PDBj

Protein Data Bank Japan

https://pdbj.org

Protein Data Bank Japan (**PDBj**) begun to accept new structures from researchers from Asia/Oceania region, from July 2000. We founded worldwide PDB (**wwPDB**: https://www.wwpdb.org/) in 2003 by collaborating with **RCSB-PDB** from the US, **PDBe-EBI** in the EU and **PDBj**, representing the Asia/Oceania region. In 2006, Biological Magnetic Resonance Data Bank (**BMRB**) joined wwPDB. The wwPDB members and experts of structural biology constitute wwPDB Advisory Committee (**wwPDBAC**) and hold regular annual meetings. We manage wwPDB in accordance with the suggestions from the meeting.

Every year, structures of more than 10,000 biological macromolecules are deposited. In May 2023, the number of total entries was over 200,000. Since the beginnig of PDBj, we processed more than 50,000 PDB entries largely from the Asian region, which constitutes approximately one-fourth of the total. Moreover, the entries are regularly inspected for quality. Furthermore, we accept experimental data from nuclear magnetic resonance (NMR) and electron microscopy experiments and provide various tools and services. Our web site is also available in mobile environments, such as Android and iOS platforms.

We occasionally hold workshops for users to promote the utilization of our services and obtain feedback to help improving them.

Our activity is supported by **JST-NBDC** (National Bioscience Database Center, Japan Science, and Technology Agency) and the **MEXT grants for joint usage and research center assigned to Institute for Protein Research (IPR), Osaka University**.

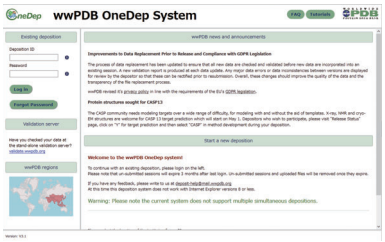
We founded Japan Alliance for Bioscience Information (**JBI**), with other databases, such as NBDC to accelerate the cooperation. We look forward to your continuous support and cooperation.

PDBj Activities

* From left to right, 1MBN, 1EMA, 2RH1, 1K4C, 1V54, 3VKH, and 1FFK.

PDB Data Deposition

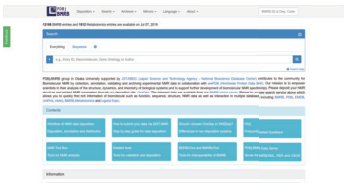
https://deposit-pdbj.wwpdb.org/deposition

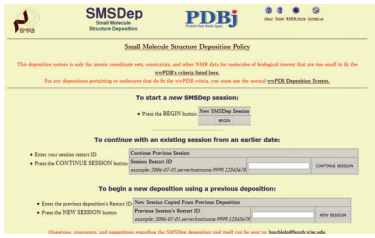


PDBj accepts data depositions largely from the Asian region. The deposited structures are released at the appointed date from each PDB partner site simultaneously.

BMRB (Biological Magnetic Resonance Data Bank)

https://bmrbj.pdbj.org/



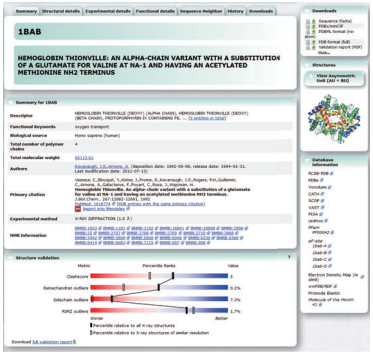


When the molecular structure is solved by NMR method, the NMR-specific information is deposited to Biological Magnetic Resonance Data Bank (**BMRB**) while atomic coordinate information is deposited to PDB. BMRB is managed by two groups: the **University of Connecticut** and **BMRBj**, subgroup of PDBj.

Small Molecule Structure Deposition (**SMSDep**), which accepts both the structural data and NMR experimental information for small biomolecules that are not accepted by PDB, is provided as BMRBj original service.

PDBj Mine (PDB Structure Search)

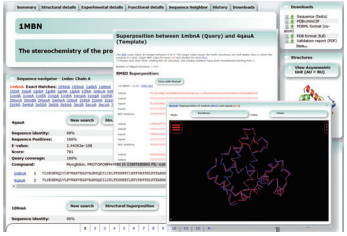
https://pdbj.org/mine



PDBj Mine is the web service for PDB entry search. In addition to keyword search, searching with detail criteria is available in **advanced** and **SQL** search. Moreover, searching with chemical components as defined in PDB, articles in PDBj site, such as news and help sections, and unreleased entries' details, such as release date and current process step, are available.

Sequence Navigator: Similar Sequence Search

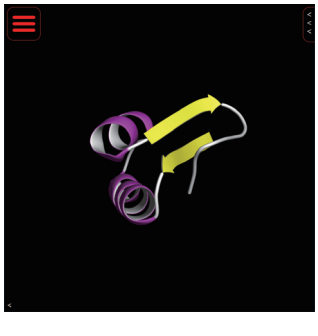
https://pdbj.org/seqnavi



Sequence Navigator is a BLAST search tool that finds PDB structures with similar amino acid sequences. It accepts two types of queries. One comprises amino acid sequences and the other consists of the concatenated string with PDB ID and Chain ID that already exist in PDB. The latter search type is also available from the **Sequence Neighbor** tab in each PDB entry page.

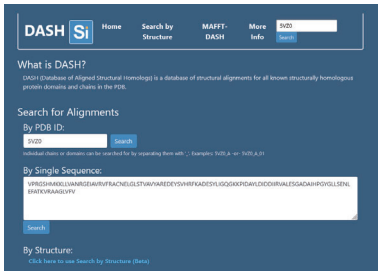
Molmil: Molecular Viewer works in Web Browsers

https://pdbj.org/help/molmil



Molmil is a molecular viewer that works in web browsers. It is available on mobile (Android and iOS) and desktop (Windows, Macintosh and Linux) platforms.

DASH: Similar Structure Search
https://sysimm.org/dash/



DASH is a tool to find molecules with similar structures from PDB. It accepts PDBID, amino acid sequence information, and structural data files written in PDB or mmCIF format as queries.

PDBj numon: Educational resource
https://numon.pdbj.org/

In addition to the main site, PDBj provides **PDBj numon**, which is dedicated for educational research purpose and helps to understand biomolecules.

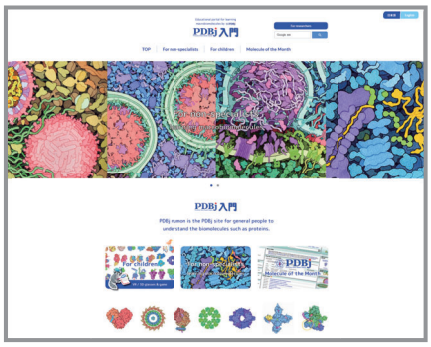
VR Molecular Viewer: Experience the molecular world with VR

Yorodumi Prime: Simple explanation and anaglyph stereo viewer for molecules

Paper models: For making molecular models using paper

Molecule of the Month: The Japanese translation of articles which introduce molecules in PDB. The original articles are provided from PDB-101 of RCSB PDB.

Games: Pelmanism of amino acids and proteins, and snake game to construct amino acid sequences.

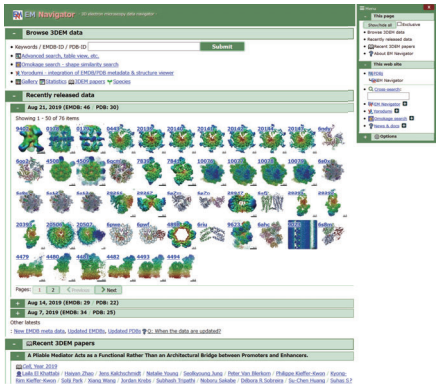


EM Navigator / Omokage Search / Yorodumi
https://pdbj.org/emnavi/
https://pdbj.org/emnavi/omo-search.php
https://pdbj.org/yorodumi/

EM Navigator is a web site to search and browse the EMDB data that include potential maps derived from electron microscopy. It can use easily without technical knowledge and experience.

Omokage Search is a service to search similar structural shapes from PDB atomic models, EMDB pottential map and Small Angle Scattering Biological Data Bank (SASBDB) molecular models.

The services described above work under the common molecular browsing service, **Yorodumi**.

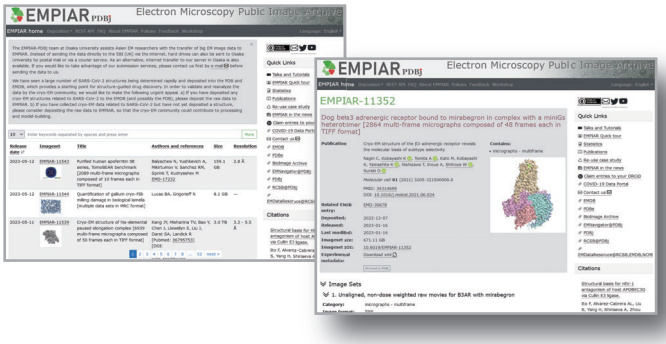


The services provided by PDBj are described in *Protein Science* (2022) vol.31, **173-186**. See also PDBj help (https://pdbj.org/help/) that includes detailed explanations and tutorial.

EMPIAR: 2D Electron Microscope Image Archive
https://empiar.pdbj.org/

EMPIAR is a database of two-dimensional electron microscope images used to solve three-dimensional molecular information (atomic structures and potential maps). It helps to access raw data obtained by using state-of-the-art technology easily and encourages method development and validation work to get better 3D structures.

PDBj manages a mirror of the main site at EBI in the UK as well as provides the information in the localized languages. In addition, since the size of the deposition data is considerably large and it takes a long time to transfer the data to the main site, we also provide a service that receive the HDDs and upload the data in place of the depositor.

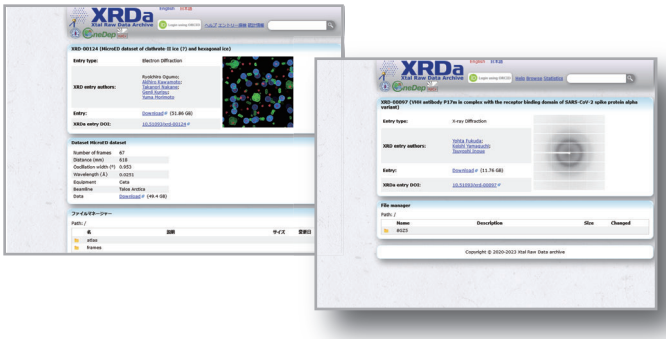


BSMA: In silico Biological Structure Archive
https://bsma.pdbj.org/

BSMA (Biological Structure Model Archive) is a database of biomacromolecule structures solved by in silico structural biology methods such as molecular dynamics and homology modeling.

XRDa: Raw Crystal Image Archive
https://xrda.pdbj.org/

XRDa (crystal Raw Data Archive) is a database of diffraction images used to solve molecular structures using crystal diffraction techniques such as X-ray, electron, and neutron.



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