

A FAIR share of crystallographic data: 17+ years of the Crystallography Open Database Saulius Gražulis Andrius Merkys Antanas Vaitkus The COD Advisory Board

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17 years ago...

... a small team of engaged scientists decided to make **all** published crystal structures available openly and free of charge to everyone.^a

The Crystallography Open Database (COD) [1] project was started by the late Michael Berndt and the current Advisory Board members Daniel Chateigner, Robert T. Downs, Armel Le Bail, Luca Lutterotti, Peter Moeck, Miguel Quirós Olozábal, F.T. Yokochi and others.

During the past decade, more than **450 000 records** were collected in a curated, versioned scientific database.

^agemstonede (Dr. Michael BERNDT) Fri Feb 14, 2003 1:26 pm

Ways to access data

Individual COD records can be inspected and downloaded using the Web interface:



What's new? 🔕

cessing COD Data

Search by structura

Home

Search

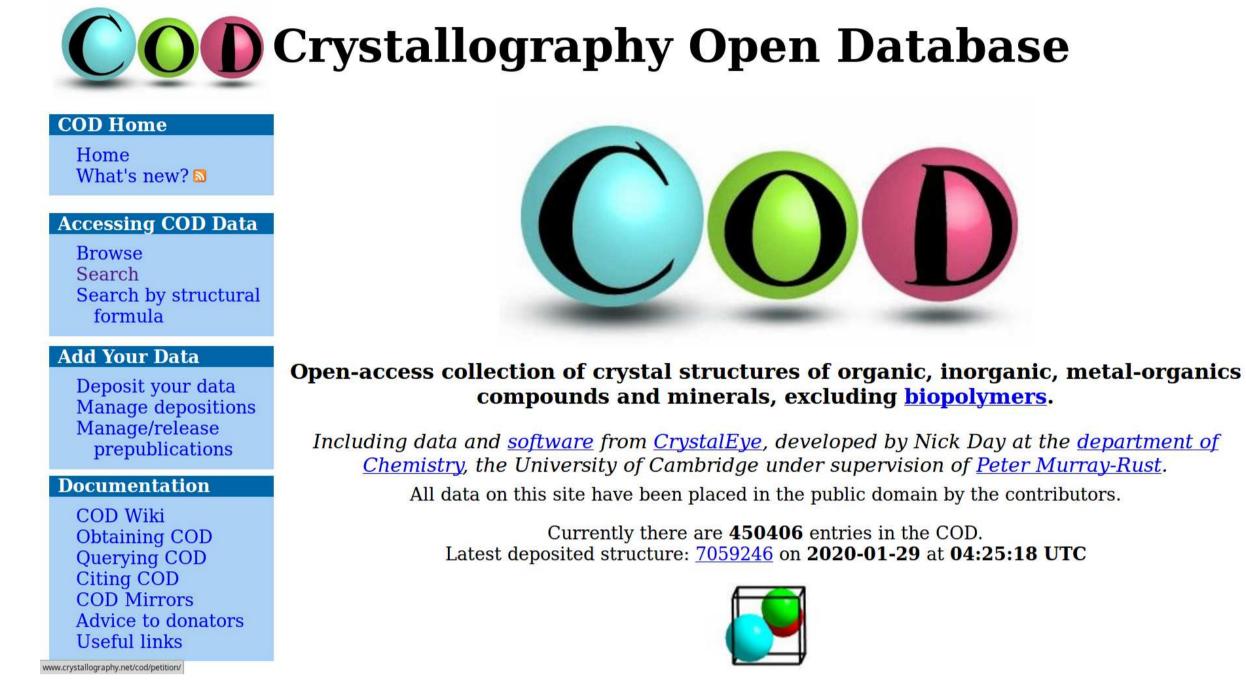
Crystallography Open Database

Information card for entry 2006278

EUROPE

The COD

COD is the largest FAIR crystal structure collection. https://www.crystallography.net/cod



The FAIRness of the COD

The COD database is:

Findable:

► Has a unique, stable identifier for every record (a record ID, e.g. COD) **2006278** [8]); Resolves record IDs to actual data (not just a landing page!); No. 1 for DuckDuckGo and Google searches for the phrase "crystallography" database" (checked 2020-01-29).



<u>2006277</u> << **2006278** >> <u>2006279</u>

Preview

HM:P 1 21/c 1 #14

2006278.cif Coordinates Original IUCr paper <u>HTML</u> ChemSpider; DrugBank; Wikipedia **External links**

Alternatively, multiple COD records can be downloaded for mass-processing using one of the available protocols: svn://crystallography.net/cod (Subversion SVN) rsync://crystallography.net/cod-cif (rsync)

Problems

- Data in many publications are not resolvable automatically (landing page instead of a data stream – not FAIR?);
- Data from some publications are behind a paywall (even less) F**A**IR?);
- Data formats and semantics not formally specified (can it still be FAIR?).

Conclusions

Using F/LOSS, Unix-architecture based tools allow one to build,

Accessible:

- Each COD ID can be resolved to a human-readable Web page: https://www.crystallography.net/cod/2006278.html
- Each COD ID can be resolved to a machine-readable data stream: https://www.crystallography.net/cod/2006278.cif
- Any previous revision of any COD record can be retrieved, at any time: https://www.crystallography.net/cod/2006278.cif@12345

Interoperable:

- The data stream is in the standard CIF [2] format and is suitable for immediate automated processing:
- curl -sSL http://crystallography.net/cod/2006278.cif | \ cif_molecule -i --p1 | buffer jmol 2> /dev/null &

Reusable:

Used in a number of scientific and industrial applications:

- as a material identification database for the EU SOLSA project [9];
- as an inter-linked resource for other databases, e.g. Raman Open Database [5];
- as a source of data for macromolecular refinement [4];
- as a source for search-match applications of macromolecular vendors;
- as data source for scientific research: see e.g. [7] and 600+ other citations (Google Scholar, checked 2020-01-29).

- curate and maintain an open scientific data collection;
- Version control systems, traditionally used for software development, are instrumental for ensuring **reproducible data** (research);
- Organised, curated databases with well-defined data semantics add value to the published data;
- Failure of some publishers to adhere to FAIR principles hampers the construction of scientifically valuable databases and obstructs the advance of science in general.

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- [5] Mendili et al. Raman open database: first interconnected raman–x-ray diffraction open-access resource for material identification. Journal of Applied Crystallography, 52(3):618-625, may 2019,

Tools and Methods

The main tools for the COD are **F**/**LOSS** software:

- Apache2 Web server hosts the Web site and the REST layer; **rewrite rules** ensure that **URIs** remain stable throughout the development of the COD;
- Jmol [3] molecule viewer is used to assess the crystal structures by the curators and users;
- Perl is an excellent tool for data processing in textual form; a strict Perl CIF parser [6] helps maintaining correct syntax.

- https://doi.org/10.1107/s1600576719004229.
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