

Electrophoretic Mobility Shift as a Detection Method for Inhibitors of Protein Kinases

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Introduction

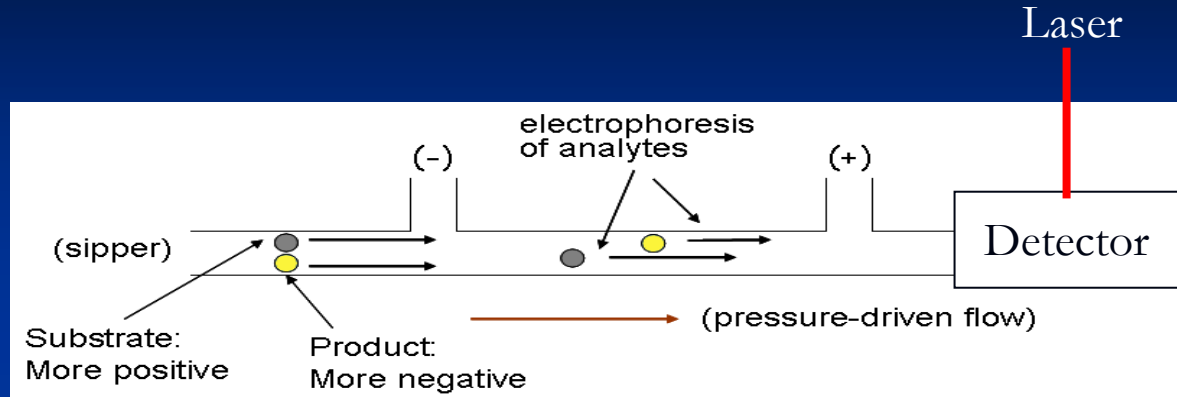
- >500 protein kinases are present in the human genome
- Protein kinases regulate significant aspects of cell life through the phosphorylation of protein substrates
 - metabolism, cell cycle progression, cytoskeletal rearrangement, cell movement, apoptosis, differentiation
- Catalytic domain
 - Bisubstrate reaction
 - ATP/divalent cation binding
 - Protein/peptide substrate binding
 - Phosphate transfer from ATP to substrate
- Common catalytic mechanism among kinase family members leads to issues with inhibitor selectivity
- In-vitro kinase selectivity of drug candidates can be monitor with simple bioassay techniques



Filtration, the 'Golden Standard'

- Separates phosphorylated product from unphosphorylated substrate with little or no interference
- Discontinuous or end-point assay
 - Assumptions:
 1. Time point measurement is within the initial velocity phase of the reaction
 2. Conditions used to stop the reaction leads to an instantaneous and permanent halt of signal production
- Laborious and require the use of ^{33}P - γATP
- It is critical to restrict the assay time to the initial velocity phase of the reaction

Electrophoretic Mobility Shift Technology

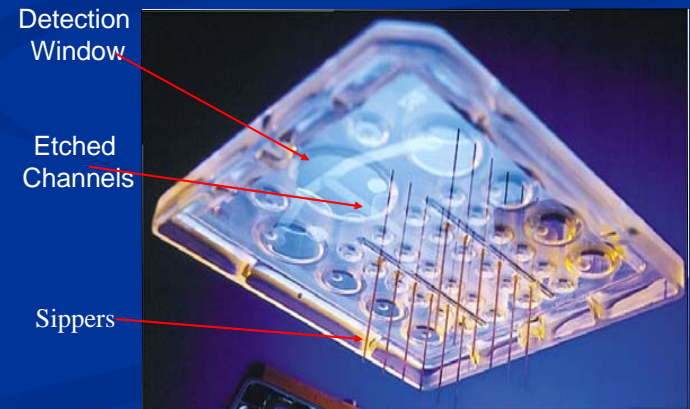


Electrophoretic separation of substrate and product

LabChip 3000



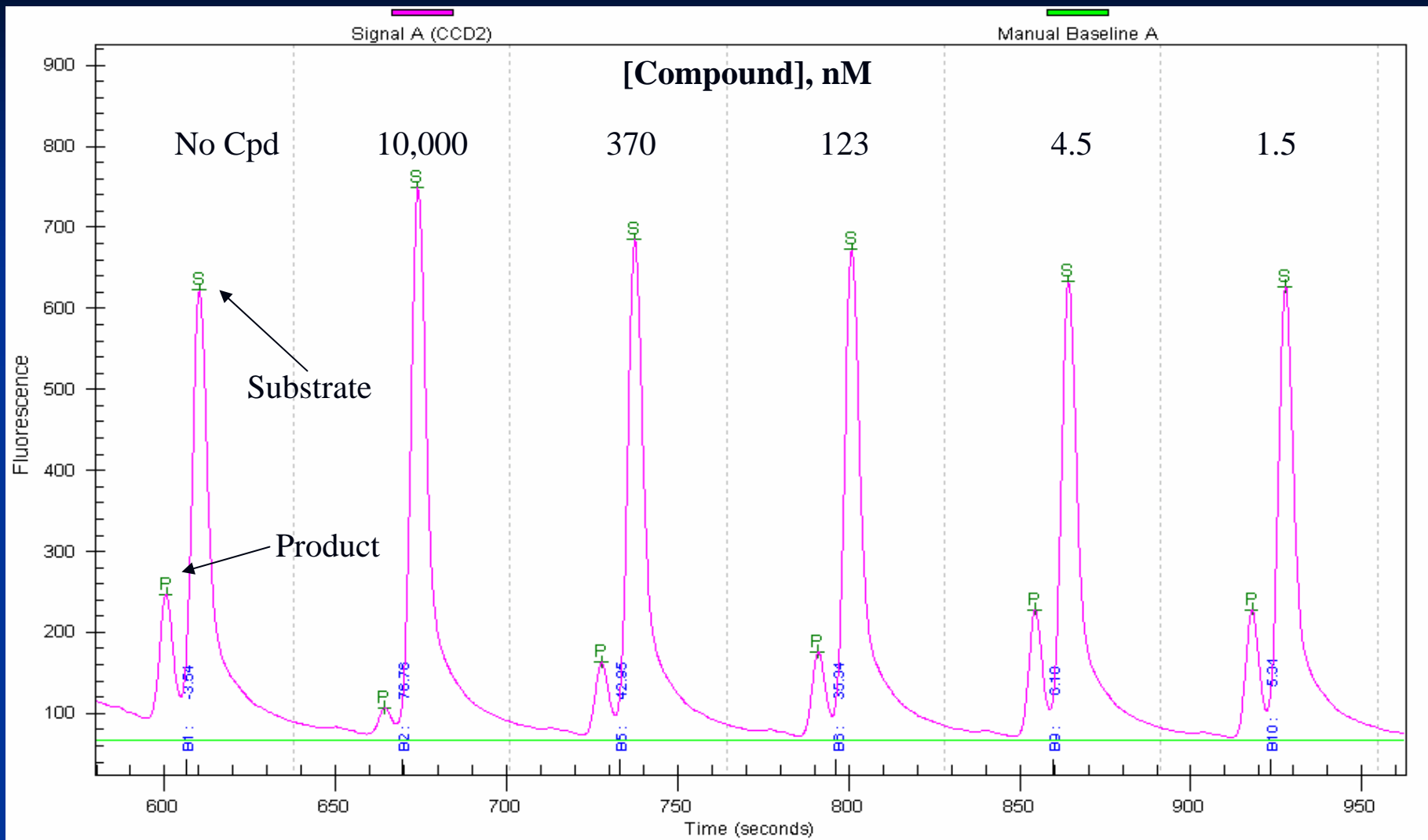
- Humidified Chamber
- Plate Stackers
- Microfluidic Chip Cartridge
- Controller and Pumps



Microfluidic Chip

Phila. LRIG Sept. 22nd 2005

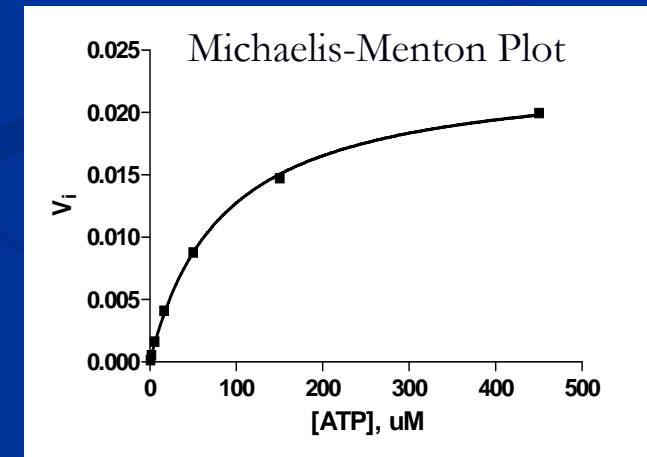
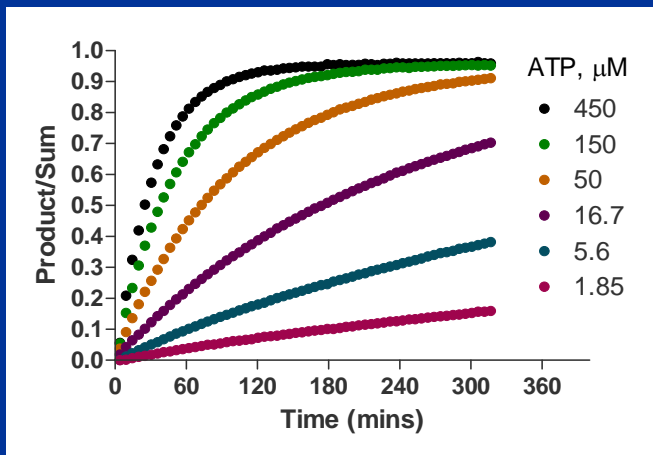
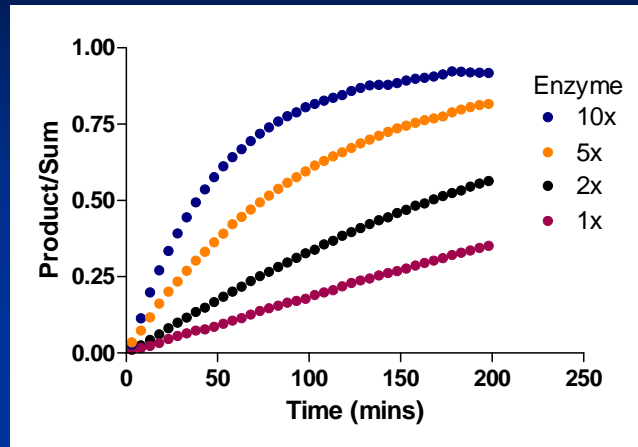
Detection of Protein Kinase Inhibition



➤ Compound inhibition is determined by calculating $P/(P+S)$ relative to control

Mobility Shift Assay Development

Enzyme Titer



➤ Continuous monitoring of the enzymatic reaction allows for accurate determination of kinetic constants under exact assay screening conditions

Correlation of ATP K_m^{app}

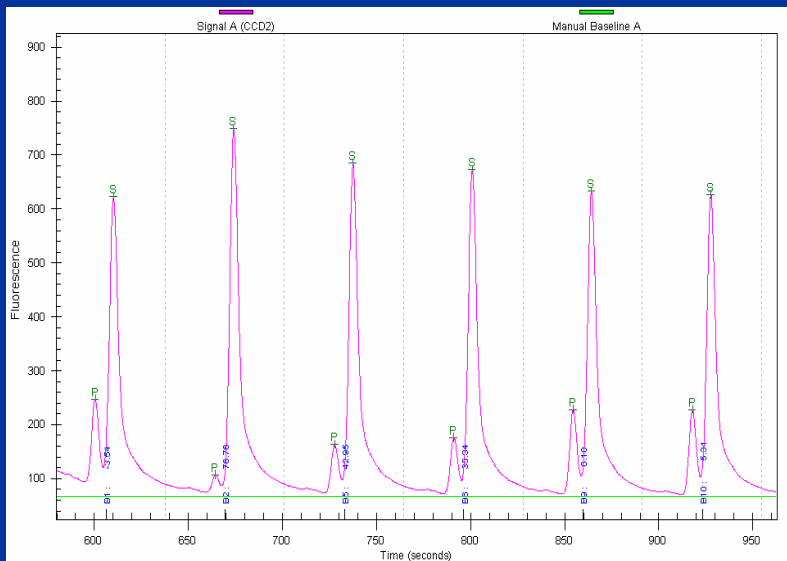
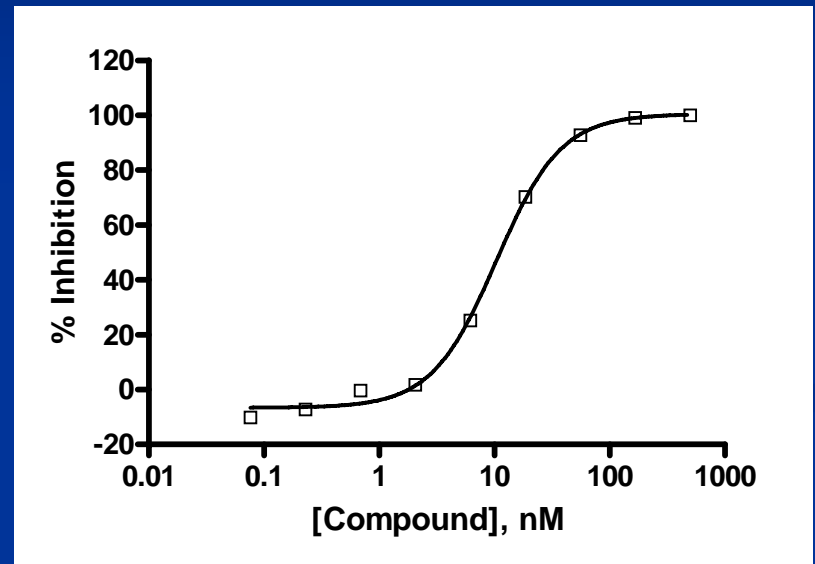
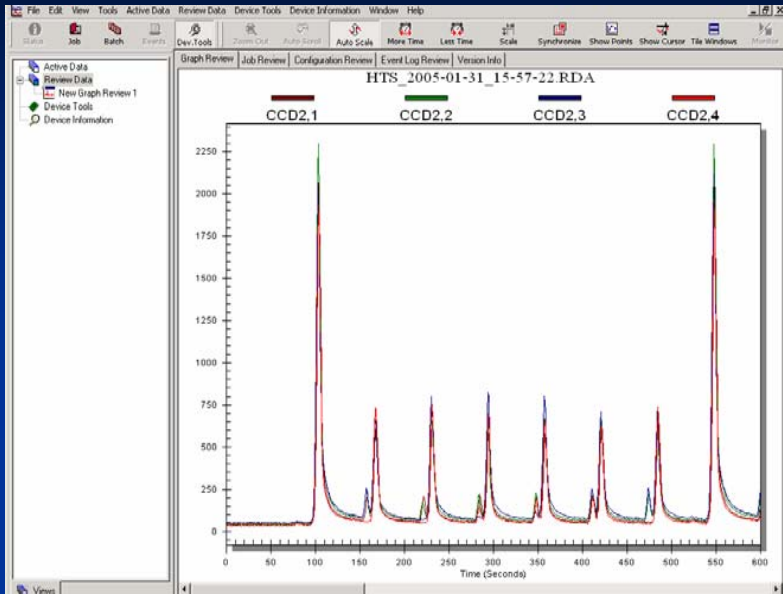
Enzyme Group	Filtration, K_m (uM)	Mobility Shift, K_m (uM)
TK	25	25
GMGC	33	84
AGC	25	25

➤ K_m values generated by mobility shift correlate with those from filtration

G. Manning, D. B. Whyte, R. Martinez, T. Hunter, S. Sudarsanam. The protein kinase complement of the human genome. *Science* 298, 1912-1914 (2002).



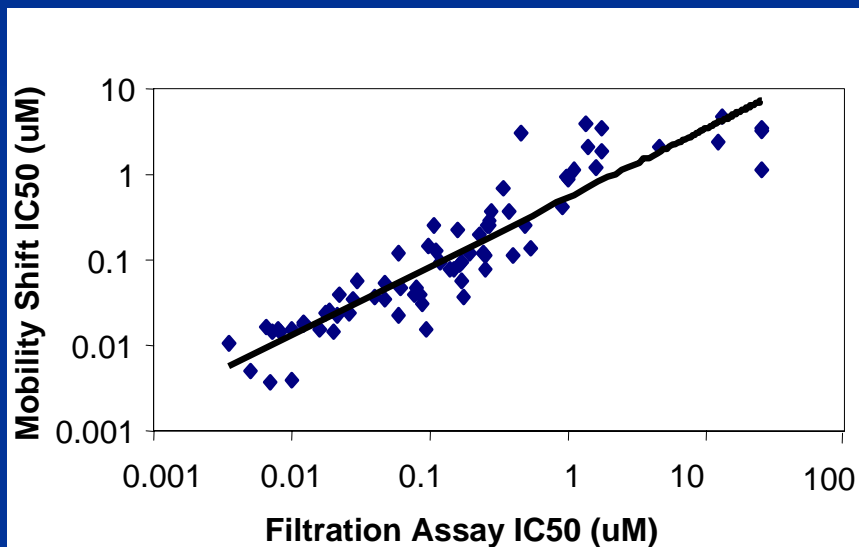
Mobility Shift Data Analysis



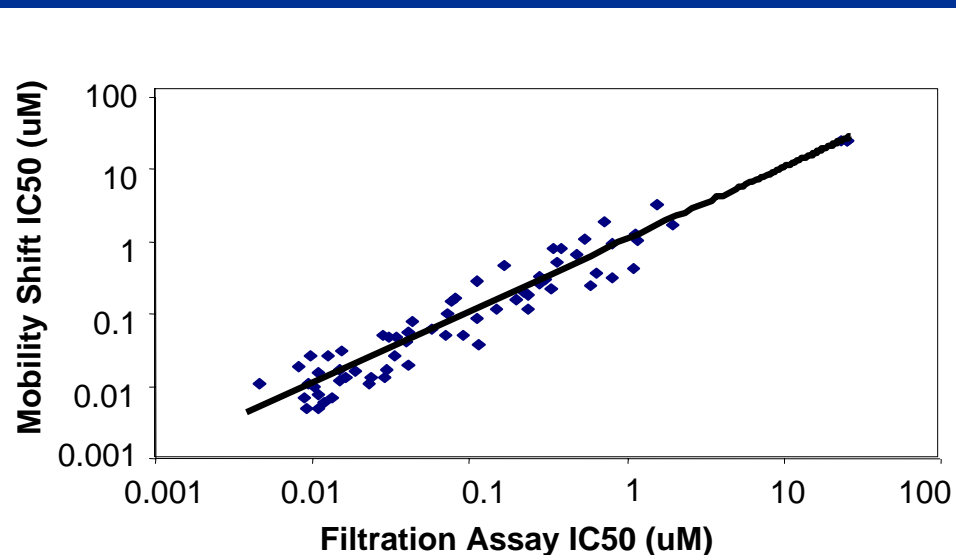
➤ Mobility shift data analysis is a multi-step process

Mobility Shift Assay Compound Validation

Tyr Kinase Inhibition

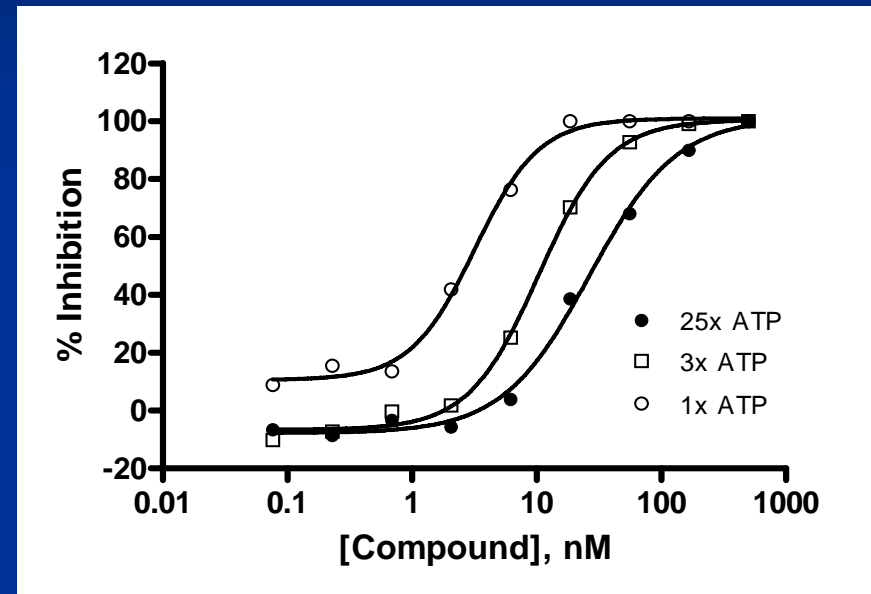
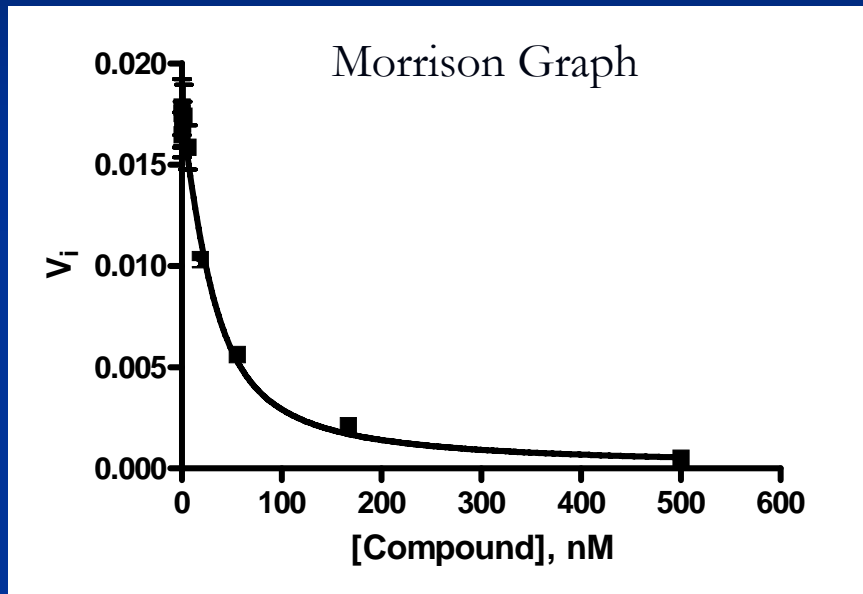


Ser/Thr Kinase Inhibition



➤ Correlation between filtration and mobility shift assays is observed for both inhibitor types

Compound Kinetic Characterization using the Mobility Shift Assay



➤ The evaluation of lead compounds using the mobility shift assay allows for steady state determination of compound potency and mechanism of action

Summary

- Filtration is a radioactive, laborious, and discontinuous assay method requiring enzyme quenching prior to signal detection
- Electrophoretic mobility shift allows for enzymatic characterization and lead compound evaluation using initial velocity measurements
- The mobility shift assay is an ideal method for measuring the initial enzymatic rate and makes subsequent analysis of reaction mechanism and inhibition modality uncomplicated and reproducible