

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

**RCSB PDB** Deposit Search Visualize Analyze Download Learn More MyPDB Login

**RCSB PDB** An Information Portal to 108789 Biological Macromolecular Structures

Advanced Search | Browse by Annotations

PDBe-101 EMDatabank Structural Biology Knowledgebase

Facebook Twitter YouTube LinkedIn

**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.

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.

**Structure and Health Focus: HIV**

HIV Resources High School Video Challenge

**May Molecule of the Month**

**Titin**

Titin is a large protein that is found in muscle tissue. It is responsible for the elasticity of muscle fibers. The image shows a 3D model of the protein structure, highlighting its long, thin, and flexible nature.

**PDB (Protein Data Bank)** یک مرکز جهانی ذخیره اطلاعات ساختاری مولکولهای زیستی بوده که هم اکنون با همکاری محققین بیوانفورماتیک ساختاری (RCSB: Research collaboration for structural bioinformatics) مدیریت میشود. هر پروتئین در PDB با یک کد ویژه که شامل حرف و ارقام است ذخیره میشود.

RCSB PDB Deposit Search Visualize Analyze Download Learn More MyPDB Login

**RCSB PDB** An Information Portal to 108789 Biological Macromolecular Structures

Advanced Search | Browse by Annotations | Search History (1) | Previous Results (1)

PDBe-101 EMDatabank Structural Biology Knowledgebase

Facebook Twitter YouTube LinkedIn

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

**CRYSTAL STRUCTURE OF THE TYROSINE KINASE DOMAIN OF FIBROBLAST GROWTH FACTOR RECEPTOR 1**

1FGK Display Files Download Files Download Citation

DOI:10.2210/pdb1fgk/pdb

**Primary Citation**

Structure of the FGF receptor tyrosine kinase domain reveals a novel autoinhibitory mechanism.

Mohammadi, M. A.; Schlessinger, J. P.; Hubbard, S. R. P.

Journal: (1999) Cell(Cambridge, Mass.) 96: 577-587

PubMed: 8752212

Search Related Articles in PubMed

**PubMed Abstract**

The crystal structure of the tyrosine kinase domain of fibroblast growth factor receptor 1 (FGFR1K) has been determined in its unliganded form to 2.0 angstroms resolution and in complex with with an ATP analog to 2.3 angstroms A resolution. Several...

[ Read More & Search PubMed Abstracts ]

**Molecular Description** Hide

Classification: Phosphotransferase

Structure Weight: 70847.88

**Biological Assembly**

3D View: JSmol or PV More Images

Symmetry: C2 view

Stoichiometry: Homo 2-mer - A2

www.rcsb.org/pdb/explore/explore.do?structureId=1FGK

RCSB PDB Deposit Search Visualize Analyze Download Learn More MyPDB Login

RCSB PDB PROTEIN DATA BANK An Information Portal to 114402 Biological Macromolecular Structures

Search by PDB ID, author, macromolecule, sequence, or ligands

Advanced Search | Browse by Annotations | Search History (1) | Previous Results (1)

Structure Summary 3D View Annotations Sequence Sequence Similarity Structure Similarity Experiment Literature

Biological Assembly 1

### 1FGK

CRYSTAL STRUCTURE OF THE TYROSINE KINASE DOMAIN OF FIBROBLAST GROWTH FACTOR RECEPTOR 1

DOI: 10.2210/pdb/1fgk/pdb

Classification: PHOSPHOTRANSFERASE

Deposited: 1997-02-08 Released: 1997-07-23

Deposition author(s): Mohammadi, M., Schlessinger, J., Hubbard, S.R.

Organism: Homo sapiens

Expression System: unidentified baculovirus

Mutation(s): 3

Structural Biology Knowledgebase: 1FGK (8 models >23 annotations) 3898 hits

Experimental Data Snapshot wwPDB Validation

Method: X-RAY DIFFRACTION

Display Files Download Files

- FASTA Sequence
- PDB File (Text)
- PDB File (gz)
- PDB/mmCIF File
- PDB/mmCIF File (gz)
- PDBML/XML File
- PDBML/XML File (gz)
- Structure Factor (Text)
- Structure Factor (gz)
- Biological Assembly (gz) (A)

طبقه بندی ساختارهای پروتئینی

RCSB PDB Deposit Search Visualize Analyze Download Learn More MyPDB Login

RCSB PDB PROTEIN DATA BANK

Structure Summary 3D View Annotations Sequence Sequence Similarity Structure Similarity Experiment Literature

### 1FGK

CRYSTAL STRUCTURE OF THE TYROSINE KINASE DOMAIN OF FIBROBLAST GROWTH FACTOR RECEPTOR 1

Macromolecule Annotations for the Entities in PDB 1FGK

Domain Annotation: SCOP Classification SCOP Database (version: 1.75) Homepage

Chains	Domain Info	Class	Fold	Superfamily	Family	Domain	Species
A	d1fgka_	Alpha and beta proteins (a+b)	Protein kinase-like (PK-like)	Protein kinase-like (PK-like)	Protein kinases, catalytic subunit	Fibroblast growth factor receptor 1	Human (Homo sapiens) [Taxid: 9606]
B	d1fgkb_	Alpha and beta proteins (a+b)	Protein kinase-like (PK-like)	Protein kinase-like (PK-like)	Protein kinases, catalytic subunit	Fibroblast growth factor receptor 1	Human (Homo sapiens) [Taxid: 9606]

Domain Annotation: CATH CATH Database (version 4.0.0) Homepage

Chains	Domain	Class	Architecture	Topology	Homology
A1	1fgkA01	Alpha Beta	2-Layer Sandwich	Phosphorylase Kinase: domain 1	Phosphorylase Kinase: domain 1

## انتخاب Sequence

CSB PDB Deposit Search Visualize Analyze Download Learn More MyPDB Login

Mouse over an annotation to see more details. Click on any annotation to enable Jmol.

Annotations	Details
Domain Assignment: <b>SCOP</b> [hide] [reference]	1F1GK Fibroblast growth factor receptor 1: 278 residues
Secondary Structure: <b>DSPP</b> [hide] [reference]	36% helical (13 helices; 114 residues) 12% beta sheet (10 strands; 39 residues)

Sequence Chain View

**PDB** PROTEIN DATA BANK

CRYSTAL STRUCTURE OF THE TYROSINE KINASE DOMAIN OF FIBROBLAST GROWTH FACTOR RECEPTOR 1

DOI: 10.2210/pdb/1fgk/pdb

Primary Citation: Structure of the FGFR tyrosine kinase domain. Mohammadi M, Sankaranarayanan V, Huber R. Journal: 1999 Cell (Cambridge Mass.) 96: 27-35. Published: 17/02/1999. Search Related Articles to: Published 2000.

Published Abstract: The crystal structure of the tyrosine kinase domain of fibroblast growth factor receptor 1 (FGFR1) is presented. The structure is a dimer of two monomers, each consisting of a tyrosine kinase domain and a fibroblast growth factor binding domain. The tyrosine kinase domain is shown in a ribbon representation, with the fibroblast growth factor binding domain shown as a surface. The structure is colored by domain.

Biological Assembly Image for 1FGK: CRYSTAL STRUCTURE OF THE TYROSINE KINASE DOMAIN OF FIBROBLAST GROWTH FACTOR RECEPTOR 1. Ribbon colors are colored from the N-terminal to the C-terminal using a rainbow (spectrum) color gradient.

Download Image

1FGK Display Files \* Download Files \* Download Citation \*

Biological Assembly 1

3D View (Jmol) or PDB-1 Images

Symmetry C2 view

کلیک بر روی ساختار سه بعدی پروتئین و مشاهده تصویر پروتئین

RCSB PDB Deposit Search Visualize Analyze Download Learn More MyPDB Login

PROTEIN DATA BANK Macromolecular Structures

Search by PDB ID, author, macromolecule, sequence, or ligands  
Advanced Search | Browse by Annotations

PDB-101 EMDatabank Structure Biology Knowledgebase

Summary 3D View Sequence Annotations Seq. Similarity 3D Similarity Literature Bib. & Chem. Methods Links

CRYSTAL STRUCTURE OF THE E. COLI TOLB PROTEIN 1CRZ

DOI:10.2210/pdb/1crz/pdb

**Primary Citation**  
Structure of the Escherichia coli TolB protein determined by MAD methods at 1.95 Å resolution.  
Abergel, C.P., Bouvet, E.P., Claverie, J.M.P., Brown, K.P., Rigal, A.P., Lazdunski, C.P., Benedetti, H.P.  
Journal: (1998) Structure Fold Des 7: 1291-1300  
PubMed: 10545334

**PubMed Abstract**  
The periplasmic protein TolB from Escherichia coli is part of the Tol-PAL (peptidoglycan-associated lipoprotein) multimeric complex used by group A colicins to penetrate and kill cells. TolB homologues are found in many gram-negative bacteria and the Tol-PAL system is thought

FASTA Sequence  
PDB File  
PDB File (Header)  
PDB File  
PDB File (Header)  
PDBML/JML File  
PDBML/JML File (Header)

www.rcsb.org/pdb/files/fasta.txt?structureIdList=1CRZ

```
>1CRZ:A|PDBID|CHAIN|SEQUENCE
DSGVDSDGRPIGVVFPQMAQPGGAAPEDIGGIVAADLRNSGKFNELDRARLPQOPGSAQEVQPAAMSAALGIDAVVYGOVTN
PDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQLRYAGHTASDEVFEKLTGKIGAFRTRIAIYVYQTNWGGQPPYELRVSIDY
DGYNQFVYHRSPOQLMSPAMSPDGSKLAVTFESGRSALVIQTLANGAVYQVASFPRHNGAPAFSPDGSKLAFALSKTGS
LMLYVMDLASGQIRQVTDGRSNWTEPTMFPDSQMLAFTSDQAGRPOYKVNINGGAPORITWEGSQWQADAVSSDGKFMW
MYSNNGGQOHIKQDLATGGVQLSSTFLDETPELAPNGTMIYSSSQMGSVLMLVSTDGRFKARLPATDGOVKFPAMS
PYL
```

RCSB PDB Deposit Search Visualize Analyze Download Learn More MyPDB Login

PROTEIN DATA BANK Macromolecular Structures

Search by PDB ID, author, macromolecule, sequence, or ligands  
Advanced Search | Browse by Annotations | Search History (1) | Previous Results (1)

PDB-101 EMDatabank Structure Biology Knowledgebase

Summary 3D View Sequence Annotations Seq. Similarity 3D Similarity Literature Bib. & Chem. Methods Links

CRYSTAL STRUCTURE OF THE E. COLI TOLB PROTEIN 1CRZ

NOTE: Use your mouse to drag, rotate, and zoom in and out of the structure.

Structure Details

Structure: Biological Assembly 1  
Symmetry Type: Global Symmetry  
Symmetry: C1  
Stoichiometry: A


Select Orientation  
Front

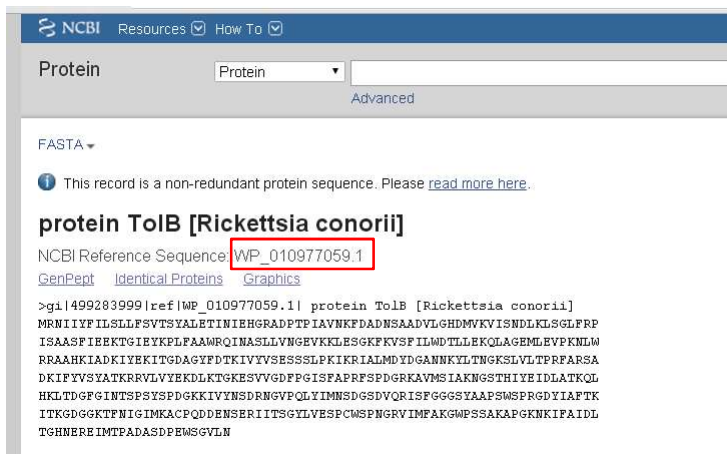
Select Display Mode

Secondary Structure  
Subunit  
Symmetry

Style: Cartoon  
Color: Secondary Structure  
Surface: None

H-Bonds  SS Bonds  
 Rotation  Black Background  
 Polyhedron  Axes





NCBI Protein Resources How To

Protein Protein Advanced

FASTA

This record is a non-redundant protein sequence. Please [read more here](#).

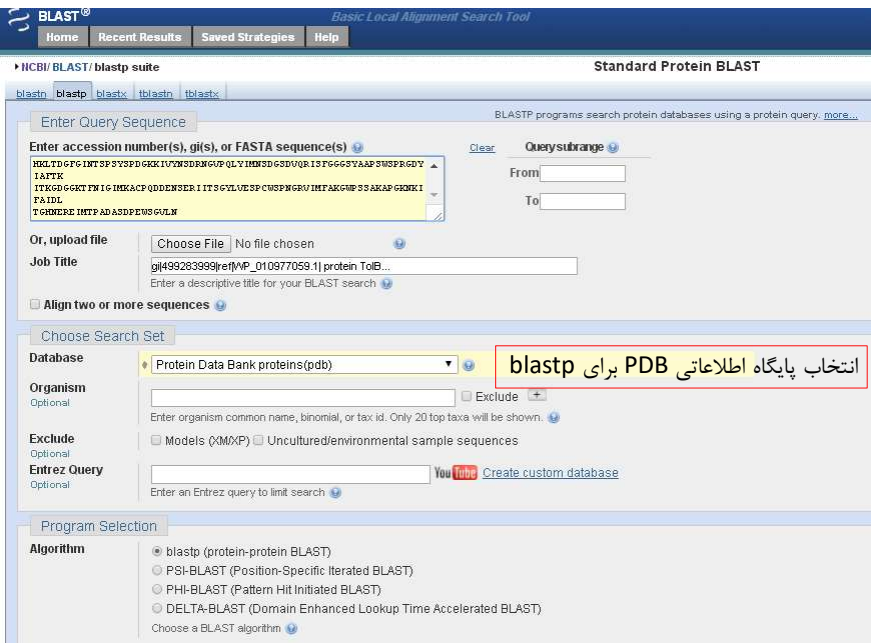
**protein TolB [Rickettsia conorii]**

NCBI Reference Sequence: **WP\_010977059.1**

[GenPept](#) [Identical Proteins](#) [Graphics](#)

```
>gi|499283999|ref|WP_010977059.1| protein TolB [Rickettsia conorii]
MRNIIYFLLSLLFSVTSYALETINIEHGRADPTPIAVNKPDAADNSAADVLGDMVKVISMDLKLSSGLFRP
ISAAASFIEBKTGIEYKELFAAWRQIMASLLVNGEVKLESQKFKVSPILMDTLLLEKQLLAGEMLEVPKMLM
RRAAHKIADKIYEKITGDAGYFDTKIVVSESSLPKIKRIALMDYDGANMKYLTNGKSLVLTFRFARSA
DKLIPVVSYATKRRVLVYEKDLTKGKESVVDPEPGEISFAPRFPDGRKAVMSIAKNGSTHIYEIDLATKQL
HKLTDGFGINTSFSYSPDGKKIVYNSDRMGVPLVIMNSDGSIVQRISFSGGSSYAAPSMSPRGDYIAFTK
ITKDGDKTFNIGIMKACPDDENSERIIITSGVLVESPCWSPNGRVIMFAKQWPSAKAPGKNKIFAILD
TGHNEREIMTFADASDFEMSGVLM
```

گرفتن توالی پروتئینی پروتئین TolB با شماره دستیابی WP\_010977059.1 از بخش پروتئین پایگاه NCBI انجام Blastp جهت یافتن پروتئین های همولوگ با این پروتئین



BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/BLAST/blastp suite Standard Protein BLAST

blastn blastp blastx tblastn tblastx

BLASTP programs search protein databases using a protein query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)  Clear

```
HKLTDSFGINTSPSYSPDGKKIVYNSDRMGVPLVIMNSDGSIVQRISFSGGSSYAAPSMSPRGDY
IATTK
ITKDGDKTFNIGIMKACPDDENSERIIITSGVLVESPCWSPNGRVIMFAKQWPSAKAPGKNKIFAILD
TGHNEREIMTFADASDFEMSGVLM
```

From

To

Or, upload file  No file chosen

Job Title  Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database  **انتخاب پایگاه اطلاعاتی PDB برای blastp**

Organism  Exclude

Exclude  Models (X/M&X/P)  Uncultured/environmental sample sequences

Entrez Query  [YouTube](#) [Create custom database](#)

Program Selection

Algorithm

- blastp (protein-protein BLAST)
- PSI-BLAST (Position-Specific Iterated BLAST)
- PHI-BLAST (Pattern Hit Initiated BLAST)
- DELTA-BLAST (Domain Enhanced Lookup Time Accelerated BLAST)

Choose a BLAST algorithm

Descriptions

Sequences producing significant alignments:  
 Select: All None Selected: 0

Alignments [Download](#) [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Chain A, Crystal Structure Of TolB Protein From <i>Yersinia Pestis</i> Co92	175	175	86%	7e-49	31%	<a href="#">4PWZ_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of TolB/tolC Complex From <i>Yersinia Pestis</i>	174	174	85%	8e-49	31%	<a href="#">4R6Q_A</a>
<input type="checkbox"/> Chain A, The Structure Of TolB, An Essential Component Of The Tol-Dependent Translocation System And Its Interactions With The Translocation Domain Of Colicin E9	169	169	89%	9e-47	29%	<a href="#">1C9K_A</a>
<input type="checkbox"/> Chain A, The Crystal Structure Of The TolB Box Of Colicin A In Complex With TolB Reveals Important Differences In The Recruitment Of The Common TolB Translocation Portal Used By Group 1	169	169	89%	1e-46	29%	<a href="#">3AX_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of The TolB(G201C)-colicinE9 The Peptide(433c) Complex	167	167	85%	3e-46	30%	<a href="#">4LM_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of Processed TolB In Complex With PstI	167	167	85%	4e-46	30%	<a href="#">2V98L_A</a>
<input type="checkbox"/> Chain B, Crystal Structure Of Processed TolB In Complex With PstI	167	167	85%	6e-46	30%	<a href="#">2V98L_B</a>
<input type="checkbox"/> Chain A, Crystal Structure Of TolBPAL COMPLEX	166	166	85%	6e-46	30%	<a href="#">2HG5_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of The E. Coli TolB Protein	160	160	78%	6e-44	30%	<a href="#">1CRZ_A</a>
<input type="checkbox"/> Chain A, The Structure Of Putative TolB From <i>Agrobacterium Tumefaciens</i>	64.3	64.3	35%	3e-11	29%	<a href="#">2QJH_A</a>
<input type="checkbox"/> Chain A, Oligosaccharyltransferase In Complex With Manganese	33.9	33.9	35%	0.31	22%	<a href="#">3PE7_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of Puromycin Hydrolase	32.7	32.7	31%	0.86	23%	<a href="#">3AZO_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of Puromycin Hydrolase S511a Mutant	32.0	32.0	31%	1.2	23%	<a href="#">3AZP_A</a>
<input type="checkbox"/> Chain A, Tricorn Protease In Complex With Tetraspide Chromomethyl Ketone Derivative	31.6	31.6	31%	1.8	22%	<a href="#">1NED_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of The Tricorn Protease	31.6	31.6	31%	1.9	22%	<a href="#">1K32_A</a>
<input type="checkbox"/> Chain A, Structural And Mechanistic Analysis Of Two Proxyl Endopeptidases: Role Of Inter-Domain Dynamics In Catalysis And Specificity	30.0	30.0	9%	4.8	30%	<a href="#">2BKJ_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of Oligosaccharyltransferase (Vpr0088) From <i>Vibrio Parahaemolyticus</i> , Northeast Structural Genomics Consortium Target Vpr198	29.3	29.3	5%	8.2	38%	<a href="#">3C5M_A</a>

**blastp خروجی**

Sequences producing significant alignments:  
 Select: All None Selected: 10

Alignments [Download](#) [GenPept](#) [Graphics](#) [Distance tree of results](#) [Multiple alignment](#)

Description	Max score	Total score	Query cover	E value	Ident	Accession
<input checked="" type="checkbox"/> Chain A, Crystal Structure Of TolB Protein From <i>Yersinia Pestis</i> Co92	175	175	86%	7e-49	31%	<a href="#">4PWZ_A</a>
<input checked="" type="checkbox"/> Chain A, Crystal Structure Of TolB/tolC Complex From <i>Yersinia Pestis</i>	174	174	85%	8e-49	31%	<a href="#">4R6Q_A</a>
<input checked="" type="checkbox"/> Chain A, The Structure Of TolB, An Essential Component Of The Tol-Dependent Translocation System And Its Interactions With The Translocation Domain Of Colicin E9	169	169	89%	9e-47	29%	<a href="#">1C9K_A</a>
<input checked="" type="checkbox"/> Chain A, The Crystal Structure Of The TolB Box Of Colicin A In Complex With TolB Reveals Important Differences In The Recruitment Of The Common TolB Translocation Portal Used By Group 1	169	169	89%	1e-46	29%	<a href="#">3AX_A</a>
<input checked="" type="checkbox"/> Chain A, Crystal Structure Of The TolB(G201C)-colicinE9 The Peptide(433c) Complex	167	167	85%	3e-46	30%	<a href="#">4LM_A</a>
<input checked="" type="checkbox"/> Chain A, Crystal Structure Of Processed TolB In Complex With PstI	167	167	85%	4e-46	30%	<a href="#">2V98L_A</a>
<input checked="" type="checkbox"/> Chain B, Crystal Structure Of Processed TolB In Complex With PstI	167	167	85%	6e-46	30%	<a href="#">2V98L_B</a>
<input checked="" type="checkbox"/> Chain A, Crystal Structure Of TolBPAL COMPLEX	166	166	85%	6e-46	30%	<a href="#">2HG5_A</a>
<input checked="" type="checkbox"/> Chain A, Crystal Structure Of The E. Coli TolB Protein	160	160	78%	6e-44	30%	<a href="#">1CRZ_A</a>
<input checked="" type="checkbox"/> Chain A, The Structure Of Putative TolB From <i>Agrobacterium Tumefaciens</i>	64.3	64.3	35%	3e-11	29%	<a href="#">2QJH_A</a>
<input type="checkbox"/> Chain A, Oligosaccharyltransferase In Complex With Manganese	33.9	33.9	35%	0.31	22%	<a href="#">3PE7_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of Puromycin Hydrolase	32.7	32.7	31%	0.86	23%	<a href="#">3AZO_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of Puromycin Hydrolase S511a Mutant	32.0	32.0	31%	1.2	23%	<a href="#">3AZP_A</a>
<input type="checkbox"/> Chain A, Tricorn Protease In Complex With Tetraspide Chromomethyl Ketone Derivative	31.6	31.6	31%	1.8	22%	<a href="#">1NED_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of The Tricorn Protease	31.6	31.6	31%	1.9	22%	<a href="#">1K32_A</a>
<input type="checkbox"/> Chain A, Structural And Mechanistic Analysis Of Two Proxyl Endopeptidases: Role Of Inter-Domain Dynamics In Catalysis And Specificity	30.0	30.0	9%	4.8	30%	<a href="#">2BKJ_A</a>
<input type="checkbox"/> Chain A, Crystal Structure Of Oligosaccharyltransferase (Vpr0088) From <i>Vibrio Parahaemolyticus</i> , Northeast Structural Genomics Consortium Target Vpr198	29.3	29.3	5%	8.2	38%	<a href="#">3C5M_A</a>

**انتخاب توالی های دارای E-value کم برای انطباق چندتایی  
 کلیک بر روی Multiple alignment**



<a href="#">4PMZ_A</a>	1	[ 3] XVRIEITQGVDSARP IGVVPPFKMXGPTTPEE IGAIVGADLRNSGKFNPIDAARXPQQPSTAAEVTPAAMTALGID	79	
<a href="#">4R40_A</a>	1	[ 3]-VRIEITQGVDSARP IGVVPPFKMXGPTTPEE IGAIVGADLRNSGKFNPIDAARXPQQPSTAAEVTPAAMTALGID	78	
<a href="#">1C5K_A</a>	1	[22] EVRIVIDSGVDSGRPIGVVPPQMAAGPGAAPED IGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAMSALGID	98	
<a href="#">3IAX_A</a>	1	[21] EVRIVIDSGVDSGRPIGVVPPQMAAGPGAAPED IGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAMSALGID	97	
<a href="#">4JML_A</a>	1	MVRIVIDSGVDSGRPIGVVPPQMAAGPGAAPED IGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAMSALGID	76	
<a href="#">2M8_B_A</a>	1	EVRIVIDSGVDSGRPIGVVPPQMAAGPGAAPED IGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAMSALGID	76	
<a href="#">2M8_B_B</a>	1	EVRIVIDSGVDSGRPIGVVPPQMAAGPGAAPED IGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAMSALGID	76	
<a href="#">2HOS_A</a>	1	MVRIVIDSGVDSGRPIGVVPPQMAAGPGAAPED IGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAMSALGID	76	
<a href="#">1CRZ_A</a>	1	-----DSGVDSGRPIGVVPPQMAAGPGAAPED IGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAMSALGID	70	
<a href="#">2OJH_A</a>		-----		
<a href="#">4PMZ_A</a>	80	AVVVGQVQPSADGSYVVSYQLVDTSGSAGS ILLAQNYKVTQMLRYSAAHTVSDEVFEKL-TG IKGAFRTR I-AYVVKTMG	157	
<a href="#">4R40_A</a>	79	AVVVGQVQPSADGSYVVSYQLVDTSGSAGS ILLAQNYKVTQMLRYSAAHTVSDEVFEKL-TG IKGAFRTR I-AYVVKTMG	156	
<a href="#">1C5K_A</a>	99	AVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQMLRYAGHTASDEVFEKL-TG IKGAFRTR I-AYVVKTMG	175	
<a href="#">3IAX_A</a>	98	AVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQMLRYAGHTASDEVFEKL-TG IKGAFRTR I-AYVVKTMG	175	
<a href="#">4JML_A</a>	77	AVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQMLRYAGHTASDEVFEKL-TG IKGAFRTR I-AYVVKTMG	154	
<a href="#">2M8_B_A</a>	77	AVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQMLRYAGHTASDEVFEKL-TG IKGAFRTR I-AYVVKTMG	154	
<a href="#">2M8_B_B</a>	77	AVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQMLRYAGHTASDEVFEKL-TG IKGAFRTR I-AYVVKTMG	154	
<a href="#">2HOS_A</a>	77	AVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQMLRYAGHTASDEVFEKL-TG IKGAFRTR I-AYVVKTMG	154	
<a href="#">1CRZ_A</a>	71	AVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQMLRYAGHTASDEVFEKL-TG IKGAFRTR I-AYVVKTMG	148	
<a href="#">2OJH_A</a>	1	-----GHXKQSTLHTRLsTGPGGSXRSS IeIFNIRTRK	33	
<a href="#">4PMZ_A</a>	158	GKFPHELRSVDYDGYNQFVHRSPPELXSPAMSPDGSKLIAYVT	FESGKSALVIQTLANGAIRQVASFPRHNGAPAF	233
<a href="#">4R40_A</a>	157	GKFPHELRSVDYDGYNQFVHRSPPELXSPAMSPDGSKLIAYVT	FESGKSALVIQTLANGAIRQVASFPRHNGAPAF	232
<a href="#">1C5K_A</a>	177	GQFPYELRSVDYDGYNQFVHRSPQPLMSPAMSPDGSKLIAYVT	FESGRSALVIQTLANGAVRQVASFPRHNGAPAF	252
<a href="#">3IAX_A</a>	176	GQFPYELRSVDYDGYNQFVHRSPQPLMSPAMSPDGSKLIAYVT	FESGRSALVIQTLANGAVRQVASFPRHNGAPAF	251
<a href="#">4JML_A</a>	155	GQFPYELRSVDYDGYNQFVHRSPQPLMSPAMSPDGSKLIAYVT	FESGRSALVIQTLANGAVRQVASFPRHNGAPAF	230
<a href="#">2M8_B_A</a>	155	GQFPYELRSVDYDGYNQFVHRSPQPLMSPAMSPDGSKLIAYVT	FESGRSALVIQTLANGAVRQVASFPRHNGAPAF	230
<a href="#">2M8_B_B</a>	155	GQFPYELRSVDYDGYNQFVHRSPQPLMSPAMSPDGSKLIAYVT	FESGRSALVIQTLANGAVRQVASFPRHNGAPAF	230

<a href="#">1C5K_A</a>	253	SPDGSKLAFALSKTGSMLLYMDLASGQIRQVTDGRSNTEPTWFPDSQNLAFSTDAQGRPVYKVINNGGAPQRITWEG	332		
<a href="#">3IAX_A</a>	252	SPDGSKLAFALSKTGSMLLYMDLASGQIRQVTDGRSNTEPTWFPDSQNLAFSTDAQGRPVYKVINNGGAPQRITWEG	331		
<a href="#">4JML_A</a>	231	SPDGSKLAFALSKTGSMLLYMDLASGQIRQVTDGRSNTEPTWFPDSQNLAFSTDAQGRPVYKVINNGGAPQRITWEG	310		
<a href="#">2M8_B_A</a>	231	SPDGSKLAFALSKTGSMLLYMDLASGQIRQVTDGRSNTEPTWFPDSQNLAFSTDAQGRPVYKVINNGGAPQRITWEG	310		
<a href="#">2M8_B_B</a>	231	SPDGSKLAFALSKTGSMLLYMDLASGQIRQVTDGRSNTEPTWFPDSQNLAFSTDAQGRPVYKVINNGGAPQRITWEG	310		
<a href="#">2HOS_A</a>	231	SPDGSKLAFALSKTGSMLLYMDLASGQIRQVTDGRSNTEPTWFPDSQNLAFSTDAQGRPVYKVINNGGAPQRITWEG	310		
<a href="#">1CRZ_A</a>	225	SPDGSKLAFALSKTGSMLLYMDLASGQIRQVTDGRSNTEPTWFPDSQNLAFSTDAQGRPVYKVINNGGAPQRITWEG	304		
<a href="#">2OJH_A</a>	137	SPDGKSFYTCGIRDQVDF IYSXD IDSGVETLTHGGRNDGPDYSPDGRWYFNSSTRGQXQIMRVRVDGSSVERITDSA	216		
<a href="#">4PMZ_A</a>	314	SQMQADVSSPDGKFLVLVSSNGGA	QHIAKQDLETGAVQVLTDTL	LDETPSLAPNGTXYIYSSSQGLGSVLLVLS	387
<a href="#">4R40_A</a>	313	SQMQADVSSPDGKFLVLVSSNGGA	QHIAKQDLETGAVQVLTDTL	LDETPSLAPNGTXYIYSSSQGLGSVLLVLS	386
<a href="#">1C5K_A</a>	333	SQMQADVSSDGKFMVMVSSNGGQ	QHIAKQDLATGGVQVLSSTF	LDETPSLAPNGTXYIYSSSQGMGSVLLVLS	406
<a href="#">3IAX_A</a>	332	SQMQADVSSDGKFMVMVSSNGGQ	QHIAKQDLATGGVQVLSSTF	LDETPSLAPNGTXYIYSSSQGMGSVLLVLS	405
<a href="#">4JML_A</a>	311	SQMQADVSSDGKFMVMVSSNGGQ	QHIAKQDLATGGVQVLSSTF	LDETPSLAPNGTXYIYSSSQGMGSVLLVLS	384
<a href="#">2M8_B_A</a>	311	SQMQADVSSDGKFMVMVSSNGGQ	QHIAKQDLATGGVQVLSSTF	LDETPSLAPNGTXYIYSSSQGMGSVLLVLS	384
<a href="#">2M8_B_B</a>	311	SQMQADVSSDGKFMVMVSSNGGQ	QHIAKQDLATGGVQVLSSTF	LDETPSLAPNGTXYIYSSSQGMGSVLLVLS	384
<a href="#">2HOS_A</a>	311	SQMQADVSSDGKFMVMVSSNGGQ	QHIAKQDLATGGVQVLSSTF	LDETPSLAPNGTXYIYSSSQGMGSVLLVLS	384
<a href="#">1CRZ_A</a>	305	SQMQADVSSDGKFXVXVSSNGGQ	QHIAKQDLATGGVQVLSSTF	LDETPSLAPNGTXYIYSSSQGMGSVLLVLS	378
<a href="#">2OJH_A</a>	217	YGDWFPHPSPSGDKVFPVSYDADV [8] VRVQLXDIDGGVETLFDLF [4] TXMSPMSPDGDEFAYRYPVEGS-----			297
<a href="#">4PMZ_A</a>	388	TDGRFKARLPATDGGVKFPAMSPYL			412
<a href="#">4R40_A</a>	387	TDGRFKARLPATDGGVKFPAMSPYL			411
<a href="#">1C5K_A</a>	407	TDGRFKARLPATDGGVKFPAMSPYL [8]			439
<a href="#">3IAX_A</a>	406	TDGRFKARLPATDGGVKFPAMSPYL [8]			438
<a href="#">4JML_A</a>	385	TDGRFKARLPATDGGVKFPAMSPYL [8]			417
<a href="#">2M8_B_A</a>	385	TDGRFKARLPATDGGVKFPAMSPYL			409
<a href="#">2M8_B_B</a>	385	TDGRFKARLPATDGGVKFPAMSPYL			409
<a href="#">2HOS_A</a>	385	TDGRFKARLPATDGGVKFPAMSPYL [6]			415
<a href="#">1CRZ_A</a>	379	TDGRFKARLPATDGGVKFPAMSPYL			403

• خروجی انطباق چندتایی  
 • مناطق قرمز رنگ نشانگر  
 یک بخش محافظت شده  
 است که در همه پروتئینهای  
 فوق وجود دارد.

اگر در صفحه نتایج انطباق چندتایی بر روی شماره دستیابی هر پروتئین کلیک کنید، وارد بخش Protein در NCBI می شود. به عنوان مثال اگر پروتئین با شماره دستیابی 4PWZ\_A انتخاب شود: وارد شدن به بخش Structure برای پروتئین

NCBI Resources How To Sign in to NCBI

Protein Search

Chain A, Crystal Structure Of Tolb Protein From Yersinia Pestis Co92  
PDB: 4PWZ\_A

Identical Proteins FASTA Graphics

Go to

LOCUS 4PWZ\_A 412 aa Linear BCT 04-APR-2014  
DEFINITION Chain A, Crystal Structure Of Tolb Protein From Yersinia Pestis Co92.  
ACCESSION 4PWZ\_A  
VERSION 4PWZ\_A GI:605604560  
DBSOURCE pdb: molecule 4PWZ, chain 65, release Apr 4, 2014;  
deposition: Mar 21, 2014;  
class: Protein Transport;  
source: Mmdb\_id: 118922, Pdb\_id 1: 4PWZ;  
Exp. method: X-Ray Diffraction.

KEYWORDS Yersinia pestis Co92  
SOURCE Yersinia pestis Co92  
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.  
REFERENCE Maltseva, N., Kim, Y., Osipiuk, J., Anderson, M.F. and Joachimiak, A.  
TITLE Crystal Structure Of Tolb Protein From Yersinia Pes

Protein 3D Structure  
Crystal Structure Of Tolb Protein From Yersinia Pestis Co92  
PDB: 4PWZ  
Source: Yersinia pestis Co92  
Method: X-Ray Diffraction  
Resolution: 1.73 Å

www.ncbi.nlm.nih.gov/Structure/mmdb/mmdbsrv.cgi?Dopt=s&uid=118922

NCBI National Center for Biotechnology Information

Structure Summary MMDB

PDB or MMDB ID Search

HOME SEARCH GUIDE Structure Home 3D Macromolecular Structures Conserved Domains Pubchem BioSystems Help

Crystal Structure of Tolb Protein From Yersinia Pestis Co92

MMDB ID: 118922 PDB ID: 4PWZ  
PDB Deposition Date: 2014/3/21  
Updated in MMDB: 04/2014  
Experimental Method: X-Ray Diffraction  
Resolution: 1.73 Å  
Source Organism: Yersinia pestis...  
Similar Structures: VAST+

Citation: Crystal structure of tol b protein from yersinia pestis co92.  
Maltseva N, Kim Y, Osipiuk J, Anderson WF, Joachimiak A  
No recorded citation in PubMed

Default: Biological Unit All Biological Units (2) Asymmetric Unit

Biological Unit: monomeric; determined by author, and by s

View structure و سپس کلیک روی Cn3D و دانلود نرم افزار Cn3D

Interactions Molecular Graphic View or Save 3D Structure

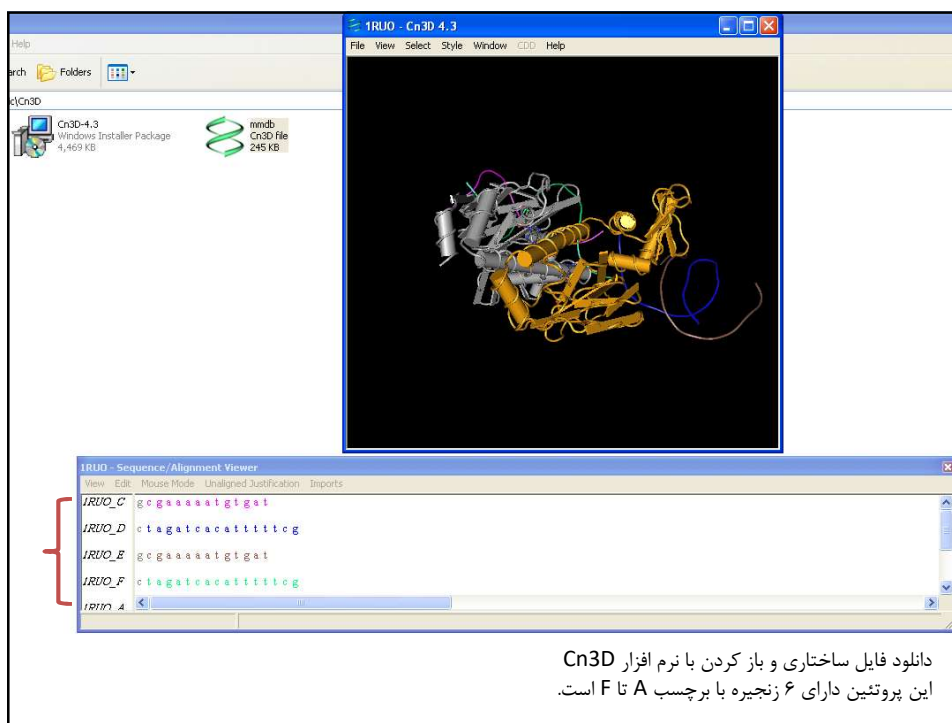
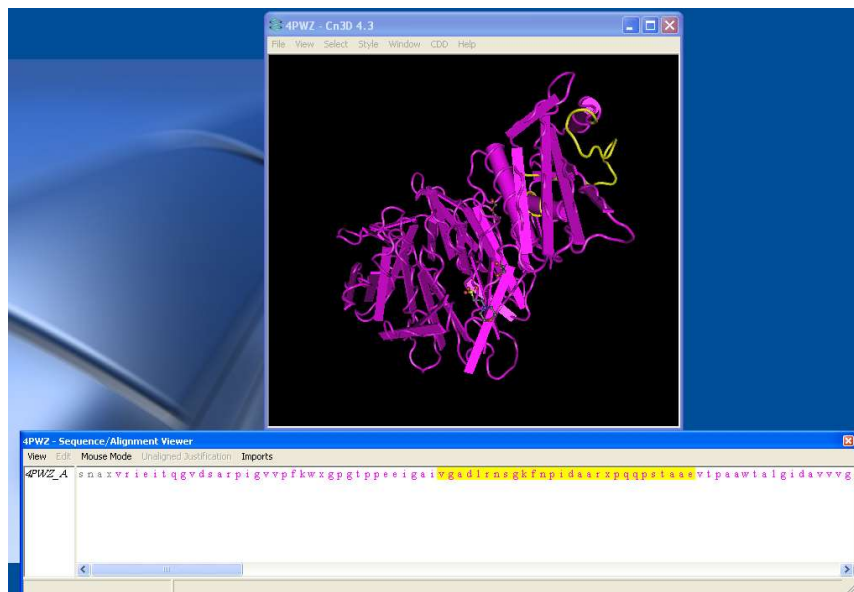
File Format: Cn3D  
Display As: 3D structure  
Data Set: Single 3D structure  
View structure  
Download Cn3D

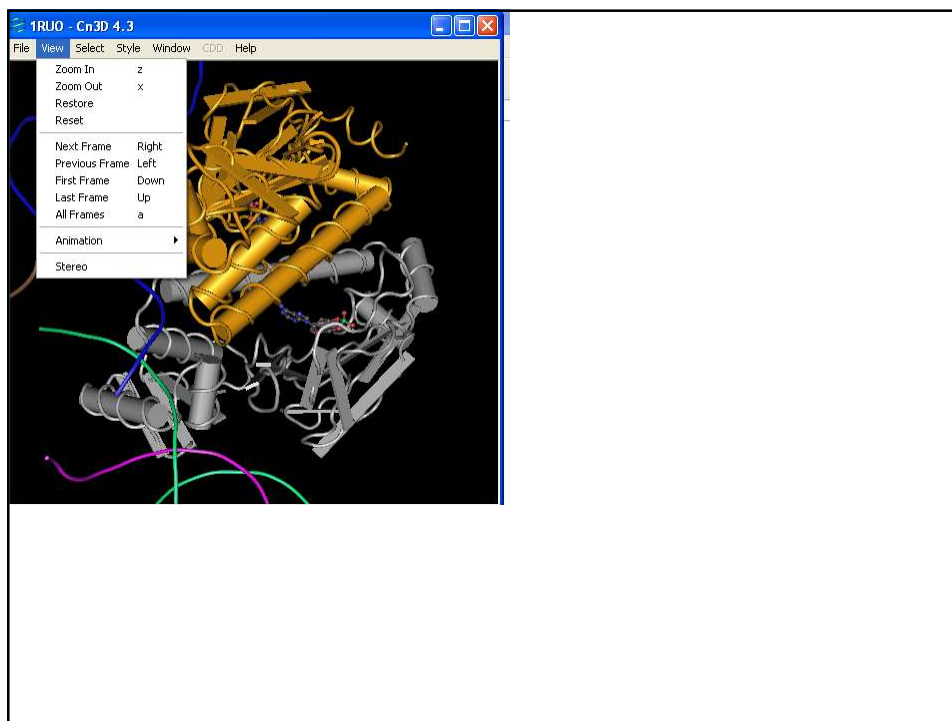
NOTICE  
In order to view this biological unit properly, please upgrade to Cn3D 4.3.

MMDB (Molecular modeling databases) یک پایگاه داده شامل ساختار سه بعدی ماکرومولکولها است. هر پروتئین در این پایگاه دارای یک کد به نام MMDB ID است. این پایگاه دارای نرم افزاری به نام Cn3D است که برای مشاهده ساختارهای سه بعدی استفاده میشود.



برای مشاهده پروتئین ابتدا با کلیک بر روی **View Structure**، فایل مربوط به اطلاعات ساختاری پروتئین دانلود می شود و به کمک نرم افزار **Cn3D** باز می شود. ابتدا باید نرم افزار دانلود و بر روی سیستم نصب گردد.





www.ncbi.nlm.nih.gov/Structure/mmdb/mmdbsrv.cgi?Doct=s&uid=118922

**NCBI** National Center for Biotechnology Information

**Structure Summary**  
MMDB

PDB or MMDB ID Search

HOME SEARCH GUIDE Structure Home 3D Macromolecular Structures Conserved Domains Pubchem BioSystems Help

MMDB ID: 118922 PDB ID: 4PWZ

PDB Deposition Date: 2014/3/21  
Updated in MMDB: 04/2014  
Experimental Method: X-Ray Diffraction  
Resolution: 1.73 Å  
Source Organism: *Yersinia pestis*...  
Similar Structures: VAST+

**Crystal Structure of TolB Protein From Yersinia Pestis Co92**

**Citation:**  
Crystal structure of tolB protein from yersinia pestis co92.  
Maltseva N, Kim Y, Osipiuk J, Anderson WF, Joachimiak A  
No recorded citation in PubMed

Default Biological Unit All Biological Units (2) Asymmetric Unit

Biological Unit: monomeric; determined by author, and by software (PISA)

کلیک بر روی VAST و یافتن ساختارهای مشابه

Interactions Molecular Graphic View or Save 3D Structure

File Format: Cn3D  
Display As: 3D structure  
Data Set: Single 3D structure  
View structure  
Download Cn3D

**NOTICE**  
In order to view this biological unit properly, please upgrade to Cn3D 4.3.

MMDB (Molecular modeling databases) یک پایگاه داده شامل ساختار سه بعدی ماکرومولکولها است. هر پروتئین در این پایگاه دارای یک کد به نام MMDB ID است. این پایگاه دارای نرم افزاری به نام Cn3D است که برای مشاهده ساختارهای سه بعدی استفاده میشود.

NCBI VAST+ Similar Structures

Crystal Structure Of Tolb Protein From Yersinia Pestic Co92

MMDb ID: 118922 (PDB ID: 4PWZ)  
 Biological unit 1: monomeric  
 Source organism: Yersinia pestis CO92  
 Number of proteins: 1 (PROTEIN TOLB)  
 Number of chemicals: 3 (Glycerol,2-(N-Morpholino)-Ethanesulfonic Acid,D... ▼)

Similar Structures

▼ Display filters

Showing 1 to 10 out of 180 structures

PDB ID	Description	Taxonomy	Aligned Protein	RMSD	Aligned Residues	Sequence Identity
1 4R40	Crystal Structure Of Tolb/pal Complex From Yersinia Pestic	Yersinia pestis C...	1	0.96Å	403	98%
2 2HQ5	Crystal Structure Of TolbPAL COMPLEX	Escherichia coli	1	1.02Å	404	84%
3 2W8B	Crystal Structure Of Processed Tolb In Complex With Pal	Others	1	1.05Å	404	83%
4 2MCS	A Bacteriophage Transcription Regulator Inhibits Bacterial Transcription Initiation ...	Xanthomonas ph...	1	1.69Å	36	13%
5 3IAX	The Crystal Structure Of The Tolb Box Of Colicin A In Complex With Tolb Reveals I...	Citrobacter freun...	1	1.73Å	395	84%

www.ncbi.nlm.nih.gov/pubmed/

PubMed

Using PubMed

- Structure
- Taxonomy
- ToolKit
- ToolKitAll
- ToolKitBook
- UniGene

PubMed Tools

- PubMed Mobile
- Single Citation Matcher
- Batch Citation Matcher
- Clinical Queries
- Topic-Specific Queries

More Resources

- MeSH Database
- Journals in NCBI Databases
- Clinical Trials
- E-Utilities (API)
- LinkOut

Structure

## جستجوی پروتئین Albumin در بخش Structure پایگاه NCBI

NCBI Resources How To Sign in to NCBI

Structure Structure albumin Search

Create alert Advanced Help


Summary 20 per page Sort by Proteins Send to: Filter your results:


All (279)  
NMR (36)  
X-ray (241)

Manage Filters

Search results

Items: 1 to 20 of 279

1.  [Crystal Structure Analysis of A 2'-O-2-\(Methylthio\)-Ethyl- Modified Oligodeoxynucleotide Duplex\(Dna\)](#)  
Taxonomy: synthetic construct  
Nucleic acids: 2 (DNA) modified: 2011-05-26  
MMDB ID: 50321 PDB ID: 1MLX  
[View in JCN3D](#) [PubMed](#)

2.  [Hsa-palmitic Acid-truc5\(ind\)2-\(Peptide Binding Protein\)](#)  
Taxonomy: Homo sapiens  
Proteins: 1 Chemicals: 9 modified: 2017-07-28  
MMDB ID: 152773 PDB ID: 5G1Y  
[View in JCN3D](#) [Similar Structures](#) [Proteins](#) [Conserved Domains](#) [PubChem Compound](#)

3.  [Human Serum Albumin-palmitic Acid-fe\(hn3pit\)2\(Immune System\)](#)  
Taxonomy: Homo sapiens  
Proteins: 1 Chemicals: 7 modified: 2017-07-28  
MMDB ID: 152772 PDB ID: 5G1X  
[View in JCN3D](#) [Similar Structures](#) [PubMed](#) [Proteins](#) [Conserved Domains](#) [PubChem Compound](#)

Refine your results - What's this?

**Protein Domain Families**  
Families (235)  
Superfamilies (259)

**Complexes**  
Protein-Protein (101)  
Protein-Chemical (203)

**Literature**  
PubMed (254)  
PMC (61)

**Taxonomy (272)**

Find related data  
Database: Select



Find related

NCBI National Center for Biotechnology Information

VAST+ Similar Structures 3D structural similarities among biological assemblies

PDB ID or MMDB ID New Search

5G1X: Human Serum Albumin-palmitic Acid-fe(hn3pit)2

Biological unit 1: monomeric  
Source organism: Homo sapiens  
Number of proteins: 1 (SERUM ALBUMIN)  
Number of chemicals: 7 (14-Piperidin-1-Yl-11-Oxa-13I^{3}-Thia-15,16I^{4}... ▼)

Similar Structures (124) Original VAST Download VAST+

Invariant substructure superposed All matching molecules superposed

Hide filters

Filter by number of matching molecules

Complete match, 1 proteins (124)

Filter by taxonomy

Eukaryota (122)

Others (2)

Apply Filter Selection

▲ Hide filters ?

Filter by number of matching molecules ?

Filter by taxonomy ?

● Complete match, 1 proteins (124)

☐ Eukaryota (122)

☐ Others (2)

Apply Filter Selection

Showing 1 to 10 out of 124 selected structures ?

Search within results: PDB ID or search word Go Reset ?

PDB ID	Description	Taxonomy	Aligned Protein	RMSD	Aligned Residues	Sequence Identity
1	SGIY Hsa-palmitic Acid-[ruc15(ind)]2-	Homo sapiens	1	0.17Å	581	100%
2	2BXP Human Serum Albumin Complexed With Myristate And Phenylbutazone	Homo sapiens	1	0.49Å	581	100%
3	5ID7 Crystal Structure Of Human Serum Albumin In Complex With Phosphorodithioate Derivative Of Myristoyl Cyclic Phosphatidic Acid (cpa)	Homo sapiens	1	0.49Å	259	100%
4	4LB9 X-ray Study Of Human Serum Albumin Complexed With Etoposide	Homo sapiens	1	0.50Å	314	100%
5	3CX9 Crystal Structure Of Human Serum Albumin Complexed With Myristic Acid And Lysophosphatidylethanolamine	Homo sapiens	1	0.51Å	581	100%
6	3UIV Human Serum Albumin-Myristate-Amantadine Hydrochloride Complex	Homo sapiens	1	0.52Å	581	100%

Filter by number of matching molecules ?

Filter by taxonomy ?

● Complete match, 1 proteins (124)

☑ Eukaryota (122)

☐ Others (2)

Apply Filter Selection

Showing 1 to 10 out of 122 selected structures ?

Search within results: PDB ID or search word Go Reset ?

PDB ID	Description	Taxonomy	Aligned Protein	RMSD	Aligned Residues	Sequence Identity
1	SGIY Hsa-palmitic Acid-[ruc15(ind)]2-	Homo sapiens	1	0.17Å	581	100%

Query structure **5GIX**      Aligned Molecules ?      Matched structure **SGIY**

SERUM ALBUMIN 581(581)

SERUM ALBUMIN 581(581)

\*Select schematic circles or highlighted molecule names to view matches

Visualize 3D structure superposition ?      View aligned sequences ?



Query ID	Query Name	Species	Query Length	Query RMSD	Match Length	Match RMSD	Match %
45	Shark Iglnar Variable Domain	Squalus acanthias/Homo sapiens	1	1.04Å	282	100%	
46	Extending The Half-life Of A Fab Fragment Through Generation Of A Humanised Anti-human Serum Albumin (hsa) Fv Domain: An Investigation Into The Correlation Between Affinity And Serum Half-life	Homo sapiens	1	1.47Å	313	98%	
47	Crystal Structure Of Equine Serum Albumin	Equus caballus	1	1.48Å	313	74%	
48	Human Serum Albumin With Bound Sulfate	Homo sapiens	1	1.49Å	321	98%	
49	Crystal Structure Of Equine Serum Albumin In Complex With Phosphorodithioate Derivative Of Myristoyl Cyclic Phosphatidic Acid (cpa)	Equus caballus	1	1.49Å	309	71%	
50	X-ray Study Of Human Serum Albumin Complexed With Idarubicin	Homo sapiens	1	1.55Å	282	90%	

بررسی ساختاری آلبومین متصل شده به یک داروی شیمی درمانی در مقایسه با آلبومین متصل به پالمیتیک اسید

این بخش از توالی از نظر ساختاری در دو پروتئین به خوبی بر هم منطبق هستند.

این بخش از توالی از نظر ساختاری در دو پروتئین به خوبی بر هم منطبق نیستند.