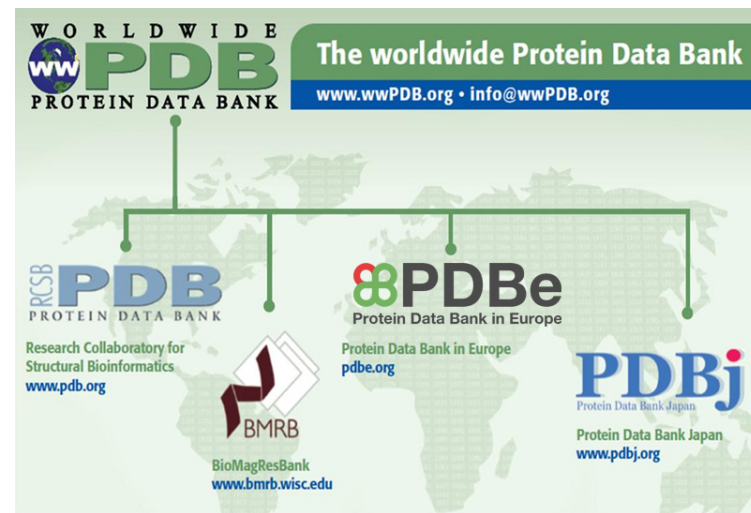




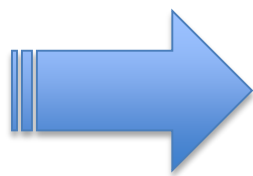
Protein Data Bank Japan

<http://pd bj.org/>

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

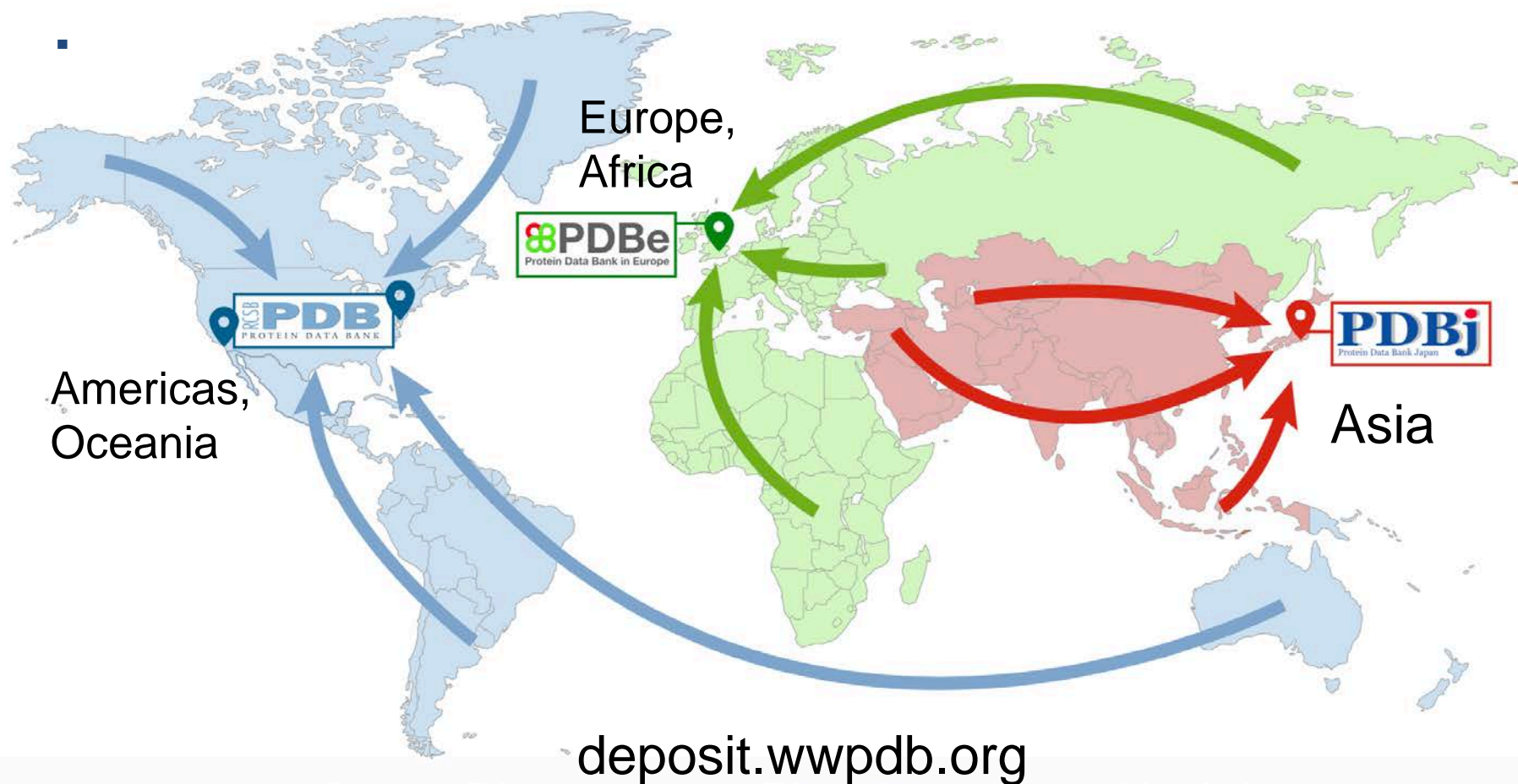


After Solving Structure, what we should do?

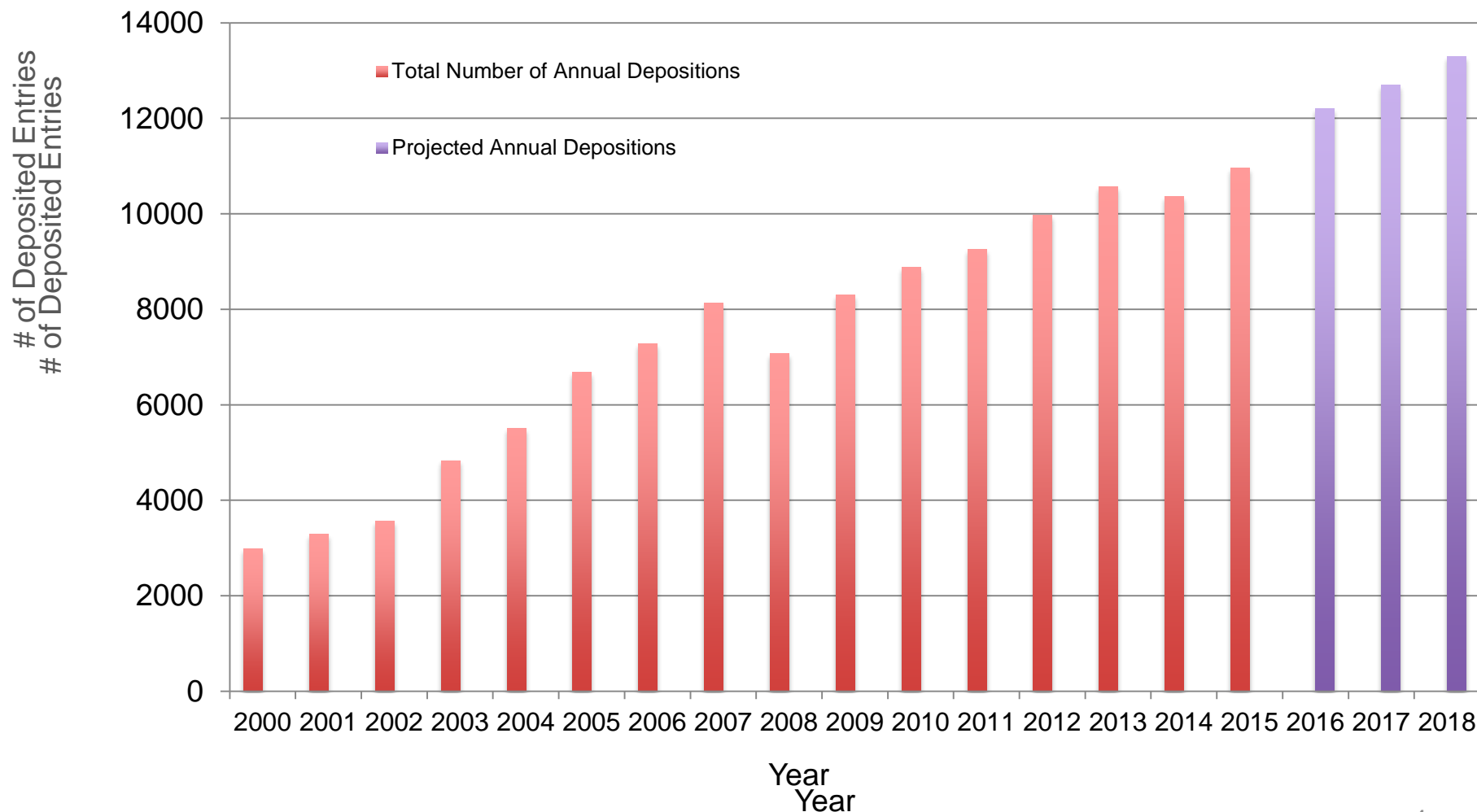


<https://wwpdb.org>

PDBj is in charge of processing and annotating the depositions from Asian and Middle-east regions

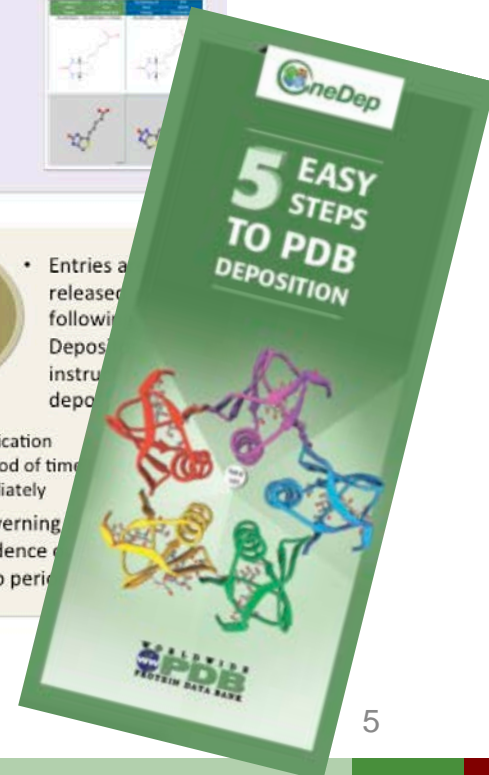
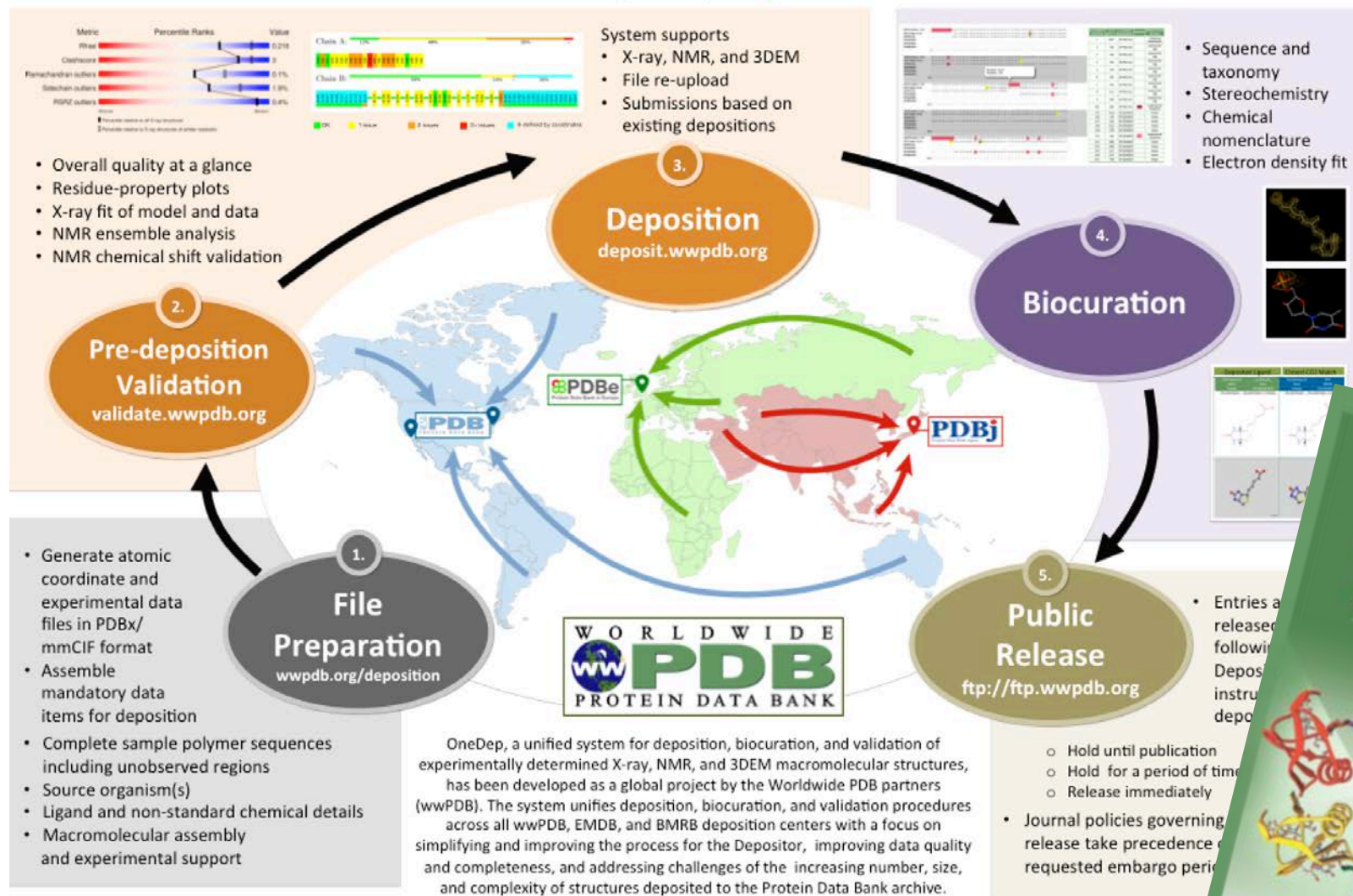


Growing Number of Depositions



OneDep: Unified Deposition Portal for the Protein Data Bank

wwPDB Partners - RCSB PDB, PDBe, PDBj, and BMRB



Collection of ORCID IDs

- Successfully Implemented Apr 11, 2016
- Metrics (Apr 11 – Aug 31, 2016):
 - ~8% of Depositions have ORCID ID (374/4713)
 - 170 unique ORCID IDs (92 identified as PIs)
- Plans to Increase ORCID Adoption
 - Expand to all entry authors to provide ORCID (2017)
 - Distribute collected ORCID IDs at ftp archive (2017)
 - Mandatory going forward (2018)

Official wwPDB Validation Report is requested for peer review



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 04:13 AM GMT

PDB ID : 3WDZ

Title : Crystal Structure of Keap1 in Complex with phosphorylated p62

Authors : Fukutomi, T.; Takagi, K.; Mizushima, T.; Tanaka, K.; Komatsu, M.; Yamamoto, M.

Deposited on : 2013-06-26

Resolution : 2.60 Å (reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

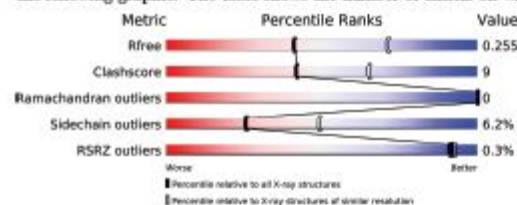
We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://www.pdb.org/ValidationPDFNotes.html>

1 Overall quality at a glance

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Kelch-like ECH-associated protein 1

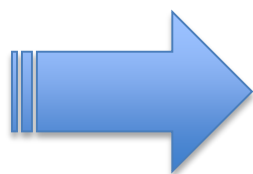


- Molecule 2: Peptide from Sequestosome-1



Example of Validation report

When you want to know the 3D structure?



<https://pdbj.org>

PDBj (Protein Data Bank Japan) maintains a centralized PDB archive and provides integrated tools, in collaboration with the [RCSB PDB](#) in EU. PDBj is supported by [JST-NBDC](#) and [Institute of Materials and Chemical Process Engineering](#).

Guide for first time visitors

For an introduction to the new web interface, please read [User's guide](#) introduction to the customization features offered by the new found [here](#). To get a more in-depth explanation on the various please take a look at the [Interactive tutorial series](#).

The [legacy PDBj website](#) will no longer be updated after July the end of August, 2017.

Find the service you need

Choose a keyword listed below or input keywords into the text list. The brief explanation of the matched services will be displayed.

- Click the 'Show all services' button to display the explanation of all services.
- Input some keywords into the 'Word Search Box' to narrow down the list.

- ☐ PDB
- ☐ BMRB
- ☐ search
- ☐ deposition
- ☐ education/dictionary
- ☐ NMR
- ☐ electron microscopy

日本蛋白質構造資料庫 (PDBj: Protein Data Bank Japan), 由 [JST-NBDC](#) 和 [大阪大学蛋白質研究所](#) 提供支援, 與美國的 [RCSB PDB](#), [BMRB](#) 和歐洲 [PDBe](#) 共同合作, 在對國際性的生物大分子立體結構資料庫的PDB檔案文件進行維護的同時, 還提供各種結構解析的應用軟體。

日本蛋白質構造データベース (PDBj: Protein Data Bank Japan), 由 [JST-NBDC](#) 和 [大阪大学蛋白質研究所](#) 提供支援, 與美國的 [RCSB PDB](#), [BMRB](#) 和歐洲 [PDBe](#) 共同合作, 在對國際性的生物大分子立體結構資料庫的PDB檔案文件進行維護的同時, 還提供各種結構解析的應用工具。

PDBj (Protein Data Bank Japan) 는 미국의 구조 생물 정보학 연구 공동체([RCSB PDB](#)), [BMRB](#) 및 유럽 생물 정보학 연구소([PDBe](#))와 협력하여 고분자 입체구조와 구조 해석 도구를 제공하고 있습니다. PDBj는 독립 행정법의 과학기술 진흥기구 [바이오사이언스데이터베이스] ([JST-NBDC](#))와 [오사카대학 단백질연구소](#)의 후원을 받고 있습니다.

日本蛋白質構造データベース (PDBj: Protein Data Bank Japan) は, [JST-NBDC](#) と [大阪大学蛋白質研究所](#) の支援を受け, 米国 [RCSB PDB](#), [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

File Versioning: Planning Process

Current Issues:

- Loss of connection between PDB ID and Publication under current wwPDB Obsolete/Supersede Policy
- Enable revisions to entries updated by the Depositor of Record (e.g., Version 1-0 → 1-1; 1-0 → 2-0)
 - wwPDB will NOT assign a new PDB ID going forward (for Depositor of Record revision only)
- Introduce new PDB ID code format
 - With PDB prefix and extension of 4 characters (e.g., from “1ABC” to “PDB_00001ABC”)
- Example: PDB_00001ABC_XYZ_V2-2.cif.gz

Nucleic Acids Research Advance Access published October 26, 2016

Nucleic Acids Research, 2016, 1
doi: 10.1093/nar/gkw962

Protein Data Bank Japan (PDBj): updated user interfaces, resource description framework, analysis tools for large structures

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Received September 15, 2016; Revised October 06, 2016; Editorial Decision October 07, 2016; Accepted October 11, 2016

ABSTRACT

The Protein Data Bank Japan (PDBj, <http://pdbj.org>), a member of the worldwide Protein Data Bank (wwPDB), accepts and processes the deposited data of experimentally determined macromolecular structures. While maintaining the archive in collaboration with other wwPDB partners, PDBj also provides a wide range of services and tools for analyzing structures and functions of proteins. We herein outline the updated web user interfaces together with RESTful web services and the backend relational database that support the former. To enhance the interoperability of the PDB data, we have previously developed PDB/RDF, PDB data in the Resource Description Framework (RDF) format, which is now a wwPDB standard called wwPDB/RDF. We have enhanced the connectivity of the wwPDB/RDF data by incorporating various external data resources. Services for searching, comparing and analyzing the ever-increasing large structures determined by hybrid methods are also described.

major changes regarding user interfaces and analysis tools as well as additional data provided. The previously described Resource Description Framework (RDF) format, PDB/RDF, is now one of the wwPDB standard formats called wwPDB/RDF and is enhanced with supplementary information in order to connect PDB data with other biological data resources.

USER INTERFACES

User interfaces include interactive (and graphical) web interfaces for humans and RESTful web services for computer programs. We also expose our backend database in the forms of web services or dump files for enabling very complex queries. These are described in turn.

Web interface

The web interface of PDBj was updated to provide a uniform integrated interface for the available services as well as to provide a scalable interface for devices ranging from smartphones to workstations. This update incorporates several innovative/renovative features as described below.

We have implemented various functionalities to ease



Tools for Protein Science

New tools and functions in Data-out activities at Protein Data Bank Japan (PDBj)

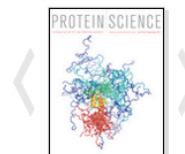
Akira R. Kinjo, Gert-Jan Bekker, Hiroshi Wako, Shigeru Endo, Yuko Tsuchiya, Hiromu Sato, Hafumi Nishi, Kengo Kinoshita, Hirofumi Suzuki, Takeshi Kawabata, Masashi Yokochi, Takeshi Iwata, Naohiro Kobayashi, Toshimichi Fujiwara, Genji Kurisu, Haruki Nakamura ✉

Accepted manuscript online: 17 August 2017 Full publication history

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More information by Drs. Kinjo & Suzuki