

Software for maintaining and expanding the (Predicted) Crystallography Open Database

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Introduction

Data are arriving in ever increasing rates. Thus, automated software tools are needed to cope with the growing amount of data, to provide consistent, uniform and accurate information.

The following goals are set by COD team:

- build automated structure deposition tools;
- build a collaboration platform for structure validation and curation;
- ensure data quality uniformity, integrity, and trustworthiness;

Deposit your data to COD for publication!

http://www.crystallography.net/

Crystallography Open Database Validation and Deposition Interface

Select CIF file for check: /home/saulius/ALL.CIF Browse.. Validate

About this Validation Interface

This interface allows you to upload, validate and edit CIF files before submitting them for deposition **Steps**

Automatic data deposition

ALL.CIFvalidEditDeposit to CODFile[ALL.CIF]iscorrect

You can now <u>check new CIF file</u>.

• make scientific data freely accessible to anyone.

The process of files deposition, after you have uploaded your data is prettty simple. First step, after files have been uploaded, is validation. Our scripts performs some validation. Results are displayed to you next to your files.

CIFParser

A new CIF parser was developed, to meet the following demands:

identify, locate and clearly show errors in the CIF source (existing parsers were found to be not adequate for this task);
callable from Perl for ultimate flexibility;
capable to correct most common CIF errors in a predictable and documented way (via extension a documented and switchable extension of the IUCr CIF grammar);
easy to extend and check against official CIF grammar for conformance – written in yapp notation, close to a Backus-Naur form.

• free software – distributable under an OSI – compatible license

cif-tools

available at <u>svn://www.crystallography.net/cif-tools</u>

A set of tools based on CIFParser was developed and deployed:
All basic programs a *x style command programs, developed for Linux;

agile development – fast deployment, automatic unit testing ensures high quality and predictability
new tools can be added as needed by environment.

• new tools can be added as needed by anybody;

• integrable into GUIs and Web applications.

Example programs:

data whatever

cell length a

cif_filter – extract uncopywritable data from CIFs, fix errors, compute missing data values; cif_cod_check – check whether a CIF satisfies COD requirements

Automatic error detection/correction

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Validation and Deposit	tion Interface	
File	Status	Actions
b407947g-DELIBERATELY-DAMAGED-FOR-TESTING.cif	warnings	Edit

The following warnings should be taken into account from file
[b407947g-DELIBERATELY-DAMAGED-FOR-TESTING.cif]:

Data block <u>b407947g 0000001</u>:

» _journal_name_full is undefined

» _journal_page_first is undefined

SMILES-building helper scripts



Remember: atomic coordinates are **not copyrightable**. The scripts introduce delays so that no noticeable charge will be put in the servers.

Automated

CIF download

COD identifies itself as the downloader.

The bibliographic information is downloaded from Openurl or Pubmed and appended to the CIF's.

atom_site_fract_x	
geom_bond_distance	
	[Pd]([P](c1cccc1)(C)C)(ON(=O)=O)

Search by SMILES

Use of available free tools: Openbabel (http://www.openbabel.org). Very compact ASCII format Human easily readable, understandable and editable.

Stores ONLY chemical connectivity, discard any other information.

Classification of structures: Is it easy to define what is the "molecule"?

Choosing between openbabel-generated connectivity and authorsupplied bonds.

Automatic fixing of some common mistakes. Removing of chirality markers in non-chiral groups. Human inspection of the results and fixing if necessary.

Expanding the PCOD

2010 update : $898.707 \operatorname{SiO}_2$ entries were added from *ZEFSAII* zeolite predictions and the contributions from *GRINSP* increased to 163.520 (silicates, phosphates, sulfates of Al, Ti, V, Ga, Nb, Zr, or zeolites, fluorides, etc). The PCOD is the first database to attain and offer more than one million of CIF entries.

Software : a new *GRINSP* version is now available [3] for parallel computing (for instance using fully the 8 processors of an INTEL core i7).

Other data from other prediction computer programs (*CASTEP*, *CERIUS2*, *CRYSTAL*, *G42*, *GULP*, *USPEX*...) are expected, just send them, please.

PCOD I

Powder P2D2

from CIF to SMILES

All powder patterns (> 1 million) were calculated and gathered in the P2D2 (Predicted Powder Diffraction Database [4]), they can be used for search-match purposes with *EVA* (Bruker), *Highscore* (Panalytical) and more soon.





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Authors thank to all CIF donators, listed on our Web page, and to numerous anonymous volunteers who help to collect data and keep COD running.

The COD Advisory Board thanks comercial supporters for donated hardware and financial support.

CONCLUSIONS

COD server is technically in position to store and serve all structures that are currently solved. COD deposition procedure ensures syntactic correctness and presence of the most essential CIF data.

COD and PCOD are constantly expanded to meet more needs of crystallographic community

We rely on the help of crystallographic community to add more data and ensure the data correctness!

Use and Add more structures to: http://www.crystallography.net/

THANK YOU !

REFERENCES

[1] http://www.crystallography.net/

[2] S. Grazulis *et al.*, (2009). J. Appl. Cryst. 42, 726-729.
[3] A. Le Bail (2010). Phys. Chem. Chem. Phys. 12, 8521-8530.
[4] A. Le Bail (2008). Powder Diffr. Suppl. 23, S5-S12.

COD/PCOD : cod@crystallography.net