



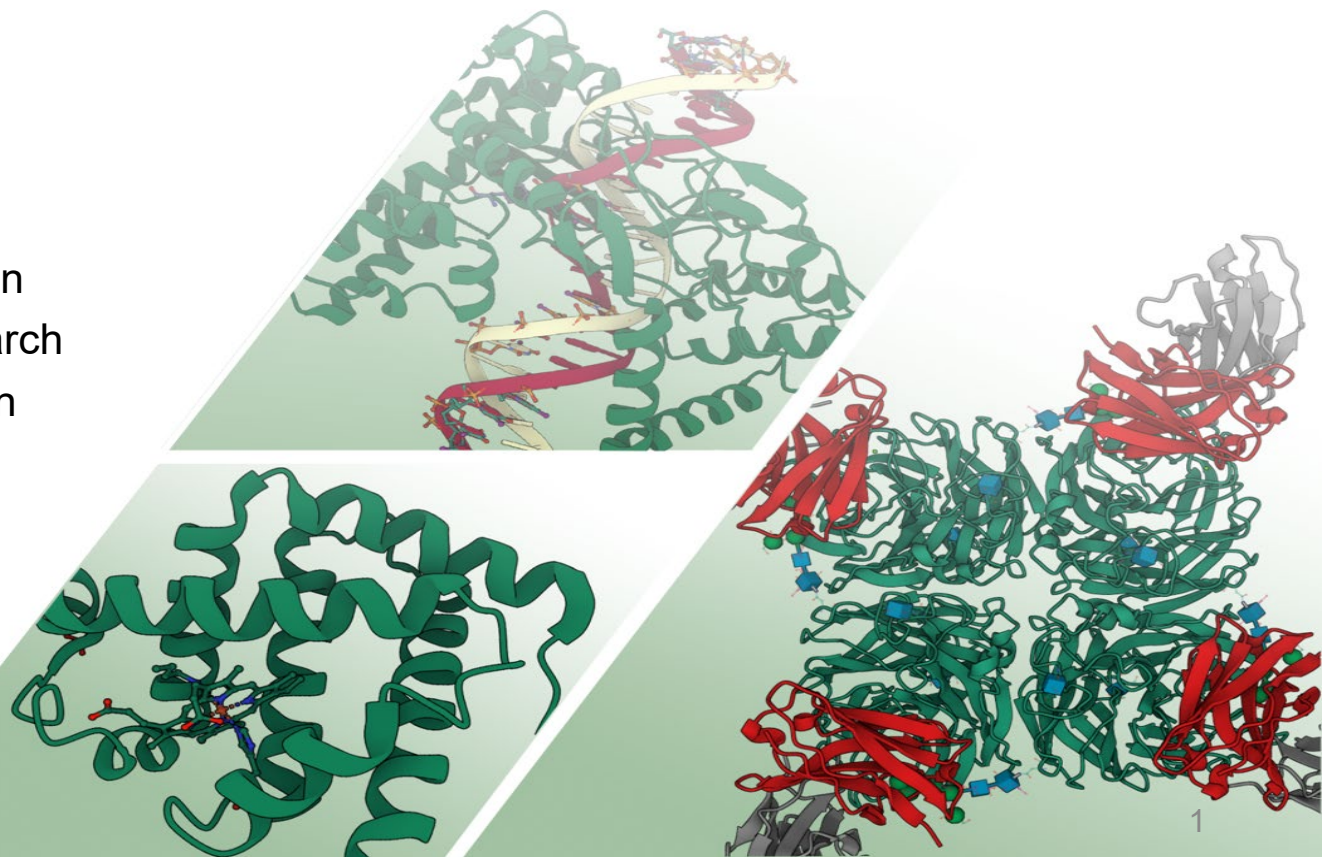
PDBj
Protein Data Bank Japan

WORLDWIDE
PDB
PROTEIN DATA BANK

Introduction to Data Deposition for PDB-Dev

Jian Yu

Protein Data Bank Japan
Institute for Protein Research
Osaka University, Japan





PDB-Dev

Prototype Archiving System for Integrative Structures

Released Entries: 171

[Home](#) [About](#) [Deposit](#) [Contact](#) [FAQ](#)

[Browse Structures](#)

Keyword Search (e.g., NPC AND 3DEM)



[Search Tips](#)

Welcome to PDB-Dev

PDB-Dev is a prototype archiving system for structural models obtained using integrative methods, funded by the NSF ABI Development Program. Structural characterization of many complex systems is increasingly carried out using integrative modeling, where a combination of computational techniques is used to determine the structure. The structural models are collected, archived and disseminated to the public through PDB-Dev. Once integrative models are fully established through PDB-Dev, the key components will be integrated into the PDB system and the PDB-Dev holdings will be moved into the PDB.

News

[All News](#)

日本語化



PDB-Dev

Prototype Archiving System for Integrative Structures

公開中のエントリー: 171

[ホーム](#) [PDB-Devについて](#) [データ登録](#) [お問い合わせ](#) [FAQ](#)

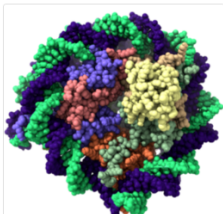
[構造を一覧する](#)

キーワード検索 (例: NPC AND 3DEM)



[検索ヒント](#)

Released PDB-Dev Structures

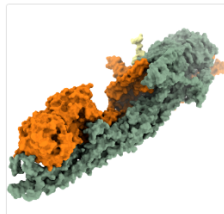


PDBDEV_00000028

RNIF168-RING domain and nucleosome complex

Release Date: 2019-04-29

Publication doi: [10.1038/s41467-019-09756-z](https://doi.org/10.1038/s41467-019-09756-z)



PDBDEV_00000030

Human Fibrin Clots

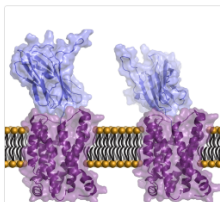
Release Date: 2020-01-10

Publication doi: [10.1073/pnas.1911785117](https://doi.org/10.1073/pnas.1911785117)

PDB-Devへようこそ

PDB-DevはNSF ABI Development Program、さらに、AMED-BINDSにより支援され、統合モデリングやハイブリッドモデリングを用いて得られた構造モデルのプロトタイプアーカイブシステムです。多くの複雑な高分子集合体の構造特性の解析は、実験と計算を補完する技術を組み合わせることで構造を決定し、統合的モデリングを用いて行われることが多くなっています。統合的モデリングによって得られた構造モデルは、PDB-Devを通じて収集・アーカイブ化され、一般に公開されています。統合モデルを処理するメカニズムがPDB-Devを通じて完全に確立されると、主要なコンポーネントはwwPDB OneDepシステムと統合し、PDB-DevのデータをPDBに移動します。

リリースされた構造



PDBDEV_00000036

Myeloid-derived growth factor with KDEI receptor

公開日: 2019-12-18

主引用文献: [10.1038/s41467-019-13577-5](https://doi.org/10.1038/s41467-019-13577-5)

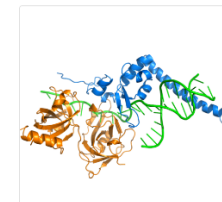


PDBDEV_00000037

Human COP9 Signalosome

公開日: 2020-01-30

主引用文献: [10.1073/pnas.1915542117](https://doi.org/10.1073/pnas.1915542117)



PDBDEV_00000039

Nucleotide excision repair complex

公開日: 2020-02-07

主引用文献: [10.1093/nar/gkz1231](https://doi.org/10.1093/nar/gkz1231)

ニュース

[全てのニュース](#)

PDB-Devで100個構造をリリースしました!

PDB-Devの重要なマイルストーンを発表します: 先着100個構造を公開しました。この成果は、PDB-Devチーム、wwPDB IHM task forceメンバー達、wwPDBリーダーシップ、RCSB PDBチームメンバー達、そして統合的構造生物学の研究結果を共有することの重要性を最初に認識したパイオニアディビジョン達を含めて、全員が継続的に協力してきた結果です。全文を読む...

PDB-Devに初めのAlphaFoldに基づく構造を登録された

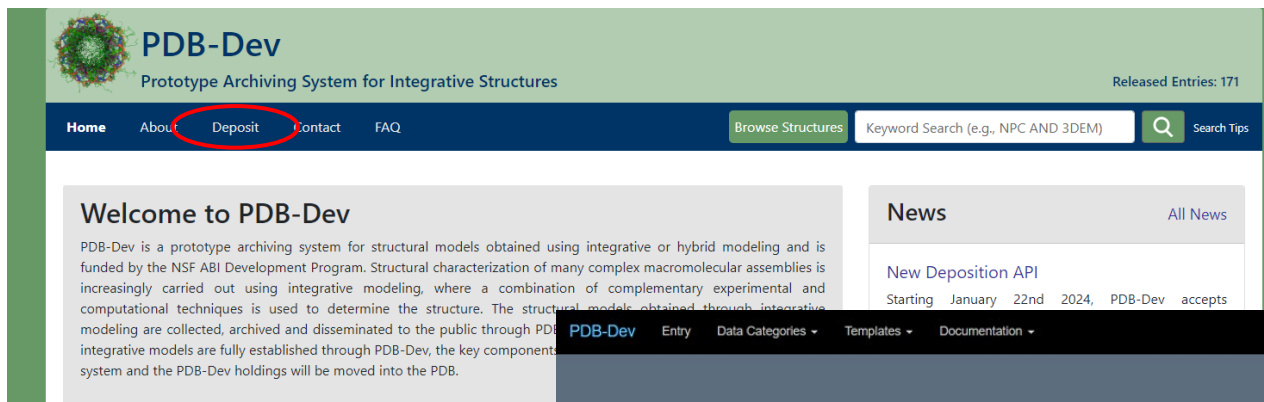
長い間で統合モデリングの初期構造の主な情報源は、Protein Data Bankからの実験構造やさまざまな比較モデリングアプローチを使用して生成された計算モデルでした。近年の機械学習革命により、AlphaFold2やRoseTTAFoldのようなモデリング手法が開発され、高品質タンパク質予測構造の新しい領域を展開しました。現在、これらの構造は最終的に統合モデリングへの道を進んでいます。全文を読む...

統合構造の検証レポート

wwPDB IHM TaskForce (Berman et al. 2019)の推奨に基づいて、PDB-Devにアーカイブされた構造の検証レポートを作成しました。検証レポートの最初バージョンは、2022年7月8日にリリースされました。全文を読む...

保留ポリシーの更新

PDB-Devに登録された構造の保留ポリシーを更新しました。wwPDBのポリシーに従い、登録日から最大1年間、エントリーを保留することが可能です。全文を読む...



PDB-Dev
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Home About **Deposit** Contact FAQ

Browse Structures Keyword Search (e.g., NPC AND 3DEM) Search Tips

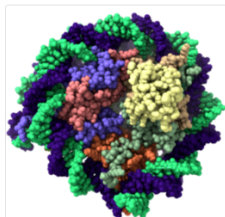
Welcome to PDB-Dev

PDB-Dev is a prototype archiving system for structural models obtained using integrative or hybrid modeling and is funded by the NSF ABI Development Program. Structural characterization of many complex macromolecular assemblies is increasingly carried out using integrative modeling, where a combination of complementary experimental and computational techniques is used to determine the structure. The structural models obtained through integrative modeling are collected, archived and disseminated to the public through PDB-Dev. As integrative models are fully established through PDB-Dev, the key components of the system and the PDB-Dev holdings will be moved into the PDB.

[PDB-Dev](#) [Entry](#) [Data Categories](#) [Templates](#) [Documentation](#)

[Go to RID](#) [Sign Up](#) [Log In](#)

Released PDB-Dev Structures

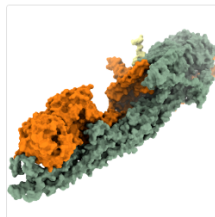


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The Data Harvesting System provides an automated mechanism for collecting diverse and heterogeneous types of integrative structures and restraint data. The system has been developed using the DERIVA scientific asset management platform and is supported by the PDBx/mmCIF dictionary, the IHM-dictionary and the python-ihm software library.

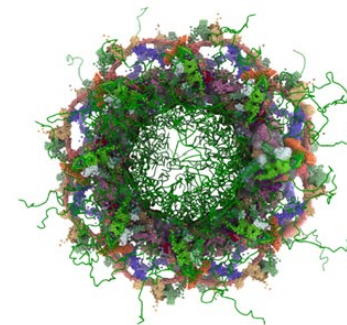
Use the links below to start exploring the system.

New Account: [Register using Globus](#)

Submit Data: [Create a New Entry](#)

Documentation: [User Guide](#)

Please report problems to pdb-dev@mail.wwpdb.org.



- Choose how to login to Globus (using organizational account, GitHub, google account or ORCID ID).



Log in to use Globus Web App

Use your existing organizational login


e.g., university, national lab, facility, project

Look-up your organization...


By selecting Continue, you agree to Globus [terms of service](#) and [privacy policy](#).

Continue

OR

 Sign in with GitHub

 Sign in with Google

 Sign in with ORCID iD

Didn't find your organization? Then use [Globus ID to sign in](#). (What's this?)



Sign in with Google account




Sign in with Google

Choose an account

to continue to globus.org



 Use another account

To continue, Google will share your name, email address, language preference, and profile picture with globus.org. Before using this app, you can review [globus.org's privacy policy](#) and [terms of service](#).

English (United States) ▾

Sign in with Google

Sign in to globus.org

By continuing, Google will share your name, email address, language preference, and profile picture with globus.org. See [globus.org's Privacy Policy](#) and [Terms of Service](#).

You can manage Sign in with Google in your [Google Account](#).

[Cancel](#) [Continue](#)

English (United States) ▾

[Help](#) [Privacy](#) [Terms](#)

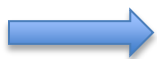
Successfully log in



Welcome – You've Successfully Logged In

This is the first time you are accessing Globus with your **Google** login.

If you have previously used Globus with another login you can link it to your **Google** login. When linked, both logins will be able to access the same Globus account permissions and history.



Continue

Link to an existing account

[Why should I link accounts?](#)

Complete a short signup form



Complete Your Sign Up For [redacted]

Name [redacted]

Email [redacted]

Organization

Account will be used for

- non-profit research or educational purposes
- commercial purposes

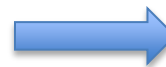
I have read and agree to the Globus [Terms of Service](#) and [Privacy Policy](#).

Please e-mail me updates about Globus

Continue

* This field is specified by the identity provider, and cannot be modified by Globus. If you change it with your identity provider, it will propagate to Globus the next time you log in.

Provide consent to
access your credentials



Provide consent to access your credentials



Account ▾

Globus Web App would like to:

- ✓ View the identities in your Globus account ⓘ
- ✓ Manage data using Globus Transfer ⓘ
- ✓ Manage your Globus groups (v2) ⓘ
- ✓ Search for data using your identities and groups ⓘ



To work, the above will need to: ▾




By clicking "Allow", you allow **Globus Web App**, in accordance with its [terms of service](#) ⓘ and [privacy policy](#) ⓘ, to use the above listed information and services. You can rescind this and other [consents](#) ⓘ at any time.


Allow

Deny

“pdb-submitter” globus group webpage

  pdb-submitter


 Overview  Members  Subgroups


Group UUID	99da042e-64a6-11ea-ad5f-0ef992ed7ca1 
Group Name	pdb-submitter
Description	pdb-submitter group is for users to submit data. Users have access to entries he/she creates and not to others.
Terms & Conditions	—
Enforce Session	false
High Assurance	false
Authentication Timeout	0 milliseconds
Group Visibility	authenticated
Membership Visibility	managers
Join Requests	true
Signup Fields	—

 [Get Shareable Link](#)

 [Join this Group](#)

- FILE MANAGER
- BOOKMARKS
- ACTIVITY
- COLLECTIONS
- GROUPS**
- CONSOLE
- FLows
- COMPUTE
- SETTINGS
- LOGOUT
- HELP & SITEMAP

- 
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- CONSOLE
- FLows
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 PDB-SUBMITTER
Join Group

Identity

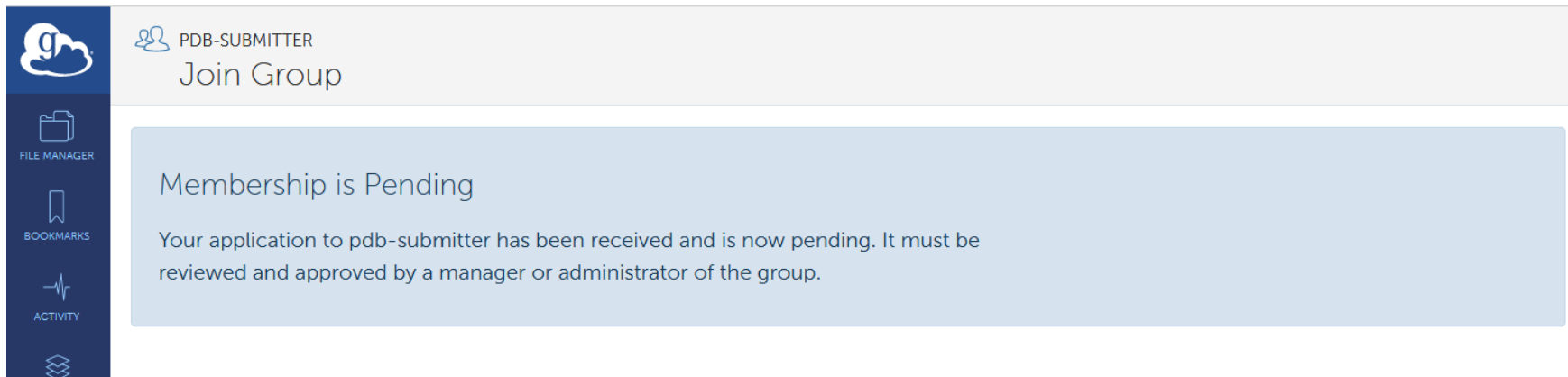
First Name


Last Name

Organization

Wait for the approval

Once the administrator has approved your join request, go to <https://data.pdb-dev.org> and login to set up the globus account.



 PDB-SUBMITTER
Join Group

Membership is Pending

Your application to pdb-submitter has been received and is now pending. It must be reviewed and approved by a manager or administrator of the group.

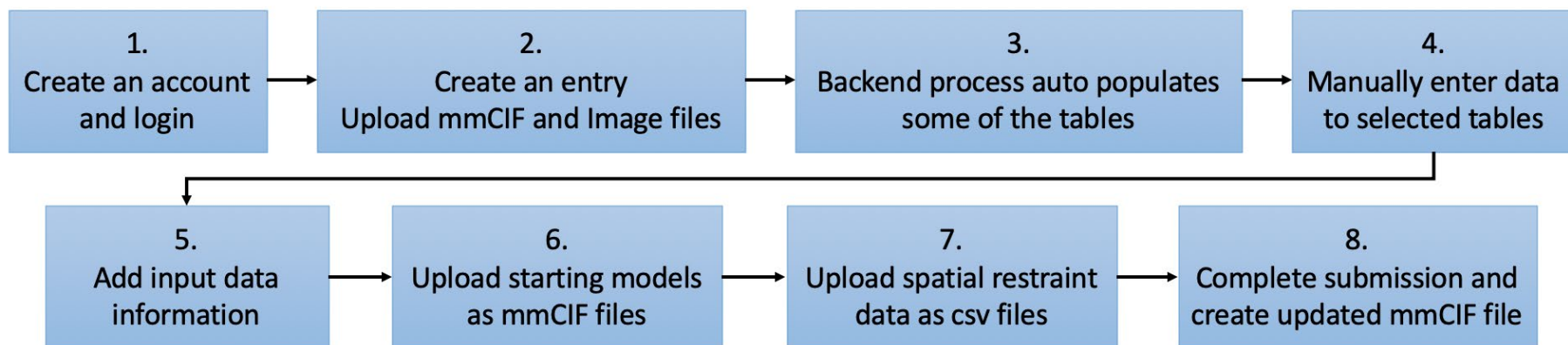
FILE MANAGER

BOOKMARKS

ACTIVITY

Workflow outline for data submission

Steps involved in creating a complete mmCIF file for PDB-Dev



Step 1: Create new entry and upload mmCIF and image files



PDB-Dev **Entry** Data Categories ▾ Templates ▾ Documentation ▾ Go to RID

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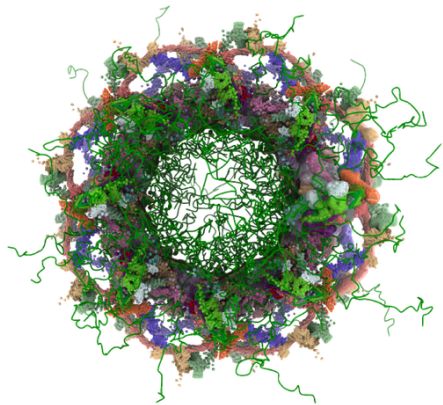
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Documentation: [User Guide](#)

Please report problems to pdb-dev@mail.wwpdb.org.



RUTGERS
THE STATE UNIVERSITY
OF NEW JERSEY

UCSF
University of California
San Francisco

USC Viterbi
School of Engineering
Information Sciences Institute

deriva

Create entry and input the data at entry page

Entry*

Export Permalink

Search all columns

Refine search

Hide panel

Displaying 0 records

+ Create

Accession Code

Search all columns

No results found

Show Details

Actions	RID	Id	User Provided mmCIF File	Last Communicated	User Provided Image File
---------	-----	----	--------------------------	-------------------	--------------------------

Previous Next



Create 1 Entry* record

Save

* Indicates required field

Qty 1 Clone

Record Number	1
* User Provided mmCIF File	<input type="text"/> Select file
User Provided Image File	<input type="text"/> Select file
* Workflow Status	Select a value ▼
* User Provided Method Details	<input type="text"/>

Input the data at entry page

Create 1 Entry* record

* indicates required field

Save Qty 1 Clone

Record Number	1
* User Provided mmCIF File ⓘ	<input type="text"/> Select file
User Provided Image File ⓘ	<input type="text"/> Select file
* Workflow Status ⓘ	Select a value ▼
* User Provided Method Details ⓘ	<input type="text"/>

Select Workflow Status for new Entry* ⓘ

X Cancel

Search all columns Q

Show filter panel

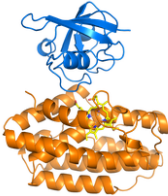
Displaying all 11 of 11 records

Select	RID ⓘ	Name ⓘ	Description ⓘ	Rank ⓘ
<input checked="" type="checkbox"/>	1-MSVE	DRAFT	User is adding/updating/removing data	1
<input checked="" type="checkbox"/>	1-MSVG	DEPO	Deposit data for automated backend process	2
<input checked="" type="checkbox"/>	1-MSVJ	RECORD READY	Automated backend process complete and ready for review	3
<input checked="" type="checkbox"/>	1-MSVM	SUBMIT	User has completed deposition and submitted the entry for processing	4
<input checked="" type="checkbox"/>	1-MSVP	mmCIF CREATED	Export to mmCIF complete	5
<input checked="" type="checkbox"/>	1-SC56	SUBMISSION COMPLETE	The curator has checked and is happy with the submission.	6
<input checked="" type="checkbox"/>	1-MSVT	HOLD	Entry is on hold for publication	7
<input checked="" type="checkbox"/>	1-SC58	RELEASE READY	The curator has triggered the release process.	8
<input checked="" type="checkbox"/>	1-MSVW	REL	Entry is released after publication	9
<input checked="" type="checkbox"/>	1-MTG0	ERROR	Error processing uploaded file	10
<input checked="" type="checkbox"/>	2-PYH8	ABANDONED	Entry abandoned by author without agreeing to delete	11

“Workflow Status” for the entry updated to “Record Ready”

Sections Hide panel **Entry**^{*} ?: D_3-7B8W + Create Copy Edit Delete

- Summary
- System Generated Files (0)
- Description of the Structure^{*} (1)**
- Authors^{*} (0)
- Citations^{*} (0)
- Authors in Citations^{*} (0)
- Software^{*} (0)
- Chemical Components^{*} (22)
- Molecular Entities^{*} (2)**
- Common Names of Entities (0)
- Systematic Names of Entities (0)
- Source of Genetically Manipulated Entities (0)
- Reference sequence information^{*} (0)
- Alignment information with the reference sequence^{*} (0)

RID ?	3-7B8W
Id ?	D_3-7B8W
RCB ?	
RMB	
User Provided mmCIF File ?	cluster1_1.cif
mmCIF File Size (Bytes) ?	354 kB ?
User Provided Image File ?	
3D Visualization	Not Available
Image File Size (Bytes) ?	1.72 MB ?
Workflow Status ?	RECORD READY
Process Status	Success
Record Status Detail ?	
Deposit Date ?	2024-03-12
User Provided Method Details ?	X-ray, NMR, HADDOCK

Step 2: Add/modify data manually

Sections

Hide panel

Summary

System Generated Files (0)

Description of the Structure* (1)

Authors* (0)

Citations* (0)

Authors in Citations* (0)

Software* (0)

Chemical Components* (22)

Molecular Entities* (2)

Common Names of Entities (0)

Systematic Names of Entities (0)

Source of Genetically Manipulated Entities (0)

Reference sequence information* (0)

Alignment information with the reference sequence* (0)

Point differences in the alignment with the reference sequence (0)

Polymeric Entities* (2)

Non-polymeric Entities

Entry*ⁱ: D_3-7B8W

[+ Create](#) [Copy](#) [Edit](#) [Delete](#)

Authors*

[+ Add records](#) [Bulk Edit](#) [Explore](#)

Authors of the structure; mmCIF category: audit_author; Example of author name format: Jones, T.J.

Displaying 0 records

Actions ⁱ	RID ⁱ	Ordinal ⁱ	Name ⁱ
No Results Found			

[Previous](#) [Next](#)

Citations*

[+ Add records](#) [Bulk Edit](#) [Explore](#)

Citation information for the primary publication as well as other relevant software and methodology; mmCIF category: citation

Displaying 0 records

Actions ⁱ	RID ⁱ	Id ⁱ	Title ⁱ	Year ⁱ	Abbreviated Journal Name (CASSI) ⁱ	Journal Volume ⁱ	Journal Issue ⁱ
No Results Found							

[Previous](#) [Next](#)

Authors in Citations*

[+ Add records](#) [Bulk Edit](#) [Explore](#)

Authors associated with publications in the citation list; mmCIF category: citation_author; Example of author name format: Jones, T.J.

Displaying 0 records

Actions ⁱ	RID ⁱ	Citation Id ⁱ	Ordinal ⁱ	Name ⁱ
No Results Found				

[Previous](#) [Next](#)

Software*

[+ Add records](#) [Bulk Edit](#) [Explore](#)

Input the starting model



Starting Structural Models*

+ Add records

Bulk Edit

Explore

Information regarding starting structural models used in the integrative modeling study; mmCIF category: ihm_starting_model_details

Displaying 0 records

Actions ⓘ	RID ⓘ ↕	Starting Model Id ⓘ ↕	Entity Id ⓘ	Entity Description ⓘ ↕	Asym Id ⓘ	Entity Poly Segment Id ⓘ
-----------	---------	-----------------------	-------------	------------------------	-----------	--------------------------



Create 1 Starting Structural Models* record

Save

* indicates required field

Qty | 1 | Clone

Record Number	1
* Structure Id ⓘ	D_3-7B8W
* Starting Model Id ⓘ	<input type="text"/>
* Entity Id ⓘ	Select a value <input type="button" value="v"/>
Entity Description ⓘ	<input type="text"/>
* Asym Id ⓘ	Select a value <input type="button" value="v"/>
Entity Poly Segment Id ⓘ	Select a value <input type="button" value="v"/>
* Starting Model Source ⓘ	Select a value <input type="button" value="v"/>
* Author Provided Chain Id for the Starting Model ⓘ	<input type="text"/>
Starting Model Sequence Offset ⓘ	<input type="text"/>
Description ⓘ	<input type="text"/>
* Dataset List Id ⓘ	Select a value <input type="button" value="v"/>
mmCIF File for the Starting Model ⓘ	<input type="text"/> <input type="button" value="Select file"/>

Experimental data



Input Datasets*

+ Add records Bulk Edit Explore

List of all input datasets used in the integrative modeling study, including data from different types of experiments and starting models from different sources; mmCIF category: ihm_dataset_list

Displaying all 1 records

Actions	RID	Id	Data Type	Database Hosted	Details
	3-7BZC	1	NMR data	NO	

Edit Input Datasets*: 1

Save Delete

Reset

* indicates required field

Record Number	1
* Structure Id	D_3-7B8W
* Id	1
* Data Type	NMR data
* Database Hosted	NO
Details	

Datasets Archived in Other Repositories

+ Add records Bulk Edit Explore

Details of input datasets archived in other repositories, including experimental data and starting structural models; mmCIF category: ihm_dataset_related_db_reference

Displaying all 1 records

Actions	RID	Id	Dataset List Id	Database Name	Accession Code	Version	Details
	3-7BZE	1	1	BMRB	BMR00000		

Edit Datasets Archived in Other Repositories: 3-7BZE

Save Delete

Reset

* indicates required field

Record Number	1
* Structure Id	D_3-7B8W
* Id	1
* Dataset List Id	1
* Database Name	BMRB
* Accession Code	BMR00000

Other restraint files



Uploaded Restraint Files

+ Add records

Bulk Edit

Explore

Uploaded restraint data files (in csv/tsv format) related to the entry. Crosslinking restraints, predicted contacts, generic distance restraints etc. can be uploaded as CSV/TSV files in the correct format. Only one file of a particular type can be uploaded. The appropriate tables will be populated based on the uploaded data. Templates for the CSV files can be downloaded from https://data.pdb-dev.org/chaise/recordset/#1/PDB:Entry_Related_File_Templates

Create 1 Uploaded Restraint Files record

Save

* indicates required field

Qty 1 Clone

Record Number	1
* Structure Id ⓘ	D_3-7B8W
* File Type ⓘ	Select a value
* File Format ⓘ	Select a value
* Uploaded File ⓘ	Select file
Description ⓘ	
* Restraint Workflow Status ⓘ	DRAFT



Displaying all 22 of 22 records

Select	RID ⓘ	Name ⓘ	Table Name	Description ⓘ	RCB	RMB	RCT ⓘ	RMT ⓘ
<input checked="" type="checkbox"/>	1-MT0J	Chemical Crosslinks from Experiments	ihm_cross_link_list	List of distance restraints derived from chemical crosslinking experiments			2020-04-15 04:02:37	2021-06-15 05:29:38
<input checked="" type="checkbox"/>	1-MT0M	Chemical Crosslinking Restraints Applied in the Modeling	ihm_cross_link_restraint	Chemical crosslinking restraints used in modeling			2020-04-15 04:02:37	2021-06-15 05:29:38
<input checked="" type="checkbox"/>	1-MT0P	Chemical Crosslink Restraint Results	ihm_cross_link_result	Results of the crosslinking restraints in integrative modeling			2020-04-15 04:02:37	2021-06-15 05:29:38
<input checked="" type="checkbox"/>	1-MT0R	Chemical Crosslink Restraint Result Parameters	ihm_cross_link_result_parameters	Parameters related to the results of crosslinking restraints			2020-04-15 04:02:37	2021-06-15 05:29:38
<input checked="" type="checkbox"/>	1-MT0T	Predicted Contact Restraints	ihm_predicted_contact_restraint	Restraints derived from predicted contacts			2020-04-15 04:02:37	2021-06-15 05:29:38
<input checked="" type="checkbox"/>	1-MT0W	Hydroxyl Radical Footprinting Restraints	ihm_hydroxyl_radical_fp_restraint	Data from hydroxyl radical footprinting experiments used as restraint in modeling			2020-04-15 04:02:37	2021-06-15 05:29:38

CSV Templates for Restraint Files



Entry Related File

CSV Templates for Restraint Files

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- 1-N0NC
- 1-N0NE
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- 1-N0NJ
- 1-N0NM
- 1-N0NP
- 1-N0NR
- 1-N0NT
- 1-N0NW
- 1-N0NY

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> File Type

View	RID	File Type	File Url	Description
	1-N0NC	Chemical Crosslinks from Experiments	Chemical-Crosslinks-from-Experiments.csv	List of distance restraints derived from chemical crosslinking experiments
	1-N0NE	Chemical Crosslinking Restraints Applied in the Modeling	Chemical-Crosslinking-Restraints-Applied-in-the-Modeling.csv	Chemical crosslinking restraints used in modeling
	1-N0NG	Chemical Crosslink Restraint Results	Chemical-Crosslink-Restraint-Results.csv	Results of the crosslinking restraints in integrative modeling
	1-N0NJ	Chemical Crosslink Restraint Result Parameters	Chemical-Crosslink-Restraint-Result-Parameters.csv	Parameters related to the results of crosslinking restraints
	1-N0NM	Predicted Contact Restraints	Predicted-Contact-Restraints.csv	Restraints derived from predicted contacts
	1-N0NP	Hydroxyl Radical Footprinting Restraints	Hydroxyl-Radical-Footprinting-Restraints.csv	Data from hydroxyl radical footprinting experiments used as restraint in modeling
	1-N0NR	Molecular Features used in Generic Restraints	Molecular-Features-used-in-Generic-Restraints.csv	List of features (atoms, residues, residue ranges, non-polymeric entities, pseudo sites) used in generic distance restraints
	1-N0NT	Molecular Features Comprising of Pseudo Sites	Molecular-Features-Comprising-of-Pseudo-Sites.csv	Details of pseudo positions used in generic distance restraints
	1-N0NW	Molecular Features Comprising of Polymeric Atoms	Molecular-Features-Comprising-of-Polymeric-Atoms.csv	Details of atomic features of polymeric entities
	1-N0NY	Molecular Features Comprising of Polymeric Residues	Molecular-Features-Comprising-of-Polymeric-Residues.csv	Details of polymeric residue features
	1-N0P0	Molecular Features Comprising of Non-polymeric Entities	Molecular-Features-Comprising-of-Non-polymeric-Entities.csv	Details of non-polymeric (ligand) features
	1-N0P2	Molecular Features Comprising of Polymeric Residues at Interfaces	Molecular-Features-Comprising-of-Polymeric-Residues-at-Interfaces.csv	Details of residues at the binding interface
	1-N0P4	Generic Distance Restraints Between Molecular Features	Generic-Distance-Restraints-Between-Molecular-Features.csv	Generic distance restraints between features (atoms, residues, non-polymeric entities, pseudo sites)
	1-N0P6	Distance Restraints between Geometric Objects and Molecular Features	Distance-Restraints-between-Geometric-Objects-and-Molecular-Features.csv	Generic distance restraints between geometric objects and molecular features (atoms, residues etc.)
	1-N0P8	Residue Positions in Polymeric Entities where Probes are Attached	Residue-Positions-in-Polymeric-Entities-where-Probes-are-Attached.csv	Specific residue positions in the polymeric entity where probes are covalently attached
	1-N0PA	Probes Attached to Residues in Polymeric Entities	Probes-Attached-to-Residues-in-Polymeric-Entities.csv	Probes that are covalently attached to residues in polymeric entities
	1-N0PC	Non-polymeric Entities used as Probes	Non-polymeric-Entities-used-as-Probes.csv	Non-covalently interacting ligands used as probes
	1-N0PE	Pseudo Site Coordinates	Pseudo-Site-Coordinates.csv	Details of pseudo sites used in restraints or model representation

Submission step

Submit entry and wait for mmCIF generation. Once all data are entered/uploaded, the “Workflow Status” column in the “Entry” table needs to be changed to “Submit” .

Accession codes

Accession codes will be provided by PDB-Dev after the submission has been processed to ensure compliance with the IHMCIF dictionary and all the necessary information has been provided. The accession code will be updated in the “entry” table under the “accession code” column.

Thanks for your attention !