



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:21 PM UTC

PDB ID : 1XC6 / pdb_00001xc6
Title : Native Structure Of Beta-Galactosidase from Penicillium sp. in complex with Galactose
Authors : Rojas, A.L.; Nagem, R.A.P.; Neustroev, K.N.; Arand, M.; Adamska, M.; Eneyskaya, E.V.; Kulminskaya, A.A.; Garratt, R.C.; Golubev, A.M.; Polikarpov, I.
Deposited on : 2004-09-01
Resolution : 2.10 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

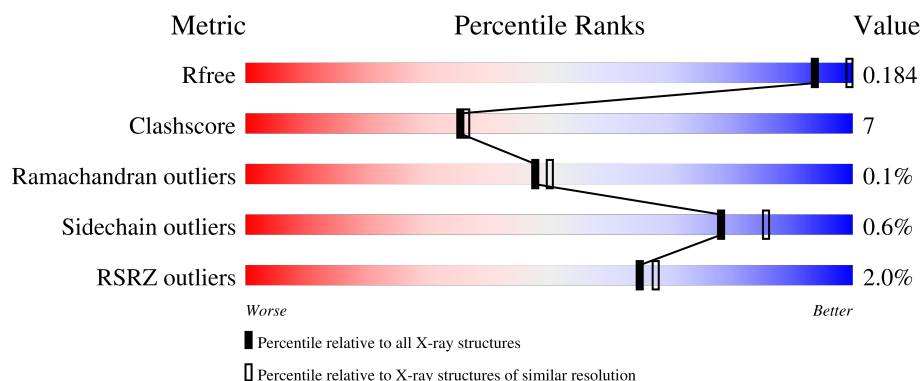
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	971	2% 86% 14%
2	B	3	100%
3	C	9	33% 56% 11%
4	D	2	50% 50%

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Mol	Chain	Length	Quality of chain
5	E	5	
6	F	7	

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
11	IOD	A	9022	-	-	X	-
11	IOD	A	9056	-	-	X	-
11	IOD	A	9057	-	-	X	-
11	IOD	A	9058	-	-	X	-
11	IOD	A	9059	-	-	X	-

2 Entry composition [i](#)

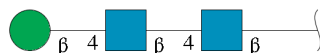
There are 13 unique types of molecules in this entry. The entry contains 8894 atoms, of which 0 are hydrogens and 0 are deuteriums.

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-Galactosidase.

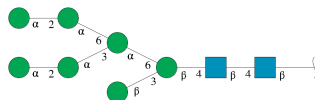
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	971	Total	C	N	O	S	24	0	0
			7484	4776	1241	1457	10			

- Molecule 2 is an oligosaccharide called 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	B	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



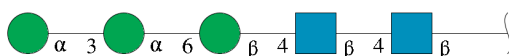
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			105	58	2	45			

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



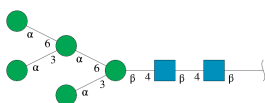
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 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
5	E	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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.



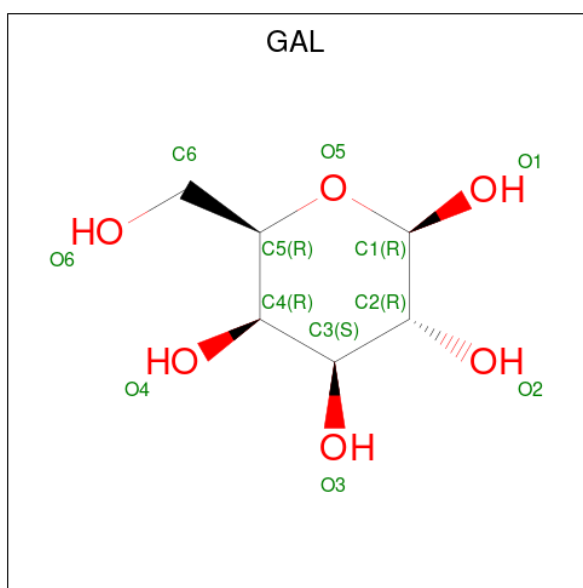
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	F	7	Total	C	N	O	0	0	0
			83	46	2	35			

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 8 is beta-D-galactopyranose (CCD ID: GAL) (formula: $C_6H_{12}O_6$).

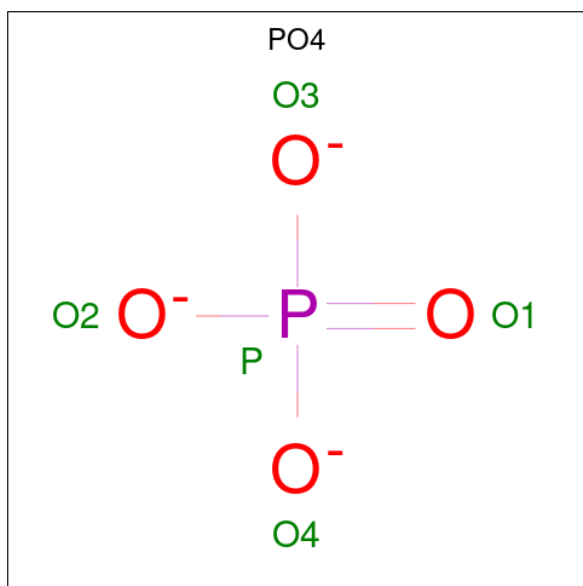


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 9 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Na	0	0
			1	1		

- Molecule 10 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

- Molecule 11 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	52	Total	I	0	0
			52	52		

- Molecule 12 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

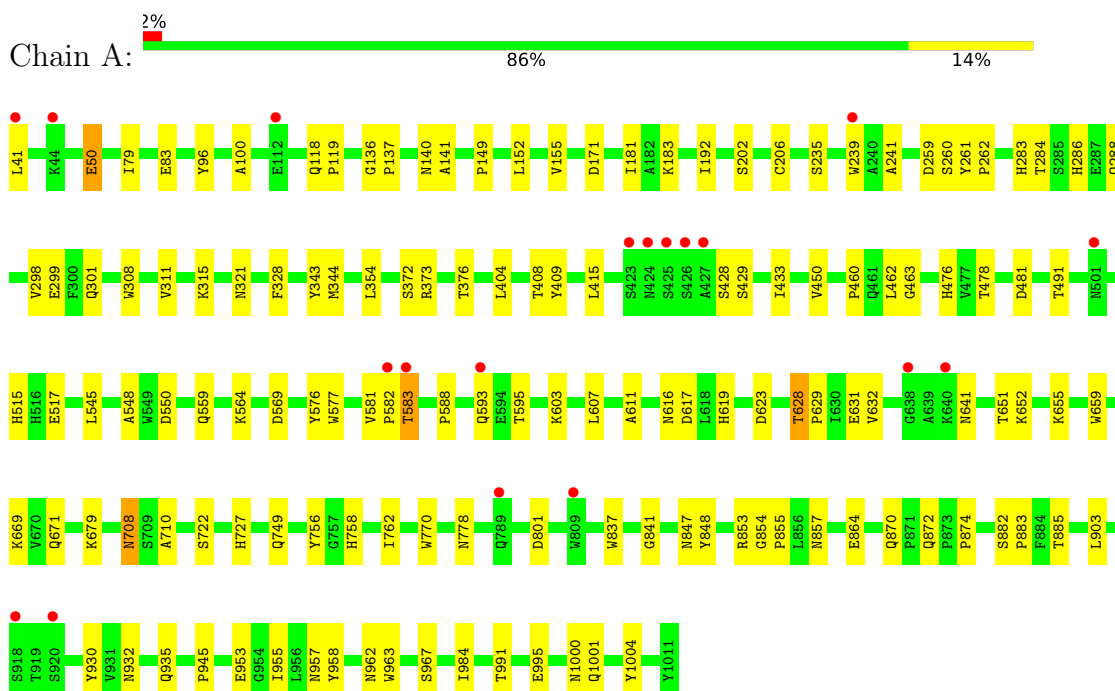
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	952	Total	O	0	0
			952	952		

3 Residue-property plots

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-Galactosidase



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



• Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[beta-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

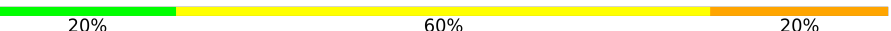


- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  50% 50%

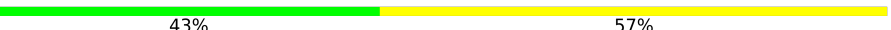
MAG1
MAG2

- Molecule 5: 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

Chain E:  20% 60% 20%

MAG1
MAG2
BMA3
MAN4
MAN5

- Molecule 6: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)-[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

Chain F:  43% 57%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7

4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	110.96Å 110.96Å 161.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.40 – 2.10 23.40 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (23.40-2.10) 99.9 (23.40-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.171 , 0.186 0.169 , 0.184	Depositor DCC
R_{free} test set	2249 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 67.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8894	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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: BMA, MAN, IOD, NAG, NA, GAL, PO4, EDO

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	0.36	0/7698	0.90	25/10501 (0.2%)

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	955	ILE	N-CA-C	-9.80	101.20	111.58
1	A	206	CYS	N-CA-C	7.24	121.45	111.90
1	A	885	THR	N-CA-C	-6.91	104.49	113.12
1	A	837	TRP	N-CA-C	6.69	120.94	110.17
1	A	953	GLU	N-CA-C	-6.66	100.58	110.23
1	A	857	ASN	N-CA-C	6.61	119.04	111.11
1	A	991	THR	N-CA-C	6.12	119.01	109.52
1	A	581	VAL	CA-C-N	5.98	125.92	119.76
1	A	581	VAL	C-N-CA	5.98	125.92	119.76
1	A	967	SER	N-CA-C	-5.82	100.22	109.59
1	A	171	ASP	N-CA-C	5.69	117.94	111.11
1	A	409	TYR	N-CA-C	5.67	121.09	113.72
1	A	628	THR	N-CA-C	5.65	119.49	107.91
1	A	569	ASP	N-CA-C	-5.49	101.34	110.17
1	A	328	PHE	N-CA-C	5.43	117.28	111.36
1	A	408	THR	N-CA-C	5.37	117.21	111.36
1	A	841	GLY	N-CA-C	-5.33	100.55	113.18
1	A	854	GLY	CA-C-N	5.33	124.94	119.56
1	A	854	GLY	C-N-CA	5.33	124.94	119.56
1	A	770	TRP	N-CA-C	-5.30	98.61	107.99
1	A	450	VAL	N-CA-C	5.27	114.77	108.45
1	A	206	CYS	N-CA-CB	-5.26	104.13	112.08
1	A	481	ASP	N-CA-C	5.16	117.16	108.96
1	A	308	TRP	N-CA-C	-5.09	102.84	110.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	847	ASN	N-CA-C	-5.08	103.62	110.68

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	7484	0	7126	99	0
2	B	39	0	34	0	0
3	C	105	0	88	2	0
4	D	28	0	25	2	0
5	E	61	0	52	5	0
6	F	83	0	70	3	0
7	A	28	0	26	1	0
8	A	12	0	12	1	0
9	A	1	0	0	0	0
10	A	5	0	0	0	0
11	A	52	0	0	25	0
12	A	44	0	66	0	0
13	A	952	0	0	23	0
All	All	8894	0	7499	114	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 7.

All (114) 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:299:GLU:OE1	8:A:9011:GAL:H1	1.60	1.02
1:A:778:ASN:HD21	5:E:1:NAG:HN2	1.24	0.83
1:A:462:LEU:HB2	11:A:9056:IOD:I	2.50	0.81
11:A:9034:IOD:I	11:A:9058:IOD:I	3.43	0.77
1:A:515:HIS:HE1	11:A:9056:IOD:I	2.38	0.76
13:A:9426:HOH:O	3:C:9:BMA:H2	1.83	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:GLU:CD	1:A:50:GLU:H	1.95	0.72
1:A:853:ARG:HH12	1:A:870:GLN:HE21	1.38	0.71
1:A:669:LYS:NZ	1:A:671:GLN:HG2	2.06	0.69
1:A:259:ASP:CG	1:A:299:GLU:HB2	2.19	0.67
1:A:629:PRO:HG3	11:A:9040:IOD:I	2.65	0.66
1:A:932:ASN:ND2	1:A:963:TRP:H	1.93	0.65
1:A:517:GLU:OE2	11:A:9056:IOD:I	2.85	0.65
1:A:582:PRO:HG3	1:A:588:PRO:HA	1.79	0.65
1:A:463:GLY:O	11:A:9056:IOD:I	2.85	0.65
1:A:778:ASN:ND2	5:E:1:NAG:HN2	1.94	0.65
13:A:9383:HOH:O	6:F:6:MAN:H61	1.97	0.64
1:A:118:GLN:OE1	11:A:9058:IOD:I	2.86	0.64
1:A:655:LYS:C	1:A:655:LYS:HD3	2.23	0.64
1:A:181:ILE:HG23	1:A:192:ILE:HD13	1.79	0.63
1:A:515:HIS:CE1	11:A:9056:IOD:I	3.22	0.63
1:A:708:ASN:HD22	1:A:710:ALA:H	1.44	0.63
1:A:576:TYR:OH	11:A:9062:IOD:I	2.91	0.59
1:A:669:LYS:HZ3	1:A:671:GLN:HG2	1.68	0.58
1:A:588:PRO:O	11:A:9059:IOD:I	2.92	0.58
1:A:582:PRO:HA	11:A:9059:IOD:I	2.74	0.58
1:A:957:ASN:HB3	11:A:9052:IOD:I	2.74	0.57
1:A:404:LEU:C	1:A:404:LEU:HD12	2.32	0.55
1:A:428:SER:HB2	13:A:9418:HOH:O	2.06	0.55
1:A:593:GLN:HG3	13:A:9579:HOH:O	2.08	0.54
11:A:9023:IOD:I	11:A:9057:IOD:I	3.66	0.54
1:A:283:HIS:HD2	13:A:9206:HOH:O	1.89	0.54
1:A:722:SER:OG	1:A:727:HIS:HD2	1.91	0.53
13:A:9842:HOH:O	4:D:2:NAG:H82	2.08	0.52
1:A:286:HIS:HE1	13:A:9163:HOH:O	1.91	0.52
1:A:616:ASN:HB3	13:A:9794:HOH:O	2.09	0.52
1:A:100:ALA:HA	1:A:149:PRO:HG3	1.92	0.52
1:A:708:ASN:ND2	1:A:710:ALA:H	2.08	0.52
1:A:41:LEU:HD12	13:A:9823:HOH:O	2.10	0.52
1:A:930:TYR:HE2	13:A:9692:HOH:O	1.93	0.51
1:A:603:LYS:HB3	1:A:631:GLU:HB2	1.91	0.51
1:A:984:ILE:HD12	1:A:984:ILE:C	2.36	0.50
1:A:415:LEU:HD13	1:A:433:ILE:HD11	1.93	0.50
1:A:583:THR:HA	13:A:9780:HOH:O	2.11	0.50
13:A:9930:HOH:O	5:E:5:MAN:H62	2.11	0.50
1:A:118:GLN:HB3	1:A:119:PRO:HD3	1.94	0.50
7:A:2001:NAG:H3	7:A:2001:NAG:H82	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ASN:HB2	11:A:9022:IOD:I	2.82	0.50
1:A:41:LEU:HA	13:A:9823:HOH:O	2.11	0.50
1:A:995:GLU:HA	13:A:9935:HOH:O	2.11	0.50
11:A:9021:IOD:I	13:A:9811:HOH:O	2.90	0.49
11:A:9022:IOD:I	13:A:9353:HOH:O	2.89	0.49
1:A:286:HIS:HD2	13:A:9222:HOH:O	1.95	0.49
1:A:79:ILE:O	1:A:83:GLU:HG3	2.13	0.49
1:A:669:LYS:HZ2	1:A:671:GLN:HG2	1.76	0.49
1:A:756:TYR:HB2	1:A:801:ASP:O	2.13	0.48
13:A:9437:HOH:O	5:E:2:NAG:H82	2.13	0.48
1:A:202:SER:HB3	13:A:9962:HOH:O	2.13	0.48
1:A:679:LYS:HD2	13:A:9792:HOH:O	2.13	0.48
1:A:762:ILE:O	1:A:762:ILE:HG23	2.14	0.48
1:A:183:LYS:HG2	11:A:9058:IOD:I	2.84	0.47
1:A:239:TRP:NE1	1:A:241:ALA:HB2	2.29	0.47
1:A:261:TYR:HA	1:A:301:GLN:HB2	1.96	0.47
1:A:708:ASN:HD22	1:A:708:ASN:C	2.22	0.47
1:A:136:GLY:HA3	1:A:137:PRO:C	2.39	0.47
1:A:882:SER:HB2	1:A:883:PRO:HD2	1.97	0.47
1:A:932:ASN:HD21	1:A:963:TRP:H	1.59	0.47
1:A:749:GLN:HE21	1:A:778:ASN:ND2	2.13	0.47
1:A:874:PRO:HD3	1:A:1004:TYR:CD2	2.50	0.46
1:A:354:LEU:C	1:A:354:LEU:HD12	2.40	0.46
1:A:548:ALA:HB2	11:A:9056:IOD:I	2.85	0.46
1:A:476:HIS:HD2	1:A:491:THR:O	1.98	0.46
1:A:758:HIS:CD2	1:A:758:HIS:C	2.94	0.46
13:A:9403:HOH:O	4:D:2:NAG:H2	2.15	0.46
1:A:515:HIS:HD2	1:A:550:ASP:OD1	1.98	0.46
1:A:853:ARG:NH1	1:A:870:GLN:HE21	2.12	0.46
1:A:311:VAL:HB	1:A:315:LYS:HD2	1.98	0.46
1:A:864:GLU:OE2	1:A:930:TYR:OH	2.30	0.46
1:A:548:ALA:CB	11:A:9056:IOD:I	3.35	0.45
1:A:429:SER:HB2	1:A:478:THR:OG1	2.16	0.45
13:A:9708:HOH:O	6:F:6:MAN:H2	2.17	0.45
1:A:874:PRO:HD3	1:A:1004:TYR:CE2	2.52	0.45
3:C:2:NAG:H62	3:C:3:BMA:C1	2.47	0.45
1:A:559:GLN:OE1	1:A:564:LYS:HG2	2.16	0.44
1:A:235:SER:O	1:A:298:VAL:HG21	2.17	0.44
1:A:149:PRO:HD2	1:A:152:LEU:HD23	2.00	0.44
1:A:239:TRP:CD1	1:A:241:ALA:HB2	2.53	0.44
1:A:617:ASP:OD1	1:A:641:ASN:HB2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:343:TYR:HA	1:A:344:MET:HA	1.83	0.43
1:A:749:GLN:HE21	1:A:778:ASN:HD22	1.65	0.43
1:A:372:SER:O	1:A:373:ARG:HB2	2.18	0.43
1:A:96:TYR:CE2	1:A:141:ALA:HB2	2.53	0.43
1:A:628:THR:HA	1:A:629:PRO:HD3	1.92	0.43
1:A:1000:ASN:HD22	1:A:1001:GLN:N	2.16	0.43
1:A:152:LEU:HD13	1:A:155:VAL:HG21	2.01	0.42
1:A:669:LYS:HE3	13:A:9913:HOH:O	2.18	0.42
1:A:595:THR:HG22	11:A:9059:IOD:I	2.90	0.42
1:A:651:THR:HG22	1:A:652:LYS:N	2.35	0.42
1:A:848:TYR:CE1	1:A:855:PRO:HB3	2.55	0.42
1:A:577:TRP:CZ2	1:A:607:LEU:HA	2.55	0.41
1:A:607:LEU:HB3	1:A:623:ASP:HB2	2.02	0.41
11:A:9053:IOD:I	6:F:7:MAN:H2	2.90	0.41
5:E:2:NAG:H83	5:E:4:MAN:O4	2.20	0.41
1:A:460:PRO:HB3	11:A:9056:IOD:I	2.90	0.41
1:A:376:THR:OG1	11:A:9057:IOD:I	3.05	0.41
1:A:284:THR:O	1:A:288:GLN:HG3	2.20	0.41
1:A:260:SER:OG	1:A:262:PRO:HD3	2.21	0.41
1:A:655:LYS:HE2	11:A:9043:IOD:I	2.91	0.41
1:A:872:GLN:NE2	11:A:9037:IOD:I	3.23	0.41
1:A:932:ASN:HD21	1:A:962:ASN:HA	1.85	0.41
1:A:632:VAL:HB	1:A:659:TRP:HB2	2.03	0.41
1:A:903:LEU:HD12	1:A:958:TYR:CD2	2.55	0.41
1:A:545:LEU:C	1:A:545:LEU:HD13	2.47	0.40
1:A:611:ALA:HA	1:A:619:HIS:O	2.21	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	969/971 (100%)	940 (97%)	28 (3%)	1 (0%)	48	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	140	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	795/795 (100%)	790 (99%)	5 (1%)	78	86

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	GLU
1	A	583	THR
1	A	708	ASN
1	A	935	GLN
1	A	945	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
1	A	140	ASN
1	A	172	ASN
1	A	188	ASN
1	A	283	HIS
1	A	286	HIS
1	A	289	GLN
1	A	476	HIS
1	A	515	HIS
1	A	621	GLN

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Mol	Chain	Res	Type
1	A	708	ASN
1	A	727	HIS
1	A	749	GLN
1	A	778	ASN
1	A	870	GLN
1	A	872	GLN
1	A	928	GLN
1	A	932	ASN
1	A	959	HIS
1	A	1000	ASN
1	A	1005	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 ⓘ

26 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	NAG	B	1	1,2	14,14,15	0.59	0	17,19,21	0.75	0
2	NAG	B	2	2	14,14,15	0.62	0	17,19,21	0.62	0
2	BMA	B	3	2	11,11,12	0.45	0	15,15,17	0.26	0
3	NAG	C	1	3,1	14,14,15	0.57	0	17,19,21	0.67	0
3	NAG	C	2	3	14,14,15	0.57	0	17,19,21	0.67	0
3	BMA	C	3	3	11,11,12	0.57	0	15,15,17	0.38	0
3	MAN	C	4	3	11,11,12	0.48	0	15,15,17	0.69	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MAN	C	5	3	11,11,12	0.48	0	15,15,17	0.54	0
3	MAN	C	6	3	11,11,12	0.45	0	15,15,17	0.58	0
3	MAN	C	7	3	11,11,12	0.51	0	15,15,17	0.66	1 (6%)
3	MAN	C	8	3	11,11,12	0.48	0	15,15,17	0.61	1 (6%)
3	BMA	C	9	3	11,11,12	0.59	0	15,15,17	0.98	1 (6%)
4	NAG	D	1	4,1	14,14,15	0.57	0	17,19,21	0.75	1 (5%)
4	NAG	D	2	4	14,14,15	0.48	0	17,19,21	0.68	1 (5%)
5	NAG	E	1	1,5	14,14,15	0.46	0	17,19,21	0.68	0
5	NAG	E	2	5	14,14,15	0.48	0	17,19,21	0.74	1 (5%)
5	BMA	E	3	5	11,11,12	0.44	0	15,15,17	0.34	0
5	MAN	E	4	5	11,11,12	0.53	0	15,15,17	0.53	0
5	MAN	E	5	5	11,11,12	0.47	0	15,15,17	0.56	0
6	NAG	F	1	1,9,6	14,14,15	0.56	0	17,19,21	0.71	1 (5%)
6	NAG	F	2	6	14,14,15	0.57	0	17,19,21	0.69	0
6	BMA	F	3	6	11,11,12	0.51	0	15,15,17	0.37	0
6	MAN	F	4	6	11,11,12	0.51	0	15,15,17	0.69	1 (6%)
6	MAN	F	5	6	11,11,12	0.51	0	15,15,17	0.41	0
6	MAN	F	6	6	11,11,12	0.53	0	15,15,17	0.49	0
6	MAN	F	7	6	11,11,12	0.46	0	15,15,17	0.53	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	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	0/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	0/1/1/1
3	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	3/6/23/26	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	-	0/2/19/22	0/1/1/1
3	MAN	C	6	3	-	0/2/19/22	0/1/1/1
3	MAN	C	7	3	-	0/2/19/22	0/1/1/1
3	MAN	C	8	3	-	0/2/19/22	0/1/1/1
3	BMA	C	9	3	-	0/2/19/22	1/1/1/1
4	NAG	D	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	E	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	0/6/23/26	0/1/1/1
5	BMA	E	3	5	-	0/2/19/22	0/1/1/1
5	MAN	E	4	5	-	0/2/19/22	0/1/1/1
5	MAN	E	5	5	-	2/2/19/22	0/1/1/1
6	NAG	F	1	1,9,6	-	0/6/23/26	0/1/1/1
6	NAG	F	2	6	-	0/6/23/26	0/1/1/1
6	BMA	F	3	6	-	0/2/19/22	0/1/1/1
6	MAN	F	4	6	-	0/2/19/22	0/1/1/1
6	MAN	F	5	6	-	0/2/19/22	0/1/1/1
6	MAN	F	6	6	-	2/2/19/22	0/1/1/1
6	MAN	F	7	6	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	9	BMA	C1-O5-C5	3.25	116.55	112.19
5	E	2	NAG	C2-N2-C7	-2.24	119.90	122.90
4	D	1	NAG	C2-N2-C7	-2.24	119.90	122.90
3	C	4	MAN	C1-O5-C5	2.18	115.11	112.19
6	F	4	MAN	C1-O5-C5	2.09	114.98	112.19
3	C	7	MAN	C1-O5-C5	2.09	114.98	112.19
6	F	1	NAG	C2-N2-C7	-2.06	120.14	122.90
3	C	8	MAN	C1-O5-C5	2.04	114.92	112.19
4	D	2	NAG	C2-N2-C7	-2.02	120.20	122.90

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	F	6	MAN	O5-C5-C6-O6
5	E	5	MAN	O5-C5-C6-O6
5	E	5	MAN	C4-C5-C6-O6
4	D	2	NAG	C8-C7-N2-C2
4	D	2	NAG	O7-C7-N2-C2
6	F	6	MAN	C4-C5-C6-O6
3	C	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
6	F	7	MAN	C4-C5-C6-O6
3	C	2	NAG	C1-C2-N2-C7

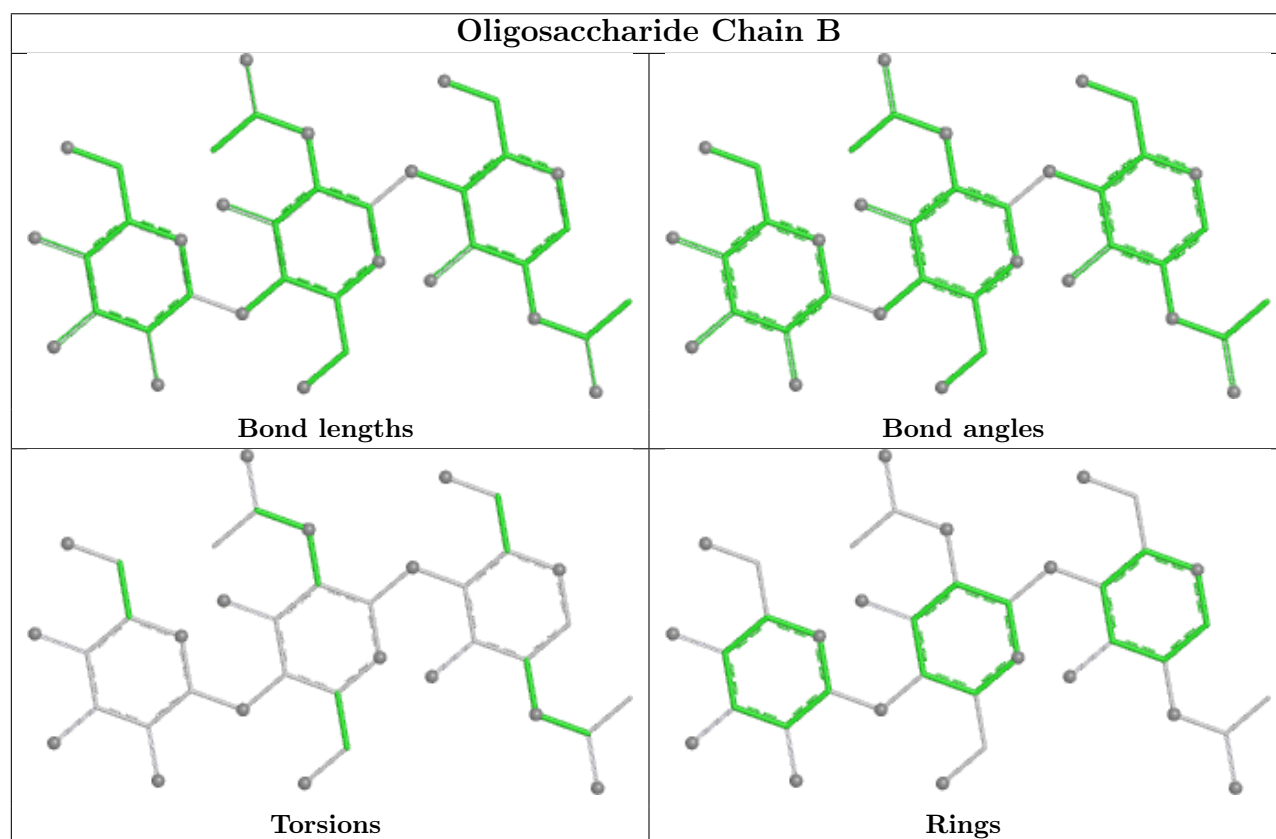
All (1) ring outliers are listed below:

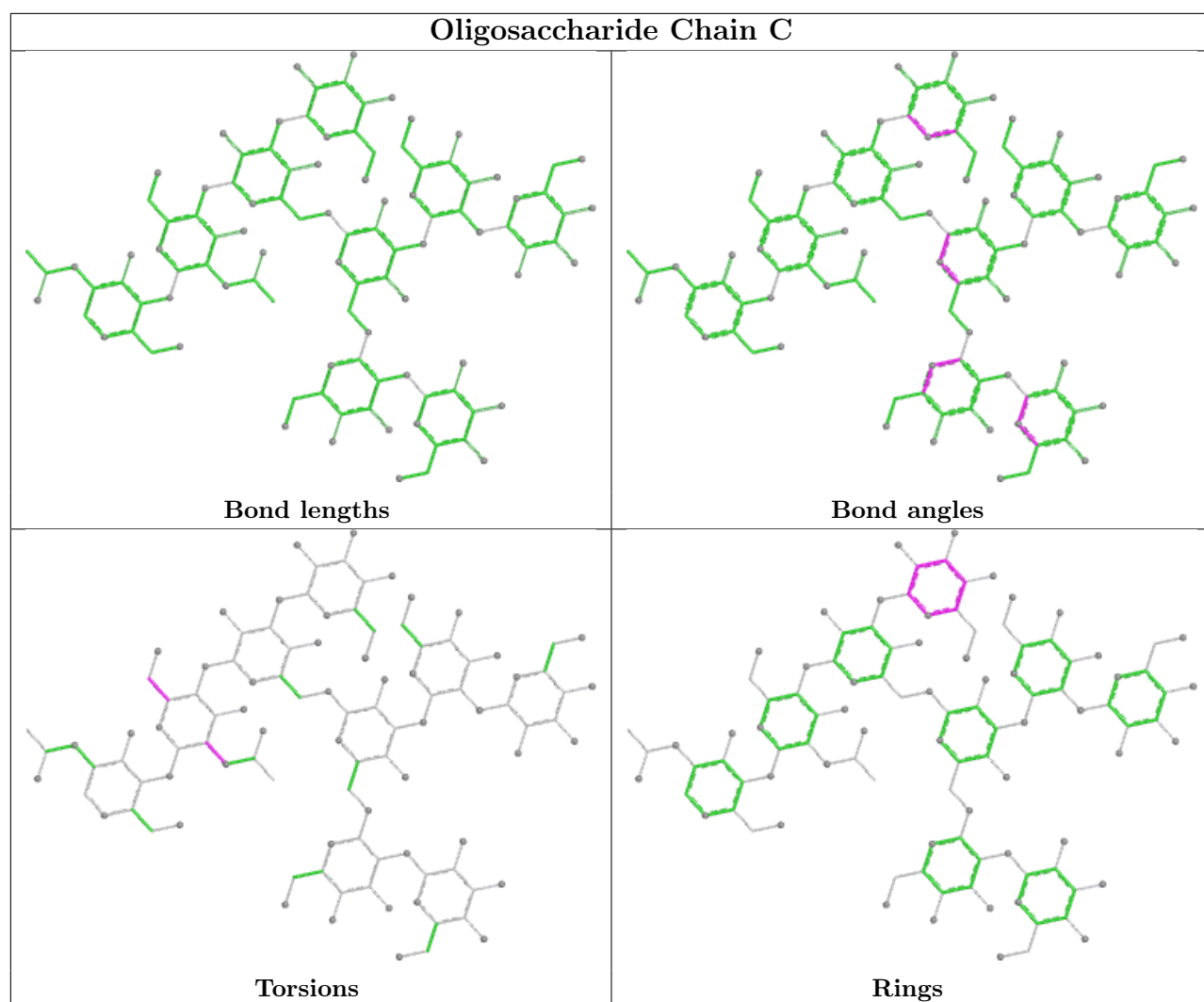
Mol	Chain	Res	Type	Atoms
3	C	9	BMA	C1-C2-C3-C4-C5-O5

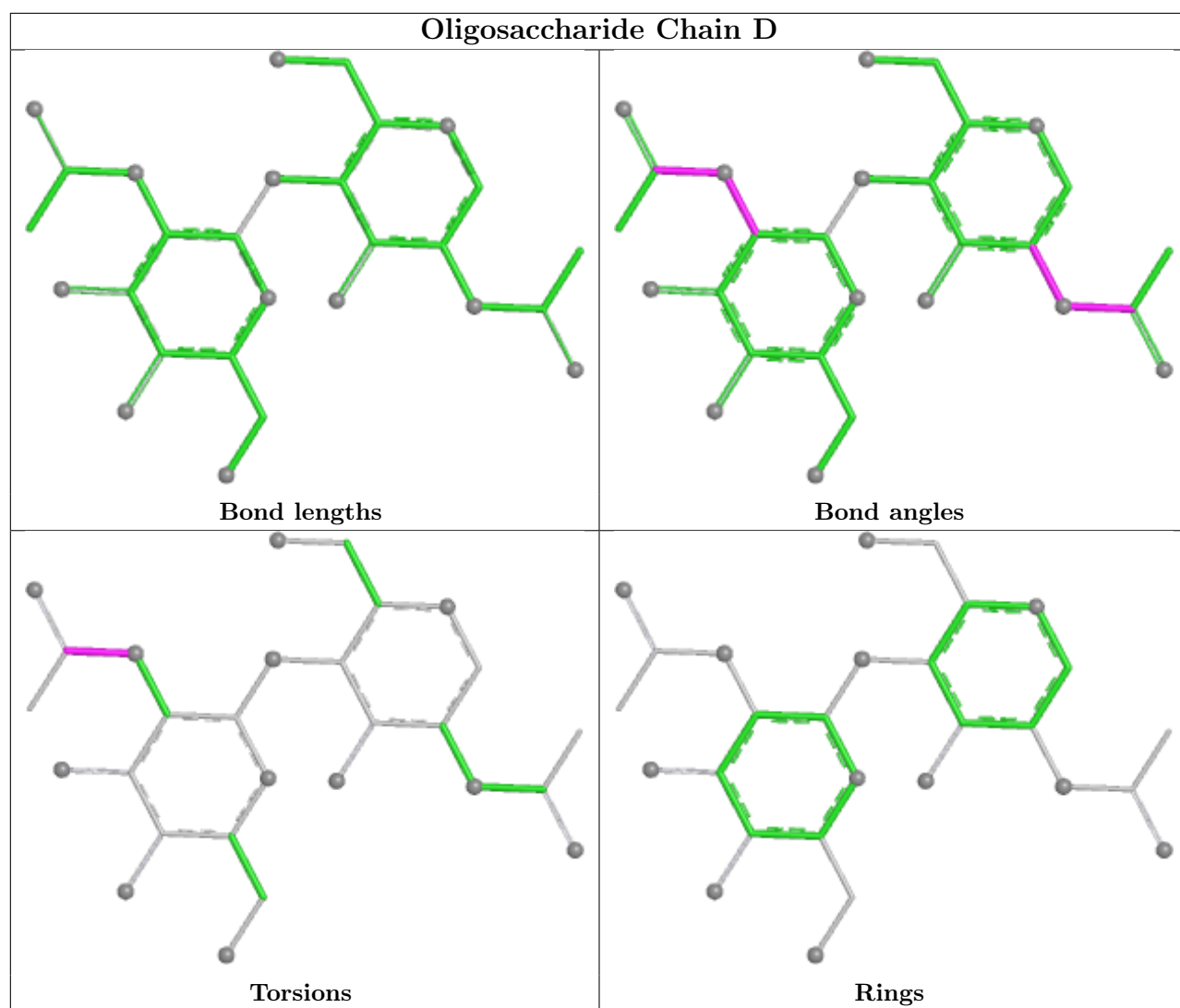
10 monomers are involved in 12 short contacts:

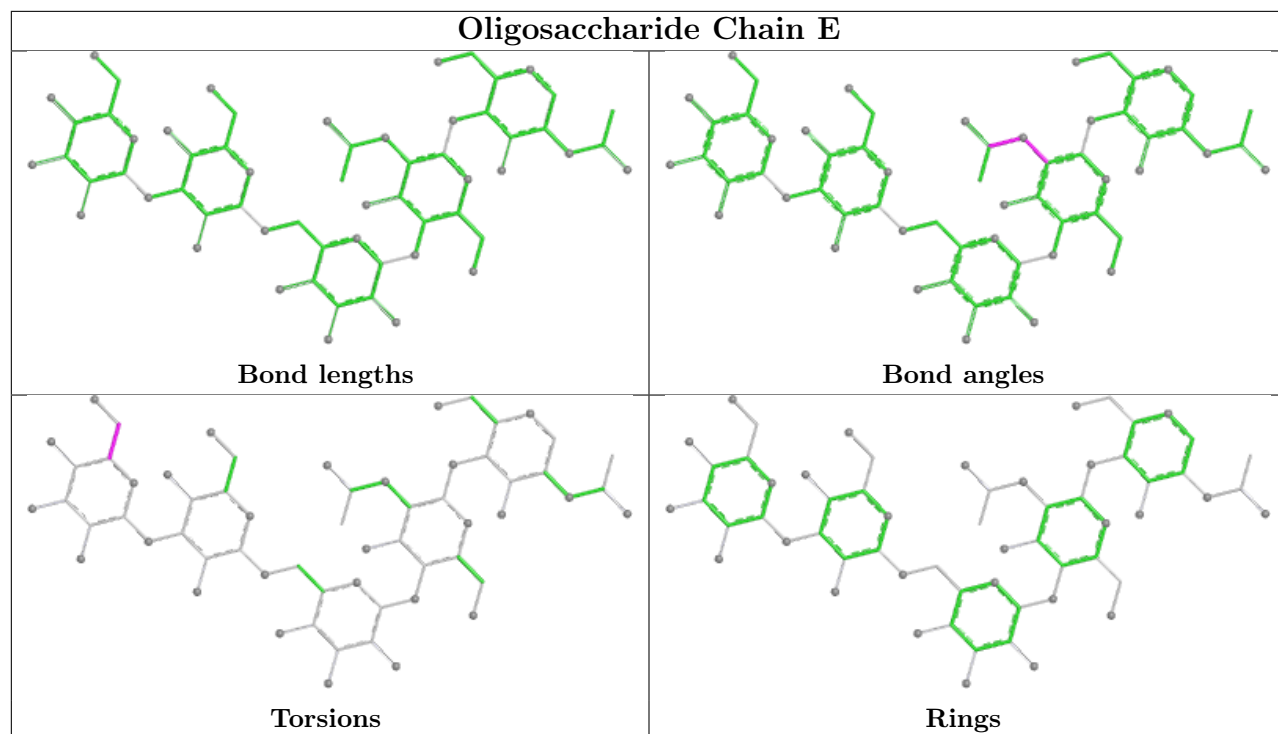
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	2	NAG	2	0
6	F	7	MAN	1	0
3	C	9	BMA	1	0
3	C	2	NAG	1	0
5	E	1	NAG	2	0
4	D	2	NAG	2	0
3	C	3	BMA	1	0
5	E	4	MAN	1	0
6	F	6	MAN	2	0
5	E	5	MAN	1	0

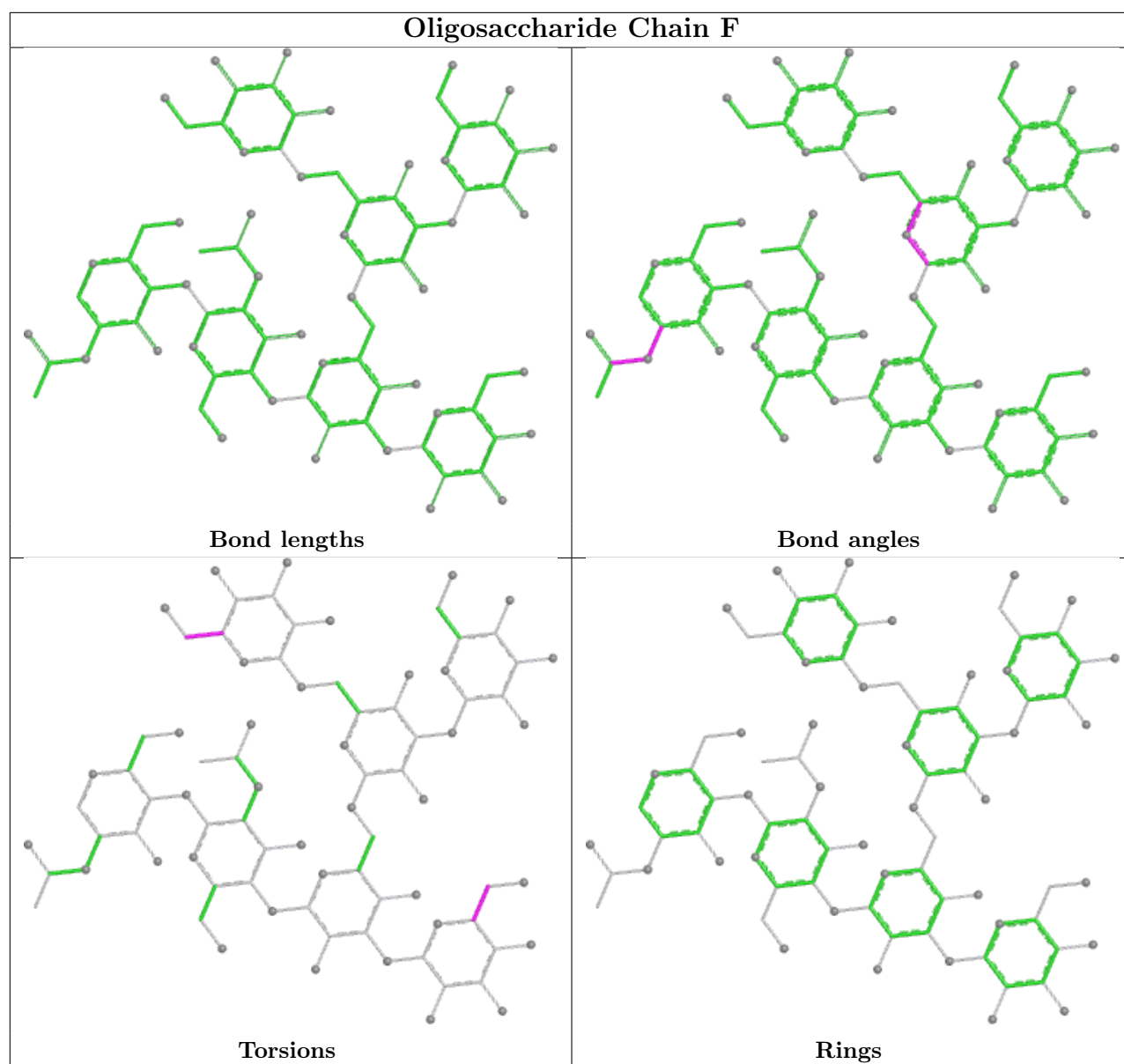
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











5.6 Ligand geometry [i](#)

Of 68 ligands modelled in this entry, 53 are monoatomic - leaving 15 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
12	EDO	A	9081	-	3,3,3	0.58	0	2,2,2	0.40	0
12	EDO	A	9080	-	3,3,3	0.50	0	2,2,2	0.40	0
7	NAG	A	4001	1	14,14,15	0.49	0	17,19,21	0.67	1 (5%)
12	EDO	A	9009	-	3,3,3	0.62	0	2,2,2	0.39	0
12	EDO	A	9006	-	3,3,3	0.54	0	2,2,2	0.40	0
12	EDO	A	9004	-	3,3,3	0.54	0	2,2,2	0.39	0
12	EDO	A	9008	-	3,3,3	0.71	0	2,2,2	0.42	0
8	GAL	A	9011	-	12,12,12	0.38	0	17,17,17	0.39	0
12	EDO	A	9007	-	3,3,3	0.59	0	2,2,2	0.41	0
12	EDO	A	9003	-	3,3,3	0.57	0	2,2,2	0.40	0
7	NAG	A	2001	1	14,14,15	0.50	0	17,19,21	0.63	0
12	EDO	A	9001	-	3,3,3	0.56	0	2,2,2	0.40	0
12	EDO	A	9002	-	3,3,3	0.55	0	2,2,2	0.39	0
12	EDO	A	9005	-	3,3,3	0.66	0	2,2,2	0.38	0
10	PO4	A	8002	-	4,4,4	1.74	1 (25%)	6,6,6	0.47	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
12	EDO	A	9081	-	-	0/1/1/1	-
12	EDO	A	9080	-	-	0/1/1/1	-
7	NAG	A	4001	1	-	0/6/23/26	0/1/1/1
12	EDO	A	9009	-	-	0/1/1/1	-
12	EDO	A	9006	-	-	0/1/1/1	-
12	EDO	A	9004	-	-	0/1/1/1	-
12	EDO	A	9008	-	-	0/1/1/1	-
8	GAL	A	9011	-	-	1/2/22/22	0/1/1/1
12	EDO	A	9007	-	-	0/1/1/1	-
12	EDO	A	9003	-	-	0/1/1/1	-
7	NAG	A	2001	1	-	6/6/23/26	0/1/1/1
12	EDO	A	9001	-	-	0/1/1/1	-
12	EDO	A	9002	-	-	0/1/1/1	-
12	EDO	A	9005	-	-	0/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	8002	PO4	P-O4	-2.01	1.48	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	4001	NAG	C2-N2-C7	-2.02	120.19	122.90

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	2001	NAG	C8-C7-N2-C2
7	A	2001	NAG	O7-C7-N2-C2
7	A	2001	NAG	C4-C5-C6-O6
8	A	9011	GAL	O5-C5-C6-O6
7	A	2001	NAG	O5-C5-C6-O6
7	A	2001	NAG	C1-C2-N2-C7
7	A	2001	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	9011	GAL	1	0
7	A	2001	NAG	1	0

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	A	971/971 (100%)	-0.35	19 (1%) 65 67	7, 18, 33, 51	18 (1%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	425	SER	4.8
1	A	918	SER	4.5
1	A	41	LEU	4.5
1	A	239	TRP	4.3
1	A	809	TRP	4.3
1	A	426	SER	4.0
1	A	583	THR	3.5
1	A	423	SER	3.3
1	A	640	LYS	3.1
1	A	789	GLN	3.0
1	A	920	SER	3.0
1	A	638	GLY	2.6
1	A	427	ALA	2.6
1	A	593	GLN	2.5
1	A	582	PRO	2.5
1	A	424	ASN	2.5
1	A	501	ASN	2.3
1	A	44	LYS	2.3
1	A	112	GLU	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

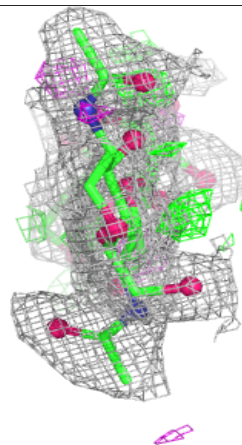
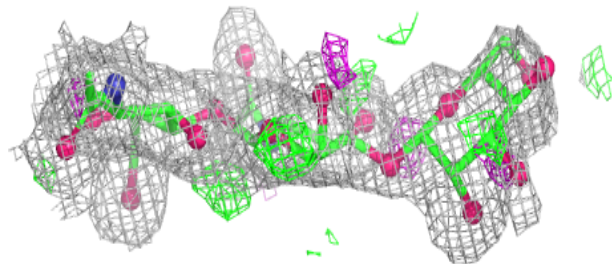
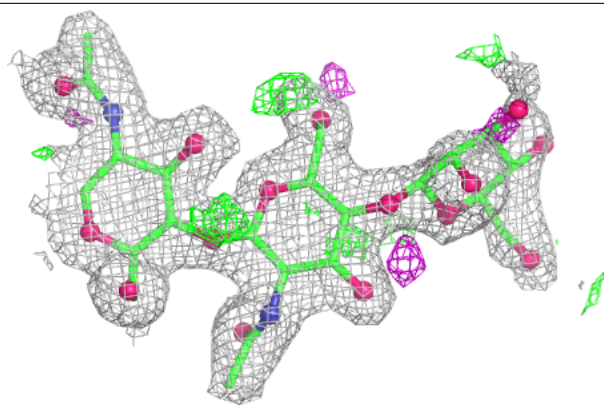
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	BMA	C	9	11/12	0.62	0.26	41,47,51,52	0
4	NAG	D	2	14/15	0.73	0.21	49,52,55,55	14
2	BMA	B	3	11/12	0.75	0.15	51,57,59,60	0
5	MAN	E	5	11/12	0.76	0.20	48,49,51,51	11
3	MAN	C	8	11/12	0.77	0.17	35,37,37,38	11
6	MAN	F	6	11/12	0.78	0.17	36,41,43,43	0
5	MAN	E	4	11/12	0.79	0.19	43,46,47,49	11
5	NAG	E	2	14/15	0.80	0.17	41,46,49,50	0
5	BMA	E	3	11/12	0.83	0.15	44,47,49,50	0
6	MAN	F	5	11/12	0.85	0.11	30,33,35,37	0
3	MAN	C	7	11/12	0.88	0.13	22,30,33,34	11
4	NAG	D	1	14/15	0.89	0.12	37,41,45,47	0
3	NAG	C	2	14/15	0.89	0.09	15,17,24,32	0
2	NAG	B	2	14/15	0.90	0.09	24,31,40,44	0
5	NAG	E	1	14/15	0.90	0.10	18,25,35,35	0
6	MAN	F	7	11/12	0.91	0.10	25,29,33,39	0
3	MAN	C	6	11/12	0.92	0.10	30,32,35,36	0
6	NAG	F	1	14/15	0.94	0.07	14,17,22,31	0
6	NAG	F	2	14/15	0.96	0.06	12,17,23,23	0
6	BMA	F	3	11/12	0.96	0.06	16,18,20,20	0
2	NAG	B	1	14/15	0.96	0.06	15,19,20,23	0
3	MAN	C	4	11/12	0.96	0.06	19,20,23,27	0
3	MAN	C	5	11/12	0.96	0.06	16,21,23,26	0
3	NAG	C	1	14/15	0.97	0.06	14,18,27,27	0
3	BMA	C	3	11/12	0.97	0.06	18,20,24,32	0
6	MAN	F	4	11/12	0.97	0.06	21,23,29,30	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.

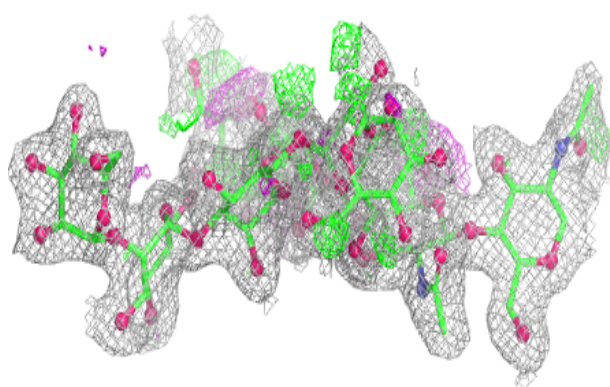
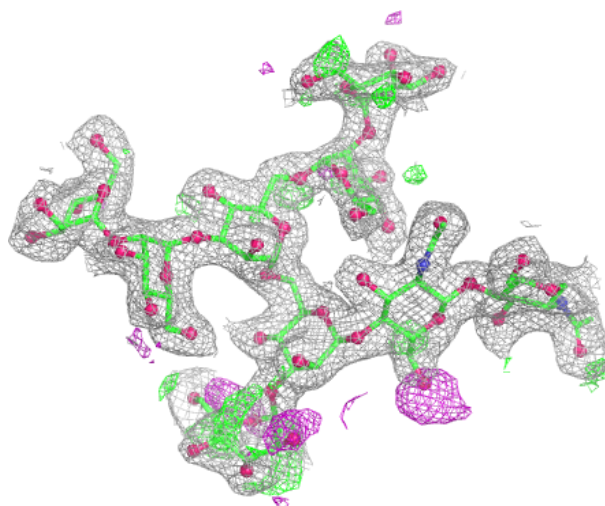
Electron density around Chain B:

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



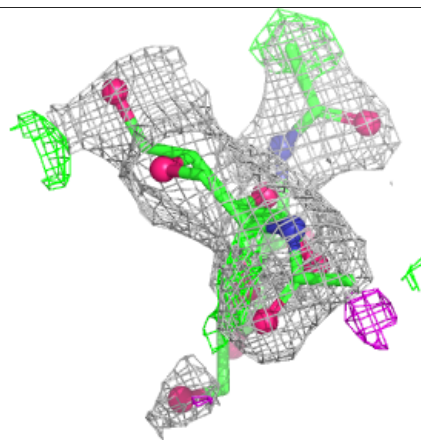
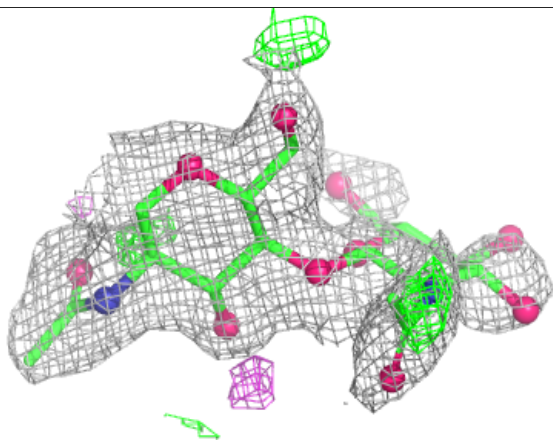
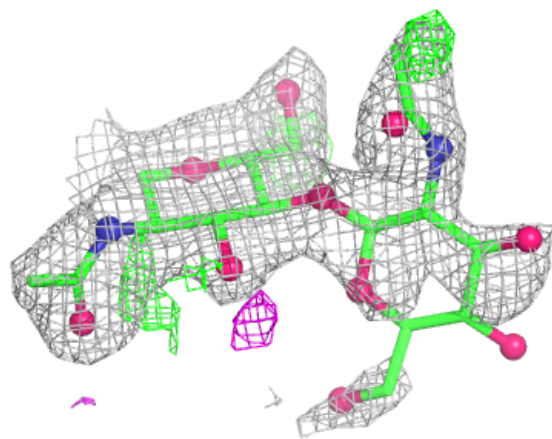
Electron density around Chain C:

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



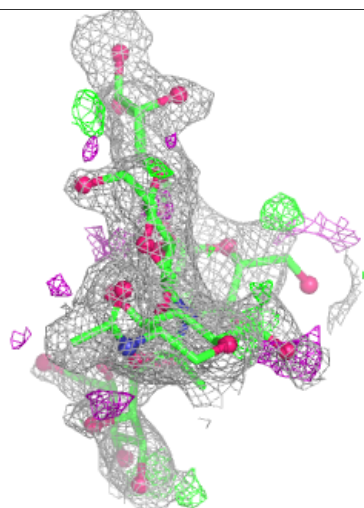
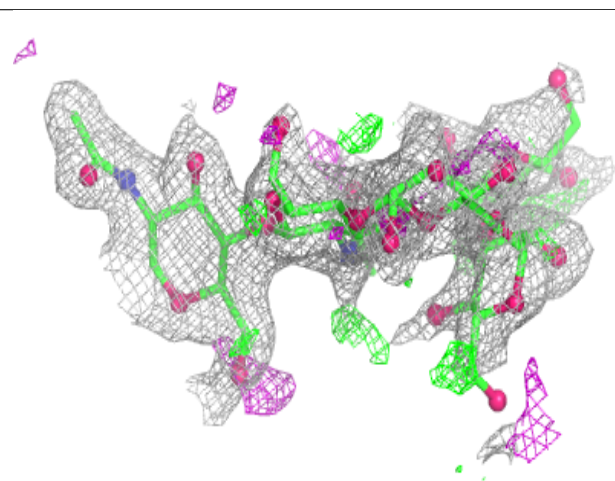
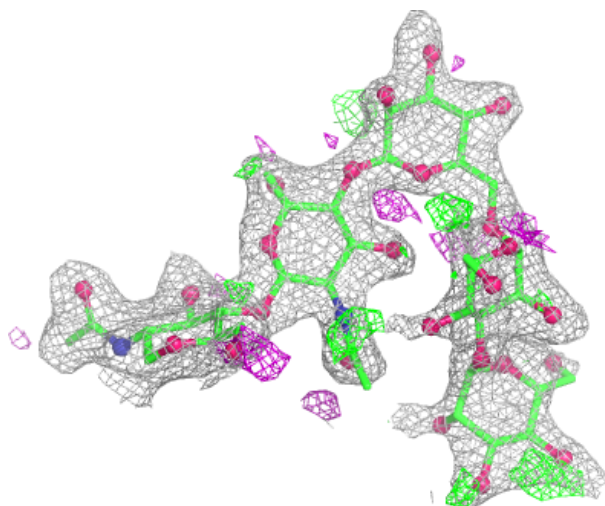
Electron density around Chain D:

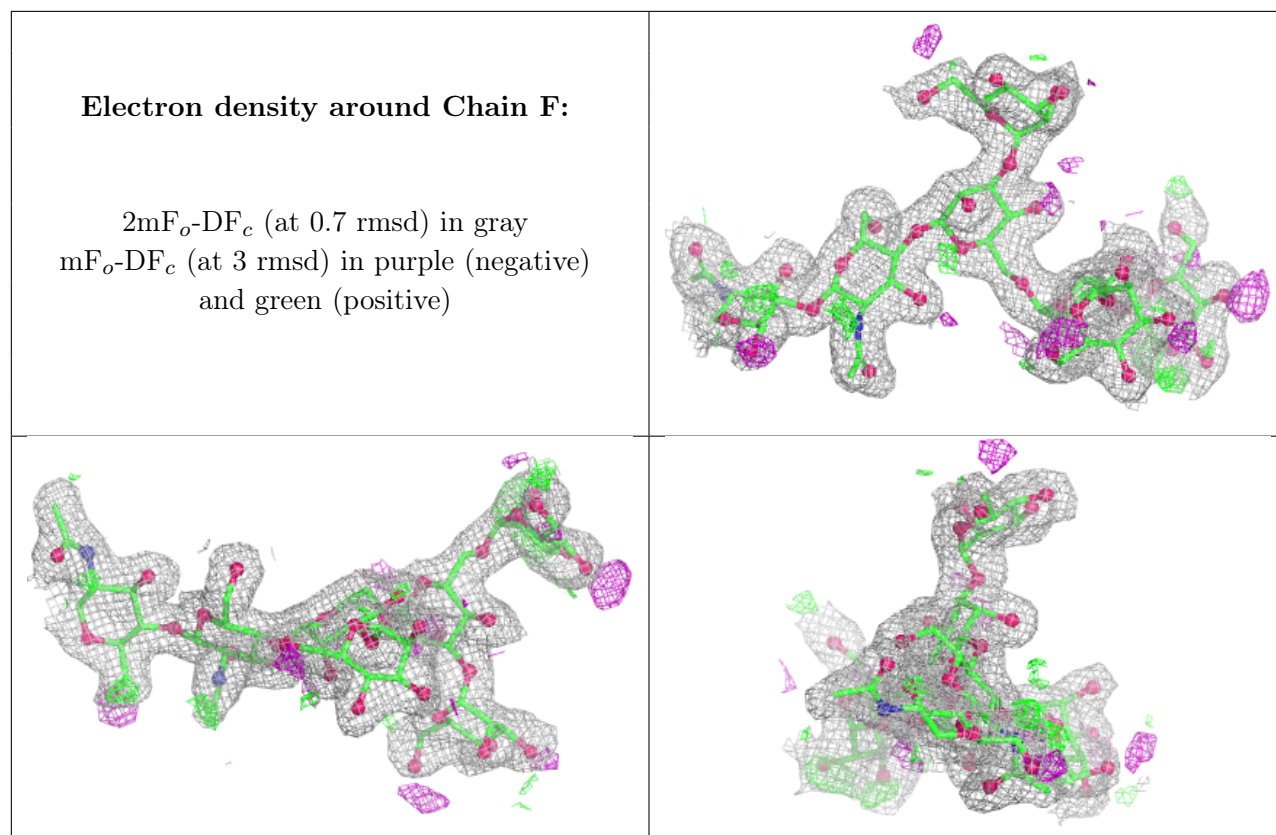
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain E:

$2mF_o-DF_c$ (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
7	NAG	A	2001	14/15	0.69	0.18	56,61,65,65	0
11	IOD	A	9070	1/1	0.71	0.24	68,68,68,68	1
11	IOD	A	9058	1/1	0.82	0.24	58,58,58,58	1
11	IOD	A	9069	1/1	0.84	0.19	65,65,65,65	1
10	PO4	A	8002	5/5	0.86	0.18	57,57,58,58	5
11	IOD	A	9063	1/1	0.86	0.47	67,67,67,67	1
12	EDO	A	9007	4/4	0.86	0.16	36,42,44,47	0
11	IOD	A	9060	1/1	0.87	0.22	59,59,59,59	1
12	EDO	A	9081	4/4	0.87	0.15	33,36,39,40	0
12	EDO	A	9006	4/4	0.88	0.14	38,39,39,42	0
7	NAG	A	4001	14/15	0.89	0.11	29,33,39,42	0
12	EDO	A	9002	4/4	0.90	0.10	25,26,27,27	0
11	IOD	A	9051	1/1	0.90	0.11	62,62,62,62	1
11	IOD	A	9059	1/1	0.90	0.20	58,58,58,58	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	IOD	A	9056	1/1	0.90	0.41	79,79,79,79	1
11	IOD	A	9072	1/1	0.91	0.16	65,65,65,65	1
11	IOD	A	9048	1/1	0.91	0.14	66,66,66,66	1
12	EDO	A	9005	4/4	0.91	0.14	30,34,35,36	0
11	IOD	A	9068	1/1	0.92	0.24	67,67,67,67	1
12	EDO	A	9003	4/4	0.92	0.15	44,44,44,46	0
11	IOD	A	9061	1/1	0.92	0.15	64,64,64,64	1
11	IOD	A	9046	1/1	0.93	0.09	45,45,45,45	1
11	IOD	A	9022	1/1	0.93	0.06	27,27,27,27	1
11	IOD	A	9028	1/1	0.93	0.09	47,47,47,47	1
12	EDO	A	9004	4/4	0.93	0.10	30,30,31,31	0
11	IOD	A	9032	1/1	0.93	0.11	56,56,56,56	1
11	IOD	A	9037	1/1	0.93	0.10	47,47,47,47	1
11	IOD	A	9045	1/1	0.93	0.10	61,61,61,61	1
11	IOD	A	9071	1/1	0.93	0.15	75,75,75,75	1
12	EDO	A	9001	4/4	0.94	0.11	34,34,35,38	0
12	EDO	A	9080	4/4	0.94	0.09	17,20,22,24	0
8	GAL	A	9011	12/12	0.94	0.09	13,18,23,25	0
11	IOD	A	9049	1/1	0.95	0.14	47,47,47,47	1
11	IOD	A	9050	1/1	0.95	0.12	68,68,68,68	1
11	IOD	A	9035	1/1	0.95	0.07	50,50,50,50	1
11	IOD	A	9064	1/1	0.95	0.21	57,57,57,57	1
11	IOD	A	9065	1/1	0.95	0.17	56,56,56,56	1
11	IOD	A	9066	1/1	0.95	0.15	72,72,72,72	1
11	IOD	A	9067	1/1	0.95	0.12	67,67,67,67	1
11	IOD	A	9052	1/1	0.96	0.11	67,67,67,67	1
11	IOD	A	9053	1/1	0.96	0.16	65,65,65,65	1
11	IOD	A	9031	1/1	0.96	0.07	23,23,23,23	1
11	IOD	A	9057	1/1	0.96	0.14	69,69,69,69	1
11	IOD	A	9025	1/1	0.96	0.07	32,32,32,32	1
9	NA	A	8001	1/1	0.96	0.10	40,40,40,40	0
11	IOD	A	9036	1/1	0.96	0.06	40,40,40,40	1
12	EDO	A	9009	4/4	0.96	0.09	25,28,29,30	0
11	IOD	A	9030	1/1	0.96	0.08	38,38,38,38	1
11	IOD	A	9038	1/1	0.96	0.07	56,56,56,56	1
11	IOD	A	9043	1/1	0.97	0.10	45,45,45,45	1
11	IOD	A	9055	1/1	0.97	0.10	68,68,68,68	1
12	EDO	A	9008	4/4	0.97	0.07	12,17,18,19	0
11	IOD	A	9044	1/1	0.97	0.05	37,37,37,37	1
11	IOD	A	9040	1/1	0.97	0.05	43,43,43,43	1
11	IOD	A	9062	1/1	0.97	0.16	59,59,59,59	1
11	IOD	A	9054	1/1	0.98	0.13	62,62,62,62	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
11	IOD	A	9039	1/1	0.98	0.04	37,37,37,37	1
11	IOD	A	9024	1/1	0.98	0.03	29,29,29,29	1
11	IOD	A	9029	1/1	0.98	0.04	29,29,29,29	1
11	IOD	A	9027	1/1	0.98	0.04	37,37,37,37	1
11	IOD	A	9042	1/1	0.99	0.05	21,21,21,21	1
11	IOD	A	9026	1/1	0.99	0.03	32,32,32,32	1
11	IOD	A	9033	1/1	0.99	0.03	28,28,28,28	0
11	IOD	A	9021	1/1	0.99	0.08	27,27,27,27	1
11	IOD	A	9023	1/1	0.99	0.06	28,28,28,28	1
11	IOD	A	9047	1/1	0.99	0.05	33,33,33,33	1
11	IOD	A	9034	1/1	1.00	0.03	20,20,20,20	1
11	IOD	A	9041	1/1	1.00	0.05	29,29,29,29	1

6.5 Other polymers [i](#)

There are no such residues in this entry.