

Recent activities of PDBj and wwPDB

Genji Kurisu
Institute for Protein Research,
Osaka University

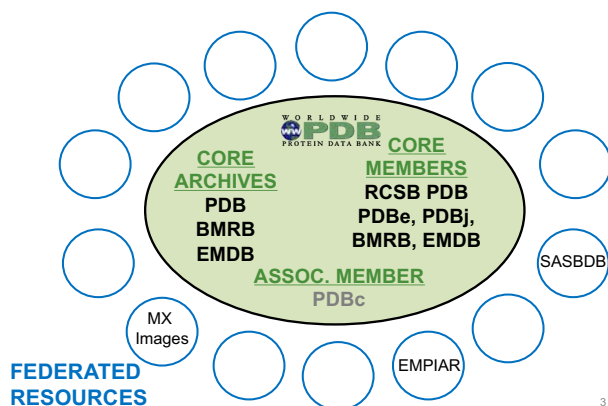
1

Protein Data Bank Japan <http://pdbj.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.

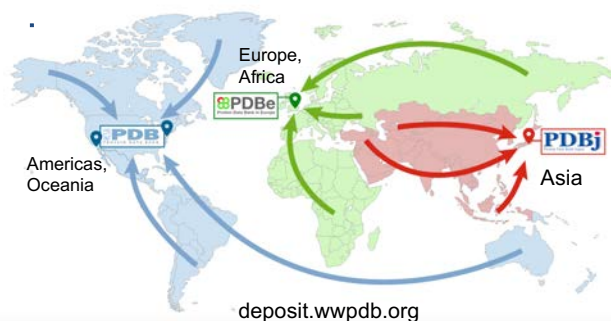


wwPDB Architecture



3

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



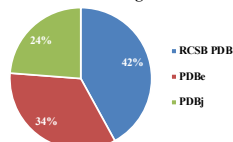
4

PDB Core Archive Depositions

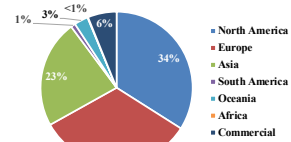
- 12,179 depositions in 2018.
- Rapid growth in 3DEM
 - Exceeded NMR depositions

Method	2017 Depositions	2018 Depositions
MX	11,889 (91.1%)	10594 (87.0%)
NMR	460 (3.5%)	418 (3.4%)
3DEM	674 (5.2%)	1140 (9.4%)
Other	26 (0.2%)	27 (0.2%)

2018 Processing Sites

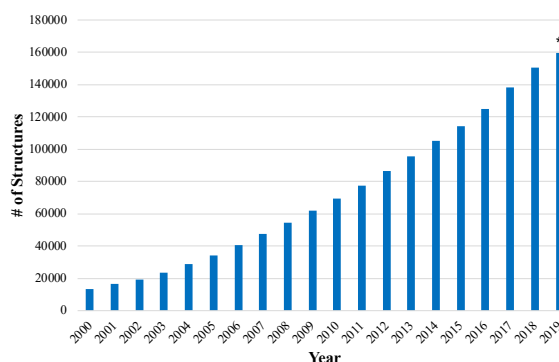


2018 Depositor Locations



5

PDB Core Archive Growth



* As of 3 Sep 2019

6

PDB Core Archive Downloads

Year	Total	Total FTP Archive	Total Website
2019	373,392,752	236,377,566	137,015,164
2018	749,356,799	N/A	N/A
2017	679,421,200	454,723,083	224,698,117
2016	591,876,087	366,677,897	225,198,190
2015	534,339,871	368,244,766	166,095,105
2014	512,227,251	339,193,721	173,033,530
2013	441,262,210	296,176,290	145,085,920
2012	376,944,070	255,837,735	121,106,335
2011	383,131,048	276,952,286	106,178,762
2010	294,326,976	213,180,966	81,146,010
2009	326,362,536	271,116,934	57,245,602

More than 1.8 million/day!

N.B.: Some 2018 data lost due to GDPR.
Hope to be back on track for 2019→.

* As of 3 Sep 2019



Geographic Origins of FTP downloads; 2012-2015

PDB Core Archive Update I

Ligand Validation

- Adapted software from Global Phasing Ltd. under a formal agreement
- Provides geometrical quality in 2D depiction
- Provides electron density fit for X-ray
- Now mandatory at deposition: identification of Ligand/s Of Interest (LOI, author's research focus)

8

Official wwPDB Validation Report is requested for peer review

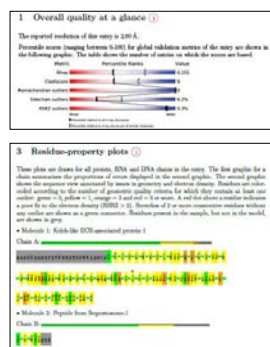
wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 - 04:13 AM GMT

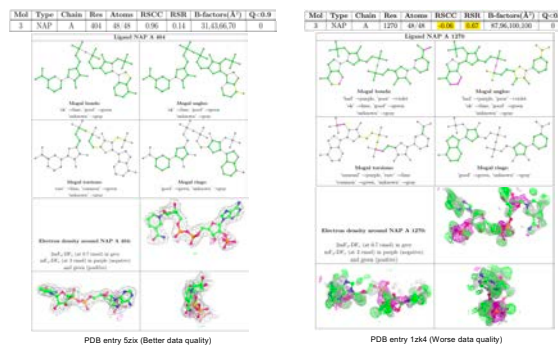
PDB ID : 3W1Z
Title : Crystal Structure of Kinetin in Complex with phosphorylated p62
Author : Fukunishi, T., Takagi, K., Mizushima, T., Tanaka, K., Komatsu, M., Yamamoto, M.
Deposited on : 2013-06-26
Resolution : 2.69 Å (reported)

This is a wwPDB validation summary report for a publicly released PDB entry. We welcome your comments at validation@wwpdb.org. A user guide is available at <http://www.pdb.org/Validation/Validation.html>

Example of Validation report



Ligand Validation- Examples on NADP



10

PDB Core Archive Update II

Coordinate Versioning

- To improve data quality in the PDB archive
- Depositors can now make corrections to existing structures in the PDB Core Archive by updating the atomic coordinates while preserving the original PDB identifier.
- Deployed on July 27th 2019 for all structures that were originally deposited via OneDep (Phase one)
- First coordinate replacement (PDB entry 5T26) versioned at FTP on August 7th 2019 following reviewers' comments based on the wwPDB validation reports
 - With PDB prefix and extension of 4 characters (e.g., from "1ABC" to "PDB_00001ABC")
 - Example: PDB_00001ABC_XYZ_V2-2.cif.gz

11

PDB Core Archive Update III

Use of ORCID

- To enable better management of incoming data
- To credit PDB entries by author unambiguously
- 25% of the unique depositors provided ORCID ids
- 3342 unique PIs with ORCID ids

ORCID
Connecting Research and Researchers

12

