



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 08:59 PM UTC

PDB ID : 3FU8 / pdb_00003fu8
Title : Melanocarpus albomyces laccase crystal soaked (10 sec) with 2,6-dimethoxyphenol
Authors : Kallio, J.P.; Hakulinen, N.; Rouvinen, J.
Deposited on : 2009-01-14
Resolution : 1.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

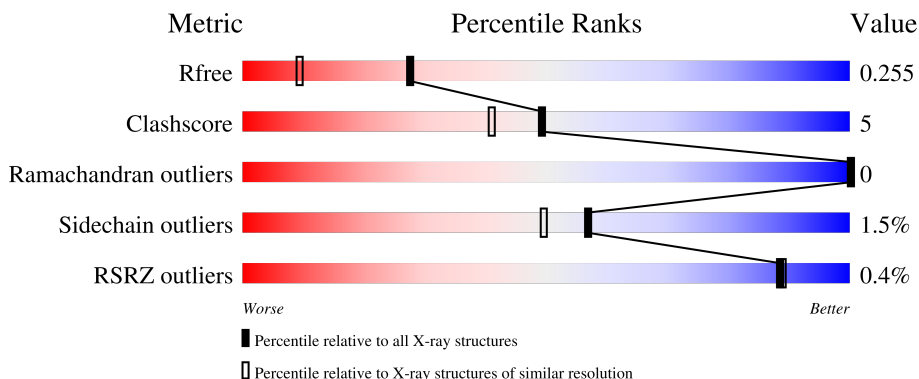
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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.



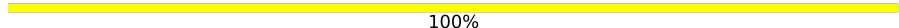
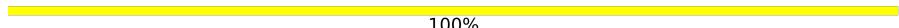

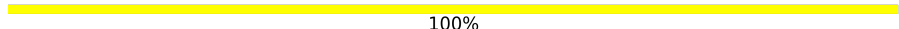
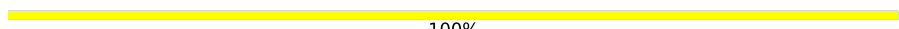
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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

Mol	Chain	Length	Quality of chain
1	A	559	
1	B	559	
2	C	4	
2	H	4	
3	D	2	

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Mol	Chain	Length	Quality of chain
3	F	2	 100%
3	G	2	 100%
3	I	2	 50% 50%
3	K	2	 100%
4	E	3	 33% 67%
4	J	3	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MAN	C	3	X	-	-	-
2	MAN	H	3	X	-	-	-
4	MAN	E	3	X	-	-	-
4	MAN	J	3	X	-	-	-
9	3DM	A	2900	-	X	-	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 10570 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 Laccase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	559	4394	2776	763	839	16	0	4	0
1	B	559	4393	2776	765	836	16	0	3	0

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



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

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



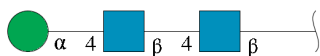
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	D	2	28	16	2	10	0	0	0
3	F	2	28	16	2	10	0	0	0

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

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	3	Total	C	N	O	0	0	0
			39	22	2	15			
4	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 5 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	Cu	0	0
			4	4		
5	B	4	Total	Cu	0	0
			4	4		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

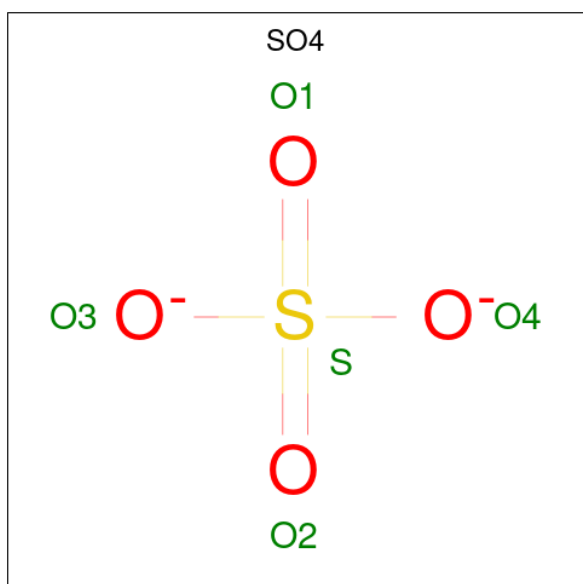
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		
6	B	1	Total	Cl	0	0
			1	1		

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



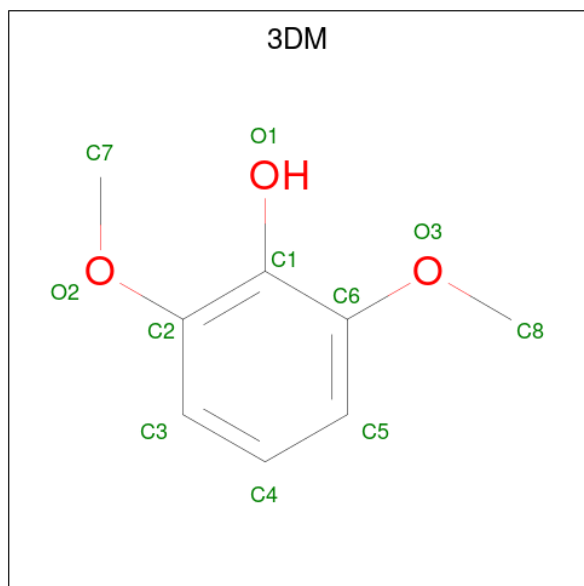
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
7	A	1	Total 14	C 8	N 1	O 5	0	0
7	A	1	Total 14	C 8	N 1	O 5	0	0
7	B	1	Total 14	C 8	N 1	O 5	0	0
7	B	1	Total 14	C 8	N 1	O 5	0	0
7	B	1	Total 14	C 8	N 1	O 5	0	0

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 9 is 2,6-dimethoxyphenol (CCD ID: 3DM) (formula: C₈H₁₀O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C O 11 8 3	0	0
9	B	1	Total C O 11 8 3	0	0

- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

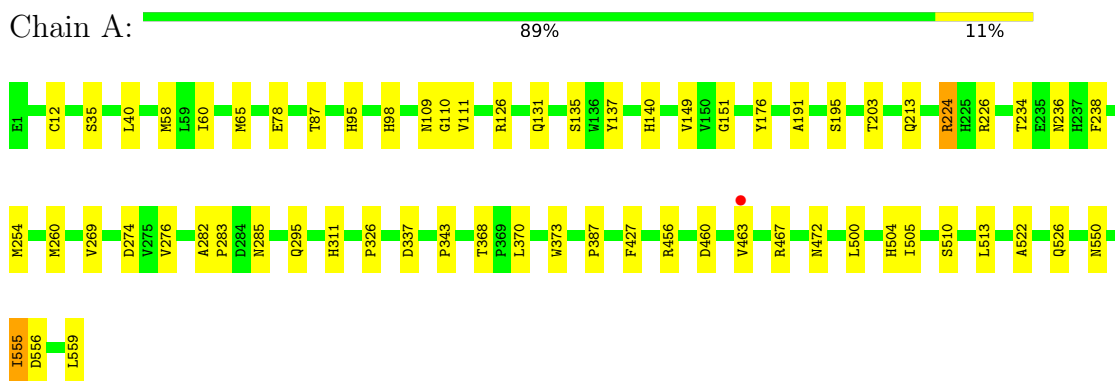
- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	677	Total O 677 677	0	0
11	B	659	Total O 659 659	0	0

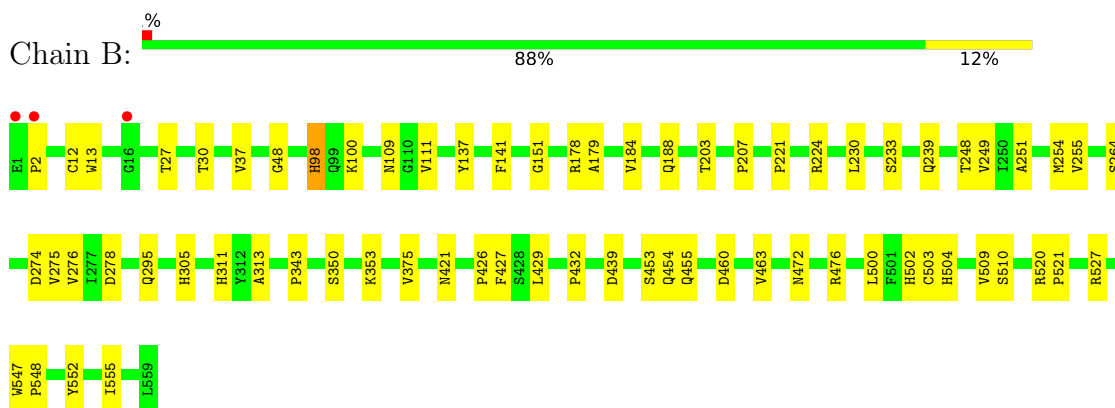
3 Residue-property plots [i](#)

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

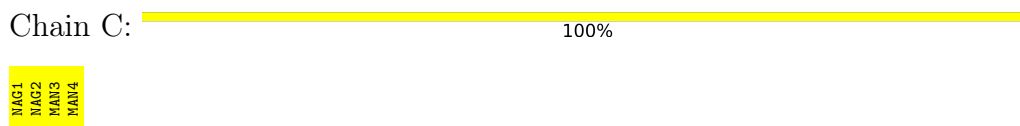
- Molecule 1: Laccase-1



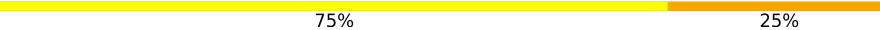
- Molecule 1: Laccase-1



- Molecule 2: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 2: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  75% 25%

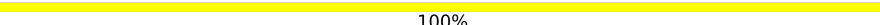
MAG1
MAG2
MAN3
MAN4

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

Chain D:  50% 50%

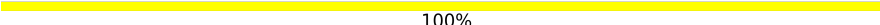
MAG1
MAG2

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

Chain F:  100%

MAG1
MAG2

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

Chain G:  100%

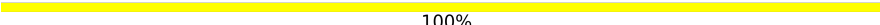
MAG1
MAG2

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

Chain I:  50% 50%

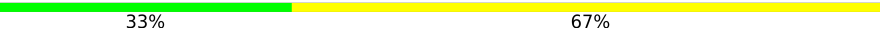
MAG1
MAG2

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

Chain K:  100%

MAG1
MAG2

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

Chain E:  33% 67%

MAG1
MAG2
MAN3

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

Chain J:

100%

MAG1
MAG2
MAG3

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	174.71Å 62.37Å 125.14Å 90.00° 96.36° 90.00°	Depositor
Resolution (Å)	19.78 – 1.80 19.78 – 1.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.78-1.80) 98.7 (19.78-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 1.80Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.203 , 0.256 0.204 , 0.255	Depositor DCC
R_{free} test set	6134 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtrriage
Anisotropy	0.017	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10570	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, OHI, NAG, MAN, CU, SO4, 3DM, GOL

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.96	1/4518 (0.0%)	0.97	3/6205 (0.0%)
1	B	0.95	1/4517 (0.0%)	0.95	7/6203 (0.1%)
All	All	0.96	2/9035 (0.0%)	0.96	10/12408 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	276	VAL	CA-CB	6.00	1.61	1.54
1	B	249	VAL	CA-CB	5.29	1.60	1.54

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	PRO	CA-C-N	-6.22	114.32	120.98
1	A	326	PRO	C-N-CA	-6.22	114.32	120.98
1	B	421	ASN	N-CA-C	6.09	118.75	109.62
1	B	255	VAL	N-CA-C	5.82	113.82	107.60
1	B	27	THR	CA-C-N	5.66	125.58	119.76

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4394	0	4124	52	0
1	B	4393	0	4127	43	0
2	C	50	0	43	0	0
2	H	50	0	42	1	0
3	D	28	0	25	1	0
3	F	28	0	25	0	0
3	G	28	0	25	0	0
3	I	28	0	25	1	0
3	K	28	0	25	0	0
4	E	39	0	34	0	0
4	J	39	0	34	0	0
5	A	4	0	0	0	0
5	B	4	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	28	0	26	0	0
7	B	42	0	39	1	0
8	A	10	0	0	0	0
8	B	5	0	0	0	0
9	A	11	0	9	2	0
9	B	11	0	9	0	0
10	A	6	0	4	1	0
10	B	6	0	4	0	0
11	A	677	0	0	24	0
11	B	659	0	0	27	0
All	All	10570	0	8620	96	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 96 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:B:141:PHE:HB2	11:B:1255:HOH:O	1.23	1.25
1:A:224:ARG:HH11	1:A:224:ARG:HG3	1.21	1.03
1:A:295:GLN:HG3	11:A:1247:HOH:O	1.59	1.02
1:A:337:ASP:HB2	11:A:1103:HOH:O	1.61	1.00
1:B:275:VAL:HB	11:B:1094:HOH:O	1.68	0.92

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	560/559 (100%)	545 (97%)	15 (3%)	0	100	100
1	B	559/559 (100%)	546 (98%)	13 (2%)	0	100	100
All	All	1119/1118 (100%)	1091 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	481/477 (101%)	473 (98%)	8 (2%)	53	45
1	B	480/477 (101%)	472 (98%)	8 (2%)	53	45
All	All	961/954 (101%)	945 (98%)	16 (2%)	57	45

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	510	SER
1	B	350	SER
1	B	12[A]	CYS
1	B	254	MET
1	A	555	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	68	ASN
1	B	84	ASN
1	B	258	ASN
1	B	190	ASN
1	B	236	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](#)

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	OHI	A	98	1	9,11,12	1.34	2 (22%)	3,14,16	2.02	1 (33%)
1	OHI	B	98	1	9,11,12	1.12	1 (11%)	3,14,16	2.00	1 (33%)

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
1	OHI	A	98	1	-	0/4/15/17	0/1/1/1
1	OHI	B	98	1	-	1/4/15/17	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	OHI	CE1-ND1	-2.66	1.31	1.39
1	B	98	OHI	CE1-ND1	-2.17	1.32	1.39
1	A	98	OHI	O12-CE1	2.02	1.29	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	OHI	O12-CE1-ND1	-3.43	117.14	125.86
1	A	98	OHI	O12-CE1-ND1	-3.38	117.26	125.86

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	98	OHI	CA-CB-CG-ND1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	98	OHI	1	0

5.5 Carbohydrates [i](#)

24 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	C	1	1,2	14,14,15	0.73	0	17,19,21	1.53	2 (11%)
2	NAG	C	2	2	14,14,15	0.69	0	17,19,21	1.47	3 (17%)
2	MAN	C	3	2	11,11,12	0.83	0	15,15,17	1.59	4 (26%)
2	MAN	C	4	2	11,11,12	0.72	0	15,15,17	1.18	2 (13%)
3	NAG	D	1	3,1	14,14,15	0.66	0	17,19,21	1.14	0
3	NAG	D	2	3	14,14,15	0.61	0	17,19,21	1.37	2 (11%)
4	NAG	E	1	4,1	14,14,15	0.73	0	17,19,21	1.11	1 (5%)
4	NAG	E	2	4	14,14,15	0.65	0	17,19,21	0.87	0
4	MAN	E	3	4	11,11,12	0.66	0	15,15,17	1.32	2 (13%)
3	NAG	F	1	3,1	14,14,15	0.62	0	17,19,21	1.51	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	F	2	3	14,14,15	0.53	0	17,19,21	1.71	2 (11%)
3	NAG	G	1	3,1	14,14,15	0.87	1 (7%)	17,19,21	1.66	1 (5%)
3	NAG	G	2	3	14,14,15	0.64	0	17,19,21	2.08	6 (35%)
2	NAG	H	1	1,2	14,14,15	0.80	0	17,19,21	1.30	2 (11%)
2	NAG	H	2	2	14,14,15	0.66	0	17,19,21	1.41	3 (17%)
2	MAN	H	3	2	11,11,12	0.68	0	15,15,17	1.86	3 (20%)
2	MAN	H	4	2	11,11,12	0.69	0	15,15,17	1.20	2 (13%)
3	NAG	I	1	3,1	14,14,15	0.62	0	17,19,21	1.28	2 (11%)
3	NAG	I	2	3	14,14,15	0.69	0	17,19,21	1.40	3 (17%)
4	NAG	J	1	4,1	14,14,15	0.64	0	17,19,21	1.34	2 (11%)
4	NAG	J	2	4	14,14,15	0.75	0	17,19,21	1.21	2 (11%)
4	MAN	J	3	4	11,11,12	0.54	0	15,15,17	1.28	2 (13%)
3	NAG	K	1	3,1	14,14,15	0.54	0	17,19,21	1.53	5 (29%)
3	NAG	K	2	3	14,14,15	0.59	0	17,19,21	1.24	2 (11%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	MAN	C	3	2	1/1/4/5	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	2/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
4	NAG	E	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1
4	MAN	E	3	4	1/1/4/5	0/2/19/22	0/1/1/1
3	NAG	F	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	NAG	G	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
2	NAG	H	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	H	2	2	-	1/6/23/26	0/1/1/1
2	MAN	H	3	2	1/1/4/5	2/2/19/22	0/1/1/1
2	MAN	H	4	2	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	0/6/23/26	0/1/1/1
4	NAG	J	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	J	2	4	-	0/6/23/26	0/1/1/1
4	MAN	J	3	4	1/1/4/5	0/2/19/22	0/1/1/1
3	NAG	K	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	K	2	3	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	1	NAG	O5-C1	-2.50	1.39	1.43

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	1	NAG	O5-C1-C2	-5.76	102.39	111.29
3	G	2	NAG	C1-O5-C5	4.59	118.34	112.19
2	H	3	MAN	C1-O5-C5	-4.33	106.38	112.19
3	F	1	NAG	C1-O5-C5	4.08	117.65	112.19
3	F	2	NAG	C2-N2-C7	-4.07	117.44	122.90

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	3	MAN	C1
2	H	3	MAN	C1
4	E	3	MAN	C1
4	J	3	MAN	C1

5 of 13 torsion outliers are listed below:

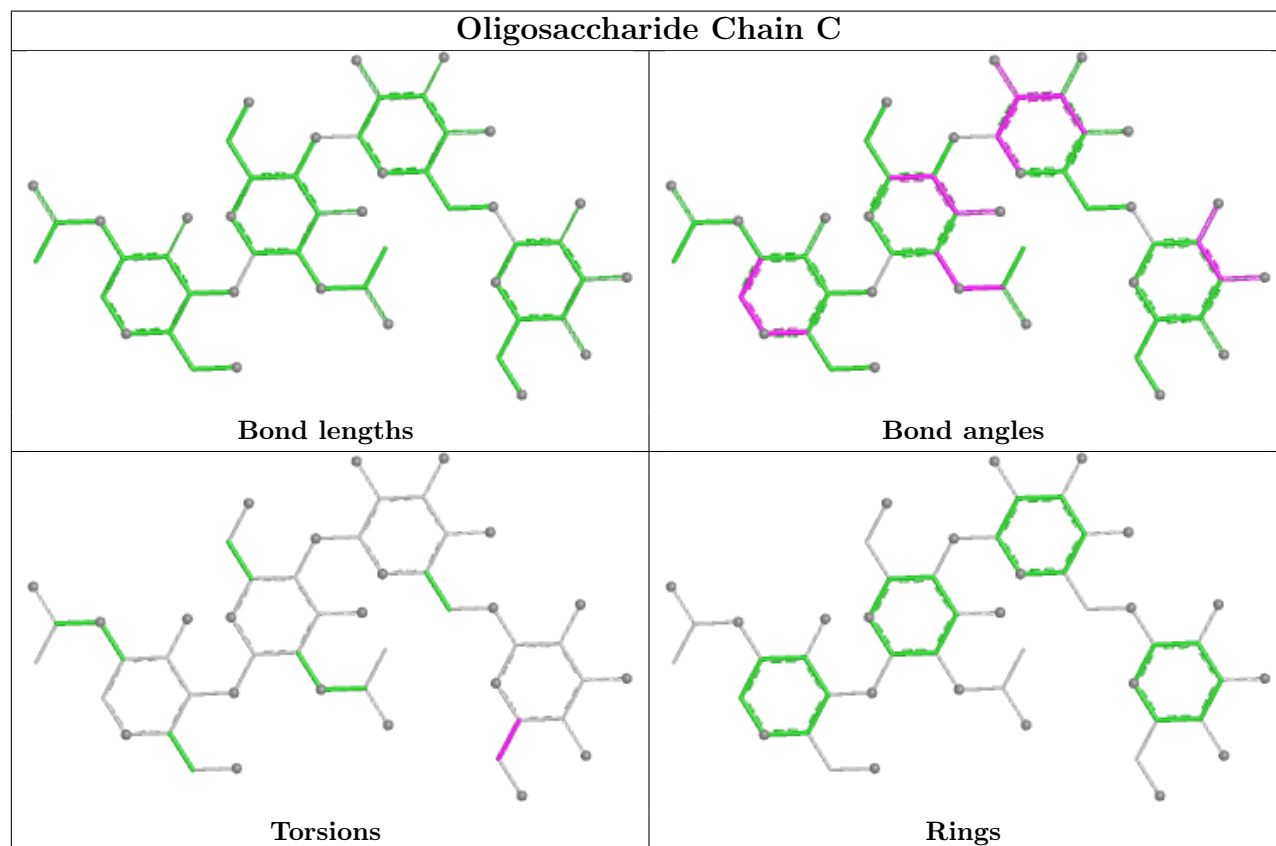
Mol	Chain	Res	Type	Atoms
3	D	1	NAG	C4-C5-C6-O6
2	C	4	MAN	C4-C5-C6-O6
2	C	4	MAN	O5-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6

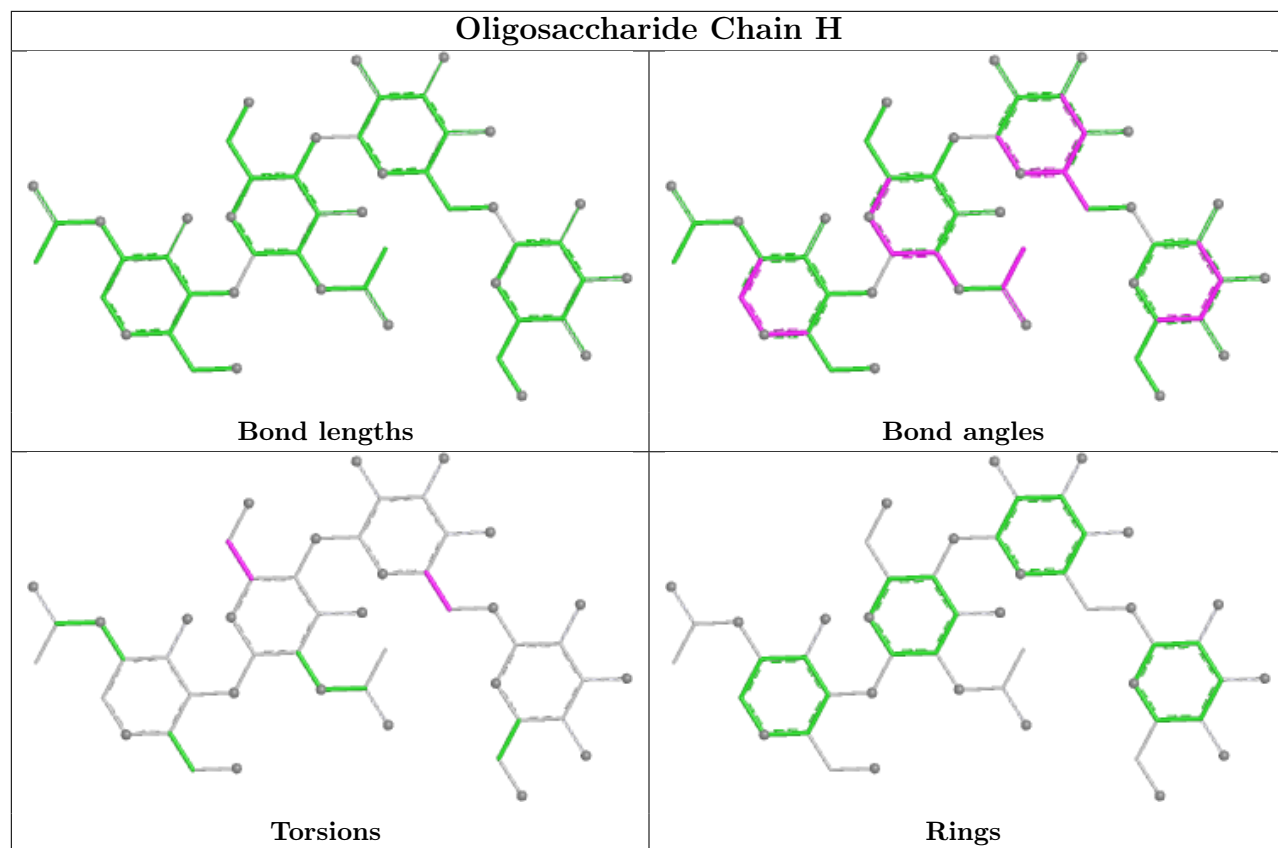
There are no ring outliers.

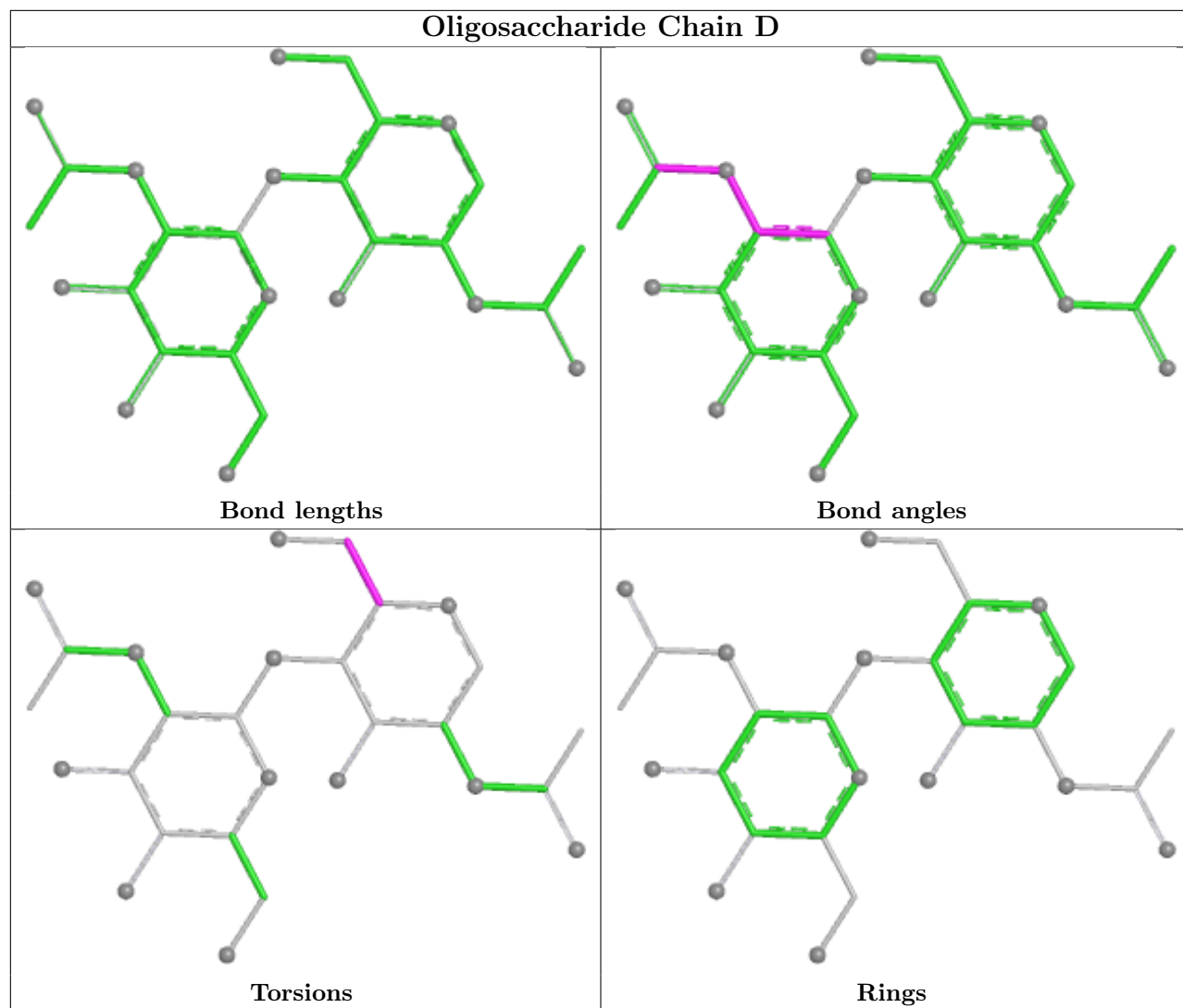
3 monomers are involved in 3 short contacts:

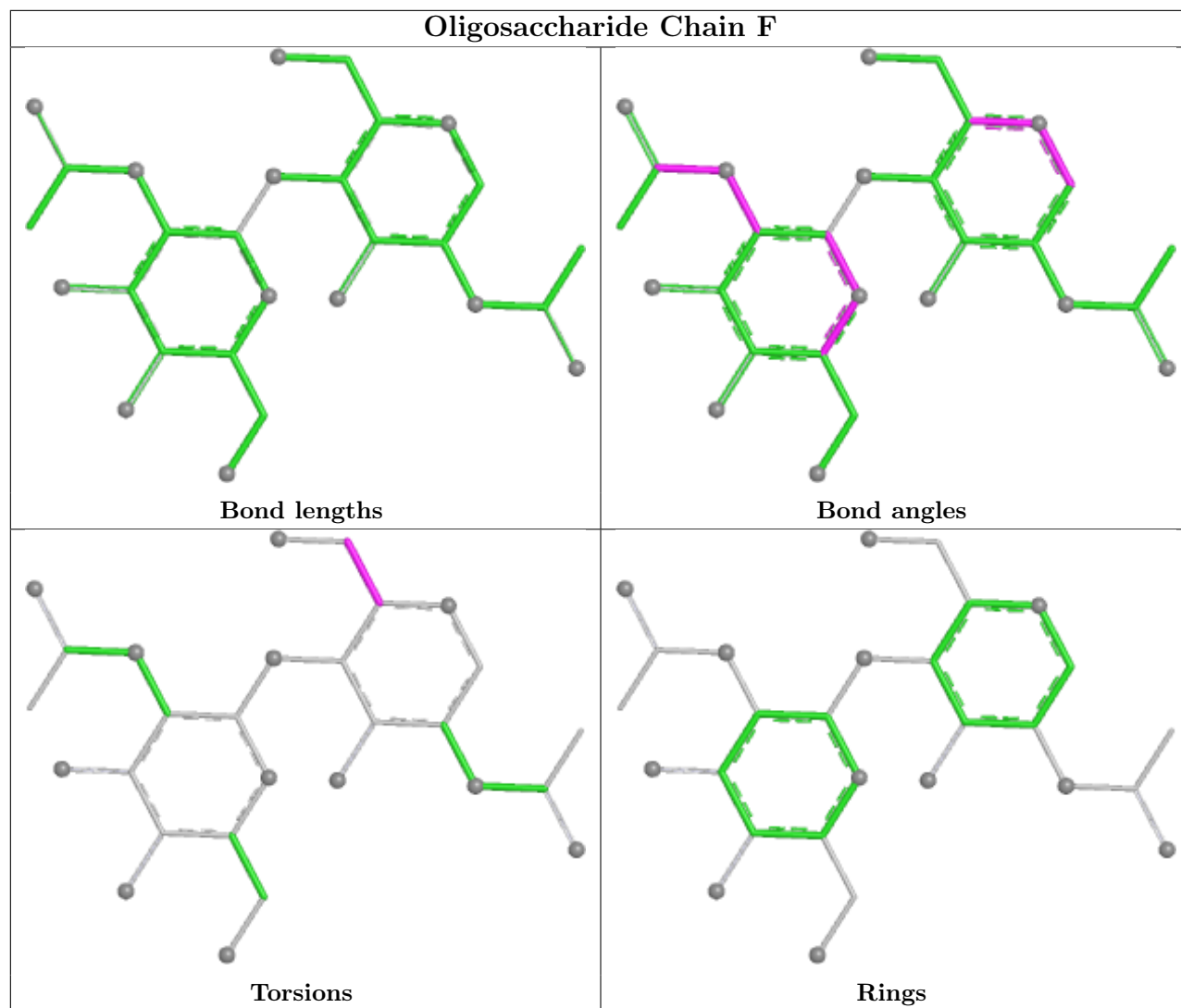
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	1	NAG	1	0
3	D	2	NAG	1	0
2	H	2	NAG	1	0

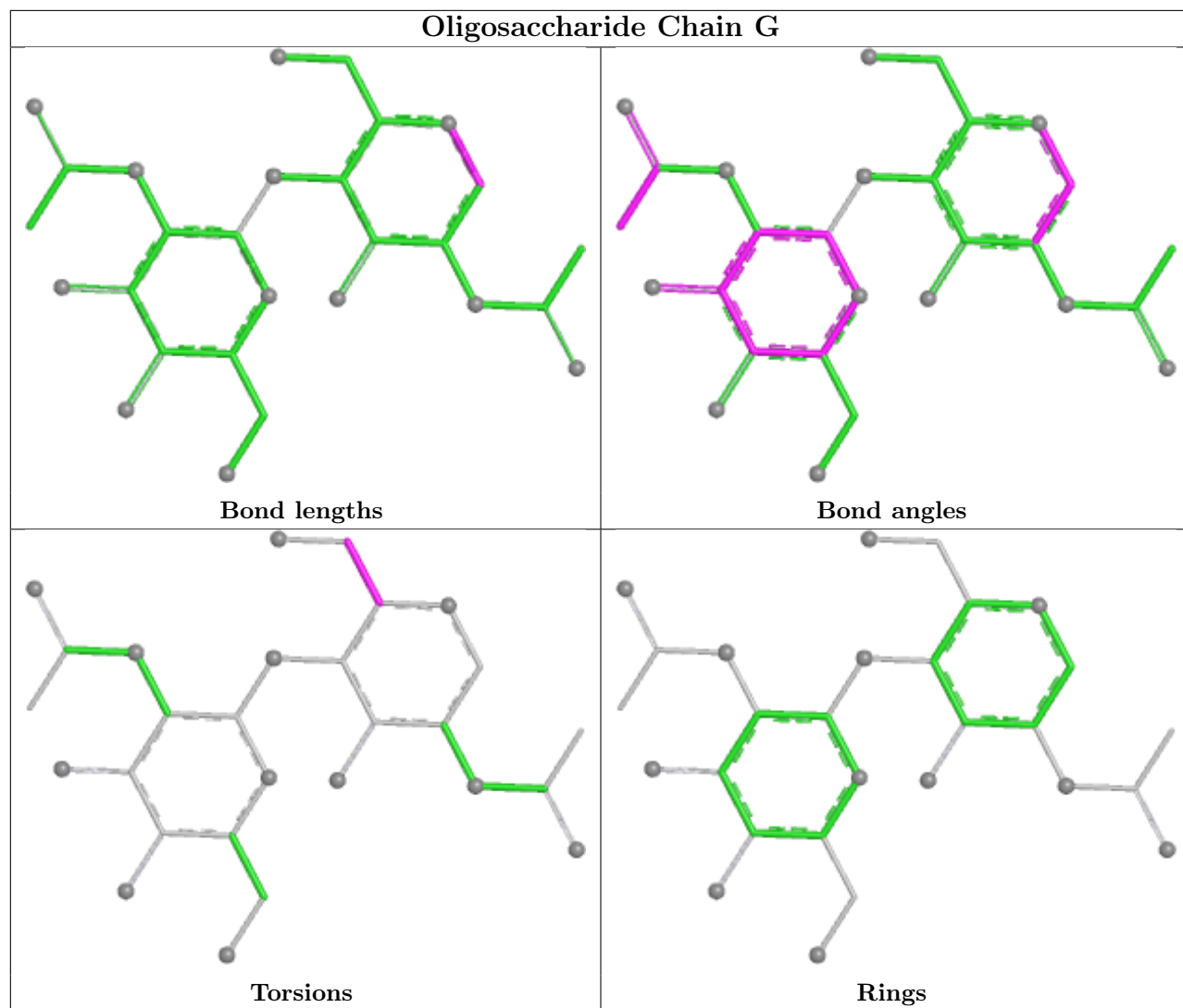
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

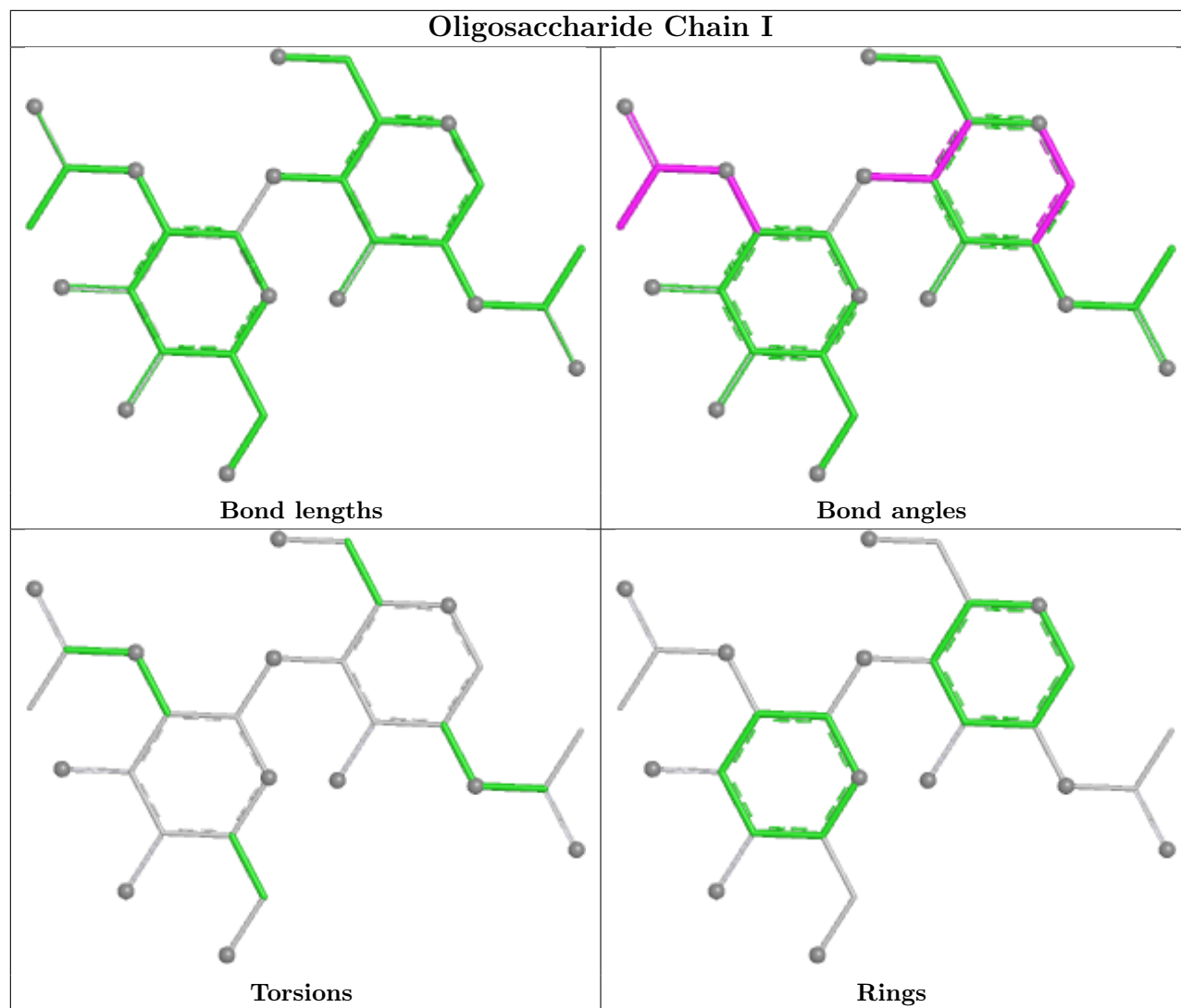


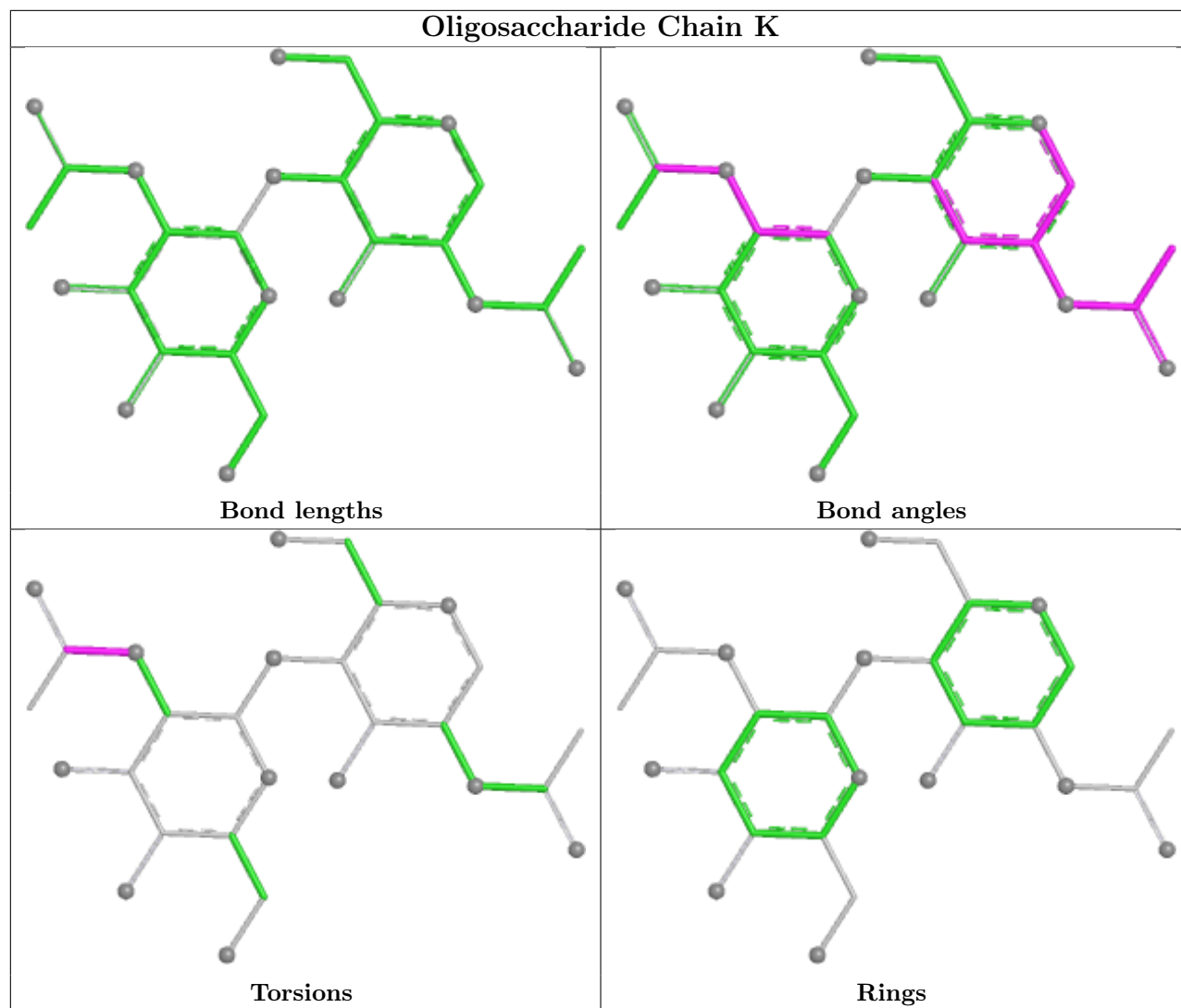


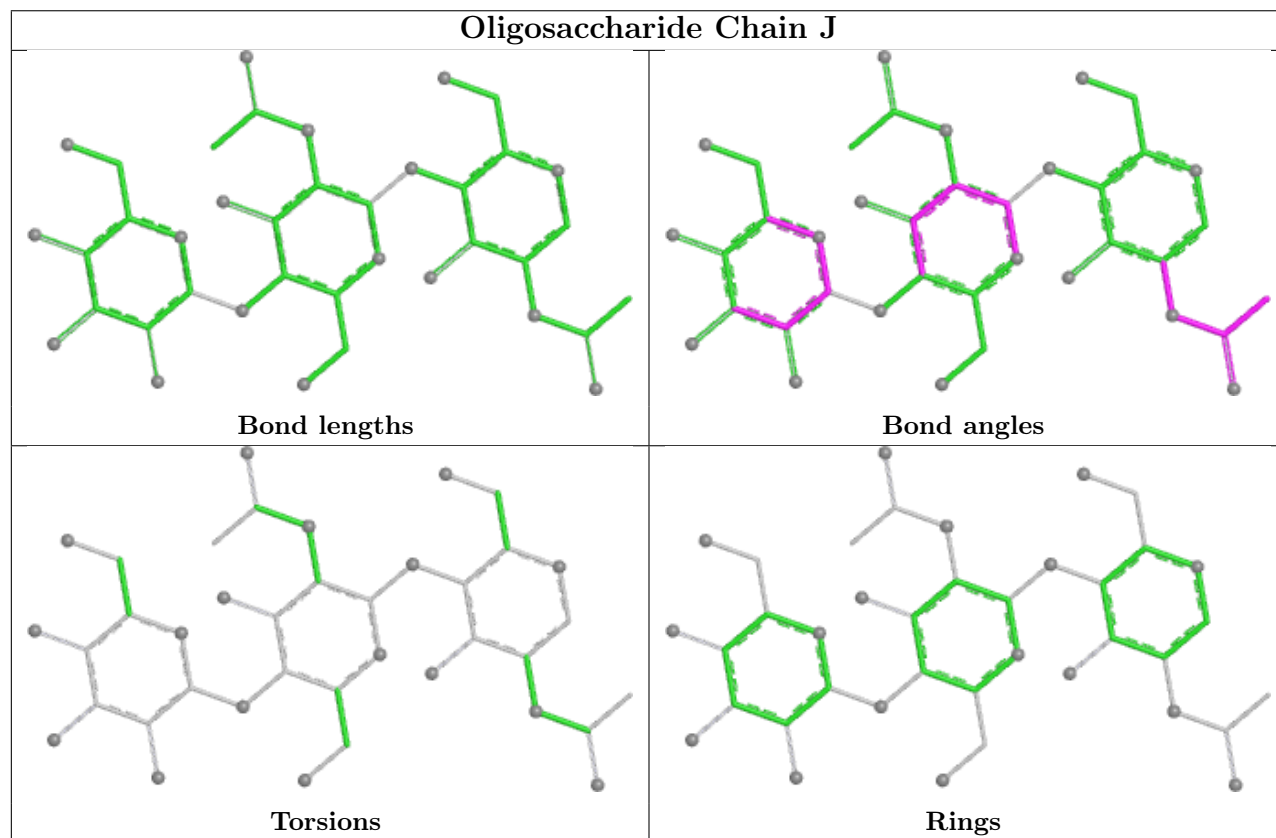
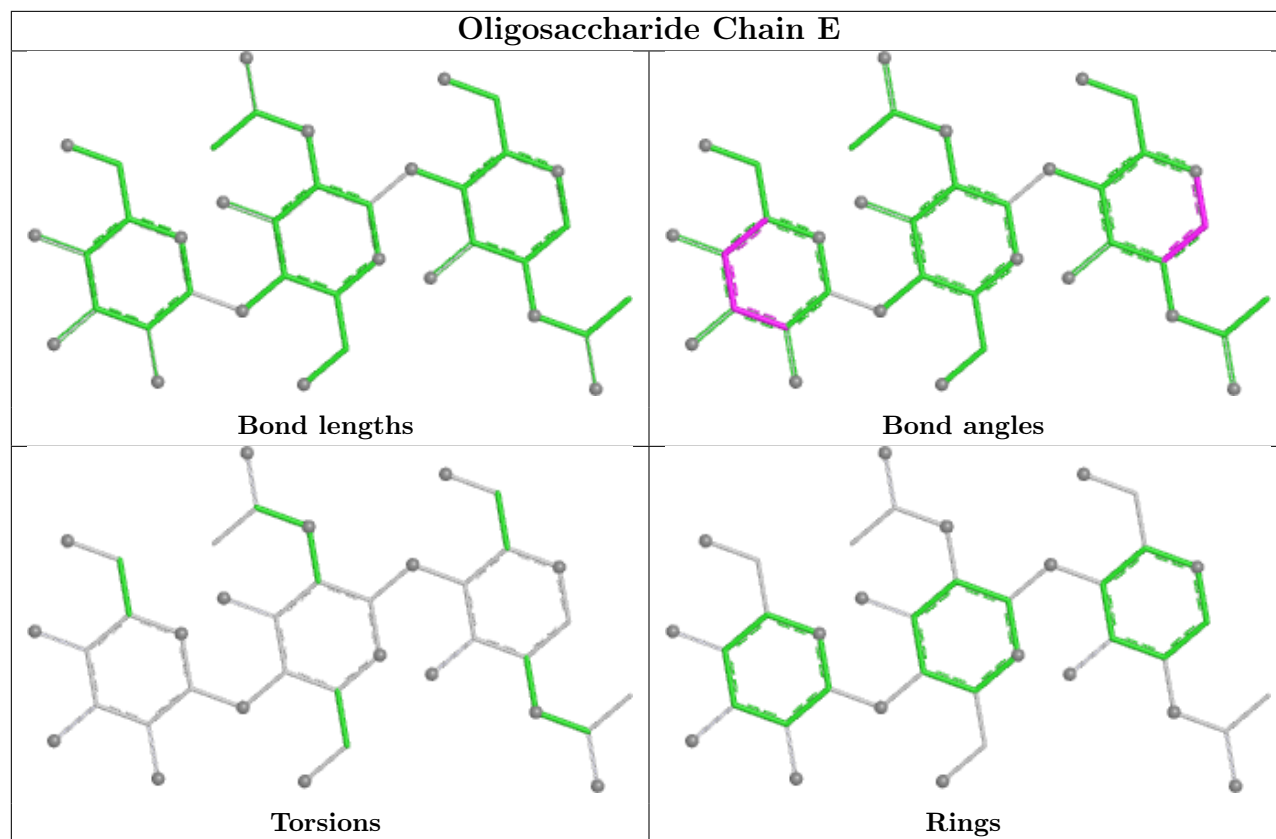












5.6 Ligand geometry

Of 22 ligands modelled in this entry, 10 are monoatomic - leaving 12 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
9	3DM	B	2910	-	11,11,11	2.78	2 (18%)	14,14,14	2.25	5 (35%)
9	3DM	A	2900	-	11,11,11	3.01	2 (18%)	14,14,14	2.74	6 (42%)
8	SO4	B	4802	-	4,4,4	0.21	0	6,6,6	0.24	0
7	NAG	A	750	1	14,14,15	0.67	0	17,19,21	1.30	3 (17%)
7	NAG	A	700	1	14,14,15	0.86	1 (7%)	17,19,21	1.51	2 (11%)
8	SO4	A	3800	-	4,4,4	0.23	0	6,6,6	0.54	0
10	GOL	A	3902[A]	-	5,5,5	0.33	0	5,5,5	0.49	0
7	NAG	B	1750	1	14,14,15	0.71	0	17,19,21	1.55	2 (11%)
10	GOL	B	3901[B]	-	5,5,5	0.34	0	5,5,5	0.43	0
7	NAG	B	2760	1	14,14,15	0.78	1 (7%)	17,19,21	1.23	1 (5%)
8	SO4	A	3801	-	4,4,4	0.31	0	6,6,6	0.32	0
7	NAG	B	700	1	14,14,15	0.61	0	17,19,21	0.93	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	3DM	B	2910	-	-	0/4/4/4	0/1/1/1
9	3DM	A	2900	-	-	4/4/4/4	0/1/1/1
7	NAG	A	750	1	-	0/6/23/26	0/1/1/1
7	NAG	A	700	1	-	2/6/23/26	0/1/1/1
10	GOL	A	3902[A]	-	-	1/4/4/4	-
7	NAG	B	1750	1	-	0/6/23/26	0/1/1/1
10	GOL	B	3901[B]	-	-	2/4/4/4	-
7	NAG	B	2760	1	-	2/6/23/26	0/1/1/1
7	NAG	B	700	1	-	0/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	2900	3DM	C6-C1	7.44	1.50	1.40
9	B	2910	3DM	C6-C1	6.61	1.49	1.40
9	A	2900	3DM	C2-C1	6.40	1.49	1.40
9	B	2910	3DM	C2-C1	6.06	1.48	1.40
7	B	2760	NAG	C1-C2	2.58	1.55	1.52

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2900	3DM	O3-C6-C1	6.84	121.68	114.53
7	B	1750	NAG	C1-O5-C5	4.94	118.81	112.19
9	A	2900	3DM	O2-C2-C1	4.87	119.63	114.53
9	B	2910	3DM	C8-O3-C6	4.84	124.61	117.51
9	B	2910	3DM	O3-C6-C1	4.37	119.10	114.53

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	3901[B]	GOL	O1-C1-C2-C3
7	A	700	NAG	O5-C5-C6-O6
7	A	700	NAG	C4-C5-C6-O6
9	A	2900	3DM	C1-C2-O2-C7
10	A	3902[A]	GOL	C1-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	2900	3DM	2	0
10	A	3902[A]	GOL	1	0
7	B	1750	NAG	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	558/559 (99%)	-0.15	1 (0%) 91 91	7, 16, 26, 40	4 (0%)
1	B	558/559 (99%)	-0.04	3 (0%) 87 88	9, 17, 27, 38	3 (0%)
All	All	1116/1118 (99%)	-0.09	4 (0%) 88 89	7, 17, 27, 40	7 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	GLU	2.9
1	A	463	VAL	2.2
1	B	2	PRO	2.1
1	B	16	GLY	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	OHI	A	98	11/12	0.87	0.11	16,19,25,26	0
1	OHI	B	98	11/12	0.88	0.10	15,18,27,31	0

6.3 Carbohydrates [i](#)

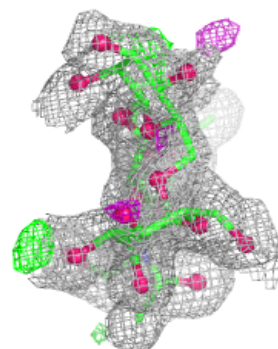
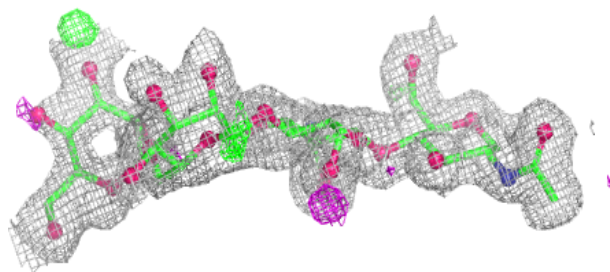
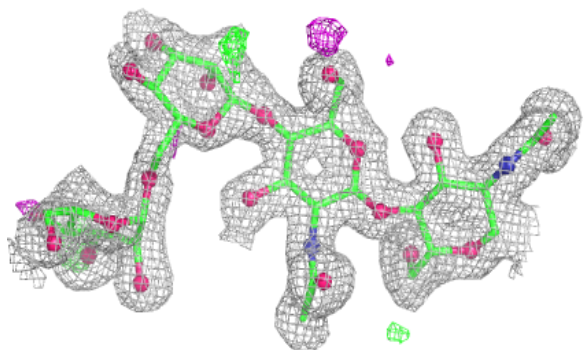
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MAN	H	4	11/12	0.69	0.14	40,45,49,52	0
4	MAN	J	3	11/12	0.73	0.12	41,45,46,46	0
3	NAG	G	2	14/15	0.74	0.12	40,44,46,47	0
2	MAN	C	4	11/12	0.75	0.15	32,36,37,40	0
2	MAN	C	3	11/12	0.75	0.13	28,32,35,38	0
4	MAN	E	3	11/12	0.76	0.12	39,43,45,48	0
3	NAG	I	1	14/15	0.81	0.12	30,32,34,34	0
2	MAN	H	3	11/12	0.82	0.11	34,39,42,43	0
3	NAG	I	2	14/15	0.83	0.11	28,37,38,39	0
3	NAG	K	2	14/15	0.83	0.11	33,37,41,41	0
3	NAG	D	1	14/15	0.84	0.12	25,27,31,34	0
3	NAG	D	2	14/15	0.86	0.10	24,31,33,34	0
3	NAG	F	2	14/15	0.86	0.10	31,35,40,40	0
3	NAG	G	1	14/15	0.86	0.10	24,30,33,36	0
3	NAG	K	1	14/15	0.89	0.09	17,21,28,29	0
4	NAG	J	2	14/15	0.90	0.09	24,29,33,36	0
4	NAG	E	2	14/15	0.91	0.09	21,27,29,33	0
3	NAG	F	1	14/15	0.91	0.08	17,19,26,29	0
2	NAG	H	2	14/15	0.93	0.08	13,21,31,32	0
2	NAG	C	2	14/15	0.94	0.07	13,18,23,26	0
4	NAG	E	1	14/15	0.95	0.06	15,19,21,21	0
2	NAG	C	1	14/15	0.96	0.05	10,12,14,14	0
4	NAG	J	1	14/15	0.96	0.06	17,20,24,24	0
2	NAG	H	1	14/15	0.97	0.05	11,13,16,18	0

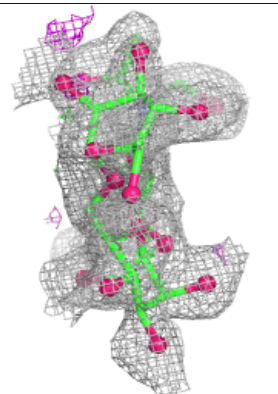
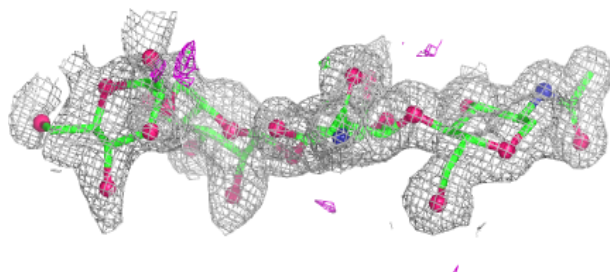
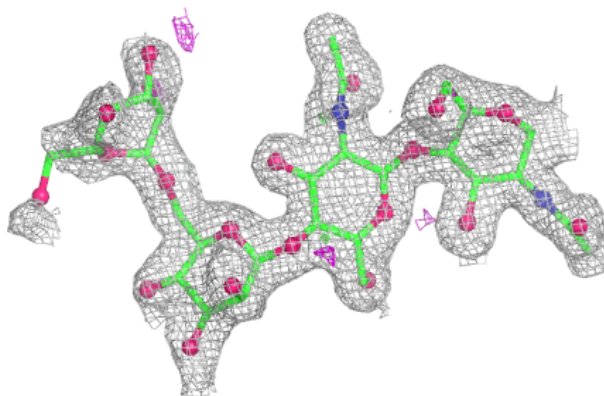
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

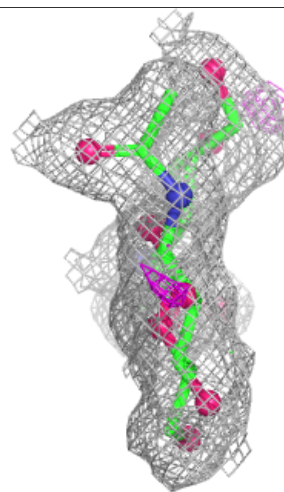
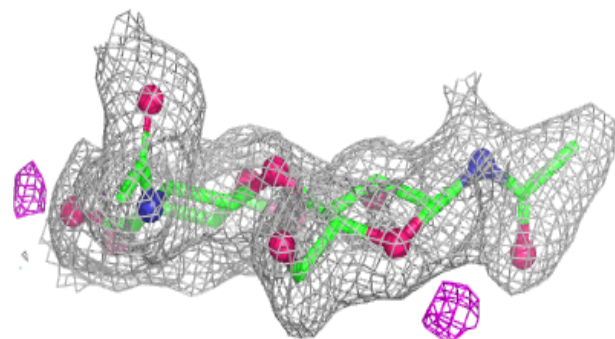
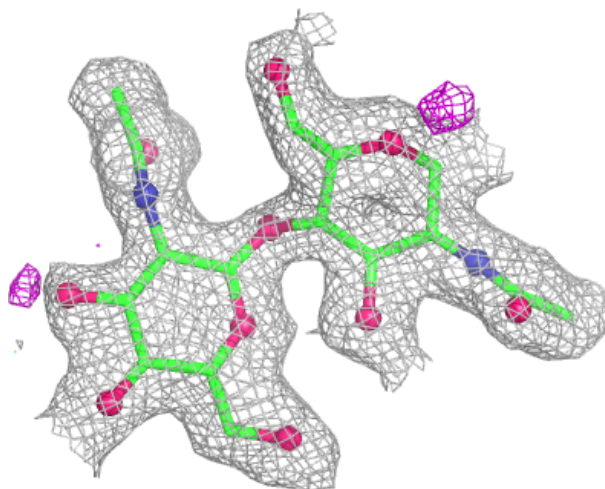
**Electron density around Chain H:**

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and green (positive)



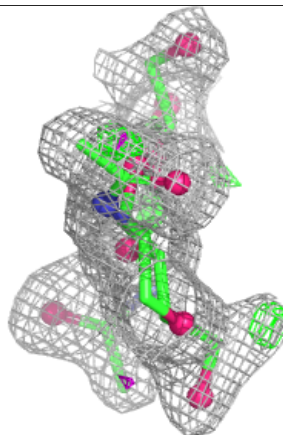
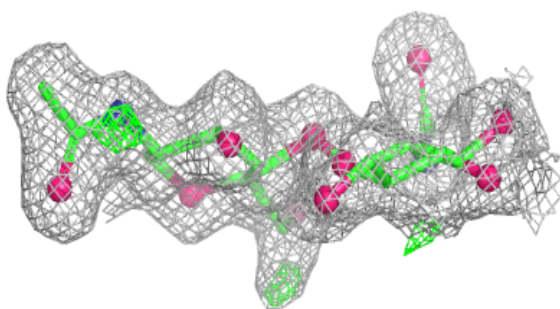
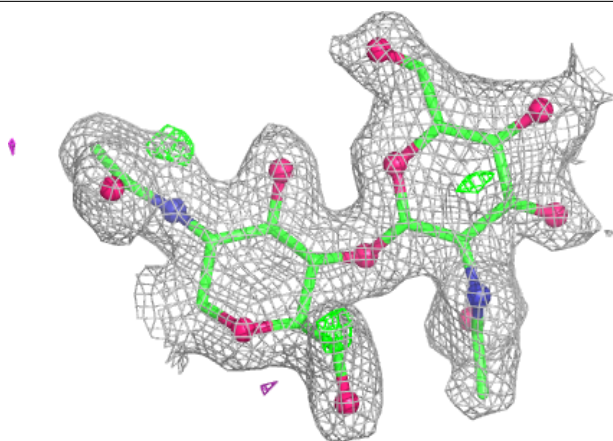
Electron density around Chain D:

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

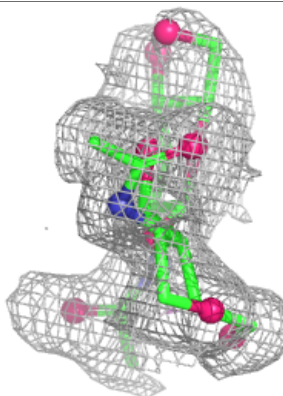
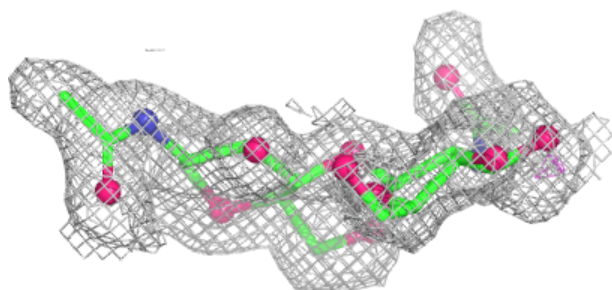
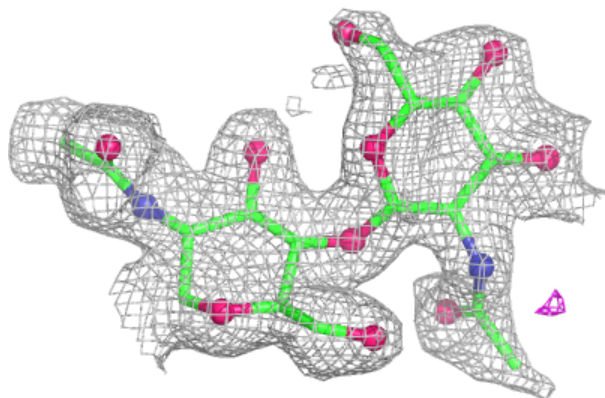


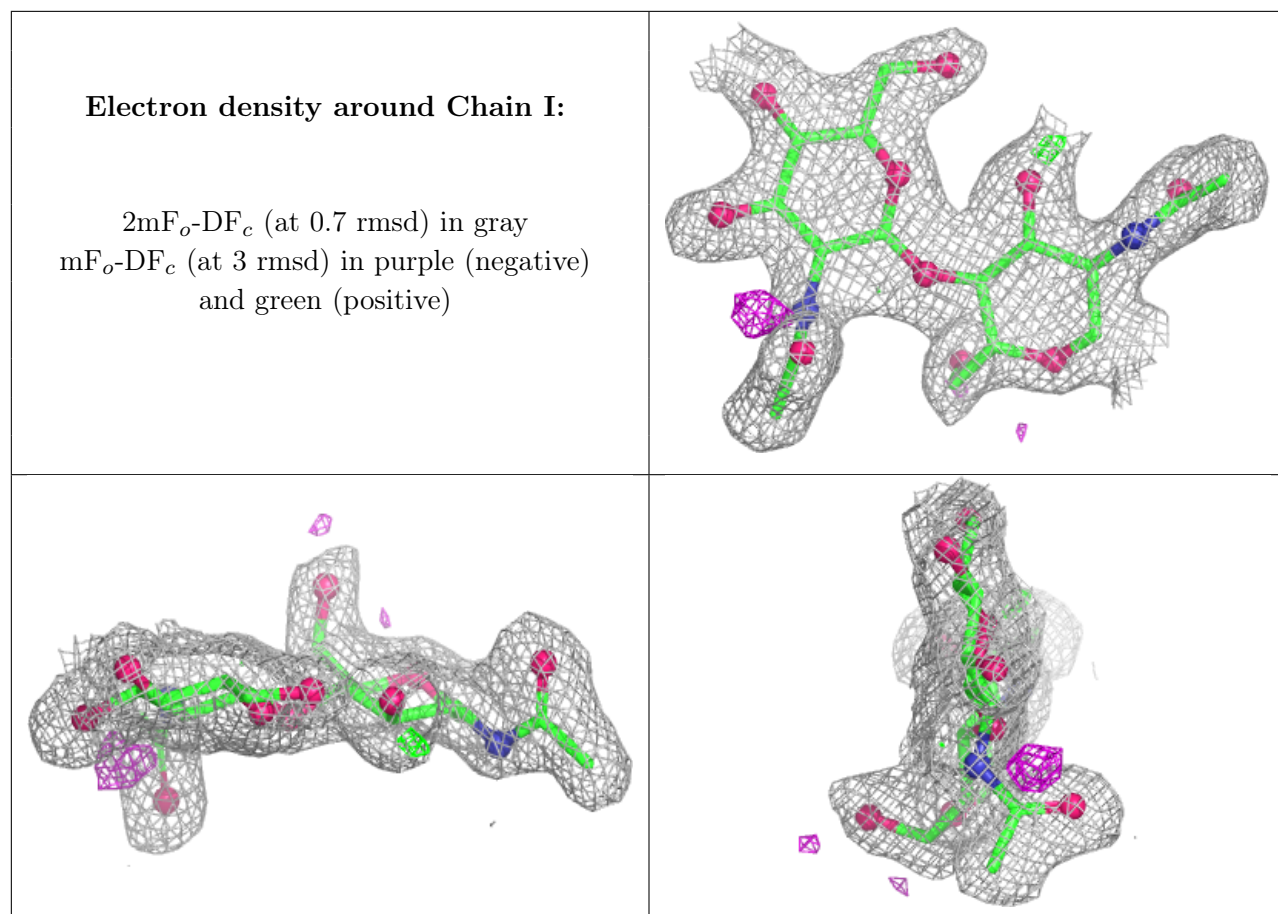
Electron density around Chain F:

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

**Electron density around Chain G:**

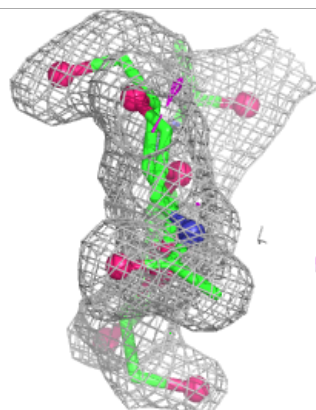
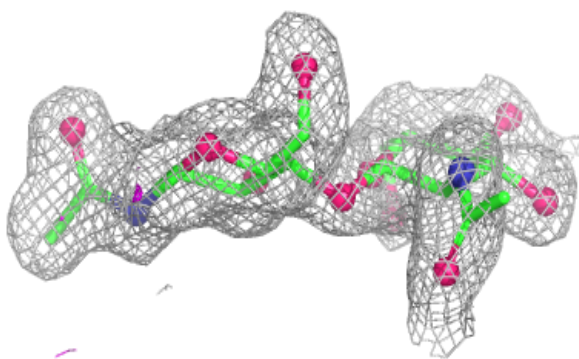
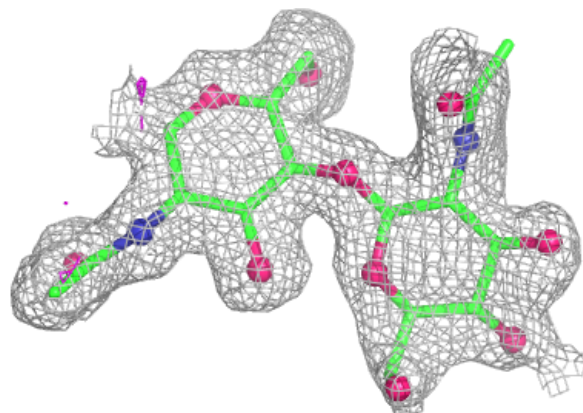
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





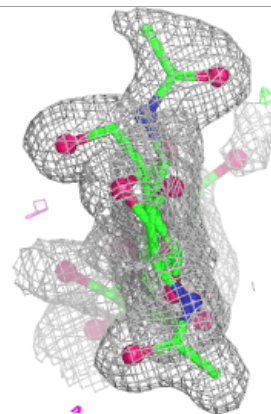
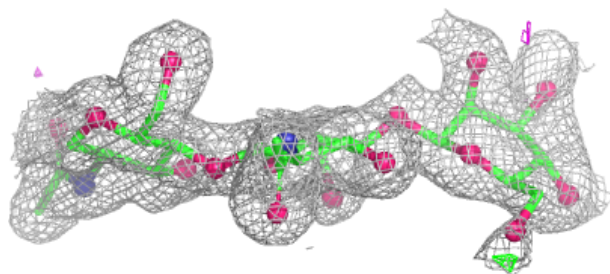
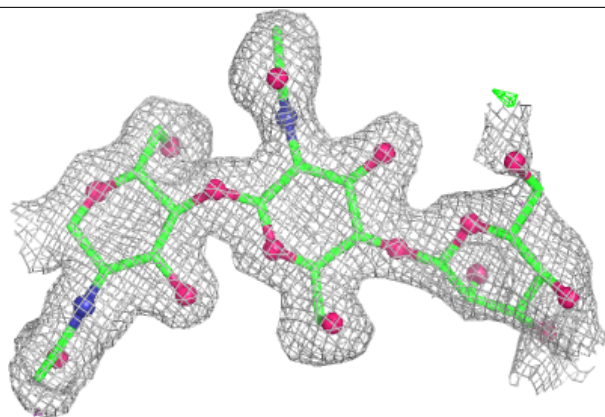
Electron density around Chain K:

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

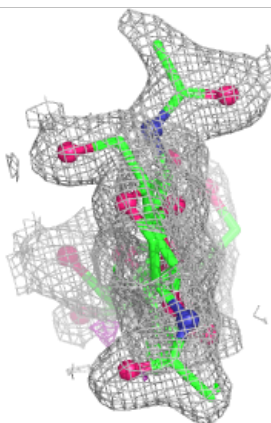
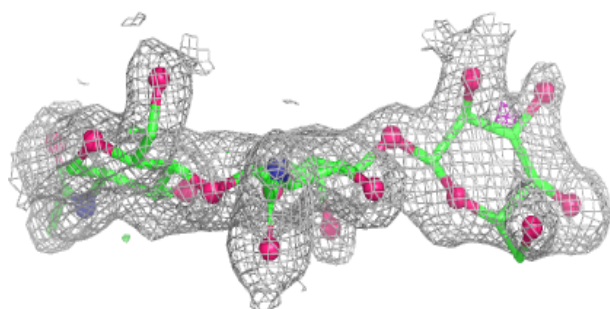
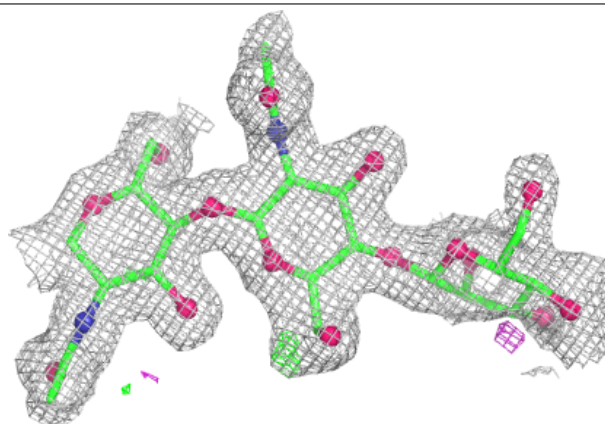


Electron density around Chain E:

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

**Electron density around Chain J:**

$2mF_o-DF_c$ (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
10	GOL	A	3902[A]	6/6	0.69	0.16	31,32,33,33	6
9	3DM	B	2910	11/11	0.72	0.17	43,46,46,46	0
10	GOL	B	3901[B]	6/6	0.72	0.15	25,26,27,27	6
9	3DM	A	2900	11/11	0.75	0.18	37,40,42,44	0
7	NAG	B	700	14/15	0.81	0.12	25,27,34,35	0
7	NAG	A	750	14/15	0.83	0.11	33,38,41,43	0
7	NAG	A	700	14/15	0.83	0.12	23,27,31,35	0
8	SO4	B	4802	5/5	0.84	0.12	53,54,55,55	0
8	SO4	A	3801	5/5	0.85	0.12	44,44,46,47	0
7	NAG	B	1750	14/15	0.86	0.10	23,25,29,29	0
7	NAG	B	2760	14/15	0.86	0.10	23,29,32,34	0
8	SO4	A	3800	5/5	0.87	0.11	44,46,47,47	0
6	CL	B	610	1/1	0.97	0.10	24,24,24,24	0
6	CL	A	610	1/1	0.99	0.07	22,22,22,22	0
5	CU	B	603	1/1	1.00	0.01	13,13,13,13	0
5	CU	B	604	1/1	1.00	0.01	17,17,17,17	0
5	CU	A	601	1/1	1.00	0.02	14,14,14,14	0
5	CU	A	602	1/1	1.00	0.01	16,16,16,16	0
5	CU	A	603	1/1	1.00	0.03	13,13,13,13	0
5	CU	A	604	1/1	1.00	0.02	17,17,17,17	0
5	CU	B	601	1/1	1.00	0.01	14,14,14,14	0
5	CU	B	602	1/1	1.00	0.03	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.