

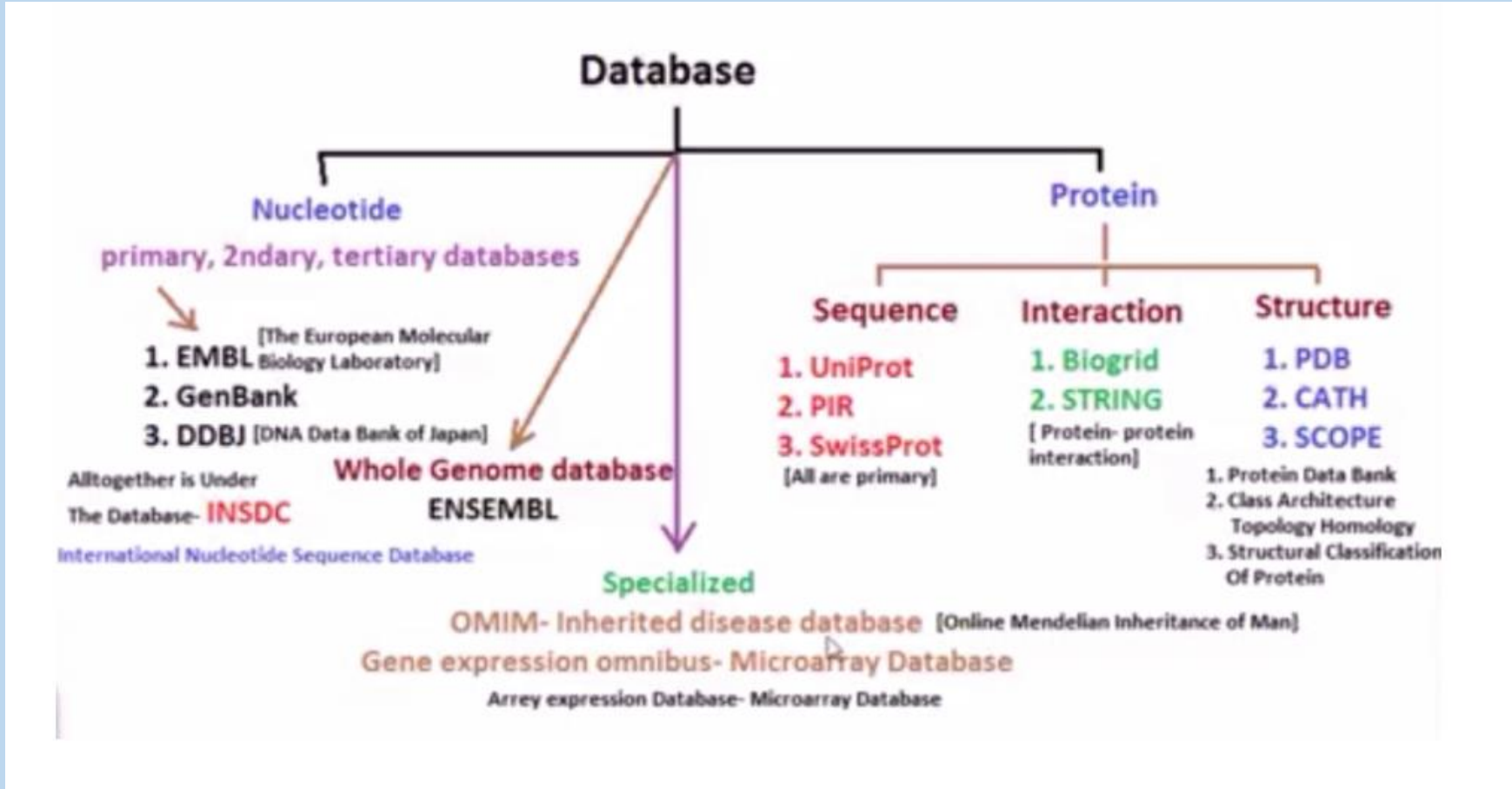
Structural Databases

MIC 405c | Microbial Genomics & Proteomics

Dr Shilpa Kaistha

Department of Microbiology

IBSBT, CSJMU, Kanpur



Structure Databases

- NDB: Nucleic Acid Structure Database
- MSD:The Macromolecular Structure Database –
A relational database representation of clean Protein Data Bank (PDB)
- 3DSeq: 3D sequence alignment server- Annotation of the alignments between sequence database and the PDB
- FSSP: Based on exhaustive all-against-all 3D structure comparison of protein structures currently in the Protein Data Bank (PDB)
- DALI: Fold Classification based on Structure-Structure Assignments
- 3Dee: Database of protein domain definitions wherein the domains have been clustered on sequence and structural similarity

Nucleic Acid Database

← → ↻ Not secure | ndbserver.rutgers.edu

Apps YouTube to Mp3 C... Sci-Hub: removing... eProMIS: Departme... Free Online Course... Microbiology Hom... Giants in genomics...

Home Mail

About NDB **Standards** **Education** **Tools** **Software** **Download**

ndb NUCLEIC ACID DATABASE

A Portal for Three-dimensional Structural Information about Nucleic Acids
As of 26-May-2021 number of released structures: 11337

Search DNA Search RNA Advanced Search

Enter an NDB ID or PDB ID
Search for released structures

Welcome to the NDB

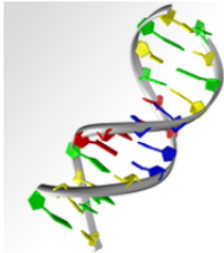
The NDB contains information about experimentally-determined nucleic acids and complex assemblies. Use the NDB to perform searches based on annotations relating to sequence, structure and function, and to download, analyze, and learn about nucleic acids.

Search Structures

Search DNA
Search DNA and its complexes

Search RNA
Search for RNA structures in the NDB archive or in the Non-Redundant list

Advanced Search
Search for structures based on structural features, chemical features, binding modes, citation and experimental information



Featured Tools

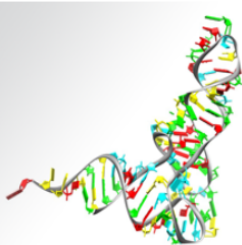
RNA 3D Motif Atlas, a representative collection of RNA 3D internal and hairpin loop motifs

Non-redundant Lists of RNA-containing 3D structures

RNA Base Triple Atlas, a collection of motifs consisting of two RNA basepairs

WebFR3D, a webserver for symbolic and geometric searching of RNA 3D structures

R3D Align, an application for detailed nucleotide to nucleotide alignments of RNA 3D structures



NDB ID: 6X1J **PDB ID: 6X1J** [🔗](#)

Title:

THE HOMING ENDONUCLEASE I-WCAI BOUND TO ITS DNA RECOGNITION SEQUENCE

Molecular Description:

Probable intron-encoded endonuclease 1/DNA Complex

Deposited:

2020-05-19

Released:

2021-05-26

Structural Keywords:

B DOUBLE HELIX

Nucleic Acid Sequence:

[Click to show/hide 2 nucleic acid sequences](#)

Protein Sequence:

[Click to show/hide 1 protein sequences](#)

Primary Citation:

Nawimanager, R., Yuan, Z., Schultz, M., Joshi, R., Lohman, J.R., Gimble, F.S.
The homing endonuclease I-WcaI bound to its DNA recognition sequence
To Be Published, , pp. - , 0.

Experimental Information:

X-RAY DIFFRACTION

Space Group:

P 1 2 1

Cell Constants:

a = 67.601 b = 37.281 c = 94.064 (Ångstroms)

α = 90.0 β = 100.44 γ = 90.0 (degrees)

Refinement:

the REFMAC program. The R value is 0.229 for 31986 reflections

as/xray/structures/6/6x1j/6X1J-biol1.jpg

Structural Features

[RNAML](#)

[Base Pair Hydrogen Bonding Classification](#)

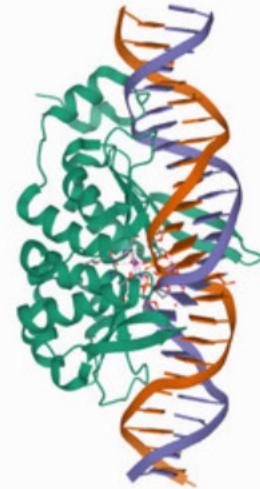
[Nucleic Acid Backbone Torsions](#)

[Base Pair Morphology Parameters](#)

[Base Pair Morphology Step Parameters](#)

[Conformer Analysis \(DNATCO\)](#)

Biological Assembly 1



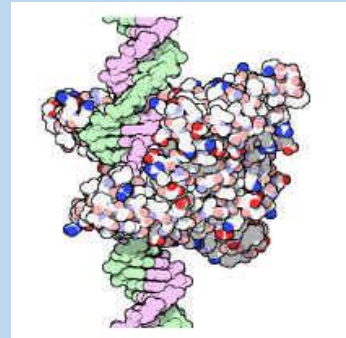
RNA View



Protein DataBank (PDB)

- Important in solving real problems in molecular biology
- Protein Databank
 - PDB Established in 1972 at Brookhaven National Laboratory (BNL)
 - Sole international repository of macromolecular structure data
 - Moved to Research Collaboratory for Structural Bioinformatics

<http://www.rcsb.org/>



PDB

Repository of

- 3D structural data of protein/protein-NA complexes (atomic coordinated, chemical data)
- Data from X ray crystallography, XRD, NMR, eM etc
- Submit Data: PDB AutoDep Input Tool
- Visualise
- Analyse



Welcome

Deposit

Search

Visualize

Analyze

Download

Learn

A Structural View of Biology

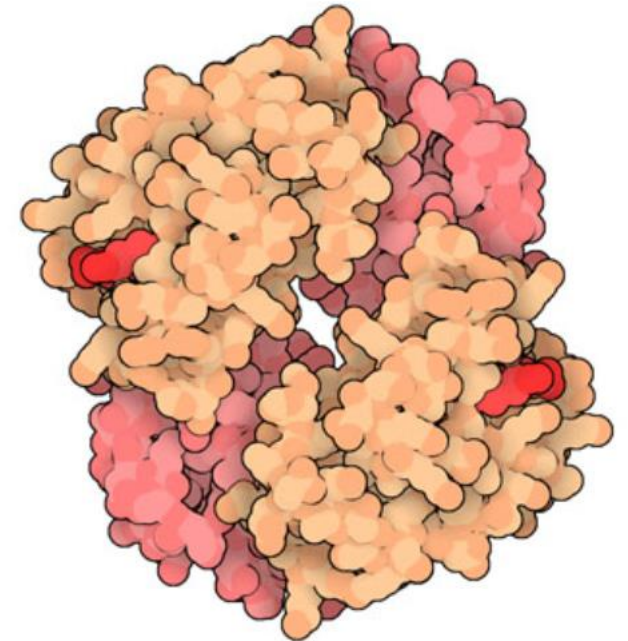
This resource is powered by the Protein Data Bank archive-information about the 3D shapes of proteins, nucleic acids, and complex assemblies that helps students and researchers understand all aspects of biomedicine and agriculture, from protein synthesis to health and disease.

As a member of the wwPDB, the RCSB PDB curates and annotates PDB data.

The RCSB PDB builds upon the data by creating tools and resources for research and education in molecular biology, structural biology, computational biology, and beyond.



May Molecule of the Month



Fetal Hemoglobin

178229

PDB entries from
2021-05-26



PDBj
Protein Data Bank Japan

English 日本語 简体中文 繁體中文 한국어

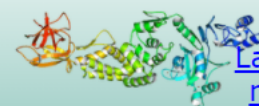
Search



[wwPDB](#) [RCSB PDB](#) [PDBe](#) [BMRB](#) [Adv. Search](#) [Search help](#)

Worldwide
Protein Data Bank
Foundation

7MSW



[Latest new entries](#)

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Data deposition (OneDep)

- Help
- Deposition to PDB, EMDB or BMRB

Download

PDBj (Protein Data Bank Japan) is a project team operating under the Joint Usage and Research activities of the [Institute for Protein Research](#), Osaka University. We maintain the single global PDB/BMRB/EMDB archives of macromolecular structures and provide integrated tools, in collaboration with [RCSB PDB](#) and [BMRB](#) in the USA, and [PDBe](#) in the EU. PDBj is supported by [JST-NBDC](#) and [AMED-BINDS](#). [PDBj's new logo](#) design incorporates cytochrome c (PDBID: [1cyc](#)), which was the first structure determined in Japan.

Guide for first time visitors

The material of this site is aimed mainly for researchers. For general people, please refer [PDBj numon](#) ("numon" means introduction or beginner) site. When accessed with old web browser, the web pages may be displayed under limited function mode. In order to use the full function mode, refer [prerequisite](#) page. For details about this site, see [interactive tutorials](#).

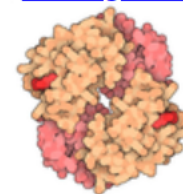
Find the service you need

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

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

Molecule of the Month

[Fetal Hemoglobin](#)



[Article List](#)

PROTEIN DATA BANK



Hot Structural News on **COVID-19**



New PDBe-KB COVID-19 Data Portal



Our new PDBe-KB [COVID-19 data portal](#) brings together all available PDB data from SARS-CoV-2 structures, to help researchers easily identify important structural features to support the development of treatments and vaccines.

[Visit the PDBe-KB COVID-19 data portal](#)

PDBe is the European resource for the collection, organisation and dissemination of data on biological macromolecular structures. [Read more about PDBe.](#)

Featured structure

The unzipping enzyme



01 May 2021

There is an enzyme that plays a role in all cellular DNA transactions, including DNA replication and repair, transcription, translation, ribosome synthesis, RNA maturation and splicing, and nuclear export processes.

[Unwind and read more...](#)

Popular

- [PDBe-KB](#)
- [EMsearch](#)
- [PDBeFold](#)
- [PDBePISA](#)
- [PDBeChem](#)
- [PDBe REST API](#)
- [EM resources](#)
- [NMR resources](#)
- [EMPIAR](#)
- [Coordinate Server](#)
- [PDB Component Library](#)
- [News](#)
- [Events](#)
- [Training](#)
- [Contact us](#)

Latest archive statistics

As of 26 May 2021 the PDB contains 178229 entries ([latest PDB entries](#), [chemistry](#), [biology](#)) and EMDB contains 15243 entries ([latest map releases](#), [latest updates](#)).



Welcome

Deposit

Search

Visualize

Analyze

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Learn

Deposit Options

- Prepare Data
- Validate Data
- Deposit Data
- Deposition Help

Documentation

- PDBx/mmCIF Dictionary Resources
- Chemical Component Dictionary
- Biologically Interesting Molecule Reference Dictionary (BIRD)
- PDB Format Guide

Deposition Preparation Tools

Data Extraction

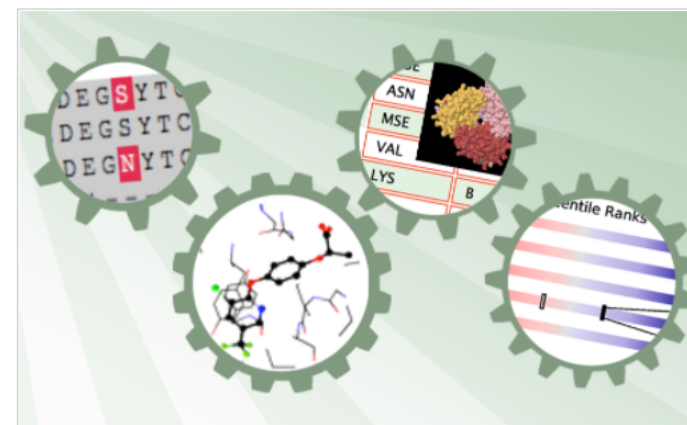
- [pdb_extract](#): Extract and harvest data in PDBx/mmCIF format from structure determination programs
- [SF-Tool](#): Convert structure factor files among various formats

Small Molecules

- [Ligand Expo](#): Search the Chemical Component Dictionary for the IDs of released ligands

Data Format Conversion

- [PDBML2CIF](#): Convert PDBML-format data into PDBx/mmCIF-format
- [PointSuite](#): Generate symmetry records for macromolecular assemblies with point and helical symmetries
- [MAXIT](#): Translate data between file formats and more



Effective use of PDB

- Queries are of three types
 - PDBid - As quoted in paper
 - Search Lite - one or more keywords
 - Search Fields - A detailed query form
- Query results
 - Structure Explorer - details of the structure
 - Query Result Browser - for multiple structures
- PDB Viewer



- Welcome
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- Viewers**
 - 3D Structure Viewers
- Sequence**
 - Protein Feature View
 - Genome View

Mol* 3D Viewer

Launch Mol* from the Structure Summary page for any entry.

A [standalone version of Mol*](#) is available. Users can upload their custom files into this tool.

A [detailed Mol* User Guide](#) is available.



PDB ID: 4HHB

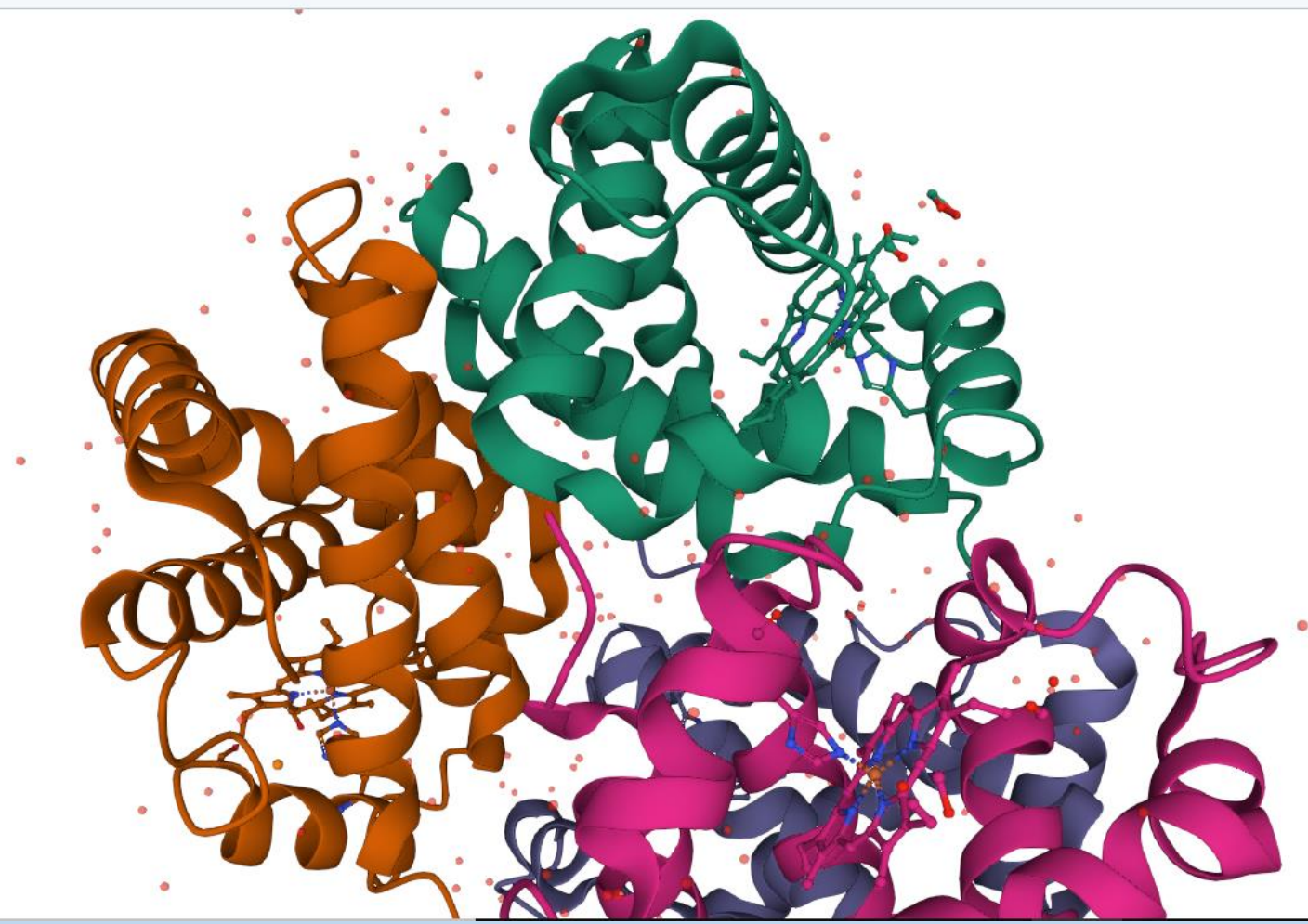


PDB ID: 3J3Q



PDB ID: 1BTN

```
1      11      21      31      41      51      61      71      81      91     101     111
VLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALS
DLHAHKLRVDPVNFKLLSHCLLVTLAAHLPE
121      131      141
AEFTPAVHASLDKFLASVSTVLTISKYR
```



↻

🔍

🔑

📏

📐

👁️

4HHB | THE CRYSTAL STRUCTURE OF...

Type	Assembly
Asm Id	1: Author And Software ...

Nothing Focused

Measurements

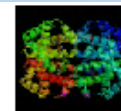
Structural Motif Search

Submit Search (3 selections required)

[Add one or more selections \(toggle mode\)](#)

Components 4HHB

Preset	+ Add	📏	🔄
Polymer	Cartoon	👁️	🗑️ ...
Ligand	Ball & Stick	👁️	🗑️ ...
Water	Ball & Stick	👁️	🗑️ ...
Ion	Ball & Stick	👁️	🗑️ ...
Unit Cell P 1 21 1		👁️	🗑️ ...



Summary Information



Summary Information

[View Structure](#)

[Download/Display File](#)

[Structural Neighbors](#)

[Geometry](#)

[Other Sources](#)

[Sequence Details](#)

[Crystallization Info](#)

[Previous version\(s\):
1HHB](#)

Explore

[SearchLite](#) [SearchFields](#)

Compound: **Hemoglobin (Deoxy)**

Authors: **G. Fermi, M. F. Perutz**

Exp. Method: **X-ray Diffraction**

Classification: **Oxygen Transport**

Source: **Homo Sapiens**

Primary Citation: **Fermi, G., Perutz, M. F., Shaanan, B., Fourme, R.: The crystal structure of human deoxyhaemoglobin at 1.74 Å resolution. *J Mol Biol* 175 pp. 159 (1984)**

[[Medline](#)]

Deposition Date: **07-Mar-1984**

Release Date: **17-Jul-1984**

Resolution [Å]: **1.74**

R-Value: **0.135**

Space Group: **P 21**

Unit Cell: dim [Å]: a 63.15 b 83.59 c 53.80

angles [°]: alpha 90.00 beta 99.34 gamma 90.00

Polymer Chains: **A, B, C, D**

Residues: **574**

Atoms: **4779**

HET groups:

ID	Name	Formula
HEM	PROTOPORPHYRIN IX CONTAINING FE	C ₃₄ H ₃₂ N ₄ O ₄ FE ₁
PO4	PHOSPHATE ION	O ₄ P ₁

Other Versions: [2HHB](#), [3HHB](#)

Cn-3D- structure viewers

The screenshot shows the NCBI Cn3D macromolecular structure viewer interface. At the top, the browser address bar shows the URL `ncbi.nlm.nih.gov/Structure/CN3D/cn3d.shtml`. Below the browser, the NCBI logo is visible on the left, and a search bar with the text "Structure" is on the right. A "Search" button and a "Help" link are also present. Below the search bar, there are three dropdown menus: "Structure Group", "3D Macromolecular Structures", and "Conserved Domains".

Cn3D macromolecular structure viewer

[ABOUT](#) [TUTORIAL](#) [FAQ](#) [INSTALL](#) [PUBLICATIONS](#) [NEWS](#) [RESOURCES](#) [DISCOVER](#)

About Cn3D

Cn3D ("see in 3D") is a helper application for your web browser that allows you to view 3-dimensional structures from NCBI's [Entrez Structure](#) database. Cn3D is provided for [Windows](#) and [Macintosh](#), and can be compiled on [Unix](#). Cn3D simultaneously displays structure, sequence, and alignment, and now has powerful annotation and alignment editing features. *(For those who prefer to view 3D structures on the web, without the need to install a separate application, [iCn3D](#) ("I see in 3D") is available as of April 2016.)*

Below is a relatively simple sample of what **Cn3D** can do. There are many more examples in the [Tutorial](#), along with instructions to help new users get started!

Highlights

Web-based Structure Viewer

- [iCn3D](#) ("I see in 3D"), released in April 2016, provides interactive views of three-dimensional macromolecular structures on the web.
- There is no need to install a separate application in order to use [iCn3D](#); you just need to use a web browser that supports [WebGL](#).
- [iCn3D](#) also allows you to customize the display of a structure and generate a URL that allows you to share the link, and to

A comprehensive help document

Cn3D FAQ

Frequently Asked Questions

Cn3D Install

Installation and Configuration

MMDB

NCBI's structure database

PDBeast

Taxonomy in MMDB

VAST

Structure comparisons

VAST Search

The image shows two overlapping software windows. The top window is titled "Cn3D 3.0" and displays a 3D ribbon model of a protein structure. The protein backbone is shown in red and yellow, with several residues highlighted in purple and green. Two specific residues are labeled: "Cys-63" and "Cys-68". The bottom window is titled "DDV" and shows a sequence alignment interface. It includes a "Go to:" field with "row:" and "col:" dropdowns, both set to "0". Below this is a sequence alignment view with two sequences: "1DOI" and "1AWD". The sequence "PTVEYLNyevvddngvdmvdddvfgeasdmldde" is shown in red, with a yellow highlight under the segment "yevvddngvdmvdddvfgeasdmldde". The sequence "YKVTLKTP" is shown in blue. A progress bar at the bottom of the DDV window shows the current position in the sequence.

Cn3D 3.0

File View Style Color Option Help

Cys-63

Cys-68

DDV

File Alignment Options Help

Go to: row: 0 col: 0

1DOI PTVEYLNyevvddngvdmvdddvfgeasdmldde

1AWD YKVTLKTP

Ready !

Rasmol/RasTop

RasMol is a molecular graphics program intended for the visualisation of proteins, nucleic acids and small molecules.

The program reads in a molecule coordinate file and interactively displays the molecule on the screen in a variety of colour schemes and molecule representations.

Currently available representations include depth-cued wireframes, 'Dreiding' sticks, spacefilling (CPK) spheres, ball and stick, solid and strand biomolecular ribbons, atom labels and dot surfaces.

Content:
[About RasTop](#)
[What's new?](#)
[Building RasTop](#)
[Translating RasTop](#)
[Comments & Bugs](#)
[About this site](#)

Authors

Source:

Herbert J. Bernstein,
Christian Duque,
Gary Grossman,
Marco Molinaro,
Arne Mueller,
Naoum Salame,
Roger Sayle,
Philippe Valadon.

Help and Translations:

Frances C. Bernstein,
Herbert J. Bernstein,
William McClure,
Eric Martz,
Naoum Salame,
Philippe Valadon,
Margaret Wong.

Open RasMol Site:

RasTop 2.2
Molecular Graphics Visualization Tool

RasTop - [Scro - 3CRD]

File Edit Molecule Atoms Bonds Ribbons Surfaces View Window Help

elements properties user sets

close-view.scr

Works Rotate Translate-Zoom Spin Reset Stop

Light

Number of Strands: 0

Number of Turns: 0

RasMol Command Line

```
Number of Chains ---- 0
Number of Groups ---- 170 (25)
Number of Atoms ---- 1856 (129)
Number of Bonds ---- 1366
Number of Helices --- 10
Number of Strands --- 0
Number of Turns ---- 0
RasTop>
```

Welcome to RasTop molecular visualization software, Version 2.2. RasTop is a graphical interface to the program RasMol. RasTop allows the viewing and the direct manipulation of macromolecules and small molecules on screen. RasMol was developed initially by Roger Sayle at the University of Edinburgh's Biocomputing Research Unit and the BioMolecular Structure Department, Glaxo Research and Development, Greenford, U.K. Many people since contributed to its code. In 1999, Herbert J. Berstein released a compiled version named Rasmol 2.7.1 of different source variants under a GPL-like license (see [NOTICE](#)). Many thanks to these people for giving RasMol freely to the community. Many thanks also to Herbert Berstein, Frances Bernstein, William McClure, Eric Marz, Margaret Wong, and Roger Sayle for their contributions to the Help and giving the permission to re-use their work. See the complete list of contributors to this version in the file [copyright](#).

NEW USERS

Expert Protein Analysis System (Original): ExPASy-integrated genomics, proteomics resource of SIB


The screenshot shows the ExPASy website interface. At the top, the browser address bar displays 'expasy.org'. Below the navigation bar, the ExPASy logo and 'Swiss Bioinformatics Resource Portal' are centered. A search bar with a red magnifying glass icon is present, with a hint 'e.g. BLAST, UniProt, MSH6, Albumin...'. On the left, a sidebar menu lists categories: Genes & Genomes (with sub-items: Genomics, Metagenomics, Transcriptomics), Proteins & Proteomes (checked), Evolution & Phylogeny (with sub-items: Evolution biology, Population genetics), and Structural Biology. The main content area is titled 'SIB Resources' and features five resource cards: STRING (Protein-protein interaction networks and enrichment analysis), SWISS-MODEL (Protein structure homology-modelling), UniProtKB/Swiss-Prot (Protein knowledgebase), neXtProt (Human protein knowledgebase), and SwissLipids (Knowledge resource for lipids). The URL 'https://www.expasy.org/resources/nextprot' is visible at the bottom left.

expasy.org

Apps YouTube to Mp3 C... Sci-Hub: removing... eProMIS: Departme... Free Online Course... Microbiology Hom... Giants in genomics...

Expasy

Swiss Bioinformatics Resource Portal

Search: 

e.g. [BLAST](#), [UniProt](#), [MSH6](#), [Albumin](#)...

- Genes & Genomes**
 - Genomics
 - Metagenomics
 - Transcriptomics
- Proteins & Proteomes**
- Evolution & Phylogeny**
 - Evolution biology
 - Population genetics
- Structural Biology**

SIB Resources ⓘ

- STRING**
Protein-protein interaction networks and enrichment analysis
- SWISS-MODEL**
Protein structure homology-modelling
- UniProtKB/Swiss-Prot**
Protein knowledgebase
- neXtProt**
Human protein knowledgebase
- SwissLipids**
Knowledge resource for lipids

https://www.expasy.org/resources/nextprot

SWISS-MODEL

is a fully automated protein structure homology-modelling server, accessible via the **Expasy web server**, or from the program DeepView (Swiss Pdb-Viewer).

The purpose of this server is to make protein modelling accessible to all life science researchers worldwide.

[Start Modelling](#)

Repository

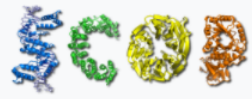
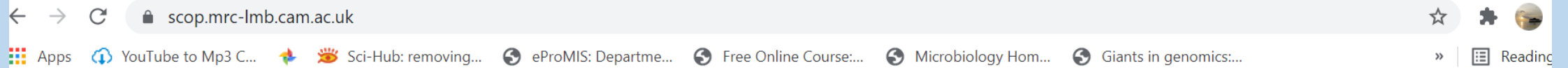
Every week we model all the sequences for thirteen core species based on the latest UniProtKB proteome. Is your protein already modelled and up to date in **SWISS-MODEL Repository**?



Selected WWW database resources for macromolecular structures.

Databases	URL
Structure and sequence/structure databases	
SCOP	http://scop.mrc-lmb.cam.ac.uk/scop/
CATH	http://www.biochem.ucl.ac.uk/bsm/cath/
FSSP	http://www2.ebi.ac.uk/dali/fssp/
Molecular Modeling Database	http://www.ncbi.nlm.nih.gov/Structure/
CAMPASS	http://www-cryst.bioc.cam.ac.uk/~campass/
ISSD	http://www.protein.bio.msu.su/issd/
Library of Protein Family Cores (LPFC)	http://WWW-SMI.Stanford.EDU/projects/helix/LPFC/
3D_ALI (a database of aligned protein structures and related sequences)	http://www.embl-heidelberg.de/argos/ali/ali_info.html
IDITIS (relational database and query tool for proteins)	http://www.oxmol.co.uk/prods/iditis/
HSSP	http://www.sander.embl-heidelberg.de/hssp/
Speciality databases	
HIV Protease Database	http://www-lbnc.ncifcrf.gov/HIVdb/
Nucleic Acid Database	http://ndbserver.rutgers.edu/
Prolysis (protease and protease inhibitor Web server)	http://delphi.phys.univ-tours.fr/Prolysis/
International Immunogenetics Database (IMGT)	http://imgt.cnusc.fr:8104/
Enzyme Structures Database	http://www.biochem.ucl.ac.uk/bsm/enzymes/
Features databases	
Molecular Movements Database	http://bioinfo.mbb.yale.edu/MolMovDB/
OLDERADO	http://neon.chem.le.ac.uk/olderado/
PROCAT	http://www.biochem.ucl.ac.uk/bsm/PROCAT/PROCAT.html
Protein Quaternary Structures (PQS)	http://pqs.ebi.ac.uk/
ReLIBase (receptor-ligand complexes database)	http://www2.ebi.ac.uk:8081/home.html
PROMISE	http://bioinf.leeds.ac.uk/promise/
PDBSum	http://www.biochem.ucl.ac.uk/bsm/pdbsum/
Biological Macromolecule Crystallization Database (BMCD)	http://h178133.nist.gov:4400/bmcd/bmcd.html
Resources	
Protein Data Bank	http://www.rcsb.org/pdb/

SCOP-Structural Classification of Proteins



[About](#)

[Contact](#)

[Download](#)

The legacy SCOP websites can be accessed at **SCOP 1.75** and **SCOP2 prototype**

SCOP 2

[Learn More](#)

SCOP: Structural Classification of Proteins

Nearly all proteins have structural similarities with other proteins and, in some of these cases, share a common evolutionary origin. The SCOP database, created by manual inspection and abetted by a battery of automated methods, aims to provide a detailed and comprehensive description of the structural and evolutionary relationships between all proteins whose structure is known. As such, it provides a broad survey of all known protein folds, detailed information about the close relatives of any particular protein, and a framework for future research and classification.

Latest update on **2021-05-27** includes **68,816** non-redundant domains representing **772,354** protein structures. Folds, superfamilies and families statistics [here](#).

SCOP

- 1995 (yearly updated) Manual classification of protein structure domains
- Class- general structural architecture of protein (β sheet, α helix, membrane protein, coiled, peptide fragments, multidomain, non natural derived)
- Fold- Similar arrangements of secondary structures
- Superfamily- structural and functional similarity
- Family- sequence similarity shared

classification.

Latest update on **2021-05-27** includes **68,816** non-redundant domains representing **772,354** protein structures. Folds, superfamilies and families statistics [here](#).

Keyword and ID search

Sequence search

Enter free text, SCOP ID, PDB ID or UniProt ID

Go

Browse by structural class

- [All alpha proteins](#)
- [All beta proteins](#)
- [Alpha and beta proteins\(a/b\)](#)
- [Alpha and beta proteins\(a+b\)](#)
- [Small proteins](#)

Browse by protein type

- [Globular proteins](#)
- [Membrane proteins](#)
- [Fibrous proteins](#)
- [Non-globular/Intrinsically unstructured proteins](#)

Please cite: Antonina Andreeva, Dave Howorth, Cyrus Chothia, Eugene Kulesha, Alexey Murzin, SCOP2 prototype: a new approach to protein structure mining. (2014) Nucl. Acid Res., 42 (D1): D310-D314 and Antonina Andreeva, Eugene Kulesha, Julian Gough, Alexey Murzin, The SCOP database in 2020: expanded classification of representative family and superfamily domains of known protein structures. (2020) Nucl. Acid Res., 48 (D1): D376-D382

Show ancestry

Families [1 entry]

- **SARS coronavirus accessory protein X4 (ORF8, ORF7a)** SCOP ID 4007538

Domains [3 entries]

	ID	Region	Links
Protein Protein 7a Species <i>Severe acute respiratory syndrome-related coronavirus</i> Representative domain 8055375 Represented structures [1]	P59635 1XAK	15-82 A:-1-67	UniProt PDBe RCSB PDB
Protein Protein 7a Species <i>Severe acute respiratory syndrome coronavirus 2</i> Representative domain 8092974	P0DTC7 6W37	16-81 A:1-66	UniProt PDBe RCSB PDB
Protein Accessory protein 7a Species <i>Severe acute respiratory syndrome coronavirus 2</i> Representative domain 8102631	A0A6C0X2S1 7CI3	14-82 A:14-82	UniProt PDBe RCSB PDB

FOLD

TIM beta/alpha-barrel

SCOP ID: 2000031

(beta-alpha)₈; parallel beta-sheet barrel, closed, n=8, S=8, strand order 12345678 (anticlockwise); the first seven superfamilies have similar phosphate-binding sites

Keywords [beta-barrel](#) [parallel beta-sheet](#) [anticlockwise](#)

Superfamilies [34 entries]

- **(Trans)glycosidases** SCOP ID 3000313 
Families: 25 
- **Metallo-dependent hydrolases** SCOP ID 3000428 
the beta-sheet barrel is similarly distorted and capped by a C-terminal helix has transition metal ions bound inside the barrel
Families: 18 
- **Xylose isomerase-like** SCOP ID 3000560 
different families share similar but non-identical metal-binding sites
Families: 9 
- **Aldolase** SCOP ID 3000445 
Common fold covers whole protein structure
Families: 8 
- **Phosphoenolpyruvate/pyruvate domain** SCOP ID 3000510 

CATH:

- University College of London
- 1990 established

- Evolutionary relationships of protein domains

The four main levels of the CATH hierarchy:

#	Level	Description
1	Class	the overall secondary-structure content of the domain. (Equivalent to the SCOP Class)
2	Architecture	high structural similarity but no evidence of homology . (Equivalent to the 'fold' level in SCOP)
3	Topology/fold	a large-scale grouping of topologies which share particular structural features
4	Homologous superfamily	indicative of a demonstrable evolutionary relationship. (Equivalent to SCOP superfamily)

CATH

- Hierarchical semi-automatic
- Classes derived from secondary protein structure and packing (all [alpha](#), all [beta](#), a mixture of alpha and beta, or little secondary structure)
- Architecture: derived from secondary structure arrangement in three-dimensional space
- Topology: information on how the secondary structure elements are connected and arranged is used
- Homology: assignments are made to the [Homologous superfamily](#) (H) level if there is good evidence that the domains are related by evolution

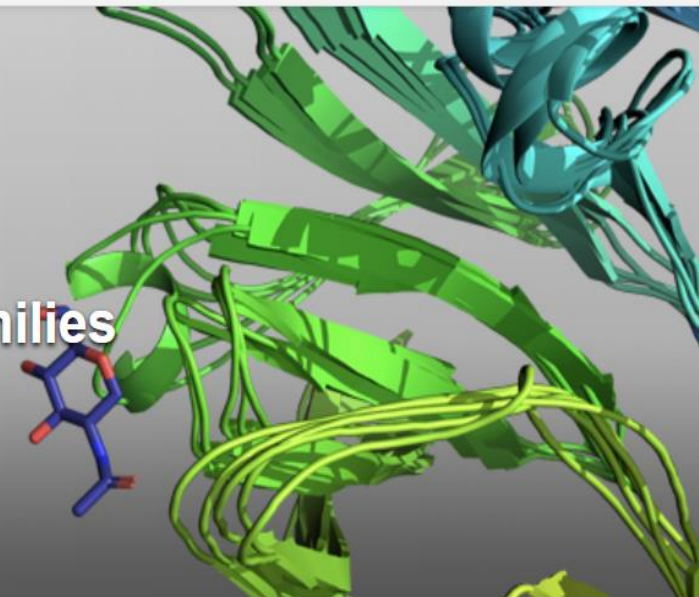


CATH / Gene3D v4.3

151 million protein domains classified into 5,481 superfamilies

Search by keywords, PDB code, GO term, etc

Search



22-23 July 2020 The CATH website experienced some technical issues during this period as a result of a power outage. Everything should now be working as expected now - apologies for the inconvenience.

Core classification files for the latest version of CATH-Plus (v4.3) are [now available to download](#). [Daily updates](#) of our very latest classifications are also available.



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