wwPDB X-ray Structure Validation Summary Report (i)

Nov 1, 2023 – 04:44 PM EDT

PDB ID	:	3TIC
Title	:	Crystal structure of 1957 pandemic H2N2 neuraminidase complexed with zanamivir
Authors	:	Vavricka, C.J.; Li, Q.; Wu, Y.; Qi, J.; Wang, M.; Liu, Y.; Gao, F.; Liu, J.; Feng, E.; He, J.; Wang, J.; Liu, H.; Jiang, H.; Gao, G.F.
Deposited on	:	2011-08-20
Resolution	:	1.89 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 (i) 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 (i)) were used in the production of this report:

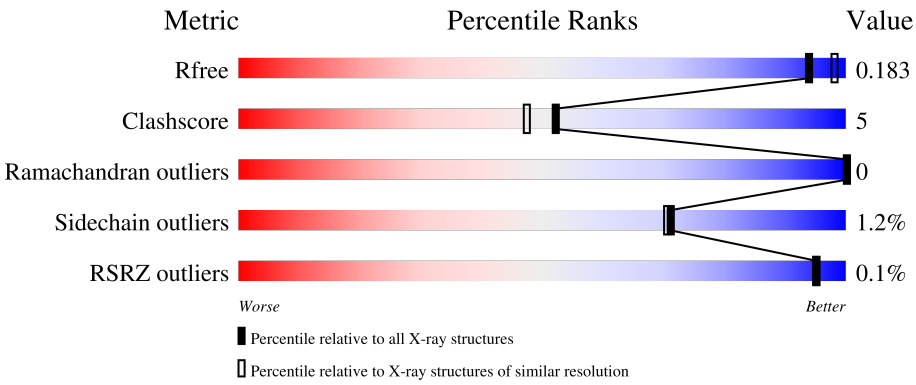
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 <=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	469	73% 9% 17%
1	B	469	73% 9% 17%
1	C	469	74% 8% • 17%
1	D	469	72% 10% 17%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	2	100%
2	H	2	100%
2	J	2	50% 50%
3	F	4	75% 25%
3	G	4	75% 25%
3	I	4	75% 25%
3	K	4	75% 25%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 14630 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 Neuraminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	388	3023	1866	543	591	23	0	1	0
1	B	388	3017	1863	542	589	23	0	0	0
1	C	388	3025	1867	544	591	23	0	1	0
1	D	388	3017	1863	542	589	23	0	0	0

- 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	E	2	28	16	2	10	0	0	0
2	H	2	28	16	2	10	0	0	0
2	J	2	28	16	2	10	0	0	0

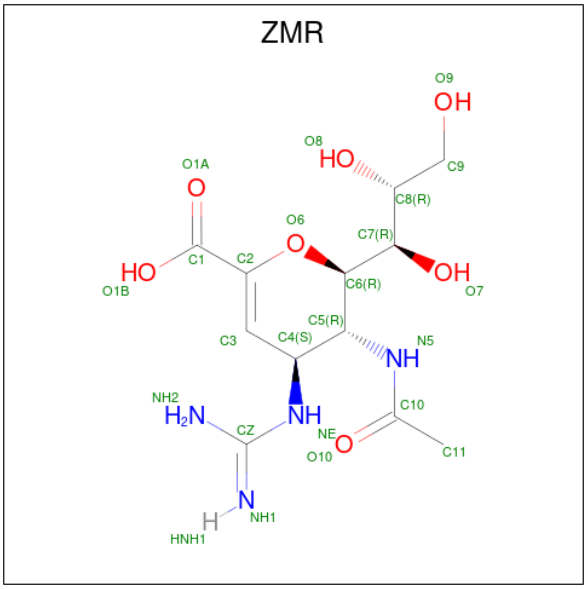
- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	F	4	50	28	2	20	0	0	0
3	G	4	50	28	2	20	0	0	0
3	I	4	50	28	2	20	0	0	0
3	K	4	50	28	2	20	0	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
4	A	1	1	1	0	0
4	B	1	1	1	0	0
4	C	1	1	1	0	0
4	D	1	1	1	0	0

- Molecule 5 is ZANAMIVIR (three-letter code: ZMR) (formula: $C_{12}H_{20}N_4O_7$).



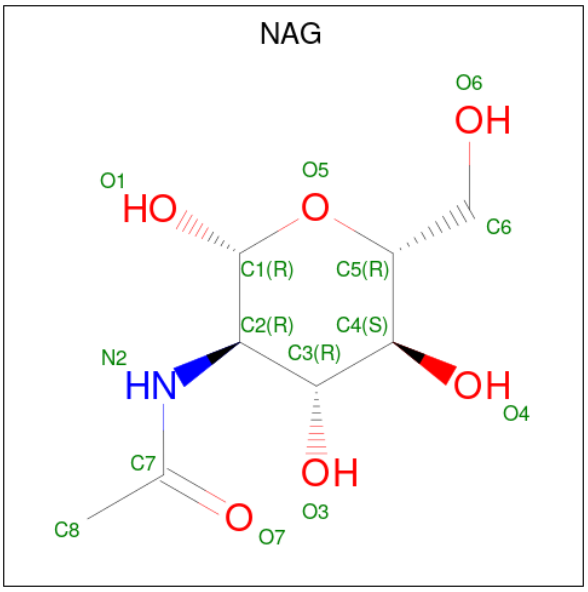
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	23	12	4	7	0	0
5	B	1	23	12	4	7	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	C	1	23	12	4	7	0	0
			Total	C	N	O		
5	D	1	23	12	4	7	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 7 is water.

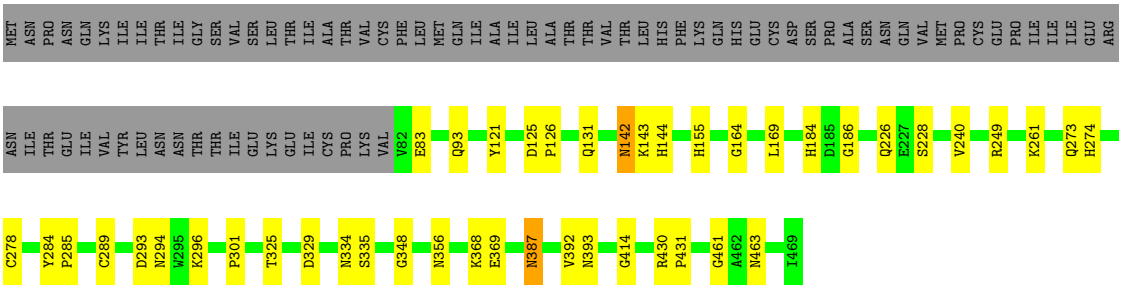
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	546	546	546	0	0
			Total	O		
7	B	528	528	528	0	0
			Total	O		
7	C	560	560	560	0	0
			Total	O		
7	D	520	520	520	0	0

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.

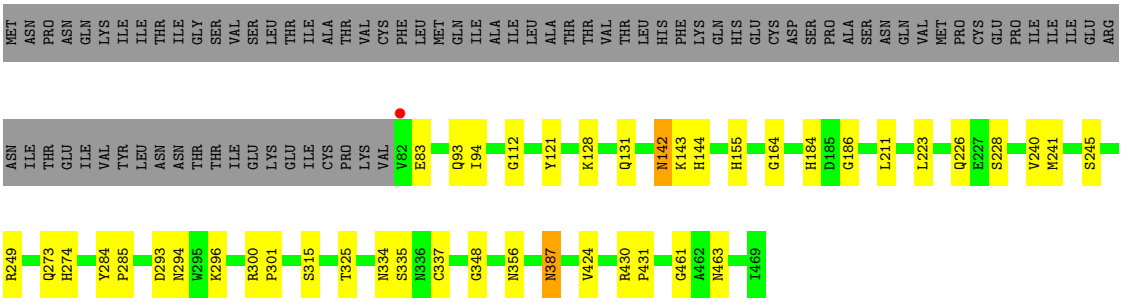
- Molecule 1: Neuraminidase

Chain A:



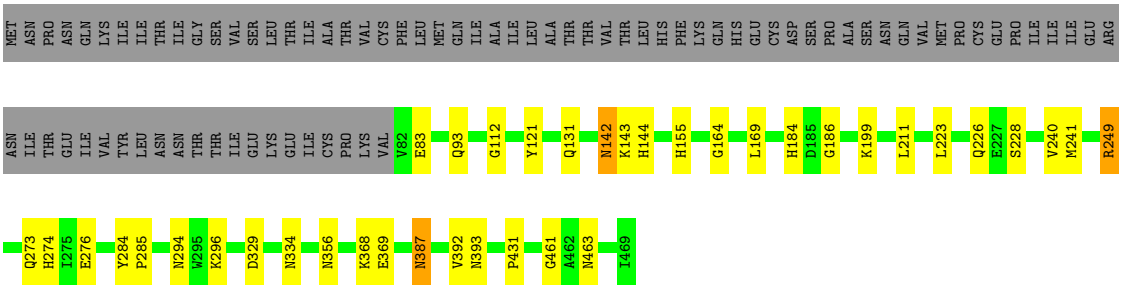
- Molecule 1: Neuraminidase

Chain B:



- Molecule 1: Neuraminidase

Chain C:



- Molecule 1: Neuraminidase

Chain D: 72% 10% 17%

MET ASN PRO ASN GLN LYS ILE ILE THR ILE GLY SER VAL SER LEU THR ILE ALA THR VAL CYS PHE LEU MET GLN ILE ALA ILE LEU ALA THR THR VAL THR LEU HIS PHE LYS GLN HIS GLU CYS ASP SER PRO ALA SER ASN GLN VAL MET PRO CYS GLU PRO ILE ILE ILE GLU ARG

ASN ILE THR GLU ILE VAL TYR LEU ASN ASN THR THR ILE GLU LYS GLU ILE CYS PRO LYS VAL V82 E83 Q93 I94 G112 Y121 D125 P126 Q131 N142 K143 H144 H155 G164 L169 H184 D185 G186 N221 T222 L223 Q226 E227 S228 C232

C237 V240 M241 G244 S245 R249 I254 L255 H264 I265 Q273 H274 Y284 P285 D293 N294 W295 K296 P301 N334 N356 W361 K378 N387 V392 N393 R430 P431 G461 A462 N463 I469

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

Chain E: 100%

NAG1 NAG2

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

Chain H: 100%

NAG1 NAG2

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

Chain J: 50% 50%

NAG1 NAG2

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

Chain F: 75% 25%

NAG1 NAG2 BMA3 MAN4

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

Chain G: 75% 25%

NAG1 NAG2 BMA3 MAN4

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

Chain I:

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

Chain K:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	90.13Å 139.99Å 90.17Å 90.00° 101.34° 90.00°	Depositor
Resolution (Å)	41.27 – 1.89 49.40 – 1.89	Depositor EDS
% Data completeness (in resolution range)	91.9 (41.27-1.89) 97.9 (49.40-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.64 (at 1.90Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.153 , 0.184 0.154 , 0.183	Depositor DCC
R_{free} test set	8553 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	14.4	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 46.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.478 for l,-k,h	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	14630	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 7.74% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: NAG, MAN, ZMR, BMA, CA

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	0.26	0/3096	0.48	0/4203
1	B	0.26	0/3090	0.48	0/4195
1	C	0.26	0/3098	0.48	0/4206
1	D	0.26	0/3090	0.48	0/4195
All	All	0.26	0/12374	0.48	0/16799

There are no bond length outliers.

There are no bond angle outliers.

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	3023	0	2836	33	0
1	B	3017	0	2832	36	0
1	C	3025	0	2837	34	0
1	D	3017	0	2832	40	0
2	E	28	0	25	0	0
2	H	28	0	25	0	0
2	J	28	0	25	0	0
3	F	50	0	43	0	0
3	G	50	0	43	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	50	0	43	0	0
3	K	50	0	43	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	23	0	14	0	0
5	B	23	0	15	0	0
5	C	23	0	14	1	0
5	D	23	0	14	0	0
6	B	14	0	13	0	0
7	A	546	0	0	5	0
7	B	528	0	0	3	0
7	C	560	0	0	6	0
7	D	520	0	0	4	0
All	All	14630	0	11654	132	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 132 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:C:463:ASN:H	1:D:144:HIS:HE2	1.17	0.92
1:B:463:ASN:H	1:C:144:HIS:HE2	1.21	0.86
1:D:226:GLN:HE21	1:D:240:VAL:H	1.20	0.86
1:A:463:ASN:H	1:B:144:HIS:HE2	1.22	0.85
1:A:226:GLN:HE21	1:A:240:VAL:H	1.22	0.84

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	387/469 (82%)	370 (96%)	17 (4%)	0	100	100
1	B	386/469 (82%)	372 (96%)	14 (4%)	0	100	100
1	C	387/469 (82%)	370 (96%)	17 (4%)	0	100	100
1	D	386/469 (82%)	370 (96%)	16 (4%)	0	100	100
All	All	1546/1876 (82%)	1482 (96%)	64 (4%)	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	339/414 (82%)	335 (99%)	4 (1%)	71	70
1	B	338/414 (82%)	334 (99%)	4 (1%)	71	70
1	C	339/414 (82%)	333 (98%)	6 (2%)	59	55
1	D	338/414 (82%)	336 (99%)	2 (1%)	86	87
All	All	1354/1656 (82%)	1338 (99%)	16 (1%)	71	70

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

Mol	Chain	Res	Type
1	D	142	ASN
1	C	431	PRO
1	C	142	ASN
1	C	387	ASN
1	B	424	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	393	ASN
1	D	274	HIS
1	C	184	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	273	GLN
1	D	393	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

22 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	E	1	1,2	14,14,15	0.59	0	17,19,21	0.72	0
2	NAG	E	2	2	14,14,15	0.57	0	17,19,21	0.69	0
3	NAG	F	1	1,3	14,14,15	0.55	0	17,19,21	0.96	1 (5%)
3	NAG	F	2	3	14,14,15	0.43	0	17,19,21	0.74	0
3	BMA	F	3	3	11,11,12	0.60	0	15,15,17	0.62	0
3	MAN	F	4	3	11,11,12	0.65	0	15,15,17	0.73	0
3	NAG	G	1	1,3	14,14,15	0.52	0	17,19,21	0.95	1 (5%)
3	NAG	G	2	3	14,14,15	0.48	0	17,19,21	0.73	0
3	BMA	G	3	3	11,11,12	0.62	0	15,15,17	0.66	0
3	MAN	G	4	3	11,11,12	0.59	0	15,15,17	0.76	0
2	NAG	H	1	1,2	14,14,15	0.59	0	17,19,21	0.73	0
2	NAG	H	2	2	14,14,15	0.54	0	17,19,21	0.74	0
3	NAG	I	1	1,3	14,14,15	0.52	0	17,19,21	1.03	2 (11%)
3	NAG	I	2	3	14,14,15	0.45	0	17,19,21	0.80	0
3	BMA	I	3	3	11,11,12	0.59	0	15,15,17	0.61	0
3	MAN	I	4	3	11,11,12	0.62	0	15,15,17	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	J	1	1,2	14,14,15	0.55	0	17,19,21	0.81	0
2	NAG	J	2	2	14,14,15	0.58	0	17,19,21	0.90	1 (5%)
3	NAG	K	1	1,3	14,14,15	0.52	0	17,19,21	1.01	2 (11%)
3	NAG	K	2	3	14,14,15	0.50	0	17,19,21	0.78	0
3	BMA	K	3	3	11,11,12	0.60	0	15,15,17	0.67	0
3	MAN	K	4	3	11,11,12	0.65	0	15,15,17	0.81	0

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

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

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	1	NAG	C1-O5-C5	2.38	115.42	112.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	2	NAG	O5-C5-C6	2.37	110.92	107.20
3	G	1	NAG	C1-O5-C5	2.30	115.31	112.19
3	K	1	NAG	C1-O5-C5	2.29	115.29	112.19
3	I	1	NAG	C2-N2-C7	-2.24	119.72	122.90

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

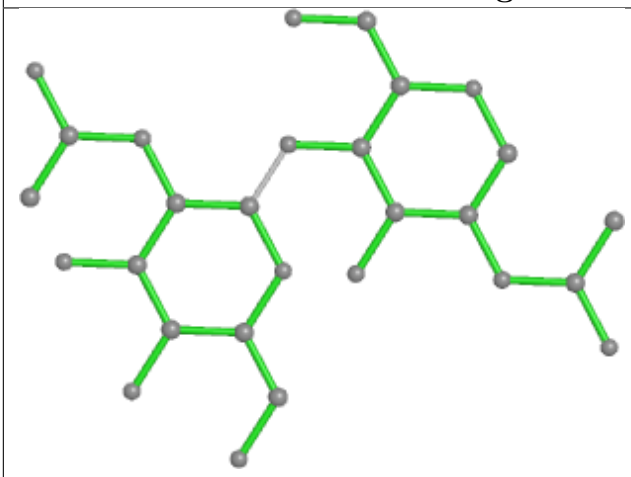
Mol	Chain	Res	Type	Atoms
3	I	1	NAG	C8-C7-N2-C2
2	J	2	NAG	O5-C5-C6-O6
2	J	2	NAG	C4-C5-C6-O6
3	I	1	NAG	O7-C7-N2-C2
3	F	1	NAG	C8-C7-N2-C2

There are no ring outliers.

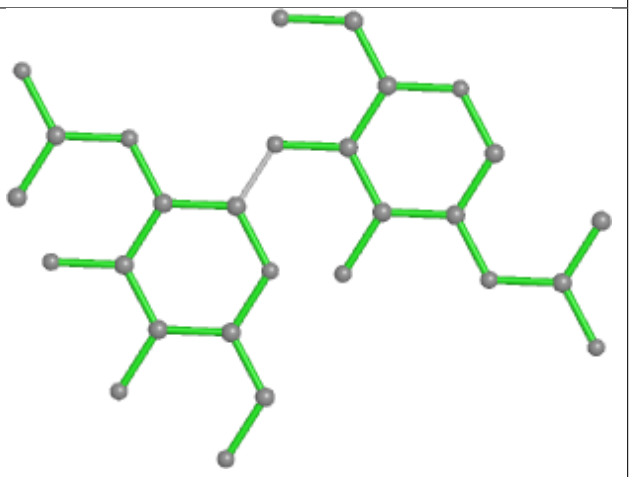
No monomer is involved in short contacts.

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

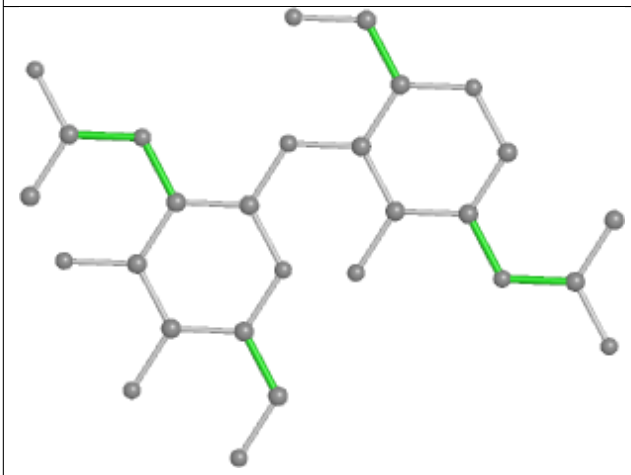
Oligosaccharide Chain E



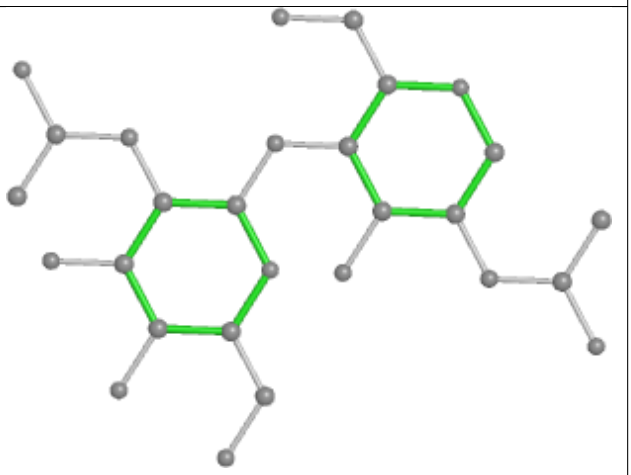
Bond lengths



Bond angles

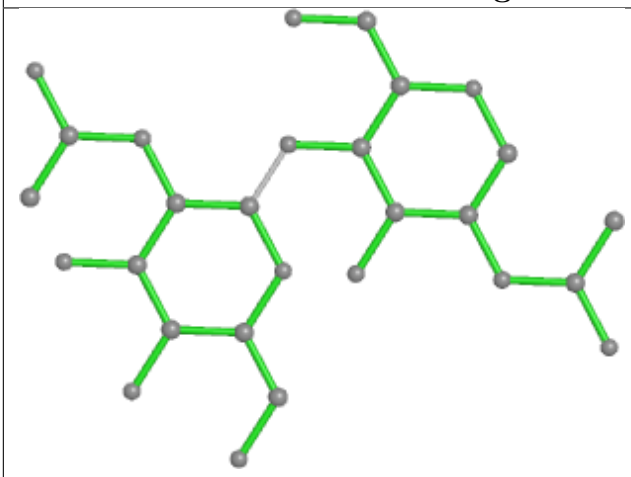


Torsions

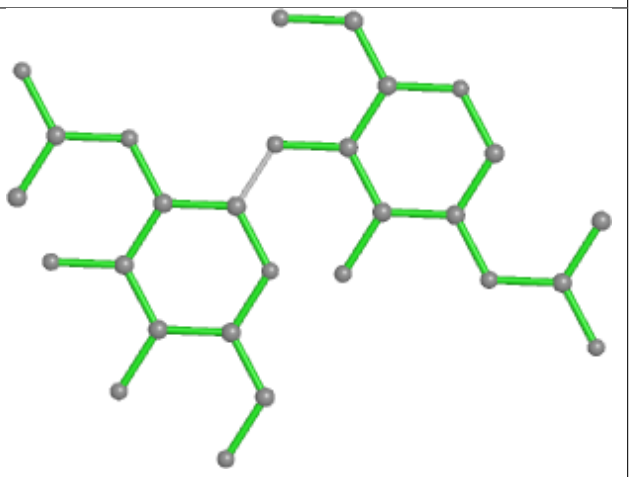


Rings

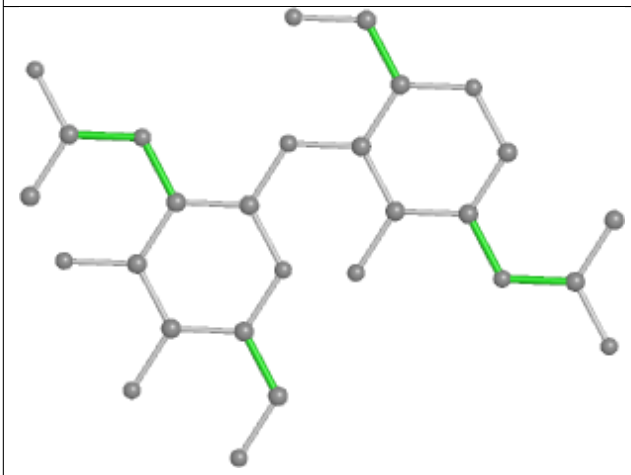
Oligosaccharide Chain H



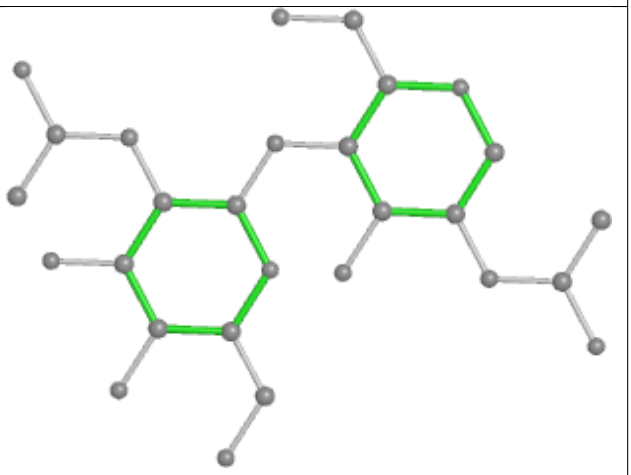
Bond lengths



Bond angles

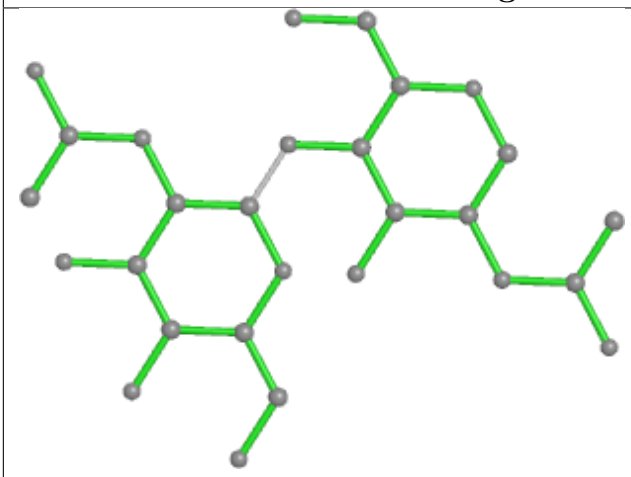


Torsions

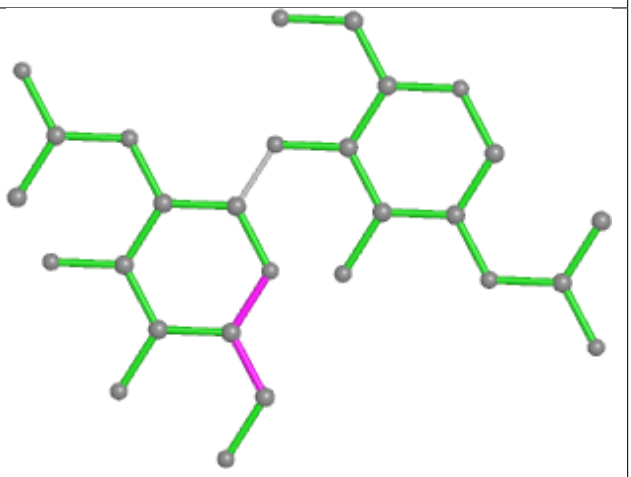


Rings

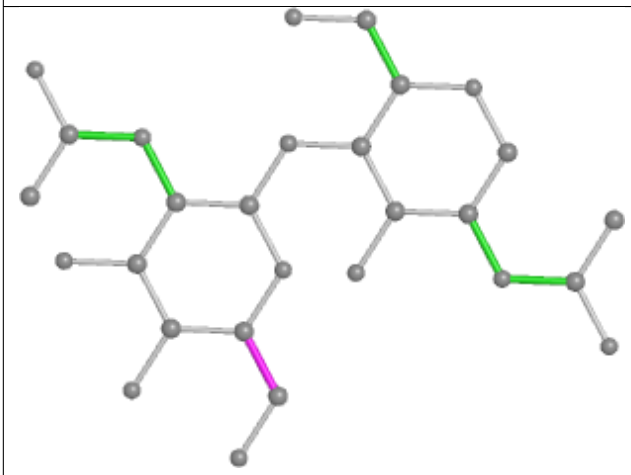
Oligosaccharide Chain J



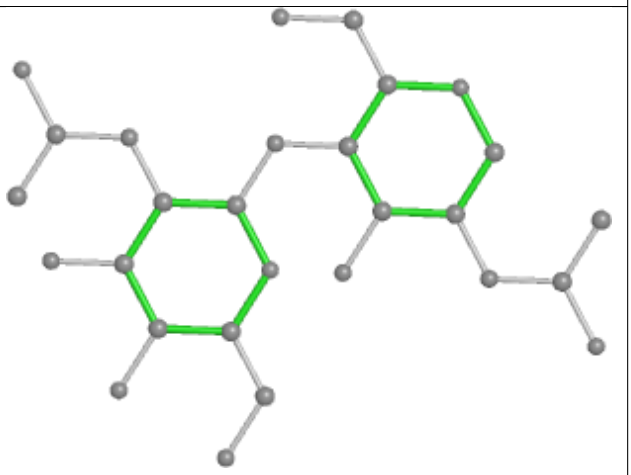
Bond lengths



Bond angles

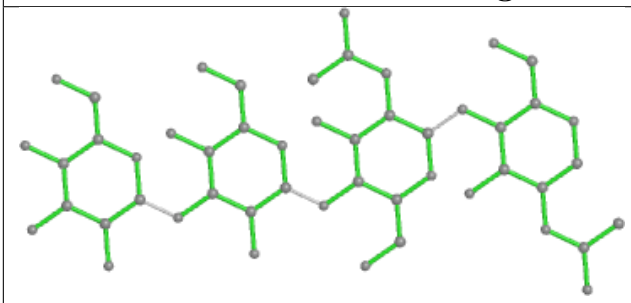


Torsions

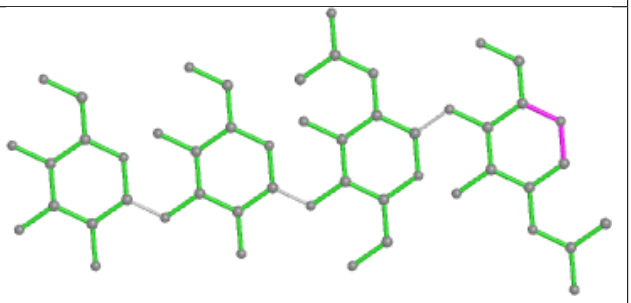


Rings

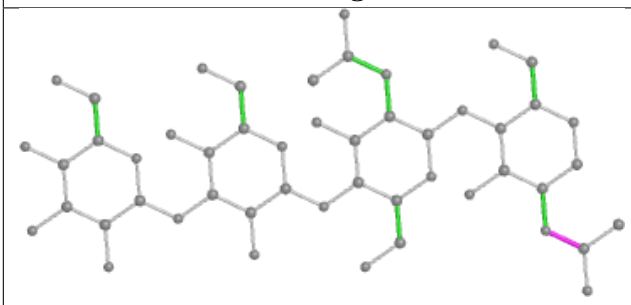
Oligosaccharide Chain F



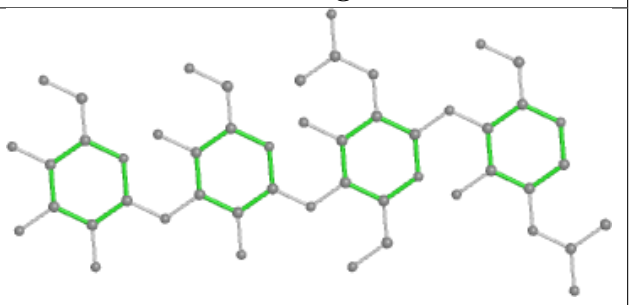
Bond lengths



Bond angles

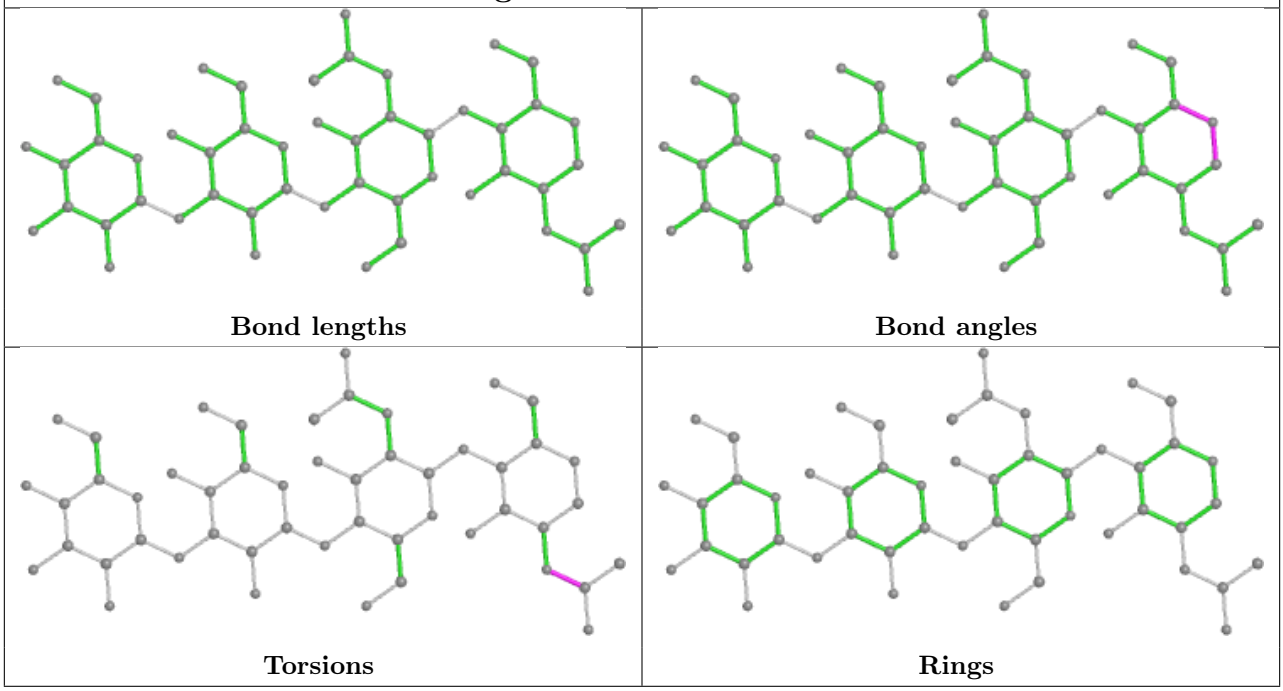


Torsions

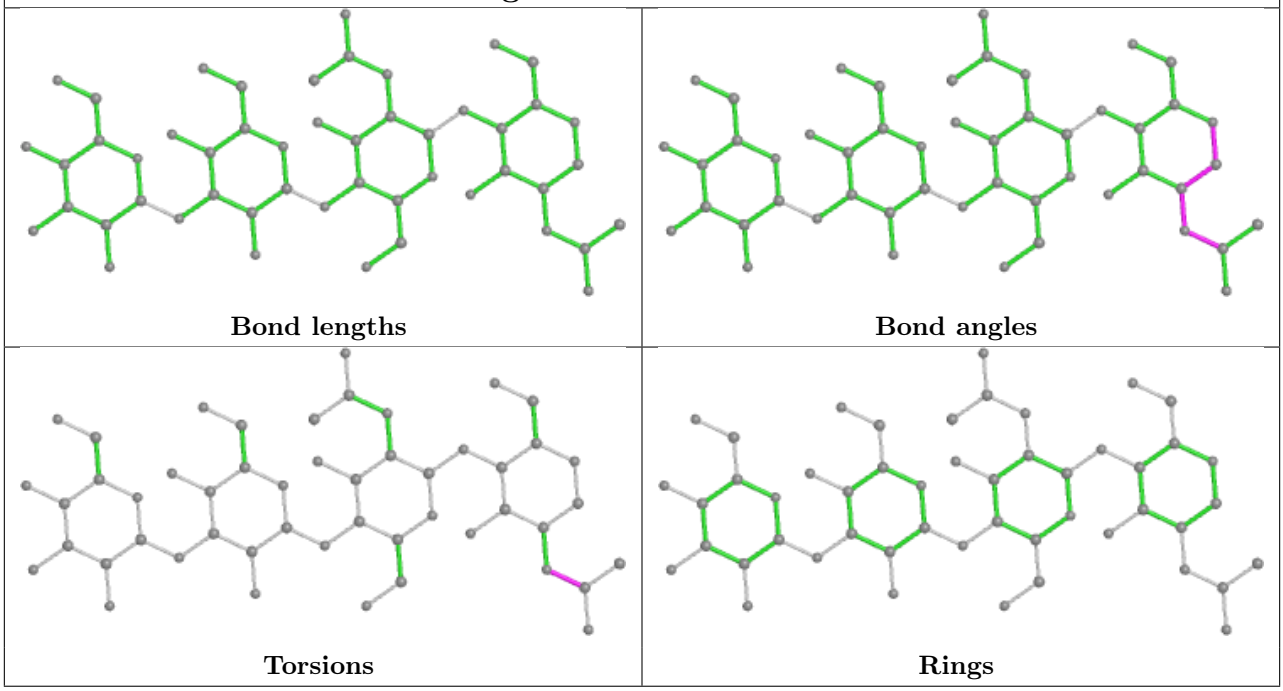


Rings

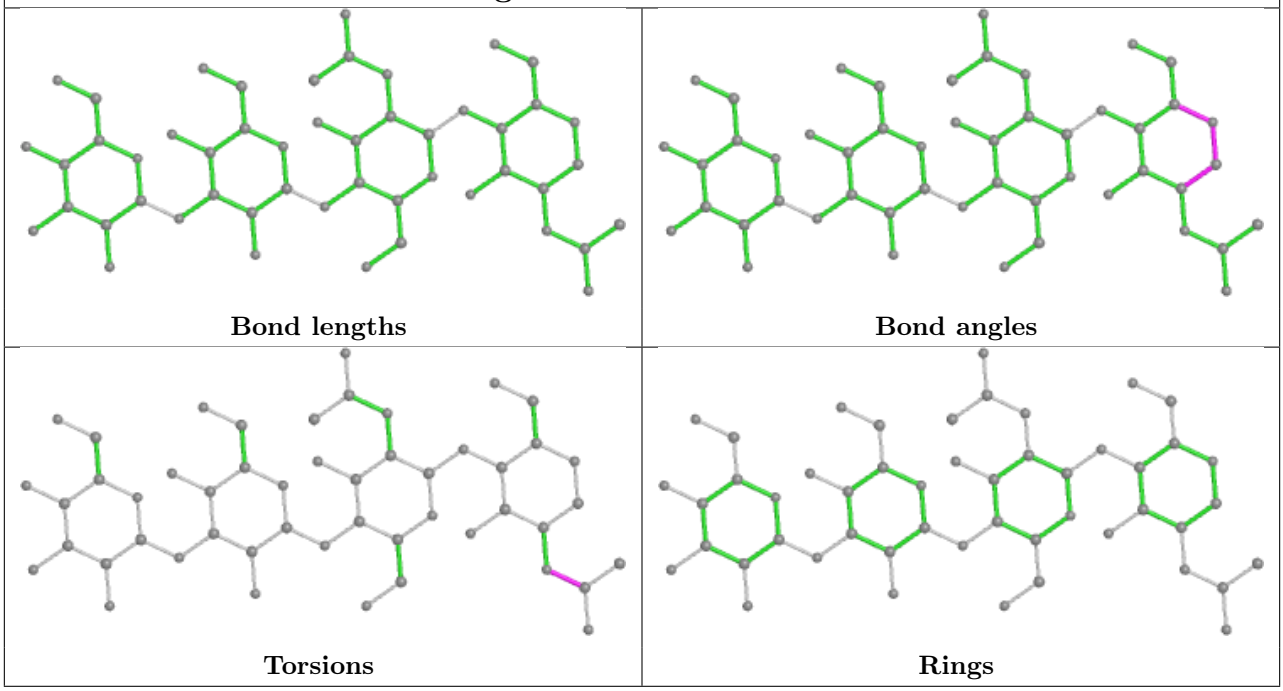
Oligosaccharide Chain G



Oligosaccharide Chain I



Oligosaccharide Chain K



5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	ZMR	A	1002	-	22,23,23	4.12	10 (45%)	24,32,32	2.31	9 (37%)
5	ZMR	C	1002	-	22,23,23	3.98	10 (45%)	24,32,32	2.14	9 (37%)
5	ZMR	B	1002	-	22,23,23	3.89	11 (50%)	24,32,32	2.00	9 (37%)
5	ZMR	D	1002	-	22,23,23	3.73	9 (40%)	24,32,32	1.98	8 (33%)
6	NAG	B	601	1	14,14,15	0.54	0	17,19,21	0.70	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
5	ZMR	A	1002	-	-	0/22/38/38	0/1/1/1
5	ZMR	C	1002	-	-	1/22/38/38	0/1/1/1
5	ZMR	B	1002	-	-	0/22/38/38	0/1/1/1
5	ZMR	D	1002	-	-	0/22/38/38	0/1/1/1
6	NAG	B	601	1	-	0/6/23/26	0/1/1/1

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1002	ZMR	C3-C2	14.81	1.56	1.33
5	C	1002	ZMR	C3-C2	14.58	1.56	1.33
5	B	1002	ZMR	C3-C2	14.56	1.55	1.33
5	D	1002	ZMR	C3-C2	14.15	1.55	1.33
5	A	1002	ZMR	O8-C8	-5.46	1.31	1.43

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1002	ZMR	O6-C2-C3	-6.12	117.47	124.61
5	C	1002	ZMR	O6-C2-C3	-6.00	117.61	124.61
5	B	1002	ZMR	O6-C2-C3	-5.61	118.06	124.61
5	D	1002	ZMR	O6-C2-C3	-4.93	118.86	124.61
5	A	1002	ZMR	C3-C4-NE	4.58	117.52	111.00

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	1002	ZMR	O10-C10-N5-C5

There are no ring outliers.

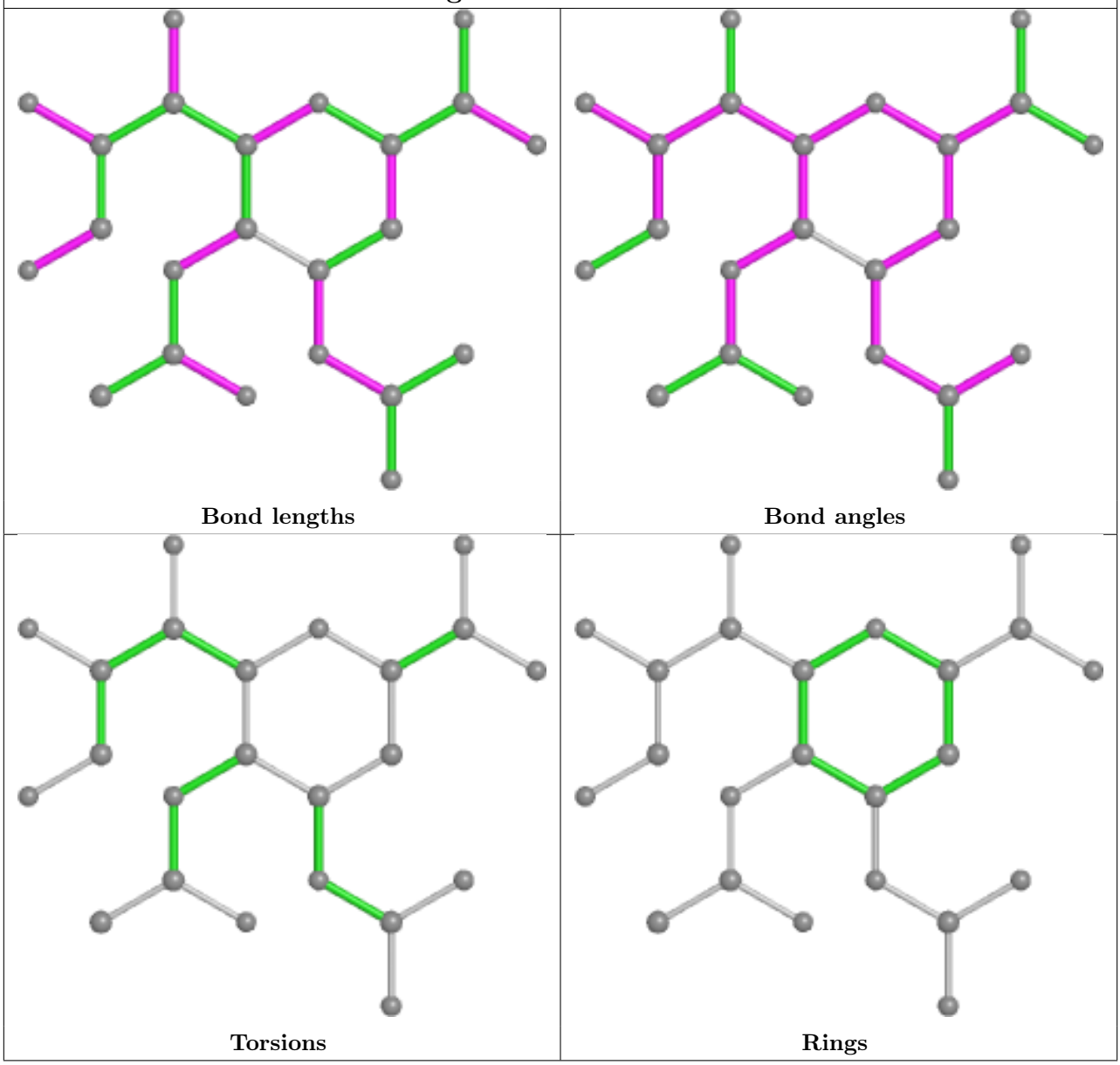
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1002	ZMR	1	0

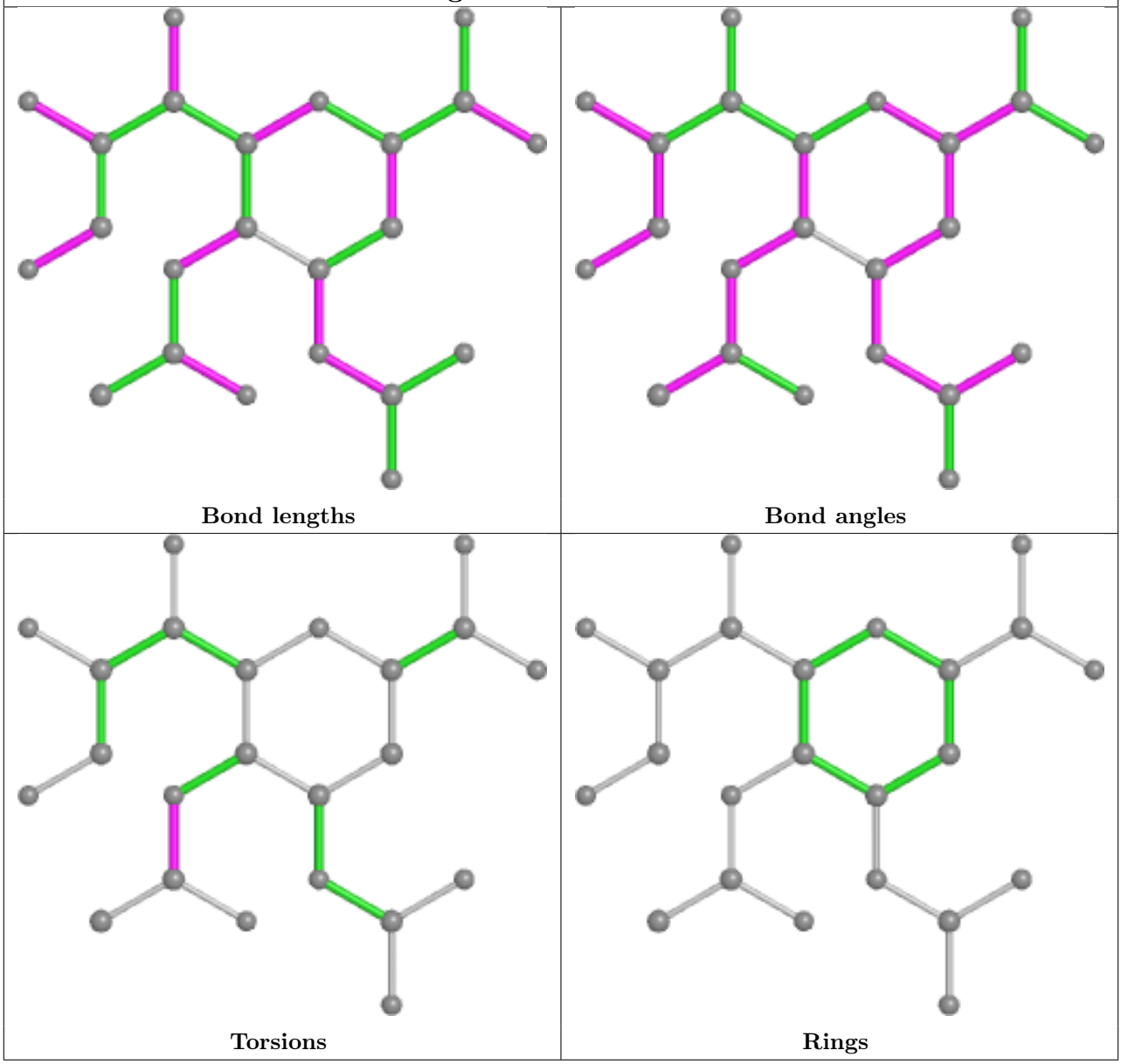
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

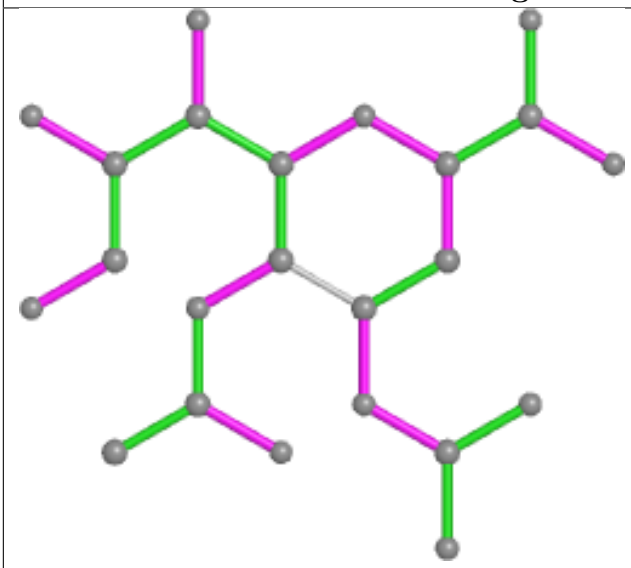
Ligand ZMR A 1002



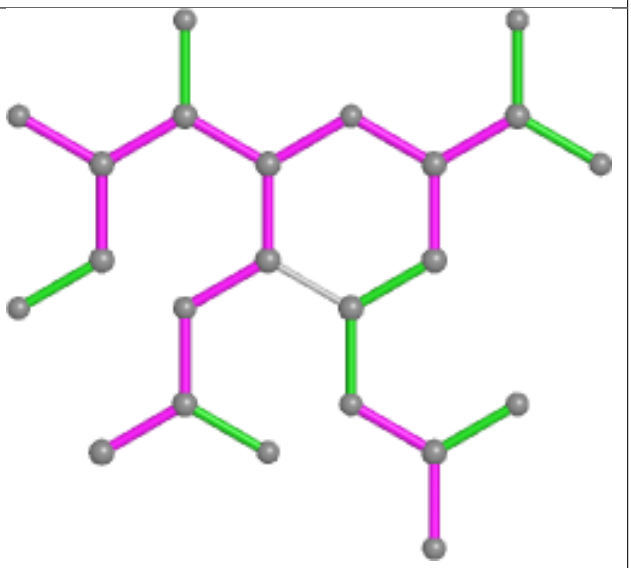
Ligand ZMR C 1002



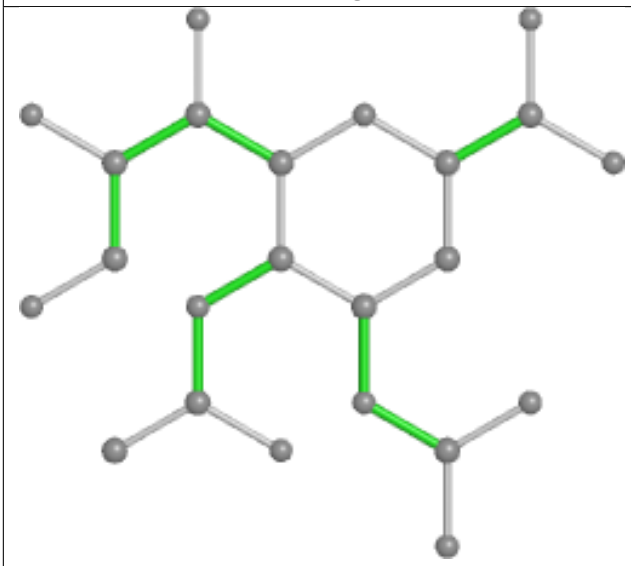
Ligand ZMR B 1002



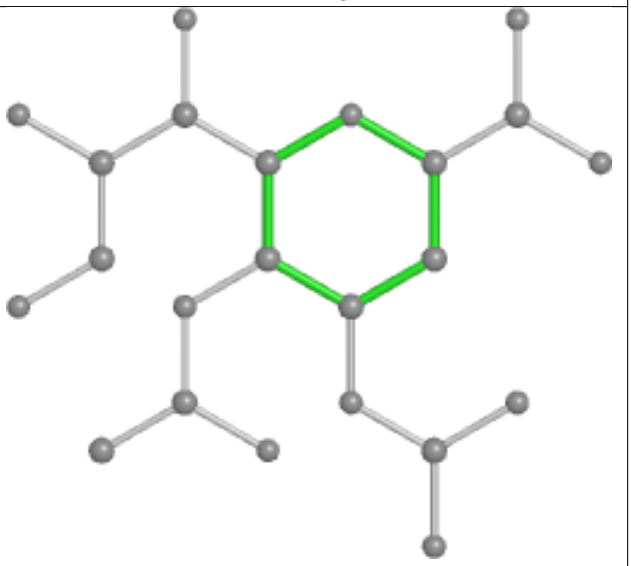
Bond lengths



Bond angles

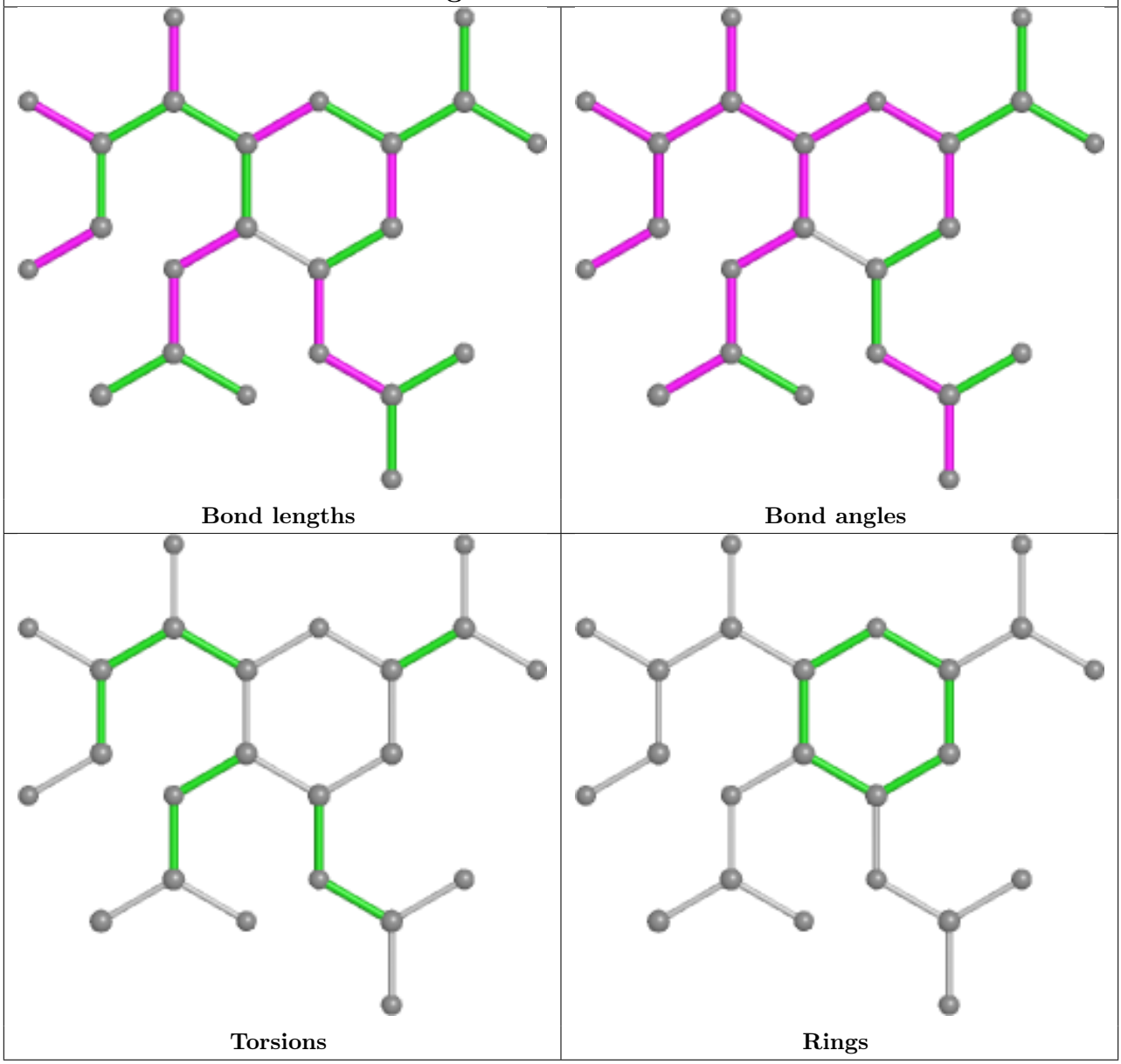


Torsions



Rings

Ligand ZMR D 1002



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	388/469 (82%)	-1.02	0 100 100	7, 13, 24, 52	0
1	B	388/469 (82%)	-1.00	1 (0%) 94 94	7, 14, 24, 60	0
1	C	388/469 (82%)	-1.02	0 100 100	7, 13, 25, 53	0
1	D	388/469 (82%)	-1.00	0 100 100	7, 13, 24, 56	0
All	All	1552/1876 (82%)	-1.01	1 (0%) 95 95	7, 13, 25, 60	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	82	VAL	2.6

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

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

6.3 Carbohydrates (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
2	NAG	E	2	14/15	0.79	0.21	63,70,79,85	0
2	NAG	H	2	14/15	0.83	0.21	64,67,81,82	0
2	NAG	J	2	14/15	0.90	0.15	41,55,70,71	0
3	NAG	G	1	14/15	0.93	0.09	15,19,33,34	0
3	NAG	K	1	14/15	0.93	0.09	14,19,34,35	0
2	NAG	E	1	14/15	0.94	0.08	21,32,45,46	0

Continued on next page...

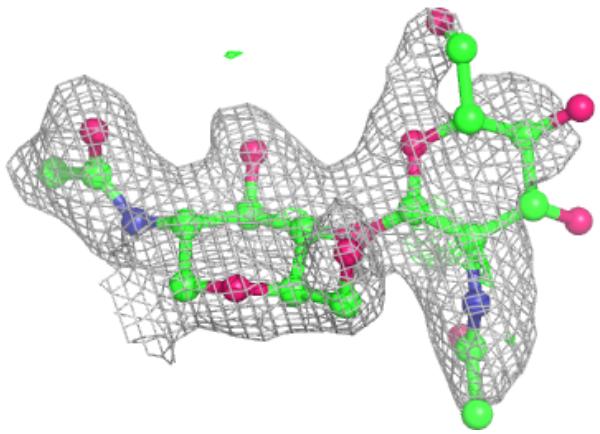
Continued from previous page...

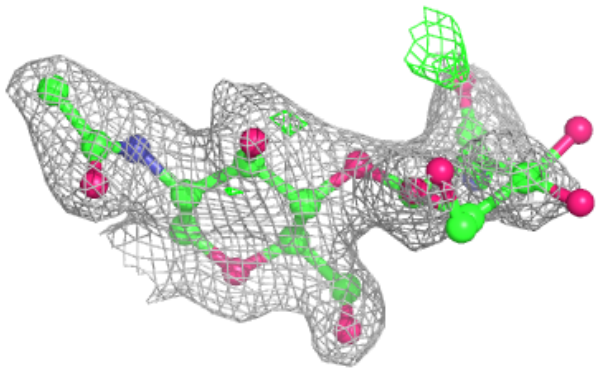
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NAG	J	1	14/15	0.95	0.08	23,31,38,38	0
3	NAG	I	1	14/15	0.95	0.08	13,20,35,41	0
2	NAG	H	1	14/15	0.95	0.09	28,36,46,49	0
3	MAN	K	4	11/12	0.95	0.06	18,19,23,27	0
3	MAN	F	4	11/12	0.96	0.07	19,20,24,24	0
3	NAG	I	2	14/15	0.96	0.05	15,18,20,22	0
3	NAG	F	1	14/15	0.96	0.08	13,20,36,44	0
3	BMA	K	3	11/12	0.96	0.06	13,18,23,23	0
3	MAN	G	4	11/12	0.96	0.06	18,20,22,29	0
3	MAN	I	4	11/12	0.97	0.06	18,20,23,28	0
3	BMA	G	3	11/12	0.97	0.05	13,19,22,23	0
3	NAG	K	2	14/15	0.97	0.06	15,16,20,21	0
3	NAG	G	2	14/15	0.97	0.06	15,17,21,23	0
3	BMA	I	3	11/12	0.97	0.07	15,17,24,27	0
3	BMA	F	3	11/12	0.98	0.05	15,19,22,24	0
3	NAG	F	2	14/15	0.98	0.05	16,18,21,21	0

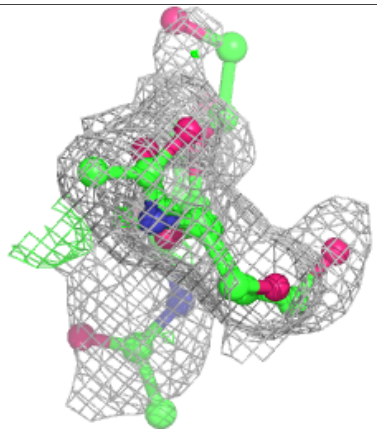
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

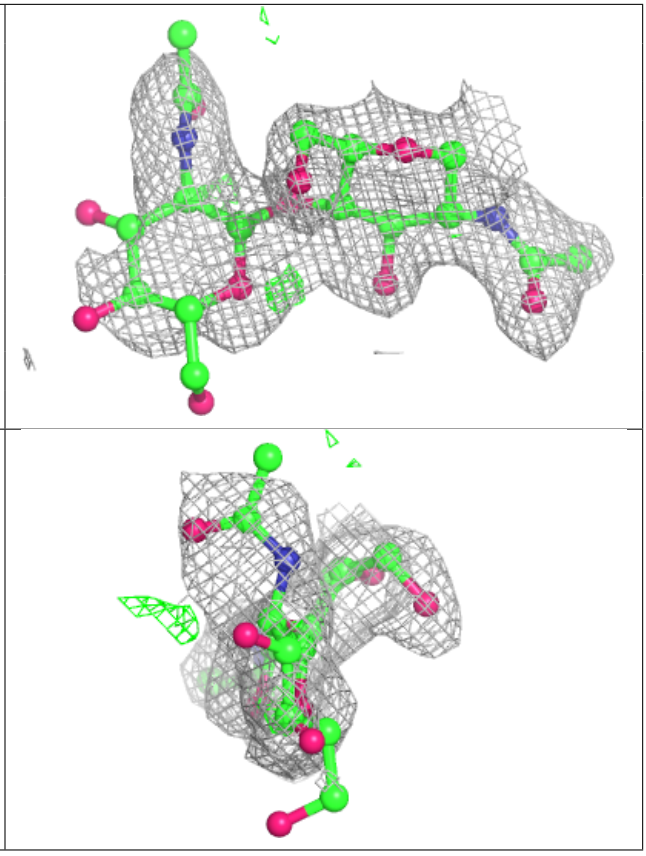


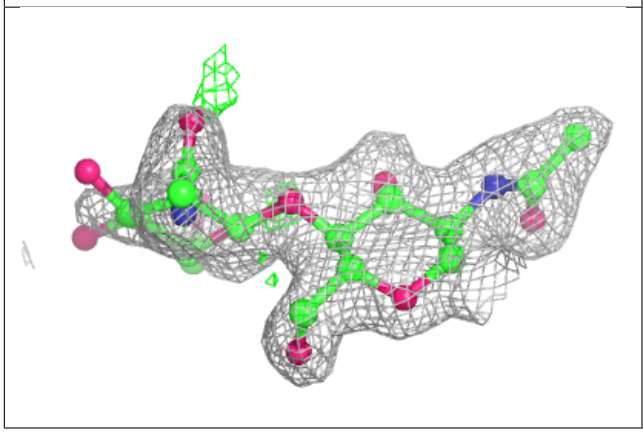




Electron density around Chain H:

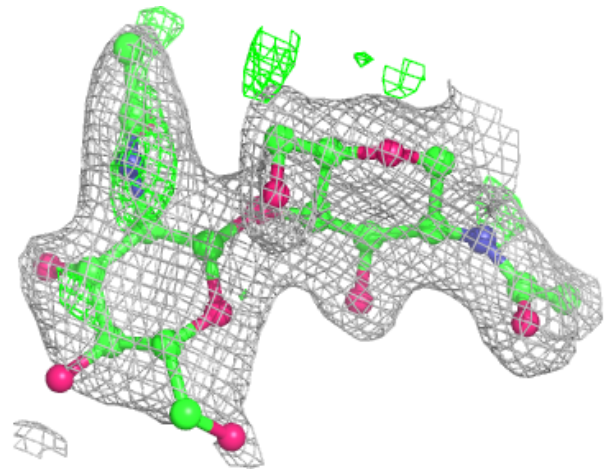
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

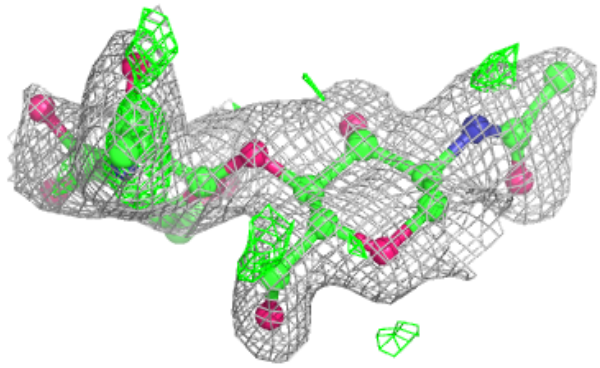


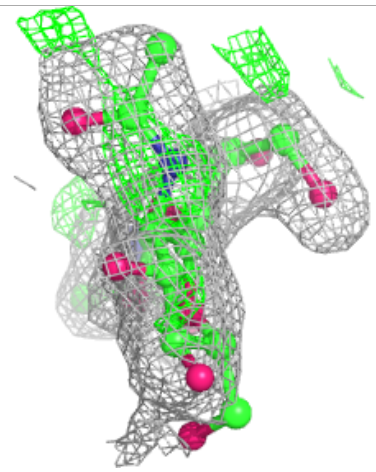


Electron density around Chain J:

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

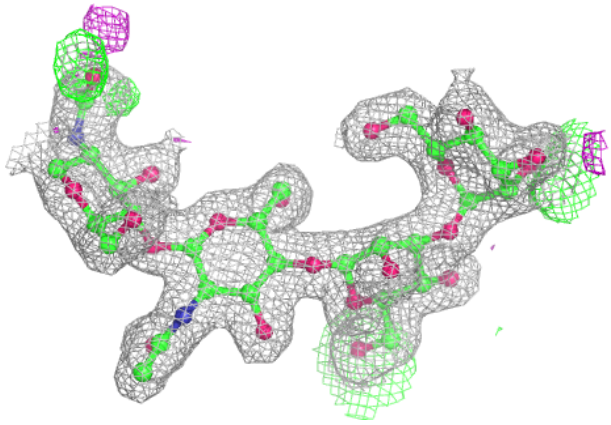


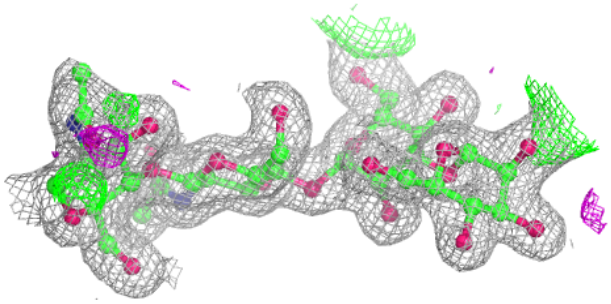


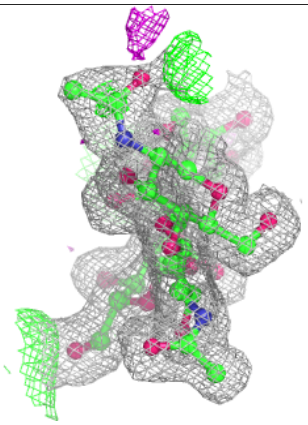


Electron density around Chain F:

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

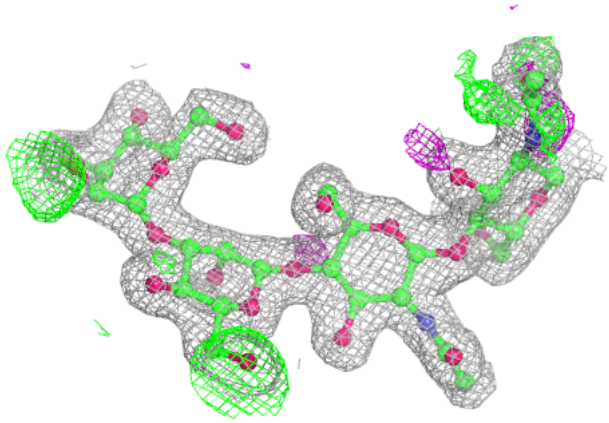


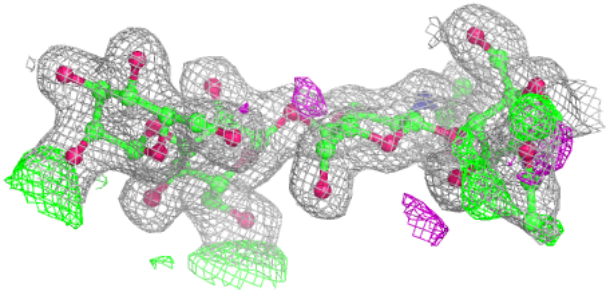


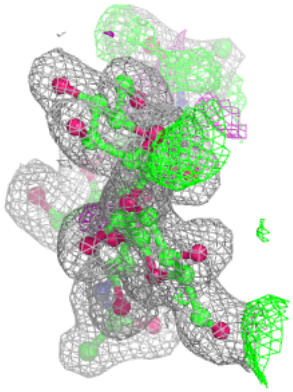


Electron density around Chain G:

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

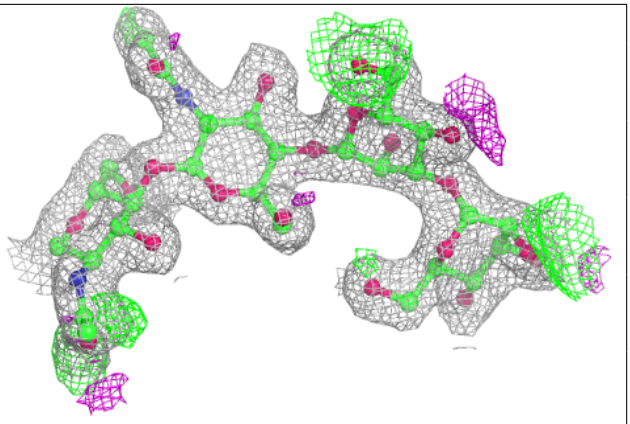


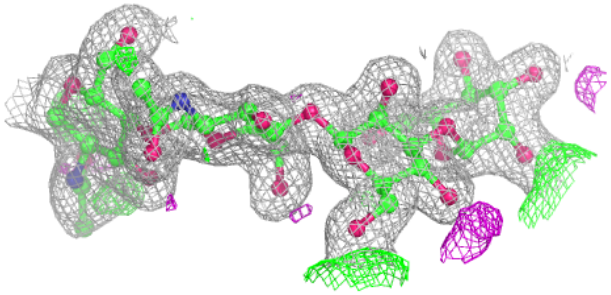


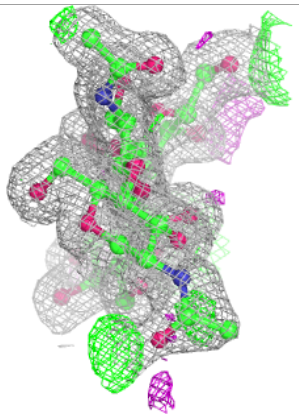


Electron density around Chain I:

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

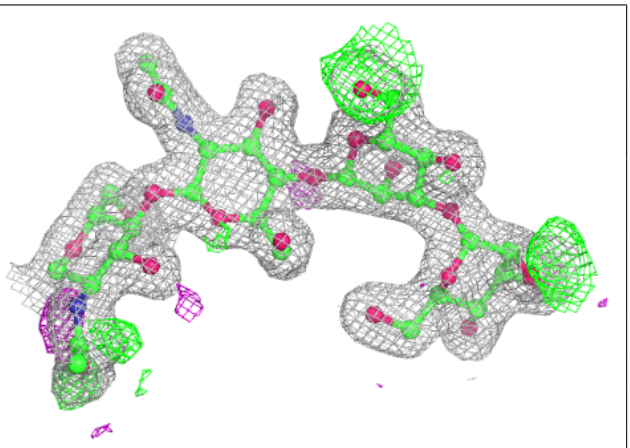


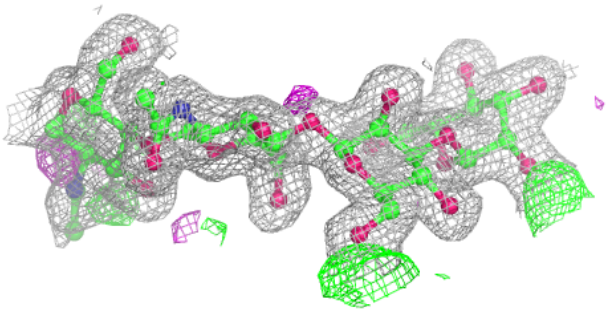


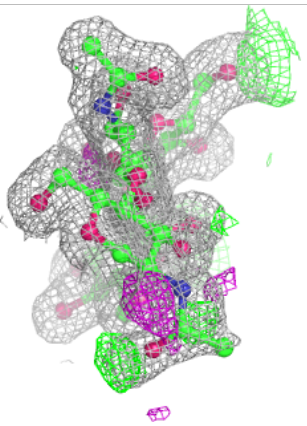


Electron density around Chain K:

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







6.4 Ligands (i)

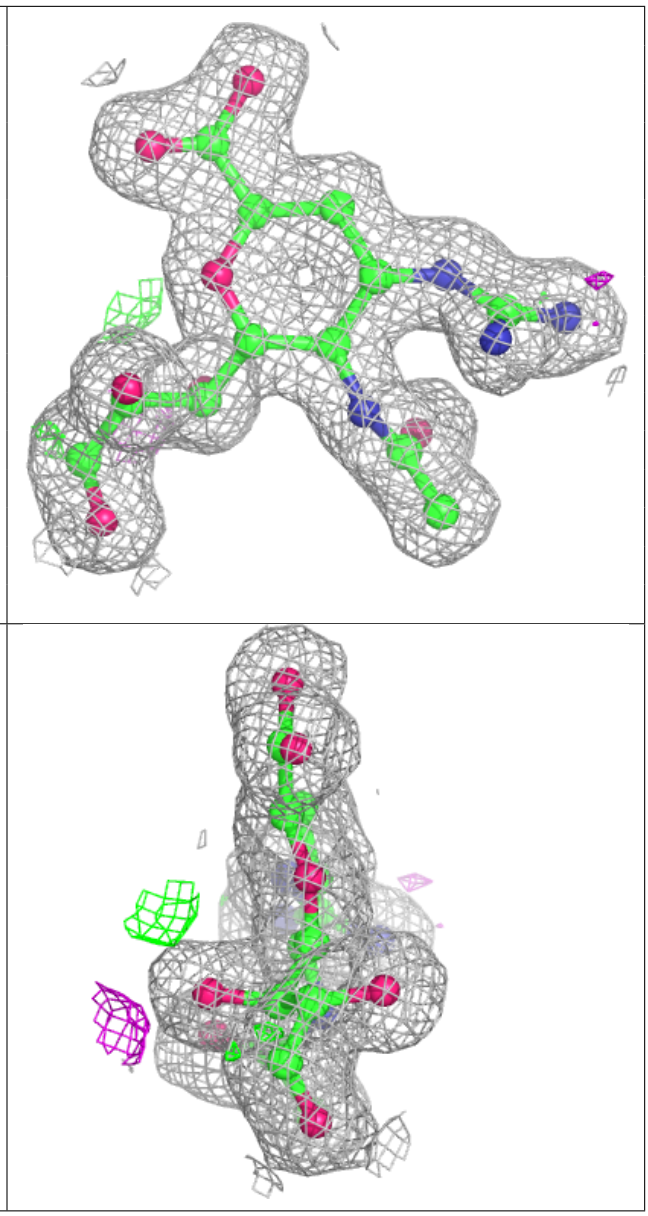
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	NAG	B	601	14/15	0.93	0.09	25,34,36,38	0
5	ZMR	B	1002	23/23	0.98	0.06	8,11,14,16	0
5	ZMR	C	1002	23/23	0.98	0.06	7,10,13,13	0
5	ZMR	D	1002	23/23	0.98	0.06	7,10,12,13	0
5	ZMR	A	1002	23/23	0.98	0.06	7,11,13,14	0
4	CA	B	501	1/1	1.00	0.07	15,15,15,15	0
4	CA	C	501	1/1	1.00	0.10	14,14,14,14	0
4	CA	D	501	1/1	1.00	0.08	14,14,14,14	0
4	CA	A	501	1/1	1.00	0.08	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.

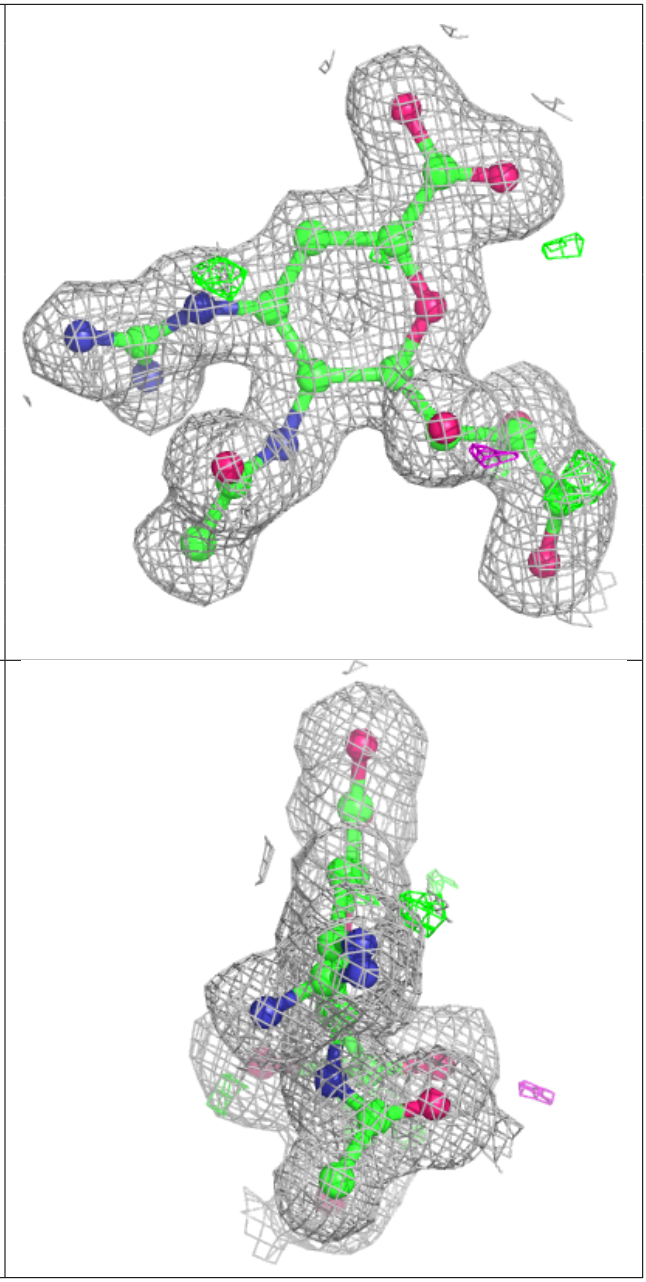
Electron density around ZMR B 1002:

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



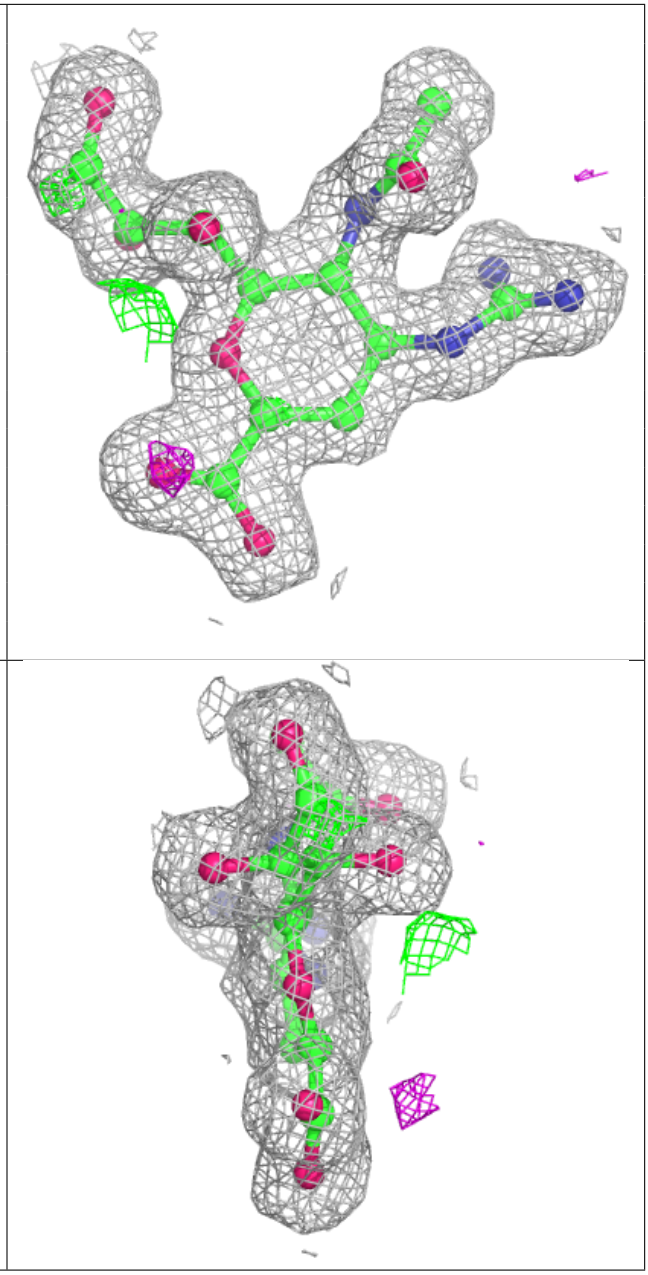
Electron density around ZMR C 1002:

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



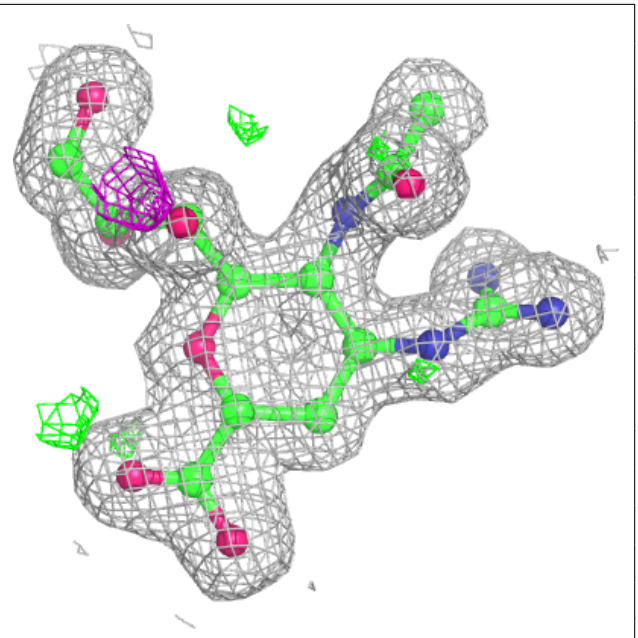
Electron density around ZMR D 1002:

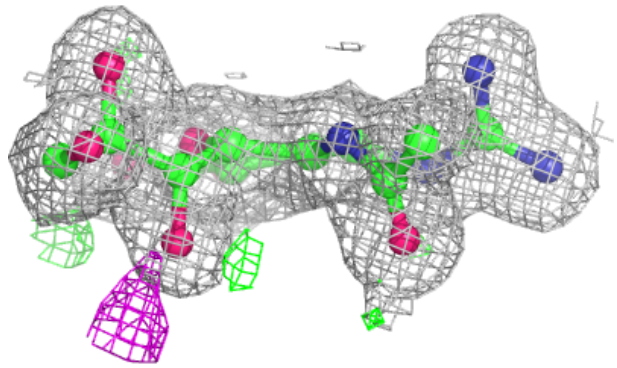
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

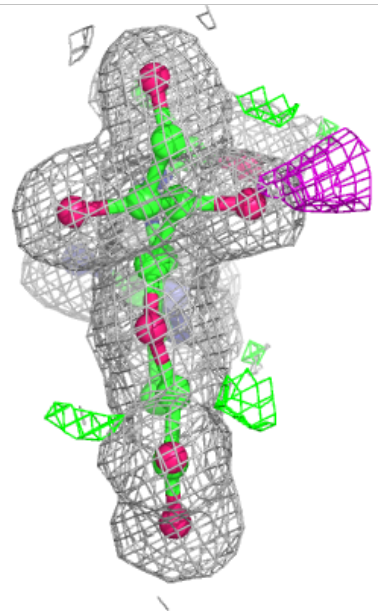


Electron density around ZMR A 1002:

$2mF_o$-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.