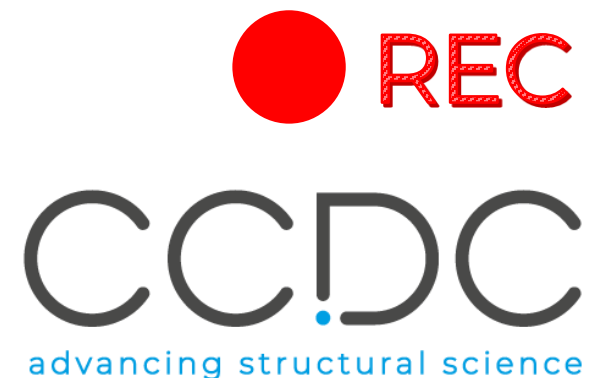


Advanced Structural Analysis of Porous Materials Using Mercury

CCDC Virtual Workshop

7th October 2025



Learning outcomes

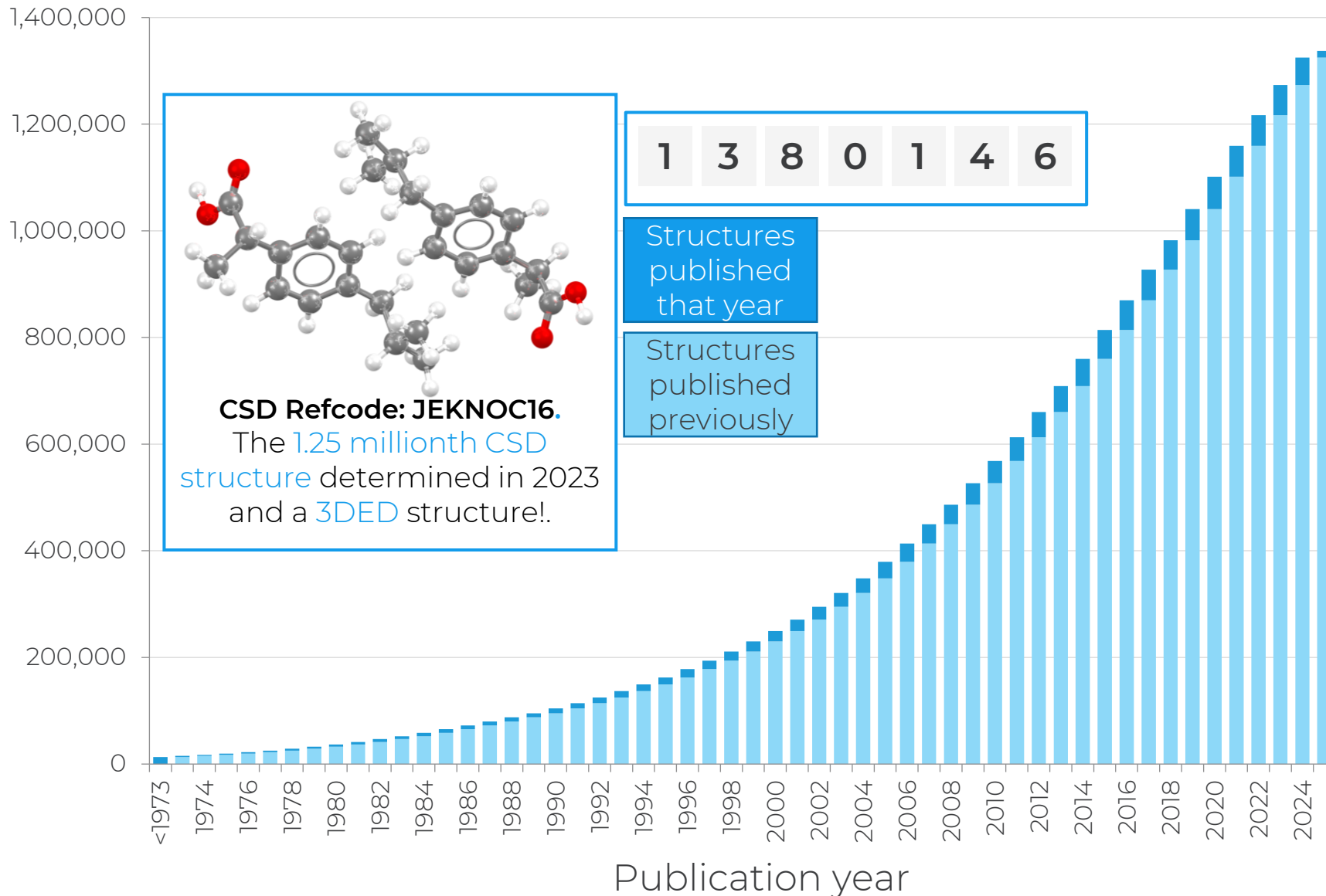
- ❑ Become familiar with the **CSD**.
- ❑ Which **subsets** of the CSD are available, how to access them in ConQuest, Mercury and the CSD Python API, and how they can help you in your research.
- ❑ How to **visualise** porous materials effectively in **Mercury**.
- ❑ How to **analyse** pore space in your structures using **Pore Analyser**.
- ❑ About applications of the **disorder visualization feature**, including recent advances and integrations with other functionality available in Mercury.
- ❑ And more Mercury **tips and tricks!**

We will make the recording available to you in the next few days.

CCDC

The Cambridge Structural Database

Number of structures in the CSD



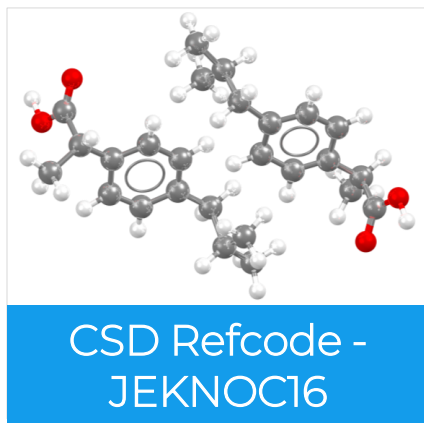
- Every published structure
 - Inc. ASAP & early view
 - *CSD Communications*
 - Patents
 - University repositories
 - Thesis
- Every entry enriched and annotated by experts
- Discoverability of data and knowledge
- Sustainable for 60 years
- A trusted CoreTrustSeal repository



Certified as Trustworthy
by CoreTrustSeal

CCDC

CSD Refcodes



What is JEKNOC16?

- A CSD Refcode
- A database reference code
- Containing 6-8 characters
- Used to identify entries in the CSD

Refcode families

- The same substances are assigned the *same* 6 letter code plus an additional 2 numbers
 - Polymorphs
 - New determinations or re-refinements of the same substance
 - Determinations at different temperatures/pressures
- Stereoisomers or different solvates, co-crystals, etc are assigned *different* refcode families

Porous materials refcode families

- Different solvents or adsorbates would be assigned to *different* refcode families, even though the framework might be the same.

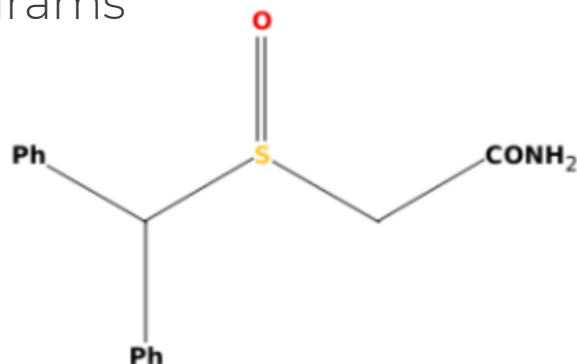
Some interesting refcodes are: KITTEN, BATMAN, DISNEY, GAUTAM, GLYCIN

Curation

A combination of manual and automated curation

Naming: 2-((Diphenylmethyl)sulfinyl)acetamide
Synonym: 2-(Benzhydrylsulfinyl)acetamide

Chemically meaningful 2D
Diagrams



Linking: DrugBank: DB00745
For Stereoisomer see [KAHVUL](#)

New for 2025

- Publication titles
- Enhanced refinement properties (including wR_2 , GooF, Max Shift, Residual density max/min)
- Predicted properties (including HOMO-LUMO gap, Singlet and Triplet state energies)
- Calculated properties (including total surface area, geometric volume, pore limiting diameter, max pore diameter)

Identifier assigned
CCDC number, CSD Refcode
CCDC [236078](#), CSD-[ETEXIK](#)

Information extracted from CIF

Spacegroup: $P2_1/n$
Cell: a 20.9610(10)Å b 9.7061(5)Å c 20.8940(10)Å,
 α 90° β 139.3360(10)° γ 90° **R factor:** 4.2%

Structural: Atom coordinates, ADPs

Experimental information: Temperature,
recrystallisation solvent, crystal colour,
crystal habit

Information added

- Melting points
- Bioactivity details
- Natural source data
- Oxidation states
- Polymorph families

Inside the Cambridge Structural Database

The CSD is a database of all the published organic and metal-organic experimental crystal structures

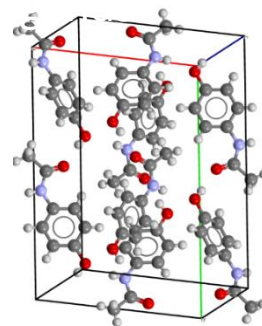
Organic
45%

Metal-Organic
55%

At least one transition metal,
lanthanide, actinide or any of Al,
Ga, In, Tl, Ge, Sn, Pb, Sb, Bi, Po

Organic

- Drugs
- Agrochemicals
- Pigments
- Explosives
- Protein ligands



Additional data

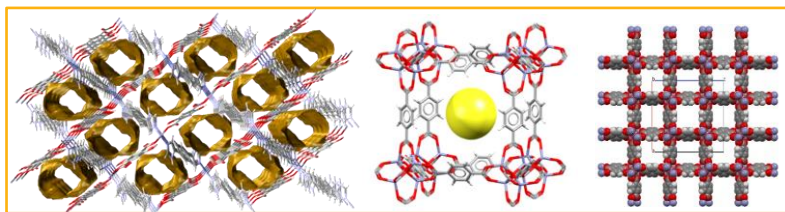
- 14,019 polymorph families
- 176,704 melting points
- 1,127,300 crystal colours
- 1,005,205 crystal shapes
- 32,100 bioactivity details
- 14,344 natural source data
- > 400,000 oxidation states

Not Polymeric
88%

Polymeric: 12%

Metal-Organic

- Metal Organic Frameworks
- Models for new catalysts
- Porous frameworks for gas storage
- Fundamental chemical bonding



Single
Component
58%

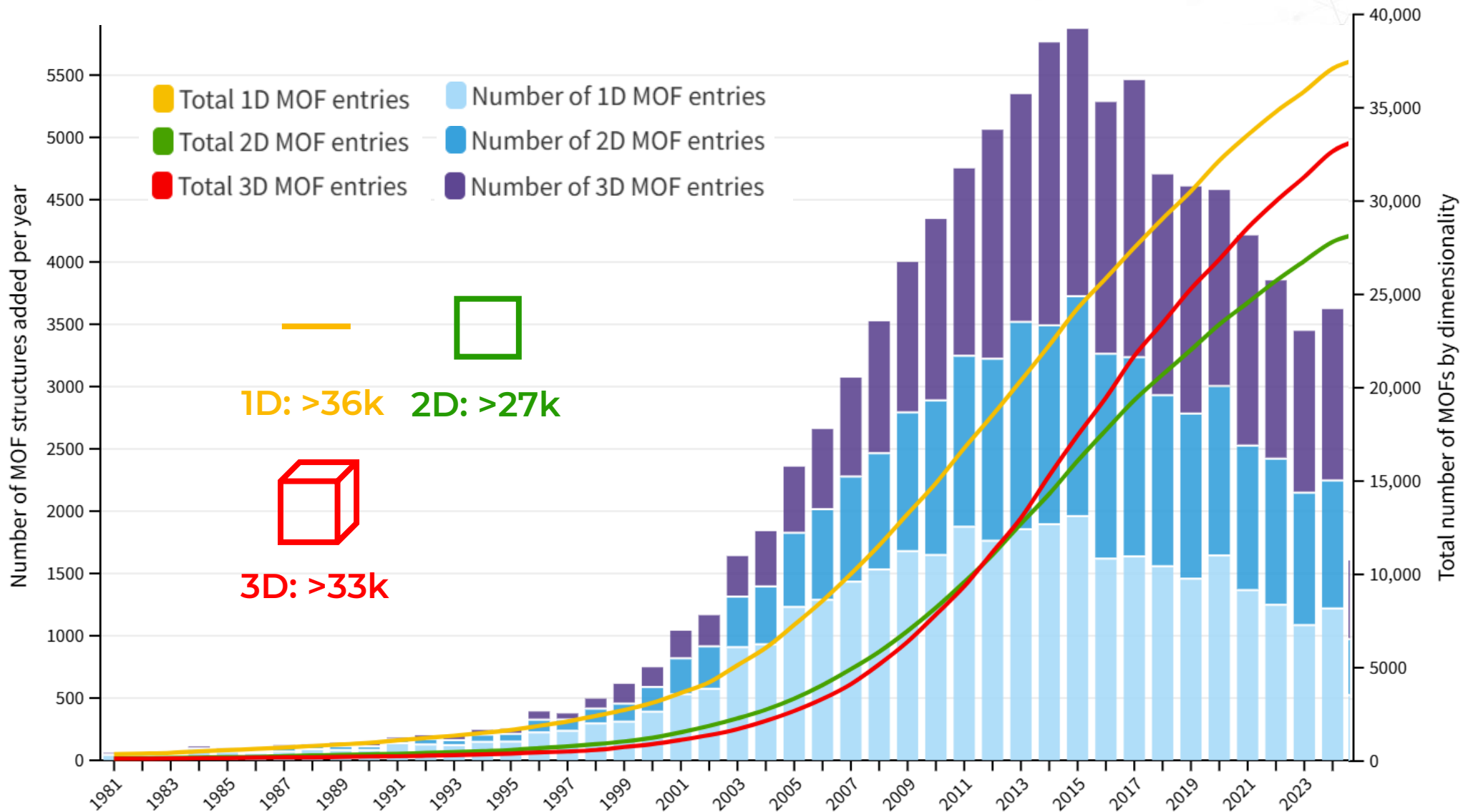
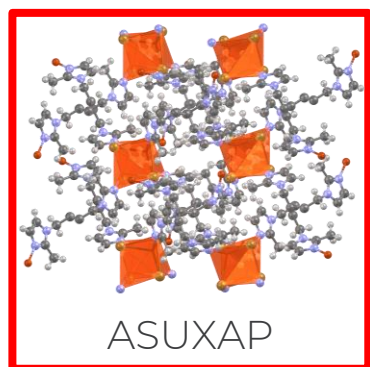
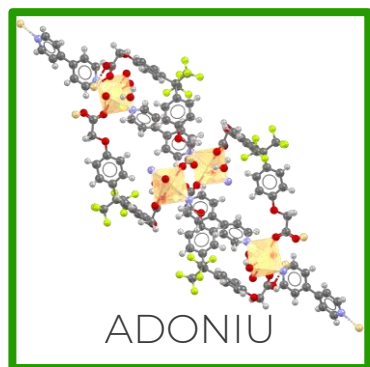
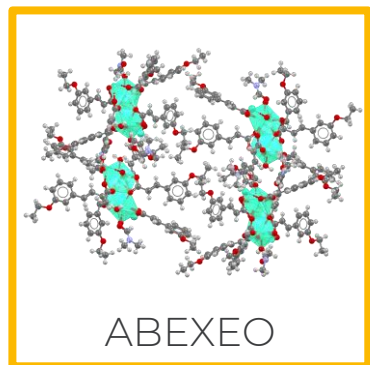
Multi
Component
42%

Links and subsets

- DrugBank
- Druglike
- MOFs
- PDB ligands
- PubChem
- ChemSpider
- Pesticide PDB

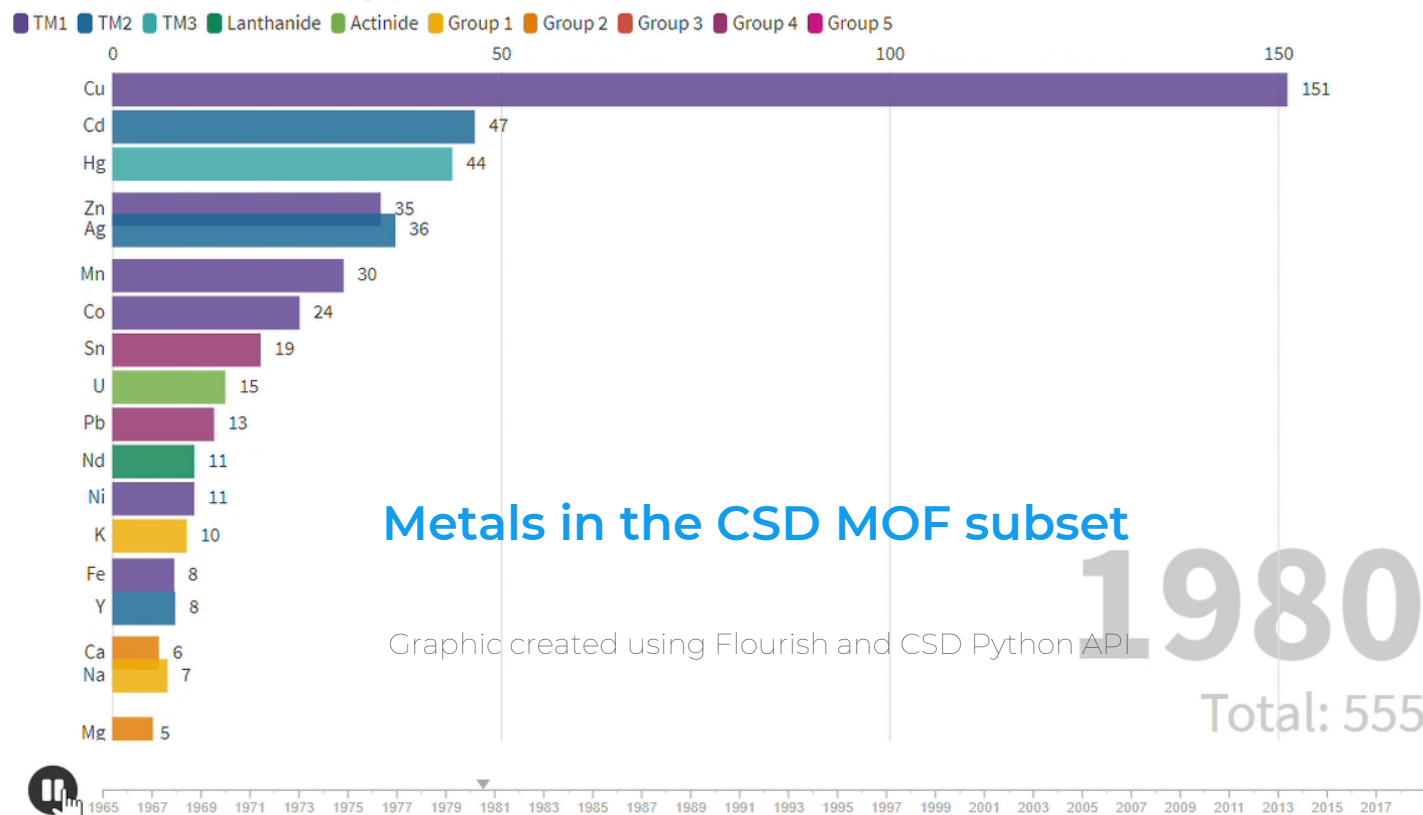


Inside the CSD



Exploring coordination polymers in the CSD

The number of structures containing a particular metal atom

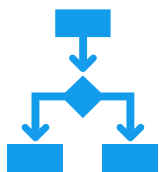


- Over **100k** have been synthesized.
- Growing **potential applications**, each with unique property requirements.
- Materials informatics using data in the CSD can help to **focus research efforts** to find the right MOFs for each application.

Industrial applications

- Energetic materials
- Batteries
- Ferroelectricity
- Drugs
- Catalysis
- Semiconductors
- Gas storage
- Filtration
- Gas separation
- Carbon capture
- Detection and sensing

Using materials informatics to support materials development



Focus
experimental
efforts



Predict future
successes and
risks



Identify **patterns**
to spark further
investigation



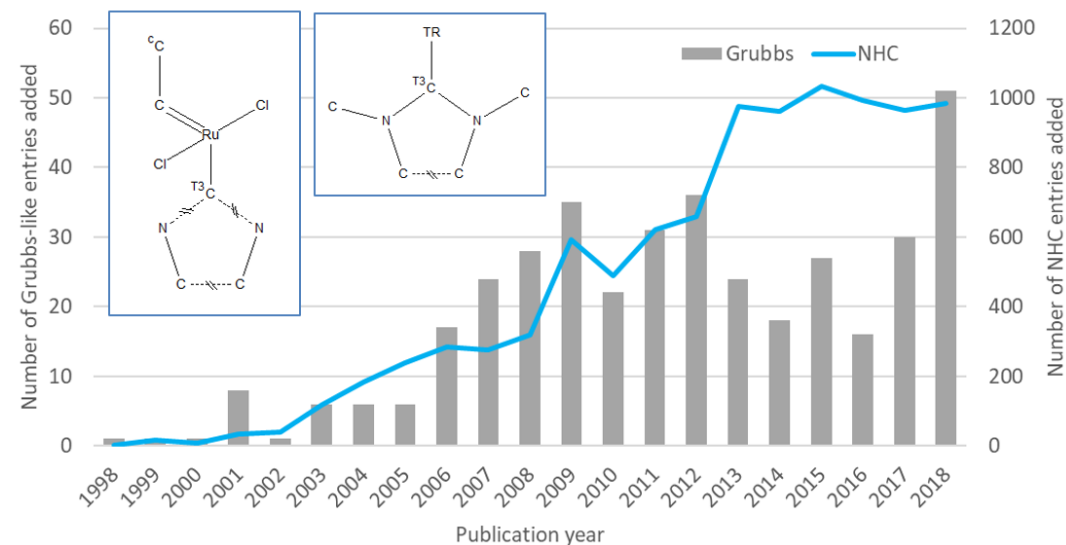
Systematically
search the
existing landscape



Data is the fuel

CCDC

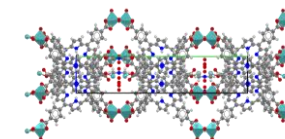
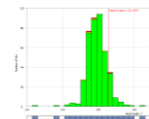
Catalysts in the CSD



The CSD Portfolio today

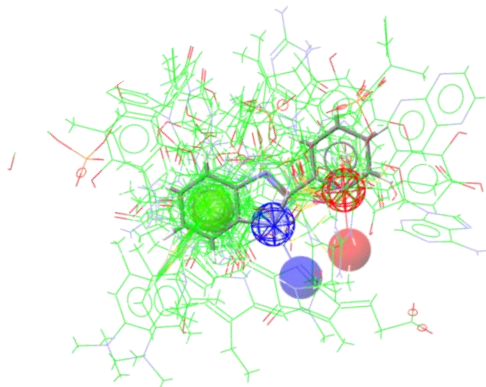
CSDCore.

*Search, visualise, analyse and communicate structural data
Insights into molecular and crystal shape and interactions*



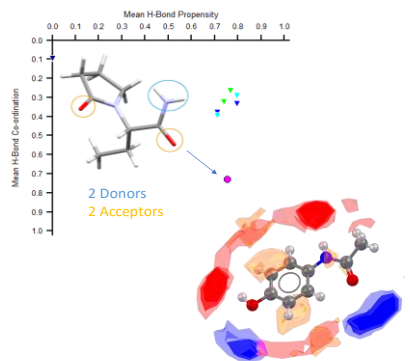
CSDDiscovery.

Design of new molecules



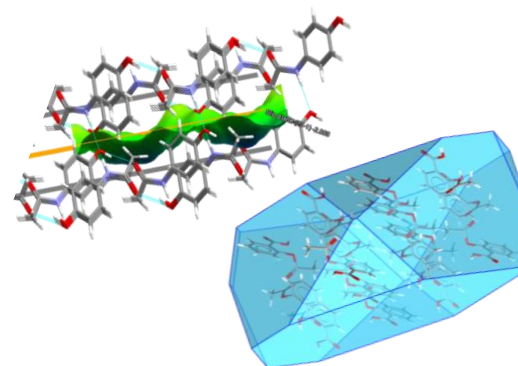
CSDMaterials.

Assessment of solid form stability and properties



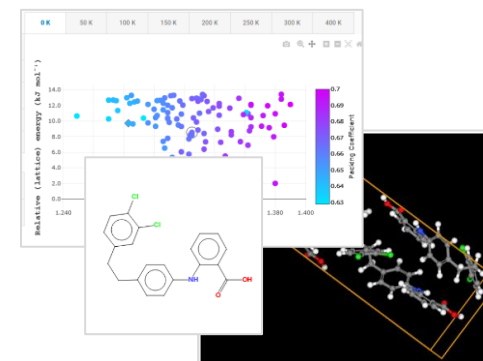
CSDParticle.

Anticipate particle properties and behaviour



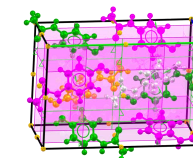
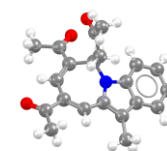
CSDTheory.

Insights from predicted structure landscapes



CSDCommunity.

*Deposit, publish, access and visualise structural data
Free functionality to share and learn from structures*



Medicinal & Computational Chemists ♦ Crystallographers & Structural Biologists ♦ Solid Form & Crystallisation Scientists ♦ Functional Materials Scientists ♦ Educators ♦ Industry and Academia

CCDC

Using the CSD for porous materials

Searching

ConQuest

WebCSD / Access Structures

Structural Analysis

Void and pore analysis

Mercury

Guest analysis

Visualisation

Mercury

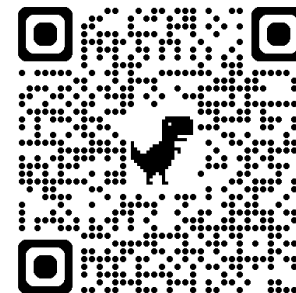
VIMRIZ

Wavelengths: 1.54056 Å

YIMRIZ simulated

CSD Python API

What can you do with a licence?



CCDC

Deposit Structures | Access Structures | Contact Us | Sign in

Home | Solutions | Communit | Discover | Consultancy Services | Research | Support and Resources | About | Contact Us

How CSD Licences Work

About CSD Licences

A licence allows you to use the Cambridge Structural Database (CSD) data and software in your research.

We offer a range of data and software to support molecular discovery, materials design, and crystallography research. This includes open source, free, and paid software.

CSD licences are available for academic universities and research institutions, government organizations, and commercial companies. The exact licence terms and what tools are included depend on the licence type. We can help advise you what licence is best for your needs.

Academic CSD Licence Types

For academic users we offer a range of free tools, including free Mercury, or a full licence enables even more search and analysis tools. The full licence is provided at a heavy discount to all academic users.

This table compares the free CSD-Community and full CSD-Enterprise licences.

[Compare Academic CSD Licences](#)

Commercial CSD Licence Types

Commercial users can select from a range of licence levels depending on your field. Specialist packages for data and search, drug discovery, materials design, crystal structure prediction, and particle / manufacturing analysis are available.

This table compares the commercial CSD licences available.

[Compare Commercial CSD Licences](#)

View Standard CSD Licence Agreement

View the standard CSD licence agreement. Note that this may not match your own agreement. If you want a copy of your personal agreement, please contact us.


[Standard CSD Licence Agreement](#)

- **Supporting research:** The CSD Python API enables bulk access to the CSD and large-scale structural surveys to advance your research.
- **Responsible data use:** We encourage and support use for research and analysis, but redistribution and large-scale publication are restricted to protect the CSD's sustainability.
- **Publication guidelines:** Small extracts and visualizations can be shared, but full datasets and CSD derived models require permission.
- **Supporting you:** More information is available on our website, but if in doubt, contact us—we're happy to help!

<https://www.ccdc.cam.ac.uk/solutions/csd-licence/>

support@ccdc.cam.ac.uk

CCDC

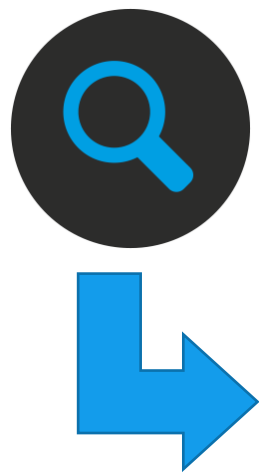


We are recording today's session and will make the recording available to you in the next few days

Agenda

- *Show One*: Introduction to the CSD and porous materials in the database
- *Show One*: Case studies from Prof. Maria Celeste Bernini
- *Show One*: Mercury functionality for porous materials
- *Try One*: Hands-on exercises
- *Explore More*: More tips and tricks for porous materials and case studies
- *Explore More*: Quiz and summary
- *Extra time*: More time for hands on and Q&A

How to search in ConQuest



File menu

Tab options/views

Search options

Learn more in this self-guided workshop

1. Build a Query: what do you want to find?
2. Click search filters: do you want to restrict your search?

Search

Search Setup

Search Name: search1

Available Databases:

CSD version 6.00 (Apr 2025)

You can search complete database(s) or a subset (e.g., hits found in a previous search)

Select Subset Clear Subset

Single query being used. Search will find structures: where this query is true: Query 1

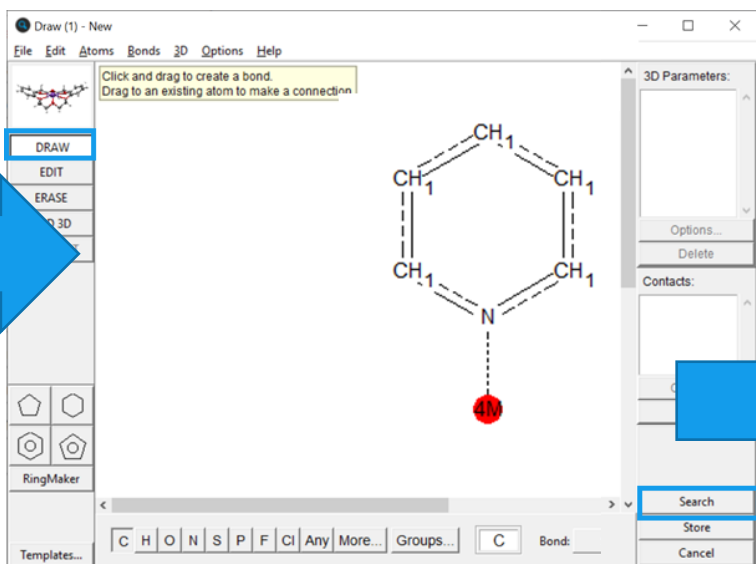
Start Search

How to search in ConQuest

1. Build a Query:
what do you
want to find?

2. Click search and select
filters: do you need to
restrict your search?

3. Visualise and analyse
results: what can you
learn from this data?



Search Setup

Search Name: search1

Available Databases:

- CSD version 6.00 (Apr 2025)

You can search complete database(s) or a subset (e.g., hits found in a previous search)

Select Subset Clear Subset

Single query being used. Search will find structures where this query is true:

Query 1

Filters Advanced Options

- 3D coordinates determined
- R factor <= 0.05 <= 0.075 <= 0.1
- Only Non-disordered Disordered
- No errors
- Not polymeric
- No ions
- Only Single crystal structures Powder structures
- Only Organics Organometallic

Start Search Cancel Reset

CCDC ConQuest (1) : search1 [Searching...]

File Edit Options View Databases Results Help

Build Queries Combine Queries Manage Hitlists View Results

Refcode: ABAFAN CSD version 5.44 (April 2023)

All Text
Author/Journal
Chemical
Crystal
Experimental
Diagram
3D Visualiser
CSD Internals
Search Overview

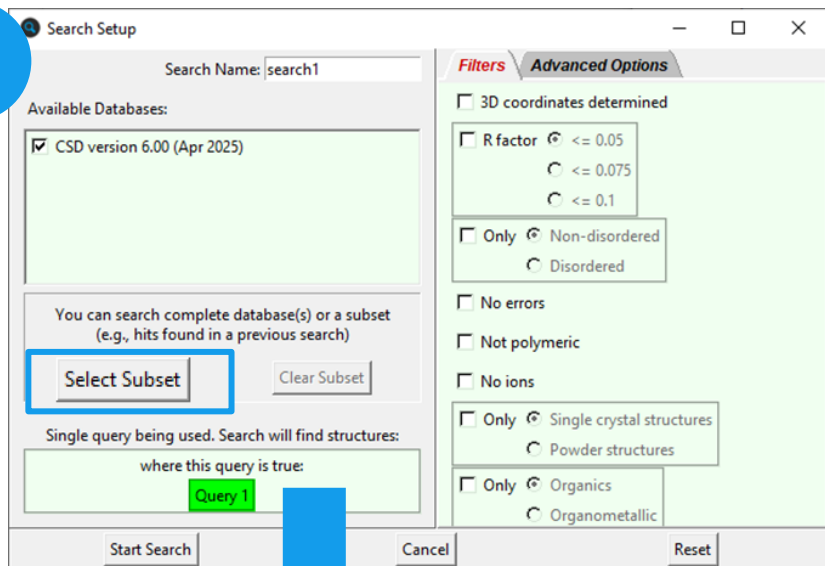
Results view options

Results

42837 hits
26%
Stop Search

Using the subsets in ConQuest

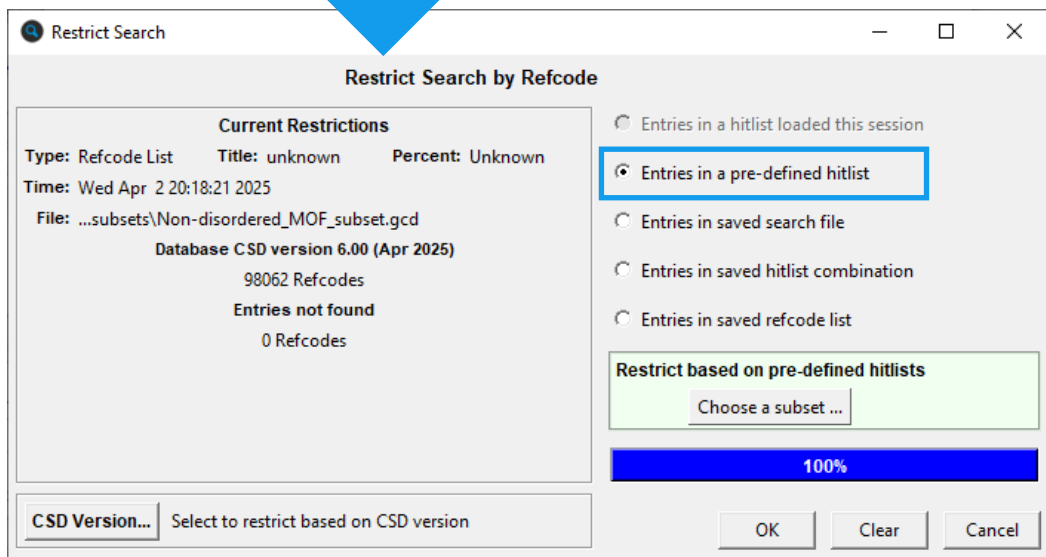
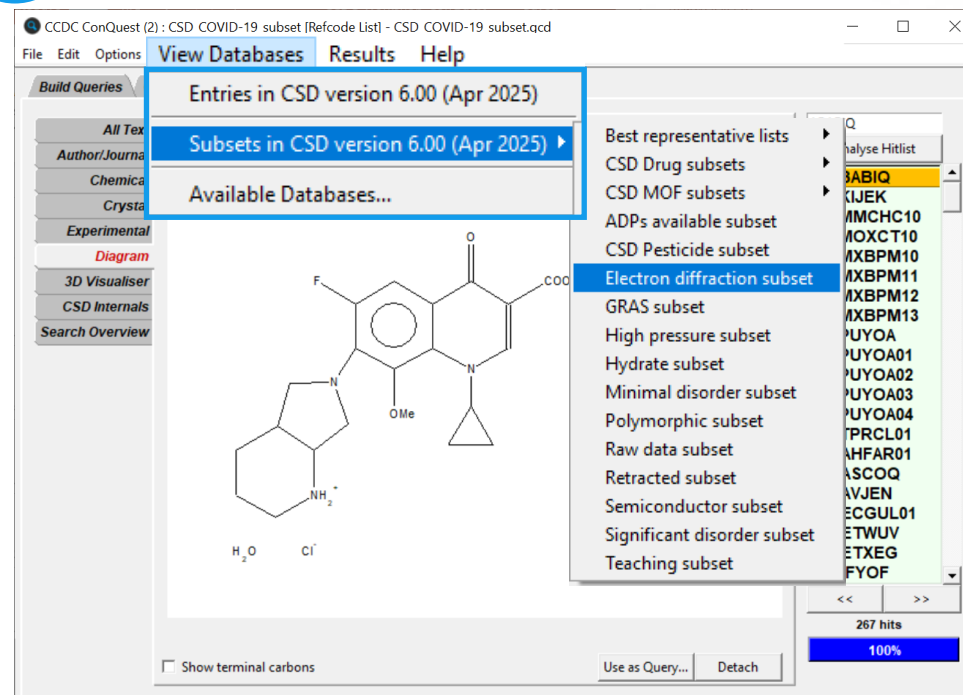
1



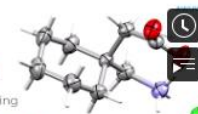
Restrict a search to a subset

2

Load a subset in the hitlists



How to:
Use CSD subsets
• Subsets in ConQuest,
accessing and searching
• Subsets in the CSD Python API
• Subsets in Mercury



CCDC

How to: Use Cambridge Structural Database Subsets

NEW!
Watch on
YouTube

CCDC

Using the subsets in the CSD Python API



Subsets

`class ccdc.io.Subsets` [\[source\]](#)

This class provides a simple way to access pre-defined CSD [subsets](#).

Example:

```
>>> mof_reader = EntryReader(subset=Subsets.MOF)
```

The returned `reader` object is the same as if the `Reader` class has been initialized with the associated GCD file directly.

Subsets available:

- ADP
- BEST_HYDROGENS
- BEST_LOW_TEMP
- BEST_RFACTOR
- BEST_ROOM_TEMP
- COVID19
- DRUG
- DRUG_SINGLE_COMPONENT
- ELECTRON
- HIGH_PRESSURE
- HYDRATE
- MOF
- MOF_NO_DISORDER
- MOF_1D
- MOF_2D
- MOF_3D
- PESTICIDE
- POLYMORPHIC
- TEACHING
- MINIMAL_DISORDER
- SIGNIFICANT_DISORDER



CSD Python API
documentation
and cookbook

Entry examples

Create indexes of useful information for subsets of CSD entries

Note that this script makes use of functionality from the `cookbook` utility module.

```
#!/usr/bin/env python
#
# This script can be used for any purpose without limitation subject to the
# conditions at http://www.ccdc.cam.ac.uk/Community/Pages/Licences/v2.aspx
#
# This permission notice and the following statement of attribution must be
# included in all copies or substantial portions of this script.
#
# 2015-06-17: created by the Cambridge Crystallographic Data Centre
#
'''
Provide information on a set of structures in the CSD.

This script takes as input a gcd file (a text file with CSD refcodes) and
writes out the identifier, author(s), literature reference, formula, compound
name and compound synonym(s). The output can be formatted as csv or html.
'''

from __future__ import division, absolute_import, print_function
import six
import sys
import os
import csv
import html
import argparse
import codecs

from ccdc.io import EntryReader

class Writer(object):
    def __init__(self, infile, out, format='csv'):
        try:
            self.rdr = EntryReader(infile, format='identifiers')
        except RuntimeError:
            print('Failed to read input file %s!' % infile)
            exit(1)

        self.out = out
        getattr(self, format + '_header')()
        for e in self.rdr:
            getattr(self, format + '_line')(e)
        getattr(self, format + '_footer')()

    def csv_header(self):
        data = ','.join([
            'Identifier',
            'Author',
            'Literature Ref',
            'Formula',
            'Compound Name',
            'Synonym'
        ])
```



Learn about searching with the CSD Python API in this free CSDU module



Mercury Overview

More advanced functionality to analyse and learn from structures

Learn on demand with the CSDU module!



Display options to visualise and navigate structures

AABHTZ (P-1) - Mercury

File Edit Selection Display Calculate CSD-Community CSD-Core CSD-Materials CSD-Theory CSD-Particle CSD-Discovery CSD Python API Help

Picking Mode: Pick Atoms Clear Measurements Show Labels for All atoms with Atom Label

Style: Ball and Stick Colour: by Element or Suppression Manage Styles... Work Atom selections:

Animate... Default view: b a b c a* b* c* x- x+ y- y+ z- z+ x-90 x+90 y-90 y+90 z-90 z+90 ← → ↓ ↑ zoom- zoom+

Select by SMARTS: [c]

Structure Navigator

Crystal Structures	Spacegroup
AABHTZ	P-1
AACANI10	P21/c
AACANI11	P21/c
AACFAZ	Pbcn
AACFAZ10	Pbcn
AACMAL	P21/c
AACMHX10	Pbca
AACRHA	Pnmc
AACRHC	P-1
AACRUB	Cc
AACRUB01	C2/c
AADAMC	P21/c
AADMPY	P-1
AADMPY10	P-1
AADRIB	P21
AAGAGG10	P212121
AAGGAG10	P21

Display Options

Display

Packing Short Contact < (sum of vdW radii) Contacts...
 Asymmetric Unit H-Bond Default definition More Info
 Auto centre Reset Powder...

Options

Show hydrogens Depth cue
 Show cell axes Z-Clipping
 Label atoms Stereo

Explore over 1.35 million curated structures

Press the left mouse button and move the mouse to rotate the structure

Using the subsets in Mercury

The screenshot displays the Mercury software interface. The main window shows a ball-and-stick model of a molecular structure. The 'CSD-Core' menu is open, showing options like 'Launch WebCSD', 'Launch ConQuest', and 'Subsets in CSD version 6.00 (Apr 2025)'. A blue arrow points from the 'Subsets in CSD version 6.00' menu item to the 'Structure Navigator' window. The 'Structure Navigator' window shows a table of crystal structures and space groups. The 'MOF_subset' is highlighted in the 'CSD_MOF_subsets' sub-menu.

File Edit Selection Display Calculate CSD-Community CSD-Core CSD-Materials CSD-Theory CSD-Particle CSD-Discovery CSD Python API Help

Picking Mode: Pick Atoms Clear Measurements

Style: Ball and Stick Colour: by Element or Suppression Manage Styles... W

Animate... Default view: b a b c a* b* c* x-

Launch WebCSD
ConQuest Hit Highlighting...
Launch ConQuest
Data Analysis Module...
Mogul Geometry Check...
Launch Mogul
Mogul Settings...
IsoStar Interaction Check...
Launch IsoStar
IsoStar Settings...
Select Databases...
Subsets in CSD version 6.00 (Apr 2025) ▶

Best_representative_lists ▶
CSD_Drug_subsets ▶
CSD_MOF_subsets ▶
ADPs_available_subset
CSD_Pesticide_subset
Electron_diffraction_subset
GRAS_subset
High_pressure_subset
Hydrate_subset
minimal_disorder_subset
Polymorphic_subset
Raw_data_subset
retracted_subset
semiconductor_subset
significant_disorder_subset
teaching_subset

1D_MOF_subset
2D_MOF_subset
3D_MOF_subset
MOF_subset
Non-disordered_MOF_subset

Structure Navigator

Crystal Structures	Spacegroup
ABACUF	P-1
ABACUF01	P-1
ABADUG	P1
ABAFUH	P212121
ABAGAO	Pbca
ABALOF	P21/c
ABALUO	P212121
ABAMOL	P21/c
ABAMOL	P21/c
ABAVOP	P21/n
ABAVOS	P-1
ABAVUV	P21/n
ABAVUY	P21/c
ABAWOT	C2/c
ABAXIN	P-1

Display Options

Display

Packing Short Contact < (sum of vdW radii) Contacts...
 Asymmetric Unit H-Bond Default definition More Info
 Auto centre
Reset

Options

Show hydrogen bonds
 Show contacts
 Label atoms
Powder...

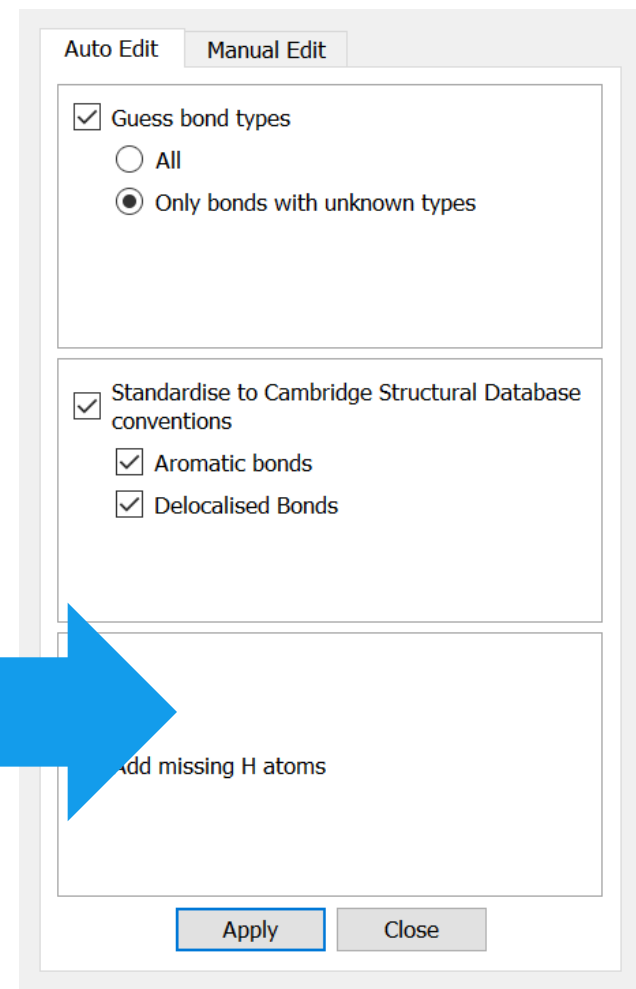
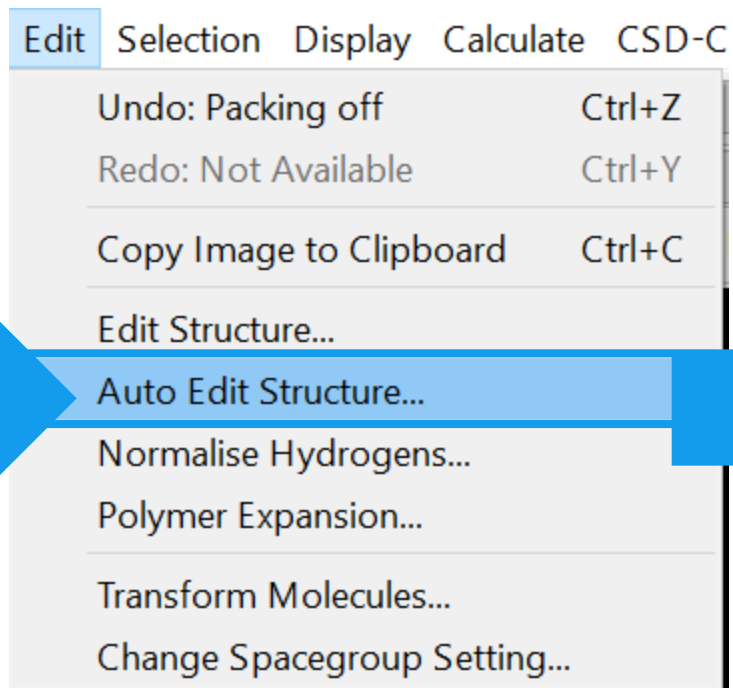
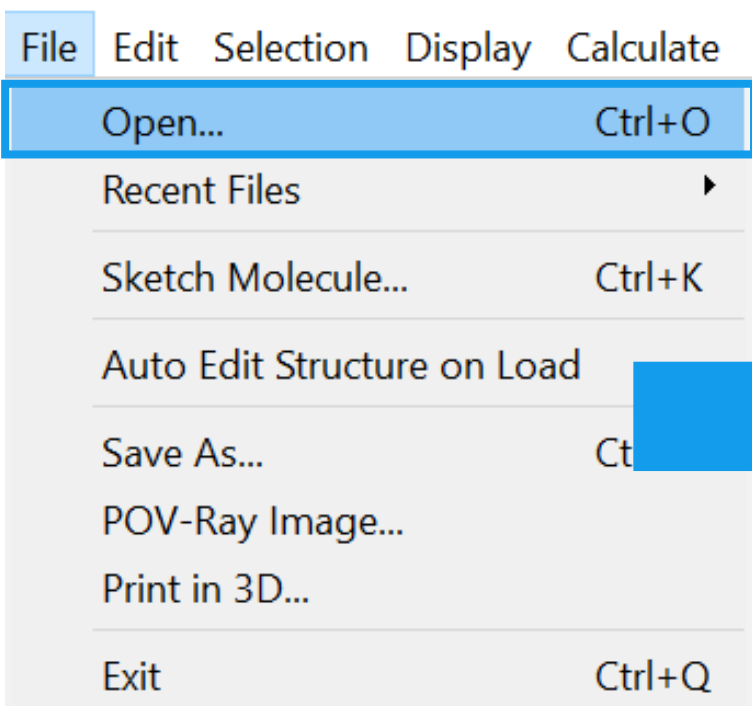
Multiple Structures
Structures...

Press the left mouse button and move the mouse to rotate the structure

Using your own file

- File > Open – to open one of your own files for example a CIF
- Edit > Auto Edit Structure to assign bond types
- File > Auto Edit Structure on Load to automate

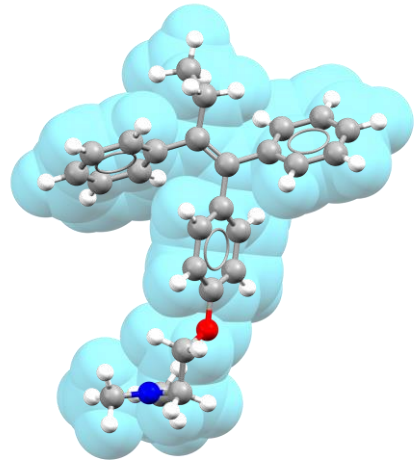
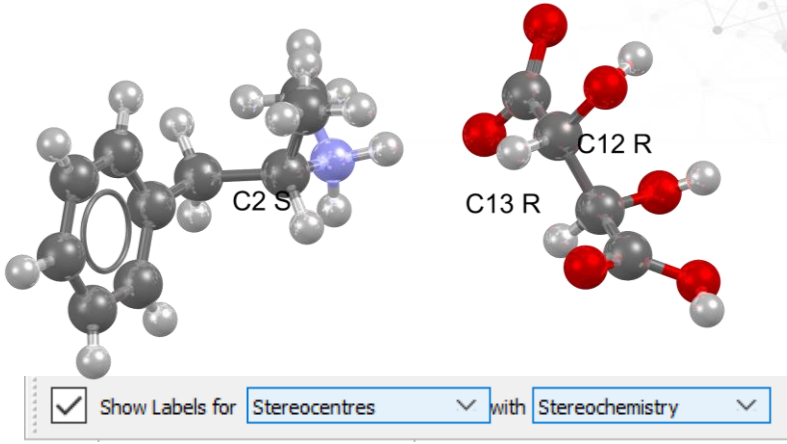
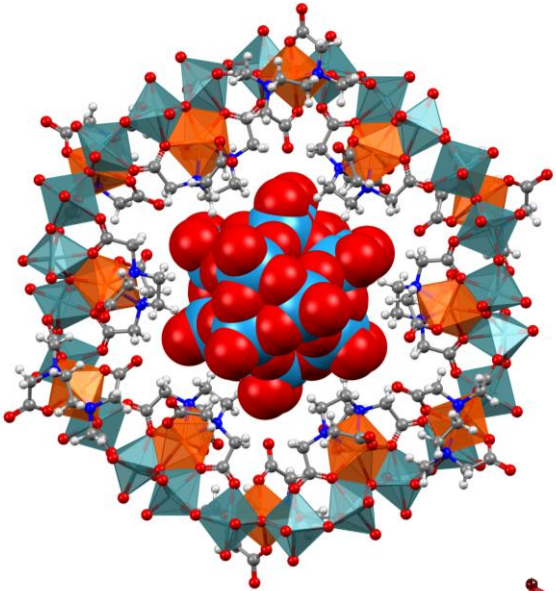
AABHTZ (P-1) - Mercury



Lots of display and analysis options!

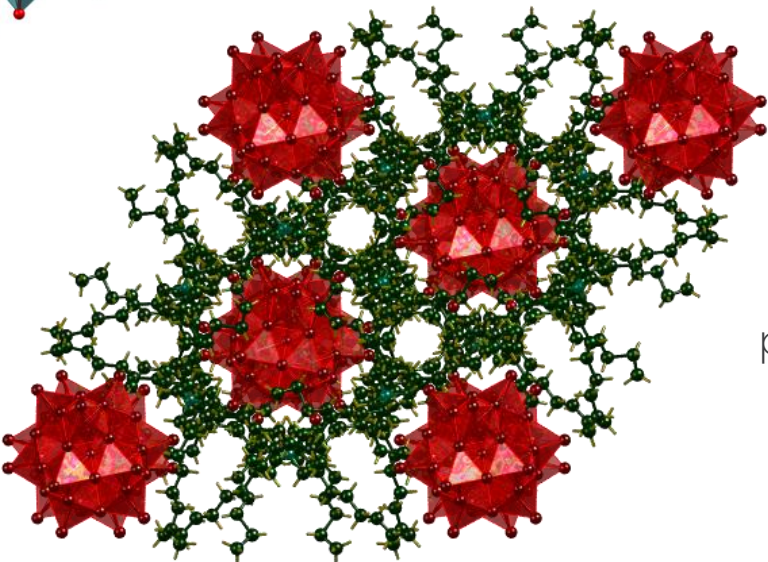
Display

Styles	Wireframe
Labels	Stick
Colours	Ball and stick
Show/Hide	Spacefill
More Information	Ellipsoid
Symmetry Elements...	Polyhedral
Voids...	Stick settings...
Display Options...	Ball and Stick settings...
Manage Styles...	Spacefill settings...
View along	Ellipsoid settings...
Dial box...	Polyhedral settings...
✓ Splash screen	Contact settings...
Toolbars	Measurement settings...
	Selected atoms



Colour: by Element

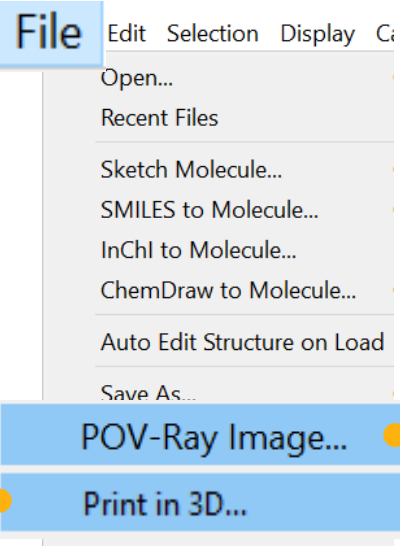
- by Element
- by Symmetry equivalence
- by Atomic displacement
- by Symmetry operation
- by Gasteiger charge
- by Partial charge
- by Element or Disorder



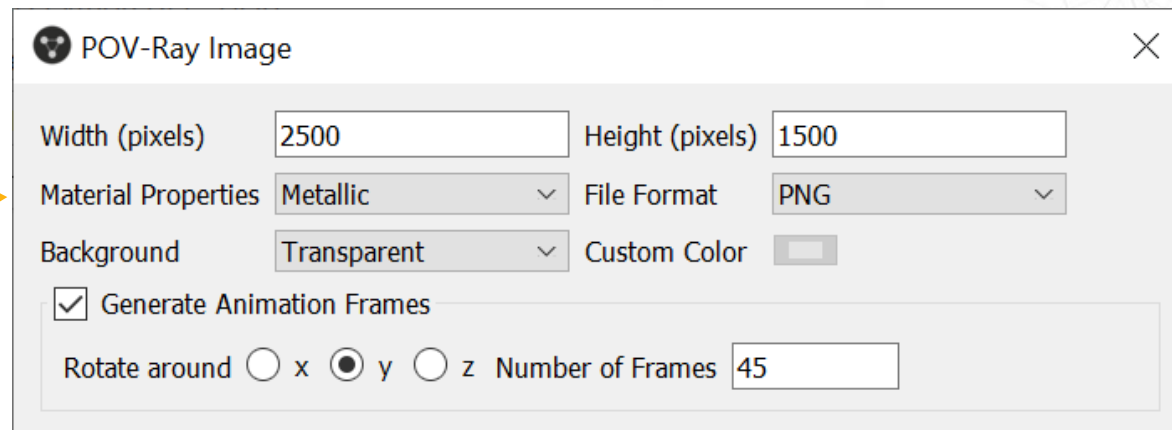
Watch the video on creating personalised styles



Features for effective visualization

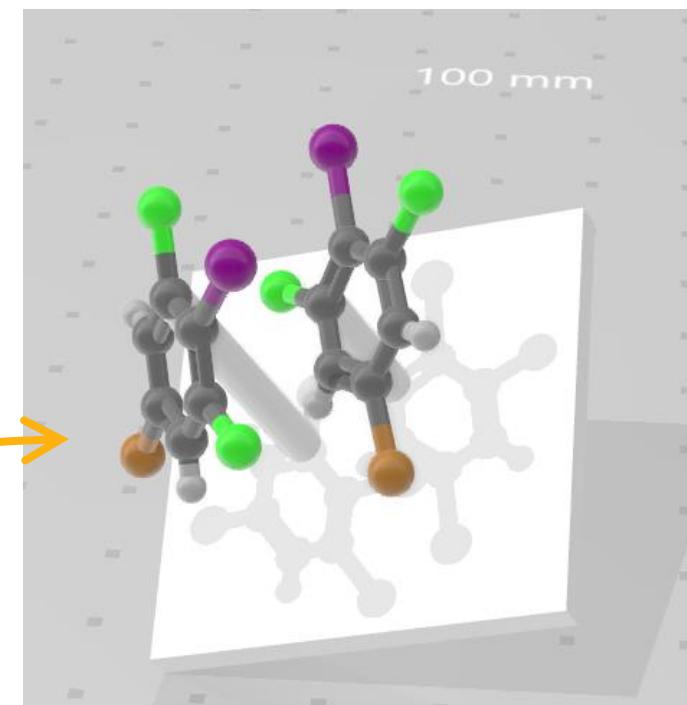
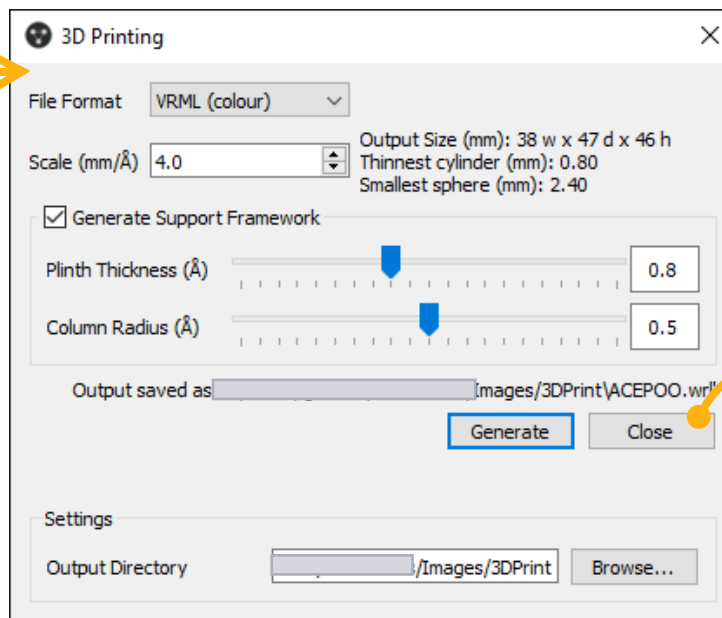
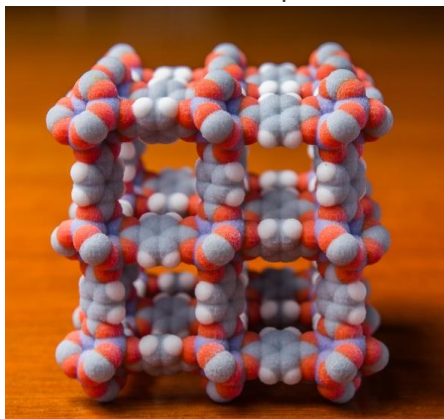


• Create high resolution images and frames for video or gifs

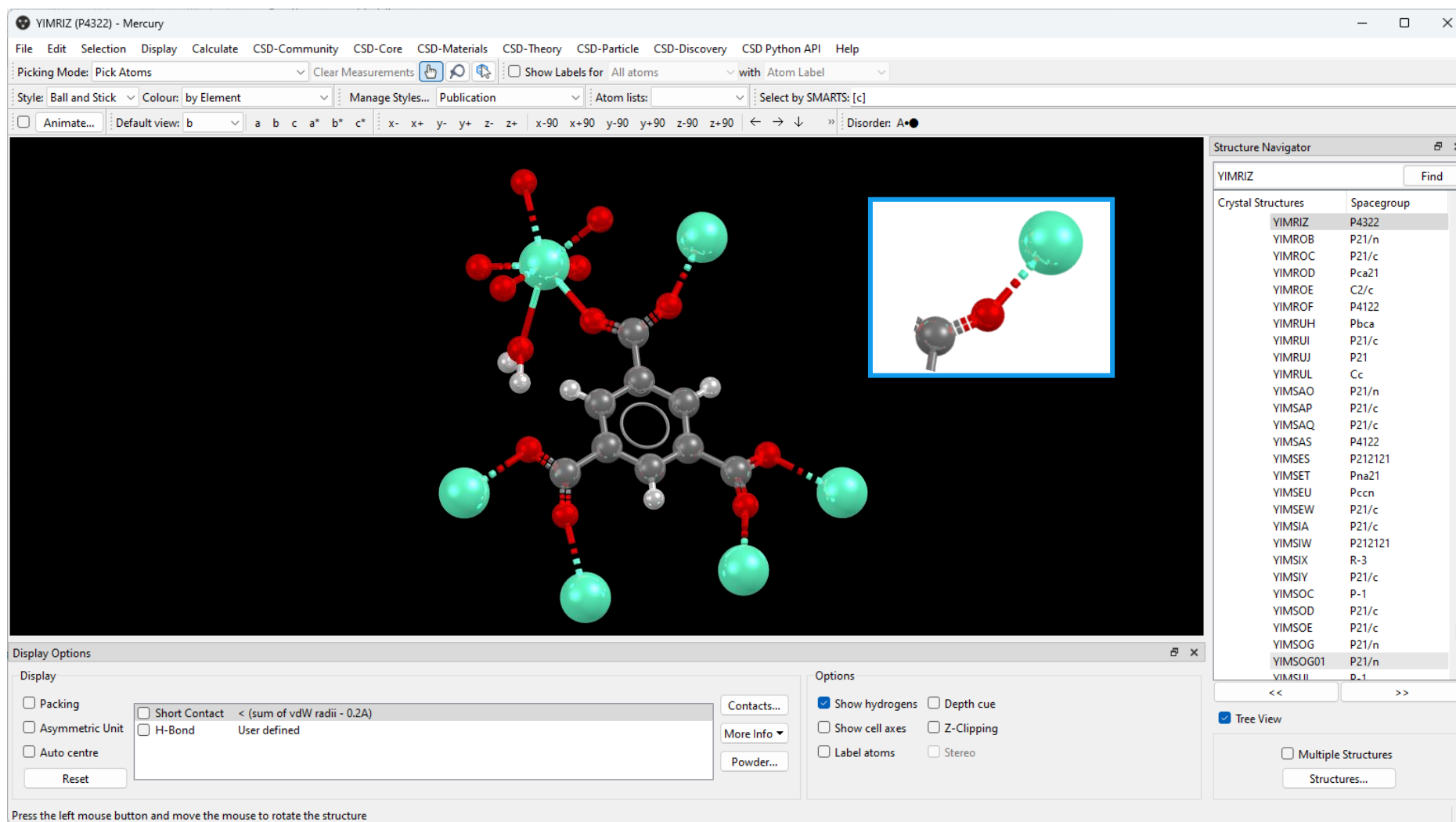


• Create files for 3D print

Example of 3D printed structure of CSD Refcode SAHYIK



Polymeric bond representations



In Mercury, polymeric bonds are drawn alternating long and short lines.

Polymer Expansion

Edit

Undo: Deselect All Ctrl+Z

Redo: Not Available Ctrl+Y

Copy Image to Clipboard Ctrl+C

Edit Structure...

Auto Edit Structure...

Normalise Hydrogens...

Polymer Expansion...

Transform Molecules...

Change Spacegroup Setting...

Invert Structure

Change Spacegroup to Subg...

Polymer Expansion

Selected atoms and bonds

Expand at selection

Expand symmetry related

Prune at selection

Expand by

Whole unit

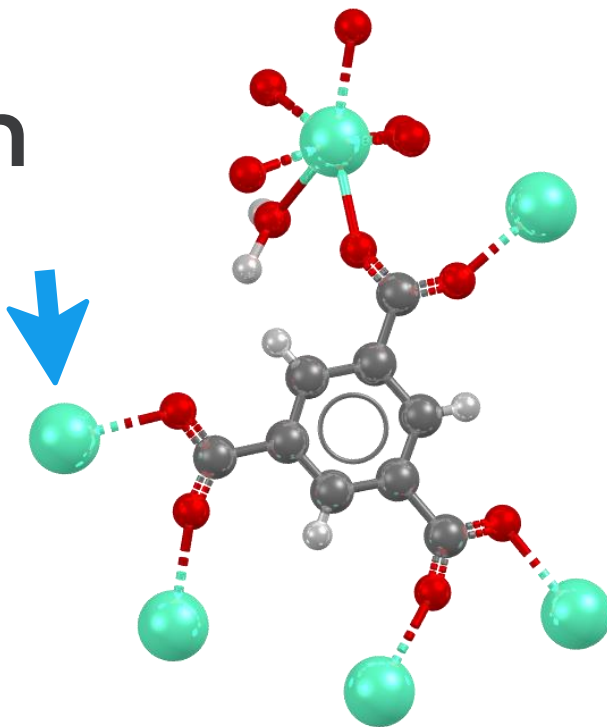
Sub unit

"Po" label on polymeric bonds

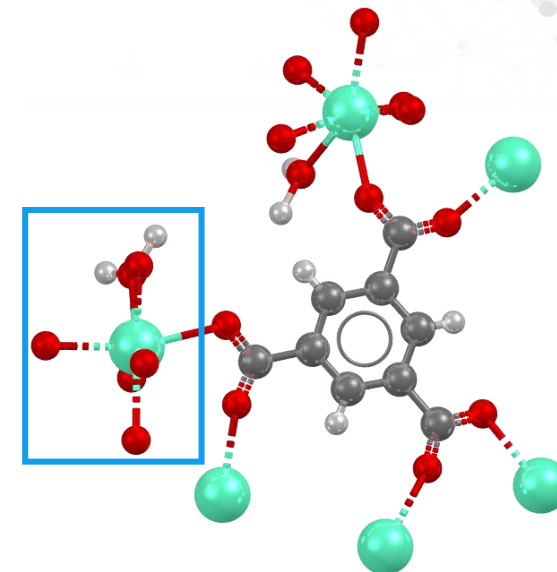
Expand All

Reset

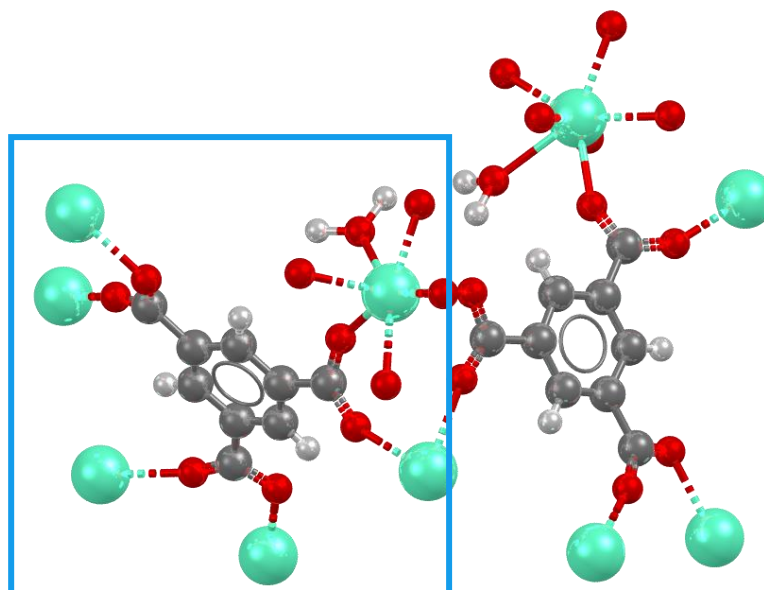
Close



By Sub unit
it will add atoms and bonds up to the next polymeric atom or bond in the structure.



By Whole unit
It will add an additional repeat of the initial crystal chemical unit to the structure



CCDC

Multiple Structures

The screenshot shows the Mercury software interface with two molecular structures displayed side-by-side. The structure on the left is YIMRIZ, colored blue, and the structure on the right is YODDOO, colored light green. The 'Multiple Structures' dialog box is open, showing a table of structures and their properties. The dialog box has a 'TOP TIP!' label pointing to the 'Local rotation centres' radio button. Another 'TOP TIP!' label points to the 'Move the structure that is nearest the mouse cursor' checkbox. The 'Colour' dropdown menu is open, showing a list of colors with 'Light Green' selected. The 'Multiple Structures' checkbox is also checked in the dialog box.

Structure	Visible	Active	Movable	Colour	Disorder
1 Delete YIMRIZ	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	by Element	A•
2 Delete YODDOO	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Blue	None

Use Multiple Structures for structure comparisons. Structures can be in different colours – helpful when overlaying structures.

Crystal Packing

The screenshot shows the Mercury software interface with the 'Packing and Slicing' dialog box open. The dialog has several sections:

- Packing:** Includes checkboxes for 'Show cell axes' and 'Label cell axes'. Below are input fields for 'Pack' with values for a, b, and c (each set to 0.0, 1.0, and +0.5). There are also buttons for '2x2x2' and '3x3x3' and a 'Reset' button.
- Include atoms:** A list of radio button options: '... that Fit', '... in molecules whose Centroids fit' (selected), '... in molecules where Any atom fits', '... in molecules where All atoms fit', and '... in molecules which occupy Unique supercell positions' (highlighted with an orange box and labeled 'NEW').
- Structure List:** A table listing various structures and their space groups.
- Options:** Checkboxes for 'Show hydrogens', 'Show cell axes', 'Label atoms', 'Depth cue', 'Z-Clipping', and 'Stereo'.

In the background, the main window shows a 3D model of a crystal structure with a unit cell box. A blue arrow points from the 'Packing/Slicing...' menu item to the dialog box. The 'Display Options' panel at the bottom left has 'Packing' checked.

Structure	Space Group
YODFAZ	C2/c
YODFAZ01	P21/c
YODFEC	P-1
YODFED	P21/c
YODFEE	P21/n
YODFEF	P212121
YODFEG	P-1
YODFIG	P-1
YODFIH	P21/c
YODFII	P2/c
YODFIJ	Pna21
YODFIK	P-1
YODFOM	P21/n
YODFON	P21/n
YODFOO	P21/n
YODFOR	P-1

Use Packing to compare larger structural units – helpful if polymer repeat unit is not identical.

Use Default view for (initial) alignment.

Structure Overlay

The screenshot shows the Mercury software interface with two crystal structures overlaid. A 'Structure Overlay' dialog box is open, displaying the following table:

	Atom1	Atom2	Distance	
1	Delete	Y5	Eu1	20.747
2	Delete	Y2	Eu5	20.585
3	Delete	C3	C12	20.574

The dialog also shows 'RMS: -' and a 'Close' button. The background shows the 'Structure Navigator' panel with a list of crystal structures and their space groups.

Crystal Structures	Spacegroup
YODFAZ	
YODDOO	P43
YODDUQ	P21/c
YODDUQ01	P21/c
YODDUR	Pca21
YODDUS	P-1
YODDUT	P-1
YODDUU	I2/c
YODFIK	P-1
YODFOM	P21/n
YODFON	P21/n
YODFOO	P21/n
YODFOP	P-1

Select pairs of atoms in the same structural environment. The more pairs you use, the more realistic the RMS value will be.

Structure Overlay

YODFAZ (C2/c) - Mercury

File Edit Selection Display Calculate CSD-Community CSD-Core CSD-Materials CSD-Theory CSD-Particle CSD-Discovery CSD Python API Help

Picking Mode: Pick Atoms Clear Measurements Show Labels for All atoms with Atom Label

Style: Ball and Stick Colour: by Element Manage Styles... Publication Atom lists: Select by SMARTS: [c]

Animate... Default view: b a b c a* b* c* x- x+ y- y+ z- z+ x-90 x+90 y-90 y+90 z-90 z+90 Disorder: A

Structure Overlay

Select pairs of atoms in any two crystal structures.

Overlay

	Atom1	Atom2	Distance
1 Delete	Y5	Eu1	0.092
2 Delete	Y2	Eu5	0.090
3 Delete	C3	C12	0.003

RMS: 0.0744

Close

Structure Navigator

YODFAZ Find

Crystal Structures	Spacegroup
YODDOO	P43
YODDUQ	P21/c
YODDUQ01	P21/c
YODDUR	Pca21
YODDUS	P-1
YODDUT	P-1
YODDUU	I2/c
YODDUU01	I2/c
YODFAA	P21/n
YODFAB	P2/a
YODFAC	Pccn
YODFAY	P-1
YODFAZ	C2/c
YODFAZ01	P21/c
YODFEC	P-1
YODFED	P21/c
YODFEE	P21/n
YODFEF	P212121
YODFEG	P-1
YODFIG	P-1
YODFIH	P21/c
YODFII	P2/c
YODFIJ	Pna21
YODFIK	P-1
YODFOM	P21/n
YODFON	P21/n
YODFOO	P21/n
YODFOQ	P-1

Display Options

Display

Packing

Asymmetric Unit

Auto centre

Reset

Short Contact < (sum of vdW radii - 0.2A)

H-Bond User defined

Contacts... More Info Powder...

Options

Show hydrogens Depth cue

Show cell axes Z-Clipping

Label atoms Stereo

Tree View

Multiple Structures

Structures...

Press the left mouse button and move the mouse to rotate the structure

Select pairs of atoms in the same structural environment. The more pairs you use, the more realistic the RMS value will be.

Exploring voids

Voids

Find any empty spaces (**voids**) in crystal unit cells that are big enough to hold a spherical "probe" of the given radius. Decrease the **Probe Radius** to find smaller spaces. Decrease the **Grid Spacing** to create smoother surfaces. To see voids in more than one unit cell, use the **Packing/Slicing** dialog to turn on packing and increase the ranges along a, b and c.

Show

Probe Radius: Å

Approx. Grid Spacing: Å

Calculate using the

Display Options

Outside Colour:

Inside Colour:

Results

Volume % of unit cell volume

Å³

YIMRIZ (P4322) - Mercury

File Edit Selection **Display** Calculate CSD-Community CSD-Cgre CSD-Materials CSD-Discovery CSD Python API Help

Picking Mode: La Styles Labels Colours Show/Hide More Information Symmetry Elements... **Voids...** Display Options... Manage Styles... View along Dial box... Splash screen Toolbars

Style: Capped Sticks Animate...

Clear Measurements Show Labels for All atoms with Atom Label

Manage Styles... Publication Atom selections:

a b c a* b* c* x- x+ y- y+ z- z+ x-90 x+90 y-90 y+90 z-90 z+90

Select by SMARTS:

YIMRIZ Find

Crystal Structures	Spacegroup
YIMRIZ	P4322
YIMROB	P21/n
YIMROC	P21/c
YIMROD	Pca21
YIMROE	C2/c
YIMROF	P4122
YIMRUH	Pbca
YIMRUI	P21/c
YIMRUJ	P21
YIMRUL	Cc
YIMSAO	P21/n
YIMSAP	P21/c
YIMSAQ	P21/c
YIMSAS	P4122
YIMSES	P212121
YIMSET	Pna21
YIMSEU	Pccn
YIMSEW	P21/c
YIMSJA	P21/c
YIMSIW	P212121
YIMSIX	R-3
YIMSIY	P21/c
YIMSOC	P-1
YIMSOD	P21/c
YIMSOE	P21/c
YIMSOG	P21/n
YIMSOG01	P21/n
YIMSLI	P-1

Display Options

Display Packing Asymmetric Unit Auto centre Short Contact < (sum of vdW radii - 0.2Å) H-Bond User defined

Options Show hydrogens Depth cue Show cell axes Z-Clipping Label atoms Stereo Tree View Multiple Structures

Press the left mouse button and move the mouse to rotate the structure

Pore Analyser

YODFAZ (C2/c) - Mercury

Calculate CSD-Community

- Centroids...
- Planes...
- Packing/Slicing...
- Contacts...
- Molecular Shell...
- Graph Sets...
- Powder Pattern...
- Pore Analyser...**
- Structure Overlay...
- Molecule Overlay...

Current Structure: YIMRIZ

Parameter	Result	Unit
1 System Volume	1506.774	Å ³
2 System Mass	1508.382	g/mol
3 System Density	1.662	g/cm ³
4 Total surface area	123.41	Å ²
5 Total surface area per volume	819.04	m ² /cm ³
6 Total surface area per mass	492.71	m ² /g
7 Network-accessible surface area	123.41	Å ²
8 Network-accessible surface area per volume	819.04	m ² /cm ³
9 Network-accessible surface area per mass	492.71	m ² /g
10 Total helium volume	653.385	Å ³
11 Total helium volume	0.261	cm ³ /g
12 Total geometric volume	761.534	Å ³

Structure Navigator

Structure	Spacegroup
YODDOO	P43
YODDUQ	P21/c
YODDUQ01	P21/c
YODDUR	Pca21
YODDUS	P-1
YODDUT	P-1
YODDUU	I2/c
YODDUU01	I2/c
YODFAA	P21/n
YODFAB	P2/a
YODFAC	Pccn
YODFAV	P-1
YODFAZ	C2/c
YODFAZ01	P21/c
YODFEC	P-1
YODFED	P21/c
YODFEE	P21/n

Materials informatics with **ForeBlazer v4.0** and the CSD MOF Database

Lev Sarkisov*, Rocio Bueno-Perez, Mythili Sutharson, and David Fairen-Jimenez

4363 16 98

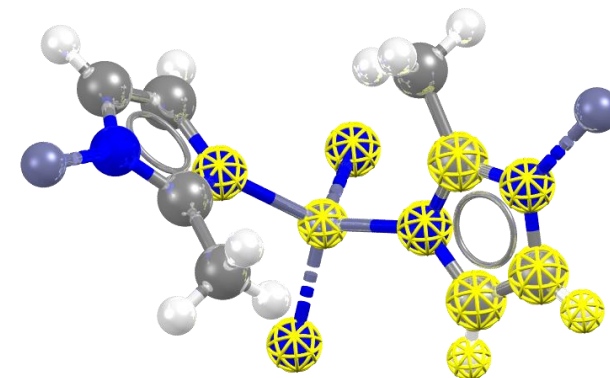
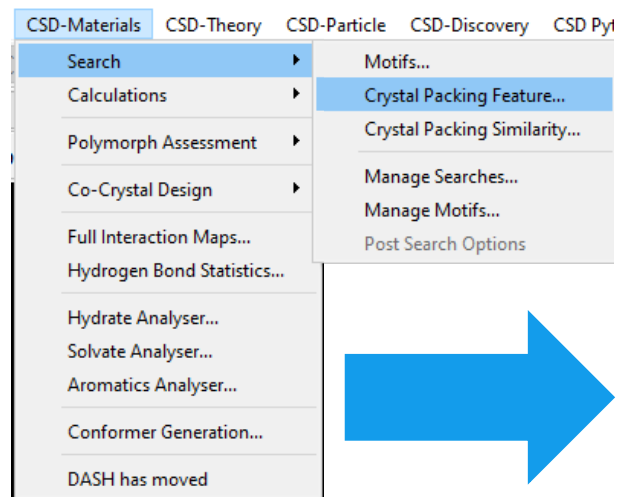
Abstract

The development of computational methods to explore crystalline materials has received significant attention in the last decades. Different codes have been reported to help researchers to evaluate and learn about the structure of materials and to understand and predict their properties. In this Methods article, we present an updated version of ForeBlazer, an open access, open source Fortran 90 code to calculate structural properties of porous materials. The article describes the properties calculated by the code, their physical meaning, and their relationship to the properties that can be measured experimentally. Here, we reflect on the methods in the code and discuss features of the most recent version. First, we demonstrate the capabilities of ForeBlazer on the prototypical metal-organic framework (MOF) materials, HKUST-1, IRMOF-1, and ZIF-8, and compare the results to those obtained with other codes, Zeo++ and RASPA. Second, we apply ForeBlazer to the recently assembled database of MOF materials—the CSD MOF subset—and compare properties such as the accessible surface area and pore volume from ForeBlazer and the two other codes, and reflect on the possible sources of the differences. Finally, we use ForeBlazer to illustrate how correlations between various structural characteristics can be mined using interactive, dynamic data visualization and how material informatics approaches—including principal component analysis and machine learning—can accelerate the discovery of new materials and new functionalities. The results of these calculations, along with the ForeBlazer code, documentation, and case studies, are available online from <https://github.com/Sarkisov-Group/ForeBlazer>. The data visualization tool is available at <https://github.com/aaal-analytics/mof-explorer>, and the principal component analysis is available at <https://github.com/aaal-analytics/pcv-explorer>.

Lev Sarkisov*, Rocio Bueno-Perez, Mythili Sutharson, and David Fairen-Jimenez, Chem. Mater. 2020, 32, 23, 9849–9867

Crystal Packing Feature Search

- Perform a substructure search.
- Investigate conformations of molecules or bonded fragments.
- Search for non-covalent interactions such as π - π or hydrogen bond interactions.
- Search for particular spatial arrangements of functional groups.
- Search for particular spatial arrangements of molecules.



← Packing Feature Search Wizard

Use this wizard to search for a crystal packing feature

Load a crystal structure in the visualizer and then **select atoms** to select the spatial arrangement of atoms you wish to search for.

Or load a previously defined feature

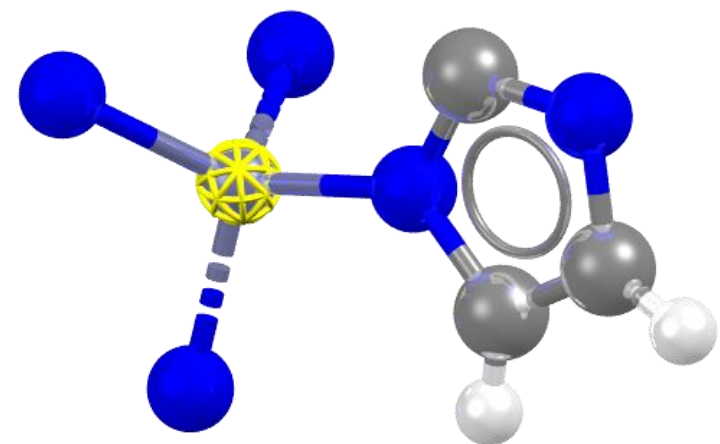
<select feature> ▾

You have selected 11 atoms of 1 molecule(s) from zif8.

Next

Cancel

Additional search functionality



← Packing Feature Search Wizard

Allow variable atom and bond types

Select the atoms and bonds you wish to vary and press 'Modify'. Or simply press 'Next'.

atoms bonds

atom	residue	element	hydroge	bonds
Zn1	1	Zn	0	4
N1	1	N	0	3
N1	1	N	0	1
C3	1	C	1	3
C1	1	C	0	3
H3	1	H		1
N1	1	N	0	3
N1	1	N	0	3
N1	1	N	0	1
H3	1	H		1
C3	1	C	1	3

Search Options

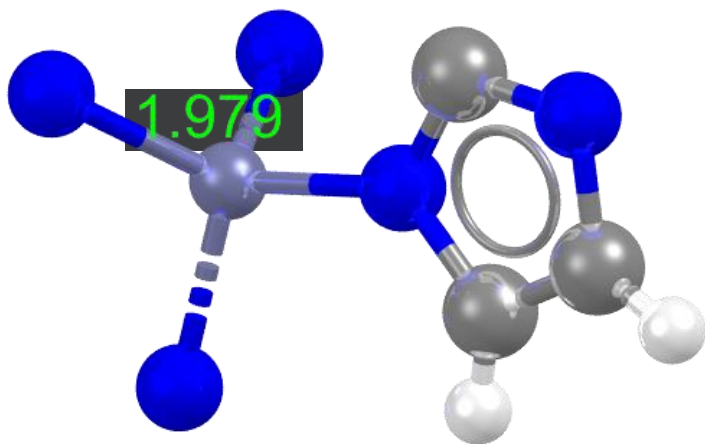
- Modify
- Element
- Hydrogens
- Charge
- Number of bonded atoms
- Cyclicity

Charge
 Cyclicity

Next

Cancel

Use for structure analysis



← Packing Feature Search Wizard

Select Parameters

Select atoms in the visualiser to select **distance**, **angle** or **torsion** parameters. Or simply press 'Next'.

Current Selection:

Add >

Parameter List

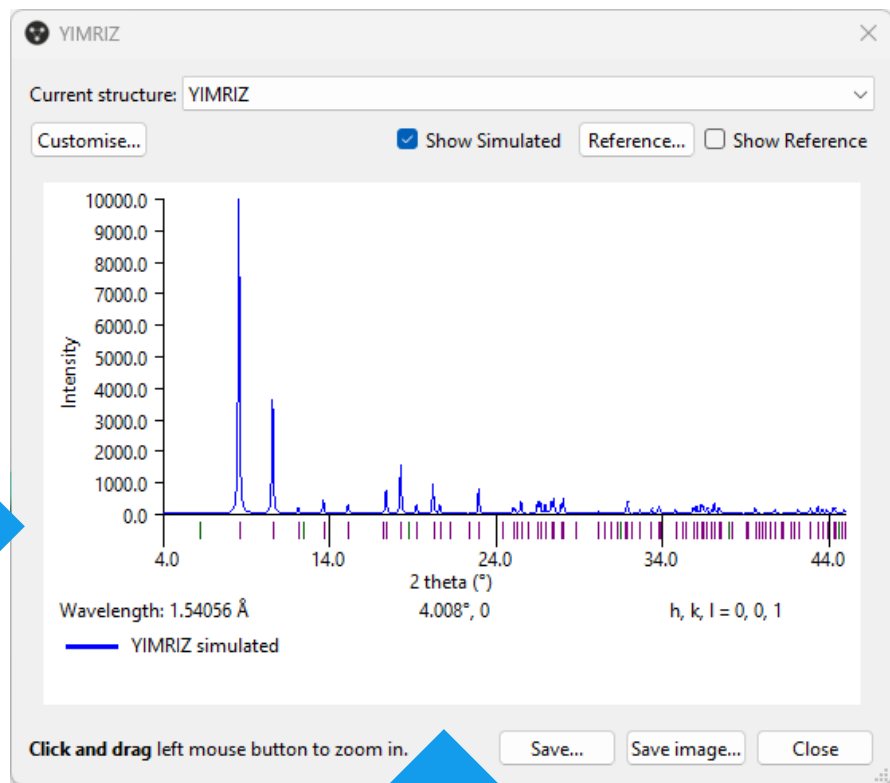
Zn1_N1	Delete
	Rename

Next Cancel

Calculate powder pattern

Calculate

- Centroids...
- Planes...
- Packing/Slicing...
- Contacts...
- Molecular Shell...
- Graph Sets...
- Powder Pattern...**
- Structure Overlay...
- Molecule Overlay...



How are the patterns calculated?

- Fundamental calculation
- No one algorithm exists
- Series of steps need to be taken based on the theories of how X-rays interact with 3D lattices.

See the book "Fundamentals of Crystallography" by C. Giacovazzo, et al. for an overview.

Display Options

Display

Packing

Asymmetric Unit

Auto centre

Reset

Short ... < (sum of vdW radii)

H-Bon... Default definition

Options

Show hydrogens Depth cue

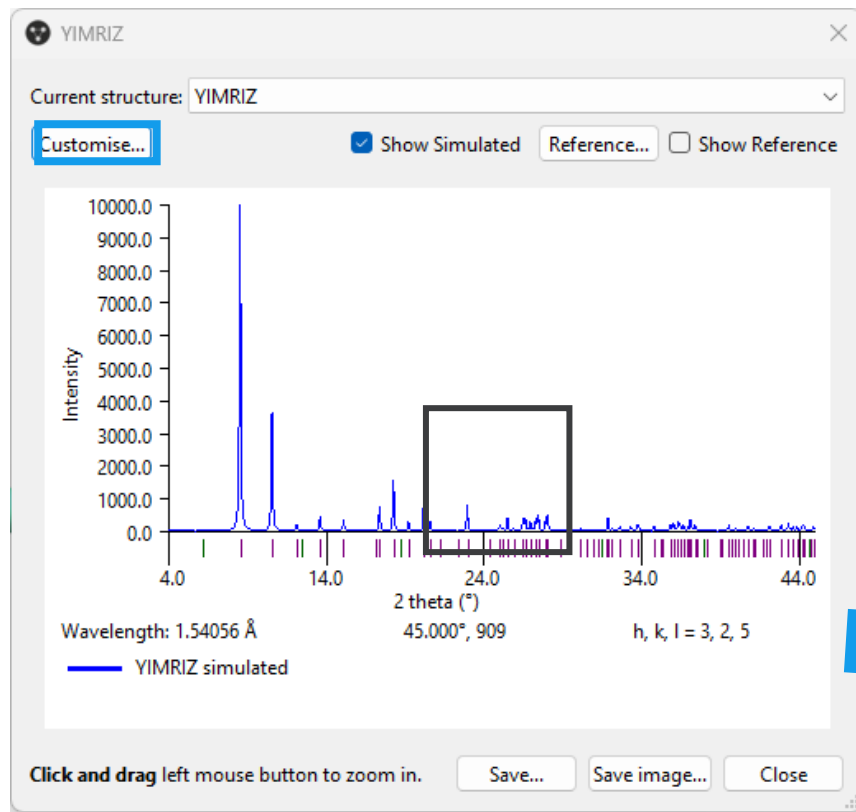
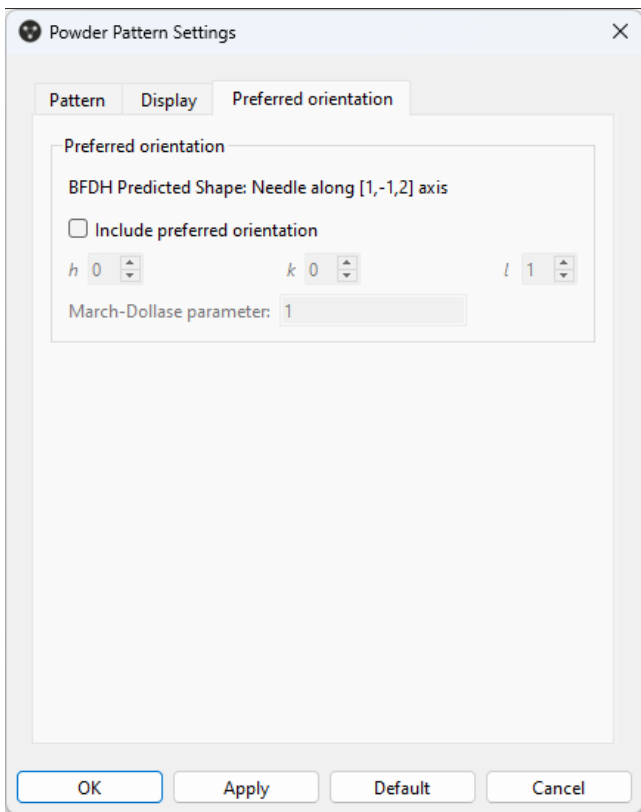
Show cell axes Z-Clipping

Label atoms Stereo

Con...
More Info
Powder..

Calculate powder pattern

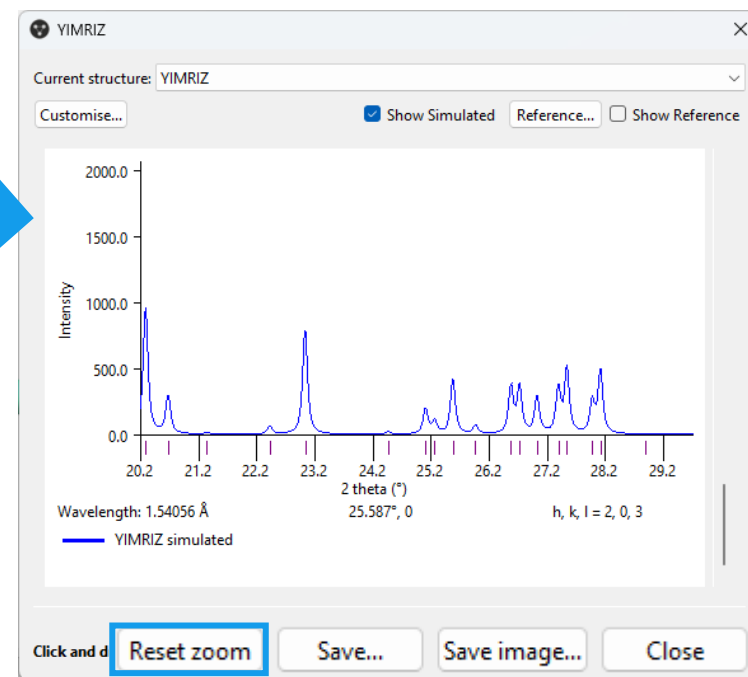
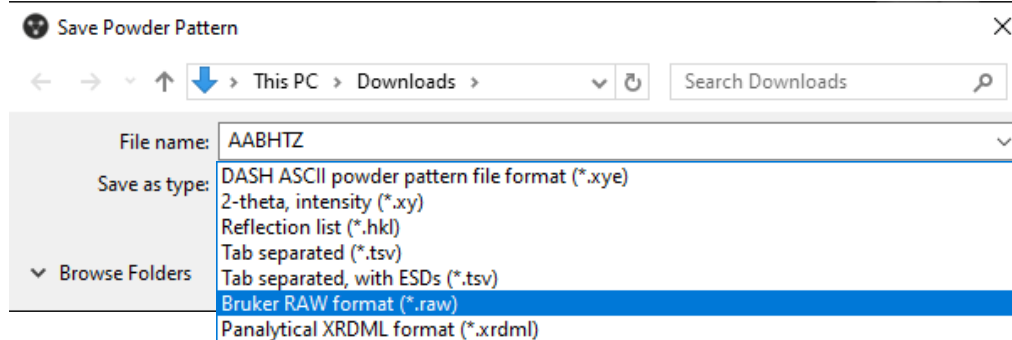
Customise...



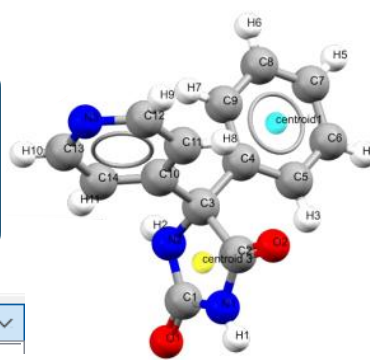
Save image...

bmp...
jpeg...
jpg...
pbm...
pgm...
png...
ppm...
tif...
tiff...
xbm...
xpm...

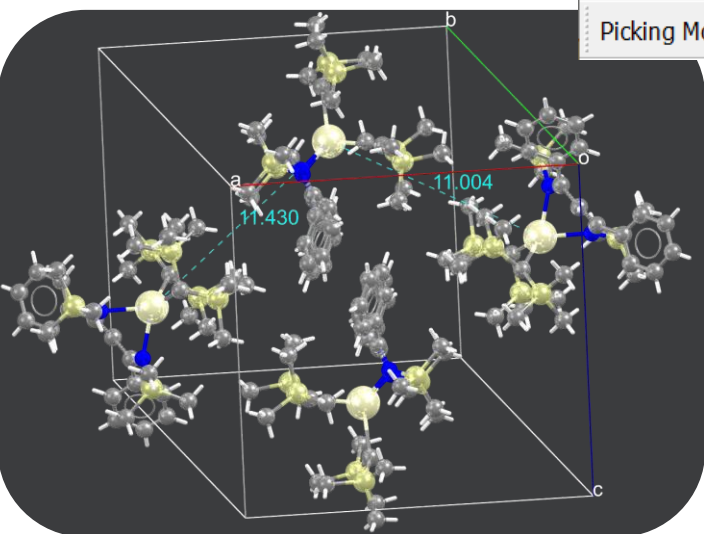
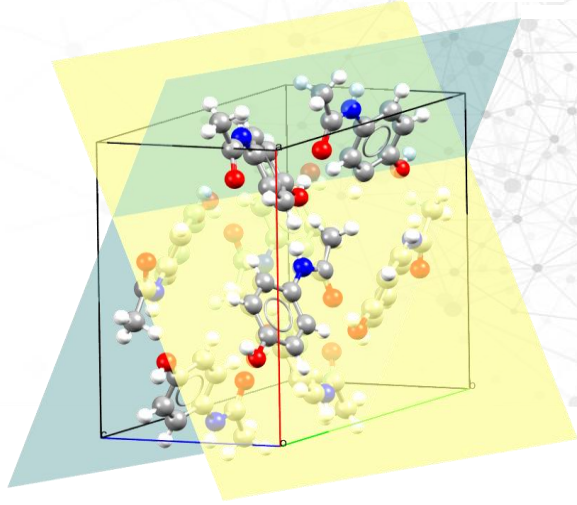
Save...



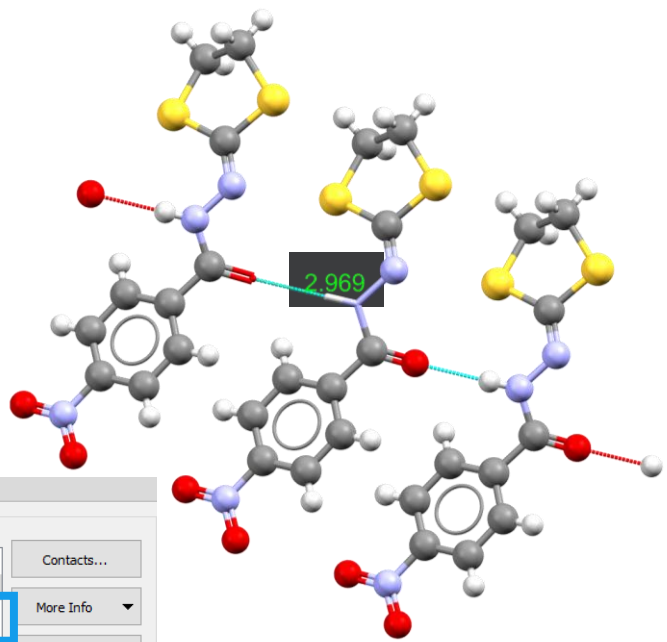
Lots of display and analysis options!



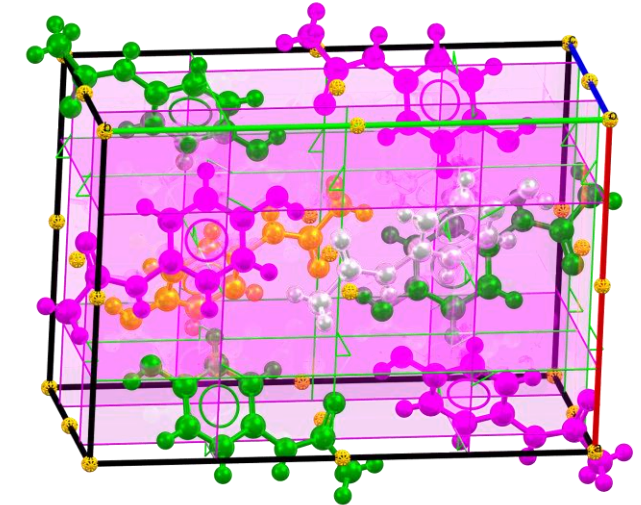
- ### Calculate
- Centroids...
 - Planes...
 - Packing/Slicing...
 - Contacts...
 - Molecular Shell...
 - Graph Sets...
 - Powder Pattern...
 - Pore Analyser...
 - Structure Overlay...
 - Molecule Overlay...



- Picking Mode: Pick Atoms
- Pick Atoms
 - Lasso Atoms
 - Expand Contacts
 - Toggle Labels
 - Move Labels
 - Measure Distances
 - Measure Angles
 - Measure Torsions
 - Reveal Symmetry-Generated Molecules



- ### Display
- Styles
 - Labels
 - Colours
 - Show/Hide
 - More Information
 - Symmetry Elements...
 - Voids...
 - Display Options...
 - Manage Styles...
 - View along
 - Dial box...
 - Splash screen
 - Toolbars



Display Options

Display

- Packing
- Asymmetric Unit
- Auto centre

Short Contact < (sum of vdW radii)

H-Bond Default definition

Reset

Contacts...

More Info

Powder...



Read the publication on symmetry tools

Data fields

1

2

3

Structure Information...
Chemical Diagram...
Atom List...
Bond List...
Contacts List...
Centroids List...
Planes List...
Symmetry Operators List...
Distances List...
Angles List...
Torsions List...
All Angles List...
All Torsions List...
More Info ▾

YODDOO

Current structure: YODDOO

Customise...

Structure
Diagram
Atoms
Bonds
Contacts
Centroids
Planes
Symmetry
Distances
Angles
Torsions
All Angles
All Torsions

Space Group	P 4 ₃ (78)
Cell Lengths	a 10.240(2) b 10.240(2) c 10.240(2)
Cell Angles	α 90 β 90 γ 90
Cell Volume	1514.67
Density (CCDC)	1.45612
Density (author)	1.3771
Z, Z'	Z : 4 Z' : 1
R-Factor (%)	4.62
Disorder	The MASK/OLEX2 program has been used to model some disorder.
Polymorph	

Close

Customise

Available Items (Right-click for options)

- 2nd Singlet State Energy (kJ/mol)
- 1st Triplet State Energy (kJ/mol)
- 2nd Triplet State Energy (kJ/mol)
- Reorganization Energy (kJ/mol)
- Transfer Integral
- HOMO-LUMO Gap (kJ/mol)
- 1st Singlet State Oscillator Stre...
- 2nd Singlet State Oscillator Stre...
- Calculated
 - Total geometric volume (Ang^3)
 - Pore limiting diameter (Ang)
 - Number of percolated dimensions

Add >>

<< Remove

Selected Items (Right-click for options)

- Bioactivity
- Remarks
- Habit
- Pressure
- Conformer
- SMILES
- InChI
- Temperature (K)
- Total surface area (Ang^2)
- Maximum pore diameter (Ang)

Up Down

4

YODDOO

Current structure: YODDOO

Customise...

Structure
Diagram
Atoms
Bonds
Contacts
Centroids
Planes
Symmetry
Distances
Angles
Torsions
All Angles
All Torsions

Reduced Cell Volume	1514.67
Bioactivity	
Remarks	
Habit	plate
Pressure	
Conformer	
SMILES	
InChI	
Temperature (K)	100
Total surface area (Ang^2)	131.844
Maximum pore diameter (Ang)	5.4096

Close

Data fields in the CSD Python API



The new properties can also be accessed using the [CSD Python API](#) from the Entry Module.

Calculated Properties

```
class ccdc.entry.CrystalCalculatedProperties(_properties=None, _entry=None) [source]
```

A container for different types of **calculated** properties of a database entry.

Currently `ccdc.descriptors.CrystalDescriptors.PoreAnalyser` is the only type implemented.

property **pore_analyser**: *PoreAnalyser* | *None*

Returns a `ccdc.descriptors.CrystalDescriptors.PoreAnalyser` with stored **calculated** properties for the entry.

The pore analyser properties stored are:

- `ccdc.descriptors.CrystalDescriptors.PoreAnalyser.total_surface_area`
- `ccdc.descriptors.CrystalDescriptors.PoreAnalyser.total_geometric_volume`
- `ccdc.descriptors.CrystalDescriptors.PoreAnalyser.pore_limiting_diameter`
- `ccdc.descriptors.CrystalDescriptors.PoreAnalyser.max_pore_diameter`
- `ccdc.descriptors.CrystalDescriptors.PoreAnalyser.num_percolated_dimensions`

Other properties of the pore analyser are not stored and will be **calculated** on demand.

property **refinement_goodness_of_fit**

Returns the refinement **goodness** of **fit**. Describes how well the structural model **fits** the experimental data.

```
>>> from ccdc.io import EntryReader
>>> csd_reader = EntryReader('CSD')
>>> arutue = csd_reader.entry('ARUTUE')
>>> arutue.refinement_goodness_of_fit
1.085
```

property **refinement_max_shift**

Returns the refinement max shift. Describes the largest ratio of the final least-squares parameter shift to the final standard uncertainty.

```
>>> from ccdc.io import EntryReader
>>> csd_reader = EntryReader('CSD')
>>> arutue = csd_reader.entry('ARUTUE')
>>> arutue.refinement_max_shift
0.001
```

property **refinement_number_of_constraints**

Returns the refinement number of constraints. Describes the number of constrained (non-refined or dependent) parameters in the least-squares process. If a model has been highly constrained users may wish to ignore this structure. Similar to No. of restraints.

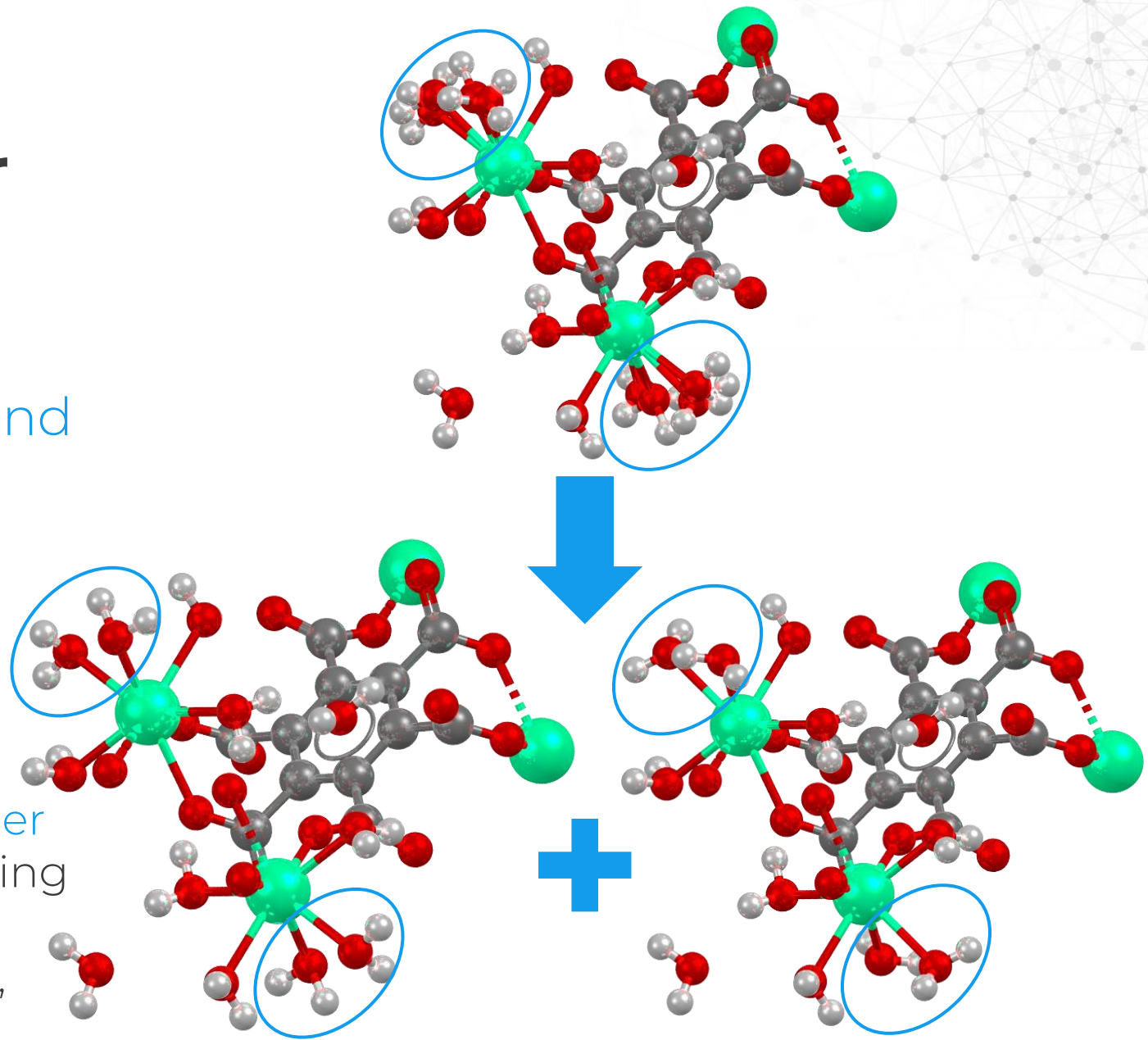
```
>>> from ccdc.io import EntryReader
>>> csd_reader = EntryReader('CSD')
>>> arutue = csd_reader.entry('ARUTUE')
>>> arutue.refinement_number_of_constraints
0
```

(Entry API Module)

https://downloads.ccdc.cam.ac.uk/documentation/API/modules/entry_api.html

Visualizing disorder

- Functionality available when you load a CIF into Mercury ^{NEW} and for structures in the CSD:
 - Visualise the different disorder models.
 - Visualise the contacts for each disorder model.
 - Works in combination with other functionality, such as Edit, viewing and selecting hydrogen bonds, displaying Voids, Pore Analyser, Mogul, CSD-Materials & CSD-Particle tools.



CCDC

Visualizing disorder

Note: you can have more disordered groups and more than two options each.

Disorder: A●● B●● C●● D●● E●● F●● All

Check CSD Entry JAZPOT!

Improved colouring and labelling options

Toggle the disorder options

Disorder: A●● All

Disorder: A●● All

by Element or Disorder
by Element
by Symmetry equivalence
by Gasteiger charge
by Element or Disorder

Show Labels for All atoms with Disorder

Stereochemistry
Occupancy
ADP type
Disorder

File Edit Selection Display Calculate CSD-Community CSD-Core CSD-Materials CSD-Theory CSD-Particle CSD-Discovery CSD Python API Help

Open... Ctrl+O

Recent Files

If cif, load from File > Open, then apply bond types via Edit > Auto-Edit

Print in 3D...

Exit Ctrl+Q

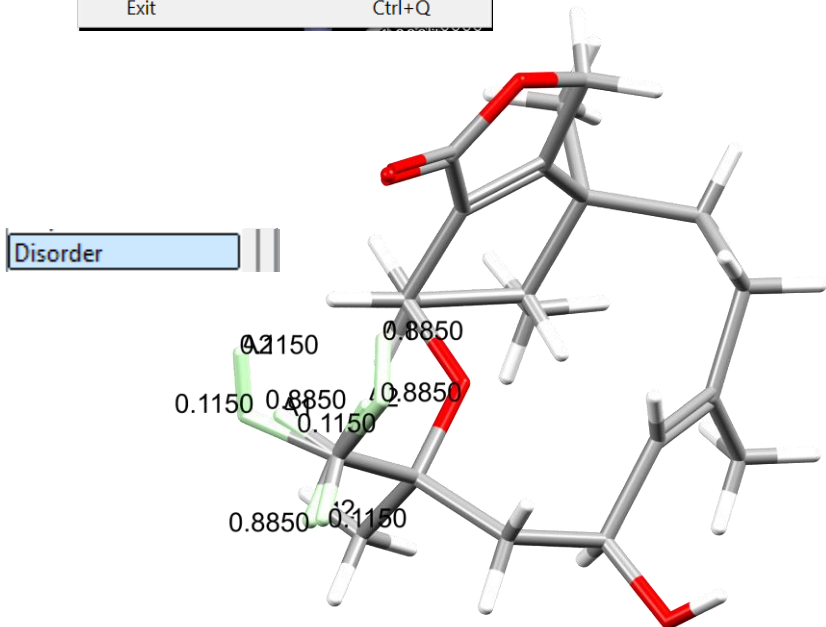
Clear Measurements

Manage Styles... Work

Atom lists:

Select by SMA

b* c* x- x+ y- y+ z- z+ x-90 x+90 y-90 y+90 z-90 z+90

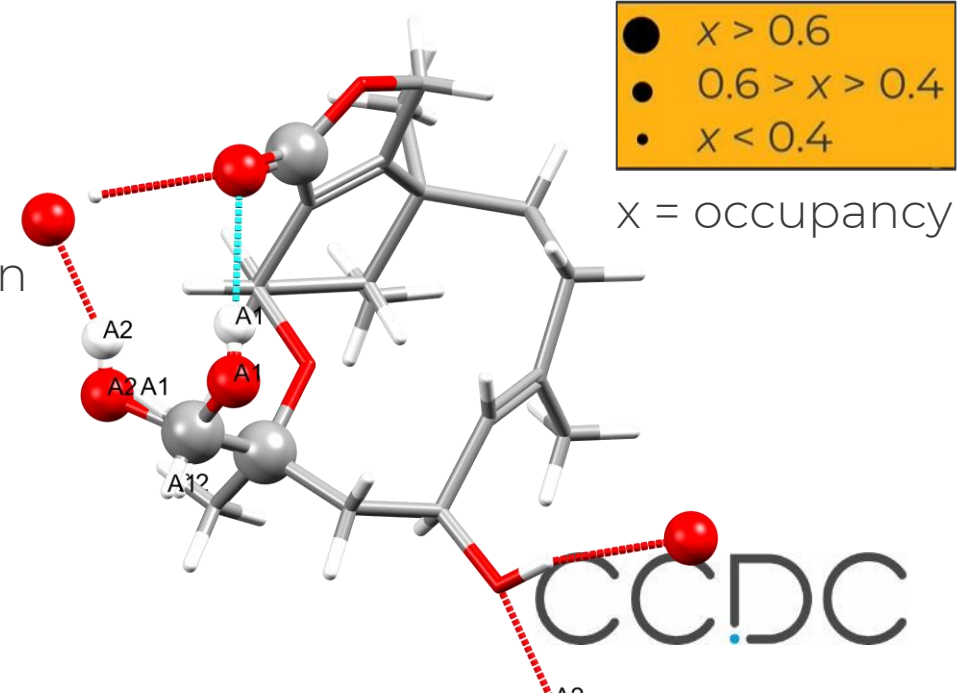


Short Contact (Sum of vdW radii +)

H-Bond User defined

Example of combination with hydrogen bonds

Disorder: A●● All

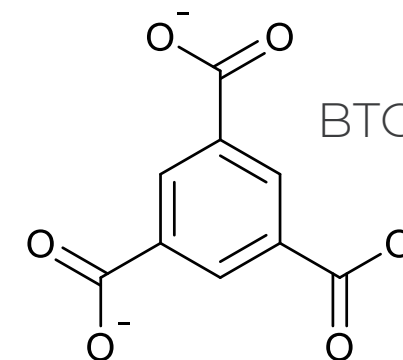


Demo of Mercury

Search and analysis of polymeric structures in Mercury

We will:

- Use Mercury to visualise the polymeric frameworks of LnBTC (Ln = lanthanoid, Y) compounds
- Compare structures with a Structure Overlay
- Calculate Pore properties
- Simulate and compare PXRD patterns



We are recording today's session and will make the recording available to you in the next few days



Try One

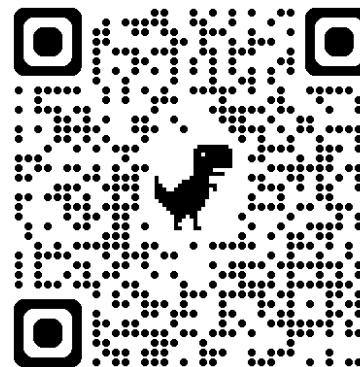
It's your turn!

- Try **one example** from the handout
- Your tutors are on hand to help you!
- To ask questions during this time **type a message in the chat box**
- **If you finish early**, try the other example or try analyse your structures

<https://info.ccdc.cam.ac.uk/2025-autumn-virtual-workshops>



link to webpage



Advanced Structural Visualization and Analysis of Porous Materials Using Mercury

Tuesday, 7th October

13:30-14:15 (BST)



Analysing Porous Materials Using Mercury

Developed using
2025.2 CSD Release
(CSD 6.00 + 1 data update)



CCDC
advancing structural science

Table of Contents

- Introduction 2
- Learning Outcomes 2
- Pre-required Skills 2
- Materials 2
- Example 1. Comparing Coordination Polymers in Mercury 3
 - Part 1: Exploring Coordination Geometry 3
 - Part 2: Structure Comparison with the Structure Overlay tool 6
 - Conclusion 8
- Example 2. Examining Porosity in a Metal-Organic Framework 9
 - Conclusion 13
- Extension Exercise: Batch Calculation of Pore Properties using the CSD Python API 14
 - Conclusion 14
- Summary 14
- Next Steps 14
- Glossary 14
- Basics of Mercury 14

link to handout



Functionality in the CSD Python API



CSD Python API 3.5.0 documentation » API documentation » Descriptors API



Descriptors API

Introduction

The `ccdc.descriptors` module contains classes for calculating descriptors.

The main classes in the `ccdc.descriptors` module are:

- `ccdc.descriptors.MolecularDescriptors`.
- `ccdc.descriptors.GeometricDescriptors`.
- `ccdc.descriptors.CrystalDescriptors.PowderPattern`.
- `ccdc.descriptors.CrystalDescriptors.Morphology`.
- `ccdc.descriptors.CrystalDescriptors.GraphSetSearch`.
- `ccdc.descriptors.CrystalDescriptors.HBondCoordination`.
- `ccdc.descriptors.CrystalDescriptors.HBondPropensities`.
- `ccdc.descriptors.StatisticalDescriptors`.

class `PoreAnalyser`(*crystal*, *settings=None*)

Calculates **Pore** Analysis. *crystal* is `ccdc.crystal.Crystal`

class `Flags`

Flags for validity of cached variables

property `calculator_is_valid`
grid spacing (A)

class `Settings`

Settings for `PoreAnalyser`

property `cutoff_distance`
Cut-off distance (A)

property `grid_spacing`
grid spacing (A)

property `he_probe_epsilon`
UFF L-J epsilon/k for He probe (K)

property `he_probe_sigma`
UFF L-J sigma for He probe (A)

property `n_probe_sigma`
UFF L-J sigma for N probe (A)

property `samples_per_atom`
Sample size for surface area calculation

Table of Contents

Descriptors API

- Introduction
- API
 - MolecularDescriptors
 - GeometricDescriptors
 - CrystalDescriptors
 - StatisticalDescriptors

Previous topic

Interaction API

Next topic

Morphology API

Quick search

Hide Search Matches

ation » API documentation » Crystal API

Crystal API

Introduction

The main class of the `ccdc.crystal` module is `ccdc.crystal.Crystal`.

`ccdc.crystal.Crystal` contains attributes and functions that relate to crystallography. An ex graphic attribute is the `ccdc.crystal.Crystal.cell_volume`.

```
>>> from ccdc.io import CrystalReader
>>> csd_crystal_reader = CrystalReader('CSD')
>>> first_csd_crystal = csd_crystal_reader[0]
>>> round(first_csd_crystal.cell_volume, 3)
769.978
```

void_volume(*probe_radius=1.2*, *grid_spacing=0.7*, *mode='contact'*)

Determine the **void** volume of the crystal.

```
>>> from ccdc.io import EntryReader
>>> entry_reader = EntryReader('CSD')
>>> abawop_crystal = entry_reader.crystal('ABAWOP')
>>> round(abawop_crystal.void_volume(), 2)
13.99
```

- Parameters:**
- **probe_radius** – float, size of the probe
 - **grid_spacing** – float, fineness of the grid on which the calculation is performed
 - **mode** – either 'accessible' or 'contact' according to whether the center of the probe must be inside the whole probe must be accommodated.

Returns: **void** volume as a percentage of the unit cell volume

Polymer Expansion

Polymeric crystals may be expanded, as in Mercury, with the method `ccdc.crystal.Crystal.polymer_expansion()`. For example:

```
>>> crystal = csd_reader.crystal('ABALOF')
>>> print(len(crystal.molecule.atoms))
36
>>> mol = crystal.polymer_expansion()
>>> print(len(mol.atoms))
100
```

There is an optional repetitions argument to `ccdc.crystal.Crystal.polymer_expansion()` to control the number of repetitions performed:

```
>>> mol = crystal.polymer_expansion(repetitions=5)
>>> print(len(mol.atoms))
356
```

There is another keyword argument to `ccdc.crystal.Crystal.polymer_expansion()`, `atoms`, to control over the expansion is required. The atoms provided will be matched by the crystal's **polymeric** bonds, so the repetitions argument can still be honoured.

```
>>> original_mol = crystal.molecule
>>> atom_to_expand = original_mol.atom('I4C')
>>> mol = crystal.polymer_expansion(atoms=[atom_to_expand])
>>> print(len(mol.atoms))
68
>>> mol = crystal.polymer_expansion(atoms=[atom_to_expand], repetitions=5)
>>> print(len(mol.atoms))
196
>>> print(len([a for a in mol.atoms if a.label == 'Cu1A']))
0
>>> print(len([a for a in mol.atoms if a.label == 'Cu3A']))
0
```

CSD Python API 3.5.0 documentation » Search

Search

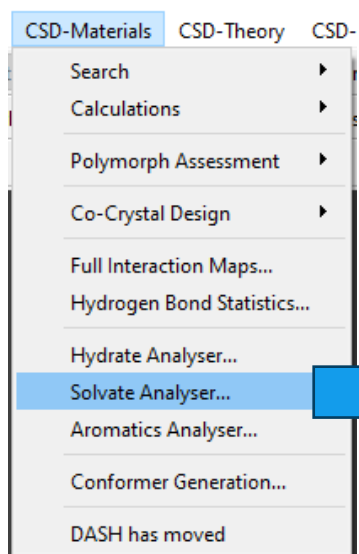
Searching for multiple words only shows matches that contain all words.

Find more functionality using the search bar!

<https://downloads.ccdc.cam.ac.uk/documentation/API/search.html?q=>

Solvate Volume

Solvate Analyser enables to visualize the volume occupied by inclusion molecules such as solvates



Solvate Analyser

Solvent Selection and Space Calculation Solvent H-Bonding Structure Summary

Add Solvent From Selected Remove Solvent Calculate Space

	1	2	3
Solvent	1	2	3
Formula	H2 O1	C2 H3 N1	C10 H8 N2
Volume (%)	2.9	3.7	6.0
Volume (Å ³)	54.31	69.35	113.97
Show Space	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Show Solvent	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Select Solvent	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Inside Colour			
Inside Opacity	<input type="range"/> 1	<input type="range"/> 1	<input type="range"/> 1
Outside Colour			
Outside Opacity	<input type="range"/> 1	<input type="range"/> 1	<input type="range"/> 1

Settings

Probe Radius: 1 Å

Approx. Grid Spacing: 0,3 Å

Calculate using the Solvent Accessible Surface

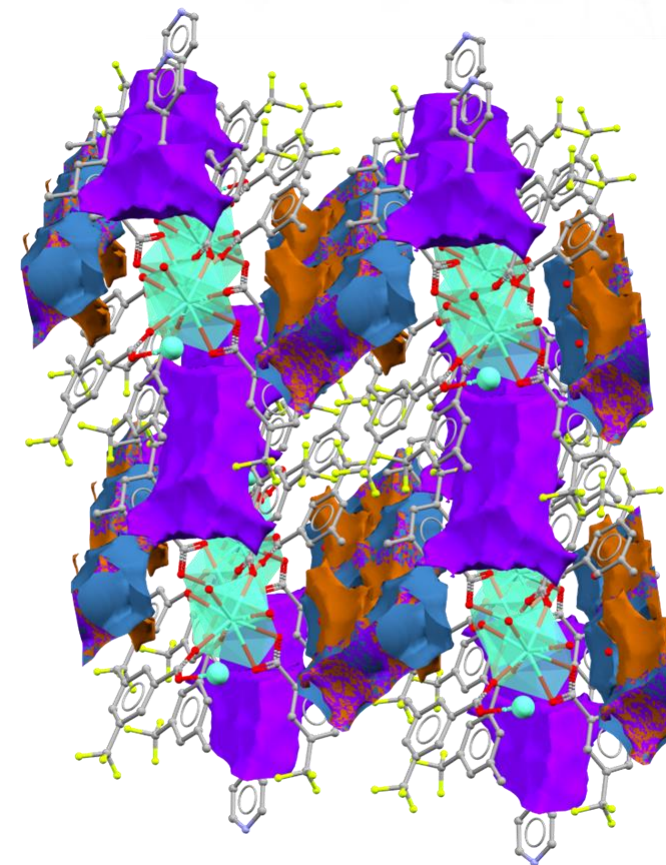
Results

Volume 12.6 % of unit cell volume

Volume 237.62 Å³

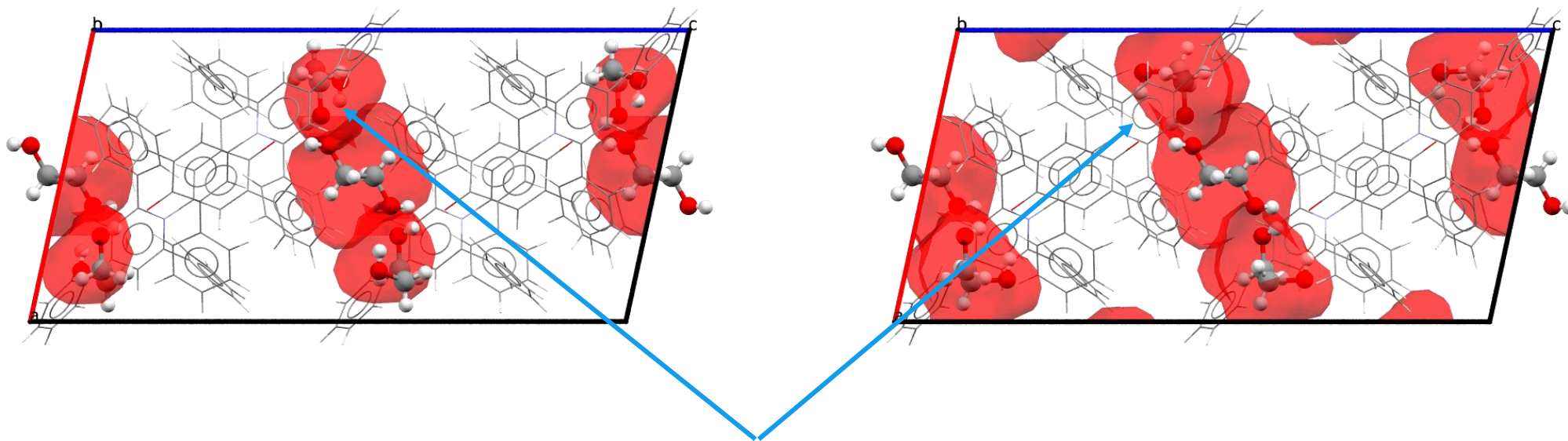
Defaults

Close



Disorder and Solvate Analyser

- Solvate Analyser works with disorder producing different results based on the disorder group selected



Space calculated with different disorder groups active.



On-demand
training
module



Disorder and Mogul

Mogul provides precise information on preferred molecular geometries.

- Enables you to **validate** the chemistry of your structure against the experimental data in **the CSD**

To see the results for different disorder options:

- Toggle the disorder button
- Then use Mogul Geometry Check as usual
- Repeat for the other options



CSD-Core CSD-Materials CSD-Disc

- Launch WebCSD
- ConQuest Hit Highlighting...
- Launch ConQuest Data Analysis Module...
- Mogul Geometry Check...**
- Launch Mogul Mogul Settings...
- IsoStar Interaction Check...
- Launch IsoStar IsoStar Settings...
- Select Databases...

Mogul Search Settings

Fragment Types

Bond Length Valence Angle Torsion Angle Ring

Search Filter Options

Available filters

R-factor <= 5.0%

Exclude Solvents

Heaviest Element U

Exclude Organometallics

Exclude Powder structures

Apply filters

Search Mode

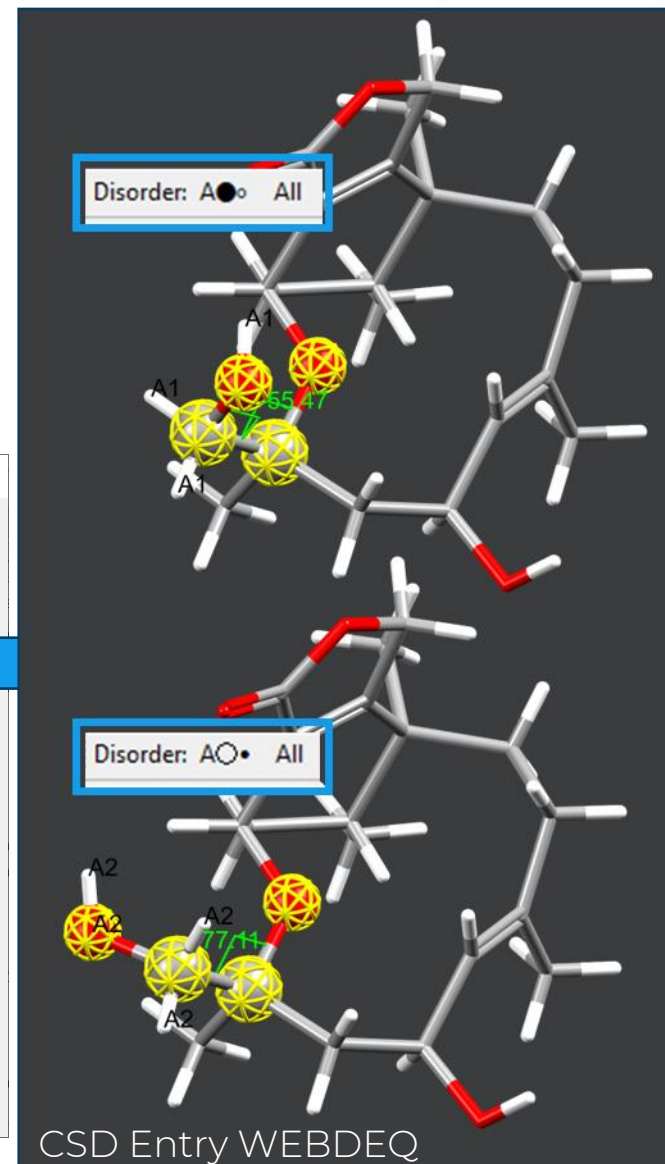
Only find fragments that match exactly

Find similar fragments if number of exact matches is less than

Bonds 15 Angles 15 Torsions 40 Rings 15

Customise fragment classification ...

Help Search Close



Mogul Results Viewer

Show / hide: Columns

Help Double click to view

Type	Molecule	Fragment
bond		
WEBDEQ		
	O3 C4	
	O4 C3	
	C3 C4	
angle		
WEBDEQ		
	O3 C4 C3	
	O4 C3 C4	
torsion		
WEBDEQ		
	O3 C4 C3 O	

Mogul Results Viewer

Show / hide: Columns

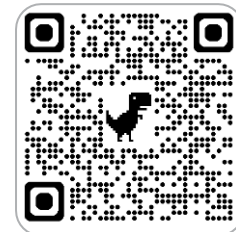
Help Double click to view

Type	Molecule	Fragment
bond		
WEBDEQ		
	O3 C4	
	C3 C4	
	O4A C3	
angle		
WEBDEQ		
	O3 C4 C3	
	O4A C3 C4	
torsion		
WEBDEQ		
	O3 C4 C3 O4	

Disorder and Mogul

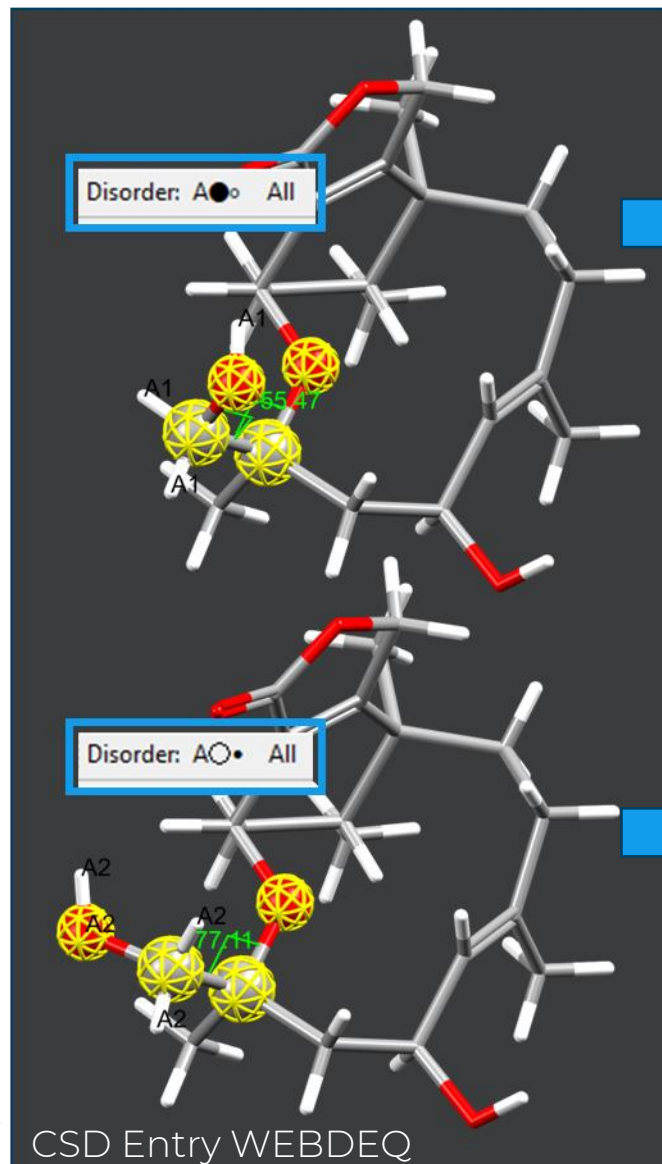


On-demand
training
module



To see the results
for different
disorder options:

- Toggle the disorder button
- Then use Mogul Geometry Check as usual
- Repeat for the other options



CSD Entry WEBDEQ

Mogul Results Viewer

Show / hide: Columns Fragments... Deselect all fragments Export...

Help Double click to view result in Mogul

Type	Molecule	Fragment
bond	WEBDEQ	O3 C4 O4 C3 C3 C4
angle	WEBDEQ	O3 C4 C3 O4 C3 C4
torsion	WEBDEQ	O3 C4 C3 O4

Results Navigator

All hits: 41
Accepted hits: 41
R-factor: Any Heaviest Element: Any
Exclude: None

Relevance	Number	Contribution
<input checked="" type="checkbox"/> 1.00	6	14.6%
<input checked="" type="checkbox"/> 0.94	2	4.9%
<input checked="" type="checkbox"/> 0.89	1	2.4%
<input checked="" type="checkbox"/> 0.84	3	7.3%
<input checked="" type="checkbox"/> 0.82	10	24.4%
<input checked="" type="checkbox"/> 0.79	3	7.3%
<input checked="" type="checkbox"/> 0.75	16	39.0%

Mogul Results Viewer

Show / hide: Columns

Help Double click to view

Type	Molecule	Fragment
bond	WEBDEQ	O3 C4 C3 C4 O4A C3
angle	WEBDEQ	O3 C4 C3 O4A C3 C4
torsion	WEBDEQ	O3 C4 C3 O4A Unusual (enough hits) 41 77.107

Statistics

Total: 41
Selected: 41
|d(min)|: 0.000°

Mogul search - Torsion angle - O3 C4 C3 O4

Value in query: 55.467° (A1)
Value in query: 77.107° (A2)

Number of hits vs Torsion angle / °

Click to (de)select bars; click and drag to (de)select a range

Results and analysis

View diagrams... More hits...

All fragments... View query...

Displayed hits: 41
Selected hits: 41

Data libraries: CSD 6.00

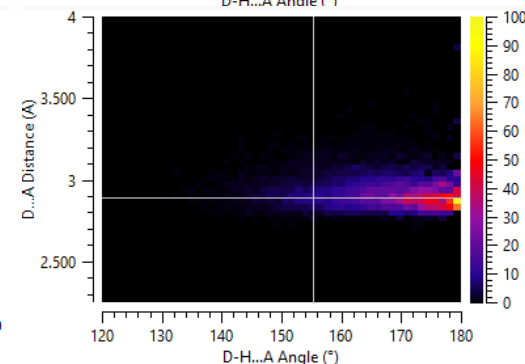
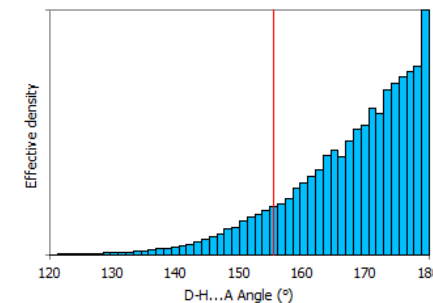
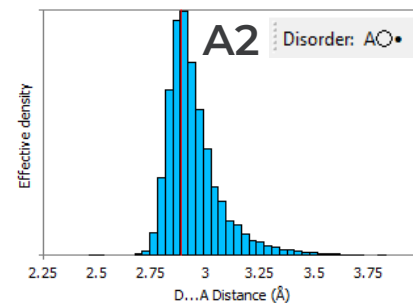
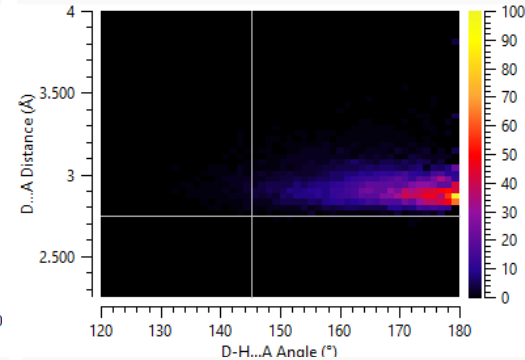
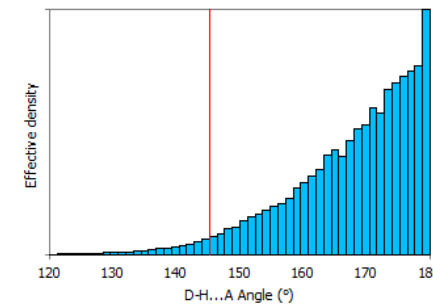
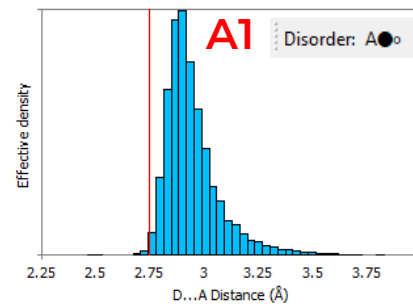
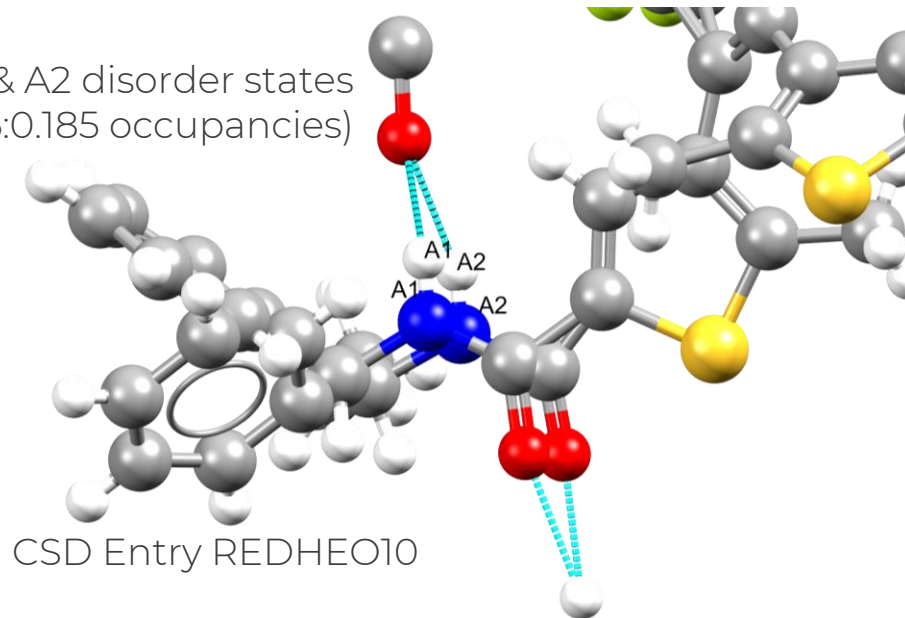
Disorder and Hydrogen Bond Statistics

Hydrogen Bond Statistics

- Interactions geometries in the context of million+ crystal structures in the CSD
- Analysis of the usual- or unusual-ness of observed hydrogen bond lengths/angles in a crystal structure

	Donor	Acceptor	Distance D-A	Distance classification	Distance threshold	Angle D-H...A	Angle classification	Angle threshold
A1	N4A (amide_carbonyl) (A1)	O1 (amide_carbonyl)	2.74	Unusual	(2.80, 3.19)	145.21	Unusual	147.52
A2	N4B (amide_carbonyl) (A2)	O1 (amide_carbonyl)	2.89	Not Unusual	(2.80, 3.19)	155.33	Not Unusual	147.52

A1 & A2 disorder states
(0.815:0.185 occupancies)



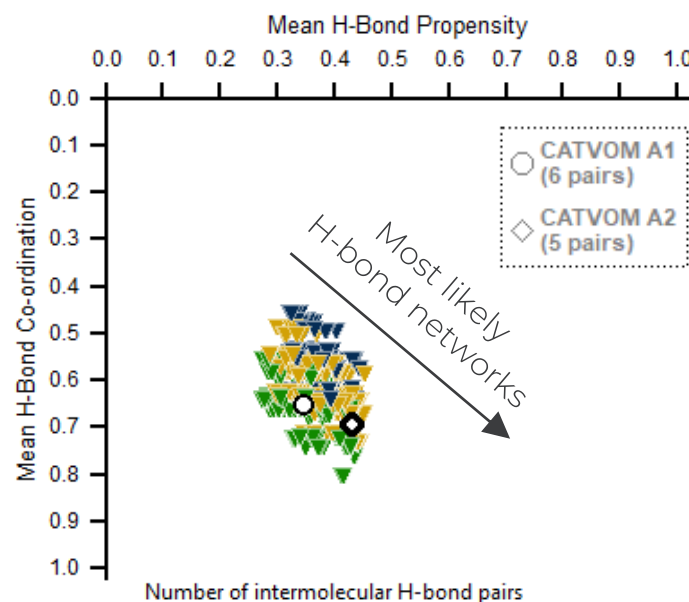
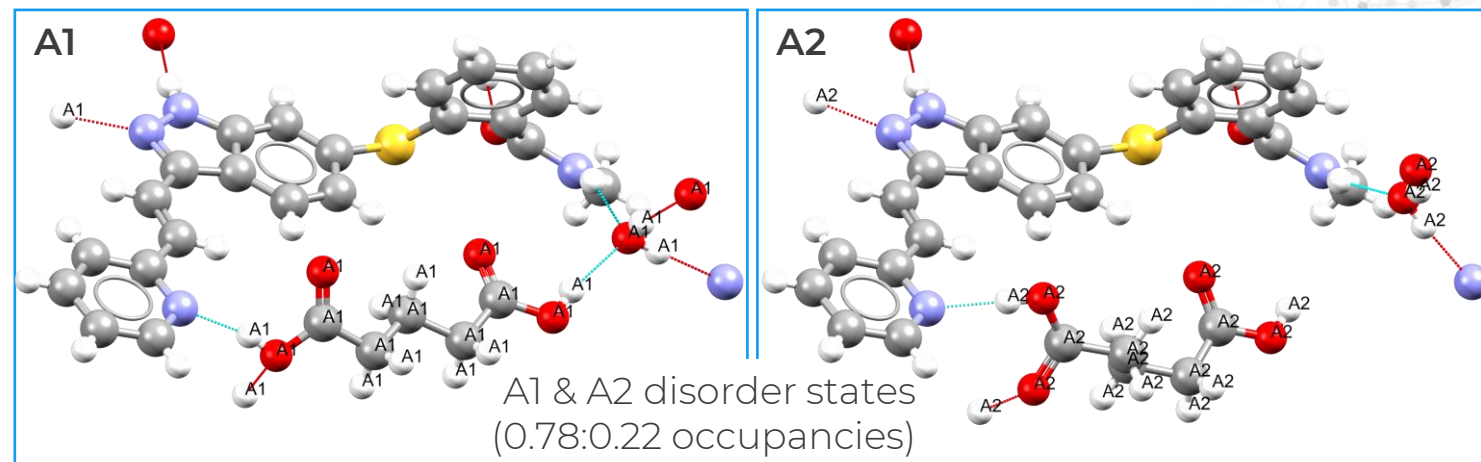
Disorder and Hydrogen Bond Propensities

• Hydrogen Bond Propensities

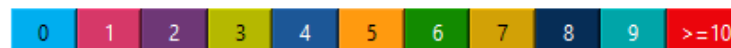
- Predict likely hydrogen bond pairings and donor/acceptor coordination likelihoods
- Assess crystal forms, e.g. identifying sub-optimal hydrogen bonding or under-/over-use of donors and acceptors
- Explore relative likelihoods of putative h-bond networks

Other tools include Full Interaction Maps (FIMs) and Aromatics Analyser

CSD Entry CATVOM



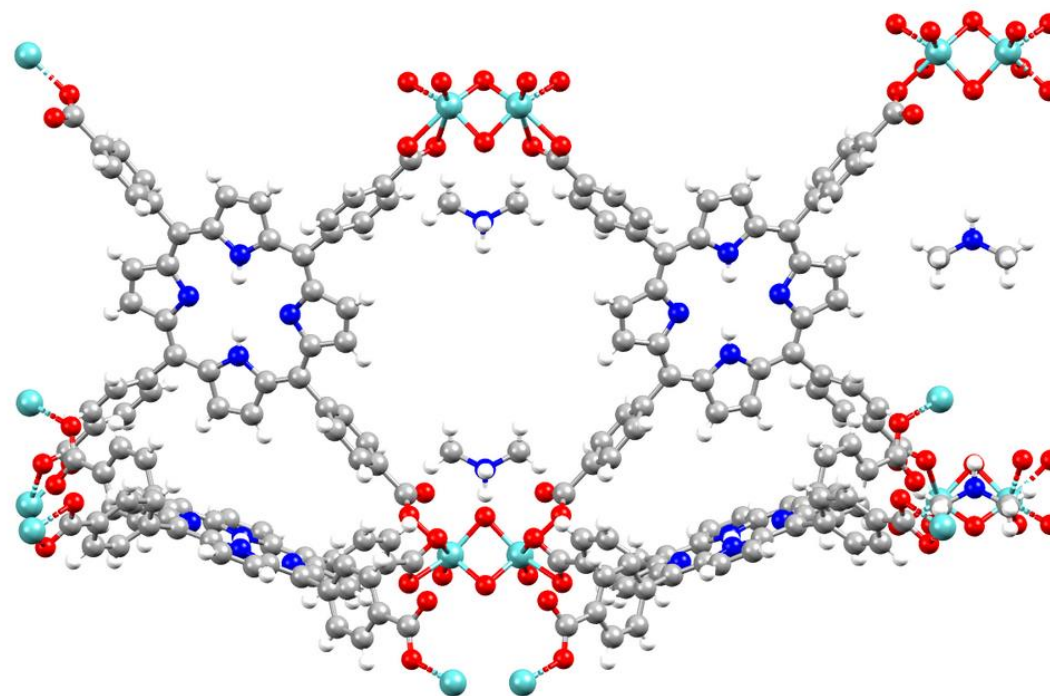
- A1 low propensity pair, donors used optimal # times
- A2 higher ranked pair, less pairs, under-used donor



CSD MOF Collection

- Complements our CSD MOF subsets embedded in CSD Portfolio
- A good starting point for high-throughput analysis
- 12,505 3D porous MOFs
 - All 3D MOFs containing over 10 % void space
 - Converted to space group P1
 - Non-bonded solvent removed
 - Missing hydrogen atoms added

CSD MOF Collection Entry



CSD MOF Collection

- The CSD MOF Collection contains reference spreadsheets
 - Allows further categorisation within the collection

CSD refcode	CIF filename	original crystal system	Sohncke space group	Percentage void space
ABAVIJ	abavij_P1	monoclinic	-	15.
ABAVOP	abavop_P1	monoclinic	-	13.
ABAYIO	abayio_P1_charged	cubic	-	62.
ABAZAF	abazaf_P1	monoclinic	-	21.
ABAZAF01	abazaf01_P1	monoclinic	-	22.

- The CSD MOF Collection has a Creative Commons licence: CC BY-NC-SA 4.0
- <https://www.ccdc.cam.ac.uk/free-products/csd-mof-collection/>
- <https://doi.org/10.1016/j.matt.2021.03.006>



Matter





Volume 4, Issue 4, 7 April 2021, Pages 1105-1106

Preview

The launch of a freely accessible MOF CIF collection from the CSD

Aurelia Li¹, Rocio Bueno Perez¹, Seth Wiggin², Suzanna C. Ward², Peter A. Wood², David Fairen-Jimenez¹  

Show more 

+ Add to Mendeley  Share  Cite

<https://doi.org/10.1016/j.matt.2021.03.006>

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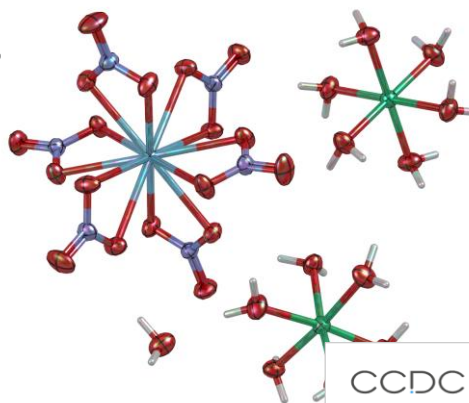
 [open archive](#)

The computational study of metal-organic frameworks (MOFs) relies heavily on the availability, quality, and simulation-readiness of MOF structural data. We announce here the release of the freely accessible and regularly updated “CSD MOF Collection,” a dataset of >10,000 3D porous computation-ready MOFs, derived from our automatically updated CSD MOF subset.

CCDC

CSD and ICSD

- Porous materials encompass structures that may be considered inorganic, metal-organic or organic
- It is possible to search for entries in both the CSD and **ICSD** using Access Structures
- Joint deposition system too!



Database to search Entire published collection CSD ICSD Teaching subset

A wealth of structures, stories and possibilities

CSD one million special issue

- 33 articles from industry and academia



**1 million structures.
stories.
possibilities.**

Cambridge Structural
Database, CSD



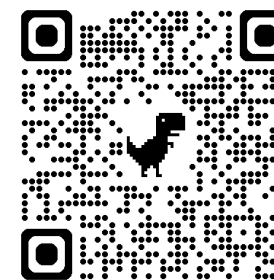
CCDC
advancing structural science

Legacy and Future Impact of the Cambridge Structural Database: A Tribute to Dr. Olga Kennard - special issue

- 29 articles from industry and academia



**CRYSTAL GROWTH
& DESIGN**



The CSD - A wealth of knowledge gained from a million structures. *CrystEngComm*, 2020,22, 7131-77502

The CSD. C.R.Groom, I.J.Bruno, M.P.Lightfoot and S.C.Ward, *Acta Cryst.* (2016). B72, 171-179 DOI: 10.1107/S2052520616003954

CCDC

More case studies



- Discover All
- Case Studies**
- Webinars
- White Papers**
- Blogs
- News
- Events
- Newsletter

Tags

- Organometallics
- Organic Crystallography
- Organometallic Complexes
- Organometallic Ligands
- Partnerships
- People
- Pharmaceutical
- Pharmaceutical Discover
- Pharmaceuticals
- Pharmacophore
- Pipeline Pilot
- Polymorph**
- Poster
- Science Communication
- Science Stories
- Scientific Research
- SCXRD
- Semiconductors
- SMARTS
- Smiles
- Software
- Solid Form**
- Solid Form Informatics**

Unlocking Solid Form Innovation in CSD-Materials

Blog Hydrogen Bond Mercury Solid Form Stability

Investigating Solid Form Stability: Understanding Hydrogen Bond Propensity in Mercury

Blog CSD Landscape Generator CSD-Theory Polymorph Solid Form Informatics

How to Generate a Solid Form Landscape without a Crystal Structure with CSD Landscape Generator

Blog CSD-Materials Solid Form Informatics

How to Analyse Hydro

Blog CSD-Materials Drug Development Matwall

Augmented reality?

DigiMOF – a database of properties for MOFs found in the CSD, data mined from journal articles using ChemDataExtractor

JCIM JOURNAL OF CHEMICAL INFORMATION AND MODELING

pubs.acs.org/jcim

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Application Note

Augmented Reality for Enhanced Visualization of MOF Adsorbents

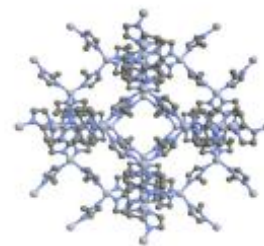
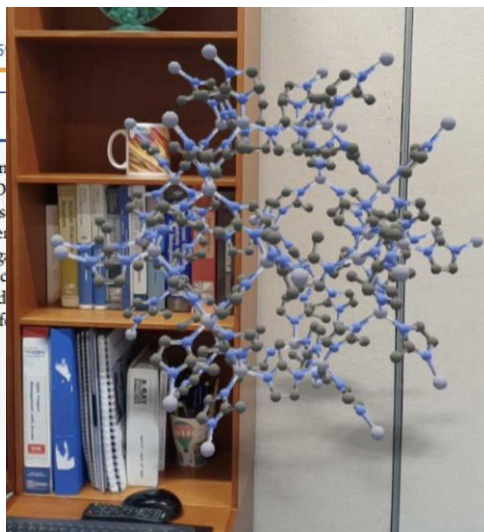
Lawson T. Glasby, Rama Oktavian, Kewei Zhu, Joan L. Cordiner, Jason C. Cole, and Peyman Z. Moghadam*

Cite This: *J. Chem. Inf. Model.* 2023, 63, 5950–5955

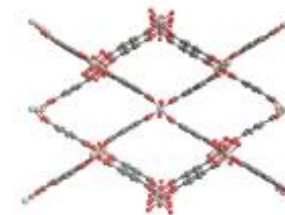
ACCESS |

Metrics & More

ABSTRACT: Augmented reality (AR) is an emerging visualization and comprehension of complex 3D applied not only in the field of chemistry but also in engineering, and many other areas. Here, we describe a free AR technique for visualization of metal-organic porous materials to investigate their crystal structures. We think this workflow will serve as an aid for experimental scientists working in the field of porous materials.



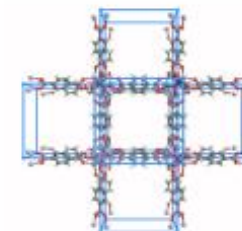
ZIF-8 (FAWCEN)



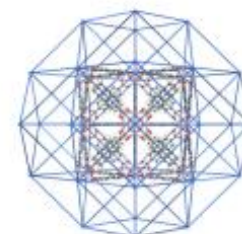
MIL-53 (ASOHUL)



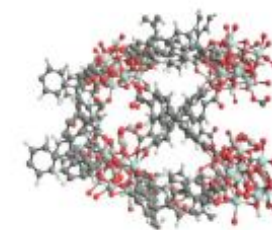
CPO-27-Co (MOHGEY)



IRMOF-1 (SAHYIK)



UIO-67 (WIZMAV)



MOF-812 (BOHWOM)



Lawson T. Glasby, Rama Oktavian, Kewei Zhu, Joan L. Cordiner, Jason C. Cole, Peyman Z. Moghadam, *J. Chem. Inf. Model.* 2023, 63, 19, 5950–5955

CCDC

How to cite the tools seen today

- **Mercury**

Mercury 4.0: from visualization to analysis, design and prediction
C. F. Macrae, I. Sovago, S. J. Cottrell, P. T. A. Galek, P. McCabe, E. Pidcock,
M. Platings, G. P. Shields, J. S. Stevens, M. Towler and P. A. Wood, *J. Appl.
Cryst.*, **53**, 226-235, 2020
[DOI: 10.1107/S1600576719014092](https://doi.org/10.1107/S1600576719014092)

- **CSD**

The Cambridge Structural Database
C. R. Groom, I. J. Bruno, M. P. Lightfoot and S. C. Ward, *Acta Cryst.*(2016).
B72, 171-179
[DOI: 10.1107/S2052520616003954](https://doi.org/10.1107/S2052520616003954)

- **MOF subset**

P. Z. Moghadam, A. Li, S. B. Wiggin, A. Tao, A. G. P. Maloney, P. A. Wood,
S. C. Ward, and D. Fairen-Jimenez, *Chemistry of Materials* **2017** 29 (7),
2618-2625
[DOI: 10.1021/acs.chemmater.7b00441](https://doi.org/10.1021/acs.chemmater.7b00441)



More reference
papers for
CSD Software

What we have learnt

- ✓ Become familiar with the **CSD**.
- ✓ Which **subsets** of the CSD are available, how to access them in ConQuest, Mercury and the CSD Python API, and how they can help you in your research.
- ✓ How to **visualise** porous materials effectively in **Mercury**.
- ✓ How to **analyse** pore space in your structures using **Pore Analyser**.
- ✓ About applications of the **disorder visualization feature**, including recent advances and integrations with other functionality available in Mercury.
- ✓ And more Mercury **tips and tricks**!

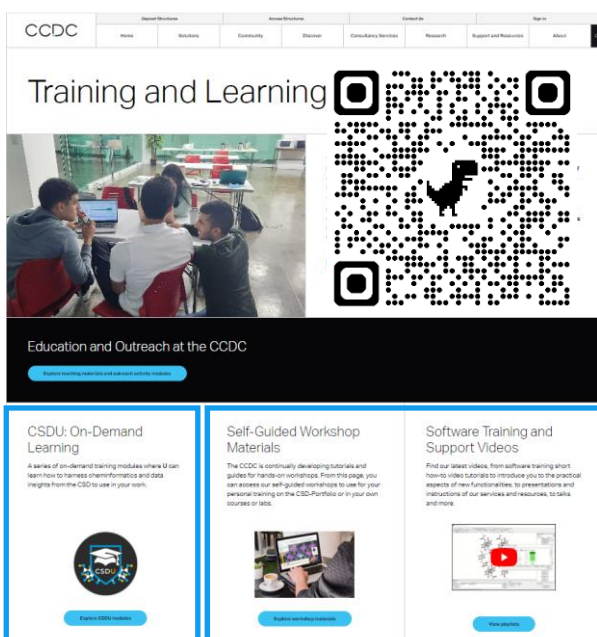
How many points did you get?

Let us know in
the chat!



Want to explore more?

Training and learning



CCDC Training and Learning

Education and Outreach at the CCDC

CSDU: On-Demand Learning

Self-Guided Workshop Materials

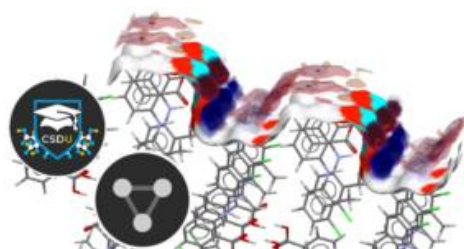
Software Training and Support Videos

- Covering use cases with guided examples.
- Including examples from today as well as other CSD Software.

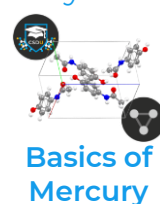


CSDU

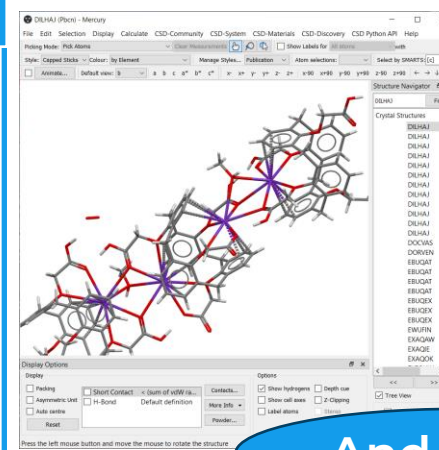
Learn on demand with free online training courses



- Free
- Completion certificate upon passing a final test.
- In-depth review of Mercury and more software and functionality.



Self-guided workshops

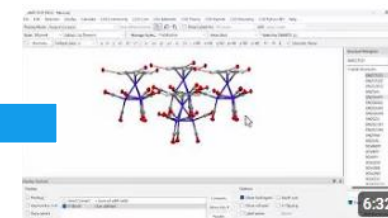


And more!

Videos



YouTube channel



How to: Explore molecules and create eye-catching graphics with Mercury



How to: Build and combine searches in ConQuest

Want to explore more?

CCDC Virtual Workshops

- **21st October** – How to Use **Particle Informatics Tools** to Connect Crystal Structure to Particle Behaviour
- **4th November** – How to Use the Docking Software **GOLD** to Perform **Virtual Screening** Simulations

CCDC Webinars

- **13th November** - Using general purpose **force fields** in solid form studies
- **20th November, Panel** – **Frontiers in MOFs**: Creating Real-World Solutions with MOFs

Check our Events online for more virtual and in person events.



Frontiers in
MOFs

CCDC **60**
advancing structural science YEARS

WEBINAR

Creating Real-World Solutions with MOFs

Panel discussion with experts from academia and industry.

20th November, 3pm GMT

[REGISTER](#)

 Lily Hunnisett
Computational Solid-State
Scientist, CCDC

Using General Purpose Force Fields in Solid Form Studies

Thursday, 13th November
15:00 (GMT)/ 10:00 (EST)

