

Lessons Learned from 30 Commercial Pharmaceutical Crystal Structure Prediction Studies

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Crystal Structure Prediction (CSP)



Crystal Structure Prediction

Also called “polymorph prediction”

In silico polymorph screening

Does not suffer from kinetics

The calculations take several months...

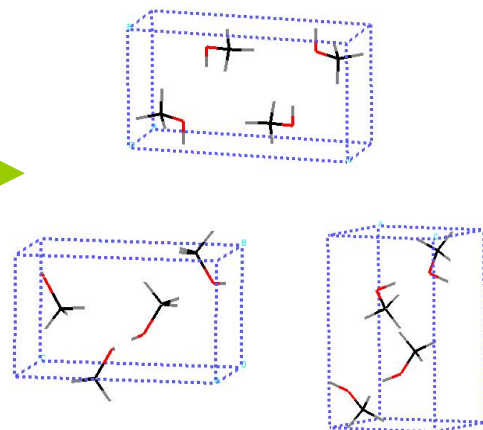
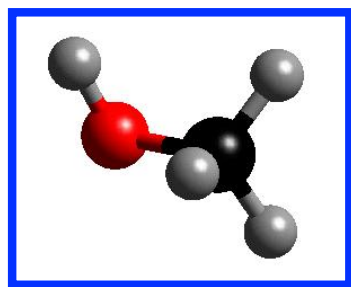


Crystal Structure Prediction

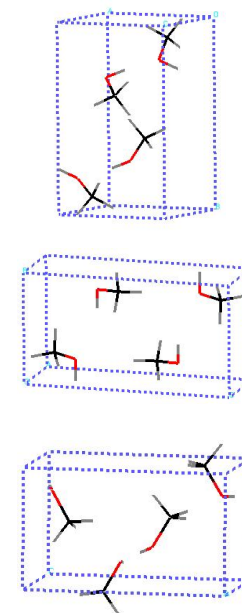
Compound

Trial structures

Predicted structures



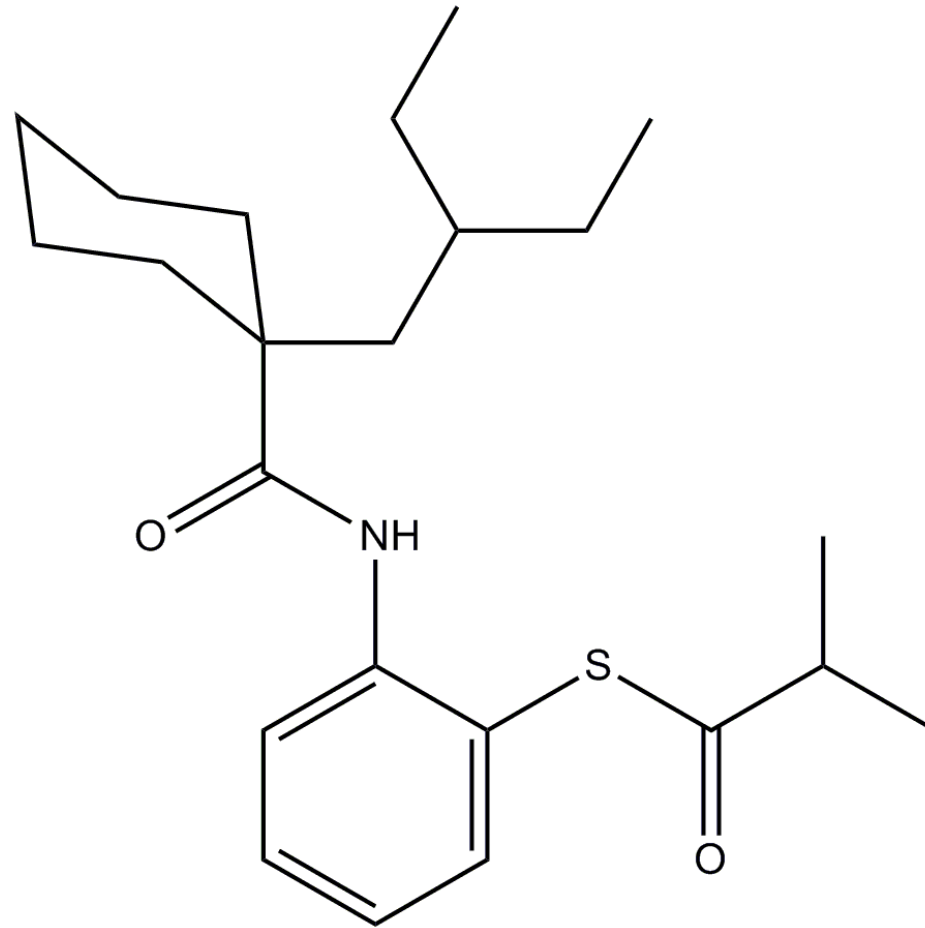
lattice energy



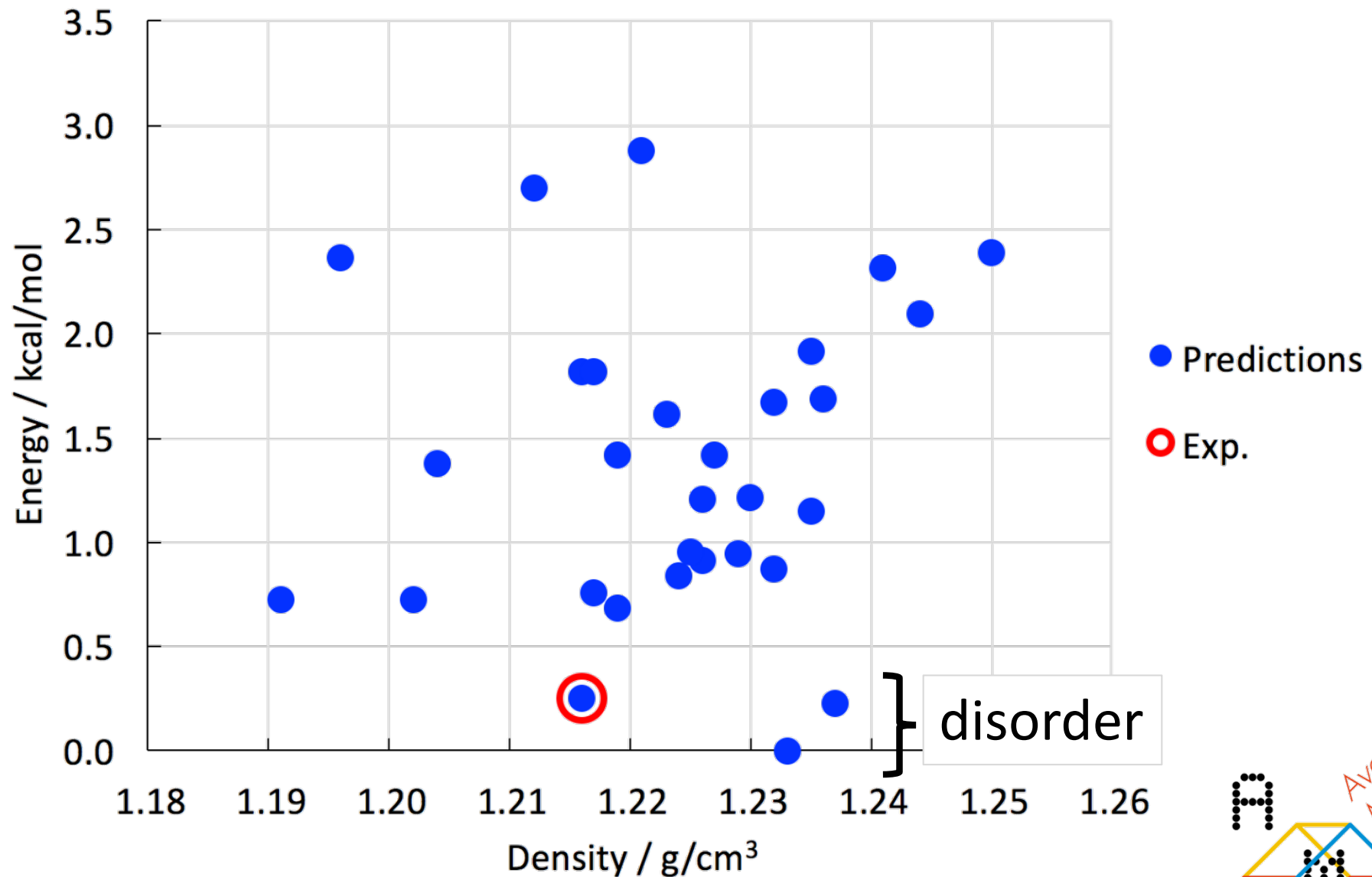
structure
generation

energy
ranking

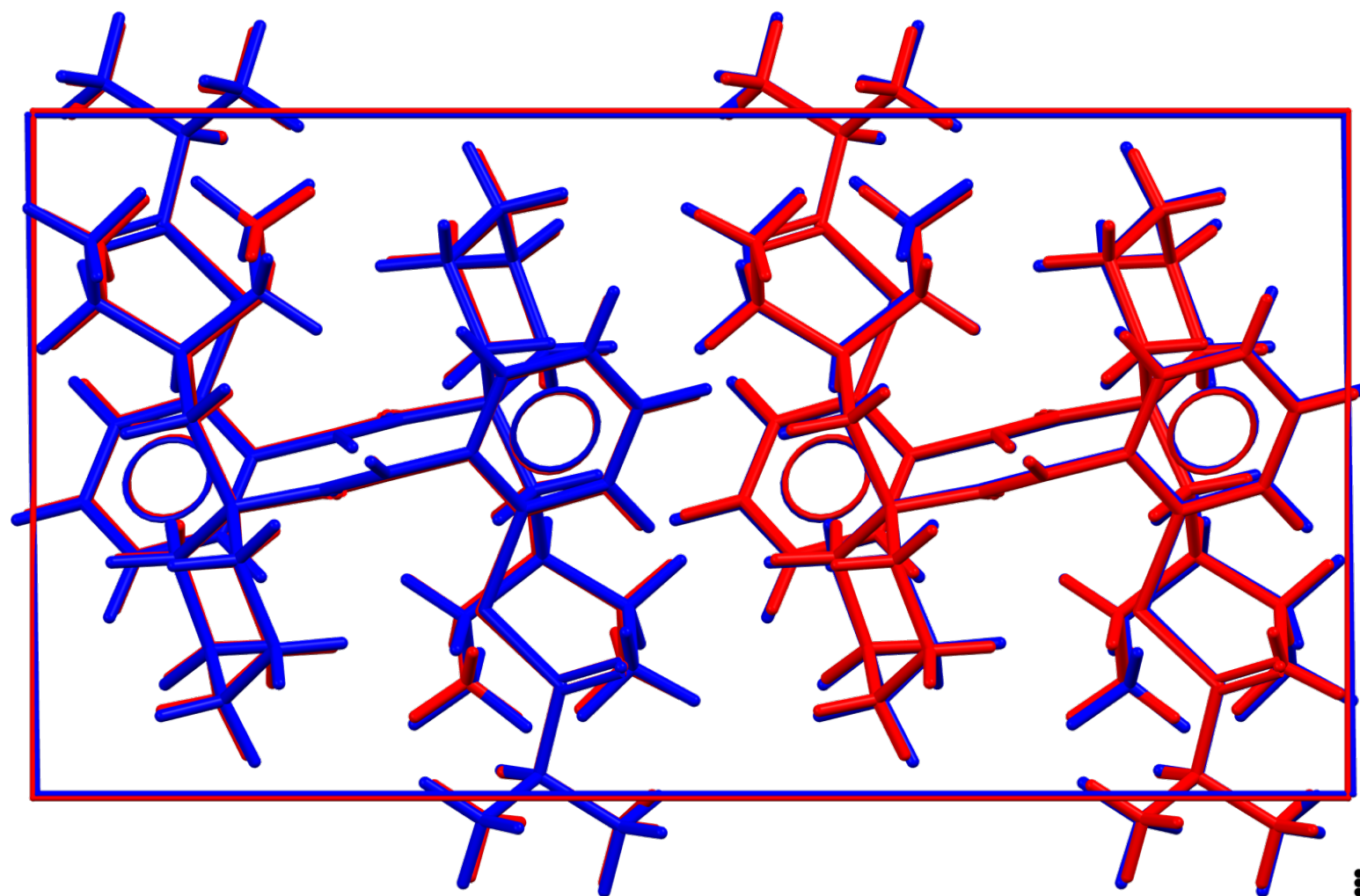
Example: CSP of Dalcetrapib



Energy Landscape of Dalcetrapib

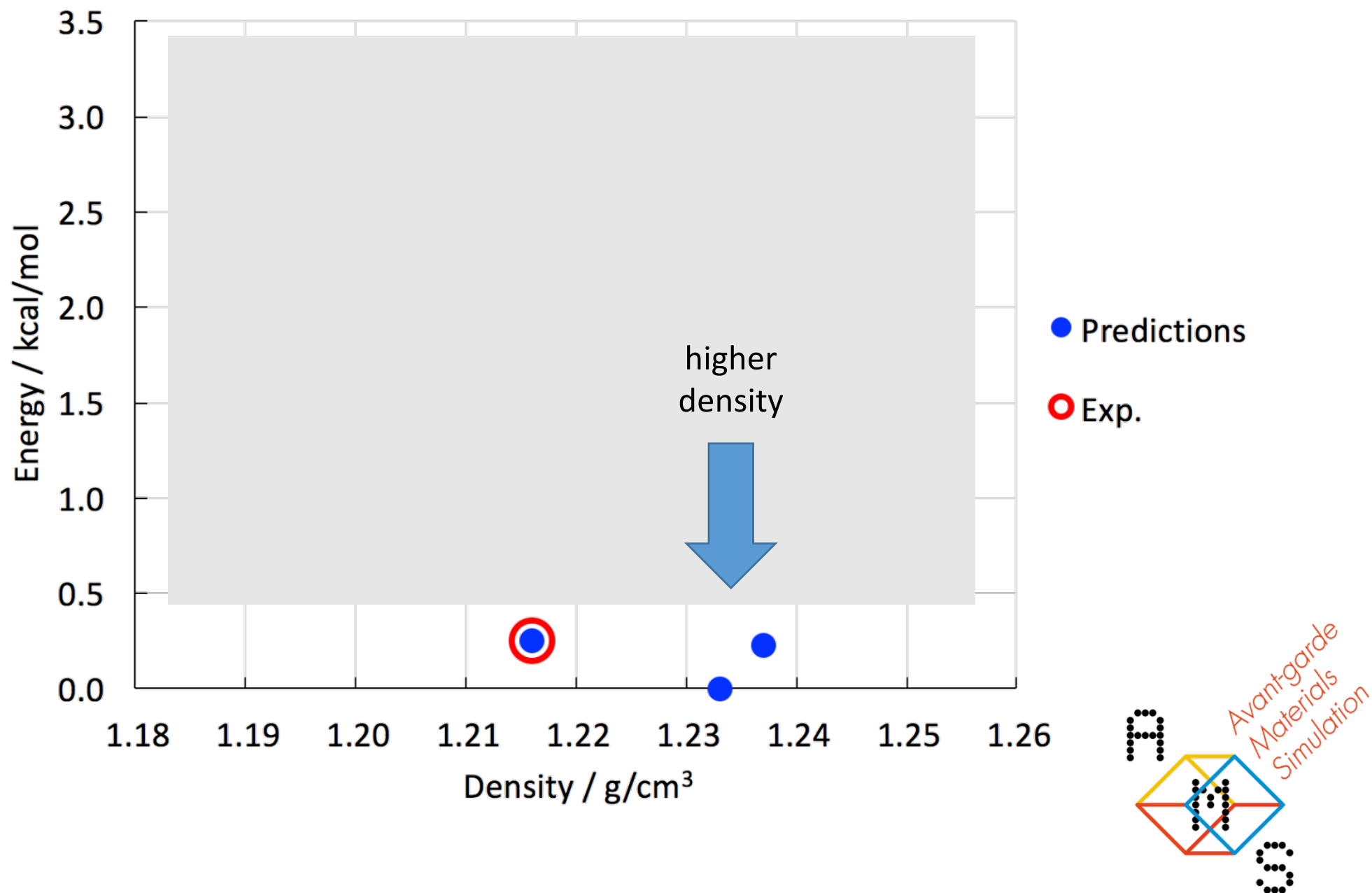


CSP of Dalcetrapib

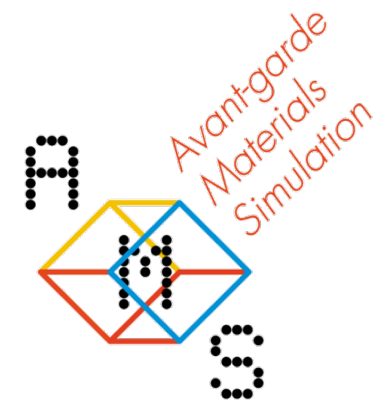
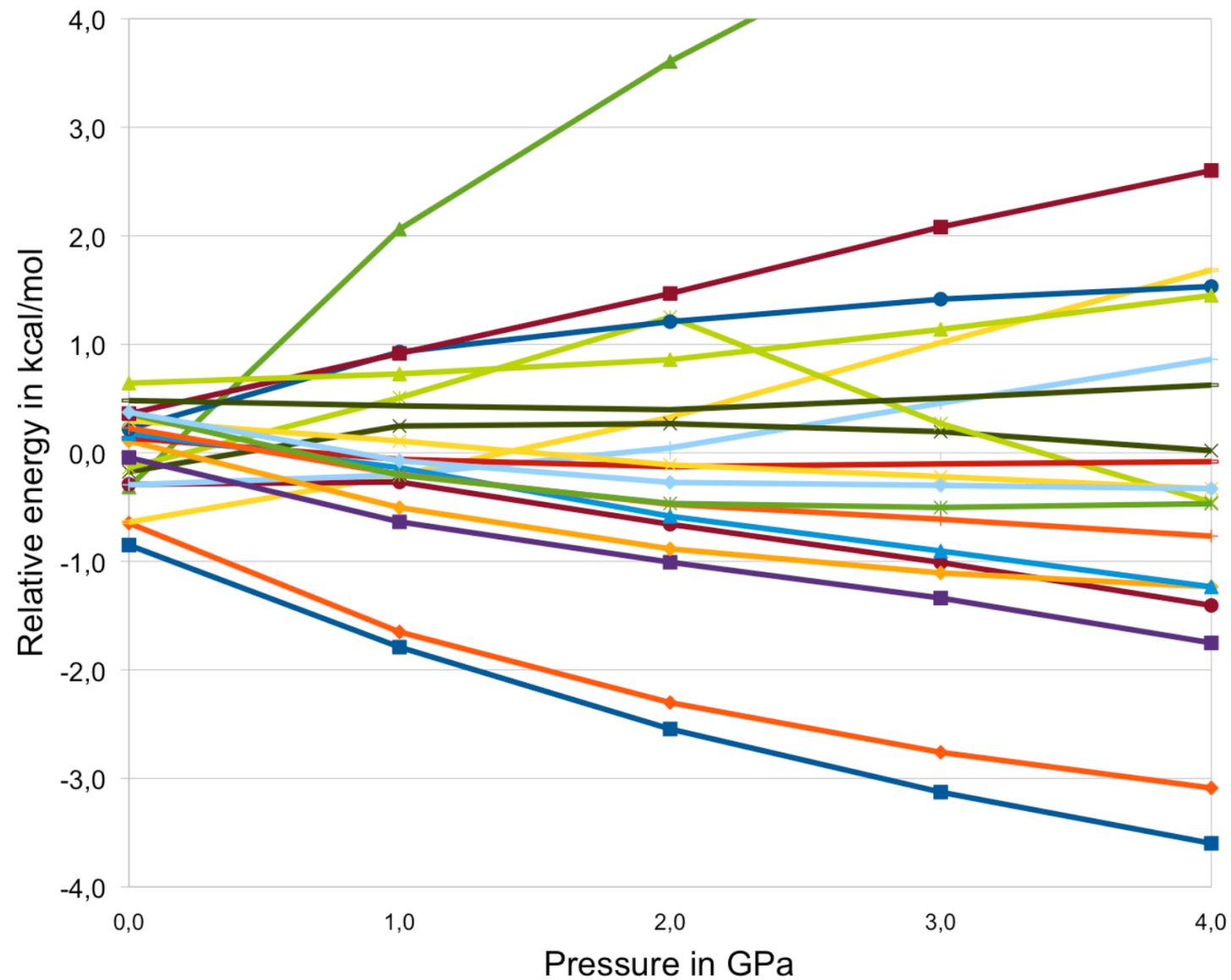


— Predicted #2
— Experiment

Energy Landscape of Dalcetrapib



Pressure Scan of Dalcetrapib



High-Pressure Crystallisation

Francesca Fabbiani crystallised Dalcetrapib at “high pressure” and found the new form (which turned out to be less stable at ambient pressure).



CCDC Blind Test Statistics



CSP Blind Tests

Crystal-structure Prediction Blind Tests:
Organised by CCDC and Dr Graeme Day

Blind Tests in 1999, 2001, 2004, 2007, 2010 and 2015

Reilly *et al.* (2016) *Acta Cryst.* B72, 439-459



CSP Blind Tests



Commercial CSP Statistics



The 30 Compounds

On average:

30 non-H atoms

23 H atoms

3 trivial flexible torsion angles (*e.g.* CH₃)

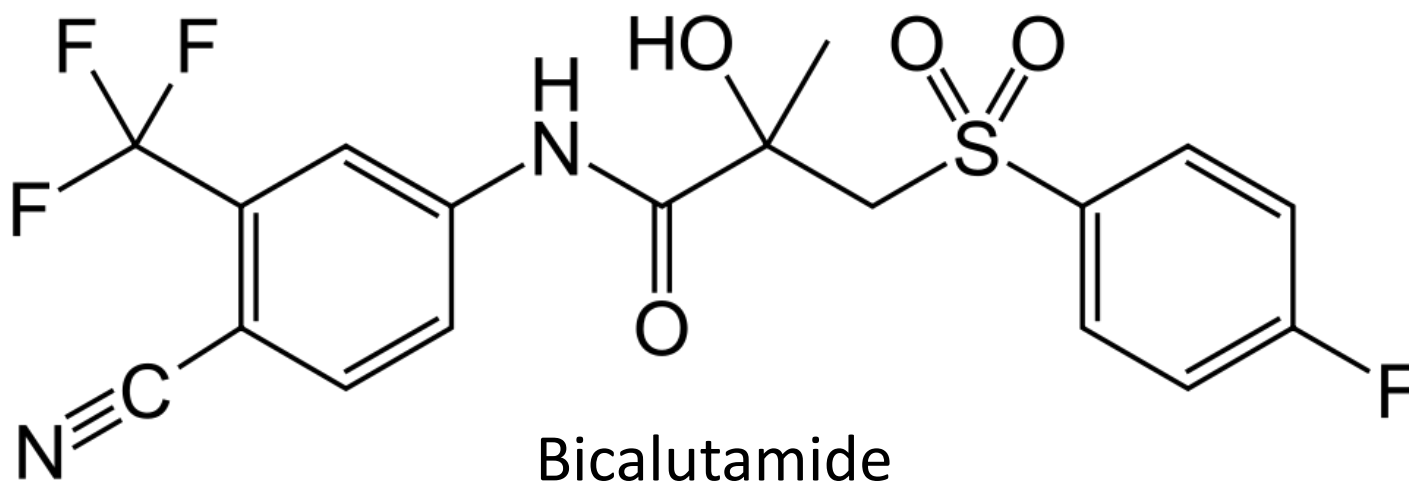
6 non-trivial flexible torsion angles

1 flexible ring

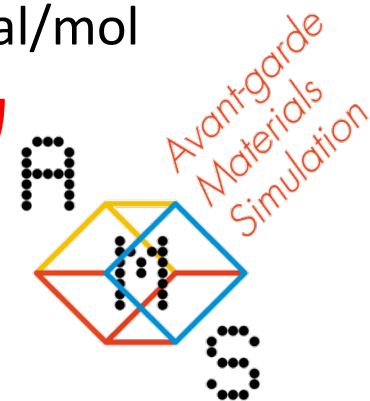
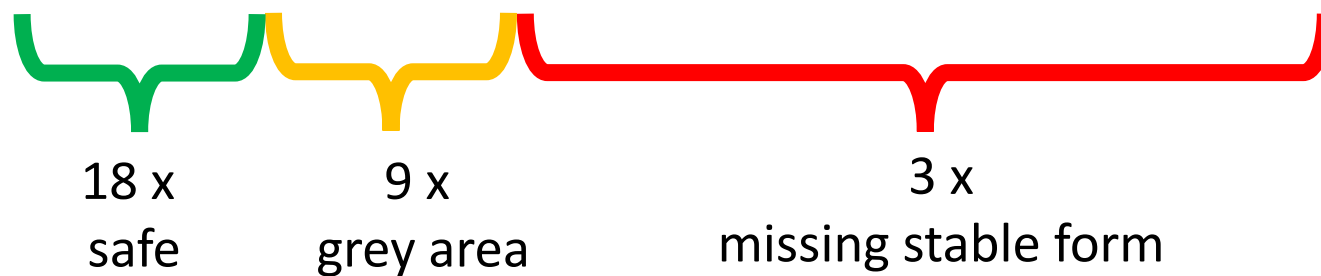
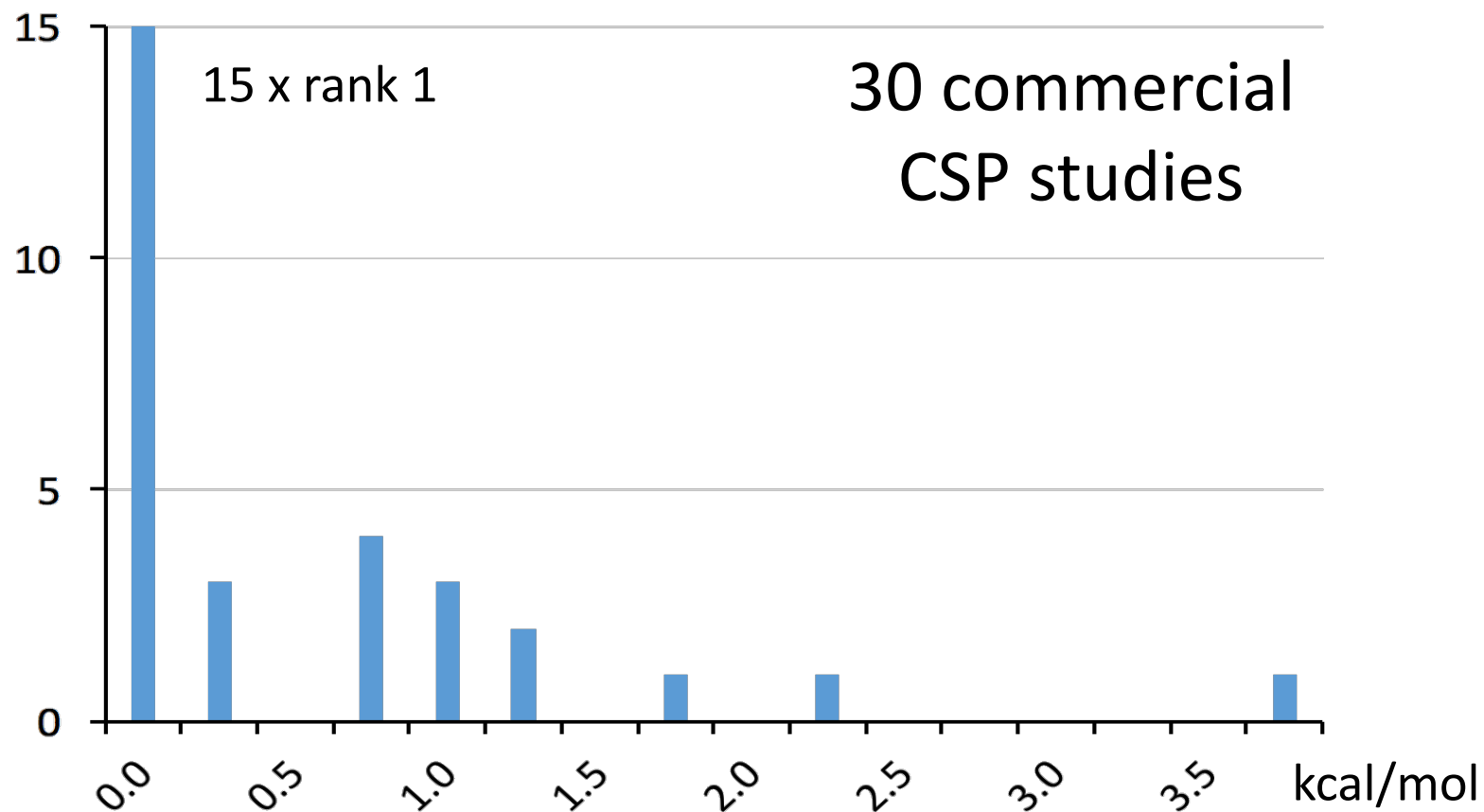
4 hydrates

2 zwitterions

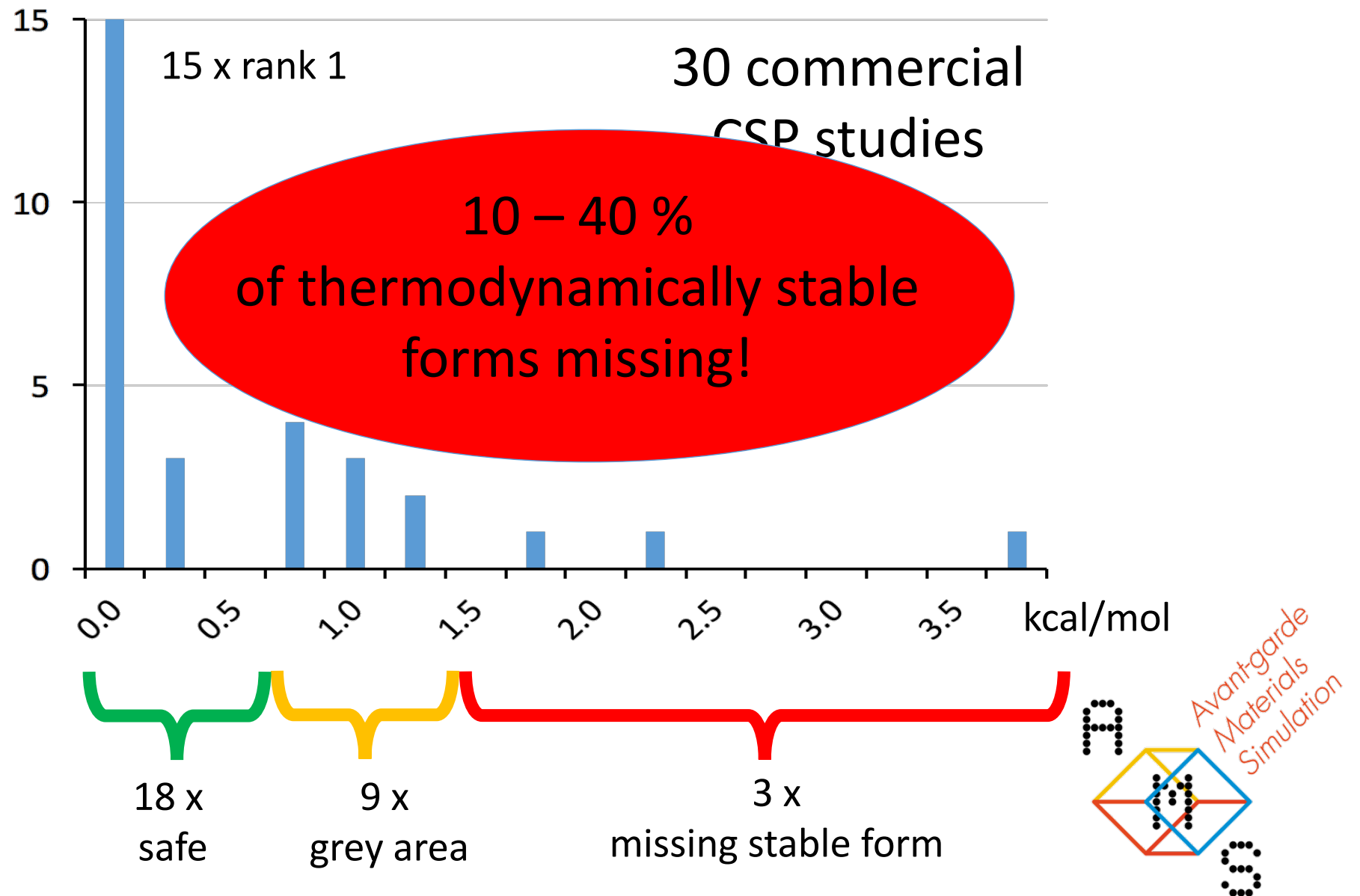
20 chiral



Energy Gap (Exp. - #1)

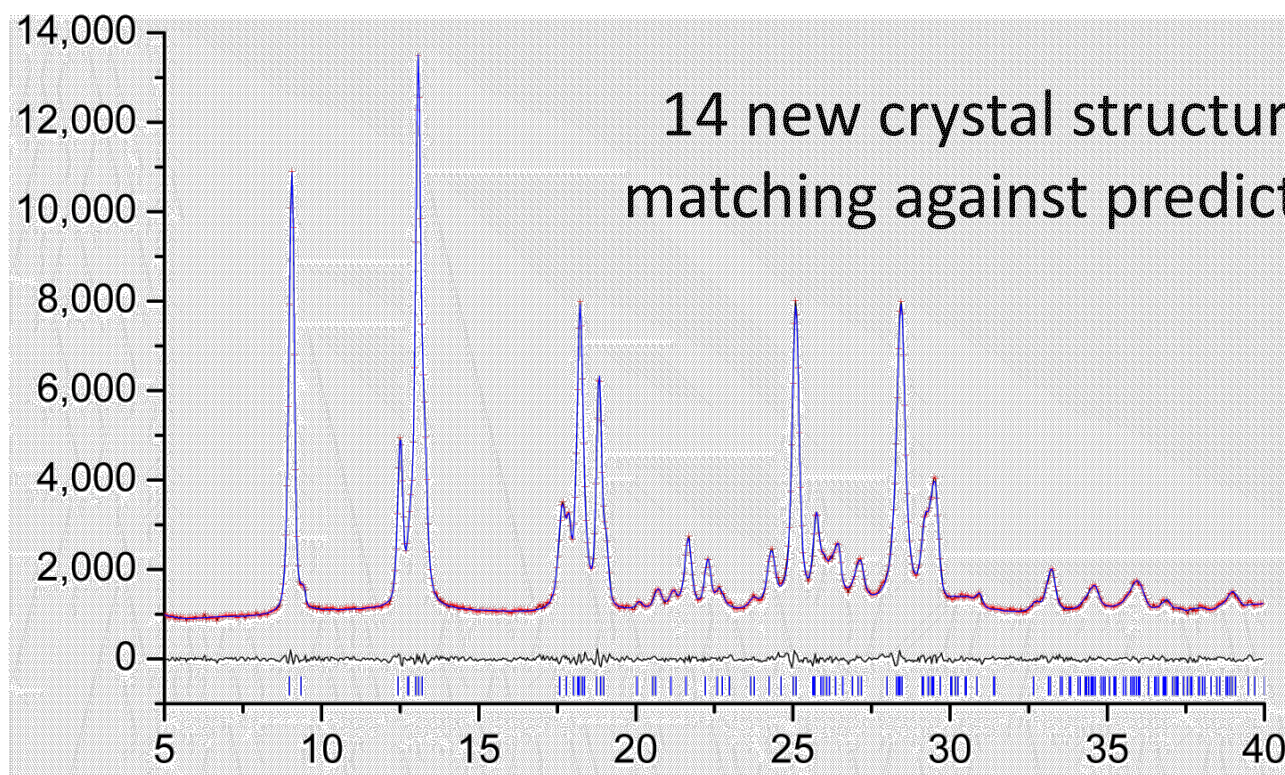


Energy Gap (Exp. - #1)



Matching XRPD Patterns

31 powder patterns made available
(including duplicates,
possible solvates,
sometimes very poor quality)



Habermehl *et al.* (2014) *Acta Cryst.* B70, 347-359.



Resources

On 384 cores (an average laptop has about 2 cores)
So roughly the equivalent of 200 laptops

Parameterising the tailor-made force field

Average: 2 weeks

Min: < 1 week

Max: > 1 month

CSP, $Z'=1$

Average: 2 weeks

Min: < 1 day

Max: > 2 months



Conclusions

At least 10% of all small-molecule drugs on the market
have an as yet unknown significantly more stable
polymorph

Crystal structure prediction can be used as a last resort
method for crystal structure solution from powder
diffraction data

