



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 13, 2026 – 01:49 pm BST

PDB ID : 9RWV / pdb_00009rwv
Title : Crystal structure of the YqiI lectin domain, in complex with oligomannose-3
Authors : D'Hondt, A.K.; Remaut, H.K.
Deposited on : 2025-07-10
Resolution : 1.30 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 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 : 4-5-2 with Phenix2.0
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

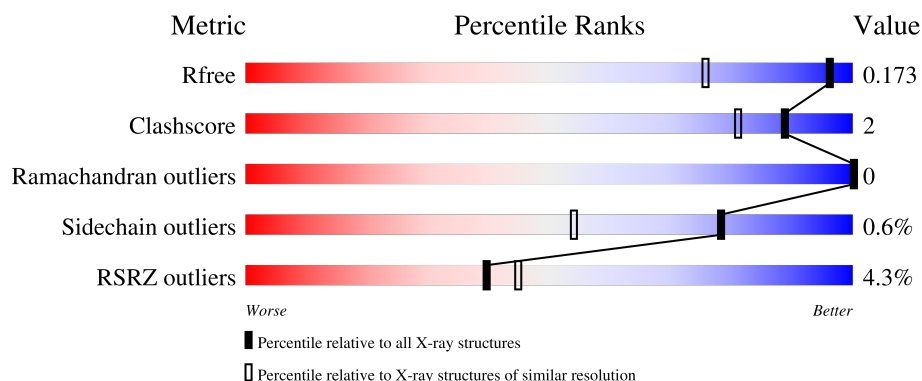
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.30 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}	180053	1553 (1.30-1.30)
Clashscore	190562	1595 (1.30-1.30)
Ramachandran outliers	187476	1551 (1.30-1.30)
Sidechain outliers	187428	1551 (1.30-1.30)
RSRZ outliers	180081	1549 (1.30-1.30)

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	A	210	5% 84% • 12%
1	B	210	3% 85% • 11%
2	D	4	50% 50%
3	C	5	20% 80%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3739 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 Pilus assembly protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	185	Total	C	N	O	S	0	14	0
			1572	992	265	306	9			
1	B	186	Total	C	N	O	S	0	16	0
			1583	1000	265	311	7			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	191	GLY	-	expression tag	UNP A0A0P7MFM4
A	192	ALA	-	expression tag	UNP A0A0P7MFM4
A	193	ALA	-	expression tag	UNP A0A0P7MFM4
A	194	ALA	-	expression tag	UNP A0A0P7MFM4
A	195	TYR	-	expression tag	UNP A0A0P7MFM4
A	196	PRO	-	expression tag	UNP A0A0P7MFM4
A	197	TYR	-	expression tag	UNP A0A0P7MFM4
A	198	ASP	-	expression tag	UNP A0A0P7MFM4
A	199	VAL	-	expression tag	UNP A0A0P7MFM4
A	200	PRO	-	expression tag	UNP A0A0P7MFM4
A	201	ASP	-	expression tag	UNP A0A0P7MFM4
A	202	TYR	-	expression tag	UNP A0A0P7MFM4
A	203	GLY	-	expression tag	UNP A0A0P7MFM4
A	204	SER	-	expression tag	UNP A0A0P7MFM4
A	205	HIS	-	expression tag	UNP A0A0P7MFM4
A	206	HIS	-	expression tag	UNP A0A0P7MFM4
A	207	HIS	-	expression tag	UNP A0A0P7MFM4
A	208	HIS	-	expression tag	UNP A0A0P7MFM4
A	209	HIS	-	expression tag	UNP A0A0P7MFM4
A	210	HIS	-	expression tag	UNP A0A0P7MFM4
B	191	GLY	-	expression tag	UNP A0A0P7MFM4
B	192	ALA	-	expression tag	UNP A0A0P7MFM4
B	193	ALA	-	expression tag	UNP A0A0P7MFM4
B	194	ALA	-	expression tag	UNP A0A0P7MFM4
B	195	TYR	-	expression tag	UNP A0A0P7MFM4

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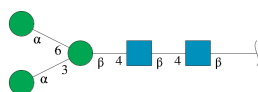
Chain	Residue	Modelled	Actual	Comment	Reference
B	196	PRO	-	expression tag	UNP A0A0P7MFM4
B	197	TYR	-	expression tag	UNP A0A0P7MFM4
B	198	ASP	-	expression tag	UNP A0A0P7MFM4
B	199	VAL	-	expression tag	UNP A0A0P7MFM4
B	200	PRO	-	expression tag	UNP A0A0P7MFM4
B	201	ASP	-	expression tag	UNP A0A0P7MFM4
B	202	TYR	-	expression tag	UNP A0A0P7MFM4
B	203	GLY	-	expression tag	UNP A0A0P7MFM4
B	204	SER	-	expression tag	UNP A0A0P7MFM4
B	205	HIS	-	expression tag	UNP A0A0P7MFM4
B	206	HIS	-	expression tag	UNP A0A0P7MFM4
B	207	HIS	-	expression tag	UNP A0A0P7MFM4
B	208	HIS	-	expression tag	UNP A0A0P7MFM4
B	209	HIS	-	expression tag	UNP A0A0P7MFM4
B	210	HIS	-	expression tag	UNP A0A0P7MFM4

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).

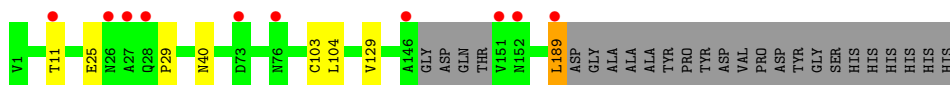


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		
4	A	1	Total	C	O	0	0
			8	6	2		
4	A	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	206	Total	O	0	0
			206	206		
5	B	211	Total	O	0	0
			211	211		

- Molecule 1: Pilus assembly protein



-

- | | |
|------|--|
| NAG1 | |
| NAG2 | |
| BMA3 | |
| MAN4 | |

- | | | | | |
|------|------|------|------|------|
| NAG1 | NAG2 | BMA3 | MAN4 | MAN5 |
|------|------|------|------|------|

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	31.03Å 69.90Å 107.35Å 90.00° 94.29° 90.00°	Depositor
Resolution (Å)	35.68 – 1.30 35.68 – 1.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (35.68-1.30) 99.8 (35.68-1.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 1.30Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.160 , 0.172 0.160 , 0.173	Depositor DCC
R_{free} test set	5599 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	14.3	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3739	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.08% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, MPD, NAG, BMA

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	0.23	0/1621	0.44	0/2208
1	B	0.25	0/1633	0.47	0/2228
All	All	0.24	0/3254	0.45	0/4436

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

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	1572	0	1469	5	0
1	B	1583	0	1473	6	0
2	D	50	0	43	0	0
3	C	61	0	52	0	0
4	A	24	0	42	1	0
4	B	32	0	56	1	0
5	A	206	0	0	0	0
5	B	211	0	0	4	0
All	All	3739	0	3135	12	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 2.

All (12) 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:40:ASN:H	4:A:301:MPD:H51	1.16	1.08
1:B:85[B]:THR:HG22	1:B:136[B]:ARG:HG2	1.55	0.87
4:B:302:MPD:HM1	5:B:494:HOH:O	2.09	0.52
1:B:11[A]:THR:HG22	5:B:569:HOH:O	2.12	0.50
1:B:85[B]:THR:CG2	1:B:136[B]:ARG:HG2	2.36	0.48
1:B:81:THR:HB	1:B:140:LYS:HB2	1.99	0.44
1:A:103:CYS:O	1:A:129[B]:VAL:HG11	2.17	0.44
1:A:104:LEU:HD21	1:A:129[B]:VAL:HG22	1.99	0.43
1:A:29[B]:PRO:HG3	5:B:407:HOH:O	2.19	0.42
1:B:31[B]:GLN:HG3	5:B:588:HOH:O	2.19	0.42
1:B:85[B]:THR:HA	1:B:89:VAL:O	2.20	0.41
1:A:25:GLU:OE2	1:A:189:LEU:HD12	2.21	0.41

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	196/210 (93%)	188 (96%)	8 (4%)	0	100	100
1	B	198/210 (94%)	192 (97%)	6 (3%)	0	100	100
All	All	394/420 (94%)	380 (96%)	14 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	173/177 (98%)	170 (98%)	3 (2%)	53	17
1	B	173/177 (98%)	173 (100%)	0	100	100
All	All	346/354 (98%)	343 (99%)	3 (1%)	78	42

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11[A]	THR
1	A	11[B]	THR
1	A	189	LEU

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

Mol	Chain	Res	Type
1	A	132	ASN
1	B	109	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

9 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
3	NAG	C	1	3	14,14,15	0.72	0	17,19,21	0.90	1 (5%)
3	NAG	C	2	3	14,14,15	0.76	0	17,19,21	0.77	0
3	BMA	C	3	3	11,11,12	1.01	0	15,15,17	1.56	2 (13%)
3	MAN	C	4	3	11,11,12	0.68	0	15,15,17	0.98	1 (6%)
3	MAN	C	5	3	11,11,12	0.61	0	15,15,17	1.90	1 (6%)
2	NAG	D	1	2	14,14,15	0.72	0	17,19,21	0.88	0
2	NAG	D	2	2	14,14,15	0.77	0	17,19,21	0.78	0
2	BMA	D	3	2	11,11,12	1.03	1 (9%)	15,15,17	1.32	1 (6%)
2	MAN	D	4	2	11,11,12	0.68	0	15,15,17	1.05	1 (6%)

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
3	NAG	C	1	3	-	1/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	0/2/19/22	0/1/1/1
3	MAN	C	4	3	-	0/2/19/22	0/1/1/1
3	MAN	C	5	3	-	1/2/19/22	0/1/1/1
2	NAG	D	1	2	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1
2	BMA	D	3	2	-	0/2/19/22	0/1/1/1
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	3	BMA	C2-C3	2.24	1.55	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	5	MAN	C1-O5-C5	6.47	120.95	112.19
3	C	3	BMA	C1-O5-C5	5.06	119.05	112.19
2	D	3	BMA	C1-O5-C5	4.43	118.19	112.19
2	D	4	MAN	C1-O5-C5	3.12	116.42	112.19
3	C	4	MAN	C1-O5-C5	2.69	115.84	112.19
3	C	3	BMA	O6-C6-C5	-2.54	102.58	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	NAG	O5-C1-C2	-2.11	107.95	111.29

There are no chirality outliers.

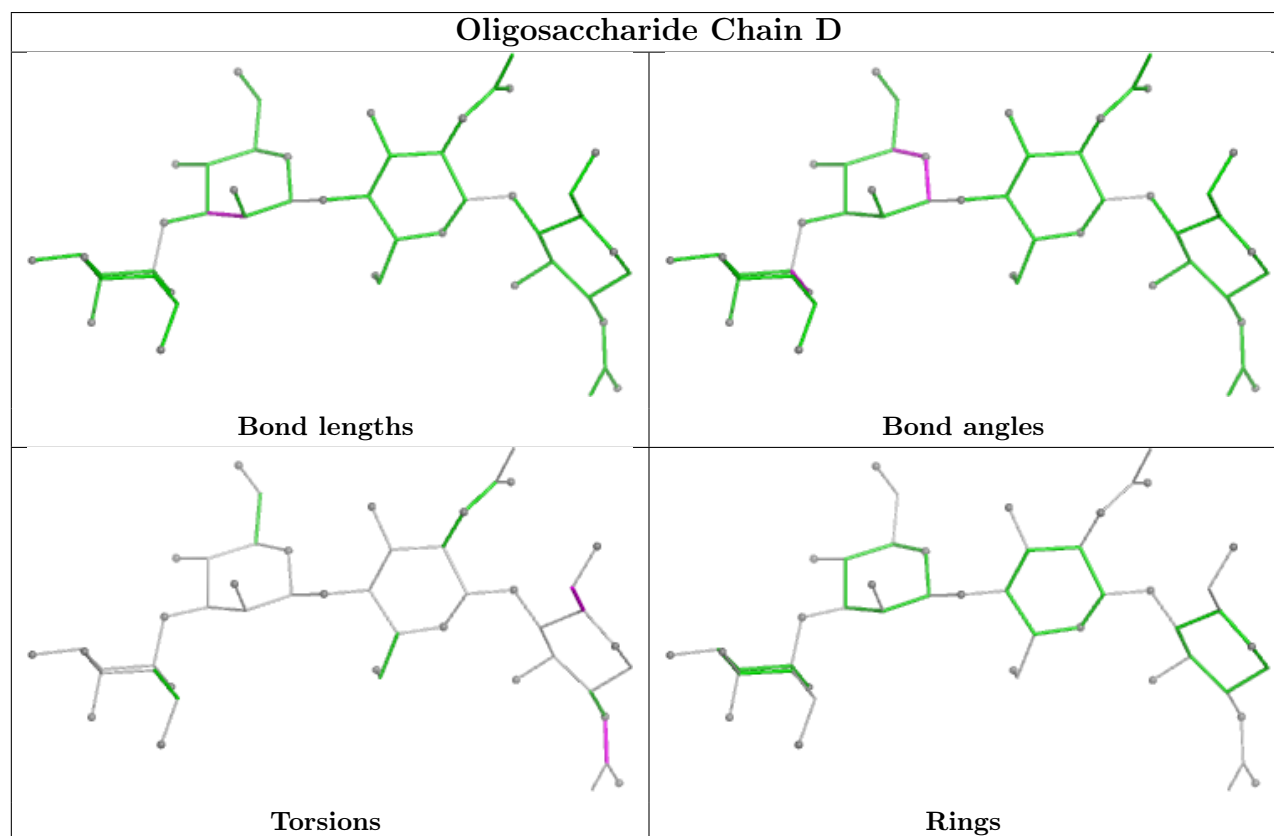
All (6) torsion outliers are listed below:

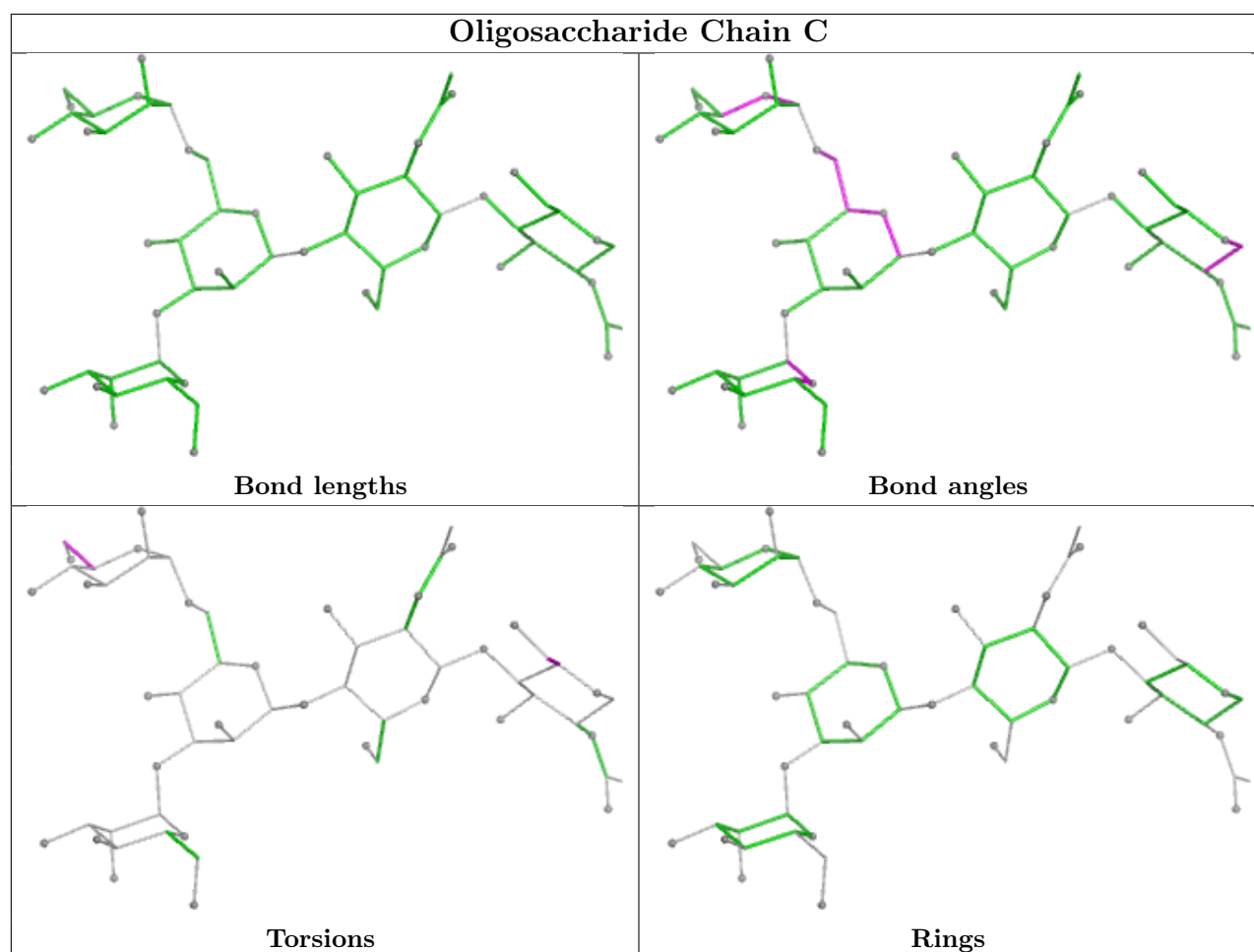
Mol	Chain	Res	Type	Atoms
2	D	1	NAG	C4-C5-C6-O6
2	D	1	NAG	C8-C7-N2-C2
2	D	1	NAG	O7-C7-N2-C2
2	D	1	NAG	O5-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
3	C	5	MAN	C4-C5-C6-O6

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.





5.6 Ligand geometry [i](#)

7 ligands 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	$\# Z > 2$
4	MPD	B	303	-	7,7,7	0.33	0	9,10,10	0.56	0
4	MPD	A	302	-	7,7,7	0.38	0	9,10,10	0.47	0
4	MPD	B	304	-	7,7,7	0.30	0	9,10,10	0.44	0
4	MPD	B	302	-	7,7,7	0.35	0	9,10,10	0.53	0
4	MPD	A	303	-	7,7,7	0.32	0	9,10,10	0.52	0
4	MPD	A	301	-	7,7,7	0.37	0	9,10,10	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MPD	B	301	-	7,7,7	0.39	0	9,10,10	0.56	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
4	MPD	B	303	-	-	0/5/5/5	-
4	MPD	A	302	-	-	0/5/5/5	-
4	MPD	B	304	-	-	0/5/5/5	-
4	MPD	B	302	-	-	0/5/5/5	-
4	MPD	A	303	-	-	0/5/5/5	-
4	MPD	A	301	-	-	1/5/5/5	-
4	MPD	B	301	-	-	4/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	301	MPD	O2-C2-C3-C4
4	B	301	MPD	C1-C2-C3-C4
4	B	301	MPD	CM-C2-C3-C4
4	A	301	MPD	C2-C3-C4-C5
4	B	301	MPD	C2-C3-C4-O4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	302	MPD	1	0
4	A	301	MPD	1	0

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	185/210 (88%)	0.21	10 (5%)	31 36	4, 16, 39, 56	14 (7%)
1	B	186/210 (88%)	0.03	6 (3%)	50 56	5, 14, 29, 54	16 (8%)
All	All	371/420 (88%)	0.12	16 (4%)	40 45	4, 15, 35, 56	30 (8%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	189	LEU	6.5
1	A	146	ALA	5.1
1	B	189	LEU	3.8
1	A	151	VAL	3.6
1	B	190	ASP	3.2
1	A	11[A]	THR	3.2
1	B	146	ALA	3.2
1	A	27	ALA	2.9
1	B	151	VAL	2.7
1	A	76	ASN	2.5
1	B	152	ASN	2.5
1	A	28	GLN	2.4
1	A	26	ASN	2.2
1	B	54	ASN	2.2
1	A	73	ASP	2.2
1	A	152	ASN	2.1

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

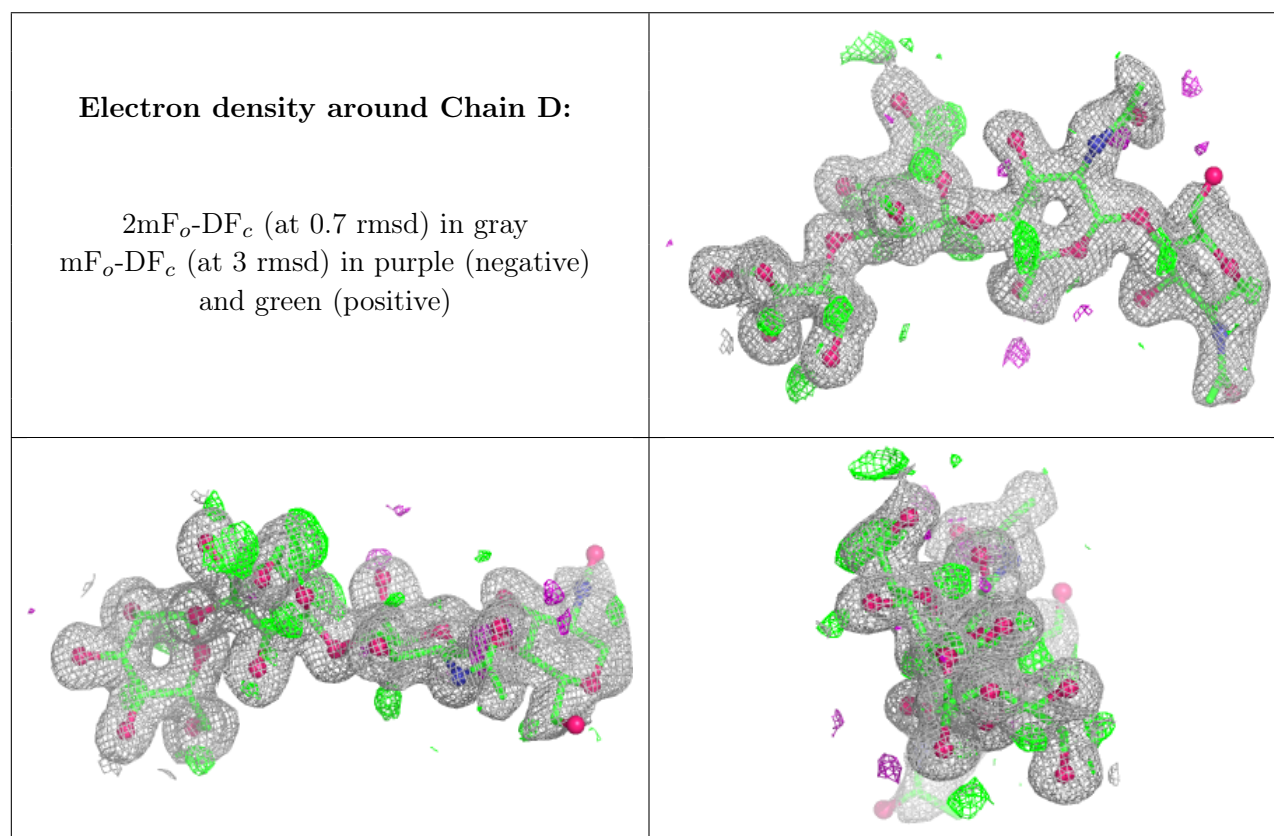
There are no non-standard protein/DNA/RNA residues in this entry.

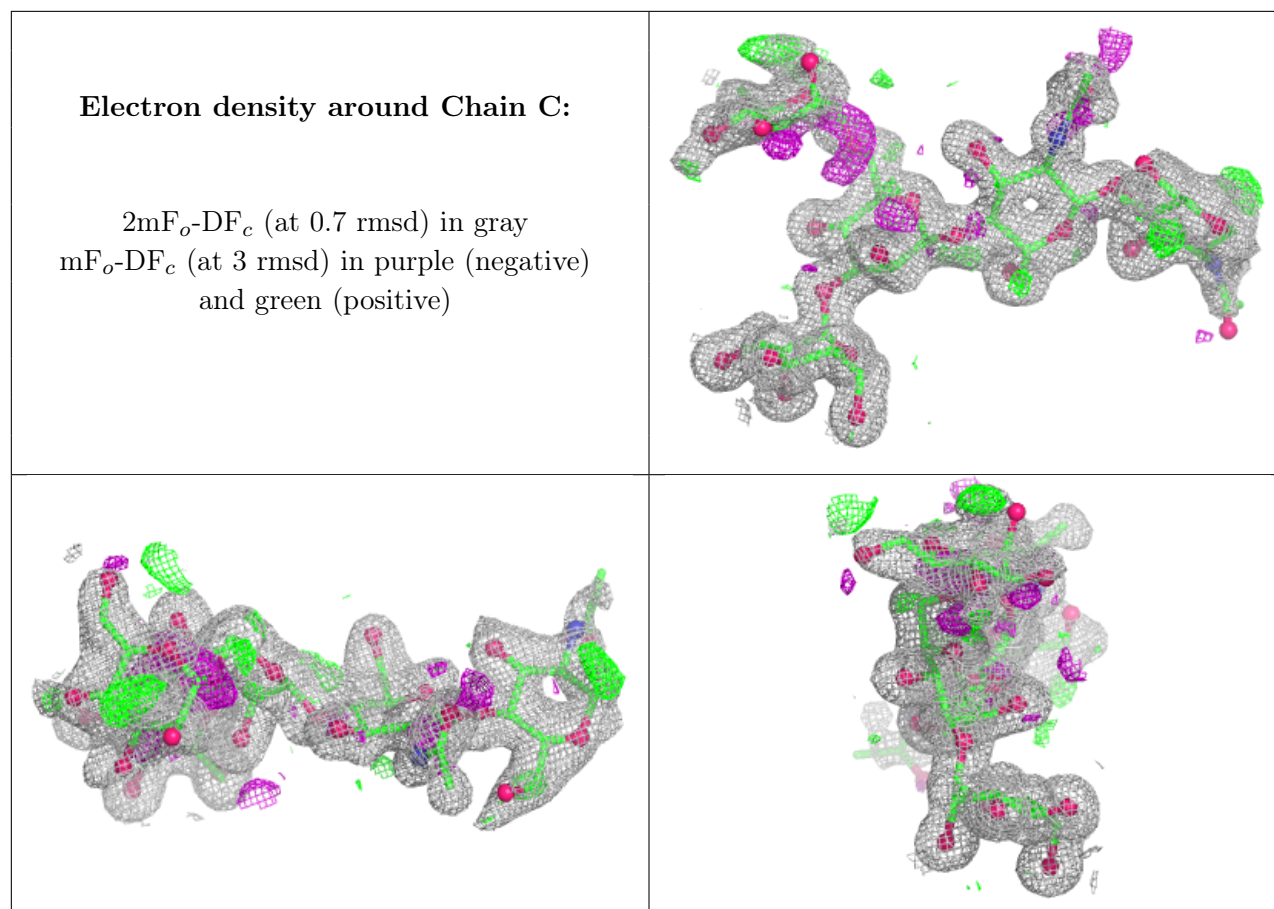
6.3 Carbohydrates [i](#)

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
2	NAG	D	1	14/15	0.73	0.17	26,47,59,65	0
3	NAG	C	1	14/15	0.83	0.15	34,53,66,66	0
2	NAG	D	2	14/15	0.88	0.13	20,24,32,35	0
3	NAG	C	2	14/15	0.92	0.11	24,30,36,39	0
3	BMA	C	3	11/12	0.93	0.09	13,17,22,37	0
2	BMA	D	3	11/12	0.95	0.08	13,15,18,23	0
3	MAN	C	4	11/12	0.98	0.05	10,11,11,12	0
2	MAN	D	4	11/12	0.99	0.04	10,11,12,12	0
3	MAN	C	5	11/12	-	-	40,48,60,64	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](#)

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($\text{\AA}^2$)	Q<0.9
4	MPD	A	302	8/8	0.87	0.12	22,25,37,41	0
4	MPD	B	303	8/8	0.87	0.13	18,22,36,36	0
4	MPD	B	304	8/8	0.87	0.14	22,26,30,31	0
4	MPD	A	303	8/8	0.90	0.12	21,23,27,28	0
4	MPD	B	301	8/8	0.91	0.11	19,22,27,30	0
4	MPD	B	302	8/8	0.91	0.11	21,23,27,33	0
4	MPD	A	301	8/8	0.92	0.10	15,22,24,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.