



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 12:22 PM BST

PDB ID : 1DWG
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

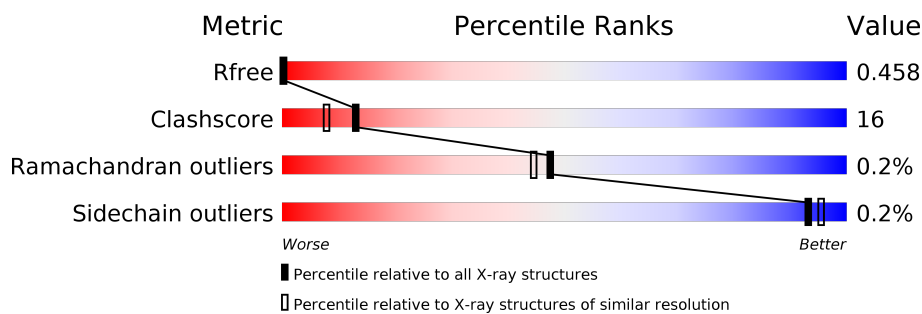
1 Overall quality at a glance

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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (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 on 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	M	499	<div> <div>81%</div> <div>16%</div> <div>.</div> </div>
2	A	2	<div> <div>50%</div> <div>50%</div> </div>
2	D	2	<div> <div>50%</div> <div>50%</div> </div>
3	B	5	<div> <div>100%</div> </div>
4	C	7	<div> <div>71%</div> <div>29%</div> </div>

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	-
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
			Total	C	N	O	S			
1	M	499	4080	2616	660	788	16	0	20	0

There is a discrepancy between the modelled and reference sequences:

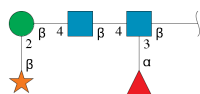
Chain	Residue	Modelled	Actual	Comment	Reference
M	497	THR	SER	SEE REMARK 999	UNP P29736

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



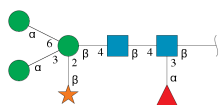
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	A	2	28	16	2	10	0	0	0
2	D	2	28	16	2	10	0	0	0

- 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.



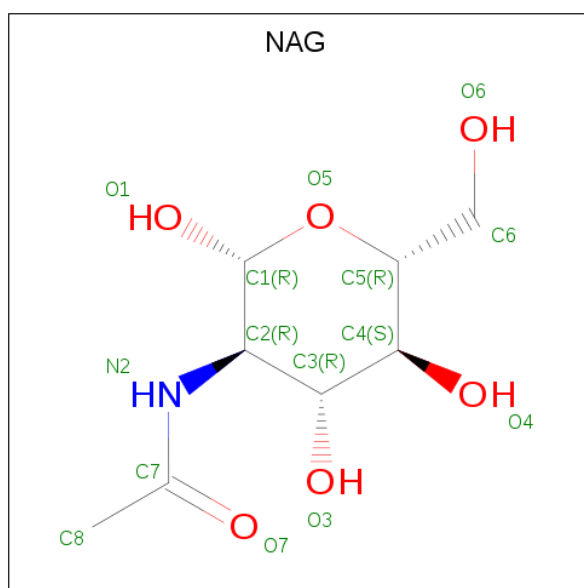
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	5	Total	C	N	O	0	0	0
			58	33	2	23			

- 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 (three-letter code: 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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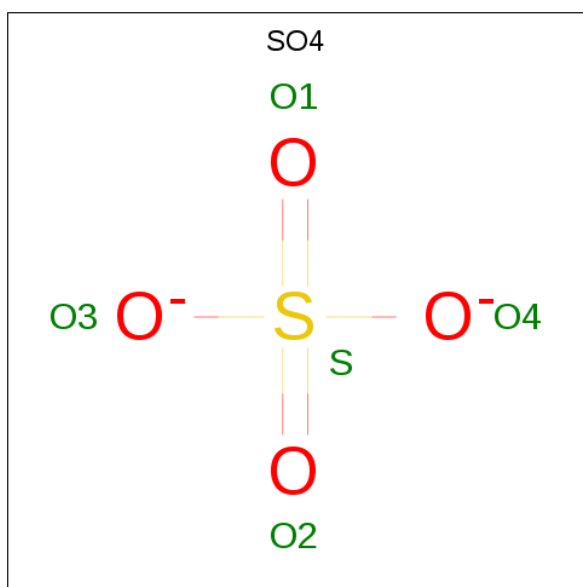
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		
5	M	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 7 is SULFATE ION (three-letter code: 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 (three-letter code: 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 [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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



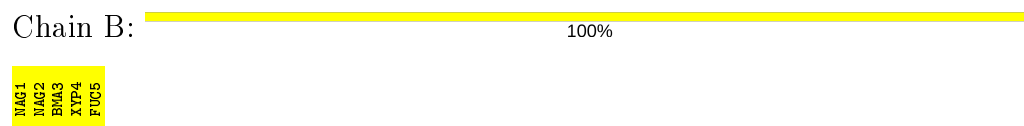
- Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



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



- 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



- 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

opyranose-(1-3)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:

71%

29%



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 9.94 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.8 (15.00-2.00) 98.4 (9.94-1.99)	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 0.440 , 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)	0.43 , 53.9	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: XYP, GOL, ZN, BMA, NAG, SO4, MAN, FUC

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	1.15	18/4283 (0.4%)	1.32	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 (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	264	TYR	CE1-CZ	-21.78	1.10	1.38
1	M	264	TYR	CZ-OH	20.20	1.72	1.37
1	M	16	ASN	CG-ND2	12.66	1.64	1.32
1	M	356	LYS	CE-NZ	-11.08	1.21	1.49
1	M	423	SER	CB-OG	9.83	1.55	1.42
1	M	13	THR	C-O	-9.72	1.04	1.23
1	M	6	CYS	CB-SG	-9.15	1.66	1.82
1	M	178	SER	CB-OG	8.91	1.53	1.42
1	M	501	PRO	CA-C	7.25	1.67	1.52
1	M	24	SER	CB-OG	7.00	1.51	1.42
1	M	115	GLU	CD-OE2	6.86	1.33	1.25
1	M	26	SER	CB-OG	5.51	1.49	1.42
1	M	413	SER	CB-OG	-5.36	1.35	1.42
1	M	246	THR	CB-CG2	-5.35	1.34	1.52
1	M	61	LYS	CD-CE	-5.18	1.38	1.51
1	M	501	PRO	N-CD	5.17	1.55	1.47
1	M	242	ARG	NE-CZ	5.11	1.39	1.33
1	M	464	GLU	CG-CD	-5.06	1.44	1.51

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	448	ASP	CB-CG-OD2	-18.65	101.51	118.30
1	M	115	GLU	OE1-CD-OE2	-15.25	105.00	123.30
1	M	264	TYR	CZ-CE2-CD2	-12.25	108.77	119.80
1	M	264	TYR	CE1-CZ-CE2	11.60	138.36	119.80
1	M	109	ARG	NE-CZ-NH1	-11.36	114.62	120.30
1	M	269	ARG	NE-CZ-NH1	10.92	125.76	120.30
1	M	372	GLU	OE1-CD-OE2	-10.19	111.07	123.30
1	M	169[A]	ASP	CB-CG-OD2	-9.73	109.55	118.30
1	M	169[B]	ASP	CB-CG-OD2	-9.73	109.55	118.30
1	M	194	ARG	NE-CZ-NH2	-9.07	115.77	120.30
1	M	242	ARG	NE-CZ-NH2	-8.74	115.93	120.30
1	M	268	ASP	CB-CG-OD1	8.74	126.17	118.30
1	M	269	ARG	NE-CZ-NH2	-8.64	115.98	120.30
1	M	266	ASP	CB-CG-OD2	-8.08	111.03	118.30
1	M	74	ASP	CB-CG-OD1	7.91	125.42	118.30
1	M	427	TYR	CG-CD1-CE1	-7.74	115.11	121.30
1	M	448	ASP	OD1-CG-OD2	7.70	137.92	123.30
1	M	264	TYR	OH-CZ-CE2	-7.51	99.82	120.10
1	M	264	TYR	CD1-CE1-CZ	-6.94	113.55	119.80
1	M	372	GLU	CG-CD-OE2	6.55	131.39	118.30
1	M	109	ARG	NH1-CZ-NH2	6.45	126.50	119.40
1	M	246	THR	OG1-CB-CG2	-6.39	95.31	110.00
1	M	482	ASN	CB-CG-OD1	6.24	134.09	121.60
1	M	76	PHE	CB-CG-CD1	-6.10	116.53	120.80
1	M	482	ASN	CA-CB-CG	-6.03	100.13	113.40
1	M	194	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	M	70	ASP	CB-CG-OD1	5.82	123.54	118.30
1	M	377	ASP	O-C-N	-5.62	113.70	122.70
1	M	497	THR	OG1-CB-CG2	-5.55	97.24	110.00
1	M	102	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	M	420	ARG	CD-NE-CZ	5.51	131.31	123.60
1	M	429	ARG	NE-CZ-NH1	5.47	123.04	120.30
1	M	420	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	M	277	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	M	427	TYR	CZ-CE2-CD2	-5.34	114.99	119.80
1	M	19	ALA	CB-CA-C	-5.24	102.24	110.10
1	M	366[A]	TYR	CB-CG-CD2	-5.22	117.87	121.00
1	M	366[B]	TYR	CB-CG-CD2	-5.22	117.87	121.00
1	M	57	ARG	NE-CZ-NH2	-5.19	117.71	120.30
1	M	473	PHE	CB-CG-CD2	5.14	124.40	120.80
1	M	478	ILE	CB-CG1-CD1	5.08	128.13	113.90

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	108	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	21	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	78	13
All	All	5217	0	4093	139	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 16.

All (139) 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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:427:TYR:HE2	9:M:1022:HOH:O	1.19	1.25
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:O3	2:A:1:NAG:C3	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: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
4:C:3:BMA:H61	4:C:6:MAN:H61	1.55	0.88
1:M:130:LYS:HB3	9:M:1579:HOH:O	1.72	0.88
1:M:215:TYR:HB2	9:M:1478:HOH:O	1.72	0.86
1:M:165:LYS:HZ1	5:M:905:NAG:H82	1.34	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:M:1578:HOH:O	2:D:2:NAG:H83	1.86	0.76
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:116:LYS:HG2	9:M:1452:HOH:O	1.92	0.70
1:M:9:ASN:HB2	9:M:1497:HOH:O	1.91	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
4:C:3:BMA:H61	4:C:6:MAN:H62	1.76	0.66
1:M:115:GLU:HG3	9:M:1020:HOH:O	1.95	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: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
7:M:926:SO4:O2	7:M:931:SO4:O3	2.15	0.63
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:115:GLU:CD	9:M:1020:HOH:O	2.42	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
1:M:21:ASN:CG	5:M:901:NAG:C1	2.67	0.56

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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:424:MET:HE3	9:M:1024:HOH:O	2.05	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
1:M:165:LYS:HZ2	5:M:905:NAG:H82	1.67	0.55
9:M:1006:HOH:O	4:C:3:BMA:C6	2.47	0.55
1:M:21:ASN:ND2	5:M:901:NAG:C2	2.58	0.54
1:M:90:ASN:CG	5:M:902:NAG:C1	2.68	0.52
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
2:A:1:NAG:C2	2:A:1:NAG:O3	2.56	0.51
1:M:472:ARG:HG2	9:M:1445:HOH:O	2.11	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:15:GLY:C	9:M:1077:HOH:O	2.34	0.48
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
9:M:1023:HOH:O	4:C:6:MAN:C5	2.62	0.47
1:M:59:PRO:HB3	9:M:1228:HOH:O	2.14	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:165:LYS:CE	5:M:905:NAG:H82	2.46	0.45
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:12:PHE:N	9:M:1025:HOH:O	2.26	0.42
1:M:4:ILE:CD1	1:M:445:LYS:HD2	2.49	0.42
5:M:918:NAG:C6	9:M:1622:HOH:O	2.41	0.41
1:M:244:ASN:ND2	5:M:905:NAG:C2	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:48:LEU:N	9:M:1032:HOH:O	2.35	0.40
1:M:111:ARG:C	9:M:1017:HOH:O	2.58	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%)	47 44

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%)	454 (100%)	1 (0%)	93	95

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	3	GLU

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

Mol	Chain	Res	Type
1	M	244	ASN
1	M	365	HIS

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 [i](#)

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	6.10	7 (50%)	17,19,21	3.46	9 (52%)
2	NAG	A	2	2	14,14,15	2.94	4 (28%)	17,19,21	4.05	9 (52%)
3	NAG	B	1	3	14,14,15	0.58	0	17,19,21	1.98	5 (29%)
3	NAG	B	2	3	14,14,15	1.03	1 (7%)	17,19,21	1.34	2 (11%)
3	BMA	B	3	3	11,11,12	1.86	2 (18%)	15,15,17	1.84	6 (40%)
3	XYP	B	4	3	9,9,10	1.34	2 (22%)	10,12,14	2.80	4 (40%)
3	FUC	B	5	3	10,10,11	1.66	3 (30%)	14,14,16	2.12	4 (28%)
4	NAG	C	1	4	14,14,15	1.84	3 (21%)	17,19,21	2.48	4 (23%)
4	NAG	C	2	4	14,14,15	1.50	3 (21%)	17,19,21	1.64	5 (29%)
4	BMA	C	3	4	11,11,12	2.49	3 (27%)	15,15,17	4.83	9 (60%)
4	XYP	C	4	4	9,9,10	1.91	3 (33%)	10,12,14	2.33	4 (40%)
4	MAN	C	5	4	11,11,12	1.95	2 (18%)	15,15,17	2.75	8 (53%)
4	MAN	C	6	4	11,11,12	3.10	7 (63%)	15,15,17	7.58	12 (80%)
4	FUC	C	7	4	10,10,11	2.72	6 (60%)	14,14,16	1.87	2 (14%)
2	NAG	D	1	1,2	14,14,15	2.41	3 (21%)	17,19,21	2.48	3 (17%)
2	NAG	D	2	2	14,14,15	1.41	3 (21%)	17,19,21	2.60	11 (64%)

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
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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1

All (52) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	NAG	O3-C3	19.82	1.89	1.43
4	C	6	MAN	O5-C5	7.85	1.59	1.43
2	A	1	NAG	O7-C7	7.52	1.40	1.23
2	A	2	NAG	O5-C5	7.10	1.57	1.43
4	C	3	BMA	C2-C3	-6.63	1.42	1.52
2	D	1	NAG	O7-C7	-6.53	1.08	1.23
2	A	2	NAG	C6-C5	-6.17	1.31	1.51
4	C	7	FUC	C4-C5	4.84	1.63	1.52
2	A	1	NAG	C7-N2	-4.81	1.17	1.34
4	C	7	FUC	C2-C3	4.80	1.59	1.52
4	C	1	NAG	C1-C2	-4.80	1.45	1.52
4	C	5	MAN	O5-C5	4.65	1.52	1.43
2	A	2	NAG	C4-C5	-4.55	1.43	1.53
2	D	1	NAG	C8-C7	4.50	1.59	1.50
3	B	3	BMA	C2-C3	-3.98	1.46	1.52
2	A	1	NAG	C3-C2	3.90	1.60	1.52
4	C	7	FUC	O4-C4	3.49	1.51	1.43
4	C	3	BMA	C4-C5	3.49	1.60	1.53
4	C	2	NAG	C3-C2	-3.43	1.45	1.52
4	C	6	MAN	C2-C3	3.43	1.57	1.52
4	C	5	MAN	C4-C5	3.25	1.59	1.53
4	C	6	MAN	O4-C4	3.15	1.50	1.43
2	A	1	NAG	C4-C5	3.12	1.59	1.53
4	C	4	XYP	C2-C3	3.07	1.57	1.52
2	A	1	NAG	O5-C5	2.93	1.49	1.43
2	D	2	NAG	C1-C2	2.89	1.56	1.52
4	C	4	XYP	O3-C3	2.88	1.49	1.43
3	B	3	BMA	O5-C5	2.81	1.49	1.43
2	A	1	NAG	O4-C4	2.78	1.49	1.43
3	B	5	FUC	C2-C3	2.73	1.56	1.52
4	C	6	MAN	C1-C2	2.69	1.58	1.52
4	C	4	XYP	O5-C5	2.58	1.47	1.42
4	C	1	NAG	O5-C1	-2.56	1.39	1.43
4	C	7	FUC	C1-C2	2.47	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1	NAG	C2-N2	-2.46	1.42	1.46
4	C	2	NAG	O7-C7	2.34	1.28	1.23
4	C	6	MAN	C6-C5	-2.34	1.44	1.51
2	D	1	NAG	O5-C1	-2.32	1.40	1.43
2	D	2	NAG	C4-C5	2.29	1.57	1.53
3	B	5	FUC	O2-C2	2.25	1.48	1.43
3	B	4	XYP	C4-C3	2.23	1.55	1.52
3	B	2	NAG	C1-C2	2.22	1.55	1.52
4	C	6	MAN	O5-C1	2.20	1.47	1.43
3	B	5	FUC	O5-C5	2.16	1.48	1.43
4	C	2	NAG	C1-C2	2.10	1.55	1.52
4	C	3	BMA	O3-C3	2.08	1.47	1.43
2	A	2	NAG	C3-C2	-2.07	1.48	1.52
4	C	6	MAN	C4-C3	2.07	1.57	1.52
3	B	4	XYP	O3-C3	2.06	1.47	1.43
4	C	7	FUC	C4-C3	-2.06	1.47	1.52
4	C	7	FUC	O5-C1	-2.03	1.40	1.43
2	D	2	NAG	C8-C7	2.02	1.54	1.50

All (97) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	6	MAN	C1-O5-C5	-15.88	90.67	112.19
4	C	6	MAN	C6-C5-C4	12.86	143.14	113.00
4	C	6	MAN	O5-C5-C6	-12.10	88.23	107.20
4	C	3	BMA	O4-C4-C5	10.01	134.15	109.30
2	A	2	NAG	C3-C4-C5	9.00	126.30	110.24
4	C	3	BMA	O5-C5-C6	-8.85	93.34	107.20
4	C	6	MAN	O4-C4-C5	8.73	130.98	109.30
2	A	2	NAG	C1-O5-C5	-7.70	101.75	112.19
2	A	1	NAG	O3-C3-C2	-7.64	93.66	109.47
4	C	6	MAN	O5-C5-C4	6.92	127.67	110.83
2	A	2	NAG	O5-C5-C4	-6.65	94.65	110.83
2	D	1	NAG	O7-C7-N2	6.61	134.11	121.95
4	C	6	MAN	O4-C4-C3	-6.37	95.62	110.35
2	A	1	NAG	C1-O5-C5	-6.29	103.67	112.19
2	D	1	NAG	C8-C7-N2	-6.24	105.54	116.10
4	C	6	MAN	C2-C3-C4	-6.18	100.20	110.89
4	C	3	BMA	C6-C5-C4	6.00	127.05	113.00
4	C	3	BMA	O4-C4-C3	-5.95	96.58	110.35
4	C	1	NAG	O5-C1-C2	5.88	120.57	111.29
4	C	1	NAG	C1-O5-C5	-5.68	104.50	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	7	FUC	C1-C2-C3	-5.65	102.72	109.67
4	C	6	MAN	C1-C2-C3	5.59	116.53	109.67
3	B	4	XYP	C5-C4-C3	-5.58	102.81	109.67
4	C	5	MAN	C1-C2-C3	5.41	116.31	109.67
4	C	3	BMA	C1-C2-C3	-5.30	103.16	109.67
2	A	1	NAG	O4-C4-C5	-5.23	96.32	109.30
3	B	5	FUC	O3-C3-C2	-4.97	100.48	109.99
4	C	3	BMA	O2-C2-C3	-4.95	100.22	110.14
4	C	4	XYP	C5-C4-C3	-4.75	103.83	109.67
2	A	2	NAG	O5-C1-C2	4.71	118.72	111.29
4	C	6	MAN	O5-C1-C2	-4.70	103.51	110.77
3	B	1	NAG	C1-O5-C5	-4.44	106.17	112.19
4	C	5	MAN	O5-C5-C6	-4.33	100.42	107.20
4	C	6	MAN	O6-C6-C5	4.29	126.02	111.29
4	C	3	BMA	O5-C5-C4	-4.27	100.44	110.83
2	D	2	NAG	C1-C2-N2	-4.21	103.29	110.49
2	A	1	NAG	C4-C3-C2	-4.20	104.86	111.02
2	D	2	NAG	O5-C1-C2	-4.16	104.72	111.29
2	A	2	NAG	O3-C3-C4	4.14	119.92	110.35
3	B	4	XYP	O2-C2-C3	-4.05	102.03	110.14
3	B	5	FUC	C1-C2-C3	-4.01	104.74	109.67
4	C	5	MAN	C3-C4-C5	-3.81	103.44	110.24
2	A	1	NAG	O7-C7-C8	-3.80	114.99	122.06
4	C	1	NAG	O5-C5-C6	-3.72	101.37	107.20
2	A	2	NAG	C4-C3-C2	-3.70	105.59	111.02
3	B	4	XYP	O3-C3-C2	-3.70	102.91	109.99
3	B	1	NAG	C2-N2-C7	-3.65	117.70	122.90
3	B	3	BMA	O5-C5-C6	-3.61	101.54	107.20
2	A	2	NAG	O5-C5-C6	-3.61	101.54	107.20
4	C	3	BMA	C3-C4-C5	3.61	116.67	110.24
4	C	5	MAN	C2-C3-C4	-3.54	104.77	110.89
2	D	2	NAG	C2-N2-C7	-3.52	117.89	122.90
4	C	5	MAN	O2-C2-C3	-3.48	103.16	110.14
4	C	4	XYP	C4-C3-C2	-3.42	106.86	110.92
3	B	4	XYP	C1-C2-C3	3.35	113.78	109.67
3	B	5	FUC	O2-C2-C3	-3.35	103.43	110.14
4	C	6	MAN	C3-C4-C5	-3.35	104.27	110.24
2	A	2	NAG	O6-C6-C5	-3.34	99.85	111.29
2	A	1	NAG	O5-C5-C4	-3.28	102.85	110.83
2	D	2	NAG	C1-O5-C5	-3.23	107.81	112.19
2	A	1	NAG	O4-C4-C3	-3.22	102.91	110.35
2	A	1	NAG	O3-C3-C4	-3.16	103.03	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	O5-C5-C4	-3.15	103.16	110.83
2	D	2	NAG	C6-C5-C4	-3.06	105.83	113.00
2	D	1	NAG	C2-N2-C7	-3.05	118.56	122.90
3	B	3	BMA	C2-C3-C4	3.05	116.17	110.89
2	D	2	NAG	C3-C4-C5	-2.94	105.00	110.24
3	B	2	NAG	C2-N2-C7	-2.90	118.77	122.90
2	D	2	NAG	O4-C4-C3	-2.89	103.67	110.35
4	C	5	MAN	O2-C2-C1	2.89	115.06	109.15
4	C	4	XYP	O4-C4-C3	-2.72	104.70	110.14
4	C	3	BMA	C1-O5-C5	-2.63	108.62	112.19
2	A	1	NAG	C8-C7-N2	2.63	120.56	116.10
4	C	2	NAG	O4-C4-C3	-2.60	104.34	110.35
4	C	6	MAN	O2-C2-C1	-2.54	103.96	109.15
3	B	1	NAG	C8-C7-N2	-2.50	111.87	116.10
4	C	5	MAN	C6-C5-C4	-2.47	107.22	113.00
3	B	1	NAG	C1-C2-N2	-2.45	106.30	110.49
3	B	3	BMA	O3-C3-C4	2.43	115.98	110.35
4	C	2	NAG	C2-N2-C7	-2.41	119.47	122.90
4	C	4	XYP	O2-C2-C3	-2.36	105.41	110.14
4	C	2	NAG	O5-C1-C2	-2.35	107.58	111.29
3	B	2	NAG	O4-C4-C3	-2.25	105.15	110.35
3	B	3	BMA	O5-C5-C4	-2.22	105.42	110.83
3	B	5	FUC	O3-C3-C4	-2.21	105.25	110.35
3	B	1	NAG	O5-C1-C2	-2.20	107.82	111.29
2	A	2	NAG	C8-C7-N2	-2.17	112.43	116.10
4	C	7	FUC	C6-C5-C4	-2.14	109.13	113.07
2	D	2	NAG	O3-C3-C2	2.12	113.86	109.47
4	C	5	MAN	C1-O5-C5	2.11	115.06	112.19
2	D	2	NAG	C4-C3-C2	-2.10	107.94	111.02
4	C	1	NAG	C2-N2-C7	2.07	125.86	122.90
4	C	2	NAG	C8-C7-N2	-2.07	112.59	116.10
2	D	2	NAG	O5-C5-C6	2.05	110.42	107.20
3	B	3	BMA	C3-C4-C5	2.05	113.89	110.24
4	C	2	NAG	C1-O5-C5	-2.04	109.42	112.19
3	B	3	BMA	O4-C4-C5	2.02	114.33	109.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	C	6	MAN	C5

All (2) torsion outliers are listed below:

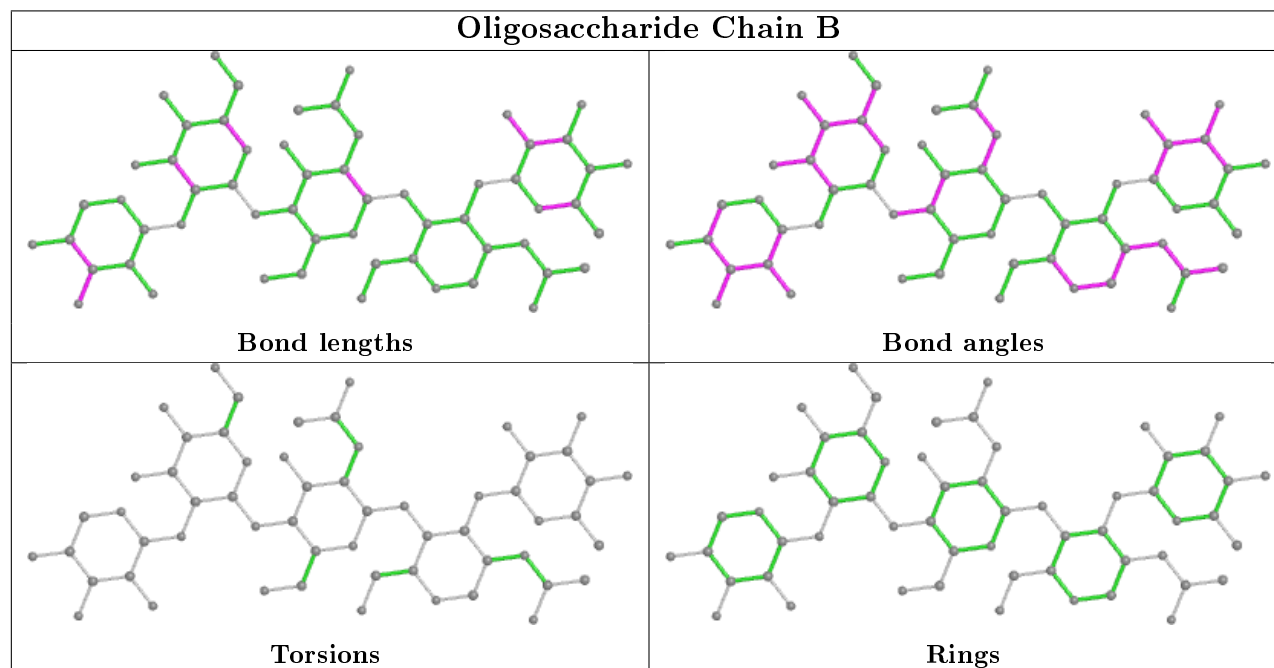
Mol	Chain	Res	Type	Atoms
4	C	6	MAN	O5-C5-C6-O6
4	C	3	BMA	C4-C5-C6-O6

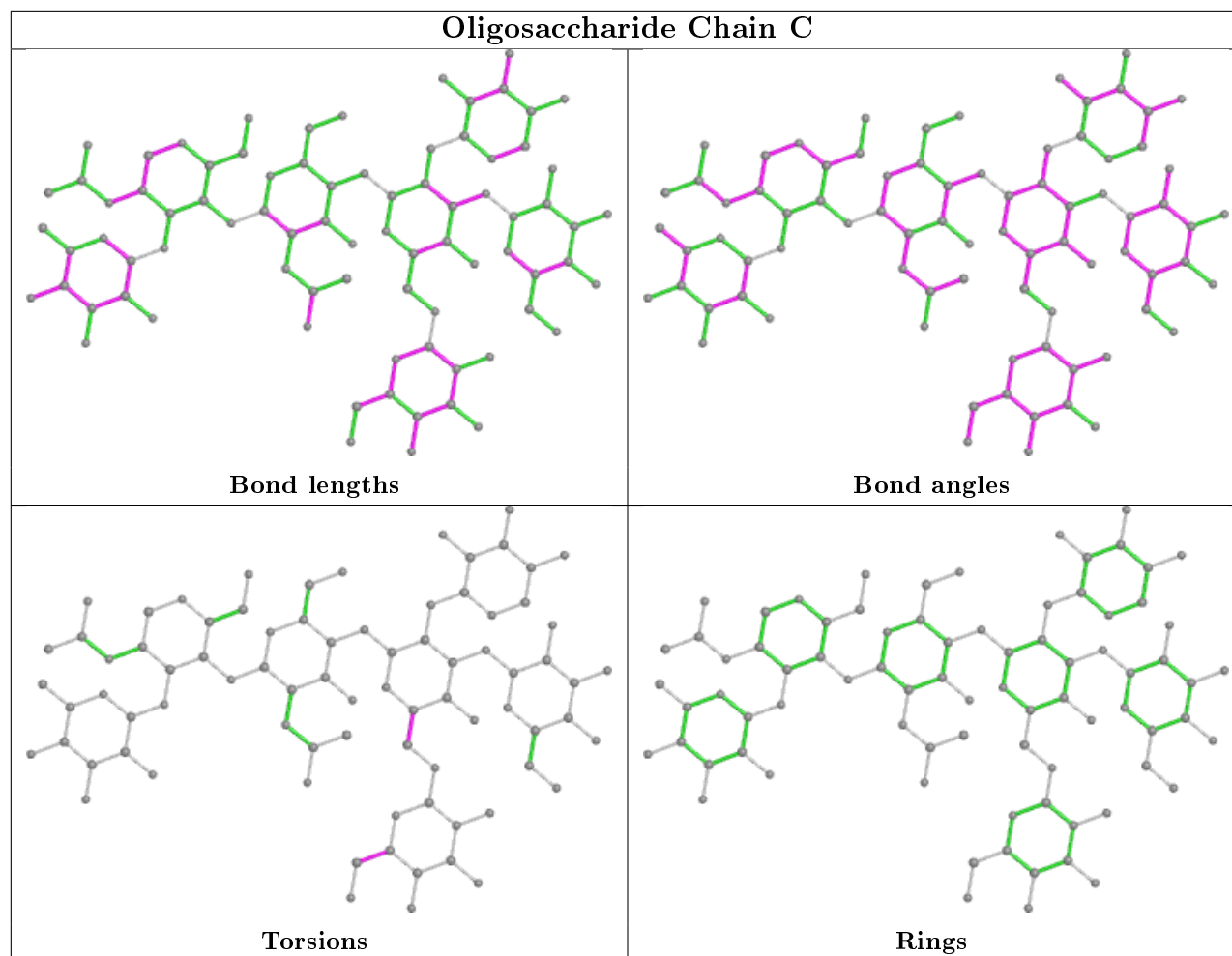
There are no ring outliers.

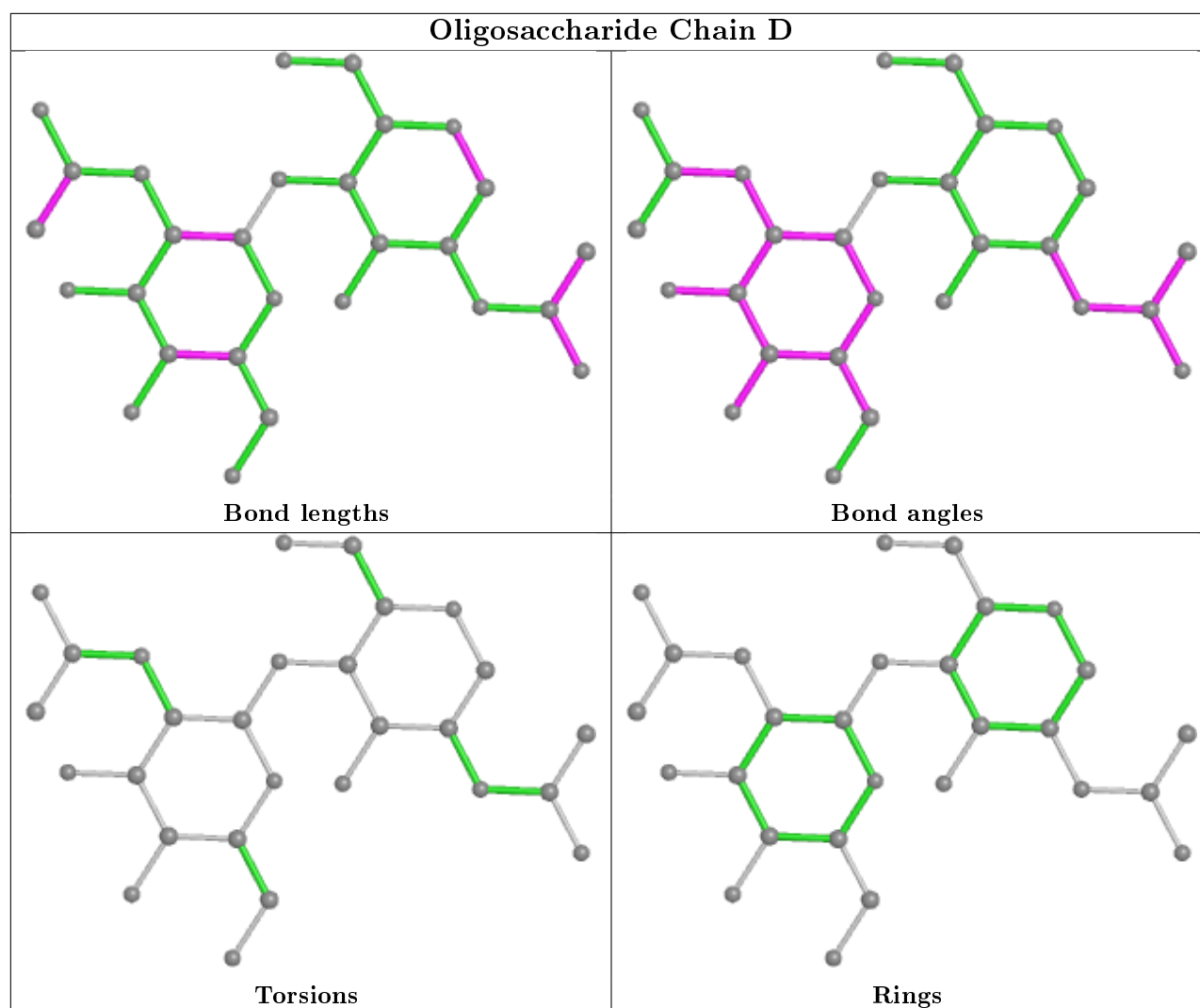
4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	3	BMA	7	0
2	A	1	NAG	3	0
2	D	2	NAG	1	0
4	C	6	MAN	8	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 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$
8	GOL	M	936	-	5,5,5	0.83	0	5,5,5	1.27	1 (20%)
5	NAG	M	901	-	14,14,15	1.21	1 (7%)	17,19,21	2.05	5 (29%)
8	GOL	M	932	-	5,5,5	0.65	0	5,5,5	1.15	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	M	922	1	14,14,15	1.25	1 (7%)	17,19,21	1.96	5 (29%)
7	SO4	M	929	-	4,4,4	1.06	0	6,6,6	1.40	1 (16%)
7	SO4	M	924	-	4,4,4	0.85	0	6,6,6	1.42	1 (16%)
7	SO4	M	930	-	4,4,4	0.76	0	6,6,6	0.36	0
7	SO4	M	928	-	4,4,4	1.93	1 (25%)	6,6,6	2.48	3 (50%)
8	GOL	M	935	-	5,5,5	0.64	0	5,5,5	1.11	1 (20%)
5	NAG	M	919	1	14,14,15	1.34	1 (7%)	17,19,21	2.51	8 (47%)
8	GOL	M	934	-	5,5,5	0.92	0	5,5,5	1.10	0
7	SO4	M	925	-	4,4,4	0.49	0	6,6,6	0.52	0
5	NAG	M	905	-	14,14,15	1.98	5 (35%)	17,19,21	8.04	13 (76%)
7	SO4	M	931	-	4,4,4	1.52	1 (25%)	6,6,6	2.98	5 (83%)
8	GOL	M	933	-	5,5,5	1.25	1 (20%)	5,5,5	1.05	0
7	SO4	M	926	-	4,4,4	1.41	1 (25%)	6,6,6	1.50	1 (16%)
5	NAG	M	918	1	14,14,15	1.38	2 (14%)	17,19,21	2.79	4 (23%)
5	NAG	M	902	-	14,14,15	1.68	2 (14%)	17,19,21	2.17	5 (29%)
7	SO4	M	927	-	4,4,4	0.24	0	6,6,6	0.38	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
8	GOL	M	936	-	-	0/4/4/4	-
5	NAG	M	901	-	-	0/6/23/26	0/1/1/1
8	GOL	M	932	-	-	4/4/4/4	-
5	NAG	M	922	1	-	0/6/23/26	0/1/1/1
8	GOL	M	935	-	-	0/4/4/4	-
5	NAG	M	919	1	-	4/6/23/26	0/1/1/1
8	GOL	M	934	-	-	0/4/4/4	-
5	NAG	M	905	-	-	2/6/23/26	0/1/1/1
8	GOL	M	933	-	-	0/4/4/4	-
5	NAG	M	918	1	1/1/5/7	0/6/23/26	0/1/1/1
5	NAG	M	902	-	-	0/6/23/26	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	902	NAG	O5-C5	4.19	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	919	NAG	O7-C7	-4.15	1.13	1.23
5	M	905	NAG	O7-C7	-3.94	1.14	1.23
5	M	922	NAG	O7-C7	-3.80	1.14	1.23
7	M	928	SO4	O2-S	3.69	1.66	1.46
5	M	902	NAG	O7-C7	-3.44	1.15	1.23
5	M	918	NAG	O7-C7	-3.38	1.15	1.23
5	M	905	NAG	C1-C2	-3.12	1.47	1.52
5	M	905	NAG	O4-C4	3.02	1.50	1.43
5	M	901	NAG	O7-C7	-2.82	1.16	1.23
5	M	905	NAG	C2-N2	-2.65	1.41	1.46
7	M	926	SO4	O1-S	2.63	1.60	1.46
7	M	931	SO4	O1-S	2.49	1.59	1.46
5	M	905	NAG	O5-C1	-2.18	1.40	1.43
5	M	918	NAG	C2-N2	2.17	1.50	1.46
8	M	933	GOL	O1-C1	2.16	1.51	1.42

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	905	NAG	C2-N2-C7	21.62	153.68	122.90
5	M	905	NAG	O5-C1-C2	14.76	134.59	111.29
5	M	905	NAG	C8-C7-N2	14.41	140.50	116.10
5	M	918	NAG	C1-O5-C5	8.43	123.61	112.19
5	M	905	NAG	O7-C7-N2	-8.36	106.58	121.95
5	M	905	NAG	C1-O5-C5	-6.67	103.16	112.19
5	M	902	NAG	C1-O5-C5	-6.24	103.74	112.19
5	M	901	NAG	C1-O5-C5	-6.12	103.90	112.19
5	M	919	NAG	O5-C1-C2	-5.91	101.95	111.29
5	M	905	NAG	O7-C7-C8	-5.00	112.77	122.06
7	M	931	SO4	O4-S-O3	4.73	129.27	109.06
5	M	922	NAG	C4-C3-C2	-4.60	104.28	111.02
5	M	918	NAG	C1-C2-N2	-4.41	102.95	110.49
5	M	918	NAG	O3-C3-C2	-4.33	100.50	109.47
5	M	905	NAG	C3-C4-C5	3.86	117.13	110.24
5	M	919	NAG	O5-C5-C6	-3.80	101.24	107.20
5	M	922	NAG	O3-C3-C2	-3.79	101.62	109.47
5	M	902	NAG	C4-C3-C2	-3.71	105.59	111.02
5	M	905	NAG	O5-C5-C6	-3.54	101.66	107.20
7	M	928	SO4	O3-S-O2	-3.49	91.08	109.31
5	M	919	NAG	O5-C5-C4	-3.48	102.37	110.83
7	M	931	SO4	O3-S-O1	-3.46	91.24	109.31
5	M	905	NAG	O4-C4-C5	-3.43	100.79	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	919	NAG	O4-C4-C3	3.23	117.82	110.35
5	M	918	NAG	O4-C4-C5	-3.20	101.36	109.30
7	M	926	SO4	O4-S-O3	3.07	122.18	109.06
7	M	928	SO4	O2-S-O1	-2.98	87.42	109.43
7	M	931	SO4	O2-S-O1	-2.90	88.00	109.43
5	M	919	NAG	O3-C3-C2	-2.86	103.55	109.47
5	M	922	NAG	O5-C1-C2	2.86	115.80	111.29
5	M	901	NAG	O5-C5-C4	-2.80	104.02	110.83
5	M	902	NAG	O5-C5-C6	-2.76	102.87	107.20
5	M	919	NAG	C1-O5-C5	2.64	115.77	112.19
5	M	901	NAG	O5-C1-C2	2.63	115.44	111.29
5	M	922	NAG	C1-C2-N2	-2.62	106.02	110.49
8	M	936	GOL	C3-C2-C1	-2.58	101.68	111.70
5	M	905	NAG	O4-C4-C3	-2.57	104.40	110.35
7	M	928	SO4	O4-S-O1	2.53	122.53	109.31
5	M	905	NAG	C4-C3-C2	-2.48	107.39	111.02
7	M	931	SO4	O4-S-O1	-2.42	96.69	109.31
7	M	924	SO4	O3-S-O2	2.41	121.88	109.31
7	M	929	SO4	O4-S-O1	2.40	121.83	109.31
5	M	922	NAG	O5-C5-C4	-2.39	105.02	110.83
5	M	919	NAG	C2-N2-C7	2.38	126.30	122.90
5	M	902	NAG	O5-C5-C4	-2.37	105.05	110.83
5	M	905	NAG	C1-C2-N2	2.28	114.39	110.49
5	M	901	NAG	O5-C5-C6	-2.26	103.66	107.20
8	M	932	GOL	O2-C2-C1	2.21	118.87	109.12
5	M	919	NAG	O7-C7-C8	2.21	126.15	122.06
5	M	901	NAG	C4-C3-C2	-2.14	107.88	111.02
7	M	931	SO4	O3-S-O2	2.13	120.41	109.31
5	M	902	NAG	O3-C3-C2	-2.09	105.13	109.47
8	M	935	GOL	C3-C2-C1	-2.01	103.88	111.70
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
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	C8-C7-N2-C2
5	M	919	NAG	O5-C5-C6-O6
5	M	905	NAG	O7-C7-N2-C2
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 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	901	NAG	6	0
8	M	932	GOL	4	0
7	M	925	SO4	2	0
5	M	905	NAG	9	0
7	M	931	SO4	8	0
7	M	926	SO4	6	0
5	M	918	NAG	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

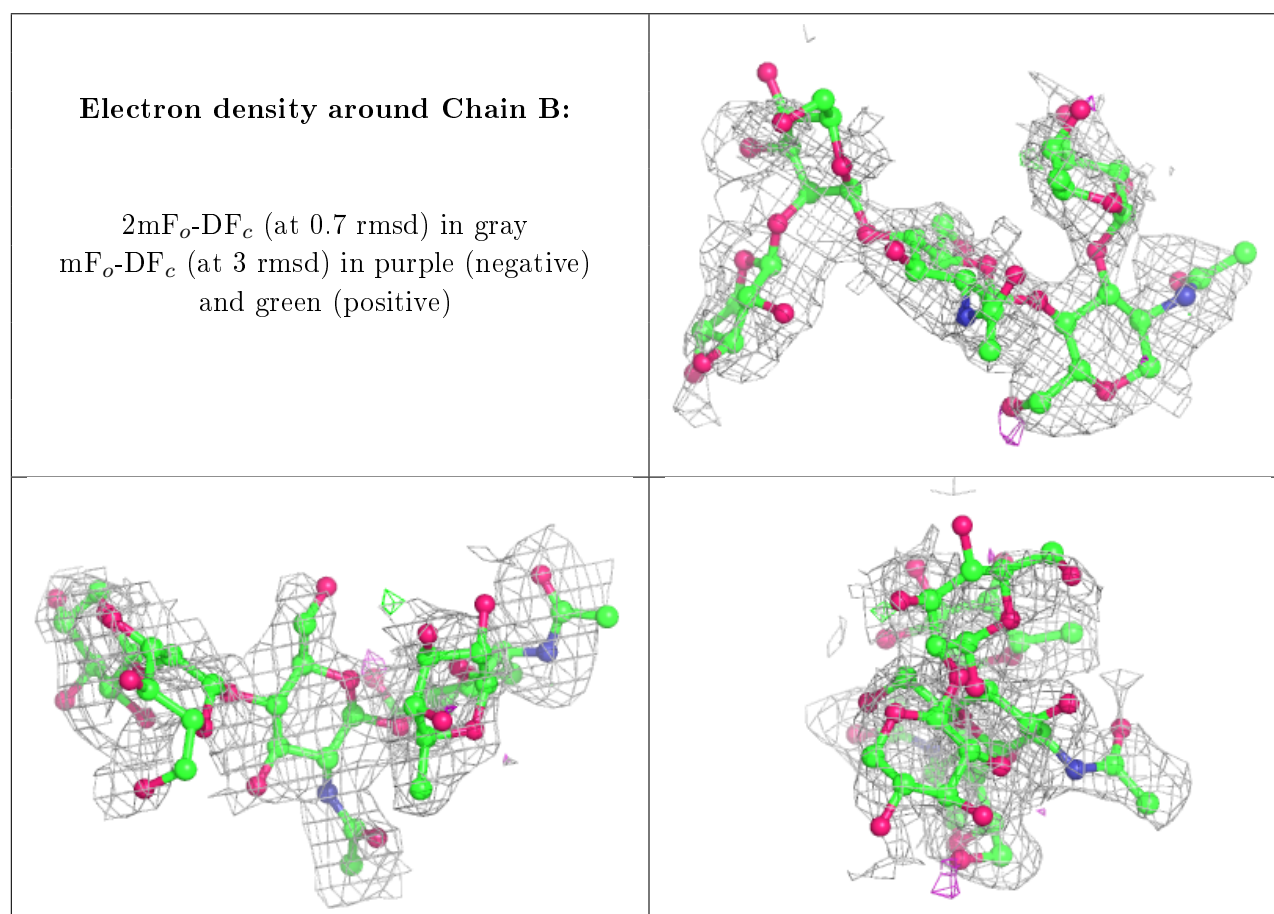
6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

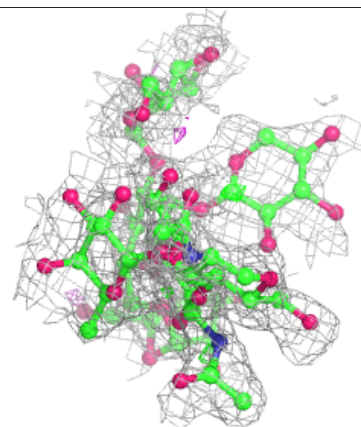
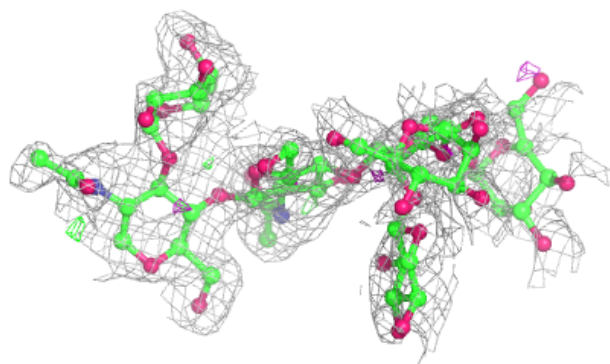
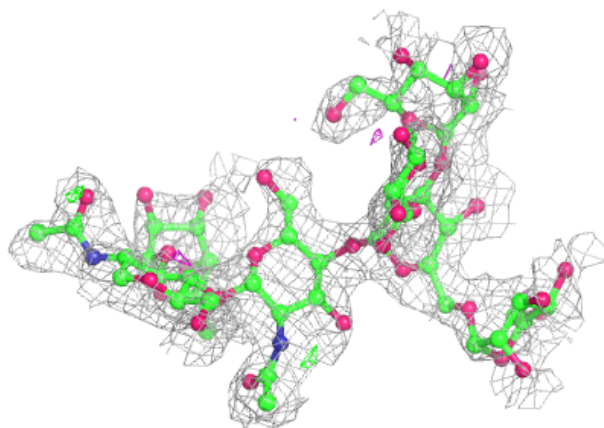
Unable to reproduce the depositors R factor - this section is therefore empty.

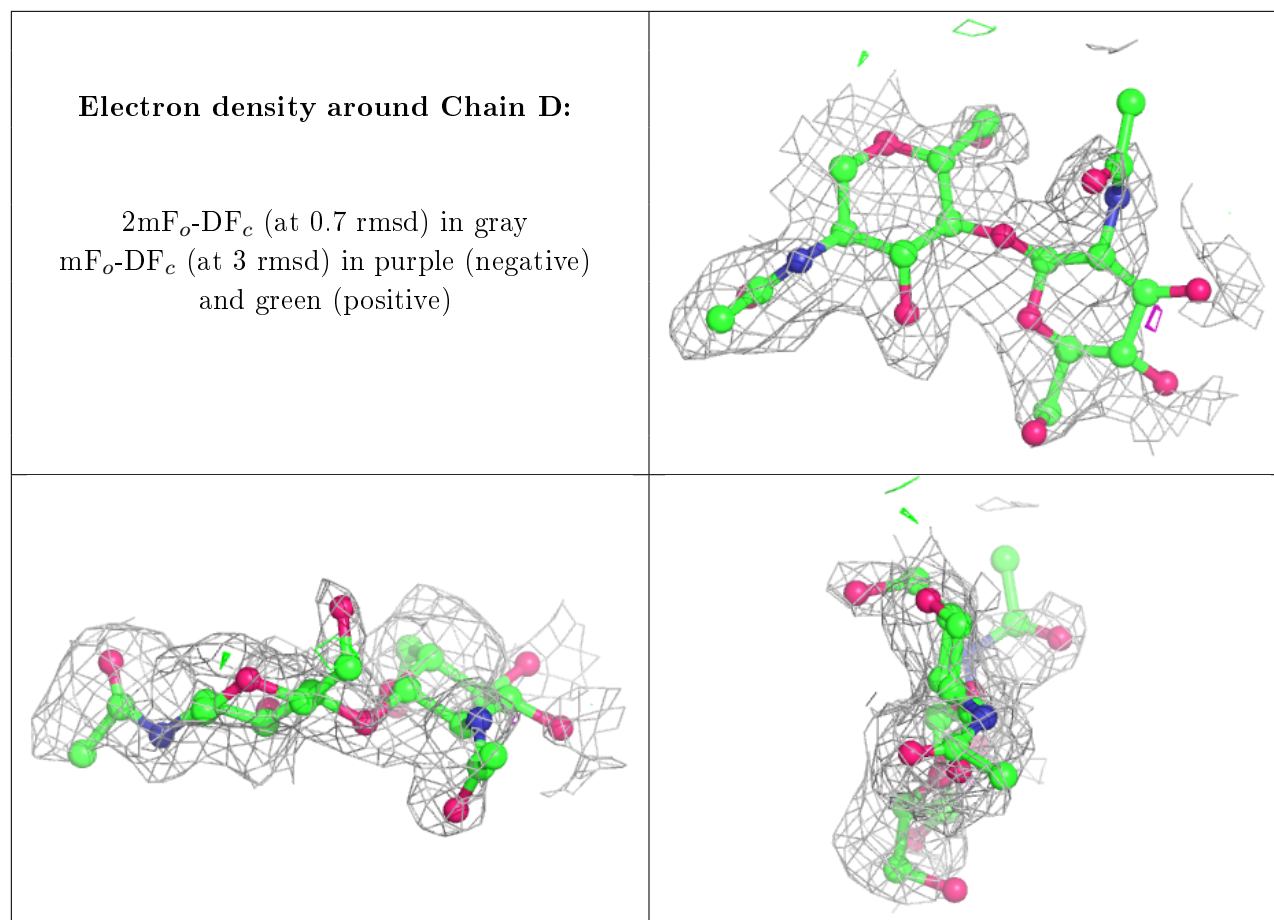
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain C:

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





6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.