



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 11:02 AM UTC

PDB ID : 2B7L / pdb_00002b7l
Title : Crystal Structure of CTP:Glycerol-3-Phosphate Cytidylyltransferase from Staphylococcus aureus
Authors : Fong, D.H.; Yim, V.C.-N.; D'Elia, M.A.; Brown, E.D.; Berghuis, A.M.
Deposited on : 2005-10-04
Resolution : 3.00 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
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

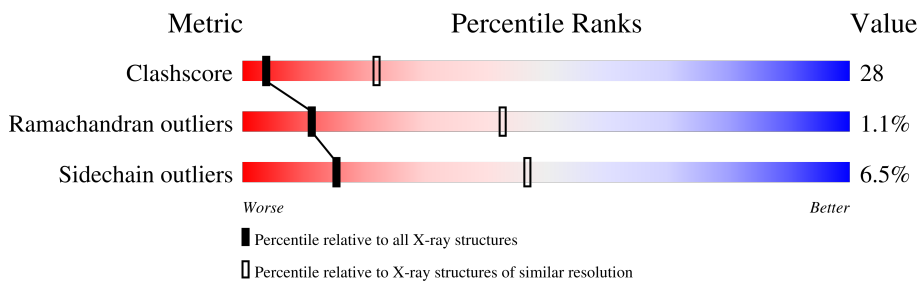
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	132	
1	B	132	
1	C	132	
1	D	132	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3880 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 glycerol-3-phosphate cytidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	115	982	632	161	183	6	9	0	0
1	B	113	966	623	159	178	6	11	0	0
1	C	113	966	623	159	178	6	10	0	0
1	D	113	966	623	159	178	6	8	0	0

F1598	I1609
F1599	Y1610
D1600	L1611
F1601	K1612
L1602	R1613
K1603	THR
D1604	GLU
	GLY
	ILE
	SER
	THR
	THR
	LYS
	ILE
	LYS
	GLN
	GLU
	LEU
	TYR
	GLY
	LYS
	LYS
	ASP
	ALA
	LYS

4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	92.15Å 92.15Å 156.12Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.08 – 3.00	Depositor
% Data completeness (in resolution range)	92.4 (46.08-3.00)	Depositor
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.239 , 0.275	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	3880	wwPDB-VP
Average B, all atoms (Å ²)	30.0	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	0.46	0/1004	0.87	2/1347 (0.1%)
1	B	0.48	0/988	0.87	1/1325 (0.1%)
1	C	0.49	0/988	0.93	2/1325 (0.2%)
1	D	0.46	0/988	0.89	0/1325
All	All	0.47	0/3968	0.89	5/5322 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	14	HIS	N-CA-C	-6.60	99.07	109.50
1	B	515	TYR	N-CA-C	6.46	119.14	111.71
1	C	1043	ILE	N-CA-C	-6.09	104.41	110.62
1	C	1013	LEU	N-CA-C	5.98	118.72	110.35
1	A	41	ASN	N-CA-C	-5.86	104.89	111.28

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	982	0	959	67	0
1	B	966	0	943	51	0
1	C	966	0	943	75	0
1	D	966	0	943	44	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3880	0	3788	215	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 28.

The worst 5 of 215 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:112:LYS:HD3	1:A:112:LYS:H	1.04	1.09
1:D:1520:LEU:HD22	1:D:1611:LEU:HD12	1.32	1.06
1:C:1023:ARG:HH22	1:C:1112:LYS:HG3	1.24	1.02
1:A:23:ARG:HH11	1:A:112:LYS:HE2	1.17	1.02
1:D:1525:ARG:HH21	1:D:1529:ASP:HA	1.28	0.96

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	113/132 (86%)	98 (87%)	13 (12%)	2 (2%)	6	31
1	B	111/132 (84%)	104 (94%)	6 (5%)	1 (1%)	14	48
1	C	111/132 (84%)	102 (92%)	9 (8%)	0	100	100
1	D	111/132 (84%)	100 (90%)	9 (8%)	2 (2%)	6	31
All	All	446/528 (84%)	404 (91%)	37 (8%)	5 (1%)	11	43

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	TYR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	113	ARG
1	B	612	LYS
1	D	1612	LYS
1	D	1544	LYS

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	106/120 (88%)	101 (95%)	5 (5%)	23	58
1	B	104/120 (87%)	96 (92%)	8 (8%)	12	40
1	C	104/120 (87%)	99 (95%)	5 (5%)	23	57
1	D	104/120 (87%)	95 (91%)	9 (9%)	9	35
All	All	418/480 (87%)	391 (94%)	27 (6%)	15	47

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1020	LEU
1	C	1039	GLU
1	D	1557	MET
1	C	1035	LEU
1	D	1503	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	554	GLN
1	C	1041	ASN
1	D	1554	GLN
1	C	1093	HIS
1	B	514	HIS

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 [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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.