Protein Data Bank & Structure Deposition at PDBj

Nobutoshi Ito

Graduate School of Biomedical Science,
Tokyo Medical and Dental University
also
Protein Bank Japan

http://www.pdbj.org

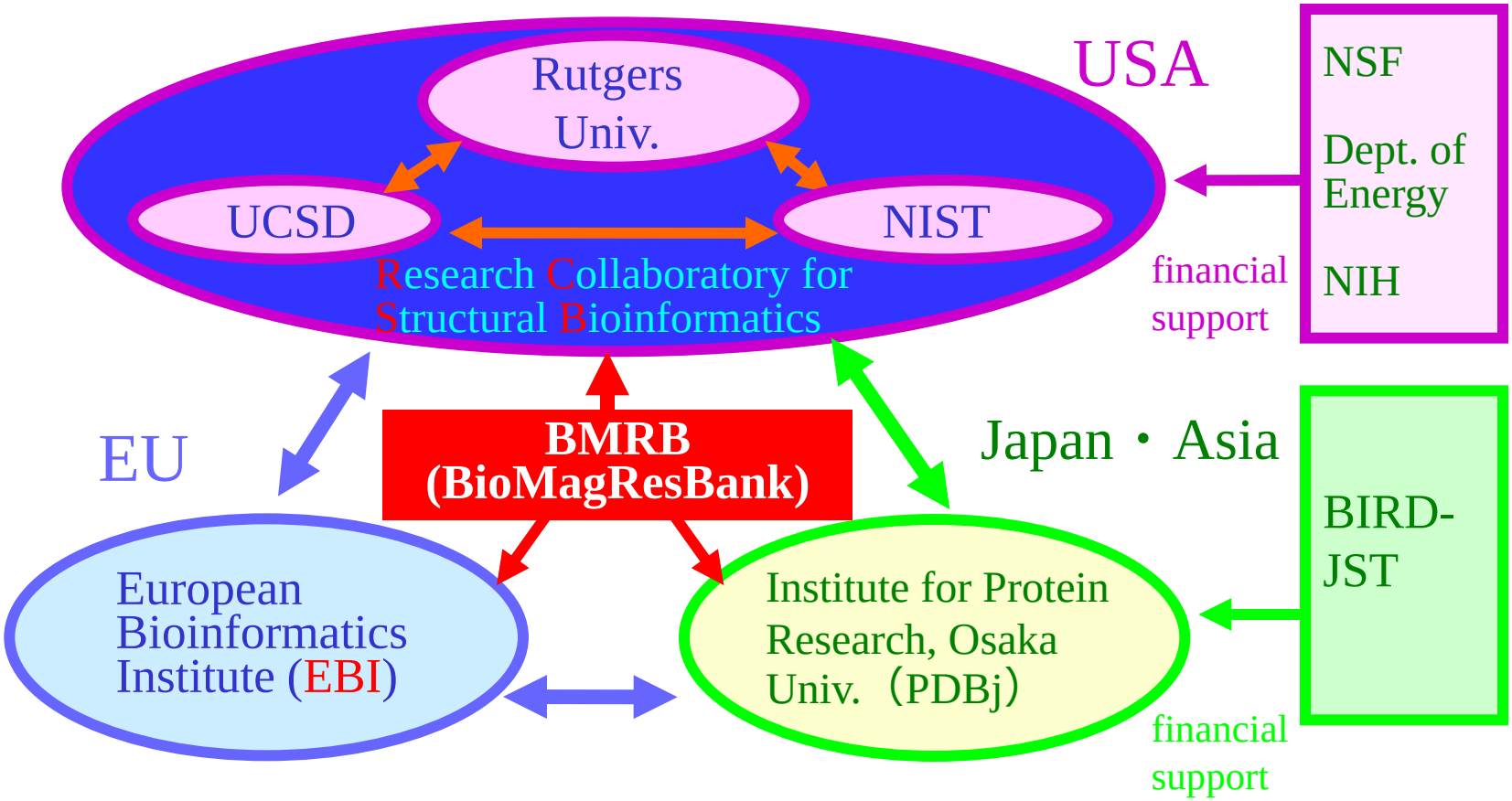
CCP4 Workshop
2 Nov 2012

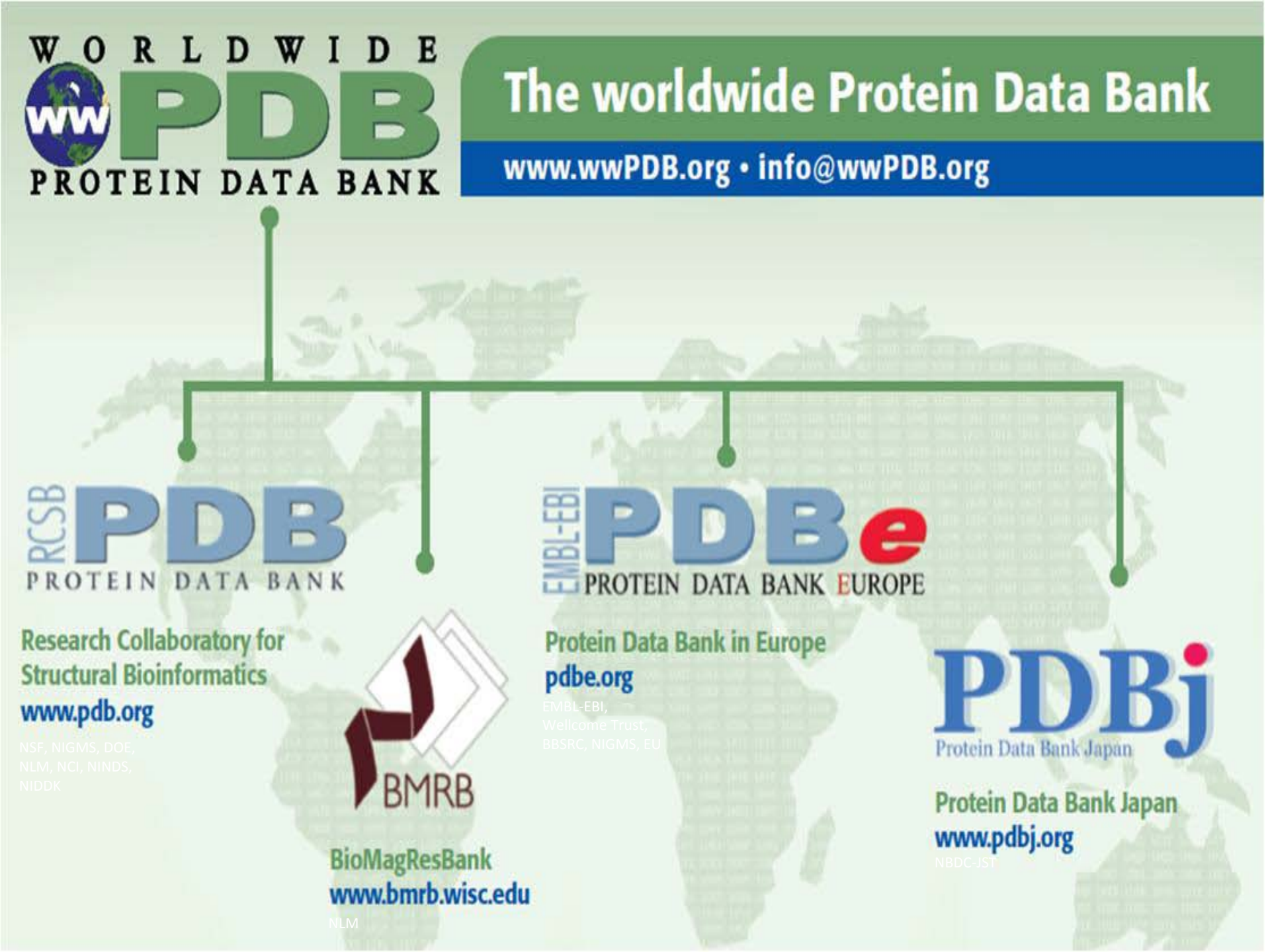
PDBj
Protein Data Bank Japan

Today’s menu

- wwPDB and PDBj
- Quick tour of deposition
- Quantity and quality of data
- Related databases etc at PDBj

Protein Data Bank (PDB)




WORLDWIDE PDB
PROTEIN DATA BANK
The worldwide Protein Data Bank
www.wwPDB.org • info@wwPDB.org
RCSB PDB
PROTEIN DATA BANK
Research Collaboratory for Structural Bioinformatics
www.pdb.org
NSF, NIGMS, DOE, NLM, NCI, NINDS, NIDDK
BMRB
BioMagResBank
www.bmrb.wisc.edu
NLM
EMBL-EBI PDBe
PROTEIN DATA BANK EUROPE
Protein Data Bank in Europe
pdbe.org
EMBL-EBI, Wellcome Trust, BBSRC, NIGMS, EU
PDBj
Protein Data Bank Japan
Protein Data Bank Japan
www.pdbj.org
NBDC-JST

WORLDWIDE PDB
PROTEIN DATA BANK

PDBe
PROTEIN DATA BANK EUROPE

PDBj
Protein Data Bank Japan

BMRB

RCSB PDB
PROTEIN DATA BANK

wwPDB and wwPDBAC members at Rutgers Univ. on 1 Oct. 2010

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 are 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)

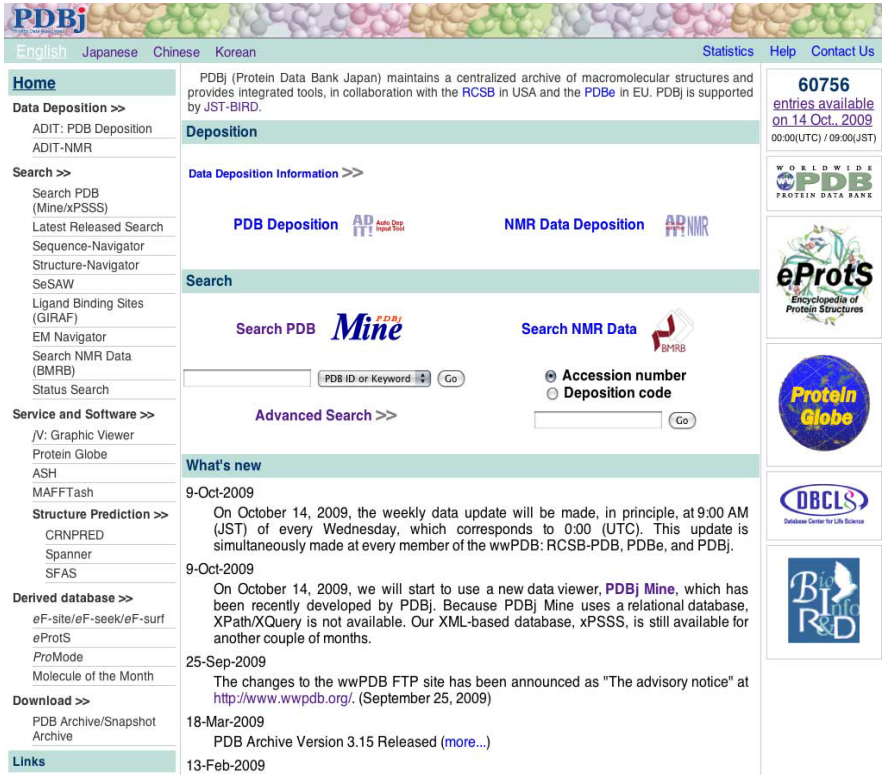
PDB FTP Traffic (July 2009 - June 2010)

219 M files were downloaded from three wwPDB members (PDBj, RCSB-PDB, PDBe) during a year.

Protein Data Bank Japan (PDBj)

http://www.pdbj.org/

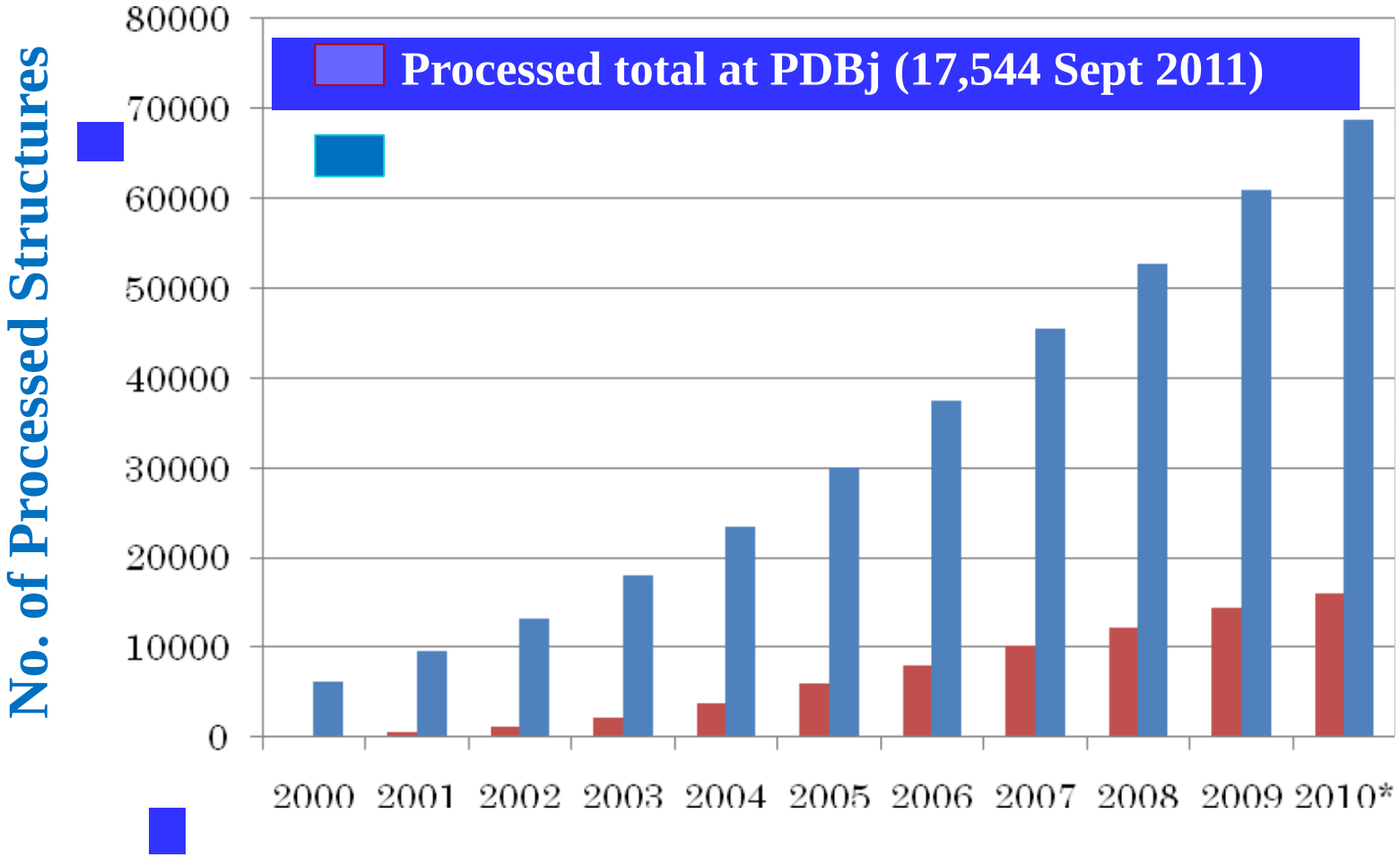
At Institute for Protein Research, Osaka Univ. since 2001.
Supported by the Institute for Bioinformatics Research and Development, Japan Science and Technology Agency (BIRD-JST).



Protein Data Bank Japan: PDBj

1. The wwPDB management as one of the members
2. Curation and data processing for the deposited data (PDB and BMRB)
3. Data remediation and development of the format for correct description
4. Addition of experimental information from literatures
5. Development of query tools and derived databases as the web service

Data Processed at PDBj and wwPDB

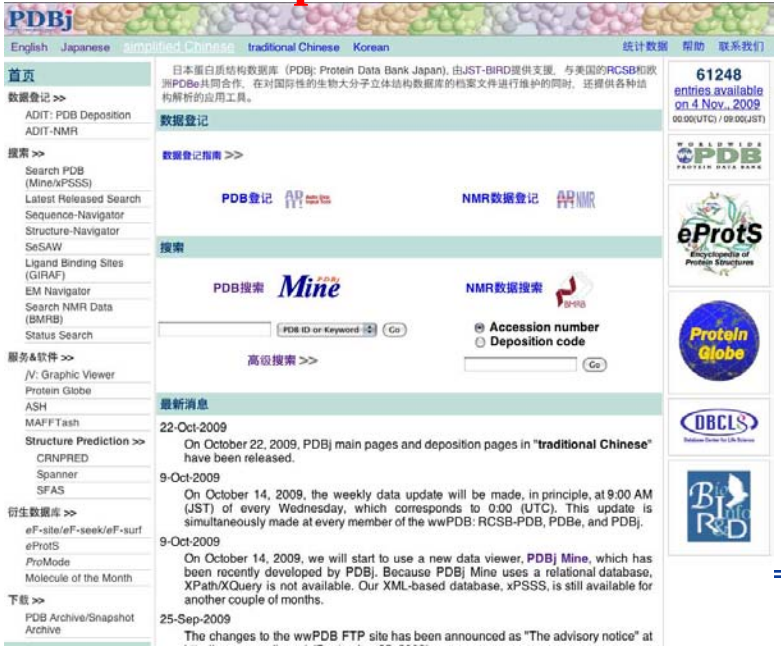


PDBj curaa Quarter of the deposited data, mainly from Asian and Oceania regions.

Japanese

Korean

Simplified Chinese



Traditional Chinese

Quick Tour of How to Deposite (X-ray) Structures with ADIT

Before deposition, please check;

- Is it the final structure?
- Coordinates and structure factors (raw images in the future?)
- You have a sequence file? (real sequence used in the experiment, one-letter code, database ID… If it's a new protein, sequence deposition is also required)
- Ligand information (IUPAC name, images…)

To make the procedure easier

- Have various log files ready (crystallisation note, data collection, scaling…)
- Run preprocessing programs (pdb_extract, deposit_mmcif, CCP4 data harvesting…)

PDBj

English Japanese simplified Chinese traditional Chinese Korean

Statistics Help FAQ Contact Us

Home

Data Deposition >>
- ADIT: PDB Deposition
- ADIT-NMR

Search >>
- Search PDB (Mine/xPSSS)
- Latest Released Search
- Sequence-Navigator
- Structure-Navigator
- SeSAW
- Ligand Binding Sites (GIRAF)
- EM Navigator
- Search NMR Data (BMRB)
- Status Search

Service and Software >>
- *j*V: Graphic Viewer
- Protein Globe
- ASH
- MAFFTash
- SEALA

Structure Prediction >>
- CRNPRED
- Spanner
- SFAS

Derived database >>
- eF-site/eF-seek/eF-surf
- eProtS
- *Pro*Mode
- Molecule of the Month

Download >>
- PDB Archive/Snapshot Archive

Links

PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB, the BMRB in USA and the PDBe in EU. PDBj is supported by JST-BIRD.

Deposition

Data Deposition Information >>

PDB Deposition (AD IT! Auto Dep Input Tool)

NMR Data Deposition (AD IT! NMR)

Search

Search PDB (Mine PDBj)

PDB ID or Keyword | Go

Advanced Search >>

Search NMR Data (BMRB)

Accession number
Deposition code

Go

What's new

6-Oct-2010
Effective December 6, 2010, deposition of chemical shift data will be mandatory when submitting NMR entries to the PDB. (more...)

19-Aug-2010
Validation Report PDFs (more...)

13-Jul-2010
The latest version of jV (jV3.8), the molecular graphics viewer developed by PDBj, has been released. A new functional command "displayatom on/off" has been added, which provides various display methods easily. Please download the newest version from **here**.

30-Jun-2010
Version 2 NMR restrain files have been released.(more...)

19-May-2010
The latest version of jV (jV3.7.1) has been released.

7-May-2010
The IP address of PDBj ftp server (ftp.pdbj.org) has been changed to 133.1.158.142. If you access to the PDBj ftp

68998
entries available on 3 Nov., 2010
00:00(UTC) / 09:00(JST)

WORLDWIDE PDB PROTEIN DATA BANK

eProtS Encyclopedia of Protein Structures

Protein Globe

DBCLS Database Center for Life Science

BioInfo R&D

PDBj

A member of the worldwide PDB

Last update: 2009-04-24

Languages: en | ja | ko | zh-cn | zh-tw

News | Deposition Tutorial (en, ja, ko, zh-cn, zh-tw) | Validation and Deposition | Policies and Procedures | Contact Us

PDBj Validation & Deposition Portal

Welcome to the PDBj validation/deposition portal.

Need help?

If you have any questions, please read "Deposition tutorial" first. If you still need help, please contact us. Questions, comments, and suggestions in validation/deposition service and tutorial are welcome.

Data Deposition Tools

Search

You may search HET groups using **Ligand Expo**. If your HET groups are ***NOT new***, you should use the existent ones.

Check sequence database references for proteins or nucleic acids in your structure at UniProtKB. The author is encouraged to submit their sequence information via SPIN (the UniProtKB submission tool) for directly sequenced proteins, or vir submission tools provided by INSDC members (SAKURA at DDBJ, Webin at EMBL, BankIt at GenBank) if the nucleotide sequence is available.

Validate

Before you deposit the structure data, validate your structure using the validation server at PDBj.

» ADIT Validation Server

Deposit

After you validate your structure data, deposit your structure using the structure deposition tool ADIT at PDBj, beta-ADIT or ADIT-NMR at PDBj (for NMR studies). For other deposition servers at wwPDB member sites, please visit from the wwPDB web site.

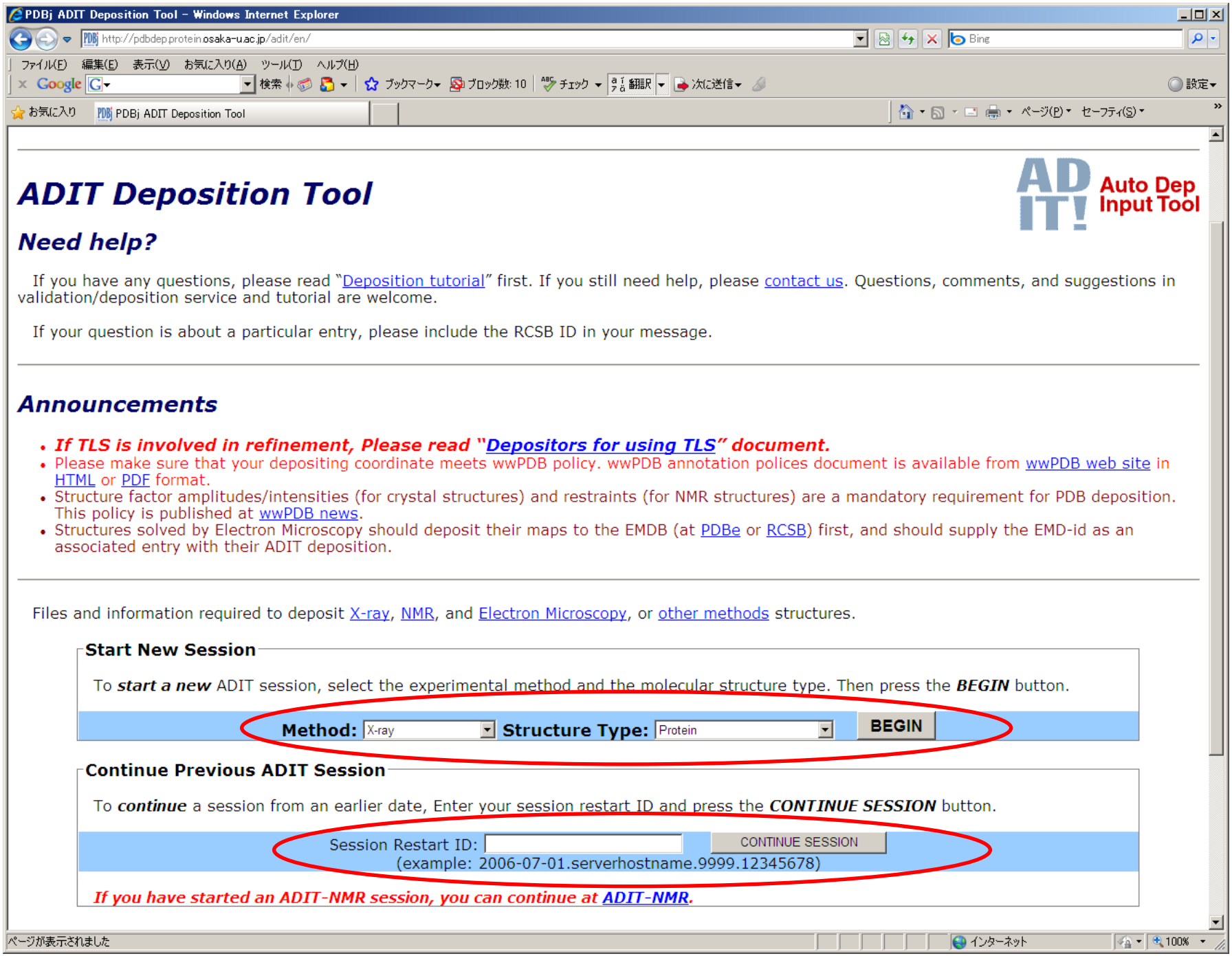
PDBj Protein Data Bank Japan — A member of the WORLDWIDE PDB PROTEIN DATA BANK

How to set the default document language

プロテインデータバンクへの構造解析データ登録のご案内

PDB (Protein Data Bank) への登録は、ウェブブラウザを利用して対話的に登録を行うことができるADIT (Auto Deposition Input Tool)を使用して行います。また、pdb_extractを使用すると、ADITで手動入力する項目を減らすことができます。このページでは登録の手順、必要なデータ類とその書式や注意事項などについてご案内いたします。

本チュートリアルは、wwPDBに構造解析データを登録する際の手引きを、日本語を用いる登録者の便宜のためにPDBjが日本語で解説するものです。PDBで公開するファイルの書式およびwwPDBへのデータ登録に関する公式文書は、"Annotation Documentation" です。また、PDBjおよびRCSB PDBによる登録データの編集方針に関する公式文書は "Data Processing and Annotation Procedures Manual" です。本チュートリアルでは公式文書に忠実に解説するよう努めていますが、万一、本チュートリアルと公式文書の間に相違が生じた場合は、公式文書の記述が優先されます。


PDBj ADIT Deposition Tool – Windows Internet Explorer
http://pdbdep.protein.osaka-u.ac.jp/adit/en/
PDBj ADIT Deposition Tool
ADIT Deposition Tool
Auto Dep Input Tool
Need help?
If you have any questions, please read "Deposition tutorial" first. If you still need help, please contact us. Questions, comments, and suggestions in validation/deposition service and tutorial are welcome.
If your question is about a particular entry, please include the RCSB ID in your message.
Announcements
If TLS is involved in refinement, Please read "Depositors for using TLS" document.
Please make sure that your depositing coordinate meets wwPDB policy. wwPDB annotation polices document is available from wwPDB web site in HTML or PDF format.
Structure factor amplitudes/intensities (for crystal structures) and restraints (for NMR structures) are a mandatory requirement for PDB deposition. This policy is published at wwPDB news.
Structures solved by Electron Microscopy should deposit their maps to the EMDB (at PDBe or RCSB) first, and should supply the EMD-id as an associated entry with their ADIT deposition.
Files and information required to deposit X-ray, NMR, and Electron Microscopy, or other methods structures.
Start New Session
To start a new ADIT session, select the experimental method and the molecular structure type. Then press the BEGIN button.
Method: X-ray
Structure Type: Protein
BEGIN
Continue Previous ADIT Session
To continue a session from an earlier date, Enter your session restart ID and press the CONTINUE SESSION button.
Session Restart ID:
CONTINUE SESSION
(example: 2006-07-01.serverhostname.9999.12345678)
If you have started an ADIT-NMR session, you can continue at ADIT-NMR.

Deposition - Windows Internet Explorer

http://pdbdep.protein.osaka-u.ac.jp/cgi-bin/adit/adit-session-driver

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An Information Portal to Biological Macromolecular Structures

PDBj | Contact Us

Validation and Deposition Services Home

Deposition Top | Tutorial | ADIT FAQ | Deposition FAQ | pdb_extract | Ligand Expo

AD IT! Auto Dep Input Tool

Running an ADIT Session

1. Please review the format requirements before starting the session.
2. You may wish to use pdb_extract to process log files for deposition.
3. Check ligands with Ligand Expo.

Coordinates

Upload coordinate file	参照... Compress (.gz or.Z files) first.	**Select file type:** ○ PDB ○ mmCIF
Upload structure factor file	参照... Compress (.gz or.Z files) first.	**Select file type:** ○ mmCIF ○ mtz ○ Other ASCII
Choose Operation:	○ Precheck ○ Validate ○ Deposit	BEGIN

Structure Factors

About ADIT

An ADIT session involves three steps:

1. A data format precheck
2. A validation check
3. The actual deposition of the structural data to the database

“Precheck” “Validate” “Deposite”

Precheck confirms that the data files you enter are in a format that can be automatically processed by our software. The format and required data items for coordinate files are described for the PDB and mmCIF formats. The required mmCIF data items for structure factor data are also described. The precheck identifies any changes that need to be made in your data files in order to obtain a validation report or to deposit your structure.

The **validation check** creates a validation report for the structure which includes an RCSB PDB Atlas page, a validation report with stereochemical checks, and, depending on the type and content of the files uploaded, produces Procheck, Molprobity, NUCheck and SFCheck reports. The validation may take a few minutes depending on the size of your

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AD IT! Auto Dep Input Tool

Data Syntax Check

Click here to e-mail the session restart ID

Coordinate format is OK!

Sequence information:

One polymer chain was extracted from the coordinate section. The detailed residue information of each chain is listed below. Standard residues are listed as one letter code sequence. Non-standard residues are included in parenthesis. Please check the sequence information carefully. If you think it was incorrctly extracted, please check if TER cards were added correctly. PDB format requires all polymer chains should have a TER card at the end and no TER cards should be included at the end of non-polymer residues (such as ions, ligands, waters).

```
CHAIN A: Total 353 residues, first residue (6 ALA), last residue (358 SER)

AAGPEMVRGQVFDVGPRYTNLSYIGEGAYGMVCSAYDNLNKVRVAIKKISPFEHQTYCQRTLREIKILLR
FRHENIIGINDIIRAPTIEQMKDVYIVQDLMETDLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLH
RDLKPSNLLLNTTCDLKICDFGLARVADPDHDHTGFL(TPO)E(PTR)VATRWYRAPEIMLNSKGYTKSI
DIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLF
PNADSKALDLLDKMLTFNPHKRIEVEQALAHPYLEQYYDPSDEPIAEAPFKFDMELDDLPKEKLKELIFE
ETARFQPGYRS
```

If a sequence above has missing residues, correct the sequence later during deposition.

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AD IT! Auto Dep Input Tool

Validation Report

Click here to e-mail the session restart ID

Please review the Validation Report carefully. If there are any outstanding issues such as sequence link problem, geometry errors, chirality errors etc., please make sure you fix the problem(s) and start a fresh session with corrected file.

Please note that the geometry errors shown in the Validation Report will also appear in the processed PDB file.

For ligands, please make sure the three letter codes are correct. Both extra and missing atoms may appear in the Validation Report if incorrect ligand three letter code was used. If only missing atoms are listed in the Validation Report, either incorrect ligand three letter code was used or part of ligand is missing coordinates (see Ligand Expo).

```
Thank you for using PDB.  The following geometrical and stereochemical
features have been calculated for your structure:

    CLOSE CONTACTS
    --------------

==> Close contacts in same asymmetric unit.  Distances smaller than 2.2
    Angstroms are considered as close contacts.

   Chain Atom    Res  Seq   Chain Atom    Res  Seq   Symm_Code         Distance
   ---------------------------------------------------------------------------
         O       HOH  542 -         O      HOH  543  (  1,  5,  5,  5)  Dist = 0.69
         O       HOH  534 -         O      HOH  537  (  1,  5,  5,  5)  Dist = 1.00
         O       HOH  551 -         O      HOH  557  (  1,  5,  5,  5)  Dist = 1.00
         O       HOH  552 -         O      HOH  554  (  1,  5,  5,  5)  Dist = 1.00
         O       HOH  585 -         O      HOH  586  (  1,  5,  5,  5)  Dist = 1.00
         O       HOH  587 -         O      HOH  588  (  1,  5,  5,  5)  Dist = 1.00

==> Close contacts based on crystal symmetry.  Distances smaller than 2.2
    Angstroms are considered as close contacts.
```

AD IT! Auto Dep Input Tool

Please input sequence(s):

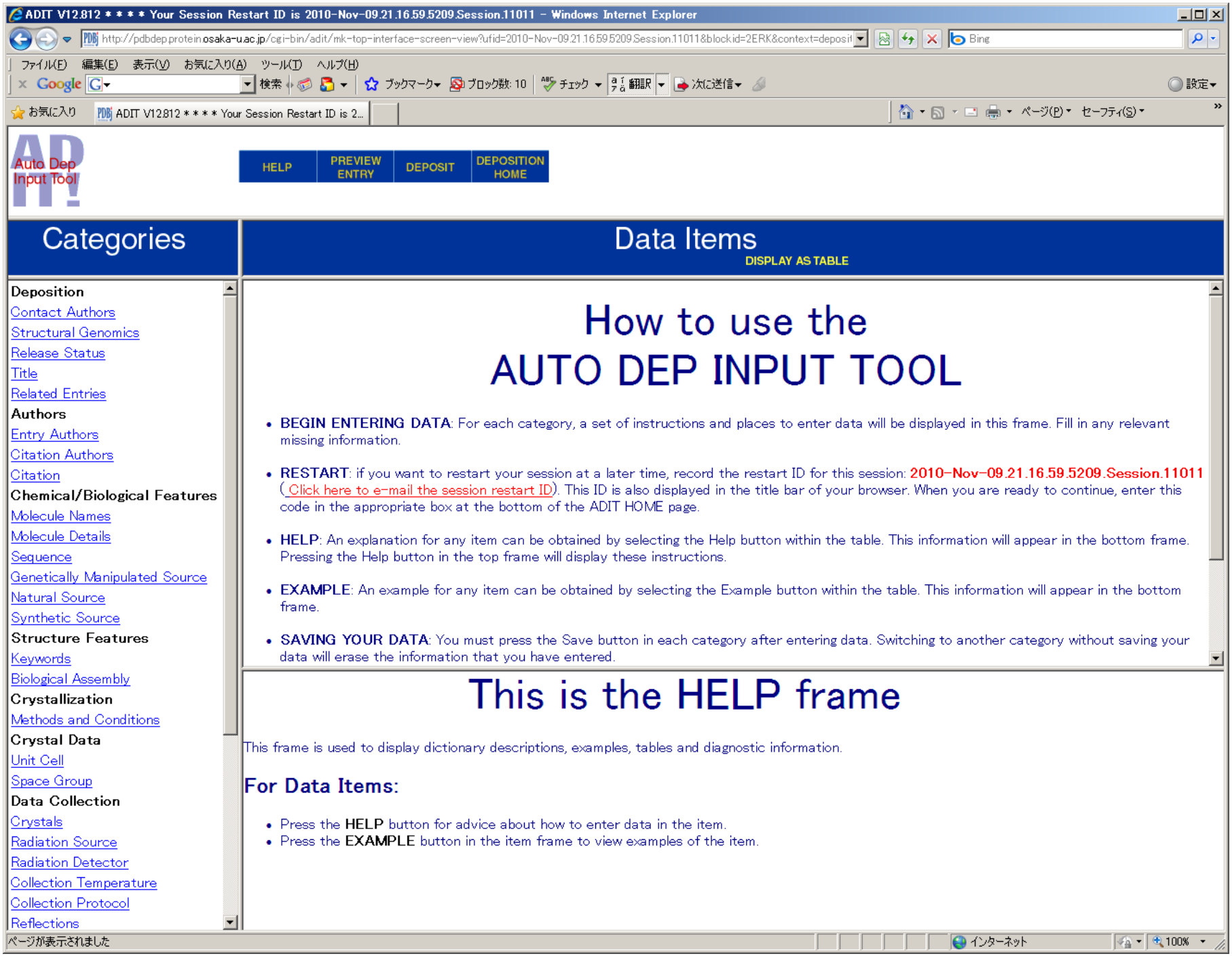
Only sequences for proteins, peptides, and nucleic acids should be entered in the boxes below.

- Please enter the sequence of each macromolecular polymer. The sequence should include all residues in the experiment including uncleaved expression tags (like his tags), as well as residues missing due to disorder.
- If a sequence applies to more than one chain, enter the sequence once and specify the chain IDs with spaces or commas in between each chain ID.
- N- and C-terminal tags can be entered in the "uncleaved N-/C-terminal HIS-tag or cloning artifact" boxes. The N- and C-terminal boxes should be left blank if no tags were used or if they are already listed in the sequence.
- To indicate a modified or non-standard residue like selenomethionine, use parenthesis: (MSE). Three letter codes can be found at Ligand Expo.
- The polymer type must be selected.
- If the sequence database reference exists, please select the database name and enter the accession code (GB (GeneBank) for nucleic acids and UNP (UniProt) protein sequence).
- For Structure Genomics, if the sequence has been or will be deposited to TargetDB, please indicate the Target ID in the "Target identifiers" box. This is for structural genomics project only.
- *One-letter code for polymer sequence INCLUDING THE RESIDUES MISSING IN THE COORDINATES (mandatory). Do not repeat terminal tags if already provided in the boxes above or below.*

Click here to e-mail the session restart ID

Save Sequence

1st sequence	
Uncleaved N-terminal HIS-tag or cloning artifact *If none, leave the box blank*	
One-letter code for polymer sequence INCLUDING THE RESIDUES MISSING IN THE COORDINATES (mandatory)	AHHHHHHMAAAAAAGPEMVRGQVFDVGPRYTNLSYIGEGA


ADIT V12.812 * * * * Your Session Restart ID is 2010-Nov-09.21.16.59.5209.Session.11011 - Windows Internet Explorer
http://pdbdep.protein.osaka-u.ac.jp/cgi-bin/adit/mk-top-interface-screen-view?ufid=2010-Nov-09.21.16.59.5209.Session.11011&block.id=2ERK&context=deposit
Bing
ファイル(F) 編集(E) 表示(V) お気に入り(A) ツール(T) ヘルプ(H)
Google 検索 ブックマーク ブロック数: 10 チェック 翻訳 次に送信 設定
お気に入り
ADIT V12.812 * * * * Your Session Restart ID is 2...
ページ(P) セーフティ(S)
Auto Dep Input Tool
HELP
PREVIEW ENTRY
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Categories
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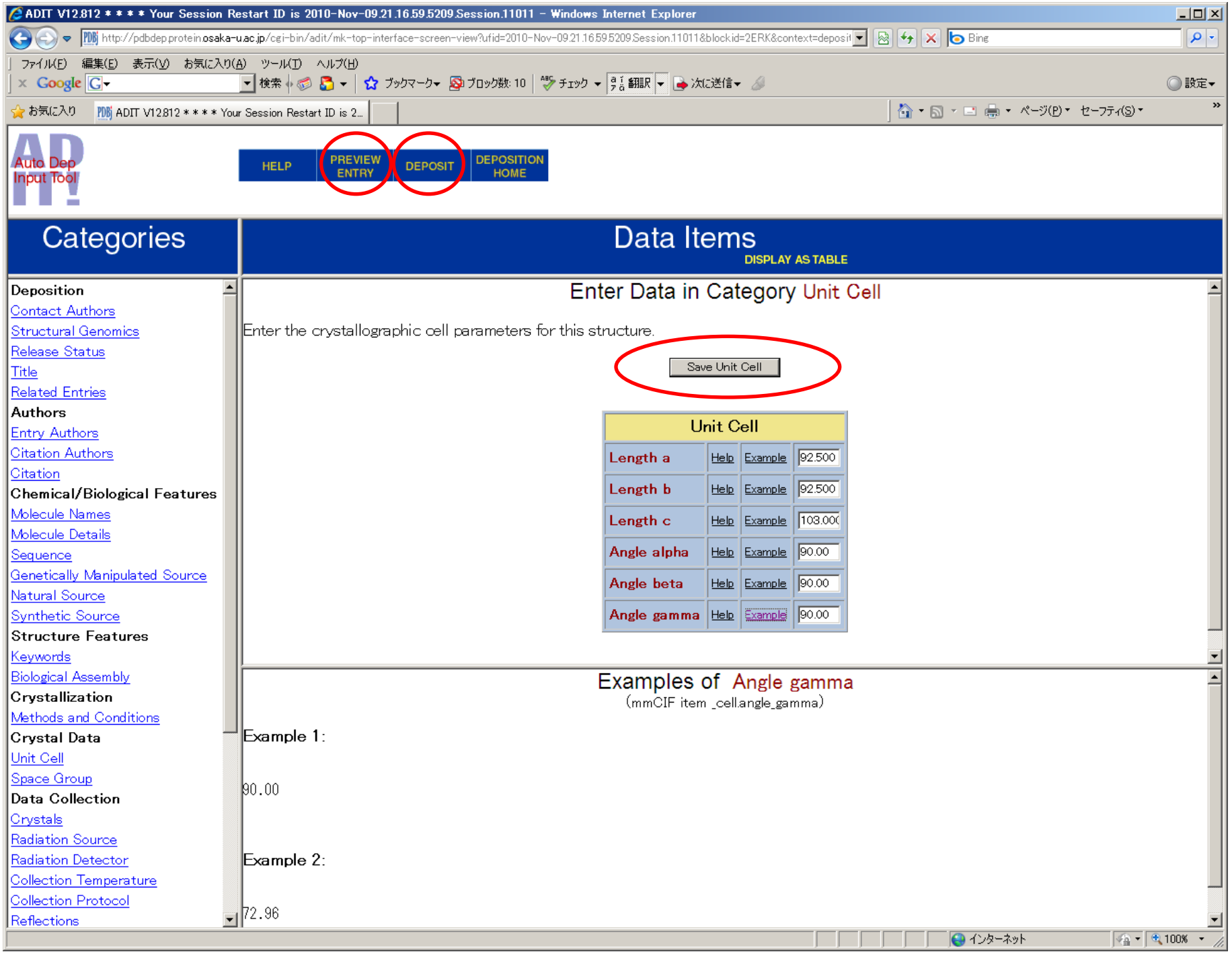
Molecule Names
Molecule Details
Sequence
Genetically Manipulated Source
Natural Source
Synthetic Source
Structure Features
Keywords
Biological Assembly
Crystallization
Methods and Conditions
Crystal Data
Unit Cell
Space Group
Data Collection
Crystals
Radiation Source
Radiation Detector
Collection Temperature
Collection Protocol
Reflections
How to use the
AUTO DEP INPUT TOOL
BEGIN ENTERING DATA: For each category, a set of instructions and places to enter data will be displayed in this frame. Fill in any relevant missing information.
RESTART: if you want to restart your session at a later time, record the restart ID for this session: 2010-Nov-09.21.16.59.5209.Session.11011 (Click here to e-mail the session restart ID). This ID is also displayed in the title bar of your browser. When you are ready to continue, enter this code in the appropriate box at the bottom of the ADIT HOME page.
HELP: An explanation for any item can be obtained by selecting the Help button within the table. This information will appear in the bottom frame. Pressing the Help button in the top frame will display these instructions.
EXAMPLE: An example for any item can be obtained by selecting the Example button within the table. This information will appear in the bottom frame.
SAVING YOUR DATA: You must press the Save button in each category after entering data. Switching to another category without saving your data will erase the information that you have entered.
This is the HELP frame
This frame is used to display dictionary descriptions, examples, tables and diagnostic information.
For Data Items:
Press the HELP button for advice about how to enter data in the item.
Press the EXAMPLE button in the item frame to view examples of the item.
ページが表示されました
インターネット
100%


ADIT V12.812 * * * * Your Session Restart ID is 2010-Nov-09.21.16.59.5209.Session.11011 - Windows Internet Explorer
http://pdbdep.protein.osaka-u.ac.jp/cgi-bin/adit/mk-top-interface-screen-view?ufid=2010-Nov-09.21.16.59.5209.Session.11011&blockid=2ERK&context=deposit
Auto Dep Input Tool
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Title
Related Entries
Authors
Entry Authors
Citation Authors
Citation
Chemical/Biological Features
Molecule Names
Molecule Details
Sequence
Genetically Manipulated Source
Natural Source
Synthetic Source
Structure Features
Keywords
Biological Assembly
Crystallization
Methods and Conditions
Crystal Data
Unit Cell
Space Group
Data Collection
Crystals
Radiation Source
Radiation Detector
Collection Temperature
Collection Protocol
Reflections
Enter Data in Category Unit Cell
Enter the crystallographic cell parameters for this structure.
Save Unit Cell
Unit Cell
Length a
Length b
Length c
Angle alpha
Angle beta
Angle gamma
Help
Example
92.500
92.500
103.000
90.00
90.00
90.00
Examples of Angle gamma
(mmCIF item _cell.angle_gamma)
Example 1:
90.00
Example 2:
72.96

Required Information

Deposition

- Contact Authors
- Structural Genomics
- Release Status
- Title
- Related Entries

Authors

- Entry Authors
- Contact Authors
- Citation

Chemical/Biological Features

- Molecule Names
- Molecule Details
- Sequence
- Genetically Manipulated Source
- Natural Source
- Synthetic Source

Structure Features

- Keywords
- Biological Assembly

Crystallization
- Methods and Conditions

Crystal Data
- Unit Cell
- Space Group

Data Collection
- Crystals
- Radiation Source
- Radiation Detector
- Collection Temperature
- Collection Protocol
- Reflections
- Reflection Shells

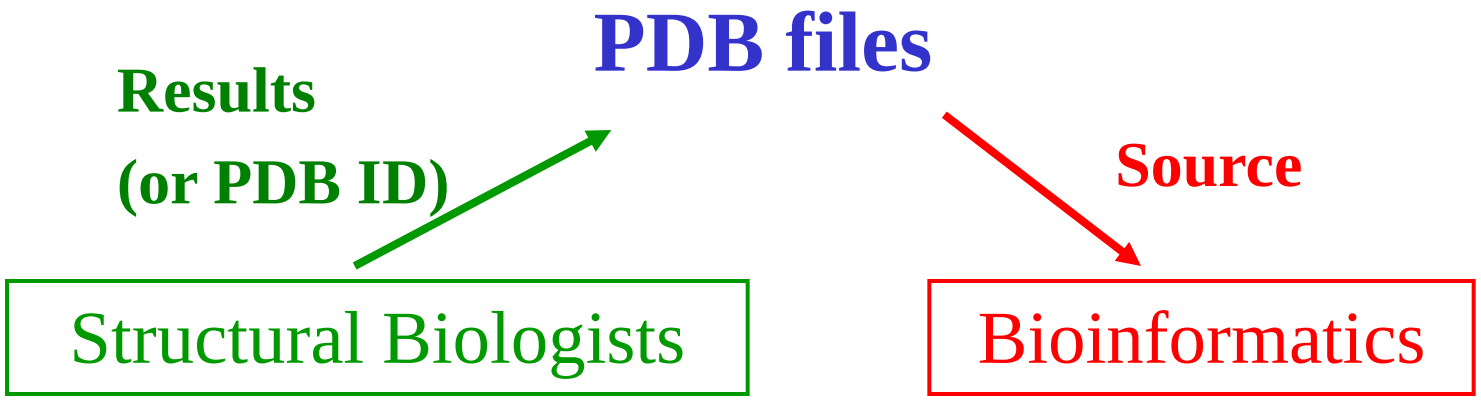
Refinement
- Refinement Statistics
- Resolution Shells
- RMS Deviations
- Coordinates Error

Software
- Programs
- Biological Assembly

Upload Supplemental Information
- Supersede/Obsolete Information
- Ligand Information
- Virus Matrices

Quantity and Quality of PDB data

Differences of views



Data Quantity

- Fill in as many data items as possible (various small tools available)
- Notify us when the paper gets published so that we can release the entry

Data Quality

It is up to depositors (you!!)…

but we have done about our part of it.

Common troubles observed…

- Wrong or missing data items

  (“to be published,” species, R-factors etc)

- Redundant definition

  (“human” or “homo sapience”)

- Ligand structure and definition

mmCIF-specific troubles

- Lack of validation program of contents

  (`_phasing.method  'MAGIC'`)
- (Inconsistent) redundancy of data items

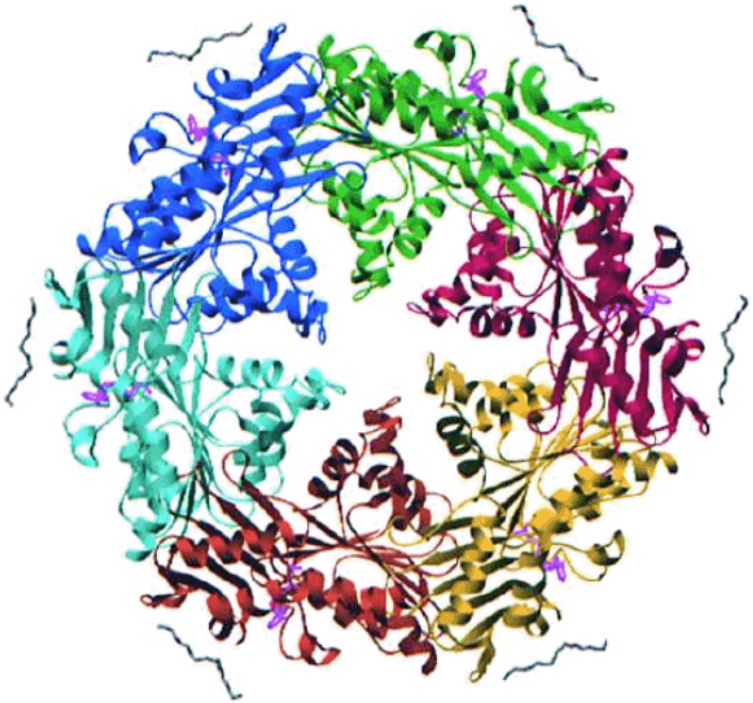
PDB Remediation Project

Thorough check of the PDB contents by all wwPDB members.

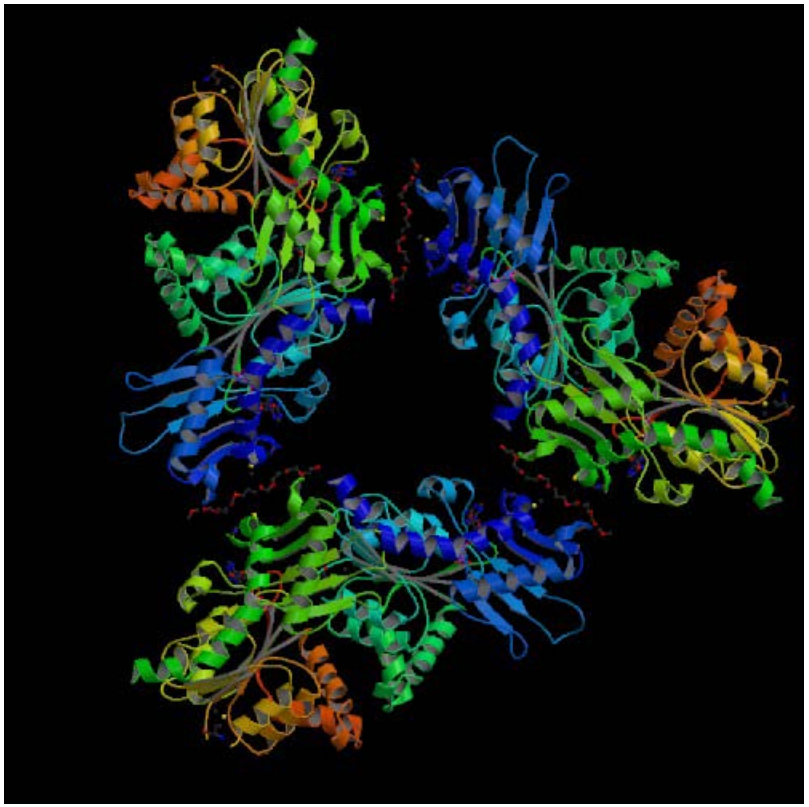
New dataset was released on 1 August 2007.

Henrick K, *et.al.*, *Nucleic Acid Res.*, **36,** D426-433 (2008)

What went wrong?



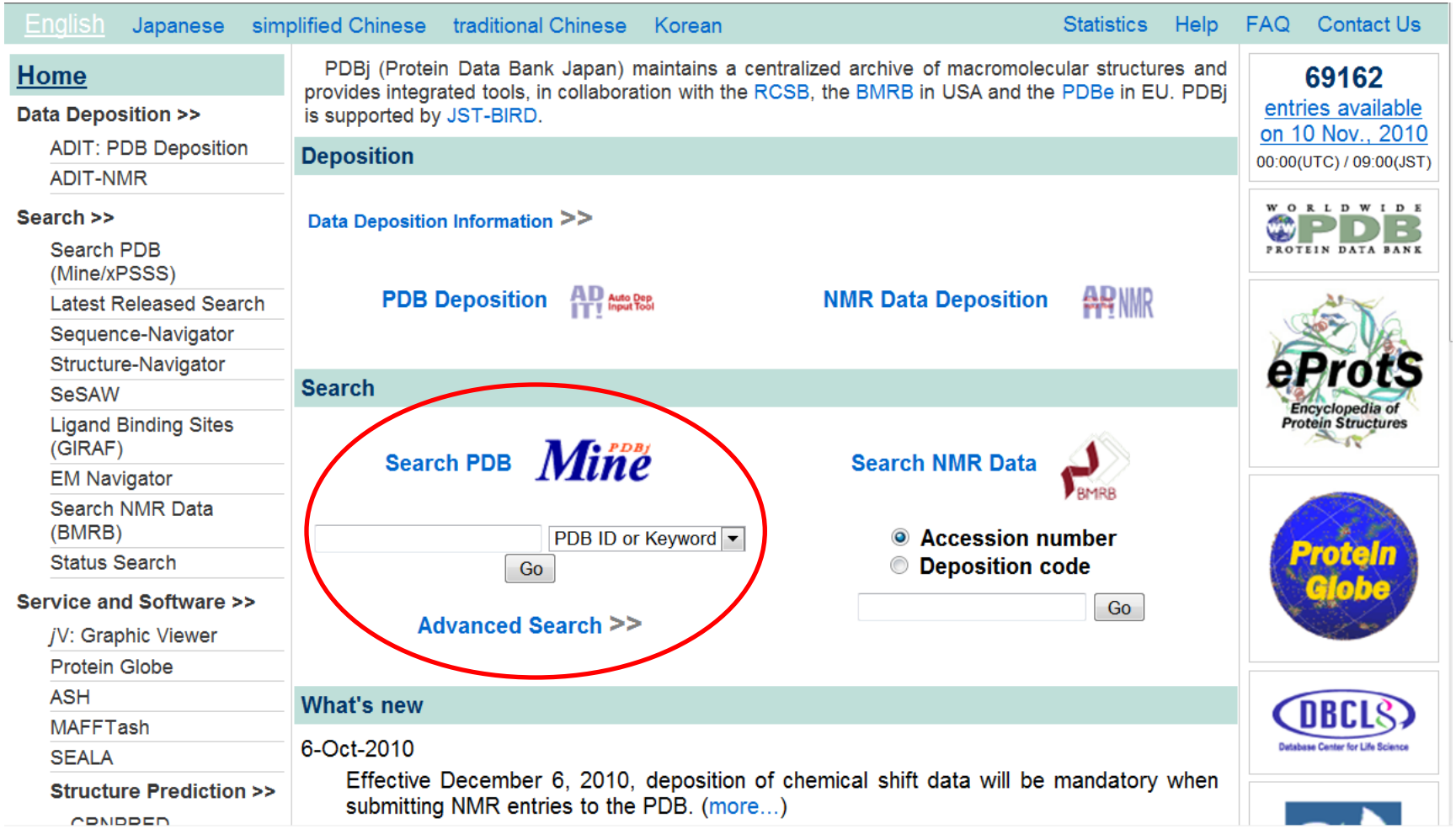
Paper



PDB

Related Database/Services at PDBj

PDBj *Mine*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PDBj (Protein Data Bank Japan) maintains a centralized archive of macromolecular structures and provides integrated tools, in collaboration with the RCSB, the BMRB in USA and the PDBe in EU. PDBj is supported by JST-BIRD.
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6-Oct-2010
Effective December 6, 2010, deposition of chemical shift data will be mandatory when submitting NMR entries to the PDB. (more...)
69162
entries available on 10 Nov., 2010
00:00(UTC) / 09:00(JST)
WORLDWIDE PDB PROTEIN DATA BANK
eProtS
Encyclopedia of Protein Structures
Protein Globe
DBCLS
Database Center for Life Science

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Mine PDBj

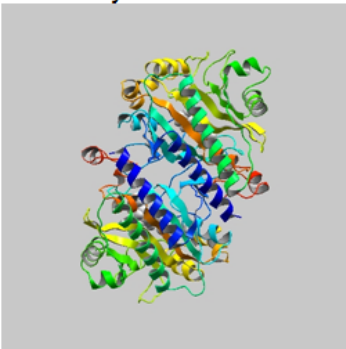
Summary [12as]

About PDBj Mine
Update Information

Summary | Structural Details | Experimental Details | Functional Details | Sequence Neighbor | Download/Display | External DB

PDB ID or Keyword search

<Asymmetric unit>



(no rotation) More images...

Structure Viewers
jV3 / Jmol
(jV3 and Jmol require Java (TM)Plug-in 1.5 or later.)

PDB ID	12as sequence information (FASTA format) download PDB format file
Descriptor	ASPARAGINE SYNTHETASE, L-ASPARAGINE, ADENOSINE MONOPHOSPHATE
Title	ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPARAGINE AND AMP
Functional Keywords	LIGASE, ASPARAGINE SYNTHETASE, NITROGEN FIXATION
Biological source	Escherichia coli K12
Cellular location	[UNP - P00963] Cytoplasm
Total number of polymer chains	2
Total molecular weight	74226 (the details in Structural Details Page)
Authors	Nakatsu, T. , Kato, H. , Oda, J. (*deposition date* : 1997-12-02, *release date* : 1998-12-30)
	Nakatsu, T. , Kato, H. , Oda, J.

Graphic viewer: *j*V version 3.8
Download from *http://www.pdbj.org/jV/*

TOP DOWNLOAD Help Links Acknowledgement

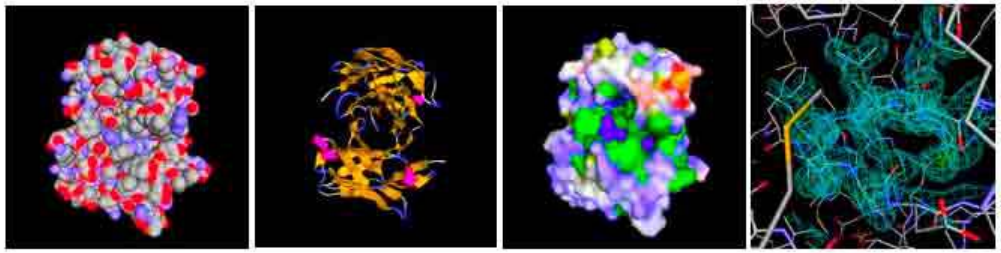
PDBj Protein Data Bank Japan

jV version 3

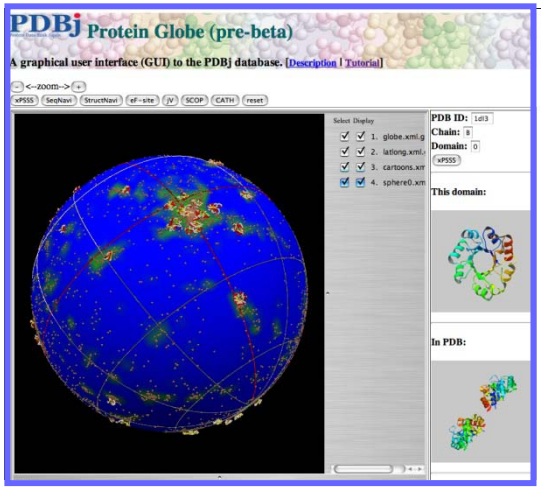
jV version 3 (formerly known as PDBjViewer) is a program to display molecular graphics of proteins and nucleic acids. jV supports the following features:

- 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.

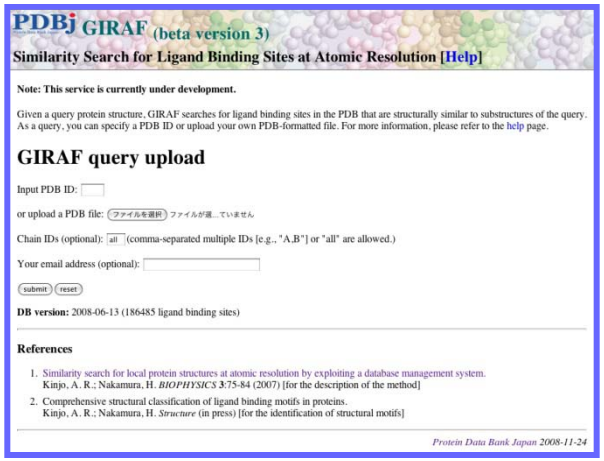
Download



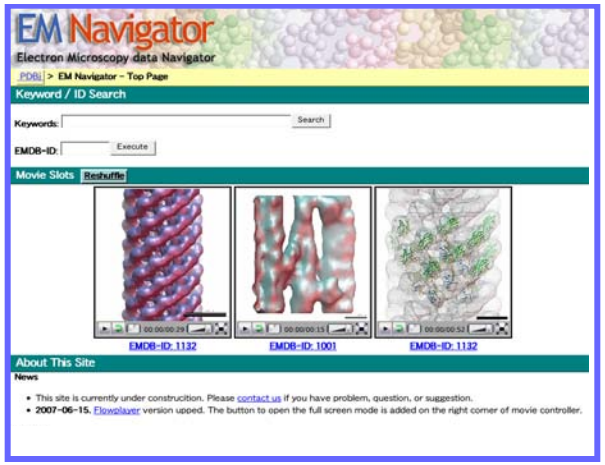
Development of other Databases & Services



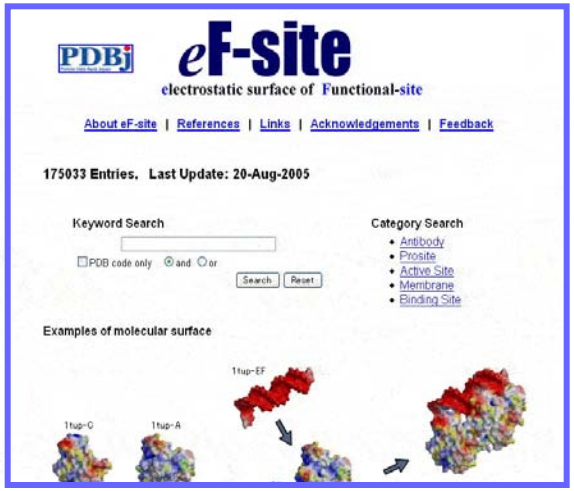
Protein Folds Browser, Protein Globe *(Kinjo & Standley)*



Ligand Binding Site Search, GIRAF *(Kinjo)*

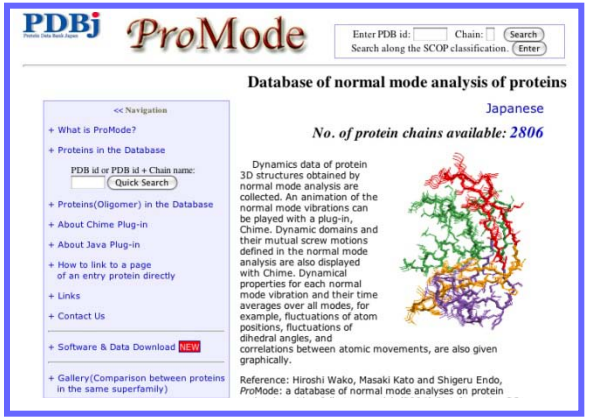


Electron Microscopy Navigator, EM-Navi *(Suzuki)*



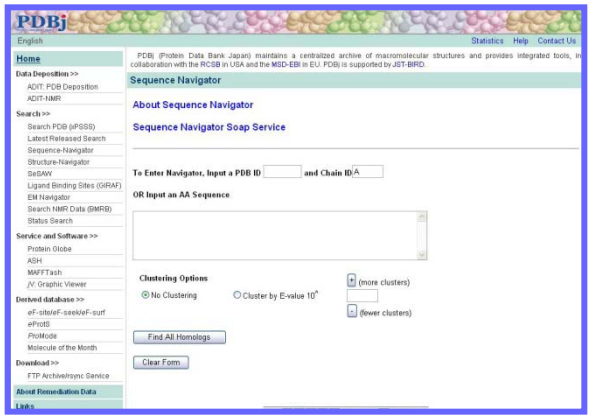
Protein Molecular Surface Database, *e*F-site *(Kinoshita & Nakamura)*

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



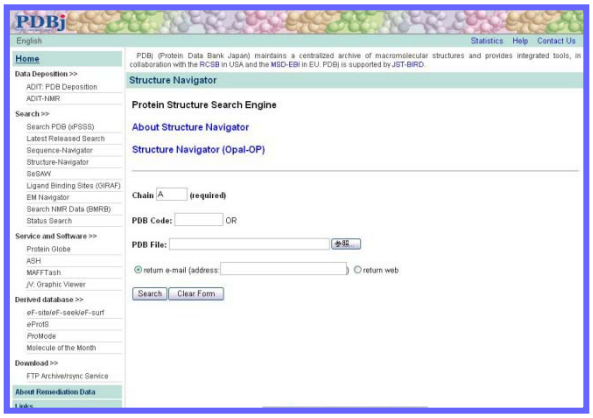
Protein Dynamics Database, *Pro*Mode *(Wako & Endo)*

Development of other Databases & Services



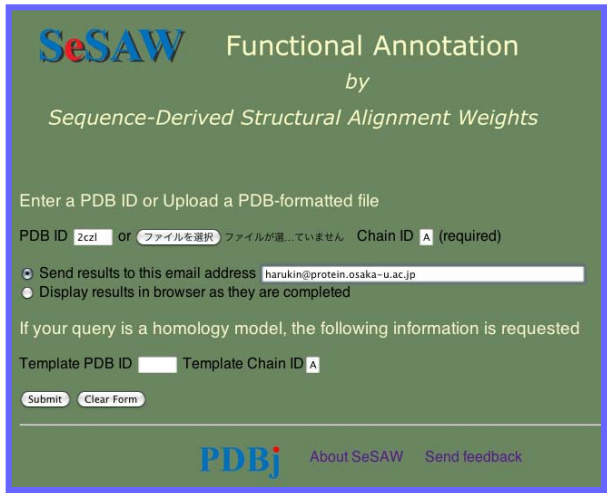
Homolog protein search,

Sequence Navigator
(Standley)



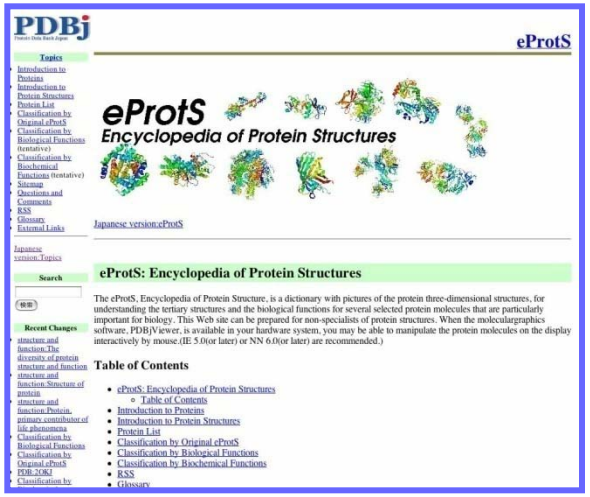
Similar fold search,

Structure Navigator
(Standley & Toh)

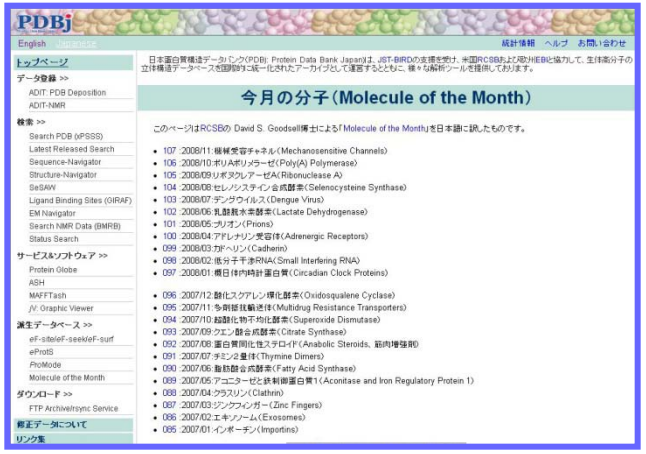


Function Annotation from Folds and Sequences, SeSAW *(Standley)*

Alignment of Sequence and Structures. MAFFTash
(Kato, Toh & Standley)



Encyclopedia of Protein Structures, eProtS
(Kinjyo, Kudo, & Ito)



Molecule of the Month, MoM
(Goodsell & Kudo)