



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:50 PM UTC

PDB ID : 4JKX / pdb_00004jkx
Title : Crystal structure Mistletoe Lectin I from Viscum album in complex with kinetin at 2.35 Å resolution.
Authors : Prokofev, I.I.; Lashkov, A.A.; Gabdoulkhakov, A.G.; Meyer, A.; Barciszewski, J.; Betzel, C.; Mikhailov, A.M.
Deposited on : 2013-03-12
Resolution : 2.35 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	:	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

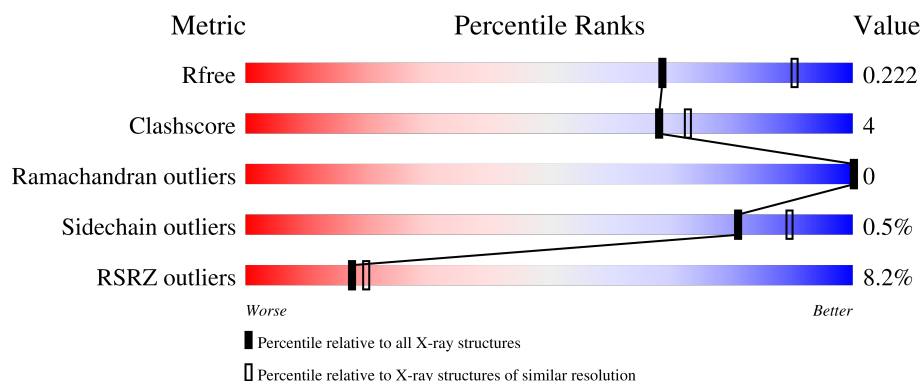
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	249	8% 92% 8%
2	B	263	9% 94% 6%
3	C	2	50% 50%
4	D	3	100%

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
12	AZI	B	301	-	X	-	-
8	H35	A	305	-	-	X	-
9	EDO	A	306	-	-	-	X

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 4402 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 Beta-galactoside-specific lectin 1 A chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	1	0
			1949	1234	339	372	4			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	15	ALA	GLU	SEE REMARK 999	UNP P81446
A	19	SER	ARG	SEE REMARK 999	UNP P81446
A	36	GLN	GLU	SEE REMARK 999	UNP P81446
A	49	GLU	ASP	SEE REMARK 999	UNP P81446
A	50	GLY	ALA	SEE REMARK 999	UNP P81446
A	61	ALA	GLU	SEE REMARK 999	UNP P81446
A	90	LYS	ARG	SEE REMARK 999	UNP P81446
A	94	ALA	ARG	SEE REMARK 999	UNP P81446
A	99	GLN	HIS	SEE REMARK 999	UNP P81446
A	100	ASP	LEU	SEE REMARK 999	UNP P81446
A	208	HIS	GLN	SEE REMARK 999	UNP P81446
A	222	LEU	ILE	SEE REMARK 999	UNP P81446
A	223	ALA	PRO	SEE REMARK 999	UNP P81446
A	225	ALA	GLY	SEE REMARK 999	UNP P81446
A	227	ILE	PHE	SEE REMARK 999	UNP P81446

- Molecule 2 is a protein called Beta-galactoside-specific lectin 1 B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	263	Total	C	N	O	S	0	1	0
			2009	1244	356	396	13			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	21	THR	CYS	SEE REMARK 999	UNP P81446

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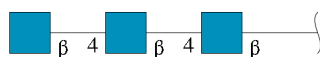
Chain	Residue	Modelled	Actual	Comment	Reference
B	54	LYS	ARG	SEE REMARK 999	UNP P81446
B	90	ILE	LEU	SEE REMARK 999	UNP P81446
B	167	ALA	ILE	SEE REMARK 999	UNP P81446
B	189	SER	ASP	SEE REMARK 999	UNP P81446
B	222	ALA	GLU	SEE REMARK 999	UNP P81446
B	242	SER	LYS	SEE REMARK 999	UNP P81446
B	244	GLN	ARG	SEE REMARK 999	UNP P81446
B	254	ASN	LYS	SEE REMARK 999	UNP P81446

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



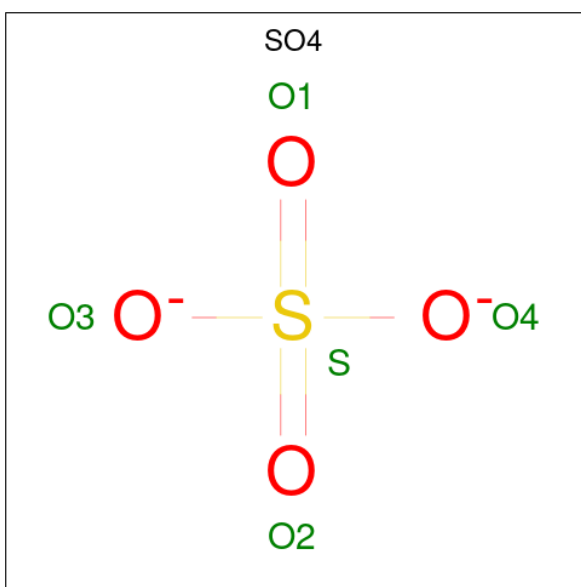
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



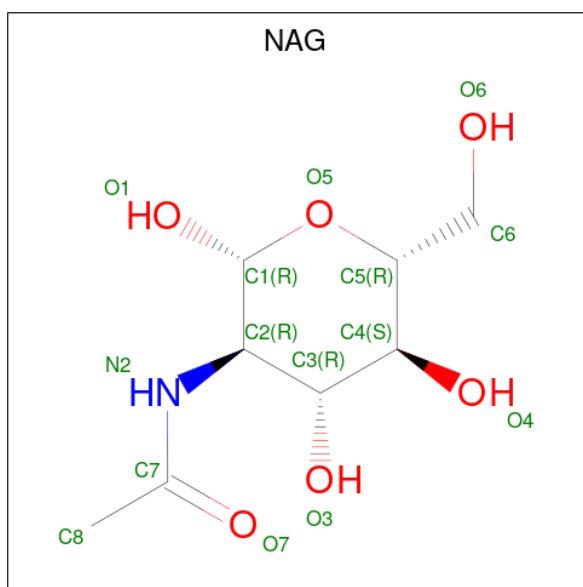
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	3	Total	C	N	O	0	0	0
			42	24	3	15			

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



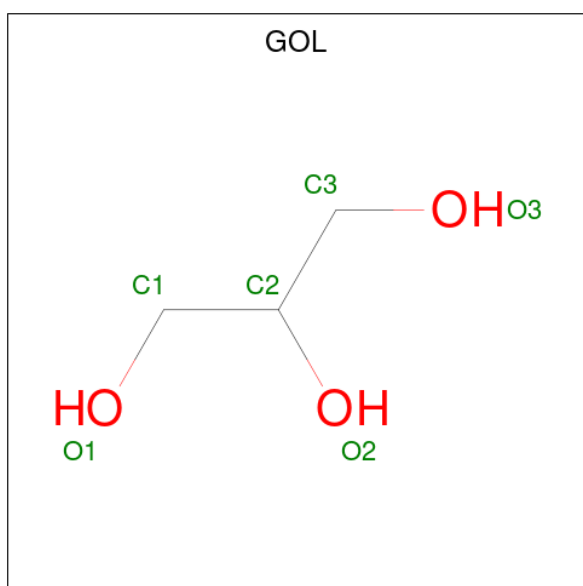
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



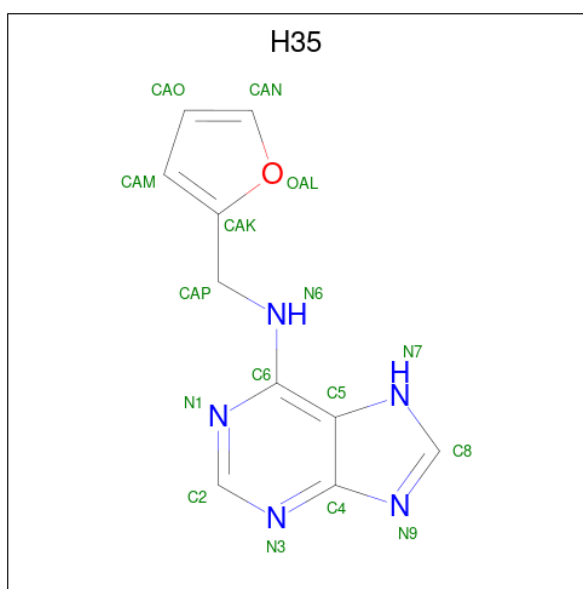
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		

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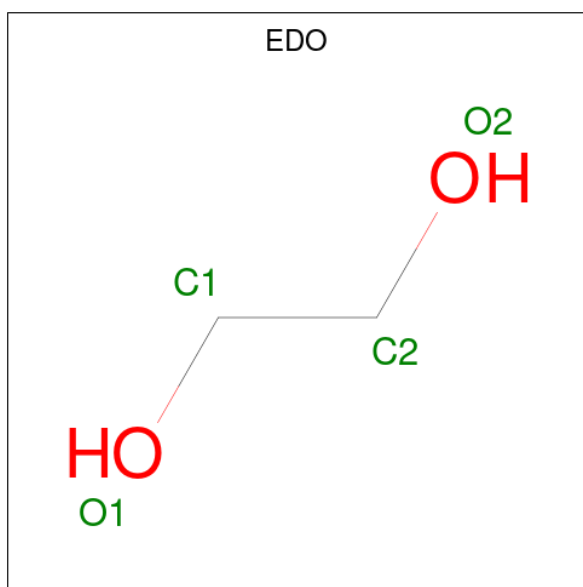
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		
7	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is N-(FURAN-2-YLMETHYL)-7H-PURIN-6-AMINE (CCD ID: H35) (formula: C₁₀H₉N₅O).



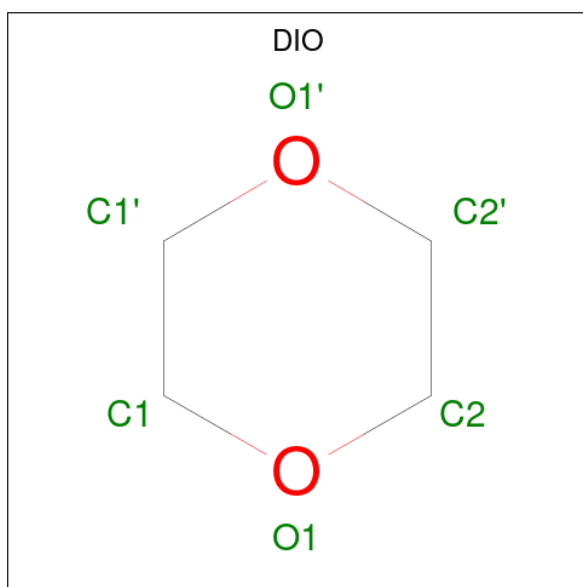
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			16	10	5	1		

- Molecule 9 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 10 is 1,4-DIETHYLENE DIOXIDE (CCD ID: DIO) (formula: C₄H₈O₂).

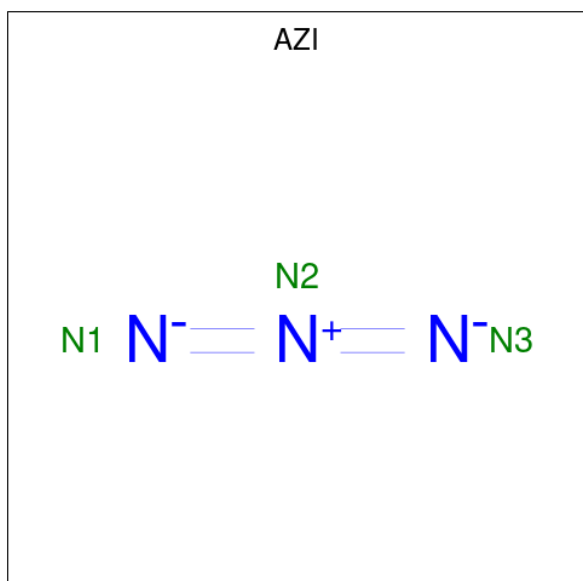


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			6	4	2		

- Molecule 11 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	1	Total	Cl	0	0
			1	1		
11	B	1	Total	Cl	0	0
			1	1		

- Molecule 12 is AZIDE ION (CCD ID: AZI) (formula: N₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	B	1	Total N 3 3	0	0

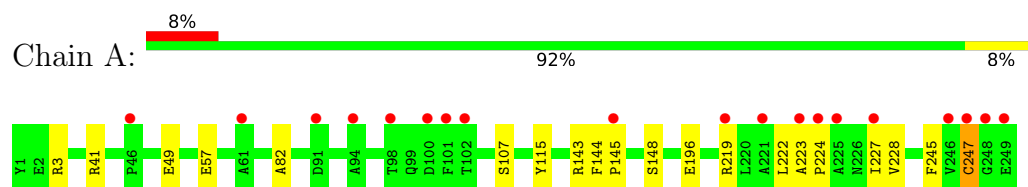
- Molecule 13 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	73	Total O 73 73	0	0
13	B	137	Total O 137 137	0	0

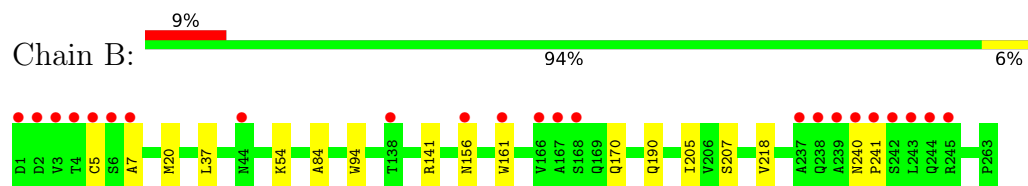
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Beta-galactoside-specific lectin 1 A chain



- Molecule 2: Beta-galactoside-specific lectin 1 B chain



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	107.01Å 107.01Å 312.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	79.70 – 2.35 79.70 – 2.35	Depositor EDS
% Data completeness (in resolution range)	100.0 (79.70-2.35) 100.0 (79.70-2.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.08Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.220 , 0.248 (Not available) , 0.222	Depositor DCC
R_{free} test set	3177 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.452	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4402	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% 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: NAG, AZI, H35, SO4, DIO, CL, EDO, GOL

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	0.51	0/1991	0.79	1/2711 (0.0%)
2	B	0.52	0/2052	0.79	1/2800 (0.0%)
All	All	0.51	0/4043	0.79	2/5511 (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	247	CYS	N-CA-C	6.14	119.54	109.72
2	B	5	CYS	N-CA-C	5.77	117.31	108.30

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	1949	0	1933	16	0
2	B	2009	0	1939	13	0
3	C	28	0	25	1	0
4	D	42	0	37	0	0
5	A	25	0	0	0	0
6	A	14	0	13	0	0
6	B	14	0	13	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	18	0	24	1	0
7	B	42	0	56	4	0
8	A	16	0	9	7	0
9	A	4	0	6	0	0
9	B	20	0	30	2	0
10	A	6	0	8	1	0
11	A	1	0	0	0	0
11	B	1	0	0	0	0
12	B	3	0	0	0	0
13	A	73	0	0	0	0
13	B	137	0	0	1	0
All	All	4402	0	4093	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 4.

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:148:SER:HB2	7:A:303:GOL:H2	1.75	0.69
1:A:245:PHE:HE1	1:A:247:CYS:O	1.77	0.66
1:A:222:LEU:HD11	1:A:228:VAL:HG13	1.77	0.66
1:A:115:TYR:HB2	8:A:305:H35:N7	2.12	0.65
1:A:115:TYR:N	8:A:305:H35:H7	1.95	0.64
2:B:170:GLN:HB2	7:B:318:GOL:H32	1.78	0.64
2:B:156:ASN:HD22	2:B:161:TRP:CD1	2.16	0.62
2:B:141:ARG:HD3	9:B:309:EDO:H12	1.85	0.59
6:B:307:NAG:H62	13:B:528:HOH:O	2.05	0.56
2:B:20:MET:HB2	2:B:37:LEU:HG	1.89	0.53
2:B:207:SER:H	9:B:311:EDO:H11	1.72	0.53
1:A:219:ARG:HH21	1:A:227:ILE:HG21	1.77	0.49
2:B:156:ASN:HD22	2:B:161:TRP:HD1	1.59	0.48
2:B:7:ALA:HB1	2:B:54:LYS:HD3	1.97	0.47
1:A:115:TYR:HB2	8:A:305:H35:H7	1.80	0.45
2:B:84:ALA:HA	7:B:315:GOL:H31	1.97	0.45
1:A:82:ALA:HB1	1:A:143:ARG:HA	1.98	0.45
1:A:144:PHE:HA	1:A:145:PRO:HD3	1.85	0.45
1:A:196:GLU:HB3	8:A:305:H35:N1	2.31	0.45
1:A:115:TYR:H	8:A:305:H35:H7	1.63	0.44
1:A:41:ARG:HE	10:A:307:DIO:H1'2	1.83	0.43
2:B:190:GLN:HB3	2:B:205:ILE:HG22	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:ARG:NH1	1:A:57:GLU:OE1	2.49	0.42
2:B:94:TRP:CG	3:C:1:NAG:H62	2.55	0.42
1:A:115:TYR:CB	8:A:305:H35:H7	2.32	0.42
1:A:115:TYR:N	8:A:305:H35:N7	2.63	0.42
2:B:170:GLN:HG2	7:B:318:GOL:H11	2.02	0.41
2:B:240:ASN:HA	2:B:241:PRO:HD2	1.96	0.41
1:A:223:ALA:HB3	1:A:224:PRO:HD3	2.03	0.41
2:B:218:VAL:HG11	7:B:319:GOL:H12	2.04	0.40

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	248/249 (100%)	239 (96%)	9 (4%)	0	100	100
2	B	262/263 (100%)	249 (95%)	13 (5%)	0	100	100
All	All	510/512 (100%)	488 (96%)	22 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	A	212/211 (100%)	210 (99%)	2 (1%)	70	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	222/221 (100%)	222 (100%)	0	100	100
All	All	434/432 (100%)	432 (100%)	2 (0%)	81	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	GLU
1	A	107	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	HIS
2	B	156	ASN
2	B	169	GLN
2	B	190	GLN
2	B	215	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 ⓘ

5 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	2,3	14,14,15	0.59	0	17,19,21	1.43	4 (23%)
3	NAG	C	2	3	14,14,15	0.49	0	17,19,21	0.61	0
4	NAG	D	1	2,4	14,14,15	0.54	0	17,19,21	0.97	1 (5%)
4	NAG	D	2	4	14,14,15	0.60	0	17,19,21	0.97	1 (5%)
4	NAG	D	3	4	14,14,15	0.57	0	17,19,21	1.41	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
3	NAG	C	1	2,3	-	3/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
4	NAG	D	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	NAG	D	3	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	3	NAG	C1-O5-C5	4.43	118.13	112.19
3	C	1	NAG	C1-O5-C5	3.14	116.39	112.19
4	D	2	NAG	O4-C4-C3	2.87	117.13	110.38
3	C	1	NAG	C1-C2-N2	2.77	114.80	110.43
4	D	1	NAG	C1-O5-C5	2.70	115.81	112.19
3	C	1	NAG	C2-N2-C7	2.37	126.07	122.90
3	C	1	NAG	O5-C1-C2	-2.10	108.04	111.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

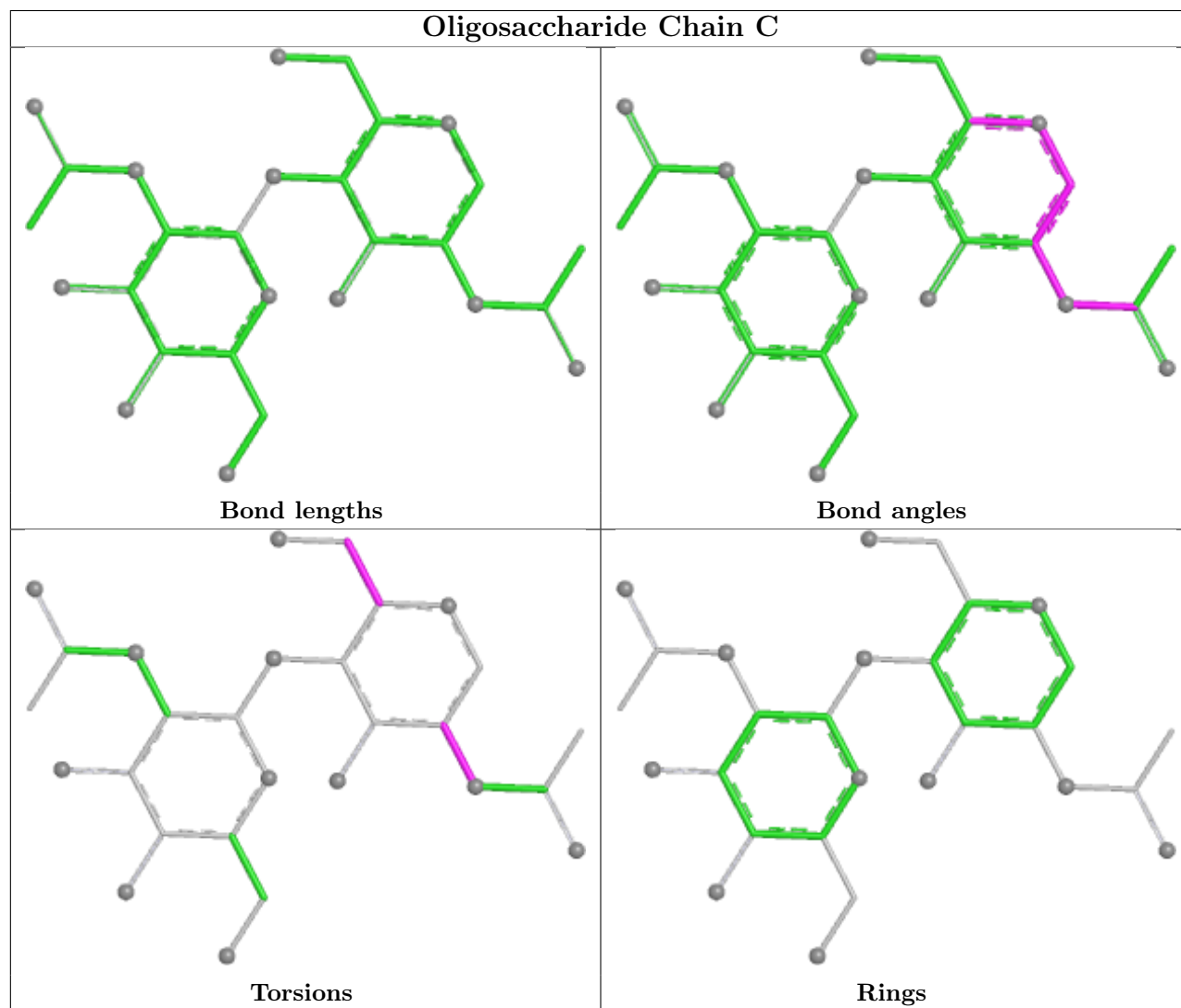
Mol	Chain	Res	Type	Atoms
4	D	3	NAG	O5-C5-C6-O6
4	D	3	NAG	C4-C5-C6-O6
3	C	1	NAG	C1-C2-N2-C7
3	C	1	NAG	C3-C2-N2-C7
3	C	1	NAG	C4-C5-C6-O6

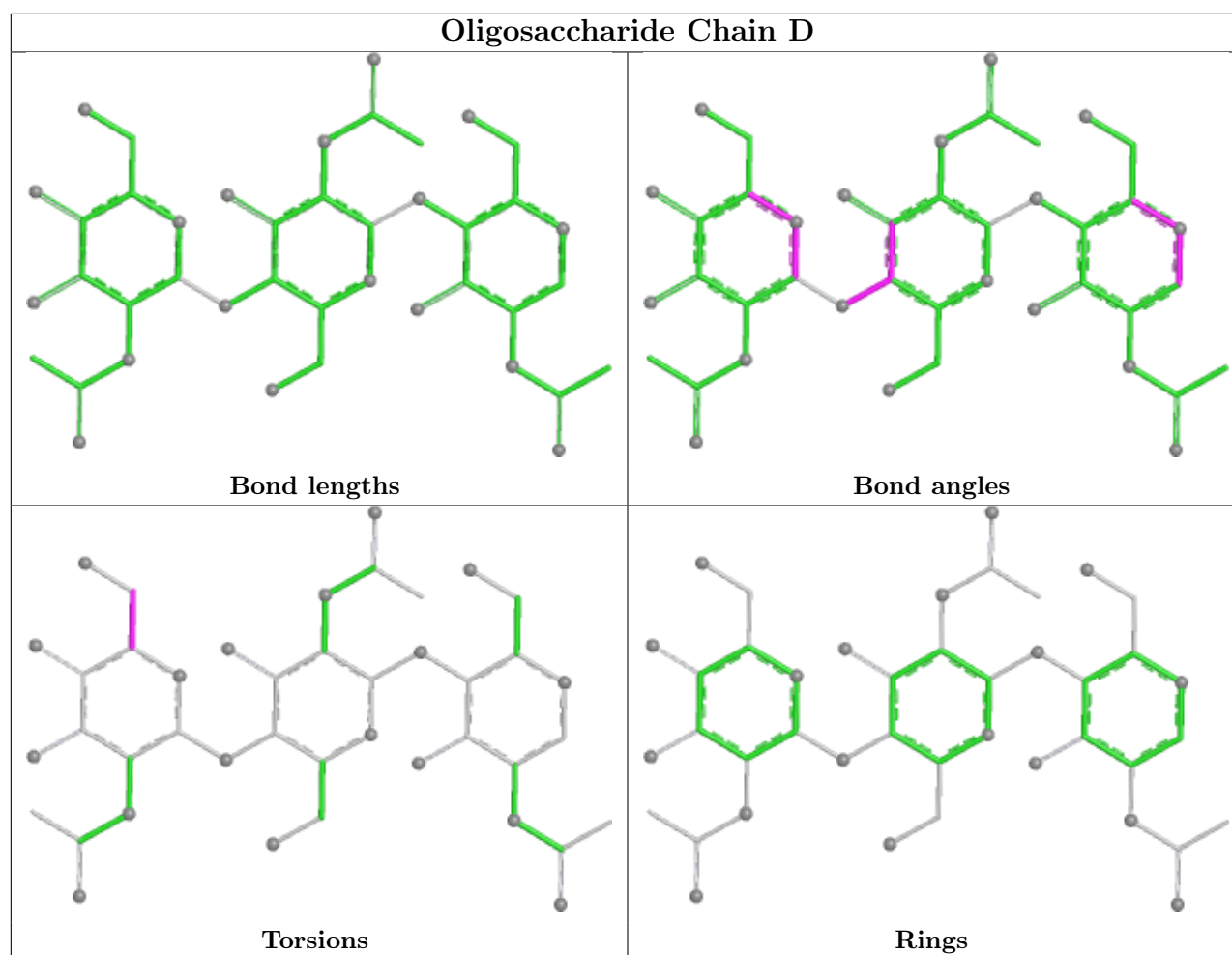
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	1	0

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](#)

Of 28 ligands modelled in this entry, 2 are monoatomic - leaving 26 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$
10	DIO	A	307	-	6,6,6	0.51	0	6,6,6	0.75	0
6	NAG	B	307	2	14,14,15	1.35	1 (7%)	17,19,21	1.71	6 (35%)
7	GOL	A	304	-	5,5,5	0.40	0	5,5,5	0.35	0
9	EDO	B	312	-	3,3,3	0.39	0	2,2,2	0.48	0
9	EDO	B	310	-	3,3,3	0.45	0	2,2,2	0.35	0
7	GOL	B	318	-	5,5,5	0.41	0	5,5,5	0.25	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	A	310	-	4,4,4	0.23	0	6,6,6	0.10	0
7	GOL	B	315	-	5,5,5	0.43	0	5,5,5	0.41	0
5	SO4	A	301	-	4,4,4	0.25	0	6,6,6	0.18	0
7	GOL	A	308	-	5,5,5	0.40	0	5,5,5	0.21	0
9	EDO	B	308	-	3,3,3	0.46	0	2,2,2	0.21	0
7	GOL	B	316	-	5,5,5	0.36	0	5,5,5	0.28	0
6	NAG	A	302	1	14,14,15	0.60	0	17,19,21	1.06	1 (5%)
5	SO4	A	311	-	4,4,4	0.23	0	6,6,6	0.11	0
7	GOL	B	314	-	5,5,5	0.41	0	5,5,5	0.19	0
7	GOL	B	313	-	5,5,5	0.54	0	5,5,5	0.59	0
5	SO4	A	309	-	4,4,4	0.23	0	6,6,6	0.12	0
9	EDO	A	306	-	3,3,3	0.44	0	2,2,2	0.45	0
7	GOL	B	317	-	5,5,5	0.37	0	5,5,5	0.26	0
9	EDO	B	311	-	3,3,3	0.42	0	2,2,2	0.44	0
8	H35	A	305	-	18,18,18	3.65	7 (38%)	24,24,24	3.53	9 (37%)
7	GOL	A	303	-	5,5,5	0.40	0	5,5,5	0.25	0
7	GOL	B	319	-	5,5,5	0.35	0	5,5,5	0.23	0
9	EDO	B	309	-	3,3,3	0.48	0	2,2,2	0.28	0
12	AZI	B	301	-	2,2,2	2.80	2 (100%)	0,1,1	-	-
5	SO4	A	312	-	4,4,4	0.25	0	6,6,6	0.09	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
10	DIO	A	307	-	-	-	0/1/1/1
6	NAG	B	307	2	-	3/6/23/26	0/1/1/1
7	GOL	A	304	-	-	0/4/4/4	-
9	EDO	B	312	-	-	0/1/1/1	-
9	EDO	B	310	-	-	1/1/1/1	-
7	GOL	B	318	-	-	0/4/4/4	-
7	GOL	B	315	-	-	0/4/4/4	-
7	GOL	A	308	-	-	1/4/4/4	-
9	EDO	B	308	-	-	0/1/1/1	-
7	GOL	B	316	-	-	2/4/4/4	-
6	NAG	A	302	1	-	2/6/23/26	0/1/1/1
7	GOL	B	314	-	-	0/4/4/4	-
7	GOL	B	313	-	-	4/4/4/4	-
9	EDO	A	306	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	B	317	-	-	0/4/4/4	-
9	EDO	B	311	-	-	1/1/1/1	-
8	H35	A	305	-	-	3/5/5/5	0/3/3/3
7	GOL	A	303	-	-	2/4/4/4	-
7	GOL	B	319	-	-	0/4/4/4	-
9	EDO	B	309	-	-	1/1/1/1	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	305	H35	C8-N7	8.09	1.54	1.35
8	A	305	H35	C5-C4	-7.66	1.27	1.40
8	A	305	H35	C8-N9	6.66	1.45	1.32
8	A	305	H35	C6-N6	6.23	1.44	1.34
6	B	307	NAG	O5-C1	-4.02	1.36	1.43
12	B	301	AZI	N1-N2	-2.85	1.17	1.23
12	B	301	AZI	N3-N2	-2.75	1.17	1.23
8	A	305	H35	C5-N7	-2.44	1.33	1.37
8	A	305	H35	OAL-CAK	2.38	1.43	1.36
8	A	305	H35	C4-N9	2.31	1.39	1.38

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	305	H35	C4-C5-N7	12.06	113.38	105.28
8	A	305	H35	N7-C8-N9	-7.05	103.13	113.87
8	A	305	H35	C6-C5-N7	-6.91	125.27	135.17
8	A	305	H35	C6-C5-C4	3.85	121.35	118.29
8	A	305	H35	C5-C4-N9	3.45	113.21	110.46
6	B	307	NAG	C4-C3-C2	-3.33	106.14	111.02
6	A	302	NAG	C1-O5-C5	3.21	116.48	112.19
6	B	307	NAG	O5-C1-C2	2.75	115.54	111.29
6	B	307	NAG	C6-C5-C4	-2.48	106.93	113.02
6	B	307	NAG	C3-C4-C5	2.29	114.38	110.23
6	B	307	NAG	C2-N2-C7	-2.20	119.95	122.90
8	A	305	H35	N6-C6-N1	2.16	121.94	118.47
8	A	305	H35	OAL-CAK-CAP	2.08	124.62	117.50
8	A	305	H35	CAP-CAK-CAM	-2.08	125.97	133.07
8	A	305	H35	C5-C6-N6	-2.06	121.03	123.42
6	B	307	NAG	O5-C5-C4	2.02	115.74	110.83

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	307	NAG	C1-C2-N2-C7
7	A	303	GOL	O1-C1-C2-C3
7	B	313	GOL	O1-C1-C2-C3
8	A	305	H35	CAK-CAP-N6-C6
8	A	305	H35	N1-C6-N6-CAP
8	A	305	H35	C5-C6-N6-CAP
6	A	302	NAG	O5-C5-C6-O6
6	A	302	NAG	C4-C5-C6-O6
7	B	313	GOL	C1-C2-C3-O3
7	B	316	GOL	O1-C1-C2-C3
7	B	313	GOL	O1-C1-C2-O2
7	B	316	GOL	O1-C1-C2-O2
9	B	311	EDO	O1-C1-C2-O2
7	A	303	GOL	O1-C1-C2-O2
9	B	310	EDO	O1-C1-C2-O2
6	B	307	NAG	C3-C2-N2-C7
9	B	309	EDO	O1-C1-C2-O2
6	B	307	NAG	O5-C5-C6-O6
7	B	313	GOL	O2-C2-C3-O3
7	A	308	GOL	C1-C2-C3-O3

There are no ring outliers.

9 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	307	DIO	1	0
6	B	307	NAG	1	0
7	B	318	GOL	2	0
7	B	315	GOL	1	0
9	B	311	EDO	1	0
8	A	305	H35	7	0
7	A	303	GOL	1	0
7	B	319	GOL	1	0
9	B	309	EDO	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 ⓘ

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	249/249 (100%)	0.59	19 (7%)	20 22	24, 52, 71, 79	1 (0%)
2	B	263/263 (100%)	0.34	23 (8%)	16 18	31, 44, 70, 85	1 (0%)
All	All	512/512 (100%)	0.46	42 (8%)	17 20	24, 49, 72, 85	2 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	243	LEU	9.0
2	B	239	ALA	6.4
1	A	247	CYS	6.0
2	B	3	VAL	4.8
2	B	6	SER	4.4
2	B	241	PRO	4.1
1	A	223	ALA	4.0
1	A	248	GLY	4.0
1	A	249	GLU	3.8
2	B	240	ASN	3.8
2	B	238	GLN	3.8
2	B	167	ALA	3.5
1	A	225	ALA	3.4
1	A	227	ILE	3.3
1	A	224	PRO	3.3
2	B	244	GLN	3.2
2	B	5	CYS	3.0
1	A	91	ASP	3.0
1	A	94	ALA	2.9
2	B	237	ALA	2.9
2	B	156	ASN	2.9
1	A	98	THR	2.8
2	B	242	SER	2.8
2	B	245	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	1	ASP	2.7
2	B	2	ASP	2.7
2	B	168	SER	2.7
1	A	246	VAL	2.7
2	B	7	ALA	2.6
2	B	4	THR	2.6
2	B	44	ASN	2.5
1	A	219	ARG	2.4
2	B	161	TRP	2.3
1	A	102	THR	2.3
2	B	138	THR	2.3
1	A	101	PHE	2.3
1	A	61	ALA	2.2
1	A	46	PRO	2.1
1	A	100	ASP	2.1
1	A	145	PRO	2.1
1	A	221	ALA	2.0
2	B	166	VAL	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](#)

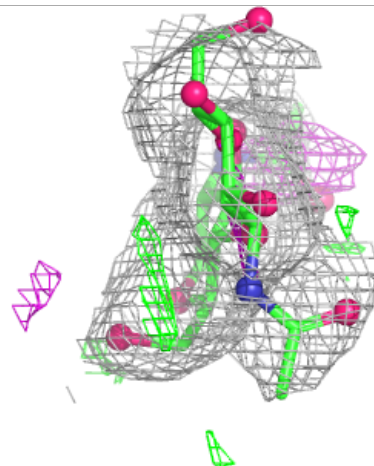
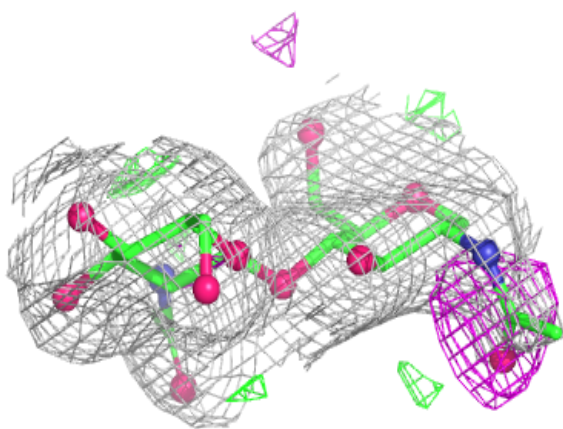
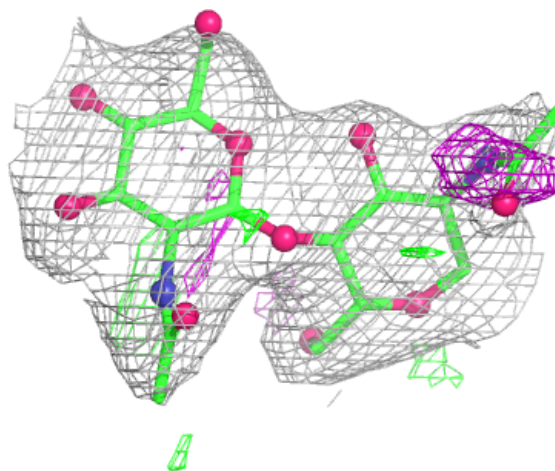
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

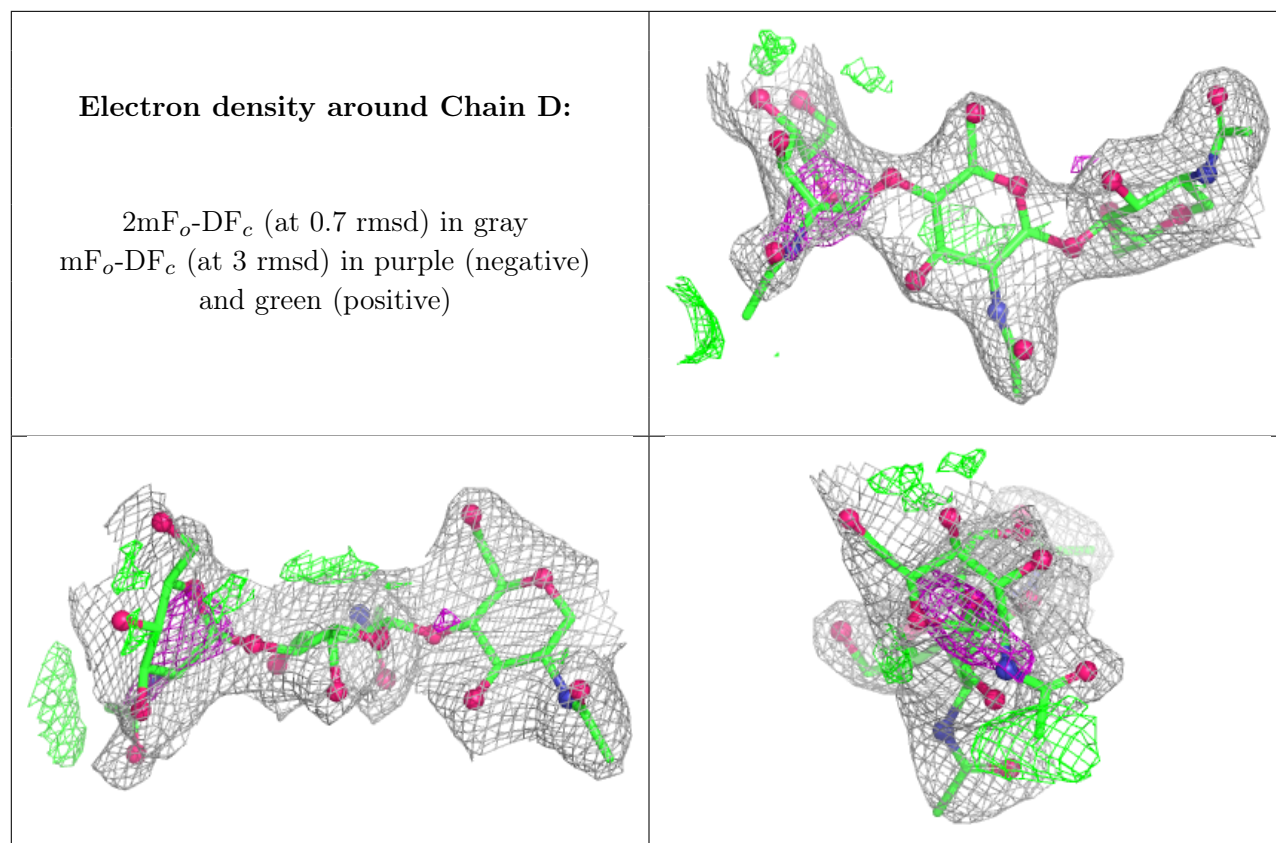
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	D	3	14/15	0.41	0.22	89,91,93,93	0
3	NAG	C	2	14/15	0.68	0.18	80,82,84,85	0
3	NAG	C	1	14/15	0.85	0.14	63,69,71,76	0
4	NAG	D	2	14/15	0.86	0.14	72,75,80,85	0
4	NAG	D	1	14/15	0.95	0.10	49,54,60,65	0

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.

Electron density around Chain C:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





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(Å ²)	Q<0.9
9	EDO	B	310	4/4	0.66	0.33	81,82,82,82	0
9	EDO	A	306	4/4	0.70	0.47	79,79,79,79	0
7	GOL	B	313	6/6	0.70	0.30	63,64,65,65	0
5	SO4	A	312	5/5	0.71	0.13	112,112,113,113	0
9	EDO	B	309	4/4	0.76	0.32	60,62,62,63	0
7	GOL	B	317	6/6	0.76	0.26	93,93,93,93	0
9	EDO	B	312	4/4	0.76	0.37	68,69,70,70	4
7	GOL	B	318	6/6	0.77	0.25	102,102,102,103	0
6	NAG	B	307	14/15	0.78	0.15	66,70,71,72	0
7	GOL	B	319	6/6	0.79	0.31	60,60,61,61	6
7	GOL	A	308	6/6	0.80	0.17	73,73,74,74	0
6	NAG	A	302	14/15	0.81	0.15	72,75,77,78	0
8	H35	A	305	16/16	0.81	0.41	112,113,113,113	16
9	EDO	B	308	4/4	0.82	0.19	51,52,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	SO4	A	309	5/5	0.82	0.13	105,105,105,106	0
12	AZI	B	301	3/3	0.82	0.19	72,72,72,73	0
9	EDO	B	311	4/4	0.84	0.30	80,81,81,81	0
7	GOL	A	303	6/6	0.86	0.20	71,71,72,73	0
11	CL	A	313	1/1	0.87	0.21	88,88,88,88	0
7	GOL	B	316	6/6	0.87	0.22	104,104,104,104	0
5	SO4	A	310	5/5	0.88	0.16	74,74,74,74	5
10	DIO	A	307	6/6	0.88	0.23	83,83,84,84	0
7	GOL	A	304	6/6	0.93	0.18	69,69,70,70	0
5	SO4	A	301	5/5	0.94	0.09	56,57,58,58	0
7	GOL	B	315	6/6	0.95	0.13	50,53,56,58	0
11	CL	B	320	1/1	0.96	0.22	70,70,70,70	0
7	GOL	B	314	6/6	0.96	0.09	55,55,56,56	0
5	SO4	A	311	5/5	0.97	0.08	56,56,57,57	5

6.5 Other polymers [i](#)

There are no such residues in this entry.