# LanthaScreen® Eu Kinase Binding Assay for IGF1R

## Overview

This protocol describes how to perform a LanthaScreen® Eu Kinase Binding Assay designed to detect and characterize kinase inhibitors. Procedure 1 describes an experiment to optimize the concentration of tracer to use with a specific kinase target (not necessary when using Invitrogen's kinase). Procedure 2 describes how to perform kinase inhibitor affinity ($IC_{50}$) measurements, using either the concentration of tracer determined by the user following Procedure 1 or using the concentration determined experimentally by Invitrogen. The protocol is accompanied by representative data generated at Invitrogen for both procedures.

LanthaScreen® Eu Kinase Binding Assays are based on the binding and displacement of a proprietary, Alexa Fluor® 647-labeled, ATP-competitive kinase inhibitor scaffold (kinase tracer) to the kinase of interest (Figure 1). Tracers based on a variety of scaffolds have been developed in order to address a wide range of kinase targets. Binding of the tracer to the kinase is detected using a europium-labeled anti-tag antibody, which binds to the kinase of interest. Simultaneous binding of both the tracer and antibody to the kinase results in a high degree of FRET (fluorescence resonance energy transfer) from the europium (Eu) donor fluorophore to the Alexa Fluor® 647 acceptor fluorophore on the kinase tracer. Binding of an inhibitor to the kinase competes for binding with the tracer, resulting in a loss of FRET.

Invitrogen's Kinase Tracers are based on ATP-competitive kinase inhibitors, making them suitable for detection of any compounds that bind to the ATP site or to an allosteric site altering the conformation of the ATP site. Inhibitors that bind the ATP site include both Type I kinase inhibitors, which bind solely to the ATP site, and Type II inhibitors (e.g., Gleevec®/Imatinib, Sorafenib, BIRB-796), which bind to both the ATP site and a hydrophobic site exposed in the DFG-out (non-active) conformation. Type III inhibitors are compounds that do not compete with ATP are loosely referred to as allosteric inhibitors. A study of 15 diverse Type III inhibitors demonstrated that all but one compound was detected in the binding assay with equivalent potency to activity assays. The sole exception was a substrate-competitive compound, and thus not a true allosteric inhibitor.

In contrast to most fluorescence-based kinase activity assays, LanthaScreen® Eu Kinase Binding Assays can be read continuously, which facilitates evaluation of compounds with slow binding kinetics. Also, unlike most activity assays, binding assays can be performed using either active or non-activated kinase preparations, which enables characterization of compounds that bind preferentially to non-activated kinases, such as Gleevec®/imatinib and some allosteric inhibitors.

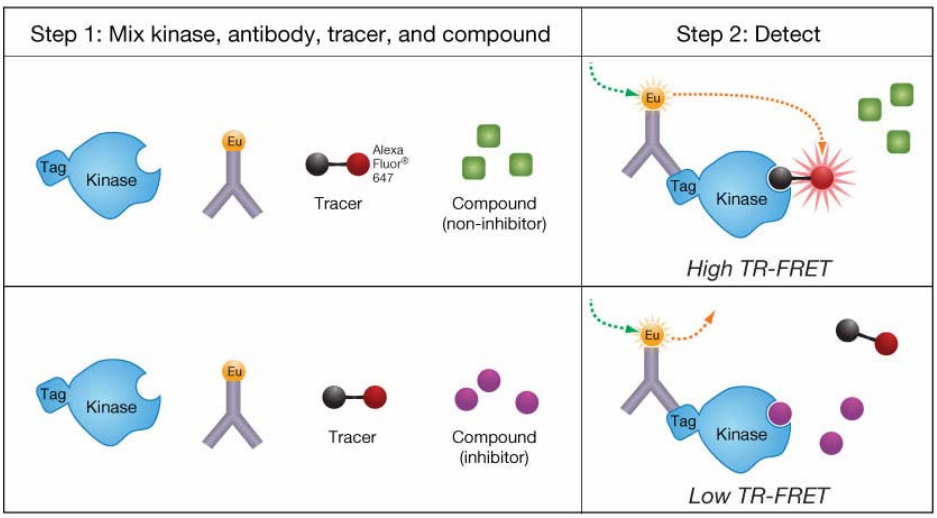


**Figure 1. Schematic of LanthaScreen® Eu Kinase Binding Assay**

## Materials required

| Product Name | Part Number | Concentration | Quantity | Notes |
|---|---|---|---|---|
| IGF1R | PV3250 | 0.1 to 0.5 mg/mL | 10 µg | (1) |
| 5X Kinase Buffer A | PV3189 | 5X | 4 mL | (2) |
| Kinase Tracer 236 | PV5592 | 50 µM in DMSO | 25 µL | (3) |
| Biotin anti-His Tag Antibody | PV6089 or PV6090 | 0.45 to 0.55 mg/mL (3.0 to 3.6 µM) | 25 µg or 1 mg | (4,5) |
| LanthaScreen® Eu-Streptavidin | PV5899 or PV6025 | 0.9 to 1.1 mg/mL (16.4 to 20 µM) | 25 µg or 1 mg | (4,5) |
| Staurosporine (optional) | PHZ1271 | N/A | 100 µg | (6) |

(1) IGF1R is supplied at a concentration between 0.1 to 0.5 mg/mL, with the exact concentration is printed on the product label. The molecular weight of the kinase is 48.9 kD, which can be found on the kinase Certificate of Analysis shipped with the product or at Invitrogen.com/kinase. The kinase molecular weight will be needed to convert the concentration to molarity as required in the following protocol.

(2) Kinase Buffer A is supplied as a 5X concentrated stock. Prepare a 1X solution by adding 4 mL of the 5X solution to 16 mL of distilled $H_2O$. The 1X kinase reaction buffer is stable at room temperature. 1X Kinase Buffer A consists of 50mM HEPES pH 7.5, 10 mM MgCl2, 1 mM EGTA, 0.01% Brij-35.

(3) Kinase Tracer 236 is supplied as a 50 µM stock in DMSO.

(4) Prior to use, the antibody tube should be centrifuged at approximately 10,000 x g for 5 minutes, and the solution needed for the assay should be aspirated from the top of the solution. This centrifugation step will eliminate spurious data points that can arise on occasion due to any particulates in the product.

(5) The LanthaScreen® Eu anti-His Tag Antibody (PV5594 or PV5595) may in some cases be used in place of the Biotin anti-His Tag Antibody, though the signal strength or "assay window" may be somewhat lower

(6) A 1 mM stock of staurosporine can be prepared by dissolving 100 µg of staurosporine in 210 µL of DMSO.

## Basic protocol for inhibitor studies

LanthaScreen® Kinase Binding Assays to evaluate inhibitors are typically performed by addition of 3 components each at 3X the final desired concentration as follows:

1. Add 5 µL of **test compound**.
2. Add 5 µL of **kinase/antibody** mixture.
3. Add 5 µL of **tracer.**
4. Incubate for 1 hour at room temperature and read plate.

## Final assay conditions for inhibitor studies

5 nM kinase[1]
2 nM Eu-Streptavidin
2 nM Biotin Anti-His Tag Antibody
250 nM Kinase Tracer 236[2]
1X Kinase Buffer A

[1]A kinase concentration of 5 nM kinase is recommended as a starting point for assay development as it typically results in a robust signal. Decreasing the kinase concentration may be necessary for accurate measurement of very tight-binding inhibitors, similar to kinase activity assays. For specific test cases, successful assays have been performed with at little as 200 pM kinase, though the assay window may be lower.
[2]A tracer concentration of 250 nM is suggested by Invitrogen, but could also be experimentally determined or optimized in Procedure 1. Optimal tracer concentrations for validated kinases typically fall within the 1 to 100 nM range.

## Plate readers

The data presented in this document were generated using a Tecan Infinite F-500 plate reader using the appropriate filters and instrument settings for europium-based LanthaScreen® assays. The assay can be performed on a variety of plate readers including those from Tecan (Ultra, Infinite F-500, Safire$^2$), Molecular Devices (Analyst and M5), BMG LABTECH (PHERAstar) and Perkin Elmer (EnVision®, Victor, and ViewLux) or any other plate reader configured for LANCE® or HTRF® assays. General instrument settings are listed in the table below:

| | |
|---|---|
| Excitation | 340 nm (30 nm bandpass) |
| Kinase Tracer Emission | 665 nm (10 nm bandpass) |
| LanthaScreen® Eu-anti-Tag Antibody Emission | 615 nm (10 nm bandpass) |
| Dichroic Mirror | Instrument dependent |
| Delay Time | 100 µs |
| Integration Time | 200 µs |

For additional assistance, ask your Invitrogen representative for instrument-specific setup guidelines, or contact Invitrogen Discovery Sciences technical support at 800-955-6288 (select option 3 and enter 40266), or email drugdiscoverytech@invitrogen.com for more information on performing these assays on your particular instrument or for a control to test an instrument.

## Plates

Assays are typically performed in white low-volume 384-well plates (Corning Part#3673 or Greiner 784207) or black, low-volume 384-well plates (Corning Part#3676). White plates are generally recommended as they yield higher quality data for many assays, especially those with a relatively low assay window (1.5 to 2 fold) or those that are being measured on monochromater-based instruments or some filter-based instruments (e.g. Perkin Elmer EnVision®). In other cases, black and white plates yield comparable data.

# Procedure 1. Optimization of tracer concentration

***Note: When using an Invitrogen kinase, this step is not necessary. One can typically proceed to inhibitor studies (Procedure 2).***

This step describes how to optimize the tracer concentration for use in subsequent inhibitor studies by performing binding assays with a 2-fold serial dilution of tracer. This experiment allows for approximation of the tracer dissociation constant ($K_d$) and evaluation of the signal strength or "assay window" as a function of tracer concentration. It is typically best to select a tracer concentration near $K_d$ or below $K_d$ to ensure sensitive detection of inhibitors. For example, the measured $IC_{50}$ value from a simple compound titration will approach $K_i$ (dissociation constant of a competitive inhibitor) if [tracer] < tracer $K_d$ and [kinase] << [tracer]. The majority of kinase assays validated by Invitrogen yield a robust signal with the tracer no more than twice the $K_d$ value. In many cases, the $K_d$ value can also be used to calculate $K_i$ from a compound titration experiment using the Cheng-Prusoff equation (see Procedure 2), which compensates for the tracer concentration being above $K_d$. The other factor to consider when selecting a tracer concentration is the signal strength or "assay window" as it correlates very well with assay robustness (i.e. Z' values). Although in many cases assay windows can exceed 10-fold, excellent Z' values are typically obtained with an assay window as low as 2-fold (See Appendix A). The specific end application may also impact the choice of tracer concentration, based on both the assay window, Z', and $K_d$ value.

The relatively simple method to determine tracer $K_d$ described in Procedure 1 is supported by data from an alternative method to calculate $K_d$ (in addition to $K_i$) as described in Appendix B. This alternative method is based on a series of inhibitor titrations performed at different tracer concentrations and the resulting $K_d$ values correlate well with those derived using the more rapid method of Procedure 1.

## Estimation of tracer $K_d$ and assay window

(1.1) Reagent preparation

1. A dilution series of tracer is prepared at 3 times the final concentration to be assayed.
    a. Dilute tracer to 3000 nM by adding 3.6 µL of 50 µM stock tracer to 56 µL of 1X Kinase Buffer A.
    b. Add 50 µL of 1X Kinase Buffer A to 6 wells in each of 2 columns of a 96-well plate.
    c. Add 50 µL of 3000 nM tracer to well A1 and mix.
    d. Remove 50 µL from well A1, transfer to well A2 and mix.
    e. Remove 50 µL from well A2, transfer to well B1 and mix.
    f. Continue process as depicted in Figure 2.

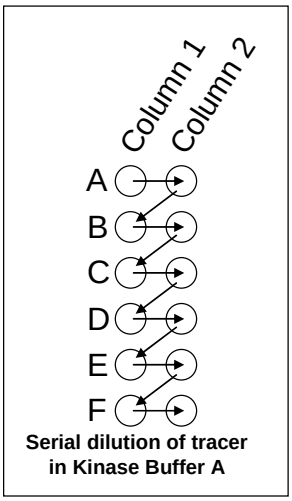


**Figure 2. Serial dilution of tracer.**

2. Prepare kinase/antibody solution at 15 nM kinase, 6 nM antibody and 6 nM Eu-Streptavidin (3X the desired final assay concentrations for each component). Centrifuge both the antibody tube and the Eu-Streptavidin tube at approximately 10,000 x g for 10 minutes and aspirate desired volume from the top of the solution. Add the volumes of reagents calculated below to the calculated volume of Kinase Buffer A.

   **Calculations (for a 1000 µL solution)**:

   **Stock kinase conc. (nM)** = $\frac{\text{stock conc. (mg/mL)} * 1{,}000{,}000{,}000 \text{ (nmol/mol)}}{48900 \text{ (g/mol)}}$ [Note: kinase MW]

   **Kinase volume needed (µL)** = $\frac{1000 \text{ µL} * 15 \text{ nM}}{\text{Stock kinase conc. (nM)}}$

   **Antibody volume needed (µL)** = $\frac{1000 \text{ µL} * 6 \text{ nM}}{\text{Stock antibody conc. (µM)} * 1000 \text{ (nmol /µmol)}}$

   **Eu-SA volume needed (µL)** = $\frac{1000 \text{ µL} * 6 \text{ nM}}{\text{Stock Eu-SA conc. (µM)} * 1000 \text{ (nmol /µmol)}}$

   **Kinase Buffer A needed (µL)** = 1000 µL – kinase volume (µL) – antibody volume (µL) – Eu-SA volume (µL)

3. Prepare 30 µM staurosporine ("competitor solution") by diluting 30 µL of 1 mM staurosporine (from a stock in DMSO) into 970 µL Kinase Buffer A.
4. Prepare 3% DMSO control solution by adding 30 µL DMSO to 970 µL Kinase Buffer A.

(1.2) Experimental procedure

1. Add 5 µL of each concentration of serially diluted tracer to six replicate assay wells in a 384-well plate (columns 1-6) as depicted in Figure 3.

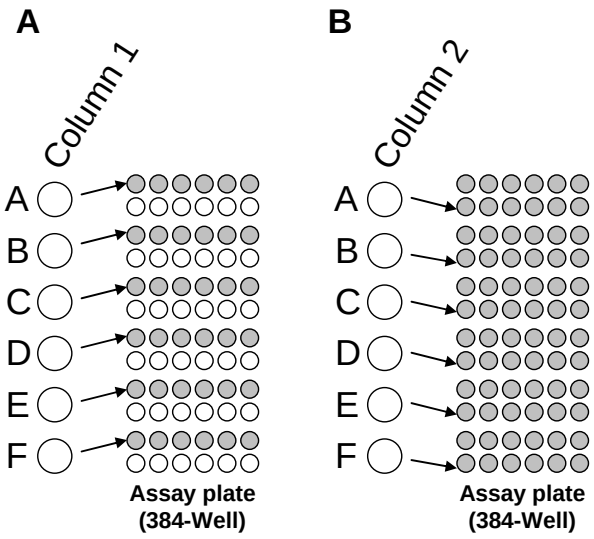


**Figure 3. Transfer of tracer dilutions from 96-well to 384-well plate.**

2. Add 5 µL of competitor solution to three wells for each tracer concentration (columns 1-3).
3. Add 5 µL of DMSO control solution to the other three wells for each tracer concentration (columns 4-6).
4. Add 5 µL of kinase/antibody solution to all wells in columns 1-6.
5. Incubate the plate at room temperature for 60 min and read plate.

(1.3) Data analysis

1. Divide the acceptor/tracer emission (665 nM) by the antibody/donor emission (615 nM) to calculate the "emission ratio".
2. Plot [tracer] versus emission ratio for the competitor (staurosporine) and control (DMSO only) (Figure 4). The sigmoidal dose-response curve with a variable slope can be fit to the data (optional). The following equation can be used with GraphPad™ Prism software:

```
F=50
logEC50=logECF-(1/HillSlope)*log(F/(100-F))
Y=Bottom+(Top-Bottom)/(1+10^((LogEC50-X)*HillSlope))
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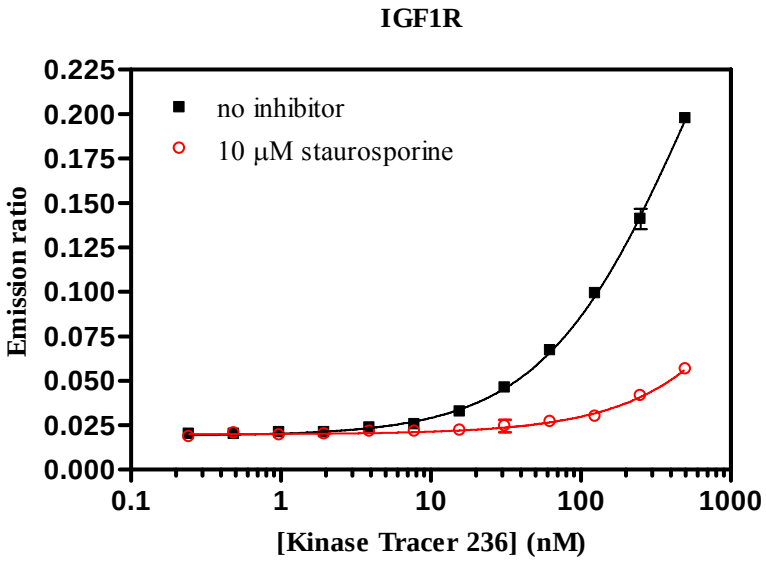



**Figure 4. Tracer titration curve.**

3. The assay window for any given tracer concentration can be calculated by dividing the signal in the absence of competitor (+ staurosporine curve) by the signal in the presence of competitor. The assay window is one of two criteria (the other being the tracer $K_d$) that are typically used to select a tracer concentration for inhibitor studies. Assays windows of ≥ 2 usually result in high Z' values (see Appendix A).
4. Subtract the competitor curve (+ staurosporine) from the control curve (DMSO only) to correct for background signal, which is typically due to diffusion enhanced FRET from Eu to unbound tracer.
5. Plot the background-corrected emission ratios versus [tracer] and fit to the one site binding (hyperbola) equation to estimate the dissociation constant (Figure 5). In some cases data at the highest one or two tracer concentrations are excluded from curve fits due to relatively high "background" signal in presence of competitor. This can be observed as these data points deviate from the one site binding model, whereas the other points align.

   The following equation can be used with GraphPad™ Prism software: $Y=Bmax*X/(K_d + X)$

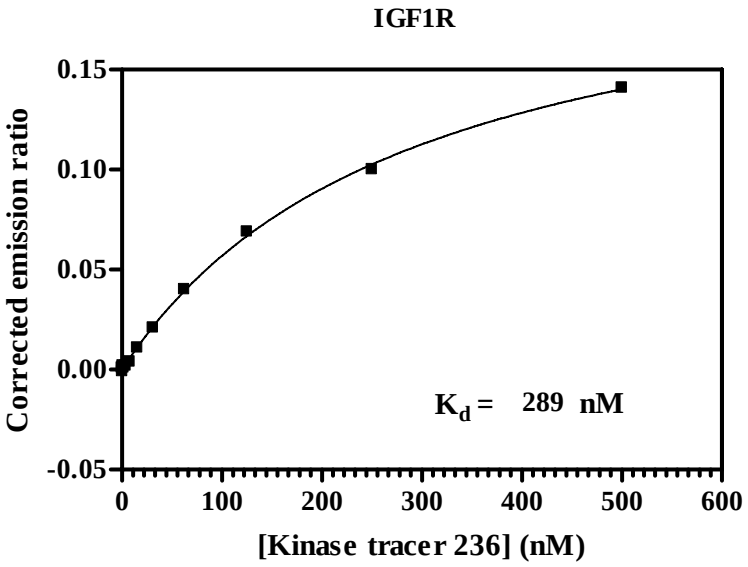



**Figure 5. Tracer $K_d$ determination.**

## Procedure 2. $IC_{50}$ determination

This procedure describes how to determine inhibitor potencies by generating a 10-point $IC_{50}$ curve from a 4-fold dilution series of test compound. The concentration of tracer used in the below protocol is based on the tracer titration from Procedure 1.

250 nM Tracer 236 was chosen by Invitrogen for inhibitor studies. Under these conditions a high Z' value of 0.86 was obtained while keeping the tracer concentration close to the $K_d$ value (290 nM).

(2.1) Reagent preparation

1. Prepare an intermediate dilution series of each test compound by 4X serial dilution in DMSO such that the top concentration is 1 mM (suggested starting point) (Figure 6, Step 1).
   a. Prepare 4 mM test compound in DMSO.
   b. Add 60 µL of DMSO to 5 wells in each of 2 columns of a 96-well plate (wells A1 to E2).
   c. Add 20 µL of 4 mM compound to well A1 and mix.
   d. Remove 20 µL from well A1, transfer to well A2 and mix.
   e. Remove 20 µL from well A2, transfer to well B1 and mix.
   f. Continue process as depicted in Step 1 of Figure 6.

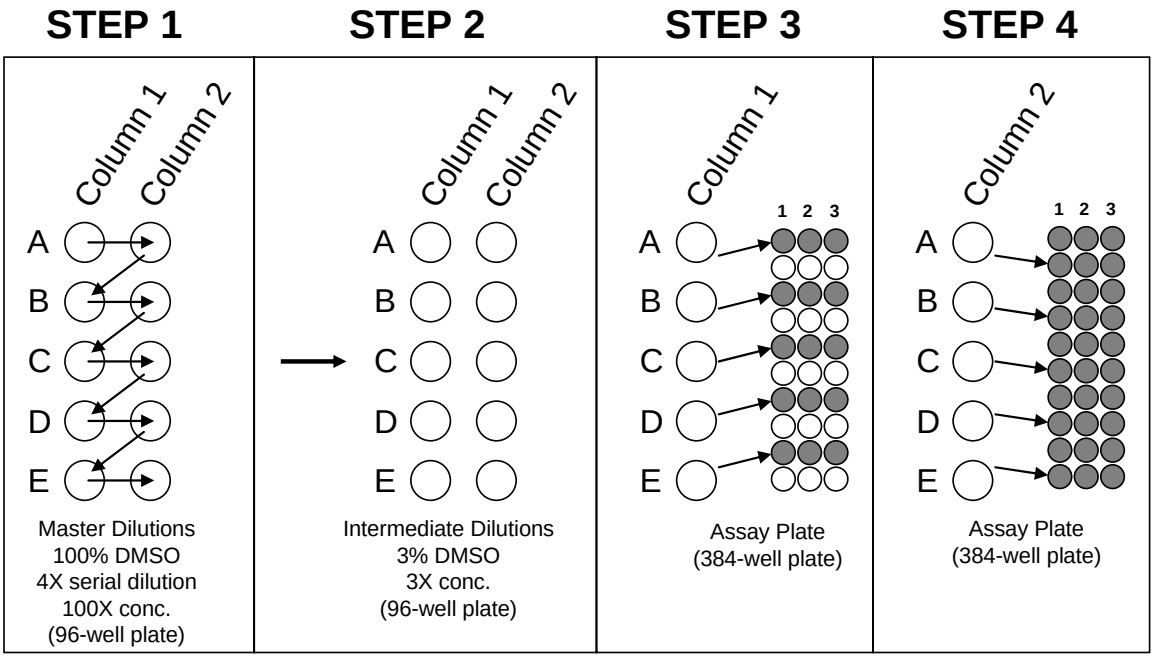



**Figure 6. Compound serial dilution.**

2. Dilute the "Master Dilution" series 33.3-fold into Kinase Buffer A. Remove 5 µL of each concentration of diluted compound, transfer to another 96-well plate, add 162 µL of Kinase Buffer A and mix (Figure 6, Step 2).
3. Prepare tracer solution in Kinase Buffer A at 750 nM tracer (3X the desired final assay concentration). Add the volumes of reagents calculated below to calculated volume of Kinase Buffer A.

   **Calculations (for a 1000 µL solution)**:

   **Tracer volume needed (µL)** = $\frac{1000\ \mu L^{1} * 750\ nM^{2}}{1000\ nM/\mu M * 50\ \mu M^{3}}$

   [1]final volume of solution
   [2]desired 3X tracer concentration
   [3]stock tracer concentration

   **Kinase Buffer A needed (µL)** = 1000 µL – tracer volume needed (µL)

4. Prepare kinase/antibody solution at 15 nM kinase, 6 nM antibody and 6 nM Eu-Streptavidin (3X the desired final assay concentrations for each component). Centrifuge both the antibody tube and the Eu-Streptavidin tube at approximately 10,000 x g for 10 minutes and aspirate desired volume from the top of the solution. Add the volumes of reagents calculated below to the calculated volume of Kinase Buffer A.

   **Calculations (for a 1000 µL solution)**:

   **Stock kinase conc. (nM)** = $\frac{\text{stock conc (mg/mL)} * 1{,}000{,}000{,}000\ \text{(nmol/mol)}}{48900\ \text{(g/mol) [Note: kinase MW]}}$

   **Kinase volume needed (µL)** = $\frac{1000\ \mu L * 15\ nM}{\text{Stock kinase conc. (nM)}}$

   **Antibody volume needed (µL)** = $\frac{1000\ \mu L * 6\ nM}{\text{Stock antibody conc (µM)} * 1000\ \text{(nmol/µmol)}}$

   **Eu-SA volume needed (µL)** = $\frac{1000\ \mu L * 6\ nM}{\text{Stock Eu-SA conc. (µM)} * 1000\ \text{(nmol /µmol)}}$

   **Kinase Buffer A needed (µL)** = 1000 µL – kinase volume (µL) – antibody volume (µL) – Eu-SA volume (µL)

(2.2) Experimental procedure

1. Add 5 µL of each concentration of serially diluted compound to triplicate assay wells in a 384-well plate (columns 1-3) as depicted in Steps 2 and 3 of Figure 6.
2. Add 5 µL of kinase/antibody solution to all wells.
3. Add 5 µL of tracer solution to all wells.
4. Incubate the plate at room temperature for 60 min and read.

   Note: 60 minutes is a general guideline for incubation. However, in some cases multiple read times or continuous measurements may be used to examine the kinetics of binding reactions as might be of interest for studies on slow-binding compounds.

(2.3) Data analysis

1. Divide the acceptor/tracer emission (665 nM) by the antibody/donor emission (615 nM) to calculate the "emission ratio".
2. Plot [test compound] versus emission ratio. The sigmoidal dose-response curve with a variable slope can be fit to the data (see section 1.3, step 2 for equation). Representative date generated by Invitrogen for a set of well-characterized kinase inhibitors is presented in Figure 7. A comparison of $IC_{50}$ values to literature and in some cases internally generated data from activity-based assays (SelectScreen® profiling service) are provided as a reference in Table 1.
3. In some cases, the Cheng-Prusoff equation[1] (equation 1) can be used to convert $IC_{50}$ to $K_i$ based on the concentration of Tracer and an accurate Tracer $K_d$ (determined by following Procedure 1 or Appendix B).

$$(1)\quad K_i = \frac{(IC_{50})}{\left(1+\left(\frac{[Tracer]}{K_d}\right)\right)}$$

This relationship holds true when the following criteria are met:

1. [kinase] << [tracer] and [kinase] << $IC_{50}$
2. [kinase] < Tracer $K_d$
3. There is a single class of binding sites

In order to determine $K_i$ values for very tight-binding compounds, it may be necessary to perform assays at lower kinase concentrations.

[1]Cheng, Y.C., Prusoff, W.H. *Biochem Pharmacol.* (22) 3099-3108 (1973).

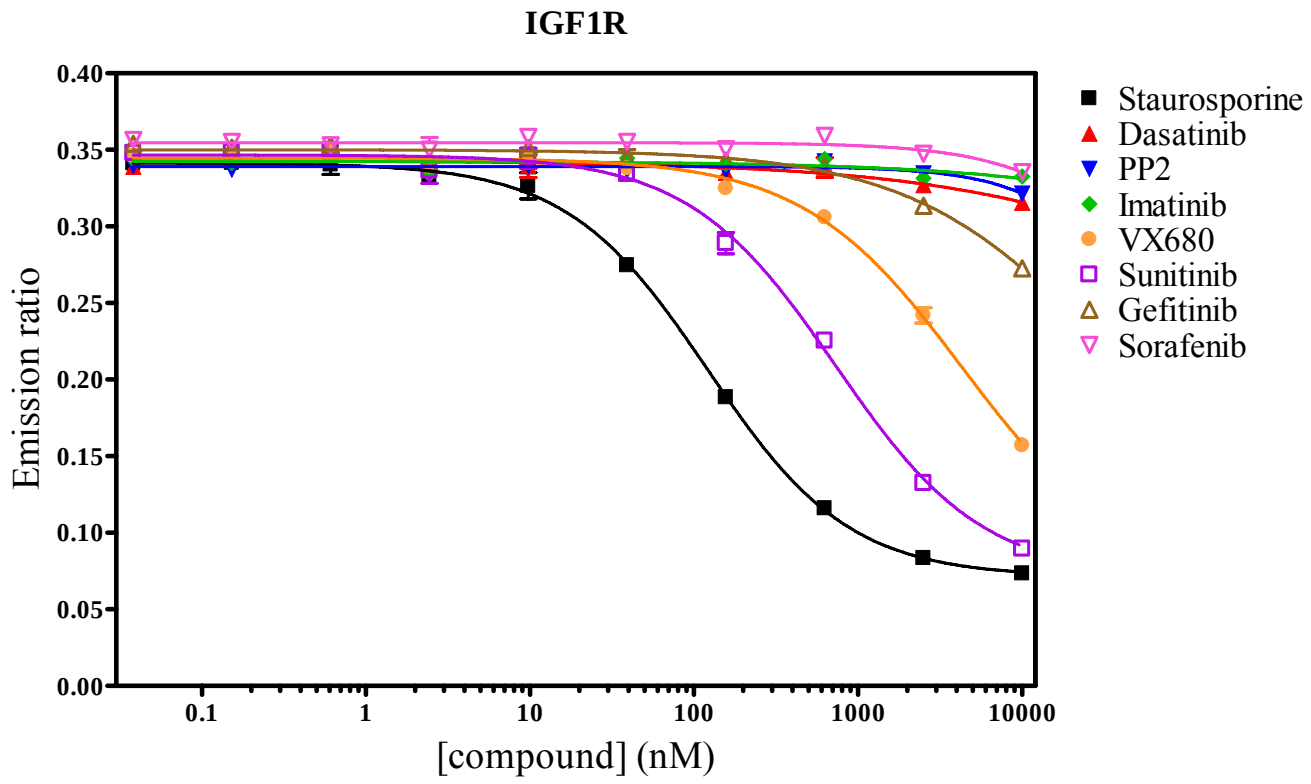



**Figure 7. Representative data generated at Invitrogen.**

**Table 1. $IC_{50}$ values (nM) and comparison to literature and activity-based data.**

| Compound | LanthaScreen® Eu Kinase Binding Assay | SelectScreen® Kinase Activity Assay | Literature $K_d$ values (Karaman et al.) |
|---|---|---|---|
| Staurosporine | 120 | 100 | 210 |
| Dasatinib | >10000 | >5000 | >10000 |
| PP2 | >10000 | >5000 | n.d. |
| Imatinib | >10000 | >5000 | >10000 |
| VX680 | 8100 | >5000 | 740 |
| Sunitinib | 790 | 610 | 2600 |
| Gefitinib | >10000 | n.d. | >10000 |
| Sorafenib | >10000 | >5000 | >10000 |

Karaman, M.Z., *et al*. *Nat. Biotechnol.* 26(1) 127-132 (2008)

Note: These data are provided for reference purposes. It is important to consider that the source of enzymes and method of detection (activity assay vs. binding assay) will affect whether measurements of $IC_{50}$ values are due to active kinase, non-activated kinase, or a combination of both.

# Appendix A. Assay robustness as a function of assay window

The Z'-factors for 215 kinase:tracer pairs were determined and plotted as a function of assay window (Figure A1). The data demonstrate excellent Z' values are typically obtained with an assay window of ≥ 2. Whereas, assay windows in the 1.5 to 2-fold range yield Z' values between 0.4 and 0.7, which may be suitable for some applications.

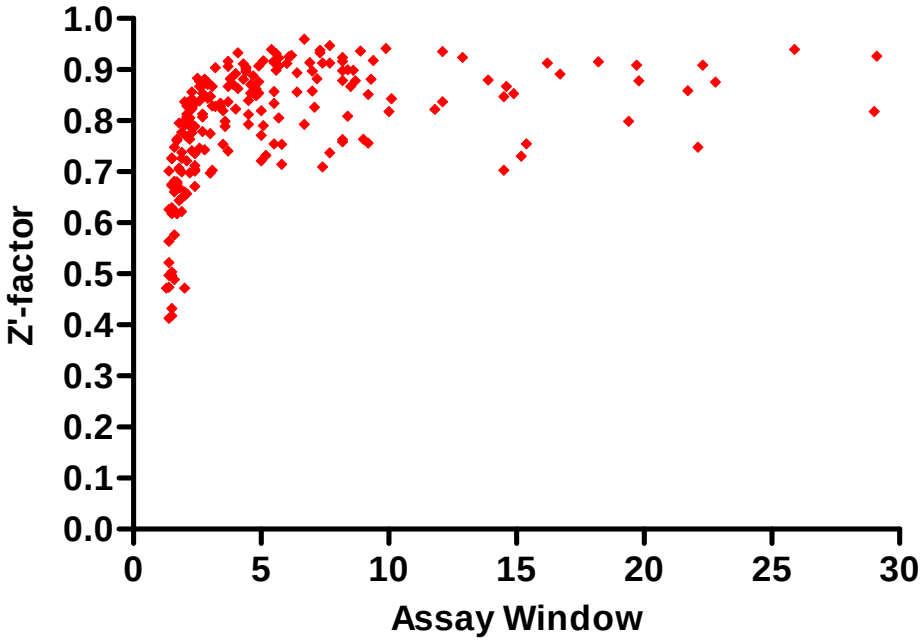



**Figure A1. Z'-factor as a function of assay window for 215 kinases.**

# Appendix B. Alternate method to determine tracer $K_d$ and $K_i$ values

A simple method to determine tracer $K_d$ values from a tracer titration is described in Procedure 1, whereas an alternate method is described here based on $IC_{50}$ curves performed at various tracer concentrations followed by analysis with the Cheng-Prusoff equation. In addition to determination of tracer $K_d$ values, this method also enables calculation of $K_i$ values (dissociation constant for the inhibitor). Rearrangement of the Cheng-Prusoff equation results in a linear relationship (i.e. the form $y = mx + b$) useful for analysis of binding data from homogenous assays (equation 2)[2]. When plotted with the $IC_{50}$ value on the y-axis and the tracer concentration of the x-axis, the $K_i$ is equal to the y-intercept and the slope equals $[K_i]/[K_d]$. Thus, the y-intercept divided by the slope equals the tracer $K_d$. This method enables calculation of the tracer $K_d$ from $IC_{50}$ curves performed at various concentrations of tracer.

(2) $$IC_{50} = \left(\left(\frac{K_i}{K_d}\right) \times [Tracer]\right) + K_i$$

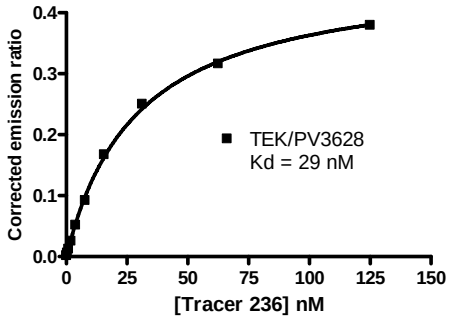
Application of the Cheng-Prusoff equation is valid if the following criteria are met:

1. There is a single class of ligand binding site
2. The is no ligand depletion (i.e. [tracer] >> [kinase])
3. The receptor concentration < $K_d$

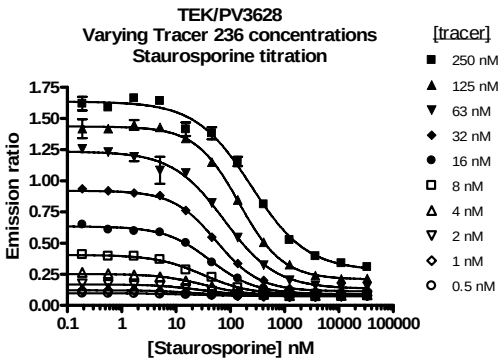
This method was applied to calculated the tracer $K_d$ for representative kinase:tracer interactions with a range of affinities and compared to the tracer titration method (Procedure 1). Example data are presented for the kinase TEK. The $K_d$ value calculated from a tracer titration is 29 nM whereas that calculated using the linearized Cheng-Prusoff equation using staurosporine as the inhibitor is 31 nM and using VX680 is 30 nM, in close agreement (Figure B1). Data for all kinases compared with both methods is in Table B1, showing close agreement between both methods and supporting use of the more simple method based on a single tracer titration.

[2]Newton, P., et al. *J Biomol Screen.* 13(7) 674-682 (2008).

**A**




**B**

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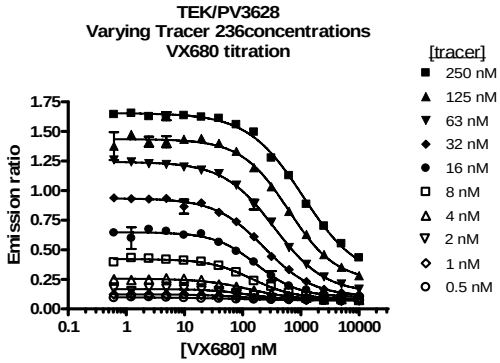


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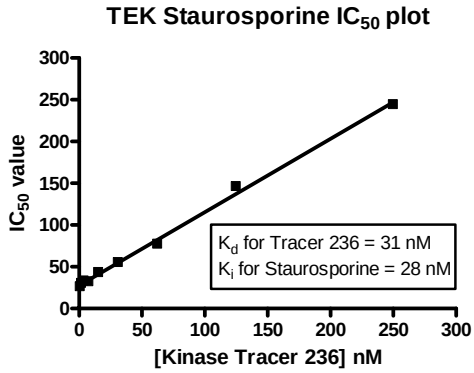


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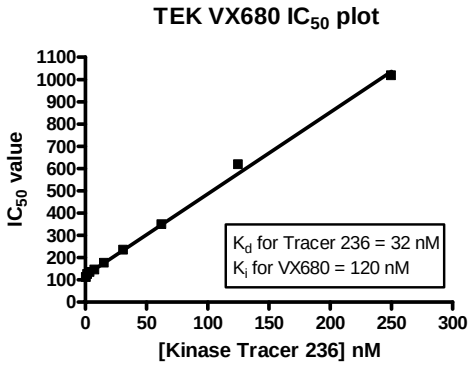


**Figure B1. Determination of tracer $K_d$ values by linearized Cheng-Prusoff equation and tracer titration method.** The tracer $K_d$ value was determined by the tracer titration method essentially as described in Procedure 1 with Kinase Tracer 236 and Eu-anti-GST antibody (A). $IC_{50}$ curves were determined for TEK for the inhibitors staurosporine (B) and VX680 (C) essentially as described in Procedure 2 with various concentrations of Kinase Tracer 236. $IC_{50}$ values were then plotted against the tracer concentration and the $K_d$ values for the Tracer and Kinase and the $K_i$ values for the inhibitor and the Kinase were determined from the slope and y-intercept.

**Table B1. Comparison of $K_d$ determination by linearized Cheng-Prusoff equation and tracer titration method.**

| | Tracer $K_d$ values (nM) | | |
|---|---|---|---|
| **Kinase** | **Tracer titration** | **Linearized Cheng-Prusoff with Staurosporine** | **Linearized Cheng-Prusoff with VX-680** |
| TEK | 29 | 31 | 30 |
| TAOK2 | 60 | 82 | 71 |
| ITK | 46 | 45 | n.d. |
| MAP3K3 | 184 | 230 | n.d. |
| MYLK2 | 237 | 299 | n.d. |