Comprehensive Protein Kinase Profiling Panels for Inhibitor Selectivity Screening

Yusuke Kawase, Hiroshi Ohmoto, Yasuyuki Kirii, Yoshimasa Inoue, and Hiroshi Ishiguro, Carna Biosciences, Inc., Kobe, Japan

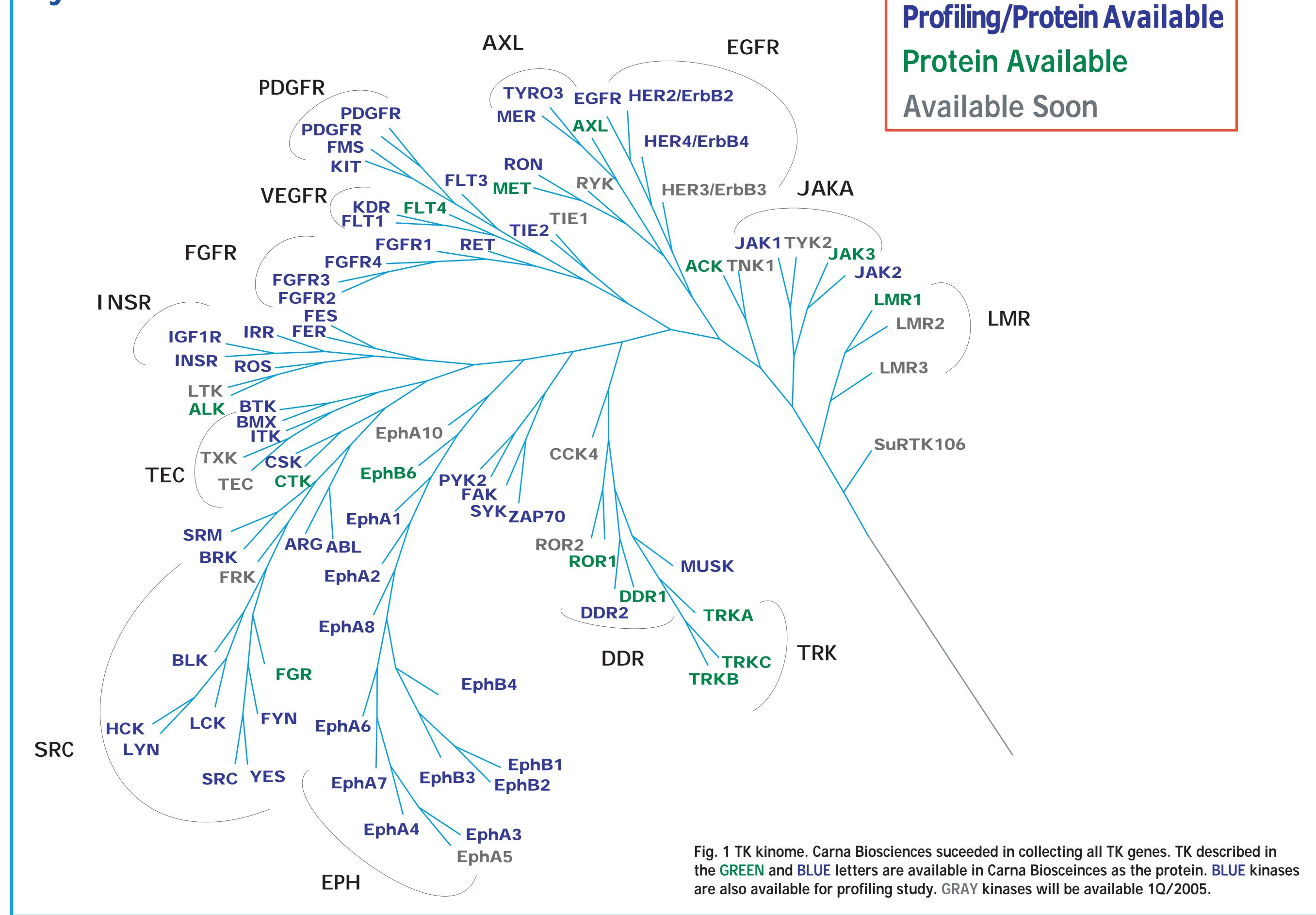
Abstract

It is well known that protein kinases are key elements in intracellular signaling pathways that control many physiological processes. Further, it has been demonstrated that the activity of protein kinases are altered in several human diseases such as cancer and autoimmune disorders. Therefore, molecules that modulate kinase functions are expected to be promising new drugs. To avoid predictable side effects of protein kinase inhibitors, determining their specificity is an important issue. Recently, Carna Biosciences have succeeded in extracting and cloning the entire (88) tyrosine kinase genes and is developing a complete tyrosine kinase assay panel for kinase inhibitor specificity profiling. A description of this panel system, as well as progress made with developing a profiling system for serine/threonine kinases will be presented. Each kinase assay will be available in homogeneous platforms using IMAPTM technology, TR-FRET and AlphaScreenTM, all of which are suitable for HTS assays.

IMAPTM technology and AlphaScreenTM are registered trademarks of Molecular Devices Corporation and PerkinElmer.

ARNA BIOSCIENCES

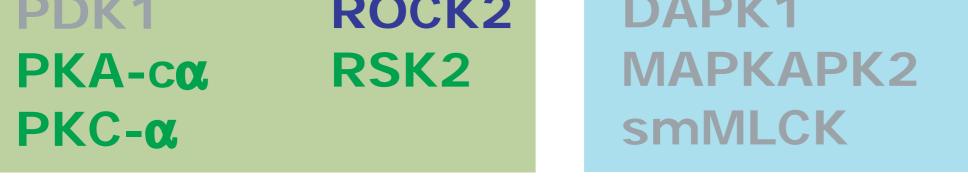
Tyrosine Kinases in Carna Biosciences

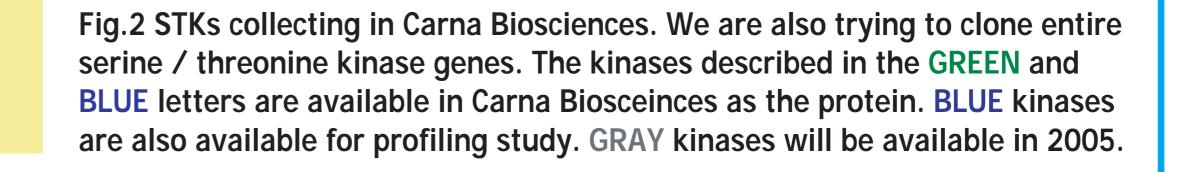


Serine/Threonine Kinases in Carna Biosciences

| AGC | | CAMK | | STE |
|-------|--------------|---------|-------|--------|
| AKT2 | ΡΚС-ε | CaMK4 | PHKg1 | MAP2K3 |
| BARK1 | ΡΚϹ-γ | CaMK2-α | PIM1 | MAP2K7 |
| BARK2 | РКС-θ | CHK1 | PKD2 | MAP3K5 |
| CRIK | ROCK1 | CHK2 | TRIO | MAP3K3 |
| | | | | |

| Profiling/Protein Available |
|------------------------------------|
| Protein Available |
| Available Soon |



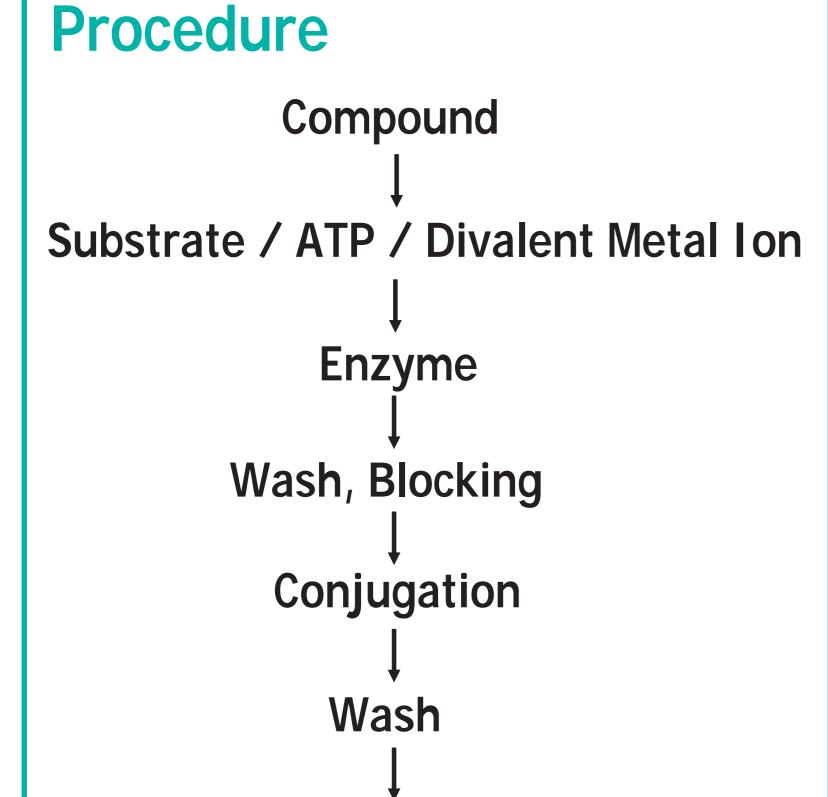






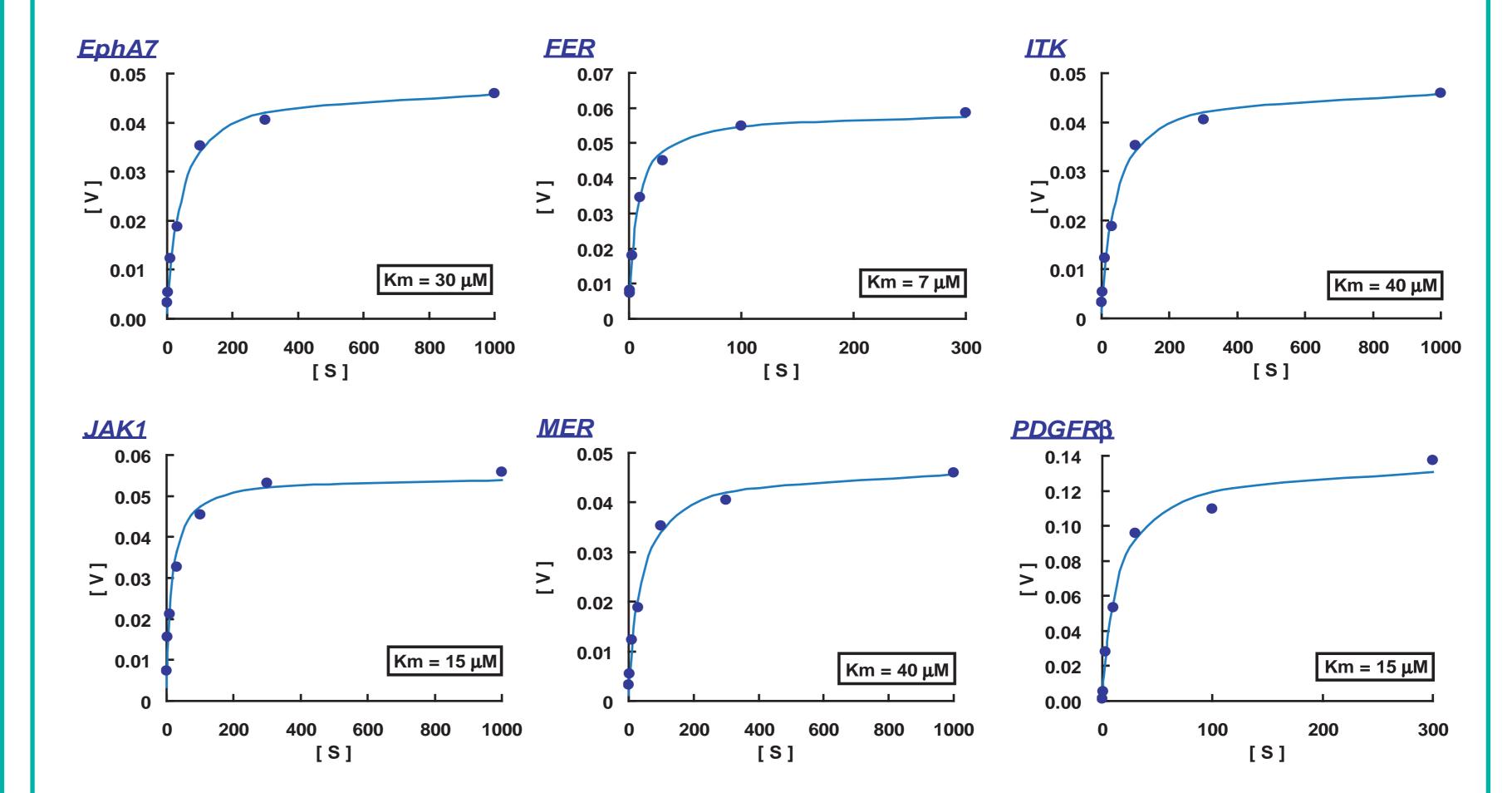
TK Profiling

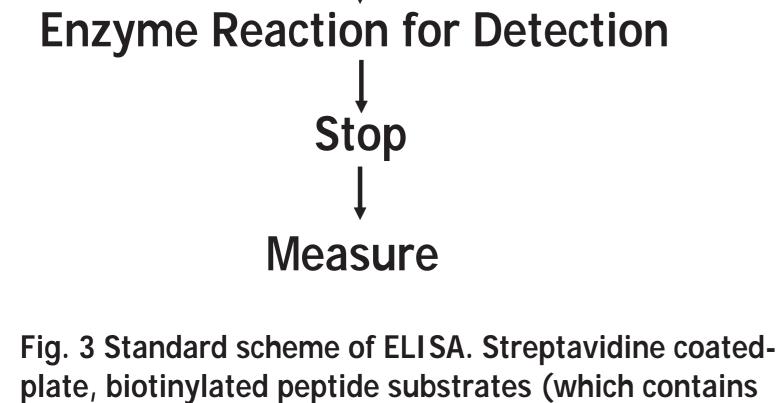
Carna Biosciences is developing entire TK profiling panel firstly with 96-well format ELISA platform to exclude potential compound interference.



Km for ATP

Carna Biosciences's standard condition to evaluate inhibitory activity of compounds is performed with ATP at the concentrarions around Km. The most of known kinase inhibitors so far are the ATP competitor. Using too much ATP may miss the positive signal.





1 tyrosine in their sequences) are used in the kinase

reaction and HRP-conjugated anti-phospho antibody

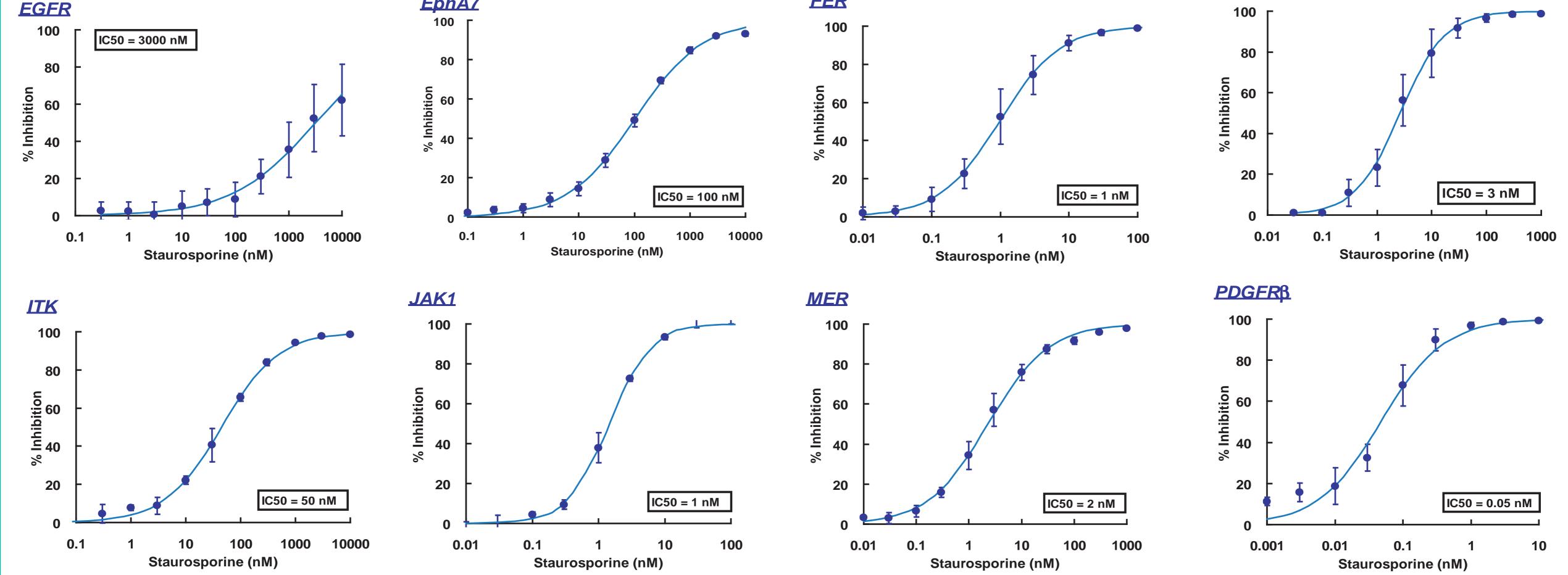
and TMB were used for detection. Absorbance at OD

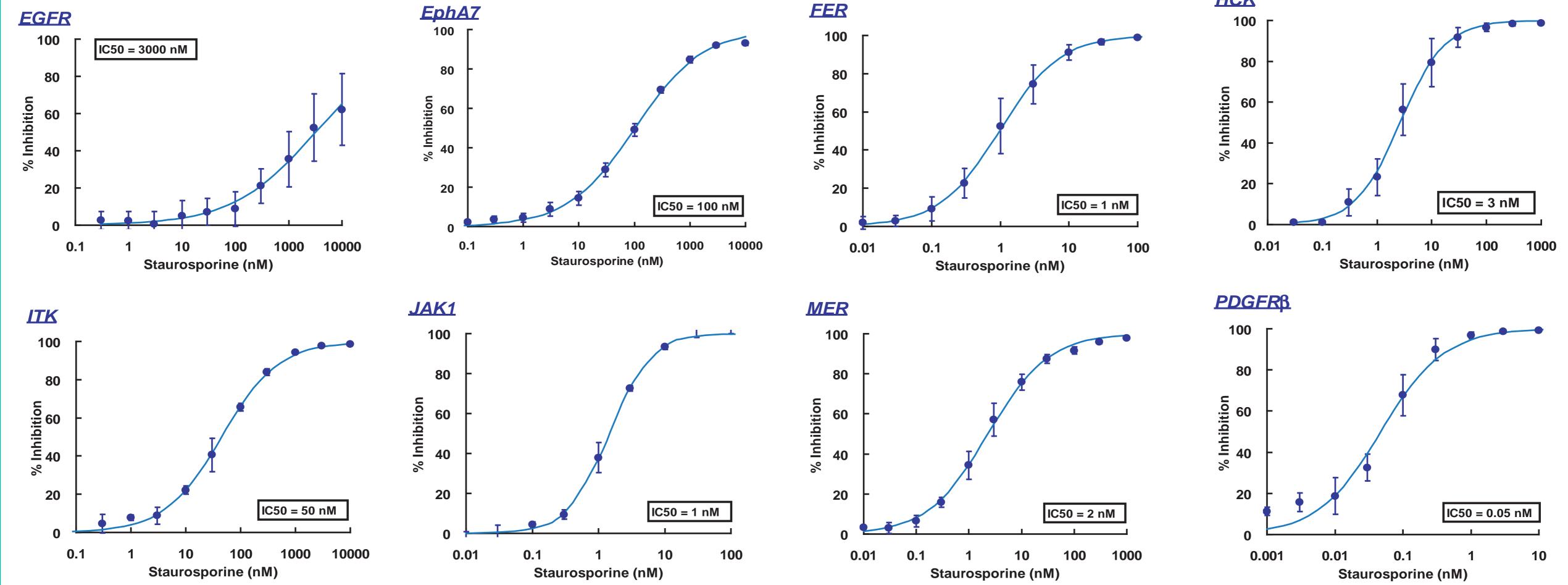
450 nm was measured.

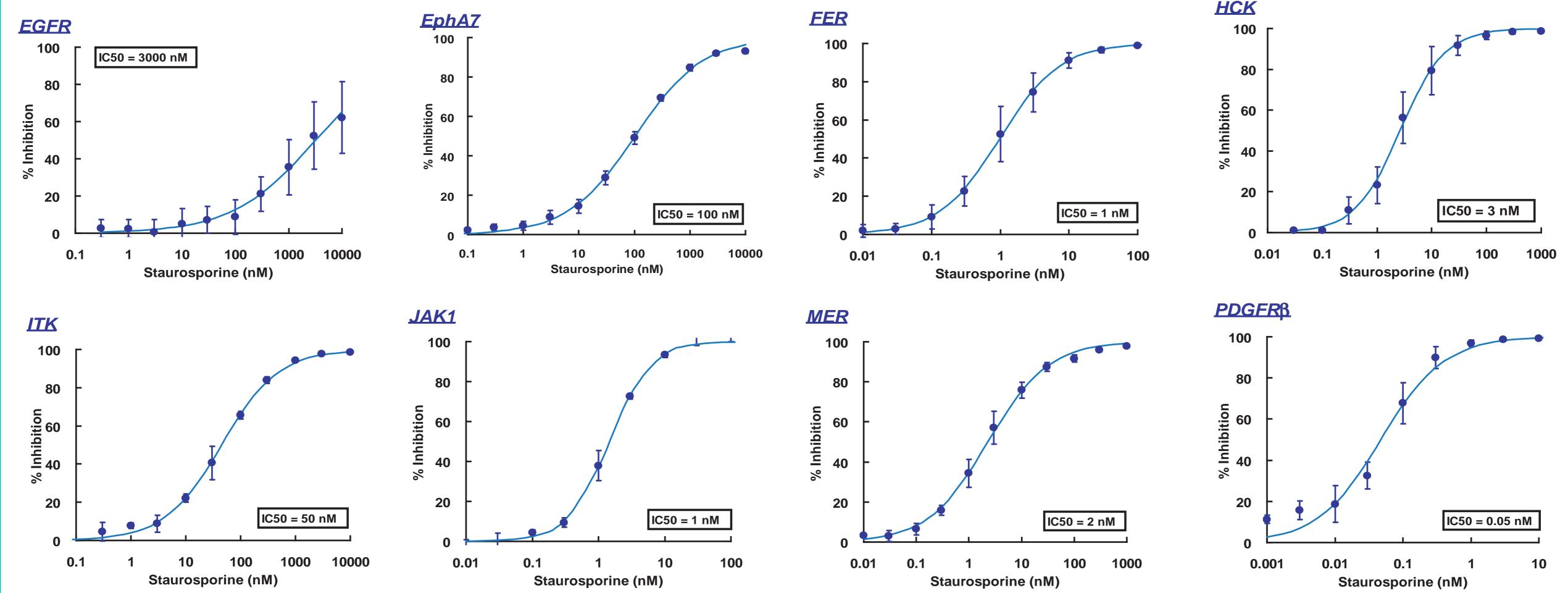
Fig.4 Representative data of Km for ATP. The Michaelis-Menten plot calculated from ATP concentrations and initial velocity values were shown. Initial velocity was determined by a linear least-squares fit from the data obtained with 5 to 30 min reaction. ATP concentrations were varied from 0.3 to 1000 nM by 3 in common ratio. The Km values for EphA7, FER, ITK, JAK1, MER and PDGFR^B were 30, 7, 40, 15, 40 and 15 µM, respectively. The values were 1 to 100 µM for the most of tested (62) TKs.

IC50 Determination (Staurosporine)

To validate the assay, IC50 for non-specific kinase inhibitor Staurosporine was determined.







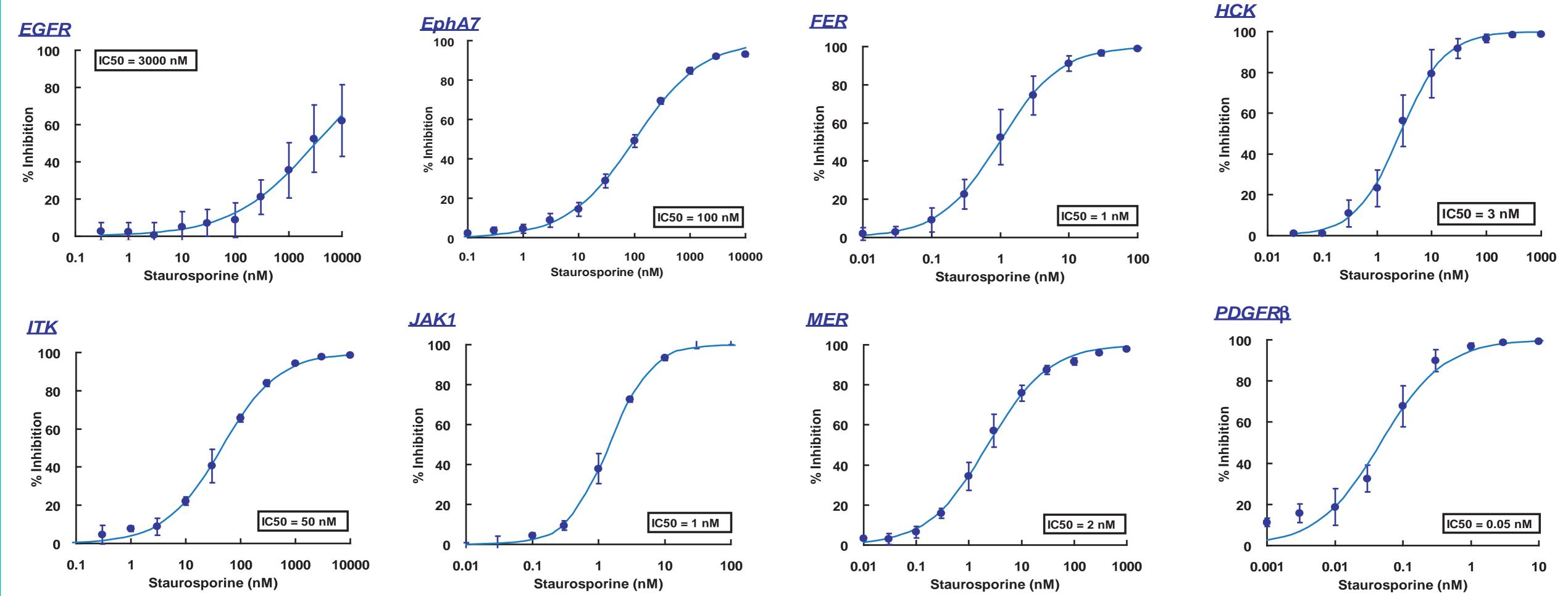


Fig.5 Representative data of IC50 values for Staurosporine. The ATP were used at the concentrations around Km for each kinase. The concentrations of each kinases were lower than 250 ng/mL. The IC50 values for EGFR, EphA7, FER, HCK, ITK, JAK1, MER and PDGFR³ were 3000, 100, 1, 3, 50, 1, 2 and 0.05 nM, respectively.

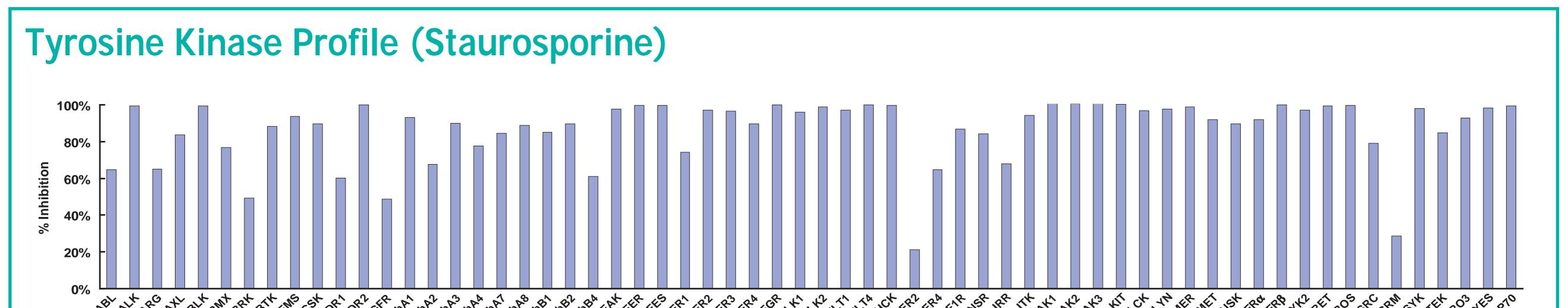


Fig.6 Inhibition study with 62 TKs were conducted with Staurosporine at 1 m. The ATP were used at the concentrations around Km for each kinase. Staurosporine showed more than 50 % inhibition on the most of tested TKs.





ΙΜΑΡ^{ΤΜ}

The IMAP^{IM} fluorescence polarization (FP) assay platform is a generic, homogeneous system applicable to a variety of enzymes, including protein kinases. IMAP^{IM} is based on the high affinity binding of phosphate to immobilized trivalent metals. It has been applied to a wide variety of kinases spanning the whole kinome.

