



No more PDB format files! Welcome to PDBx/mmCIF ecosystem

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wwPDB data deposition

Model File

CPDBx/mmCIF
coordinate data and meta
data

Experimental File

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

wwPDB accept data coming from structure determination studies where as BMRB accepts all kinds of NMR data including raw experimental data.

PDBx/mmCIF Format

PDBx(Protein Data Bank exchange)/mmCIF(macromolecular Crystallographic Information File) is the master archival format of the PDB since 2014

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

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

Metadata

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
metal1 metalc D ZN . ZN 1_555 C HIS 25 NE2 C ZN 201 C HIS 25 1_555 2.138
metal2 metalc D ZN . ZN 1_555 C CYS 7 SG C ZN 201 C CYS 7 1_555 2.232
metal3 metalc D ZN . ZN 1_555 C CYS 12 SG C ZN 201 C CYS 12 1_555 2.440
metal4 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				0.000000				
SCALE2	0.000000	0.017794	0.000000				0.000000				
SCALE3	0.000000	0.000000	0.007645				0.000000				

(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 sidechains 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

NMR-STAR is the archival format for NMR data at wwPDB and BMRB.



NMR-STAR Resource

- Dictionary resource <https://bmr.io/dictionary/>
- Parser <https://pypi.org/project/pynmrstar/>
- Data visualization <https://pypi.org/project/pybmr/>

Why PDBx/mmCIF and NMR-STAR?

Integrative and hybrid methods have become more common and model files are required to carry the necessary meta data from different experiments in addition to the coordinate information. The complexity of the information like multiple conformations, ligand interactions, screening studies require proper data modeling with can only be possible using PDBx/mmCIF and NMR-STAR.

Join Us!

If you are a software developer and your software is capable of generating model data and NMR data then join us as a NMR mmCIF working group member and contribute to the data modeling and software development.

Contact: help@bmr.io

- Westbrook, *et al.*, (2022) PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology *JMB* 434: 167599 doi: [10.1016/j.jmb.2022.167599](https://doi.org/10.1016/j.jmb.2022.167599)
- 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](https://doi.org/10.1007/s10858-018-0220-3)