

wwPDB X-ray Structure Validation Summary Report (i)

Oct 17, 2023 – 07:07 PM EDT

PDB ID : 1WVC

Title: alpha-D-glucose-1-phosphate cytidylyltransferase complexed with CTP

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Deposited on : 2004-12-14

Resolution : 2.50 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 (i) 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 (1)) were used in the production of this report:

MolProbity: 4.02b-467

Mogul : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

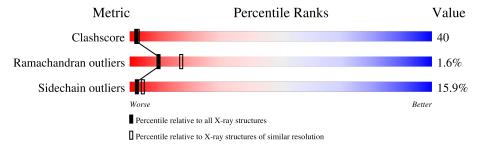
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 2.50 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	Similar resolution		
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$		
Clashscore	141614	5346 (2.50-2.50)		
Ramachandran outliers	138981	5231 (2.50-2.50)		
Sidechain outliers	138945	5233 (2.50-2.50)		

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 <=5%

Mol	Chain	Length	Quality of chain					
1	٨	250						
1	A	259	35%	49%	12% • •			



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2119 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 Glucose-1-phosphate cytidylyltransferase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	٨	254	Total	С	N	О	S	0	0	0
1	A	204	1996	1287	332	364	13	0	0	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	cloning artifact	UNP P26396
A	2	ALA	-	cloning artifact	UNP P26396
A	3	SER	-	cloning artifact	UNP P26396

• Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

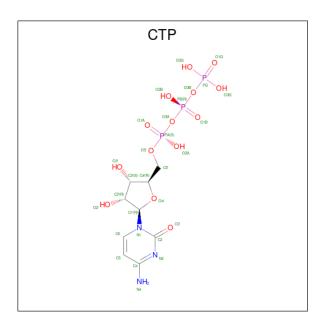
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0

• Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ni 1 1	0	0

• Molecule 4 is CYTIDINE-5'-TRIPHOSPHATE (three-letter code: CTP) (formula: $C_9H_{16}N_3O_{14}P_3$).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	A	1	Total	С	N	О	Р	0	0
1	11	*	29	9	3	14	3		

• Molecule 5 is water.

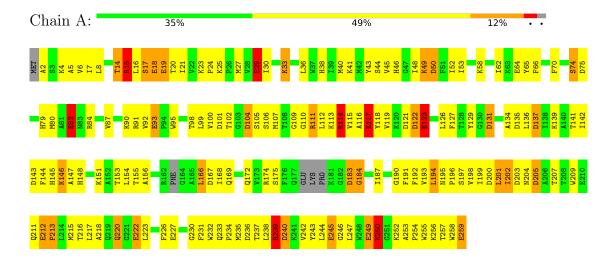
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	91	Total O 91 91	0	0



3 Residue-property plots (i)

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. 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. 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: Glucose-1-phosphate cytidylyltransferase





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 63 2 2	Depositor	
Cell constants	84.20Å 84.20Å 157.40Å	D	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	25.00 - 2.50	Depositor	
rtesolution (A)	19.83 - 2.50	EDS	
% Data completeness	97.4 (25.00-2.50)	Depositor	
(in resolution range)	97.8 (19.83-2.50)	EDS	
R_{merge}	(Not available)	Depositor	
R_{sym}	0.06	Depositor	
$< I/\sigma(I) > 1$	0.90 (at 2.50Å)	Xtriage	
Refinement program	TNT	Depositor	
R, R_{free}	0.199 , 0.272	Depositor	
It, It free	0.297 , (Not available)	DCC	
R_{free} test set	No test flags present.	wwPDB-VP	
Wilson B-factor (\mathring{A}^2)	41.4	Xtriage	
Anisotropy	0.201	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.30, 94.9	EDS	
L-test for twinning ²	$ < L > = 0.48, < L^2> = 0.31$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.88	EDS	
Total number of atoms	2119	wwPDB-VP	
Average B, all atoms (\mathring{A}^2)	44.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.21% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CTP, NI

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	Bo	nd lengths	Bond angles		
		Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
	1	A	0.98	16/2048 (0.8%)	1.42	32/2768 (1.2%)	

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$Ideal(\AA)$
1	A	117	GLU	CD-OE2	7.14	1.33	1.25
1	A	259	GLU	CD-OE2	7.07	1.33	1.25
1	A	64	GLU	CD-OE2	7.04	1.33	1.25
1	A	212	GLU	CA-C	-6.96	1.34	1.52
1	A	183	ASP	N-CA	-6.42	1.33	1.46

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	A	183	ASP	CB-CA-C	-9.17	92.06	110.40
1	A	101	ASP	CB-CG-OD1	8.69	126.12	118.30
1	A	205	ASP	CB-CG-OD2	-8.24	110.89	118.30
1	A	236	ASP	CB-CG-OD1	8.00	125.50	118.30
1	A	135	ASP	CB-CG-OD2	-7.51	111.54	118.30

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	1996	0	1948	158	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	29	0	10	4	0
5	A	91	0	0	3	0
All	All	2119	0	1958	158	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 40.

The worst 5 of 158 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)	
1:A:211:GLN:O	1:A:215:MET:SD	2.15	1.04	
1:A:212:GLU:H	1:A:213:PRO:HD2	1.27	0.99	
1:A:43:TYR:HB3	1:A:48:ILE:HB	1.46	0.97	
1:A:212:GLU:N	1:A:213:PRO:HD2	1.90	0.86	
1:A:183:ASP:OD1	1:A:184:GLY:N	2.15	0.79	

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	248/259 (96%)	207 (84%)	37 (15%)	4 (2%)	9 17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	117	GLU
1	A	250	LYS
1	A	230	GLY

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Mol	Chain	Res	Type
1	A	213	PRO

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	207/215~(96%)	174 (84%)	33 (16%)	2 4	

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	202	ILE
1	A	220	GLN
1	A	259	GLU
1	A	91	ARG
1	A	82	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	GLN
1	A	177	GLN
1	A	195	ASN
1	A	219	GLN
1	A	233	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
MIOI		Chain		Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	СТР	A	401	2	26,30,30	1.26	2 (7%)	39,47,47	1.73	7 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	CTP	A	401	2	-	4/22/38/38	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(Å)	$\operatorname{Ideal}(ext{\AA})$
4	A	401	CTP	C4-N4	-4.59	1.23	1.33
4	A	401	CTP	C4-N3	2.23	1.39	1.34

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
4	A	401	CTP	C5-C4-N3	-5.14	112.58	121.33
4	A	401	CTP	C5-C4-N4	4.77	128.08	120.57
4	A	401	CTP	C4-N3-C2	4.50	127.52	120.25
4	A	401	CTP	C6-C5-C4	2.78	121.99	117.50
4	A	401	CTP	O2-C2-N1	2.71	124.48	118.89

There are no chirality outliers.



All (4) torsion outliers are listed below:

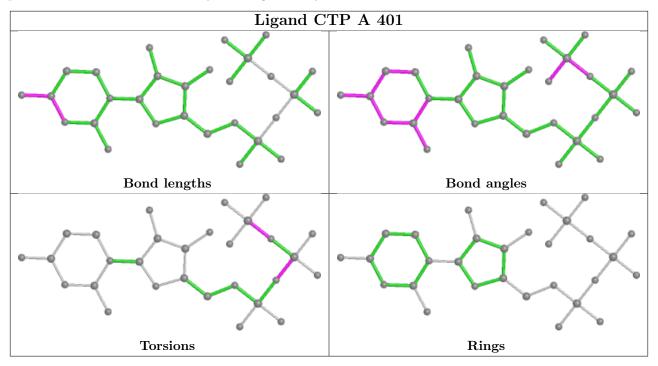
Mol	Chain	Res	Type	Atoms
4	A	401	CTP	PB-O3B-PG-O1G
4	A	401	CTP	PA-O3A-PB-O2B
4	A	401	CTP	PB-O3B-PG-O2G
4	A	401	CTP	PB-O3B-PG-O3G

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	CTP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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 (i)

6.1 Protein, DNA and RNA chains (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

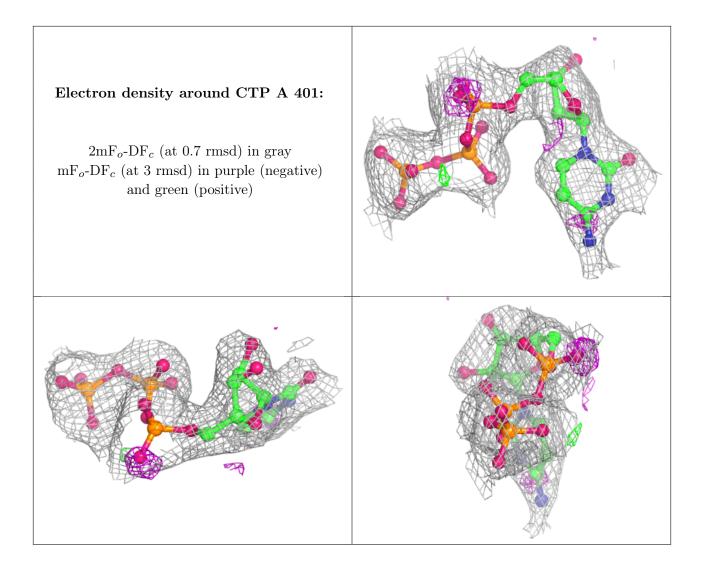
Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

