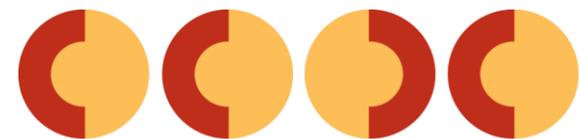




ADVANCED DIGITAL DESIGN OF PHARMACEUTICAL THERAPEUTICS



The Cambridge Crystallographic
Data Centre

Applying structural informatics approaches to pharmaceutical supply chain processes

Andrew G.P. Maloney, Mathew J. Bryant and Ian J. Bruno

The Cambridge Crystallographic Data Centre

Thursday 12th April 2018



The ADDoPT Project

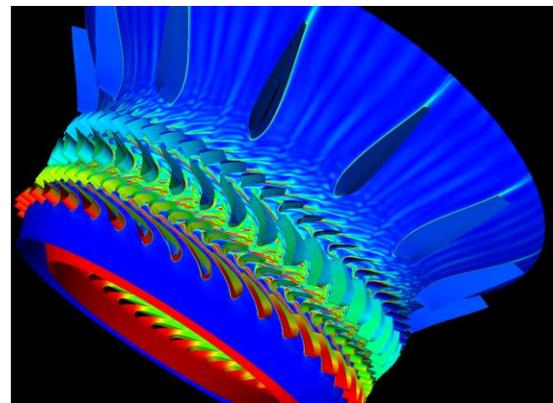
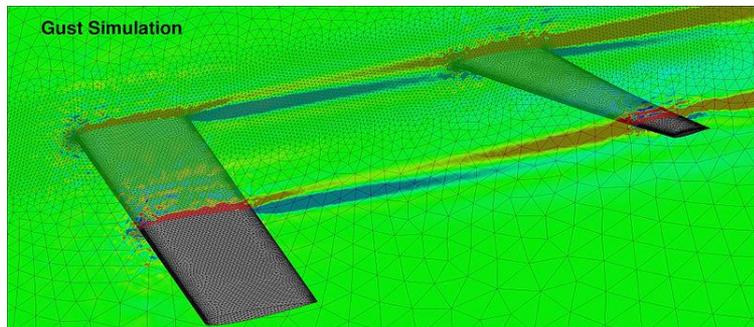
- **Advanced Digital Design of Pharmaceutical Therapeutics**
 - Four year collaboration between government, industry and academia
 - Instigated by the Medicines Manufacturing Industry Partnership and part funded under the **Advanced Manufacturing Supply Chain Initiative**





Digital Design

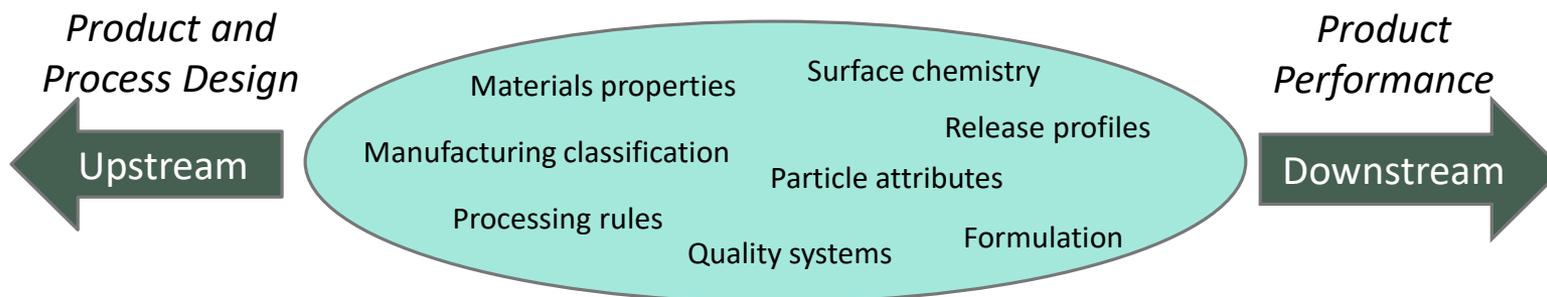
If we designed drugs like we design airplanes...



“Why has pharmaceutical research and development lagged so far behind other industries in the development and application of simulation and modelling for research and development?”



Digital Design: Molecules to medicines



Primary Manufacturing - Secondary Manufacturing

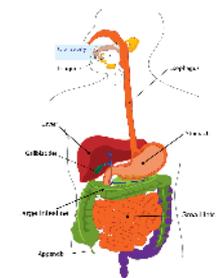
Active Ingredient (API)



Crystallisation
Filtration
Washing
Drying



Milling
Blending
Compaction
Coating



Processes

Products

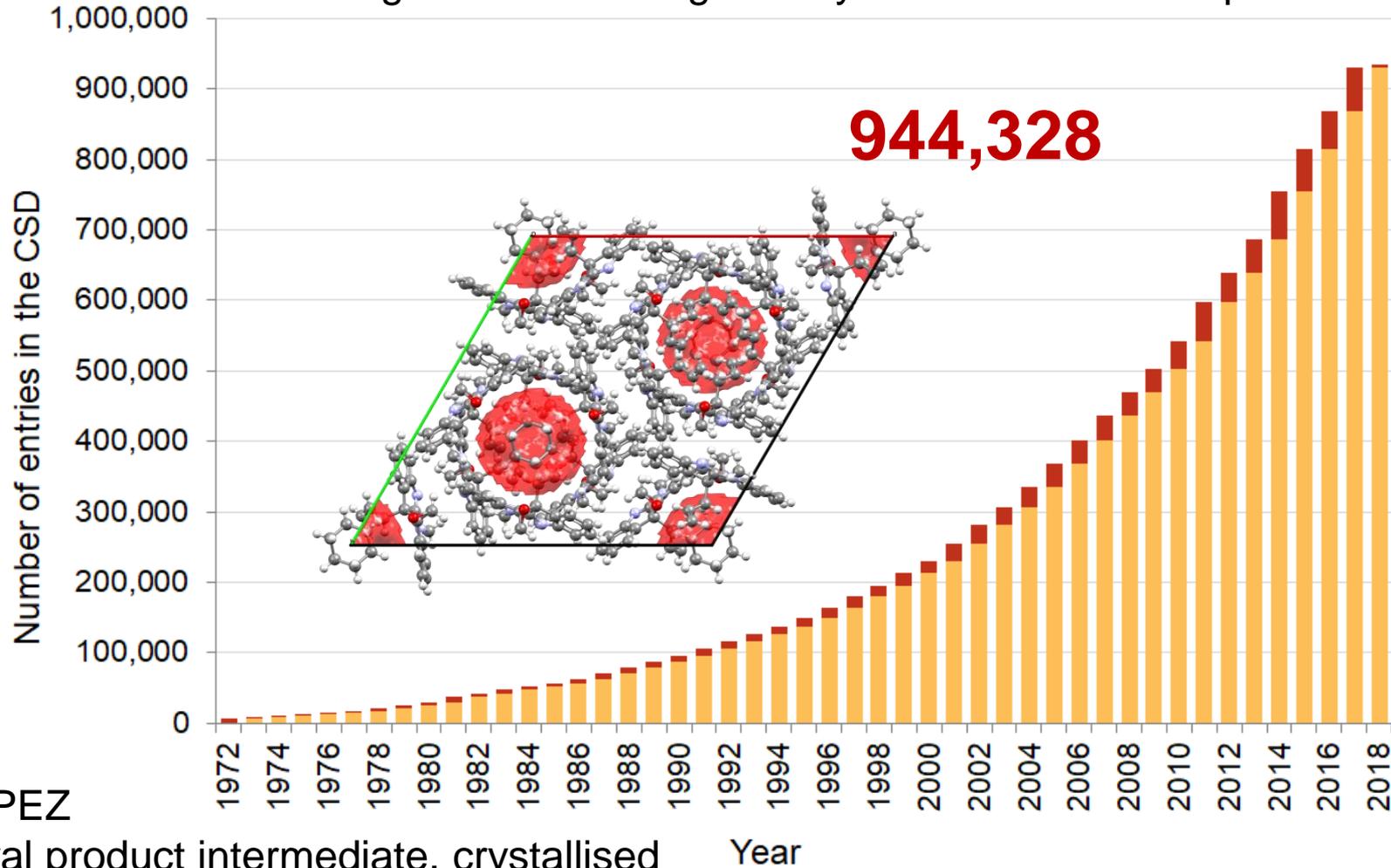
Performance

Design and control of optimised development & manufacturing processes through data analysis and first principle models



The Cambridge Structural Database

All small-molecule organic & metal-organic crystal structures ever published.



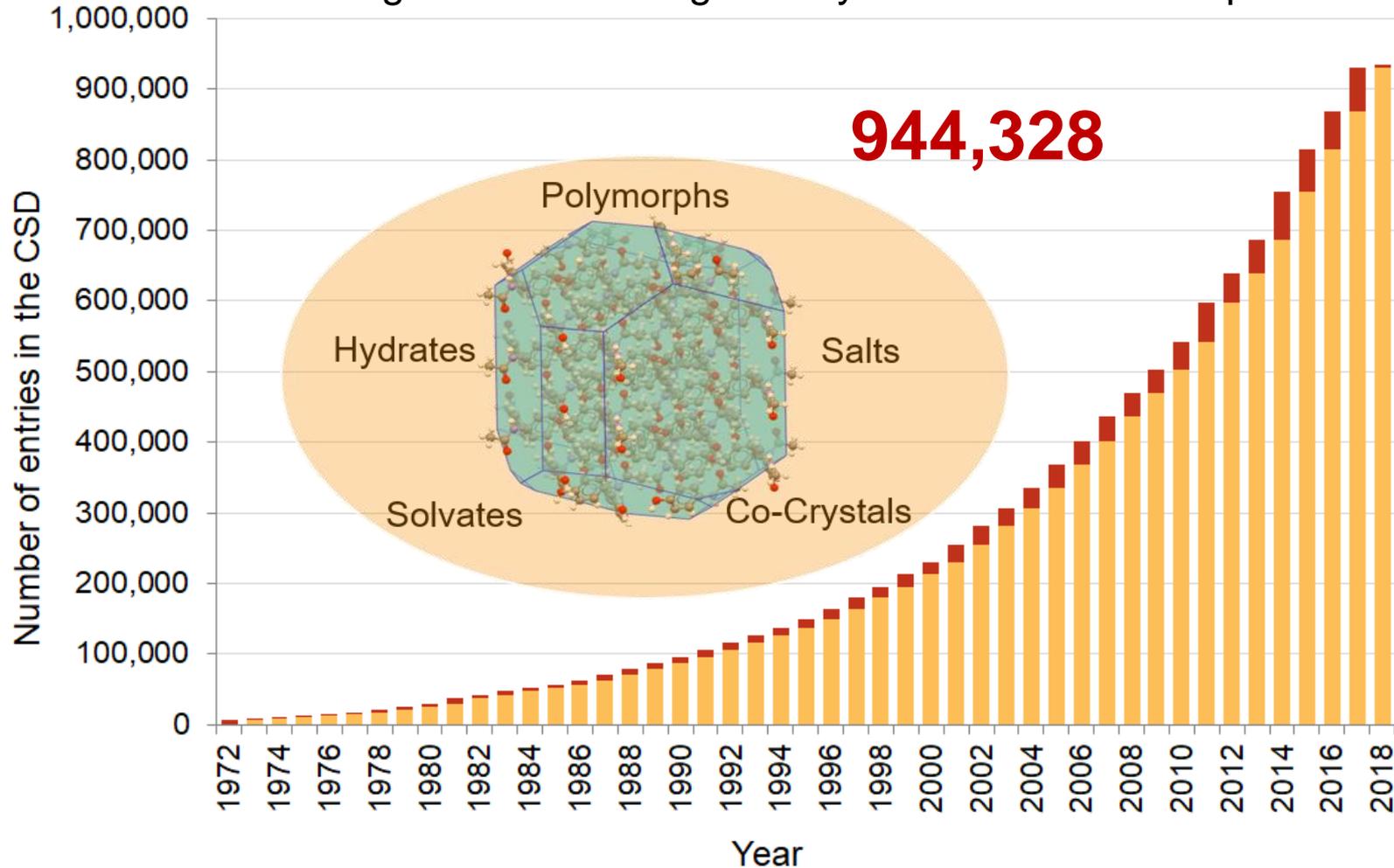
USOPEZ

Natural product intermediate, crystallised
as a cyclohexane solvate



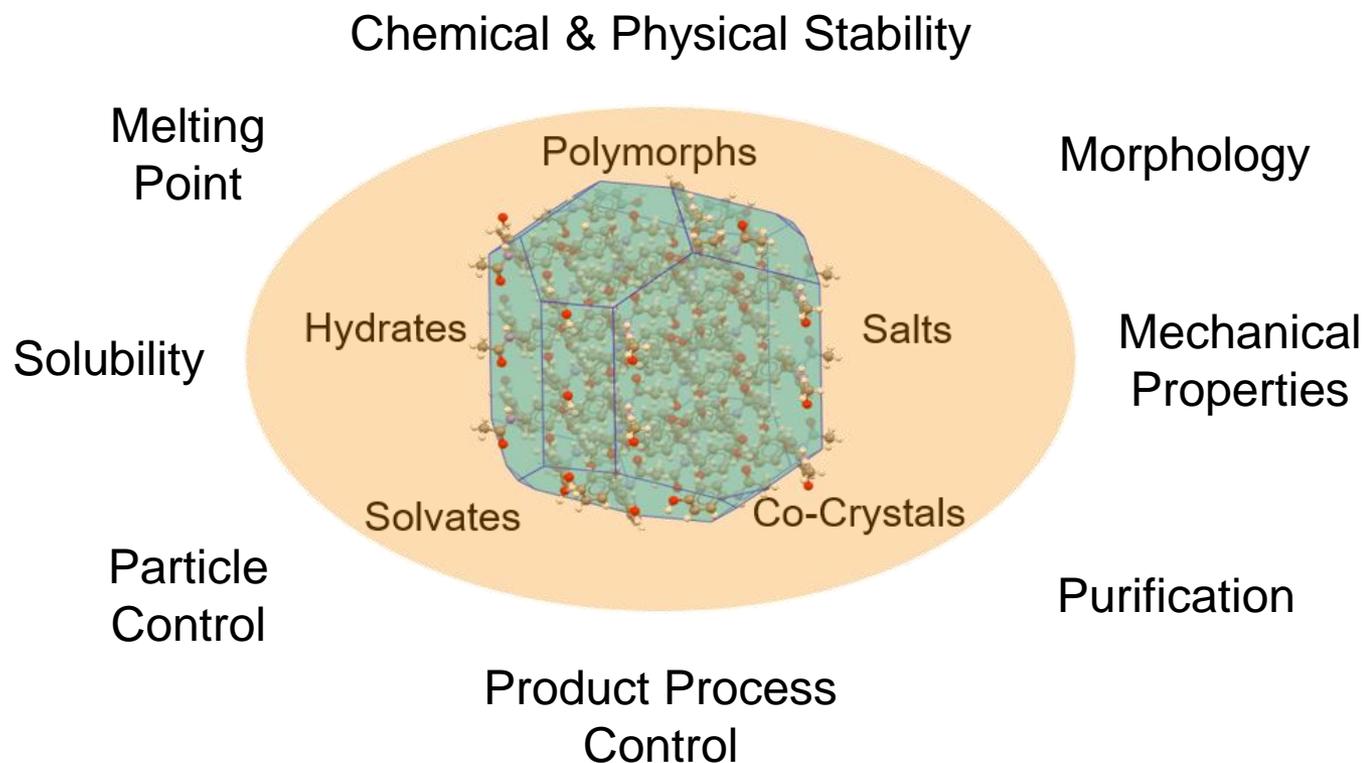
The Cambridge Structural Database

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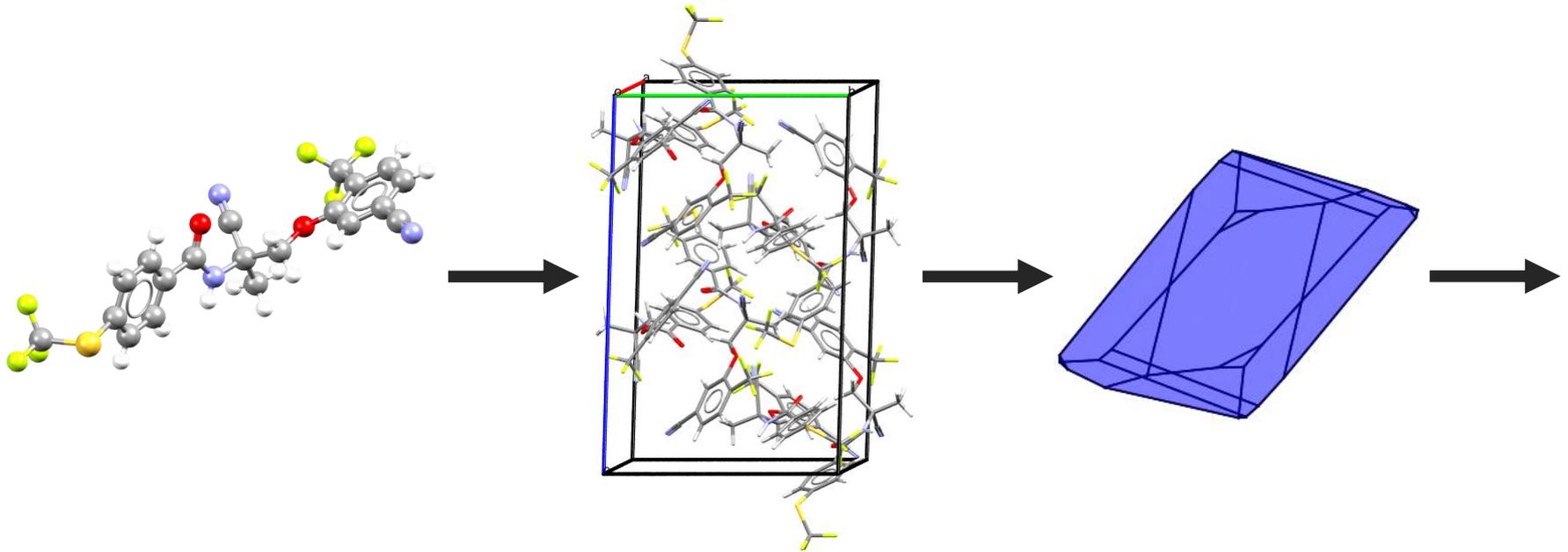


Crystal structure is important...





Drug product design and development



Molecule

Form

Particle

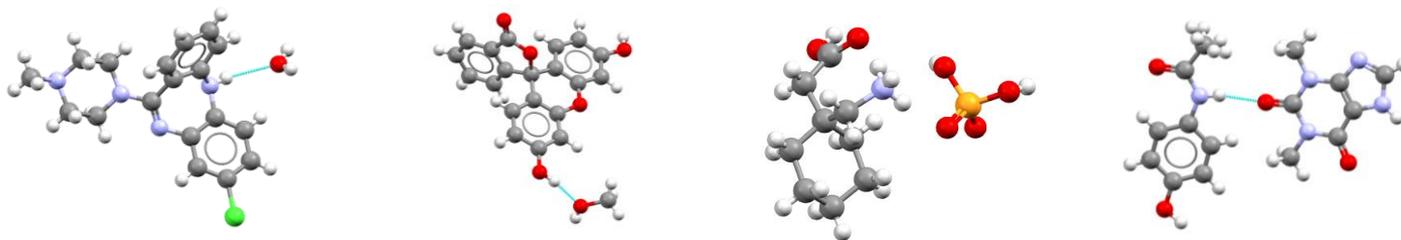


Making a CSD Drug Subset

- Drug definition taken from the approved drug database of Drugbank.ca

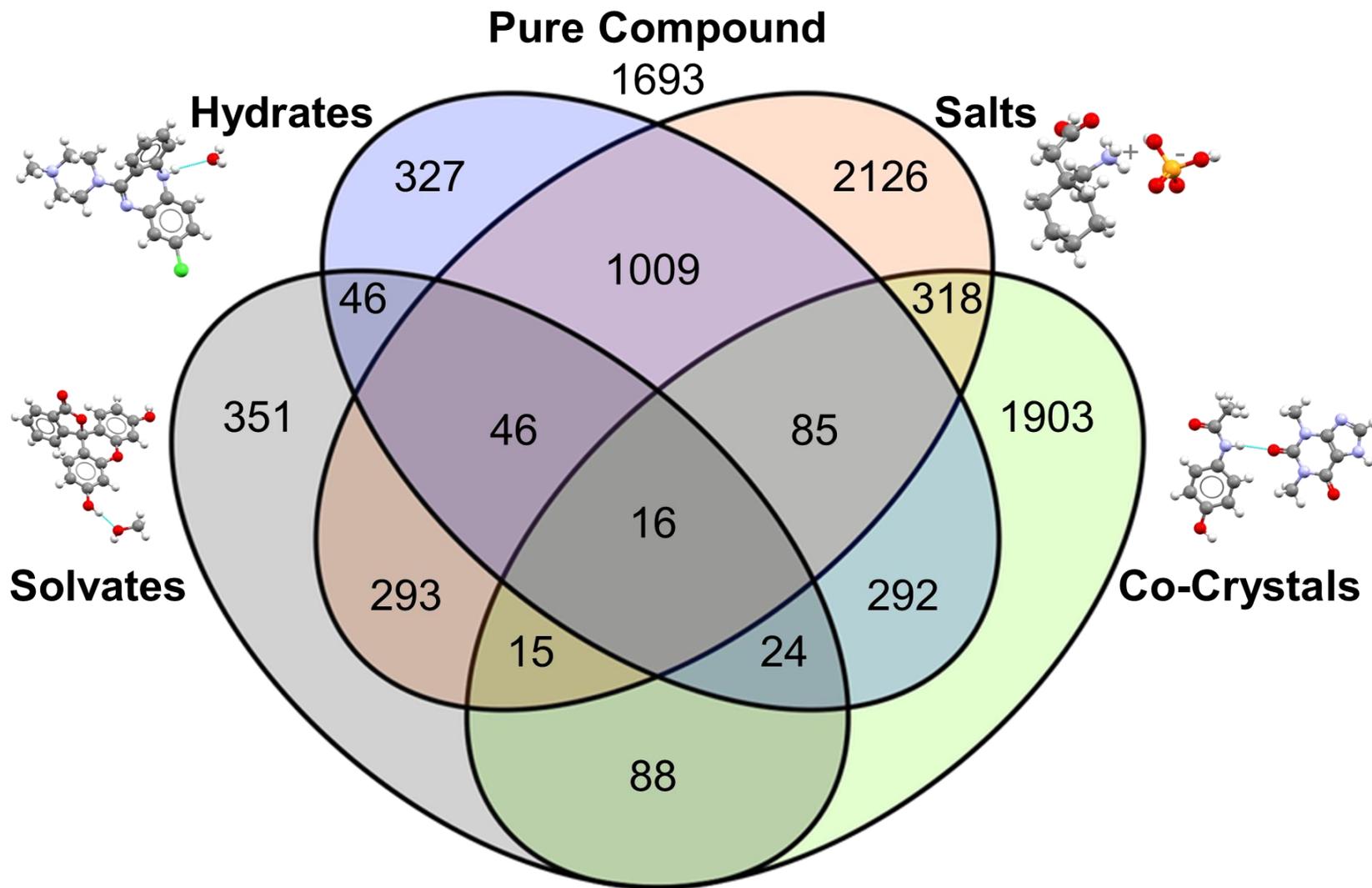


- Generated using InChI strings and the CSD Python API
- 8632 crystal structures representing 785 drug molecules
- Searchable and sortable by categories like hydrates, solvates, salts, co-crystals, pure drug (or any combination of these)



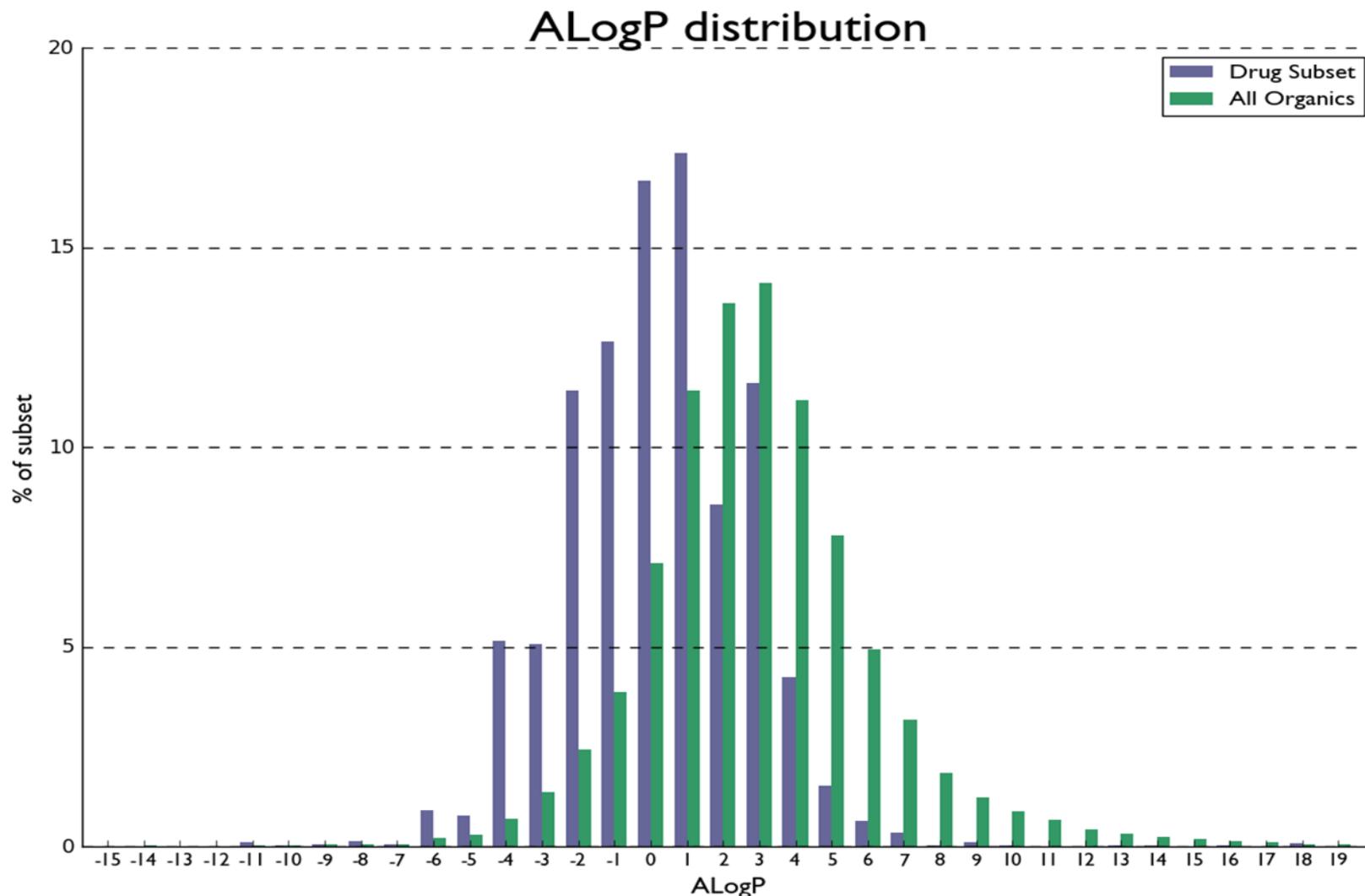


Making a CSD Drug Subset





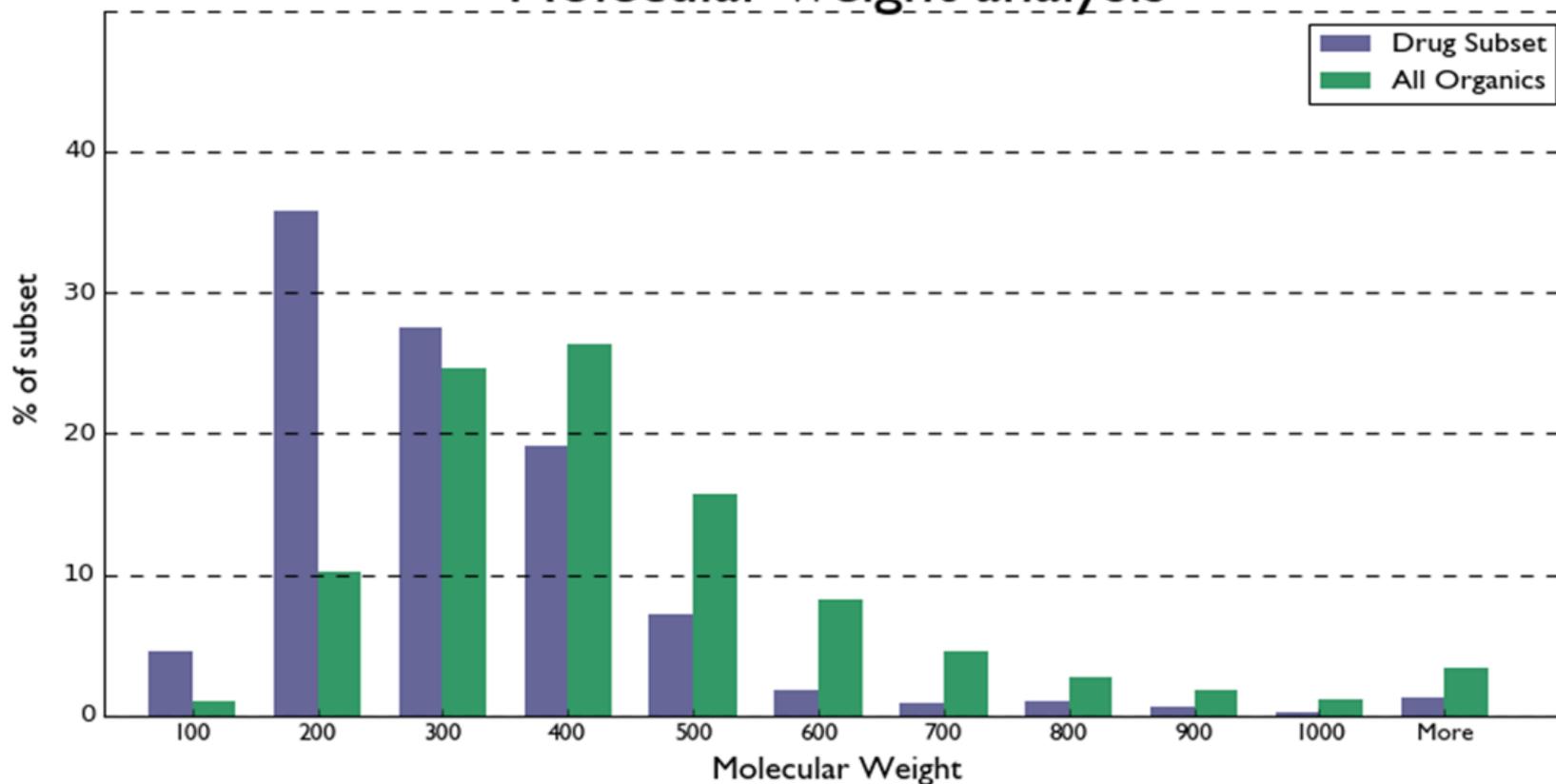
Comparison to organic molecules in the CSD





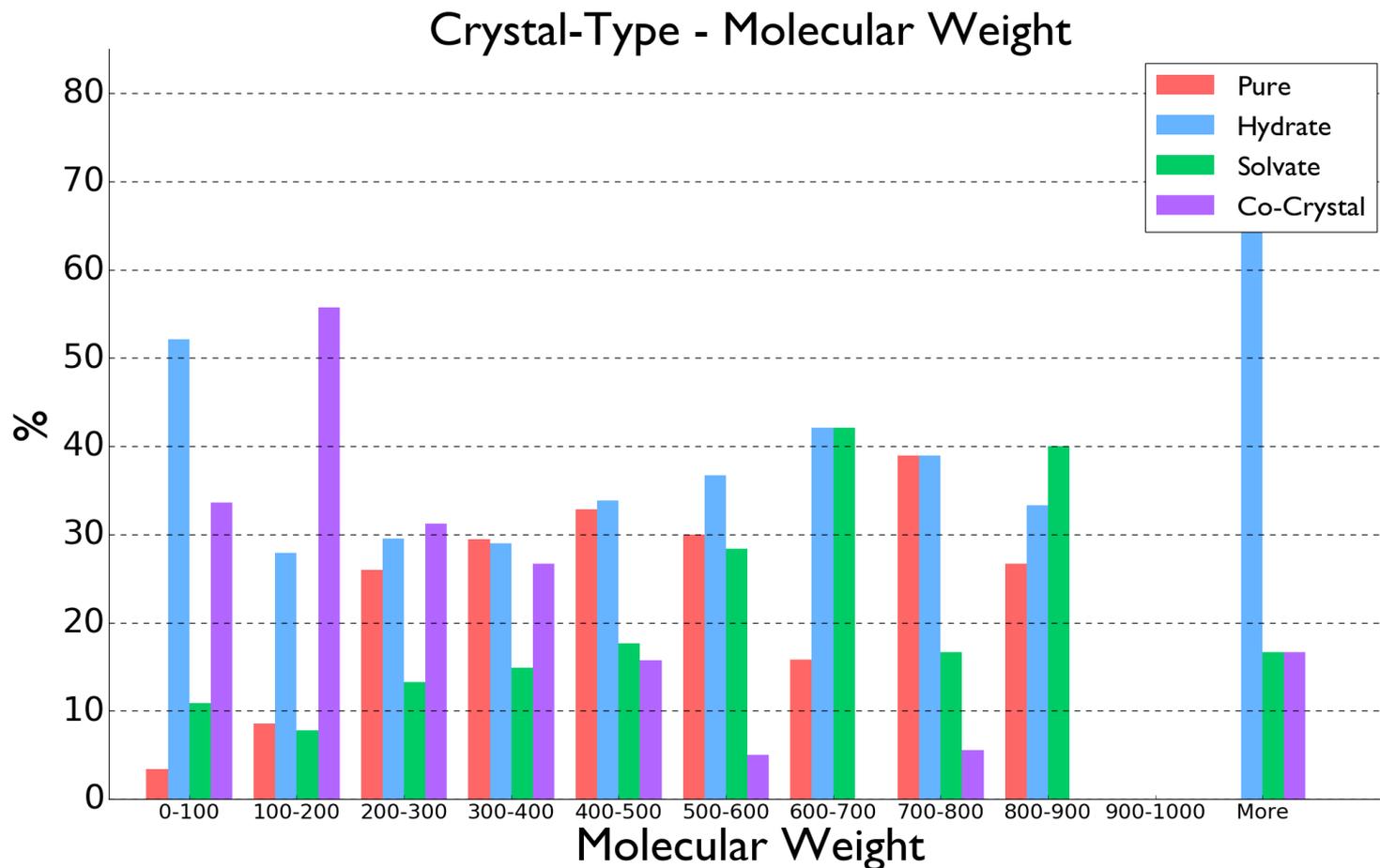
Comparison to organic molecules in the CSD

Molecular weight analysis





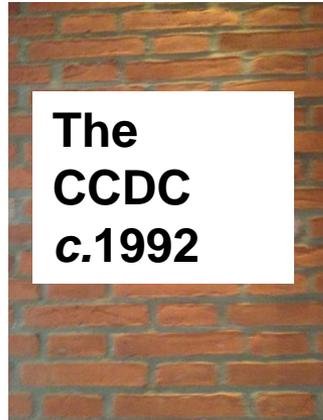
Solid form and molecular descriptors



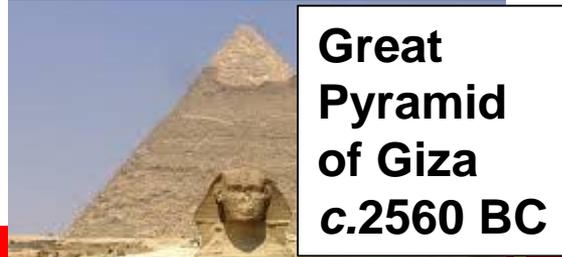


Structural Informatics

Which is the stable wall?



The
CCDC
c.1992



Great
Pyramid
of Giza
c.2560 BC



Hadrian's Wall
c.122



Great
Wall
of China
c.1368

A

B



My
House
c.1988

The database of walls indicates that A is the frequently observed arrangement and therefore the one that achieves stability.



Crystal Structure Characteristics that Influence Stability

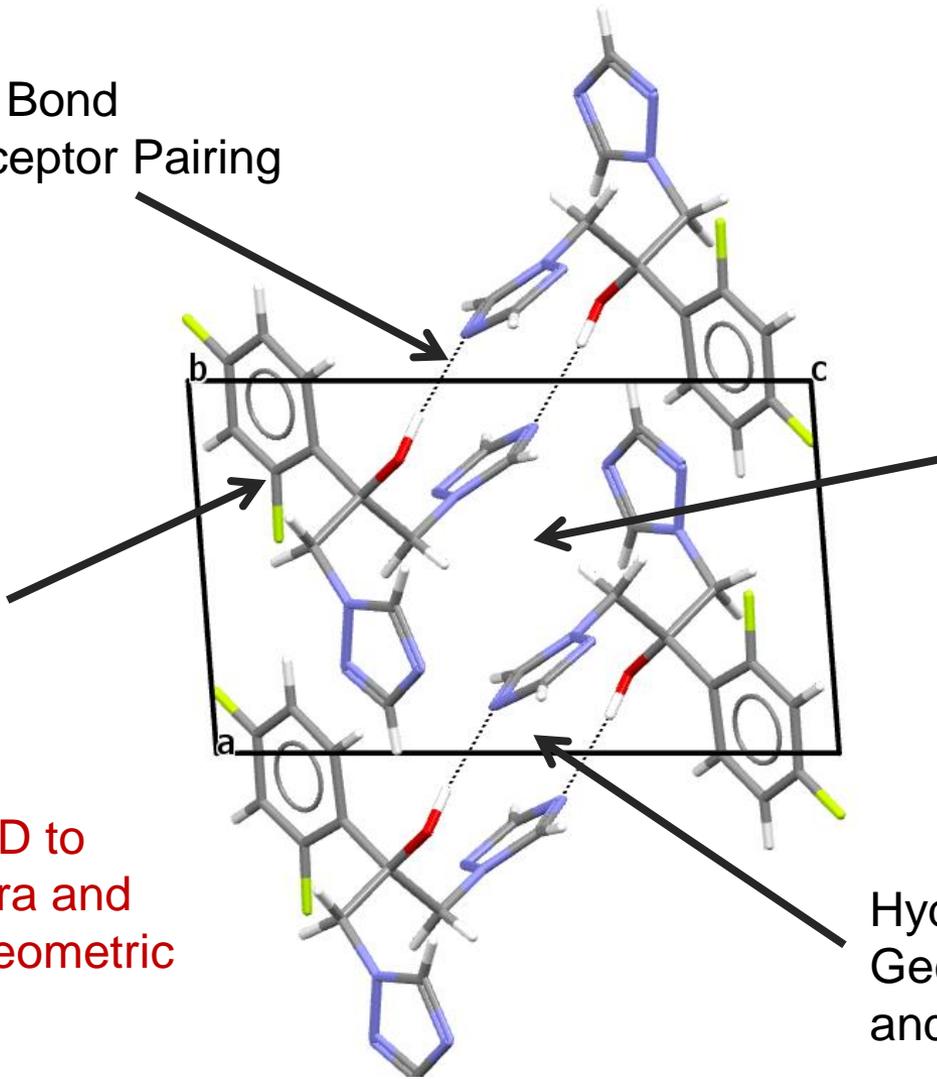
Hydrogen Bond Donor/Acceptor Pairing

'Non-Hydrogen Bond' Intermolecular Interactions

Molecular Conformation

Hydrogen Bond Geometry, Symmetry and Motif

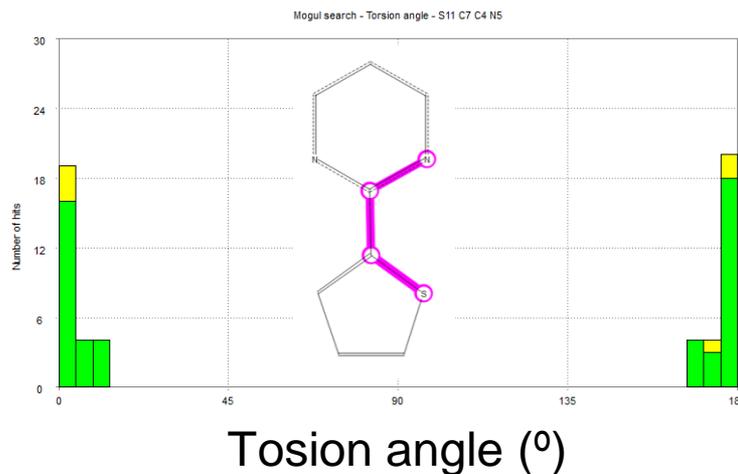
We mine the CSD to identify these intra and intermolecular geometric preferences.





CSD derived knowledge bases

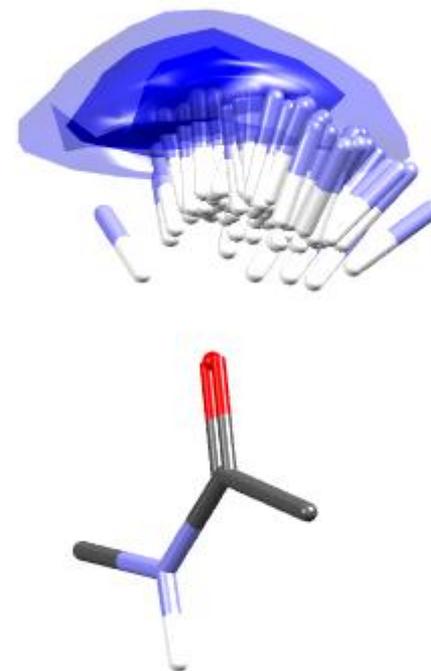
Number of hits



Mogul

Molecular geometry distributions

- Bond lengths
- Valence angles
- Torsion angles
- Rings



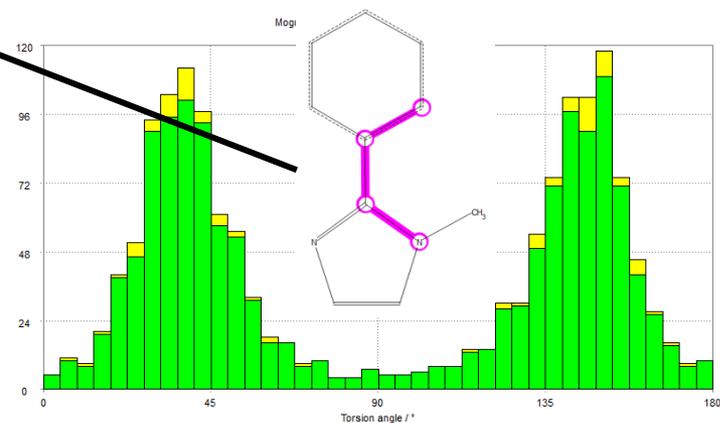
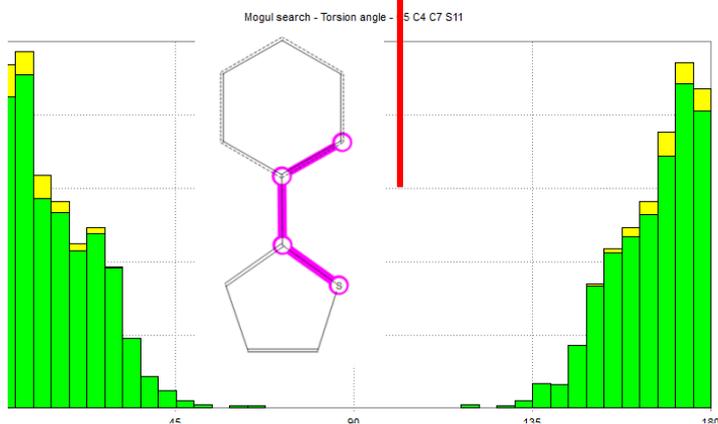
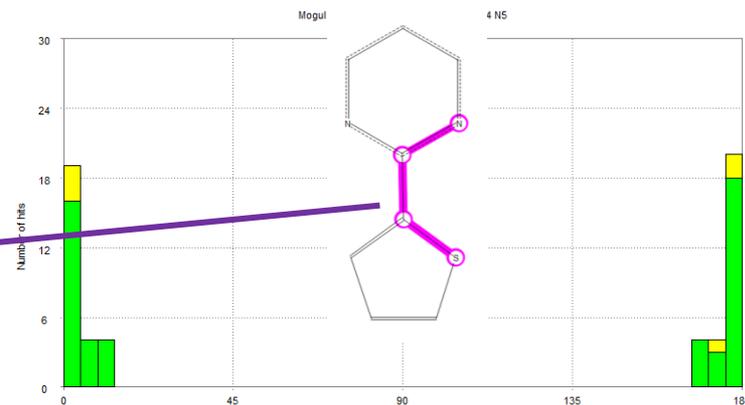
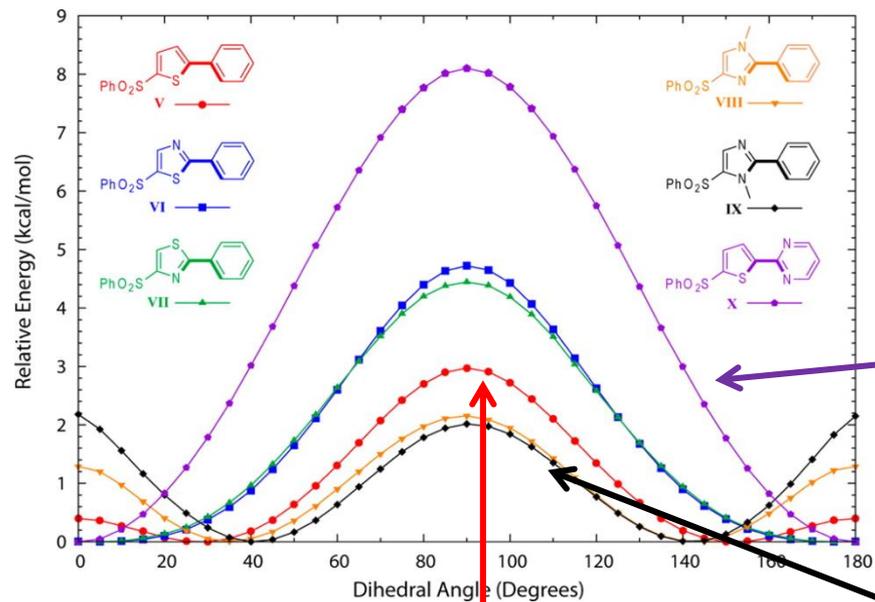
IsoStar

Intermolecular geometry analysis

- Interaction distributions displayed as scatterplots or contour surfaces
- 18,000 pre defined interaction scatter plots



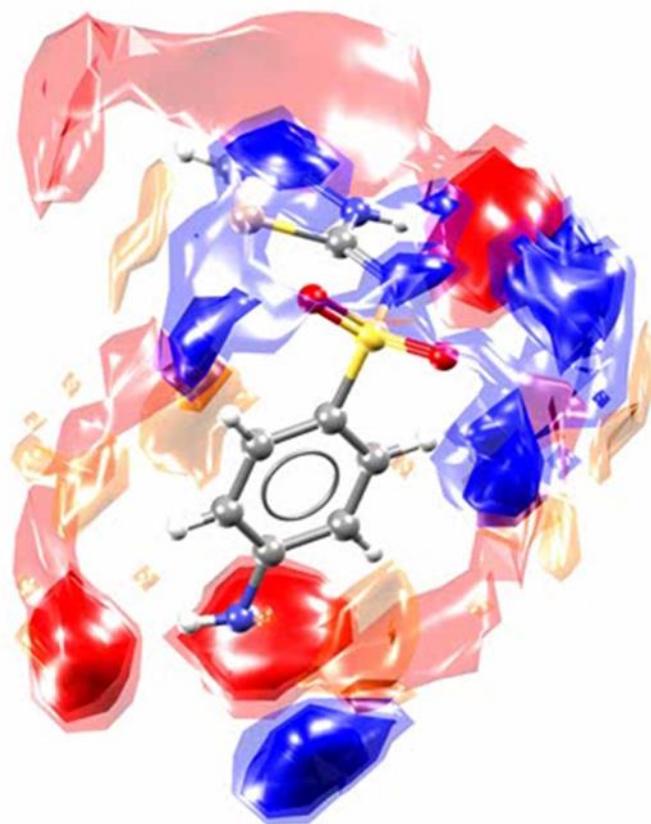
Understanding conformational complexity





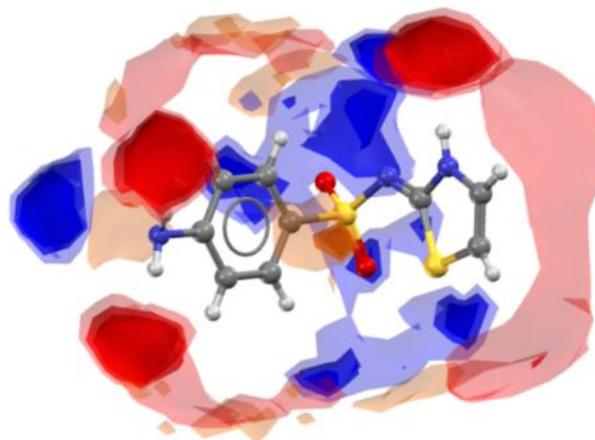
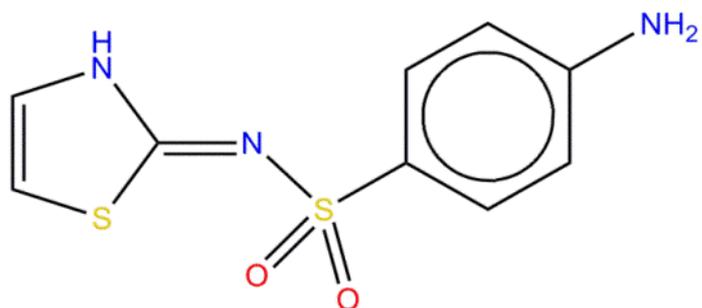
Full Interaction Maps (FIMs)

- IsoStar libraries used to map interaction preferences around complete molecules in a crystal structure
- The satisfaction of the Full Interactions Maps by the packing shell of the crystal structure can then be used to assess stability



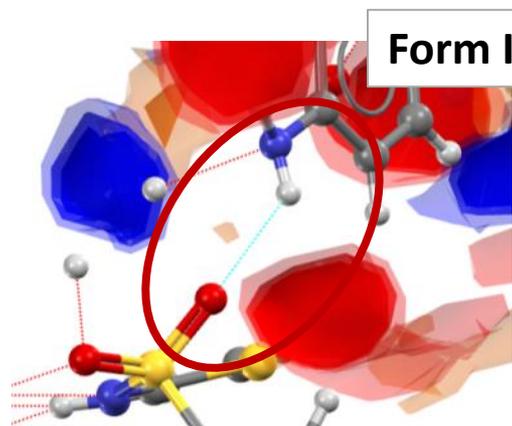


Using FIMs to assess stability



Donor probe
Acceptor Probe
Hydrophobic Probe

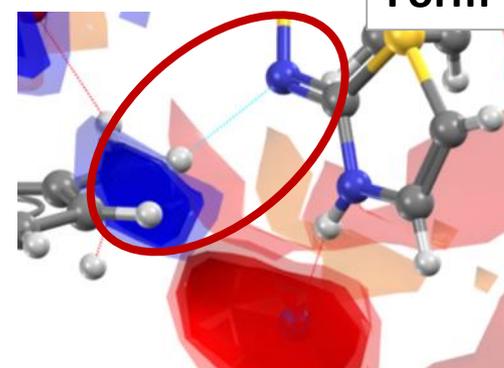
SUTHAZ16



Form I

Low satisfaction – Metastable

SUTHAZ19

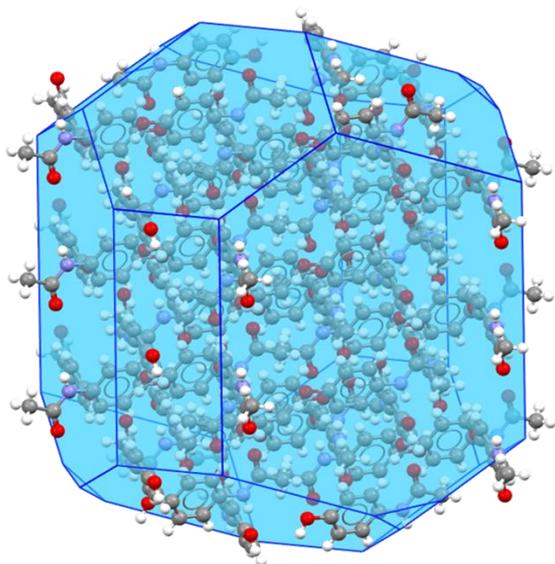


Form V

High satisfaction – Stable



Crystal structure directs...



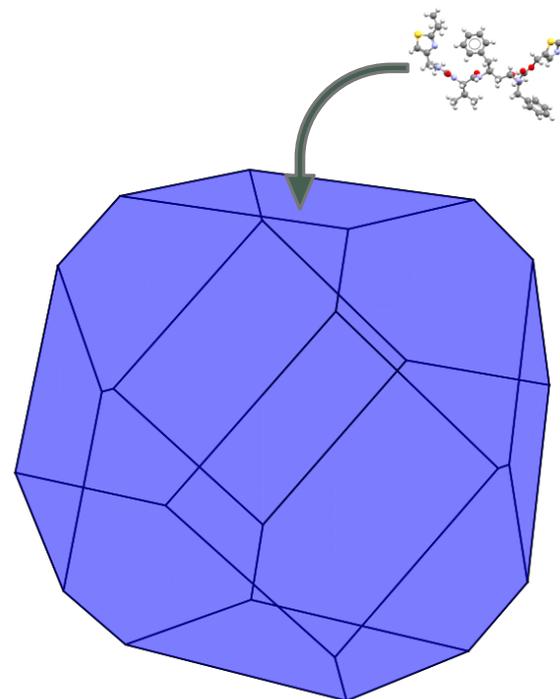
- Morphology/crystal growth
- Surface chemistry
- Mechanical properties
- Solubility
- Stability
- Melting point





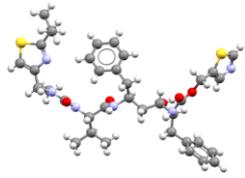
Predicting morphologies

- Start from a base morphology prediction
- Assume nucleation onto existing faces to be the rate limiting step in further crystal growth
- Use a forcefield to quantify the most favourable site of interaction
- As growth rate is proportional to the nucleation rate, this allows us to use nucleation kinetics, including a term for supersaturation

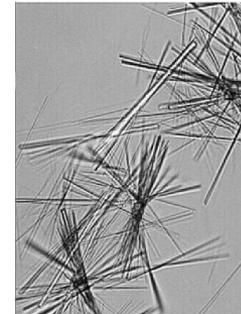
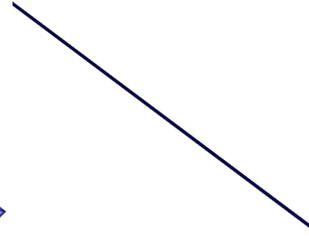
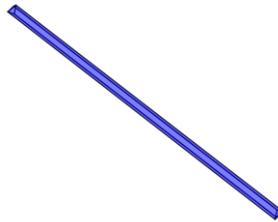
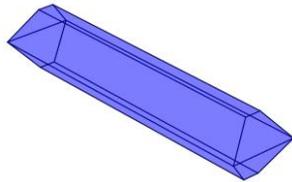
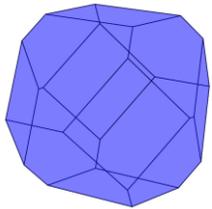




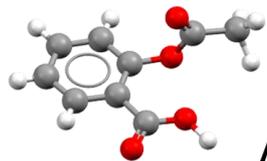
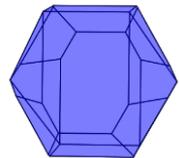
Predicting morphologies



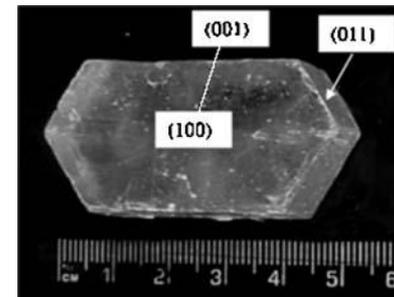
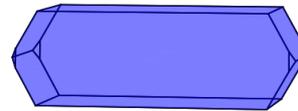
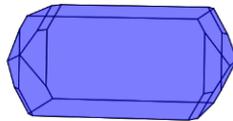
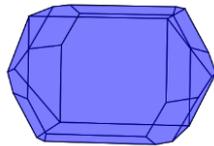
Ritonavir Form-II



Supersaturation



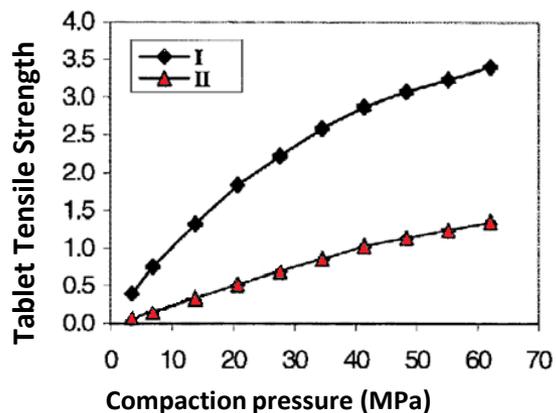
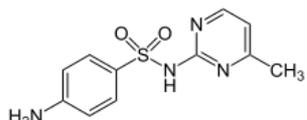
Aspirin



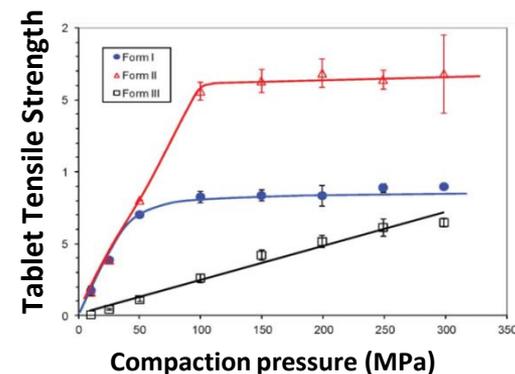
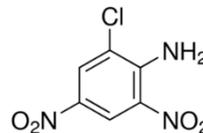


Mechanical properties from structure

Sulfamerazine

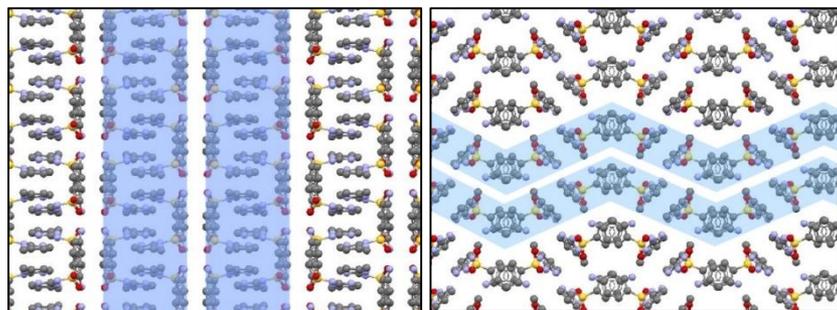


6-chloro-2,4-dinitroaniline

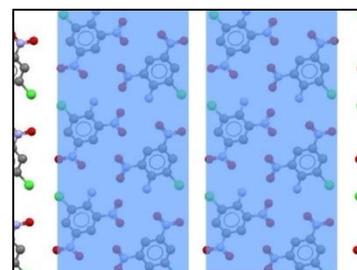


Form-I

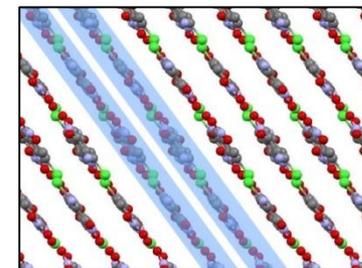
Form-II



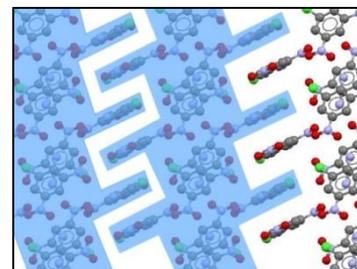
Form-I



Form-II

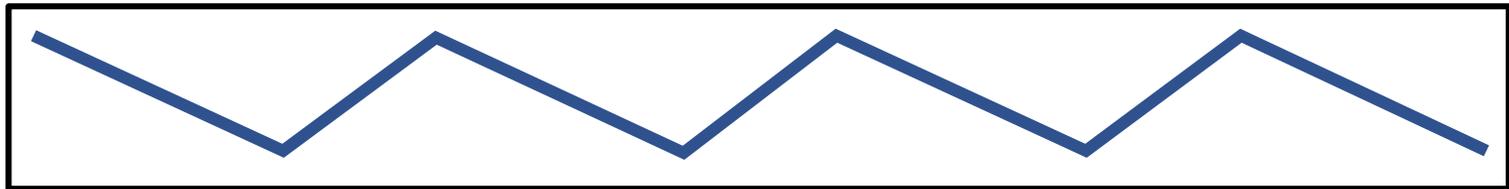
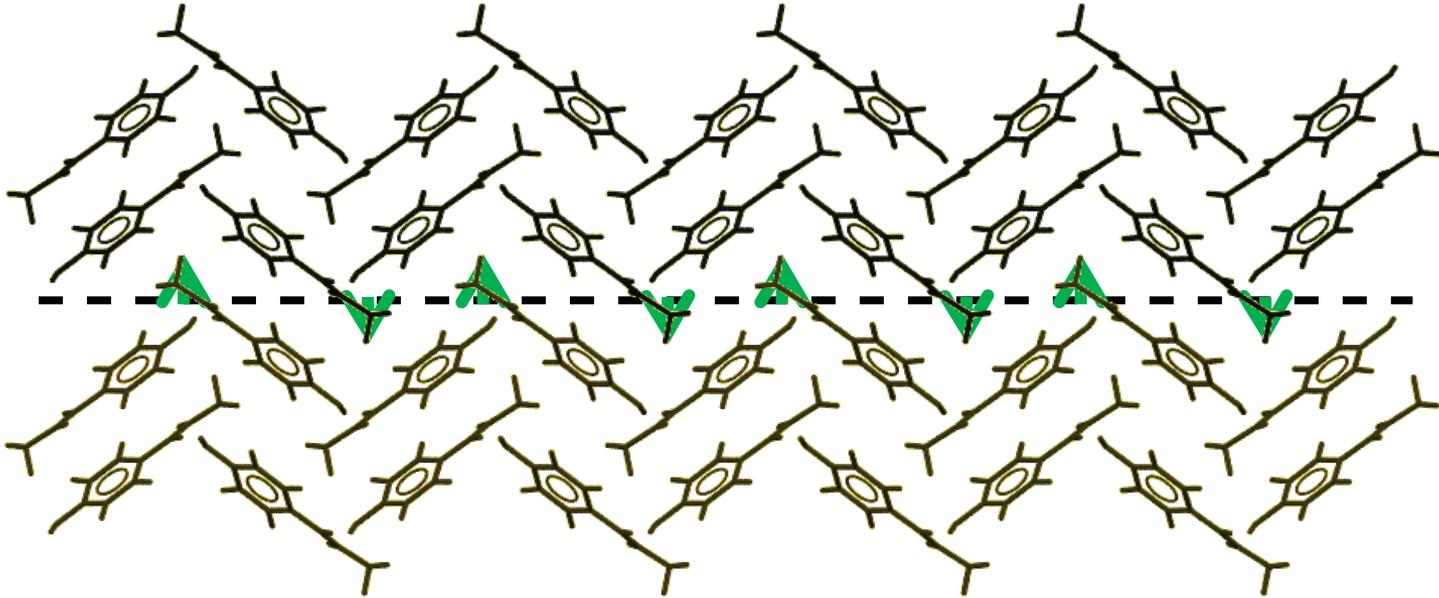


Form-III





Predicting slip planes

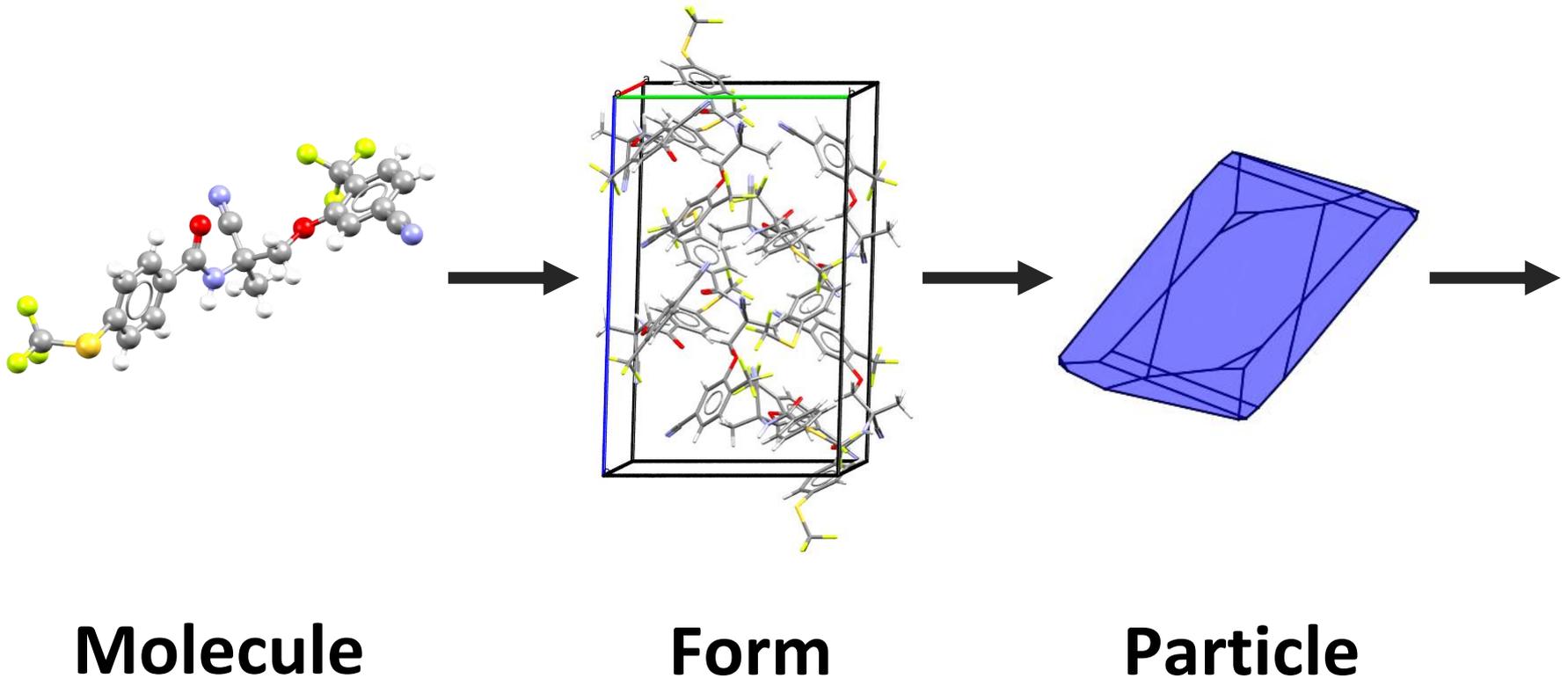




Predicting slip planes

Crystal	Observed	Dreiding	cvff	compass	CCDC Rugosity tool
SLFNMA01	020	002	002	002	010
SLFNMA02	020	020	020	020	010
260457 (UCECAG03)	001	001	001	001	001
CITRAC10	002	002	002	002	001
260456 (UCECAG02)	001	001	001	001	001
PUPBAD01	10-2	10-2	020	011	10-2
PUPBAD02	101	10-1	011	020	101
HXACAN	002	002	200	200	001
HXACAN01	010	110	110	110	010
DIJVOH	002	200	200	200	001
260455 (UCECAG01)	10-1	100	100	100	10-1
ethyl paraben (FEGLEI)	101	100	100	100	101
propyl paraben (DUPKAB)	101	100	100	100	101

Making the most of every crystal structure ever published





Acknowledgements

- Mat Bryant
- Mat.Sci. Team at CCDC
- Members of the ADDoPT Consortium

