

Not for Circulation

# MedChemica

CREATING A STEP CHANGE IN MEDICINAL CHEMISTRY

## Practical Drug Discovery using Explainable AI

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Managing Director, MedChemica Ltd

**Available on Slideshare - search for Dossetter**  
<https://www.slideshare.net/AlDossetter/practical-drug-discovery-using-explainable-artificial-intelligence>

**Twitter @MedChemica**  
**Twitter @covid\_moonshot**  
**Twitter #BucketListPapers**  
<https://www.medchemica.com/bucket-list/>

June2021

# Agenda

- What is Explainable AI and What does it mean to MedChem?
- Designing AI systems to **enable** the chemist
- How do you get new ideas from a computer?
  - About Generative SMILE systems.....
  - Matched Molecular Pair analysis (MMPA)
    - Enumeration with MMPA
    - Drilling back to source data, to *explain* the origin of the Rules
- Explainable AI with ML Models
- Project Examples (6 projects including Covid Moonshot)
  - Please request extended version of the talk for your institute
- Future vision – A view on further AI supported chemistry



# What is Explainable AI and What does it mean to MedChem?

# What is Artificial Intelligence (AI)?

## What is Explainable AI?

- **The Turing test**, originally called the **Imitation game** by Alan Turing in 1950, is a test of a machine's ability to exhibit intelligent behaviour equivalent to, or indistinguishable from, that of a human.
- An Artificial Intelligence (AI) systems provides (or performs) *Actions*, either fully automated or with additional human experience and final decision making.
- AI **does not** mean Machine Learning (ML)
- Machine Learning (ML) is the collective term for algorithms that can analyse a dataset to create a 'model' that can perform predictions or generate options [they save humans from having to work out the 'Rules' governing a dataset and custom write a program]
- The 'models' (produced by ML and other techniques) are often called 'blackbox' – we, as humans, have no idea how they work...
- Explainable AI are systems (or models) where the human can “see” how they work and can link the Actions back to original data  
→ **For chemists it means we can see (sub)structures / measurements**

# The 5 Levels of AI

Level	Label	Description
Level 5	Fully Automated	Never requires human intervention
Level 4	Automation	Runs itself unless it hits an 'extreme' situation
Level 3	Semi-Autonomous	Running and monitoring a system – e.g. auto trading on the stock exchange
Level 2	Close supervision	Routine stuff administered uses humans for difficult situations
Level 1	Simple Augmentation	Data entry, processing, identifying cluster of activity, profiling
Level 0	No automation	Human powered only

For Drug Discovery we can see that somewhere between Level 1 and Level 2 would be very useful given the current high volume of data and diversity

# Designing AI systems to **enable** the chemist

A bit about MedChemica and how the computer can work with the chemists

## ...9 Years of working with pharma companies

“Our median number of compounds per LO project is 3000 - this is unsustainable... [it should be] 300”

– Director of Chemistry (large pharma)

“Can we define the text book of medicinal chemistry?”

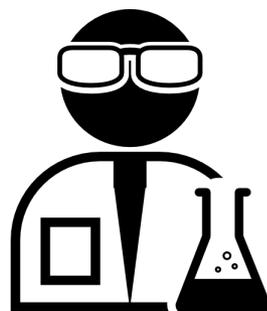
– Director of Comp Chem (large pharma)

“We are aiming at 300 compound per project – currently we are about 400, we will get better”

– ExSciencia scientist at SCI ‘What can BigData do for chemistry’ –  
London Oct 2017

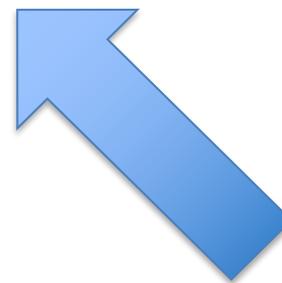
MedChemica: Using knowledge extraction techniques to build Augmented Intelligence systems to increase success and reduce the time and cost in Drug Discovery.

# Augmenting the Medicinal Chemist

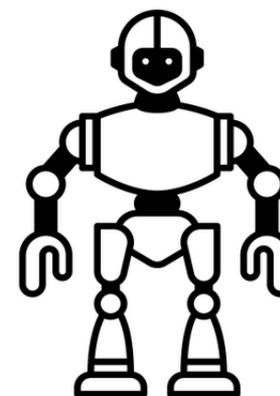


Sets goals  
Makes  
Decisions

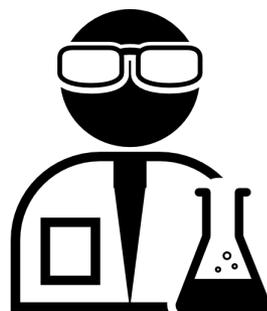
Data is organized  
and summarized



Prioritizes  
options



# Augmenting the Medicinal Chemist



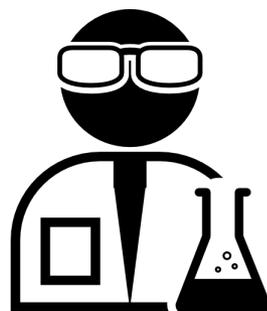
Sets goals  
Makes  
Decisions

Data is organized  
and summarized



Data normalization  
Pattern Recognition  
Visualisation

# Augmenting the Medicinal Chemist

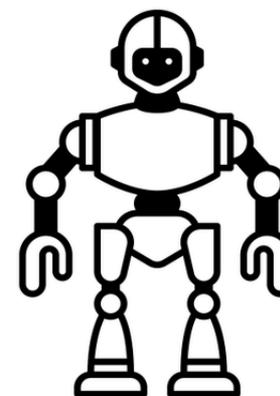


Sets goals  
Makes  
Decisions

Makes proposals from information + goals  
Automated improvement & Active  
Learning ..... *Situational awareness?*



Prioritizes  
options



# What does AI mean to Medicinal Chemistry?

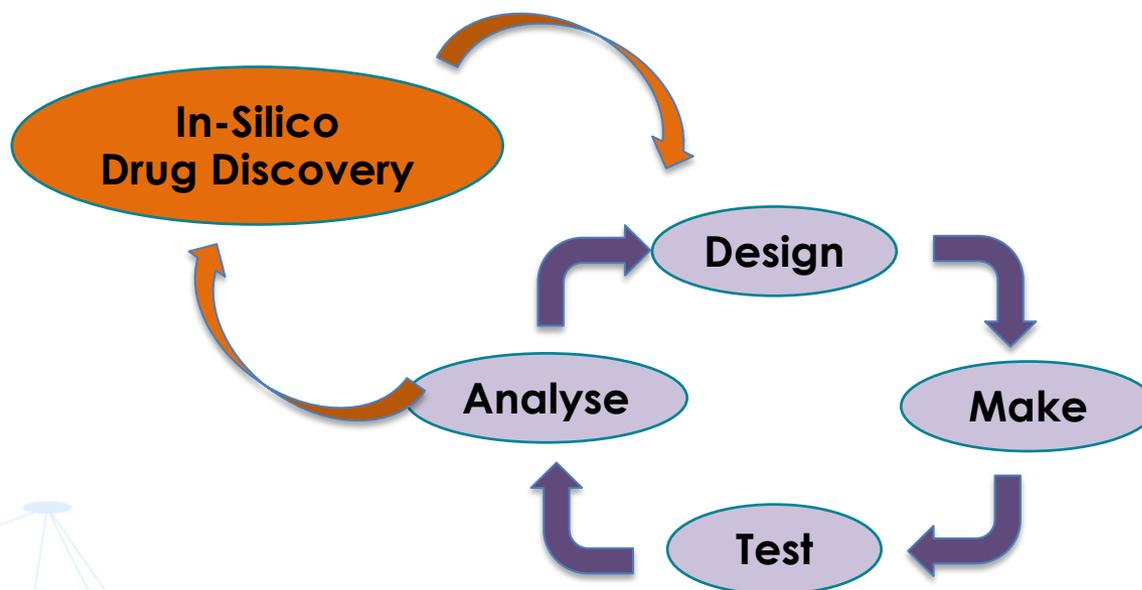
- So it is more helpful to consider Augmenting Intelligence in Medicinal Chemistry....
- The quality of an AI model depends on the number of times the machine can learn from success and failure.
  - Alpha-Go
    - fast to learn because a computer can play another computer
    - Clear success and failure
  - Drug Discovery 
    - Fully documented discovery projects (all cmpds/all measurements) in short supply
    - DTMA too long for many iterations?
    - Unclear success / failure in early research

*"Can we accelerate medicinal chemistry by augmenting the chemist with BigData and Artificial Intelligence?"* Griffen E.J. et al **Drug Disco. Today**, **2018**, 23, 7, 1373-1384.

*"Chemists: AI Is Here; Unite To Get the Benefits"* Griffen, E.J.\*; Dossetter, A.G.; Leach, A.G.; **J. Med. Chem.** **2020**, 63, 16, 8695–8704 <https://doi.org/10.1021/acs.jmedchem.0c00163>

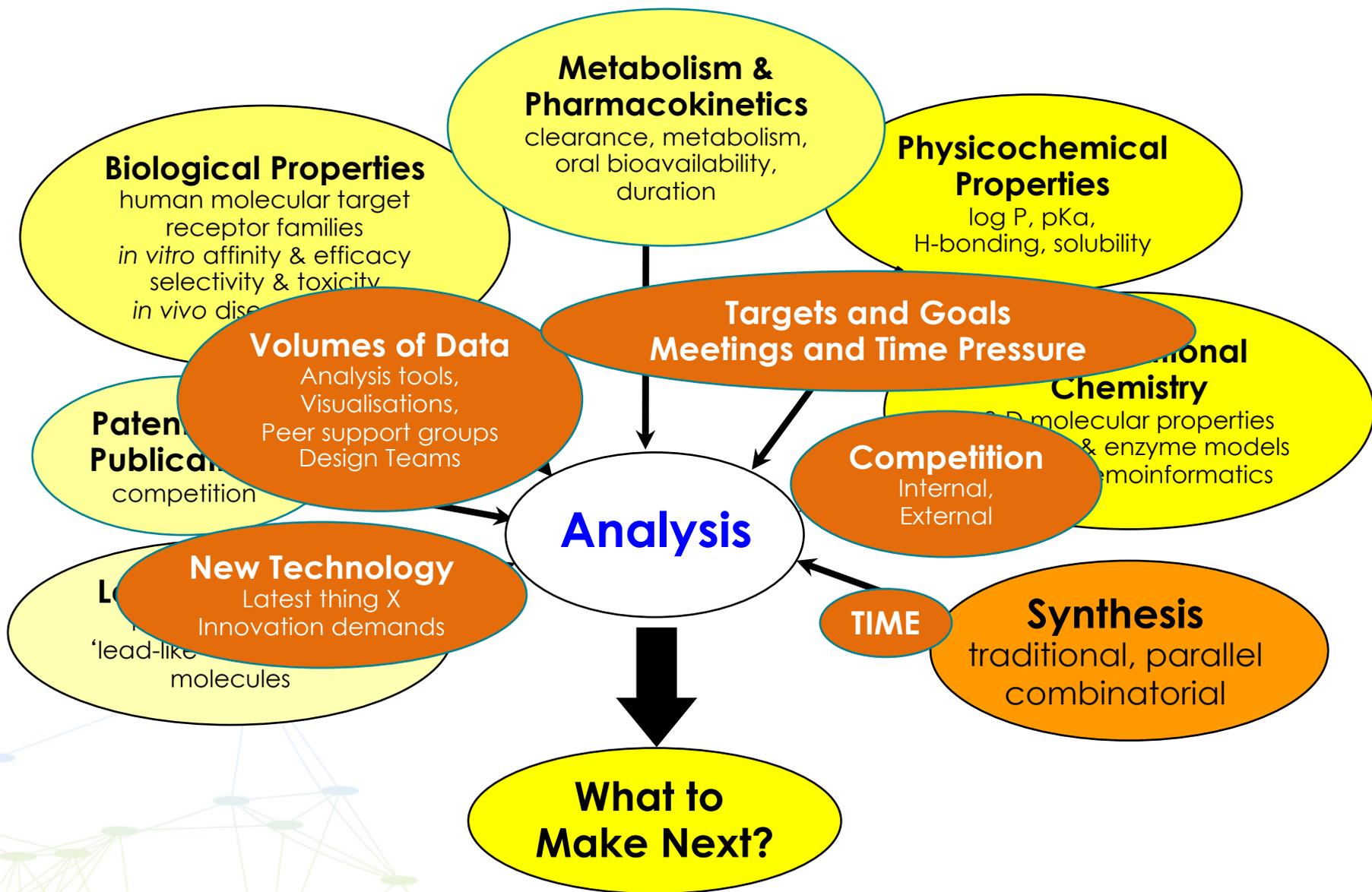
# AI or In-Silico Drug Discovery

- In small molecule Drug Discovery Med Chem controls the productivity.
- Better Analysis and Design is the the only way to Making and Testing fewer compounds.
- In-Silico Drug Discovery covers both Analysis and Design
- AI techniques are being applied to improve In-Silico DD with unbiased analysis and recommendation systems (Level 1 and 2)



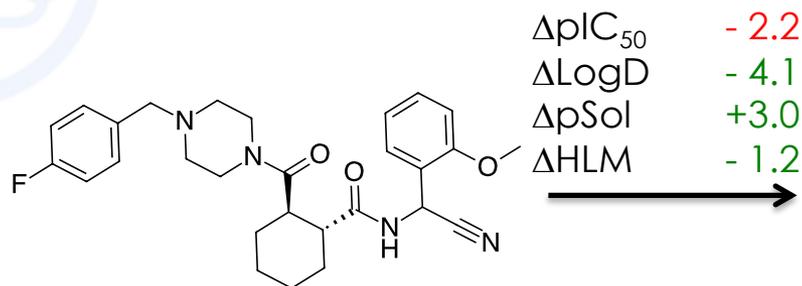
- **Omission** – New ML models have been built on synthetic chemistry routes to produce new route recommenders – not covered in this talk.

# For the jobbing Med Chemist what does this mean?

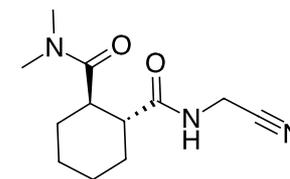


# CD1 - Cathepsin K Inhibitors for OE – AZD4996

pIC <sub>50</sub>	8.70
LogD	3.6
HLM	127
Solubility	99µM
DTM	
<b>Potent</b>	
<b>High Clearance / 0 F%</b>	



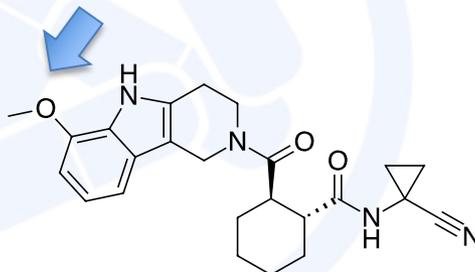
Molecular Simplification



43 Compounds made

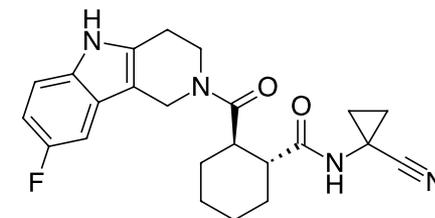
pIC <sub>50</sub>	9.1
LogD	2.8
HLM	<2.0
Solubility	>1000µM
DTM	0.05 mg/kg UID
High F% / stability maximised	

Unusual structural change



$\Delta pIC_{50}$  ~ 0.0  
 $\Delta \text{LogD}$  - 0.1  
 $\Delta p\text{Sol}$  + 0.1  
 $\Delta \text{HLM}$  - 0.4

$\Delta pIC_{50}$  + 2.3  
 $\Delta \text{LogD}$  + 3.2  
 $\Delta p\text{Sol}$  - 1.0  
 $\Delta \text{HLM}$  + 1.0



Dossetter, A.G. *et al Bioorg Med Chem Lett.* **2012**, 22(17), 5563 - 5568.

Dossetter, A.G. *et al J Med Chem.* **2012**, 55(14), 6363 - 6374.

# CD2 - Cathepsin K Inhibitors for OE

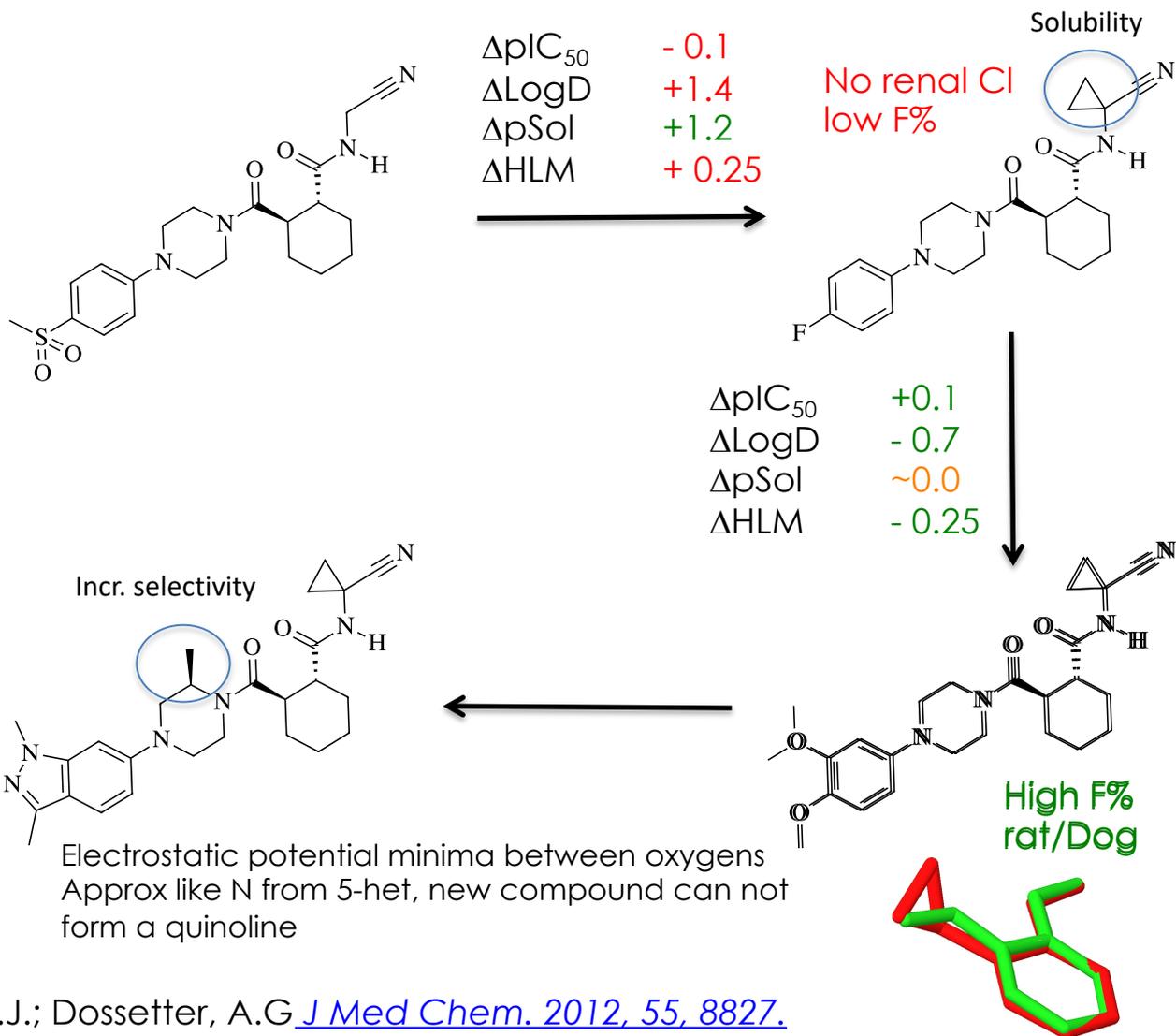
pIC <sub>50</sub>	7.95
LogD	0.67
HLM	<2.0
Solubility	280μM
DTM	~1.0 mg/kg UID

**Potent**  
**Too polar / Renal Cl**

Increase in LogP,  
Properties improved

pIC <sub>50</sub>	8.2
LogD	2.8
HLM	<1.0
Solubility	>1400μM
DTM	0.01 mg/kg UID

High F% / stability  
maximised

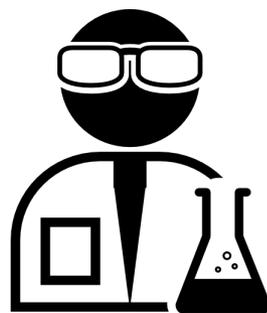


Crawford, J.J.; Dossetter, A.G [J Med Chem. 2012, 55, 8827.](#)

Dossetter, A. G. [Bioorg. Med. Chem. 2010, 4405](#)

PDB - 97% of structures

# Augmenting the Medicinal Chemist



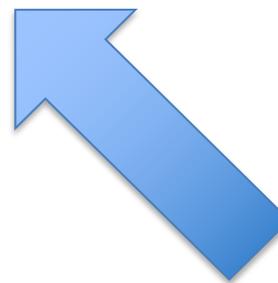
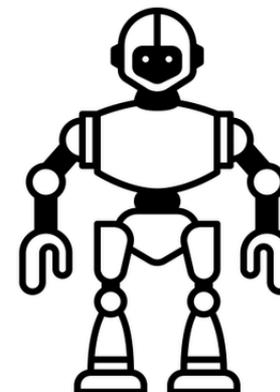
Sets goals  
Makes  
Decisions

How do you get a computer to make sensible compound suggestions, aligned to a strategy, and where we can see where the idea has come from?

- *Generative SMILES models*
- *Matched Molecular Pair Models*



What to make next?

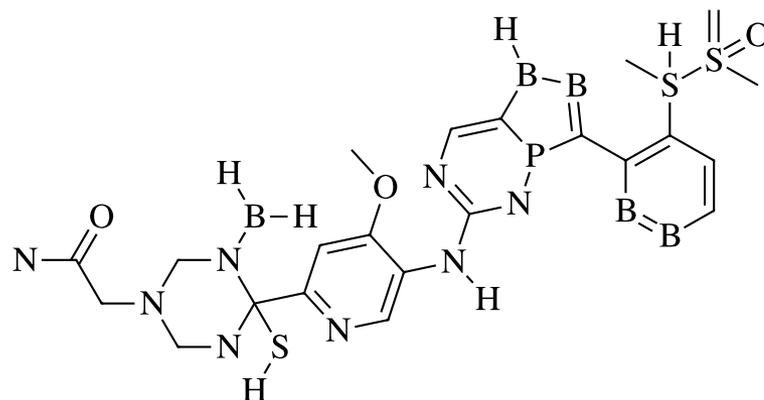


# How do you get new ideas from a computer?

About Generative SMILE systems  
Matched Molecular Pair analysis (MMPA)  
Enumeration with MMPA  
Drilling back to source data, to *explain* the origin of the Rules

# About Generative SMILES models

- Compounds can be represented as SMILES notation e.g. benzene c1ccccc1
- Use ML (or DL) 'model' to how SMILES strings are constructed
- With the model we can then ask it produce 'novel' compounds
  - They can do this in their billions.....



SMILES string

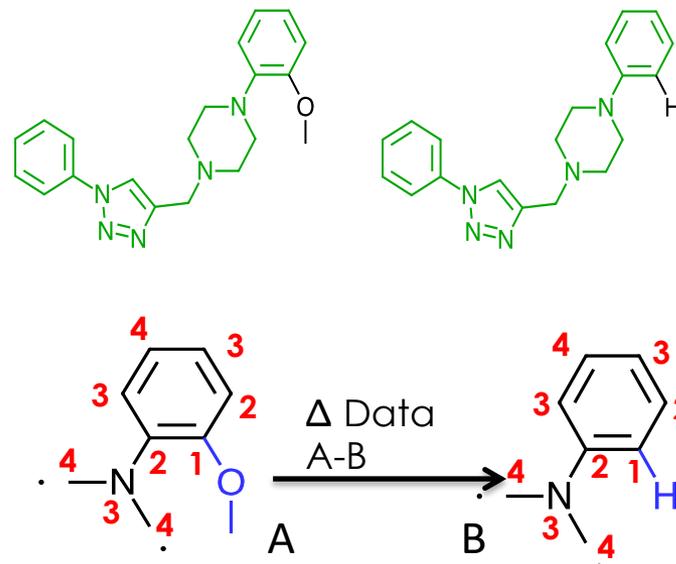
B1C(C(=BB2)P(C2=CN2)NC=2NC(=CN2)C(=CC=2C(S)(N)N(B)C2)OC)=C(C=CB=1)S(S(=C)(C)=O)C

De novo molecular design and generative models, Meyers, J.; Fabian, B.; Brown, N.;  
**Drug Discovery Today, June 2021**, <https://doi.org/10.1016/j.drudis.2021.05.019>

# Fully Automated Matched Molecular Pair Analysis (MMPA)

## What is this form of Artificial Intelligence?

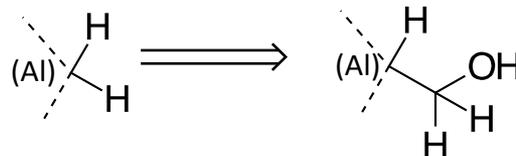
- **Matched Molecular Pairs** – Molecules that differ only by a particular, well-defined structural transformation
- **Capture the change and environment** – MMPs can be recorded as transformations from A → B
- **Statistical analysis to define “medicinal chemistry rules”**  
Defined transformations with high probability of improving properties of molecules
- **Store in a high performance database and provide an intuitive user interface**

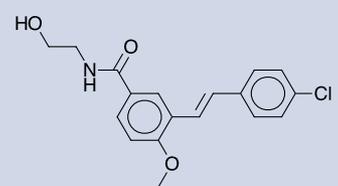
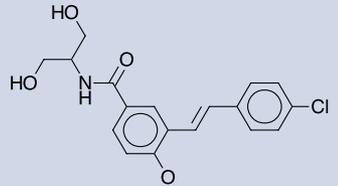
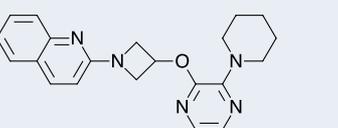
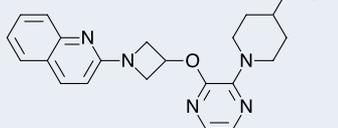
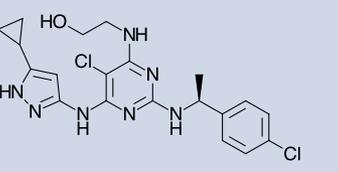
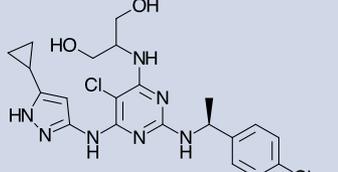


Griffen, E. *et al.* *J. Med. Chem.* **2011**, **54**(22), pp.7739 - 7750.

Leach *et al.* *J. Chem. Inf. Model.* **2017**, **57**, 2424 - 2436

# From SAR to MMPA.....

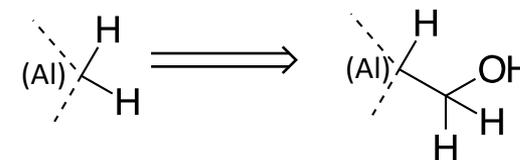


A	B	pSol A ( $\mu\text{M}$ )	pSol B ( $\mu\text{M}$ )	$\Delta\text{pSol}$
 CHEMBL1949786	 CHEMBL1949790	- 4.3 (48 $\mu\text{M}$ )	- 3.2 (700 $\mu\text{M}$ )	1.1
 CHEMBL3356658	 CHEMBL218767	- 6.0 (1.0 $\mu\text{M}$ )	- 3.7 (178 $\mu\text{M}$ )	2.3
 CHEMBL456802	 CHEMBL456322	-5.7 (2.0 $\mu\text{M}$ )	- 4.1 (82 $\mu\text{M}$ )	1.6
				3 pairs +ve Sol Median 1.6

MCPairs Rule finder required 6 matched pairs for 95% confidence

# The Matched Pairs leading to Rule.....

compound name A	compound name B	Depiction A	Depiction B	log10(M)	=	-1.6042	=	-1.2971	0.3071
				Aqueous Solubility at pH 7.4		Aqueous Solubility at pH 7.4		Aqueous Solubility at pH 7.4	Aqueous Solubility at pH 7.4
				solubility [CHEMBL2362975]		solubility [CHEMBL2362975]		solubility [CHEMBL2362975]	solubility [CHEMBL2362975]
				unit		measurement A		measurement B	measurement delta
CHEMBL104459	CHEMBL316800			log10(M)	=	-1.6042	=	-1.2971	0.3071
CHEMBL118022	CHEMBL115462			log10(M)	=	-4.63875	=	-4.3343	0.30445
CHEMBL161956	CHEMBL165547			log10(M)	=	-9.9586	=	-9.7447	0.2139
CHEMBL165864	CHEMBL166093			log10(M)	=	-10.699	=	-9.6778	1.0212
CHEMBL184	CHEMBL182			log10(M)	=	-5.2353	=	-4.7115	0.5238
CHEMBL184521	CHEMBL439660			log10(M)	=	-5.0168	=	-3.3704	1.6464
CHEMBL1949786	CHEMBL1949790			log10(M)	=	-4.31675	=	-3.1588	1.15795



Actual Rule from MCPairs  
Endpoint:  
Aqueous Solubility at pH 7.4  
[CHEMBL2362975]

n-qual	69
n-qual-up	47
n-qual-down	21
median $\Delta$ pSol	0.26
std dev +/-	0.636

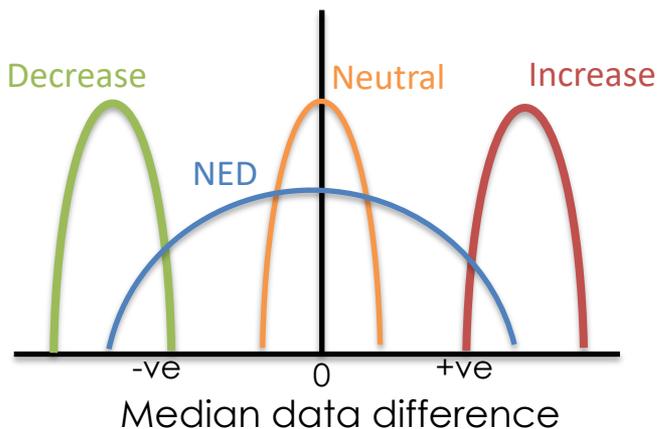
Explainable

- Drill back to real world examples and measured data

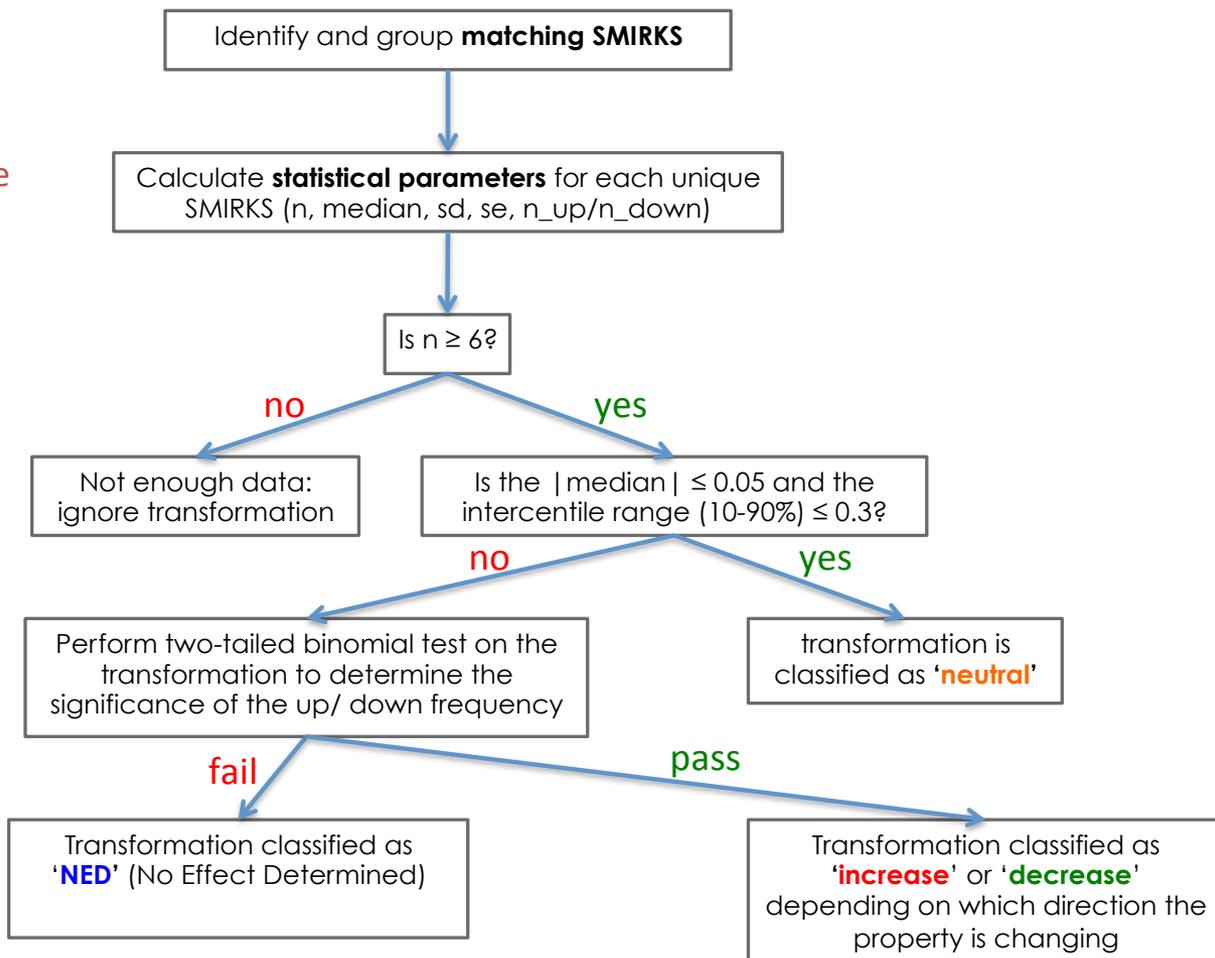
Actionable

- Clear decision to make the compound

# Rule selection



- No assumption of normal distribution
- Manages 'censored' = qualified / out-of-range data

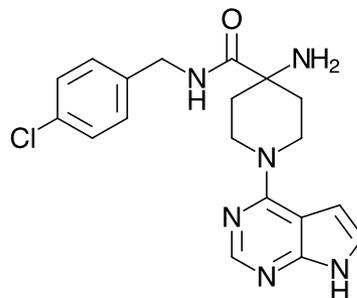


Leach et al. *J. Chem. Inf. Model.* **2017**, *57*, 2424 - 2436

# Capivasertib (AZD5363) – AKT inhibitors

AKT pIC<sub>50</sub> 7.89 (13nM)  
 LogD 2.9  
 Sol (pSol) -5.3 (5 – 150µM)  
 hERG pIC<sub>50</sub> 5.2 (5.2 µM)

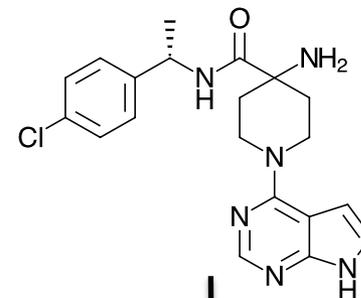
**Potent enough**  
**hERG and improved**  
**solubility**



CHEMBL598194

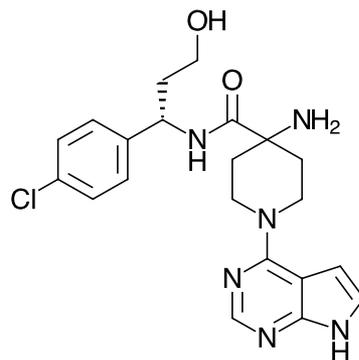
$\Delta$ pIC<sub>50</sub> + 0.2  
 $\Delta$ LogD - 0.2 (?)  
 $\Delta$ pSol + 0.5  
 $\Delta$ hERG ~ 0.2

CHEMBL2325742

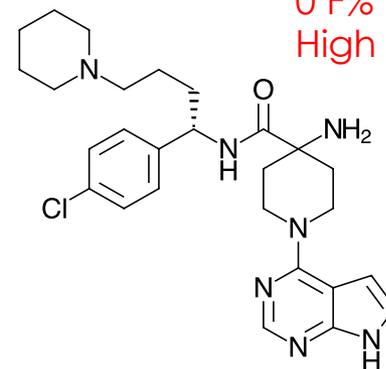


$\Delta$ pIC<sub>50</sub> ~ 0.0  
 $\Delta$ LogD - 0.3  
 $\Delta$ pSol + 1.4  
 $\Delta$ hERG - 0.5

0 F%  
 High Cl



CHEMBL2325741



CHEMBL2325729

AKT pIC<sub>50</sub> 8.4 (3nM)  
 LogD 2.5  
 Sol (pSol) -3.1 (780µM)  
 hERG pIC<sub>50</sub> <4.0 (>100 µM)

**Potent**  
**No hERG and improved**  
**solubility**

Kettle, J.G. et al ; J. Med. Chem. **2013**, **56**, 5, 2059–2073. <http://dx.doi.org/10.1021/jm301762v>

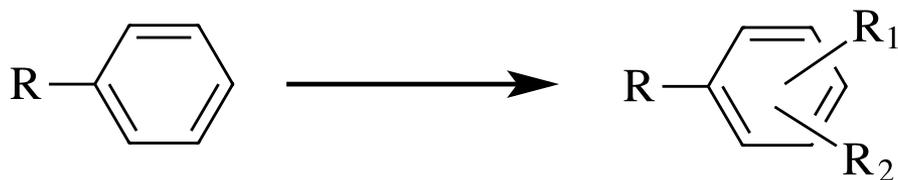
# MMPA Enables knowledge sharing



Kramer, Robb, Ting, Zheng, Griffen, et al. *J. Med. Chem.* **2018**, **61(8)**, 3277-3292  
<http://pubs.acs.org/doi/10.1021/acs.jmedchem.7b00935>

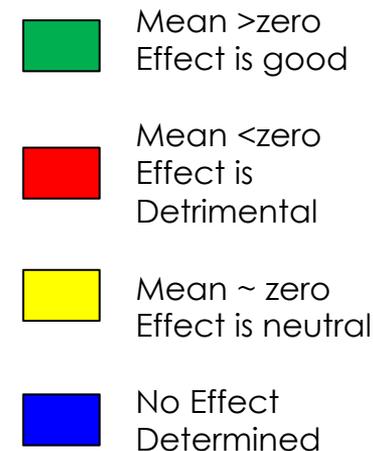
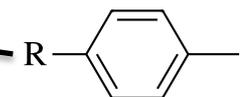
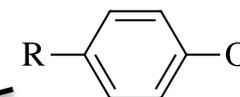
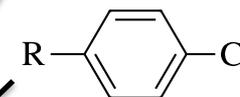
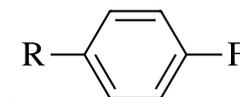
**Our MMPA technology enabled knowledge sharing between multiple organisations (AstraZeneca, Hoffman La Roche and Genentech)**

# Most common phenyl substitutions

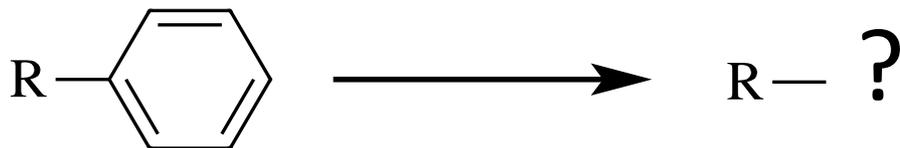


\* - Only the highest specificity data was used

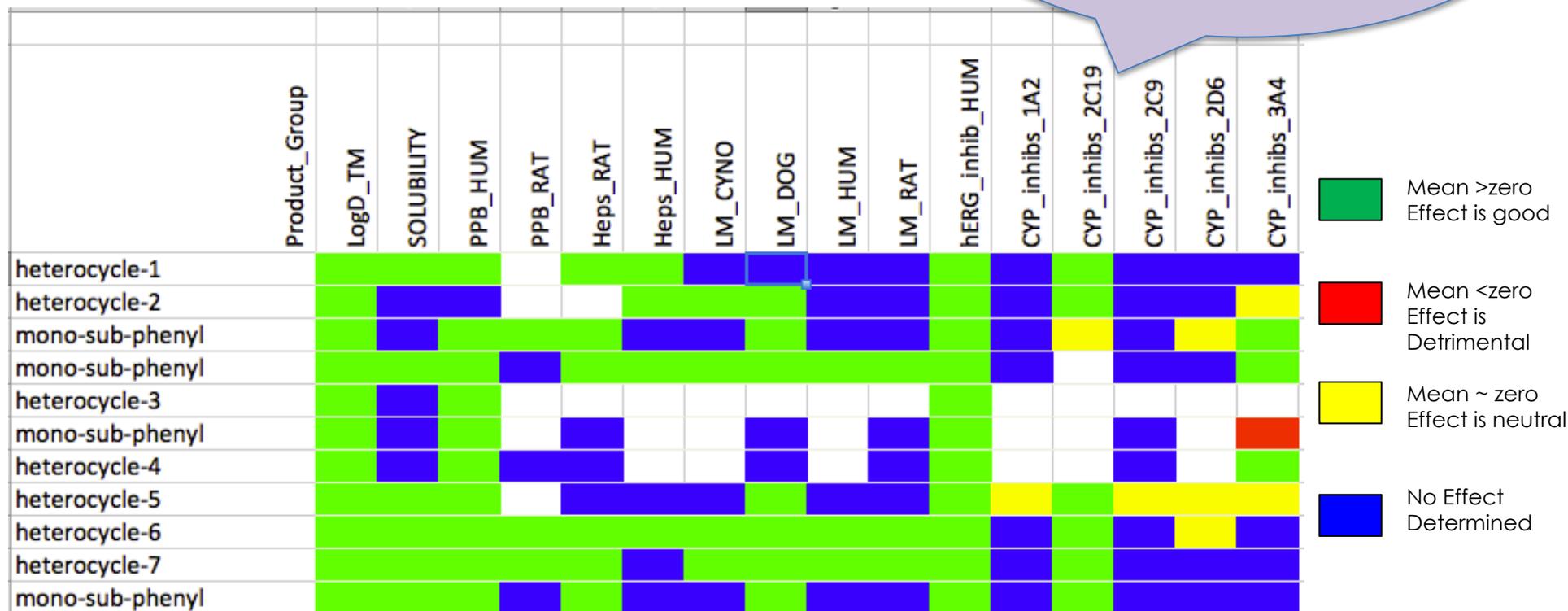
Product_Group	no_of_MPs	LogD_TM	SOLUBILITY	PPB_HUM	PPB_RAT	Heps_HUM	Heps_RAT	LM_HUM	LM_RAT	hERG_inhib_HUM	CYP_inhibs_1A2	CYP_inhibs_2C19	CYP_inhibs_2C9	CYP_inhibs_2D6	CYP_inhibs_3A4
c1cc(cc[c]1)F	5894	Red	Red	Red	Red	Blue	Green	Blue	Green	Blue	Blue	Blue	Blue	Blue	Green
c1cc(cc[c]1)Cl	4431	Red	Red	Red	Red	Blue	Green	Blue	Green	Red	Blue	Blue	Blue	Blue	Blue
COc1cc[c]cc1	3595	Blue	Red	Red	Red	Blue	Red	Red	Red	Blue	Blue	Blue	Blue	Blue	Blue
Cc1cc[c]cc1	2525	Red	Red	Red	Red	Blue	Red	Red	Red	Red	Blue	Blue	Blue	Blue	Blue
c1cc(cc[c]1)C#N	1921	Green	Blue	Green	Blue	Green	Green	Green	Green	Red	Blue	Yellow	Blue	Yellow	Green
c1cc(cc[c]1)O	732	Green	Blue	Green	Blue	White	Blue	Green	Blue	Blue	Blue	Green	Blue	Blue	Blue
c1cc(cc[c]1)C(F)(F)F	684	Red	Red	Red	Red	Blue	Green	Green	Blue	White	Blue	Blue	Blue	Blue	Blue
c1cc(cc[c]1)Br	512	Red	Red	Red	Red	White	Blue	Blue	Blue	Red	Blue	Blue	Blue	Blue	Blue
mono_sub_phenyl	472	Green	Green	Green	Blue	White	Green	Blue	Green	Blue	Green	Blue	Blue	Blue	Blue
mono_sub_phenyl	392	Green	Green	Green	Blue	White	Green	Blue	Green	Blue	White	Blue	Blue	Blue	Green
mono_sub_phenyl	383	Green	Blue	Green	Blue	White	Green	Blue	Green	Blue	Yellow	Blue	Blue	Blue	Green
mono_sub_phenyl	278	Green	Green	Green	Blue	White	Green	Blue	Green	Blue	Green	Blue	Blue	Blue	Blue
mono_sub_phenyl	237	Blue	Blue	Blue	Blue	White	Blue	Blue	Green	Blue	Blue	Blue	Blue	Blue	Blue
mono_sub_phenyl	223	Red	Red	Red	Red	White	Blue	Green	Blue	Blue	Blue	Blue	Blue	Blue	Blue
mono_sub_phenyl	222	Red	Blue	Red	Red	White	Blue	Blue	Blue	Blue	Yellow	Blue	Blue	Blue	Yellow
mono_sub_phenyl	208	Red	Blue	Red	Red	White	Blue	Blue	Blue	Blue	Green	Blue	Blue	Yellow	Blue
mono_sub_phenyl	159	Red	Blue	Red	Red	White	Blue	Blue	Red	Blue	Blue	Blue	Blue	Blue	Blue
mono_sub_phenyl	153	Green	Blue	Blue	Blue	White	Green	Blue	Blue	Blue	Blue	Blue	Blue	Blue	Blue
mono_sub_phenyl	129	Red	Blue	Red	Red	White	Blue	Blue	Green	Blue	Blue	Blue	Blue	Green	Blue
mono_sub_phenyl	106	Green	Blue	Green	Blue	White	Blue	Blue	Green	Blue	Blue	Blue	Blue	Blue	Red
mono_sub_phenyl	103	Blue	Red	Red	Red	White	Blue	Red	Blue	Blue	Blue	Blue	Blue	Blue	Blue



# Are there great changes from Phenyl?



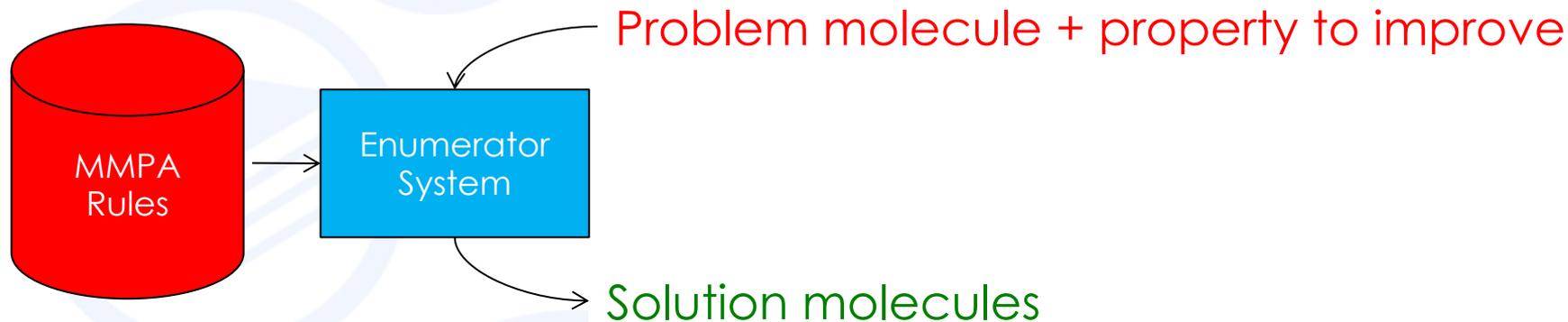
“I want rules that fix a couple of problems but leave lots of things alone” (MPO)



There are 25 thousand reasonable heterocycles for Med Chem

Tu, M. et al. *J. Chem. Inf. Model.* (2012), 52, 1114–1123

\* - Only the highest specificity data was used



RuleDesign® (enumerate “Compounds From Rules”)

- User enters in a sub-optimal molecule with a property they wish to improve – e.g. solubility, metabolism, hERG....
- System suggests new molecules considering the context of the changes (**Level 1 / 2**)

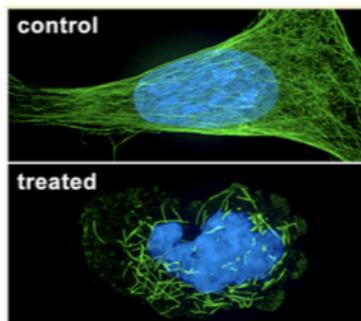
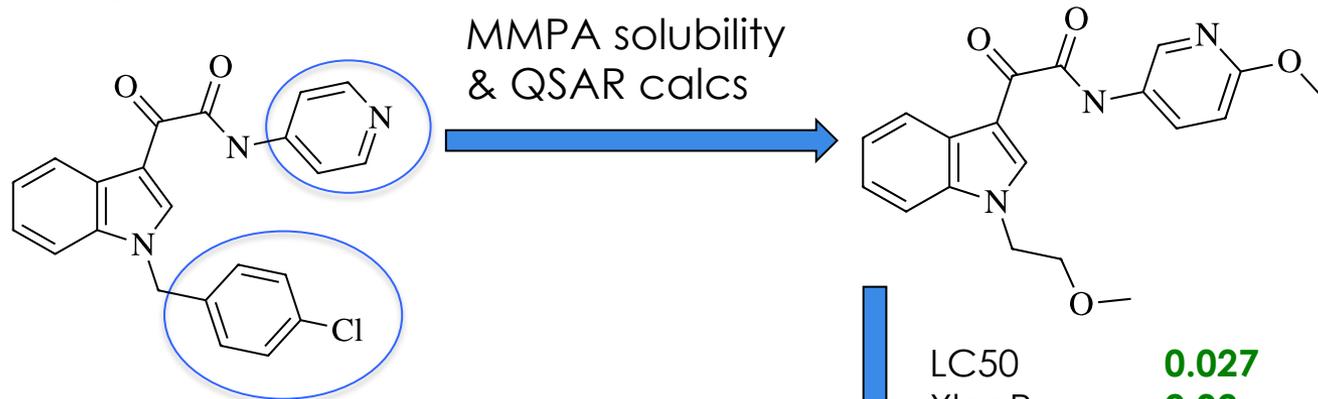
**“..it’s like asking 150 of your peers for ideas in just a few seconds”**  
**- Principal Scientist (large pharma)**

**A Turing test for molecular generators** Darren Green D.; *et al*  
*J. Med. Chem.* 2020, 2020, 63, 20, 11964–11971

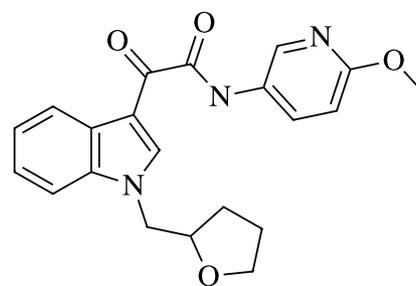
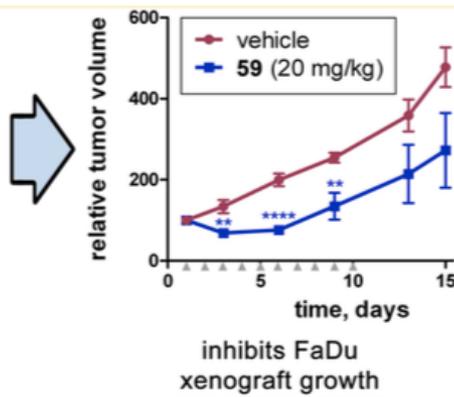
# Indole-3-glyoxylamide Based Series of Tubulin Polymerization Inhibitors

- Increase potency, solubility and reduce metabolism
- Enable in-vivo xenograft studies

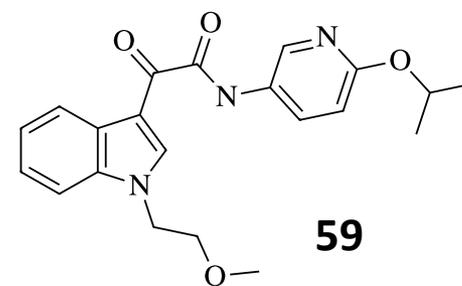
Indibulin D-24851  
 LC50 **0.032**  
 XlogP **3.35**  
 ~ **potent**  
**In-vivo activity**  
**poor solubility (~ 1uM)**



disruption of cellular microtubule network



LC50 **0.031**  
 XlogP **2.57**  
**solubility (~10-80uM)**



LC50 **0.055**  
 XlogP **2.91**  
**solubility (~10-80uM)**

Thompson, M. et al J. Med. Chem., 2015, 58 (23), pp 9309-9333

AI design → synthesis → In-vivo → publication 1 year

Journal of  
**Medicinal  
Chemistry**

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Article

pubs.acs.org/jmc

## An Orally Bioavailable, Indole-3-glyoxylamide Based Series of Tubulin Polymerization Inhibitors Showing Tumor Growth Inhibition in a Mouse Xenograft Model of Head and Neck Cancer

Helen E. Colley,<sup>\*,†,∇</sup> Munitta Muthana,<sup>‡,∇</sup> Sarah J. Danson,<sup>§</sup> Lucinda V. Jackson,<sup>||</sup> Matthew L. Brett,<sup>||</sup> Joanne Harrison,<sup>||</sup> Sean F. Coole,<sup>||</sup> Daniel P. Mason,<sup>||</sup> Luke R. Jennings,<sup>†</sup> Melanie Wong,<sup>⊥,∇</sup> Vamshi Tulasi,<sup>⊥</sup> Dennis Norman,<sup>⊥</sup> Peter M. Lockey,<sup>⊥</sup> Lynne Williams,<sup>‡</sup> Alexander G. Dossetter,<sup>#</sup> Edward J. Griffen,<sup>#,∇</sup> and Mark J. Thompson<sup>\*,||,∇</sup>

<sup>†</sup>School of Clinical Dentistry, University of Sheffield, 19 Claremont Crescent, Sheffield S10 2TA, U.K.

<sup>‡</sup>Department of Oncology, The University of Sheffield, Medical School, Beech Hill Road, Sheffield S10 2RX, U.K.

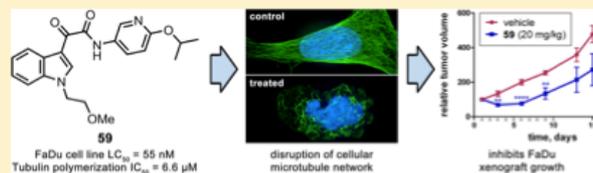
<sup>§</sup>Academic Unit of Clinical Oncology and Sheffield Experimental Medicine Centre, Weston Park Hospital, Whitham Road, Sheffield S10 2SJ, U.K.

<sup>||</sup>Department of Chemistry, University of Sheffield, Brook Hill, Sheffield S3 7HF, U.K.

<sup>⊥</sup>Charles River, 8–9 Spire Green Centre, Harlow, Harlow, Essex CM19 5TR, U.K.

<sup>#</sup>MedChemica Limited, Ebenezer House, Ryecroft, Newcastle-Under-Lyme, Staffordshire ST5 2BE, U.K.

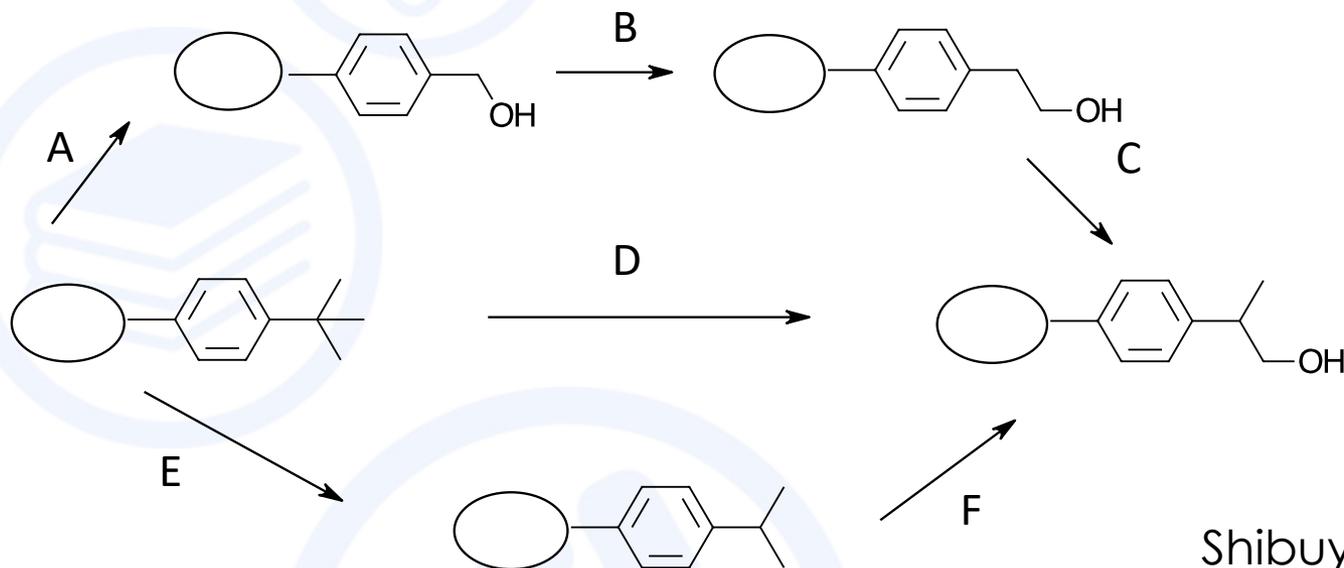
### Supporting Information



**ABSTRACT:** A number of indole-3-glyoxylamides have previously been reported as tubulin polymerization inhibitors, although none has yet been successfully developed clinically. We report here a new series of related compounds, modified according to a strategy of reducing aromatic ring count and introducing a greater degree of saturation, which retain potent tubulin polymerization activity but with a distinct SAR from previously documented libraries. A subset of active compounds from the reported series is shown to interact with tubulin at the colchicine binding site, disrupt the cellular microtubule network, and exert a cytotoxic effect against multiple cancer cell lines. Two compounds demonstrated significant tumor growth inhibition in a mouse xenograft model of head and neck cancer, a type of the disease which often proves resistant to chemotherapy, supporting further development of the current series as potential new therapeutics.

Thompson, M. J.; *J. Med. Chem.*,  
**2015**, 58 (23), 9309 – 9333

# “Multi-Step” transformations



Shibuya Crossing Tokyo



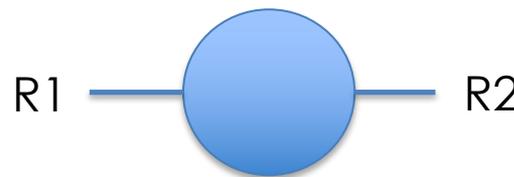
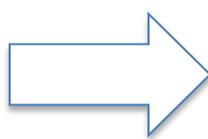
Would you go steps via A -> B -> C  
 How would you go know to go E -> F  
 Or go straight there via D  
 - if the data said it was good?

# Example - <sup>t</sup>Bu metabolism issue

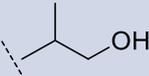
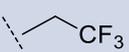
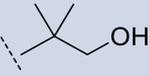
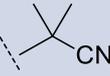
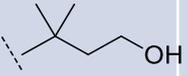
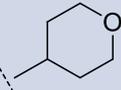
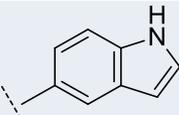
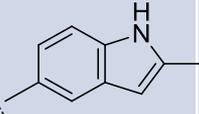
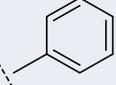


CANCER  
RESEARCH  
UK

MedChemical<sup>RY</sup>  
MANCHESTER  
INSTITUTE



Roger Butlin  
Rebecca Newton  
Allan Jordan

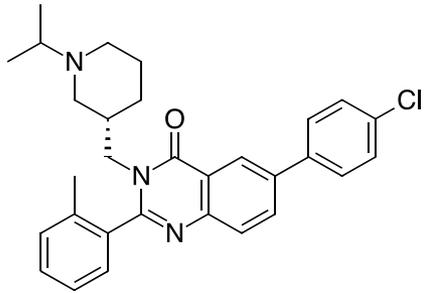
		Benchmark compound	Predicted to offer most improvement in microsomal stability (in at least 1 species / assay)									
												
R2 \ R1		<sup>t</sup> Bu				Me				Et	iPr	
		99 392	16 64	78 410	53 550	99 288	78 515	41 35	98 327		92 372	24 247
		35 128				24 62				60 395		
		39 445	3 21			20 27			57 89		54 89	

- Data shown are  $Cl_{int}$  for HLM and MLM (top and bottom, respectively)

# Project 4 – Ghrelin Inverse agonists – CNS target

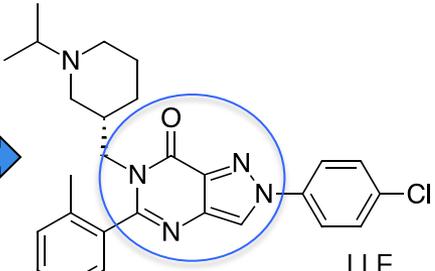
- Novel more efficient core required, improve hERG for CD
- CNS penetration, good potency and deliver tool for in vivo testing

pIC <sub>50</sub>	9.9
logD	5.0
hERG pIC <sub>50</sub>	5.0
LLE	4.9
<b>very potent</b>	
<b>very lipophilic</b>	



MMPA Cores

$\Delta$ pIC <sub>50</sub>	-0.4
$\Delta$ logD	-1.8
$\Delta$ hERG pIC <sub>50</sub>	+0.4

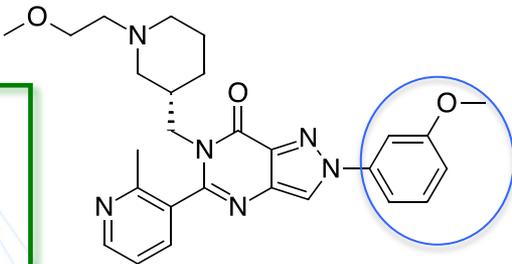


LLE	6.4
-----	-----

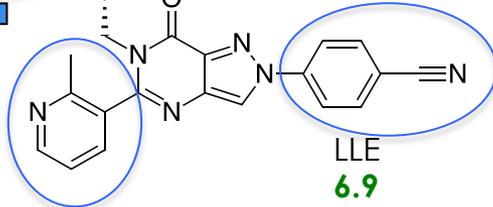
$\Delta$ pIC <sub>50</sub>	-2.2
$\Delta$ logD	-2.2
$\Delta$ hERG pIC <sub>50</sub>	-0.7

100 compounds made

pIC <sub>50</sub>	8.2
logD	1.3
hERG pIC <sub>50</sub>	4.4
LLE	6.9



$\Delta$ pIC <sub>50</sub>	+0.9
$\Delta$ logD	+0.2
$\Delta$ hERG pIC <sub>50</sub>	-0.3



LLE	6.9
-----	-----

McCoull, W.M.; Dossetter A.G.; et al, Med. Chem. Commun., (2013), 4, 456

LLE = lipophilic ligand efficiency: LLE=pIC<sub>50</sub>-logD

# What makes MMPA Explainable?

The screenshot displays the 'Rule to Pairs' interface in the MedChemica software. It features a table with columns for 'A', 'B', and 'Aqueous Solubility at pH 7.4 solubility [CHEMBL2362975]'. The table lists three pairs of chemical structures (A and B) with their corresponding solubility values and fold change. A text box on the right explains that users can click through the structures to see the original compounds and measured data, making the rule's origin fully explainable.

Transformation Information		Aqueous Solubility at pH 7.4 solubility [CHEMBL2362975]				
A	B	Qual A	A	Qual B	B	Fold Change
		=	39.264	=	84.850	~ 2.2 ↑
		=				
		=				

In just a few clicks we arrive back at the original compounds and measured data to see where the Rule has come from. Fully explained because we can see the structures!

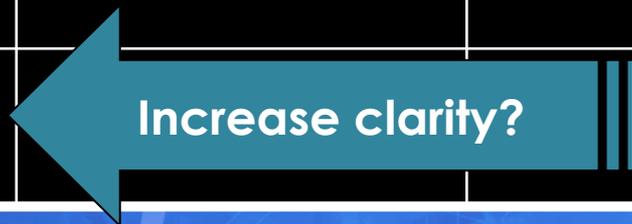
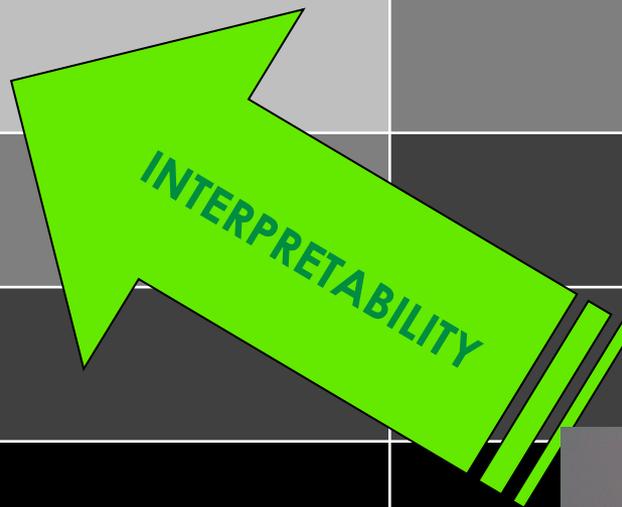
## Explaining AI with ML Models

It is possible to produce a potency prediction with ML models  
AND  
show the chemist how that prediction is derived

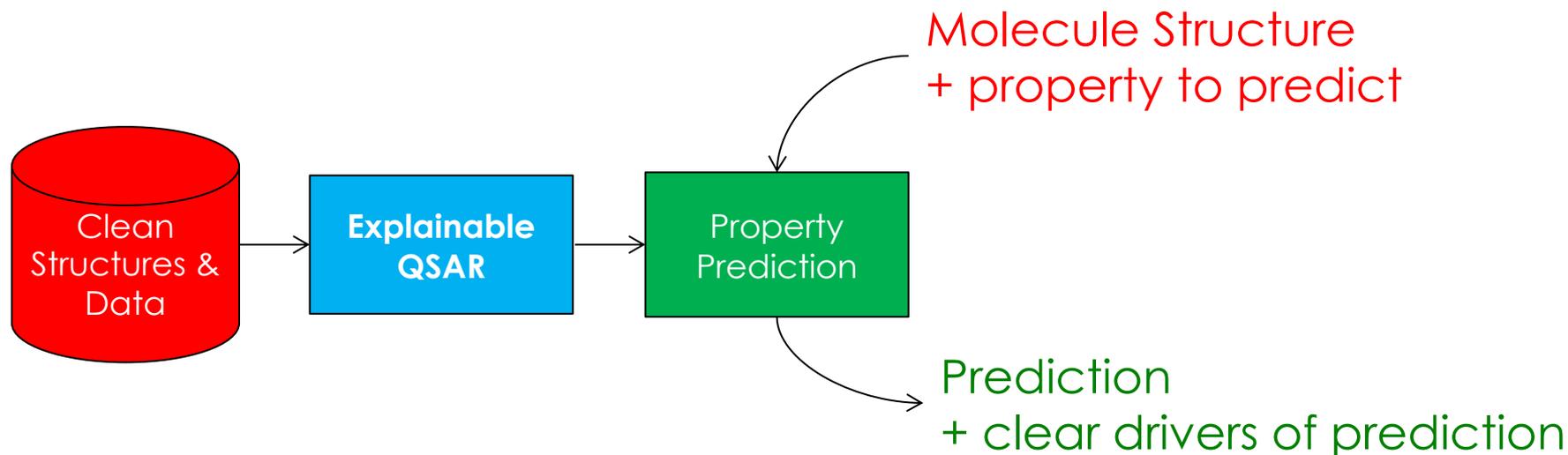
# What does Explainable AI mean?

About compound descriptors and Methods...

Method \ Descriptors	substructures	Physical chemistry descriptors (Hansch, Taft, Fujita, Abraham)	Atomic, pair, triplet descriptors	Indices
(M)LR				
PLS				
Trees / Forests				
SVM				
Bayesian NN				
Deep Learning				



# Property Prediction and Explainable AI Models



## Automated Explainable QSAR

Chemists get predictions with the substructures highlighted that are driving prediction and the molecules used to support that part of the model – transparent / explainable AI.

## Muscarinic acetylcholine receptor M1 Homo sapiens pIC50 [CHEMBL216]

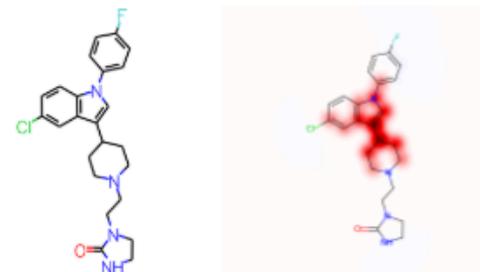
c1cc(ccc1n2cc(c3c2ccc(c3)Cl)C4CCN(CC4)CCN5CCNC5=O)F

### Explainable

- Highlighted features show the chemist the contribution to the prediction

### Actionable

- Which parts should be optimized to achieve the Goal



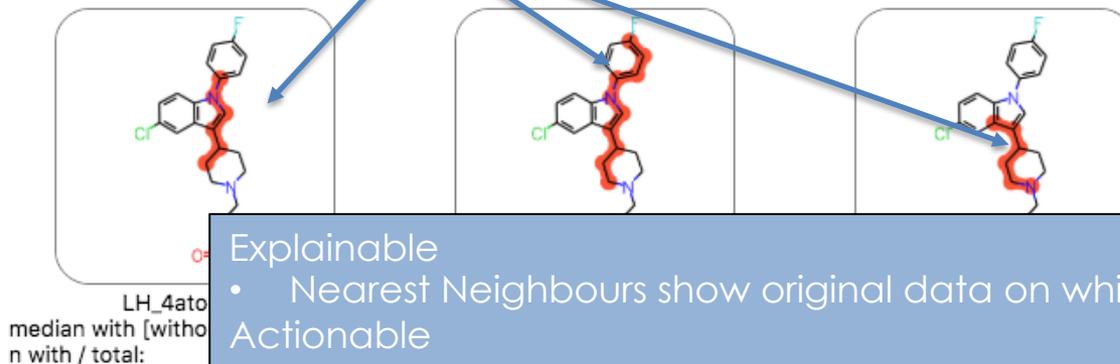
### 3 Pharmacophore(s)

Active

In domain

**uM: 0.096**

**Range: 0.321 - 0.028**



### Explainable

- Nearest Neighbours show original data on which model is built

### Actionable

- What weight do I put on this results? How likely is it? Do we test?

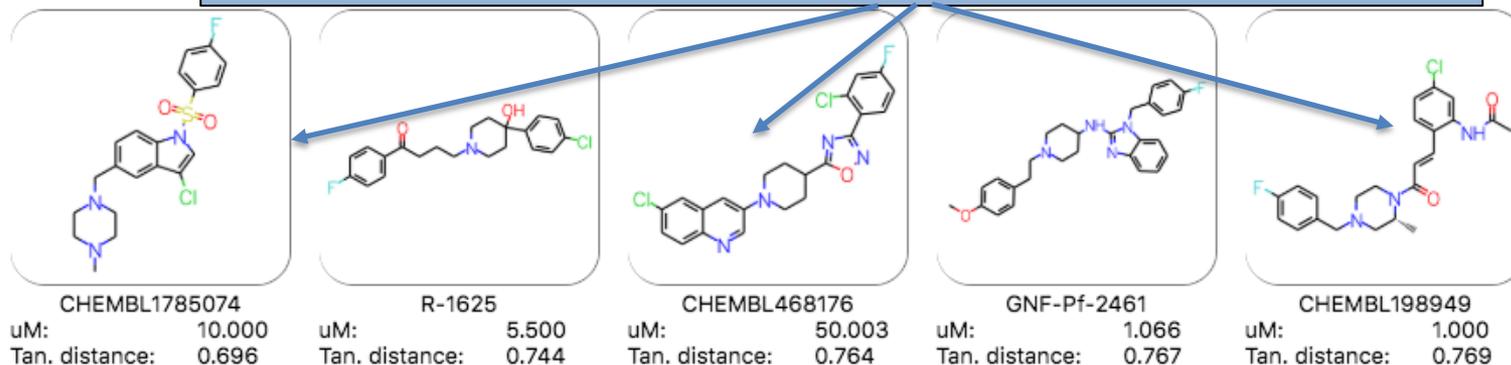
### 10 Nearest Neighbour(s)

Active

Out of domain

**uM: 2.555**

**Range: 3.584 - 1.821**



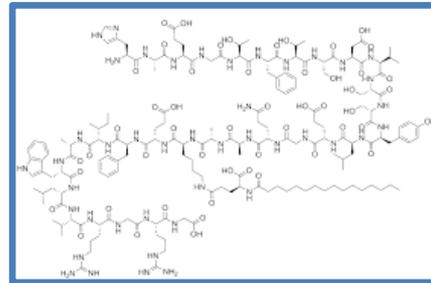


# Future vision – A view on further AI supported chemistry

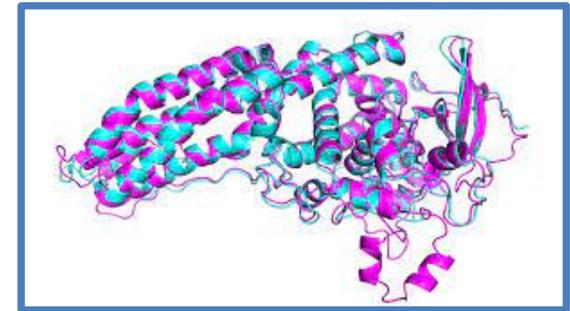
# Future of Augmented Intelligence in Drug Discovery?



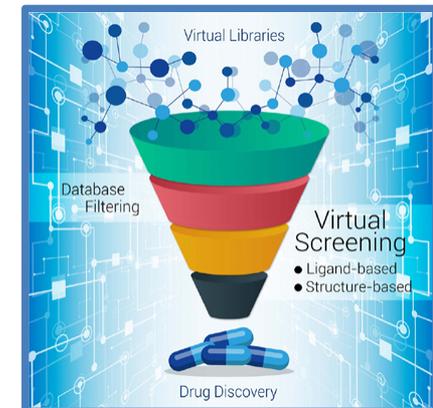
Genome Sequence



Peptide sequence



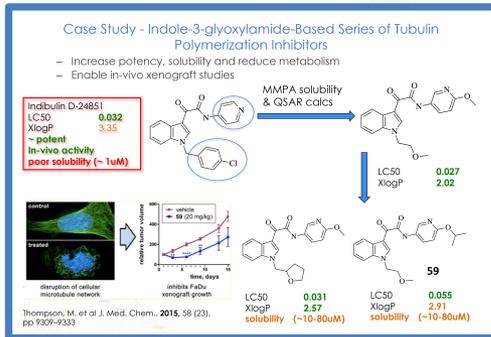
3D peptide folding  
Identify binding pockets



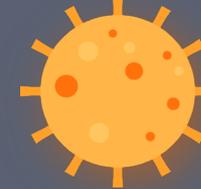
Virtual Screen – 2000 hits



Biochemical Screening



Lead Optimisation  
100 compounds



# THE COVID MOONSHOT

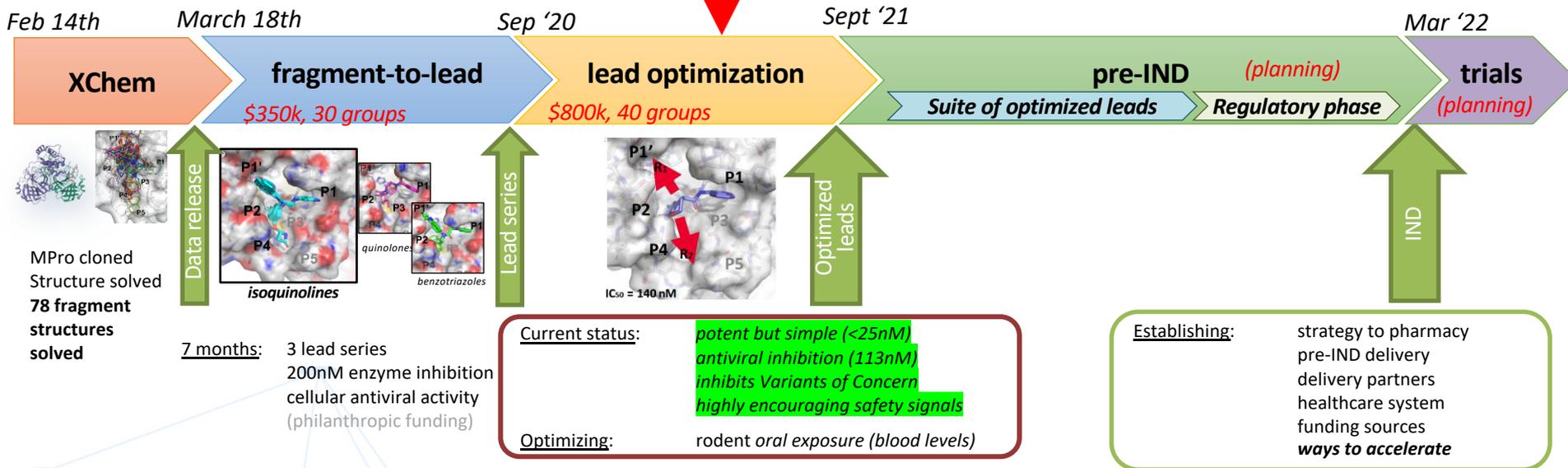
**Goal:** new potent antiviral: therapeutic & prophylactic

- simple synthesis
- orally potent, 3x daily for 5 days
- very safe
- simple tablet

**Strategy:** work fully open to enable rapid global availability

- data and compound designs immediately public
- no IP filed
- generic drug "straight from pipeline"
- (unprecedented – no template available)

June



<https://www.diamond.ac.uk/covid-19/for-scientists/Main-protease-structure-and-XChem.html>

<https://www.nature.com/articles/d41586-021-01571-1>

# Conclusions

- What is AI, Explainable AI and What does it mean to MedChem?
  - Think Augmented Intelligence (Level 1 and 2)
  - Viewing (sub)structures and measurements *explains* the computer's thinking
- Designing AI systems to **enable** the chemist
  - Sensible compound suggestions with simple interfaces
- How do you get new ideas from a computer?
  - Matched Molecular Pair analysis (MMPA)
    - Suggests compounds with decisions made by the chemists (Level 2)
    - Drilling back to source data, to *explain* the origin of the Rules (Level 1)
    - Permutative MMPA to ensure all the gaps are filled (Level 2)
    - ML models with substructural features – where do we need to focus (Level 1)
- Project Examples (6 projects including Covid Moonshot)
- Future vision – A view on further AI supported chemistry
  - Invest in Data there is still lots of chemical space we do not understand
  - Compute methods are improving all the time...

# Thank you

- Dr Alexander G. Dossetter
- Managing Director, MedChemica Ltd
- [al.dossetter@medchemic.com](mailto:al.dossetter@medchemic.com)
  
- **Available on Slideshare - search for Dossetter**
  
- **Twitter @MedChemica**
- **Twitter @covid\_moonshot**
- **Twitter #BucketListPapers**
- <https://www.medchemica.com/bucket-list/>

## About MedChemica

>10 experience in building A.I. Systems for drug discovery



Genentech  
A Member of the Roche Group

syngenta



HEPTARES  
therapeutics

Alkermes®  
Patient inspired®



REVOLUTION  
MEDICINES

BenevolentAI



bugworks



Exscientia

CATAPULT  
Medicines Discovery



Galapagos



CANCER  
RESEARCH  
UK



astex®  
pharmaceuticals



ROYAL SOCIETY  
OF CHEMISTRY



UNICAMP

ICR The Institute of  
Cancer Research

BLUEBERRY THERAPEUTICS



insight through  
communication



Medicines for Malaria Venture



SGC



THE UNIVERSITY  
of LIVERPOOL



AMR  
CENTRE

The UK R&D  
Centre for  
Antimicrobial  
Resistance

MANCHESTER  
1824

The University  
of Manchester



Liverpool  
John Moores  
University



The  
University  
Of  
Sheffield.

THE UNIVERSITY OF  
WARWICK

UNIVERSITY OF  
DUNDEE



- Founded in 2012 by AZ AP Medicinal / Computational chemists to accelerate drug hunting by exploiting data driven knowledge
- Domain leaders in SAR knowledge extraction and knowledge based design
- > 11 years experience of building AI systems that suggest actions to chemists (7 years as MedChemica)
- Creators of largest ever documented database of medicinal chemistry ADMET knowledge

[MedChemica Publications](#)

# AI Software Platforms



## **MCPAIRS** ENTERPRISE

- Complete In-house platform
- Analysis of own data and automated updating
- Design tool access to all chemists
- Custom fitting (Software-as-a-Service)

Medium to large pharma,  
agrochemical and  
materials research



## **MCPAIRS** ONLINE

- Secure web-based AI design platform
- ChEMBL, Patent data analysed
- Merged into one knowledgebase

One stop GUI  
Design tool  
Biotech, Universities and  
Foundations

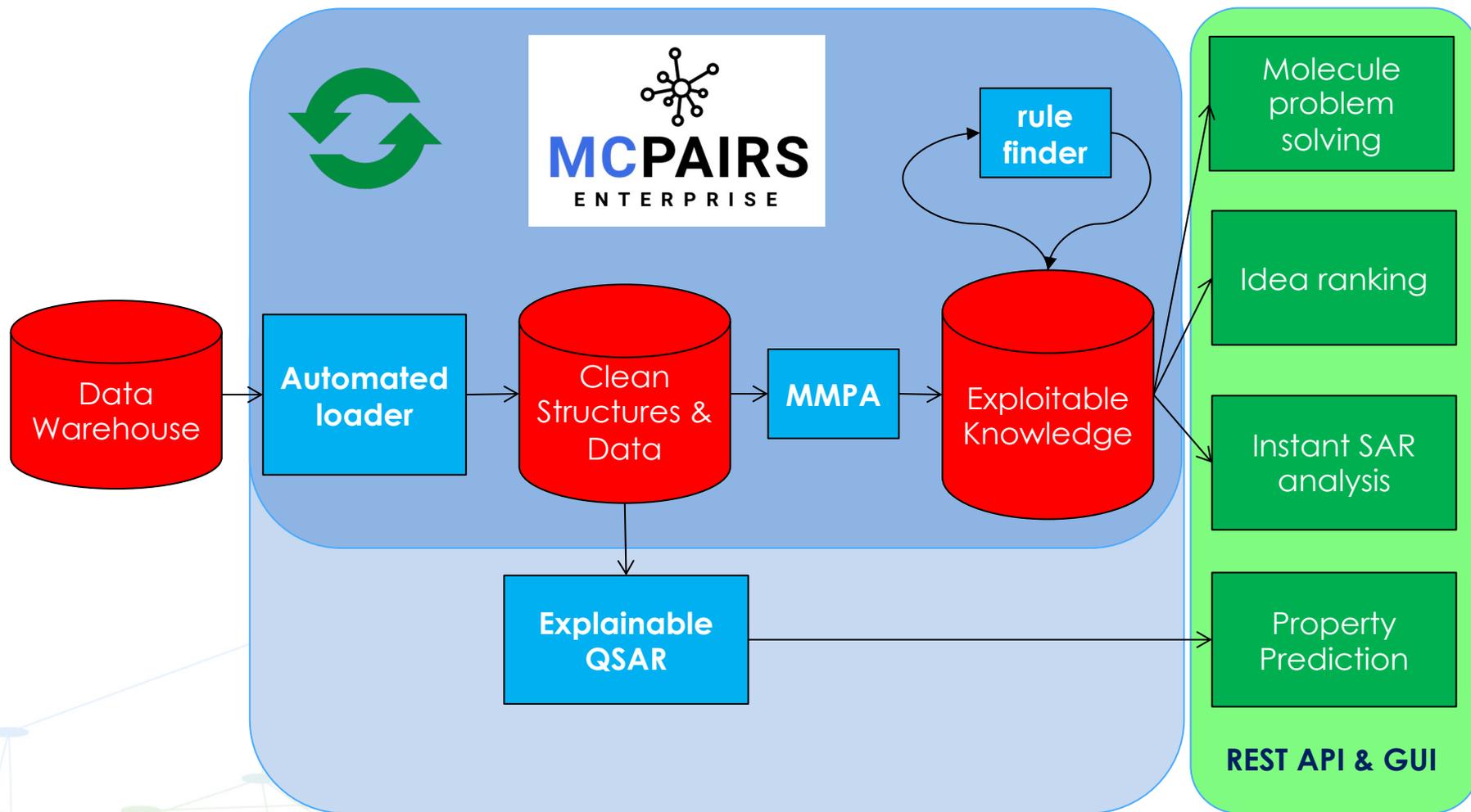
# AI systems that enhance Chemists

- Principles:
  - Evaluate with directly observable data
  - Expose conflicting views
  - Continuous learning and improvement
  - Place in context



- Translating into practice:
  - Methods that directly connect to chemical structures & data
  - Make all methods auditable
  - Automate updates and track metrics
  - Integrate automated systems and chemists ideas

# Explainable AI for Medicinal Chemistry Design



# Simple submission and control of the Goal

MedChemica

[Home](#)   [Log Out](#)   [Modules](#)

Rule Design

Input Molecule\*

**Compound Name:**

**SMILES\*:**

JSME Molecular Editor by Peter Ertl and Bruno Bienfait

Sub-structure Lock

**SMARTS:**

**Goal\***

**Direction\*:** Increase

**Endpoint\*:** solubility

Submit

Advanced Filters

- Molecular charge:
- HBA:
- HBD:
- CLogP:
- RMM:
- PSA:
- Specificity:** [ 1 - 4 ]

#	Timestamp	Status	Number of Products	
0	Jan 28, 2020, 1:32:48 PM	Complete	1	<a href="#">Save</a>
1	Jan 28, 2020, 1:33:27 PM	Complete	139	<a href="#">Save</a>

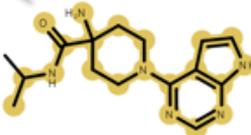
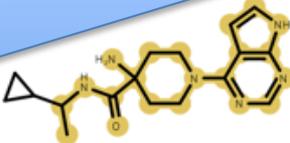
# Looking at the results

Results sorted in increasing RMM (Mol Weight)

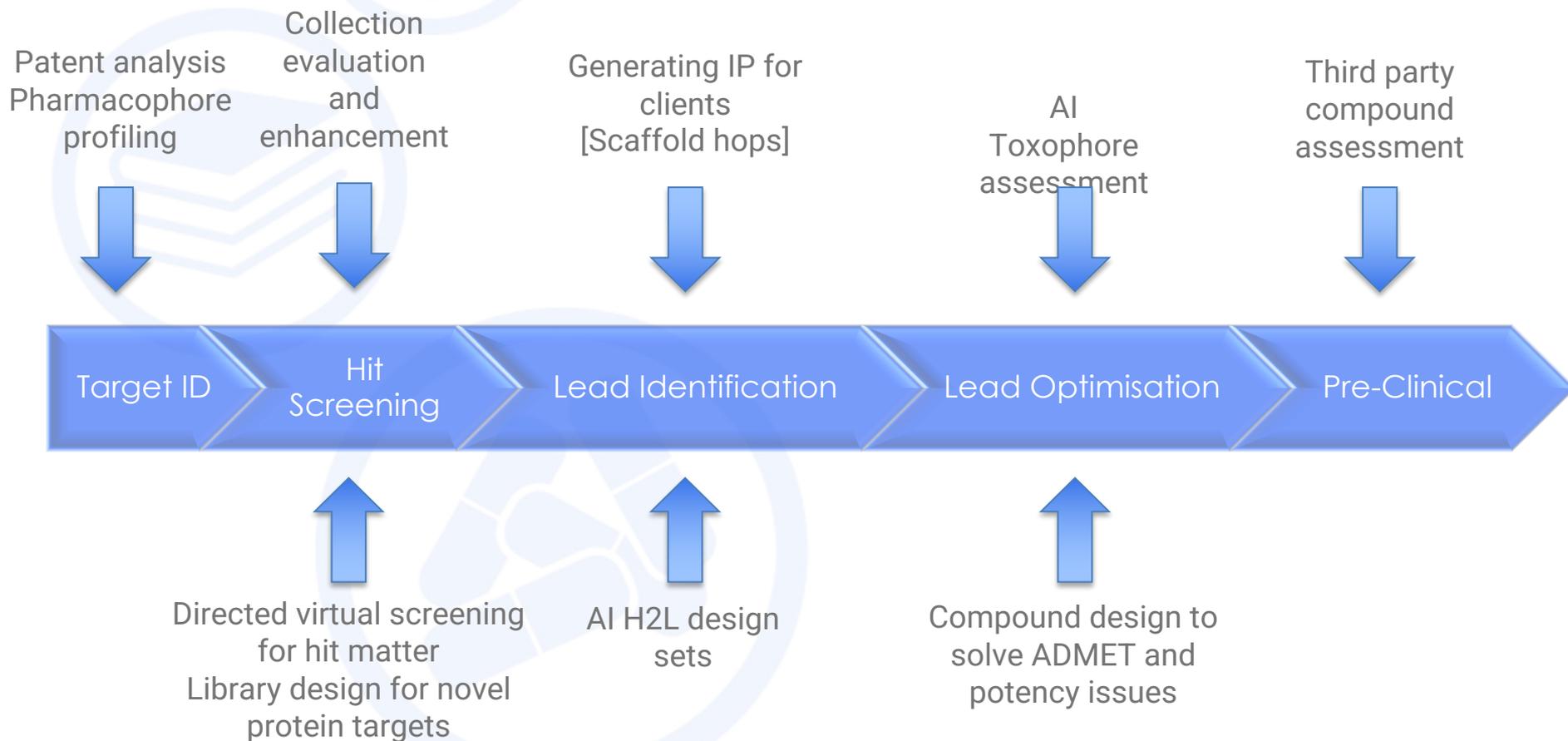
One column per assay  
- colour and direction  
- LogD decrease, Sol increase

Yellow highlight is the overlap with the input compound

Hyperlink to "Drill back" to the original data

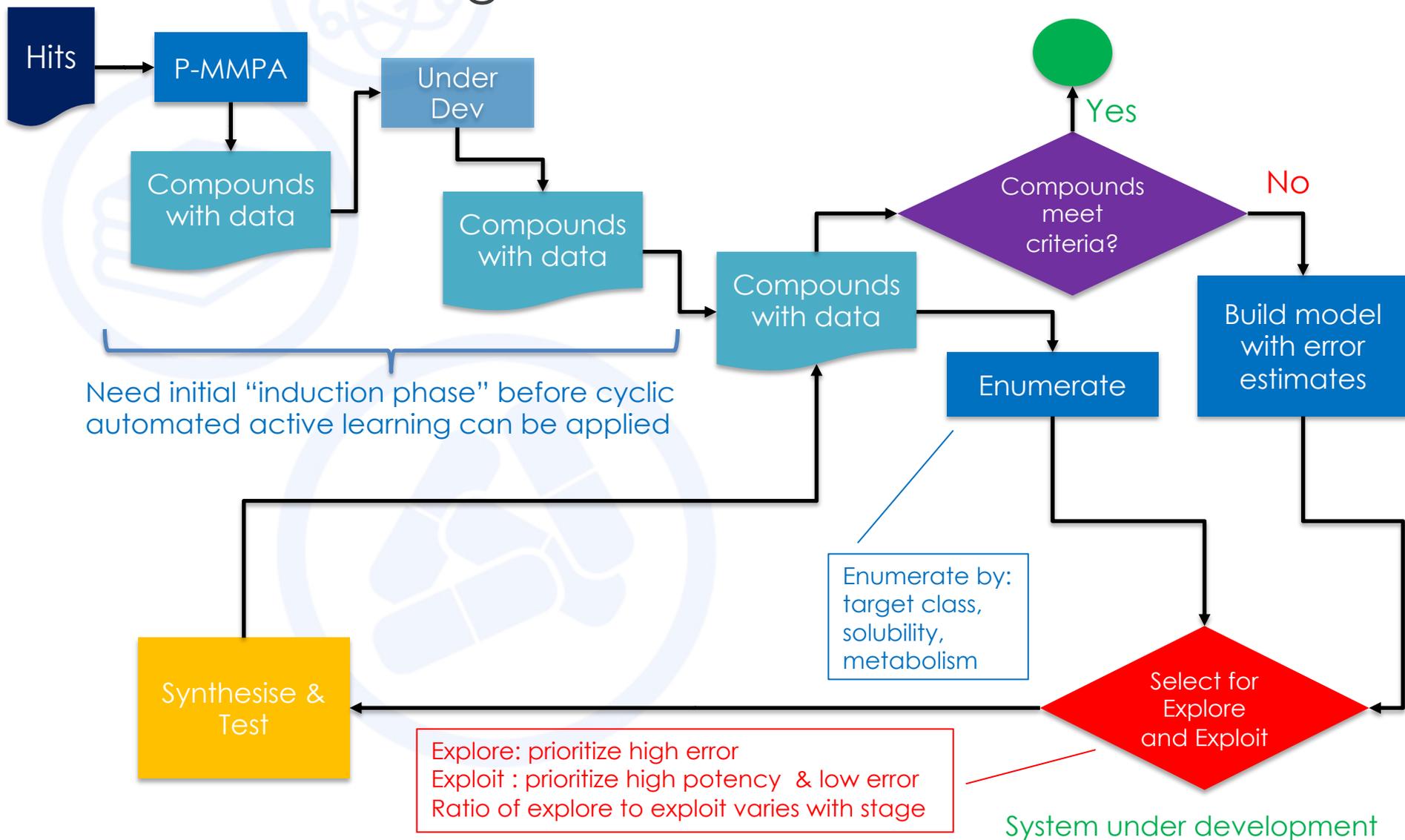
	H	I	J	K	L	M	AD	AT	BJ		
function	pair data	ClongP	HBA	HBD	PSA	RMM	LogD TM direction	Aq Solubility pH 7.4 [CHEMBL236 2975] direction	Aq Solubility pH 7.4 [CHEMBL612 558] direction	Aq Solubility comb patent data log(M) direction	PP rat log on Fri dir
	<a href="#">matched pair</a>	0.4	7	3	100	302.4	decrease	.	.	increase	.
<chem>.(CCN(CC1)c2c3cc[nH]c3ncn2)N</chem>											
	<a href="#">matched pair</a>	0.7	7	3	100	328.4	NED	.	.	increase	.
<chem>.(CCN(CC1)c2c3cc[nH]c3ncn2)N</chem>											

# Science As A Service (SaaS)



Bespoke Advanced Analytics and Computational Chemistry services through-out the research phase

# Active Learning v2



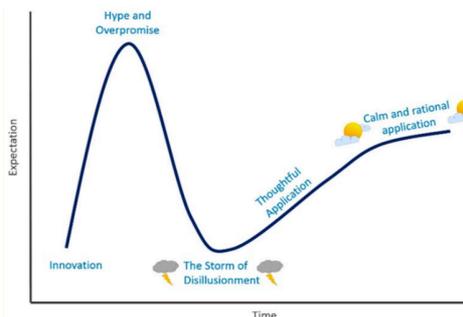
## Project examples

An illustration of how MCPairs saves time and money  
“Leap-frogging to the best the molecule”

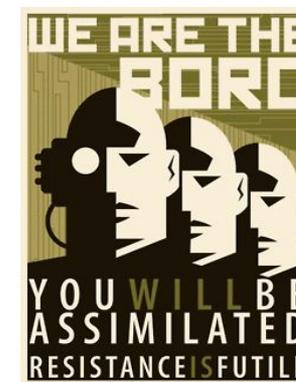
## Resistance is Futile Rational

- Is all this AI stuff going to be just another spin round the hype cycle?
  - Artificial Intelligence in Drug Design -The Storm Before the Calm?

Allan M. Jordan [ACS Med. Chem. Lett. 2018, 9, 12, 1150-1152](#)



- What's our defense reaction?
  - **Avoid embarrassment**
  - Unilateral control – 'I'm in charge'
  - Win-lose conflict framing – 'if I'm better - that is rubbish'
  - Emphasize rationality
  - Avoid inquiry – 'nothing to learn from the past– move on'
- How to Engage Constructively?
  - Define common goals
  - Evaluate with directly observable data
  - Expose conflicting views
  - Continuous learning and improvement
  - Place in context



Argyris C.  
Schein EH.

Organizational traps: leadership, culture, organizational design. Oxford University Press; 2010.

Organizational culture and leadership, Chapter 10: How Leaders Embed and Transmit Culture. 5th Edition. Wiley; 2017.

# Project Example 1 – GPR 119 anatagonists

## Changing view of SO<sub>2</sub>CH<sub>3</sub> on solubility

Leach *et al* 2006

ArH → ArSO<sub>2</sub>CH<sub>3</sub> ↑ solubility in line with ↓ logP

Leach *et al* 2012

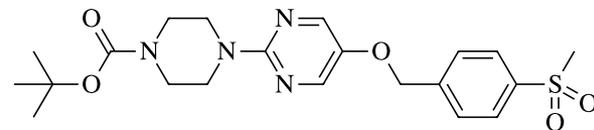
SO<sub>2</sub>CH<sub>3</sub> was found to contribute to tight crystal packing via small molecule single crystal x-ray structure determination

5 years of combined data and the application of MMPA

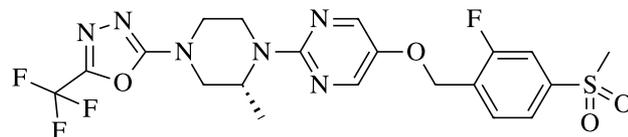
ArH → ArSO<sub>2</sub>CH<sub>3</sub> ↓ solubility with ↓ logP

Initial dataset was too small (28 pairs) and unrepresentative and did not include environment

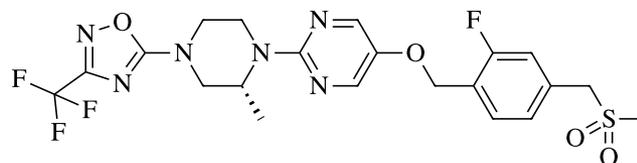
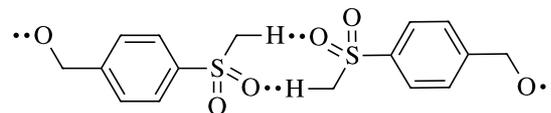
## GPR119 - Project



pEC<sub>50</sub> 7.2 (83%); Sol 0.03 μM



pEC<sub>50</sub> 7.6 (121%); Sol 1.0 μM; hERG 7 μM



pEC<sub>50</sub> 8.1 (84%); Sol 1.8 μM; hERG >33 μM

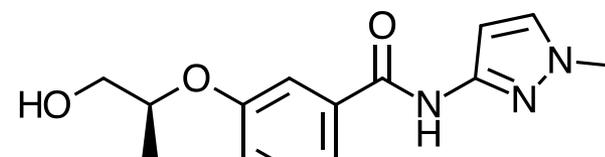
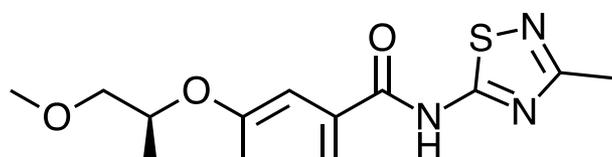
Scott, J.; Leach, A.G.; *et al* *Med. Chem. Commun.*, **2013**, 4, 95-100  
Scott, J.; Leach, A.G.; *et al* *J. Med. Chem.* **2012**, 55, 5361-5379.  
Oxadiazoles in medicinal chemistry. Boström, J. *et al.* (2012) *J. Med. Chem.* 55, 1817–1830

## Project example 2 - Glucokinase Activators

- Fix hERG problem whilst maintaining potency

**pEC<sub>50</sub>: 7.0**  
**logD: 2.9**  
**hERG pIC<sub>50</sub>: 5.1**

MMPA  
 $\Delta pEC_{50}$ : **-0.1**  $\Delta \log D$ : **-0.6**  $\Delta hERG$  pIC<sub>50</sub>: **-0.5**  
*n*=27      *n*=27      *n*=7



MMPA  
 $\Delta pEC_{50}$ : **-0.1**  $\Delta \log D$ : **-0.6**  $\Delta hERG$  pIC<sub>50</sub>: **-0.5**  
*n*=33      *n*=32      *n*=22

**pEC<sub>50</sub>: 7.5**  
**logD: 1.8**  
**hERG pIC<sub>50</sub>: 4.2**

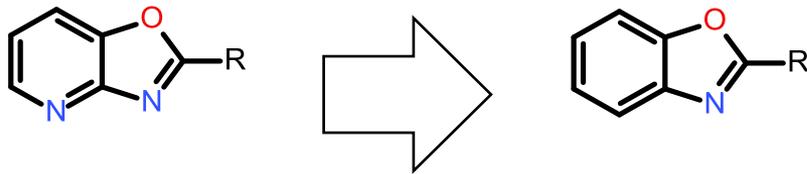
MMPA  
 $\Delta pEC_{50}$ : **+0.3**  $\Delta \log D$ : **+0.3**  $\Delta hERG$  pIC<sub>50</sub>: **-0.3**  
*n*=20      *n*=23      *n*=19

Waring *et al*, *Med. Chem. Commun.*,  
**2011**, 2, 775

# Project 7 - A Less Simple Example

## Increase $\log D$ and gain solubility

**Question:**

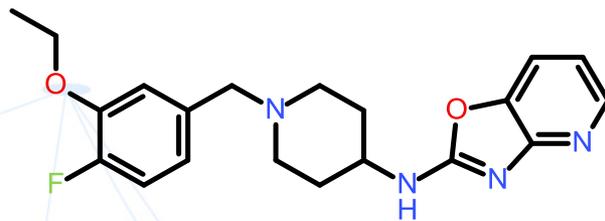


What is the effect on lipophilicity and solubility?  
Roche data is inconclusive! (2 pairs for  $\log D$ , 1 pair for solubility)

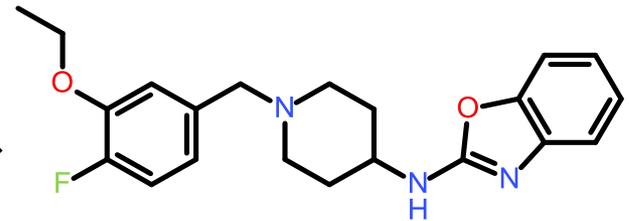
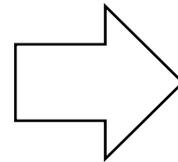
**Available Statistics:**

Property	Number of Observations	Direction	Mean Change	Probability
$\log D$	8	Increase	1.2	100%
Log(Solubility)	14	Increase	1.4	92%

**Roche Example:**

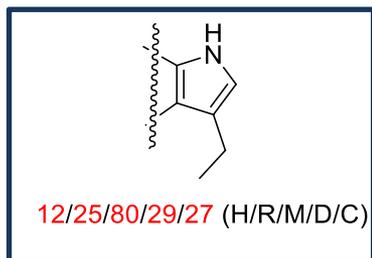


$\log D = 2.65$   
Kinetic solubility = 84  $\mu\text{g/ml}$   
 $\text{IC}_{50} \text{ SST5} = 0.8 \mu\text{M}$



$\log D = 3.63$   
Kinetic solubility = >452  $\mu\text{g/ml}$   
 $\text{IC}_{50} \text{ SST5} = 0.19 \mu\text{M}$

# Project 8 - Base of Success Story from Genentech



100 cmpds x (\$2K make + \$1K test) = \$ 300 000  
8 cmpds x (\$2K make + \$1K test) = \$ 24 000

Enumeration

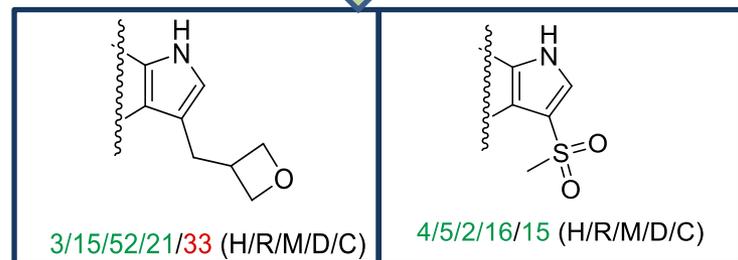
193 compounds  
Enumerated

Objective:  
improve  
metabolic  
stability

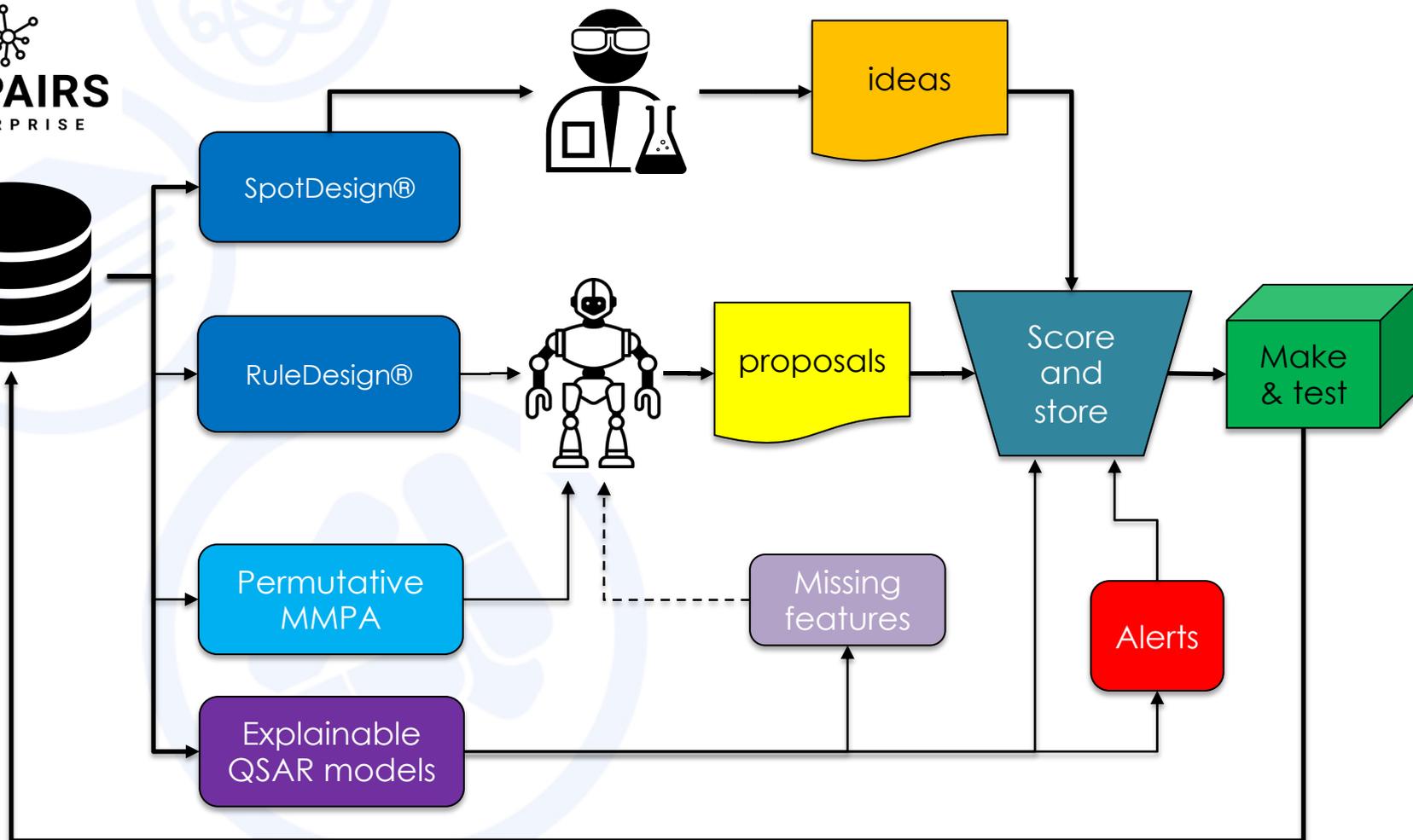
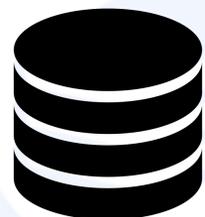
Calculated Property  
Docking

8 compounds  
synthesized

It is not just money, it is actually time  
100 cmpds make & test ~ 15 – 25 weeks  
8 cmpds make & test ~ 2 – 4 weeks



# Augmented Chemists – Data is everything!

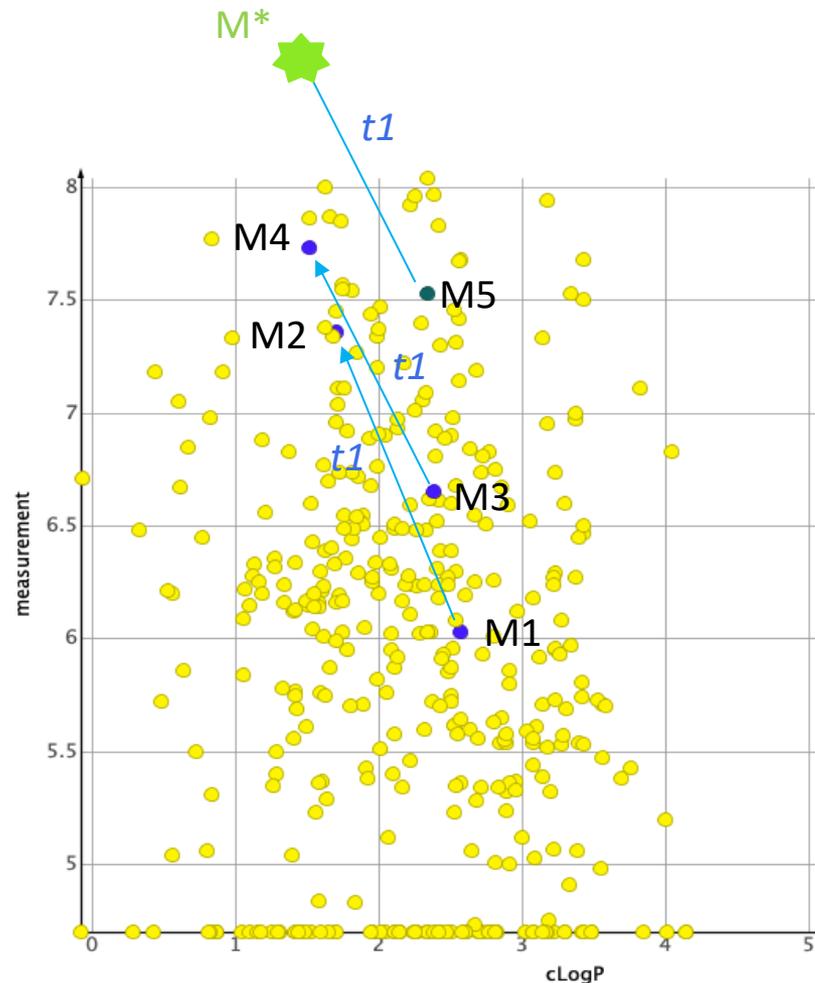


Missing features

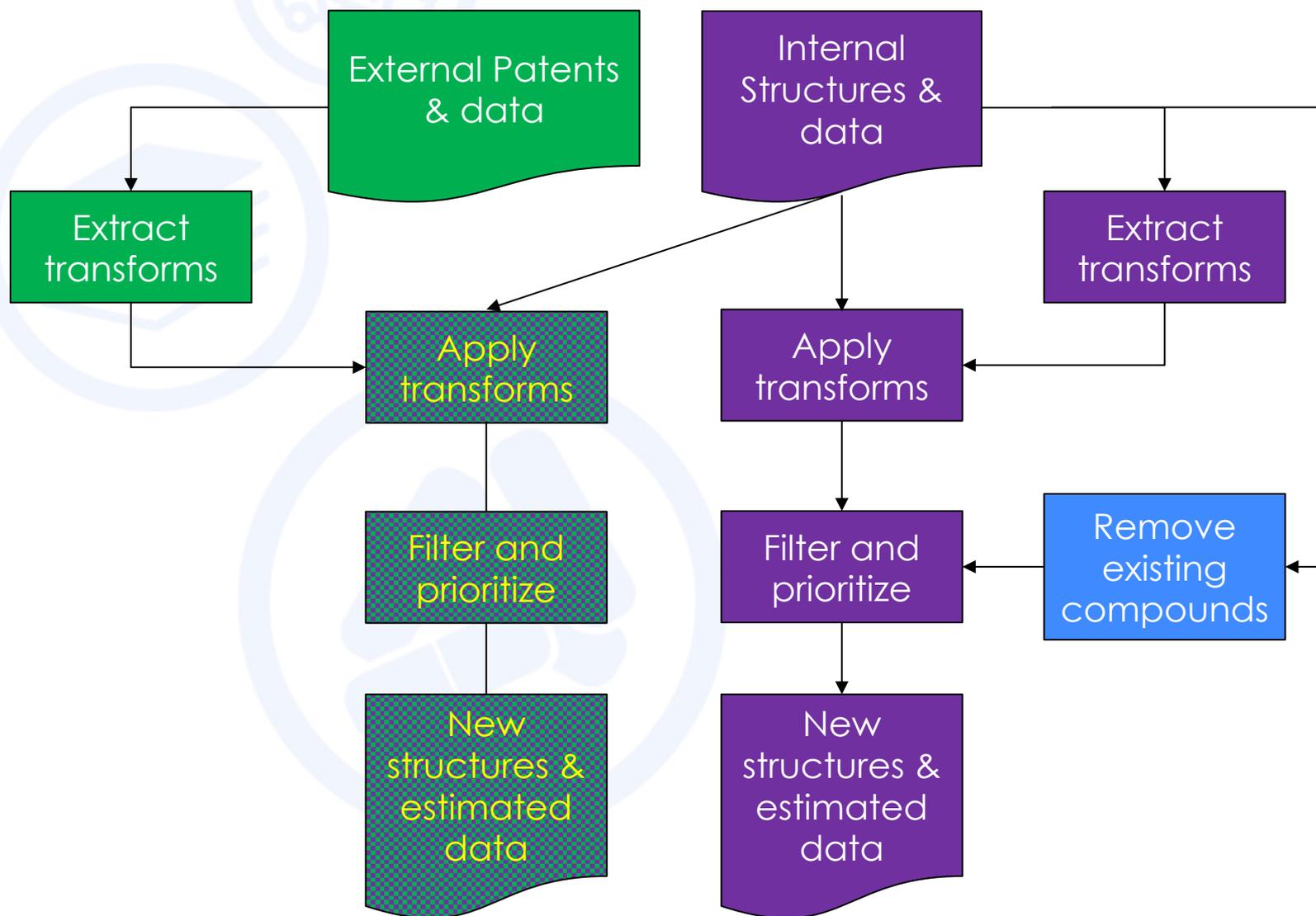
The company that invests in data is the going to be the company that wins in AI

# Permutative MMPA (like Free-Wilson)

- **Level 1 - Augmentation**
- Find all matched pairs of a given dataset & extract  $\Delta pIC50$  and the transforms between them
- Aggregate transformations with median  $\Delta pIC50$  and count of pairs
- Apply all transformations back to the initial compounds in the data set (at the most specific environment level) **NO R GROUP MAPPING REQUIRED !!!**
- Predicted  $pIC50 = \text{substrate } pIC50 + \text{median } \Delta pIC50$
- Remove existing compounds
- Prioritize new compounds by  $pIC50$  estimate



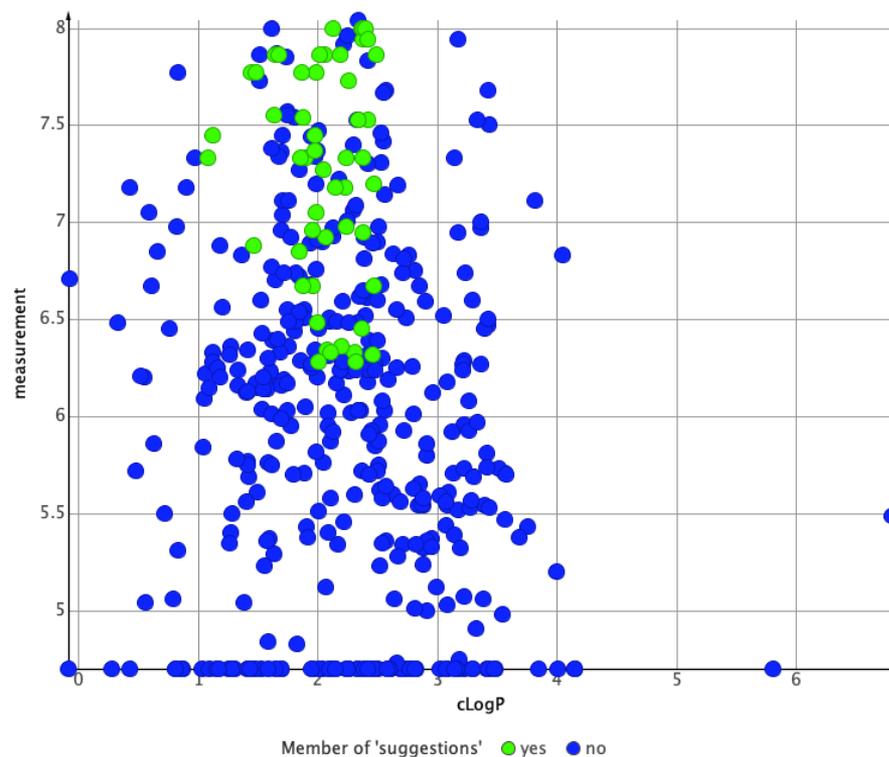
# Exploit Internal and Patent Data



# Client Oncology PPI project example

- 386 patent compounds analyzed
- 6024 pair relationships found (39% - good number of MMPs)
- Permutative MMPA process:
  - Apply to own series,
  - Then filter:
    - remove undesirable substructure
    - Estimated potency  $\geq 6.5$ ,  $\text{clogP} \leq 2.5$
- 52 suggestions

Measurement =  $p(\text{TR-FRET nucleotide exchange assay pIC50})$  or estimated  $\text{pIC50}$  from seed value +  $\Delta\text{pIC50}$



## Explainable

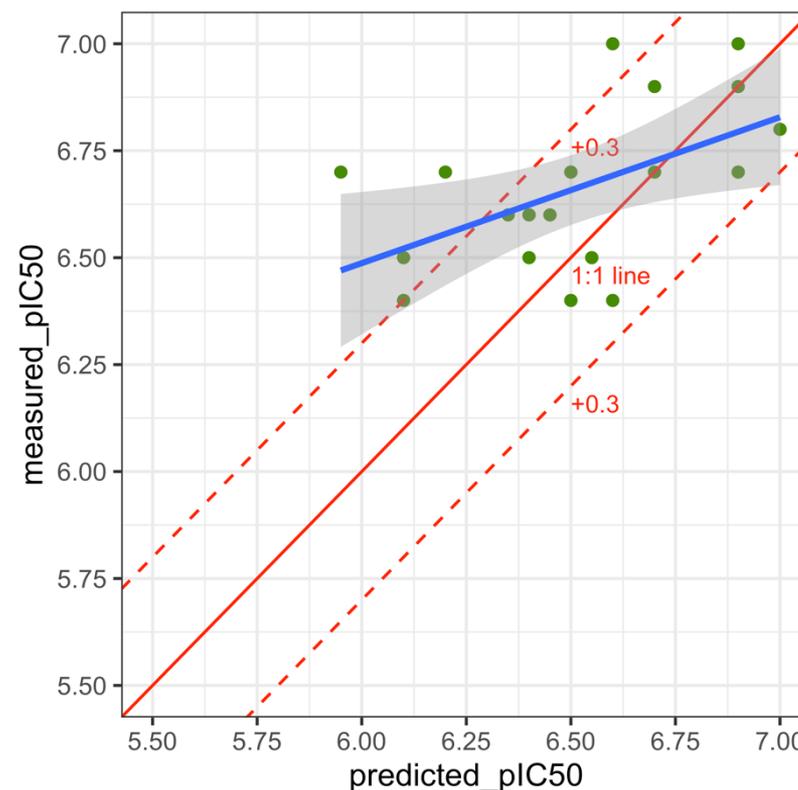
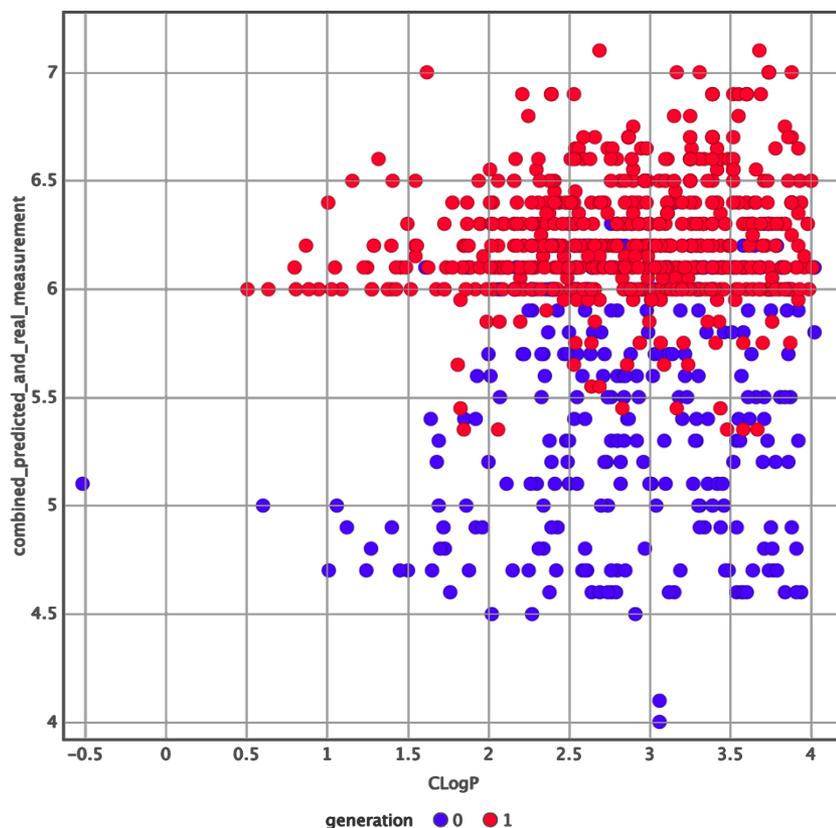
- Visible, original real world compounds and measurement

## Actionable

- Prioritises 'realistic' next step compounds.

# Covid Moonshot - pMMPA example

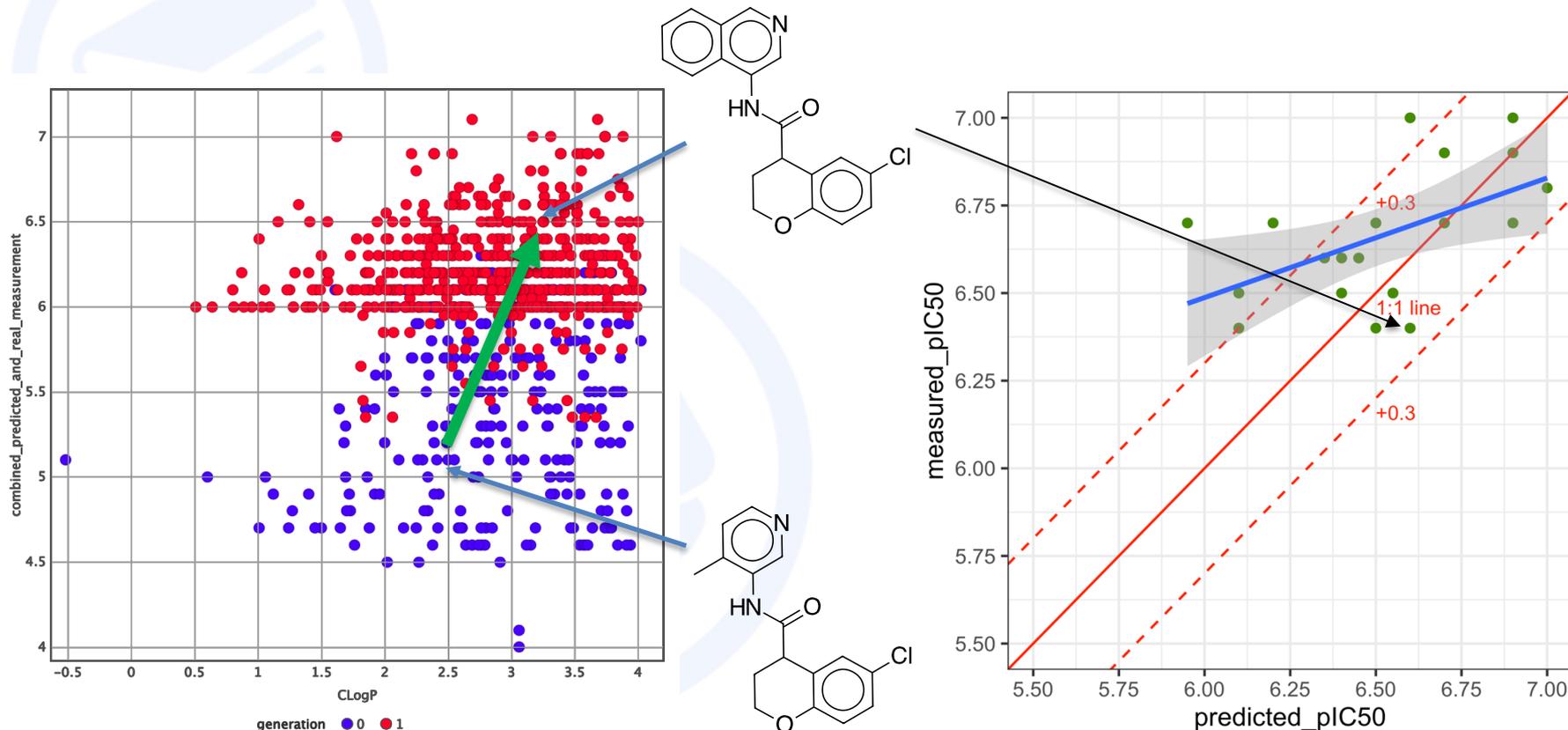
- 313 Compounds from Covid Moonshot lead series all with  $pIC_{50} < 6.3$  (500nM) fed into pMMPA process,
- New compounds are shown in red, compounds from the input data set in blue
- 671 suggestions ( $clogP \leq 4$ ,  $RMM \leq 550$ ), 18 with predicted  $pIC_{50} > 6$  synthesised



Griffen, E.J.; Full Covid Moonshot talk - Cambridge Med Chem – Sept 2021

# Covid Moonshot - pMMPA example

- 313 Compounds from Covid Moonshot lead series all with pIC50 <6.3 (500nM) fed into pMMPA process,
- Compounds from the input data set in blue, new compounds are shown in red,
- 671 suggestions(clogP <=4, RMM <=550), 18 with predicted pIC50 > 6 synthesised



Griffen, E.J.; Full Covid Moonshot talk - Cambridge Med Chem – Sept 2021