



Protein Data Bank

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Protein data bank is a data archive. The database include two sequences there are:

- Protein sequence
- Nucleic acids sequence

These sequences are large biological macromolecules and protein and nucleic acids shapes are Three-Dimensional structure. The protein data bank was Entrenched at Brookhaven National Laboratory (BNL: Bernstein *et al.*1977) i.e.,1971 annals for macromolecular translucent anatomy.

The protein and nucleic acids archive captured by three main methods are:

- ❖ X - ray crystallography
- ❖ Nuclear Magnetic Resonance (NMR) Spectroscopy
- ❖ Cry - electron Microscopy

The protein data bank is an openly obtainable on the cyberspace via the web page. The protein data bank affiliated managements are PROTEIN DATA BANK Europe (PDBe), PROTEIN DATA BANK Japan (PDBj), RESEARCH COLLOBORATORY STRUCTURAL BIOINFRMATICS (RCSB), BIOLOGICAL MAGNETIC RESONANCE DATA BANK (BMRB).




The Research Collaboratory structural Bioinformatics gained responsibility for risk administration of the protein data bank in October 1998. In principle the RCSB's mission is to provide a resource focused on the modern technology that makes structural data easier to access and analyze. The PDB is also called as global protein data. The protein data bank information was

carried out by Worldwide Protein Data Bank (wwPDB). There are several information facilities are included in PDB homepage will be given in the table 1:

S. No	Sections	PDB Advanced facilities
1.	Deposit	Data Extraction Short Molecule Data format conversion
2.	Search	Basic Advanced Sequence search chemical sketch tool Unreleased & New Browse by annotation PDB Data Distribution Statistics Ligands Drugs
3.	Visualization	3-dimentional structure Protein future view Genome view
4.	Analyze	Pairwise structure alignment Protein symmetry Structure quality Map genomic position to protein PDB Statistics EPPIC Biological Assemblies PDB citation Integrated Resources Additional resources
5.	Learn	Molecule of the month Browse all resources Educational System Curricula Guide to PDB data News and events
6.	More	About RCSB PDB Policies PDB History Advisory committee Publication Service status
7.	Documentation	Chemical components dictionary Biological interesting molecule reference PDB format guide

The database sequence structure and annotation similarities, NMR verification, Primary and secondary protein structure prediction.

Protein can be elucidated at three mains aligned

-  Atomic
-  Amino acid
-  Exclusive protein

There are three structure prediction tools are available in PDB,

- PDBePISA
- PDBeMODIF
- PDBeFold

The PDB annotation is usually deposit in different file format:

- ✓ PDB file format
- ✓ mmCIF Crystallographic Information File
- ✓ PDBML –The Protein Databank Markup Language
- ✓ XML Format

Atomic coordinate file format

Atom	Atom number	Element name	Residue (amino acid)	Chain name	Residue number	Coordinates		
						X	Y	Z
Atom	1	H	SER	A	1	12.345	4.567	32.546
Atom	2	O	SER	A	1	45.345	12.897	32.456
Atom	3	CA	ASP	A	2	8.325	8.657	9.456
Atom	4	C	ASP	A	2	34.658	23.456	5.657
Atom	5	CD1	VAL	A	3	5.455	7.453	8.877
Atom	6	N	ARG	A	4	3.435	22.675	6.546
Atom	7	P	ARG	A	4	9.657	4.786	2.786
Atom	8	N2	GLN	A	5	5.698	3.546	23.678

PDB ID is an individual Identifier, Protein data bank ID is the four letter code word, to enter the unique code word for PDB Search Bar.

Example for PDB ID,

- 2HHB
- 4RCO
- 5CZA
- 4INR

There are certain microorganisms used in protein and nucleic acids sequence.

S. No	Microorganisms
1.	<i>Bacillus anthracis</i>
2.	<i>Vibrio cholera</i>
3.	<i>Clostridium perfringens</i>
4.	<i>Anguilla japonica</i>
5.	<i>Dania rerio</i>
6.	<i>Bacillus anthracis</i>
7.	<i>Vibrio cholera</i>
8.	<i>Clostridium perfringens</i>

All PDB deposition data was include their several protein data bank organization links,

Protein Data Bank Source links

1. <http://www.rcsb.org/pdb/>
2. <http://www.rcsb.org/pdb/neswletter/index.html>
3. <http://rutgers.rcsb.org/pdb/mirrors.html>
4. <http://nist.rcsb.org/pdb/>

All areas of statistics acquisition are being enhanced and developed by the protein data bank. these would be fascinating and demanding times for all those in control of supramolecular structure data analysis, archiving as well as dissemination.

Conclusion

The gathering, archiving, and sharing of complex molecular data are all difficulties in structural biology, which is rapidly evolving field. The estimated value of testimony per week has been around fifty. This makes fast transmission difficult while keeping outstanding services.

Reference

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