



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:14 AM GMT

PDB ID : 2CAU  
Title : CANAVALIN FROM JACK BEAN  
Authors : Ko, T.-P.; Day, J.; Macpherson, A.  
Deposited on : 1998-11-20  
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

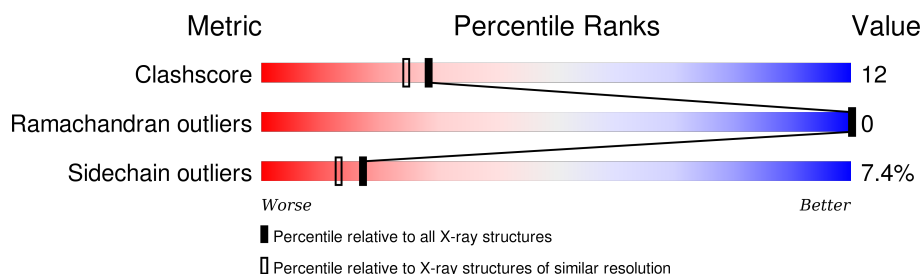
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	445	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2865 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PROTEIN (CANAVALIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	344	Total	C	N	O	S	0	0	0
			2764	1751	473	535	5			

- Molecule 2 is water.

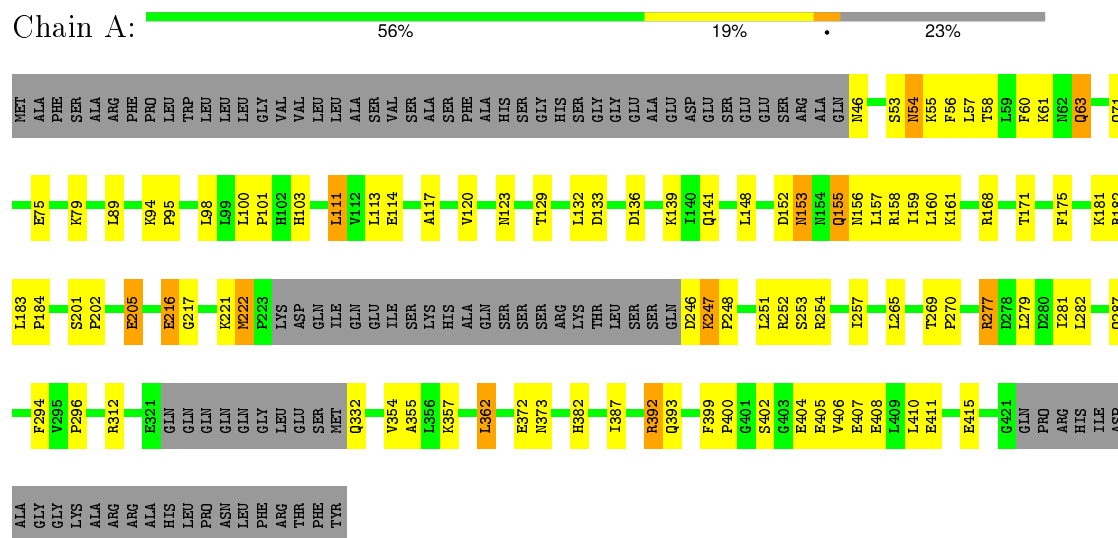
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	101	Total	O	0	0
			101	101		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

#### • Molecule 1: PROTEIN (CAVAVALIN)



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.99 Å   105.99 Å   105.99 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	40.00 – 2.10	Depositor
% Data completeness (in resolution range)	84.0 (40.00-2.10)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, $R_{free}$	0.175 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2865	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.50	0/2815	0.72	1/3812 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	362	LEU	CA-CB-CG	5.12	127.08	115.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2764	0	2733	64	0
2	A	101	0	0	7	0
All	All	2865	0	2733	64	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (64) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:LYS:HD2	1:A:216:GLU:HG2	1.37	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ASN:HD22	1:A:54:ASN:C	1.72	0.93
1:A:407:GLU:O	1:A:411:GLU:HG2	1.83	0.78
1:A:393:GLN:HG2	2:A:578:HOH:O	1.90	0.71
1:A:183:LEU:HD12	1:A:184:PRO:HD2	1.74	0.70
1:A:54:ASN:ND2	1:A:54:ASN:C	2.43	0.68
1:A:46:ASN:HA	2:A:587:HOH:O	1.94	0.67
1:A:404:GLU:O	1:A:408:GLU:HG3	1.95	0.66
1:A:46:ASN:N	2:A:587:HOH:O	2.30	0.65
1:A:155:GLN:NE2	1:A:156:ASN:H	2.00	0.60
1:A:246:ASP:C	1:A:247:LYS:HD3	2.24	0.58
1:A:79:LYS:HD2	2:A:542:HOH:O	2.05	0.57
1:A:181:LYS:CD	1:A:216:GLU:HG2	2.24	0.56
1:A:114:GLU:HB3	1:A:158:ARG:HB2	1.87	0.56
1:A:253:SER:O	1:A:254:ARG:HG3	2.06	0.56
1:A:46:ASN:CA	2:A:587:HOH:O	2.54	0.55
1:A:54:ASN:HD22	1:A:55:LYS:N	2.05	0.55
1:A:153:ASN:N	1:A:153:ASN:HD22	2.06	0.54
1:A:392:ARG:CZ	1:A:404:GLU:OE1	2.55	0.54
1:A:277:ARG:HD3	1:A:277:ARG:C	2.28	0.54
1:A:406:VAL:O	1:A:410:LEU:HG	2.09	0.53
1:A:399:PHE:HB3	1:A:400:PRO:HD2	1.89	0.53
1:A:53:SER:O	1:A:56:PHE:HB2	2.09	0.52
1:A:114:GLU:OE1	1:A:158:ARG:HD3	2.08	0.52
1:A:415:GLU:OE1	2:A:599:HOH:O	2.19	0.52
1:A:252:ARG:HH22	1:A:287:GLN:HE21	1.58	0.51
1:A:247:LYS:HD3	1:A:247:LYS:N	2.25	0.51
1:A:60:PHE:CZ	1:A:217:GLY:HA3	2.46	0.51
1:A:60:PHE:HZ	1:A:217:GLY:HA3	1.76	0.50
1:A:168:ARG:HB3	1:A:171:THR:HB	1.94	0.50
1:A:181:LYS:HZ2	1:A:216:GLU:HG3	1.78	0.49
1:A:202:PRO:HG2	1:A:205:GLU:HB2	1.95	0.48
1:A:402:SER:OG	1:A:405:GLU:HG3	2.13	0.48
1:A:120:VAL:HG22	1:A:129:THR:HG23	1.95	0.48
1:A:71:GLN:NE2	1:A:75:GLU:HB3	2.28	0.48
1:A:269:THR:HB	1:A:270:PRO:HD2	1.96	0.48
1:A:296:PRO:HA	1:A:354:VAL:O	2.15	0.47
1:A:113:LEU:HD11	1:A:160:LEU:HB2	1.96	0.47
1:A:181:LYS:NZ	1:A:216:GLU:CG	2.78	0.46
1:A:139:LYS:NZ	1:A:141:GLN:HG2	2.31	0.46
1:A:57:LEU:HD12	1:A:58:THR:N	2.30	0.46
1:A:148:LEU:HD21	1:A:159:ILE:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:LYS:HZ1	1:A:216:GLU:HB2	1.81	0.45
1:A:63:GLN:HE21	1:A:63:GLN:HB3	1.66	0.44
1:A:103:HIS:CE1	1:A:175:PHE:HB2	2.53	0.44
1:A:133:ASP:O	1:A:136:ASP:HB2	2.18	0.44
1:A:222:MET:O	1:A:222:MET:HG3	2.17	0.44
1:A:354:VAL:HG22	1:A:355:ALA:N	2.33	0.43
1:A:181:LYS:NZ	1:A:216:GLU:HG3	2.33	0.43
1:A:257:ILE:HD11	1:A:265:LEU:HD23	2.01	0.42
1:A:89:LEU:HB2	1:A:161:LYS:HB2	2.02	0.42
1:A:282:LEU:HD12	1:A:282:LEU:C	2.40	0.42
1:A:161:LYS:HE3	2:A:528:HOH:O	2.20	0.41
1:A:372:GLU:O	1:A:373:ASN:HB3	2.20	0.41
1:A:132:LEU:HD21	1:A:248:PRO:HG3	2.00	0.41
1:A:282:LEU:HD12	1:A:282:LEU:O	2.20	0.41
1:A:61:LYS:HE3	1:A:61:LYS:HB3	1.74	0.41
1:A:279:LEU:HB3	1:A:281:ILE:HD12	2.03	0.41
1:A:100:LEU:HA	1:A:101:PRO:HD3	1.97	0.40
1:A:148:LEU:HD21	1:A:159:ILE:HD13	2.03	0.40
1:A:117:ALA:HB2	1:A:157:LEU:CD2	2.51	0.40
1:A:111:LEU:HD21	1:A:251:LEU:HD11	2.03	0.40
1:A:332:GLN:OE1	1:A:332:GLN:HA	2.22	0.40
1:A:94:LYS:HB3	1:A:95:PRO:HD2	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	338/445 (76%)	330 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.



### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	309/392 (79%)	286 (93%)	23 (7%)	17	13

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	63	GLN
1	A	98	LEU
1	A	111	LEU
1	A	123	ASN
1	A	152	ASP
1	A	153	ASN
1	A	155	GLN
1	A	182	ARG
1	A	201	SER
1	A	205	GLU
1	A	216	GLU
1	A	221	LYS
1	A	222	MET
1	A	247	LYS
1	A	277	ARG
1	A	294	PHE
1	A	312	ARG
1	A	357	LYS
1	A	362	LEU
1	A	382	HIS
1	A	387	ILE
1	A	392	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	A	63	GLN

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Mol	Chain	Res	Type
1	A	153	ASN
1	A	155	GLN
1	A	193	ASN
1	A	287	GLN
1	A	370	ASN
1	A	373	ASN
1	A	412	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers

EDS was not executed - this section will therefore be empty.