



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3RCE
Title : Bacterial oligosaccharyltransferase PglB
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Deposited on : 2011-03-31
Resolution : 3.40 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

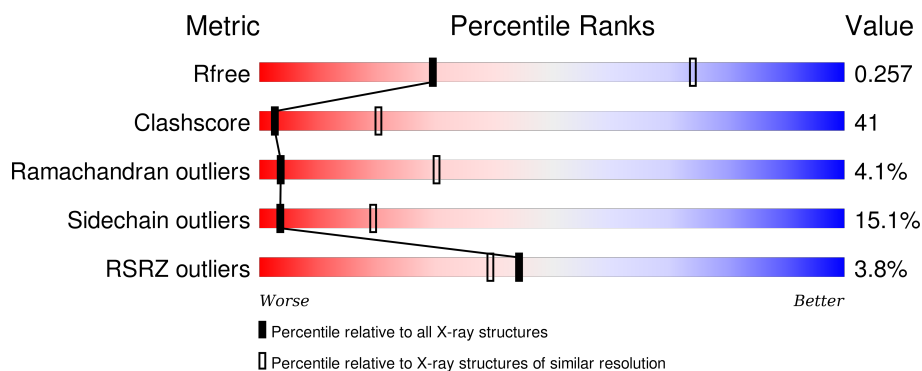
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

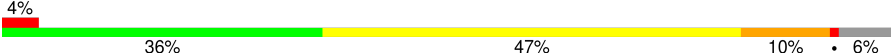

The reported resolution of this entry is 3.40 Å.

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}	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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. 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	724	 4% 36% 47% 10% • 6%
2	B	8	 63% 25% 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MG	A	725	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5668 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 Oligosaccharide transferase to N-glycosylate proteins.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	683	Total	C	N	O	S	0	0	0
			5606	3730	857	990	29			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLU	LYS	ENGINEERED MUTATION	UNP B9KDD4
A	108	THR	ALA	SEE REMARK 999	UNP B9KDD4
A	187	ILE	VAL	SEE REMARK 999	UNP B9KDD4
A	227	ALA	THR	SEE REMARK 999	UNP B9KDD4
A	275	SER	LEU	SEE REMARK 999	UNP B9KDD4
A	536	GLN	LYS	SEE REMARK 999	UNP B9KDD4
A	550	ASN	ASP	SEE REMARK 999	UNP B9KDD4
A	681	ALA	SER	SEE REMARK 999	UNP B9KDD4
A	699	VAL	ILE	SEE REMARK 999	UNP B9KDD4
A	713	GLU	-	EXPRESSION TAG	UNP B9KDD4
A	714	PHE	-	EXPRESSION TAG	UNP B9KDD4
A	715	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	716	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	717	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	718	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	719	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	720	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	721	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	722	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	723	HIS	-	EXPRESSION TAG	UNP B9KDD4
A	724	HIS	-	EXPRESSION TAG	UNP B9KDD4

- Molecule 2 is a protein called Substrate Mimic Peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	8	Total	C	N	O	5	0	0
			59	33	11	15			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	O	0	0
			1	1		

- Molecule 2: Substrate Mimic Peptide

Chain B:  63% 25% 13%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.06 Å 116.10 Å 175.04 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.98 – 3.40 29.98 – 3.40	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.98-3.40) 97.4 (29.98-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 3.39 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.238 , 0.271 0.228 , 0.257	Depositor DCC
R_{free} test set	1999 reflections (8.39%)	DCC
Wilson B-factor (Å ²)	112.7	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 71.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 23843 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5668	wwPDB-VP
Average B, all atoms (Å ²)	129.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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, PPN

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	0.53	0/5752	0.71	2/7791 (0.0%)
2	B	0.53	0/43	0.83	0/55
All	All	0.53	0/5795	0.71	2/7846 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	337	LEU	CA-CB-CG	5.76	128.54	115.30
1	A	246	LEU	CA-CB-CG	5.10	127.03	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	5606	0	5628	465	0
2	B	59	0	42	3	0
3	A	2	0	0	0	0
4	A	1	0	0	0	0
All	All	5668	0	5670	466	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 41.

The worst 5 of 466 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:169:THR:HG21	1:A:185:SER:HB3	1.22	1.14
1:A:488:LYS:HD3	1:A:488:LYS:O	1.47	1.09
1:A:20:ILE:HG13	1:A:119:ILE:HD11	1.25	1.06
1:A:329:MET:HE1	1:A:336:VAL:HG13	1.39	1.03
1:A:173:LEU:HB2	1:A:181:THR:HG21	1.41	0.98

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	677/724 (94%)	533 (79%)	117 (17%)	27 (4%)	4	31
2	B	5/8 (62%)	3 (60%)	1 (20%)	1 (20%)	0	1
All	All	682/732 (93%)	536 (79%)	118 (17%)	28 (4%)	3	30

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	335	SER
1	A	549	LYS
1	A	590	GLU
1	A	103	ILE
1	A	142	ASN

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	607/646 (94%)	515 (85%)	92 (15%)	3	19
2	B	4/4 (100%)	4 (100%)	0	100	100
All	All	611/650 (94%)	519 (85%)	92 (15%)	3	19

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	273	SER
1	A	327	VAL
1	A	596	SER
1	A	277	LEU
1	A	317	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	203	ASN
1	A	353	HIS
1	A	583	ASN
1	A	176	ASN
1	A	485	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PPN	B	16	2	11,14,15	0.96	1 (9%)	13,18,20	1.91	3 (23%)

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
2	PPN	B	16	2	-	0/8/10/12	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	16	PPN	CB-CA	-2.48	1.48	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	16	PPN	CG-CB-CA	-4.35	104.39	114.21
2	B	16	PPN	O-C-CA	-3.61	116.08	125.49
2	B	16	PPN	CE1-CZ-N1	3.23	122.09	119.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	16	PPN	1	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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	683/724 (94%)	-0.10	26 (3%) 44 39	73, 119, 191, 321	0
2	B	7/8 (87%)	0.04	0 100 100	88, 113, 133, 140	2 (28%)
All	All	690/732 (94%)	-0.10	26 (3%) 44 39	73, 119, 191, 321	2 (0%)

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	259	GLU	5.9
1	A	493	SER	4.7
1	A	622	PHE	3.6
1	A	258	GLU	3.3
1	A	537	THR	3.2

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	PPN	B	16	14/15	0.89	0.28	-	111,118,131,135	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	MG	A	725	1/1	0.96	0.76	9.16	78,78,78,78	0
3	MG	A	726	1/1	0.98	0.18	0.94	65,65,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.