



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 10, 2020 – 10:41 AM BST

PDB ID : 3FU7
Title : Melanocarpus albomyces laccase crystal soaked (4 sec) with 2,6-dimethoxyphenol
Authors : Kallio, J.P.; Hakulinen, N.; Rouvinen, J.
Deposited on : 2009-01-14
Resolution : 1.67 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 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
buster-report : 1.1.7 (2018)
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

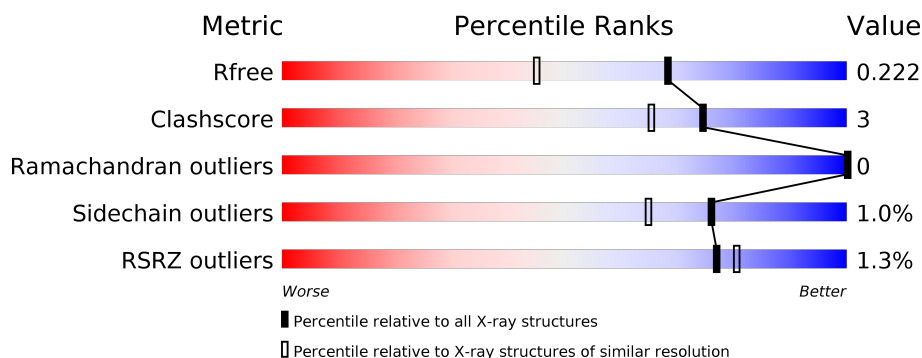
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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.



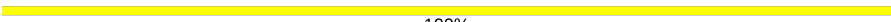
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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 $\leq 5\%$. 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	<div> <div>%</div> <div> <div></div> <div>94%</div> <div>6%</div> </div> </div>
2	B	559	<div> <div>%</div> <div> <div></div> <div>96%</div> <div>.</div> </div> </div>
3	C	4	<div> <div></div> <div>50%</div> <div>50%</div> </div>
3	H	4	<div> <div></div> <div>50%</div> <div>25%</div> <div>25%</div> </div>
4	D	2	<div> <div></div> <div>100%</div> </div>
4	F	2	<div> <div></div> <div>100%</div> </div>

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Mol	Chain	Length	Quality of chain
4	G	2	 100%
4	I	2	 100%
4	K	2	 100%
5	E	3	 100%
5	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
12	D2M	B	2100[A]	-	-	X	-
3	MAN	C	3	X	-	-	-
3	MAN	H	3	X	-	-	-
5	MAN	E	3	X	-	-	-
5	MAN	J	3	X	-	-	-

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 10365 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
1	A	559	Total	C	N	O	S	0	13	0
			4478	2823	785	853	17			

- Molecule 2 is a protein called Laccase-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	559	Total	C	N	O	S	0	13	0
			4472	2822	782	851	17			

- Molecule 3 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
3	C	4	Total	C	N	O	0	0	0
			50	28	2	20			
3	H	4	Total	C	N	O	0	0	0
			50	28	2	20			

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



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

- Molecule 5 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
5	E	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

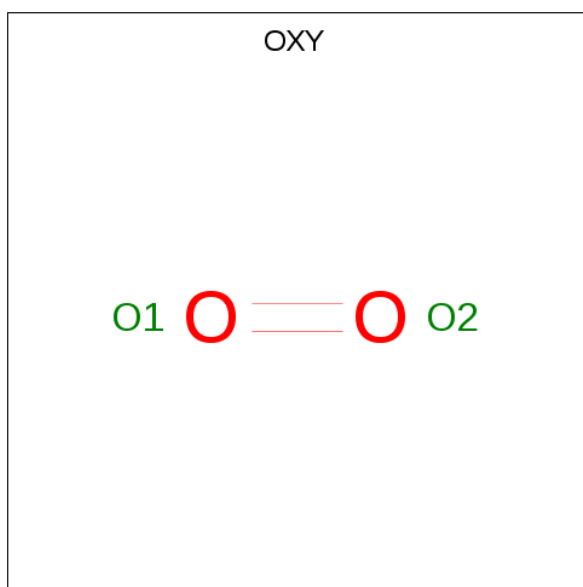
- Molecule 6 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

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

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 8 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	O	0	0
			2	2		
8	B	1	Total	O	0	0
			2	2		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



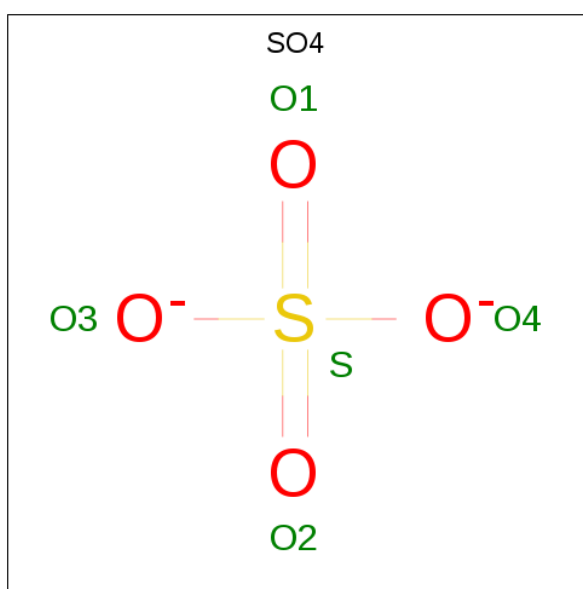
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			14	8	1	5		

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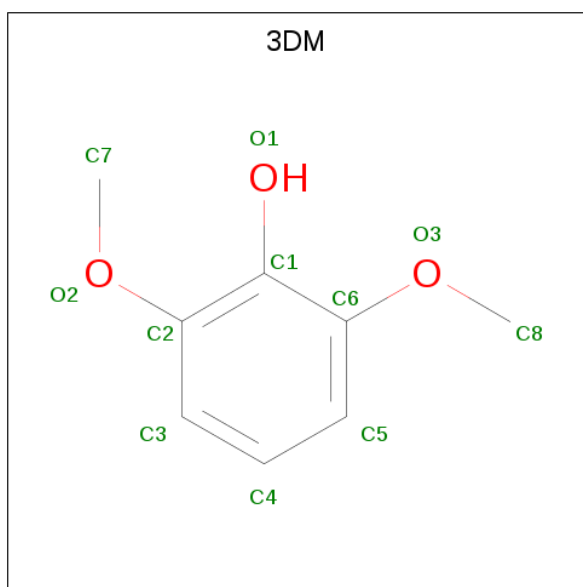
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



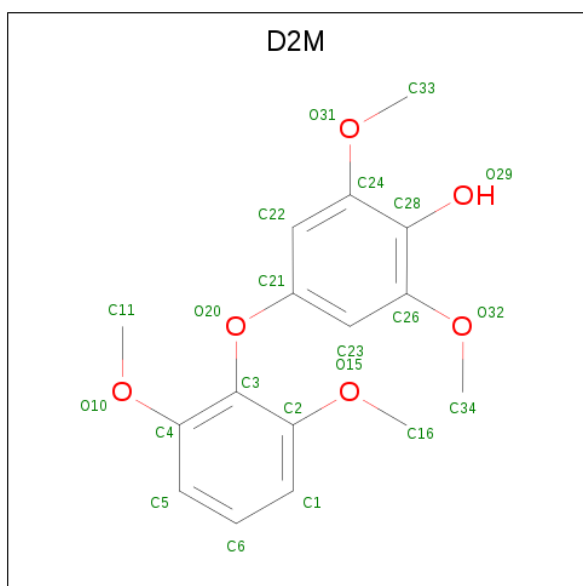
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	O	S	0	0
			5	4	1		
10	A	1	Total	O	S	0	0
			5	4	1		
10	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 11 is 2,6-dimethoxyphenol (three-letter code: 3DM) (formula: C₈H₁₀O₃).



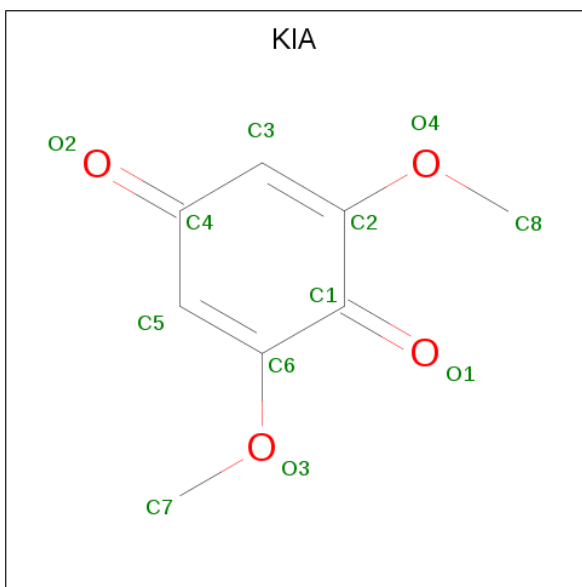
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	1
			11	8	3		

- Molecule 12 is 4-(2,6-dimethoxyphenoxy)-2,6-dimethoxyphenol (three-letter code: D2M) (formula: $C_{16}H_{18}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	C	O	0	1
			22	16	6		

- Molecule 13 is 2,6-dimethoxycyclohexa-2,5-diene-1,4-dione (three-letter code: KIA) (formula: $C_8H_8O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	C	O	0	1
			12	8	4		

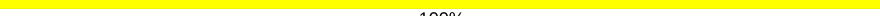
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	506	Total	O	0	0
			506	506		
14	B	447	Total	O	0	0
			447	447		

Chain D:  100%

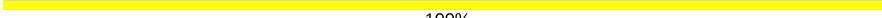
MAG1
MAG2

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

Chain F:  100%

MAG1
MAG2

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

Chain G:  100%


MAG1
MAG2

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

Chain I:  100%

MAG1
MAG2

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

Chain K:  100%

MAG1
MAG2

- Molecule 5: alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:  100%

MAG1
MAG2
MAG3

- Molecule 5: 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	174.12Å 62.10Å 124.63Å 90.00° 96.36° 90.00°	Depositor
Resolution (Å)	19.61 – 1.67 19.60 – 1.67	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.61-1.67) 97.5 (19.60-1.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 1.67Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.189 , 0.220 0.190 , 0.222	Depositor DCC
R_{free} test set	7468 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	13.7	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10365	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% 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: OHI, CL, OXY, D2M, SO4, 3DM, KIA, MAN, CU, NAG

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	0.55	0/4603	0.69	2/6316 (0.0%)
2	B	0.54	0/4610	0.67	0/6329
All	All	0.54	0/9213	0.68	2/12645 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	ASP	CB-CG-OD2	-5.28	113.55	118.30
1	A	174	ASP	CB-CG-OD1	5.10	122.89	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4478	0	4201	27	0
2	B	4472	0	4199	29	0
3	C	50	0	43	0	0
3	H	50	0	43	3	0
4	D	28	0	25	1	0
4	F	28	0	25	0	0
4	G	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	28	0	25	0	0
4	K	28	0	25	0	0
5	E	39	0	34	0	0
5	J	39	0	34	0	0
6	A	4	0	0	0	0
6	B	4	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	2	0	0	0	0
8	B	2	0	0	0	0
9	A	28	0	26	0	0
9	B	42	0	39	0	0
10	A	10	0	0	0	0
10	B	5	0	0	0	0
11	A	11	0	3	3	0
12	B	22	0	13	9	0
13	B	12	0	8	5	0
14	A	506	0	0	6	0
14	B	447	0	0	6	0
All	All	10365	0	8768	58	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 3.

The worst 5 of 58 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)
2:B:68[A]:ASN:OD1	14:B:880:HOH:O	1.62	1.14
1:A:224:ARG:HH11	1:A:224:ARG:HG3	1.27	0.98
2:B:427[A]:PHE:CZ	12:B:2100[A]:D2M:O15	2.17	0.97
2:B:30[A]:THR:HG21	2:B:75:ASP:OD1	1.72	0.89
1:A:505:ILE:HA	14:A:986:HOH:O	1.73	0.88

There are no symmetry-related clashes.

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	A	569/559 (102%)	555 (98%)	14 (2%)	0	100	100
2	B	570/559 (102%)	554 (97%)	16 (3%)	0	100	100
All	All	1139/1118 (102%)	1109 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	490/477 (103%)	486 (99%)	4 (1%)	81	72
2	B	491/478 (103%)	484 (99%)	7 (1%)	67	51
All	All	981/955 (103%)	970 (99%)	11 (1%)	76	61

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	100	LYS
2	B	109	ASN
2	B	244	ASN
1	A	224	ARG
2	B	140	HIS

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

Mol	Chain	Res	Type
1	A	311	HIS
1	A	550	ASN
2	B	99	GLN
2	B	144	GLN
2	B	455	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	8,11,12	1.51	2 (25%)	5,14,16	1.77	2 (40%)

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	-	0/3/15/17	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	OHI	O12-CE1	3.20	1.28	1.24
1	A	98	OHI	CE1-ND1	-2.10	1.33	1.39

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	98	OHI	O12-CE1-ND1	-2.83	118.80	126.01
1	A	98	OHI	CB-CA-C	-2.07	107.59	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

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	$\# Z > 2$
3	NAG	C	1	1,3	14,14,15	0.75	0	17,19,21	0.82	0
3	NAG	C	2	3	14,14,15	0.50	0	17,19,21	0.93	1 (5%)
3	MAN	C	3	3	11,11,12	0.53	0	15,15,17	1.28	2 (13%)
3	MAN	C	4	3	11,11,12	0.67	0	15,15,17	0.89	0
4	NAG	D	1	1,4	14,14,15	0.56	0	17,19,21	1.31	2 (11%)
4	NAG	D	2	4	14,14,15	0.52	0	17,19,21	0.87	0
5	NAG	E	1	1,5	14,14,15	0.73	1 (7%)	17,19,21	0.88	0
5	NAG	E	2	5	14,14,15	0.51	0	17,19,21	1.14	1 (5%)
5	MAN	E	3	5	11,11,12	0.67	0	15,15,17	1.48	3 (20%)
4	NAG	F	1	1,4	14,14,15	0.55	0	17,19,21	1.35	2 (11%)
4	NAG	F	2	4	14,14,15	0.55	0	17,19,21	1.01	1 (5%)
4	NAG	G	1	1,4	14,14,15	0.76	0	17,19,21	1.02	1 (5%)
4	NAG	G	2	4	14,14,15	0.50	0	17,19,21	1.01	1 (5%)
3	NAG	H	1	3,2	14,14,15	0.48	0	17,19,21	1.03	1 (5%)
3	NAG	H	2	3	14,14,15	0.63	0	17,19,21	0.94	0
3	MAN	H	3	3	11,11,12	0.60	0	15,15,17	1.00	0
3	MAN	H	4	3	11,11,12	0.60	0	15,15,17	1.50	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	I	1	2,4	14,14,15	0.54	0	17,19,21	1.13	2 (11%)
4	NAG	I	2	4	14,14,15	0.55	0	17,19,21	1.03	1 (5%)
5	NAG	J	1	2,5	14,14,15	0.63	0	17,19,21	1.05	1 (5%)
5	NAG	J	2	5	14,14,15	0.65	0	17,19,21	0.96	1 (5%)
5	MAN	J	3	5	11,11,12	0.58	0	15,15,17	1.07	1 (6%)
4	NAG	K	1	2,4	14,14,15	0.56	0	17,19,21	1.27	1 (5%)
4	NAG	K	2	4	14,14,15	0.52	0	17,19,21	0.96	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. '-' means no outliers of that kind were identified.

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	1	NAG	O5-C1	-2.18	1.40	1.43

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	3	MAN	C1-O5-C5	4.03	117.66	112.19
5	E	3	MAN	C3-C4-C5	3.55	116.57	110.24
4	F	1	NAG	C1-O5-C5	3.46	116.88	112.19
4	G	1	NAG	O5-C1-C2	-3.32	106.05	111.29
3	H	4	MAN	C1-C2-C3	3.10	113.48	109.67

All (4) chirality outliers are listed below:

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

5 of 11 torsion outliers are listed below:

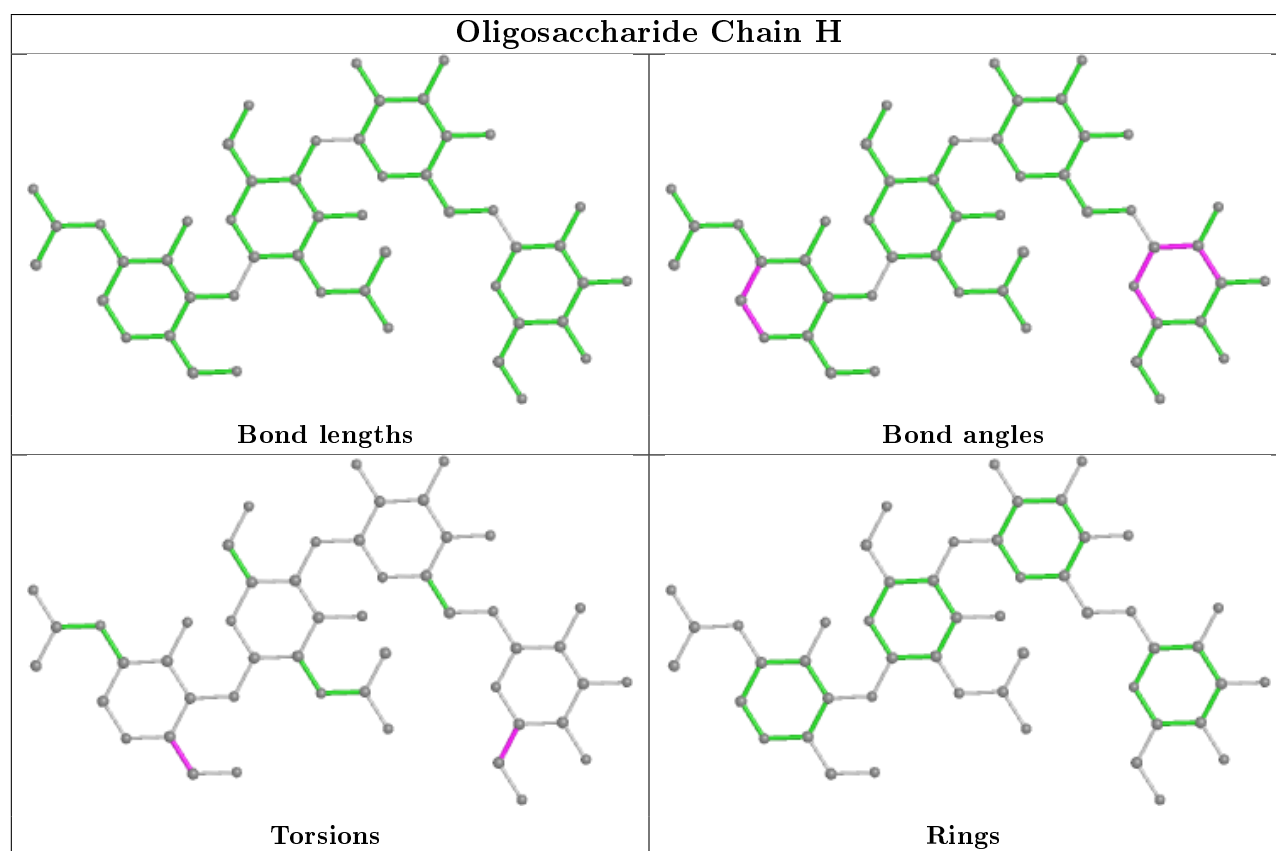
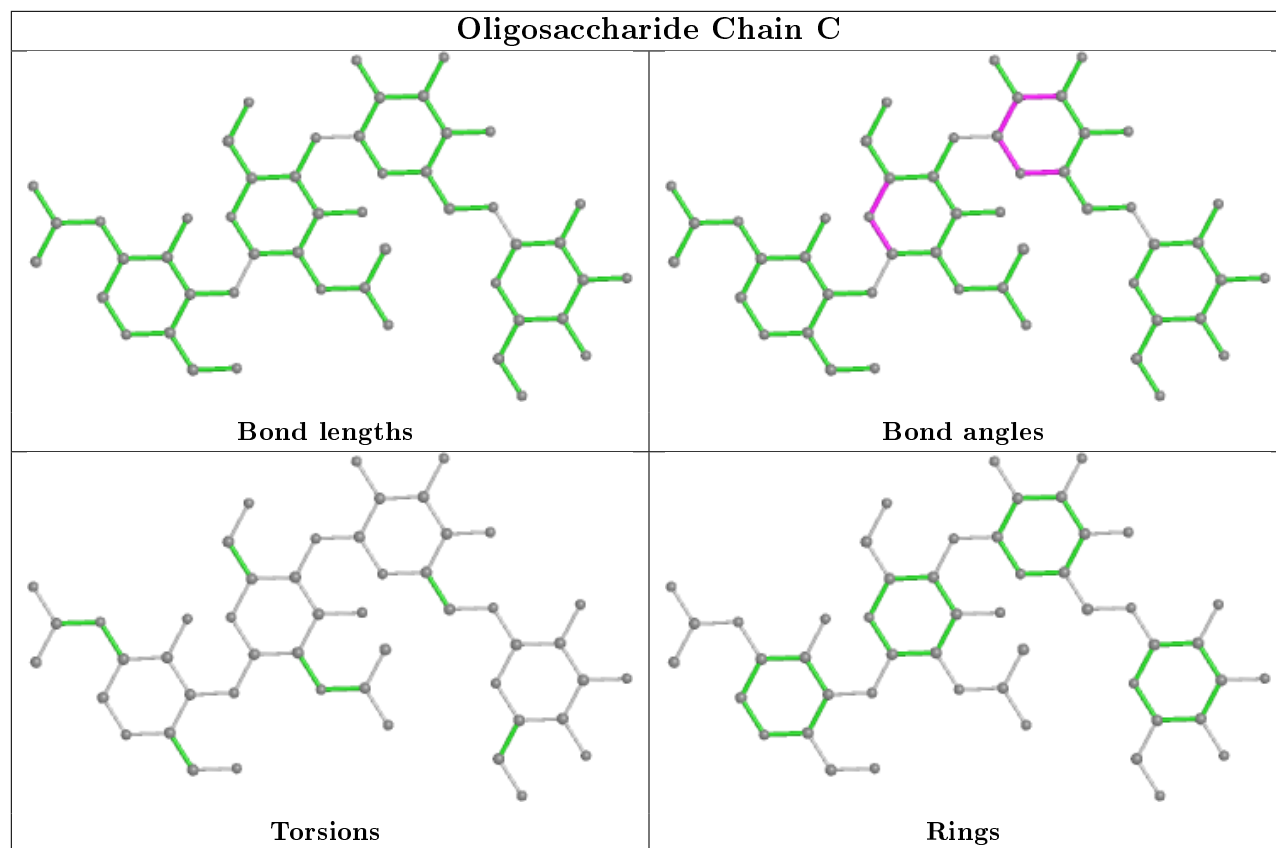
Mol	Chain	Res	Type	Atoms
4	G	1	NAG	O5-C5-C6-O6
5	E	3	MAN	C4-C5-C6-O6
4	D	1	NAG	C4-C5-C6-O6
4	G	1	NAG	C4-C5-C6-O6
5	E	3	MAN	O5-C5-C6-O6

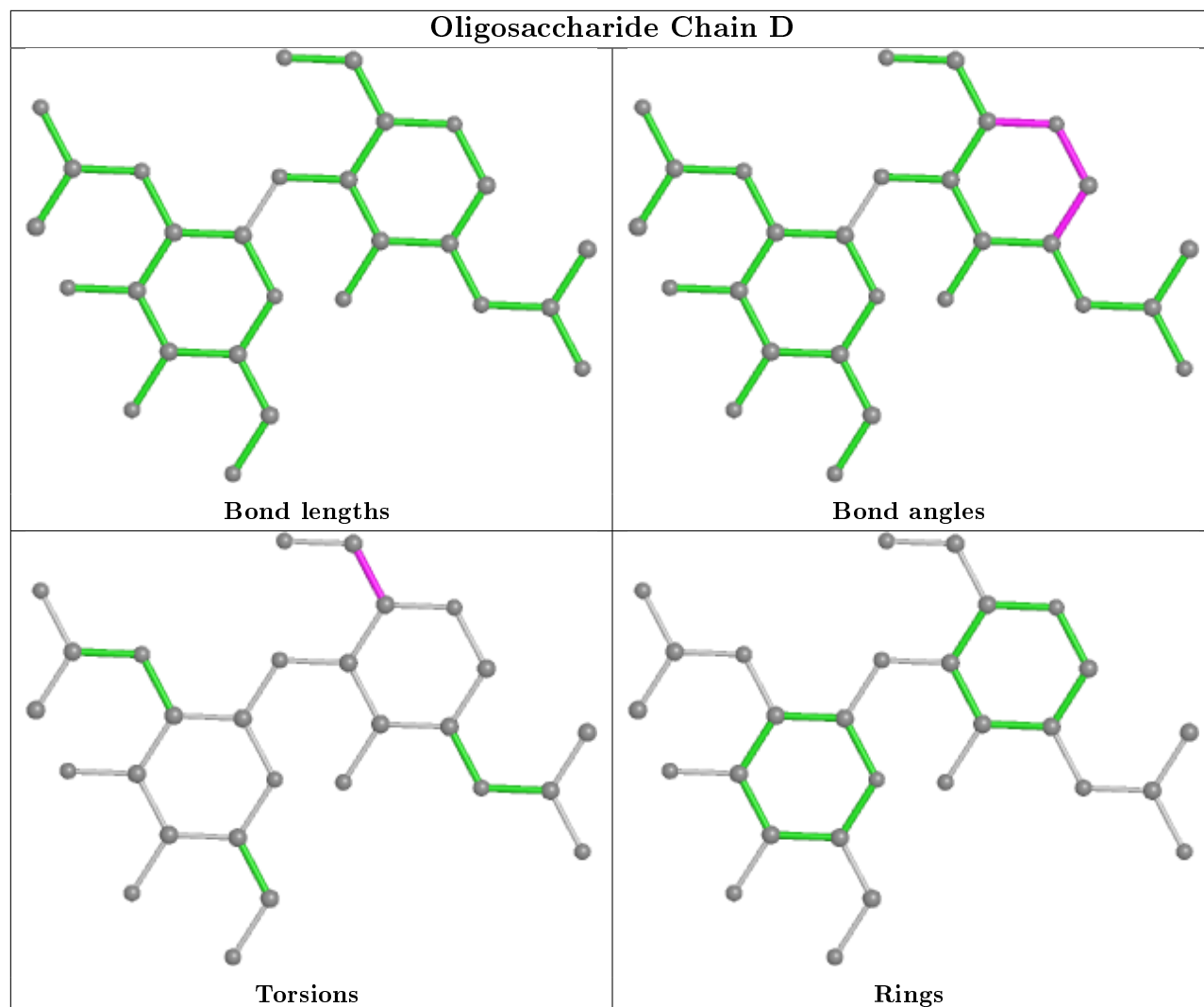
There are no ring outliers.

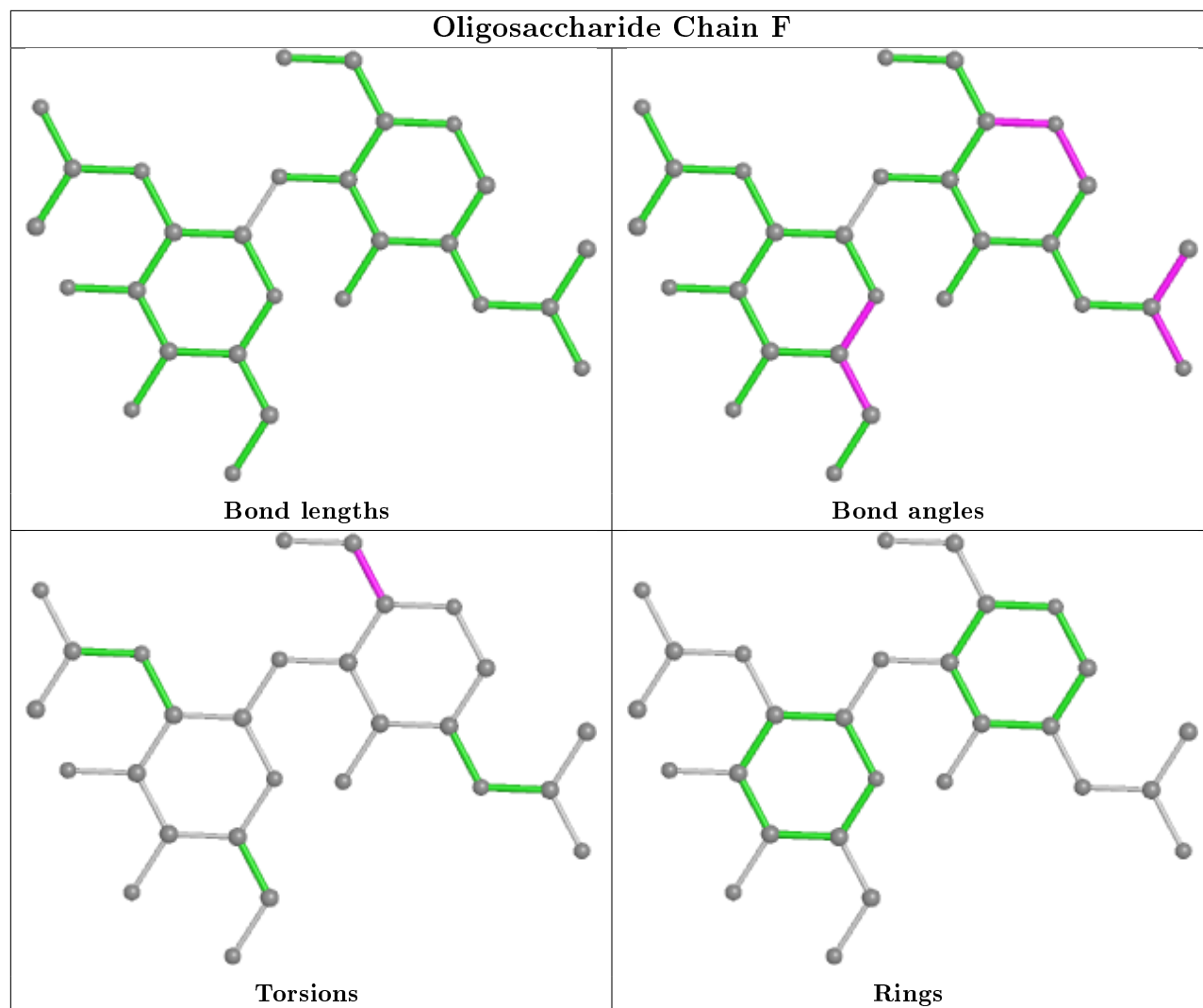
2 monomers are involved in 4 short contacts:

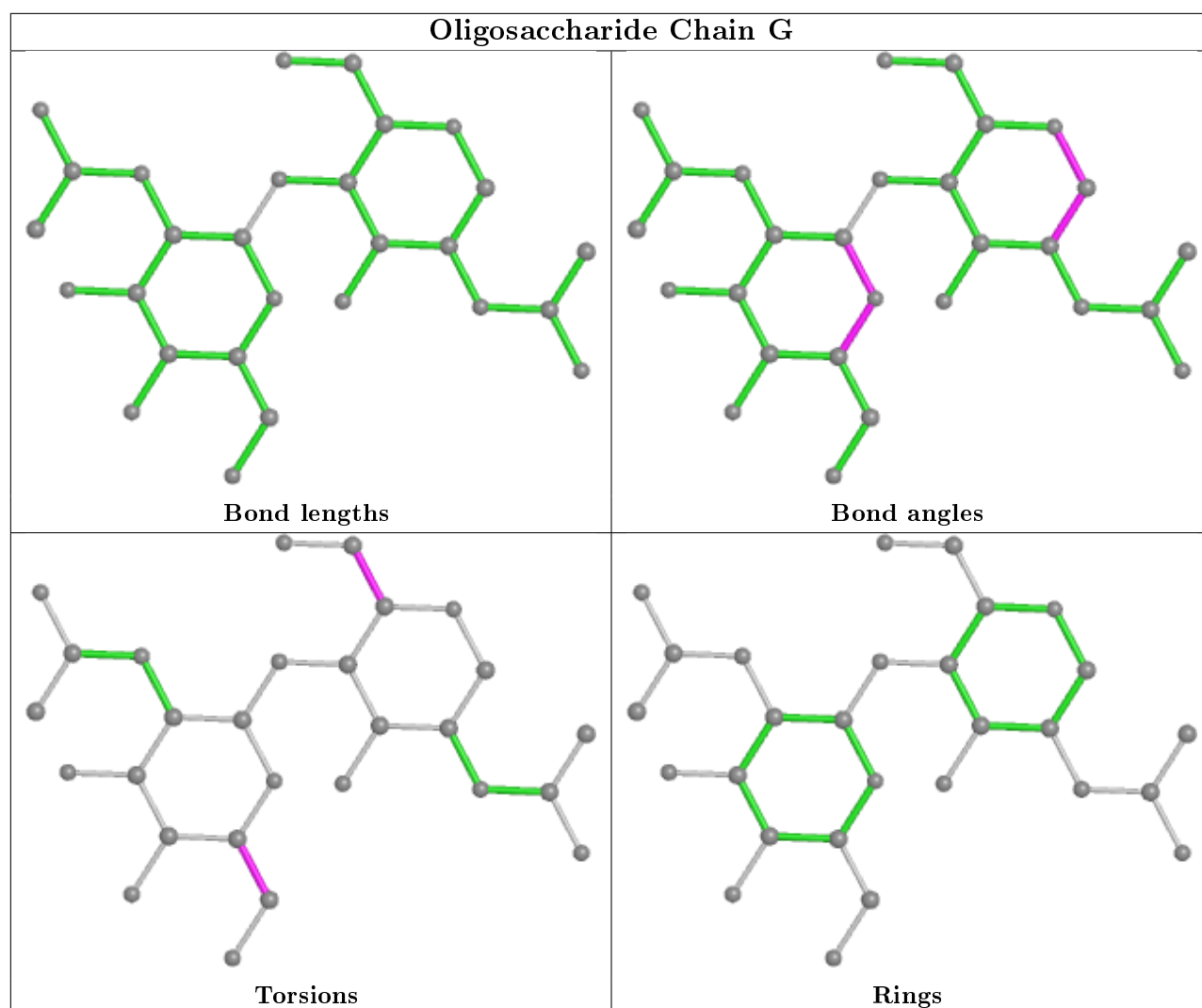
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2	NAG	1	0
3	H	4	MAN	3	0

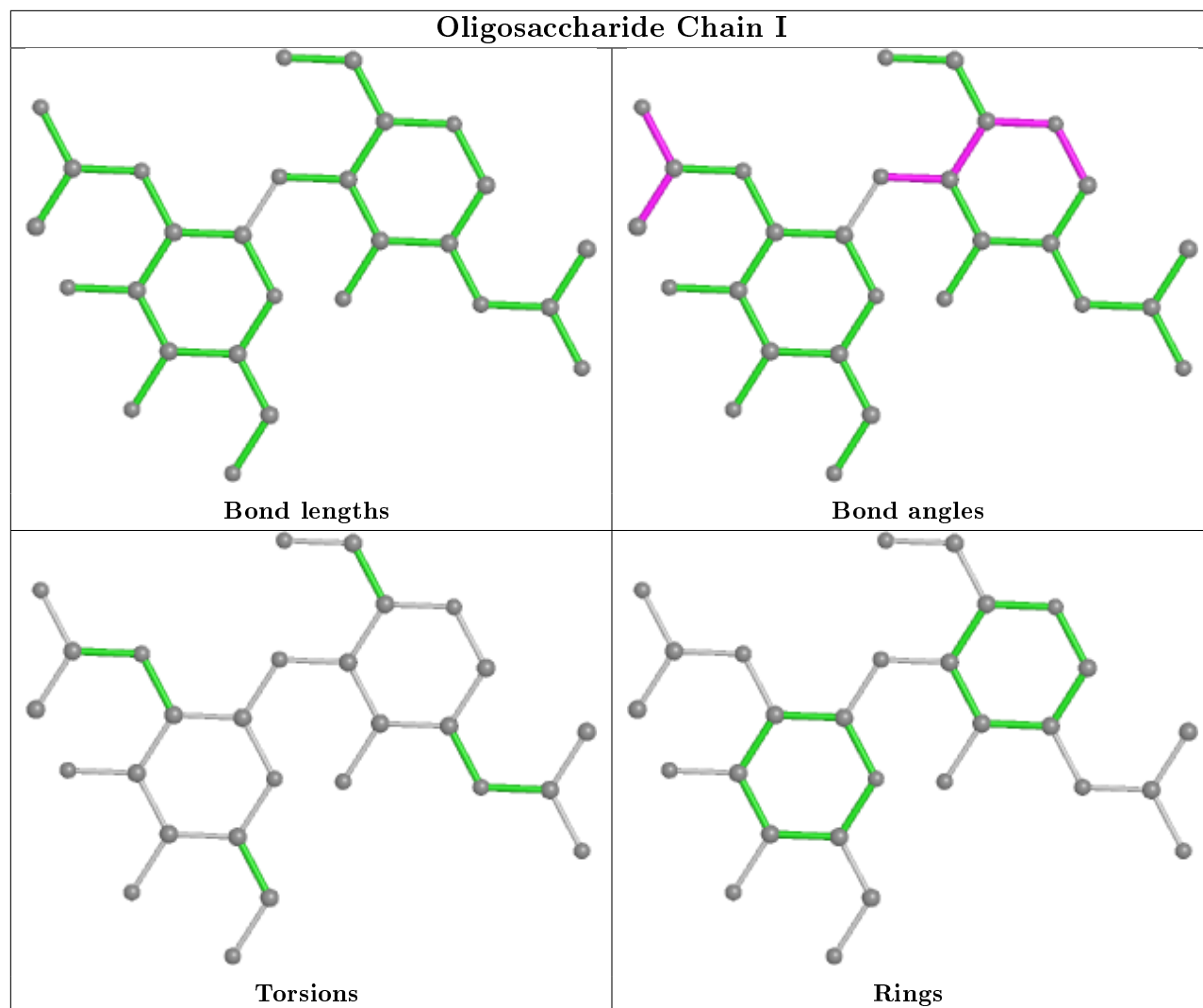
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

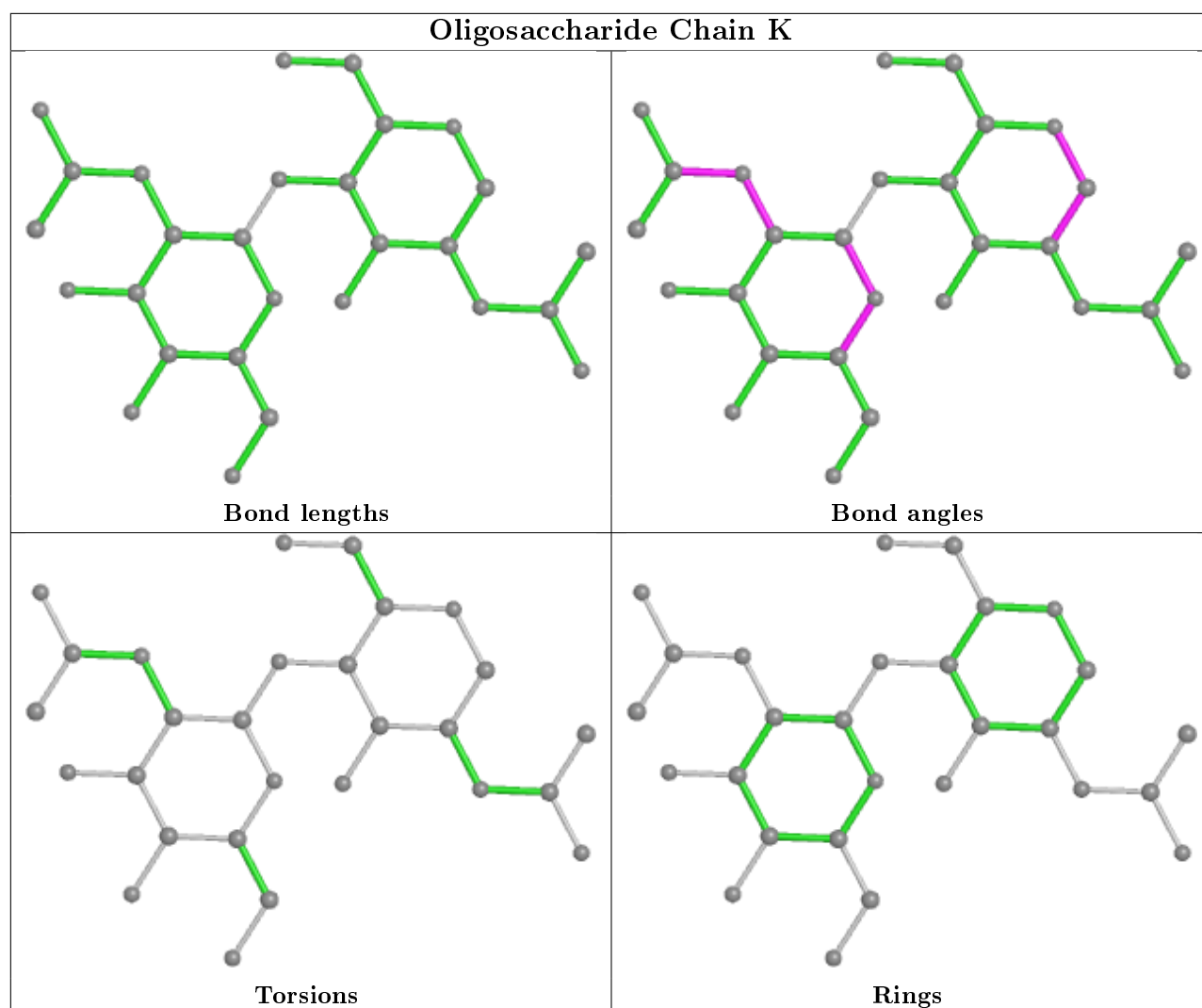


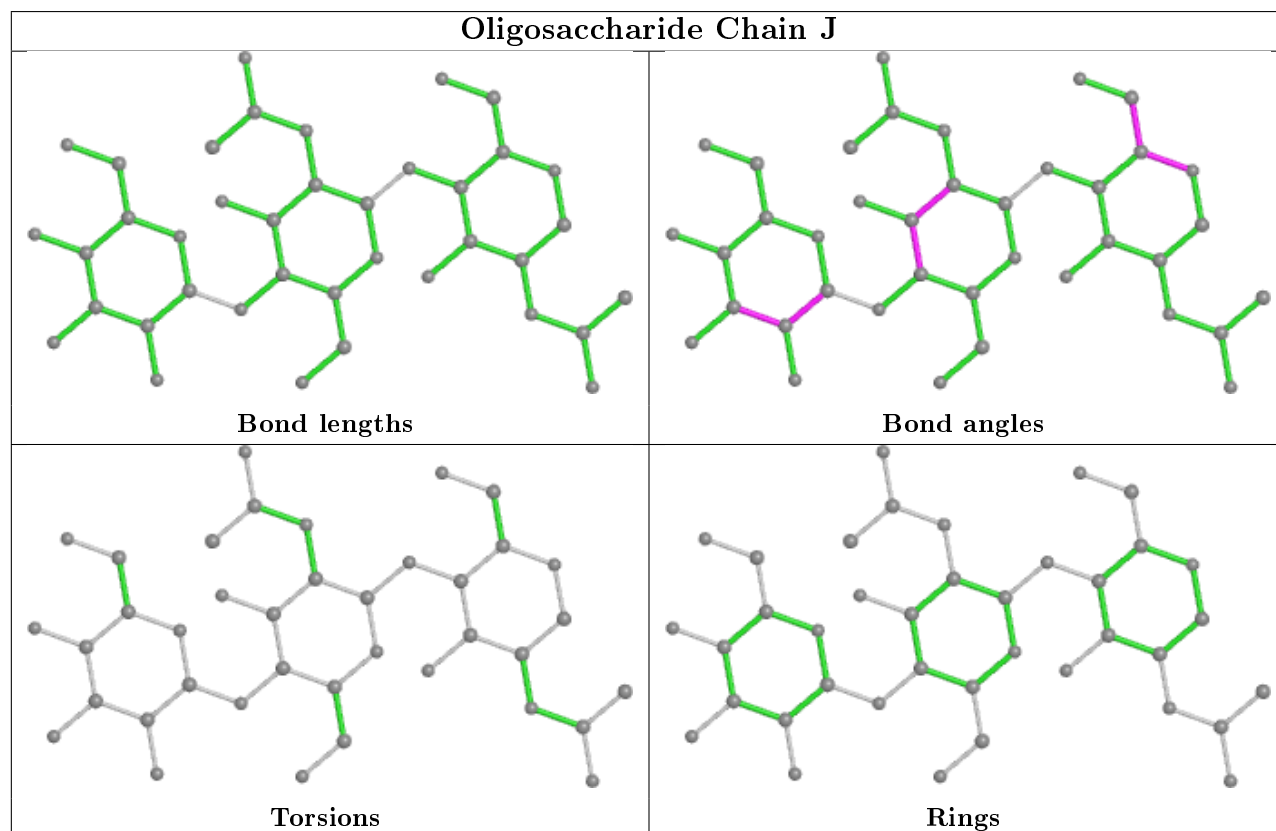
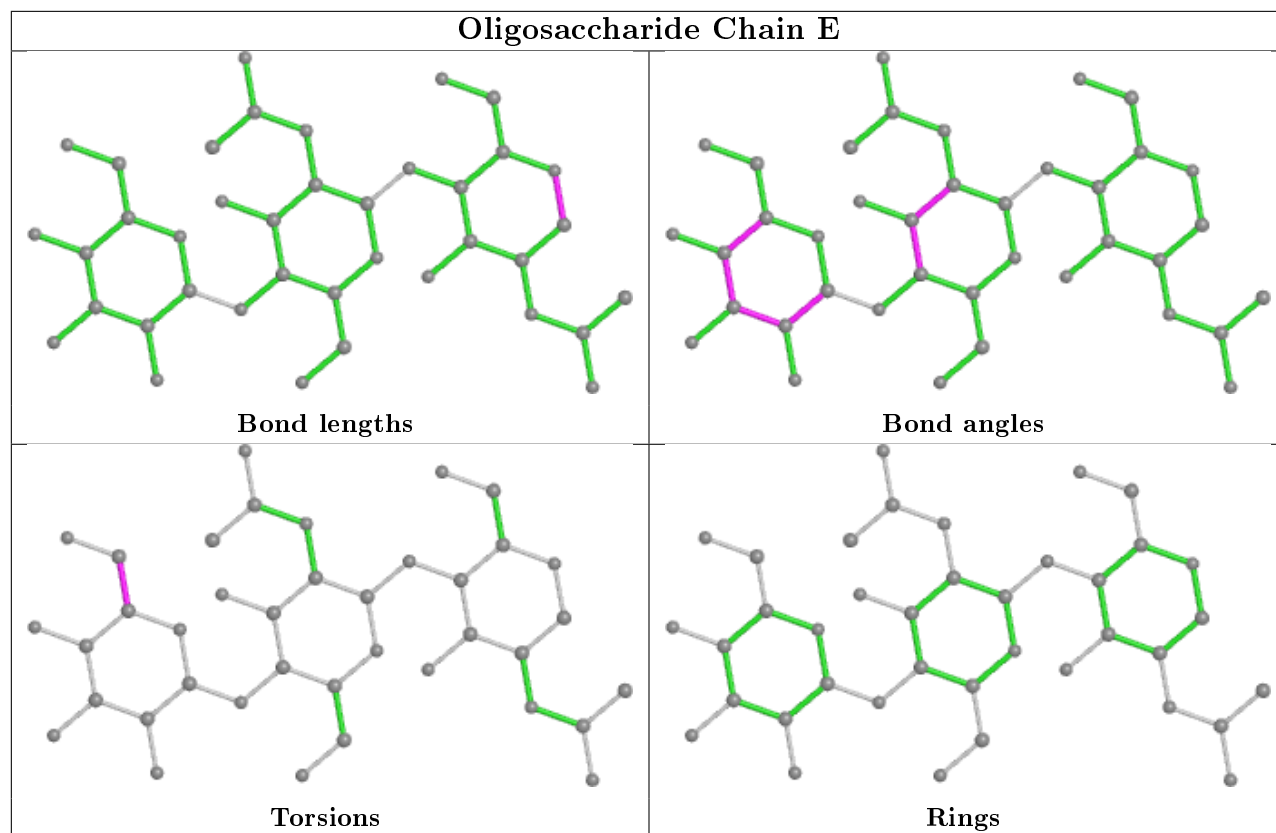












5.6 Ligand geometry

Of 23 ligands modelled in this entry, 10 are monoatomic - leaving 13 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	NAG	B	2760	2	14,14,15	0.60	0	17,19,21	1.04	1 (5%)
11	3DM	A	3900[B]	-	11,11,11	3.08	2 (18%)	14,14,14	3.94	5 (35%)
8	OXY	A	1620	6	1,1,1	0.91	0	-		
10	SO4	A	3801	-	4,4,4	0.15	0	6,6,6	0.12	0
9	NAG	B	700	2	14,14,15	0.68	0	17,19,21	0.99	1 (5%)
10	SO4	A	3800	-	4,4,4	0.14	0	6,6,6	0.11	0
12	D2M	B	2100[A]	-	23,23,23	0.58	0	31,31,31	2.29	13 (41%)
9	NAG	A	750	1	14,14,15	0.62	0	17,19,21	0.94	0
8	OXY	B	1620	6	1,1,1	0.90	0	-		
9	NAG	B	1750	2	14,14,15	0.60	0	17,19,21	1.26	2 (11%)
10	SO4	B	4802	-	4,4,4	0.13	0	6,6,6	0.10	0
9	NAG	A	700	1	14,14,15	0.69	0	17,19,21	1.02	1 (5%)
13	KIA	B	2910[B]	-	12,12,12	1.15	2 (16%)	15,16,16	2.07	7 (46%)

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	NAG	B	2760	2	-	2/6/23/26	0/1/1/1
9	NAG	B	1750	2	-	0/6/23/26	0/1/1/1
9	NAG	A	750	1	-	0/6/23/26	0/1/1/1
9	NAG	B	700	2	-	1/6/23/26	0/1/1/1
12	D2M	B	2100[A]	-	-	8/12/12/12	0/2/2/2
11	3DM	A	3900[B]	-	-	4/4/4/4	0/1/1/1
9	NAG	A	700	1	-	0/6/23/26	0/1/1/1
13	KIA	B	2910[B]	-	-	4/4/20/20	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	3900[B]	3DM	C6-C1	7.57	1.50	1.40
11	A	3900[B]	3DM	C2-C1	6.65	1.49	1.40
13	B	2910[B]	KIA	C3-C4	-2.23	1.40	1.45
13	B	2910[B]	KIA	C5-C4	-2.15	1.40	1.45

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	3900[B]	3DM	O3-C6-C1	10.60	125.23	114.54
12	B	2100[A]	D2M	O31-C24-C28	6.68	121.28	114.54
11	A	3900[B]	3DM	C8-O3-C6	6.01	126.60	117.53
12	B	2100[A]	D2M	O32-C26-C28	5.32	119.91	114.54
11	A	3900[B]	3DM	O2-C2-C1	5.15	119.74	114.54

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	B	2910[B]	KIA	C5-C6-O3-C7
13	B	2910[B]	KIA	C1-C6-O3-C7
13	B	2910[B]	KIA	C1-C2-O4-C8
13	B	2910[B]	KIA	C3-C2-O4-C8
11	A	3900[B]	3DM	C1-C6-O3-C8

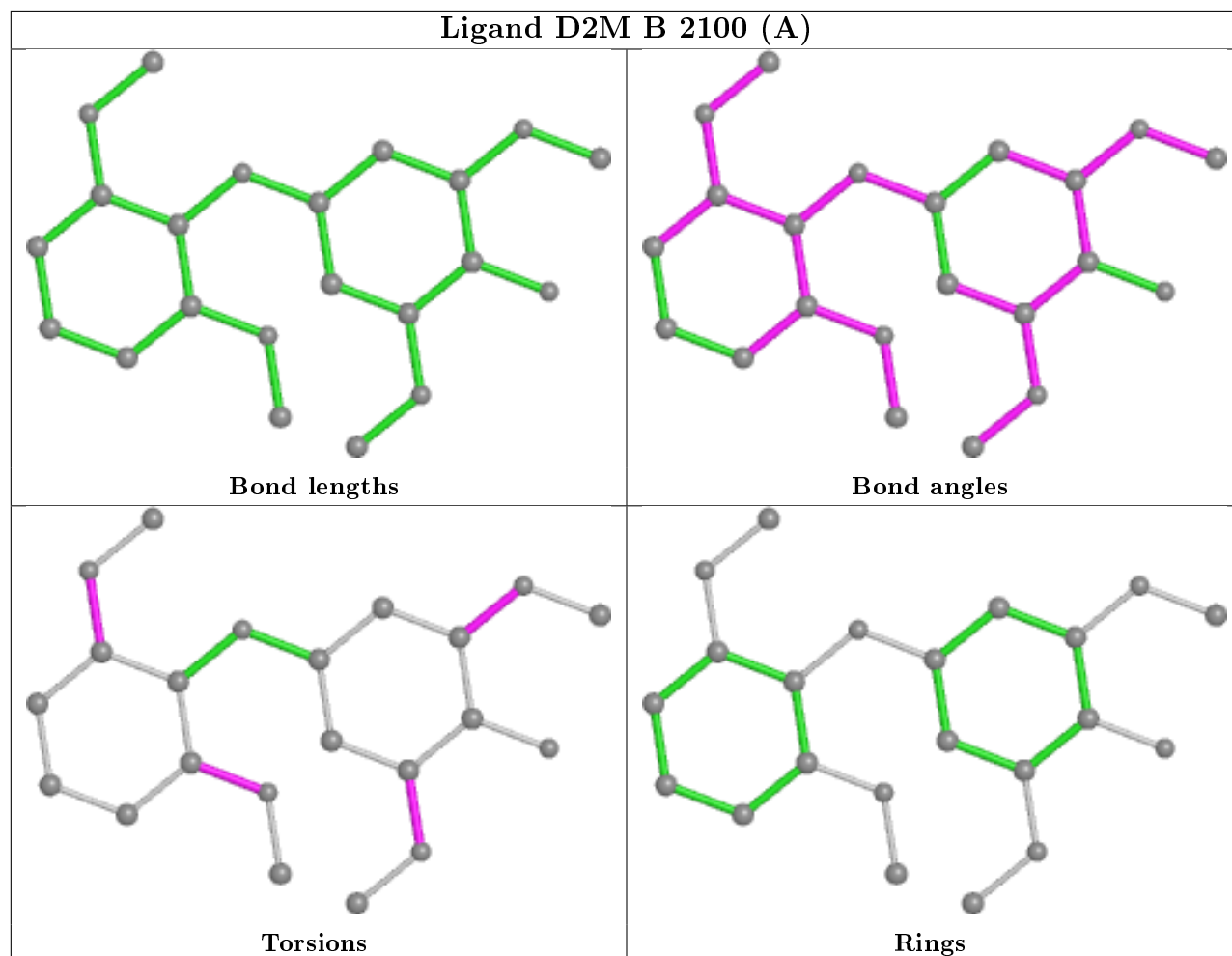
There are no ring outliers.

3 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	3900[B]	3DM	3	0
12	B	2100[A]	D2M	9	0
13	B	2910[B]	KIA	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	558/559 (99%)	-0.11	6 (1%) 80 83	7, 14, 24, 36	0
2	B	559/559 (100%)	-0.03	8 (1%) 75 79	8, 15, 26, 36	0
All	All	1117/1118 (99%)	-0.07	14 (1%) 77 80	7, 14, 25, 36	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	462	ALA	5.0
2	B	1	GLU	4.0
1	A	368	THR	3.7
1	A	463	VAL	3.4
1	A	462	ALA	3.3

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	0.90	0.12	14,18,24,25	0

6.3 Carbohydrates [i](#)

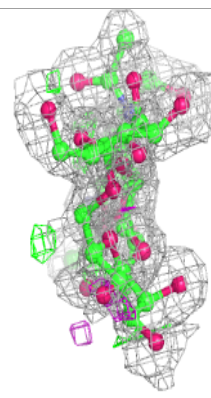
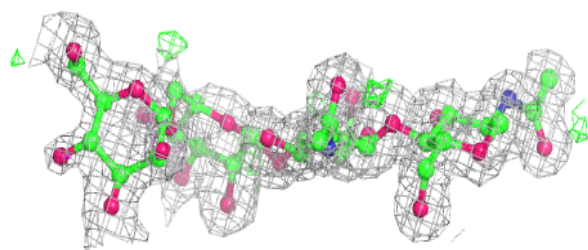
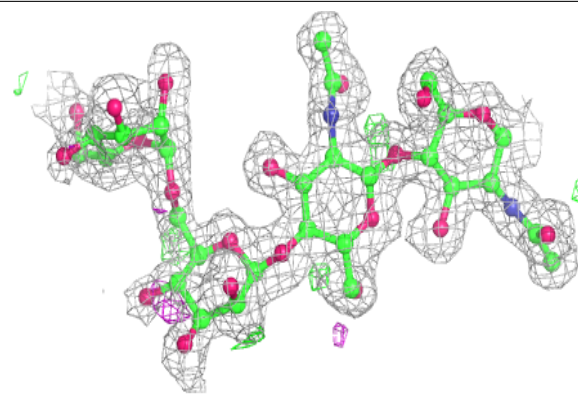
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MAN	H	4	11/12	0.66	0.27	43,44,45,46	0
3	MAN	C	3	11/12	0.71	0.27	29,34,35,36	0
3	MAN	H	3	11/12	0.72	0.23	31,35,38,40	0
5	MAN	E	3	11/12	0.74	0.29	36,39,42,43	0
3	MAN	C	4	11/12	0.74	0.24	35,36,37,37	0
4	NAG	G	2	14/15	0.78	0.40	37,41,43,44	0
5	MAN	J	3	11/12	0.79	0.36	37,40,41,41	0
4	NAG	K	2	14/15	0.79	0.29	32,36,39,39	0
4	NAG	F	2	14/15	0.83	0.26	30,33,38,39	0
4	NAG	D	1	14/15	0.84	0.15	22,25,28,32	0
4	NAG	I	2	14/15	0.84	0.20	28,33,36,36	0
4	NAG	I	1	14/15	0.85	0.13	25,28,29,31	0
4	NAG	G	1	14/15	0.87	0.16	21,24,31,32	0
4	NAG	F	1	14/15	0.88	0.11	15,18,26,28	0
4	NAG	D	2	14/15	0.89	0.15	24,28,30,31	0
5	NAG	J	2	14/15	0.89	0.15	22,27,30,32	0
4	NAG	K	1	14/15	0.90	0.10	18,21,25,27	0
5	NAG	E	2	14/15	0.90	0.13	19,23,29,32	0
5	NAG	E	1	14/15	0.93	0.09	14,16,20,21	0
3	NAG	C	2	14/15	0.94	0.10	15,19,25,29	0
3	NAG	H	2	14/15	0.96	0.06	16,19,26,29	0
3	NAG	C	1	14/15	0.97	0.08	9,10,14,14	0
5	NAG	J	1	14/15	0.97	0.07	16,19,22,22	0
3	NAG	H	1	14/15	0.97	0.06	10,13,15,15	0

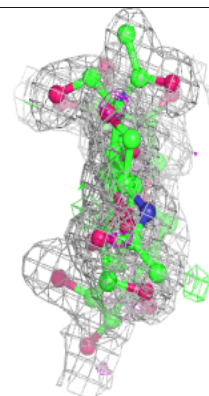
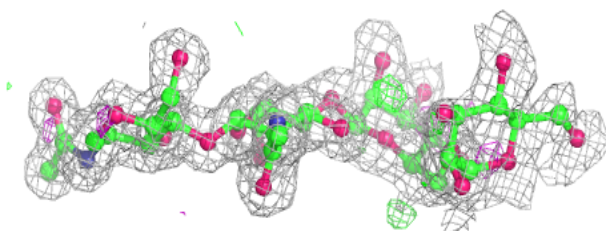
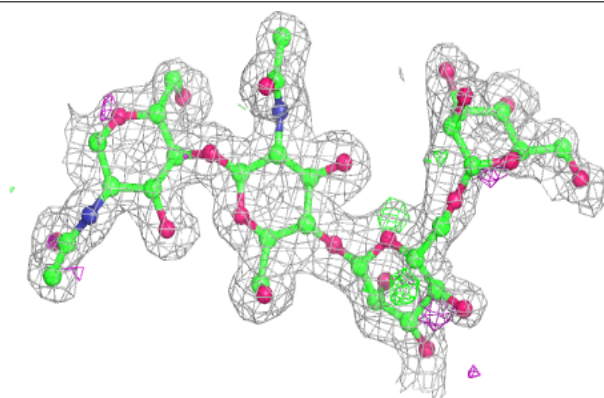
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

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)

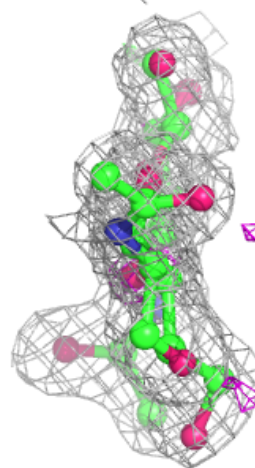
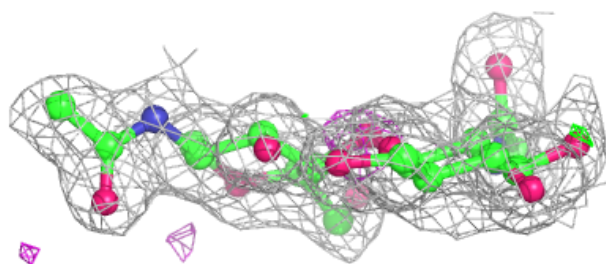
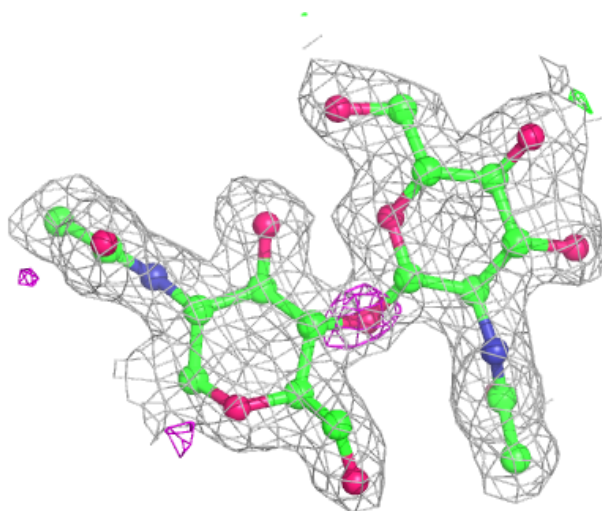
**Electron density around Chain H:**

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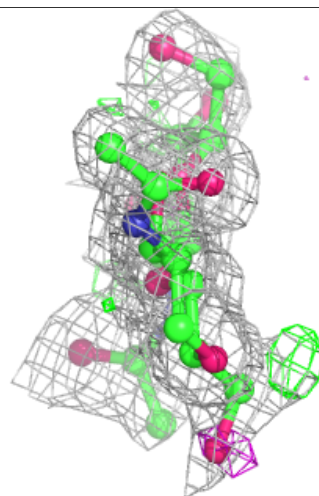
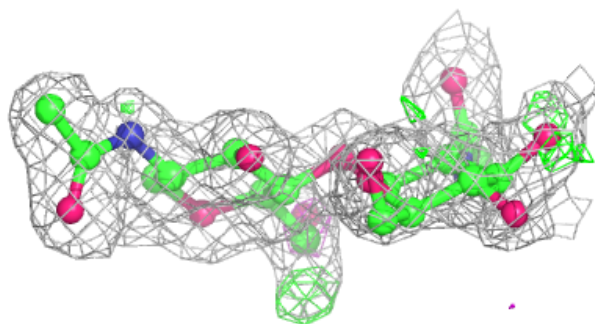
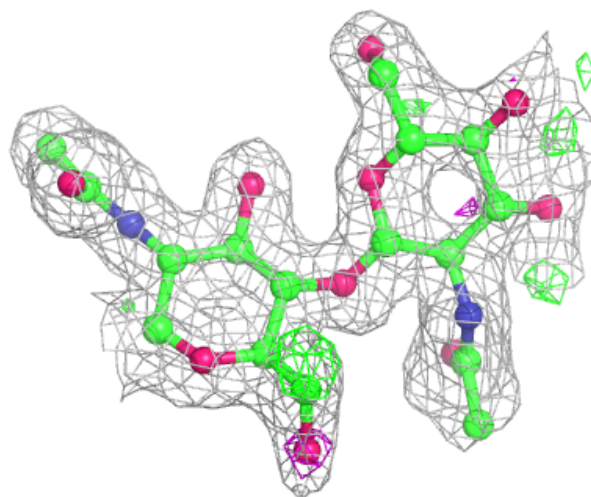
Electron density around Chain D:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



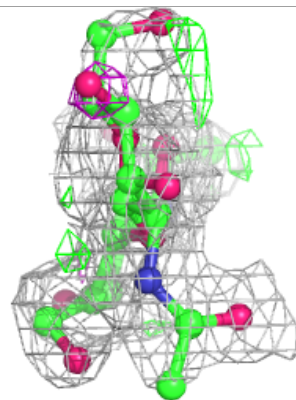
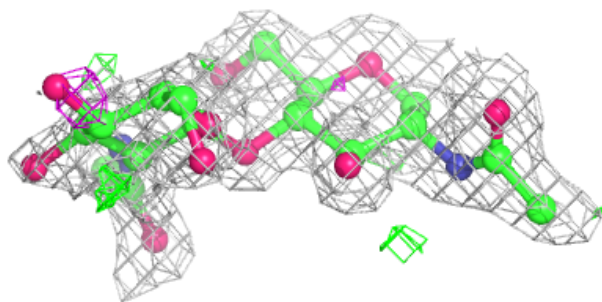
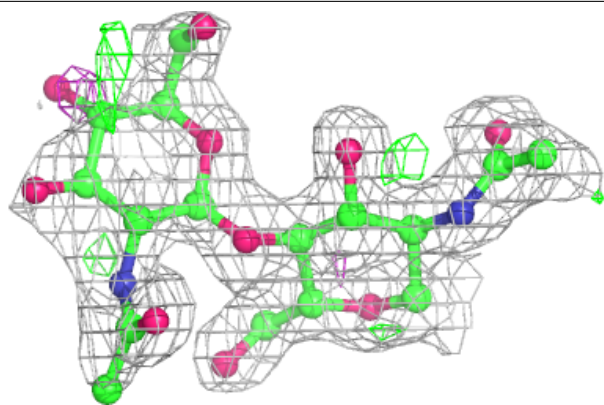
Electron density around Chain F:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



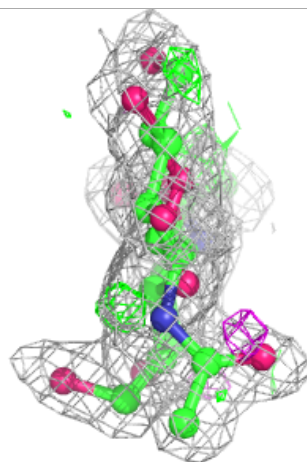
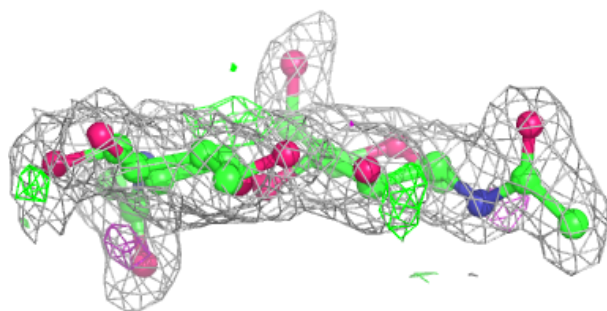
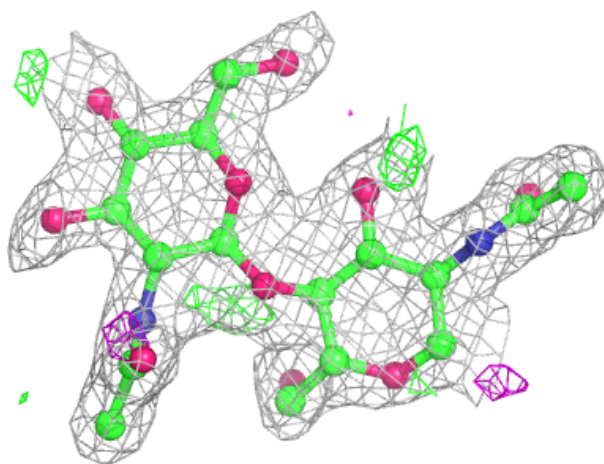
Electron density around Chain G:

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and green (positive)



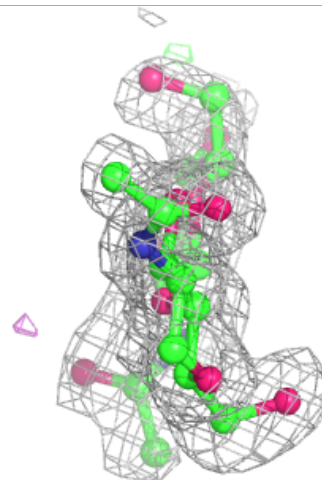
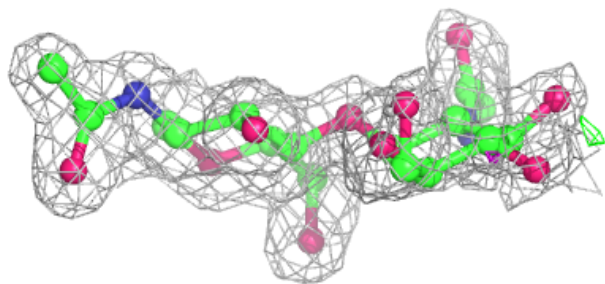
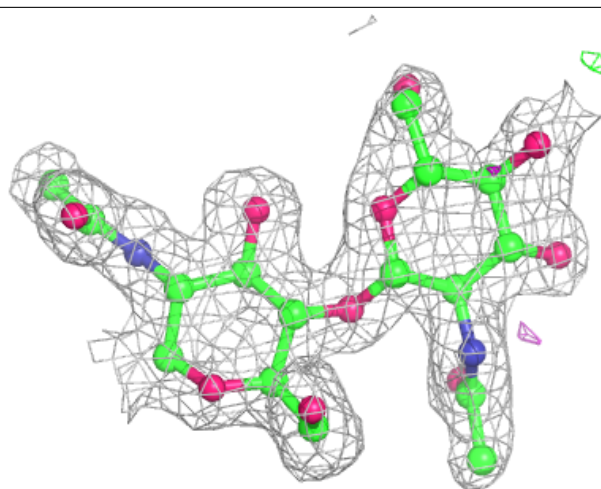
Electron density around Chain I:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



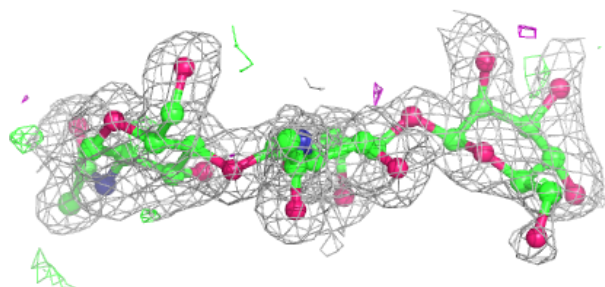
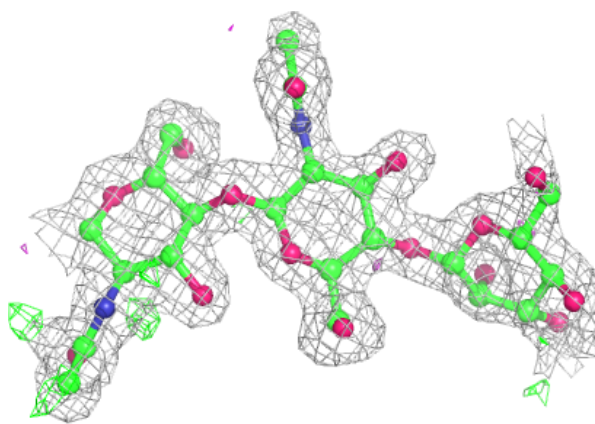
Electron density around Chain K:

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

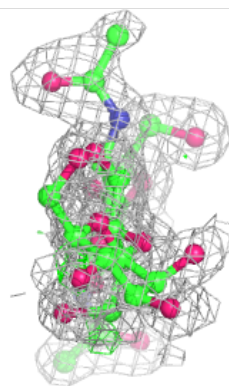
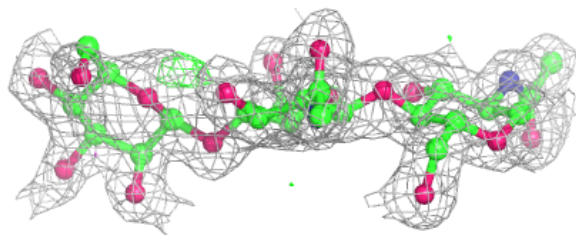
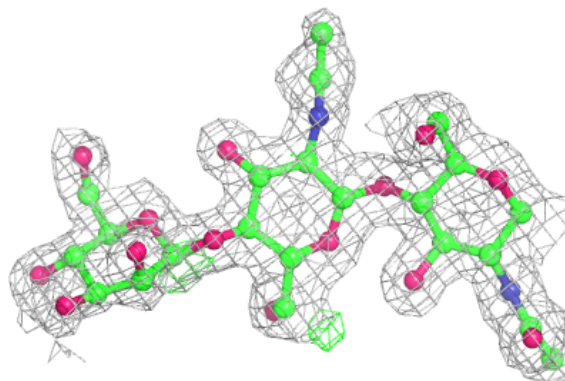


Electron density around Chain E:

$2mF_o-DF_c$ (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 ⓘ

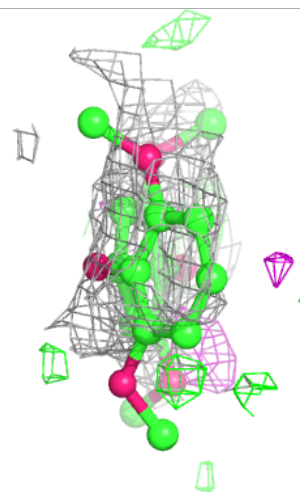
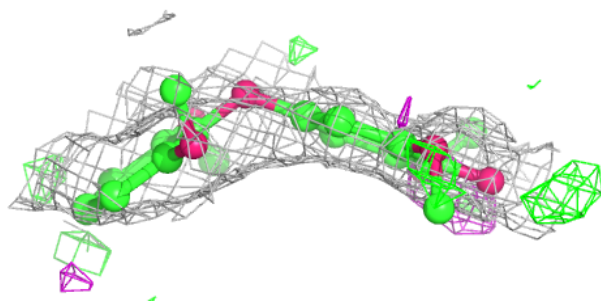
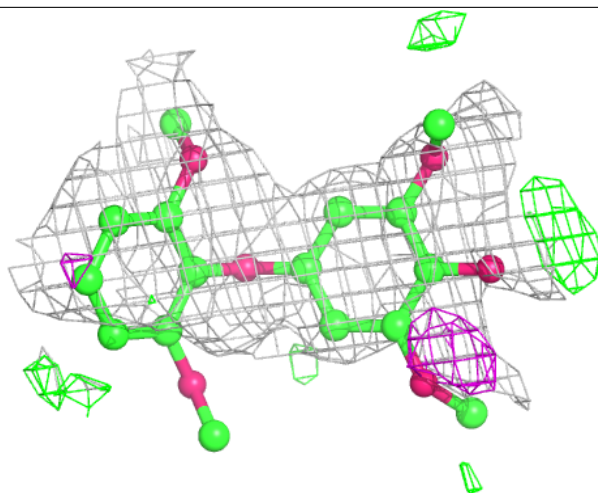
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
11	3DM	A	3900[B]	11/11	0.55	0.26	24,26,28,28	11
13	KIA	B	2910[B]	12/12	0.80	0.16	28,29,29,29	12
12	D2M	B	2100[A]	22/22	0.83	0.23	62,62,62,62	22
9	NAG	A	750	14/15	0.84	0.21	28,33,36,36	0
9	NAG	B	2760	14/15	0.85	0.15	22,25,29,31	0
9	NAG	A	700	14/15	0.87	0.16	19,22,26,28	0
9	NAG	B	700	14/15	0.89	0.15	21,24,27,31	0
10	SO4	B	4802	5/5	0.91	0.13	62,62,62,62	0
9	NAG	B	1750	14/15	0.93	0.09	14,18,21,23	0
10	SO4	A	3800	5/5	0.93	0.09	58,59,59,59	0
10	SO4	A	3801	5/5	0.95	0.10	45,46,46,46	0
8	OXY	B	1620	2/2	0.98	0.24	20,20,20,21	0
8	OXY	A	1620	2/2	0.98	0.30	22,22,22,24	0
7	CL	B	610	1/1	0.99	0.15	22,22,22,22	0
7	CL	A	610	1/1	1.00	0.08	20,20,20,20	0
6	CU	B	601	1/1	1.00	0.02	14,14,14,14	0
6	CU	B	604	1/1	1.00	0.04	18,18,18,18	0
6	CU	A	603	1/1	1.00	0.02	13,13,13,13	0
6	CU	B	602	1/1	1.00	0.06	17,17,17,17	0
6	CU	A	602	1/1	1.00	0.04	16,16,16,16	0
6	CU	A	604	1/1	1.00	0.03	16,16,16,16	0
6	CU	A	601	1/1	1.00	0.02	13,13,13,13	0
6	CU	B	603	1/1	1.00	0.02	15,15,15,15	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around D2M B 2100 (A):

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



6.5 Other polymers [i](#)

There are no such residues in this entry.