

## Supplementary Note

### Test compounds do not need to be linked or immobilized

A key feature of our approach is that any molecule can be tested for binding against the entire set of assays described here without the need to be linked, labeled, immobilized or chemically modified in any way (**Fig. 1a**). This provides a critical advantage over alternative strategies that require chemical modification and immobilization of each small molecule of interest to identify proteins from cell lysates that bind to the immobilized inhibitor. While it is often claimed that these alternative strategies can identify 'all' kinases that bind the compound, in practice they are generally limited to non-membrane proteins that are abundant in the particular lysates employed. Furthermore, alternative affinity-based methods require difficult protein identification steps, negatives can not be interpreted, and they do not directly yield quantitative information.

### Allosteric interactions can be detected

To compete with the interaction between immobilized SB202190 and tagged p38, compounds must either bind directly at the ATP site, or allosterically alter the ATP site conformation. Both modes of action are observed. SB203580 is known to bind directly in the ATP site (Tong, L. *et al. Nat. Struct. Biol.* **4**, p.311; Fitzgerald C. E. *et al. Nat. Struct. Biol.* **10**, p.764), while BIRB-796 binds predominantly in an adjacent position and indirectly affects the conformation of the ATP site (Pargellis, C. *et al. Nat. Struct. Biol.* **9**, p.268). Both compounds are potent inhibitors of p38 (Lee, J. C. *et al. Nature* **372**, p.739; Pargellis, C. *et al. Nat. Struct. Biol.* **9**, p.268). Furthermore, binding of BIRB-796 requires a specific conformational change in the p38 protein that results in very slow association kinetics, while SB203580 binding does not require this conformational change and has a rapid on-rate (Pargellis, C. *et al. Nat. Struct. Biol.* **9**, p.268). The competition binding assay

yielded accurate binding constants for both compounds (**Supplementary Table 2**), and the distinct binding kinetics for BIRB-796 and SB203580 are also observed in the competition assays (data not shown). The detailed behavior of the kinase is therefore faithfully recapitulated by the tagged p38 protein.

### **Binding constants for test compounds are independent of the affinity of the immobilized ligand for the kinase**

The binding assays are performed under conditions in which binding constants measured for the interaction between kinases and test compounds are independent of the affinity of the immobilized ligand for the kinase (see 'Methods'). We have experimentally verified this by measuring binding constants for several kinase/test compound combinations using two different immobilized ligands (for some of the kinases, more than one immobilized ligand can be used to build an assay). Test compound binding affinity did not change with the immobilized ligand used, confirming that the results are independent of the affinity of the immobilized ligand for the kinase (data not shown).

### **Assay validation**

#### *Comparison between binding and enzymatic activity assays*

To assess the correlation between binding measured with the competition assays and inhibition observed in enzyme activity assays, we determined  $K_d$ 's for 41 known interactions with reported  $IC_{50}$ 's or  $K_i$ 's below 1  $\mu$ M and compared them to published results (**Supplementary Table 2**). A good correlation between binding constants measured here and published  $IC_{50}$  values was observed. Every known interaction tested was detected with the binding assay, and for 28 of the 41 interactions the binding constants were within five-fold of published values. For ten of the thirteen comparisons where there was a greater

than five-fold difference, the binding constant measured here was lower than the published value. This is not unexpected because  $IC_{50}$ 's derived from activity assays depend on the concentration of ATP and enzyme, and can be significantly higher than the intrinsic binding constant. We also tested 77 compound/kinase combinations for which no evidence of inhibition was reported in the literature and observed no evidence of binding for 74 of these 77. For the remaining three interactions we observed relatively weak binding ( $K_d > 1 \mu M$ ).

One of the few apparent discrepancies between our results and published data is the interaction of ZD-6474 with EGFR (measured  $K_d$  of 17 nM, compared to a published  $IC_{50}$  of 500 nM) and VEGFR2 (measured  $K_d$  of 470 nM, compared to a published  $IC_{50}$  of 40 nM). To resolve this apparent discrepancy, we tested ZD-6474 in enzyme activity assays for inhibition of EGFR and VEGFR2 (Upstate Biotechnology). The new enzyme activity results showed  $IC_{50}$ 's of 50 nM for EGFR and 300 nM for VEGFR2, in good agreement with our binding results. We do not know the reason for the discrepancy between the new enzyme activity results and the published activity data, but believe the observed differences highlight the often large variability in conventional kinase enzyme activity assays performed under different conditions by different groups at different times. The consistent agreement between the results obtained in our binding assays and the results from activity assays indicates that ATP-site competitive binding in our system is a reliable predictor of inhibitory activity, and can be used to discover new interactions and assess the specificity of kinase inhibitors.

While *in vitro* enzyme activity assays generally require a pre-activated form of the kinase, our tagged kinases are produced in bacteria at very low concentrations and are therefore in an unphosphorylated, unactivated form. It is important to note that several clinical kinase inhibitors bind to the unactivated form of their target, and that this state is at

least as relevant as the activated form for therapeutic intervention (Schindler, T. *et al. Science* **289**, p. 1938; Pargellis, C. *et al. Nat. Struct. Biol.* **9**, p. 268; Wan, P. T. *et al. Cell* **116**, p. 855; Manley, P. W. *et al. Biochim. Biophys. Acta* **1697**, p. 17). Because results from our binding assays agree very well with results from activity assays, many compounds appear to bind with similar affinities to phosphorylated and unphosphorylated kinases.

#### *Validation of results in cell-based assays*

To determine whether novel interactions identified in the binding assays also occur in intact cells, we tested ZD-6474 and BAY-43-9006 in a cell-based assay for FLT3 inhibition. ZD-6474 and BAY-43-9006 were not previously known as inhibitors of FLT3, but were identified in our assays to bind FLT3 with  $K_d$ 's of 1.2  $\mu$ M and 20 nM, respectively. As controls, Vatalanib and Gleevec, two compounds that do not bind FLT3 in our assays, were also tested. We found that the  $IC_{50}$ 's for ZD-6474 (0.76  $\mu$ M) and BAY-43-9006 (1.2 nM) determined in cell-based assays were consistent with the binding constants measured in the binding assays, and there was no evidence for inhibition by Vatalanib or Gleevec (**Supplementary Table 3**).

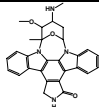
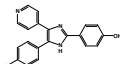
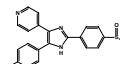
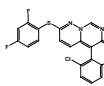
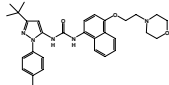

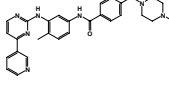
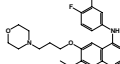
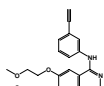
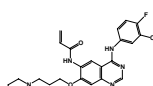
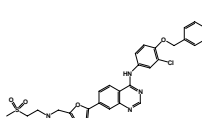
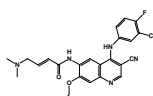
To further determine the ability of our assays to identify novel inhibitors of important kinases, we screened a library of small molecules against FLT3 and EGFR. We found compounds that bind tightly to FLT3, and compounds that bind tightly to EGFR (**Supplementary Table 3**). These were then tested in cell-based assays for FLT3 and EGFR inhibition. For every compound tested, the  $IC_{50}$  in the cell-based assay was consistent with the  $K_d$  measured in the binding assay (**Supplementary Table 3**) (the compounds will be described in more detail elsewhere). While the results of cell-based assays can be influenced by additional factors that may obscure the fundamental ATP site dependent binding events, such as the ability of compounds to get into cells, these results

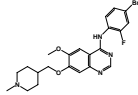
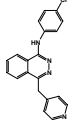
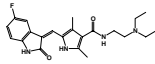
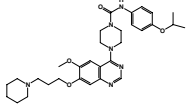
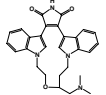
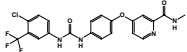
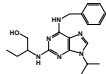
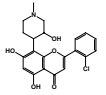
confirm that binding observed in the *in vitro* competition assays is generally predictive of kinase inhibition in intact cells.

#### *Methods for cell-based assays*

To determine the ability of compounds to inhibit FLT3 in intact cells we used the well-characterized FLT3-dependent human cell line MV4,11, which contains an activating mutation in FLT3 (Yee, K. W. *et al. Blood* **100**, p. 2941). MV4,11 cells were plated at 10,000 cells per well in DMEM (10% FBS), and cell proliferation was measured after 72 hours in the presence of varying inhibitor concentrations using a standard MTS assay (Promega). To assess inhibition of EGFR kinase activity in intact cells, we measured inhibition of EGFR autophosphorylation in A431 cells (Trinks, U. *et al. J. Med. Chem.* **37**, p. 1015). A431 cells were plated at 40,000 cells per well in DMEM (0.5% FBS), and phosphorylation of Tyr-1173 was measured by ELISA (Biosource) after stimulation with EGF (5 minutes, 5 ng/mL) in the presence of varying inhibitor concentrations.

**Supplementary Table 1. Kinase inhibitors for which specificity profiles were determined<sup>a</sup>.**

Inhibitor	Primary Targets	Status	Chemical Structure
Staurosporine	Pan-inhibitor	Research compound	
SB202190	p38 $\alpha$	Research compound	
SB203580	p38 $\alpha$	Research compound	
VX-745	p38 $\alpha$	Phase II (discont.)	
BIRB-796	p38 $\alpha$	Phase III	
SP600125	JNK	Research compound	
Gleevec	ABL, KIT, PDGFR	Approved	
Iressa	EGFR	Approved	
Tarceva	EGFR	Approved	
CI-1033	EGFR subfamily	Phase II	
GW-2016	EGFR, ERBB2, ERBB4	Phase III	
EKB-569	EGFR, ERBB2	Phase II	

Inhibitor	Primary Targets	Status	Chemical Structure
ZD-6474	VEGFR2, EGFR	Phase II	
Vatalanib/PTK-787	VEGFR2	Phase III	
SU11248	VEGFR2, PDGFR, FLT3, KIT	Phase III	
MLN-518	FLT3	Phase I	
LY-333531	PKC $\beta$	Phase III	
BAY-43-9006	RAF1	Phase III	
Roscovitine/CYC202	CDK2	Phase II	
Flavopiridol	CDK1, CDK2, CDK4	Phase II (discont.)	

<sup>a</sup>Source: Pharmaprojects database, V5 (PJB Publications, [www.pjbpubs.com](http://www.pjbpubs.com)).

Supplementary Table 2. Comparison of binding constants measured in the competition binding assays to published results.

Compound	Kinase	K <sub>d</sub> (μM)	Published IC <sub>50</sub> /K <sub>i</sub> /K <sub>d</sub> (μM)	Literature Assay Format	Reference
Gleevec	ABL	0.0022	0.037	in vitro	Science (2000) vol. 289, p.1938
MLN-518	ABL	>10	>30	in vitro	Cancer Cell (2002) vol. 1, p.421
Roscovitin	ABL	>10	>1000	in vitro	Eur. J. Biochem. (1997) vol. 243, p.527
SU11248	ABL	1.0	0.8	in vitro	Clin. Cancer Res. (2003) vol. 9, p.327
Tarceva	ABL	0.77	1	in vitro	Cancer Res. (1997) vol. 57, p.4838
Vatalanib	ABL	>10	>10	in vitro	Cancer Res. (2000) vol. 60, p.2178
CI-1033	CDK2	>10*	>50	in vitro	Semin. Oncol. (2002) vol. 29, Suppl. 11, p. 11
Flavopiridol	CDK2	0.20*	0.1	in vitro	Cancer Res. (1996) vol. 56, p.2973
GW-2016	CDK2	>10*	>10	in vitro	Mol. Cancer Ther. (2001) vol. 1, p.85
LY333531	CDK2	>10*	5	in vitro	Structure (2004) vol. 12, p.215
Roscovitin	CDK2	2.9*	0.7	in vitro	Eur. J. Biochem. (1997) vol. 243, p.527
SB203580	CDK2	>10*	>100	in vitro	FEBS Lett. (1995) vol. 364, p.229
SU11248	CDK2	>10*	>10	in vitro	Clin. Cancer Res. (2003) vol. 9, p.327
ZD-6474	CDK2	>10*	>10	in vitro	Cancer Res. (2002) vol. 62, p.4645
Roscovitin	CDK5	2.0*	0.2	in vitro	Eur. J. Biochem. (1997) vol. 243, p.527
LY333531	CSK	>10	10	in vitro	Structure (2004) vol. 12, p.215
Roscovitin	CSK	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
Gleevec	CSNK1	>10	>100	in vitro	Biochim. Biophys. Acta (2001) vol. 1551, p.M11-M18
LY333531	CSNK1	>10	>10	in vitro	Structure (2004) vol. 12, p.215
BIRB-796	EGFR	>10	>20	not reported	Nature Struct. Biol. (2002) vol. 9, p.268
SP600125	EGFR	>10	>10	in vitro	Proc. Natl. Acad. Sci. USA (2001) vol. 98, p.13681
CI-1033	EGFR	0.0014	0.0008	in vitro	Semin. Oncol. (2002) vol. 29, Suppl. 11, p. 11
EKB-569	EGFR	0.0010	0.038	in vitro	Nature Med. (2000) vol. 6, p.1024
Flavopiridol	EGFR	>10	25	not reported	Biochem. Biophys. Res. Comm. (1994) vol. 201, p.589
Gleevec	EGFR	>10	>100	in vitro	Bioorg. Med. Chem. Lett. (1997) vol. 7, p.187
GW-2016	EGFR	0.0055	0.011	in vitro	Mol. Cancer Ther. (2001) vol. 1, p.85
Iressa	EGFR	0.0018	0.0021	in vitro	Cancer Res. (2002) vol. 62, p.5749
MLN-518	EGFR	>10	>30	cell-based	Cancer Cell (2002) vol. 1, p.421
SU11248	EGFR	>10	>10	in vitro	Clin. Cancer Res. (2003) vol. 9, p.327
Tarceva	EGFR	0.0014	0.0027	in vitro	Cancer Res. (1997) vol. 57, p.4838
Vatalanib	EGFR	>10	>10	in vitro	Cancer Res. (2000) vol. 60, p.2178
ZD-6474	EGFR	0.017	0.5	in vitro	Cancer Res. (2002) vol. 62, p.4645
CI-1033	ERBB2	0.0084	0.019	in vitro	Semin. Oncol. (2002) vol. 29, Suppl. 11, p. 11
GW-2016	ERBB2	0.011	0.0092	in vitro	Mol. Cancer Ther. (2001) vol. 1, p.85
MLN-518	FGFR	>10	>30	cell-based	Cancer Cell (2002) vol. 1, p.421
CI-1033	FGFR1	>10	>50	in vitro	Semin. Oncol. (2002) vol. 29, Suppl. 11, p. 11
Gleevec	FGFR1	>10	>100	in vitro	Biochim. Biophys. Acta (2001) vol. 1551, p.M11-M18
SU11248	FGFR1	1.8	0.83	in vitro	Clin. Cancer Res. (2003) vol. 9, p.327
Vatalanib	FGFR1	>10	>10	in vitro	Cancer Res. (2000) vol. 60, p.2178
ZD-6474	FGFR1	5.3	3.6	in vitro	Cancer Res. (2002) vol. 62, p.4645
Gleevec	FGR	>10	>100	in vitro	Biochim. Biophys. Acta (2001) vol. 1551, p.M11-M18
Gleevec	FLT3	>10	>10	cell-based	J. Pharm. Expt. Ther. (2000) vol. 295, p.139
MLN-518	FLT3	0.0035	0.22	cell-based	Cancer Cell (2002) vol. 1, p.421
SU11248	FLT3	0.0008	<0.010	cell-based	Blood (2003) vol. 101, p.3597
Vatalanib	FLT4	0.19	0.66	in vitro	Cancer Res. (2000) vol. 60, p.2178
ZD-6474	FLT4	0.30	0.11	in vitro	Cancer Res. (2002) vol. 62, p.4645
BIRB-796	FYN	>10	24	not reported	Nature Struct. Biol. (2002) vol. 9, p.268
CI-1033	INSR	>10	>50	in vitro	Semin. Oncol. (2002) vol. 29, Suppl. 11, p. 11
Gleevec	INSR	>10	>100	cell-based	Biochim. Biophys. Acta (2001) vol. 1551, p.M11-M18
MLN-518	INSR	>10	>30	in vitro	Cancer Cell (2002) vol. 1, p.421
Roscovitin	INSR	>10	70	in vitro	Eur. J. Biochem. (1997) vol. 243, p.527
Tarceva	INSR	>10	>10	in vitro	Cancer Res. (1997) vol. 57, p.4838
Gleevec	JAK2	>10	>10	in vitro	J. Pharm. Expt. Ther. (2000) vol. 295, p.139
SP600125	JNK1	0.10	0.11	in vitro	J. Clin. Invest. (2001) vol. 108, p.73
LY333531	JNK1	>10	>10	in vitro	Structure (2004) vol. 12, p.215
Roscovitin	JNK1	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	JNK1	3.1	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
SB203580	JNK1	1.2	20	in vitro	J. Neurosci. (2002) vol. 22, p.4335
VX-745	JNK1	>10	>1	not reported	Bioorg. Med. Chem. Lett. (2003) vol. 13, p.277
BIRB-796	JNK2	0.0056	0.098	not reported	Nature Struct. Biol. (2002) vol. 9, p.268
SP600125	JNK2	0.084	0.11	in vitro	J. Clin. Invest. (2001) vol. 108, p.73
SB203580	JNK2	0.095	1	in vitro	J. Neurosci. (2002) vol. 22, p.4335
SP600125	JNK3	0.022	0.15	in vitro	J. Clin. Invest. (2001) vol. 108, p.73
SB203580	JNK3	0.045	1	in vitro	J. Neurosci. (2002) vol. 22, p.4335
VX-745	JNK3	>10	>1	not reported	Bioorg. Med. Chem. Lett. (2003) vol. 13, p.277
Gleevec	KIT	0.83	0.3	cell-based	J. Pharm. Expt. Ther. (2000) vol. 295, p.139
MLN-518	KIT	0.12	0.17	cell-based	Cancer Cell (2002) vol. 1, p.421
SU11248	KIT	0.00071	0.001	cell-based	Mol. Cancer Ther. (2003) vol. 2, p.471
Vatalanib	KIT	0.70	0.73	in vitro	Cancer Res. (2000) vol. 60, p.2178
ZD-6474	KIT	1.1	>20	in vitro	Cancer Res. (2002) vol. 62, p.4645
BIRB-796	LCK	1.1	35	not reported	Nature Struct. Biol. (2002) vol. 9, p.268
SP600125	LCK	>10	4.3	in vitro	Proc. Natl. Acad. Sci. USA (2001) vol. 98, p.13681
Gleevec	LCK	0.062	9	in vitro	Biochim. Biophys. Acta (2001) vol. 1551, p.M11-M18
LY333531	LCK	1.3	10	in vitro	Structure (2004) vol. 12, p.215
Roscovitin	LCK	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	LCK	>10	10	in vitro	Biochem. J. (2000) vol. 351, p.95
SB203580	LCK	>10	10	in vitro	Biochem. J. (2000) vol. 351, p.95
VX-745	LCK	1.8	>1	not reported	Bioorg. Med. Chem. Lett. (2003) vol. 13, p.277
Gleevec	LYN	>10	>100	in vitro	Biochim. Biophys. Acta (2001) vol. 1551, p.M11-M18
Roscovitin	MYLK2	>10	90	in vitro	Eur. J. Biochem. (1997) vol. 243, p.527

Supplementary Table 2. Comparison of binding constants measured in the competition binding assays to published results.

Compound	Kinase	K <sub>d</sub> (μM)	Published IC <sub>50</sub> /K <sub>i</sub> /K <sub>d</sub> (μM)	Literature Assay Format	Reference
LY333531	NEK6	>10	>10	in vitro	Structure (2004) vol. 12, p.215
BIRB-796	p38-alpha	0.00024	0.0001	in vitro	Nature Struct. Biol. (2002) vol. 9, p.268
GW-2016	p38-alpha	>10	>10	in vitro	Mol. Cancer. Ther. (2001) vol. 1, p.85
LY333531	p38-alpha	>10	>10	in vitro	Structure (2004) vol. 12, p.215
MLN-518	p38-alpha	>10	>30	in vitro	Cancer Cell (2002) vol. 1, p.421
Roscovitine	p38-alpha	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	p38-alpha	0.013	0.037	in vitro	Biochemistry (1998) vol. 37, p.13850
SB203580	p38-alpha	0.017	0.04	in vitro	Biochemistry (1998) vol. 37, p.13850
VX-745	p38-alpha	0.0032	0.0008	in vitro	Nature Struct. Biol. (2003) vol. 10, p.764
SP600125	p38-beta	>10	>30	in vitro	J. Clin. Invest. (2001) vol. 108, p.73
LY333531	p38-beta	>10	>10	in vitro	Structure (2004) vol. 12, p.215
Roscovitine	p38-beta	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	p38-beta	0.12	0.1	in vitro	Biochem. J. (2000) vol. 351, p.95
SB203580	p38-beta	0.25	0.1	in vitro	Biochem. Biophys. Res. Comm. (1997) vol. 235, p.533
LY333531	p38-gamma	>10	>10	in vitro	Structure (2004) vol. 12, p.215
Roscovitine	p38-gamma	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	p38-gamma	9.4	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
SB203580	p38-gamma	1.7	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
CI-1033	PDGFRB	>10	>50	in vitro	Semin. Oncol. (2002) vol. 29, Suppl. 11, p. 11
Gleevec	PDGFRB	0.028	0.05	in vitro	Bioorg. Med. Chem. Lett. (1997) vol. 7, p.187
MLN-518	PDGFRB	0.0078	0.20	cell-based	Cancer Cell (2002) vol. 1, p.421
SU11248	PDGFRB	0.00021	0.008	in vitro	Clin. Cancer Res. (2003) vol. 9, p.327
Vatalanib	PDGFRB	0.058	0.58	in vitro	Cancer Res. (2000) vol. 60, p.2178
ZD-6474	PDGFRB	0.25	1.1	in vitro	Cancer Res. (2002) vol. 62, p.4645
LY333531	PRKAA1	>10	5	in vitro	Structure (2004) vol. 12, p.215
Roscovitine	PRKAA1	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	PRKAA1	>10	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
SB203580	PRKAA1	>10	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
BIRB-796	PRKACA	>10	>20	not reported	Nature Struct. Biol. (2002) vol. 9, p.268
SP600125	PRKACA	>10	>10	in vitro	Proc. Natl. Acad. Sci. USA (2001) vol. 98, p.13681
Flavopiridol	PRKACA	>10	145	not reported	Biochem. Biophys. Res. Comm. (1994) vol. 201, p.589
Gleevec	PRKACA	>10	>100	in vitro	Bioorg. Med. Chem. Lett. (1997) vol. 7, p.187
LY333531	PRKACA	>10	>10	in vitro	Structure (2004) vol. 12, p.215
MLN-518	PRKACA	>10	>30	in vitro	Cancer Cell (2002) vol. 1, p.421
Roscovitine	PRKACA	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	PRKACA	>10	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
SB203580	PRKACA	>10	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
ZD-6474	PTK2	>10	>20	in vitro	Cancer Res. (2002) vol. 62, p.4645
LY333531	RPS6KA5	2.0	1	in vitro	Structure (2004) vol. 12, p.215
Roscovitine	RPS6KA5	>10	>10	in vitro	Biochem. J. (2003) vol. 371, p.199
SB202190	RPS6KA5	>10	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
SB203580	RPS6KA5	>10	>10	in vitro	Biochem. J. (2000) vol. 351, p.95
EKB-569	SRC	0.12	0.28	not reported	Nature Med. (2000) vol. 6, p.1024
Gleevec	SRC	>10	>100	in vitro	Bioorg. Med. Chem. Lett. (1997) vol. 7, p.187
GW-2016	SRC	>10	3.5	in vitro	Mol. Cancer. Ther. (2001) vol. 1, p.85
LY333531	SRC	>10	>100	in vitro	J. Med. Chem. (1996) vol. 39, p. 2664
MLN-518	SRC	>10	30	in vitro	Cancer Cell (2002) vol. 1, p.421
Roscovitine	SRC	>10	250	in vitro	Eur. J. Biochem. (1997) vol. 243, p.527
SU11248	SRC	3.1	0.6	in vitro	Clin. Cancer Res. (2003) vol. 9, p.327
Tarceva	SRC	1.9	1	in vitro	Cancer Res. (1997) vol. 57, p.4838
Vatalanib	SRC	>10	>10	in vitro	Cancer Res. (2000) vol. 60, p.2178
VX-745	SRC	0.98	>1	not reported	Bioorg. Med. Chem. Lett. (2003) vol. 13, p.277
BIRB-796	SYK	>10	>20	not reported	Nature Struct. Biol. (2002) vol. 9, p.268
Gleevec	SYK	>10	>100	in vitro	Biochim. Biophys. Acta (2001) vol. 1551, p.M11-M18
Gleevec	TEK	>10	>10	in vitro	J. Pharm. Expt. Ther. (2000) vol. 295, p.139
GW-2016	TEK	>10	>10	in vitro	Mol. Cancer. Ther. (2001) vol. 1, p.85
Vatalanib	TEK	>10	>10	in vitro	Cancer Res. (2000) vol. 60, p.2178
ZD-6474	TEK	3.6	2.5	in vitro	Cancer Res. (2002) vol. 62, p.4645
Gleevec	VEGFR2	>10	>10	in vitro	J. Pharm. Expt. Ther. (2000) vol. 295, p.139
GW-2016	VEGFR2	>10	>10	in vitro	Mol. Cancer. Ther. (2001) vol. 1, p.85
Iressa	VEGFR2	>10	3.7-10	in vitro	Cancer Res. (2002) vol. 62, p.5749
MLN-518	VEGFR2	>10	>30	cell-based	Cancer Cell (2002) vol. 1, p.421
SU11248	VEGFR2	0.00023	0.009	in vitro	Clin. Cancer Res. (2003) vol. 9, p.327
Vatalanib	VEGFR2	0.070	0.037	in vitro	Cancer Res. (2000) vol. 60, p.2178
ZD-6474	VEGFR2	0.47	0.04	in vitro	Cancer Res. (2002) vol. 62, p.4645

\* There is no added human cyclin present in the competition binding assays for CDK's.

Binding constants are averages of at least two independent experiments.

Published results are IC<sub>50</sub>'s, K<sub>i</sub>'s or K<sub>d</sub>'s reported in the literature.

Supplementary Table 3. Comparison of the results of cell-based assays and binding assays for FLT3 and EGFR inhibitors.

Compound	Target	K <sub>d</sub> (μM)	Cell line	Cell-based IC <sub>50</sub> (μM)
ZD-6474	FLT3	1.2	MV4,11	0.76
BAY-43-9006	FLT3	0.020	MV4,11	0.0012
Vatalanib	FLT3	> 10	MV4,11	> 10
Gleevec	FLT3	> 10	MV4,11	> 10
AB200289	FLT3	0.010	MV4,11	0.027
AB200382	FLT3	0.0010	MV4,11	0.0040
AB200440	FLT3	0.0020	MV4,11	0.0035
AB400171	EGFR	0.048	A431	0.050
AB400277	EGFR	0.0060	A431	0.034

Each value was measured at least in duplicate.

Supplementary Table 4. Complete quantitative results of screening twenty kinase inhibitors against 119 protein kinases. Blank fields indicate combinations that were tested, but for which no evidence of binding was observed in a primary screen (10 uM).

Accession #	Gene Symbol (LocusLink)	Gene Symbol	Staurosporine	SB202190	SB203580	VX-745	BIRB-796	SP600125	Gleevec	Iressa	Tarceva	ZD-6474	CI-1033
NM_014911.1	AAK1	AAK1	0.013					0.035			4.4		
XM_033355.1	ABL1	ABL1	0.41			0.87	1.5		0.0022		0.77	0.27	0.34
XM_033355	ABL1	ABL1(E255K)	2.8			7.2			0.11		2.4	0.68	2.9
XM_033355	ABL1	ABL1(H396P)	0.34			1.2			0.062		0.69	0.12	0.32
XM_033355	ABL1	ABL1(M351T)	0.4			1.8	2.2		0.014		0.73	0.17	0.56
XM_033355	ABL1	ABL1(Q252H)	0.5			1.7	4.2		0.024		0.28	0.18	0.47
XM_033355	ABL1	ABL1(T315I)	0.038				0.041		6.2		0.6	0.12	0.29
XM_033355	ABL1	ABL1(Y253F)	0.17			0.71	2.3		0.044		0.54	0.16	0.42
NM_007314.1	ABL2	ABL2	0.16			0.22			0.013		0.3	0.13	1.3
NM_005781.2	ACK1	ACK1	0.017										
NM_003600.1	STRK6	Aurora2	0.016					0.98			3.8		
NM_003160.1	AURKC	Aurora3	0.011										3.5
NM_017593.2	BMP2K	BIKE	0.0037					0.025			1.8		1.6
NM_001721.2	BMX	BMX	0.41										1.2
NM_000061.1	BTX	BTX	0.71										0.75
NM_003656.3	CAMK1	CAMK1	0.03						4.1				
NM_020397.1	CAMK1D	CAMK1D	0.002						1.4				
NM_020439.1	CAMK1G	CAMK1G	0.053						4.2				
NM_015981.1	CAMK2A	CAMK2A	0.0001										
NM_001220.2	CAMK2B	CAMK2B	0.003										
NM_001221.1	CAMK2D	CAMK2D	0.0005										
BC034044.1	CAMK2G	CAMK2G	0.0005										
NM_032294.1	CAMKK1	CAMKK1	0.00005										
NM_006549.2	CAMKK2	CAMKK2	0.00005					7.5					
NM_001798.2	CDK2	CDK2	0.0081					3.2					
NM_004935.1	CDK5	CDK5	0.089				0.39						
NM_004071.1	CLK1	CLK1	0.027						4.5				
NM_003993.1	CLK2	CLK2	0.012					0.3					
NM_003992.1	CLK3	CLK3	3.5										
NM_020666.1	CLK4	CLK4	0.015					0.26	4.2				
NM_004383.1	CSK	CSK	0.44									3.7	2.9
NM_001894.2	CSNK1E	CSNK1E	0.69	0.4	0.22			3.1		2		1.5	
NM_022048.1	CSNK1G1	CSNK1G1						3.7					
NM_001319.5	CSNK1G2	CSNK1G2	1.4										
NM_014326.2	DAPK2	DAPK2	0.003					0.61					
NM_001348.1	DAPK3	DAPK3	0.001					0.41					
NM_005228.1	EGFR	EGFR	0.07	4.6	2.9				0.0018	0.0014	0.017	0.014	
NM_004431.1	EPHA2	EPHA2	0.87			2.1	3.1					1.9	
NM_005233.2	EPHA3	EPHA3	0.055				0.58	4				1.8	0.85
NM_004438.1	EPHA4	EPHA4	0.71			10	3.9					4.3	0.31
NM_004439.3	EPHA5	EPHA5	0.15			1.9	1.3					0.31	0.27
SK646	EPHA6	EPHA6	0.24				0.43			1.4	0.93	0.065	0.072
NM_004440.1	EPHA7	EPHA7	0.69				0.22					3.4	1.5
NM_020526.2	EPHA8	EPHA8	0.3			3.1	0.14		2.1			0.16	0.79
NM_004441.2	EPHB1	EPHB1	0.59			1.6	4.2			7.3		0.54	1.4
NM_004444.2	EPHB4	EPHB4				1						2.6	5
NM_004448.1	ERBB2	ERBB2								1.1	5.1		0.0084
NM_005246.1	FER	FER	0.03										
NM_000604.2	FGFR1	FGFR1	0.06									5.3	
NM_000141.2	FGFR2	FGFR2	0.16					1.9				5.5	
NM_000142.2	FGFR3	FGFR3	0.11									0.24	
NM_005248.1	FGR	FGR	0.03									2.2	1.7
NM_004119.1	FLT3	FLT3	0.0018			1.2						1.2	
NM_002020.1	FLT4	FLT4	0.031				2.5					0.3	
NM_002031.1	FRK	FRK	0.26	6	4.4	3.3	0.36		3.5			0.48	8.1
NM_153047.1	FYN	FYN	0.051						5.5			5.7	
NM_005255.1	GAK	GAK	0.068	0.65	0.039			0.038	3.6	0.007	0.04	0.33	0.044
NM_002110.1	HCK	HCK	0.012			10						4.2	5.7
NM_000208.1	INSR	INSR	0.073										
NM_002227.1	JAK1	JAK1 (Kin.Dom.1)											
NM_004972.2	JAK2	JAK2 (Kin.Dom.2)	0.011										
NM_002750.2	MAPK8	JNK1	0.52	3.1	1.2			0.1	3.2				
NM_139068.1	MAPK9	JNK2	1.1	0.12	0.095		0.0056	0.084	5.2	1.4	4		1.1
NM_002753.2	MAPK10	JNK3	0.34	0.051	0.045		0.062	0.022	3.3	2.3			2.8
NM_000222.2	KIT	KIT	0.1						0.63			1.1	
NM_005356.2	LCK	LCK	0.02			1.8	1.1		0.062	1.1	0.53	0.061	0.56
NM_002314.2	LIMK1	LIMK1	0.69									0.71	0.78
NM_002350.1	LYN	LYN	0.21									4.8	2
NM_005922.1	MAP3K4	MAP3K4	2.2										
NM_005923.3	MAP3K5	MAP3K5	0.12										
NM_006575.2	MAP4K5	MAP4K5	0.026									0.51	1.3
NM_017490.1	MARK2	MARK2	0.0001					1.8					
NM_017572.1	MKNK2	MKNK2	0.022				1.1	1		0.36	1.6	3.4	1.3
NM_033118.2	MYLK2	MYLK2	0.11										
NM_002497.1	NEK2	NEK2	0.74										
NM_014397.2	NEK6	NEK6											
NM_033116.3	NEK9	NEK9	6.7										
NM_002529.2	NTRK1	NTRK1	0.002				0.77						
NM_139012.1	MAPK14	p38-alpha		0.013	0.017	0.0032	0.00024						
NM_002751.4	MAPK11	p38-beta	0.12	0.25	0.16		0.22						
NM_002969.2	MAPK12	p38-gamma	0.092	9.4	1.7		0.014	2.4					
NM_002576.2	PAK1	PAK1	0.002										
NM_002578.1	PAK3	PAK3	0.0005										
NM_005884.2	PAK4	PAK4	0.008										
NM_020168.3	PAK6	PAK6	0.0004										
NM_020341.1	PAK7	PAK7/PAK5	0.003										
NM_006201.2	PCTK1	PCTK1	0.025					0.18					
NM_002609.2	PDGFRB	PDGFRB	0.0027			0.87	1		0.028			0.25	
NM_006213.1	PHK31	PHK31	0.0005									7.1	
NM_000294.1	PHK32	PHK32	0.001					0.48		6.4		9.5	
NM_002548.1	PIM1	PIM1	0.015										
NM_006875.1	PIM2	PIM2	0.004					0.46					
NM_004203.2	PKMYT1	PKMYT1											
NM_006251.1	PRKAA1	PRKAA1	0.009									10	
NM_002730.1	PRKACA	PRKACA	0.05										
NM_005607.3	PTK2	PTK2	0.068										
NM_005975.2	PTK6	PTK6		3	9							0.033	1.1
NM_003821.2	RIPK2	RIPK2	5.1	0.35	2.1					0.8	0.41	0.031	0.33
NM_021135.2	RPS6KA2	RPS6KA2 (Kin.Dom.1)	0.01					2.2					
NM_004586.1	RPS6KA3	RPS6KA3 (Kin.Dom.1)	0.06										
NM_004755.1	RPS6KA5	RPS6KA5 (Kin.Dom.1)	0.02					1.7					
NM_014720.1	SLK	SLK	0.00002		4.6		0.096	2.3		1.1	0.11	0.096	0.44
NM_005417.2	SRC	SRC	0.1			0.98				5	1.9	0.17	0.76
NM_005990.1	STK10	STK10	0.00003				0.0071			0.87	0.083	2.4	0.43
NM_003691.1	STK16	STK16	0.2					0.51					
NM_004760.1	STK17A	STK17A	0.023					2.1	2.8		2.9		3.8
NM_004226.1	STK17B	STK17B	0.026							6.5			
NM_014264.2	STK18	STK18	0.00075						9			1.5	
NM_019635.1	Stk3_mouse	STK3_m	0.00015					0.22					
NM_015690.1	STK36	STK36	2.9	3.8	0.86								2.7
NM_015000.1	STK38L	STK38L	0.077					2.3					
NM_006282.1	STRK4	STRK4	0.0002					2.2					
NM_003177.2	SYK	SYK	0.007										
NM_006459.1	TEK	TEK	0.24				0.011					3.6	
AF17254.1	KIAA0551	TNIK	0.006	10	1.5		0.0099	0.48				3.9	
NM_003319.2	TTK	TTK	0.1					1.2					
XM_134854.1	1200015E14Rik	ULK3_m	0.003							1.4	0.63		
NM_002253.1	KDR	VEGFR2	0.27									0.47	
NM_005433.2	YES1	YES	0.049			2.6						0.28	2.5

All binding constants are given in micromolar, and values are the average from at least two independent experiments.

Supplementary Table 4. Complete quantitative results of screening twenty kinase inhibitors against 119 protein kinases. Blank fields indicate combinations that were tested, but for which no evidence of binding was observed in a primary screen (10 uM).

Accession #	Gene Symbol (LocusLink)	Gene Symbol	GW-2016	EKB-569	Vatalanib	SU11248	MLN-518	LY-333531	BAY-43-9006	Roscovitine	Flavopiridol
NM_014911.1	AAK1	AAK1		2.3		0.13		0.96			
XM_033355.1	ABL1	ABL1		0.22		1			0.13		
XM_033355	ABL1	ABL1(E255K)		0.54					4.4		
XM_033355	ABL1	ABL1(H396P)		0.17		0.87			1.2		
XM_033355	ABL1	ABL1(M351T)		0.13		0.53			0.23		
XM_033355	ABL1	ABL1(Q252H)		0.16		2.3			0.45		
XM_033355	ABL1	ABL1(T315I)		0.3		0.21			0.17		
XM_033355	ABL1	ABL1(Y253F)		0.11		0.72			0.58		
NM_007314.1	ABL2	ABL2		0.16		1.2			1.3		
NM_005781.2	ACK1	ACK1		0.89		2.2					
NM_003600.1	STK6	Aurora2				6.6					
NM_003160.1	AURKC	Aurora3				0.31		3			
NM_017593.2	BMP2K	BIKE		0.54		0.038		2.5			
NM_001721.2	BMX	BMX									
NM_000061.1	BTX	BTX		1.5							
NM_003556.3	CAMK1	CAMK1				2					
NM_020397.1	CAMK1D	CAMK1D		3.8		1.1		2.6			
NM_020439.1	CAMK1G	CAMK1G				0.99					
NM_015981.1	CAMK2A	CAMK2A				0.37		9.6			1.3
NM_001220.2	CAMK2B	CAMK2B				3.2					2.6
NM_001221.1	CAMK2D	CAMK2D				1.1					
BC034044.1	CAMK2G	CAMK2G				0.76					
NM_032294.1	CAMKK1	CAMKK1				0.9		1.5			0.019
NM_006549.2	CAMKK2	CAMKK2		2.2		5.8		1.1			0.32
NM_001798.2	CDK2	CDK2								2.9	0.2
NM_004935.1	CDK5	CDK5							6.2	2	0.043
NM_004071.1	CLK1	CLK1		1		0.1	1.4			2.1	2.2
NM_003993.1	CLK2	CLK2		0.7		0.19	1.9			0.47	1.4
NM_003992.1	CLK3	CLK3		2.1			9				1
NM_020666.1	CLK4	CLK4		2.9		0.08		8.3		4.5	
NM_004383.1	CSK	CSK		2.3							
NM_001894.2	CSNK1E	CSNK1E		0.097						0.16	
NM_022048.1	CSNK1G1	CSNK1G1								3.3	
NM_001319.5	CSNK1G2	CSNK1G2								1.4	
NM_014326.2	DAPK2	DAPK2				0.47		2.6			
NM_001348.1	DAPK3	DAPK3		4.1		0.3		1.3			
NM_005228.1	EGFR	EGFR	0.0055	0.001							
NM_004431.1	EPHA2	EPHA2							4.8		
NM_005233.2	EPHA3	EPHA3		4.1					6.4		
NM_004438.1	EPHA4	EPHA4							1.3		
NM_004439.3	EPHA5	EPHA5		0.71		5.9			0.35		4
SK648	EPHA6	EPHA6		4.1		2			0.24		
NM_004440.1	EPHA7	EPHA7				0.71			0.67		
NM_020526.2	EPHA8	EPHA8		0.4					0.96		
NM_004441.2	EPHB1	EPHB1		4.2		0.96			1.7		2.2
NM_004444.2	EPHB4	EPHB4		1.3		2.2			3.9		
NM_004448.1	ERBB2	ERBB2	0.011	0.077							
NM_005246.1	FER	FER		0.25		1.4					
NM_000604.2	FGFR1	FGFR1				1.8		5.1	2.5		
NM_000141.2	FGFR2	FGFR2				0.53					
NM_000142.2	FGFR3	FGFR3				0.3					
NM_005248.1	FGR	FGR				0.29					
NM_004119.1	FLT3	FLT3			0.19	0.0008	0.0035	0.27	0.02		
NM_002020.1	FLT4	FLT4				0.035			0.016		
NM_002031.1	FRK	FRK		0.19					0.44		
NM_153047.1	FYN	FYN		1.6		3.9					
NM_005255.1	GAK	GAK		0.0015		0.12		1.3			1.1
NM_002110.1	HCK	HCK		2.3		3.3		2.8			
NM_000208.1	INSR	INSR				0.18					
NM_002227.1	JAK1	JAK1 (Kin.Dom.1)				0.0092					
NM_004972.2	JAK2	JAK2 (Kin.Dom.2)		2		0.94					
NM_002750.2	MAPK8	JNK1									
NM_139068.1	MAPK9	JNK2							3.6		
NM_002753.2	MAPK10	JNK3									
NM_000222	KIT	KIT			0.7	0.00071	0.12	0.38	0.74		
NM_005356.2	LCK	LCK		0.044		1.2		1.3	6.9		
NM_002314.2	LIMK1	LIMK1							2.2		
NM_002350.1	LYN	LYN		0.96		0.54					
NM_005922.1	MAP3K4	MAP3K4		0.13		3.3					
NM_005923.3	MAP3K5	MAP3K5									
NM_006575.2	MAP4K5	MAP4K5		0.0037		0.077	2.5	8.4	1.7		
NM_017490.1	MARK2	MARK2				0.32		2.3			
NM_017572.1	MKNK2	MKNK2							0.25		1.9
NM_033118.2	MYLK2	MYLK2		1.8		0.057			1.3		
NM_002497.1	NEK2	NEK2		0.14		0.5					
NM_014397.2	NEK6	NEK6									
NM_033116.3	NEK9	NEK9									
NM_002529.2	NTRK1	NTRK1				0.22	0.2		3.6		
NM_139012.1	MAPK14	p38-alpha							0.26		
NM_002751.4	MAPK11	p38-beta							0.2		
NM_002969.2	MAPK12	p38-gamma							9.9		
NM_002576.2	PAK1	PAK1		2.1							
NM_002578.1	PAK3	PAK3									
NM_005884.2	PAK4	PAK4									
NM_020168.3	PAK6	PAK6									
NM_020341.1	PAK7	PAK7/PAK5									
NM_006201.2	PCTK1	PCTK1		10		0.13	2.4	8		0.99	0.18
NM_002609.2	PDGFRB	PDGFRB			0.058	0.00021	0.0078	7	0.041		
NM_006213.1	PHKG1	PHKG1		1.5		0.07		2.7			
NM_000294.1	PHK2	PHK2		2.5		0.039					2
NM_002548.1	PIM1	PIM1						0.055			0.52
NM_006875.1	PIM2	PIM2				5		0.13			0.65
NM_004203.2	PKMYT1	PKMYT1		0.93							
NM_006251.1	PRKAA1	PRKAA1				0.052					6.6
NM_002730.1	PRKACA	PRKACA				6					
NM_005607.3	PTK2	PTK2		4.4		0.61					
NM_005975.2	PTK6	PTK6			2.7						
NM_003821.2	RIPK2	RIPK2							2.9		
NM_021135.2	RPS6KA2	RPS6KA2 (Kin.Dom.1)		8.1		0.058		1.5		3.2	1.6
NM_004586.1	RPS6KA3	RPS6KA3 (Kin.Dom.1)				0.055		2.2			
NM_004755.1	RPS6KA5	RPS6KA5 (Kin.Dom.1)				0.25		2			2
NM_014720.1	SLK	SLK	9.3	0.25		0.081	4.2	0.94	1.6		
NM_005417.2	SRC	SRC		0.12		3.1					
NM_005990.1	STK10	STK10	2.6	0.11		0.64		1.1	0.14		
NM_003691.1	STK16	STK16				0.36					
NM_004760.1	STK17A	STK17A		0.057		0.021					
NM_004226.1	STK17B	STK17B		1.3		0.22					5.1
NM_014264.2	STK18	STK18				0.38		0.37	3.4		3.1
NM_019635.1	Stk3_mouse	STK3_m		1.1		0.16		0.09			
NM_015690.1	STK36	STK36		1.2					5.4		
NM_015000.1	STK38L	STK38L				1.5					
NM_006282.1	STR4	STR4		3.9		0.1		0.22			
NM_003177.2	SYK	SYK		1.2							
NM_009459.1	TEK	TEK		2.9				3			
AF17284.1	KIAA0551	TNIK		0.045		0.025		5.8			
NM_003319.2	TTK	TTK				0.23				2.1	
XM_134854.1	1200015E14Rik	ULK3_m		3.8		0.11					
NM_002253.1	KDR	VEGFR2			0.07	0.00023			0.093		
NM_005433.2	YES1	YES1		0.84		0.24					

All binding constants are given in micromolar, and values are the average from at least two independent experiments.

Supplementary Table 5. Binding constants for eight small molecules binding to ten EGFR variants. Binding constant values are in nanomolar.

Compound	Iressa	Tarceva	PKI-166	CI-1033	GW-2016	EKB-569	SU-11464	ZD-6474
Primary Target(s)	EGFR	EGFR	EGFR	EGFR, ERBB2, ERBB4	EGFR, ERBB2, ERBB4	EGFR, ERBB2	EGFR, ERBB2	EGFR, VEGFR2
Chemical Class	quinazoline	quinazoline	pyrrolo-pyrimidine	quinazoline	quinazoline	quinoline	indolinone	quinazoline
EGFR Variant								
wild type	0.90	0.67	1.9	0.24	2.3	0.44	2.2	9.5
L747-S752del P753S	0.50	0.47	0.93	0.17	3.9	0.27	1.6	7.9
L747-E749del A750P	0.69	0.52	1.3	0.16	2.2	0.24	1.4	12
L747-T751del insS	0.62	0.35	1.3	0.22	3.5	0.23	1.6	8.9
L861Q	1.4	1.2	2.4	0.22	1.2	0.44	1.7	11
G719C	2.6	0.85	1.2	0.13	0.92	0.24	15	9.6
L858R	1.3	0.97	0.81	0.25	2.8	0.41	2.4	8.7
E746-A750del	0.54	0.48	1.3	0.27	8.6	0.38	2.3	4.8
G719S	1.4	0.52	0.78	0.19	2.1	0.42	8.2	5.9
S752-I759del	0.98	1.6	1.9	0.19	4.2	0.33	2.0	12

Binding constants are the average of at least two experiments, performed independently from the experiments reported in Supplementary Table 4.

Supplementary Table 6. List of clone type used for each kinase assay. Domain clones include the complete kinase catalytic domain along with flanking sequences.

Accession #	Gene Symbol (LocusLink)	Gene Symbol	Clone Type
NM_014911.1	AAK1	AAK1	Domain
XM_033355.1	ABL1	ABL1	Domain
XM_033355	ABL1	ABL1(E255K)	Domain
XM_033355	ABL1	ABL1(H396P)	Domain
XM_033355	ABL1	ABL1(M351T)	Domain
XM_033355	ABL1	ABL1(Q252H)	Domain
XM_033355	ABL1	ABL1(T315I)	Domain
XM_033355	ABL1	ABL1(Y253F)	Domain
NM_007314.1	ABL2	ABL2	Domain
NM_005781.2	ACK1	ACK1	Domain
NM_003600.1	STK6	Aurora2	Domain
NM_003160.1	AURKC	Aurora3	Full-length
NM_017593.2	BMP2K	BIKE	Domain
NM_001721.2	BMX	BMX	Full-length
NM_000061.1	BTX	BTX	Full-length
NM_003656.3	CAMK1	CAMK1	Full-length
NM_020397.1	CAMK1D	CAMK1D	Domain
NM_020439.1	CAMK1G	CAMK1G	Domain
NM_015981.1	CAMK2A	CAMK2A	Domain
NM_001220.2	CAMK2B	CAMK2B	Domain
NM_001221.1	CAMK2D	CAMK2D	Domain
BC034044.1	CAMK2G	CAMK2G	Domain
NM_032294.1	CAMKK1	CAMKK1	Domain
NM_006549.2	CAMKK2	CAMKK2	Domain
NM_001798.2	CDK2	CDK2	Full-length
NM_004935.1	CDK5	CDK5	Full-length
NM_004071.1	CLK1	CLK1	Full-length
NM_003993.1	CLK2	CLK2	Domain
NM_003992.1	CLK3	CLK3	Full-length
NM_020666.1	CLK4	CLK4	Domain
NM_004383.1	CSK	CSK	Full-length
NM_001894.2	CSNK1E	CSNK1E	Full-length
NM_022048.1	CSNK1G1	CSNK1G1	Domain
NM_001319.5	CSNK1G2	CSNK1G2	Full-length
NM_014326.2	DAPK2	DAPK2	Full-length
NM_001348.1	DAPK3	DAPK3	Domain
NM_005228.1	EGFR	EGFR	Domain
NM_004431.1	EPHA2	EPHA2	Domain
NM_005233.2	EPHA3	EPHA3	Domain
NM_004438.1	EPHA4	EPHA4	Domain
NM_004439.3	EPHA5	EPHA5	Domain
SK648	EPHA6	EPHA6	Domain
NM_004440.1	EPHA7	EPHA7	Domain
NM_020526.2	EPHA8	EPHA8	Domain
NM_004441.2	EPHB1	EPHB1	Domain
NM_004444.2	EPHB4	EPHB4	Domain
NM_004448.1	ERBB2	ERBB2	Domain
NM_005246.1	FER	FER	Domain
NM_000604.2	FGFR1	FGFR1	Domain
NM_000141.2	FGFR2	FGFR2	Domain
NM_000142.2	FGFR3	FGFR3	Domain
NM_005248.1	FGR	FGR	Full-length
NM_004119.1	FLT3	FLT3	Domain
NM_002020.1	FLT4	FLT4	Domain
NM_002031.1	FRK	FRK	Domain
NM_153047.1	FYN	FYN	Full-length
NM_005255.1	GAK	GAK	Domain
NM_002110.1	HCK	HCK	Full-length
NM_000208.1	INSR	INSR	Domain
NM_002227.1	JAK1	JAK1 (Kin.Dom.1)	Domain
NM_004972.2	JAK2	JAK2 (Kin.Dom.2)	Domain
NM_002750.2	MAPK8	JNK1	Full-length
NM_139068.1	MAPK9	JNK2	Full-length
NM_002753.2	MAPK10	JNK3	Domain
NM_000222	KIT	KIT	Domain
NM_005356.2	LCK	LCK	Domain
NM_002314.2	LIMK1	LIMK1	Full-length
NM_002350.1	LYN	LYN	Full-length
NM_005922.1	MAP3K4	MAP3K4	Domain
NM_005923.3	MAP3K5	MAP3K5	Domain
NM_006575.2	MAP4K5	MAP4K5	Domain
NM_017490.1	MARK2	MARK2	Domain
NM_017572.1	MKNK2	MKNK2	Domain
NM_033118.2	MYLK2	MYLK2	Domain
NM_002497.1	NEK2	NEK2	Domain
NM_014397.2	NEK6	NEK6	Full-length
NM_033116.3	NEK9	NEK9	Domain
NM_002529.2	NTRK1	NTRK1	Domain
NM_139012.1	MAPK14	p38-alpha	Full-length
NM_002751.4	MAPK11	p38-beta	Full-length
NM_002969.2	MAPK12	p38-gamma	Full-length
NM_002576.2	PAK1	PAK1	Domain
NM_002578.1	PAK3	PAK3	Full-length
NM_005884.2	PAK4	PAK4	Domain
NM_020168.3	PAK6	PAK6	Domain
NM_020341.1	PAK7	PAK7/PAK5	Domain
NM_006201.2	PCTK1	PCTK1	Domain
NM_002609.2	PDGFRB	PDGFRB	Domain
NM_006213.1	PHKG1	PHKG1	Full-length
NM_000294.1	PHK32	PHK32	Domain
NM_002548.1	PIM1	PIM1	Domain
NM_006875.1	PIM2	PIM2	Domain
NM_004203.2	PKMYT1	PKMYT1	Full-length
NM_006251.1	PRKAA1	PRKAA1	Domain
NM_002730.1	PRKACA	PRKACA	Domain
NM_005607.3	PTK2	PTK2	Domain
NM_005975.2	PTK6	PTK6	Full-length
NM_003821.2	RIPK2	RIPK2	Domain
NM_021135.2	RPS6KA2	RPS6KA2 (Kin.Dom.1)	Domain
NM_004586.1	RPS6KA3	RPS6KA3 (Kin.Dom.1)	Domain
NM_004755.1	RPS6KA5	RPS6KA5 (Kin.Dom.1)	Domain
NM_014720.1	SLK	SLK	Domain
NM_005417.2	SRC	SRC	Domain
NM_005990.1	STK10	STK10	Domain
NM_003691.1	STK16	STK16	Domain
NM_004760.1	STK17A	STK17A	Domain
NM_004226.1	STK17B	STK17B	Full-length
NM_014264.2	STK18	STK18	Domain
NM_019635.1	Stk3_mouse	STK3_m	Domain
NM_015690.1	STK36	STK36	Domain
NM_015000.1	STK38L	STK38L	Domain
NM_006282.1	STK4	STK4	Full-length
NM_003177.2	SYK	SYK	Domain
NM_000459.1	TEK	TEK	Domain
AF172284.1	KIAA0551	TNIK	Domain
NM_003319.2	TTK	TTK	Domain
XM_134854.1	1200015E14Rik	ULK3_m	Domain
NM_002253.1	KDR	VEGFR2	Domain
NM_005433.2	YES1	YES	Domain