



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 10:06 AM UTC

PDB ID : 1AA5 / pdb_00001aa5
Title : VANCOMYCIN
Authors : Loll, P.J.; Bevivino, A.E.; Korty, B.D.; Axelsen, P.H.
Deposited on : 1997-01-23
Resolution : 0.89 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 : **FAILED**
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

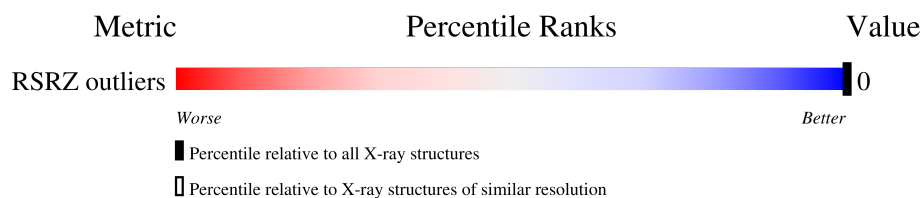
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 0.89 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))
RSRZ outliers	180081	1363 (1.00-0.80)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition [i](#)

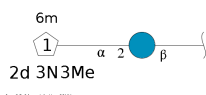
There are 5 unique types of molecules in this entry. The entry contains 461 atoms, of which 177 are hydrogens and 0 are deuteriums.

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 VANCOMYCIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	Cl	H	N				O
1	A	7	Total 139	C 55	Cl 2	H 57	N 8	O 17	0	1	0
1	B	7	Total 141	C 55	Cl 2	H 56	N 9	O 19	0	2	0

- Molecule 2 is an oligosaccharide called vancosamine-(1-2)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
2	C	2	Total 47	C 13	H 25	N 1	O 8	0	1	0
2	D	2	Total 67	C 19	H 35	N 1	O 12	0	1	0

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
3	A	1	8	2	4	2	0	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
4	A	2	2	2	0	0
4	B	2	2	2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	34	34	34	0	7
5	B	21	21	21	0	7

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3 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	28.45Å 28.45Å 65.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	4.00 – 0.89 4.00 – 0.91	Depositor EDS
% Data completeness (in resolution range)	80.0 (4.00-0.89) 85.6 (4.00-0.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	29.86 (at 0.91Å)	Xtrriage
Refinement program	SHELXL-93	Depositor
R, R_{free}	0.124 , (Not available) 0.165 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	6.9	Xtrriage
Anisotropy	0.321	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.20 , 211.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	461	wwPDB-VP
Average B, all atoms (Å ²)	8.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.47% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

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4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

14 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	MLU	B	1	1	7,8,9	1.47	1 (14%)	7,9,11	0.94	1 (14%)
1	GHP	A	4	2,1	10,11,12	0.85	0	11,14,16	0.38	0
1	GHP	A	5	1	10,11,12	1.06	1 (10%)	11,14,16	1.30	2 (18%)
1	MLU	A	1[B]	-	7,8,9	0.95	0	7,9,11	0.94	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLU	A	1[A]	-	7,8,9	0.97	0	7,9,11	0.90	0
1	OMY	A	6	1	12,14,15	1.09	1 (8%)	17,19,21	1.44	1 (5%)
1	3FG	A	7	1	12,13,13	1.34	1 (8%)	14,18,18	1.11	0
1	OMY	B	6	1	12,14,15	1.31	1 (8%)	17,19,21	1.28	1 (5%)
1	3FG	B	7	1	12,13,13	1.44	2 (16%)	14,18,18	1.41	3 (21%)
1	GHP	B	5	1	10,11,12	1.21	1 (10%)	11,14,16	1.19	1 (9%)
1	GHP	B	4[A]	2	10,11,12	0.86	0	11,14,16	1.00	1 (9%)
1	GHP	B	4[B]	2	10,11,12	2.58	1 (10%)	11,14,16	1.56	3 (27%)
1	OMZ	A	2	1	12,14,15	1.07	1 (8%)	17,19,21	0.88	1 (5%)
1	OMZ	B	2	1	12,14,15	0.68	0	17,19,21	0.99	1 (5%)

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
1	MLU	B	1	1	-	0/5/8/10	-
1	GHP	A	4	2,1	-	0/4/6/8	0/1/1/1
1	GHP	A	5	1	-	0/4/6/8	0/1/1/1
1	MLU	A	1[B]	-	-	2/5/8/10	-
1	MLU	A	1[A]	-	-	0/5/8/10	-
1	OMY	A	6	1	-	1/9/10/12	0/1/1/1
1	3FG	A	7	1	-	4/8/8/8	0/1/1/1
1	OMY	B	6	1	-	1/9/10/12	0/1/1/1
1	3FG	B	7	1	-	3/8/8/8	0/1/1/1
1	GHP	B	5	1	-	0/4/6/8	0/1/1/1
1	GHP	B	4[A]	2	-	0/4/6/8	0/1/1/1
1	GHP	B	4[B]	2	-	0/4/6/8	0/1/1/1
1	OMZ	A	2	1	-	1/9/10/12	0/1/1/1
1	OMZ	B	2	1	-	1/9/10/12	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	4[B]	GHP	O4-C4	7.81	1.54	1.37
1	B	7	3FG	OXT-C	-3.26	1.20	1.30
1	A	2	OMZ	CZ-CE1	-2.96	1.36	1.39
1	B	5	GHP	CA-C	2.96	1.56	1.51
1	A	7	3FG	OXT-C	-2.90	1.21	1.30

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	OMY	CG-CB-CA	-4.98	105.04	111.58
1	B	6	OMY	CG-CB-CA	-4.17	106.10	111.58
1	B	7	3FG	CD2-CG2-CB	3.40	123.02	120.09
1	B	4[B]	GHP	O4-C4-C3	-3.07	111.46	120.00
1	B	4[B]	GHP	O4-C4-C5	2.64	127.37	120.00

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2	OMZ	O-C-CA-CB
1	B	2	OMZ	O-C-CA-CB
1	A	6	OMY	O-C-CA-CB
1	B	6	OMY	O-C-CA-CB
1	A	7	3FG	C-CA-CB-CG1

There are no ring outliers.

No monomer is involved in short contacts.

4.5 Carbohydrates [i](#)

6 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
2	BGC	C	1	2,1	11,11,12	1.30	2 (18%)	15,15,17	1.00	1 (6%)
2	RER	C	2[A]	-	7,10,11	1.67	1 (14%)	6,15,17	1.69	1 (16%)
2	RER	C	2[B]	-	7,10,11	3.42	1 (14%)	6,15,17	2.27	2 (33%)
2	BGC	D	1[A]	2,1	11,11,12	1.00	1 (9%)	15,15,17	1.06	1 (6%)
2	BGC	D	1[B]	2,1	11,11,12	1.41	1 (9%)	15,15,17	1.47	3 (20%)
2	RER	D	2	2	7,10,11	0.85	0	6,15,17	0.82	0

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	BGC	C	1	2,1	-	0/2/19/22	0/1/1/1
2	RER	C	2[A]	-	-	-	0/1/1/1
2	RER	C	2[B]	-	-	-	0/1/1/1
2	BGC	D	1[A]	2,1	-	0/2/19/22	0/1/1/1
2	BGC	D	1[B]	2,1	-	2/2/19/22	0/1/1/1
2	RER	D	2	2	-	-	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2[B]	RER	O4-C4	8.75	1.60	1.42
2	C	2[A]	RER	O4-C4	3.75	1.50	1.42
2	D	1[A]	BGC	O2-C2	2.66	1.48	1.43
2	D	1[B]	BGC	O2-C2	2.63	1.48	1.43
2	C	1	BGC	O5-C1	-2.12	1.40	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2[A]	RER	O5-C1-C2	3.95	116.74	111.38
2	C	2[B]	RER	O5-C1-C2	3.95	116.74	111.38
2	C	2[B]	RER	O4-C4-C5	-3.75	103.00	109.46
2	D	1[B]	BGC	C1-C2-C3	3.13	114.20	109.64
2	D	1[B]	BGC	O2-C2-C3	-2.85	104.26	110.15

There are no chirality outliers.

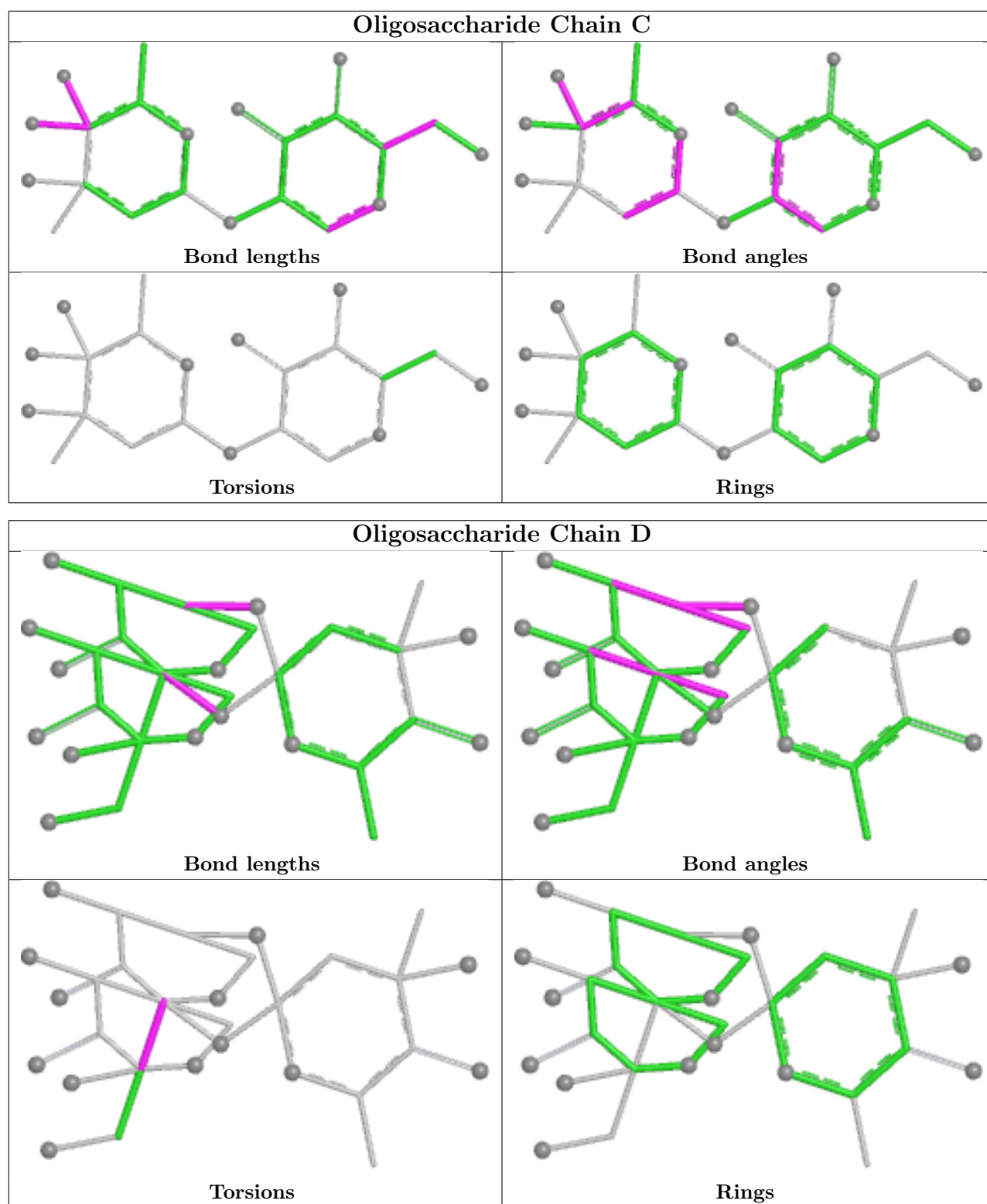
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1[B]	BGC	O5-C5-C6-O6
2	D	1[B]	BGC	C4-C5-C6-O6

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.



4.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 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		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	ACY	A	11	-	3,3,3	1.27	0	3,3,3	1.65	1 (33%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	11	ACY	O-C-CH3	-2.25	113.32	122.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 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	1/7 (14%)	-1.02	0 100 100	4, 4, 4, 4	0
1	B	1/7 (14%)	-0.45	0 100 100	5, 5, 5, 5	1 (100%)
All	All	2/14 (14%)	-0.74	0 100 100	4, 4, 4, 5	1 (50%)

There are no RSRZ outliers to report.

5.2 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. 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.

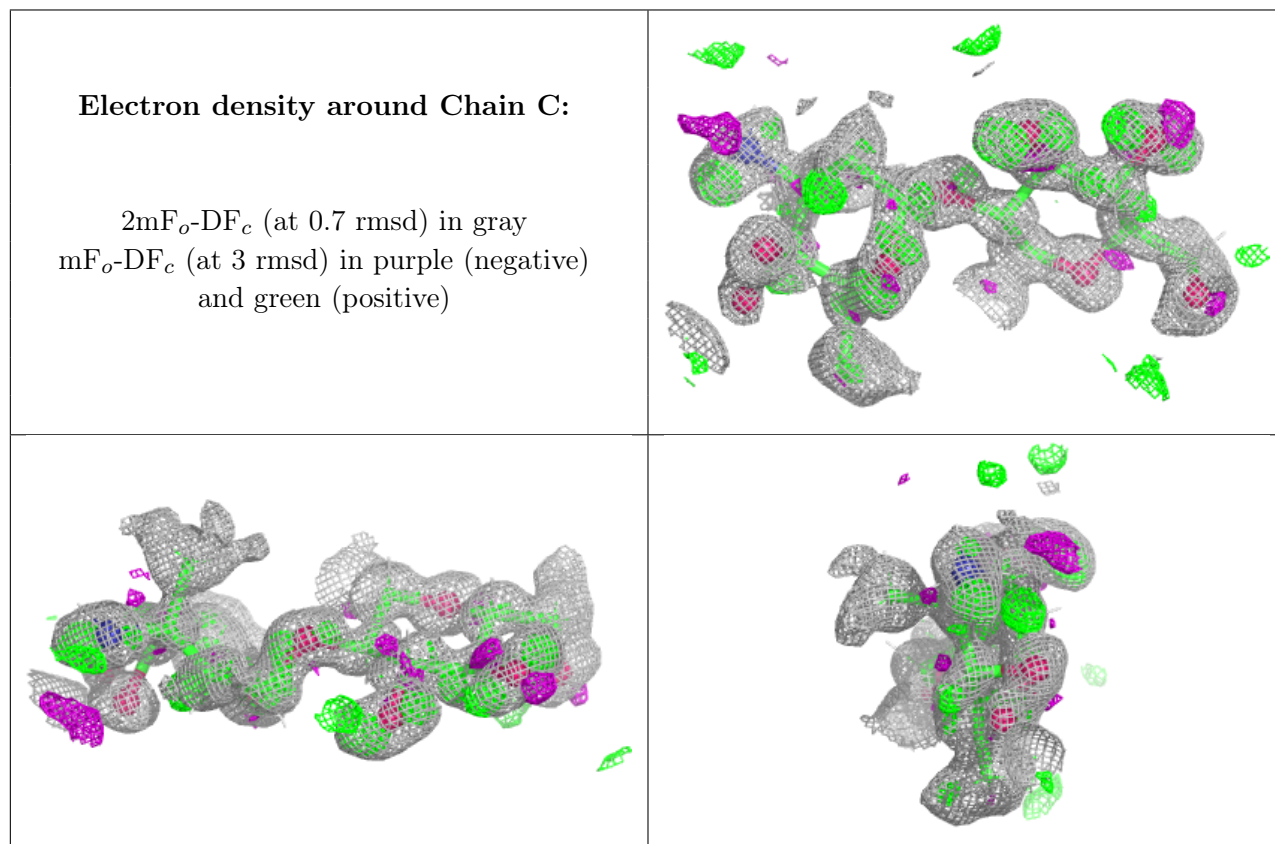
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	3FG	B	7	13/13	0.89	0.07	4,9,17,20	0
1	MLU	B	1	9/10	0.96	0.04	5,8,16,16	0
1	MLU	A	1[A]	9/10	0.98	0.03	3,7,11,11	8
1	GHP	B	4[A]	11/12	0.98	0.03	3,4,6,6	1
1	GHP	B	4[B]	11/12	0.98	0.03	3,4,6,6	1
1	GHP	A	5	11/12	0.98	0.03	2,3,7,8	0
1	GHP	B	5	11/12	0.98	0.03	3,5,7,10	0
1	OMY	B	6	14/15	0.98	0.03	3,5,7,8	0
1	3FG	A	7	13/13	0.98	0.03	3,4,7,9	0
1	MLU	A	1[B]	9/10	0.98	0.03	3,6,10,10	7
1	OMY	A	6	14/15	0.99	0.03	3,4,5,6	0
1	OMZ	B	2	14/15	0.99	0.04	4,5,8,12	0
1	GHP	A	4	11/12	0.99	0.02	2,3,5,5	0
1	OMZ	A	2	14/15	0.99	0.03	3,4,6,7	0

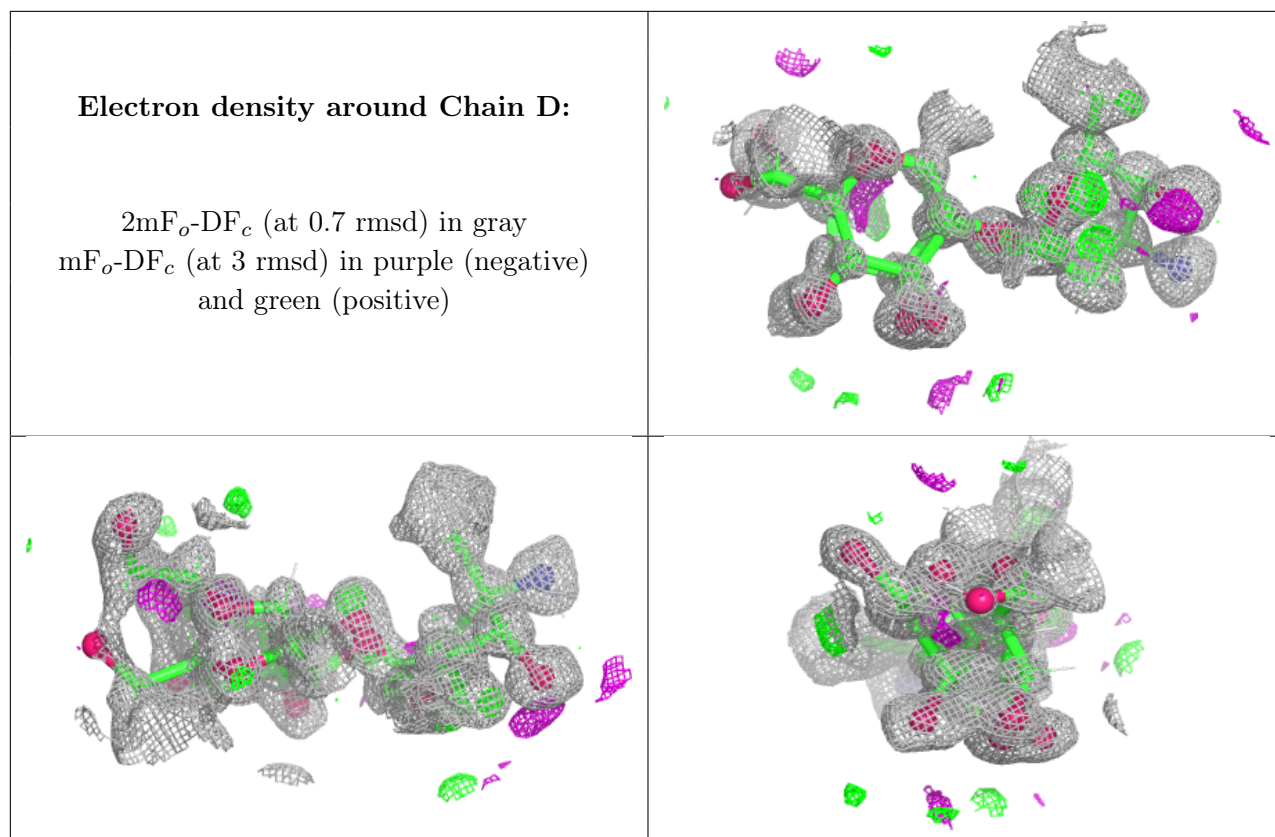
5.3 Carbohydrates [i](#)

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
2	RER	C	2[A]	10/11	0.87	0.08	7,11,18,18	2
2	RER	C	2[B]	10/11	0.87	0.08	6,11,18,18	1
2	BGC	C	1	11/12	0.90	0.08	6,11,20,22	0
2	BGC	D	1[A]	11/12	0.94	0.06	5,8,12,14	21
2	BGC	D	1[B]	11/12	0.94	0.06	4,7,12,17	21
2	RER	D	2	10/11	0.96	0.04	3,6,10,10	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.





5.4 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. 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
4	CL	A	22	1/1	0.91	0.07	15,15,15,15	0
4	CL	B	21	1/1	0.94	0.04	8,8,8,8	0
4	CL	B	22	1/1	0.96	0.05	10,10,10,10	0
3	ACY	A	11	4/4	0.98	0.05	8,10,16,16	0
4	CL	A	21	1/1	0.99	0.02	4,4,4,4	0

5.5 Other polymers [i](#)

There are no such residues in this entry.