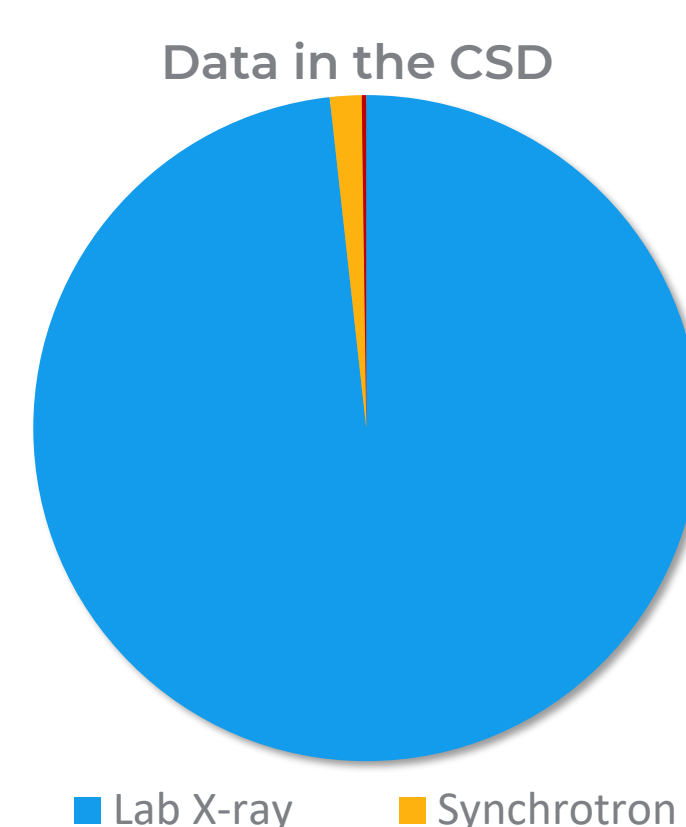


From Structure to Publication: How to Utilise Your FAIRE License

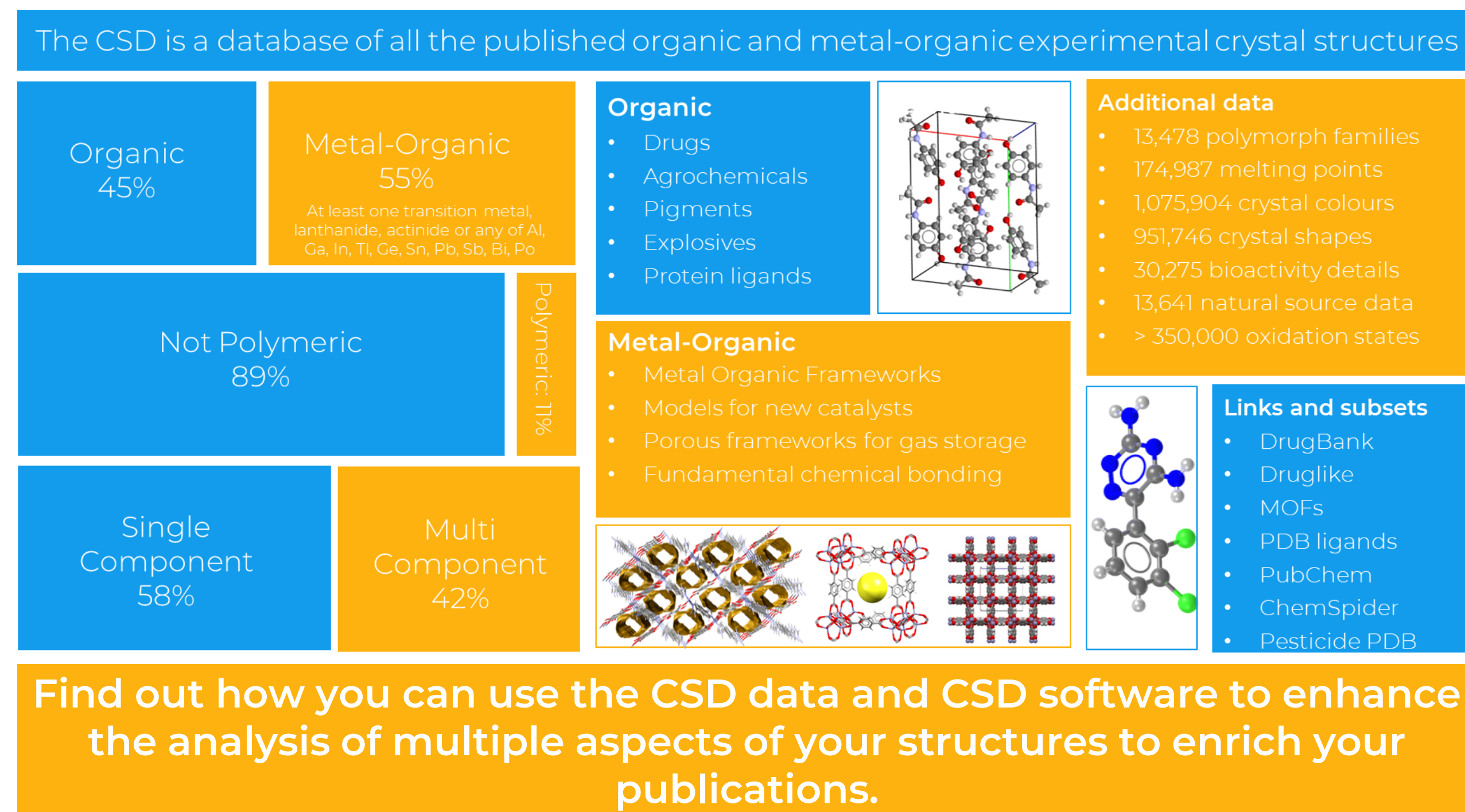
FAIRE and the Cambridge Structural Database

The Frank H. Allen International Research and Education programme (FAIRE)¹ provides a campus-wide Academic CSD-Enterprise license, free of charge, to researchers in parts of the world with demonstrable need. Your FAIRE license gives you access to the [Cambridge Structural Database](#) (CSD) and [CSD Software](#). The CSD is a curated database of over 1.25 million small molecule organic and metal-organic experimental crystal structures.² Data is curated in house, validated and stored in a standardised format so that the structures are searchable, reusable and easily findable.



The [CSD](#) contains a wealth of structural information from drugs, pigments, and protein ligands, to metal organic frameworks, large clusters, and catalyst structures. These structures are enriched with bibliographic information, 2D structural diagrams, and experimental details, as well as physical and chemical properties. This can be invaluable for your research whether it is experimental or computational.

[CSD Software](#) is included with your license, giving you access to the desktop software [ConQuest](#) and [Mercury](#), which provide you with all the core functionality you need to search the CSD and analyse crystal structures. If you work in life sciences, then you can explore [GOLD](#) and [CSD-CrossMiner](#) to perform protein-ligand docking and pharmacophore searching. As a companion to CSD desktop software, [WebCSD](#) provides you with flexible online searching capability. [CSD-Python API](#) is also provided which allows you to harness these programs' functionality programmatically.



Find out how you can use the CSD data and CSD software to enhance the analysis of multiple aspects of your structures to enrich your publications.

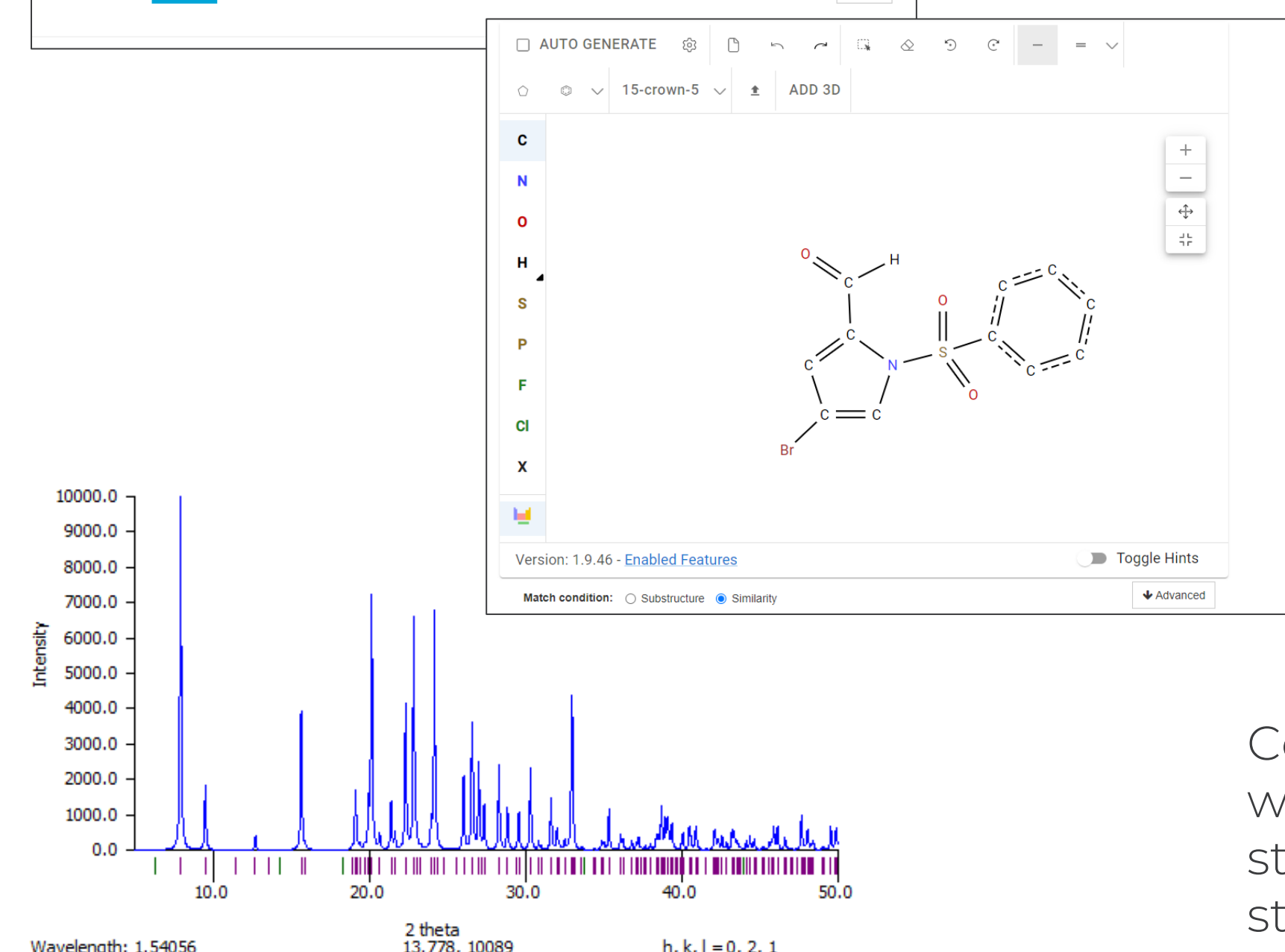
Here we use CSD entry UNOYEE³ to demonstrate how you could perform crystal structure analysis using CSD Software for a publication in a journal such as *Acta Crystallographica E*.

Is my compound novel?

The first thing you will want to know is if your structure is novel. Has it been published before? Are there many similar compounds? You can use [ConQuest](#) and [WebCSD](#) to check this.

Screen the CSD for **unit cell hits** as you collect your data using [WebCSD](#). You can also use [CellCheckCSD](#) during data collection.

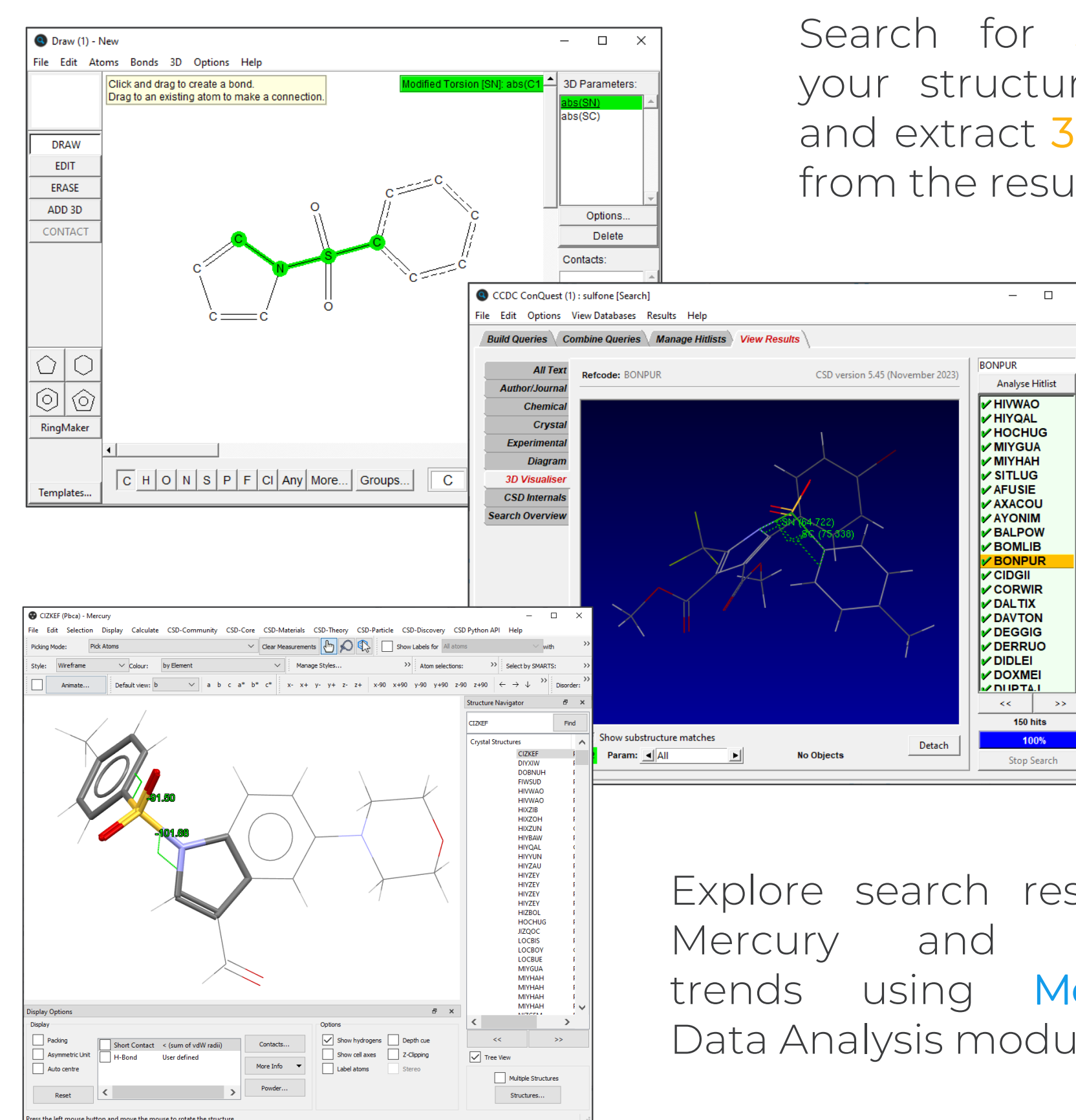
Find comparable structures using **substructure** or **similarity** searching with [WebCSD](#).



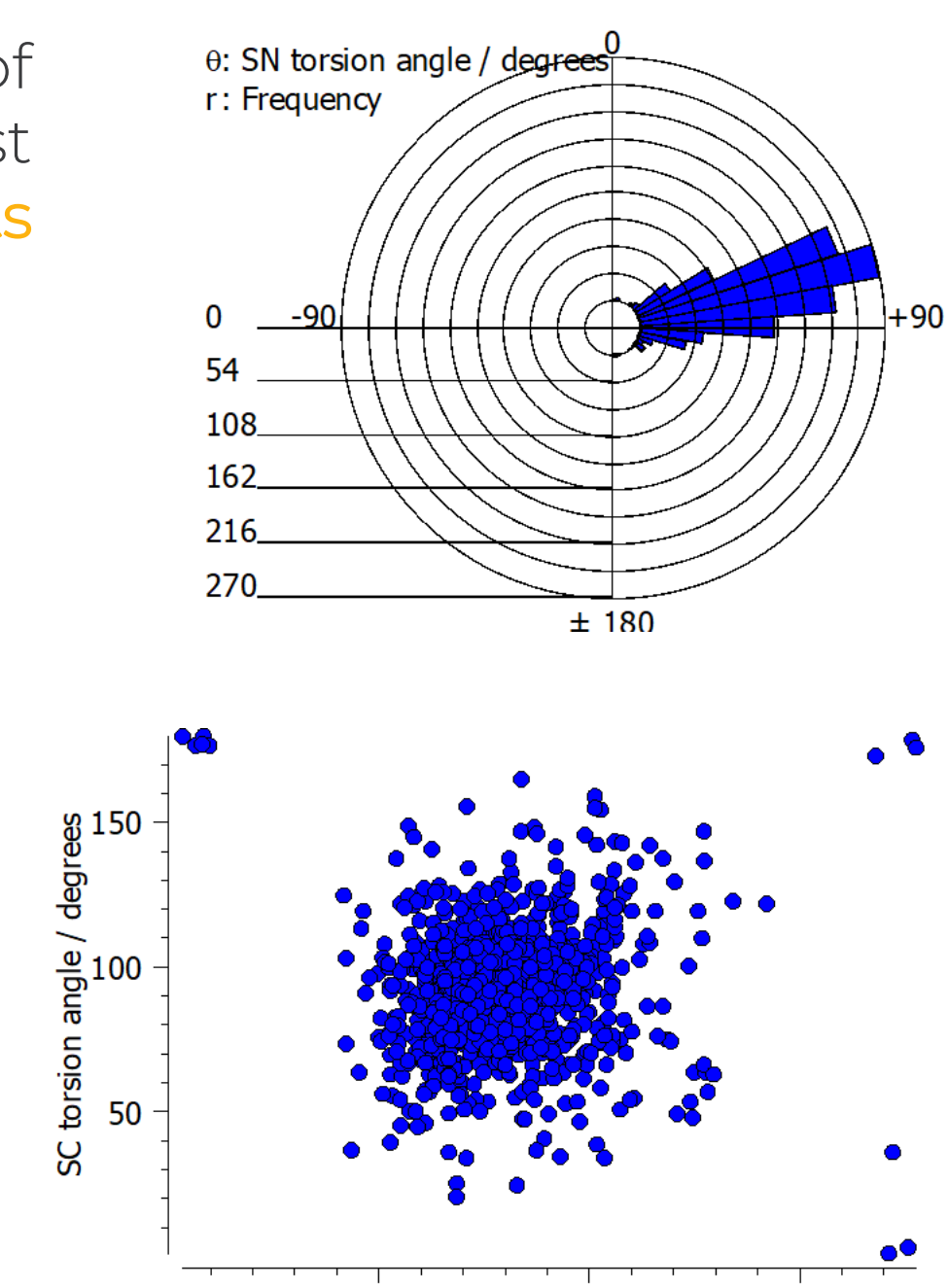
Compare experimental powder patterns with **simulated powder patterns** from CSD structures or your own single crystal structures using [Mercury](#).

Database surveys and analysis

Search the CSD for structures related to yours using [ConQuest](#). Identify relevant **literature** from bibliographic records, discover chemical, physical and biological properties, and explore **3D** structure.



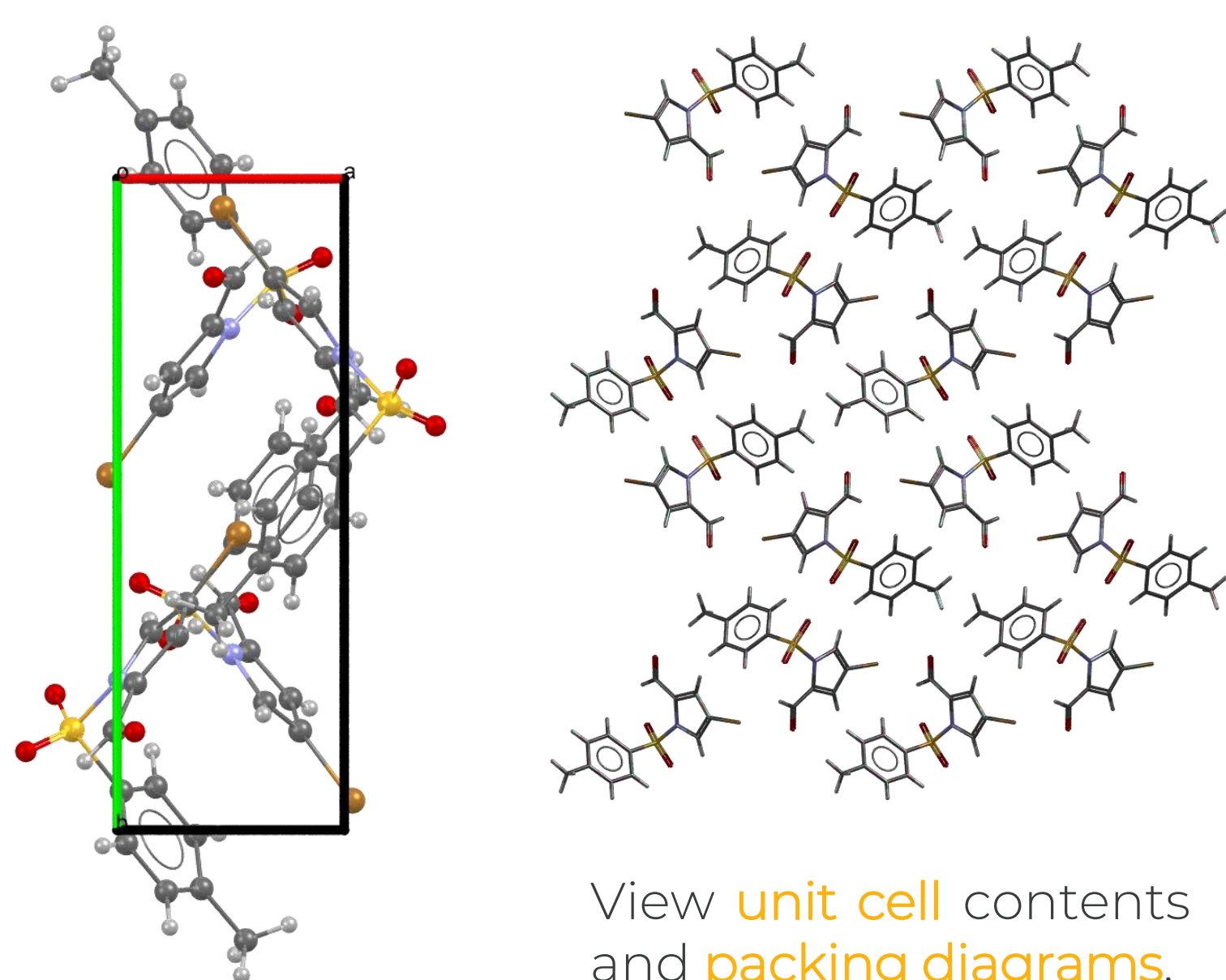
Search for **substructures** of your structures in ConQuest and extract **3D measurements** from the results.



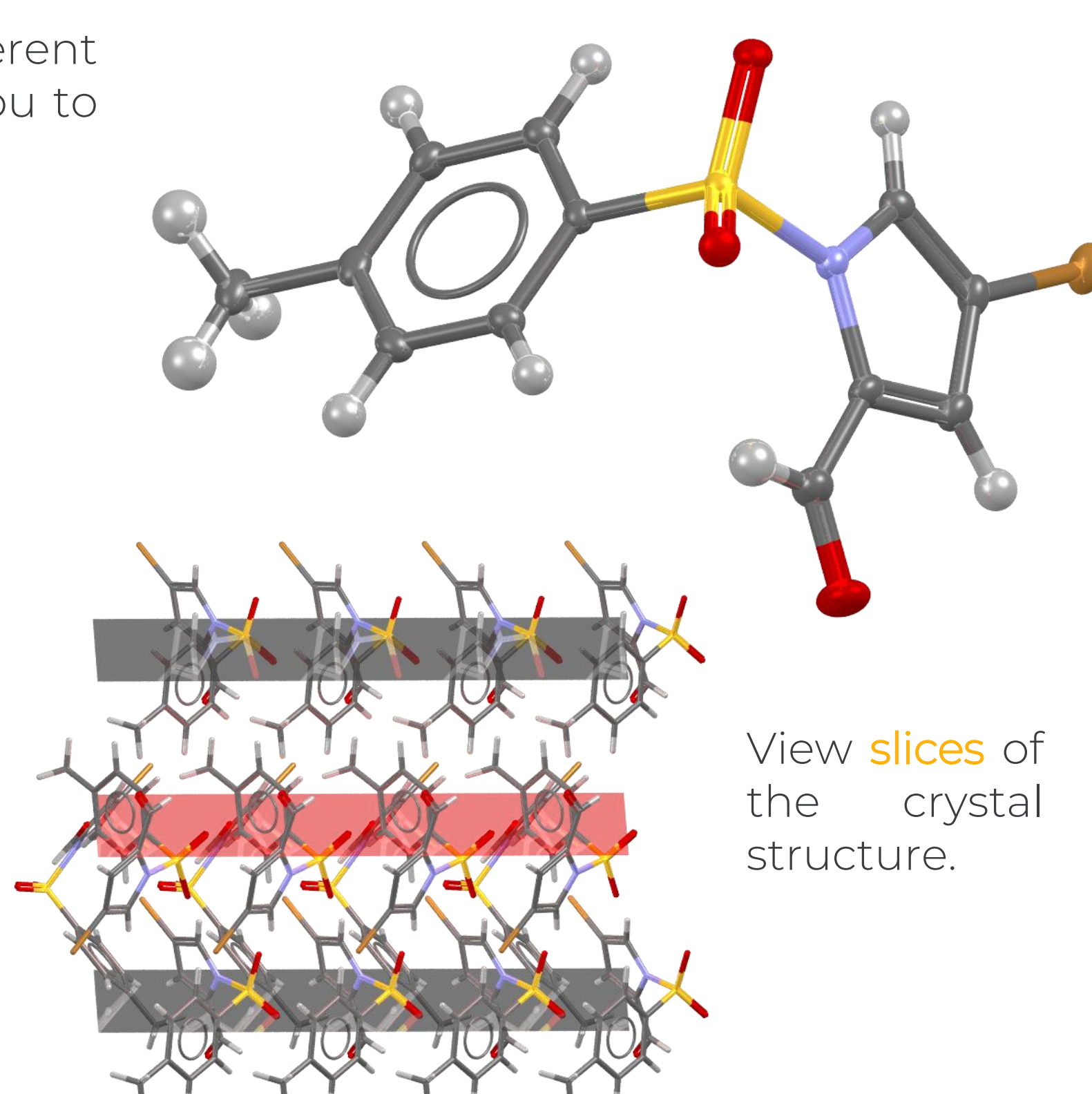
Create **plots** or **export data** for analysis in other software.

Structure visualisation

Structures can be **visualised** in [Mercury](#). Different styles are available and customisable allowing you to make **publication quality images**.



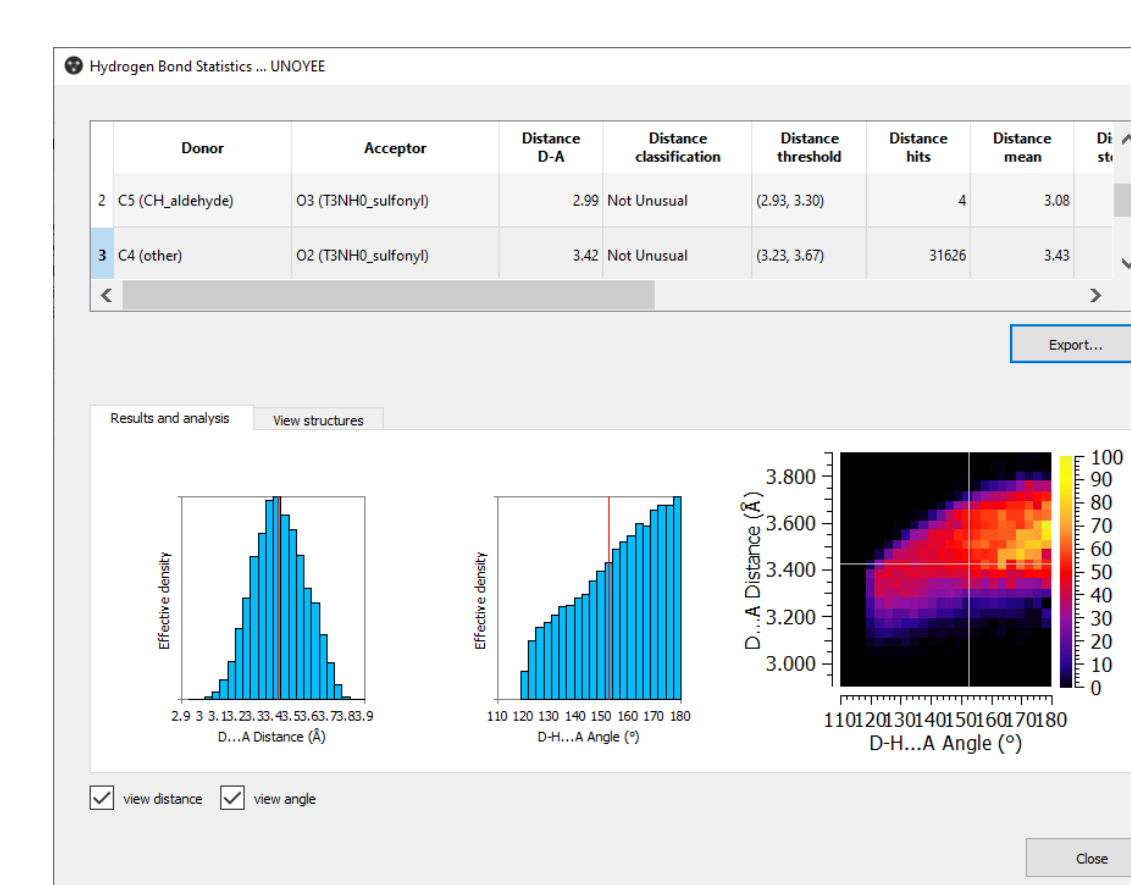
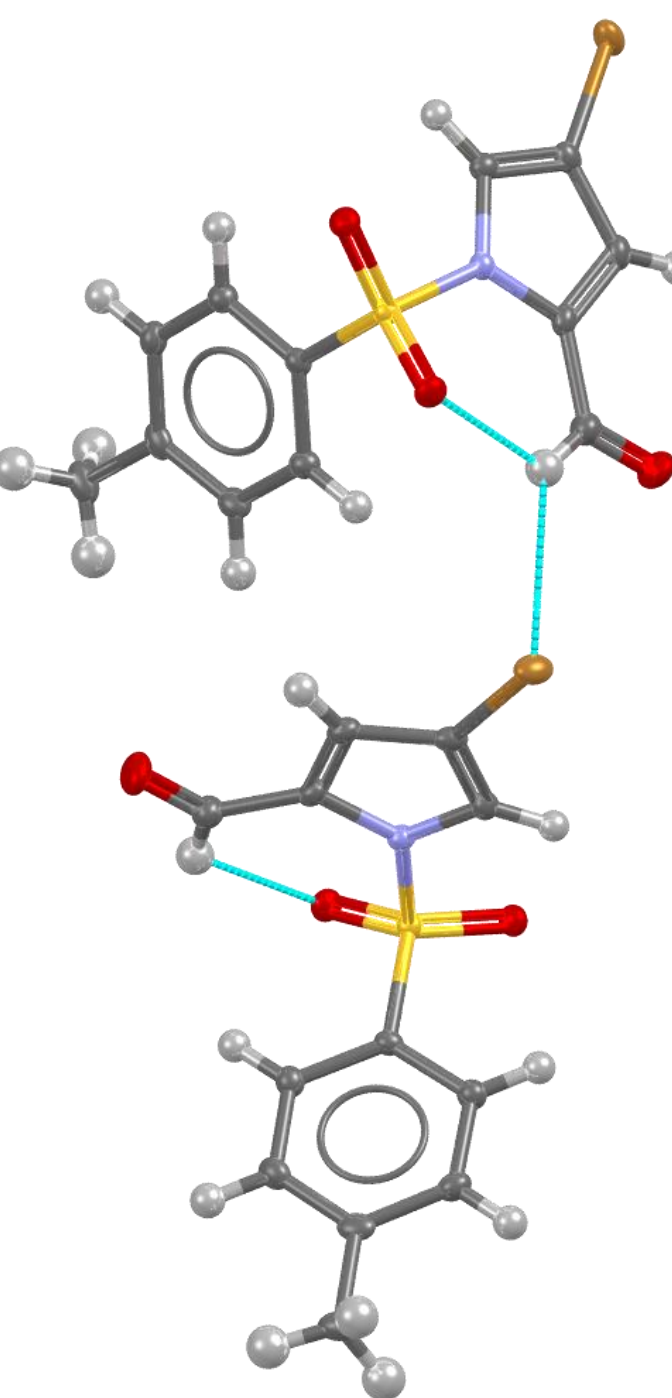
View **unit cell** contents and **packing diagrams**.



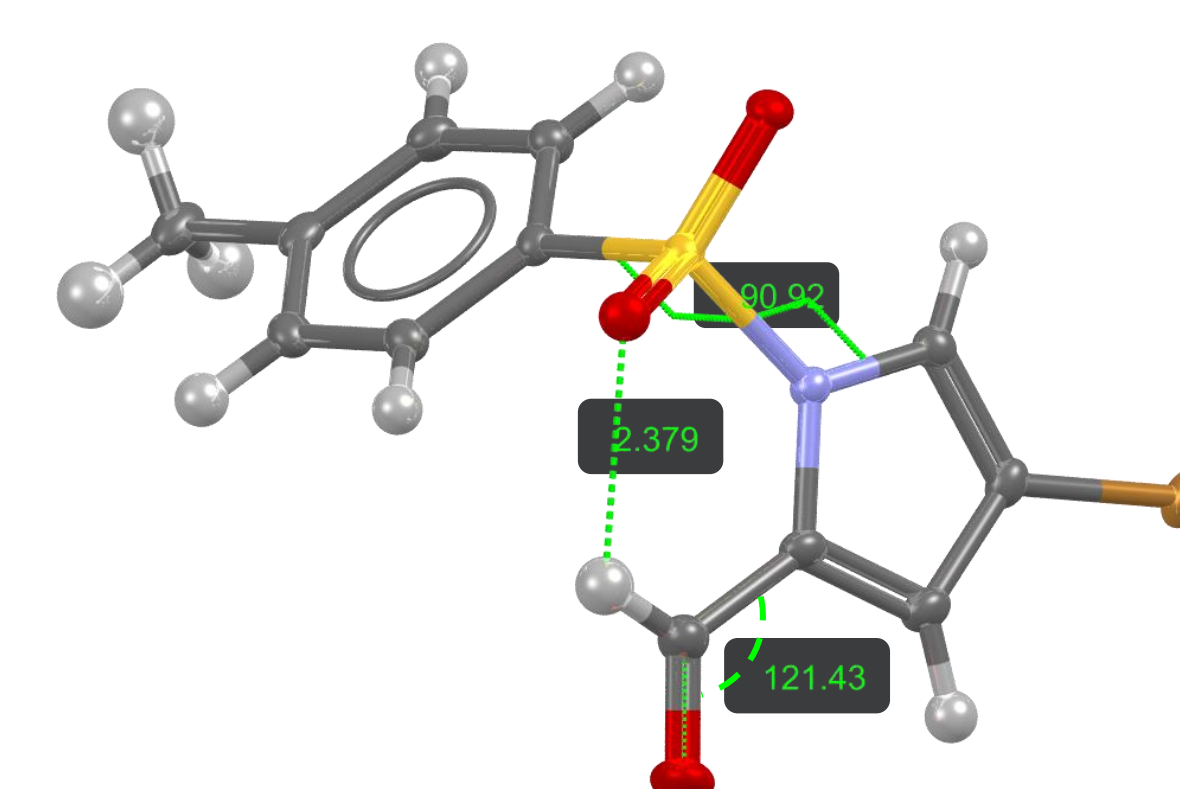
View **slices** of the crystal structure.

Structure analysis

Analyse your structures in [Mercury](#) to uncover **intermolecular** and **intramolecular interactions**.



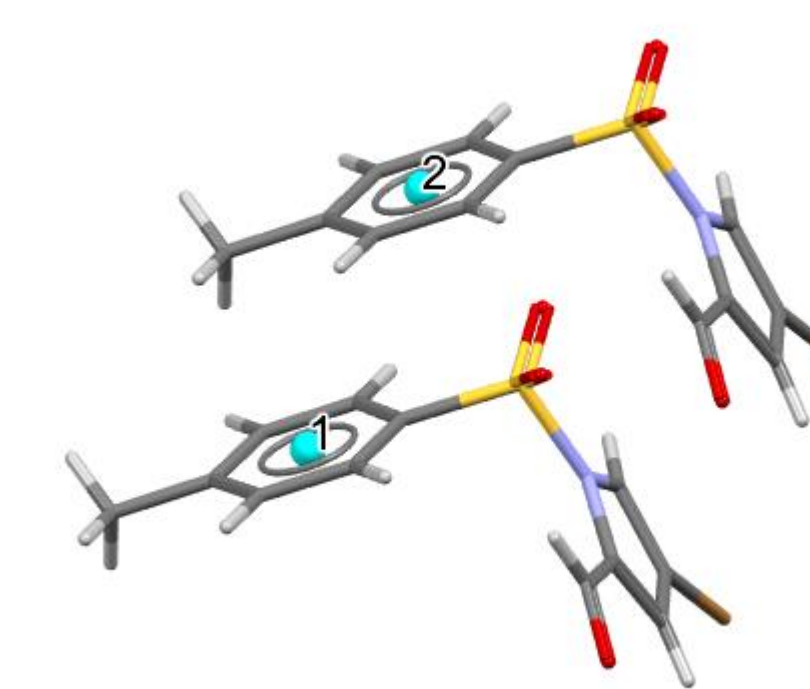
Automatic **Hydrogen Bond Statistics** calculations.



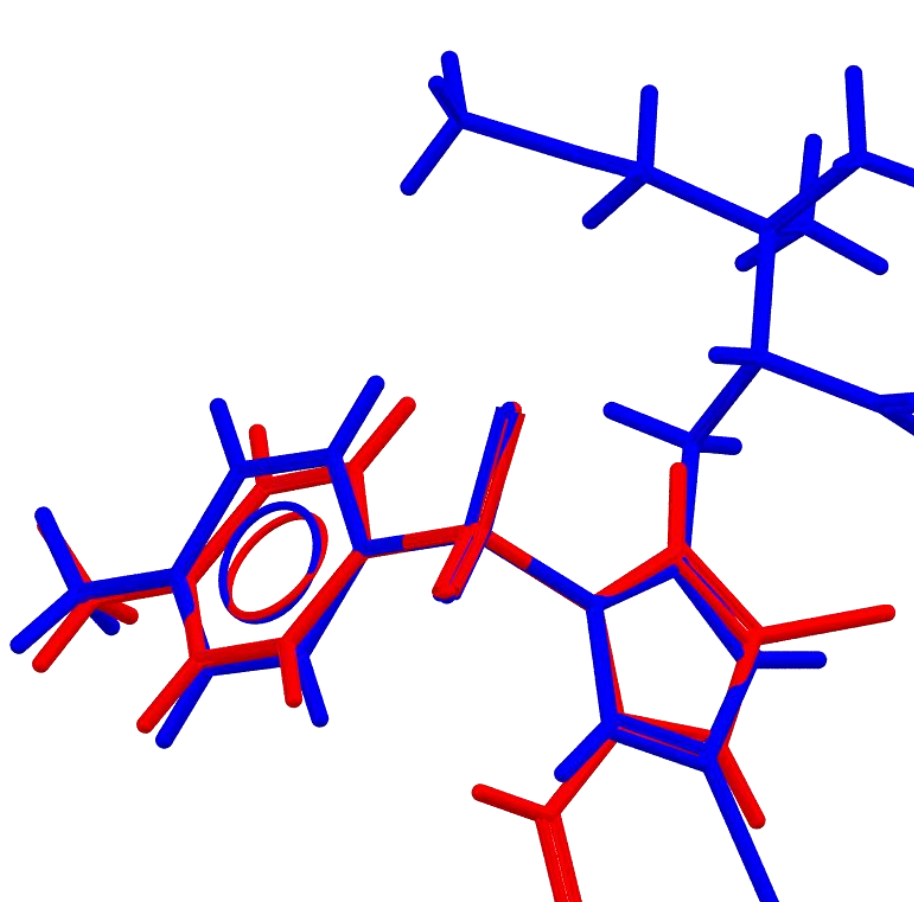
Measure and visualise distances, angles and torsions.

Explore **hydrogen bond networks** with customisable hydrogen bond definitions.

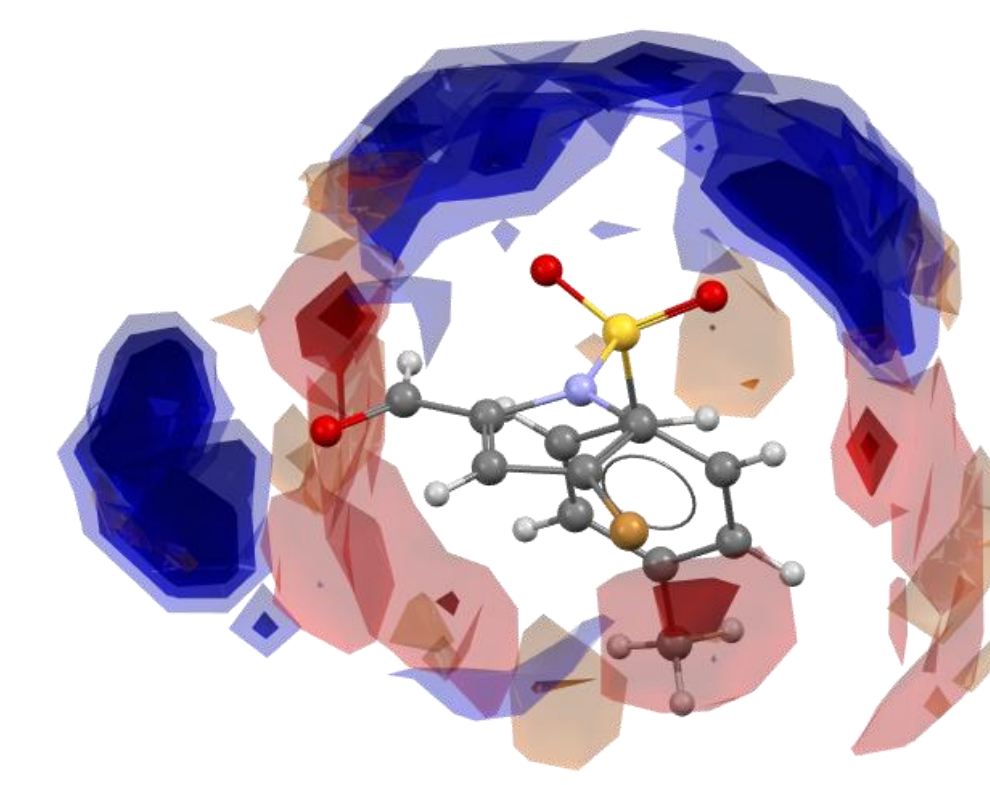
Distance	Relative Orientation	Inter-molecular	Score	Assessment
1	0	Yes	7	Strong
2	0	Yes	7	Strong
3	83.37	Yes	1.2	Weak
4	83.37	Yes	1.2	Weak



Uncover and evaluate **aromatic interactions** with [Aromatics Analyser](#).



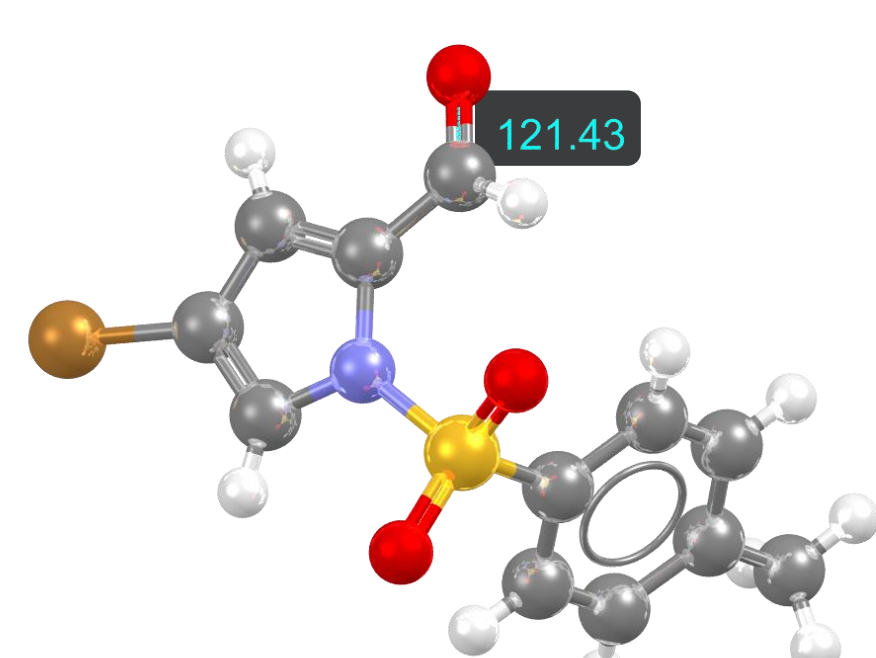
Assess conformational and **structural similarities** with similar molecules using [Structure/Molecule Overlay](#).



Predict and assess **intermolecular interactions** with a range of functional groups using [Full Interaction Maps](#).

Structure validation

Check for **unusual geometric features** which might point to interesting chemistry or suggest improvements to the structural model using [Mogul](#) to assess bond length, valence angles, torsion angles and rings.



Item	Molecule	Fragment	Classification	No. of hits	Query value	Mean	Std. Dev.
01 CSD 01	Not unusual	Length 101	101	101	101	101	101
01 CSD 02	Not unusual	Length 102	102	102	102	102	102
01 CSD 03	Not unusual	Length 103	103	103	103	103	103
01 CSD 04	Not unusual	Length 104	104	104	104	104	104
01 CSD 05	Not unusual	Length 105	105	105	105	105	105
01 CSD 06	Not unusual	Length 106	106	106	106	106	106
01 CSD 07	Not unusual	Length 107	107	107	107	107	107
01 CSD 08	Not unusual	Length 108	108	108	108	108	108
01 CSD 09	Not unusual	Length 109	109	109	109	109	109
01 CSD 10	Not unusual	Length 110	110	110	110	110	110
01 CSD 11	Not unusual	Length 111	111	111	111	111	111
01 CSD 12	Not unusual	Length 112	112	112	112	112	112
01 CSD 13	Not unusual	Length 113	113	113	113	113	113
01 CSD 14	Not unusual	Length 114	114	114	114	114	114
01 CSD 15	Not unusual	Length 115	115	115	115	115	115
01 CSD 16	Not unusual	Length 116	116	116	116	116	116
01 CSD 17	Not unusual	Length 117	117	117	117	117	117
01 CSD 18	Not unusual	Length 118	118	118	118	118	118
01 CSD 19	Not unusual	Length 119	119	119	119	119	119
01 CSD 20	Not unusual	Length 120	120	120	120	120	120



Don't forget to cite the CSD and acknowledge the FAIRE programme in any publications that use the CSD Portfolio. Find more information on how to cite the CSD in our FAQ's here: <https://ccdc-info.com/3yBbTXt>