

PDBj: Protein Data Bank Japan

「日本蛋白質構造データバンク」

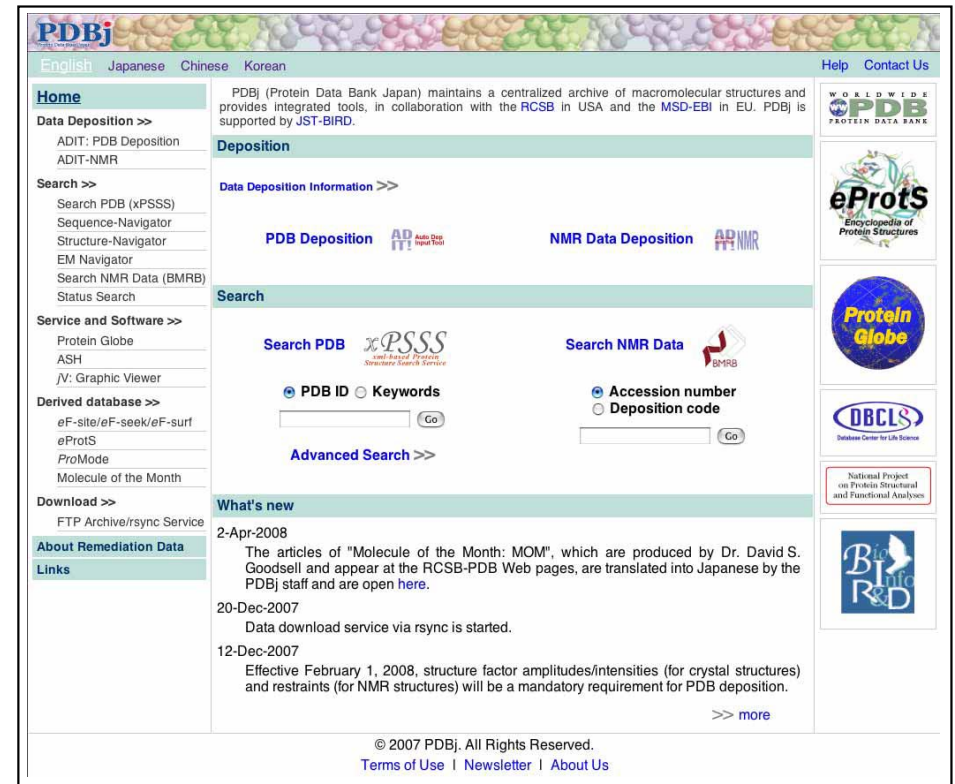
活動とサービスについて

中村春木



大阪大学蛋白質研究所

<http://www.pdbj.org/>



- Structure Data curation and editing
- Structure Data browsing and downloading

PDBj members at IPR, Osaka Univ.





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wwPDB Agreement

Statistics

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Access the PDB FTP:

RCSB PDB

MSD EBI

PDBj

Deposit Data to the PDB:

RCSB PDB

MSD EBI

PDBj

BMRB

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PDB Archive Snapshots

PDB Remediation

Description

Chemical Component

The Worldwide Protein Data Bank (wwPDB) consists of organizations that act as deposition, data processing and distribution centers for PDB data. The founding members are **RCSB PDB** (USA), **MSD EBI** (Europe) and **PDBj** (Japan). The **BMRB** (USA) group joined the wwPDB in 2006. The mission of the wwPDB is to maintain a single Protein Data Bank Archive of macromolecular structural data that is freely and publicly available to the global community.

This site provides information about services provided by the individual member organizations and about projects undertaken by the wwPDB.

22-January-2008

Time-stamped Copies of PDB Archive Available via FTP

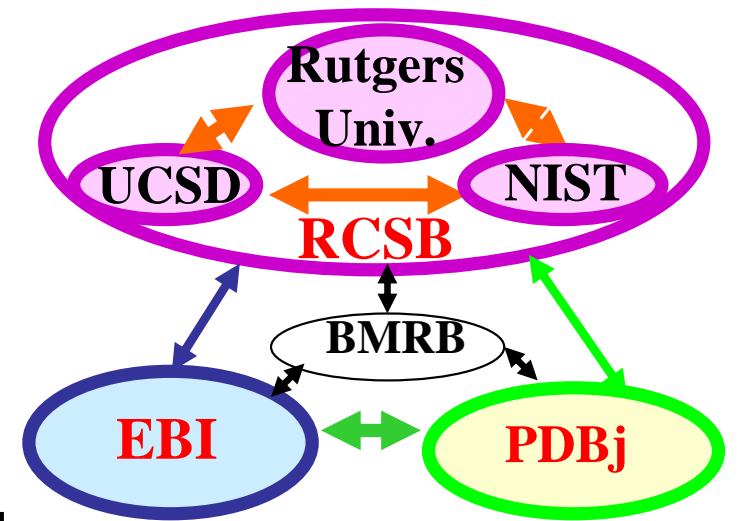
A time-stamped snapshot of the PDB archive (<ftp://ftp.wwpdb.org>) as of January 7, 2008 has been added to <ftp://snapshots.rcsb.org/>.

Snapshots of the PDB have been archived annually since 2004. It is hoped that these snapshots will provide readily identifiable data sets for research on the PDB archive.

The script at <ftp://snapshots.rcsb.org/rsyncSnapshots.sh> may be used to make a local copy of a snapshot or sections of the snapshot.

The directory 20080107 includes the 48,161 experimentally-determined coordinate files that were current as of January 7, 2008. Coordinate data are available in PDB, mmCIF, and XML formats. The date and time stamp of each file indicates the last time the file was modified.

International collaboration in wwPDB



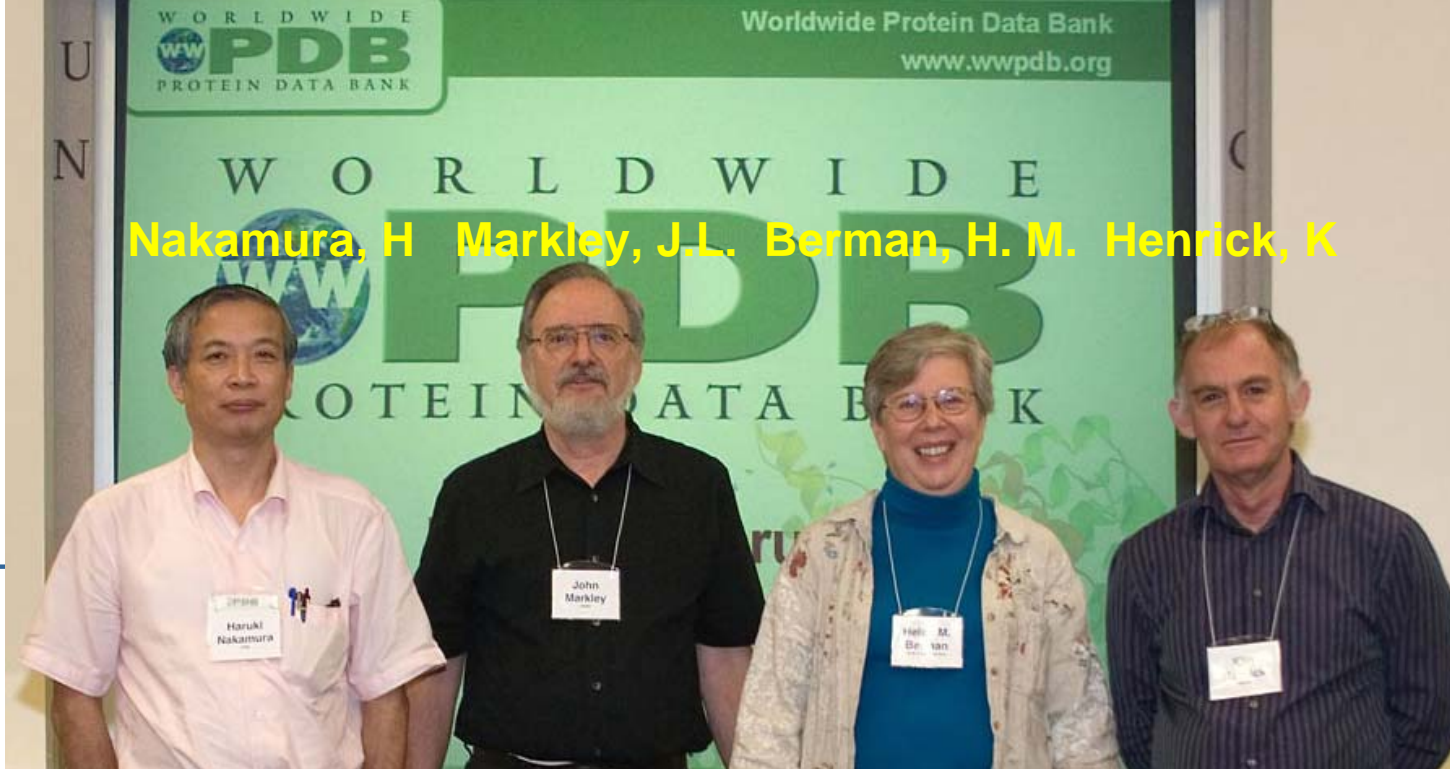
1) Curation, data processing, and registration are made by all the members, collaborating with each other.

2) We have a single data archive, which is looked after by one “archive keeper (RCSB)”.

3) Data format and new descriptions will be discussed among the members.

4) Members are encouraged to develop their own browsers, viewers, and other APIs and services.

(Berman, Henrick & Nakamura (2003) Nat. Struct. Biol. 10, 980)





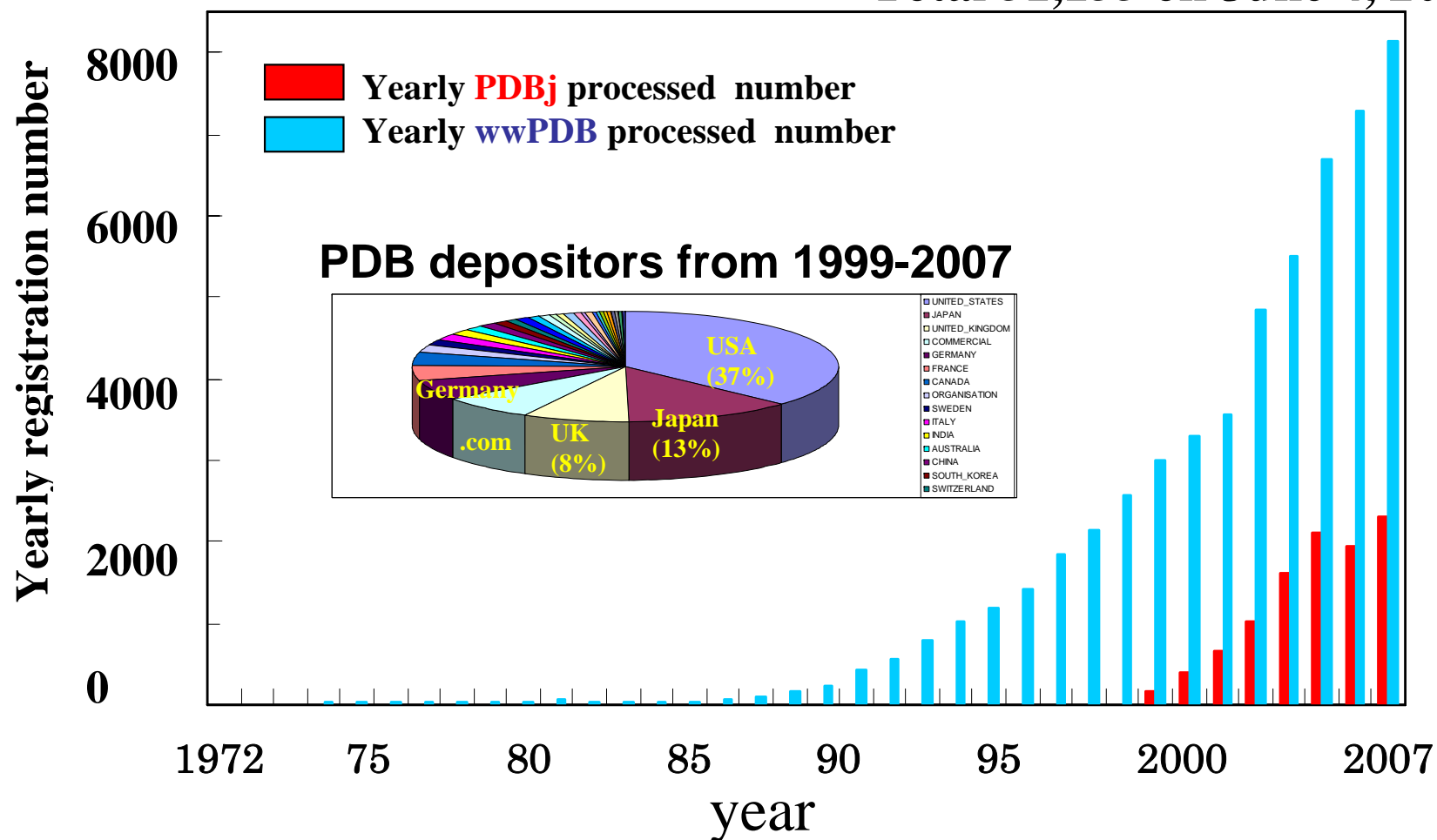
Hybrid

PDB depositories from 1999-2007



Processed data numbers at PDBj

Total 51,155 on June 4, 2008



We process **25-30 %** deposited data of the entire world, mainly from Asian and Oceania regions

wwPDB FTP Traffic



- Approximately **6,235,000** files were downloaded in **June 2007** (RCSB PDB, EBI-MSD, and PDBj)

How are the data qualities kept?

- **Quality of each structure is strictly examined when deposited.** Both the depositor himself/herself and our primary annotators examine it. Without the approval, the PDBID cannot be authorized.
- **Experimental information** (Structure Factors/ Distance Restraints) **are mandatory** to be deposited together with the atom coordinates from February 1st, 2008.

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ADIT-NMR

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(BMRB)

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修正データについて

リンク集

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-BIRDの支援を受け、米国RCSBおよび欧州EBIと協力して、生体高分子の立体構造データベースを国際的に統一化されたアーカイブとして運営するとともに、様々な解析ツールを提供しております。

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PDB登録



構造解析データ登録のご案内 >>

NMRデータ登録



検索

PDB検索



☒ PDB ID ☐ Keywords

詳細条件検索 >>

NMRデータ検索



☒ Accession number

☐ Deposition code

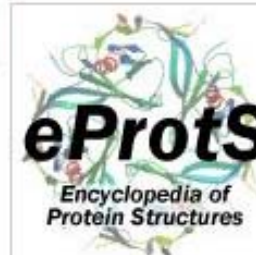
最新情報

2008/1/10

2008年3月3日に、PDBj講習会を大阪大学中之島センターで開催いたします。(お申し込み/詳細)

2007/12/20

rsyncによるPDBアーカイブのダウンロードサービスを始めました。



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NMRデータ登録 

検索

PDB検索 
xml-based Protein
Structure Search Service

☒ PDB ID ☐ Keywords

詳細条件検索 >>

NMRデータ検索



☒ Accession number

☐ Deposition code

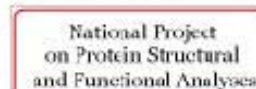
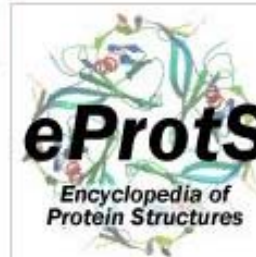
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Graphic viewer: jV version 3.5

Access to <http://www.pdbj.org/jV/>

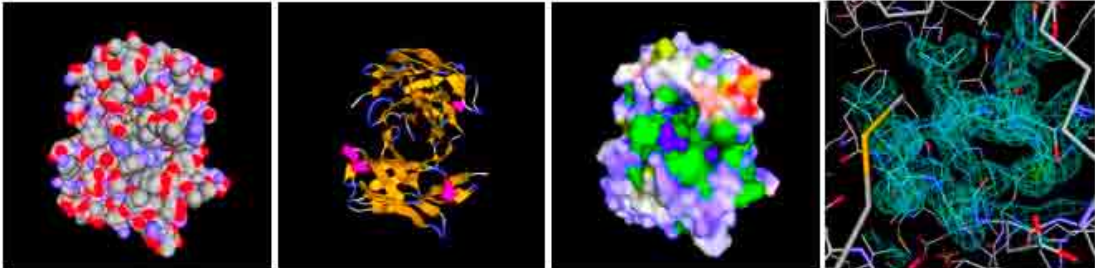
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 **jV version 3** 

jV version 3 (formerly known as PDBjViewer) is a program to display molecular graphics of proteins and nucleic acids. jV supports the following features:

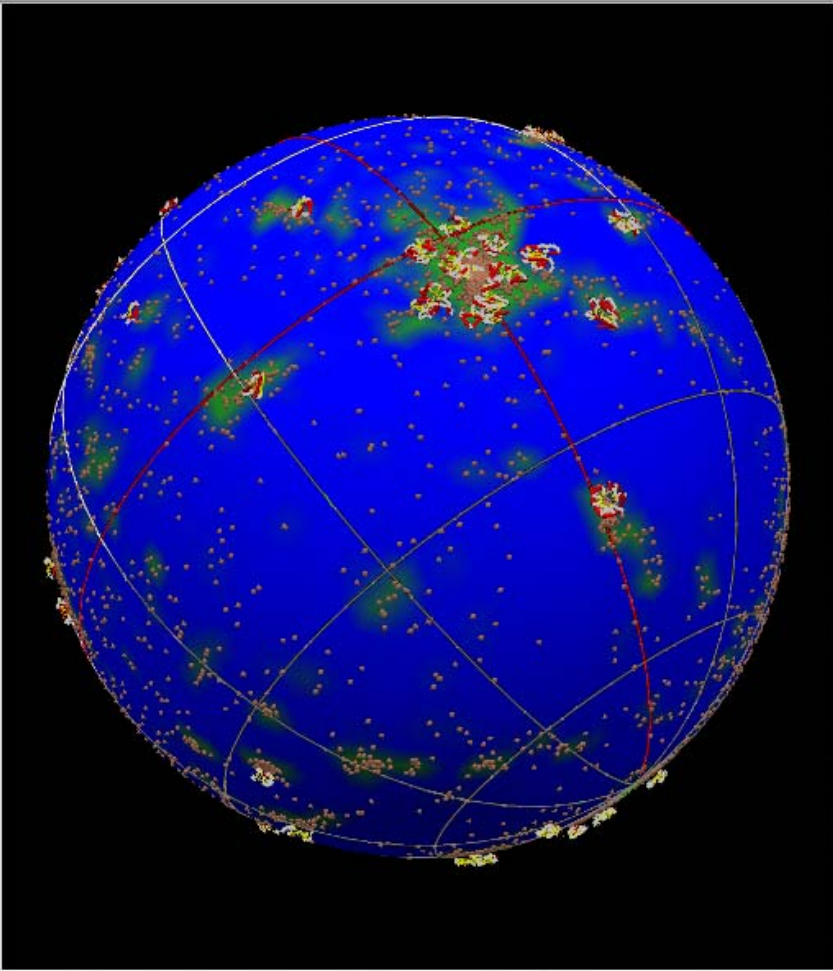
- jV can read and display PDBML files, the canonical XML format for the Protein Data Bank.
- Of course, jV can read and display the traditional PDB format files, too.
- RasMol-like usability.
- jV can process more than one molecules.
- jV can display polygons specified by XML. ([XML Schema for polygons](#) is available.)
- Multiple polygons can be processed simultaneously, and be superimposed onto molecular images.
- Animation can be realized.
- jV runs on the Java Runtime Environment ([JRE](#)) so that it can work as a stand-alone application as well as [an applet](#).
- The graphics of jV is based on OpenGL (JOGL), thereby producing fairly beautiful pictures.

[Download](#)



Protein Globe

By Akira Kinjo &
Daron Standley



Select Display


- ☒ ☒ 1. globe.xml.g
- ☒ ☒ 2. latlong.xml.g
- ☒ ☒ 3. cartoons.xrr
- ☒ ☒ 4. sphere0.xml

PDB ID:


Chain:

Domain:

This domain:



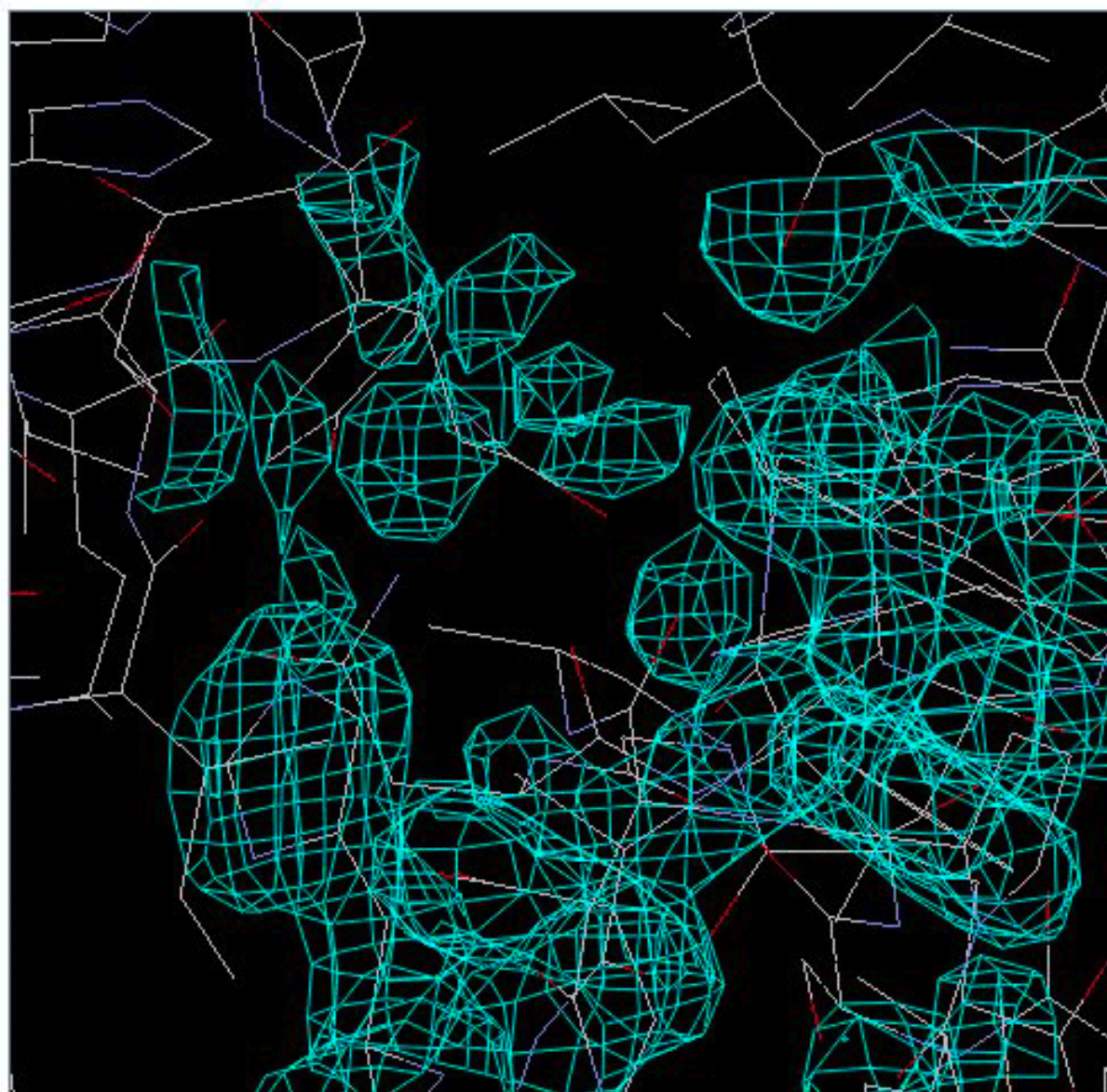
In PDB:



```

jV>
Welcome to PDBj Globe!
jV>
1 Atom Selected.
jV>
Atom: 1dl3 1647  Group: sco 1647  Chain: B  Model: 0  File: 1
jV>

```



http://133.1.158.159 - EDM (Electron Densit...

Options for Electron Density Map (EDM)

Type of the map

☒ contour mesh
☐ iso surface

Map position

☒ atom nearest to the center of the map

☐ Atom ID: Chain Residue Atom

(you can select by clicking in the viewer)

☐ coordinates: (x, y, z)

mapped area: Å
(this is the length of edge of a cube)

contour level: σ

color: R G B

isosurface transparency level:

ページが表示されました インターネット

jV>

Additional Information in our XML database:

PDBMLplus

Total number in PDBMLplus	51,155
GO Information (Biological Process, Molecular Function, Cellular Component)	20,186
Extracted from Literatures by Annotators	19,697
Information of binding site residues from HETATM	28,143
Function Information from Uni-Prot (ACT_SITE, BINDING, DNA_BIND, NP_BIND, ZN_FING, TRANSMEM)	27,573
Function Information from CATRES/extCATRES-EBI-CSA-EBI-	2,621 18,578
Primary Citation Information	45,268

(as of June 4, 2008)

Development of other Databases and Services

Protein Molecular Surface Database, *eF-site*
(Kinoshita & Nakamura)

Search for Similar Surface, *eF-seek* (Kinoshita & Nakamura)

Protein Dynamics Database, *ProMode*
(Wako & Endo)

Encyclopedia of Protein Structures, *eProtS*
(Kinjo, Kudo, & Ito)

Electron Microscopy Navigator, *EM-Navi* (Suzuki)

BioMagResBank-NMR experimental data
(Akutsu, Harano & Nakatani)