

日本蛋白質科学会 年会2012年、名古屋国際会
議場、PDBjランチョンセミナー 2012年6月20日

PDBj : PDB japan

(日本蛋白質構造データバンク) の データベース高度化・統合化について

Haruki Nakamura

中村 春木



Institute for Protein Research

大阪大学蛋白質研究所

<http://pdbj.org/>

<http://wwpdb.org/>



Protein Data Bank Japan

日本蛋白質構造データバンク

<http://pdbj.org/>

Since 2001, PDBj has been managed at Institute for Protein Research, Osaka University as a member of the wwPDB, to curate, edit and process the deposited data for an open, public, and single archive of the wwPDB.

The screenshot shows the PDBj homepage with a navigation bar in English, Japanese, simplified Chinese, traditional Chinese, and Korean. It features a search bar for PDB ID or keyword, and options for Accession number or Deposition code. The page also displays news items from 2012, such as the launch of PDBMine and the addition of EM entries to the PDB archive. A sidebar on the right lists various protein structure databases and resources.



阪大蛋白研・データベース開発研究室のスタッフ

PDBj is a member of NBDC, Japan

JST-バイオサイエンスデータベースセンター

<http://biosciencedbc.jp/>

The screenshot shows the NBDC website's "Organization" page. At the top, there is a navigation bar with links to Home, About Us, Contact Us, and Link. On the right side of the header, there is a "Font size" dropdown menu with options L, M, S and a search bar. The main content area features a large organizational chart. At the top of the chart is the "Council for Science and Technology Policy (CSTP)" with two branches: "Life Science Project Team" and "DB Integration Promotion Task Force". Below this is the "National Bioscience Database Center (NBDC)". Inside NBDC, there are several boxes: a pink box for "Director-General Michio Oishi, Ph.D." and "Deputy Director-General Toshihisa Takagi, Ph.D.", a yellow box for the "Steering Committee", a green box for "Program Concerning Technology Development for Database Integration" with three research advisors and one research subject, and a blue box for "Program for Coordination Toward Integration of Related Databases" with three research advisors and three research subjects. To the left of NBDC, there are two green boxes: "Department of Planning and Management" and "Researchers". Arrows indicate interactions between these entities. At the bottom of the page, there is a section titled "About the Director-General (Michio Oishi, Ph.D.)" with a photo of him and a "Education:" section listing his academic degrees.

National Bioscience Database Center

Japanese | Sitemap | Site search

Font size L M S

search

Organization

Council for Science and Technology Policy (CSTP)

Life Science Project Team DB Integration Promotion Task Force

National Bioscience Database Center (NBDC)

Director-General Michio Oishi, Ph.D.
Deputy Director-General Toshihisa Takagi, Ph.D.

Steering Committee

Program Concerning Technology Development for Database Integration

Research Supervisor Takeshi Nagase, Ph.D.
Research Advisor
Research Advisor
Research Advisor

Research Subject

Program for Coordination Toward Integration of Related Databases

Research Supervisor Toshihisa Takagi, Ph.D.
Research Advisor
Research Advisor
Research Advisor

Research Subject Research Subject Research Subject

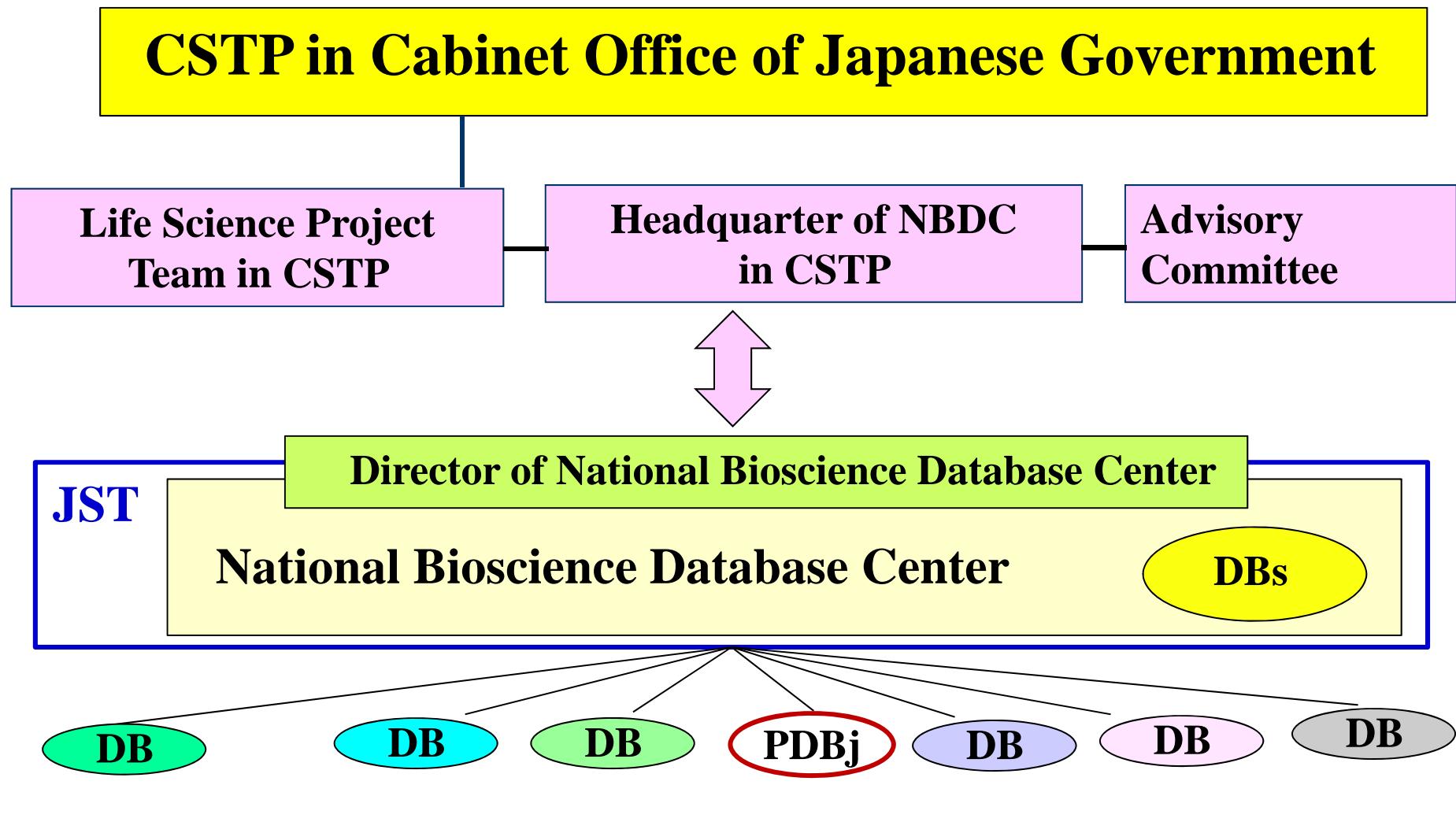
About the Director-General (Michio Oishi, Ph.D.)

Education :

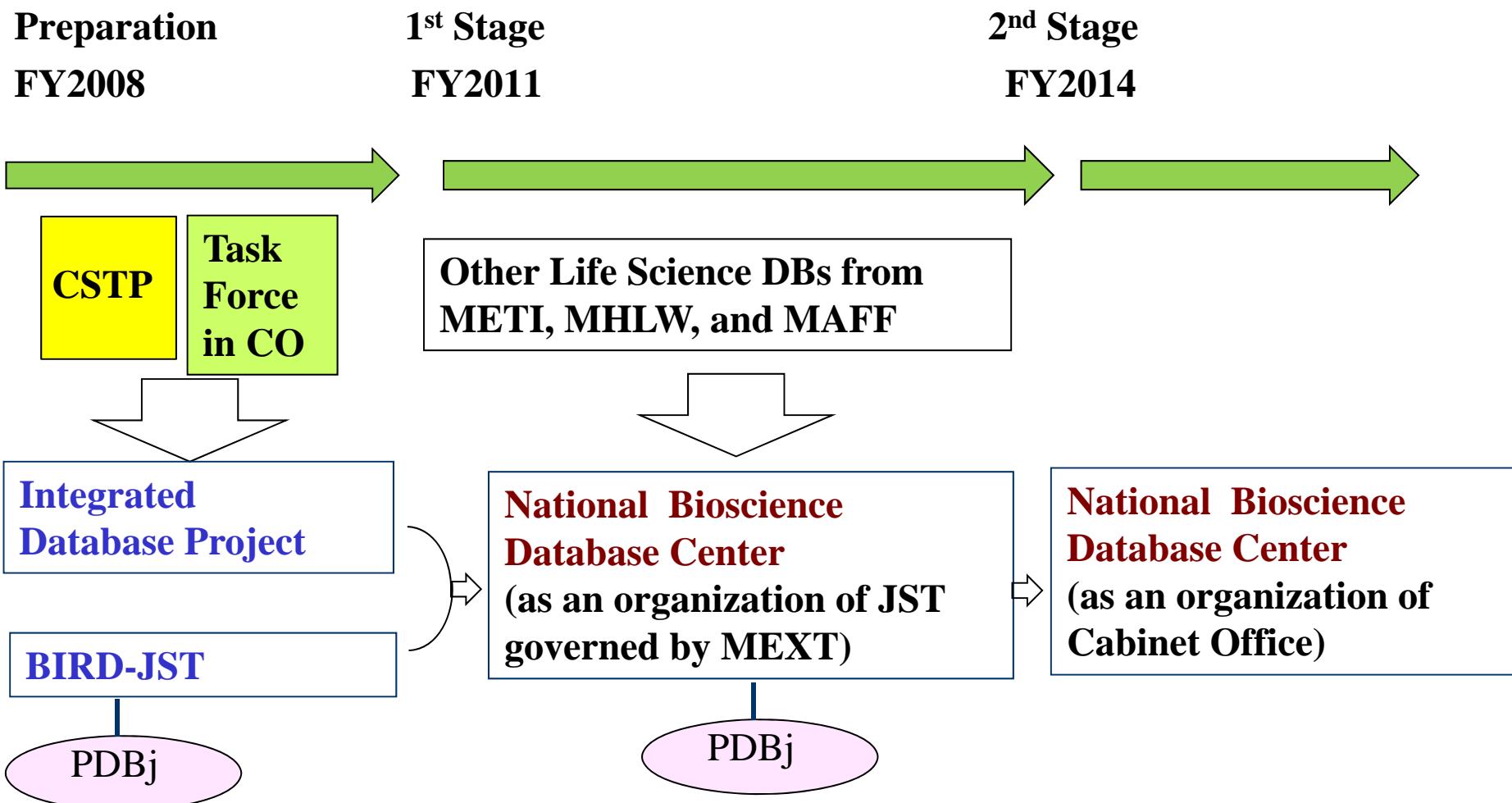
1958 B. S. Dept. of Biology, Faculty of Sciences, The University of Tokyo

1963 Ph.D. Dept. of Biochemistry and Biophysics, Faculty of Sciences, The University of Tokyo

Organization of National Bioscience Database Center (NBDC)



Roadmap for Foundation of National Bioscience Database Center (NBDC)



- **Head**

- Nakamura, Haruki, Ph. D. (Prof., IPR, Osaka Univ.)

- **Group for PDB Database Curation**

- Nakagawa, Atsushi, Ph. D. (Group Leader, Prof., IPR, Osaka Univ.)
 - Matsuda, Makoto (IPR, Osaka Univ.)
 - Igarashi, Reiko (IPR, Osaka Univ.)
 - Kengaku, Yumiko (IPR, Osaka Univ.)
 - Cho, Hasumi (IPR, Osaka Univ.)
 - Ikegawa, Yasuyo (IPR, Osaka Univ.)
 - Sato, Junko (IPR, Osaka Univ.)

- **Group for Development of new tools and services**

- Kinjo, Akira, Ph. D. (IPR, Osaka Univ.)
 - Iwasaki, Kenji, Ph. D. (IPR, Osaka Univ.)
 - Suzuki, Hirofumi, Ph. D. (IPR, Osaka Univ.)
 - Yamashita, Reiko (IPR, Osaka Univ.)
 - Kudou, Takahiro (IPR, Osaka Univ.)
 - Nishikawa, Ken, Ph. D. (Guest Prof., IPR, Osaka Univ.)
 - Bekker, Gert-Jan (IPR, Osaka Univ.)

- **Group for BMRB**

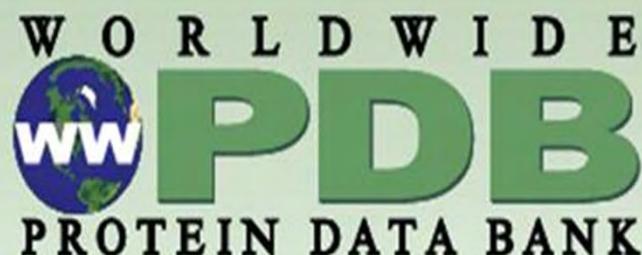
- Fujiwara, Toshimichi, Ph. D. (Group Leader, Prof. Osaka Univ.)
 - Akutsu, Hideo, Ph. D. (Prof., IPR, Osaka Univ.)
 - Kojima, Chojiro (IPR, Osaka Univ.)
 - Kobayashi, Naohiro (IPR, Osaka Univ.)
 - Iwata, Takeshi (IPR, Osaka Univ.)
 - Takahashi, Ami (IPR, Osaka Univ.)

- **Collaboratory Researchers**

- Wako, Hiroshi, Ph. D. (Prof., Waseda Univ.) (**for Pro Mode**)
 - Ito, Nobutoshi, Ph. D. (Prof., Tokyo Medical and Dental Univ.)
 - Kinoshita, Kengo, Ph.D. (Prof., Tohoku Univ.) (**for eF-site**)
 - Standley, Daron, Ph. D. (IFReC, Osaka Univ.) (**for SeqNavi, StructNavi, SeSAW, and ASH**)
 - Katoh, Kazutaka, Ph. D. (IFReC, Osaka Univ.) (**for ASH**)

- **Secretary**

- Haruki, Nahoko (IPR, Osaka Univ.)



The worldwide Protein Data Bank

www.wwPDB.org • info@wwPDB.org



Research Collaboratory for
Structural Bioinformatics
www.pdb.org

NSF, NIGMS, DOE,
NLM, NCI, NINDS,
NIDDK



BioMagResBank
www.bmrb.wisc.edu

NLM



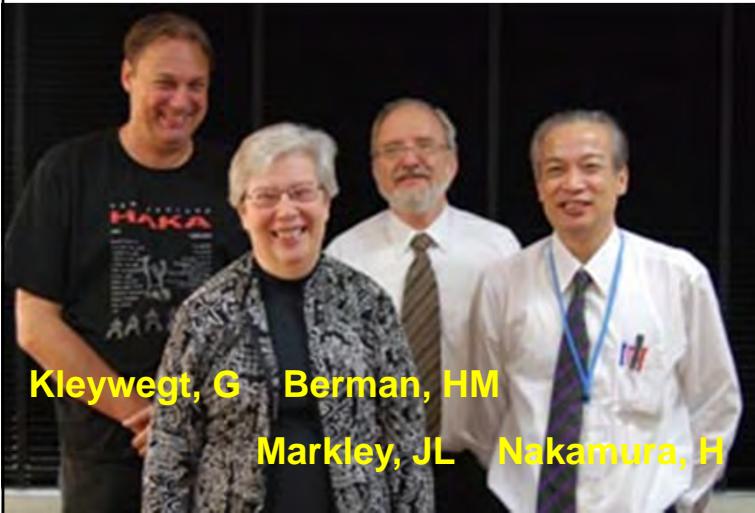
Protein Data Bank in Europe
pdbe.org

EMBL-EBI,
Wellcome Trust,
BBSRC, NIGMS, EU



Protein Data Bank Japan
www.pdbj.org

NBDC-JST



Kleywegt, G Berman, HM

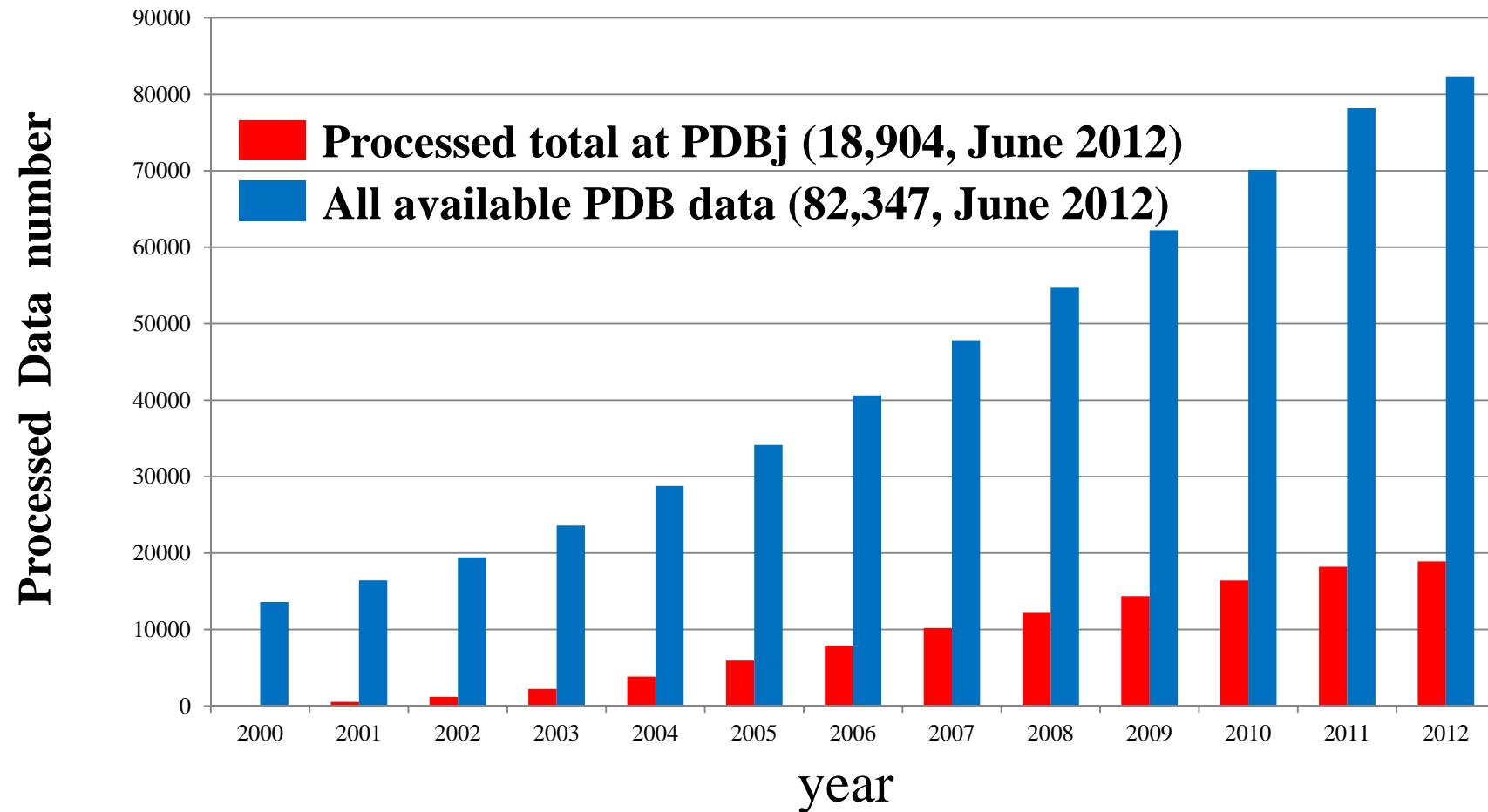
Markley, JL Nakamura, H



**wwPDB and wwPDBAC members
at EBI, Hinxton, on Sept. 30 2011**

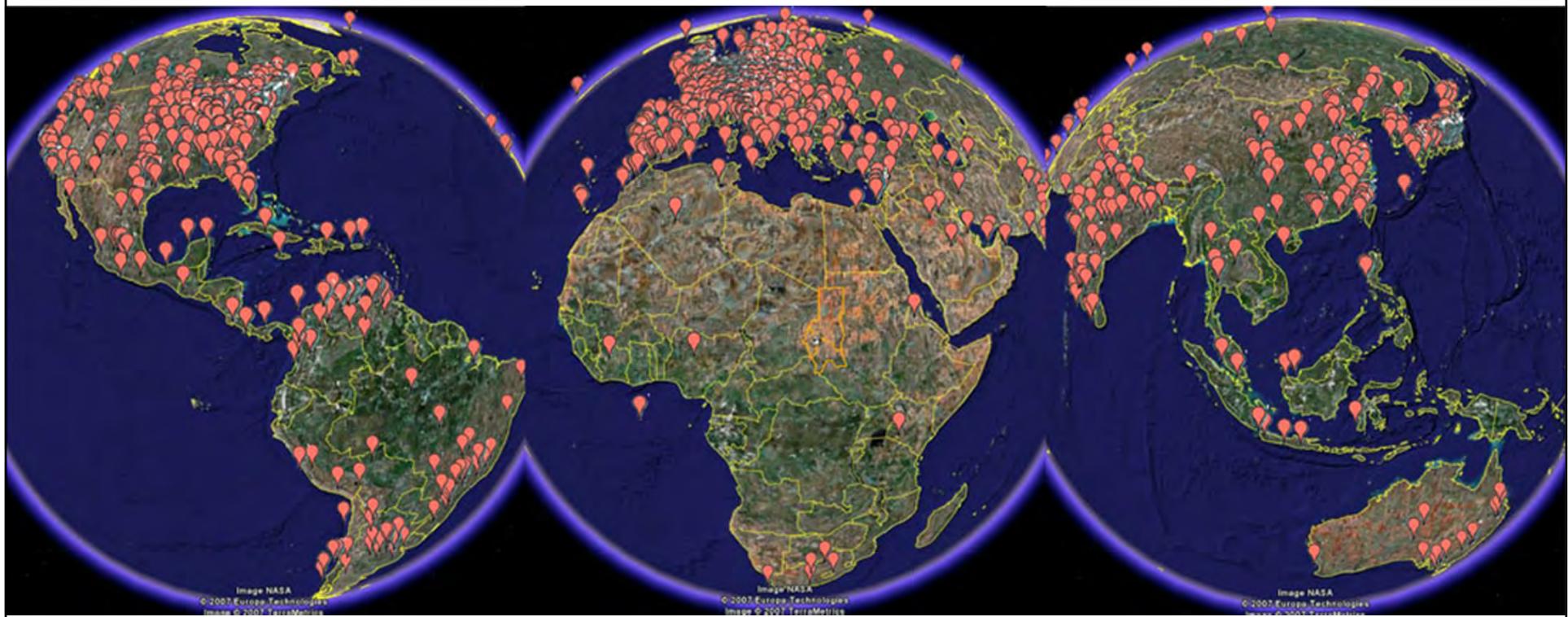


Data Processed at PDBj and wwPDB



PDBj curates and processes about a Quarter of the deposited data, mainly from Asian and Oceania regions.

wwPDB FTP Traffic



30,627,357 files were downloaded during March 2012 from the wwPDB member sites (RCSB-PDB, EBI-PDBe, and PDBj).

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ADIT: PDB Deposition

ADIT-NMR

検索 >>

Search PDB (Mine/xPSSS)

PDB/RDF, chem_comp/RDF

Latest Release Search

Sequence-Navigator

Structure-Navigator

SeSAW

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Search NMR Data (BMRB)

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Structure Prediction >>

CRNPRED

Spanner

SFAS

二次データベース >>

eF-site/eF-seek/eF-surf

eProtS

ProMode / ProMode Elastic /
ProMode Oligomer

ダウンロード >>

PDB Archive/Snapshot Archive

日本蛋白質構造データバンク(PDBj: Protein Data Bank Japan)は、JST-NBDCと大阪大学の支援を受け、米国RCSB、BMRB、および
欧州PDBe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PDB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。

データ登録

データ登録のご案内 >>

PDB登録 NMRデータ登録 

検索

PDB検索 

Mine日本語ページについて

PDB IDまたはキーワード

検索

詳細条件検索 >>

NMRデータ検索 

- Accession number
 Deposition code

 Go

最新情報

2012/4/18

2012年6月20日(水)に、第12回蛋白質科学会年会にて、ランチョンセミナーを開催いたします。(詳細...)

2012/4/16

2012年4月30日をもちまして、xPSSSサービスを終了させていただきます。それに伴いSOAPサービスも終了となります。今後は、PDBj Mine のRESTサービスをご利用ください。

2012/3/26

JVの最新版(JV4.2)がリリースされました。eF-siteで配布されるPyMOL用ポリゴンファイル(CGQファイル)の読み込み機能
が加わり、コマンド「load polygon_cgq」が追加されました。詳細はリリースノートをご覧ください。

2012/3/16

PDBで公開済みのエントリー数が、8万件を超過しました。また、PDB40シンポジウムの報告書が掲載されました。(詳細...)

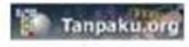
EMデータバンクがPDBアーカイブに追加されました

2012年3月7日に、EMデータバンク(EMDB)がPDBアーカイブに追加されました。今後はPDBjのftpサイト(
[ftp://pdb.protein.osaka-u.ac.jp/pub/emdb](http://pdb.protein.osaka-u.ac.jp/pub/emdb))からお使い頂けます。(詳細...)

80850

entries available
on 18 Apr., 2012

00:00(UTC) / 09:00(JST)



Get Entry Data from our browser

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



The screenshot shows the PDBj homepage in Japanese. A red circle highlights the search bar where the keyword "トリプトファン合成酵素" has been entered. Below the search bar, there are two search options: "PDB検索" and "NMRデータ検索". To the right of the search bar, there are fields for "Accession number" and "Deposition code". The main content area displays a list of search results for "tryptophan synthase". Each result includes the PDB ID, title, authors, experimental details, and download links. The results are paginated at the top right.

PDBj
English Japanese simplified Chinese traditional Chinese Korean
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PDB/RDF, chem_comp/RDF
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PDB登録 NMRデータ登録
検索
PDB検索 Mine
Mine日本語ページについて
PDB IDまたはキーワード 検索
詳細条件検索 >>
最新情報
2012/4/18 2012年6月20日(水)に、第12回蛋白質学会年会にて、ランチョンセミナーを開催いたします。(詳細...)
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統計情報 ヘルプ お問い合わせ
データ登録
PDBj Mine
検索結果ページ
(PDB-IDをクリックすると、詳細情報をご覧いただけます)
1 - 16 / 148
1 2 3 4 5 6 ... 10 次へ
クエリ : トリプトファン合成酵素 PDB ID or Keyword 表示数 一覧表示
実行クエリ : (tryptophan synthase) | (tryptophan synthetase)
リセット 検索

分子名稱	TRYPTOPHAN SYNTHASE ALPHA CHAIN (E.C.4.2.1.20), TRYPTOPHAN SYNTHASE BETA CHAIN (E.C.4.2.1.20)
タイトル	:TRYPTOPHAN SYNTHASE IN COMPLEX WITH (NAPHTHALENE-2-SULFONYL)-2-AMINO-1-ETHYLPHOSPHATE (F19)
著者	:Ngo, H., Harris, R., Kimminich, N., Casino, P., Niks, D., Blumenstein, L., Barends, T.R., Kulk, V., Weyand, M., Schlichting, I., Dunn, M.F..
実験手法	:X-RAY DIFFRACTION
登録日	:2008-04-27
公開日	:2007-06-12
分子名稱	TRYPTOPHAN SYNTHASE ALPHA CHAIN (E.C.4.2.1.20), TRYPTOPHAN SYNTHASE BETA CHAIN (E.C.4.2.1.20)
タイトル	:TRYPTOPHAN SYNTHASE IN COMPLEX WITH D-GLYCERALDEHYDE 3-PHOSPHATE (G3P)
著者	:Ngo, H., Harris, R., Kimminich, N., Casino, P., Niks, D., Blumenstein, L., Barends, T.R., Kulk, V., Weyand, M., Schlichting, I., Dunn, M.F..
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日本語のキーワード
を入力

→ 検索結果ページ

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PDBj

English Japanese simplified Chinese traditional Chinese Korean

統計情報 ヘルプ FAQ お問い合わせ

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リンク集

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検索

PDB検索 Mine 日本語ページについて

NMRデータ検索

検索

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PDBj

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日本語 ページについて PDBj Mineについて 更新情報

80850 entries available on 18 Apr, 2012 00:00 (UTC) / 09:00 (JST)

WORLDWIDE PROTEIN DATA BANK

eProtS Encyclopedia of Protein Structures

Protein Globe

OBCLS Database Center for Life Science

Tanpaku.org

NBDC New Protein Database

非対称単位

エンタリーID (PDB ID) 12as 配列情報 (FASTA形式) PDBファイルのダウンロード

分子名稱 ASPARAGINE SYNTHETASE, L-ASPANINE, ADENOSINE MONOPHOSPHATE

タイトル ASPARAGINE SYNTHETASE MUTANT C51A, C315A COMPLEXED WITH L-ASPANINE AND AMP

機能のキーワード LIGASE, ASPARAGINE SYNTHETASE, NITROGEN FIXATION

由来する生物種 Escherichia coli K12

細胞内の位置 [UNP - P00963] Cytoplasm

オリマー鎖の合計数 2

分子量の合計 74226 (詳細は 構造情報のページ)

著者 Nakatsu, T., Kato, H., Oda, J. (登録日 : 1997-12-02, 公開日 : 1998-12-30)

引用文献 Nakatsu, T., Kato, H., Oda, J. Crystal structure of asparagine synthetase reveals a close evolutionary relationship to class II aminoacyl-tRNA synthetase. *Nature Struct. Biol.*, 5:15 - 19, 1998. (Published: 9437423) (DOI: 10.1038/nsb0198-15)

実験手法 X-RAY DIFFRACTION (2.2Å)

他のデータベース情報 CATH, CE, FSSP, SCOP, VAST, UniProt (P00963), eF-site, KEGG (EC 6.3.1.1), GDB, EzCatDB, PISA, PQS

3次元構造ビューア JV3 / Jmol (JV3とJmolにはJava(TM)Plug-in 1.5以上が必要です)

(回転なし) 他の画像...

→ Summary for each PDBID is displayed.

PDBID (e.g. 12as) is input
in a box and GO

Summary for each PDBID is
displayed.

Summary for each PDBID

<http://pdbj.org/>

PDBj

English

Home

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- ADIT-NMR

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Derived database >>

 - eF-site/eF-seek/eF-surf
 - eProtS
 - ProMode

Mine

Summary [1gof]

About PDBj Mine
Update Information

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

PDB ID or Keyword search

PDB ID 1gof sequence information (FASTA format) download PDB format file

Descriptor GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5)

Title NOVEL THIOETHER BOND REVEALED BY A 1.7 ANGSTROMS CRYSTAL STRUCTURE OF GALACTOSE OXIDASE

Functional Keywords OXIDOREDUCTASE(OXYGEN(A))

Biological source Hypomyces rosellus

Cellular location [UNP - Q01745] Secreted

Total number of polymer chains 1

Total molecular weight 68785.9 (the details in Structural Details Page)

Authors Ito, N. , Phillips, S.E.V. , Knowles, P.F. (deposition date : 1993-09-30, release date : 1994-01-31)

Primary citation Ito, N. , Phillips, S.E. , Stevens, C. , Ogel, Z.B. , McPherson, M.J. , Keen, J.N. , Yadav, K.D. , Knowles, P.F. Novel thioether bond revealed by a 1.7 Å crystal structure of galactose oxidase. *Nature*, 350:87 - 90, 1991. (PubMed : 2002850) (DOI: 10.1038/350087a0)

Experimental method X-RAY DIFFRACTION (1.7[Å])

Other Database Information CATH , CE , FSSP , SCOP , VAST , UniProt (Q01745) , eF-site , KEGG (EC 1.1.3.9) , EzCatDB , PISA , PQS

Asymmetric unit

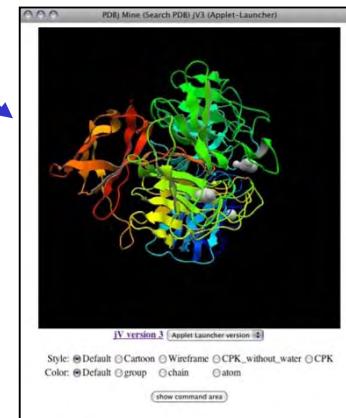
(no rotation) More images

Structure Viewers JV3 / Jmol (JV3 and Jmol require Java(TM)Plug-in 1.5 or later.)

Data viewer at PDBj

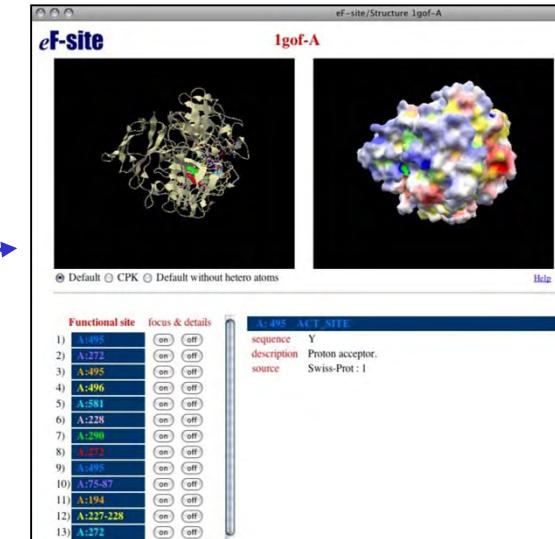
Graphic viewer: JV

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



Amino acid sequence (FASTA)

```
ftp://ftp.pdbj.org/XML/pdbmlplus/fasta_seq_data/1gof_seq.txt
>1gofA:GALACTOSE_OXIDASE
ASAPIGSAISRINNAWATCDSAQSGNECNKAIQDGKUDTPWHFTFYVGANGDPKPPTYTYIDMK
TTONVNGLNSMLPFDQDQNQNGWIGRIEVLYLSSDCTNNGSPVAGSGFADFDTTKYSNFETRP
ARYVRLVAITEANGQWTISIAEINVQASYTAPQFLGRNGCPIDLPFLPVAAAIEPTS
GRVLWLMSSRNDAFGPSGGITLTLSWDFSTGIVSDRRTVTVKHOMFCPGISMDQHNGQIV
VTGDNADAKTSLVQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQGKQ
VQFPEPSSPQELPAKVNRLPMLTADQQLYRSEPLGWKEKESVQGKQGKQGKQGKQGKQGKQGKQ
GECDVFKACHEGSGNSHNSVAFDAMCGNNWVHDNAYNKGLIPFGCSPDQYQPSAINTHNTIZLG
EPGTSPTVTVASNLGLYFARTHHTSVVLPDGSTF1TGQQRGQIPPESTDTPVFTPEIYVPEQ
DTTYKQNPNISIVRVYHSISLLLPDRVRVNGGGCLGCDCTTNNHFDQIIFTPNYLNSNGNL
ATRKIITRTSOSVXVGR1T1STSSISKAISLRYGTATHTVNTDQRRIPLTLTHNGGN
SYSFQVPSDSGVALFGYWMFLVINSAGUPSVASTIKVTQ
```



Molecular surface DB: eF-site

<http://ef-site.hgc.jp/eF-site/>

Annotation of Protein Function from Molecular Surface Similarity: eF-site / eF-seek

PDBj **eF-site**
electrostatic surface of Functional-site

[About eF-site](#) | [References](#) | [Links](#) | [Acknowledgements](#) | [Feedback](#)

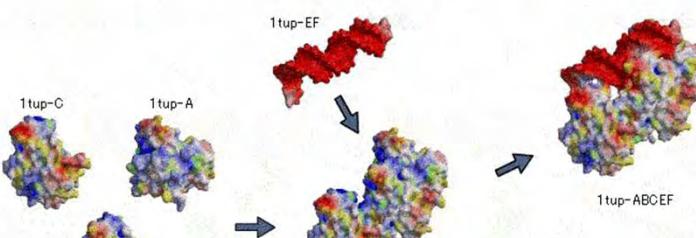
175033 Entries, Last Update: 20-Aug-2005

Keyword Search
 PDB code only and or

Category Search

- Antibody
- Prosite
- Active Site
- Membrane
- Binding Site

Examples of molecular surface



1tup-C 1tup-A 1tup-EF 1tup-ABCEF

Protein Molecular Surface DB

TOP Help FAQ References Llinks

PDBj **eF-seek**

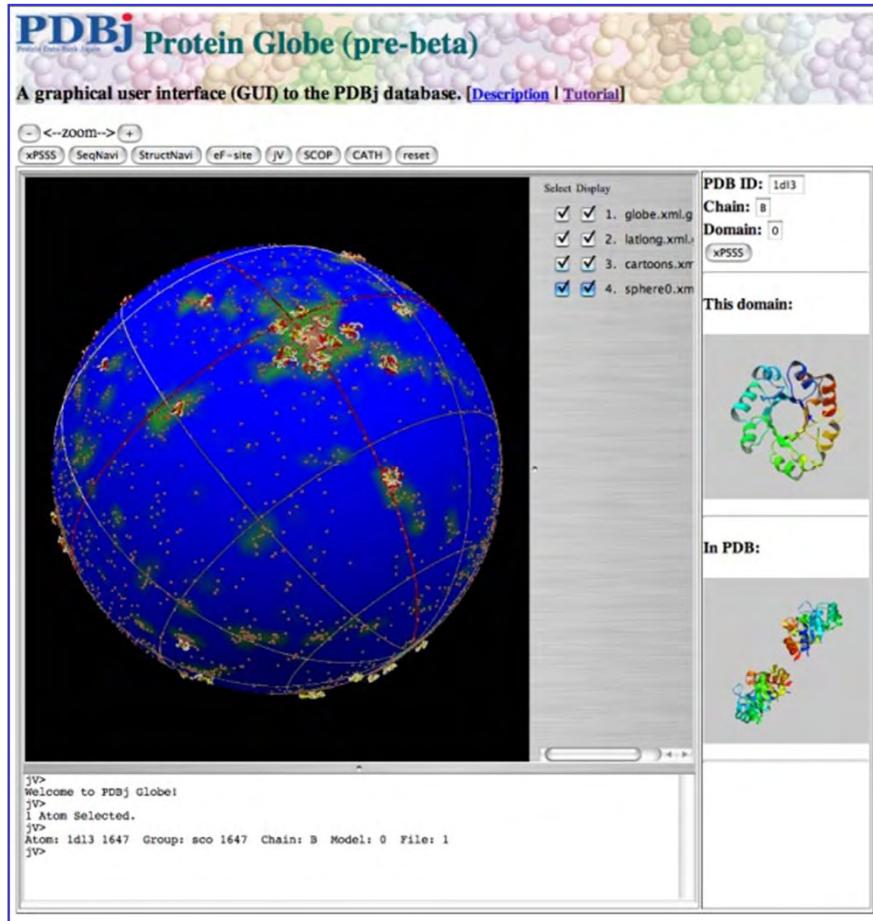
ABOUT eF-seek:
Molecular function of proteins are determined by their three dimensional structures, thus the similarity of protein structure can give some clues to infer their functions. In many cases, the molecular function are begun with the molecular interaction with small molecules (ligands). **eF-seek** is a web server to search for the similar ligand binding sites for the uploaded coordinate file with PDB format. The representative binding sites in eF-site database are search by our own algorithm based on the clique search algorithm.



Submission STEP-1:
Specify a PDB format file:
E-mail address:
Keyword: *
Title: (optional)

Search for Similar Surface

Viewing Folds and Dynamics @ PDBj



PDBj Protein Data Bank Japan **ProMode Elastic** **ProMode** **ProMode Oligomer**

Database of normal mode analysis of PDB data using elastic network model in torsional angle space

Home | What is ProMode-Elastic | Help Japanese No.of entries 13

PDB code (4 chars) Find Example 1abc

Select from a list of entries

Submission of your data to be analyzed. (In preparation)

Download of

ProMode-Elastic using the protein backbone atoms in PDB files for ligand molecules and reference molecules.

Reference: 1

TOPICS 2009.12.12

PDB id: 7rsa Name: Hydrolase (phosphoric diester) Title: Structure of phosphate-free ribonuclease a refined at 1.26 angstroms. Structure: Ribonuclease A Chain: a Function: Enzyme

*Click on image for an enlarged image and more information.

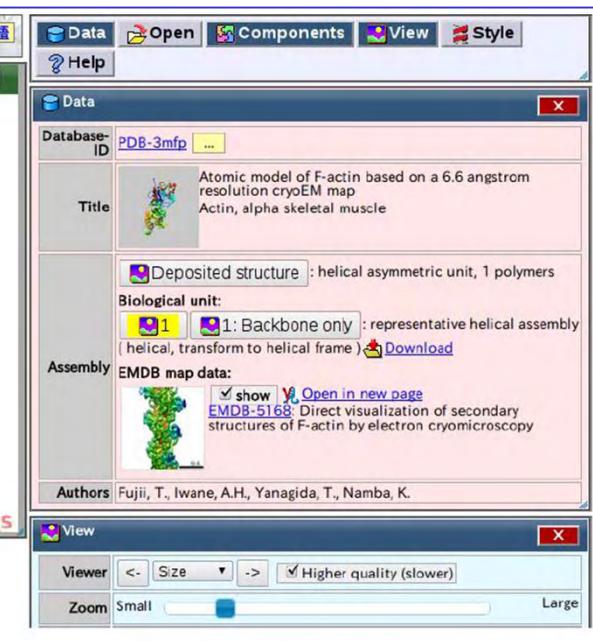
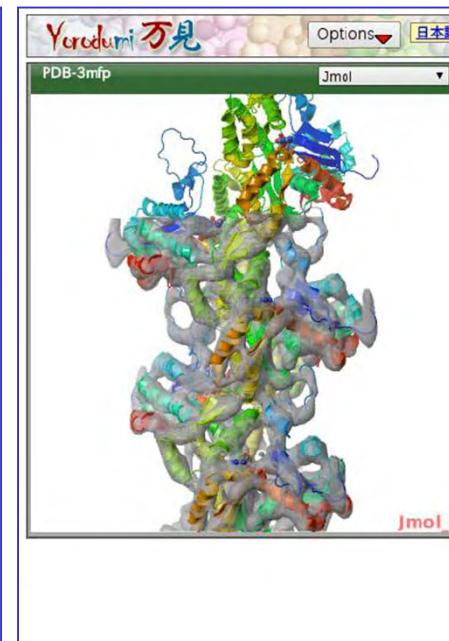
PageTop | Back (Latest update 2009.12.21)

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Protein Globe: Protein Folds Browser

ProMode: Protein Dynamics Database by NMA

Viewing both EM Image and Atomic Structure



EM Navigator: Viewer of
Images of EM-DB

Yorodumi: Viewer of both
Image and Atomic Structure

PDB/RDF for Semantic Web

(Recently developed by PDBj: Akira R. Kinjo et al.)

<http://pdbj.org/rdf>

PDB/RDF

*About PDB/RDF
chem_comp/RDF Search*

PDB ID: (e.g., '7RSA')

property: (e.g.,
'PDBo:entity.pdbx_description')

keywords: (e.g., 'alcohol')

Download XSLT stylesheet for converting PDBML to RDF: [PDBML2rdf.xsl.gz](#)
(gzipped 22KB)

*) Some web browsers such as Internet Explorer will display the plain XML file. Please use other browsers that can handle XSLT, e.g. Firefox, Google Chrome, or Safari etc..

PDB data in the Resource Description Framework (RDF) format for the Semantic Web.

Kinjo et al. (2012) Nucl. Acids Res. 40, D453-D460.

Development of other Databases and Services

This screenshot shows the Sequence Navigator page. It includes a search bar for PDB ID and Chain ID, clustering options (no clustering or cluster by E-value 10⁻⁴), and a 'Find All Homologs' button. The sidebar contains links for Data Deposition, Structure Navigator, Sequence Navigator, and various search and download options.

Homolog protein search,
Sequence Navigator
(Standley)

This screenshot shows the Structure Navigator page. It features a search bar for PDB Code or File, and a 'Search' button. The sidebar includes links for Protein Structure Search Engine, Structure Navigator, and various search and download options.

Similar fold search,
Structure Navigator
(Standley & Toh)

This screenshot shows the Spanner interface. It has sections for Input (upload template and alignment files), Link (Lab homepage at JFCG and Protein Data Bank Japan), and Advanced Parameters. A sidebar lists various tools like SeqAlign, IBD Navigator, and MAFFT.

Hybrid Template Homology
Modeling, Spanner
(Lis, Standley, Nakamura)

This screenshot shows the MAFFTash interface. It includes a sequence input area with an example sequence, a file upload section, and a search form. The sidebar provides links for Data Deposition, Structure Navigator, and various search and download options.

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

This screenshot shows the eProtS Encyclopedia of Protein Structures. It features a grid of protein structures, a search bar, and a table of contents. The sidebar includes links for Data Deposition, Structure Navigator, and various search and download options.

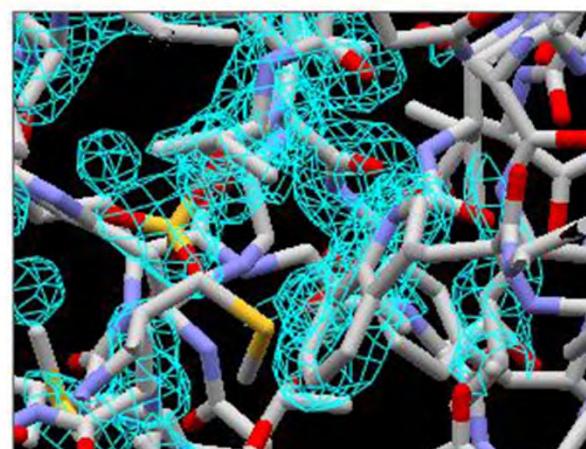
Encyclopedia of Protein
Structures, eProtS
(Kinjyo, Kudo, & Ito)

This screenshot shows the MoM interface. It displays a list of molecules of the month from 2008, with a link to the Japanese version. The sidebar includes links for Data Deposition, Structure Navigator, and various search and download options.

Molecule of the Month, MoM
(Goodsell & Kudo)

[Home](#)[Data Deposition >>](#)[ADIT: PDB Deposition](#)[ADIT-NMR](#)[Search >>](#)[Search PDB \(Mine/xPSSS\)](#)[PDB/RDF,](#)[chem_comp/RDF](#)[Latest Release Search](#)[Sequence-Navigator](#)[Structure-Navigator](#)[SesAW](#)[Ligand Binding Sites
\(GIRAF\)](#)[EM Navigator](#)[Search NMR Data \(BMRB\)](#)[Status Search](#)[Service and Software >>](#)[JV: Graphic Viewer](#)[Yorodumi](#)[Protein Globe](#)[ASH](#)[MAFFtash](#)[SEALA](#)[Structure Prediction >>](#)[CRNPRED](#)[Spanner](#)[SFAS](#)[Derived database >>](#)[eF-site/eF-seek/eF-surf](#)[ePrntS](#)

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-NBDC and Osaka University.

Mine**Electron Density Map [2xvy]**[About PDBj Mine](#)
[Update Information](#)**About the PDBj Electron Density Map Viewer**

```
jV>
Atom: S 2075 Group: S04 1272 Chain: A
File: 1
jV>
```

jV version 4

Applet Launcher (new Java Plug-in) version

Style: Cartoon Backbone Wireframe
 Color: group chain atom

When the mouse right button is clicked in the jV4 window, it
 For a trouble to display a picture, please retry selecting
 "Applet Launcher (new Java Plug-in) version" or
 "Applet Launcher (classic Java Plug-in) version" from the above pull-down menu.
 You may also refer the [known problems page](#).

Here,

Applet Launcher (classic Java Plug-in) version: for Mac OS X or for Windows
 Applet Launcher (new Java Plug-in) version: for Windows or Linux with JRE 1.6

Parameters for Electron Density Map**Type of the map:** contour mesh iso surface**Map position:** atom nearest to the center of the map

Chain: , Residue: , Atom:

(you can select "Atom ID" by clicking in the viewer)

 coordinates: (x , y , z)

mapped area: 10 Å

(this is the length of edge of a cube)

contour level: 1 σ

color: R 0.0 G 1.0 B 1.0

isosurface transparency level: 0.5

Electron Density Map Download/Delete ... <
>

service.pdbj.org/mine_test/jsp/download_map2.jsp

Electron Density Map Download/Delete Page

file format	filename	download
structure factor	r2xvysfent.gz	<input type="button" value="download"/>
refinement file	2xvy.reftar.gz	<input type="button" value="download"/>
edmap file	20111122111327_2xvy.xml.gz	<input type="button" value="delete"/> <input type="button" value="download"/>

配列情報を入力とした、構造情報に基づく機能の解析・推定パイプラインの構築

- Multiple Sequence Alignment (MSA) for query (MAFFT) and templates (MAFFTash)
- MSA-profile alignment (MSThread)
- Fragment-based structural modeling (Spanner)
- Function prediction (SeSAW)

Structure & Function Prediction Pipeline

Input Progress Alignments Spanner Sesaw About

Query Sequence

```
>sp|Q5D1E7|ZC12A_MOUSE Ribonuclease ZC3H12A OS=Mus musculus GN=Zc3h12a PE=1
SV=2MSDPCGTKPVQESNPTMSLWSLEDRHSSQRPQDPQDPAKEAPTSELQMVKDFRKLGYSSSEIHSVLQKLGVQADNTVLGELVKHGSATER
ECQALTAPSPQPPLVPRGGSTPKPSTLEPSPEEDREGSDLRPVVIDGSNVAMSHGNKEVFSCRGILLA VNWFLERGHTIDITVFVPSWRKEQPRPDVPIT
DQHILRELEKKKILVFTPSRRVGGKRVVCYDDRFIVKLAFESDGVVVNSNDTYRDLQGERQEWKRFIEERLLMYSFVNDFKMPDDPLGRHGPSLDNFL
RKKPLPSEHRKQPCPYGKKCTYGIKCRFFHPERPSRPQRSVADELRLANALLSPRTPVKDKSSQRSPASQSSSVSLEAEPGSLDGKKGARSSPGHRE
GSPQTCAPIAGRSLPVSGGSFGPTEWAHTQDSLPTSQECLDSIGSLESQMSSELWGVRGGSPGESGPTRGPYAGYHSYGSKVPAAPSFPFRPAMGA
GHFSVPTDYVPPPTTYPSPREYWSEPYPLPPPTPVLQEPRPSPGAGGGPWGRVGDLAKERAVYT KLCGVFPPLVEAMMRRFPQLLDPQQLAAEILSY
KSQHLSE
```

Structure & Function Prediction Pipeline

Input Progress Alignments Spanner Sesaw About

Alignment methods

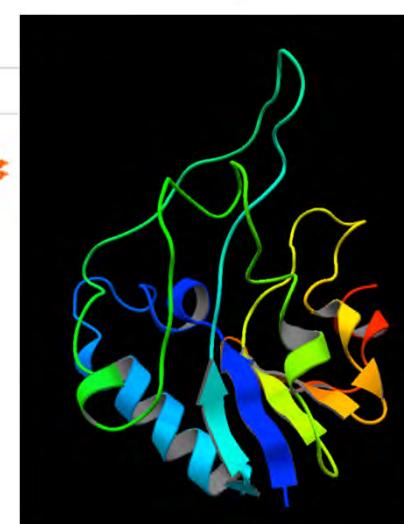
hhpred options
 ffas options
 forte options
 msthread options
 psiblast
 blast

E-Mail

Job id (optional)

Run!

1ixs_A 1exn_A 2cqe_A
2w84_ 3h7i_A 2cqe_
3oq9_A 3ix7_A 1n9o_
1tte_A 1o4w_A 2rhk_
1cuk_A 2qip_A 1n9o_
2dna_A 3i8_ 2d9n_
3a1y_ 3cq5_A 1axh_
3d0w_A 3e3n_A 2d9n_
1fad_A 1byk_A 2e5s_A
1wxp_A 3fdb_A 2e5s_
2ztd_A 2x5d_A 2r_
2lbf_ 1c7n_A 1_
3t15_ 2hsg_A
1d2f_A



Spanner Model

生体系NMRデータ群の登録

