



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2024 – 02:48 PM JST

PDB ID : 4XIG
Title : Crystal structure of bacterial alginate ABC transporter determined through humid air and glue-coating method
Authors : Kaneko, A.; Maruyama, Y.; Mizuno, N.; Baba, S.; Kumasaka, T.; Mikami, B.; Murata, K.; Hashimoto, W.
Deposited on : 2015-01-07
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

<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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

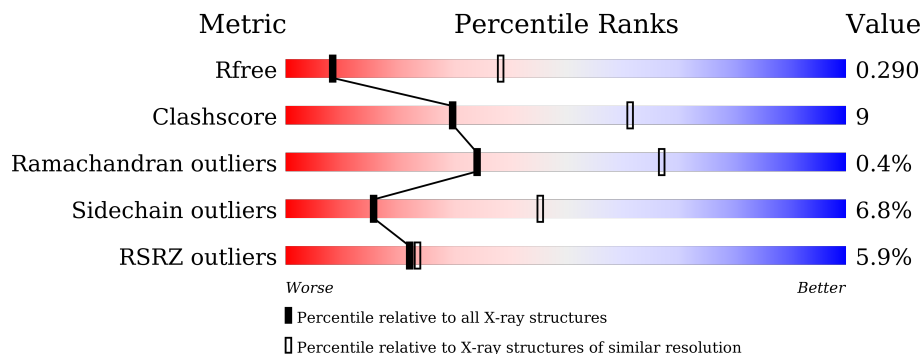
1 Overall quality at a glance

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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (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 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	M	301	 5% 69% 26% . .
2	N	305	 4% 74% 18% . 5%
3	S	363	 6% 71% 24% .
3	T	363	 9% 63% 33% .
4	Q	516	 5% 71% 22% . 5%
5	A	4	 50% 50%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 14266 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 AlgM1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	M	288	2323	1554	369	390	10	0	0	0

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	?	-	THR	deletion	UNP Q9KWT8
M	?	-	SER	deletion	UNP Q9KWT8
M	?	-	ALA	deletion	UNP Q9KWT8
M	?	-	THR	deletion	UNP Q9KWT8
M	?	-	LYS	deletion	UNP Q9KWT8
M	?	-	ALA	deletion	UNP Q9KWT8
M	?	-	GLN	deletion	UNP Q9KWT8
M	?	-	SER	deletion	UNP Q9KWT8
M	?	-	ILE	deletion	UNP Q9KWT8
M	?	-	PRO	deletion	UNP Q9KWT8
M	?	-	LEU	deletion	UNP Q9KWT8
M	?	-	PRO	deletion	UNP Q9KWT8
M	?	-	ALA	deletion	UNP Q9KWT8
M	?	-	ALA	deletion	UNP Q9KWT8
M	?	-	THR	deletion	UNP Q9KWT8
M	?	-	LEU	deletion	UNP Q9KWT8
M	?	-	ASP	deletion	UNP Q9KWT8
M	?	-	VAL	deletion	UNP Q9KWT8
M	?	-	ARG	deletion	UNP Q9KWT8
M	?	-	SER	deletion	UNP Q9KWT8
M	?	-	LYS	deletion	UNP Q9KWT8
M	?	-	PRO	deletion	UNP Q9KWT8
M	?	-	LEU	deletion	UNP Q9KWT8

- Molecule 2 is a protein called AlgM2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	N	290	2293	1530	365	385	13	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	294	LEU	-	expression tag	UNP Q9KWT7
N	295	GLU	-	expression tag	UNP Q9KWT7
N	296	HIS	-	expression tag	UNP Q9KWT7
N	297	HIS	-	expression tag	UNP Q9KWT7
N	298	HIS	-	expression tag	UNP Q9KWT7
N	299	HIS	-	expression tag	UNP Q9KWT7
N	300	HIS	-	expression tag	UNP Q9KWT7
N	301	HIS	-	expression tag	UNP Q9KWT7
N	302	HIS	-	expression tag	UNP Q9KWT7
N	303	HIS	-	expression tag	UNP Q9KWT7
N	304	HIS	-	expression tag	UNP Q9KWT7
N	305	HIS	-	expression tag	UNP Q9KWT7

- Molecule 3 is a protein called AlgS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	S	363	2777	1745	503	518	11	0	0	0
3	T	363	2777	1745	503	518	11	0	0	0

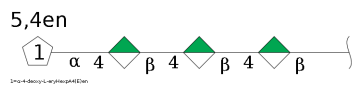
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	160	GLN	GLU	engineered mutation	UNP Q9KWT9
T	160	GLN	GLU	engineered mutation	UNP Q9KWT9

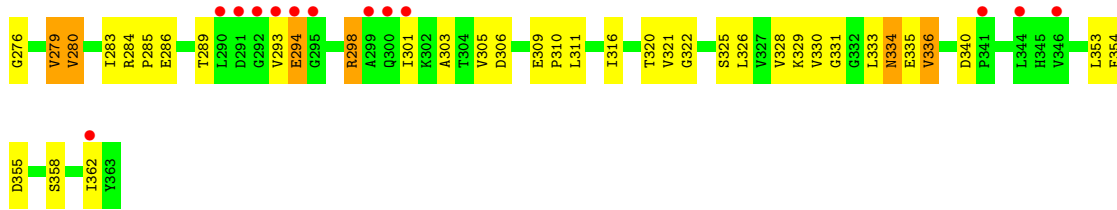
- Molecule 4 is a protein called AlgQ2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	Q	492	4048	2604	693	735	16	0	0	0

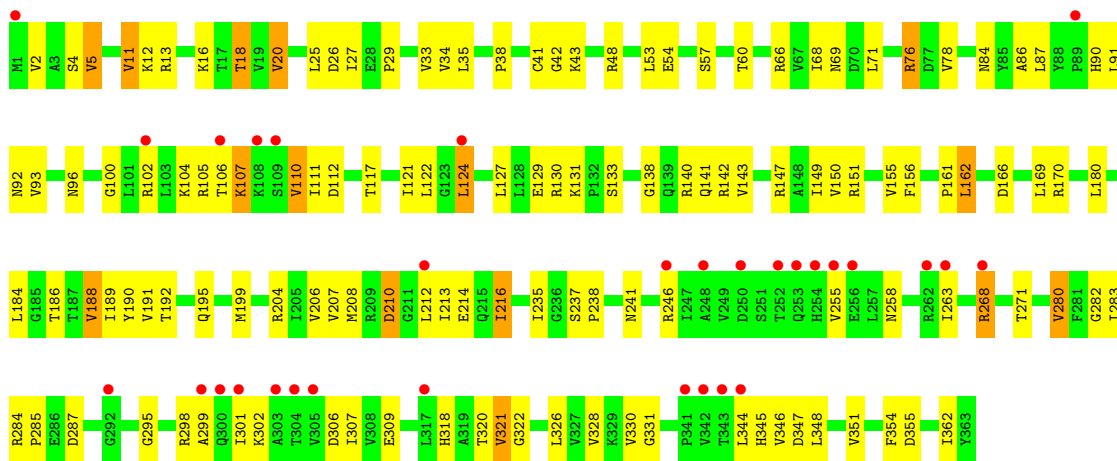
- Molecule 5 is an oligosaccharide called 4-deoxy-alpha-L-erythro-hex-4-enopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid.



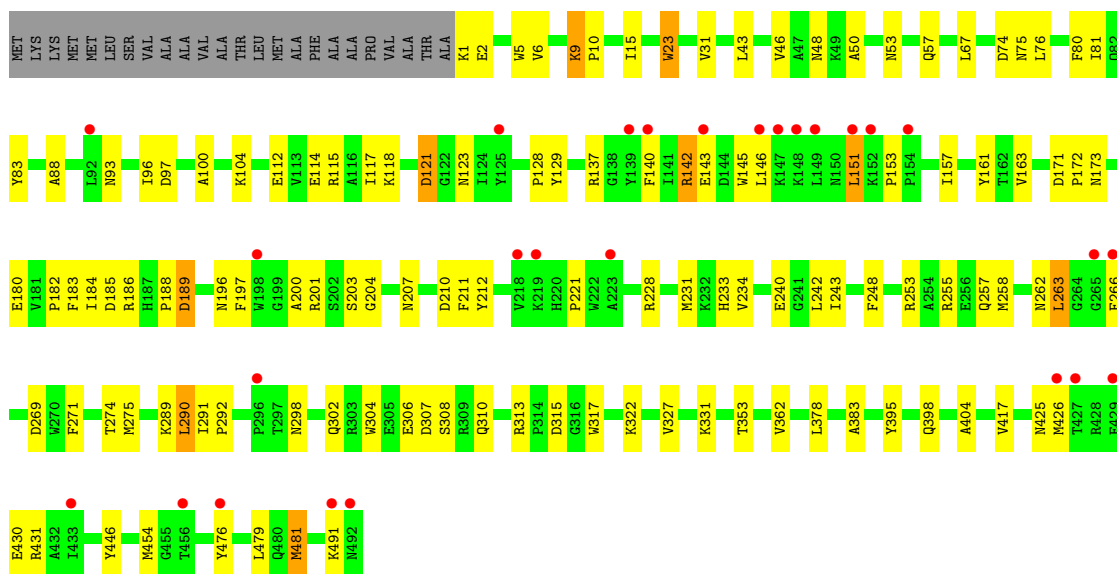
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
5	A	4	48	24	24	0	0	0



• Molecule 3: AlgS



• Molecule 4: AlgQ2



• Molecule 5: 4-deoxy-alpha-L-erythro-hex-4-enopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.17Å 133.41Å 272.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.56 – 3.40 37.56 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (37.56-3.40) 99.7 (37.56-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.29 (at 3.40Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.236 , 0.289 0.239 , 0.290	Depositor DCC
R_{free} test set	1846 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	110.5	Xtrriage
Anisotropy	0.356	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 68.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	14266	wwPDB-VP
Average B, all atoms (Å ²)	128.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MAW, BEM

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	M	0.23	0/2384	0.42	0/3250
2	N	0.25	0/2352	0.44	0/3198
3	S	0.23	0/2822	0.50	0/3826
3	T	0.22	0/2822	0.48	0/3826
4	Q	0.21	0/4168	0.37	0/5640
All	All	0.23	0/14548	0.44	0/19740

There are no bond length outliers.

There are no bond angle outliers.

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	M	2323	0	2412	43	0
2	N	2293	0	2362	41	0
3	S	2777	0	2854	58	0
3	T	2777	0	2854	80	0
4	Q	4048	0	3920	67	0
5	A	48	0	25	0	0
All	All	14266	0	14427	270	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 9.

The worst 5 of 270 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)
3:S:43:LYS:HD3	3:S:44:SER:H	1.43	0.84
3:T:34:VAL:HG22	3:T:190:TYR:HB3	1.68	0.75
3:T:48:ARG:HG3	3:T:53:LEU:HB2	1.69	0.75
3:S:34:VAL:HG22	3:S:190:TYR:HB3	1.69	0.74
3:T:141:GLN:NE2	3:T:161:PRO:O	2.24	0.71

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	M	284/301 (94%)	268 (94%)	16 (6%)	0	100	100
2	N	288/305 (94%)	258 (90%)	28 (10%)	2 (1%)	22	55
3	S	361/363 (99%)	330 (91%)	27 (8%)	4 (1%)	14	44
3	T	361/363 (99%)	334 (92%)	25 (7%)	2 (1%)	25	57
4	Q	490/516 (95%)	460 (94%)	30 (6%)	0	100	100
All	All	1784/1848 (96%)	1650 (92%)	126 (7%)	8 (0%)	34	67

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	N	59	ILE
3	T	111	ILE
2	N	52	VAL
3	S	249	VAL
3	S	336	VAL

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	M	251/260 (96%)	236 (94%)	15 (6%)	19	49
2	N	243/258 (94%)	229 (94%)	14 (6%)	20	50
3	S	307/307 (100%)	280 (91%)	27 (9%)	10	33
3	T	307/307 (100%)	281 (92%)	26 (8%)	10	35
4	Q	424/440 (96%)	402 (95%)	22 (5%)	23	53
All	All	1532/1572 (98%)	1428 (93%)	104 (7%)	16	45

5 of 104 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	Q	9	LYS
4	Q	317	TRP
3	T	321	VAL
4	Q	46	VAL
4	Q	185	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	S	258	ASN
3	S	324	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

4 monosaccharides are 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
5	BEM	A	1	5	13,13,13	0.72	0	18,19,19	1.16	2 (11%)
5	BEM	A	2	5	12,12,13	0.66	0	14,17,19	0.69	0
5	BEM	A	3	5	12,12,13	0.71	0	14,17,19	0.69	0
5	MAW	A	4	5	10,11,12	2.14	1 (10%)	13,15,17	1.74	5 (38%)

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
5	BEM	A	1	5	-	0/4/24/24	0/1/1/1
5	BEM	A	2	5	-	0/4/21/24	0/1/1/1
5	BEM	A	3	5	-	0/4/21/24	0/1/1/1
5	MAW	A	4	5	-	2/4/17/20	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	4	MAW	O5-C5	6.01	1.45	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	4	MAW	O5-C5-C6	4.09	117.66	111.52
5	A	1	BEM	C3-C4-C5	2.59	113.69	109.25
5	A	1	BEM	O5-C5-C4	2.36	113.79	109.57
5	A	4	MAW	C2-C3-C4	-2.31	109.16	112.32
5	A	4	MAW	O5-C5-C4	-2.15	122.99	124.81

There are no chirality outliers.

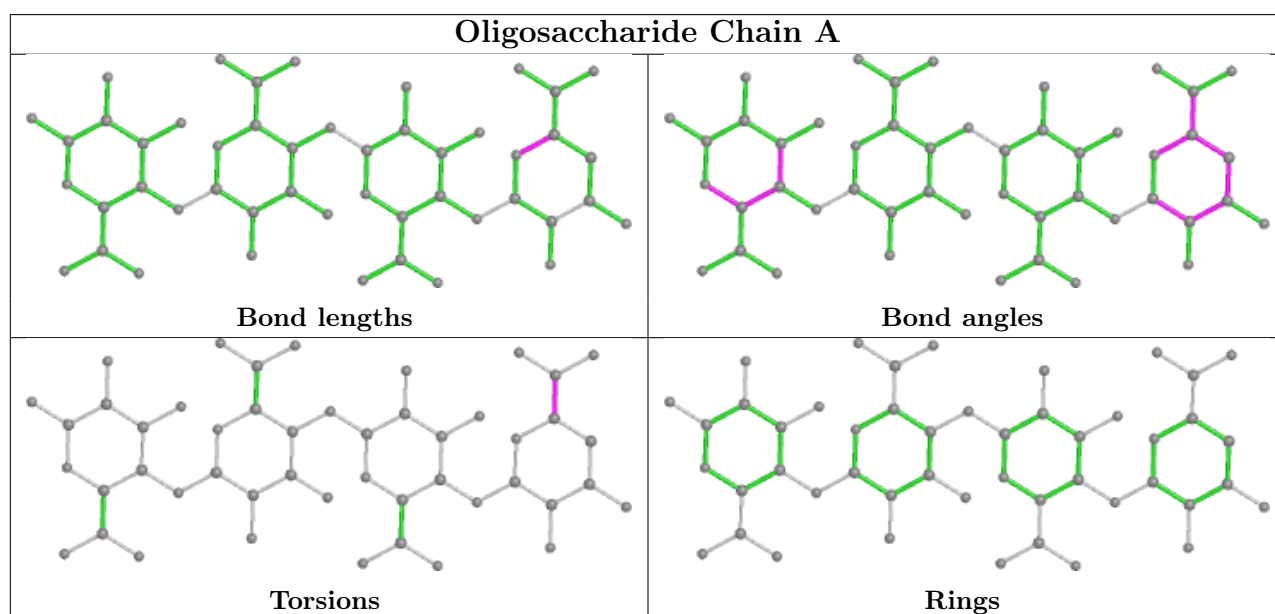
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	4	MAW	O5-C5-C6-O6A
5	A	4	MAW	O5-C5-C6-O6B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



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 [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	M	288/301 (95%)	0.28	16 (5%) 24 25	63, 110, 183, 249	0
2	N	290/305 (95%)	0.12	11 (3%) 40 39	70, 108, 157, 223	0
3	S	363/363 (100%)	0.30	21 (5%) 23 24	64, 113, 172, 276	0
3	T	363/363 (100%)	0.41	31 (8%) 10 12	86, 130, 214, 269	0
4	Q	492/516 (95%)	0.30	27 (5%) 25 25	95, 140, 195, 254	0
All	All	1796/1848 (97%)	0.29	106 (5%) 22 23	63, 123, 192, 276	0

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	Q	492	ASN	6.1
2	N	289	GLY	5.0
4	Q	429	GLU	4.8
3	S	290	LEU	4.7
1	M	65	GLN	4.4

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](#)

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. 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.

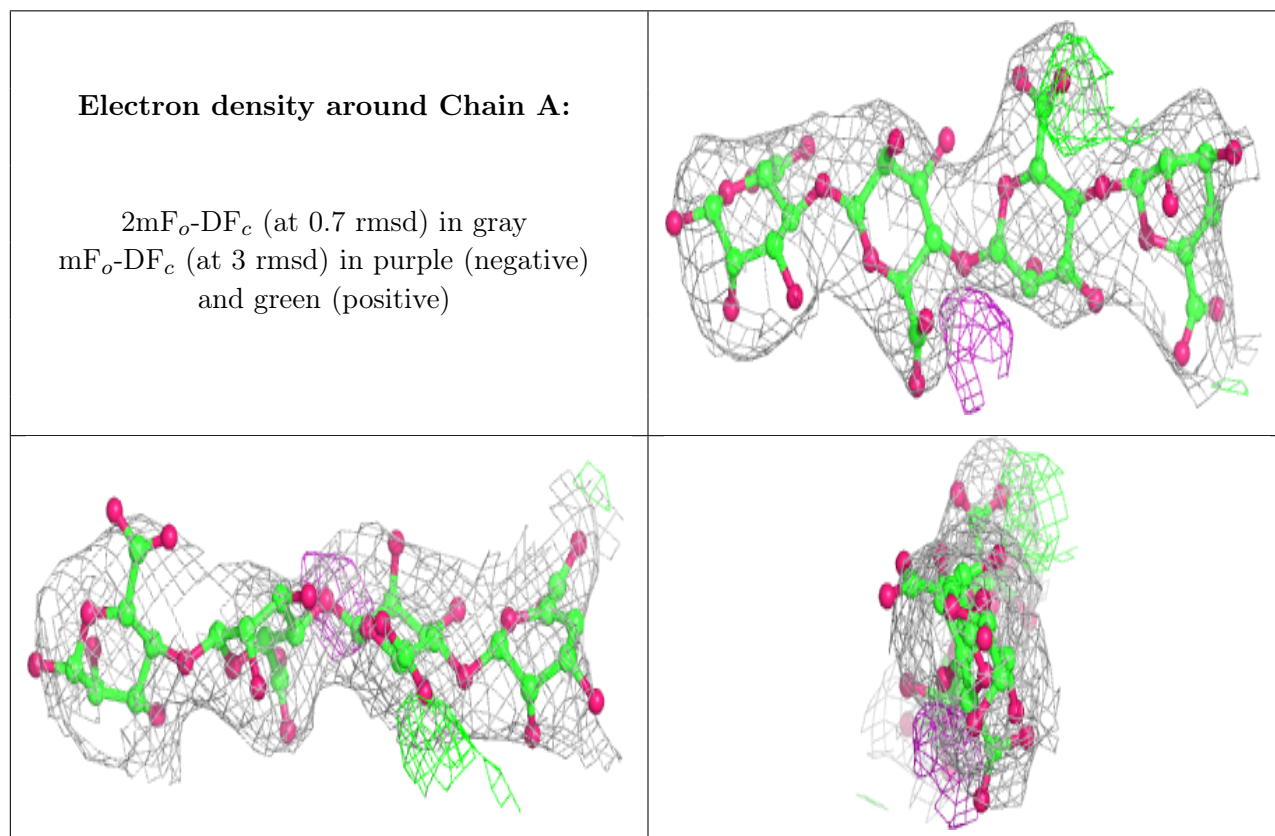
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	BEM	A	2	12/13	0.87	0.38	86,120,150,188	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	BEM	A	1	13/13	0.88	0.52	87,140,163,172	0
5	BEM	A	3	12/13	0.88	0.38	117,126,145,155	0
5	MAW	A	4	11/12	0.91	0.33	133,137,149,155	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.