

Life Science Informatics



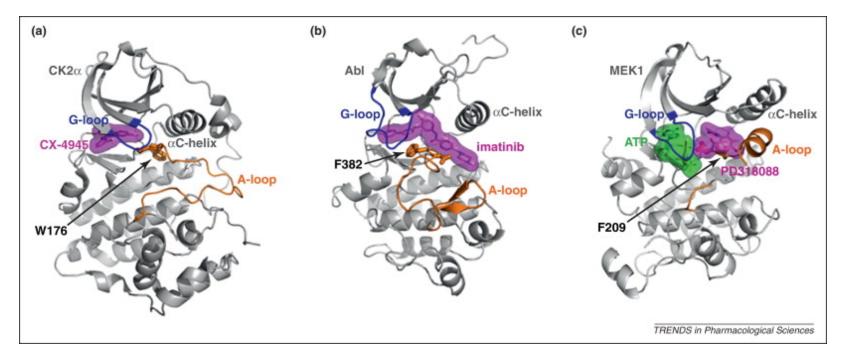
Emerging Big Data: Chemoinformatics-Driven View of Kinase Drug Discovery

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Protein Kinases

Kinases and G protein coupled receptors currently are the most intensely investigated drug targets



Kinases play a key role in native and aberrant signaling pathways and are prime targets in oncology, immunology/inflammation etc.

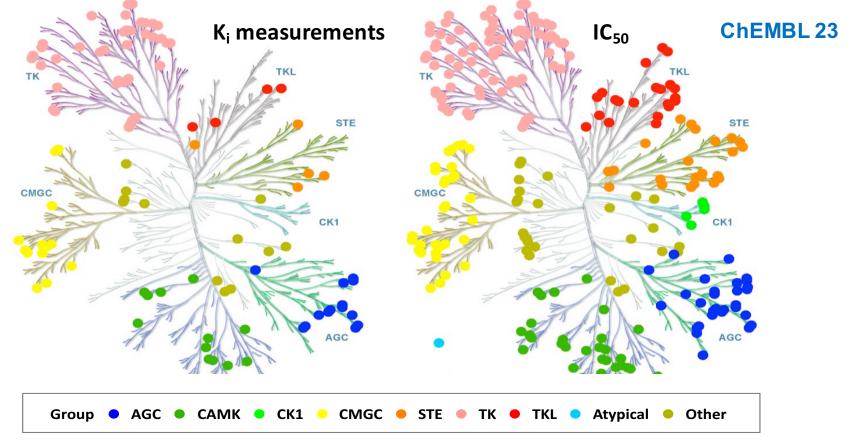






Inhibitor Coverage of the Kinome

- Human kinome comprises 518 kinases
- Inhibitors with high-confidence data are available for 286 kinases

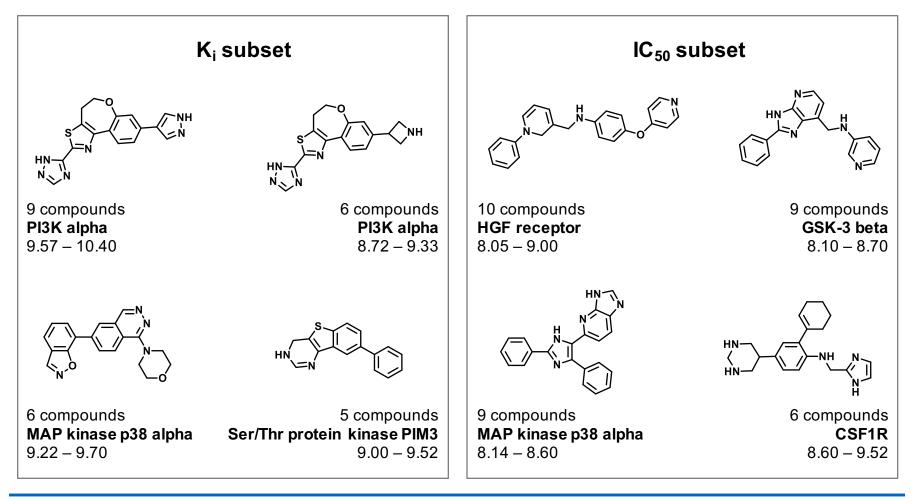








Scaffolds of structurally diverse and potent inhibitors









Big Compound Data

Compound activity data from biological screening and medicinal chemistry increasingly meet Big Data criteria

Heterogeneity (across databases) *Complexity* (multi-layered data structures) *Confidence* (experimental stringency)

(Hu & Bajorath, 2017)

(Van Rijmenam, 2013)

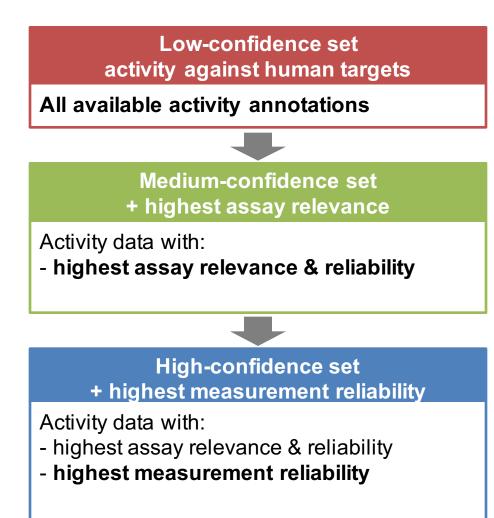
Kinase inhibitors are a representative example







Activity Data Confidence Levels









Data Growth

• Kinase inhibitors with **high-confidence** activity data

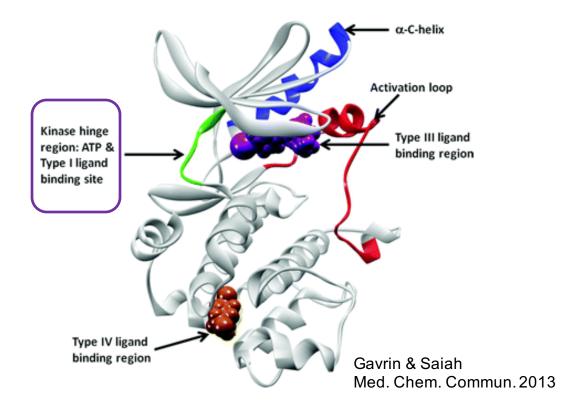
ChEMBL 23	ChEMBL 18
2017	2015
 45,728 kinase inhibitors 286 kinases 12 kinase groups 	 18,951 kinase inhibitors 266 kinases 10 kinase groups







More than 95% of current kinase inhibitors target the largely conserved ATP (cofactor) binding site (type I)

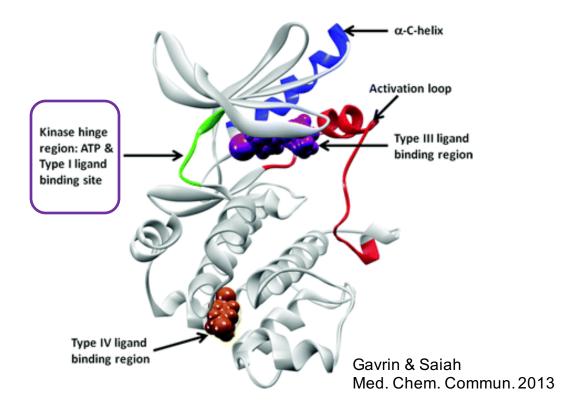








 Type I inhibitors are expected to be promiscuous (active against multiple kinases)









Promiscuity degrees (high-confidence data)

ChEMBL 23	ChEMBL 18	
2017	2015	
 45,728 kinase inhibitors 286 kinases 12 kinase groups 	 18,951 kinase inhibitors 266 kinases 10 kinase groups 	
 33,157 (76.5%)	 14,892 (78.6%)	
single-kinase inhibitors 504 (1.2%) with activity	single-kinase inhibitors 353 (1.9%) with activity	
against ≥ 5 kinases	against ≥ 5 kinases	







• Low detectable promiscuity due to **data sparseness?**

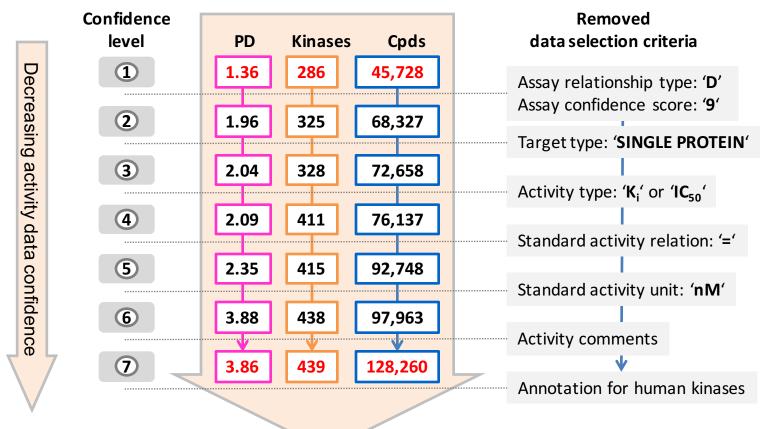
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Iterative removal of confidence criteria leads to increasing data volumes and kinome coverage



PD: mean promiscuity degree



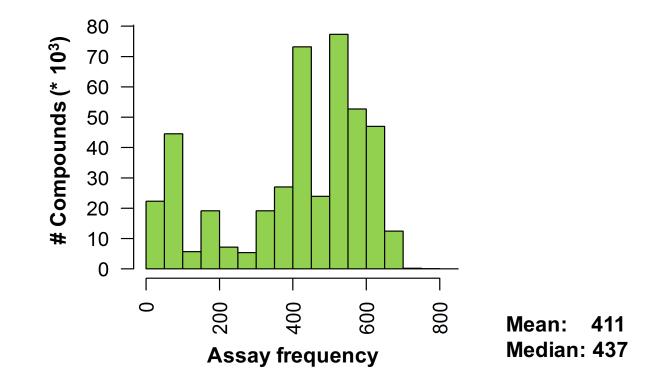


ChEMBL 23



Extensively Assayed Compounds

 437,257 screening compounds assembled from PubChem BioAssays tested in both primary and confirmatory assays (> 800 targets)

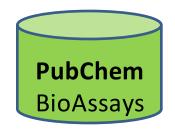








Subset of 437,257 extensively assayed screening compounds contains 28,172 inhibitors of a total of 43 human kinases

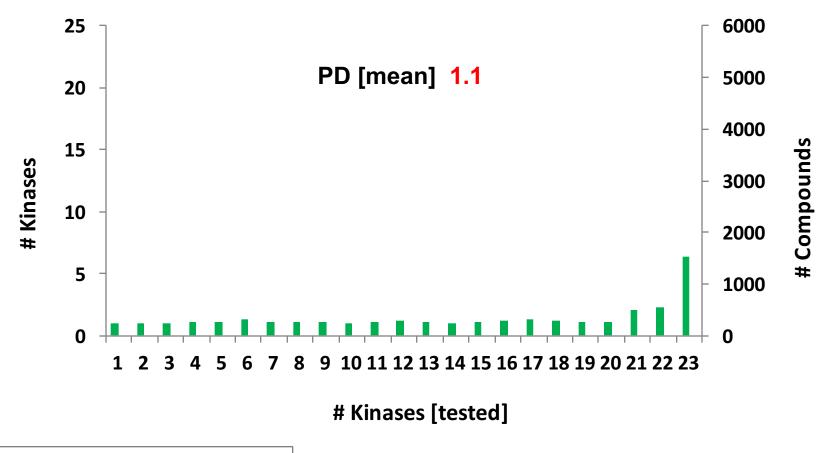


Extensively assayed screening compounds		
# Kinase inhibitors	28,172	
# Kinase targets	43	
Promiscuity degree (PD)	1 – 11	
PD [mean]	1.1	
# Kinases [tested]	1 – 23 (mean 14)	







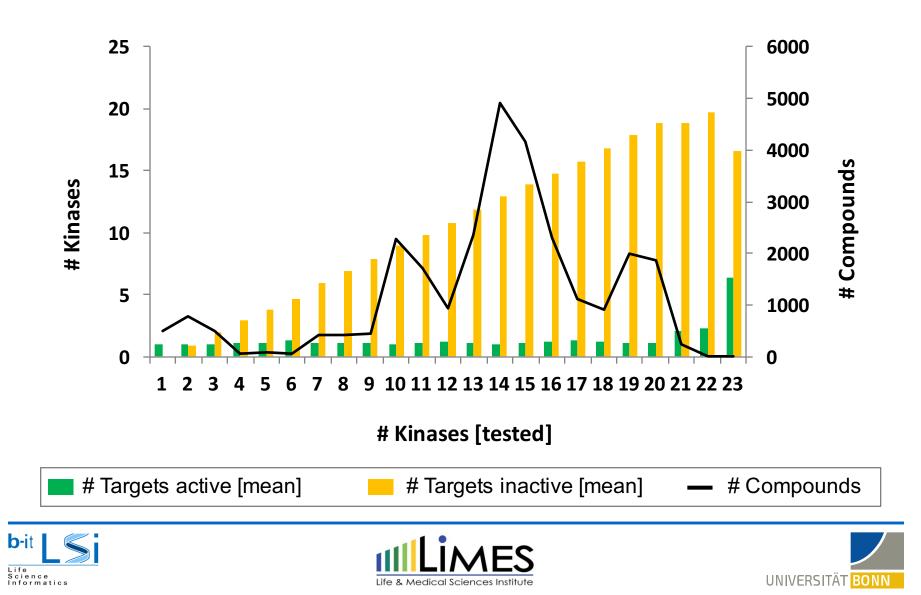


Targets active [mean]

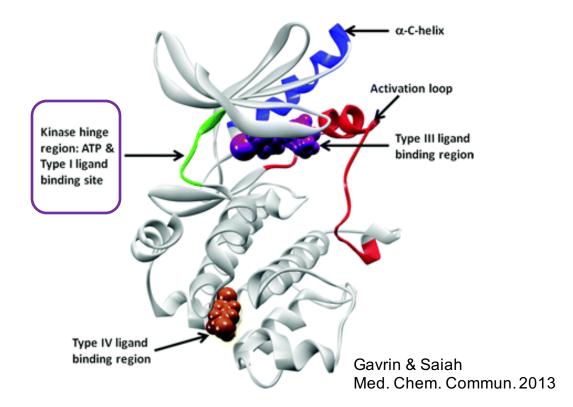








Type I inhibitors are expected to have limited selectivity for individual kinases – promiscuous inhibitors should be least selective



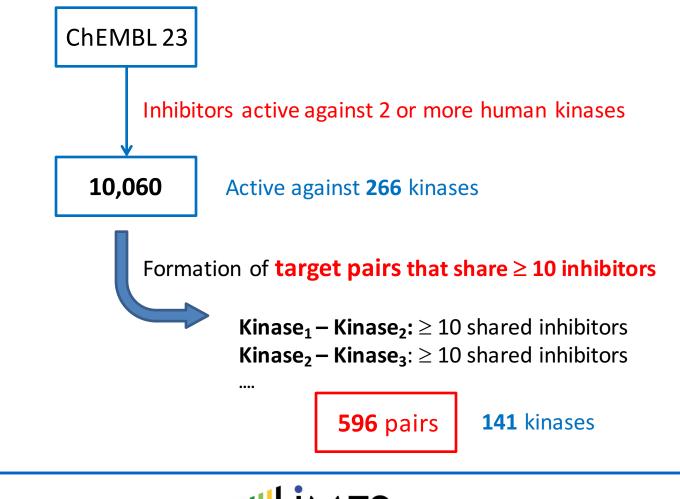






Kinase Inhibitors - Selectivity

• **Promiscuous** human kinase inhibitors with high-confidence data









Kinase Pair Categories

- 596 protein kinase pairs sharing at least 10 inhibitors (median value of 18 compounds per pair)
- 3 different **pair categories** according to their phylogenetic distance¹⁻³

(i)	same family	132 pairs
(ii)	different families	262 pairs
(iii)	different groups	202 pairs

¹UniProt Consortium. *Nucleic Acids Res.* 2015, *43*, D204. ²Miranda-Saavedra, D.; Barton, G. J. *Proteins* 2007, *68*, 893-914. ³Manning, G. *et al. Science* 2002, *298*, 1912-1934.







Selectivity Analysis

- By kinase pair-based analysis, all possible selectivity relationships for kinases and inhibitors were quantified
- For each kinase pair, potency differences (ΔpIC₅₀) between shared inhibitors were calculated as a measure of selectivity

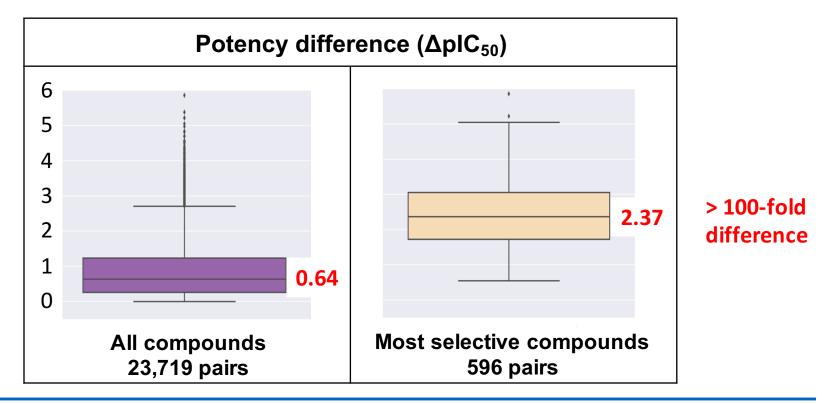






Kinase Inhibitors - Selectivity

- Small global potency differences (median ΔpIC₅₀ value 0.64)
- Different result for most selective inhibitors per pair (median 2.37)



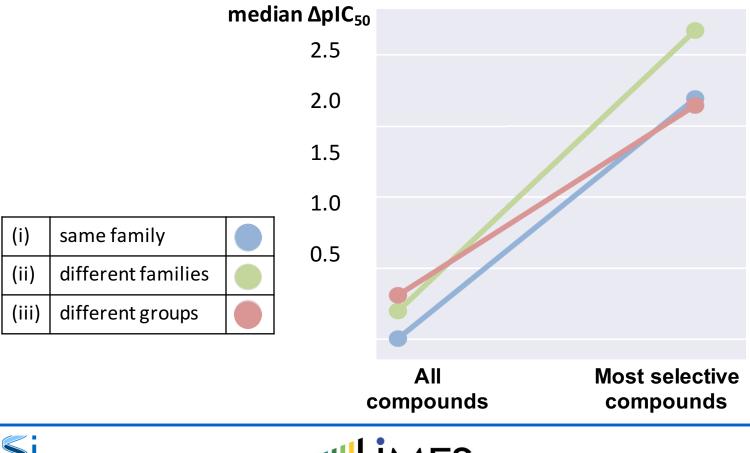






Kinase Inhibitors - Selectivity

Similar differences for pairs with increasing phylogenetic distances









Selectivity Analysis

- Pair-based selectivity profiles: recording inhibitors with largest potency differences per kinase pair
- Compound-based selectivity profiles: ordering available inhibitors according to increasing potency differences between paired kinases

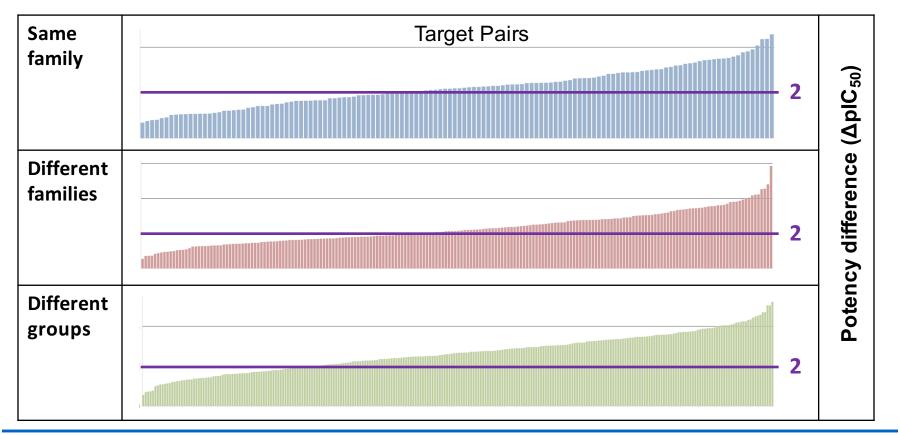






Category-Based Selectivity Profiles

More than 50% of kinase pairs from each category have inhibitors with more than 100-fold potency differences



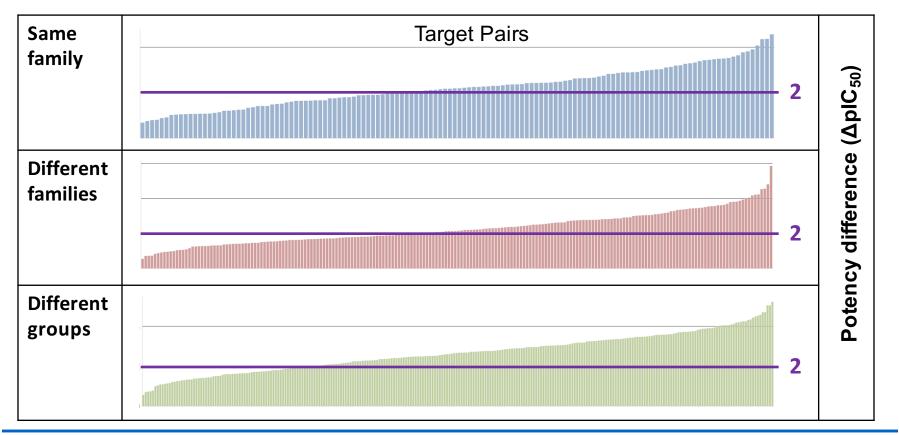




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Kinase Inhibitors - Selectivity

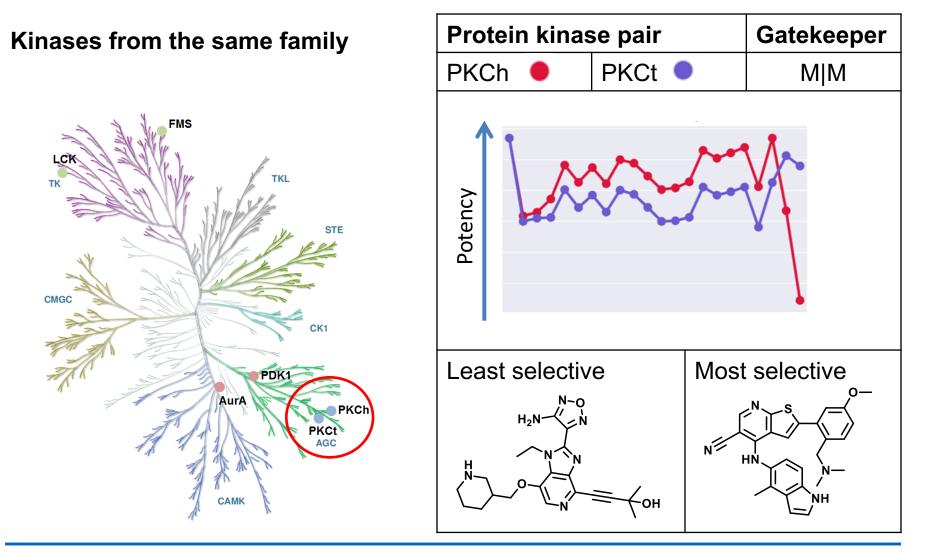
Unexpected selectivity among promiscuous kinase inhibitors







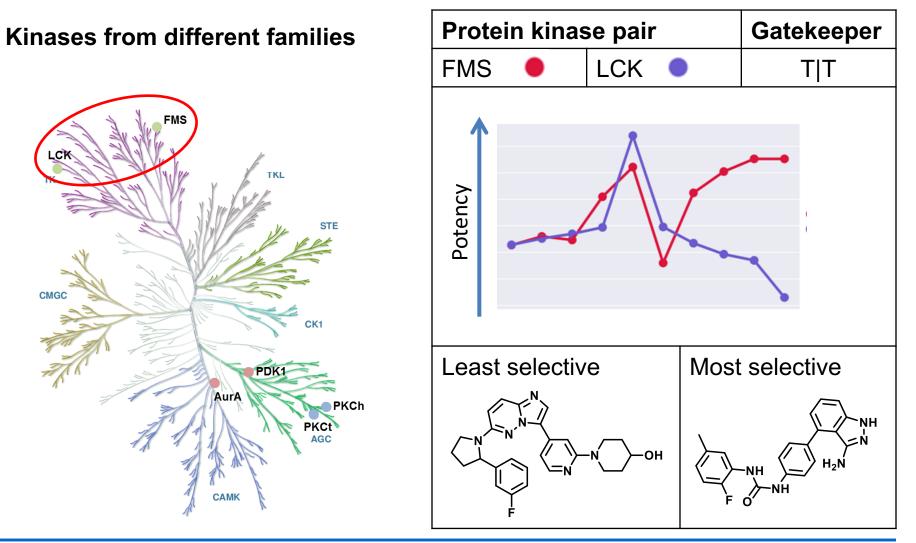
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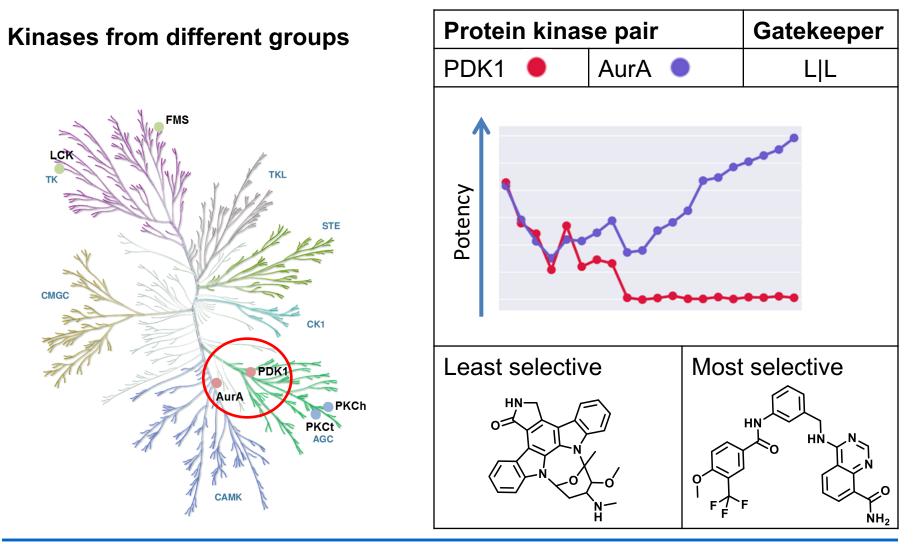


















Profiling Clinical Kinase Inhibitors

- Most comprehensive kinase inhibitor profiling study currently available¹
- Cell-based profiling of 243 clinical kinase inhibitors
- "Kinobeads" assays, followed by qMS
- Cellular interactions with 253 human kinases detected

Chemoinformatics perspective:

Reconciling observed promiscuity vs. selectivity trends on the basis of compound activity data from medicinal chemistry

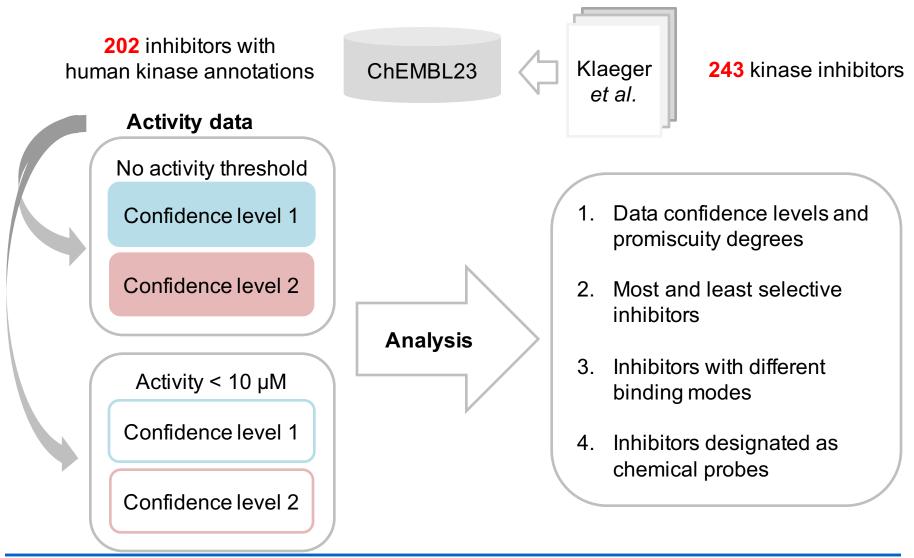
¹Klaeger et al. Science 2017, 358, eaan4368.





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Activity Data



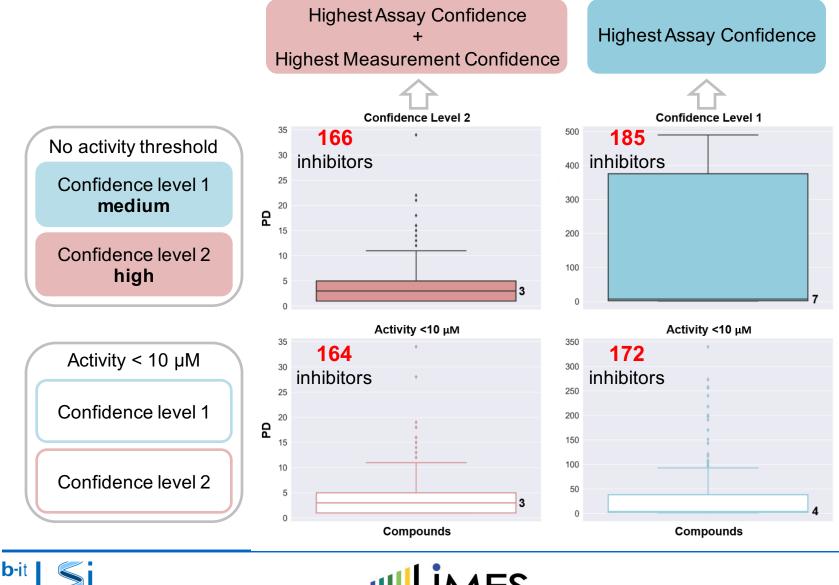






Promiscuity Degrees (PDs)

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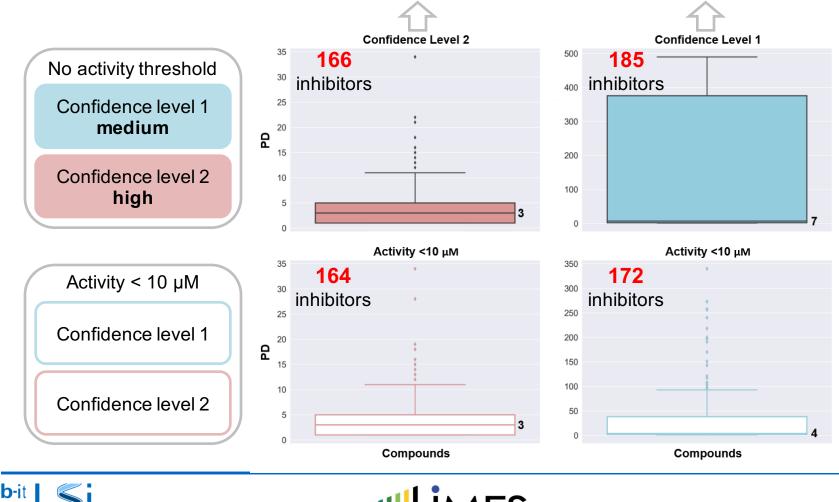
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Promiscuity Degrees (PDs)

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Strong influence of data confidence criteria Small median PD values

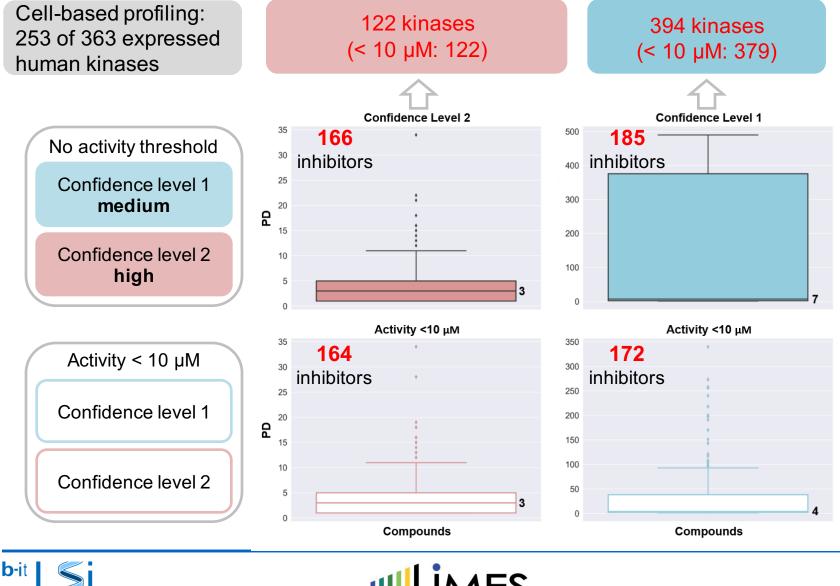


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Kinome Coverage

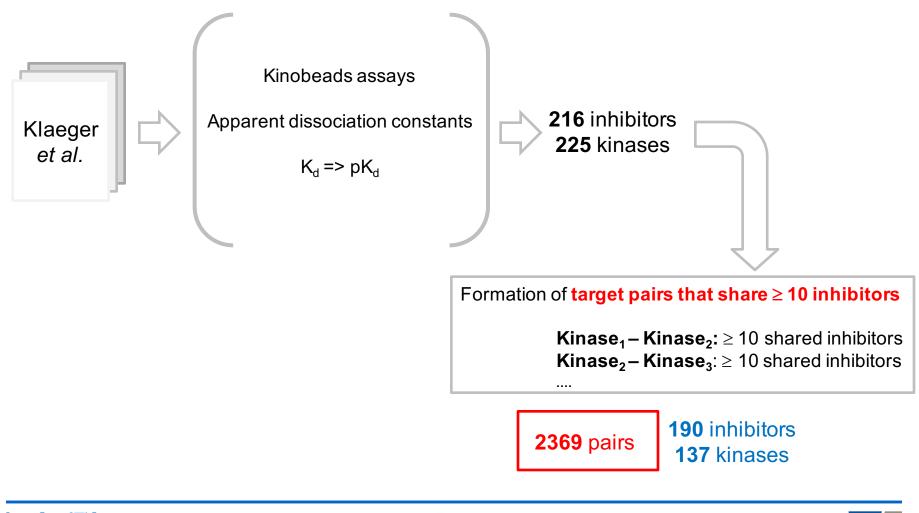
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Kinase Pair-Based Selectivity Analysis





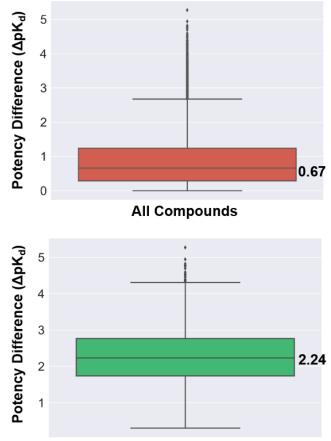




Kinase Inhibitors - Selectivity

 Small global potency differences: median ΔpK_d value 0.67 (med. chem. data: median ΔpIC₅₀ 0.69)

 Different picture for most selective inhibitors: median ΔpK_d value 2.24 (med. chem. data: median ΔpIC₅₀ 2.37) Potency differences between shared inhibitors per pair



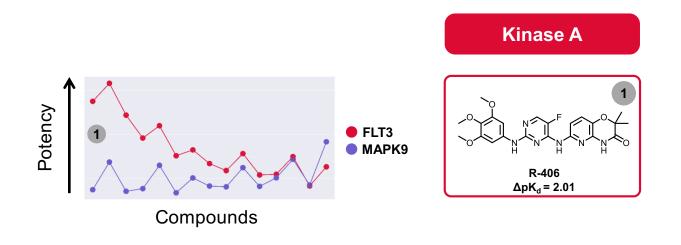
Most Selective Compounds







 Uni-directional selectivity profiles revealed inhibitors with exclusive selectivity for one kinase over the other



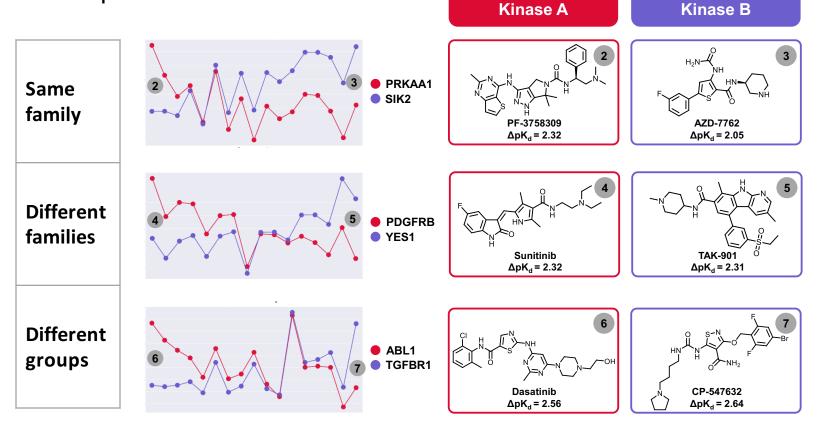
Compounds are ordered according to increasing potency differences for each kinase from the left to right and vice versa







 Bi-directional profiles uncovered inhibitors with inverted selectivity for paired kinases









Conclusions

- Advent of the 'big data' era in medicinal chemistry
- Kinase inhibitors as a representative example
- Most kinase inhibitors target the largely conserved ATP binding site
- Promiscuity and lack of selectivity are anticipated
- Systematic activity data analysis is strongly influenced by data confidence criteria
- Varying confidence criteria and inclusion of screening data put the data sparseness issue into perspective







Conclusions

- Data analysis reveals that ATP site-directed kinase inhibitors are less promiscuous and more specific than often assumed
- In part surprising agreement of computational selectivity analysis on the basis of activity data from medicinal chemistry and cell-based profiling





