

Structural Bioinformatics

- # **Elucidation of the 3D structures of biomolecules.**
- # **Analysis and comparison of biomolecular structures.**
- # **Prediction of biomolecular recognition.**
- # *Handles three-dimensional (3-D) structures.*

Why bother with structures when we have sequences ?

- # In evolutionary related proteins structure is much better preserved than sequence.
 - # Structural motifs may predict similar biological function .
 - # Getting insight into protein folding.
Recovering the limited (?) number of protein folds.
-

Applications

- # Classification of protein databases by structure.
 - # Search of **partial and disconnected** structural patterns in large databases.
 - # Extracting Structure information is difficult, we want to extract "new" folds.
-

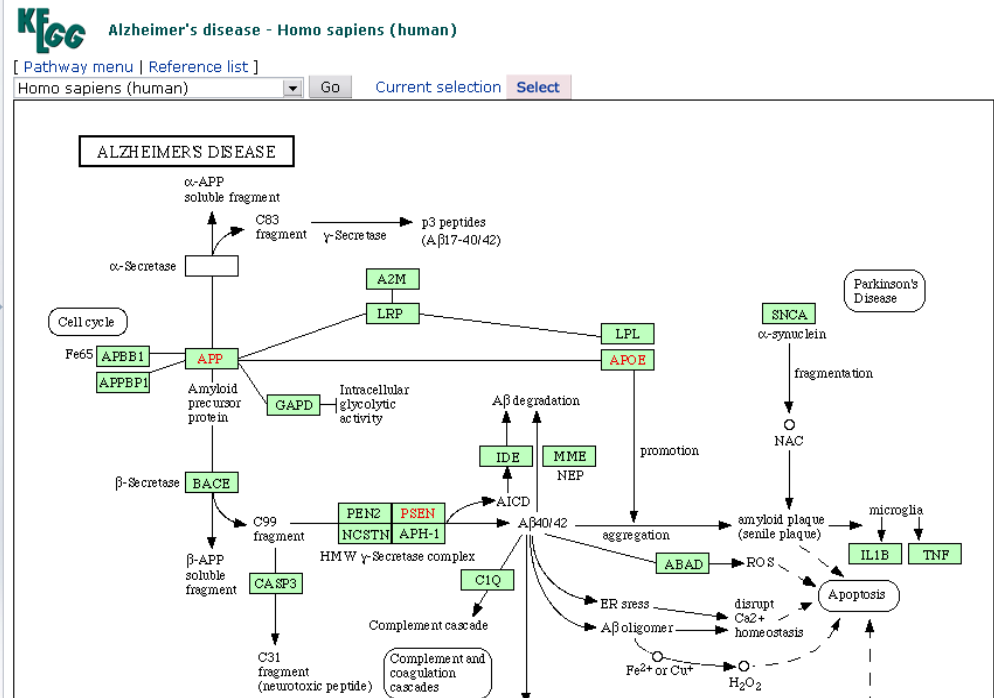
Applications (continued)

- # Speed up of drug discovery.
 - # Detection of structural pharmacophores in an ensemble of drugs (similar substructures in drugs acting on a given receptor - pharmacophore).
 - # Comparison and detection of drug receptor *active sites* (structurally similar receptor cavities could bind similar drugs).
-

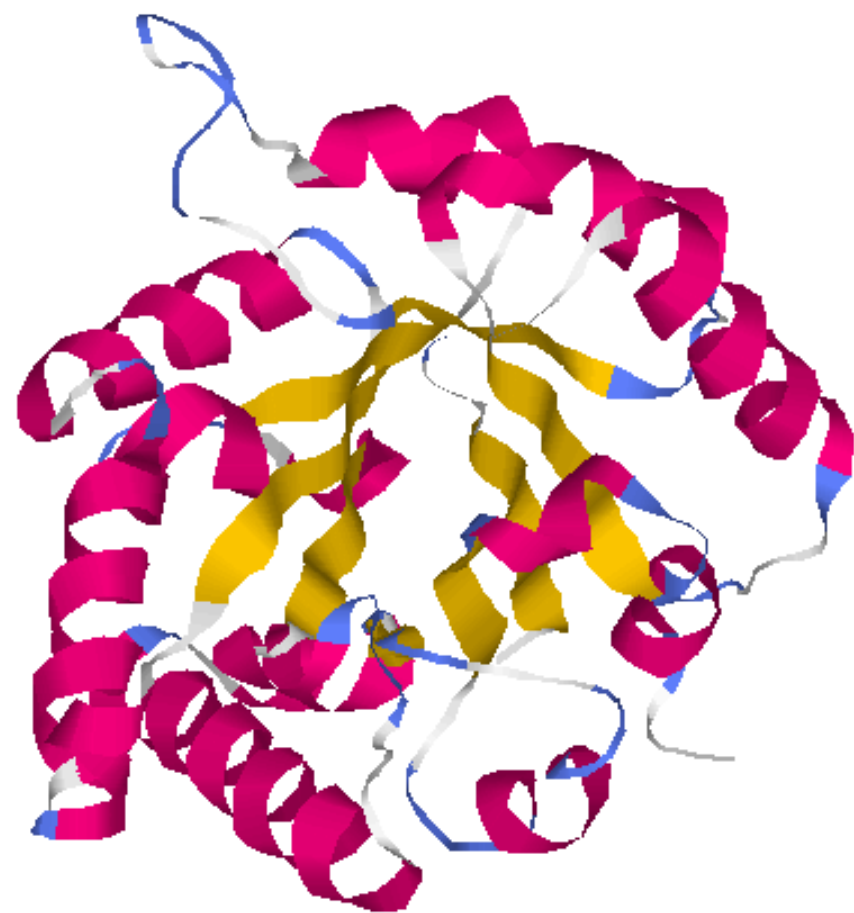
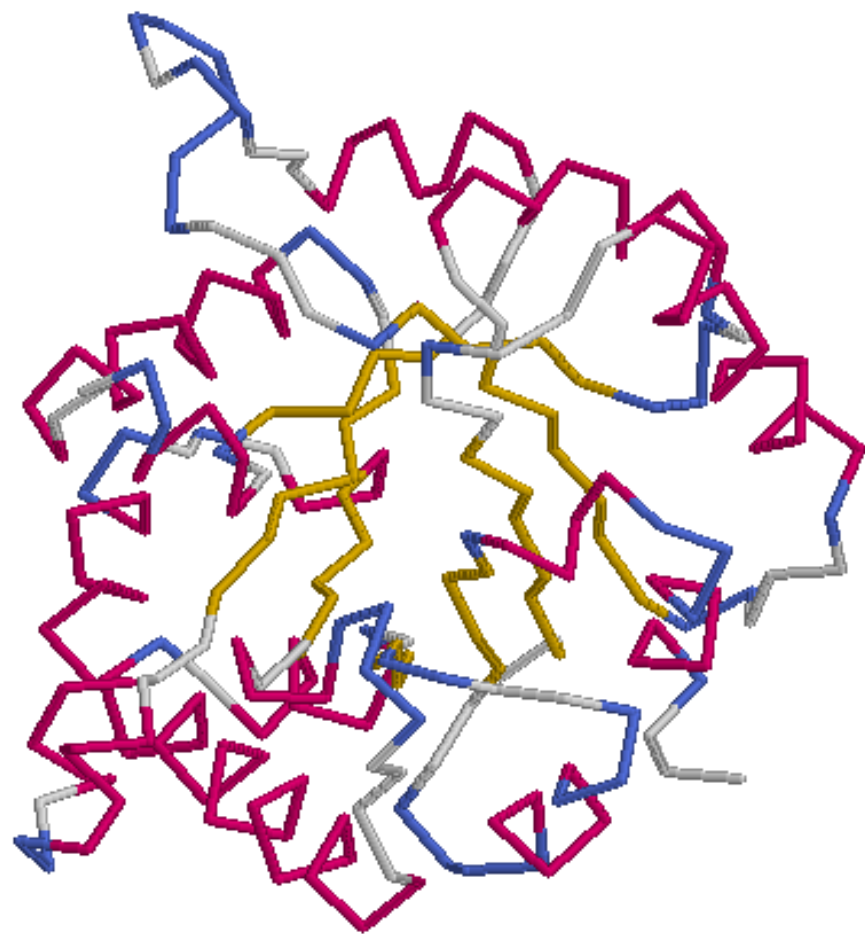
A Life Sciences Data Integration Problem



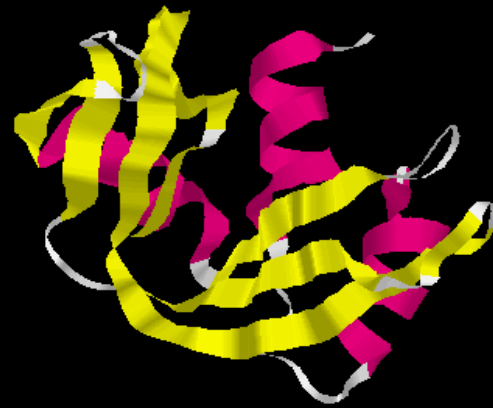
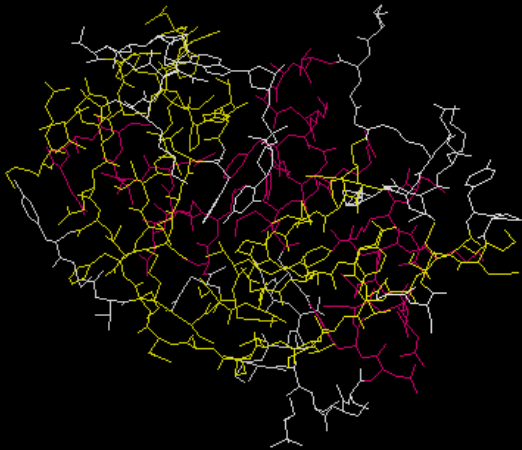
3D Structure

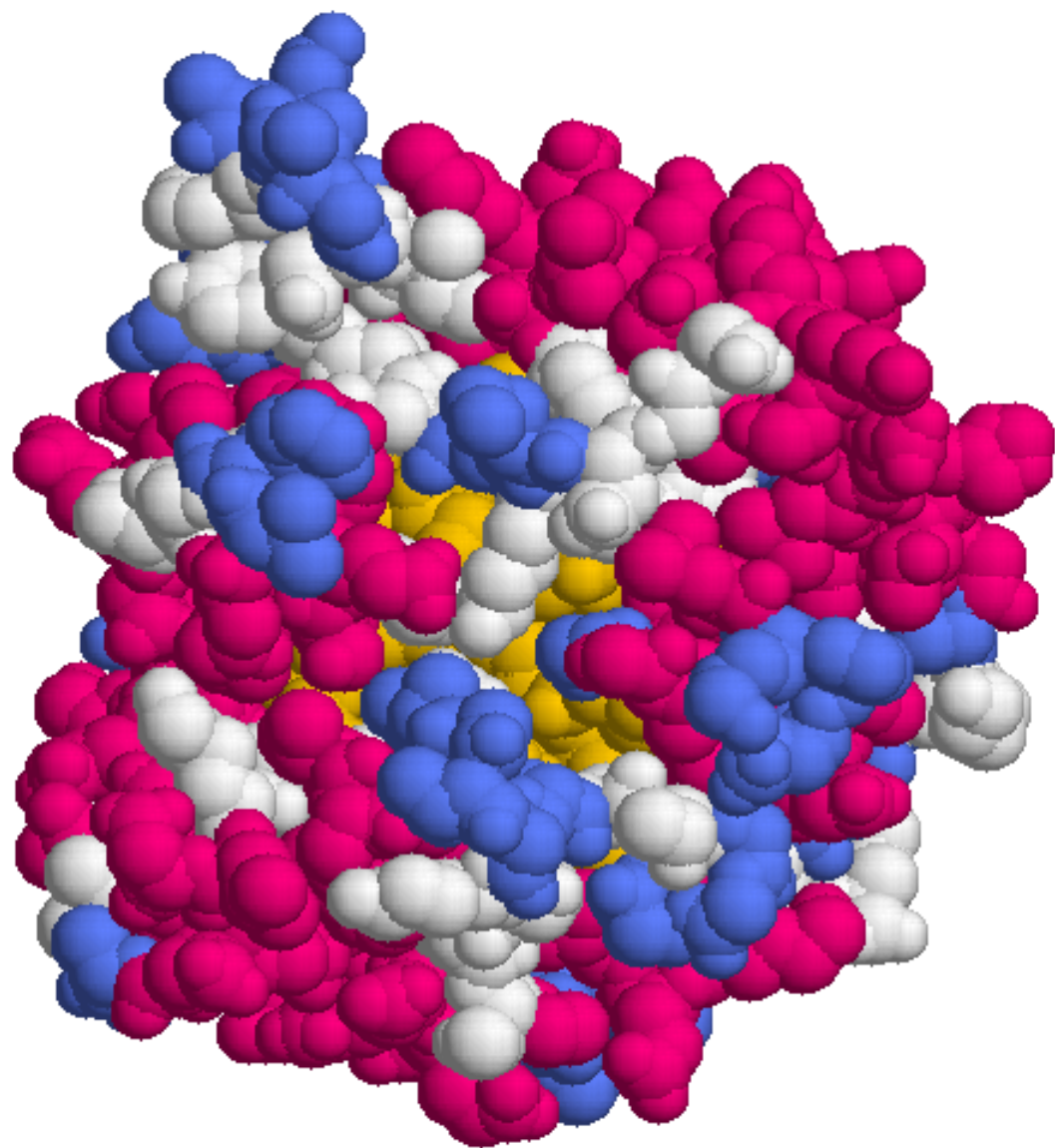


Pathways



Wire-frame or ribbons display







RCSB Protein Data Bank Agenda

- Introduction & Credits
- Basic Searching & Browsing
- Result Options
- Structure Summary Page
- Advanced Searching
- Tools & Education
- Summary
- Exercises

Introduction & Credits



PROTEIN DATA BANK

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- Advanced Search
- Latest Release
- New Structure Papers
- Sequence Search
- Chemical Components
- Unreleased Entries
- Browse Database
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Deposit

All Deposit

Electron Microscopy

A Resource Macromolecules

The PDB archive contains structures of proteins, nucleic acids, and small molecules. The **wwPDB**, the **RCSB PDB**, and the **PDBe** have agreed upon standards.

The RCSB PDB also provides a variety of tools and resources to perform simple and advanced searches based on annotation, sequence, structure and function. These molecules are viewed and analyzed by users who range from students to scientists.

Hide Welcome Message

Featured Molecules

Structural View of Biology

The Research Collaboratory for Structural Bioinformatics (RCSB) is a non-profit consortium dedicated to improving our understanding of the function of biological macromolecules. We work cooperatively and equally with our partners to secure grants and subsequently produce resources and publications to further the fields of bioinformatics and structural biology.

RUTGERS
THE STATE UNIVERSITY OF NEW JERSEY

The RCSB-Rutgers group is located in the Department of Chemistry and Chemical Biology and the Biomaps Institute for Quantitative Biology at Rutgers, The State University of New Jersey.

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Piscataway, NJ 08854-6007
phone: 732 445 1313
fax: 732 445 4320

UCSD
SKAGGS SCHOOL OF PHARMACY and PHARMACEUTICAL SCIENCES

The RCSB-SDSC group is located in at the San Diego Supercomputer Center (SDSC) and the Skaggs School of Pharmacy and Pharmaceutical Sciences (SSPPS) at the University of California, San Diego (UCSD).

RCSB-SDSC
San Diego Supercomputer Center and Skaggs School of Pharmacy and Pharmaceutical Sciences
Pharmaceutical Sciences Building
University of California, San Diego (UCSD)
9500 Gilman Drive, Mailcode 0259
La Jolla, CA 92093-0743

Easy to navigate & customize

The RCSB PDB is managed by 2 members of RCSB

WORLDWIDE PDB PROTEIN DATA BANK

Welcome to the Worldwide Protein Data Bank

nitroglycerin will slowly break down and release

Contact Us | Print

PDB ID or Text PDB ID lookup or Text search of the complete structure file

Search ? | Advanced Search

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Website FAQ

A Resource for Studying Biological Macromolecules

The PDB archive contains information about experimentally-determined structures of proteins, nucleic acids, and complex assemblies. As a member of the wwPDB, the RCSB PDB curates and annotates PDB data according to agreed upon standards.

The RCSB PDB also provides a variety of tools and resources. Users can

Customize This Page

New Features

Ligand Images on Structure Summary Page

Latest features released:

Website Release Archive:

RCSB PDB News

Happy Holidays

Deposition Session Restart

Annual Report Published

Statement on Retraction of PDB Entries

From 7 to 70,000: The PDB Reaches a New Milestone

Advanced Notification

Advisory Committee Meeting

Full wwPDB News

FTP Archives

Current PDB FTP Archive:

ftp.wwpdb.org

Yearly FTP Snapshots:

ftp://snapshots.wwpdb.org

New Features Hide

Ligand Images on Structure Summary Page

Latest features released:

Website Release Archive:

RCSB PDB News Hide

Weekly | Quarterly | Yearly

2011-01-04

Structural Biology Knowledgebase Widget

A new widget loads SBKB data about available models, targets,

wwPDB News Hide

Statement on Retraction of PDB Entries

2010-12-21

From 7 to 70,000: The PDB Reaches a New Milestone

Advanced Notification

Advisory Committee Meeting

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ftp.wwpdb.org

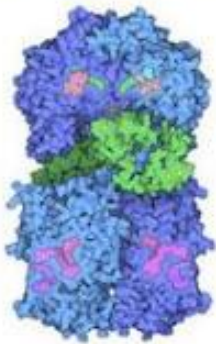
Yearly FTP Snapshots:

ftp://snapshots.wwpdb.org

Featured Molecules Hide

List View of Archive By: Title | Date | Category

Structural View of Biology



Molecule of the Month: Nitric Oxide Synthase

Nitroglycerin is a powerful explosive, detonating when exposed to heat or pressure. The same molecule, however, can save your life if you're experiencing a heart attack. A small dose of nitroglycerin will slowly break down and release nitric oxide (NO), which then spreads to the muscle cells surrounding blood vessels, telling them to relax.

Full Article...

Protein Structure Initiative Featured Molecule:
CXCR4



PSI | nature
StructuralBiology Knowledgebase

Full Article | PSI Featured Molecule Archive |
PSI Structural Biology Knowledgebase

Structural Diversity - Constantly

Increasing

Glucagon

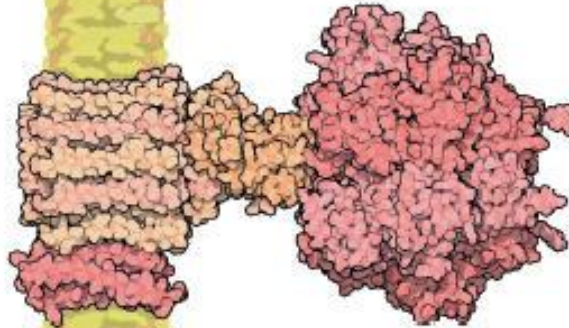
Insulin

Many
Enzymes

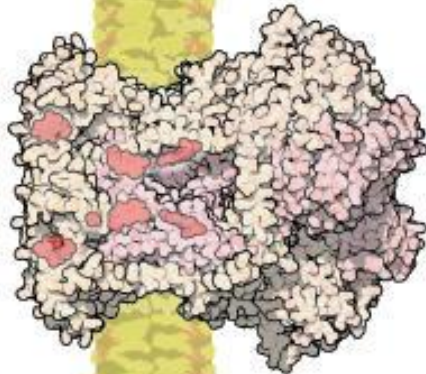


1dhf Dihydrofolate Reductase

Complexes



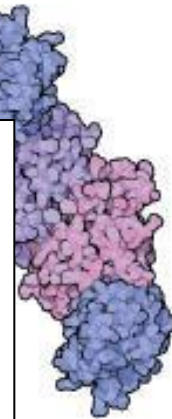
1c17+1e79 ATP Synthase



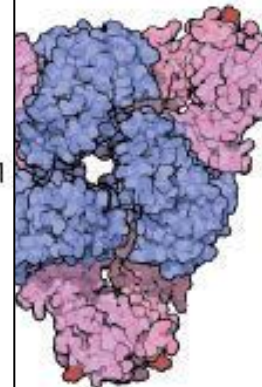
1bg9 Cytochrome b-c1
Complex



Cytochrome c

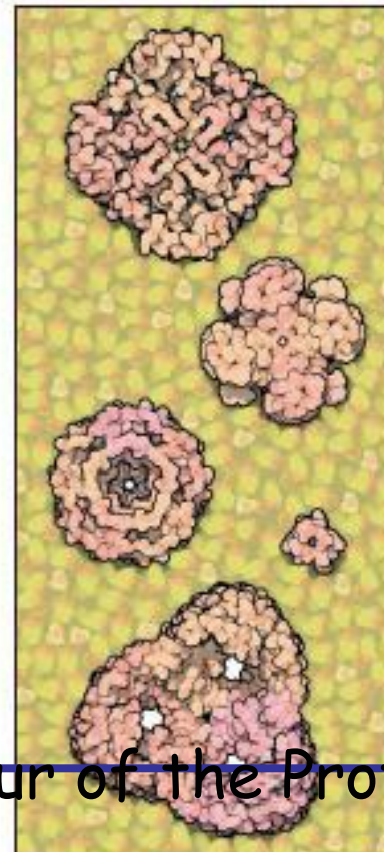


Tryptophan Synthase



Aspartate Carbamoyltransferase

Channels



1fqy Aquaporin

1bl8 Potassium Channel

1msl Mechanosensitive Channel

1gm Gramicidin

2por Porin

"Molecular Machinery: A Tour of the Protein
Data Bank"

http://www.rcsb.org/pdb/structure_education_discussion/educational_resources/index.html

An Example of a Structure

Summary Page

Explore next

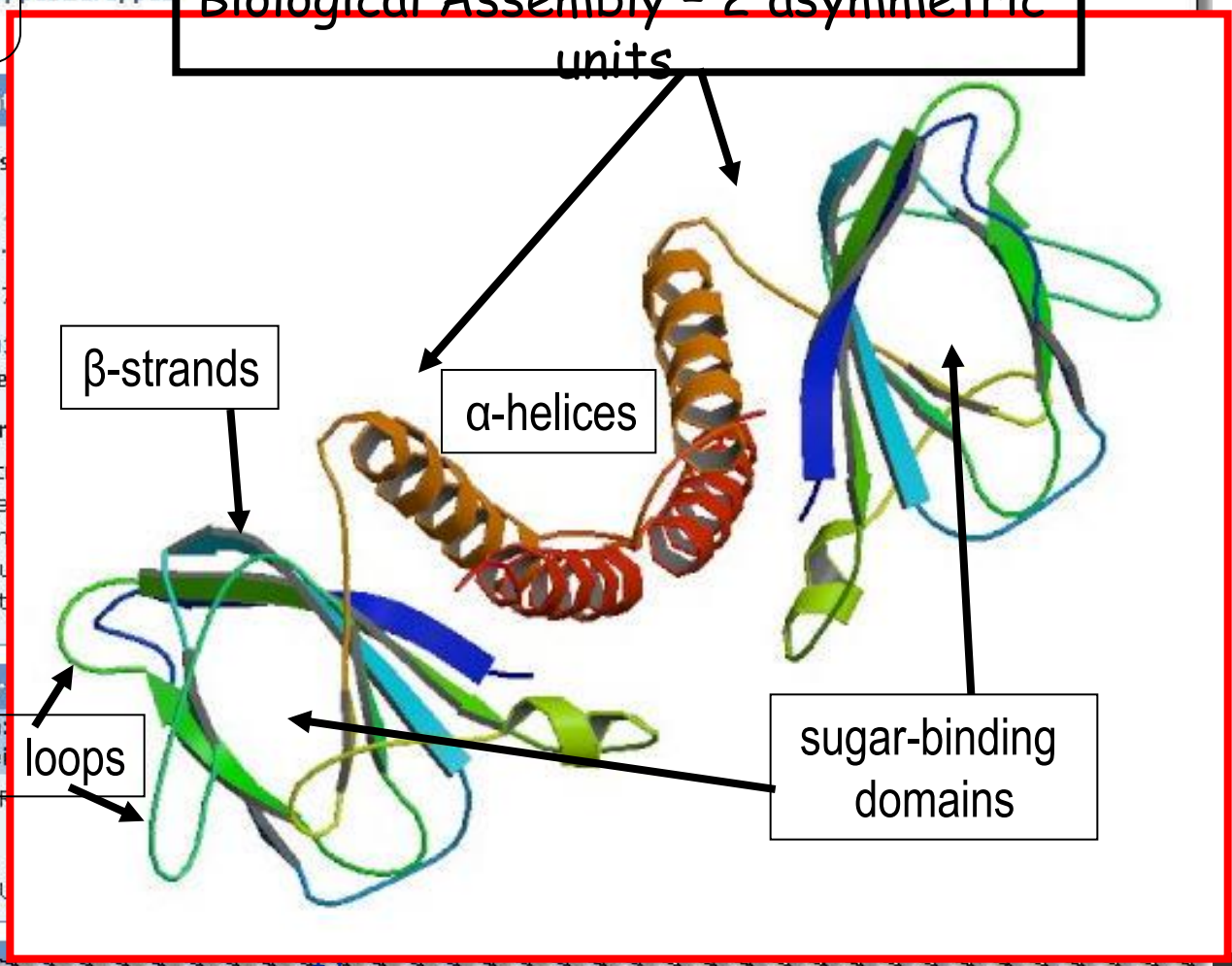
Biological Assembly - 2 asymmetric units

β -strands

α -helices

loops

sugar-binding domains



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Summary Sequence Annotations Seq. Similarity 3D Similarity Literature Biol. & Chem. Methods Geometry Links

APO FORM OF ESCHERICHIA COLI REGULATORY PROTEIN ARAC

DOI:10.2210/pdb2ara/pdb

2ARA

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Explorer

Last Structure: 2ARA

Tools Hide

Primary Citation

Structural basis for the function of the APO FORM OF ESCHERICHIA COLI REGULATORY PROTEIN ARAC

Soisson, S.M.
Wolberger, C.

Journal: (1997)

PubMed: 9101234

Search Related

PubMed Abstracts

The crystal structure of the APO FORM OF ESCHERICHIA COLI REGULATORY PROTEIN ARAC determined in 1.8 angstrom resolution. The protein adopts a dimeric structure with two asymmetric units.

Molecular Classification

Structure Weight

Molecule: APO FORM OF ESCHERICHIA COLI REGULATORY PROTEIN ARAC

Polymer: 1

Chains: A

Fragment: S1

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More Background Information

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PDB ID of

Policies & References

Usage Policies

Frequently Asked Questions About this Website

This page contains a number of frequently asked questions and answers. If this page does not address your questions, please contact us at info@rcsb.org.

Contact Us

Help Desk

Please use the adjacent form

Questions and Comments

Please use this form to send any questions, bug reports, or suggestions about what you

About the PDB Archive and the RCSB PDB

The Protein Data Bank (PDB) archive is the single worldwide repository of information about the structure of large biological molecules, including proteins and nucleic acids. These are the molecules of life, and their study helps to understand how they work. This information is vital to understanding health and disease, and in drug development. The PDB archive is available at no cost to users.

The PDB archive is available at no cost to users. The PDB was established in 1971 at Brookhaven National Laboratory, and is now a part of the Research Collaboratory for Structural Bioinformatics (RCSB).

The PDB was established in 1971 at Brookhaven National Laboratory, and is now a part of the Research Collaboratory for Structural Bioinformatics (RCSB).

RCSB PDB Sitemap

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Getting Started: Organization, Icons & Help

Click to return to homepage

Access from homepage

Icons

Help widget

The screenshot shows the RCSB PDB website. Annotations include:

- A red circle around the top right navigation icons (help, molecular viewer, search, etc.).
- A red box around the "Browser Compatibility Check" section, which includes a table of browser status.
- A red box around the "Help" widget in the bottom left.

Browser Compatibility Check

Browser Info: Mozilla Firefox 3.0.15

Description	Status	Details
JavaScript	✓ Pass	JavaScript is enabled in your browser.
Cookies	✓ Pass	Cookies are enabled in your browser.
Java	✓ Pass	Java version 1.6.0_05
Popup windows	✓ Pass	Popup windows are enabled in your browser.
Adobe Flash	✓ Pass	Adobe Flash is installed and working in your browser.

Help

- Launch Help System
- Video Tutorials
- Glossary of Terms
- PDBMobile FAQ

Icons are used to indicate links to pages or actions; holding your mouse over a search field or link option will display more information. Icons include help pages (?), molecular viewers (🔍), database searches (🔍), external sites (🌐), viewing lists (📄), downloading (📁), and reports (📊).

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RCSB Protein Data Bank Agenda

- Introduction & Credits
- **Basic Searching & Browsing**
- Result Options
- Structure Summary Page
- Advanced Searching
- Tools & Education
- Summary
- Exercises

Structure Deposition & Unique

PDB Identifiers

The screenshot shows the PDB website homepage. A red circle highlights the 'PDB ID or Text' search field. A red box highlights the 'Deposition' menu, which includes links for 'All Deposit Services', 'Electron Microscopy', 'X-ray | NMR', 'Validation Server', 'BioSync Beamline', and 'Related Tools'. A red box highlights the 'PDB ID examples' section, which lists '2ara' (AraC transcription factor), '1lr5' (Auxin Binding Protein), and '1e5s' (Proline hydroxylase), with a note '(not case-sensitive)'. A blue box highlights the 'Customize your homepage' section, which includes a 'Customize This Page' panel with checkboxes for 'Main Panels' (Featured Molecules, Download Files, Structure Comparison, Sequence Search, Latest Structures) and 'Side Panels' (New Features, RCSB PDB News, wwPDB News, FTP Archives, ADIT Deposition). A blue box highlights the 'Molecule of the Month' section. A blue box highlights the 'www.pdb.org' URL. A blue box highlights the 'Deposit your structural data from the homepage' text. A blue box highlights the 'Data will be validated and assigned a unique PDB ID' text.

PDB ID examples:

2ara
AraC transcription factor

1lr5
Auxin Binding Protein

1e5s
Proline hydroxylase
(not case-sensitive)

Customize your homepage view

Customize This Page

Main Panels

- ☒ Featured Molecules
- ☐ Download Files
- ☐ Structure Comparison
- ☐ Sequence Search
- ☒ Latest Structures

Side Panels

- ☒ New Features
- ☒ RCSB PDB News
- ☒ wwPDB News
- ☒ FTP Archives
- ☐ ADIT Deposition

Presets

- ☐ Default

Close This Panel

www.pdb.org

Deposit your structural data from the homepage

Data will be validated and assigned a unique PDB ID

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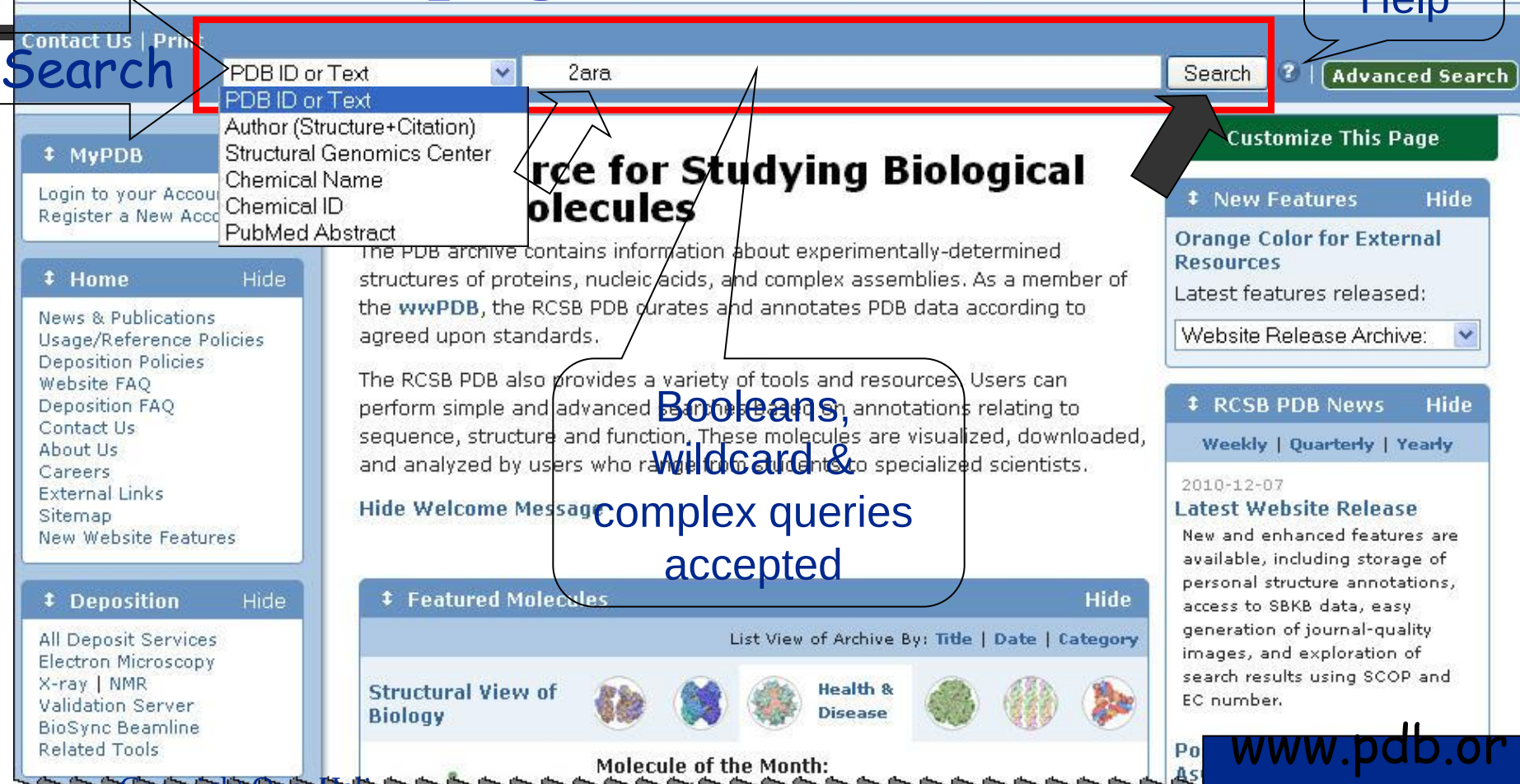
9

10

Basic Search Methods – From the Homepage

Search

Search Help



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Many search methods in Top Bar Search

www.pdb.org

A PDB ID Search Returns

Structure Summary Page

more data

Structure title, ID, citations, descriptions, sources, methodology, structure & more

Easy access to all search methods

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Browse Database
Histograms

Explorer:
Last Structures: 2ARA

Tools Hide

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APO FORM OF ESCHERICHIA COLI REGULATORY PROTEIN ARAC

DOI: 10.2210/pdb2ara/pdb

2ARA

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Primary Citation

Structural basis for ligand-regulated oligomerization of AraC.

Soisson, S.M., MacDougall-Shackleton, B., Schleif, R., Wolberger, C.

Journal: (1997) Science 275: 421-425

PubMed: 9103202

Search Related Articles in PubMed

PubMed Abstract:

The crystal structure of the arabinose-binding and dimerization domain of the Escherichia coli gene regulatory protein AraC was determined in the presence and absence of L-arabinose. The 2.5 angstrom structure of the arabinose-bound molecule shows that the protein adopts an...

[Read More & Search PubMed Abstracts]

Biological Assembly ?

View in Jmol SimpleViewer
Other Viewers ▾ Protein Workshop

Biological assembly assigned by authors

More Images...

MyPDB Personal Annotations Hide

To save personal annotations, please

A Structure Summary page for every structure

Advanced Search & Latest Release

74 Structure Hits | 20 Citations | 102 Ligand Hits

Query Parameters:
This week's new structures

Query Refinements ?

Organism

- Homo sapiens (man) (16)
- Oryctolagus cuniculus (rabbits) (14)
- Streptococcus mutans (7)
- Escherichia coli O157:H7 (4)
- Bacillus subtilis (4)
- Mus musculus (mouse) (3)
- Hepatitis C virus subtype 1b (3)
- Other (21)

Taxonomy

- Eukaryota (37)
- Bacteria (30)**
- Viruses (6)
- Unassigned (4)
- Archaea (1)

Experimental Method

- X-RAY (69)
- Solution NMR (1)

X-Ray Resolution

- less than 1.5 Å (9)
- 1.5 - 2.0 Å (20)
- 2.0 - 2.5 Å (24)
- 2.5 - 3.0 Å (10)
- 3.0 and more Å (6)
- more choices...

Release Date

- Jan 2011 (74)
- this month (74)
- more choices...

Polymer Type

- Protein (67)
- RNA (4)
- Mixed (3)

Enzyme Classification

- 2: Transferases (18)
- 3: Hydrolases (10)
- 1: Oxidoreductases (8)
- 4: Lyases (2)
- 5: Isomerases (1)

Refine Query

Remove Similar: Select Percent Similarity

Display/Download: [v] Generate Reports: [v] Sort by: Release

Displaying results 1 - 25 of 74 total | Page 1 of 3

2KTG Calmodulin like protein from Entamoeba histolytica: solution binding properties of a partially folded protein

Authors: Rout, A.K., Padhan, N., Barnwal, R.P., Bhattacharya, A., Ghaly, K.V.

↑ Search

Advanced Search

Latest Release

New Structure Papers

Sequence Search

Chemical Components

Unreleased Entries

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Histograms

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Mouse over

Click to see
data
distribution
summary for
this subset

- Select Percent Similarity
- 95% Seq. Similar
 - 90% Seq. Similar
 - 70% Seq. Similar
 - 50% Seq. Similar
 - 40% Seq. Similar
 - 30% Seq. Similar

Latest Release Search

181 Structure Hits | 35 Citations | 151 Ligand Hits

Query Parameters:
This week's new structures

Query Refinements ? Show

Organism **Taxonomy** **Exp. Method** **X-Ray Resolution** **Release Date**
Polymer Type **Enzyme Classification**

Refine Query Remove Similar: Select Percent Similarity ▾

☒ Display/Download: ▾ Generate Reports: ▾ Sort by: ▾ Release Date ▾ Results per Page: ▾

Displaying results 1 - 25 of 181 total | Page 1 of 8 | Jump to page:

☒ **2KIC** n-NaF_Y. N-terminal domain of NaF_Y
Authors: Phillips, A.H. Hernandez, J.A. Erbil, K. Pelton, J.G. Wemmer, D.E. Rubio, L.M.
Release Date: 2010-12-08 **Classification:** Protein Binding Metal Transport
Experiment: SOLUTION NMR
Compound: L-Polymer [[Display Full Polymer Details](#) | [Display for All Results](#)]
Citation: Not Available.



☒ **2L3P** Structure of the prolyl cis isomer of the Crk Protein
Authors: Kishimoto, A. Sarkar, P. Saleh, T. Tzeng, S.R. Birge, R.
Release Date: 2010-12-08 **Classification:** Structural Protein

↑ Search

Advanced Search
Latest Release
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Left hand
Search
menu

Jump to a
results
page

Click PDB ID,
structure or title
to go to Structure
Summary

↑ Search

Advanced Search

Latest Release

New Structure Papers

New Structure Papers Search

Query Parameters:

Publications newly associated with PDB structures during the latest weekly update

Display/Download:

Sort by: ↓ Publication Year

Results per Page:

Displaying results 1 - 25 of 61 total

Page 1 of 3

Jump to page:

GO



Related ID:
3PD2

Mechanistic insights into cognate substrate discrimination during proofreading in translation.

Hussain T., Kamarthapu V., Kruparani S.P., Deshmukh M.V., Sankaranarayanan R.

Proc Natl Acad Sci U S A 2010 Nov 22;().

PMID: 21098258 [Read Abstract](#) [PubMed](#)

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related
structures.

[Related Articles](#)



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Structural and Functional Conservation of Mycobacterium tuberculosis GroEL Paralogs Suggests that GroEL1 Is a Chaperone

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Nat Biotechnol 2010 Nov 19;().

PMID: 21094166 [Read Abstract](#) [PubMed](#)

To searchable PubMed
abstract & NCBI
PubMed abstract

To related
structures &
articles

Sequence Search

↑ Search

Advanced Search
Latest Release
New Structure Papers
Sequence Search

Advanced Search Interface

Sequence (BLAST/FASTA/PSI-BLAST) ▼

Sequence search (BLAST or FASTA)

Structure Id

Chain Id

Sequence

Search Tool

Mask Low
Complexity

E Cut Off

BLAST ▼

BLAST
FASTA
PSI-BLAST

10.0



Result Count

Input PDB ID
& chain ID or
paste
sequence

Search methods

Add Search Criteria +

☐ Return Similar Sequences at 90% ▼ Identity ?

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Clear All Parameters

Submit Query

BLAST vs. FASTA: See RCSB PDB Help or OpenHelix tutorials

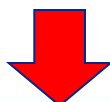
Chemical Components Search

↑ Search

Advanced Search
Latest Release
New Structure Papers
Sequence Search
Chemical Components

Chemical component search

The **Chemical Component Dictionary** gives detailed chemical descriptions of all residue and small molecule components found in PDB entries including standard and modified amino acids/nucleotides, small molecule ligands and solvent molecules.



Structure

Name/Identifier

Formula/Weight

Formula

e.g. C10-12 N* O4 S

Launch formula
expression editor

Molecular weight

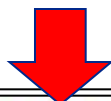
From:

To:

Clear All Parameters

Submit Query

10364 chemical components - **10359** as free ligands in **49378** PDB files - **0** as non-standard polymeric components in **0** PDB files



Ligand Expo  is another browser for the Chemical Component Dictionary and supports searches for current and obsolete chemical components.

Search Unreleased Structures

Unreleased Entries Search

Use this form to find structures that are being processed, on hold waiting for release, or have been withdrawn.

Status codes:

HPUB: processing complete, entry on hold until publication;	REPL: author sent new coordinates, entry to be reprocessed;
HOLD: processing complete, entry on hold until a certain date;	POLC: waiting for a policy decision;
PROC: to be processed;	REFI: re-refined entry;
WAIT: processing started, waiting for author input to continue processing;	WDRN: deposition withdrawn;
AUTH: processed, waiting for author review and approval;	

The **full listing** of all unreleased entries is also available for **viewing in your browser** or for **download as comma delimited text**.

Click [here](#) for all sequences cleared for **immediate release**.

New structures are released each Wednesday between 00:00 UTC and 02:00 UTC.

PDB ID:	
Author:	e.g., Matthews or Matthews, B.W.
Title:	e.g., Actin
Status:	— select one — HPUB - hold until publication HOLD - hold until a certain date PROC - to be processed WAIT - processing started, waiting for author input to continue processing WDRN - deposition withdrawn AUTH - processed, waiting for author review and approval POLC - waiting for a policy decision REPL - author sent new coordinates, entry to be reprocessed REFI - re-refined entry
Sequence Availability:	
Deposition Date:	
Structural Genomics Project Name:	
Structural Genomics Center Initials:	
Has structure factors deposited:	
Sort by:	Status
Display: ☐ Web Page ☐ TEXT (CSV) Download ☐ Pre-released Sequences Download	
Search	

- Find the current status of a structure
- On hold, processing, withdrawn, & more

Understanding Your Results & Options

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PROTEIN DATA BANK

A MEMBER OF THE PDB

An Information Portal to Biological Macromolecular Structures

As of Tuesday Dec 07, 2010 at 4 PM PST there are 69834 Structures | PDB Statistics

Contact Us | Print

PDB ID or

MyPDB Hide

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Search

Advanced Search
Latest Release
New Structure Papers
Sequence Search
Chemical Components

Query Details

Query	Structures Found	Conjunction	Structures Displayed	Search time (seconds)
Text Search for: "TRANSCRIPTION FACTOR"	719		719	0.069

Query History

All queries performed during the current web session are shown.

Session Query
Text Search "FACTOR"

Refine / Modify

Save Query to MyPDB

Clear Query History

Page 1 of 29 | Jump to page: | GO

Results:

Query (719):

- Query Results
- Query Details
- Query History (1)
- Save Query to MyPDB

MyPDB Login

What is a MyPDB Account?

A MyPDB account lets you save custom queries that you frequently use. You can assign queries to be executed during each weekly update of the RCSB PDB. Email notifications about new structures matching your queries are sent on either a weekly or monthly schedule based on your account settings. Queries can for example be keyword, sequence, ligand, advanced searches, or composite queries with multiple sub queries.

MyPDB login & registration

Upper Tabs & More Options

Results breakdown

52 Web Page Hits

14 Unreleased Structures

You may also have these tabs

Select All/None

Next slide

719 Structure Hits 32 Citations 175 Ligand Hits 50 Hits SCOP Hits CATH Hits

Query Parameters
Text Search for: "TRANSCRIPTION FACTOR"

Query Refinements ?

Organism Taxonomy Exp. Method X-Ray Resolution Release Date
Polymer Type Enzyme Classification SCOP Classification

Refine Query Remove Similar: Select Percent Similarity

Display/Download: ☒ Display/Download: View IDs Selected Display Selected Download Selected

Sort by: Release Date Results per Page:
Page 1 of 29 Jump to page: GO

1BIX 1C7U 1C8Z 1C04 1E50 1E00 1GD2 1HKS 1HKT 1I7E 1K1A 1K1B 1K3Z 1L3A 1LE5

Authors: Consani Textor
Release Date: 2010-12-08
Experiment: X-RAY DIFFRACTION
Compound: 3 Polymers (1 Polymer) 1 Ligand (1 Ligand)
Citation: Not Available

RNA polymerase-Gfh1 complex
Authors: Tagami, S., S., RIKEN
Release Date: 2010-12-08

Classification: Transcription
Resolution of 2.90 Å
Polymer Details | Display for All Results
Ligand Details | Display for All Results

Crystal type 1)
Kumarevel, T., Yamamoto, M., Yokoyama,
omics/Proteomics Initiative (RSGI)

Classification: Transcription

Downloading

Structure Download

Structure Download

Use the form below to download the coordinates or experimental data for one or more structures. Multiple PDB IDs should be separated by **commas or spaces**. For other download services [click here](#).

Note:

- This tool requires the Java Runtime Environment ([Browser compatibility check](#))
- Experimental data files (Structure Factors, NMR Restraints) and biological assembly files are not deposited for all structures so experimental data will only be downloaded when it is available.
- Some biological models have been removed from the main archive and are not available from this download. Click [here](#) for more information.

Enter PDB IDs:

1A02, 1A0A, 1A3Q, 1A66, 1AIS, 1AM9, 1AN2, 1ARD, 1ARE, 1ARF,
1AU7, 1AUZ, 1AWC, 1B00, 1B8X, 1BF5, 1BFS, 1BFT, 1BG1, 1BGF,
1BHI, 1BJA, 1BM8, 1BOR, 1BUZ, 1BVO, 1C7U, 1C9B, 1CDW, 1CF7,
1CI6, 1CIT, 1CMO, 1CQG, 1CQH, 1CQT, 1D3U, 1D5V, 1D5Y, 1D8J,
1D8K, 1DH3, 1DL6, 1DN6, 1DP7, 1DXS, 1E17, 1E2X, 1E3O, 1E5O,
1EAN, 1EAO, 1EAQ, 1EDU, 1EGW, 1ERE, 1ERR, 1EXE, 1F62, 1FBQ,

Download Type:

☐ PDB Format

☒ mmCIF Format

☐ PDBML/XML Format

☐ Structure Factors

☐ NMR Restraints

☐ Biological Assemblies

Compression Type:

☐ uncompressed

☒ gzipped

PDB IDs entered

FASTA file Download

FASTA File Download

Use the form below to download a FASTA file containing the sequences for one or more structures. Multiple PDB IDs should be separated by **commas or spaces**. For other download services [click here](#).

1A02, 1A0A, 1A3Q, 1A66, 1AIS, 1AM9, 1AN2, 1ARD, 1ARE, 1ARF,
1AU7, 1AUZ, 1AWC, 1B00, 1B8X, 1BF5, 1BFS, 1BFT, 1BG1, 1BGF,
1BHI, 1BJA, 1BM8, 1BOR, 1BUZ, 1BVO, 1C7U, 1C9B, 1CDW, 1CF7,
1CI6, 1CIT, 1CMO, 1CQG, 1CQH, 1CQT, 1D3U, 1D5V, 1D5Y, 1D8J,
1D8K, 1DH3, 1DL6, 1DN6, 1DP7, 1DXS, 1E17, 1E2X, 1E3O, 1E5O,
1EAN, 1EAO, 1EAQ, 1EDU, 1EGW, 1ERE, 1ERR, 1EXE, 1F62, 1FBQ,

☐ uncompressed

☒ gzipped

PDB IDs entered

Download Services

RCSB PDB File Download Services

- HTTP Services:** PDB data files, chemical component files, and more are available for download via http. These URLs are useful in scripted downloads using utilities such as wget.
- Summary of FTP Services**
- Theoretical Models**
- Archival Snapshots:** time-stamped copies of the FTP archive
- Download a FASTA file containing **all** PDB sequences: **uncompressed** | **gzipped**

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Report Generation

713 Structure Hits 432 Citations 175 Ligand Hits 60 Hits 50

Query Parameters:

Text Search for: "TRANSCRIPTION FACTOR"

Query Refinements ?



Organism



Taxonomy



Exp. Method



X-ray



Polymer Type



Enzyme Classification



SCOP Class

Refine Query

Generate Reports:

Custom Reports

Image Collage

Customizable Table

Summary Reports

Structure

Sequence

Ligands

Structural Genomics Center

Primary Citation

Biological Details

Experimental Reports

X-ray

Crystallization

Data Collection

Refinement

Refinement Parameters

Unit Cell

NMR

Representative Model

Image Collage

Page 1 of 8

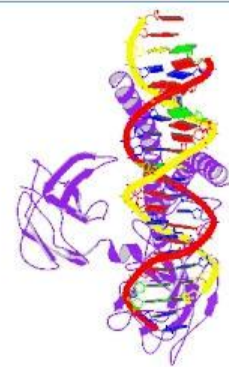
Image Size:

80px

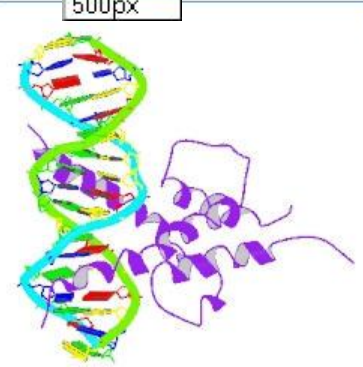
250px

500px

Images per page: 100



1A02



1A0A

Image Collage

Customizable Table

2WTY

CRYSTAL

T-MARE E

Experimental

Authors:

Release D

Experimen

Compound

Citation:

RNA poly

Authors

Requirements

Selection

Custom Tabular Report

Please choose from the following: (All choices will be included in the report)

☐ Structure Summary

☐ Structure Title

☐ Experimental

☐ Deposition Date

☐ Release Date

☐ NDB ID

☐ Resolution

Crystallization Report

Click on column headers to sort up/down. Click again to reverse order. Download options:

Type value in text boxes under column headers to filter the data set. ?

PDB ID	Crystallization Me	Temp (K)	pH Value	Matthews	Percent S	Crystal
1A02	VAPOR DIFFUSION,		7.50	3.54	68.00	THE COMPLEX WAS CR
1A0A	vapor diffusion		3.60	4.20	71.00	VAPOR DIFFUSION ME
1A3Q	vapor diffusion - ha		6.00	2.40	48.70	THE PROTEIN-DNA COM
1AIS	vapor diffusion - ha		7.40	3.34	64.00	HANGING DROP METHO
1AM9	VAPOR DIFFUSION,		5.60	4.30	74.21	PROTEIN WAS CRYSTAL
1AN2	VAPOR DIFFUSION,	277.00	5.50	3.60	61.48	pH 5.50, VAPOR DIFFU
1AU7	vapor diffusion - ha		4.00	2.14	33.00	A 28 BP DNA DUPLEX I

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Sorting, Displaying & More

Result Options

719 Structure Hits 432 Citations 175 Ligand Hits GO Hits SCOP Hits CATH Hits

Query Parameters:
Text Search for: "TRANSCRIPTION FACTOR"

Query Refinements ? Show

Organism Taxonomy Exp. Method X-Ray Resolution Release Date

Polymer Type Enzyme Classification SCOP Classification

Refine Query

Sort by: Release Date Select Percent Similarity

Display/Download: Generate Reports: Results per Page:

Displaying results 1 - 25 of 719 total | Page 1 of 29 | Jump to page: GO

☒ 2WTY CRYSTAL STRUCTURE OF THE HOMODIMERIC MAFB IN COMPLEX WITH THE T-MARE BINDING SITE

 ☒ 2WTY    Consani Textor, L., Holton, S., Wilmanns, M.

2010-12-08 Classification: Transcription

X-RAY DIFFRACTION with resolution of 2.90 Å

Compound: 3 Polymers [Display Full Polymer Details | Display for All Results]

1 Ligand [Display Full Ligand Details | Display for All Results]

Citation: Not Available.

RNA polymerase-Gfh1 complex (Crystal type 1)

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Basic Entry Information &

Access to More

719 Structure Hits 432 Citations 175 Ligand Hits GO Hits SCOP Hits CATH Hits

Query Parameters
Text Search for: "TRANSCRIPTION FACTOR"

Query Refinements ?

Organism Taxonomy Exp. Method Polymer Type Enzyme Classification SCOP

Refine Query

☒ Display/Download: Displaying results 1 - 25 of 719

☒ 2WTY CRYSTAL STRUCTURE OF THE HOMOTETRAMER BINDING SITE

Authors: Consani Textor, L., Holton, S., Wilmanns, M.

Release Date: 2010-12-01

Experiment: X-RAY DIFFRACTION with resolution of 2.90 Å

Compound: 3 Polymers [[Display Full Polymer Details](#) | [Display for All Results](#)]
1 Ligand [[Display Full Ligand Details](#) | [Display for All Results](#)]

Citation: Not Available.

Classification: Transcription

Download DNA polymerase-Gfh1 complex (Crystal type 1)

Display full polymer or ligand details for this entry or all results

Molecule: TRANSCRIPTION FACTOR MAFB
Polymer: 1 Type: polypeptide(L) Length: 97
Chains: A, B
Fragment: RESIDUES 211-306
Mutation: YES

Molecule: DNA (5'-D(*TP*AP*AP*TP*TP*GP*CP*TP*GP*AP*CP*TP*CP*AP*GP*CP*AP*AP*AP*T)-3')
Polymer: 2 Type: polydeoxyribonucleotide Length: 20
Chains: C

Molecule: DNA (5'-D(*TP*AP*TP*TP*TP*GP*CP*TP*GP*AP*GP*TP*CP*AP*GP*CP*AP*AP*TP*T)-3')
Polymer: 3 Type: polydeoxyribonucleotide Length: 20
Chains: D

Helix. induction

less written

32

RCSB Protein Data Bank Agenda

- Introduction & Credits
- Basic Searching & Browsing
- Result Options
- **Structure Summary Page**
- Advanced Searching
- Tools & Education
- Summary
- Exercises

Structure Summary

One for every structure

Organized similarly

It provides access to a wealth of data

Customizable with a widget framework

Re-arranged sections in red

Use Reset Layout to return to default

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Reset Layout

The screenshot displays the PDB Structure Summary page for entry 2AAR. The page is organized into a grid of sections. A custom layout is shown with several sections highlighted in red boxes, indicating they have been re-arranged. The sections include:

- Report tabs Title & ID**: Located at the top right, showing the structure name and ID.
- Primary Citation**: Located in the middle left, providing the primary citation for the structure.
- Molecular Description**: Located in the middle left, providing a brief description of the molecule.
- Ligand Chemical Component**: Located in the middle left, showing the chemical component of the ligand.
- Source**: Located in the middle left, showing the source of the protein.
- Experimental Details**: Located in the middle right, showing details about the experimental method used.
- MyPDB**: Located in the middle right, showing the user's MyPDB information.
- Related Entries**: Located in the bottom left, showing related entries.
- External Data (orange)**: Located in the bottom left, showing external data sources.
- Deposition Summary**: Located in the bottom right, showing the deposition summary.

The page also includes a sidebar on the left with navigation links and a footer with copyright information.

Structure Summary Page - Top

RCSB PDB
PROTEIN DATA BANK

An Information Portal to Biological Macromolecular Structures
As of Tuesday Dec 07, 2010 at 4:04 PM PST there are 69634 Structures

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PDB ID or Text PDB ID lookup or Text search of the complete structure file

Reports

MyPDB
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Title, ID

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Sitemap
New Website Features

Citation

Search
Advanced Search
Latest Release
New Structure Papers
Sequence Search
Chemical Components
Unreleased Entries
Browse Database
Histograms

Explorer:
Last Structure: 2ARC

Deposition
All Deposit Services
Electron Microscopy
X-ray
Validation Server
BioSync Beamlines
Related Tools

Summary | Sequence | Annotations | Seq. Similarity | 3D Similarity | Literature | Biol. & Chem. | Methods | Geometry | Links

ESCHERICHIA COLI REGULATORY PROTEIN ARAC COMPLEXED WITH L-ARABINOSE **2ARC**

DOI:10.2210/pdb2arc/pdb

Primary Citation

Structural basis for ligand-regulated oligomerization of the Escherichia coli gene regulatory protein AraC

Soisson, S.M., MacDougall-Shackleton, B., Wolberger, C.

Journal: (1997) Science **276**: 421-425

PubMed: 9103202

Search Related Articles in PubMed

PubMed Abstract:

The crystal structure of the arabinose-binding and dimerization domain of the Escherichia coli gene regulatory protein AraC was determined in the presence and absence of L-arabinose. The 1.5 angstrom structure of the arabinose-bound molecule shows that the protein adopts an... [Read More & Search PubMed Abstracts]

FASTA Sequence
PDB File
PDB File (Header)
mmCIF File
mmCIF File (Header)
PDBML/XML File
PDBML/XML File (Header)

Display Files
Download Files
Share this Page

Email
Delicious
Stumble
Google
More...

Link this Page
<http://www.rcsb.org/pdb/>

Click on abstract words and keywords to add them to the search box.

AraC AND L-arabinose

Search PubMed Abstracts

Structure Summary Page - Top,

Part 2

RCSB PDB PROTEIN DATA BANK

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Home Hide

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Usage/Reference Policies
Deposition Policies
Website FAQ
Deposition FAQ
Contact Us
About Us
Careers

Deposition Hide

All Deposit Services
Electron Microscopy
X-ray
Validation Server
BioSync Beamlines
Related Tools

Tools Hide

Summary Sequence

ESCHERICHIA PROTEIN ARABINOSIDE BINDING PROTEIN L-ARABINOSE

DOI:10.2210/pdb2arc/pdb

Primary Citation

Regulation of the arabinose-binding and dimerization of AraC.
Dougall-Shackleton, B., Schleif, R.,
e 276: 421-425
es in PubMed

of the arabinose-binding and dimerization
hia coli gene regulatory protein AraC was
sence and absence of L-arabinose. The 1.5
the arabinose-bound molecule shows that the
protein adopts an... [Read More & Search PubMed Abstracts]

Biological Assembly

The biological assembly (also sometimes referred to as the biological unit) is the macromolecular assembly that has either been shown to be or is believed to be the functional form of the molecule. For example, the functional form of hemoglobin has four chains.

Depending on the particular crystal structure, symmetry operations consisting of rotations, translations or their combinations may need to be performed in order to obtain the complete biological assembly. Alternately, a subset of the deposited coordinates may need to be selected to represent the biological assembly. Thus, a biological assembly may be built from:

- one copy of the asymmetric unit
- multiple copies of the asymmetric unit
- a portion of the asymmetric unit

Asymmetric Unit options:

close

KING
WebMol
QuickPDB
FirstGlance
Kiosk

Toggle through views

Click here

Molecular Description

Classification: Transcription Factor

Structure Weight: 38441.66

Molecule: ARABINOSE OPERON REGULATORY PROTEIN

Polymer: 1 **Type:** polypeptide(L) **Length:** 164

Chains: A, B

Fragment: SUGAR-BINDING/DIMERIZATION DOMAIN

Biological Assembly ?

Larger image

View in Jmol SimpleViewer
Other Viewers Protein Workshop
Kiosk

MyPDB Personal Annotations Hide

Jmol View

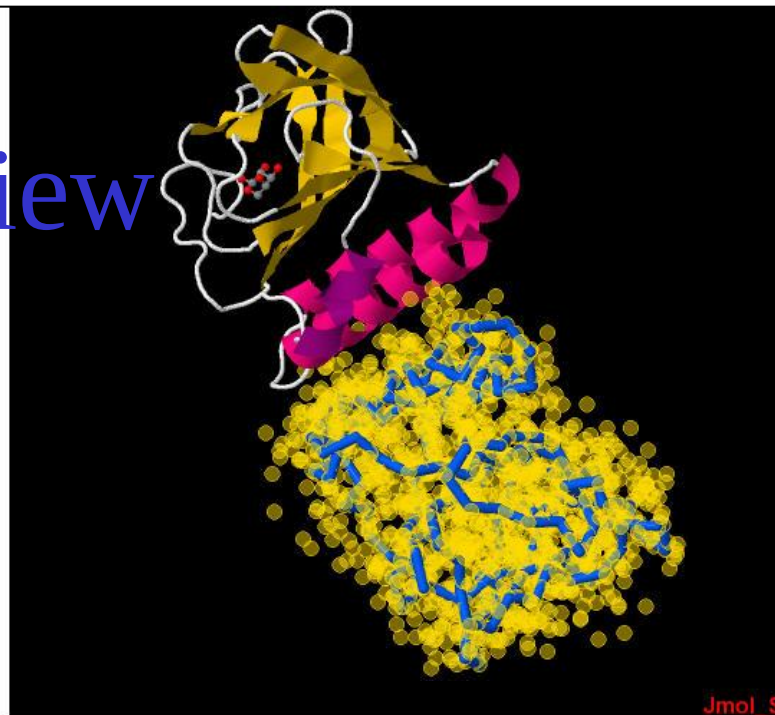
Menus to easily change coloring & display styles

Scripting box

Mouse over for info & click to display

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Right click

- model 1/1
- Configurations (2)
- Select (3,124)
- View
- Style
- Color
- Surfaces
- Symmetry
- Zoom
- Spin
- Vibration
- Animation
- Measurements
- Set picking
- Console
- Show
- File
- Computation
- Language
- About...

Tip: right-mouse click on Jmol to get access to additional Jmol functionality.

Display Style: Cartoon Color: Secondary Structure Surface: None

Toggle: ☐ Selection ☐ H-Bonds ☐ SS Bonds ☐ Rotation ☒ Antialias Display (nicer) ☒ Black Background

Reset Display Export Image Slab

Help tab

Annotations

History

Console

Help

Help tab

Domain Assignment

Classification

Location

Name

Link Out

(click to display in Jmol)

SCOP ?

Regulatory protein AraC

b.82.4.1

A:

d2arca_

in SCOP

Regulatory protein AraC

Class

All beta proteins

d2arcb_

in SCOP

DP ?

Fold

Double-stranded beta-helix

2ARCA0

Superfamily

Regulatory protein AraC

2ARCB0

Family

Regulatory protein AraC

PDP ?

Protein

Regulatory protein AraC

2ARCAa

Species

Escherichia coli [TaxId: 562]

http://jmol.s

<http://jmol.sourceforge.net/>

Structure Summary Page -

Bottom Source

Related PDB Entries

Ligand Component

External Annotations

To move sections to

customiz

MyPDB

Deposition Summary

Experimental Details

Return to default

Tools: Download, Export, Upload, Compare Structures, PDB Services, File Formats, Services: RESTful, SOAP, Widgets

Education: Launch Help System, Video Tutorials, Glossary of Terms

Help: Launch Help System, Video Tutorials, Glossary of Terms

Fragment: SUGAR-BINDING/DIMERIZATION DOMAIN

Source

Polymer: 1

Scientific Name: [Escherichia coli](#) [Taxonomy](#) Expression System: [Escherichia coli](#)

Related PDB Entries

Id	Details
1XJA	
2AAC	
2ARA	
2K9S	

Ligand Chemical Component

Identifier	Formula	Name	Interactions
ARA Search Download	<chem>C5 H10 O5</chem>	ALPHA-L ...	Ligand Explorer

External Ligand Annotations

Identifier	Binding Affinity data from BindingDB	Binding Affinity data from BindingMOAD
ARA Search Download	N/A	Kd: 1000000 nM

External Domain Annotations

- SCOP Classification v1.75: **2 Domains** - data from [SCOP](#)
- CATH Classification v3.3.0: **2 Domains** - data from [CATH](#)
- PFAM Classification: **2 Domains** - data from [PFAM](#)

Structural Biology Knowledgebase Data

Information from the [Structural Biology Knowledgebase](#)

- Models from the Protein Model Portal: **299 models**
- Protein Targets from TargetDB: **0 targets**
- Related Biological Annotations: **>14 annotations**
- Related Clones from PSI:Biology Materials Repository: **0 clones**
- Related Protocols from PeptideDB: **0 protocols**

MyPDB Personal Annotations

To save personal annotations, please [login](#) to your MyPDB account.

Deposition Summary

Authors: [Soisson, S.M.](#), [Wolberger, C.](#)

Deposition: 1996-10-29

Release: 1997-05-15

Last Modified (REVDAT): 2010-02-16

Experimental Details

Method: X-RAY DIFFRACTION

Exp. Data: [Structure Factors](#) [EDS](#)

Resolution[Å]: 1.50

R-Value: 0.179 (obs.)

R-Free: 0.232

Space Group: [P 21](#)

Unit Cell:

Length [Å]	Angles [°]
a = 39.75	α = 90.00
b = 93.84	β = 95.62
c = 50.33	γ = 90.00

Data in orange boxes are gathered from external resources (when available).

Reset Layout

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Sequence Report

Graphic of
secondary
structures

Choose domain
assignments or
annotations from
dropdown menu

Specify how you
want to view
graphic

Set viewing preferences

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Summary **Sequence** Annotations Seq. Similarity 3D Similarity Literature Biol. & Chem. Methods Geometry Links

ESCHERICHIA COLI REGULATORY PROTEIN ARAC COMPLEXED WITH L-ARABINOSE

2ARC

Display Files ▾
Download Files ▾
Share this Page ▾

Results Tabs

Redundancy Reduction and Sequence Clustering

View the clustering results for 2ARC.

Sequence Display ⓘ

The structure 2ARC has in total 2 chains. Out of these 1 are sequence-unique.
Currently viewing **unique chains** only. [[show all chains](#)] [[Show 3D in Jmol](#)]

Chain Display

Chain A (polymer 1) [[help](#)] [[fasta](#)] [[sequence & DSSP](#)]

Description ARABINOSE OPERON REGULATORY PROTEIN

Identical chains B

[[show all chains](#)]

Chain Type polypeptide(L)

UniProtKB reference POA9E0

Select

domain assignment from sequence

pfam

interpro

secondary structure

Preferences

Jmol - 3D parameters

show Jmol No ▾

Jmol width 450 Jmol height 450

Page parameters

Sequence to view PDB SEQRES sequence ▾ Label residue ids by ATOM record only ▾

Font size 12 ▾ Residues per row 60 ▾

Chains to view Unique chains (1 chains) ▾

Submit

Annotations Report

Summary Sequence **Annotations** Seq. Similarity 3D Similarity Literature Biol. & Chem. Methods Geometry Links

ESCHERICHIA COLI REGULATORY PROTEIN ARAC COMPLEXED WITH L-ARABINOSE

2ARC

Display Files
Download Files
Share this Page

Database links

Annotation data related to this entry.

SCOP

Domain Annotation: SCOP Classification (version 1.75) Hide

Domain Info	Class	Fold	Superfamily	Family	Domain	Species
d2arca_	All beta proteins	Double-stranded beta-helix	Regulatory protein AraC	Regulatory protein AraC	Regulatory protein AraC	Escherichia coli [TaxId: 562]
d2arcb_	All beta proteins	Double-stranded beta-helix	Regulatory protein AraC	Regulatory protein AraC	Regulatory protein AraC	Escherichia coli [TaxId: 562]

CATH

Domain Annotation: CATH Classification (version 3.3.0) Hide

Domain	Class	Architecture	Topology	Homology
2arcA00	Mainly Beta	Sandwich	Jelly Rolls	
2arcB00	Mainly Beta	Sandwich		

PFAM

Protein Family Annotation: PFAM Classification

Chain	PFAM Accession	PFAM ID	Description
A	PF02311	AraC_binding	AraC-like ligand binding domain
B	PF02311	AraC_binding	AraC-like ligand binding domain

SBKB

Structural Biology Knowledgebase Data

Information from the Structural Biology Knowledgebase

- Models from the Protein Model Portal: 299 models
- Protein Targets from TargetDB: 0 targets
- Related Clones from PSI:Biological Annotations: >14 annotations
- Related Clones from PSI:Biological Materials Repository: 0 clones
- Related Protocols from PepcDB: 0 protocols

Annotations in orange boxes have been gathered from external re

1169 Structure Hits 588 Citations 313 Ligand Hits GO Hits SCOP Hits CATH Hits

Query Parameters:
CathTree Search for Jelly Rolls (2.60.120)

Query Refinements ?

Organism Taxonomy Exp. Method X-Ray Resolution

Enzyme Classification SCOP Classification

Refine Query

Display/Download: Generate Reports: Sort by

Displaying results 1 - 25 of 1169 total | Page

3D4K Concanavalin A Complexed to a Synthetic Analog of the

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Sequence Similarity Report

ESCHERICHIA COLI REGULATORY PROTEIN ARAC
COMPLEXED WITH L-ARABINOSE

2ARC

Display Files
Download Files
Share this Page

Sequence Clustering and Redundancy Reduction Results

Cluster # 3319 Members. Sequence cutoff: 95% Cluster size: 4 sequences

Sequence Clusters

Entity #1: Chains:

Cluster Sequence Similarity

100%

95%

90%

70%

50%

40%

30%

Rank	PDB id	Entity id	Chains	Description	Details	EC Number	Taxonomy
Select for download / view details OR: Select two chains for comparison							
☐	Download	Details	— Select Comparison Method — Submit				
☐ 1	2ARC	1	A, B	ARABINOSE OPERON REGULATORY PROTEIN	SUGAR-BINDING/DIMERIZATION DOMAIN		562
☐ 2	2AAC	1	A, B	ARAC	SUGAR-		562

Redundancy in the Protein Data Bank

As the single worldwide repository for macromolecular structures, the Protein Data Bank holds a body of data that contains considerable redundancy in regard to both sequence and structure. We have incorporated into the query interface the ability to select a subset of structures from which similar sequences have been largely removed. In most cases, the selected subset will contain far fewer structures than the complete result set. However, the following caveats should be kept in mind:

- Sequence similarity is defined on a chain basis, but results are returned on a structure basis.

Statistics

The following table shows the number of non-redundant sequences as determined by blastclust at several levels of sequence identity.

Method	Description	# of Clusters
blast	100% identity	40231
blast	95% identity	28822
blast	90% identity	27708

Documentation

[Click here for more detailed documentation](#)

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3D Similarity Report

ESCHERICHIA COLI
COMPLEXED WITH L-

Structure Alignment View

Pre-calculated jFATCAT_rigid results for 2ARC.B vs. 3FJS.D .

This page provide a summary view of the protein structure alignment.

Structural Similarity

The following structural similarities have
40% sequence identity clustering has

Entity # 1: Chains: A,B

Description: ARABINOSE OPERC

Length: 164

2ARC.B (chain 1) vs. representatives of other

Rank	Result	Chain 2	Title
1	view	20A2.A	BH2720 protein
2	view	3H8U.B	uncharacterized cons
3	view	3J5.D	uncharacterized pro
4	view	2B8M.A	Hypothetical protein
5	view	1VJ2.B	novel manganese-cont
6	view	1V70.A	probable antibiotics
7	view	2VPV.B	PROTEIN MIF2
8	view	3LWC.A	Uncharacterized pro
9	view	2K9Z.A	uncharacterized pro
10	view	20ZJ.B	Cupin 2, conserved b
11	view	3CEW.D	Uncharacterized cup
12	view	2D7D.B	40-mer from UvrABC
13	view	2GU9.B	tetracenomycin polyk
14	view	1H1P.A	hypothetical protein
15	view	1YSM.A	Calcyclin-binding pro

Text representation of the alignment.

Align 2ARC.B.pdb Length1: 164 with 3FJS.D.pdb Length2: 102

P-value: 1.45e-04

Equ: 82

RMSD: 3.07

Score: 155.59

Align-len: 94

Gaps: 12 (12.77%)

Identity: 11.00%

Similarity: 18.00%

7:B	20:B	30:B	40:B	50:B	60:B	70:B
-----	------	------	------	------	------	------

DPLLPGYSFNAHLVAGLTPIEANGYLDFFIDRPLGMKGYILNLTIRGQGVVKNQGREFVCRPGDILLFPP

PSAALF--KEHRLEVMR-VLPAG---KQVGSH--SVAGPSTIQCLEGEVEIGVDGAQRRRLHQGDL-YLGA

25:D	50:D	60:D	70:D	80:D
------	------	------	------	------

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Literature Report

Summary Sequence Annotations Seq. Similarity **Literature** Biol. & Chem. Methods Geometry Links

ESCHERICHIA COLI REGULATORY PROTEIN ARAC COMPLEXED WITH L-ARABINOSE

2ARC

Display Files

BioLit

Primary Citation and Related **Related articles from PubMedCentral (provided by BioLit)**

Primary Citation

Structural basis for ligand-

Soisson, S.M., MacDougal

Journal: (1997) Science 276:

PubMed: 9103202

Search Related Articles in

PubMed Abstract:

The crystal structure of the ar...
determined in the presence a...
that the protein adopts an...



Phylogenomic identification of five new human homologs of the DNA repair enzyme AlkB

Michal A Kurowski, Ashok S Bhagwat, Grzegorz Papaj, Janusz M Bujnicki

BMC Genomics 2003; 4():48ff.

BioLit: 317286 PubMedCentral: 317286 PubMed: 14667252 DOI: 10.1186/1471-2164-4-48

Abstract Context Copyright



DNA tape measurements of AraC

Michael E. Rodgers, Robert Schleif

Nucleic Acids Research 2008; 36(2):404ff.

BioLit: 2241862 PubMedCentral: 2241862 PubMed: 18039712 DOI: 10.1093/nar/gkm1030

Abstract Context Copyright

Publication Details

MeSH Terms (Primary C

Pubmed 9103202
ID

MeSH
Terms

Arac

Crystallography
Protein Conforma

Other PDB IDs found in the above articles ?

Image	PDB ID	Structure Title	Sequence Similarity
	1BK0	ISOPENICILLIN N SYNTHASE FROM ASPERGILLUS NIDULANS (ACV-FE COMPLEX)	-
	1GP4	ANTHOCYANIDIN SYNTHASE FROM ARABIDOPSIS THALIANA (SELENOMETHIONINE	-

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Biology & Chemistry Report

ESCHERICHIA COLI REGULATORY PROTEIN ARAC
COMPLEXED WITH L-ARABINOSE

2ARC

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Biology and Chemistry Report

Structure Details ?

Help

Hide

Structure Keywords

Keywords
Text

Polymeric Molecule

Chain A,B

Description

Fragment

Nonstandard Linkage

Nonstandard Monomers

Polymer Type

Formula Weight

Source Method

Entity Name

Ligands and Prosthetic

ID Name
ARA ALPHA-L-ARABINOSE

Protein Details ?

Help

Hide

UniProtKB Information

Chain	SWS/UNP ID	SWS/UNP Accession(s)
A,B	ARAC_ECOLI	P0A9E0

Keywords and Names

Chain(s)	RCSB Name	UniProtKB Name	UniProtKB Keywords
A,B	ARABINOSE OPERON REGULATORY PROTEIN	Arabinose operon regulatory protein	3D-structure , Activator , Arabinose catabolism , Carbohydrate metabolism , Complete proteome , Cytoplasm , DNA-binding , Repressor , Transcription , Transcription regulation

Gene Details ?

Help

Hide

Genetic Source

Chain A,B	Scientific name of the organism.
Scientific Name	ESCHERICHIA COLI
Genus	HOMO SAPIENS
Host Scientific Name	SACCHAROMYCES CEREVISIAE
Host Genus	

Mouse over
for details

Escherichia coli
Escherichia
Escherichia coli
Escherichia

Methods Report

Precise
experimental
details

Organized
similarly

Mouse over to
read

definitions

Sections
depend on
methodology

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SummarySequenceAnnotationsSeq. Similarity3D SimilarityLiteratureBiol. & Chem.**Methods**GeometryLinks

X-RAY DIFFRACTION2ARC

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Materials and Methods page

Crystallization

Hide

Crystallization Experiments

pH7.25

DetailsPROTEIN WAS CRYSTALLIZED BY MICROSEEDING FROM 18-20% PEG 8000, 100 MM TRIS-HCL, PH 7.25, 40 MM MAGNESIUM ACETATE AND 0.2% (W/V) L-ARABINOSE

Crystal Data

Hide

Unit Cell

Length	(Å)	Angle	(°)
a =	39.75	α =	90
b =	93.84	β =	95.62
c =	50.33	γ =	90

Space Group

Space Group Name:

Hermann-Mauguin space-group symbol. Note that the Hermann-Mauguin symbol does not necessarily contain complete information about the symmetry and the space-group origin. If used, always supply the FULL symbol from International Tables for Crystallography Vol. A (2002) and indicate the origin and the setting if it is not implicit. If there is any doubt that the equivalent positions can be uniquely deduced from this symbol, specify the attribute pos_as_xyz in category symmetry_equiv or attribute space_group_name_Hall in category symmetry data items as well. Leave spaces between symbols referring to different axes.
P 1 21/m 1
P 2/n 2/n 2/n (origin at -1)
R -3 2/m

Diffraction

Hide

Diffraction Experiment

Diffn ID

Data Collection Temperature

Diffraction Detector

DetectorIMAGE PLATE

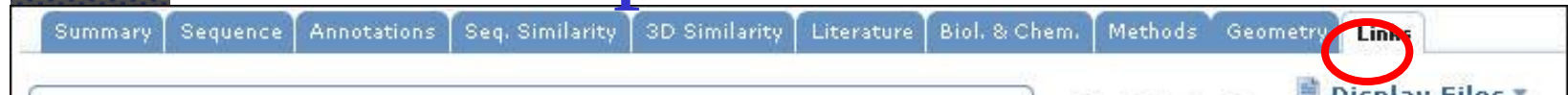
TypeFUJI

DetailsSPHERICAL RH COATED MIRROR

Collection Date1995-09

45

Links Report



ESCHERICHIA COLI REGULATORY PROTEIN COMPLEXED WITH L-ARABINOSE

SCOP & CATH

External Links

STRUCTURE SUMMARY

- Protein Databank in Europe (PDBe)
- Protein Data Bank Japan (wwPDB Partner) (PDBj)
- PSI Structural Biology Knowledgebase (PSI/KB)
- Protein Interfaces, Surfaces and Assemblies (PISA)
- Molecular Modeling DataBase (NCBI/Entrez) (MMDB)
- PDBsum
- Jena Library
- PDBWiki
- Proteopedia
- OCA Browser (OCA)

Scroll down to

STRUCTURE FEATURES

- Homology derived Secondary Structure of Protein
- Analysis of Ligand-Protein Contacts (LPC)
- Analysis of interatomic Contacts of Structural Unit
- Computed Atlas of Surface Topography of protein
- Gaussian Network Model (GNM)

LIGAND FEATURES

- BindingDB - No external link available
- Ligand
- ChemBL
- PubChem
- DrugBank

STRUCTURE CLASSIFICATION AND COMPARISON

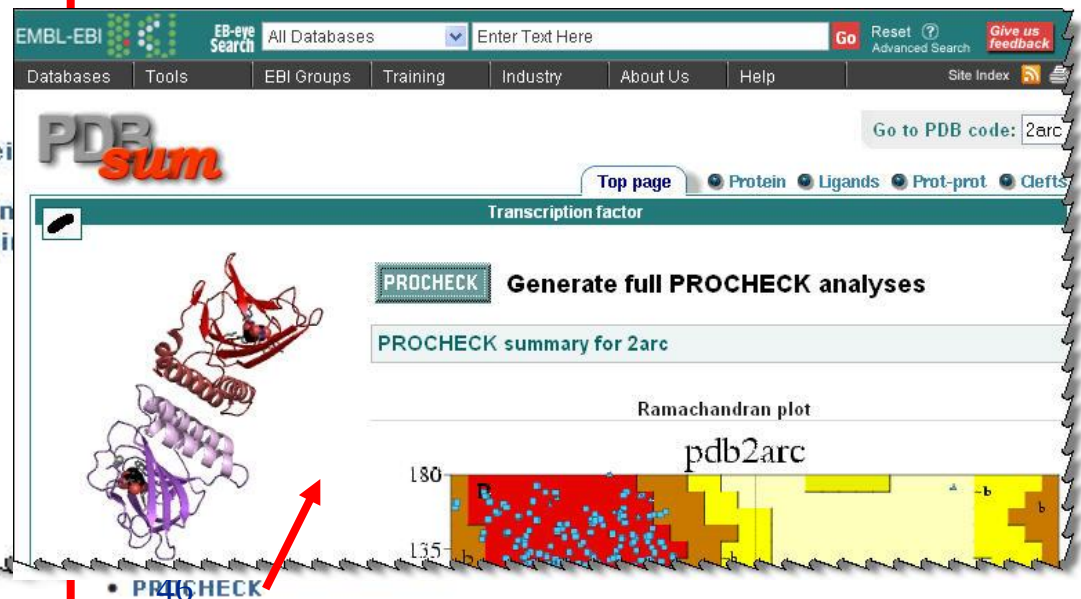
- Structural Classification of Proteins (SCOP)
- Protein Structure Classification (CATH)
- Vector Alignment Search Tool (VAST)
- Flexible structure Alignment by Chaining Aligned fragment pairs allowing Twists (FATCAT)
- DALI
- SUPERFAMILY

SECONDARY STRUCTURE

- Secondary Structure Assignments (DSSP)

EXPERIMENTAL DATA

- Electron Density Server (EDS)



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RCSB Protein Data Bank Agenda

- Introduction & Credits
- Basic Searching & Browsing
- Result Options
- Structure Summary Page
- **Advanced Searching**
- Tools & Education
- Summary
- Exercises

Advanced Search Access & Basics

The screenshot displays the RCSB PDB Protein Data Bank homepage. At the top, it states 'A MEMBER OF THE PDB' and 'An Information Portal to Biological Macromolecular Structures'. Below this, a status bar indicates 'As of Tuesday Dec 14, 2010 at 4 PM PST there are 69967 Structures'. The main navigation bar includes 'Contact Us | Print' and a search input field with a dropdown menu set to 'PDB ID or Text'. A red circle highlights the 'Advanced Search' button. On the left, a 'MyPDB' sidebar contains links for account management and a 'Search' section with a red circle around 'Advanced Search'. A large black arrow labeled 'Query Types' points to the 'Advanced Search Interface' dropdown menu. This menu lists various search criteria categories: 'ID(s) and Keywords', 'Structure Annotation', 'Deposition', 'Structure Features', 'Sequence Features', 'Chemical Components', 'Biology', and 'Methods'. The 'Enzyme Classification' option under the 'Biology' section is circled in red.

RCSB PDB PROTEIN DATA BANK

A MEMBER OF THE PDB

An Information Portal to Biological Macromolecular Structures

As of Tuesday Dec 14, 2010 at 4 PM PST there are 69967 Structures | PDB Statistics

Contact Us | Print

PDB ID or Text PDB ID lookup or Text search of the complete structure file Search ? **Advanced Search**

MyPDB Hide

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Deposition Policies
Website FAQ
Deposition FAQ
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Careers
External Links
Sitemap
New Website Features

Search Hide

Advanced Search
Latest Release
New Structure Papers
Sequence Search

Advanced Search Interface

Choose a Query Type:

- ID(s) and Keywords**
 - PDB ID(s)
 - PubMed ID(s)
 - UniProt Accession Number
 - Keyword(s)
- Structure Annotation**
 - Structure Title
 - Structure Description
 - Macromolecule Name
- Deposition**
 - Author Name
 - Deposit Date
 - Release Date
 - Latest Released Structure
 - Latest Modified Structures
 - Structural Genomics Project
- Structure Features**
 - Macromolecule Type
 - Number of Chains (Asymmetric Unit)
 - Number of Chains (Biological Assembly)
- Sequence Features**
 - Number of Chains (Biological Assembly)
 - Number of Entities
 - Number of Models
 - Number of Disulfide Bonds
 - Molecular Weight (Structure)
 - Secondary Structure Content
 - Secondary Structure Length
 - SCOP Classification Browser (opens popup)
 - CATH Classification Browser (opens popup)
 - Taxonomy Browser (opens popup)
- Chemical Components**
 - Chemical Name
 - Chemical ID
 - InChI Descriptor
- Biology**
 - Source Organism Browser (NCBI) (opens popup)
 - Expression Organism
 - Enzyme Classification Browser (opens popup)
 - Enzyme Classification**
 - Biological Process Browser (GO) (opens popup)
 - Cell Component Browser (GO) (opens popup)
 - Molecular Function Browser (GO) (opens popup)
 - Transporter Classification Browser (opens popup)
- Methods**
 - Experimental Method
 - X-Ray Resolution
 - X-Ray Refinement R Factors
 - X-Ray Diffraction Source
 - X-Ray Reflections
 - X-Ray Cell Dimensions
 - X-Ray Software
 - Space Group
 - Crystal Properties
 - EM Assembly

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Access from homepage top or left side search menu

Advanced Search - Number of Entities Query

Advanced Search Interface

Number of Entities ▼

Search by number of entities (e.g. 4HHB contains 2 protein entities)

Entity Type: Any Protein ?

Between: 5 and 5

Result Count
168
PDB Entries

Add Search Criteria +

☐ Remove Similar Sequences at 90% ▼ Identity

Match all ▼ of the above conditions.

Clear All Parameters Submit Query

Use Result Count to see how many results you will obtain

Click on Add Search Criteria to add a query box

CATH Classification Browser (opens popup)
Taxonomy Browser (opens popup)
Sequence Features
Sequence (BLAST/FASTA/PSI-BLAST)
Translated Nucleotide Sequence (BLASTX)
Sequence Motif
Chain Length
Genome Location Browser (opens popup)

Chemical Components
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Advanced Search Methods - Adding Query Boxes

Advanced Search Interface

Number of Entities

Search by number of entities (e.g. 4HHB contains 2 protein entities)

Entity Type

Between: and

168 PDB Entries

AND

Has Ligand(s)

Search based on whether or not the structure contains any free ligands

Has Ligands

☐ Remove Similar Sequences at Identity

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Results

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Adding More Query Boxes

Macromolecule
Type

Experimental
Method

Remove Similar &
Match ALL or ANY

Advanced Search Interface

Number of Entities 168 PDB Entries

Search by number of entities (e.g. 4HHB contains 2 protein entities)

Entity Type

Between: and

AND

Has Ligand(s)

Search based on whether or not the structure contains any free ligands

Has Ligands

AND

Macromolecule Type

Search based on whether the structure contains chains of certain molecule types (e.g. protein vs. DNA)

Contains Protein

Contains DNA

Contains RNA

Contains DNA/RNA Hybrid

AND

Experimental Method

Search by the experimental method used to determine the structure, e.g. X-ray vs. NMR

Experimental Method

Has Experimental Data

Remove Similar & Match ALL or ANY

☒ Remove Similar Sequences at identity

Match of the above conditions.

Results

Add Search Criteria

Structur
es vs.
ligands,
start
over,
or submit
query

27 Structure Hits 23 Citations 51 Ligand Hits GO Hits SCOP Hits CATH Hits

Advanced Search Results

Query Parameters
 Number of Entities Search : Entity Type=Protein Min Number of Entities=5 Max Number of Entities=5 and Ligand Search : Has free ligands=yes and Chain Type: there is a Protein chain but not any DNA or RNA or Hybrid and Experimental Method is X-RAY and has Experimental Data and Homologue Removal - 95% Identity Cutoff

Query Refinements ? Show

Organism Taxonomy Exp. Method X-Ray Resolution Release Date

Polymer Type Enzyme Classification SCOP Classification

Refine Query Remove Similar: Select Percent Similarity

Display/Download: Generate Reports: Sort by: Release Date Results per Page:

Displaying results 1 - 25 of 27 total | Page 1 of 2 | Jump to page: GO

☒ 3P8C Structure and Control of the Actin Regulatory WAVE Complex

Authors: Rosen, M.K.

Release Date: 2010-12-01 Classification: Protein Binding

Experiment: X-RAY DIFFRACTION with resolution of 2.29 Å

Compound: 5 Polymers [Display Full Polymer Details | Display for All Results]
 3 Ligands [Display Full Ligand Details | Display for All Results]

Citation: Not Available.

20FF Structure of four mutant forms of yeast F1-ATPase: alpha-F405S

Our query

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RCSB Protein Data Bank Agenda

- Introduction & Credits
- Basic Searching & Browsing
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Tools & Educational Resources

Structure Download

Use the form below to download the coordinates or experimental data for one or more structures. Multiple PDB IDs should be separated by **commas or spaces**. For other download services [click here](#).

FTP Services

FTP Access

File Formats

Overview

RCSB PDB - SOAP Web Services:

RCSB PDB Widgets

A resource for web developers

The RCSB PDB provides web widgets, small bits of code, which provide PDB functionality that you can embed in your own website. All of the widgets that we provide on our site are 100% self contained JavaScript files which we maintain. When using any of these widgets, please make sure to remote link to our libraries instead of downloading and hosting them yourself. This will insure that any updates or changes we make to our site are automatically reflected in your usage.

RCSB PDB Widgets

- [Comparison Tool Widget](#)
- [Molecule of the Month Widget](#)

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Download: Entries | Ligands
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Understanding PDB Data
Molecule of the Month
Educational Resources

Click on
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Structures

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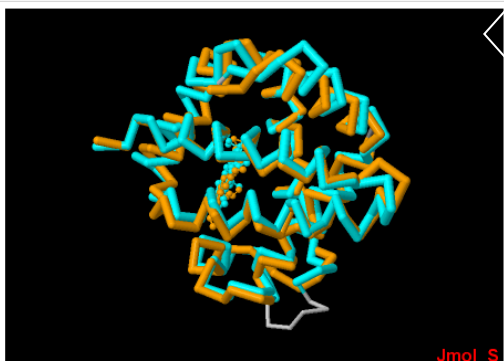
The RCSB PDB Comparison

RCSB PDB Protein Comparison Tool

Structure Alignment Results

Alignment Details: ■ Query: (orange/dark grey) HEMOGLOBIN (DEOXY) (ALPHA CHAIN)		■ Subject: (cyan/light grey) HEMOGLOBIN (DEOXY) (BETA CHAIN)	
P-value: 0.00e+00 Score: 364.84 RMSD: 1.49 %Id: 41.0%	PDB ID: 4HHB Chain ID: A Length: 141 Similarity: 99%		PDB ID: 4HHB Chain ID: B Length: 146 Similarity: 95%

Jmol Version 12.0.18



Tip: right-mouse click on Jmol to get access to additional Jmol functionality. You may also drag the right-bottom corner of the Jmol area to resize it.

Text representation of the alignment.

```

Align 4HHB.A.pdb Length1: 141 with 4HHB.B.pdb Length2: 146
P-value: 0.00e+00
Equ: 139
RMSD: 1.49
Score: 364.84
Align-len: 147
Gaps: 8 (5.44%)

Identity: 41.00%
Similarity: 58.00%
            
```

1:A	10:A	20:A	30:A	40:A	50:A	60:A
VLSPADKINVKAAWGKVG	HAHAGEYGAELERN	FLSPTTKTYFPHFDL	-----	SHGSAQVKHGKQKQAD		
.....						
HLTPEEKSAVTALWGKV	--NVDEYGEALGRLLV	YPTQRFESFGDLSTPD	AVMGKPKVKAHGKKVLG			
2:B	20:B	30:B	40:B	50:B	60:B	

Example

Alignment Options

Align custom files (Launches a Java Web Start application)

Show Example (4HHB.A vs 4HHB.B Java-FATCAT, rigid)

More documentation on the RCSB PDB protein structure alignments

Acknowledgements

Click Here to show the acknowledgements

Acknowledgements

RCSB PDB Comparison Tool Reference

Andreas Prlic; Spencer Bliven; Peter W. Rose; Wolfgang F. Bluhm; Chris Bizon; Adam Godzik; Philip E. Bourne (2010)
 Pre-calculated protein structure alignments at the RCSB PDB website
 Bioinformatics 26: 2983-2985
[\[PubMed\]](#)

Smith & Waterman algorithm

T.F. Smith, M.S. Waterman (1981)
 Identification of Common Molecular Subsequences
 Journal of Molecular Biology 147: 195-197
[\[PubMed\]](#)

Needleman & Wunsch algorithm

S.B. Needleman & C.D. Wunsch (1970)

To Expert mode - vary parameters

Read more

Understanding PDB Data: Looking at Structures

The PDB archive is a repository of atomic coordinates and other information describing proteins and other important biological macromolecules. Structural biologists use methods such as **X-ray crystallography**, **NMR spectroscopy**, and **cryo-electron microscopy** to determine the location of each atom relative to each other in the molecule. They then deposit this information, which is then annotated and publicly released into the archive by

Looking at Structures

- [Introduction](#)
- [Biological Assemblies](#)
- [Dealing with Coordinates](#)
- [Methods for Determining Structure](#)
- [Missing Coordinates and Biological Assemblies](#)
- [Molecular Graphics Programs](#)
- [Resolution](#)
- [R-value and R-free](#)

Educational Resources

[Kiosk Viewer](#) | [Posters](#) | [Website Tutorials](#) | [Animations](#) | [Activities/Lessons](#) | [Exhibit Materials](#) | [Events](#) | [Poster Prize](#)

These Educational Resources are aimed at teachers and students interested in learning about protein and nucleic acid structures, and how to use the RCSB PDB site ([PDF Overview](#)). For researchers and educators interested in how to understand PDB data, how to visualize structures, how to read coordinate files, and potential challenges in exploring the archive, please see the [Looking at Structures](#) feature.



Molecules in Motion Kiosk Viewer

The **Molecules in Motion Kiosk Viewer** is a full-screen animation program that displays structures from different angles and perspectives, and focuses on chemical components within the structure ([PDF flyer](#)).

The Kiosk program runs on Mac, Windows and some versions of Linux (i.e. CentOS).

Click on
Molecule of
the Month

Education
Understanding PDB Data
Molecule of the Month
Educational Resources

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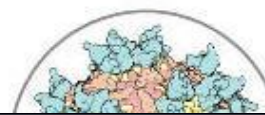
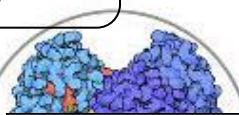
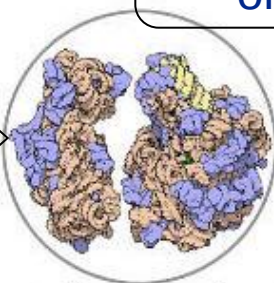
Molecule of the Month

Molecule of the Month: Structural View of Biology

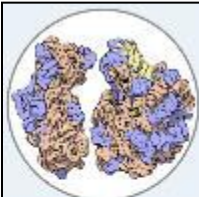
View by Title, Date
or Category

List View of Archive By: Title | Date | Category

Click on



Transcription



Protein Synthesis

The major molecules of protein synthesis, ribosomes to folded proteins, are available

Structure of Nucleic Acids

DNA Maintenance

Replication

Transcription

Translation

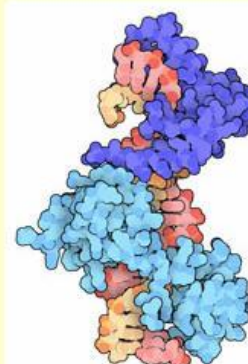
Protein Folding - Modification - D

Enhanceosome

Oct and Sox
Transcription

Poly(A)
Polymerase

Oct and Sox Transcription Factors



The development of a complete human being from a single cell is one of the great miracles of life. A human egg cell contains about 30,000 genes that encode proteins, and of these, about 3,000 of these genes encode transcription factors. Transcription factors determine when genes will be turned on and turned off, orchestrating the many processes involved in the development of an embryo and the many tasks performed by each cell after a child is born. Amazingly, there is only about 1

transcription factor for every 10 genes, posing a puzzle: how does this limited set of proteins control the many genes and processes that must be regulated?

[Click to Read More.](#)

Aconitase and
Iron Regulatory
Protein 1



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The RCSB PDB's Molecule of the Month series by is intended for all types of users, but especially for those interested in the structure and function of the molecule, a discussion

Community Publications

An Information Portal to Biological Macromolecular Structures

A MEMBER OF THE PDB

Published quarterly by the Research Collaboratory for Structural Bioinformatics Protein Data Bank

Fall 2010
Number 47

NEWSLETTER

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PDB ID or Text PDB ID lookup or Text search of the

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Histograms

Deposition

News and Publications

News

The RCSB PDB releases weekly information about r

Year: 2010 (Latest News) | 2009 | 2008 | 2007 |

RCSB PDB Newsletter

A newsletter is published quarterly online and in p Corner is also archived. To request the printed ver Readers can also subscribe to the electronic versi

Publications

The RCSB PDB has published several journal artic publications.

Annual Reports

Our annual reports describe the history, mission,

Year: 2010 | 2009 | 2008 | 2007 | 2006 | 200

Flyers and Brochures

- Molecules in Motion Kiosk Viewer [pdf]
- Comparison Tool [pdf]
- Widgets Information [pdf]
- Birch Aquarium Exhibit [pdf]
- Educational Resources Highlights [pdf]
- General Information [pdf]
- ImmersivePDB [pdf]
- Molecule of the Month 2006 Highlights [pdf]
- Structure Deposition: 5 Easy Steps [pdf]
- New Searching [pdf]

Discussion Groups

proteins is an open discussion forum for protein structure, analysis, and related topics. [A

Contents

Message from the RCSB PDB

Data Deposition

New Release of pdb_extract Available Online and for Download

Redesigned BioSync

Deposition Statistics

Structural Genomics in the News

wwPDB News: Get the Latest wwPDB News

Data Query, Reporting and Access

Latest Website Release

Analyze small molecule interactions in the PDB with Ligand Explorer

dConsensus

Home | Newsletter Archive | PDF Version

Message from the RCSB PDB

The RCSB PDB's **Molecule of the Month** introduces readers to the structure and function of specific molecules, and shows how the structures function and their importance in our lives. Each entry is illustrated through descriptive text and pictures, with links to specific PDB entries, discussion questions, and interactive 3D molecular views. As of October 2010, there are now 130 articles describing everything from **AAA+ proteases** to **zinc fingers**.

These columns have been organized to help users explore the **Molecule of the Month** and the PDB archive in the context of biology. Major functional categories can be browsed by areas of interest. Within each topic, descriptive subcategories lead to the relevant **Molecule of the Month** features.

The major topic categories include:

Snapshot: October 1, 2010

68288 released atomic coordinate entries

Molecule Type

63236 proteins, peptides, and viruses
2173 nucleic acids
2841 protein/nucleic acid complexes
38 other

Experimental Technique

59210 X-ray
8596 NMR
308 electron microscopy

Electronic Mailing List: pdb-l@rcsb.org

The RCSB PDB electronic mailing list, pdb-l@rcsb.org, is maintained as an open forum for information exchange related to macromolecular structures. Topics include the PDB, as well as problems in structure analysis, job ads, and requests for information relating to protein structure.

For-profit use of the list, such as for advertising, is prohibited, except for occasional brief announcements of relevant products or services. Subscribers with commercial affiliations are welcome, as is their participation in educational/research discussions, including such discussions which may concern their commercial products. Personal messages, abuse, and messages of unrelated commercial nature are not acceptable.

Please note that only subscribers are able to post messages to this list.

- [Subscription Information and Management](#)
- [Archives](#)

Related Newsgroups and Lists

- [BIOSI/Bionet](#) contains a wide variety of newsgroup archives, including, [BIOPHYSICS](#), [COMPUTATIONAL-BIOLOGY](#), and [X-PLOR](#)
- [CCP4 Bulletin Board](#)

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An Information Portal

Summary



RCSB
PDB
PROTEIN DATA BANK

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An Information Portal to Biological Macromolecular Structures

As of Tuesday Dec 14, 2010 at 4 PM PST there are 69967 Structures | [PDB Statistics](#)

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PDB ID or Text

Author (Structure+Citation)
Structural Genomics Center
Chemical Name
Chemical ID
PubMed Abstract

PDB ID lookup or Text search of the complete structure file



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Source for Studying Biological Molecules

The PDB archive contains information about experimentally-determined structures of proteins, nucleic acids, and complex assemblies. As a member of the **wwPDB**, the RCSB PDB curates and annotates PDB data according to agreed-upon standards.

The RCSB PDB also provides a variety of tools and resources. Users can perform simple and advanced searches based on annotations relating to sequences, structure and function. These molecules are visualized, downloaded, and analyzed by users who range from students to specialized scientists.

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Structural View of
Biology

Health &
Disease

Molecule of the Month:
Adenovirus

Viruses are one of the most dangerous enemies to our health, attacking cells and causing deadly diseases like AIDS and influenza. However, scientists are currently discovering ways to trick



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Summary Page

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Weekly Monthly Yearly

2010-12-14
Annual Report 2010



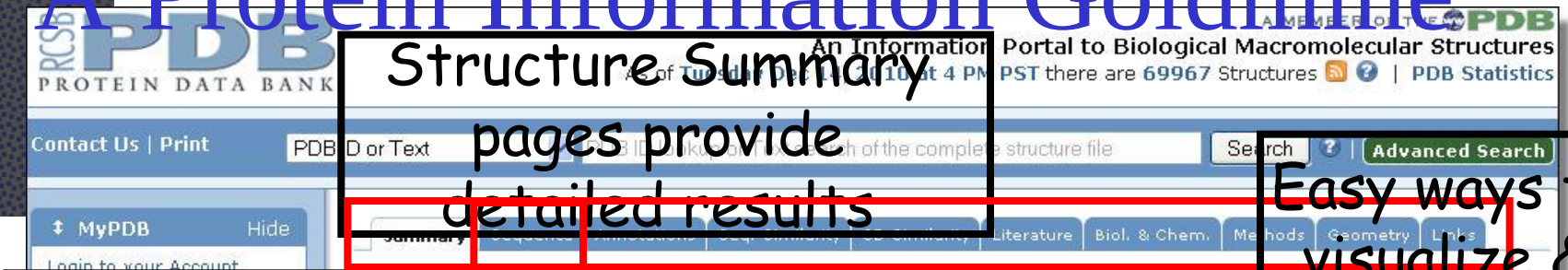
www.pdb.org

A Protein Information Goldmine

Structure Summary

pages provide
detailed results

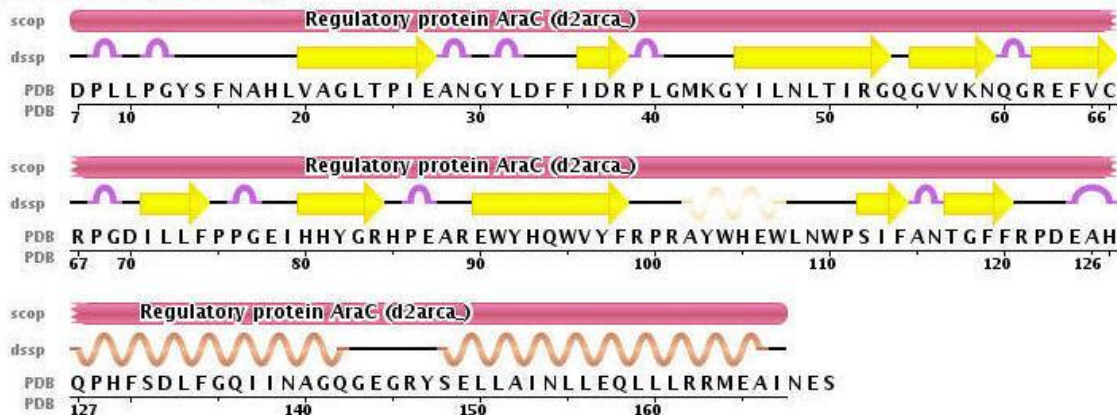
Easy ways to
visualize &
manipulate
structures



Chain A (polymer 1) [help] [fasta] [sequence & DSSP]	
Description	ARABINOSE OPERON REGULATORY PROTEIN
Identical chains	B
[show all chains]	
Chain Type	polypeptide(L)
UniProtKB reference	P0A9E0
Length	164 residues
scop domain assignment	d2arca Regulatory protein AraC: 161 residues
[hide] [reference]	
dssp secondary structure	25% helical (3 helices; 41 residues) 33% beta sheet (10 strands; 55 residues)
[hide] [reference]	
More annotations	
Select	

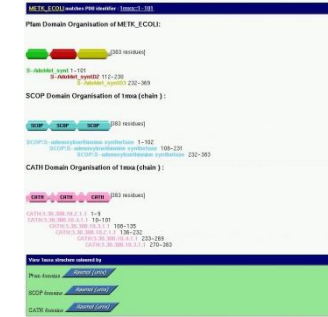
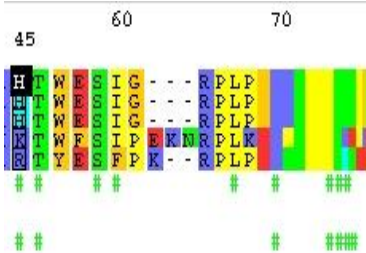
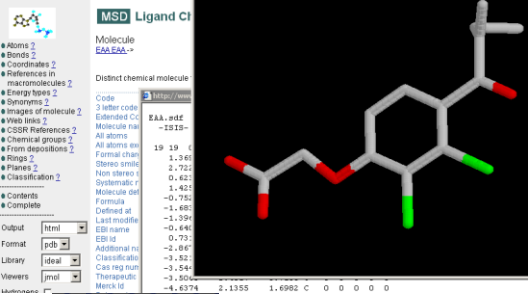
Currently displayed: SEQRES sequence. [display external (UniProtKB) sequence]

Sequence Details [View image]



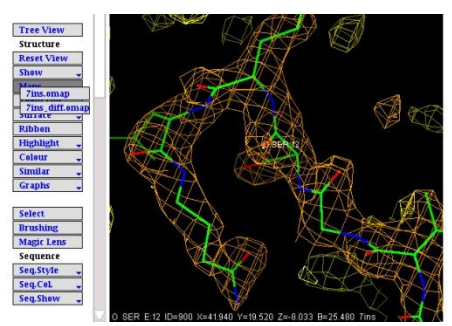
RCSB Protein Data Bank Agenda

- Introduction & Credits
- Basic Searching & Browsing
- Result Options
- Structure Summary Page
- Advanced Searching
- Tools & Education
- Summary
- Exercises



Linking to Domain data, eFamily

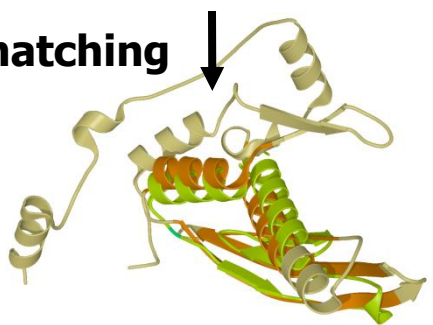
PDBChem ligand data



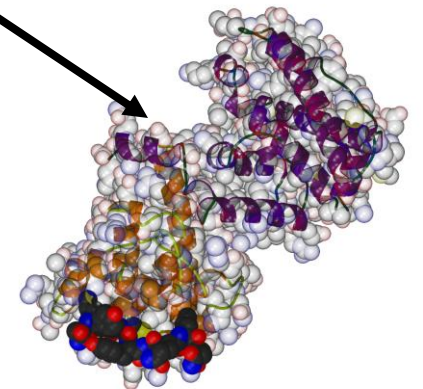
Electron Density Visualisation



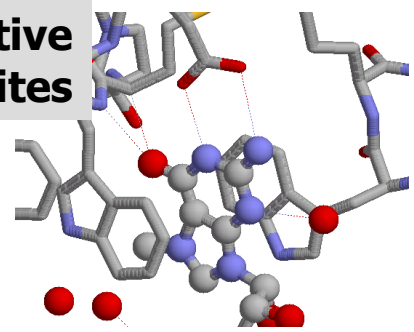
Fold matching



PISA biological assemblies



Active sites



Surface Matching

Protein Databank in Europe (PDBe) group

- Is one of the [four sites](#) around the world that where 3D structures may be deposited.
- Provides [stable](#) and [clean repository](#) of macromolecular structure data.
- [Has services](#) that allow users [to access, search and retrieve](#) structural data from a single web access point.

P D B *e*
PROTEIN DATA BANK **E**UROPE