



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 12:40 am BST

PDB ID : 5WCE
Title : Caulobacter crescentus pol III beta
Authors : Oakley, A.J.
Deposited on : 2017-06-30
Resolution : 1.90 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	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)	:	2.11

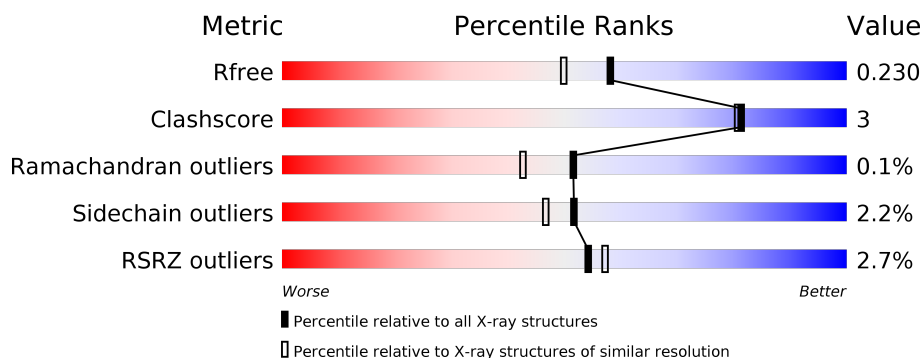
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 ≥ 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	379	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div>••</div> </div> </div>
1	B	379	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>7%</div> <div>••</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6185 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 DNA polymerase III subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	370	Total	C	N	O	S	0	5	0
			2827	1794	481	542	10			
1	B	369	Total	C	N	O	S	0	8	0
			2822	1793	481	537	11			

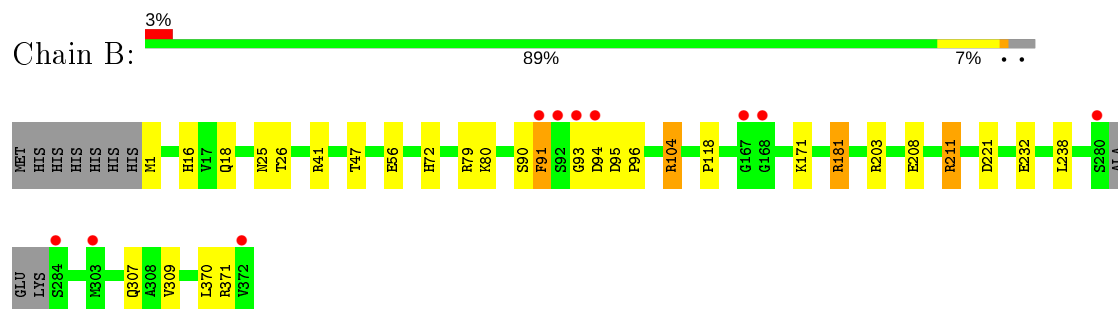
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP P0CAU5
A	-5	HIS	-	expression tag	UNP P0CAU5
A	-4	HIS	-	expression tag	UNP P0CAU5
A	-3	HIS	-	expression tag	UNP P0CAU5
A	-2	HIS	-	expression tag	UNP P0CAU5
A	-1	HIS	-	expression tag	UNP P0CAU5
A	0	HIS	-	expression tag	UNP P0CAU5
B	-6	MET	-	initiating methionine	UNP P0CAU5
B	-5	HIS	-	expression tag	UNP P0CAU5
B	-4	HIS	-	expression tag	UNP P0CAU5
B	-3	HIS	-	expression tag	UNP P0CAU5
B	-2	HIS	-	expression tag	UNP P0CAU5
B	-1	HIS	-	expression tag	UNP P0CAU5
B	0	HIS	-	expression tag	UNP P0CAU5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	254	Total	O	0	0
			254	254		
2	B	282	Total	O	0	0
			282	282		

- Molecule 1: DNA polymerase III subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.86Å 59.57Å 86.49Å 90.00° 92.89° 90.00°	Depositor
Resolution (Å)	86.38 – 1.90 31.81 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.9 (86.38-1.90) 92.9 (31.81-1.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.187 , 0.226 0.195 , 0.230	Depositor DCC
R_{free} test set	3082 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.419	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.019 for h,-k,-l 0.014 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6185	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 55.45 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.1582e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

5.1 Standard geometry

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	0.77	0/2890	0.92	9/3930 (0.2%)
1	B	0.79	0/2891	0.97	11/3933 (0.3%)
All	All	0.78	0/5781	0.94	20/7863 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	211[A]	ARG	NE-CZ-NH2	-8.87	115.87	120.30
1	B	211[B]	ARG	NE-CZ-NH2	-8.87	115.87	120.30
1	B	104	ARG	NE-CZ-NH1	8.72	124.66	120.30
1	A	104	ARG	NE-CZ-NH2	-8.42	116.09	120.30
1	B	104	ARG	NE-CZ-NH2	-8.41	116.09	120.30
1	B	91	PHE	CB-CA-C	7.93	126.25	110.40
1	A	104	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	A	95	ASP	CB-CA-C	7.24	124.87	110.40
1	A	203	ARG	NE-CZ-NH1	7.10	123.85	120.30
1	B	211[A]	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	B	211[B]	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	B	203	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	A	211	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	B	79	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	B	95	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A	265	ASP	CB-CG-OD1	5.53	123.28	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	181	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	A	301	ARG	NE-CZ-NH1	5.11	122.86	120.30
1	A	55	ASP	CB-CG-OD1	5.10	122.89	118.30
1	A	86	ASP	CB-CG-OD2	-5.06	113.75	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	93	GLY	Peptide

5.2 Too-close contacts

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	2827	0	2855	16	0
1	B	2822	0	2851	16	0
2	A	254	0	0	2	0
2	B	282	0	0	5	0
All	All	6185	0	5706	30	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 3.

All (30) 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:279:ILE:HD11	1:A:300:VAL:HG12	1.51	0.93
1:A:313:GLU:OE2	1:B:104:ARG:NH2	2.22	0.73
1:B:25[A]:ASN:OD1	2:B:401:HOH:O	2.07	0.72
1:B:1:MET:N	2:B:402:HOH:O	2.29	0.66
1:A:279:ILE:HD11	1:A:300:VAL:CG1	2.26	0.61
1:A:341:GLN:NE2	2:A:402:HOH:O	2.35	0.59
1:A:108:ASN:ND2	2:A:403:HOH:O	2.40	0.55
1:B:41:ARG:NH1	1:B:56:GLU:OE1	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:GLN:OE1	1:B:72[A]:HIS:ND1	2.35	0.53
1:A:280:SER:HB3	1:A:285[B]:ARG:HG2	1.90	0.52
1:A:120:MET:SD	1:A:228:LYS:HE2	2.49	0.52
1:A:41:ARG:NH2	1:A:56:GLU:OE2	2.42	0.52
1:B:171:LYS:NZ	2:B:404:HOH:O	2.35	0.52
1:B:211[B]:ARG:NH2	2:B:408:HOH:O	2.43	0.51
1:A:278:THR:O	1:A:278:THR:HG22	2.10	0.51
1:A:67:ILE:CD1	1:A:98:LEU:HD13	2.42	0.50
1:B:307:GLN:HE21	1:B:309:VAL:CG2	2.25	0.49
1:B:371:ARG:NH2	2:B:405:HOH:O	2.37	0.49
1:A:278:THR:OG1	1:B:80:LYS:HD2	2.13	0.49
1:B:208:GLU:OE1	1:B:211[A]:ARG:NH1	2.48	0.46
1:B:16:HIS:O	1:B:211[A]:ARG:NH2	2.47	0.46
1:A:279:ILE:CD1	1:A:300:VAL:HG12	2.35	0.45
1:B:307:GLN:HE21	1:B:309:VAL:HG23	1.82	0.45
1:B:47:THR:HG21	1:B:118:PRO:HG2	2.00	0.44
1:B:221:ASP:HB2	1:B:232:GLU:HB3	2.00	0.44
1:A:18:GLN:OE1	1:A:72[A]:HIS:ND1	2.37	0.43
1:B:91:PHE:HE1	1:B:96:PRO:O	2.01	0.43
1:A:307:GLN:HE21	1:A:309:VAL:HG23	1.84	0.43
1:A:307:GLN:HE21	1:A:309:VAL:CG2	2.32	0.42
1:A:33:ILE:HG13	1:A:71:ALA:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	371/379 (98%)	362 (98%)	9 (2%)	0	100	100
1	B	373/379 (98%)	361 (97%)	11 (3%)	1 (0%)	41	31
All	All	744/758 (98%)	723 (97%)	20 (3%)	1 (0%)	51	43

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	94	ASP

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	303/314 (96%)	294 (97%)	9 (3%)	41	33
1	B	302/314 (96%)	297 (98%)	5 (2%)	60	57
All	All	605/628 (96%)	591 (98%)	14 (2%)	52	45

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	THR
1	A	90	SER
1	A	95	ASP
1	A	181	ARG
1	A	238	LEU
1	A	285[A]	ARG
1	A	285[B]	ARG
1	A	301	ARG
1	A	370	LEU
1	B	26	THR
1	B	90	SER
1	B	181	ARG
1	B	238	LEU
1	B	370	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	108	ASN
1	A	307	GLN
1	B	307	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 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 ⓘ

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	370/379 (97%)	-0.07	10 (2%) 54 57	16, 28, 52, 68	4 (1%)
1	B	369/379 (97%)	-0.09	10 (2%) 54 57	16, 26, 49, 69	4 (1%)
All	All	739/758 (97%)	-0.08	20 (2%) 54 57	16, 27, 50, 69	8 (1%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	168	GLY	5.4
1	B	372	VAL	5.1
1	A	281	ALA	5.1
1	B	284	SER	4.5
1	A	167	GLY	4.1
1	B	91	PHE	3.8
1	A	303	MET	3.5
1	A	24	ARG	3.3
1	A	94	ASP	3.3
1	B	94	ASP	3.1
1	B	303	MET	3.1
1	B	93	GLY	3.0
1	A	91	PHE	3.0
1	A	153	ARG	2.7
1	B	167	GLY	2.6
1	A	372	VAL	2.3
1	A	283	LYS	2.1
1	B	168	GLY	2.1
1	B	92	SER	2.1
1	B	280	SER	2.0

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 carbohydrates 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.