	1	11	13
RPS6KA1 (RSK1)	Activity	Km app	1	0	4	4	1
RPS6KA2 (RSK3)	Activity	Km app	4	3	3	-5	-6
RPS6KA3 (RSK2)	Activity	Km app	3	4	2	4	2
RPS6KA4 (MSK2)	Activity	Km app	25	12	11	3	8
RPS6KA5 (MSK1)	Activity	Km app	5	2	6	8	10
RPS6KA6 (RSK4)	Activity	Km app	1	5	6	2	7
RPS6KB1 (p70S6K)	Activity	Km app	4	4	4	0	-1
SGK (SGK1)	Activity	Km app	0	2	1	-9	-8
SGK2	Activity	Km app	6	5	0	-2	-7
SGKL (SGK3)	Activity	Km app	-1	-1	-1	-5	-3
SLK	Binding					5	5
SNF1LK2	Activity	Km app				9	7
SPHK1	Activity	Km app				-4	-2
SPHK2	Activity	10				-36	2
SPHK2	Activity	100					
SRC	Activity	Km app	65	27	36	16	7
SRC N1	Activity	Km app	61	21	28	23	13
SRMS (Srm)	Activity	Km app	22	7	11	22	21
SRPK1	Activity	Km app	5	5	4	6	4
SRPK2	Activity	Km app	0	0	3	-3	1

STK16 (PKL12)	Binding					11	3
STK17A (DRAK1)	Binding					10	6
STK22B (TSSK2)	Activity	Km app	2	4	2	6	4
STK22D (TSSK1)	Activity	Km app	5	4	5	0	1
STK23 (MSSK1)	Activity	Km app	6	5	6	4	3
STK24 (MST3)	Activity	Km app	22	9	9	0	4
STK25 (YSK1)	Activity	Km app	11	1	5	-2	-3
STK3 (MST2)	Activity	Km app	13	4	3	5	8
STK33	Binding					3	1
STK4 (MST1)	Activity	Km app	14	8	5	12	18
SYK	Activity	Km app	7	10	4	-10	-3
ΤΑΟΚ2 (ΤΑΟ1)	Activity	Km app	3	-1	1	-4	2
TAOK3 (JIK)	Binding					9	6
ТВК1	Activity	Km app	7	8	5	9	9
TEC	Binding					3	3
TEK (Tie2)	Activity	Km app	-2	0	-4	-5	3
TGFBR1 (ALK5)	Binding						
TNK2 (ACK)	Binding					29	31
ттк	Binding					0	0
тхк	Activity	Km app					
ТҮК2	Activity	Km app	0	0	1	10	10
TYRO3 (RSE)	Activity	Km app	9	3	2	24	21
WEE1	Binding		7777777			-3	-1
WNK2	Binding					-3	-4
YES1	Activity	Km app	54	42	52	42	39
ΖΑΚ	Binding					1	1

ZAP70 Activity	Km app	-7	-5	-6	14	10
----------------	-----------	----	----	----	----	----

Supplementary Table S2. Kinase inhibitor profiling data was provided by SelectScreen® Kinase Profiling Services from Life Technologies. 1 μ M of each inhibitor (1NA-PP1, 1NM-PP1, 3MB-PP1, 17 and 18) was screened against a panel of several hundred protein kinases in duplicate. The average % activity inhibited is listed for each compound against each kinase.

Data Collection

Structure	Src-1NA	Src-1NM	Src-3MB
Space Group	P212121	P1	P1
Unit Cell Dimensions	$\begin{array}{l} a = 50.96, \\ b = 72.72, \\ c = 171.98, \\ \alpha = 90, \\ \beta = 90, \gamma \\ = 90 \end{array}$	$\begin{array}{c} a{=}42.3 \ , \\ b{=}62.7 \ , \\ c{=}74.3 \ , \\ \alpha{=}100.4 \ , \\ \beta{=}91.0 \ , \\ \gamma{=}90.1 \end{array}$	$\begin{array}{l} a{=}42.0 \ , \\ b{=}55.8 \ , \\ c{=}63.0 \ , \\ \alpha{=}90.0 \ , \\ \beta{=}90.1 \ , \\ \gamma{=}88.9 \end{array}$
Number protein molceules/assymetric unit	1	2	2
X-ray Source	CHESS A1	ALS 5.0.1	ALS 5.0.1
Resolution (Å)	2.3	2.84	2.4
Total Reflections	101969	16738	21085
Unique Reflections	28882	16738	18807
Completeness (%)	98.7 (99.6 in 2.38-2.3 shell)	94.7	95.1
Mo	del Refineme	nt	
Resolution (Å)	25-2.3	32.93-2.84	33.87-2.41
Rwork/Rfree	0.213/0.25	0.230/0.287	0.232/0.281
Rmsd from ideality in bond length (Å)	0.018	0.008	0.014
Rmsd from ideality in Angles (°)	1.38	1.12	1.4
Number of Protein Atoms In Model	3607	3874	7685
Number of Drug atoms In Model	24	50	43

Number of waters	278	37	46
Favored/Allowed/Outliers in the Ramachandran Plot (%)	97.3/2.7/0	95.6/4.4/0	96.6/3.4/0

Supplemental Table S3. Data collection and refinement statistics for X-ray crystal structures of Src(T338G) in complex with PP inhibitors.

Supplementary Experimental

Compound Characterization

1-*tert*-**Butyl-3**-(**2**,**3**-dimethylphenyl)-1*H*-pyrazolo[**3**,**4**-*d*]pyrimidin-4-ylamine (1). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.81 (s, 9H), 2.17 (s, 3H), 2.33 (s, 3H), 5.25 (br s, 2H), 7.20 (m, 3H), 8.31 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 16.5, 20.6, 29.3, 60.3, 100.9, 125.9, 127.9, 130.7, 132.6, 136.2, 138.2, 142.0, 153.7, 154.6, 157.8; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅ 295.17970, found 295.17968.

3-Benzyl-1*tert***-butyl-1***H***-pyrazolo**[**3**,**4***-d*]**pyrimidin-4-ylamine (2).** White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 4.29 (s, 2H), 4.89 (br s, 2H), 7.20 (d, J = 7 Hz, 2H), 7.25 (t, J = 7 Hz, 1H), 7.32 (t, J = 7 Hz, 2H), 8.23 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.2, 35.2, 59.9, 100.7, 127.3, 128.4, 129.4, 138.2, 140.9, 154.5, 154.7, 157.6; HRMS (EI) molecular ion calculated for C₁₆H₁₉N₅ 281.16405, found 281.16410.

1-*tert*-Butyl-3-phenethyl-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (3). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.74 (s, 9H), 3.11 (t, 2H), 3.22 (t, 2H), 6.32 (s, 2H), 7.17 (d, 2H), 7.25 (m, 3H), 8.17 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.2, 31.3, 34.8, 61.1, 99.7, 126.7, 128.5, 128.8, 140.6, 143.2, 147.8, 152.3, 155.1; HRMS (EI) molecular ion calculated for $C_{17}H_{21}N_5$ 295.17970, found 295.17888.

1-*tert*-**Butyl-3**-cyclopentylmethyl-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (4). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.28 (m, 2H), 1.53 (m, 2H), 1.65 (m, 2H), 1.71 (m, 2H), 1.73 (s, 9H), 2.28 (m, 1H), 2.86 (d, J = 8 Hz, 2H), 5.69 (br s, 2H), 8.25 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 25.0, 29.2, 32.4, 35.2, 39.7, 59.7, 100.5, 142.1, 153.0, 154.0, 158.0; HRMS (EI) molecular ion calculated for C₁₅H₂₃N₅ 273.19535, found 273.19565.

1-*tert*-Butyl-3-(1-phenethyl)-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (5). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.71 (d, J = 7 Hz, 3H), 1.79 (s, 9H), 4.38 (q, J = 7 Hz, 1H), 5.06 (br s, 2H), 7.19 (d, J = 7 Hz, 2H), 7.22 (m, 1H), 7.30 (t, J = 7 Hz, 2H), 8.16 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 21.0, 29.1, 40.1, 60.0, 100.0, 127.2, 127.4, 129.3, 144.5, 145.2, 153.6, 154.5, 157.3; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅ 295.17970, found 295.18043.

1-*tert*-**Butyl-3**-(2-methylbenzyl)-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (6). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.77 (s, 9H), 2.30 (s, 3H), 4.25 (s, 2H), 5.09 (br s, 2H), 6.98 (d, J = 8 Hz, 1H), 7.14 (m, 3H), 8.20 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 19.8, 29.1, 33.1, 59.9, 100.9, 126.7, 127.3, 128.3, 130.8, 136.1, 136.8, 140.6, 154.3, 154.5, 157.8; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅ 295.17970, found 295.17922.

1-*tert*-**Butyl-3**-(**2**-**chlorobenzyl**)-1*H*-**pyrazolo**[**3**,**4**-*d*]**pyrimidin**-**4**-**ylamine** (**7**). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.78 (s, 9H), 4.38 (s, 2H), 5.41 (br s, 2H), 7.00 (dd, J₁ = 7 Hz, J₂ = 2 Hz, 1H), 7.15 (m, 2H), 7.39 (dd, J₁ = 8 Hz, J₂ = 2 Hz, 1H), 8.22 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.1, 31.9, 60.0, 100.7, 127.4, 128.4, 129.6, 130.1, 133.3, 135.6, 139.4, 154.4, 154.5, 157.7; HRMS (EI) molecular ion calculated for C₁₆H₁₈N₅Cl 315.12507, found 315.12449.

1*-tert***-Butyl-3-(2-methoxybenzyl)-1***H***-pyrazolo**[**3**,**4***-d*]**pyrimidin-4-ylamine (8).** White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.77 (s, 9H), 3.89 (s, 3H), 4.25 (s, 2H), 5.77 (br s, 2H), 6.89 (m, 2H), 7.18 (m, 2H), 8.20 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 27.4, 29.2,

55.5, 59.8, 100.4, 110.8, 121.5, 126.5, 128.0, 130.6, 141.1, 154.3, 154.3, 155.7, 158.0; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅O 311.17461, found 311.17545.

1-*tert*-**Butyl-3**-(**3**-methylbenzyl)-1*H*-pyrazolo[**3**,**4**-*d*]pyrimidin-**4**-ylamine (**3**MB). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 2.29 (s, 3H), 4.24 (s, 2H), 4.95 (br s, 2H), 6.99 (d, J = 7 Hz, 1H), 7.00 (s, 1H), 7.06 (d, J = 8 Hz, 1H), 7.20 (t, J = 8 Hz, 1H), 8.22 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 21.4, 29.2, 35.1, 59.9, 100.7, 125.4, 128.1, 129.1, 138.1, 139.0, 141.1, 154.4, 154.7, 157.7; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅ 295.17970, found 295.17981.

1-(*tert*-**butyl**)-**3-**(**3-**chlorobenzyl)-1*H*-**pyrazolo**[**3**,**4**-*d*]**pyrimidin-4-amine (10).** White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 3.79 (s, 3H), 3.25 (s, 2H), 7.06 (d, 1H), 7.19 (m, 3H), 8.26 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.2, 34.8, 60.1, 77.2, 100.6, 126.4, 127.5, 128.5, 130.4, 135.1, 139.8, 140.2, 154.6, 157.5; HRMS (EI) molecular ion calculated for C₁₆H₁₉N₅³⁵Cl 316.1324, found 316.1314.

3-(3-Methoxybenzyl)-1*-tert*-butyl-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (11). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 3.74 (s, 3H), 4.25 (s, 2H), 4.89 (s, 2H), 6.72 (s, 1H), 6.79 (m, 2H), 7.22 (s, 1H), 8.24 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.4, 35.4, 55.4, 60.1, 100.9, 112.5, 114.7, 120.8, 130.5, 140.1, 141.0, 154.7, 154.9, 157.8, 160.5; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅O 311.1824, found 311.1835.

1-*tert*-Butyl-3-(4-methylbenzyl)-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (12). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 2.30 (s, 3H), 4.24 (s, 2H), 4.94 (br s, 2H), 7.08 (d, J = 8 Hz, 2H), 7.11 (d, J = 8 Hz, 2H), 8.21 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 21.0, 29.2, 34.8, 59.9, 100.6, 128.3, 130.0, 135.1, 136.9, 141.3, 154.5, 154.7, 157.7; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅ 295.17970, found 295.18068.

1-*tert*-**Butyl-3**-(**4**-**chlorobenzyl**)-1*H*-**pyrazolo**[**3**,**4**-*d*]**pyrimidin**-**4**-**ylamine** (**13**). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.77 (s, 9H), 4.25 (s, 2H), 5.16 (br s, 2H), 7.11 (d, J = 8 Hz, 2H), 7.27 (d, J = 8 Hz, 2H), 8.22 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.1, 34.5, 60.0, 100.6, 129.3, 129.6, 133.1, 136.6, 140.1, 154.5, 154.6, 157.6; HRMS (EI) molecular ion calculated for C₁₆H₁₈N₅Cl 315.12507, found 315.12545.

1-tert-Butyl-3-(4-methoxybenzyl)-1H-pyrazolo[3,4-d]pyrimidin-4-ylamine (14).

White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.78 (s, 9H), 3.76 (s, 3H), 4.22 (s, 2H), 4.91 (br s, 2H), 6.84 (d, J = 9 Hz, 2H), 7.11 (d, J = 9 Hz, 2H), 8.22 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.2, 34.3, 55.2, 59.9, 100.6, 114.6, 129.4, 130.0, 141.4, 154.5, 154.7, 157.6, 158.7; HRMS (EI) molecular ion calculated for C₁₇H₂₁N₅O 311.17461, found 311.17454.

3-(3-Trifluoromethylbenzyl)-1-tert-butyl-1H-pyrazolo[3,4-d]pyrimidin-4-ylamine

(15). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.789 (s, 9H), 4.349 (s, 2H), 4.917 (s, 2H), 7.360 (d, 1H), 7.430 (t, 1H), 7.506 (s, 1H), 7.516 (d, 1H), 8.262 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.144, 34.961, 60.172, 77.205, 100.601, 124.108, 125.042, 129.640, 131.265, 131.652, 139.124, 139.474, 154.646, 154.699, 157.387; ESI-HRMS [MH]⁺ calculated for C₁₇H₁₈ F₃N₅ 350.1587, found 350.1581.

3-(3-Bromobenzyl)-1-*tert*-**butyl-1***H*-**pyrazolo**[**3**,**4**-*d*]**pyrimidin-4-ylamine (16).** White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 4.28 (s, 2H), 5.73 (s, 2H), 7.13 (d, 1H), 7.20 (t, 1H), 7.36 (s, 1H), 7.40 (d, 1H), 8.21 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.2, 34.7, 60.8, 100.1, 123.5, 126.9, 130.7, 130.8, 131.4, 140.0, 141.0, 151.5, 153.8, 156.0; HRMS (EI) molecular ion calculated for C₁₆H₁₈BrN₅ 359.07456, found 359.07423.

3-(3-Iodobenzyl)-1*tert*-butyl-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (17). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 4.24 (s, 2H), 4.90 (s, 2H), 7.04 (t, 1H), 7.13 (d, 1H), 7.58 (s, 1H), 7.60 (d, 1H), 8.26 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.4, 34.9, 60.3, 95.4, 100.8, 127.8, 131.0, 136.6, 137.5, 140.0, 140.8, 154.8, 154.9, 157.7; HRMS (EI) molecular ion calculated for C₁₆H₁₈IN₅ 407.0685, found 407.0705.

3-(3-Methylthiolbenzyl)-1*-tert*-butyl-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (18). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.791 (s, 9H), 2.414 (s, 3H), 4.250 (s, 2H), 4.886 (s, 2H), 6.937 (d, 1H), 7.097 (s, 1H), 7.123 (d, 1H), 7.225 (t, 1H), 8.243 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 15.567, 29.190, 35.105, 60.013, 77.205, 100.685, 124.924, 125.076, 126.283, 129.602, 138.942, 139.853, 140.468, 154.585, 154.767, 157.585; HRMS (EI) [MH]⁺ calculated for C₁₇H₂₁N₅S 328.1577, found 328.1583.

27

1-*tert*-**Butyl-3**-(**2**,**3**-dimethylbenzyl)-1*H*-pyrazolo[**3**,**4**-*d*]pyrimidin-4-ylamine (19). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.78 (s, 9H), 2.19 (s, 3H), 2.28 (s, 3H), 4.28 (s, 2H), 4.86 (s, 2H), 6.88 (d, 1H), 7.02 (t, 1H), 7.08 (d, 1H), 8.23 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 15.3, 20.6, 29.2, 34.0, 59.9, 100.9, 126.1, 126.3, 129.2, 135.7, 136.0, 137.8, 141.1, 154.4, 154.6, 157.7; HRMS (EI) molecular ion calculated for C₁₈H₂₃N₅ 309.19535, found 309.19515.

1-*tert*-**Butyl-3**-(**3**,**4**-dimethylbenzyl)-1*H*-pyrazolo[**3**,**4**-*d*]pyrimidin-4-ylamine (**20**). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 2.20 (s, 3H), 2.21 (s, 3H), 4.21 (s, 2H), 5.45 (s, 2H), 6.91 (d, 1H), 6.96 (s, 1H), 7.07 (d, 1H), 8.18 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 19.4, 19.8, 29.2, 34.8, 60.4, 100.2, 125.7, 129.6, 130.6, 135.0, 136.0, 137.9, 142.4, 151.5, 153.9, 156.4; HRMS (EI) molecular ion calculated for $C_{18}H_{23}N_5$ 309.19535, found 309.19542.

1-*tert*-Butyl-3-(2,5-dimethylbenzyl)-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (21). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 2.20 (s, 3H), 2.25 (s, 3H), 4.22 (s, 2H), 4.94 (s, 2H), 6.81 (s, 1H), 6.98 (d, 1H), 7.08 (d, 1H), 8.23 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 19.3, 21.0, 29.2, 33.1, 59.9, 100.9, 128.1, 129.1, 130.9, 133.6, 135.9, 136.3, 140.9, 154.3, 154.6, 157.7; HRMS (EI) molecular ion calculated for C₁₈H₂₃N₅ 309.19535, found 309.19386.

1-*tert*-Butyl-3-(3,5-dimethylbenzyl)-1*H*-pyrazolo[3,4-*d*]pyrimidin-4-ylamine (22). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.80 (s, 9H), 2.25 (s, 6H), 4.20 (s, 2H), 5.00 (s, 2H), 6.80 (s, 2H), 6.88 (s, 1H), 8.22 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 21.3, 29.2, 35.1, 59.9, 100.7, 126.2, 129.0, 138.0, 138.9, 141.3, 154.4, 154.7, 157.7; HRMS (EI) molecular ion calculated for C₁₈H₂₃N₅ 309.19535, found 309.19439.

1-*tert*-**Butyl-3**-(**3**,**4**-dichlorobenzyl)-1*H*-pyrazolo[**3**,**4**-*d*]pyrimidin-4-ylamine (23). White powder; ¹H NMR (CDCl₃, 400 MHz) δ 1.79 (s, 9H), 4.24 (s, 2H), 5.07 (s, 2H), 7.02 (dd, 1H), 7.29 (d, 1H), 7.37 (d, 1H), 8.26 (s, 1H); ¹³C NMR (CDCl₃, 100 MHz) δ 29.1, 34.3, 60.2, 100.6, 127.6, 130.2, 131.0, 131.4, 133.2, 138.4, 139.2, 154.6, 154.7, 157.5; HRMS (EI) molecular ion calculated for C₁₆H₁₇N₅Cl₂ 349.08610, found 349.08621.

Kinase inhibition assays in vitro

Fyn Kinase. Glutathione S-transferase (GST) fused Fyn proteins were expressed in *E. coli* and purified on glutathione beads as described previously³⁵. In the Fyn kinase assay, various concentrations of inhibitor were incubated with 50 mM Tris (pH 8.0), 10 mM MgCl₂, 1.6 mM glutathione, 1 mg/mL BSA, 0.1 mg/mL peptide substrate (IYGEFKKK), 3.3% DMSO, and 11 nM (2 μ Ci) [γ -³²P]ATP (6000 Ci/mmol, NEN), and Fyn kinase in a total volume of 30 μ L for 30 min. Reaction mixtures (27 μ L) were spotted onto a phosphocellulose disk, and washed with 0.5% H₃PO₄. The transfer of ³²P was measured by standard scintillation counting. IC₅₀ values were defined to be the concentration of inhibitor at which the radioactivity counts remaining on the phosphocellulose disk were inhibited by 50%.

Src Kinase. 6xHis-tagged Src (257-533) was expressed in BL-21 *ecoli* cells as previously described⁷². Kinase reaction was carried out as described for Fyn kinase above.

CK1δ and CK1ε. Casein Kinase 1δ (catalog # PV3665) and Casein Kinase 1ε (catalog # PV3500) were purchased from Life Technologies and assayed under the following conditions: 50mM TRIS (pH 8.0), 10mM MgCl₂, 0.4 mg/mL casein, 2.5 mM DTT, 2% DMSO, 5nM kinase, 100μM ATP, 0.1 mg/mL BSA, 1μCi ³²P-ATP and various concentrations of inhibitors.

PKD1 and PKD2. PKD1 (catalog # PV3791) and PKD2 (catalog # PV3758) were purchased from Life Technologies and assayed under the following conditions: 50 mM TRIS (pH 8.0), 10 mM MgCl₂, 2mM DTT, 2% DTT, 0.1 mg/mL BSA, 100 μ M ATP, 3 μ Ci ³²P-ATP, 7 nM kinase and various concentrations of inhibitors.

RET and ACK. RET (catalog # PV3819) and ACK (catalog # PV4807) were purchase from Life Technologies and assayed under the following conditions: 50 mM TRIS (pH 8.0), 10 mM MgCl₂, 2 mM DTT, 0.1 mg/mL BSA, 2% DMSO, 200 μ M Abltide, 10 nM kinase, 100 μ M ATP, 1 μ Ci ³²P-ATP and variable concentrations of inhibitors. **EPHA1 and PTK6.** EPHA1 (catalog # 3841) and PTK6 (catalog # 3291) were purchased from Life Technologies and assayed under the following conditions: 50 mM TRIS (pH 8.0), 10 mM MgCl₂, 2.5 mM DTT, 0.1 mg/mL BSA, 2% DMSO, 0.2 mg/mL poly[Glu, Tyr] 4:1, 2 nM kinase, 100 μM ATP, 1μCi ³²P-ATP and variable concentrations of inhibitors.

- Carroll, A. S., Bishop, A. C., DeRisi, J. L., Shokat, K. M. & O'Shea, E. K. Chemical inhibition of the Pho85 cyclin-dependent kinase reveals a role in the environmental stress response. *Proceedings of the National Academy of Sciences* 98, 12578–12583 (2001).
- Kung, C., Kenski, D. M., Krukenberg, K., Madhani, H. D. & Shokat, K. M. Selective kinase inhibition by exploiting differential pathway sensitivity. *Chem. Biol.* 13, 399–407 (2006).
- 3. Sreenivasan, A., Bishop, A. C., Shokat, K. M. & Kellogg, D. R. Specific inhibition of Elm1 kinase activity reveals functions required for early G1 events. *Mol. Cell. Biol.* **23**, 6327–6337 (2003).
- 4. Liu, Y. *et al.* Two cyclin-dependent kinases promote RNA polymerase II transcription and formation of the scaffold complex. *Mol. Cell. Biol.* **24**, 1721–1735 (2004).
- 5. Drubin, D. G., Weiss, E. L., Bishop, A. C. & Shokat, K. M. Chemical genetic analysis of the budding-yeast p21-activated kinase Cla4p. *Nat. Cell Biol.* **2**, 677–685 (2000).
- 6. D'Aquino, K. E. *et al.* The protein kinase Kin4 inhibits exit from mitosis in response to spindle position defects. *Mol. Cell* **19**, 223–234 (2005).
- 7. Shokat, K. M. *et al.* A chemical switch for inhibitor-sensitive alleles of any protein kinase. *Nature* **407**, 395–401 (2000).
- 8. Jones, M. H., Huneycutt, B. J., Pearson, C. G. & Zhang, C. Chemical genetics reveals a role for Mps1 kinase in kinetochore attachment during mitosis. *Current* ... (2005).
- 9. Pinsky, B. A., Kung, C., Shokat, K. M. & Biggins, S. The Ipl1-Aurora protein kinase activates the spindle checkpoint by creating unattached kinetochores. *Nat. Cell Biol.* **8**, 78–83 (2006).
- Benjamin, K. R., Zhang, C., Shokat, K. M. & Herskowitz, I. Control of landmark events in meiosis by the CDK Cdc28 and the meiosis-specific kinase Ime2. *Genes Dev.* 17, 1524–1539 (2003).
- 11. Niu, H. *et al.* Regulation of meiotic recombination via Mek1-mediated Rad54 phosphorylation. *Mol. Cell* **36**, 393–404 (2009).
- 12. Wan, L., de los Santos, T., Zhang, C., Shokat, K. & Hollingsworth, N. M. Mek1 kinase activity functions downstream of RED1 in the regulation of meiotic double

strand break repair in budding yeast. (2004).

- 13. Papa, F. R., Zhang, C., Shokat, K. & Walter, P. Bypassing a kinase activity with an ATP-competitive drug. *Science* **302**, 1533–1537 (2003).
- 14. Sekiya-Kawasaki, M. *et al.* Dynamic phosphoregulation of the cortical actin cytoskeleton and endocytic machinery revealed by real-time chemical genetic analysis. *J. Cell Biol.* **162**, 765–772 (2003).
- Abeliovich, H., Zhang, C., Dunn, W. A., Shokat, K. M. & Klionsky, D. J. Chemical genetic analysis of Apg1 reveals a non-kinase role in the induction of autophagy. *Mol. Biol. Cell* 14, 477–490 (2003).
- 16. Weiss, E. L. The Saccharomyces cerevisiae Mob2p-Cbk1p kinase complex promotes polarized growth and acts with the mitotic exit network to facilitate daughter cell-specific localization of Ace2p transcription factor. *J. Cell Biol.* **158**, 885–900 (2002).
- 17. Kurischko, C. *et al.* The yeast LATS/Ndr kinase Cbk1 regulates growth via Golgidependent glycosylation and secretion. *Mol. Biol. Cell* **19**, 5559–5578 (2008).
- 18. Westfall, P. J. & Thorner, J. Analysis of mitogen-activated protein kinase signaling specificity in response to hyperosmotic stress: use of an analog-sensitive HOG1 allele. *Eukaryotic Cell* **5**, 1215–1228 (2006).
- 19. Klein, M. *et al.* Design, synthesis and characterization of a highly effective inhibitor for analog-sensitive (as) kinases. *PLoS ONE* **6**, e20789 (2011).
- 20. Ramachandran, V. & Herman, P. K. Antagonistic interactions between the cAMPdependent protein kinase and Tor signaling pathways modulate cell growth in Saccharomyces cerevisiae. *Genetics* **187**, 441–454 (2011).
- 21. Ramachandran, V., Shah, K. H. & Herman, P. K. The cAMP-dependent protein kinase signaling pathway is a key regulator of P body foci formation. *Mol. Cell* **43**, 973–981 (2011).
- 22. Stephan, J. S., Yeh, Y.-Y., Ramachandran, V., Deminoff, S. J. & Herman, P. K. The Tor and cAMP-dependent protein kinase signaling pathways coordinately control autophagy in Saccharomyces cerevisiae. *Autophagy* **6**, 294–295 (2010).
- Budhwar, R., Lu, A. & Hirsch, J. P. Nutrient control of yeast PKA activity involves opposing effects on phosphorylation of the Bcy1 regulatory subunit. *Mol. Biol. Cell* 21, 3749–3758 (2010).
- 24. Yorimitsu, T., Zaman, S., Broach, J. R. & Klionsky, D. J. Protein kinase A and Sch9 cooperatively regulate induction of autophagy in Saccharomyces cerevisiae. *Mol. Biol. Cell* **18**, 4180–4189 (2007).
- 25. Lee, J., Moir, R. D. & Willis, I. M. Regulation of RNA polymerase III transcription involves SCH9-dependent and SCH9-independent branches of the target of rapamycin (TOR) pathway. *J. Biol. Chem.* **284**, 12604–12608 (2009).
- 26. Rubenstein, E. M. *et al.* Access denied: Snf1 activation loop phosphorylation is controlled by availability of the phosphorylated threonine 210 to the PP1 phosphatase. *J. Biol. Chem.* **283**, 222–230 (2008).
- Wan, L., Zhang, C., Shokat, K. M. & Hollingsworth, N. M. Chemical inactivation of cdc7 kinase in budding yeast results in a reversible arrest that allows efficient cell synchronization prior to meiotic recombination. *Genetics* 174, 1767–1774 (2006).
- 28. Zhang, C. et al. A second-site suppressor strategy for chemical genetic analysis of

diverse protein kinases. Nat. Methods 2, 435-441 (2005).

- 29. Snead, J. L. *et al.* A coupled chemical-genetic and bioinformatic approach to Pololike kinase pathway exploration. *Chem. Biol.* **14**, 1261–1272 (2007).
- Young, E. T., Zhang, C., Shokat, K. M., Parua, P. K. & Braun, K. A. The AMPactivated protein kinase Snf1 regulates transcription factor binding, RNA polymerase II activity, and mRNA stability of glucose-repressed genes in Saccharomyces cerevisiae. J. Biol. Chem. 287, 29021–29034 (2012).
- 31. Shirra, M. K. *et al.* A chemical genomics study identifies Snf1 as a repressor of GCN4 translation. *J. Biol. Chem.* **283**, 35889–35898 (2008).
- 32. Liu, Y. *et al.* Phosphorylation of the transcription elongation factor Spt5 by yeast Bur1 kinase stimulates recruitment of the PAF complex. *Mol. Cell. Biol.* **29**, 4852– 4863 (2009).
- 33. Cipak, L. *et al.* Generation of a set of conditional analog-sensitive alleles of essential protein kinases in the fission yeast Schizosaccharomyces pombe. *Cell Cycle* **10**, 3527–3532 (2011).
- 34. Hauf, S. *et al.* Aurora controls sister kinetochore mono-orientation and homolog bi-orientation in meiosis-I. *EMBO J* **26**, 4475–4486 (2007).
- 35. Bishop, A. C., Kung, C., Shah, K. & Witucki, L. Generation of monospecific nanomolar tyrosine kinase inhibitors via a chemical genetic approach. *Journal of the* ... (1999).
- 36. Schoenborn, J. R., Tan, Y. X., Zhang, C., Shokat, K. M. & Weiss, A. Feedback circuits monitor and adjust basal Lck-dependent events in T cell receptor signaling. *Sci Signal* **4**, ra59 (2011).
- 37. Denzel, A. *et al.* Cutting Edge: A Chemical Genetic System for the Analysis of Kinases Regulating T Cell Development. *The Journal of* ... (2003).
- 38. Chen, X. *et al.* A chemical-genetic approach to studying neurotrophin signaling. *Neuron* **46**, 13–21 (2005).
- 39. Wong, S. Sole BCR-ABL inhibition is insufficient to eliminate all myeloproliferative disorder cell populations. *Proceedings of the National Academy of Sciences* **101**, 17456–17461 (2004).
- Fan, Q.-W., Zhang, C., Shokat, K. M. & Weiss, W. A. Chemical genetic blockade of transformation reveals dependence on aberrant oncogenic signaling. *Curr. Biol.* 12, 1386–1394 (2002).
- Haan, C., Rolvering, C., Raulf, F., Kapp, M. & Drückes, P. Jak1 has a dominant role over Jak3 in signal transduction through γc-containing cytokine receptors. *Chem. Biol.* (2011).
- 42. Au-Yeung, B. B. *et al.* A genetically selective inhibitor demonstrates a function for the kinase Zap70 in regulatory T cells independent of its catalytic activity. *Nat. Immunol.* **11**, 1085–1092 (2010).
- Miller, A. L., Zhang, C., Shokat, K. M. & Lowell, C. A. Generation of a novel system for studying spleen tyrosine kinase function in macrophages and B cells. J. *Immunol.* 182, 988–998 (2009).
- 44. Soskis, M. J. *et al.* A chemical genetic approach reveals distinct EphB signaling mechanisms during brain development. *Nat. Neurosci.* **15**, 1645–1654 (2012).
- 45. Savitt, J. *et al.* The in vivo response of stem and other undifferentiated spermatogonia to the reversible inhibition of glial cell line-derived neurotrophic

factor signaling in the adult. *Stem Cells* **30**, 732–740 (2012).

- 46. Su, T. *et al.* A kinase cascade leading to Rab11-FIP5 controls transcytosis of the polymeric immunoglobulin receptor. *Nat. Cell Biol.* **12**, 1143–1153 (2010).
- 47. Gravells, P., Tomita, K., Booth, A., Poznansky, J. & Porter, A. C. G. Chemical genetic analyses of quantitative changes in Cdk1 activity during the human cell cycle. *Human Molecular Genetics* (2013). doi:10.1093/hmg/ddt133
- 48. Merrick, K. A. *et al.* Switching Cdk2 On or Off with Small Molecules to Reveal Requirements in Human Cell Proliferation. *Mol. Cell* **42**, 624–636 (2011).
- 49. Merrick, K. A. *et al.* Distinct activation pathways confer cyclin-binding specificity on Cdk1 and Cdk2 in human cells. *Mol. Cell* **32**, 662–672 (2008).
- 50. Niswender, C. M. *et al.* Protein engineering of protein kinase A catalytic subunits results in the acquisition of novel inhibitor sensitivity. *J. Biol. Chem.* **277**, 28916–28922 (2002).
- 51. Qi, Z.-H. *et al.* Protein kinase C epsilon regulates gamma-aminobutyrate type A receptor sensitivity to ethanol and benzodiazepines through phosphorylation of gamma2 subunits. *J. Biol. Chem.* **282**, 33052–33063 (2007).
- 52. Kenski, D. M., Zhang, C., Zastrow, von, M. & Shokat, K. M. Chemical genetic engineering of G protein-coupled receptor kinase 2. *J. Biol. Chem.* **280**, 35051–35061 (2005).
- 53. Das, M. *et al.* Suppression of p53-dependent senescence by the JNK signal transduction pathway. *Proc. Natl. Acad. Sci. U.S.A.* **104**, 15759–15764 (2007).
- 54. Jaeschke, A. *et al.* JNK2 is a positive regulator of the cJun transcription factor. *Mol. Cell* **23**, 899–911 (2006).
- Wei, F. *et al.* Forebrain overexpression of CaMKII abolishes cingulate long term depression and reduces mechanical allodynia and thermal hyperalgesia. *Mol Pain* 2, 21 (2006).
- 56. Wang, H. *et al.* Inducible protein knockout reveals temporal requirement of CaMKII reactivation for memory consolidation in the brain. *Proc. Natl. Acad. Sci.* U.S.A. **100**, 4287–4292 (2003).
- 57. Lin, J. H. *et al.* IRE1 signaling affects cell fate during the unfolded protein response. *Science* **318**, 944–949 (2007).
- 58. Burkard, M. E. *et al.* Chemical genetics reveals the requirement for Polo-like kinase 1 activity in positioning RhoA and triggering cytokinesis in human cells. *Proc. Natl. Acad. Sci. U.S.A.* **104**, 4383–4388 (2007).
- 59. Burkard, M. E. *et al.* Plk1 self-organization and priming phosphorylation of HsCYK-4 at the spindle midzone regulate the onset of division in human cells. *PLoS Biol.* **7**, e1000111 (2009).
- 60. Maciejowski, J. *et al.* Mps1 directs the assembly of Cdc20 inhibitory complexes during interphase and mitosis to control M phase timing and spindle checkpoint signaling. *J. Cell Biol.* **190**, 89–100 (2010).
- 61. Sliedrecht, T., Zhang, C., Shokat, K. M. & Kops, G. J. P. L. Chemical genetic inhibition of Mps1 in stable human cell lines reveals novel aspects of Mps1 function in mitosis. *PLoS ONE* **5**, e10251 (2010).
- 62. Lo, B. *et al.* Lkb1 regulates organogenesis and early oncogenesis along AMPK-dependent and -independent pathways. *The Journal of cell* ... (2012).
- 63. Okuzumi, T. et al. Inhibitor hijacking of Akt activation. Nat. Chem. Biol. 5, 484-

493 (2009).

- 64. Okuzumi, T. *et al.* Synthesis and evaluation of indazole based analog sensitive Akt inhibitors. *Mol Biosyst* **6**, 1389–1402 (2010).
- 65. Tamgüney, T., Zhang, C., Fiedler, D., Shokat, K. & Stokoe, D. Analysis of 3phosphoinositide-dependent kinase-1 signaling and function in ES cells. *Experimental Cell Research* **314**, 2299–2312 (2008).
- 66. Hengeveld, R. C. C. *et al.* Development of a Chemical Genetic Approach for Human Aurora B Kinase Identifies Novel Substrates of the Chromosomal Passenger Complex. *Mol. Cell Proteomics* **11**, 47–59 (2012).
- 67. Ultanir, S. K. *et al.* Chemical genetic identification of NDR1/2 kinase substrates AAK1 and Rabin8 Uncovers their roles in dendrite arborization and spine development. *Neuron* **73**, 1127–1142 (2012).
- 68. Brodersen, P. *et al.* Arabidopsis MAP kinase 4 regulates salicylic acid- and jasmonic acid/ethylene-dependent responses via EDS1 and PAD4. *Plant J.* **47**, 532–546 (2006).
- 69. Salomon, D. *et al.* Bypassing kinase activity of the tomato Pto resistance protein with small molecule ligands. *J. Biol. Chem.* **284**, 15289–15298 (2009).
- Salomon, D., Zhang, C., Shokat, K. M. & Sessa, G. Sensitizing plant protein kinases to specific inhibition by ATP-competitive molecules. *Methods Mol. Biol.* 779, 185–197 (2011).
- 71. Kim, J. S. M. *et al.* A chemical-genetic strategy reveals distinct temporal requirements for SAD-1 kinase in neuronal polarization and synapse formation. *Neural Dev* **3**, 23 (2008).
- 72. Seeliger, M. A. *et al.* High yield bacterial expression of active c-Abl and c-Src tyrosine kinases. *Protein Sci.* **14**, 3135–3139 (2005).