



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:19 PM UTC

PDB ID : 1DWG / pdb_00001dwg
Title : STUDY ON RADIATION DAMAGE ON A CRYOCOOLED CRYSTAL:
PART 3 STRUCTURE AFTER IRRADIATION WITH 18.2*10E15 PHO-
TONS/MM2.
Authors : Burmeister, W.P.
Deposited on : 1999-12-05
Resolution : 2.00 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

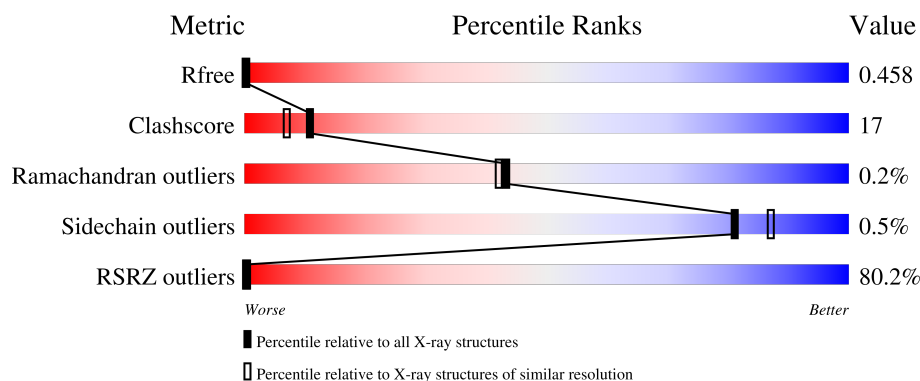
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	M	499	80% 80%18%.
2	A	2	50%50%
2	D	2	50%50%
3	B	5	100%
4	C	7	71%29%

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
4	BMA	C	3	-	-	X	-
4	MAN	C	6	X	X	X	-
5	NAG	M	905	-	-	X	-
5	NAG	M	918	X	-	-	-
7	SO4	M	925	-	-	X	-
7	SO4	M	926	-	-	X	-
7	SO4	M	928	-	X	-	-
7	SO4	M	931	-	X	X	X
8	GOL	M	932	-	-	X	-

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 5217 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 MYROSINASE MA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	M	499	Total	C	N	O	S	0	20	0
			4080	2616	660	788	16			

There is a discrepancy between the modelled and reference sequences:

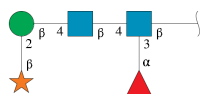
Chain	Residue	Modelled	Actual	Comment	Reference
M	497	THR	SER	SEE REMARK 999	UNP P29736

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



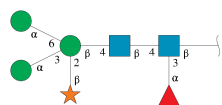
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	A	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



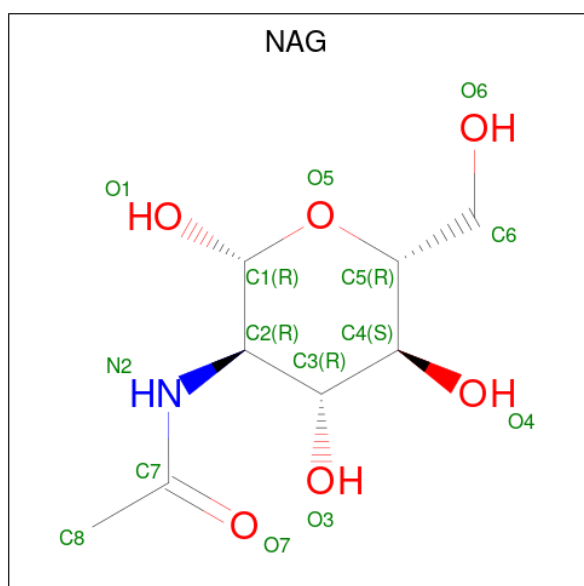
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	5	Total	C	N	O	0	0	0
			58	33	2	23			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	C	7	Total	C	N	O	0	0	0
			80	45	2	33			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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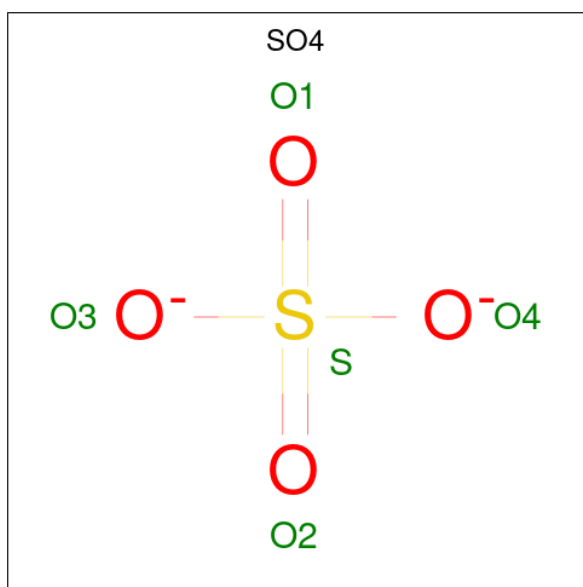
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	M	1	Total	Zn	0	0
			1	1		

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



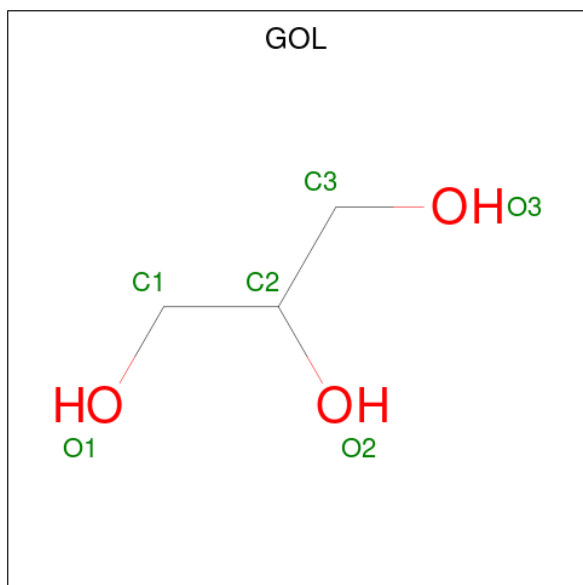
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		
7	M	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	M	1	Total	C	O	0	0
			6	3	3		
8	M	1	Total	C	O	0	0
			6	3	3		
8	M	1	Total	C	O	0	0
			6	3	3		
8	M	1	Total	C	O	0	0
			6	3	3		
8	M	1	Total	C	O	0	0
			6	3	3		

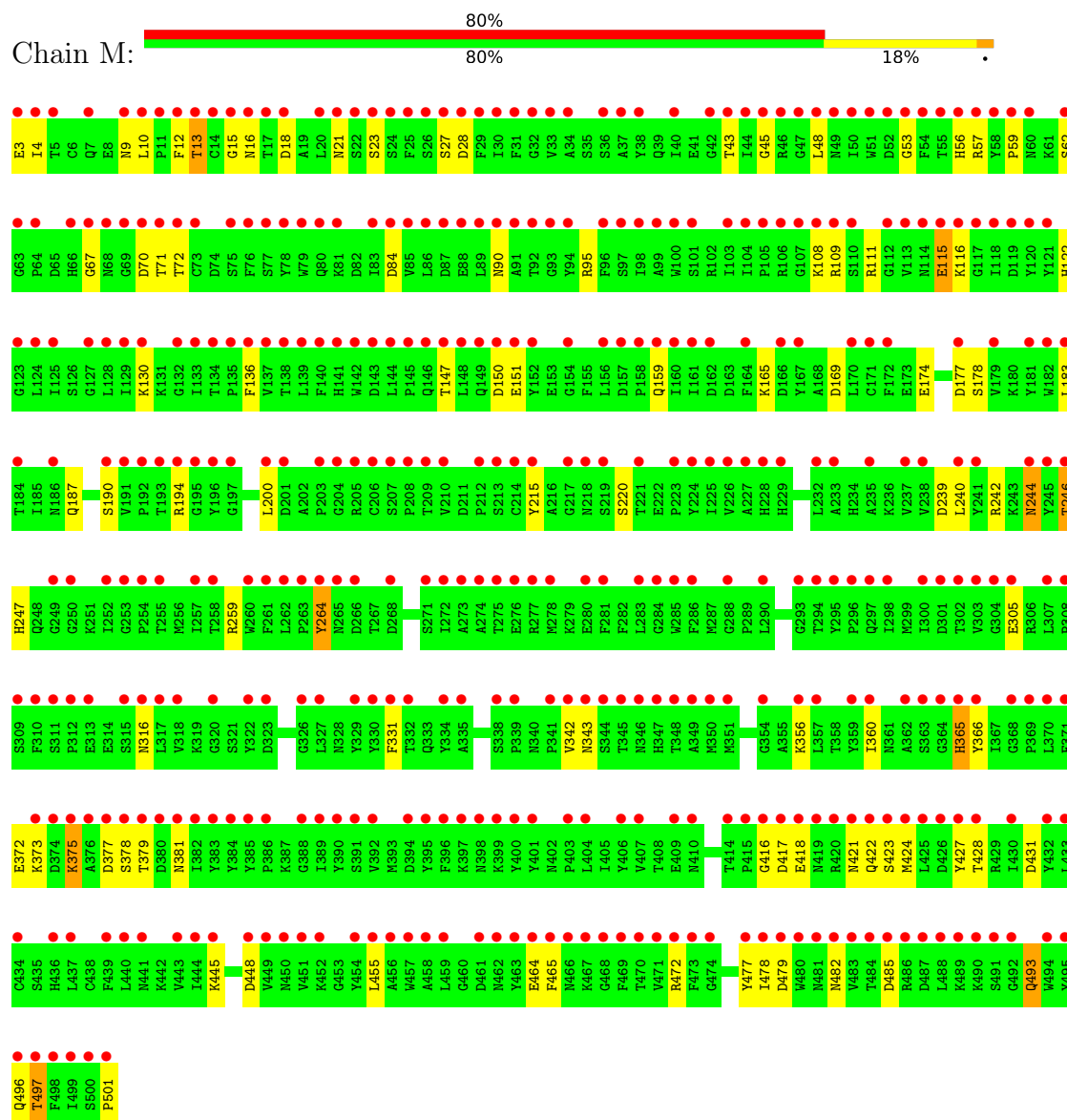
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	M	788	Total	O	0	0
			788	788		

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: MYROSINASE MA1



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

Chain A:  50% 50%

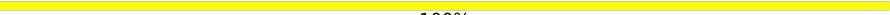
NAG1
NAG2

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

Chain D:  50% 50%

NAG1
NAG2

- Molecule 3: beta-D-xylopyranose-(1-2)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:  100%

NAG1
NAG2
BMA3
XYP4
FUC5

- Molecule 4: beta-D-xylopyranose-(1-2)-[alpha-D-mannopyranose-(1-3)][alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  71% 29%

NAG1
NAG2
BMA3
XYP4
MAN5
MAN6
FUC7

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	134.30Å 136.40Å 80.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.00 15.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (15.00-2.00) 98.0 (15.00-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.22 (at 1.99Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.184 , 0.193 0.441 , 0.458	Depositor DCC
R_{free} test set	2572 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	19.4	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.68	EDS
Total number of atoms	5217	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 5.20% 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: FUC, SO4, MAN, GOL, NAG, BMA, ZN, XYP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	M	1.25	16/4283 (0.4%)	1.34	41/5824 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	M	0	1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	264	TYR	CZ-OH	16.26	1.72	1.38
1	M	16	ASN	CG-ND2	14.88	1.64	1.33
1	M	13	THR	C-O	-12.91	1.04	1.24
1	M	264	TYR	CE1-CZ	-11.67	1.10	1.38
1	M	356	LYS	CE-NZ	-9.33	1.21	1.49
1	M	501	PRO	CA-C	6.86	1.67	1.52
1	M	423	SER	CB-OG	6.44	1.55	1.42
1	M	416	GLY	C-O	-6.22	1.17	1.24
1	M	242	ARG	NE-CZ	6.04	1.39	1.33
1	M	178	SER	CB-OG	5.84	1.53	1.42
1	M	147	THR	CB-OG1	5.48	1.52	1.43
1	M	246	THR	CB-CG2	-5.41	1.34	1.52
1	M	242	ARG	CD-NE	-5.38	1.38	1.46
1	M	497	THR	C-O	-5.38	1.17	1.24
1	M	501	PRO	N-CD	5.24	1.55	1.47
1	M	247	HIS	CE1-NE2	5.07	1.37	1.32

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	482	ASN	CA-CB-CG	-12.47	100.13	112.60
1	M	482	ASN	OD1-CG-ND2	-10.79	111.81	122.60
1	M	264	TYR	CE1-CZ-CE2	9.03	138.36	120.30
1	M	16	ASN	CA-CB-CG	-8.60	104.00	112.60
1	M	115	GLU	OE1-CD-OE2	-7.46	105.00	122.90
1	M	377	ASP	O-C-N	-7.37	113.70	123.14
1	M	448	ASP	CB-CG-OD2	-7.34	101.51	118.40
1	M	421	ASN	CA-C-O	-7.21	112.78	120.42
1	M	246	THR	OG1-CB-CG2	-7.00	95.31	109.30
1	M	109	ARG	NE-CZ-NH1	-6.88	114.62	121.50
1	M	478	ILE	CB-CG1-CD1	6.82	128.13	113.80
1	M	239	ASP	CA-CB-CG	6.80	119.40	112.60
1	M	264	TYR	OH-CZ-CE2	-6.70	99.82	119.90
1	M	482	ASN	CB-CG-OD1	6.64	134.09	120.80
1	M	496	GLN	OE1-CD-NE2	-6.26	116.34	122.60
1	M	448	ASP	OD1-CG-OD2	6.26	137.92	122.90
1	M	418	GLU	CA-C-O	-6.24	114.76	121.56
1	M	377	ASP	CA-C-O	6.14	128.76	120.47
1	M	422	GLN	OE1-CD-NE2	-6.09	116.51	122.60
1	M	497	THR	OG1-CB-CG2	-6.03	97.24	109.30
1	M	264	TYR	CZ-CE2-CD2	-6.01	108.77	119.60
1	M	493	GLN	OE1-CD-NE2	-5.92	116.68	122.60
1	M	316	ASN	OD1-CG-ND2	5.90	128.50	122.60
1	M	244	ASN	OD1-CG-ND2	-5.76	116.84	122.60
1	M	18	ASP	CA-C-O	-5.75	113.36	119.97
1	M	23	SER	CA-CB-OG	-5.68	99.74	111.10
1	M	416	GLY	N-CA-C	-5.68	108.42	114.67
1	M	365	HIS	CB-CG-ND1	5.65	131.17	122.70
1	M	372	GLU	CG-CD-OE2	5.65	131.39	118.40
1	M	417	ASP	CA-CB-CG	5.61	118.21	112.60
1	M	183	LEU	CD1-CG-CD2	5.59	123.09	110.80
1	M	109	ARG	NH1-CZ-NH2	5.54	126.50	119.30
1	M	84	ASP	CA-CB-CG	5.48	118.08	112.60
1	M	423	SER	CA-CB-OG	-5.31	100.49	111.10
1	M	485	ASP	CA-CB-CG	5.30	117.90	112.60
1	M	72	THR	CB-CA-C	5.28	120.92	110.42
1	M	479	ASP	CA-CB-CG	5.21	117.81	112.60
1	M	343	ASN	OD1-CG-ND2	5.17	127.77	122.60
1	M	177	ASP	CA-CB-CG	-5.15	107.45	112.60
1	M	27	SER	CA-CB-OG	-5.10	100.90	111.10
1	M	190	SER	N-CA-C	5.01	116.56	111.14

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	M	13	THR	Mainchain

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	M	4080	0	3828	110	4
2	A	28	0	24	3	0
2	D	28	0	25	1	0
3	B	58	0	42	0	0
4	C	80	0	58	9	0
5	M	84	0	77	20	0
6	M	1	0	0	0	1
7	M	40	0	0	10	0
8	M	30	0	39	4	0
9	M	788	0	0	79	13
All	All	5217	0	4093	141	17

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 17.

All (141) 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:M:244:ASN:HD21	5:M:905:NAG:C1	0.96	1.56
1:M:90:ASN:ND2	5:M:902:NAG:C1	1.72	1.53
1:M:21:ASN:HD21	5:M:901:NAG:C1	0.90	1.52
1:M:244:ASN:ND2	5:M:905:NAG:C1	1.77	1.46
1:M:264:TYR:OH	1:M:264:TYR:CZ	1.72	1.42
1:M:21:ASN:ND2	5:M:901:NAG:C1	1.75	1.42
1:M:360[B]:ILE:HD11	1:M:366[B]:TYR:CZ	1.57	1.37
8:M:932:GOL:C1	9:M:1011:HOH:O	1.71	1.34
1:M:360[B]:ILE:CD1	1:M:366[B]:TYR:CZ	2.14	1.30
1:M:15:GLY:HA3	9:M:1077:HOH:O	1.25	1.28
1:M:427:TYR:HE2	9:M:1022:HOH:O	1.19	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:360[B]:ILE:HD11	1:M:366[B]:TYR:OH	1.33	1.24
1:M:428:THR:HG23	9:M:1109:HOH:O	1.27	1.24
1:M:360[B]:ILE:CG1	1:M:366[B]:TYR:CE2	2.22	1.23
2:A:1:NAG:C3	2:A:1:NAG:O3	1.89	1.19
1:M:477:TYR:HE1	9:M:1021:HOH:O	1.21	1.18
1:M:360[B]:ILE:HD11	1:M:366[B]:TYR:CE2	1.78	1.17
1:M:431:ASP:OD1	9:M:1004:HOH:O	1.66	1.10
1:M:477:TYR:CE1	9:M:1021:HOH:O	1.94	1.08
8:M:932:GOL:H11	9:M:1011:HOH:O	1.27	1.08
1:M:360[B]:ILE:CD1	1:M:366[B]:TYR:CE2	2.33	1.07
1:M:215:TYR:O	9:M:1005:HOH:O	1.69	1.07
1:M:360[B]:ILE:HG12	1:M:366[B]:TYR:CD2	1.92	1.05
8:M:932:GOL:C2	9:M:1011:HOH:O	1.91	1.04
1:M:360[B]:ILE:CD1	1:M:366[B]:TYR:OH	2.03	1.03
1:M:360[B]:ILE:HG12	1:M:366[B]:TYR:CE2	1.91	1.02
1:M:427:TYR:CE2	9:M:1022:HOH:O	1.95	1.01
7:M:926:SO4:O2	7:M:931:SO4:S	2.19	1.00
1:M:165:LYS:NZ	5:M:905:NAG:H82	1.76	0.99
5:M:918:NAG:H61	9:M:1622:HOH:O	1.62	0.98
1:M:259:ARG:HG2	9:M:1061:HOH:O	1.64	0.96
1:M:165:LYS:HZ1	5:M:905:NAG:H82	1.24	0.96
1:M:472:ARG:CZ	9:M:1021:HOH:O	2.12	0.95
1:M:246:THR:HG22	9:M:1309:HOH:O	1.66	0.94
1:M:150:ASP:OD2	9:M:1007:HOH:O	1.88	0.91
1:M:379:THR:HG23	9:M:1573:HOH:O	1.71	0.90
1:M:53:GLY:O	9:M:1008:HOH:O	1.90	0.89
4:C:3:BMA:H61	4:C:6:MAN:C6	2.03	0.89
7:M:926:SO4:O2	7:M:931:SO4:O2	1.91	0.88
1:M:130:LYS:HB3	9:M:1579:HOH:O	1.72	0.88
4:C:3:BMA:H61	4:C:6:MAN:H61	1.55	0.88
1:M:215:TYR:HB2	9:M:1478:HOH:O	1.72	0.86
1:M:130:LYS:HG3	9:M:1387:HOH:O	1.76	0.84
1:M:15:GLY:CA	9:M:1077:HOH:O	1.93	0.84
1:M:21:ASN:HD21	5:M:901:NAG:C2	1.88	0.83
1:M:151:GLU:OE1	9:M:1009:HOH:O	1.97	0.82
4:C:3:BMA:C6	4:C:6:MAN:H61	2.11	0.81
1:M:381:ASN:ND2	9:M:1018:HOH:O	2.14	0.79
1:M:360[B]:ILE:CG1	1:M:366[B]:TYR:CD2	2.61	0.78
7:M:931:SO4:O1	9:M:1010:HOH:O	2.00	0.78
1:M:70:ASP:HB3	9:M:1540:HOH:O	1.83	0.76
9:M:1578:HOH:O	2:D:2:NAG:H83	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:3:BMA:C6	4:C:6:MAN:C6	2.65	0.74
1:M:373:LYS:NZ	9:M:1018:HOH:O	2.21	0.74
1:M:130:LYS:HB3	9:M:1675:HOH:O	1.87	0.74
1:M:360[B]:ILE:HD13	1:M:366[B]:TYR:CZ	2.22	0.74
1:M:90:ASN:ND2	5:M:902:NAG:C2	2.53	0.72
1:M:264:TYR:OH	1:M:264:TYR:CE2	2.42	0.71
1:M:360[B]:ILE:HG13	1:M:366[B]:TYR:CE2	2.24	0.71
1:M:9:ASN:HB2	9:M:1497:HOH:O	1.91	0.70
1:M:116:LYS:HG2	9:M:1452:HOH:O	1.92	0.70
9:M:1013:HOH:O	2:A:1:NAG:O3	2.10	0.70
1:M:472:ARG:NE	9:M:1021:HOH:O	2.20	0.70
1:M:360[B]:ILE:CG1	1:M:366[B]:TYR:CZ	2.67	0.69
1:M:493:GLN:NE2	9:M:1024:HOH:O	2.24	0.69
7:M:926:SO4:S	7:M:931:SO4:O3	2.51	0.68
1:M:45:GLY:HA2	9:M:1180:HOH:O	1.93	0.68
1:M:70:ASP:OD2	9:M:1014:HOH:O	2.11	0.68
7:M:925:SO4:O2	9:M:1016:HOH:O	2.14	0.66
1:M:115:GLU:HG3	9:M:1020:HOH:O	1.95	0.66
4:C:3:BMA:H61	4:C:6:MAN:H62	1.76	0.66
1:M:111:ARG:O	9:M:1017:HOH:O	2.14	0.66
1:M:71:THR:HG23	9:M:1651:HOH:O	1.94	0.65
1:M:169[B]:ASP:HB2	1:M:240:LEU:HD21	1.78	0.65
1:M:90:ASN:CG	5:M:902:NAG:C1	2.68	0.65
1:M:472:ARG:NH2	9:M:1021:HOH:O	2.26	0.65
1:M:220[A]:SER:OG	9:M:1019:HOH:O	2.15	0.64
1:M:4:ILE:HD11	1:M:445:LYS:HD2	1.80	0.64
7:M:925:SO4:O4	9:M:1016:HOH:O	2.16	0.63
1:M:200:LEU:HB3	9:M:1222:HOH:O	1.98	0.63
1:M:115:GLU:CD	9:M:1020:HOH:O	2.42	0.63
7:M:926:SO4:O2	7:M:931:SO4:O3	2.15	0.63
1:M:21:ASN:CG	5:M:901:NAG:C1	2.67	0.61
8:M:932:GOL:O2	9:M:1011:HOH:O	2.01	0.61
7:M:926:SO4:O1	7:M:931:SO4:O3	2.20	0.60
1:M:365:HIS:HE1	9:M:1216:HOH:O	1.83	0.60
1:M:342[A]:VAL:HG13	9:M:1019:HOH:O	2.02	0.60
7:M:926:SO4:S	7:M:931:SO4:S	3.00	0.59
1:M:45:GLY:HA2	9:M:1079:HOH:O	2.03	0.58
1:M:159:GLN:NE2	9:M:1034:HOH:O	2.36	0.58
1:M:360[B]:ILE:HG12	1:M:366[B]:TYR:CZ	2.33	0.58
1:M:90:ASN:ND2	5:M:902:NAG:O5	2.36	0.58
1:M:115:GLU:OE2	9:M:1020:HOH:O	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:360[B]:ILE:HG12	1:M:366[B]:TYR:CG	2.40	0.56
1:M:194:ARG:NH1	7:M:931:SO4:O4	2.40	0.55
1:M:331:PHE:CD1	9:M:1061:HOH:O	2.53	0.55
9:M:1006:HOH:O	4:C:3:BMA:C6	2.47	0.55
1:M:15:GLY:C	9:M:1077:HOH:O	2.34	0.54
1:M:21:ASN:ND2	5:M:901:NAG:C2	2.58	0.54
1:M:424:MET:HE3	9:M:1024:HOH:O	2.06	0.54
1:M:4:ILE:HD11	1:M:445:LYS:CD	2.39	0.52
1:M:244:ASN:HD21	5:M:905:NAG:C2	1.98	0.52
9:M:1023:HOH:O	4:C:6:MAN:C4	2.58	0.52
1:M:472:ARG:HG2	9:M:1445:HOH:O	2.11	0.51
2:A:1:NAG:O3	2:A:1:NAG:C2	2.56	0.51
1:M:21:ASN:ND2	5:M:901:NAG:O5	2.40	0.51
1:M:130:LYS:CB	9:M:1579:HOH:O	2.43	0.51
1:M:28:ASP:HA	9:M:1604:HOH:O	2.10	0.51
1:M:115:GLU:CG	9:M:1020:HOH:O	2.56	0.50
1:M:360[A]:ILE:HG23	9:M:1628:HOH:O	2.10	0.50
1:M:10:LEU:HD23	9:M:1025:HOH:O	2.12	0.49
1:M:108:LYS:HD2	9:M:1124:HOH:O	2.12	0.49
1:M:70:ASP:CB	9:M:1540:HOH:O	2.51	0.48
1:M:360[A]:ILE:CG2	9:M:1628:HOH:O	2.61	0.48
1:M:95:ARG:HA	1:M:136:PHE:O	2.14	0.47
1:M:59:PRO:HB3	9:M:1228:HOH:O	2.14	0.47
9:M:1023:HOH:O	4:C:6:MAN:C5	2.62	0.47
4:C:3:BMA:O6	4:C:6:MAN:C6	2.49	0.46
1:M:12:PHE:HD2	9:M:1025:HOH:O	2.00	0.45
1:M:111:ARG:C	9:M:1017:HOH:O	2.58	0.45
1:M:165:LYS:CE	5:M:905:NAG:H82	2.46	0.45
1:M:53:GLY:C	9:M:1008:HOH:O	2.52	0.44
1:M:373:LYS:NZ	1:M:378:SER:OG	2.46	0.44
1:M:45:GLY:CA	9:M:1180:HOH:O	2.57	0.44
1:M:122:HIS:HE1	1:M:174:GLU:O	1.99	0.44
1:M:95:ARG:HB2	1:M:455:LEU:HD13	2.00	0.43
1:M:360[B]:ILE:HD13	1:M:366[B]:TYR:OH	2.05	0.43
1:M:497:THR:HG23	9:M:1584:HOH:O	2.19	0.42
1:M:59:PRO:HG3	9:M:1640:HOH:O	2.19	0.42
1:M:244:ASN:ND2	5:M:905:NAG:O5	2.42	0.42
1:M:4:ILE:CD1	1:M:445:LYS:HD2	2.49	0.42
1:M:12:PHE:N	9:M:1025:HOH:O	2.26	0.42
1:M:62[B]:SER:OG	1:M:67:GLY:O	2.31	0.41
5:M:918:NAG:C6	9:M:1622:HOH:O	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:244:ASN:ND2	5:M:905:NAG:C2	2.68	0.41
1:M:464:GLU:O	1:M:465:PHE:C	2.64	0.41
1:M:48:LEU:N	9:M:1032:HOH:O	2.35	0.40

All (17) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:M:923:ZN:ZN	6:M:923:ZN:ZN[3_656]	1.10	1.10
9:M:1009:HOH:O	9:M:1009:HOH:O[3_656]	1.10	1.10
9:M:1720:HOH:O	9:M:1720:HOH:O[4_576]	1.42	0.78
9:M:1576:HOH:O	9:M:1576:HOH:O[4_576]	1.44	0.76
9:M:1174:HOH:O	9:M:1174:HOH:O[4_576]	1.63	0.57
9:M:1663:HOH:O	9:M:1663:HOH:O[4_576]	1.63	0.57
9:M:1046:HOH:O	9:M:1075:HOH:O[6_564]	1.71	0.49
9:M:1436:HOH:O	9:M:1629:HOH:O[3_656]	1.76	0.44
1:M:45:GLY:N	1:M:57:ARG:O[3_656]	1.95	0.25
9:M:1330:HOH:O	9:M:1461:HOH:O[4_576]	2.01	0.19
1:M:375:LYS:O	1:M:375:LYS:CD[4_576]	2.04	0.16
9:M:1496:HOH:O	9:M:1620:HOH:O[6_564]	2.06	0.14
1:M:379:THR:CG2	9:M:1108:HOH:O[4_576]	2.07	0.13
9:M:1174:HOH:O	9:M:1519:HOH:O[4_576]	2.08	0.12
1:M:43:THR:OG1	1:M:56:HIS:O[3_656]	2.10	0.10
9:M:1180:HOH:O	9:M:1555:HOH:O[3_656]	2.12	0.08
9:M:1497:HOH:O	9:M:1497:HOH:O[4_576]	2.12	0.08

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	M	517/499 (104%)	503 (97%)	13 (2%)	1 (0%)	43 42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	187	GLN

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	455/435 (105%)	453 (100%)	2 (0%)	84	89

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

Mol	Chain	Res	Type
1	M	3	GLU
1	M	375	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	M	122	HIS
1	M	230	GLN
1	M	244	ASN
1	M	365	HIS
1	M	402	ASN
1	M	410	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

16 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	A	1	2	14,14,15	5.90	7 (50%)	17,19,21	3.46	9 (52%)
2	NAG	A	2	2	14,14,15	2.98	4 (28%)	17,19,21	4.02	9 (52%)
3	NAG	B	1	3	14,14,15	0.59	0	17,19,21	2.03	5 (29%)
3	NAG	B	2	3	14,14,15	1.06	1 (7%)	17,19,21	1.36	2 (11%)
3	BMA	B	3	3	11,11,12	1.83	2 (18%)	15,15,17	1.74	6 (40%)
3	XYP	B	4	3	9,9,10	1.30	1 (11%)	10,12,14	2.51	4 (40%)
3	FUC	B	5	3	10,10,11	1.65	3 (30%)	14,14,16	1.97	4 (28%)
4	NAG	C	1	4	14,14,15	1.93	3 (21%)	17,19,21	2.47	4 (23%)
4	NAG	C	2	4	14,14,15	1.53	3 (21%)	17,19,21	1.65	5 (29%)
4	BMA	C	3	4	11,11,12	2.41	2 (18%)	15,15,17	4.55	9 (60%)
4	XYP	C	4	4	9,9,10	1.87	4 (44%)	10,12,14	2.15	4 (40%)
4	MAN	C	5	4	11,11,12	1.97	2 (18%)	15,15,17	2.53	8 (53%)
4	MAN	C	6	4	11,11,12	3.13	7 (63%)	15,15,17	7.21	12 (80%)
4	FUC	C	7	4	10,10,11	2.66	5 (50%)	14,14,16	1.65	2 (14%)
2	NAG	D	1	2,1	14,14,15	2.41	3 (21%)	17,19,21	2.56	3 (17%)
2	NAG	D	2	2	14,14,15	1.46	3 (21%)	17,19,21	2.62	10 (58%)

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	A	1	2	-	0/6/23/26	0/1/1/1
2	NAG	A	2	2	-	0/6/23/26	0/1/1/1
3	NAG	B	1	3	-	0/6/23/26	0/1/1/1
3	NAG	B	2	3	-	0/6/23/26	0/1/1/1
3	BMA	B	3	3	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	XYP	B	4	3	-	-	0/1/1/1
3	FUC	B	5	3	-	-	0/1/1/1
4	NAG	C	1	4	-	0/6/23/26	0/1/1/1
4	NAG	C	2	4	-	0/6/23/26	0/1/1/1
4	BMA	C	3	4	-	1/2/19/22	0/1/1/1
4	XYP	C	4	4	-	-	0/1/1/1
4	MAN	C	5	4	-	0/2/19/22	0/1/1/1
4	MAN	C	6	4	1/1/4/5	1/2/19/22	0/1/1/1
4	FUC	C	7	4	-	-	0/1/1/1
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1

All (50) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	NAG	O3-C3	18.86	1.89	1.43
4	C	6	MAN	O5-C5	8.17	1.59	1.43
2	A	1	NAG	O7-C7	7.59	1.40	1.23
2	A	2	NAG	O5-C5	7.39	1.57	1.43
2	D	1	NAG	O7-C7	-6.60	1.08	1.23
4	C	3	BMA	C2-C3	-6.35	1.42	1.52
2	A	2	NAG	C6-C5	-6.16	1.31	1.51
4	C	1	NAG	C1-C2	-5.28	1.45	1.52
2	A	1	NAG	C7-N2	-5.12	1.17	1.34
4	C	7	FUC	C4-C5	4.86	1.63	1.52
4	C	5	MAN	O5-C5	4.84	1.52	1.43
4	C	7	FUC	C2-C3	4.63	1.59	1.52
2	D	1	NAG	C8-C7	4.50	1.59	1.50
2	A	2	NAG	C4-C5	-4.49	1.43	1.53
2	A	1	NAG	C3-C2	3.96	1.60	1.52
3	B	3	BMA	C2-C3	-3.80	1.46	1.52
4	C	2	NAG	C3-C2	-3.48	1.45	1.52
4	C	3	BMA	C4-C5	3.45	1.60	1.53
4	C	7	FUC	O4-C4	3.33	1.51	1.43
4	C	6	MAN	C2-C3	3.31	1.57	1.52
4	C	5	MAN	C4-C5	3.22	1.59	1.53
2	D	2	NAG	C1-C2	3.16	1.56	1.52
2	A	1	NAG	C4-C5	3.09	1.59	1.53
2	A	1	NAG	O5-C5	3.06	1.49	1.43
4	C	6	MAN	O4-C4	3.00	1.50	1.43
4	C	4	XYP	C2-C3	2.97	1.57	1.52
3	B	3	BMA	O5-C5	2.93	1.49	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	4	XYP	O3-C3	2.74	1.49	1.43
2	A	1	NAG	O4-C4	2.65	1.49	1.43
3	B	5	FUC	C2-C3	2.64	1.56	1.52
4	C	4	XYP	O5-C5	2.60	1.47	1.43
4	C	6	MAN	C1-C2	2.57	1.58	1.52
4	C	1	NAG	C2-N2	-2.50	1.42	1.46
3	B	2	NAG	C1-C2	2.43	1.55	1.52
4	C	1	NAG	O5-C1	-2.43	1.39	1.43
4	C	2	NAG	O7-C7	2.36	1.28	1.23
4	C	7	FUC	C1-C2	2.36	1.57	1.52
4	C	6	MAN	C6-C5	-2.33	1.44	1.51
3	B	5	FUC	O5-C5	2.32	1.48	1.43
4	C	2	NAG	C1-C2	2.29	1.55	1.52
3	B	5	FUC	O2-C2	2.28	1.48	1.43
2	D	2	NAG	C4-C5	2.27	1.57	1.53
2	D	1	NAG	O5-C1	-2.19	1.40	1.43
3	B	4	XYP	C4-C3	2.16	1.55	1.52
2	A	2	NAG	C3-C2	-2.11	1.48	1.52
4	C	6	MAN	O5-C1	2.10	1.47	1.43
4	C	6	MAN	C4-C3	2.03	1.57	1.52
4	C	7	FUC	C4-C3	-2.02	1.47	1.52
2	D	2	NAG	C8-C7	2.02	1.54	1.50
4	C	4	XYP	O5-C1	-2.01	1.39	1.43

All (96) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	6	MAN	C1-O5-C5	-16.05	90.67	112.19
4	C	6	MAN	C6-C5-C4	12.27	143.14	113.02
4	C	3	BMA	O4-C4-C5	10.08	134.15	109.32
4	C	6	MAN	O5-C5-C6	-9.98	88.23	107.66
2	A	2	NAG	C3-C4-C5	8.86	126.30	110.23
4	C	6	MAN	O4-C4-C5	8.79	130.98	109.32
2	A	2	NAG	C1-O5-C5	-7.78	101.75	112.19
2	A	1	NAG	O3-C3-C2	-7.58	93.66	109.40
4	C	3	BMA	O5-C5-C6	-7.36	93.34	107.66
4	C	6	MAN	O5-C5-C4	6.92	127.67	110.83
2	D	1	NAG	O7-C7-N2	6.86	134.11	121.98
2	A	2	NAG	O5-C5-C4	-6.65	94.65	110.83
2	D	1	NAG	C8-C7-N2	-6.38	105.54	116.12
2	A	1	NAG	C1-O5-C5	-6.36	103.67	112.19
4	C	6	MAN	O4-C4-C3	-6.26	95.62	110.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	6	MAN	C2-C3-C4	-6.06	100.20	110.86
4	C	1	NAG	O5-C1-C2	6.00	120.57	111.29
4	C	3	BMA	O4-C4-C3	-5.85	96.58	110.38
4	C	1	NAG	C1-O5-C5	-5.74	104.50	112.19
4	C	3	BMA	C6-C5-C4	5.71	127.05	113.02
2	A	1	NAG	O4-C4-C5	-5.28	96.32	109.32
2	A	2	NAG	O5-C1-C2	4.80	118.72	111.29
4	C	3	BMA	O2-C2-C3	-4.79	100.22	110.15
4	C	7	FUC	C1-C2-C3	-4.76	102.72	109.64
4	C	6	MAN	C1-C2-C3	4.73	116.53	109.64
3	B	4	XYP	C5-C4-C3	-4.69	102.81	109.64
3	B	5	FUC	O3-C3-C2	-4.69	100.48	110.05
4	C	5	MAN	C1-C2-C3	4.58	116.31	109.64
2	D	2	NAG	C1-C2-N2	-4.53	103.29	110.43
3	B	1	NAG	C1-O5-C5	-4.49	106.17	112.19
4	C	3	BMA	C1-C2-C3	-4.46	103.16	109.64
4	C	6	MAN	O6-C6-C5	4.31	126.02	111.33
4	C	3	BMA	O5-C5-C4	-4.27	100.44	110.83
2	D	2	NAG	O5-C1-C2	-4.25	104.72	111.29
2	A	1	NAG	C4-C3-C2	-4.20	104.86	111.02
2	A	2	NAG	O3-C3-C4	4.05	119.92	110.38
4	C	4	XYP	C5-C4-C3	-4.00	103.83	109.64
2	A	1	NAG	O7-C7-C8	-3.96	114.99	122.05
3	B	4	XYP	O2-C2-C3	-3.92	102.03	110.15
3	B	1	NAG	C2-N2-C7	-3.88	117.70	122.90
4	C	5	MAN	C3-C4-C5	-3.75	103.44	110.23
2	D	2	NAG	C2-N2-C7	-3.74	117.89	122.90
4	C	5	MAN	O5-C5-C6	-3.72	100.42	107.66
2	A	2	NAG	C4-C3-C2	-3.70	105.59	111.02
4	C	3	BMA	C3-C4-C5	3.55	116.67	110.23
3	B	4	XYP	O3-C3-C2	-3.50	102.91	110.05
4	C	5	MAN	C2-C3-C4	-3.47	104.77	110.86
4	C	4	XYP	C4-C3-C2	-3.42	106.86	110.92
4	C	5	MAN	O2-C2-C3	-3.37	103.16	110.15
2	A	2	NAG	O6-C6-C5	-3.37	99.85	111.33
3	B	5	FUC	C1-C2-C3	-3.37	104.74	109.64
4	C	6	MAN	C3-C4-C5	-3.29	104.27	110.23
2	A	1	NAG	O5-C5-C4	-3.28	102.85	110.83
2	D	2	NAG	C1-O5-C5	-3.26	107.81	112.19
3	B	5	FUC	O2-C2-C3	-3.25	103.43	110.15
2	D	1	NAG	C2-N2-C7	-3.24	118.56	122.90
4	C	1	NAG	O5-C5-C6	-3.23	101.37	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	NAG	O4-C4-C3	-3.17	102.91	110.38
2	D	2	NAG	O5-C5-C4	-3.15	103.16	110.83
3	B	3	BMA	O5-C5-C6	-3.15	101.54	107.66
2	A	2	NAG	O5-C5-C6	-3.14	101.54	107.66
2	A	1	NAG	O3-C3-C4	-3.12	103.03	110.38
3	B	2	NAG	C2-N2-C7	-3.08	118.77	122.90
4	C	6	MAN	O5-C1-C2	-3.05	103.51	110.79
3	B	3	BMA	C2-C3-C4	3.02	116.17	110.86
2	D	2	NAG	C6-C5-C4	-2.93	105.83	113.02
2	D	2	NAG	C3-C4-C5	-2.89	105.00	110.23
2	D	2	NAG	O4-C4-C3	-2.85	103.67	110.38
3	B	4	XYP	C1-C2-C3	2.84	113.78	109.64
2	A	1	NAG	C8-C7-N2	2.68	120.56	116.12
4	C	3	BMA	C1-O5-C5	-2.66	108.62	112.19
4	C	4	XYP	O4-C4-C3	-2.63	104.70	110.15
3	B	1	NAG	C1-C2-N2	-2.62	106.30	110.43
3	B	1	NAG	C8-C7-N2	-2.56	111.87	116.12
4	C	2	NAG	O4-C4-C3	-2.56	104.34	110.38
4	C	2	NAG	C2-N2-C7	-2.56	119.47	122.90
4	C	5	MAN	O2-C2-C1	2.55	115.06	109.22
4	C	2	NAG	O5-C1-C2	-2.40	107.58	111.29
3	B	3	BMA	O3-C3-C4	2.38	115.98	110.38
4	C	5	MAN	C6-C5-C4	-2.36	107.22	113.02
4	C	6	MAN	O2-C2-C1	-2.30	103.96	109.22
4	C	4	XYP	O2-C2-C3	-2.29	105.41	110.15
3	B	1	NAG	O5-C1-C2	-2.24	107.82	111.29
2	A	2	NAG	C8-C7-N2	-2.23	112.43	116.12
3	B	3	BMA	O5-C5-C4	-2.22	105.42	110.83
3	B	2	NAG	O4-C4-C3	-2.22	105.15	110.38
4	C	1	NAG	C2-N2-C7	2.20	125.86	122.90
3	B	5	FUC	O3-C3-C4	-2.18	105.25	110.38
4	C	7	FUC	C6-C5-C4	-2.16	109.13	113.08
2	D	2	NAG	O3-C3-C2	2.14	113.86	109.40
4	C	5	MAN	C1-O5-C5	2.14	115.06	112.19
4	C	2	NAG	C8-C7-N2	-2.13	112.59	116.12
2	D	2	NAG	C4-C3-C2	-2.10	107.94	111.02
4	C	2	NAG	C1-O5-C5	-2.06	109.42	112.19
3	B	3	BMA	O4-C4-C5	2.03	114.33	109.32
3	B	3	BMA	C3-C4-C5	2.02	113.89	110.23

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	6	MAN	C5

All (2) torsion outliers are listed below:

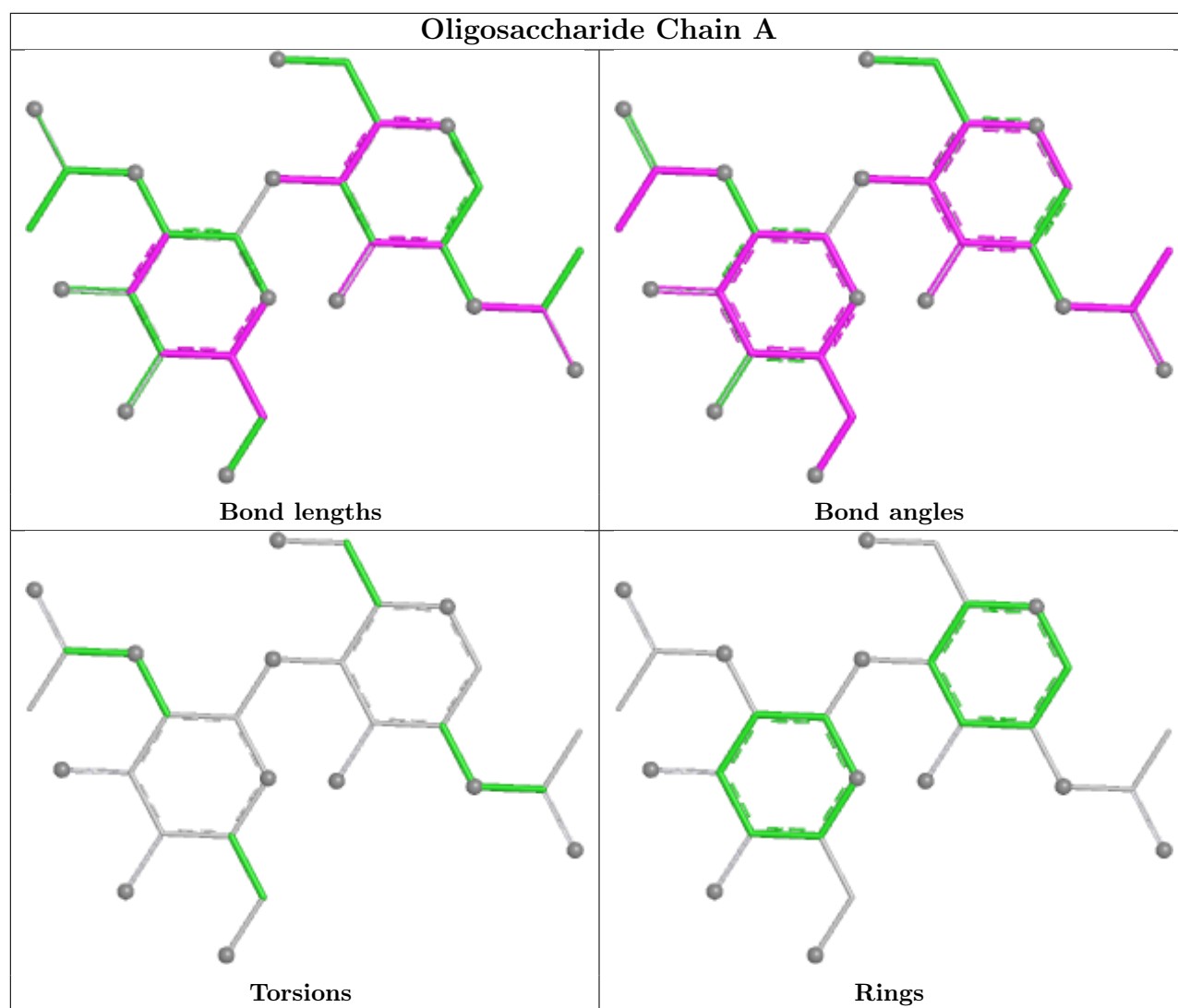
Mol	Chain	Res	Type	Atoms
4	C	6	MAN	O5-C5-C6-O6
4	C	3	BMA	C4-C5-C6-O6

There are no ring outliers.

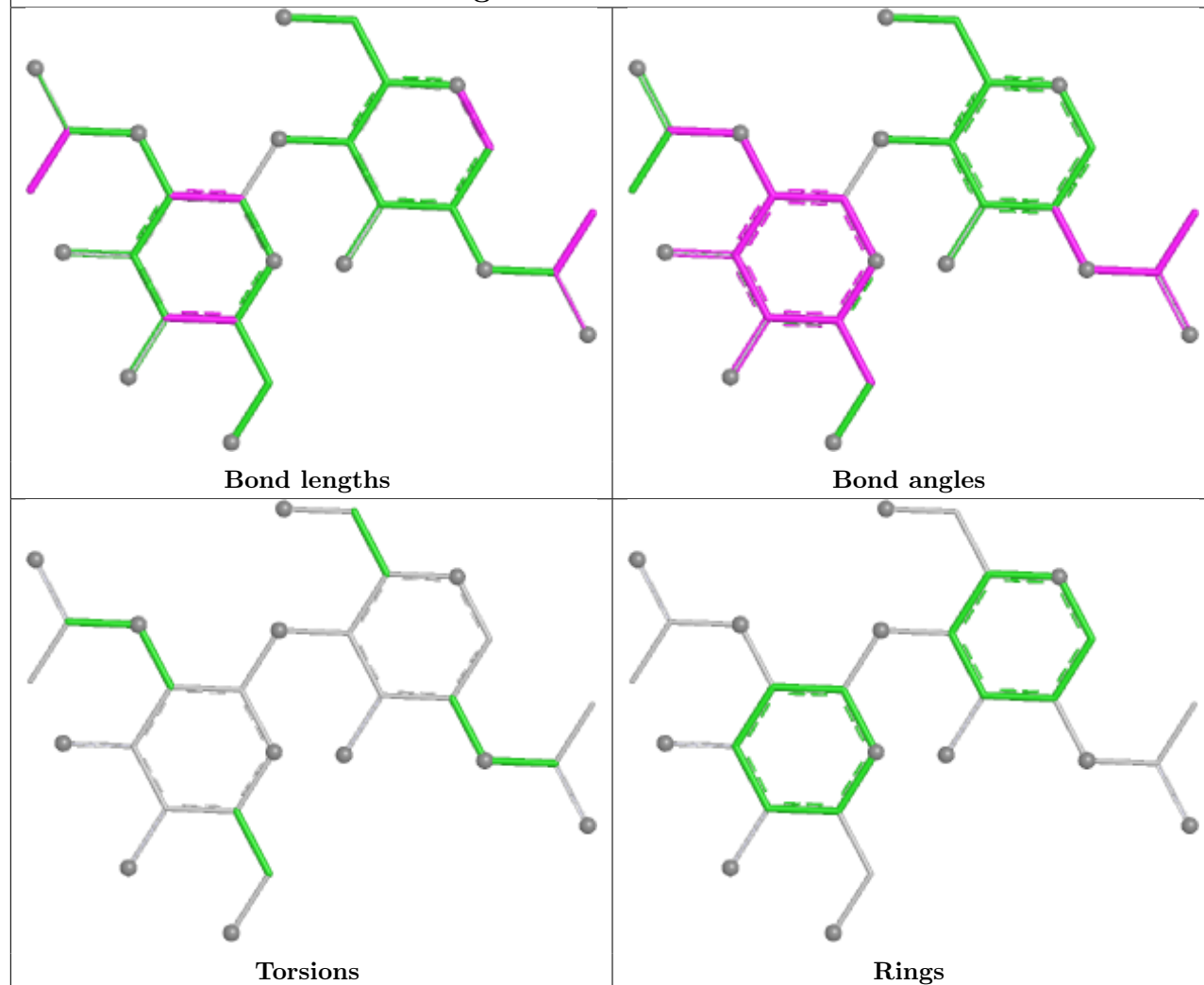
4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	3	BMA	7	0
2	D	2	NAG	1	0
4	C	6	MAN	8	0
2	A	1	NAG	3	0

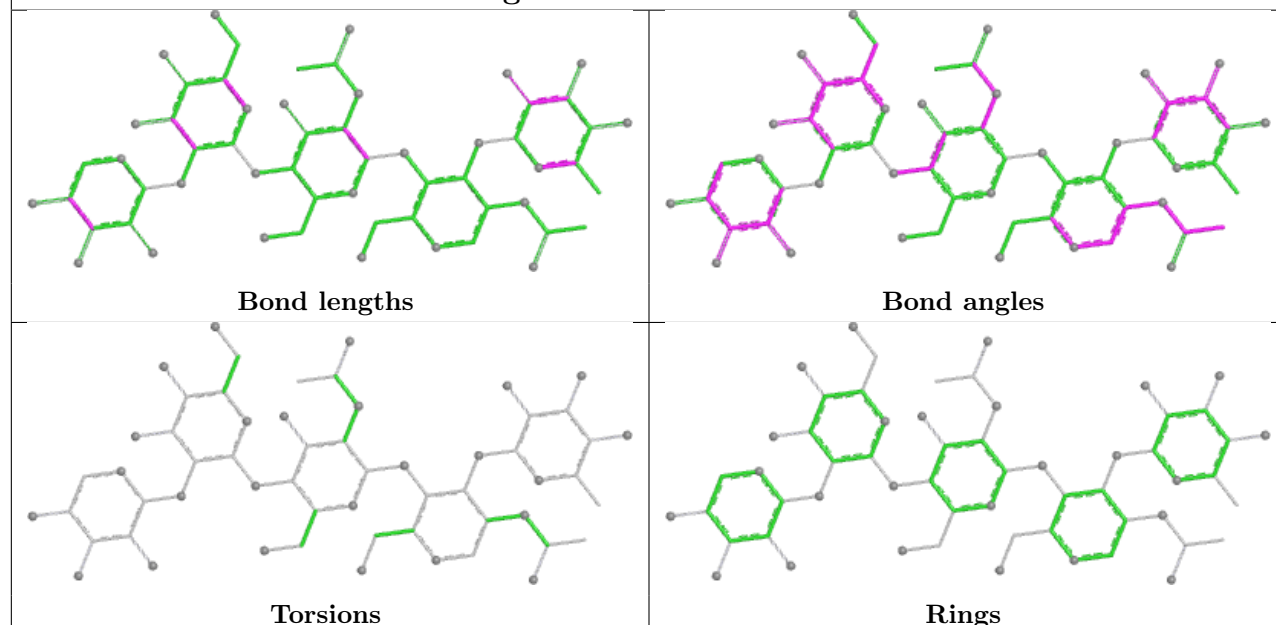
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

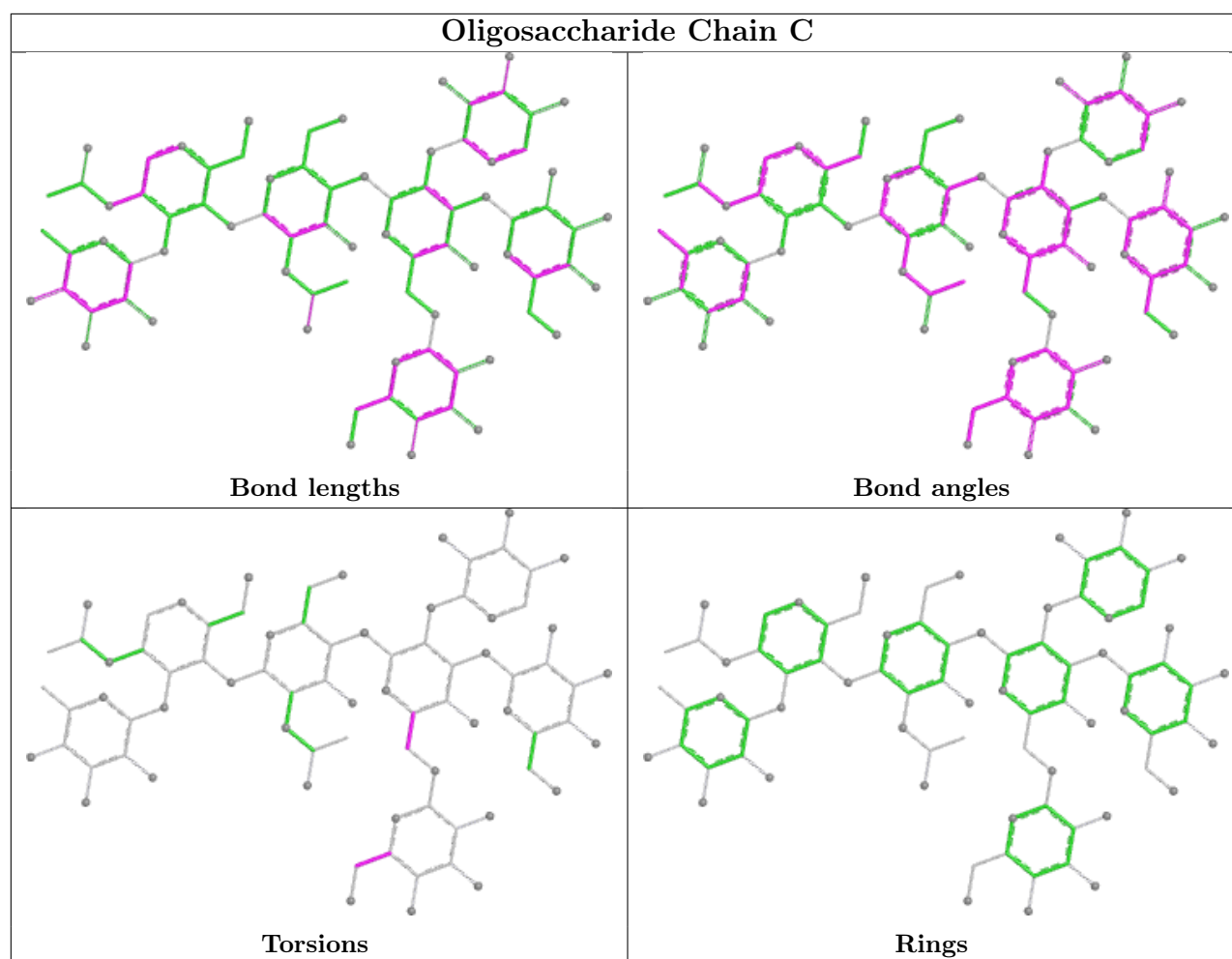


Oligosaccharide Chain D



Oligosaccharide Chain B





5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 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	$\# Z > 2$
5	NAG	M	901	-	14,14,15	1.21	1 (7%)	17,19,21	2.06	5 (29%)
8	GOL	M	932	-	5,5,5	0.68	0	5,5,5	1.21	1 (20%)
7	SO4	M	927	-	4,4,4	0.27	0	6,6,6	0.32	0
7	SO4	M	926	-	4,4,4	1.42	1 (25%)	6,6,6	1.31	1 (16%)
7	SO4	M	930	-	4,4,4	0.81	0	6,6,6	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	SO4	M	929	-	4,4,4	1.10	0	6,6,6	1.36	1 (16%)
8	GOL	M	935	-	5,5,5	0.66	0	5,5,5	1.19	1 (20%)
7	SO4	M	925	-	4,4,4	0.57	0	6,6,6	0.51	0
5	NAG	M	905	-	14,14,15	2.01	5 (35%)	17,19,21	8.34	13 (76%)
8	GOL	M	933	-	5,5,5	1.28	1 (20%)	5,5,5	1.12	0
8	GOL	M	936	-	5,5,5	0.87	0	5,5,5	1.37	1 (20%)
7	SO4	M	924	-	4,4,4	0.88	0	6,6,6	1.39	1 (16%)
8	GOL	M	934	-	5,5,5	0.94	0	5,5,5	1.15	1 (20%)
5	NAG	M	918	1	14,14,15	1.40	2 (14%)	17,19,21	2.84	4 (23%)
7	SO4	M	931	-	4,4,4	1.53	1 (25%)	6,6,6	2.76	5 (83%)
7	SO4	M	928	-	4,4,4	1.88	1 (25%)	6,6,6	2.46	3 (50%)
5	NAG	M	922	1	14,14,15	1.26	1 (7%)	17,19,21	1.97	5 (29%)
5	NAG	M	902	-	14,14,15	1.72	2 (14%)	17,19,21	2.16	5 (29%)
5	NAG	M	919	1	14,14,15	1.36	1 (7%)	17,19,21	2.50	8 (47%)

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
8	GOL	M	936	-	-	0/4/4/4	-
5	NAG	M	901	-	-	0/6/23/26	0/1/1/1
5	NAG	M	922	1	-	0/6/23/26	0/1/1/1
8	GOL	M	935	-	-	0/4/4/4	-
5	NAG	M	902	-	-	0/6/23/26	0/1/1/1
8	GOL	M	934	-	-	0/4/4/4	-
5	NAG	M	918	1	1/1/5/7	0/6/23/26	0/1/1/1
5	NAG	M	919	1	-	4/6/23/26	0/1/1/1
5	NAG	M	905	-	-	2/6/23/26	0/1/1/1
8	GOL	M	933	-	-	0/4/4/4	-
8	GOL	M	932	-	-	4/4/4/4	-

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	902	NAG	O5-C5	4.36	1.51	1.43
5	M	919	NAG	O7-C7	-4.20	1.13	1.23
5	M	905	NAG	O7-C7	-3.99	1.14	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	922	NAG	O7-C7	-3.84	1.14	1.23
7	M	928	SO4	O2-S	3.57	1.66	1.44
5	M	902	NAG	O7-C7	-3.48	1.15	1.23
5	M	905	NAG	C1-C2	-3.43	1.47	1.52
5	M	918	NAG	O7-C7	-3.41	1.15	1.23
5	M	905	NAG	O4-C4	2.88	1.50	1.43
5	M	901	NAG	O7-C7	-2.85	1.16	1.23
5	M	905	NAG	C2-N2	-2.69	1.41	1.46
7	M	926	SO4	O1-S	2.59	1.60	1.44
7	M	931	SO4	O1-S	2.47	1.59	1.44
5	M	918	NAG	C2-N2	2.26	1.50	1.46
8	M	933	GOL	O1-C1	2.17	1.51	1.42
5	M	905	NAG	O5-C1	-2.06	1.40	1.43

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	905	NAG	C2-N2-C7	22.97	153.68	122.90
5	M	905	NAG	O5-C1-C2	15.06	134.59	111.29
5	M	905	NAG	C8-C7-N2	14.70	140.50	116.12
5	M	905	NAG	O7-C7-N2	-8.72	106.58	121.98
5	M	918	NAG	C1-O5-C5	8.53	123.61	112.19
5	M	905	NAG	C1-O5-C5	-6.73	103.16	112.19
5	M	902	NAG	C1-O5-C5	-6.30	103.74	112.19
5	M	901	NAG	C1-O5-C5	-6.18	103.90	112.19
5	M	919	NAG	O5-C1-C2	-6.04	101.95	111.29
5	M	905	NAG	O7-C7-C8	-5.21	112.77	122.05
5	M	918	NAG	C1-C2-N2	-4.75	102.95	110.43
5	M	922	NAG	C4-C3-C2	-4.60	104.28	111.02
5	M	918	NAG	O3-C3-C2	-4.28	100.50	109.40
5	M	905	NAG	C3-C4-C5	3.81	117.13	110.23
7	M	931	SO4	O4-S-O3	3.76	129.27	108.54
5	M	922	NAG	O3-C3-C2	-3.75	101.62	109.40
5	M	902	NAG	C4-C3-C2	-3.71	105.59	111.02
7	M	928	SO4	O3-S-O2	-3.53	91.08	109.56
7	M	931	SO4	O3-S-O1	-3.50	91.24	109.56
5	M	919	NAG	O5-C5-C4	-3.48	102.37	110.83
5	M	905	NAG	O4-C4-C5	-3.47	100.79	109.32
5	M	919	NAG	O5-C5-C6	-3.30	101.24	107.66
5	M	918	NAG	O4-C4-C5	-3.23	101.36	109.32
5	M	919	NAG	O4-C4-C3	3.16	117.82	110.38
5	M	905	NAG	O5-C5-C6	-3.08	101.66	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	928	SO4	O2-S-O1	-3.07	87.42	109.06
7	M	931	SO4	O2-S-O1	-2.99	88.00	109.06
5	M	922	NAG	O5-C1-C2	2.92	115.80	111.29
5	M	919	NAG	O3-C3-C2	-2.82	103.55	109.40
5	M	922	NAG	C1-C2-N2	-2.80	106.02	110.43
5	M	901	NAG	O5-C5-C4	-2.80	104.02	110.83
8	M	936	GOL	C3-C2-C1	-2.76	101.68	111.80
5	M	901	NAG	O5-C1-C2	2.68	115.44	111.29
5	M	919	NAG	C1-O5-C5	2.67	115.77	112.19
5	M	905	NAG	O4-C4-C3	-2.54	104.40	110.38
5	M	919	NAG	C2-N2-C7	2.53	126.30	122.90
5	M	905	NAG	C1-C2-N2	2.51	114.39	110.43
7	M	928	SO4	O4-S-O1	2.48	122.53	109.56
5	M	905	NAG	C4-C3-C2	-2.48	107.39	111.02
7	M	926	SO4	O4-S-O3	2.47	122.18	108.54
7	M	931	SO4	O4-S-O1	-2.46	96.69	109.56
5	M	902	NAG	O5-C5-C6	-2.46	102.87	107.66
5	M	922	NAG	O5-C5-C4	-2.39	105.02	110.83
5	M	902	NAG	O5-C5-C4	-2.37	105.05	110.83
7	M	924	SO4	O3-S-O2	2.36	121.88	109.56
7	M	929	SO4	O4-S-O1	2.35	121.83	109.56
8	M	932	GOL	O2-C2-C1	2.34	118.87	109.18
5	M	919	NAG	O7-C7-C8	2.30	126.15	122.05
8	M	935	GOL	C3-C2-C1	-2.16	103.88	111.80
5	M	901	NAG	C4-C3-C2	-2.14	107.88	111.02
7	M	931	SO4	O3-S-O2	2.08	120.41	109.56
5	M	901	NAG	O5-C5-C6	-2.06	103.66	107.66
5	M	902	NAG	O3-C3-C2	-2.05	105.13	109.40
8	M	934	GOL	O2-C2-C3	2.00	117.48	109.18
5	M	905	NAG	O5-C5-C4	-2.00	105.95	110.83

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	M	918	NAG	C1

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	M	905	NAG	C8-C7-N2-C2
8	M	932	GOL	O1-C1-C2-O2
8	M	932	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
5	M	905	NAG	O7-C7-N2-C2
5	M	919	NAG	O5-C5-C6-O6
5	M	919	NAG	C4-C5-C6-O6
8	M	932	GOL	C1-C2-C3-O3
8	M	932	GOL	O2-C2-C3-O3
5	M	919	NAG	O7-C7-N2-C2
5	M	919	NAG	C8-C7-N2-C2

There are no ring outliers.

8 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	901	NAG	6	0
8	M	932	GOL	4	0
7	M	926	SO4	6	0
7	M	925	SO4	2	0
5	M	905	NAG	8	0
5	M	918	NAG	2	0
7	M	931	SO4	8	0
5	M	902	NAG	4	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

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	M	499/499 (100%)	2.78	400 (80%) 0 0	10, 16, 29, 57	29 (5%)

All (400) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	378	SER	6.9
1	M	23	SER	6.6
1	M	212	PRO	6.4
1	M	345	THR	6.0
1	M	376	ALA	5.9
1	M	12	PHE	5.7
1	M	469	PHE	5.5
1	M	138	THR	5.3
1	M	4	ILE	5.3
1	M	380	ASP	5.2
1	M	305[A]	GLU	5.2
1	M	374	ASP	5.2
1	M	364	GLY	5.1
1	M	313	GLU	5.0
1	M	375	LYS	5.0
1	M	388	GLY	4.9
1	M	43	THR	4.8
1	M	335	ALA	4.8
1	M	421	ASN	4.7
1	M	497	THR	4.7
1	M	419	ASN	4.7
1	M	349	ALA	4.6
1	M	112	GLY	4.6
1	M	9	ASN	4.6
1	M	28	ASP	4.5
1	M	152	TYR	4.5
1	M	245	TYR	4.5

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Mol	Chain	Res	Type	RSRZ
1	M	363[A]	SER	4.5
1	M	18	ASP	4.4
1	M	409	GLU	4.4
1	M	326	GLY	4.4
1	M	89	LEU	4.4
1	M	492	GLY	4.3
1	M	457	TRP	4.3
1	M	404	LEU	4.3
1	M	17	THR	4.3
1	M	480	TRP	4.2
1	M	450	ASN	4.2
1	M	132	GLY	4.2
1	M	219	SER	4.2
1	M	3	GLU	4.2
1	M	300	ILE	4.1
1	M	465	PHE	4.1
1	M	377	ASP	4.1
1	M	223	PRO	4.1
1	M	482	ASN	4.1
1	M	197	GLY	4.1
1	M	210	VAL	4.1
1	M	417	ASP	4.1
1	M	448	ASP	4.1
1	M	206	CYS	4.0
1	M	63	GLY	4.0
1	M	390	TYR	4.0
1	M	339	PRO	4.0
1	M	478	ILE	4.0
1	M	458	ALA	4.0
1	M	20	LEU	4.0
1	M	167	TYR	4.0
1	M	203	PRO	4.0
1	M	415	PRO	3.9
1	M	115	GLU	3.9
1	M	195	GLY	3.9
1	M	36	SER	3.9
1	M	318	VAL	3.9
1	M	53	GLY	3.9
1	M	400	TYR	3.8
1	M	50	ILE	3.8
1	M	420	ARG	3.8
1	M	55	THR	3.8

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Mol	Chain	Res	Type	RSRZ
1	M	183	LEU	3.8
1	M	154	GLY	3.8
1	M	16	ASN	3.8
1	M	37	ALA	3.8
1	M	209	THR	3.8
1	M	262	LEU	3.8
1	M	379	THR	3.8
1	M	52	ASP	3.8
1	M	371	PHE	3.8
1	M	45	GLY	3.7
1	M	25	PHE	3.7
1	M	213[A]	SER	3.7
1	M	151	GLU	3.7
1	M	196	TYR	3.7
1	M	275	THR	3.7
1	M	142	TRP	3.7
1	M	10	LEU	3.7
1	M	423	SER	3.7
1	M	418	GLU	3.6
1	M	140	PHE	3.6
1	M	79	TRP	3.6
1	M	343	ASN	3.6
1	M	30[A]	ILE	3.6
1	M	83	ILE	3.6
1	M	235	ALA	3.6
1	M	293	GLY	3.6
1	M	396	PHE	3.6
1	M	341	PRO	3.6
1	M	365	HIS	3.6
1	M	432	TYR	3.6
1	M	311	SER	3.6
1	M	362	ALA	3.5
1	M	42	GLY	3.5
1	M	150	ASP	3.5
1	M	147	THR	3.5
1	M	470	THR	3.5
1	M	320	GLY	3.5
1	M	310	PHE	3.5
1	M	144	LEU	3.5
1	M	27	SER	3.5
1	M	359	TYR	3.5
1	M	401	TYR	3.5

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Mol	Chain	Res	Type	RSRZ
1	M	356	LYS	3.5
1	M	129	ILE	3.4
1	M	99	ALA	3.4
1	M	164	PHE	3.4
1	M	304	GLY	3.4
1	M	264	TYR	3.4
1	M	118[A]	ILE	3.4
1	M	22	SER	3.4
1	M	162	ASP	3.4
1	M	80	GLN	3.4
1	M	215	TYR	3.4
1	M	265	ASN	3.4
1	M	330	TYR	3.4
1	M	143	ASP	3.4
1	M	257	ILE	3.4
1	M	274	ALA	3.4
1	M	298	ILE	3.4
1	M	444	ILE	3.4
1	M	170	LEU	3.4
1	M	357	LEU	3.4
1	M	145	PRO	3.4
1	M	15	GLY	3.4
1	M	468	GLY	3.4
1	M	501	PRO	3.3
1	M	226	VAL	3.3
1	M	160	ILE	3.3
1	M	283	LEU	3.3
1	M	33	VAL	3.3
1	M	471	VAL	3.3
1	M	98	ILE	3.3
1	M	414	THR	3.2
1	M	443	VAL	3.2
1	M	449[A]	VAL	3.2
1	M	73	CYS	3.2
1	M	159	GLN	3.2
1	M	103	ILE	3.2
1	M	479	ASP	3.2
1	M	51	TRP	3.1
1	M	100	TRP	3.1
1	M	179	VAL	3.1
1	M	58	TYR	3.1
1	M	94	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	M	334	TYR	3.1
1	M	436	HIS	3.1
1	M	249	GLY	3.1
1	M	381	ASN	3.1
1	M	434	CYS	3.1
1	M	46	ARG	3.1
1	M	191	VAL	3.1
1	M	201	ASP	3.1
1	M	156	LEU	3.1
1	M	490	LYS	3.1
1	M	5	THR	3.1
1	M	92	THR	3.1
1	M	403	PRO	3.1
1	M	48	LEU	3.1
1	M	66	HIS	3.1
1	M	430	ILE	3.1
1	M	26	SER	3.1
1	M	284	GLY	3.1
1	M	221	THR	3.1
1	M	64	PRO	3.0
1	M	266	ASP	3.0
1	M	91	ALA	3.0
1	M	225	ILE	3.0
1	M	491	SER	3.0
1	M	47	GLY	3.0
1	M	93	GLY	3.0
1	M	368	GLY	3.0
1	M	260	TRP	3.0
1	M	54	PHE	3.0
1	M	148	LEU	3.0
1	M	338[A]	SER	3.0
1	M	360[A]	ILE	3.0
1	M	441	ASN	3.0
1	M	466	ASN	3.0
1	M	241	TYR	3.0
1	M	57	ARG	3.0
1	M	268	ASP	3.0
1	M	467	LYS	3.0
1	M	141	HIS	3.0
1	M	424	MET	3.0
1	M	14	CYS	2.9
1	M	114	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	M	290	LEU	2.9
1	M	113	VAL	2.9
1	M	342[A]	VAL	2.9
1	M	489	LYS	2.9
1	M	308	PRO	2.9
1	M	120	TYR	2.9
1	M	204	GLY	2.9
1	M	250	GLY	2.9
1	M	354	GLY	2.9
1	M	474	GLY	2.9
1	M	461	ASP	2.9
1	M	329	TYR	2.9
1	M	49	ASN	2.9
1	M	494	TRP	2.9
1	M	200	LEU	2.9
1	M	137	VAL	2.9
1	M	297	GLN	2.9
1	M	428	THR	2.9
1	M	97	SER	2.9
1	M	370	LEU	2.8
1	M	437	LEU	2.8
1	M	90	ASN	2.8
1	M	238	VAL	2.8
1	M	294	THR	2.8
1	M	263	PRO	2.8
1	M	157	ASP	2.8
1	M	217	GLY	2.8
1	M	13	THR	2.8
1	M	71	THR	2.8
1	M	255	THR	2.8
1	M	11	PRO	2.8
1	M	149	GLN	2.8
1	M	347	HIS	2.8
1	M	70	ASP	2.8
1	M	177	ASP	2.8
1	M	281	PHE	2.8
1	M	498	PHE	2.8
1	M	295	TYR	2.8
1	M	386	PRO	2.8
1	M	56	HIS	2.7
1	M	87	ASP	2.7
1	M	60	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	M	316	ASN	2.7
1	M	346	ASN	2.7
1	M	389	ILE	2.7
1	M	101[A]	SER	2.7
1	M	500	SER	2.7
1	M	84	ASP	2.7
1	M	130	LYS	2.7
1	M	184	THR	2.7
1	M	327	LEU	2.7
1	M	78	TYR	2.7
1	M	406	TYR	2.7
1	M	495	TYR	2.7
1	M	485	ASP	2.7
1	M	484	THR	2.7
1	M	272	ILE	2.7
1	M	124	LEU	2.6
1	M	128	LEU	2.6
1	M	208	PRO	2.6
1	M	312	PRO	2.6
1	M	38	TYR	2.6
1	M	366[A]	TYR	2.6
1	M	108	LYS	2.6
1	M	399	LYS	2.6
1	M	422	GLN	2.6
1	M	34	ALA	2.6
1	M	398	ASN	2.6
1	M	29	PHE	2.6
1	M	76	PHE	2.6
1	M	240	LEU	2.6
1	M	307	LEU	2.6
1	M	425	LEU	2.6
1	M	75	SER	2.6
1	M	166	ASP	2.6
1	M	224	TYR	2.6
1	M	7	GLN	2.6
1	M	229	HIS	2.6
1	M	459	LEU	2.6
1	M	104	ILE	2.6
1	M	384	TYR	2.6
1	M	395	TYR	2.6
1	M	32	GLY	2.6
1	M	373	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	M	72	THR	2.6
1	M	59	PRO	2.6
1	M	105	PRO	2.6
1	M	62[A]	SER	2.6
1	M	207	SER	2.6
1	M	285	TRP	2.6
1	M	331	PHE	2.5
1	M	44	ILE	2.5
1	M	237	VAL	2.5
1	M	21	ASN	2.5
1	M	456	ALA	2.5
1	M	426	ASP	2.5
1	M	88[A]	GLU	2.5
1	M	192	PRO	2.5
1	M	439	PHE	2.5
1	M	121	TYR	2.5
1	M	171	CYS	2.5
1	M	477	TYR	2.5
1	M	85	VAL	2.4
1	M	276	GLU	2.4
1	M	317	LEU	2.4
1	M	473	PHE	2.4
1	M	186	ASN	2.4
1	M	125	ILE	2.4
1	M	146	GLN	2.4
1	M	315	SER	2.4
1	M	383	TYR	2.4
1	M	348	THR	2.4
1	M	486	ARG	2.4
1	M	481	ASN	2.4
1	M	119	ASP	2.4
1	M	252	ILE	2.4
1	M	24	SER	2.4
1	M	110	SER	2.4
1	M	106	ARG	2.4
1	M	258	THR	2.4
1	M	322	TYR	2.4
1	M	369	PRO	2.4
1	M	427	TYR	2.4
1	M	227	ALA	2.4
1	M	139	LEU	2.4
1	M	136	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	M	382	ILE	2.4
1	M	246	THR	2.4
1	M	69	GLY	2.3
1	M	96	PHE	2.3
1	M	344[A]	SER	2.3
1	M	158	PRO	2.3
1	M	410	ASN	2.3
1	M	487	ASP	2.3
1	M	277	ARG	2.3
1	M	397	LYS	2.3
1	M	445	LYS	2.3
1	M	286	PHE	2.3
1	M	77	SER	2.3
1	M	135	PRO	2.3
1	M	302	THR	2.3
1	M	214	CYS	2.3
1	M	244	ASN	2.3
1	M	86	LEU	2.3
1	M	323	ASP	2.3
1	M	433	LEU	2.3
1	M	454	TYR	2.3
1	M	463	TYR	2.3
1	M	472	ARG	2.3
1	M	488	LEU	2.3
1	M	116	LYS	2.3
1	M	172	PHE	2.3
1	M	332	THR	2.3
1	M	68	ASN	2.3
1	M	233	ALA	2.3
1	M	273	ALA	2.3
1	M	181	TYR	2.3
1	M	385	TYR	2.3
1	M	391	SER	2.2
1	M	31	PHE	2.2
1	M	254	PRO	2.2
1	M	392	VAL	2.2
1	M	451	VAL	2.2
1	M	81	LYS	2.2
1	M	278	MET	2.2
1	M	351	MET	2.2
1	M	205	ARG	2.2
1	M	133	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	M	218	ASN	2.2
1	M	483	VAL	2.2
1	M	67	GLY	2.2
1	M	117	GLY	2.2
1	M	288	GLY	2.2
1	M	440	LEU	2.2
1	M	462[A]	ASN	2.2
1	M	296	PRO	2.2
1	M	107	GLY	2.2
1	M	123	GLY	2.2
1	M	127	GLY	2.2
1	M	416	GLY	2.2
1	M	190	SER	2.1
1	M	452	LYS	2.1
1	M	280	GLU	2.1
1	M	496	GLN	2.1
1	M	261	PHE	2.1
1	M	350	MET	2.1
1	M	464	GLU	2.1
1	M	193	THR	2.1
1	M	228	HIS	2.1
1	M	109	ARG	2.1
1	M	499	ILE	2.1
1	M	407	VAL	2.1
1	M	232	LEU	2.1
1	M	309[A]	SER	2.1
1	M	455	LEU	2.1
1	M	301	ASP	2.1
1	M	253	GLY	2.1
1	M	161	ILE	2.1
1	M	182	TRP	2.1
1	M	271[A]	SER	2.1
1	M	394	ASP	2.0
1	M	194	ARG	2.0
1	M	134	THR	2.0
1	M	40	ILE	2.0
1	M	303	VAL	2.0

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

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

6.3 Carbohydrates

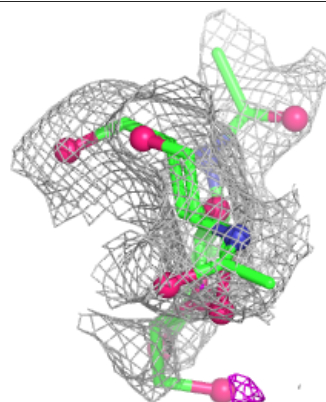
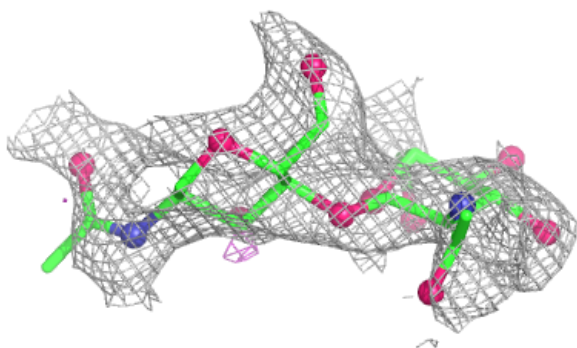
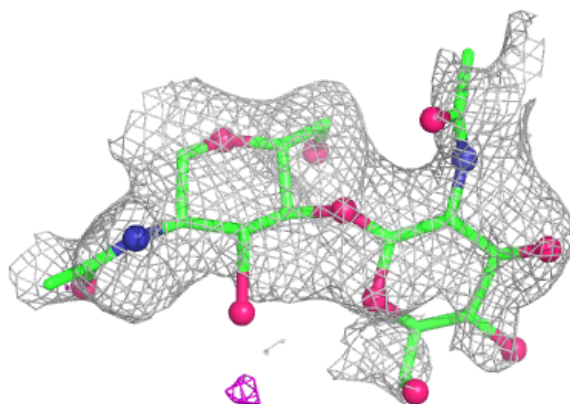
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NAG	A	1	14/15	-	-	20,24,33,38	0
2	NAG	A	2	14/15	-	-	38,46,58,60	0
4	BMA	C	3	11/12	0.33	0.27	26,31,36,48	0
4	XYP	C	4	9/10	0.41	0.20	33,39,44,64	0
3	NAG	B	2	14/15	0.48	0.22	22,28,34,39	0
3	NAG	B	1	14/15	0.61	0.19	15,23,27,28	0
3	BMA	B	3	11/12	-	-	39,44,49,53	0
3	XYP	B	4	9/10	-	-	42,48,53,54	0
3	FUC	B	5	10/11	-	-	25,33,40,48	0
4	NAG	C	1	14/15	0.61	0.23	18,21,27,29	0
2	NAG	D	1	14/15	0.64	0.18	10,17,22,24	0
2	NAG	D	2	14/15	0.68	0.16	27,32,50,57	0
4	NAG	C	2	14/15	0.68	0.17	21,24,29,33	0
4	MAN	C	5	11/12	-	-	26,40,52,57	0
4	MAN	C	6	11/12	-	-	34,44,55,56	0
4	FUC	C	7	10/11	-	-	19,22,34,34	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.

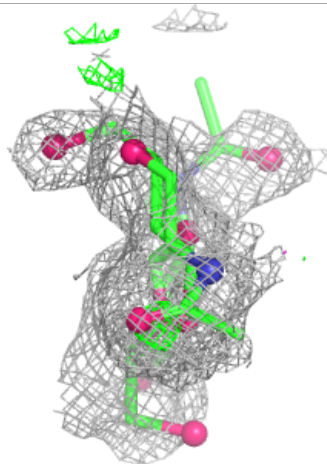
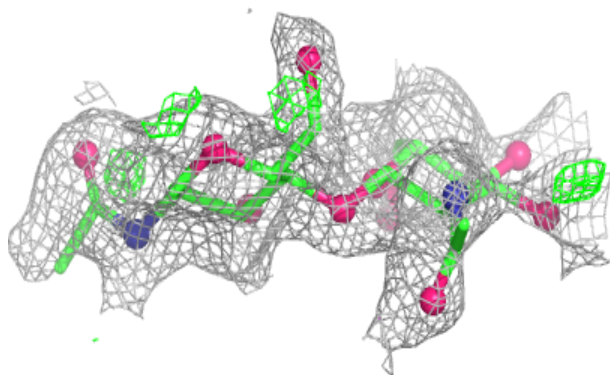
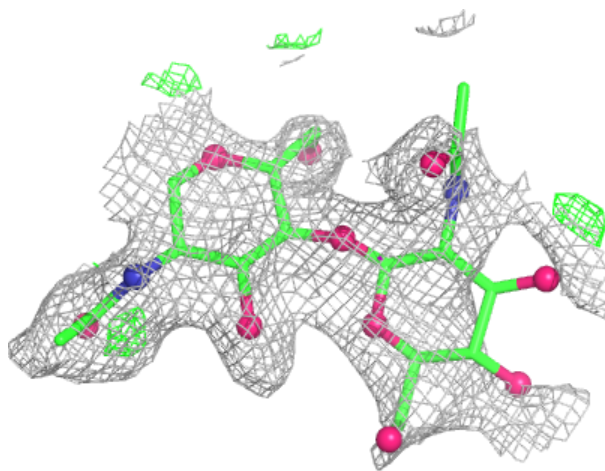
Electron density around Chain A:

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



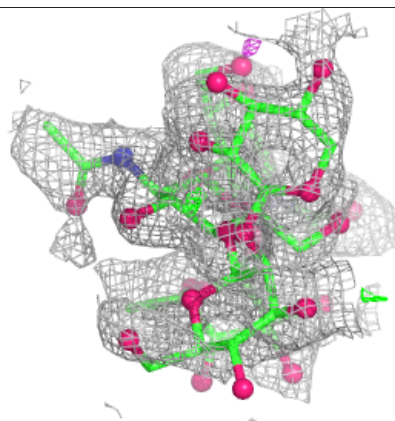
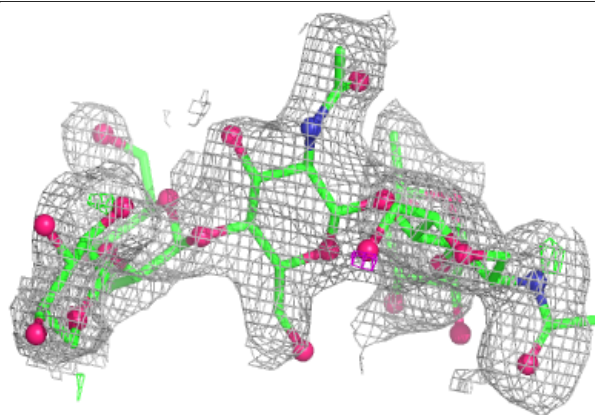
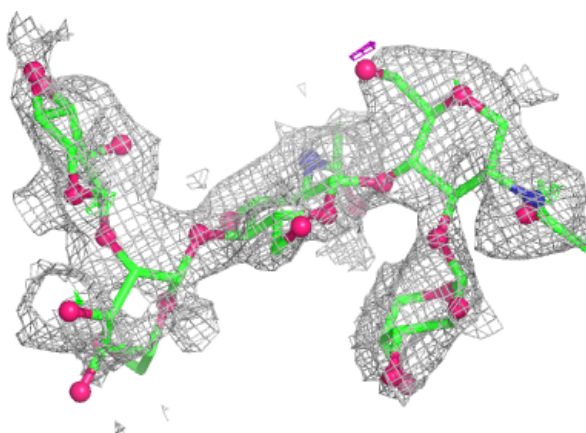
Electron density around Chain D:

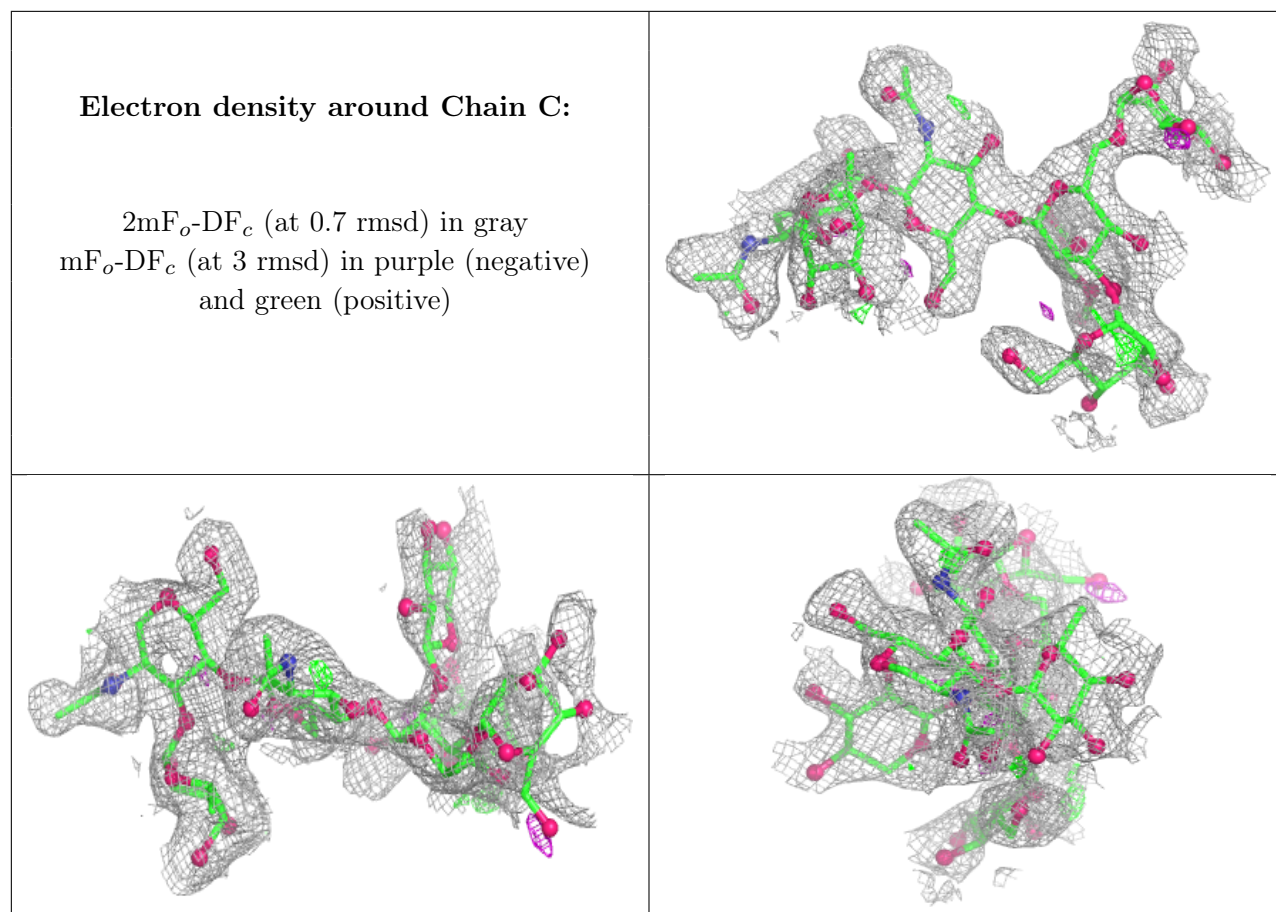
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain B:

$2mF_o-DF_c$ (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
8	GOL	M	932	6/6	0.32	0.34	36,43,45,52	6
5	NAG	M	918	14/15	0.45	0.23	44,51,63,69	0
5	NAG	M	922	14/15	0.47	0.23	35,41,54,57	0
5	NAG	M	901	14/15	0.49	0.23	26,35,47,49	0
5	NAG	M	919	14/15	0.49	0.31	57,65,70,71	0
7	SO4	M	931	5/5	0.51	0.41	39,40,47,60	1
8	GOL	M	933	6/6	0.54	0.22	6,15,19,19	1
8	GOL	M	935	6/6	0.54	0.32	31,32,43,46	6
5	NAG	M	905	14/15	0.55	0.19	36,43,49,50	0
7	SO4	M	925	5/5	0.56	0.25	26,29,36,37	5
5	NAG	M	902	14/15	0.61	0.18	25,28,37,46	0
8	GOL	M	936	6/6	0.63	0.15	16,17,23,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	GOL	M	934	6/6	0.67	0.14	12,22,27,32	6
7	SO4	M	930	5/5	0.68	0.28	34,36,39,39	5
7	SO4	M	927	5/5	0.69	0.20	18,22,27,29	0
7	SO4	M	929	5/5	0.76	0.17	14,34,35,38	5
7	SO4	M	924	5/5	0.77	0.23	27,30,33,38	5
7	SO4	M	926	5/5	0.78	0.14	15,28,31,35	5
7	SO4	M	928	5/5	0.81	0.27	26,31,35,36	5
6	ZN	M	923	1/1	0.83	0.16	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.