



INTRODUCTION TO “FBDD”

BACKGROUND

Thorsten Nowak

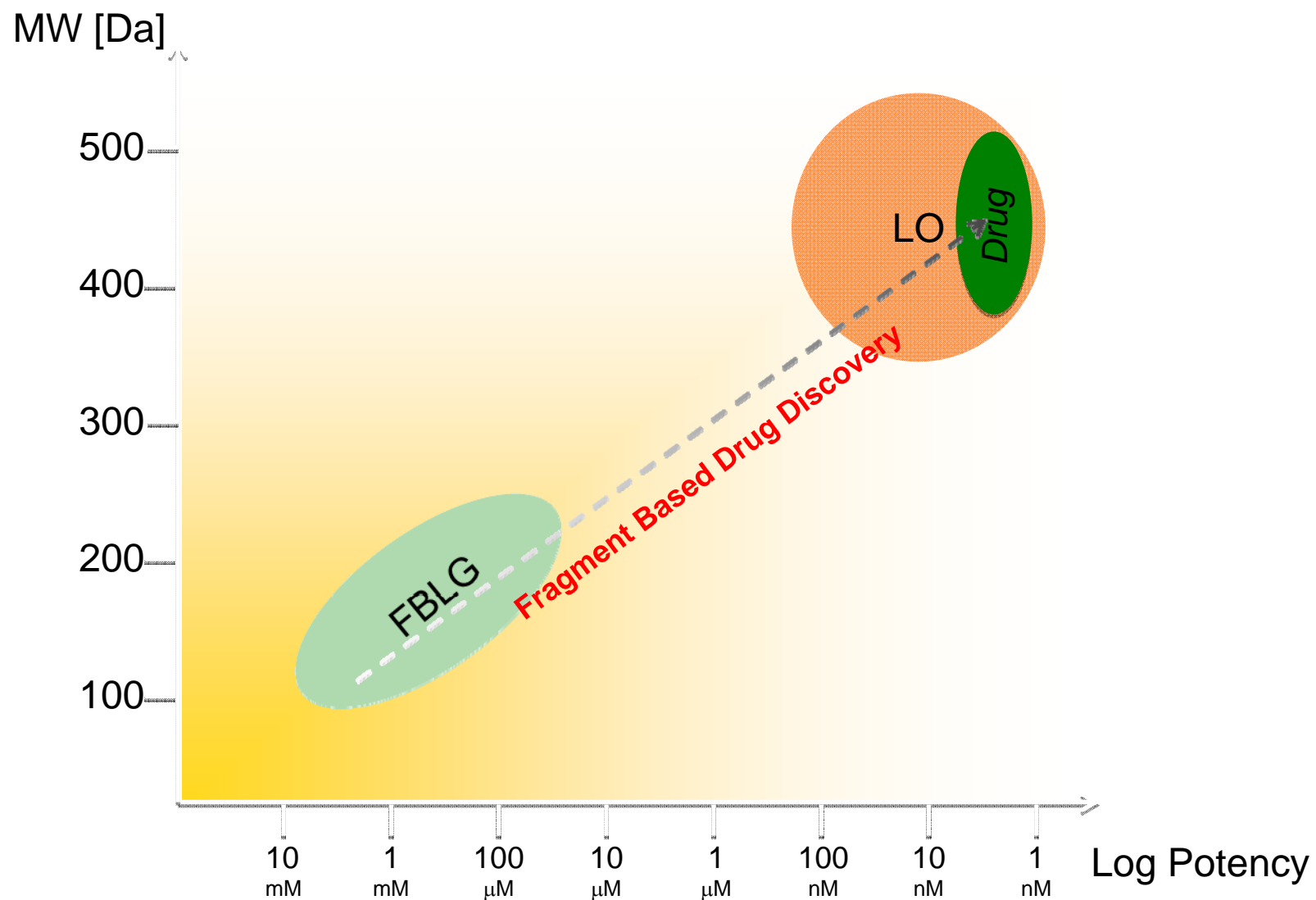


What is FBDD all About?





What is "FBDD"?





Where Does “FBDD” Come From?

- By early 1980s
 - ✓ Jencks “On the Attribution and Additivity of Binding Energies”
 - *Proc. Nat. Acad. Sci. USA* (1981), **78** (7). 4046-4050.
 - $\Delta G = -RT \ln K \Rightarrow$ twice the energy – square the affinity



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 - ✓ Peter Goodford and GRID – computation to map where functional groups could bind to active sites
 - Goodford, *J. Med. Chem.* (1985), **28**, 849
 - Example of OH probe on surface of lysozyme





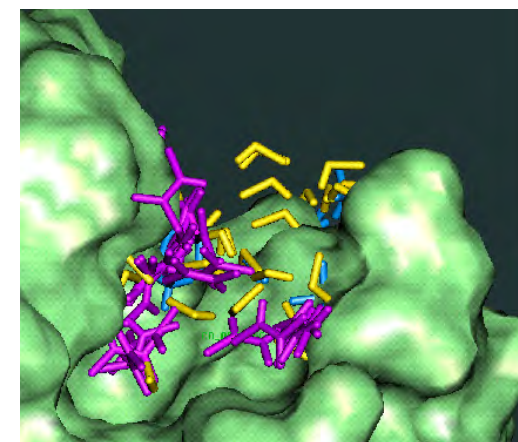
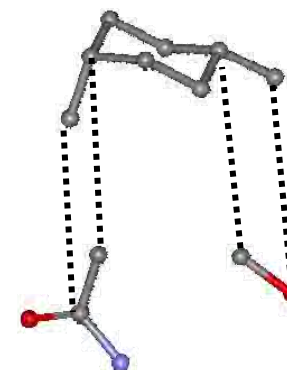
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 - ✓ Peter Andrews – ascribing binding affinity to particular groups
 - ✓ Abrahams and Perutz – bezafibrate variants binding in crystals



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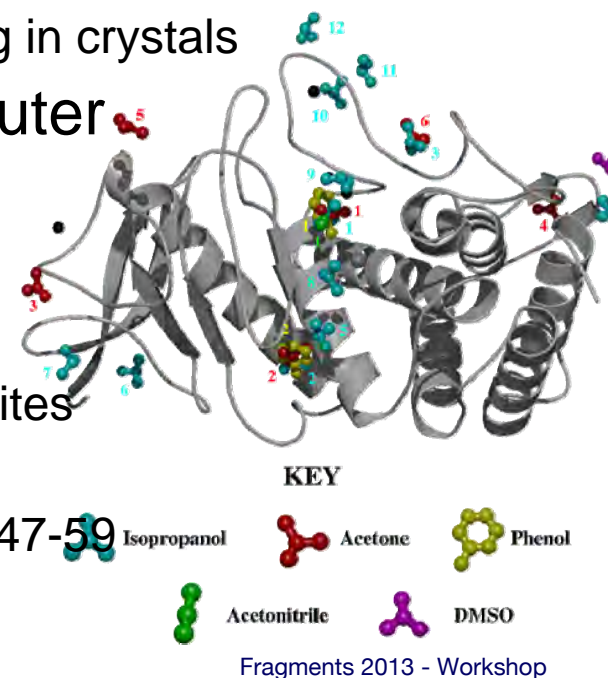
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- Early 1990s – linking fragments by computer
 - ✓ Bartlett - the Caveat program
 - ✓ Karplus, Miranker, Eisen, Hubbard – MCSS / Hook
 - Karplus and Miranker, *Proteins* (1991), **11**, 29.
 - Eisen et al. *Proteins* (1994), **19**, 119.
 - English, Groom & Hubbard, *Prot Eng*, (2001), **14**, 47.





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- 1990s
 - ✓ Ringe – Xray mapping of solvent binding to active sites
 - ✓ Extended to other systems and titrated (affinity?)
 - ✓ English, Groom & Hubbard, *Prot. Eng.*, (2001), **14**, 47-59





Where Does “FBDD” Come From?

- 1996 - SAR by NMR from Abbott group (Fesik and Hajduk)
- 1999 - SAR by Xray from Abbott group (Nienaber)
- Late 1990s / early 2000s
 - ✓ Big pharma for targets that failed HTS
 - Roche, Novartis, AZ
 - Small technology oriented companies started developing the methods (Astex, Vertex, RiboTargets (Vernalis), SGX, Plexxikon,
- Additional conceptual framework developed
 - ✓ Hann et al analysis of compound size, complexity and finding hits (*J. Chem. Inf. Comp. Sci.* **2001**, *41*, 856-864.)
 - ✓ Ligand efficiency
 - ✓ Kuntz and maximal affinity – (*PNAS*, **1999**, *96*, 9997-10002.)
 - ✓ Ligand Efficiency – DG / HAC – (*Drug Disc Today*, **2004**, *9*, 430-431.)
- Mid-2000s
 - ✓ A number of fragment-derived compounds selected for clinical trials
 - ✓ Unlike many other technologies – methods developed and relevance understood (with minimal hype) before large-scale take-up



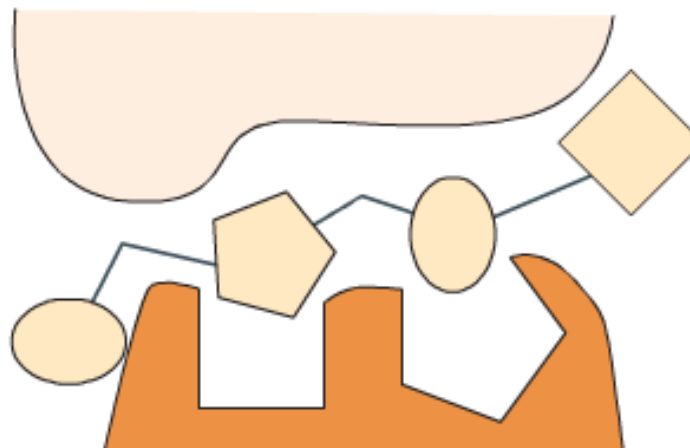
Why Do “FBDD”?

Potency

$\mu\text{M} \rightarrow \text{nM}$

Properties

ADMET What is a real hit



Poor Fit to Target

Need to “deconstruct”

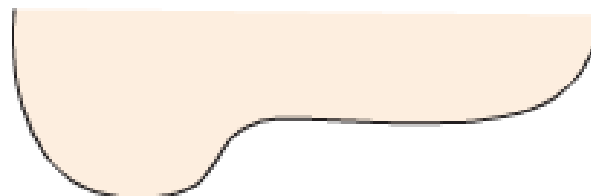
Relevance of
Chemical Space

Need for millions..

Low absolute Potency

High Lig. Eff.

$\text{mM} \rightarrow \mu\text{M}$

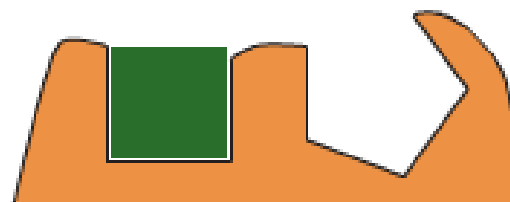


Poor Fit to **any** Target

Need to “construct”

Excellent Properties

ADMET What is a real hit



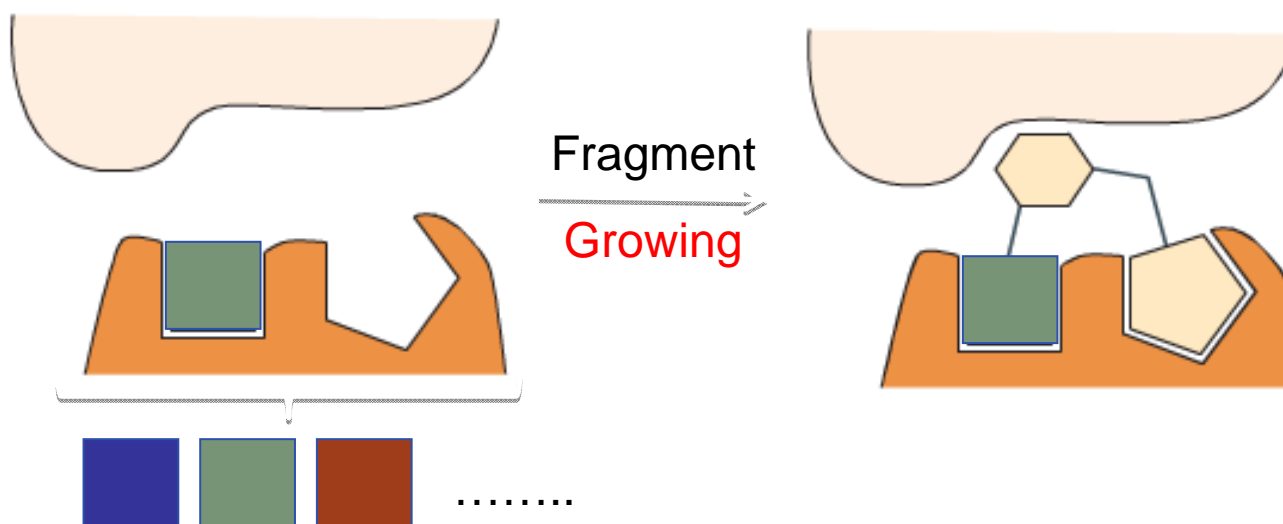
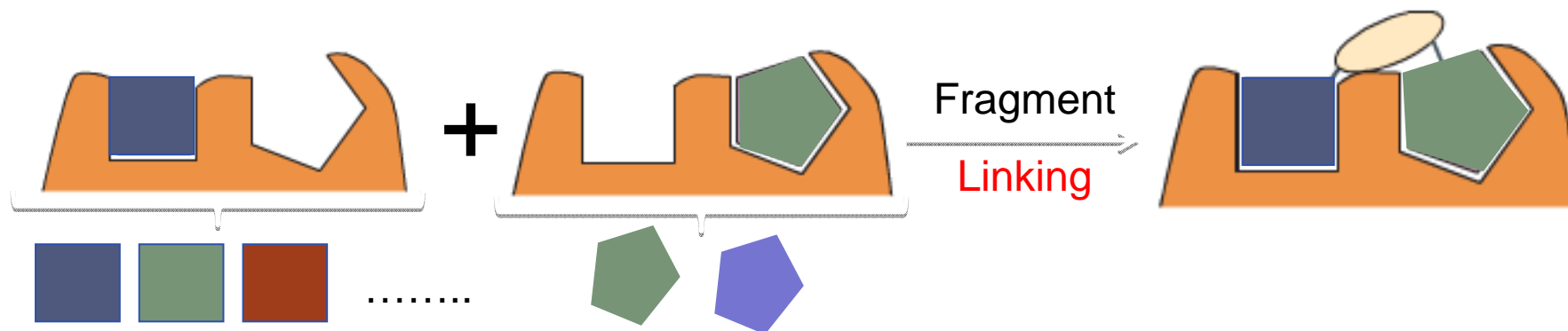
Ultimate Relevance of
Chemical Space

Hundreds -> Thousands

Rees, D.; Congreve, M.; Murray, C.; Carr, R. Fragment-based lead discovery. Nature reviews. Drug discovery (2004), **3**, 660–72.



Strategy of Fragment Exploitation



Rees, D.; Congreve, M.; Murray, C.; Carr, R. Fragment-based lead discovery. *Nature reviews. Drug discovery* (2004), **3**, 660–72.



What Are The Advantages & Principles Of FBDD?

- Complexity of large molecules
- Coverage of chemical space with conventional lead like libraries
- Ligand Efficiency and other considerations
- Fragment expansion strategies

Molecular Complexity: Hann, M.; Leach, A.; Harper, G. Journal of chemical information and computer sciences (2001), **41**, 856–64.

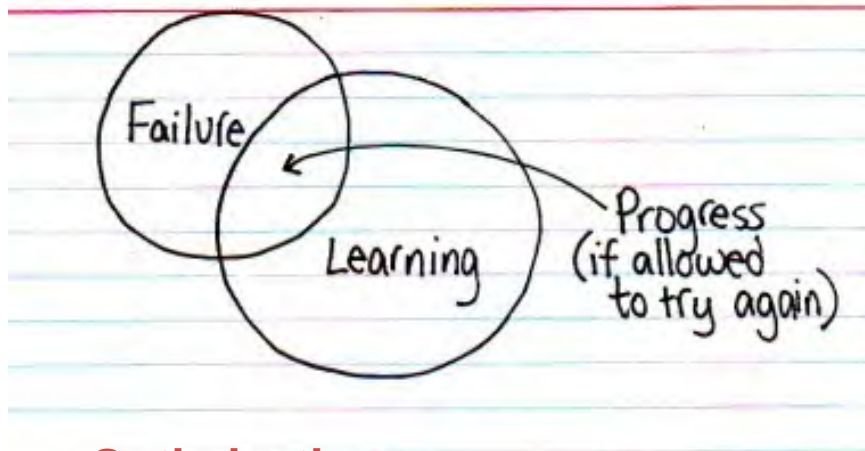


What Do You Need?

Target



Library



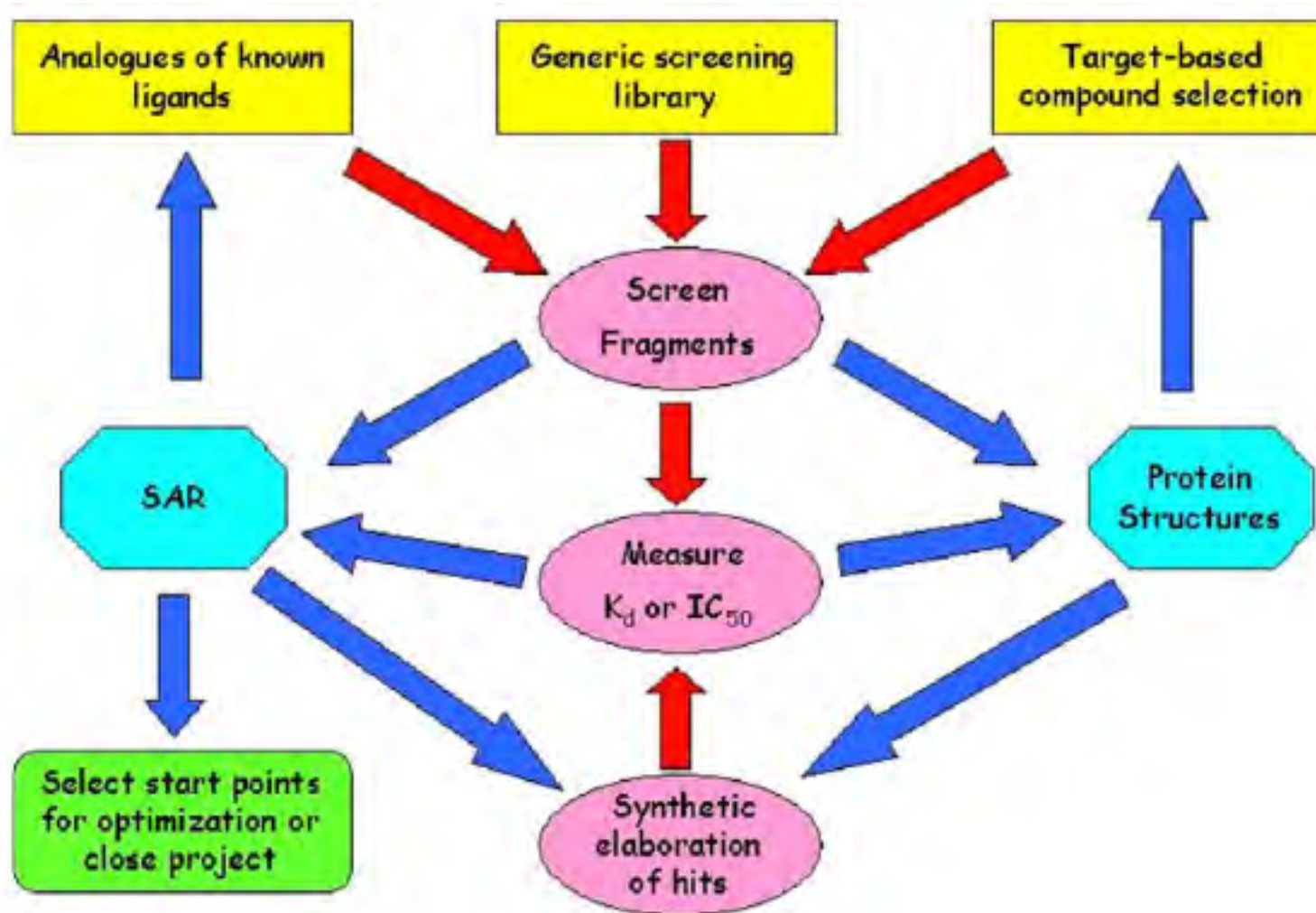
conducting an experiment to test the discoveries were hit on by accident"

Screening

Optimisation



How Is It Done? – Principal Workflow



Blomberg, N.; Cosgrove, D.; Kenny, P.; Kolmodin, K. *Journal of computer-aided molecular design* (2009), **23**, 513–25.



What Are The Main Pitfalls?

- Reliable assessment of technical feasibility of a new target
- Time from Gen-to-Structure
- Need for reliable affinity and high concentration biochemical assay
- SBDD – expertise



- **LE** = Ligand Efficiency
- **LLE** = Lipophilicity Ligand Efficiency
- **SBDD** = Structure Based Drug Design
- **FBDD** = Fragment Based Drug Discovery
- **FBLG** = Fragment Based Lead Generation



Ligand Efficiency

- ✓ Scaling factor to correct affinity/potency for size

Fragment Growing

- ✓ Building new interactions into fragment start points; expanding into neighbouring pockets

Fragment Linking

- ✓ Tether fragment screening hits together that bind in adjacent pockets, thus adding the affinities of the individual fragments -> Potency jumps

Affinity Screening

- ✓ Screening of molecule applying a biophysical approach which will determine the dissociation constant (k_D) as a measure of affinity i.e. how tightly a molecule binds to a target.



“Efficiency” Indices

Type	Metrics	Definition	Use	Reference
Ligand efficiency	LE	$-RT\ln(K_d \text{ or } pK_i)/HA$	Prioritization of starting points, early optimization	Hopkins AL, Groom CR, Alex A. <i>Drug Discov Today</i> 2004;9(10):430-1
	BEI	$(pK_i \text{ or } pK_d)/MW$		Abad-Zapatero C, Metz JT. <i>Drug Discov Today</i> 2005;10(7):464-9
Size independent ligand efficiency	FQ	$LE/(0.0715 + 7.5328/HA + 25.7079/(HA)^2 + -361.4722/(HA)^3)$	Size unbiased comparison of compounds in early optimization	Reynolds CH, Toungue BA, Bembenek SD. <i>J Med Chem</i> 2008;51(8):2432-8
	%LE	$LE/(1.614^{\log_2(10/HA)}) * 100$		Orita M, Ohno K, Niimi T. <i>Drug Discov Today</i> 2009;14(5-6):321-8
	SILE	$-RT\ln(pK_i)/(HA)^{0.3}$		Nissink JWM. <i>J Chem Inf Model</i> 2009;49(6):1617-22
Lipophilic ligand efficiency	LLE	$pK_i - cLogP \text{ (or LogD)}$	Control of lipophilicity in lead optimization	Leeson PD, Springthorpe B. <i>Nat Rev Drug Discov</i> 2007;6(11):881-90
	LLE _{Astex}	$0.11 * \ln(10) * RT(\log P - \log(K_d \text{ or } pK_i \text{ or } IC_{50}))/HA$	Lipophilic efficiency assessment for fragments	Paul N. Mortenson • Christopher W. Murray <i>J Comput Aided Mol Des</i> DOI 10.1007/s10822-011-9435-z
	LELP	$\log P/LE$	Control lipophilicity in optimization, assessment of druglikeness	Keseru GM, Makara GM. <i>Nat Rev Drug Discov</i> 2009;8(3):203-12
Enthalpic efficiency	EE	$\Delta H/HA$	Enthalpy driven potency optimization	J. E. Ladbury, G. Klebe, E. Freire <i>Nature Rev. Drug Disc.</i> 2010 , 9, 23-27
	SIHE	$(-\Delta H/40 * 2.303 * RT) * HA^{0.3}$	Size independent assessment of binding enthalpy contributions	G. G. Ferenczy, G. M. Keserü, <i>J. Chem. Inf. Comput. Sci.</i> 2010 , 50, 1536-1541
Complex metrics	MPO	$clogP, clogD \text{ pH}=7.4, MW, TPSA, HBD, pK_a$	Supporting the optimization of CNS compounds	Travis T. Wager, Xinjun Hou, Patrick R. Verhoest, and Anabella Villalobos <i>ACS Chem. Neurosci.</i> (2010), 1, 435-449
	CSE	in vitro promiscuity and toxicity data, cLogP, TPSA and pK _a	Control toxicity related attrition	Kevin Dack, <i>Designing Safer Medicines in Discovery symposium, SCI</i> , , 17th March 2011
	DRUGeff	Biophase Concentration * 100/Dose	Estimation of in vivo efficacy in combination with <i>in vitro</i> potency	Expert Opinion on Drug Discovery 2010, 5(7), 609-618; S Braggio, D Montanari, T Rossi & E. Ratti

Hann, M.; Keserü, G. Finding the sweet spot: the role of nature and nurture in medicinal chemistry. *Nature reviews. Drug discovery* (2012), **11**, 355-65.



Some Literature

- **Web Resources:** Fragment Blog Practical Fragment by Dan Erlanson: <http://practicalfragments.blogspot.co.uk>
- **Web Resources:** Fragment-Based Drug Discovery & Molecular Design by Pete Kenny: <http://fbdd-lit.blogspot.co.uk>
- **General Review:** Rees, D.; Congreve, M.; Murray, C.; Carr, R. Fragment-based lead discovery. *Nature reviews. Drug discovery* (2004), **3**, 660–72.
- **General Review:** Albert, J.; Blomberg, N.; Breeze, A.; Brown, A.; Burrows, J.; Edwards, P.; Folmer, R.; Geschwindner, S.; Griffen, E.; Kenny, P.; Nowak, T.; Olsson, L.-L.; Sanganee, H.; Shapiro, A. An integrated approach to fragment-based lead generation: philosophy, strategy and case studies from AstraZeneca's drug discovery programmes. *Current topics in medicinal chemistry* (2007), **7**, 1600–29.
- **Molecular Complexity:** Hann, M.; Leach, A.; Harper, G. Molecular complexity and its impact on the probability of finding leads for drug discovery. *Journal of chemical information and computer sciences* (2001), **41**, 856–64.
- **Fragment Library Design:** Blomberg, N.; Cosgrove, D.; Kenny, P.; Kolmodin, K. Design of compound libraries for fragment screening. *Journal of computer-aided molecular design* (2009), **23**, 513–25.
- **Fragment Library Design:** Brewer, M.; Ichihara, O.; Kirchhoff, C.; Schade, M.; Whittaker, M. Assembling a Fragment Library. *Fragment-Based Drug Discovery: A Practical Approach* (2008), 39–62.
- **Critical retrospective:** Hajduk, P.; Greer, J. A decade of fragment-based drug design: strategic advances and lessons learned. *Nature reviews. Drug discovery* (2007), **6**, 211–9.
- **Efficiency indices:** Hann, M.; Keserü, G. Finding the sweet spot: the role of nature and nurture in medicinal chemistry. *Nature reviews. Drug discovery* (2012), **11**, 355–65.
- **Efficiency indices:** Andrew L. Hopkins, Colin R. Groom, Alexander Alex, Ligand efficiency: a useful metric for lead selection, *Drug Discovery Today*, (2004) **9**, 430.
- **Structure Based Drug Design:** Böhm, H.-J.; Klebe, G.; What Can We Learn from Molecular Recognition in Protein–Ligand Complexes for the Design of New Drugs?. *Angew. Chem. Int. Ed. Engl.* (1996), **35**, 2588
- **Structure Based Drug Design:** Bissantz, C.; Kuhn, B.; Stahl, M. A medicinal chemist's guide to molecular interactions. *Journal of medicinal chemistry* (2010), **53**, 5061–84.