



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:33 PM UTC

PDB ID : 2J42 / pdb_00002j42
Title : low quality crystal structure of the transport component C2-II of the C2-toxin from Clostridium botulinum
Authors : Schleberger, C.; Hochmann, H.; Barth, H.; Aktories, K.; Schulz, G.E.
Deposited on : 2006-08-24
Resolution : 3.13 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

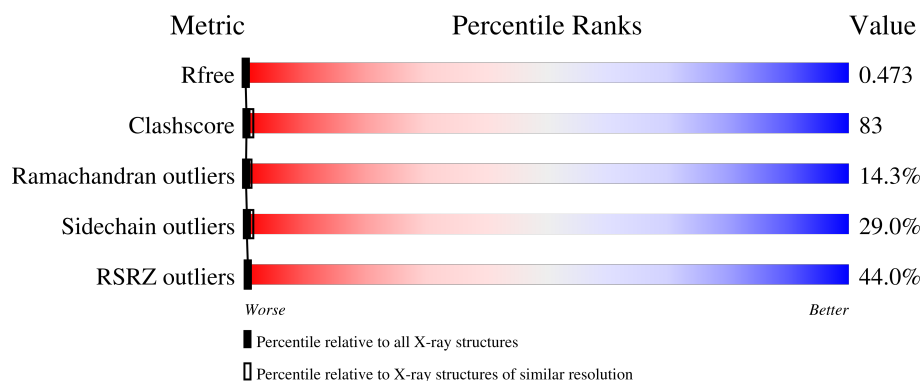
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.13 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))
R_{free}	180053	2351 (3.18-3.10)
Clashscore	190562	2452 (3.18-3.10)
Ramachandran outliers	187476	2324 (3.18-3.10)
Sidechain outliers	187428	2324 (3.18-3.10)
RSRZ outliers	180081	2351 (3.18-3.10)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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.

Mol	Chain	Length	Quality of chain
1	A	721	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3948 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 C2 TOXIN COMPONENT-II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	505	Total	C	N	O	S	0	0	1
			3948	2493	654	786	15			

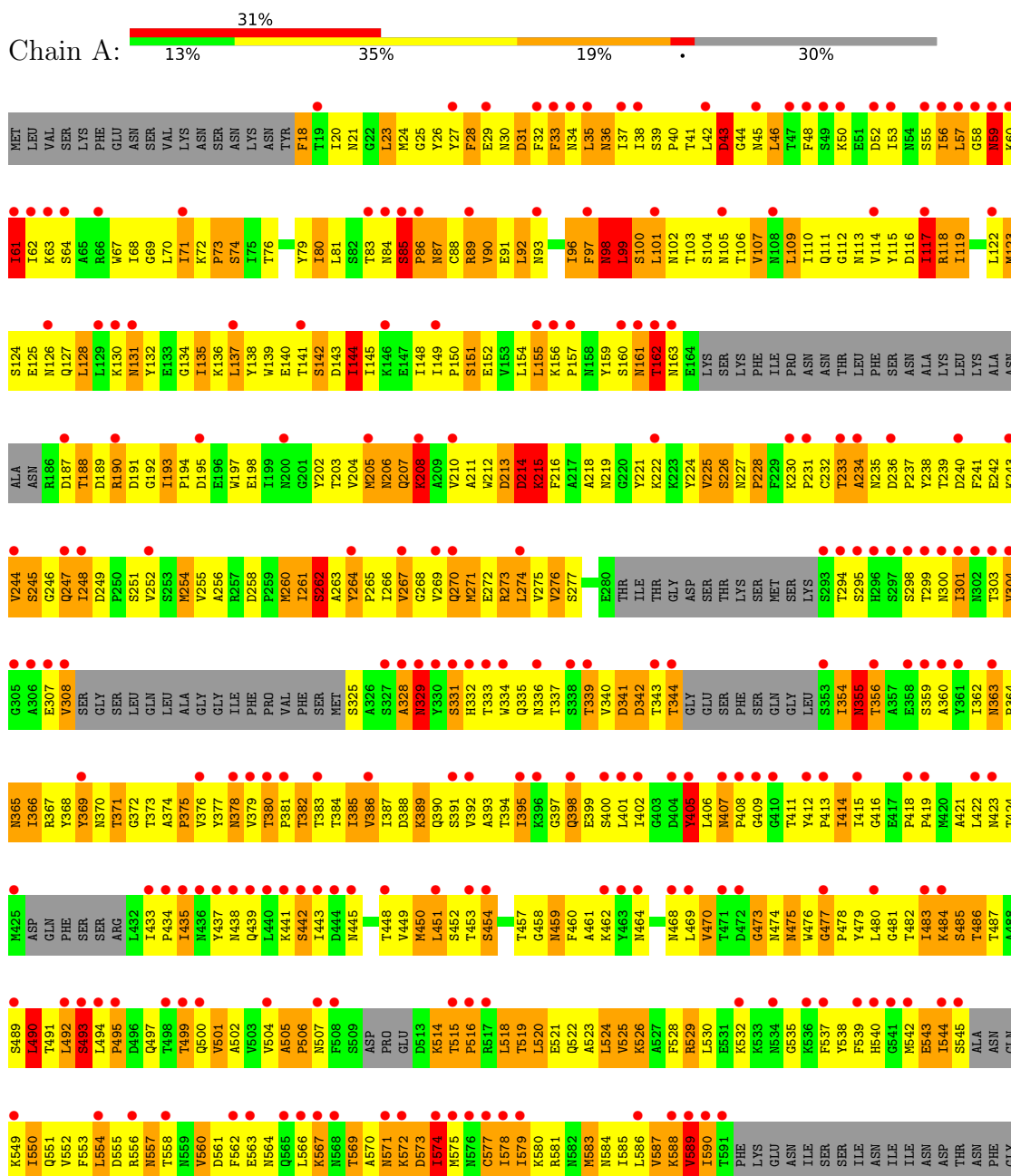
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	357	ALA	GLY	conflict	UNP O86171
A	494	LEU	PHE	conflict	UNP O86171
A	495	PRO	SER	conflict	UNP O86171
A	496	ASP	GLY	conflict	UNP O86171
A	517	ARG	LYS	conflict	UNP O86171
A	529	ARG	ALA	conflict	UNP O86171
A	542	MET	LEU	conflict	UNP O86171
A	556	ARG	SER	conflict	UNP O86171
A	560	VAL	ASN	conflict	UNP O86171
A	571	ASN	ASP	conflict	UNP O86171
A	576	ASN	HIS	conflict	UNP O86171

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

• Molecule 1: C2 TOXIN COMPONENT-II



VAL	GLU	SER	THR	GLY	LEU	SER	LYS	ARG	ILE	TYR	LYS	GLY	ASN	ASP	GLY	ILE	TYR	ARG	ALA	SER	LYS	SER	PHE	SER	PHE	ASP	LYS	SER	ILE	LYS	GLU	ILE	LYS	TYR	PRO	GLU	GLY	PHE	TYR	ARG	LEU	SER	GLY	VAL	PHE	VAL	ILE	GLN	SER	GLU	TYR	GLU	ASP	LYS	PRO	PHE	THR	CYS	ASN	PHE	LYS	LEU	PHE	ASN	ASN
LEU	ILE	TYR	SER	ASN	SER	PHE	ASP	ILE	GLY	TYR	ASP	GLU	PHE	PHE	TYR	PHE	TYR	CYS	ASN	GLY	SER	LYS	SER	PHE	PHE	ASP	ILE	SER	ILE	CYS	ASP	ILE	ILE	ASN	ASN	SER	ILE	ASN	ARG	LEU	SER	GLY	VAL	PHE	LEU	ILE	GLN	SER	GLU	LEU	ASP	LYS	LEU	ILE	ILE										

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	104.40Å 104.40Å 153.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.13 30.00 – 3.13	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-3.13) 99.5 (30.00-3.13)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.99 (at 3.13Å)	Xtriage
Refinement program	TNT BUSTER/TNT	Depositor
R, R_{free}	0.413 , 0.433 0.447 , 0.473	Depositor DCC
R_{free} test set	775 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	84.0	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.64	EDS
Total number of atoms	3948	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.32	1/4019 (0.0%)	0.81	4/5461 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	590	ILE	C-N	-5.70	1.25	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	SER	C-N-CD	-19.14	46.52	125.00
1	A	395	ILE	N-CA-C	6.03	112.66	106.21
1	A	374	ALA	C-N-CD	-5.31	103.23	125.00
1	A	97	PHE	N-CA-C	5.13	115.31	108.23

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	3948	0	3888	652	0
All	All	3948	0	3888	652	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 83.

The worst 5 of 652 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:83:THR:HG23	1:A:98:ASN:HD21	1.10	1.16
1:A:586:LEU:HD21	1:A:588:LYS:HE2	1.31	1.11
1:A:507:ASN:HB2	1:A:581:ARG:HD2	1.36	1.08
1:A:461:ALA:HB1	1:A:470:VAL:HG13	1.36	1.07
1:A:528:PHE:HB2	1:A:530:LEU:HD11	1.38	1.04

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	489/721 (68%)	311 (64%)	108 (22%)	70 (14%)	0 1

5 of 70 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	PHE
1	A	57	LEU
1	A	85	SER
1	A	86	PRO
1	A	213	ASP

5.3.2 Protein sidechains [i](#)

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	451/648 (70%)	320 (71%)	131 (29%)	0 1

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	538	TYR
1	A	554	LEU
1	A	589	VAL
1	A	245	SER
1	A	244	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	ASN
1	A	507	ASN
1	A	500	GLN
1	A	551	GLN
1	A	200	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 oligosaccharides 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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	505/721 (70%)	2.09	222 (43%) 0 0	22, 43, 63, 71	0

The worst 5 of 222 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	562	PHE	8.6
1	A	566	LEU	8.5
1	A	344	THR	7.8
1	A	62	ILE	7.1
1	A	48	PHE	6.9

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.