PDBx/mmCIF Ecosystem for NMR Structures

Hamid R. Eghbalnia, Kumaran Baskaran, Jonathan R. Wedell, Hongyang Yao, Dimitri Maziuk, Michael M. Gryk, and Jeffrey C. Hoch

Department of Molecular Biology and Biophysics, UConn Health,
263 Farmington Avenue, Farmington, CT 06030, USA

The Macromolecular Crystallographic Information File (mmCIF), also known as PDBx/mmCIF[1], is a standard text file format for representation and exchange of experimentally determined three-dimensional (3D) macromolecular structure data. It is the adopted standard for all data processing and annotation by the Worldwide Protein Data Bank (wwPDB, wwpdb.org). Because mmCIF can be easily extended to include representations that characterize unique structural features such as disorder, multiple conformers, and dynamic parameters, it is extremely well-suited for aligning data from NMR studies with atomic coordinates. PDB-Dev (https://pdb-dev.wwpdb.org) uses the mmCIF ecosystem to represent biological assemblies derived using integrative and hybrid methods. The dictionary and format are machine-readable, assuring that the wwPDB partners can more effectively represent, biocurate, validate and distribute structural biology data.

wwPDB data deposition

Model data
PDBx/mmCIF coordinate data and meta data

Experimental data
NMR-STAR/NEF Chemical shifts, restraints, peak list and other experimental data

wwPDB accepts data coming from structure determination studies whereas BMRB accepts all additional NMR related data including raw experimental data.

PDBx/mmCIF format

Standardization
Format, syntax and data standards

Extensibility
Easily extendable to support different methods like NMR, EM, etc..

PDBx/mmCIF

Metadata
Dictionary can be extended to support any type of metadata

FAIR
Findable, Accessible, Interoperable and Reusable

PDF version of the poster

Limitations of legacy PDB format

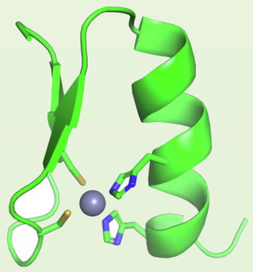
- Fixed size columns
- Column informations hard coded
- Limited scope for meta data
- Can't be used represent large molecules like viruses
- No support to define biological assemblies
- No way define ligand interaction
- No way to define ensemble properties
- No way to represent conformers

PDBx/mmCIF example

The figure below illustrates a partial mapping between the legacy PDB and PDBx/mmCIF file formats with a canonical zinc finger domain structure from PDB ID 1ZAA.

A

```
loop_
_struct_conn.id
_struct_conn.conn_type_id
_struct_conn.ptnr1_label_asym_id
_struct_conn.ptnr1_label_comp_id
_struct_conn.ptnr1_label_seq_id
_struct_conn.ptnr1_label_atom_id
_struct_conn.ptnr1_symmetry
_struct_conn.ptnr2_label_asym_id
_struct_conn.ptnr2_label_comp_id
_struct_conn.ptnr2_label_seq_id
_struct_conn.ptnr2_label_atom_id
_struct_conn.ptnr1_auth_asym_id
_struct_conn.ptnr1_auth_comp_id
_struct_conn.ptnr1_auth_seq_id
_struct_conn.ptnr2_auth_asym_id
_struct_conn.ptnr2_auth_comp_id
_struct_conn.ptnr2_auth_seq_id
_struct_conn.ptnr2_symmetry
_struct_conn.pdbx_dist_value
_struct_conn.pdbx_value_order
metalc1 metalc D ZN . ZN 1_555 C HIS 25 NE2 C ZN 201 C HIS 25 1_555 2.138
metalc2 metalc D ZN . ZN 1_555 C CYS 7  SG  C ZN 201 C CYS 7  1_555 2.232
metalc3 metalc D ZN . ZN 1_555 C CYS 12 SG  C ZN 201 C CYS 12 1_555 2.440
metalc4 metalc D ZN . ZN 1_555 C HIS 29 NE2 C ZN 201 C HIS 29 1_555 1.876
. . .
#
_cell.entry_id           1ZAA
_cell.length_a           45.400
_cell.length_b           56.200
_cell.length_c           130.800
_cell.angle_alpha        90.00
_cell.angle_beta         90.00
_cell.angle_gamma        90.00
_cell.Z_PDB              8
#
_atom_sites.entry_id                    1ZAA
_atom_sites.fract_transf_matrix[1][1]   0.022026
_atom_sites.fract_transf_matrix[1][2]   0.000000
_atom_sites.fract_transf_matrix[1][3]   0.000000
. . .
```



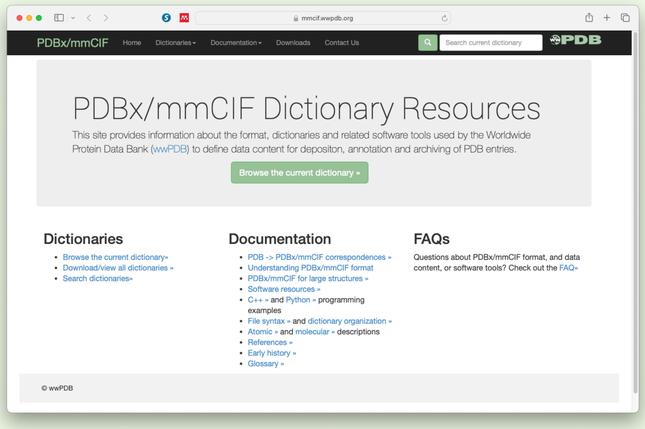
B

```
LINK         ZN    ZN C 201                NE2 HIS C  25     1555   1555  2.14
LINK         ZN    ZN C 201                SG  CYS C   7     1555   1555  2.23
LINK         ZN    ZN C 201                SG  CYS C  12     1555   1555  2.44
LINK         ZN    ZN C 201                NE2 HIS C  29     1555   1555  1.88
. . .

CRYST1   45.400   56.200  130.800  90.00  90.00  90.00 C 2 2 21       8

SCALE1      0.022026  0.000000  0.000000        0.00000
SCALE2      0.000000  0.017794  0.000000        0.00000
SCALE3      0.000000  0.000000  0.007645        0.00000
```

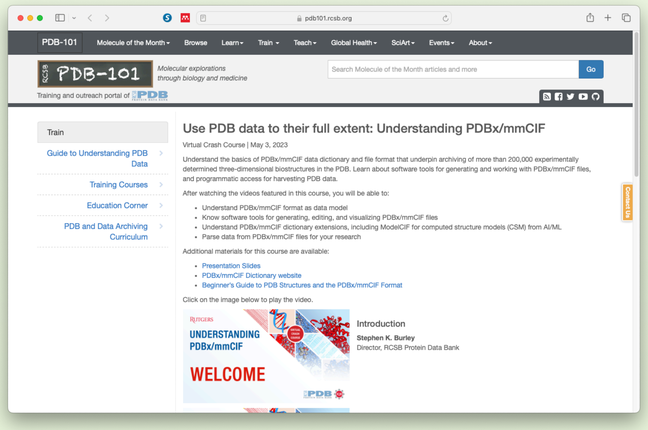
(A) Partial PDBx/mmCIF file for PDB ID 1ZAA. N.B.: Every data value has a key and multiple rows of data may be described in a table. The yellow highlighting describes the category and attributes. For the _struct_conn category, green depicts the residue numbers and cyan the component type. (B) Equivalent metadata records in legacy PDB format. Similar color coding depicts the mapping between category keys and record names as in (A), with LINK records highlighting the residue number and cyan the chemical component type. Inset figure, one of the zinc finger domains in 1ZAA depicting the side-chains that interact with the bound zinc ion codified in (A) and (B).

PDBx/mmCIF resource

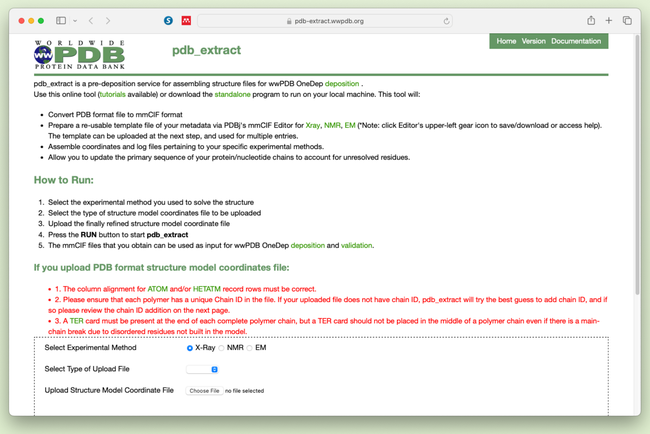
Dictionary resource https://mmcif.wwpdb.org/



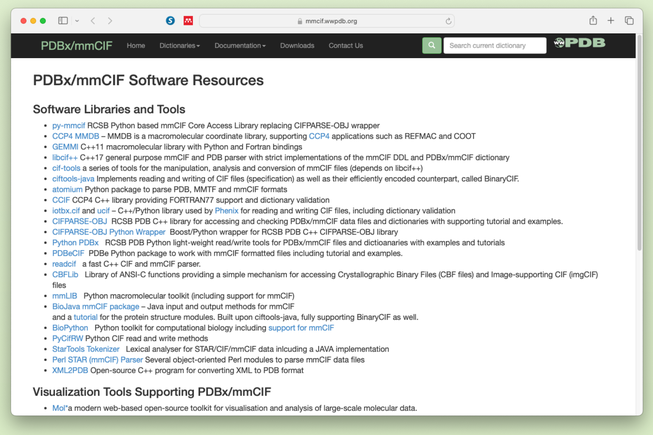
Virtual crash course https://pdb101.rcsb.org/train/training-events/mmcif



Create your mmCIF https://pdb-extract.wwpdb.org/



Software resource https://mmcif.wwpdb.org/docs/software-resources.html



NMR-STAR data model

BMRB uses NMR-STAR[2] data model to represent NMR data derived from various NMR experiments. NMR-STAR is a tag-value format similar to PDBx/mmCIF driven by NMR-STAR data dictionary. The PDBx/mmCIF and the NMR-STAR data dictionaries share common tags used to represent structure models. The NMR-STAR dictionary is focused more towards modeling NMR experimental data and PDBx/mmCIF dictionary includes data models relevant to other experimental techniques like X-Ray crystallography and Cryo-EM. The only difference between NMR-STAR and PDBx/mmCIF is that NMR-STAR uses save frames to organize and group data items.

NMR-STAR is the archival format for NMR data at the world wide Protein Data Bank

Why PDBx/mmCIF?

- **Flexibility**: mmCIF format allows for more flexibility in representing complex structural data
- **Richer Metadata**: mmCIF provides a more extensive set of data fields and metadata descriptors
- **Improved Representation of Biomolecular Assemblies**: mmCIF supports more sophisticated descriptions of macromolecular assemblies, including quaternary structures and complexes
- **Support for Large Structures**: mmCIF is better suited for representing large and complex structures, such as those determined by NMR spectroscopy
- **Future-Proofing**: mmCIF is a more modern and extensible format compared to the PDB format, which has limitations in representing certain types of structural data. By adopting mmCIF, researchers can future-proof their data and ensure compatibility with evolving standards and technologies

Overall, the mmCIF format offers a more comprehensive and flexible framework for representing NMR structures, allowing for better integration, analysis, and exchange of structural data within the scientific community.

Join us!

BMRB is leading the effort to extend the PDBx/mmCIF data model to faithfully represent the structure models derived from NMR studies. In association with wwPDB partners, BMRB is in the process of forming a PDBx/mmCIF working group for the NMR community. If you interested to contribute to the data modeling efforts and become a NMR PDBx/mmCIF working group member, feel free to contact BMRB at help@bmrb.io

BMRB is supported by NIGMS through grant R24GM150793

1. Westbrook, et al., (2022) PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology JMB 434: 167599 doi: 10.1016/j.jmb.2022.167599

2. Ulrich, et al. NMR-STAR: comprehensive ontology for representing, archiving and exchanging data from nuclear magnetic resonance spectroscopic experiments. J Biomol NMR 73, 5–9 (2019). doi: 10.1007/s10858-018-0220-3