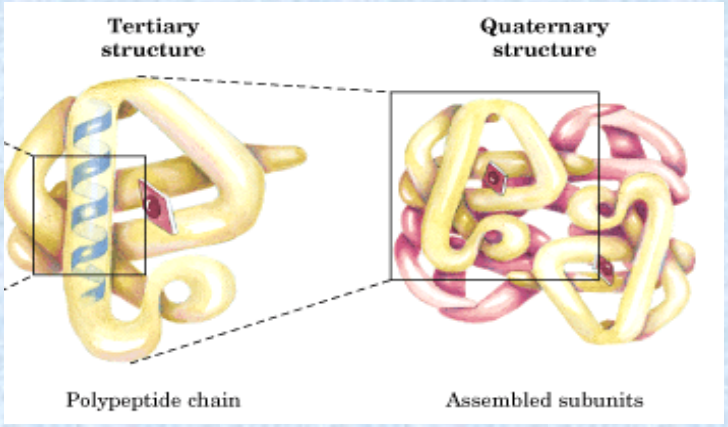
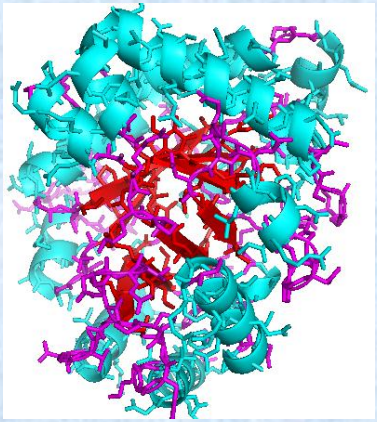
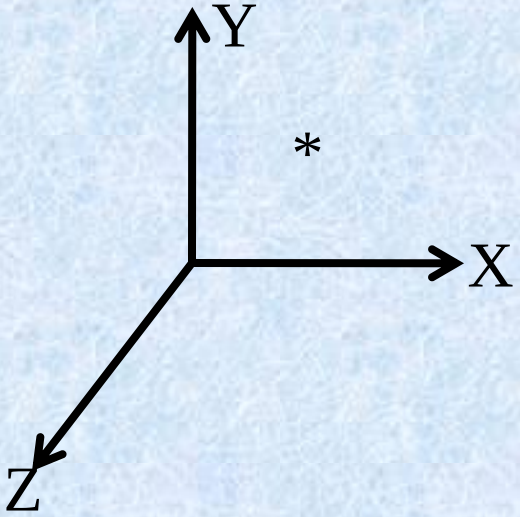
Tertiary and quaternary structures

Tertiary structure provides the information about the three-dimensional structure of a protein with atomic details; the positions of each atom in Cartesian coordinate system.







3D structure of a protein contains the complete information.

3D structure determination

Experiment

X-ray crystallography

Protein purification

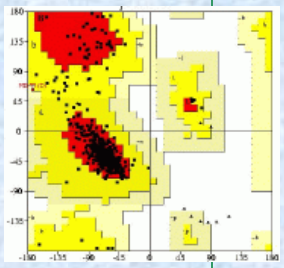
Protein crystallization

Crystal mounting

Data collection

distribution of electrons in the molecule,

i.e. an electron density map.

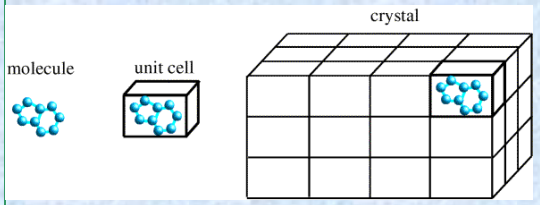


Data processing

Structure solution

Structure refinement

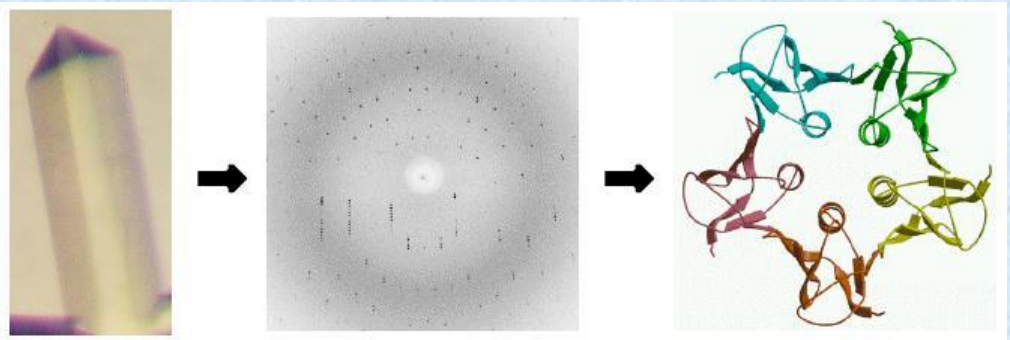
Structure analysis



NMR spectroscopy

Electron microscopy

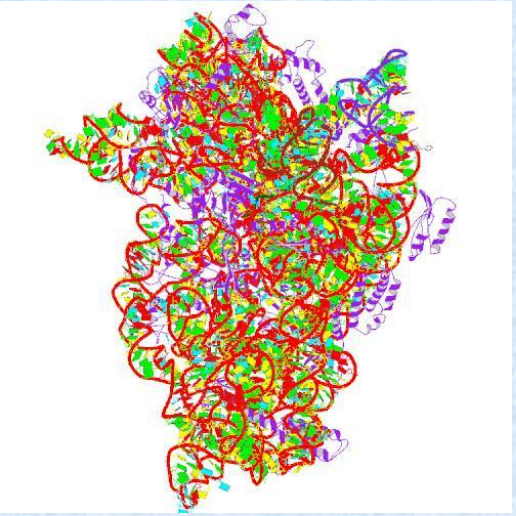
It is based on the quantum mechanical properties of atoms, particularly spin, and it determines information about atoms from the fact that their local environment influences how they respond to applied magnetic fields.



All available structures are stored in Protein Data Bank (PDB).

Protein Data Bank

Myoglobin, Kendrew (1958)



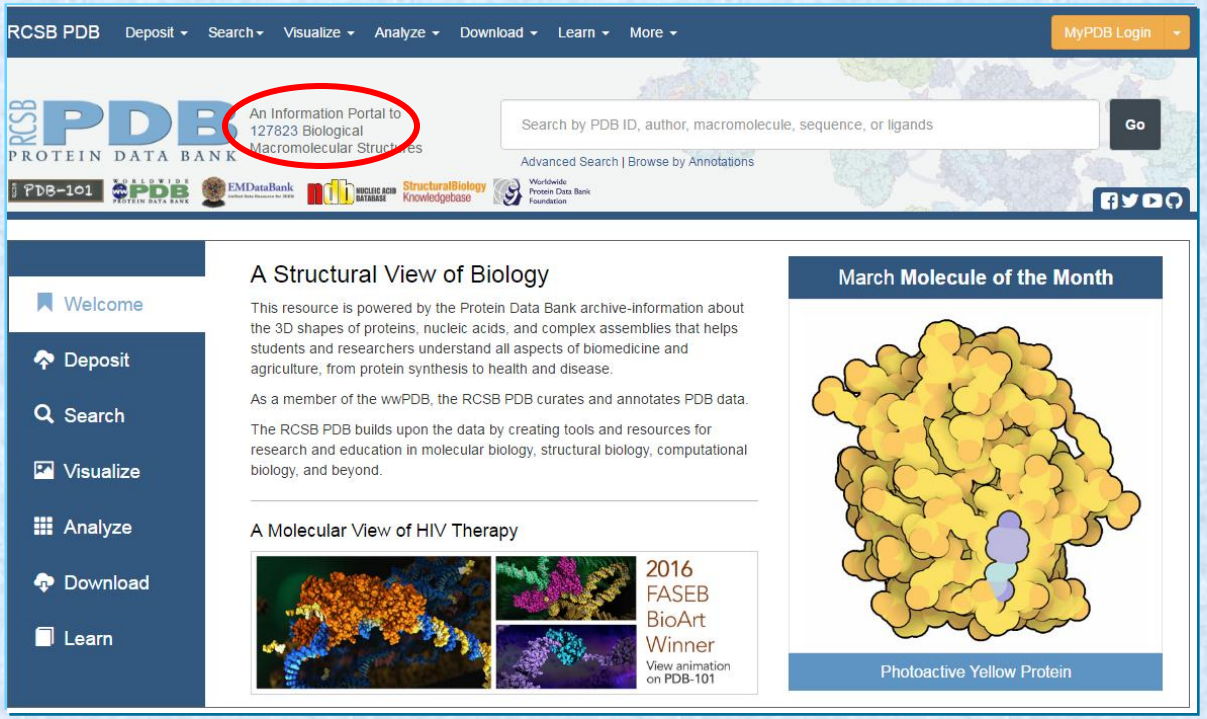
PDB (USA), PDB (Europe) and PDB (**Japan**)

World wide Protein Data Bank: Organizations that act as deposition, data processing and distribution centers for PDB data.

2009 **Nobel Prize for Chemistry** has been awarded to Venki Ramakrishnan (UK), Tom Steitz (USA) and Ada Yonath (Israel). These three crystallographers have contributed enormously to our understanding of how the protein production machinery works at the atomic level by **determining the detailed three-dimensional structure** of so-called ribosomes.

Protein Data Bank

CODE
2LZMA



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NMR	10300	1190	241	8	11739
ELECTRON MICROSCOPY	1022	30	367	0	1419
HYBRID	99	3	2	1	105
other	181	4	6	13	204
Total	118663	3047	6087	26	127823

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

STRUCTURE OF BACTERIOPHAGE T4 LYSOZYME REFINED AT 1.7 ANGSTROMS RESOLUTION

2LZM

Display Files

close

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

DOI: 10.2210/pdb2lzm/pdb

ENTRY 2LZM SUPERSEDES 1LZM

Primary Citation

Structure of bacteriophage T4 lysozyme refined at 1.7 A resolution.

Weaver, L.H., Matthews, B.W.

Journal: (1987) J.Mol.Biol. **193:** 189-199

PubMed: 3586019
Search Related Articles in PubMed

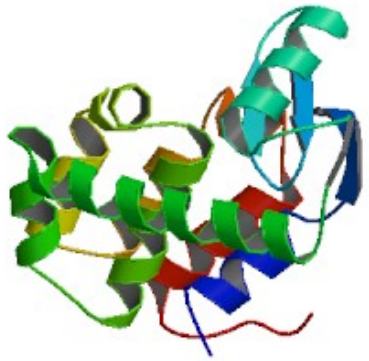
PubMed Abstract:

The structure of the lysozyme from bacteriophage T4 has been refined at 1.7 A resolution to a crystallographic residual of 19.3%. The final model has bond lengths and bond angles that differ from "ideal" values by 0.019 A and 2.7... [Read More & Search PubMed Abstracts]

Related Citations in PDB Entry (REMARK 1) Hide

Temperature-Sensitive Mutations of Bacteriophage T4 Lysozyme Occur at Sites with Low Mobility and Low Solvent Accessibility in the Folded Protein
Alber, T., Dao-Pin, S., Nye, J.A., Muchmore, D.C., Matthews, B.W.
(1987) *Biochemistry* ***26:*** *3754*

Biol



More Images...

View in Jmol | Simple Viewer
Other Viewers | Protein Workshop

Biological assembly 1 assigned by authors

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>2LZM:A|PDBID|CHAIN|SEQUENCE
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YKNL
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Protein Data Bank

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TITLE    2 RESOLUTION
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COMPND   2 MOLECULE: T4 LYSOZYME;
COMPND   3 CHAIN: A;
COMPND   4 EC: 3.2.1.17;
COMPND   5 ENGINEERED: YES
SOURCE    MOL_ID: 1;
SOURCE   2 ORGANISM_SCIENTIFIC: ENTEROBACTERIA
SOURCE   3 ORGANISM_TAXID: 10665;
SOURCE   4 ORGAN: EGG
KEYWDS    HYDROLASE (O-GLYCOSYL)
EXPDTA    X-RAY DIFFRACTION
AUTHOR    L.H.WEAVER,B.W.MATTHEWS
REVDAT   7   13-JUL-11 2LZM    1       VERSN
REVDAT   6   24-FEB-09 2LZM    1       VERSN
REVDAT   5   01-APR-03 2LZM    1       JRNL
REVDAT   4   16-APR-88 2LZM    1       REMARK
REVDAT   3   16-OCT-87 2LZM    1       REMARK
REVDAT   2   16-APR-87 2LZM    1       JRNL
REVDAT   1   24-OCT-86 2LZM    0
SPRSDE     24-OCT-86 2LZM      1LZM
JRNL        AUTH   L.H.WEAVER,B.W.MATTHEWS
JRNL        TITL   STRUCTURE OF BACTERIOPHAGE T
JRNL        TITL 2 RESOLUTION.
JRNL        REF    J.MOL.BIOL.
JRNL        REFN                   ISSN 0022-28
JRNL        PMID   3586019
JRNL        DOI    10.1016/0022-2836(87)90636-X
REMARK   1
REMARK   1 REFERENCE 1
REMARK   1  AUTH   T.ALBER,S.DAO-PIN,J.A.NYE,D.
REMARK   1  TITL   TEMPERATURE-SENSITIVE MUTATI
REMARK   1  TITL 2 OCCUR AT SITES WITH LOW MOBI
REMARK   1  TITL 3 ACCESSIBILITY IN THE FOLDED
REMARK   1  REF    BIOCHEMISTRY
REMARK   1  REFN                   ISSN 0006-29
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REMARK   2
REMARK   2 RESOLUTION.    1.70 ANGSTROMS.
REMARK   3
REMARK   3 REFINEMENT.
REMARK   3   PROGRAM     : TNT
REMARK   3   AUTHORS     : TRONRUD,TEN EYCK,MATTHEWS
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SEQRES   6 A  164  LEU PHE ASN GLN ASP VAL ASP ALA ALA VAL ARG GLY ILE
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HELIX    5  H5 ALA A   93  MET A  106  1                                  14
HELIX    6  H6 GLU A  108  GLY A  113  5                                   6
HELIX    7  H7 THR A  115  GLN A  123  1                                   9
HELIX    8  H8 TRP A  126  ALA A  134  1                                   9
HELIX    9  H9 ARG A  137  GLN A  141  1                                   5
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SHEET    3  S1 4 TYR A  24  ILE A  27 -1  O  TYR A  24   N  ASP A  20
SHEET    4  S1 4 HIS A  31  THR A  34 -1  N  HIS A  31   O  ILE A  27
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Protein Data Bank

Sample entry in PDB

X Y Z

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Occupancy

Macromolecular crystals are composed of many individual molecules packed into a symmetrical arrangement.

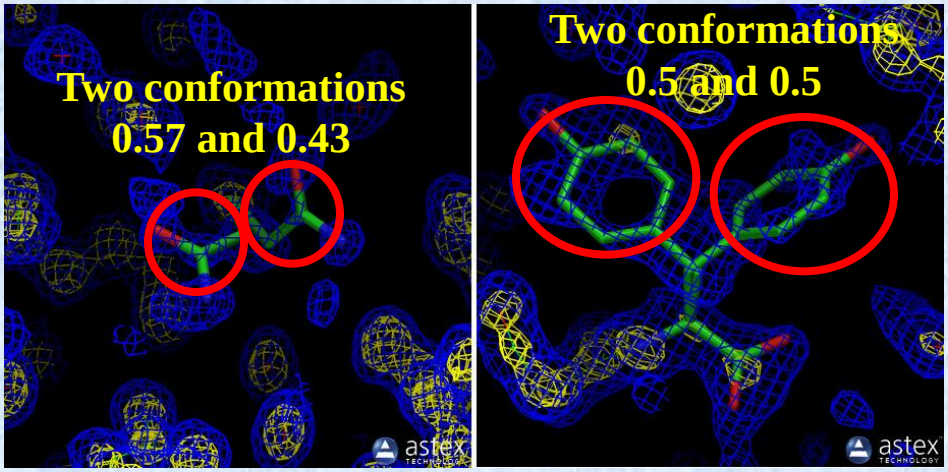
A sidechain on the surface may wag back and forth between several conformations, or a substrate may bind in two orientations in an active site, or a metal ion may be bound to only a few of the molecules.

When building the atomic model of these portions, the occupancy can be used to estimate the amount of each conformation that is observed in the crystal.

For most atoms, the occupancy is given a value of 1, indicating that the atom is found in all of the molecules in the same place in the crystal.

However, if a metal ion binds to only half of the molecules in the crystal, the researcher will see a weak image of the ion in the electron density map, and can assign an occupancy of 0.5 in the PDB structure file for this atom.

The occupancy value is used to indicate the fraction of molecules that have each of the conformations. Two (or more) atom records are included for each atom, with occupancies like 0.5 and 0.5, or 0.4 and 0.6, or other fractional occupancies that sum to a total of 1.



Gln8 (0.57 and 0.43) and Tyr151 in 1A6M

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ATOM     65  C   GLN A   8       7.602  12.149  22.631  1.00  8.08           C
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ATOM     69  CG AGLN A   8       7.030  11.303  25.500  0.57 16.30           C
ANISOU   69  CG AGLN A   8    2914   1636   1644    -[illegible]   -429    642       C
ATOM     70  CG BGLN A   8       6.967  12.094  25.680  0.43 12.07           C
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ATOM     76  NE2BGLN A   8       7.067  11.762  28.084  0.43 14.03           N
ANISOU   76  NE2BGLN A   8    2245   1968   1117    -[illegible]   -7      225       N
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ATOM     79  C   LEU A   9       9.080  11.630  20.080  1.00  7.19           C
ANISOU   79  C   LEU A   9    1008   1038    685     70     41      2       C
ATOM     80  O   LEU A   9      10.311  11.526  19.962  1.00  7.98           O
ANISOU   80  O   LEU A   9    1019   1097    915    232    143     83       O
ATOM     81  CB  LEU A   9       7.677   9.576  19.969  1.00  9.04           C
ANISOU   81  CB  LEU A   9    1440    983   1012    -45    222     79       C
ATOM     82  CG  LEU A   9       7.090   8.338  20.698  1.00 10.56           C
ANISOU   82  CG  LEU A   9    1658    982   1370    -49    291     80       C
ATOM     83  CD1 LEU A   9       6.290   7.498  19.721  1.00 12.91           C
ANISOU   83  CD1 LEU A   9    2111   1030   1763   -292    327   -155       C
ATOM     84  CD2 LEU A   9       8.189   7.510  21.315  1.00 16.75           C
ANISOU   84  CD2 LEU A   9    2279   1349   2735     -8   -215    792       C
ATOM     85  N   VAL A  10       8.391  12.589  19.483  1.00  6.70           N
ANISOU   85  N   VAL A  10     931    934    681     29     49     12       N
ATOM     86  CA  VAL A  10       9.019  13.628  18.670  1.00  6.25           C
ANISOU   86  CA  VAL A  10     822    859    692     15    113      1       C
```

Temperature factor

If we were able to hold an atom rigidly fixed in one place, we could observe its distribution of electrons in an ideal situation.

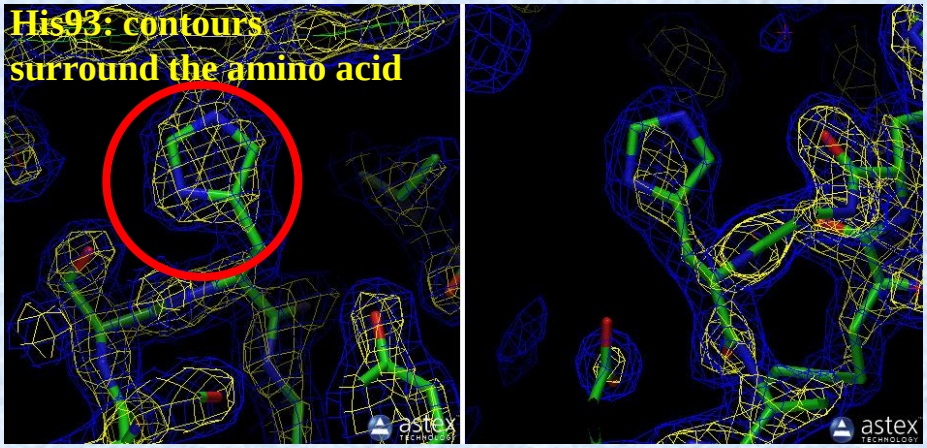
The image would be dense towards the center with the density falling off further from the nucleus.

The electrons usually have a wider distribution than this ideal. This may be due to vibration of the atoms, or differences between the many different molecules in the crystal lattice. The observed electron density will include an average of all these small motions, yielding a slightly smeared image of the molecule.

These motions, and the resultant smearing of the electron density, are incorporated into the atomic model by a B-value or temperature factor.

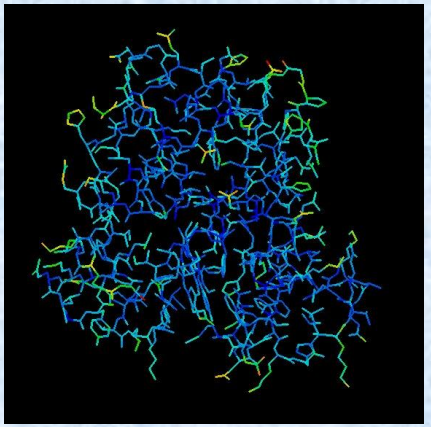
Values under 10 create a model of the atom that is very sharp, indicating that the atom is not moving much and is in the same position in all of the molecules in the crystal.

Values greater than 50 or so indicate that the atom is moving so much that it can barely been seen. This is often the case for atoms at the surface of proteins, where long sidechains are free to wag in the surrounding water.




```
ATOM   737  ND1 HIS A  93      11.243  30.390   4.397  1.00 12.73           N
ATOM   738  CD2 HIS A  93      12.005  28.593   3.361  1.00 20.40           C
ATOM   739  CE1 HIS A  93      12.419  30.059   4.926  1.00 15.17           C
ATOM   740  NE2 HIS A  93      12.897  28.963   4.332  1.00 16.09
```

```
ATOM   642  ND1 HIS A  81      -2.541  24.541  20.570  1.00 72.63           N
ATOM   643  CD2 HIS A  81      -0.874  23.158  20.970  1.00 54.37           C
ATOM   644  CE1 HIS A  81      -3.006  23.416  21.159  1.00 53.46           C
ATOM   645  NE2 HIS A  81      -2.022  22.561  21.396  1.00 73.87           N
```



High values, indicating lots of motion, are in red and yellow, and low values are in blue.

STRUCTURE OF BACTERIOPHAGE T4 LYSOZYME REFINED AT 1.7 ANGSTROMS RESOLUTION

2LZM

FASTA | Sequence & DSSP | Image

Polymer 1
Length: 164 residues
Chain Type: polypeptide(L)
Reference: **UniProtKB** P00720

Display Parameters

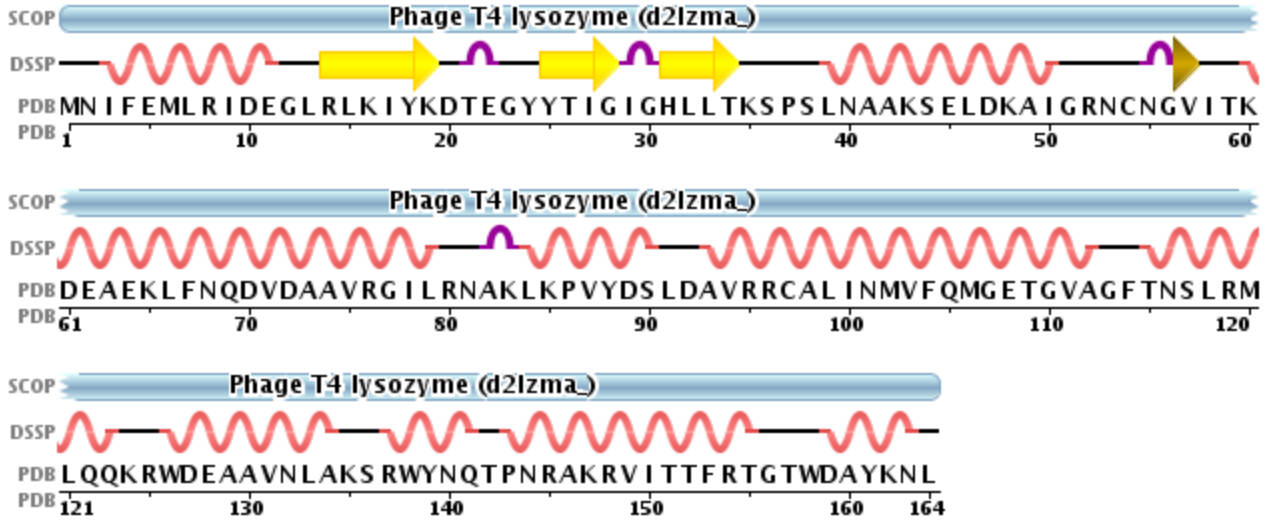
Currently displayed: **SEQRES sequence.**
Display external (UniProtKB) sequence
Mouse over an annotation to see details.

Annotations *Add Annotations*

Select

Domain Assignment:**SCOP** d2lzma_ Phage T4 lysozyme: 164 residues
[hide] [reference]

Secondary Structure:**DSSP** 66% helical (10 helices; 109 residues)
[hide] [reference] 9% beta sheet (4 strands; 15 residues)



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

STRUCTURE OF BACTERIOPHAGE T4 LYSOZYME REFINED AT 1.7 ANGSTROMS RESOLUTION

2LZM

Domain Annotation: SCOP Classification (version 1.75) Hide

Domain Info	Class	Fold	Superfamily	Family	Domain	Species
d2lzma_	Alpha and beta proteins (a+b)	Lysozyme-like	Lysozyme-like	Phage lysozyme	Phage T4 lysozyme	Bacteriophage T4 [TaxId: 10665]

Domain Annotation: CATH Classification (version 3.4.0) Hide

Domain	Class	Architecture	Topology	Homology
2lzmA00	Mainly Alpha	Orthogonal Bundle	Lysozyme	

Protein Family Annotation: PFAM Classification Hide

Chain	PFAM Accession	PFAM ID	Description	Type	Clan ID
A	PF00959	Phage_lysozyme	Phage lysozyme	Domain	

Gene Product Annotation: GO Terms Hide

Polymer	Molecular Function	Biological Process	Cellular Component
T4 LYSOZYME (2LZM:A)	• lysozyme activity • catalytic activity • hydrolase activity • hydrolase activity, acting on glycosyl bonds	• metabolic process • peptidoglycan catabolic process • cell wall macromolecule catabolic process • cytolysis • defense response to bacterium	• none

Structural Biology Knowledgebase Data Hide

Information from the Structural Biology Knowledgebase

- Protein Targets from TargetDB: 0 targets
- Related Biological Annotations: >21 annotations
- Related Clones from PSI:Biology Materials Repository: 0 clones
- Related Protocols from PepcDB: 0 protocols

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

STRUCTURE OF BACTERIOPHAGE T4 LYSOZYME REFINED AT 1.7 ANGSTROMS RESOLUTION

2LZM

Cluster # 3648 Members. Sequence cutoff: 100% Cluster size: 9 sequences

Rank	PDB id	Entity id	Chains	Description	Details	Taxonomy	EC Number
Select for download / view details OR: Select two chains for comparison							
☐	Download	Details		--- Select Comparison Method ---	Submit		
☐ 1	3FA0	1	A	Lysozyme		10665	3.2.1.17
☐ 2	3LZM	1	A	T4 LYSOZYME		10665	3.2.1.17
☐ 3	4LZM	1	A	T4 LYSOZYME		10665	3.2.1.17
☐ 4	7LZM	1	A	T4 LYSOZYME		10665	3.2.1.17
☐ 5	5LZM	1	A	T4 LYSOZYME		10665	3.2.1.17
☐ 6	6LZM	1	A	T4 LYSOZYME		10665	3.2.1.17
☐ 7	2LZM	1	A	T4 LYSOZYME		10665	3.2.1.17
☐ 8	1T6H	1	A	Lysozyme		10665	3.2.1.17
☐ 9	1LYD	1	A	T4 LYSOZYME		10665	

Sequence Clusters for the Sequence Entities in PDB 2LZM

Entity #1: Chains: A - T4 LYSOZYME protein, length: 164 [Blast]

Cluster Sequence Similarity Cutoff	Rank	Nr. of chains in Cluster	Cluster Nr.
100%	7	9	3648
95%	199	522	2
90%	200	530	2
70%	200	530	6
50%	200	530	8
40%	200	530	9
30%	200	530	14

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

STRUCTURE OF BACTERIOPHAGE T4 LYSOZYME REFINED AT 1.7 ANGSTROMS RESOLUTION

2LZM

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Structural Similarities for the Entities in PDB 2LZM

The following structural similarities have been found using the jFATCAT-rigid algorithm. In order to reduce the number of hits, a 40% sequence identity clustering has been applied and a representative chain is taken from each cluster.

Entity #1: Chains: A

Description: T4 LYSOZYME protein

Length: 164

No structure alignment results are available for 2LZM.A explicitly.

It is represented by chain **1SX7.A** which has more than 95% sequence similarity.

▾ **Click here to hide the structure comparison results for representative 1SX7.A**

1SX7.A (chain 1) vs. representatives of other sequence clusters (chain 2)

Rank	Results	Chain 2	Title	P-value	Score	Rmsd	Len1	Len2	%ID	%Cov1	%Cov2
1	view	2QB0.B	TELSAM domain - Lysozym	0.0	477.58	1.29	164	241	96	98	67
2	view	2O7A.A	Lysozyme	0.0	301.62	0.47	164	116	97	59	83
3	view	3SN6.R	Lysozyme, Beta-2 adrene	1.14E-10	457.36	1.62	443	164	97	36	97
4	view	1WTH.A	Tail-associated lysozyme	5.0E-10	442.54	1.16	164	571	43	99	28
5	view	2RH1.A	beta-2-adrenergic recept	1.55E-9	471.90	2.22	164	443	96	100	37
6	view	3HDE.A	Lysozyme	2.48E-8	270.98	2.99	164	165	17	83	82

Results options Hide

Currently viewing only **significant results** (P-value < 0.001).
Show all available results

Update Status Hide

The data on this page are up to date as of: Oct 04 2011

Table Legend Hide

- **Rank**: current row position. Changes with different sorting orders and filter rules
- **Chain 2**: PDB chain name
- **Title**: Protein chain description
- **P-value**: P-value of this alignment (FATCAT) (default sorted by this)
- **Score**: Raw alignment score (FATCAT)
- **RMSD**: RMSD value of the

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

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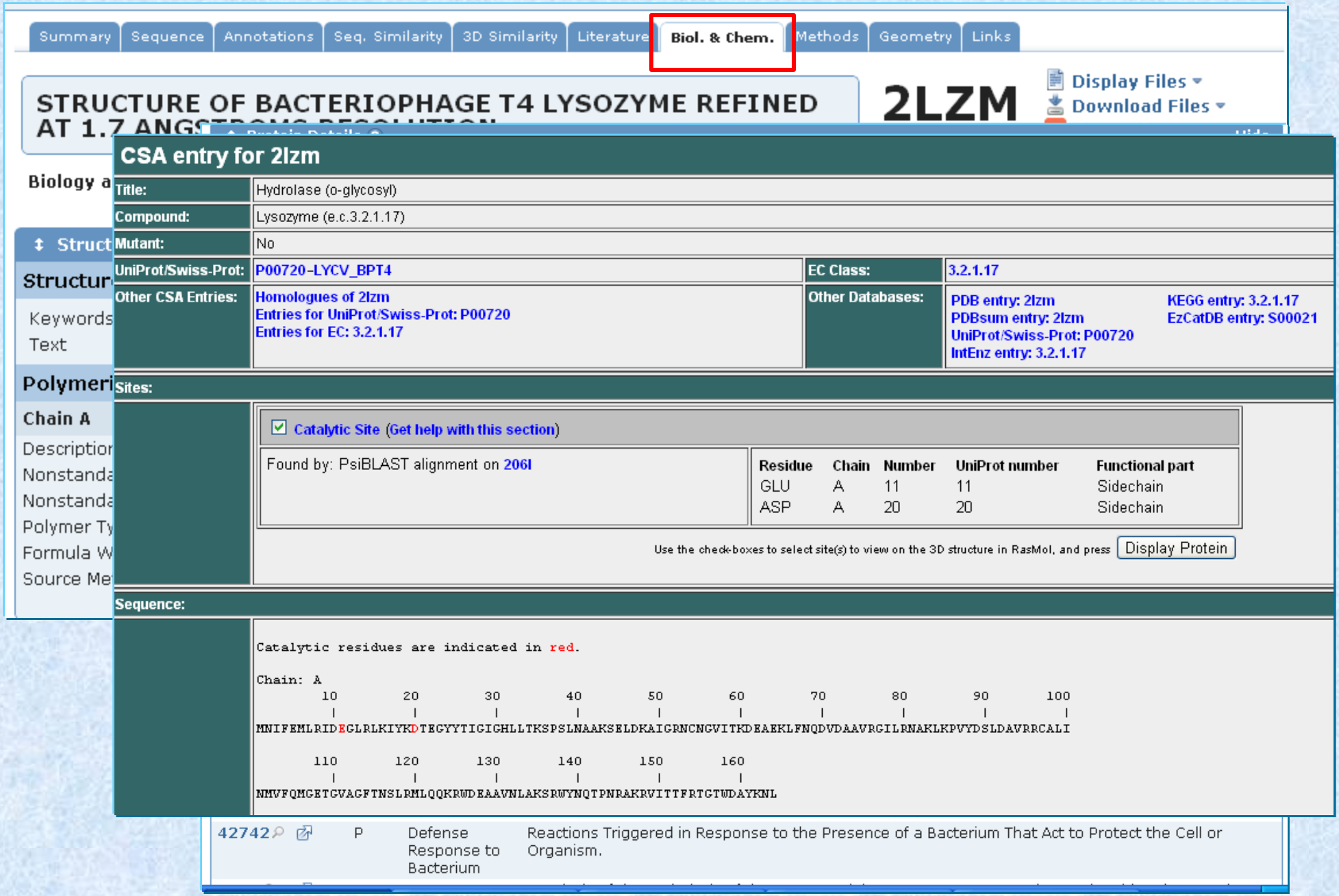
Related articles from PubMedCentral (provided by BioLit) Hide

FOLD-RATE: prediction of protein folding rates from amino acid sequence

M. Michael Gromiha, A. Mary Thangakani, S. Selvaraj

Other PDB IDs found in the above articles

Image	PDB ID	Structure Title	Sequence Similarity
	1A6N	DEOXY-MYOGLOBIN, ATOMIC RESOLUTION	-
	1AON	CRYSTAL STRUCTURE OF THE ASYMMETRIC CHAPERONIN COMPLEX GROEL/GROES/(ADP)7	-
	1BNI	BARNASE WILDTYPE STRUCTURE AT PH 6.0	-
	1CBI	APO-CELLULAR RETINOIC ACID BINDING PROTEIN I	-
	1CEI	STRUCTURE DETERMINATION OF THE COLICIN E7 IMMUNITY PROTEIN (IMME7) THAT BINDS SPECIFICALLY TO THE DNASE-TYPE COLICIN E7 AND INHIBITS ITS BACTERIOCIDAL ACTIVITY	-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STRUCTURE OF BACTERIOPHAGE T4 LYSOZYME REFINED
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CSA entry for 2lzm
Title: Hydrolase (o-glycosyl)
Compound: Lysozyme (e.c.3.2.1.17)
Mutant: No
UniProt/Swiss-Prot: P00720-LYCV_BPT4
EC Class: 3.2.1.17
Other CSA Entries: Homologues of 2lzm
Entries for UniProt/Swiss-Prot: P00720
Entries for EC: 3.2.1.17
Other Databases: PDB entry: 2lzm
PDBsum entry: 2lzm
UniProt/Swiss-Prot: P00720
IntEnz entry: 3.2.1.17
KEGG entry: 3.2.1.17
EzCatDB entry: S00021
Sites:
Catalytic Site (Get help with this section)
Found by: PsiBLAST alignment on 206l
Residue Chain Number UniProt number Functional part
GLU A 11 11 Sidechain
ASP A 20 20 Sidechain
Use the check-boxes to select site(s) to view on the 3D structure in RasMol, and press
Display Protein
Sequence:
Catalytic residues are indicated in red.
Chain: A
MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSLDAVRRCALI
NMVFQMGETGVAGFTNSLRMLQQKRWDEAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYKNL
42742
P
Defense Response to Bacterium
Reactions Triggered in Response to the Presence of a Bacterium That Act to Protect the Cell or Organism.

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

X-RAY DIFFRACTION

2LZM

Materials and Methods page

Crystal Data

Unit Cell

Length	(Å)	Angle	(°)
a =	61.2		
b =	61.2		
c =	96.8		

Space Group

Space Group Name:

Diffraction

Refinement

Refinement Statistics

reflnsShellList

R-Factor(Observed)

RMS Deviations

Parameter Type	Deviation from Ideal
t_angle_deg	2.7
t_bond_d	0.019

Number of Non-Hydrogen Atoms Used in Refinement

Protein Atoms	1309
Nucleic Acid Atoms	0
Heterogen Atoms	0
Solvent Atoms	118

Software and Computing

Computing

Structure Refinement	TNT

Software

refinement	TNT

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

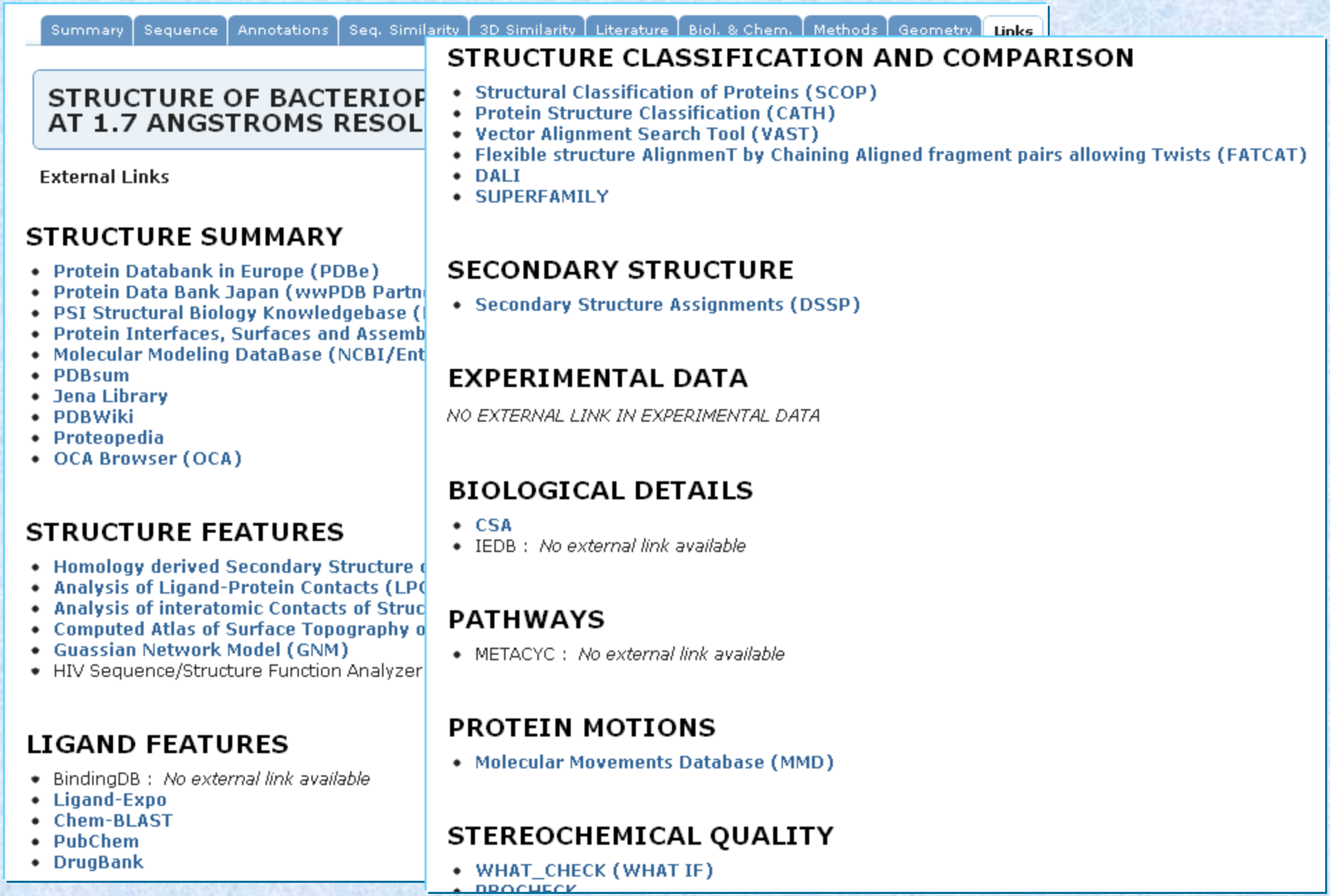
Bond Length

Bond Type	Chain Id	Tot Num	Cal Ave	Cal StdDev	Std Val	Std StdDev	Minimum	Maximum
C-N	A	160	1.33	0.020	1.329	0.014	1.27	1.38
C-N(P)	A	3	1.33	0.014	1.341	0.016	1.31	1.34
C-O	A	164	1.23	0.017	1.231	0.02	1.19	1.27
CA-C	A	153	1.53	0.020	1.525	0.021	1.47	1.58
CA-C(G)	A	11	1.53	0.014	1.516	0.018	1.51	1.56
CA-CB	A	108	1.53	0.025	1.53	0.02	1.43	1.61
CA-CB(A)	A	15	1.53	0.010	1.521	0.033	1.51	1.55
CA-CB(I,T,V)	A	30	1.55	0.021	1.54	0.027	1.51	1.61
N-CA	A	150	1.45	0.018	1.458	0.019	1.40	1.50

Dihedral Angle

Dihedral Angle	Chain Id	Tot Num	Cal Ave	Cal StdDev	Std Val	Std StdDev	Minimum	Maximum
Chi1 g(+)	A	78	-71.67	18.724	-66.7	15.0	-115.50	-3.60
Chi1 g(-)	A	18	60.64	29.323	64.1	15.7	0.70	116.10
Chi1 trans	A	42	184.84	16.233	183.6	16.8	144.40	237.90
Omega	A	163	179.68	3.595	180	5.8	169.30	189.80
Phi	A	53	-71.51	72.347	-65.3	11.9	-157.70	88.50
Phi helix	A	109	-63.55	17.101	-65.3	11.9	-106.90	77.20
Phi(P)	A	1	-69.50	0.000	-65.4	11.2	-69.50	-69.50
Psi	A	46	94.20	72.308	-39.4	11.3	-48.60	175.00
Psi helix	A	109	-38.07	21.279	-39.4	11.3	-61.30	157.70
Psi(G)	A	8	-26.81	76.181	-39.4	11.3	-177.40	31.70

Save Dihedral Angle Summary in: ◉ CSV (Excel) Format Save Report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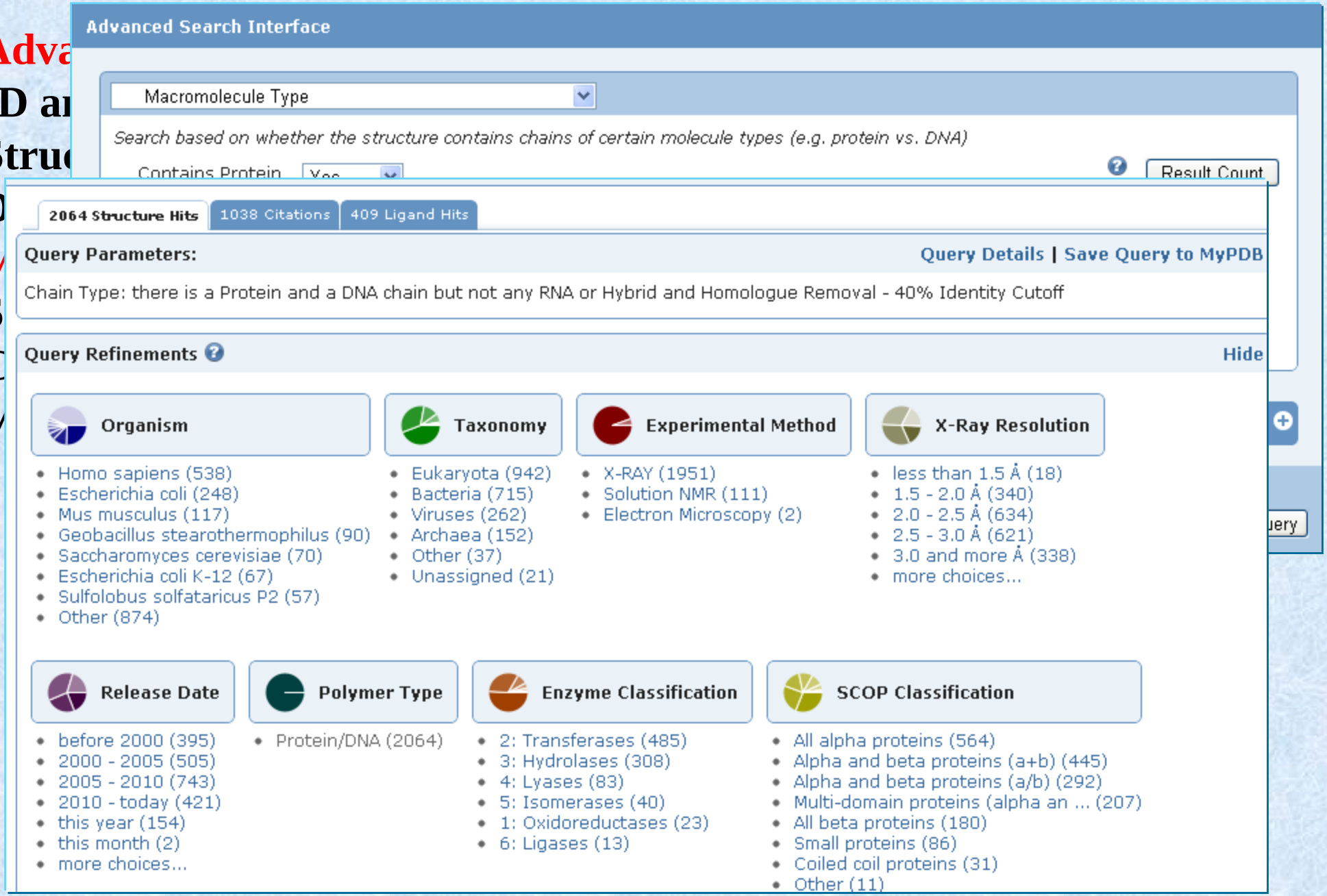
External Links
STRUCTURE SUMMARY
Protein Databank in Europe (PDBe)
Protein Data Bank Japan (wwPDB Partn
PSI Structural Biology Knowledgebase (
Protein Interfaces, Surfaces and Assemb
Molecular Modeling DataBase (NCBI/Ent
PDBsum
Jena Library
PDBWiki
Proteopedia
OCA Browser (OCA)
STRUCTURE FEATURES
Homology derived Secondary Structure
Analysis of Ligand-Protein Contacts (LP
Analysis of interatomic Contacts of Struc
Computed Atlas of Surface Topography o
Guassian Network Model (GNM)
HIV Sequence/Structure Function Analyzer
LIGAND FEATURES
BindingDB : No external link available
Ligand-Expo
Chem-BLAST
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
NO EXTERNAL LINK IN EXPERIMENTAL DATA
BIOLOGICAL DETAILS
CSA
IEDB : No external link available
PATHWAYS
METACYC : No external link available
PROTEIN MOTIONS
Molecular Movements Database (MMD)
STEREOCHEMICAL QUALITY
WHAT_CHECK (WHAT IF)


Advanced Search Interface
Macromolecule Type
Search based on whether the structure contains chains of certain molecule types (e.g. protein vs. DNA)
Contains Protein
Result Count
2064 Structure Hits
1038 Citations
409 Ligand Hits
Query Parameters:
Query Details | Save Query to MyPDB
Chain Type: there is a Protein and a DNA chain but not any RNA or Hybrid and Homologue Removal - 40% Identity Cutoff
Query Refinements
Hide
Organism
Homo sapiens (538)
Escherichia coli (248)
Mus musculus (117)
Geobacillus stearothermophilus (90)
Saccharomyces cerevisiae (70)
Escherichia coli K-12 (67)
Sulfolobus solfataricus P2 (57)
Other (874)
Taxonomy
Eukaryota (942)
Bacteria (715)
Viruses (262)
Archaea (152)
Other (37)
Unassigned (21)
Experimental Method
X-RAY (1951)
Solution NMR (111)
Electron Microscopy (2)
X-Ray Resolution
less than 1.5 Å (18)
1.5 - 2.0 Å (340)
2.0 - 2.5 Å (634)
2.5 - 3.0 Å (621)
3.0 and more Å (338)
more choices...
Release Date
before 2000 (395)
2000 - 2005 (505)
2005 - 2010 (743)
2010 - today (421)
this year (154)
this month (2)
more choices...
Polymer Type
Protein/DNA (2064)
Enzyme Classification
2: Transferases (485)
3: Hydrolases (308)
4: Lyases (83)
5: Isomerases (40)
1: Oxidoreductases (23)
6: Ligases (13)
SCOP Classification
All alpha proteins (564)
Alpha and beta proteins (a+b) (445)
Alpha and beta proteins (a/b) (292)
Multi-domain proteins (alpha an ... (207)
All beta proteins (180)
Small proteins (86)
Coiled coil proteins (31)
Other (11)

Protein visualization

Pymol

Rasmol

Jmol

KING

Webmol

SWISS-PDB viewer