



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 02:33 PM BST

PDB ID : 3MPH
Title : The structure of human diamine oxidase complexed with an inhibitor aminoguanidine
Authors : McGrath, A.P.; Guss, J.M.
Deposited on : 2010-04-27
Resolution : 2.05 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

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

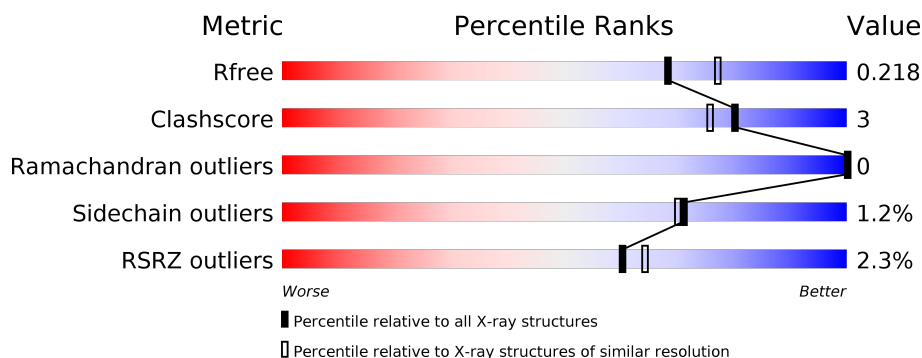
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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.



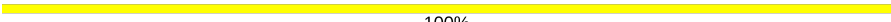

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	731	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>6%</div> <div></div> </div> </div>
1	B	731	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>7%</div> <div></div> </div> </div>
2	C	3	<div> <div>33%</div> <div>67%</div> </div>
3	D	2	<div> <div>100%</div> </div>
3	E	2	<div> <div>50%</div> <div>50%</div> </div>
3	F	2	<div> <div>50%</div> <div>50%</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	2	 100%
3	H	2	 50% 50%

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
3	NAG	E	2	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 12719 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 Amiloride-sensitive amine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	714	Total	C	N	O	S	0	14	0
			5789	3735	997	1039	18			
1	B	710	Total	C	N	O	S	0	12	0
			5748	3712	988	1031	17			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ARG	PRO	engineered mutation	UNP P19801
A	592	SER	THR	SEE REMARK 999	UNP P19801
A	645	ASP	HIS	SEE REMARK 999	UNP P19801
B	21	ARG	PRO	engineered mutation	UNP P19801
B	592	SER	THR	SEE REMARK 999	UNP P19801
B	645	ASP	HIS	SEE REMARK 999	UNP P19801

- Molecule 2 is an oligosaccharide called 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
2	C	3	Total	C	N	O	0	0	0
			39	22	2	15			

- 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
3	D	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cu	0	0
			1	1		
4	A	1	Total	Cu	0	0
			1	1		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Ca	0	0
			2	2		
5	A	2	Total	Ca	0	0
			2	2		

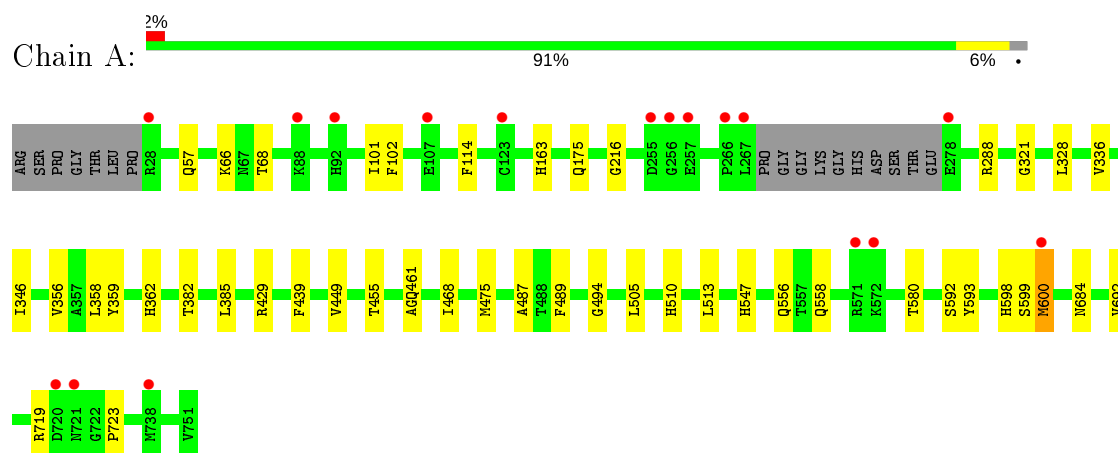
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	515	Total	O	0	0
			515	515		
6	B	482	Total	O	0	0
			482	482		

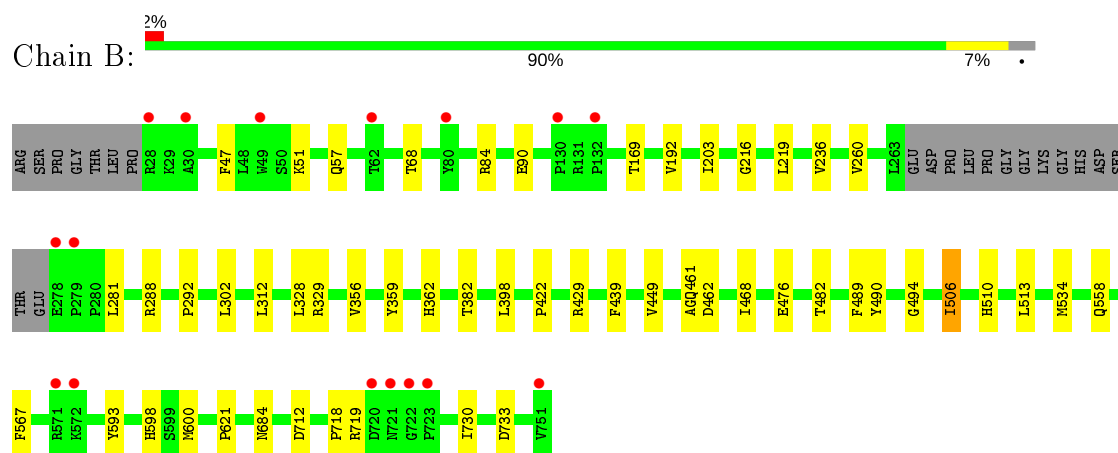
3 Residue-property plots

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

- Molecule 1: Amiloride-sensitive amine oxidase



- Molecule 1: Amiloride-sensitive amine oxidase



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



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

Chain D:  100%

NAG1
NAG2

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

Chain E:  50% 50%

NAG1
NAG2

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

Chain F:  50% 50%

NAG1
NAG2

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

Chain G:  100%

NAG1
NAG2

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

Chain H:  50% 50%

NAG1
NAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.69Å 94.60Å 196.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.13 – 2.05 31.13 – 2.05	Depositor EDS
% Data completeness (in resolution range)	97.5 (31.13-2.05) 97.5 (31.13-2.05)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.05Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.177 , 0.215 0.182 , 0.218	Depositor DCC
R_{free} test set	5416 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	18.2	Xtriage
Anisotropy	0.122	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12719	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 3.32% 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: CA, BMA, CU, NAG, AGQ

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	0.47	0/6005	0.61	0/8203
1	B	0.46	0/5962	0.61	0/8145
All	All	0.46	0/11967	0.61	0/16348

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	5789	0	5484	31	0
1	B	5748	0	5444	32	0
2	C	39	0	34	1	0
3	D	28	0	25	0	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
3	G	28	0	25	0	0
3	H	28	0	25	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	2	0	0	0	0
6	A	515	0	0	1	0
6	B	482	0	0	3	0
All	All	12719	0	11087	61	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.

All (61) 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:A:328:LEU:HD21	1:A:382:THR:HG21	1.58	0.86
1:B:328:LEU:HD21	1:B:382:THR:HG21	1.70	0.72
1:A:449[B]:VAL:HG21	1:A:468:ILE:CG2	2.27	0.64
1:B:84:ARG:CZ	1:B:90:GLU:OE1	2.45	0.64
1:B:449[B]:VAL:HG21	1:B:468:ILE:CG2	2.28	0.63
1:A:598[B]:HIS:ND1	1:B:598[B]:HIS:CE1	2.70	0.59
1:B:312:LEU:HD21	1:B:398[A]:LEU:HD21	1.82	0.59
1:B:302:LEU:HD21	1:B:422:PRO:CD	2.35	0.57
1:A:356[B]:VAL:HG22	1:A:513:LEU:HB2	1.86	0.57
1:B:718:PRO:O	1:B:719:ARG:NH1	2.38	0.56
1:B:57:GLN:O	1:B:68[B]:THR:HG22	2.04	0.56
1:A:216:GLY:HA2	1:A:489:PHE:CG	2.42	0.55
1:A:57:GLN:O	1:A:68[B]:THR:HG22	2.07	0.54
1:B:219:LEU:HD23	1:B:236:VAL:HG22	1.89	0.54
1:A:66:LYS:CE	1:A:68[B]:THR:HG21	2.37	0.53
1:B:449[B]:VAL:HG21	1:B:468:ILE:HG23	1.92	0.52
1:B:203:ILE:HD11	1:B:219:LEU:HD12	1.92	0.52
1:B:302:LEU:HD21	1:B:422:PRO:HD2	1.92	0.52
1:A:321:GLY:HA2	1:B:292:PRO:HD2	1.93	0.50
1:A:359:TYR:CD1	1:A:510:HIS:HB3	2.46	0.50
1:A:68[A]:THR:HG22	1:A:102:PHE:HB2	1.92	0.50
1:B:169:THR:HG22	1:B:260:VAL:CG1	2.42	0.50
1:A:66:LYS:HE2	1:A:68[B]:THR:HG21	1.94	0.49
1:B:449[B]:VAL:CG2	1:B:468:ILE:HG23	2.42	0.49
1:B:216:GLY:HA2	1:B:489:PHE:CG	2.48	0.48
1:B:169:THR:HG22	1:B:260:VAL:HG13	1.94	0.48
1:B:712:ASP:OD1	1:B:730:ILE:HD12	2.13	0.48
1:B:490:TYR:HA	1:B:506:ILE:HG13	1.95	0.47
1:B:558:GLN:NE2	6:B:1096:HOH:O	2.44	0.47
1:B:356[B]:VAL:HG22	1:B:513:LEU:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:487:ALA:HB1	1:A:505:LEU:HD11	1.96	0.47
1:B:362:HIS:CG	1:B:494:GLY:HA2	2.50	0.47
1:B:359:TYR:CD1	1:B:510:HIS:HB3	2.50	0.47
1:A:598[B]:HIS:ND1	1:B:598[B]:HIS:HE1	2.11	0.47
1:A:163:HIS:ND1	1:A:175:GLN:HG2	2.30	0.47
1:A:719[B]:ARG:HD3	1:A:723:PRO:O	2.15	0.46
1:A:487:ALA:CB	1:A:505:LEU:HD11	2.47	0.45
2:C:2:NAG:H4	2:C:3:BMA:O2	2.15	0.45
1:A:547:HIS:CE1	1:B:192:VAL:HG21	2.53	0.44
1:A:356[B]:VAL:CG2	1:A:513:LEU:HB2	2.48	0.44
1:A:449[B]:VAL:CG2	1:A:468:ILE:CG2	2.95	0.44
1:A:599:SER:HA	1:A:600:MET:HE3	2.01	0.43
1:A:449[B]:VAL:CG2	1:A:468:ILE:HG23	2.48	0.43
1:B:329:ARG:NH2	6:B:892:HOH:O	2.51	0.43
1:B:449[B]:VAL:CG2	1:B:468:ILE:CG2	2.95	0.43
1:B:462:ASP:HB2	1:B:482:THR:HG23	2.00	0.42
1:A:600:MET:HE3	1:A:692:VAL:HG12	1.99	0.42
6:B:1075:HOH:O	3:H:1:NAG:H81	2.19	0.42
1:A:449[B]:VAL:HG21	1:A:468:ILE:HG23	2.00	0.42
1:A:336:VAL:HG21	1:A:475[B]:MET:HE3	2.02	0.42
1:A:346[A]:ILE:HD12	1:A:593:TYR:CE1	2.55	0.42
1:A:556:GLN:HG2	1:A:558:GLN:OE1	2.20	0.42
1:B:47:PHE:CZ	1:B:51:LYS:HE2	2.55	0.41
6:A:1243:HOH:O	1:B:534:MET:HE3	2.19	0.41
1:A:356[A]:VAL:HG12	1:A:358:LEU:HG	2.02	0.41
1:B:468:ILE:HB	1:B:476:GLU:HB3	2.01	0.41
1:A:580:THR:HG22	1:A:592[A]:SER:OG	2.21	0.41
1:A:362:HIS:CG	1:A:494:GLY:HA2	2.56	0.41
1:A:385:LEU:HD21	1:A:455:THR:HG23	2.03	0.41
1:A:101:ILE:HD12	1:A:114:PHE:CE1	2.55	0.40
1:B:567:PHE:O	1:B:621:PRO:HD2	2.21	0.40

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	723/731 (99%)	700 (97%)	23 (3%)	0	100	100
1	B	717/731 (98%)	694 (97%)	23 (3%)	0	100	100
All	All	1440/1462 (98%)	1394 (97%)	46 (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	614/634 (97%)	609 (99%)	5 (1%)	81	82
1	B	611/634 (96%)	602 (98%)	9 (2%)	65	63
All	All	1225/1268 (97%)	1211 (99%)	14 (1%)	71	73

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	288	ARG
1	A	429	ARG
1	A	439	PHE
1	A	600	MET
1	A	684	ASN
1	B	281	LEU
1	B	288	ARG
1	B	429	ARG
1	B	439	PHE
1	B	506	ILE
1	B	593	TYR
1	B	600	MET
1	B	684	ASN
1	B	733	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	AGQ	A	461	1	16,18,19	2.92	5 (31%)	13,24,26	1.42	2 (15%)
1	AGQ	B	461	1	16,18,19	2.90	6 (37%)	13,24,26	1.71	3 (23%)

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	AGQ	A	461	1	-	3/10/27/29	0/1/1/1
1	AGQ	B	461	1	-	3/10/27/29	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	461	AGQ	N6-N5	-7.87	1.24	1.38
1	A	461	AGQ	N6-N5	-7.86	1.24	1.38
1	A	461	AGQ	CG-CD1	-6.69	1.39	1.49
1	B	461	AGQ	CG-CD1	-6.69	1.39	1.49
1	A	461	AGQ	CE1-CZ	3.26	1.40	1.35
1	B	461	AGQ	CE1-CZ	3.23	1.40	1.35
1	A	461	AGQ	CE2-N5	2.22	1.35	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	461	AGQ	CE2-N5	2.19	1.35	1.31
1	A	461	AGQ	CE1-CD1	-2.04	1.39	1.44
1	B	461	AGQ	CD2-CG	2.01	1.39	1.34
1	B	461	AGQ	CE1-CD1	-2.00	1.39	1.44

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	461	AGQ	CD2-CG-CD1	4.74	122.28	118.64
1	A	461	AGQ	CD2-CG-CD1	3.52	121.34	118.64
1	B	461	AGQ	CB-CA-C	-2.88	106.08	111.47
1	A	461	AGQ	CB-CA-C	-2.70	106.41	111.47
1	B	461	AGQ	CE2-N5-N6	2.07	122.54	118.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	461	AGQ	CE2-N5-N6-C7
1	A	461	AGQ	N8-C7-N6-N5
1	A	461	AGQ	N9-C7-N6-N5
1	B	461	AGQ	CE2-N5-N6-C7
1	B	461	AGQ	N8-C7-N6-N5
1	B	461	AGQ	N9-C7-N6-N5

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

13 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	0.50	0	17,19,21	0.80	1 (5%)
2	NAG	C	2	2	14,14,15	0.65	0	17,19,21	1.31	3 (17%)
2	BMA	C	3	2	11,11,12	0.41	0	15,15,17	1.65	1 (6%)
3	NAG	D	1	1,3	14,14,15	0.44	0	17,19,21	1.13	1 (5%)
3	NAG	D	2	3	14,14,15	0.52	0	17,19,21	0.89	1 (5%)
3	NAG	E	1	1,3	14,14,15	0.75	1 (7%)	17,19,21	1.20	1 (5%)
3	NAG	E	2	3	14,14,15	0.54	0	17,19,21	1.02	0
3	NAG	F	1	1,3	14,14,15	0.63	0	17,19,21	1.10	1 (5%)
3	NAG	F	2	3	14,14,15	0.51	0	17,19,21	0.94	0
3	NAG	G	1	1,3	14,14,15	0.58	0	17,19,21	1.08	2 (11%)
3	NAG	G	2	3	14,14,15	0.55	0	17,19,21	1.25	1 (5%)
3	NAG	H	1	1,3	14,14,15	0.56	0	17,19,21	1.11	1 (5%)
3	NAG	H	2	3	14,14,15	0.69	0	17,19,21	0.98	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
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	BMA	C	3	2	-	1/2/19/22	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	0/6/23/26	0/1/1/1
3	NAG	G	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	0/6/23/26	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	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)
3	E	1	NAG	O5-C1	-2.08	1.40	1.43

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	3	BMA	O5-C5-C6	4.77	114.68	107.20
3	G	2	NAG	C1-O5-C5	3.63	117.11	112.19
3	H	1	NAG	C1-O5-C5	3.44	116.85	112.19
2	C	2	NAG	C4-C3-C2	3.04	115.47	111.02
3	D	1	NAG	C1-O5-C5	2.73	115.89	112.19
3	G	1	NAG	C1-O5-C5	2.63	115.75	112.19
2	C	2	NAG	O3-C3-C2	-2.56	104.17	109.47
3	F	1	NAG	C4-C3-C2	2.49	114.66	111.02
3	G	1	NAG	O5-C1-C2	-2.27	107.70	111.29
3	D	2	NAG	C1-O5-C5	2.25	115.23	112.19
2	C	1	NAG	O5-C5-C6	2.19	110.64	107.20
3	H	2	NAG	O5-C5-C4	-2.11	105.69	110.83
3	E	1	NAG	C1-C2-N2	-2.11	106.89	110.49
2	C	2	NAG	O5-C1-C2	-2.05	108.05	111.29

There are no chirality outliers.

All (3) torsion outliers are listed below:

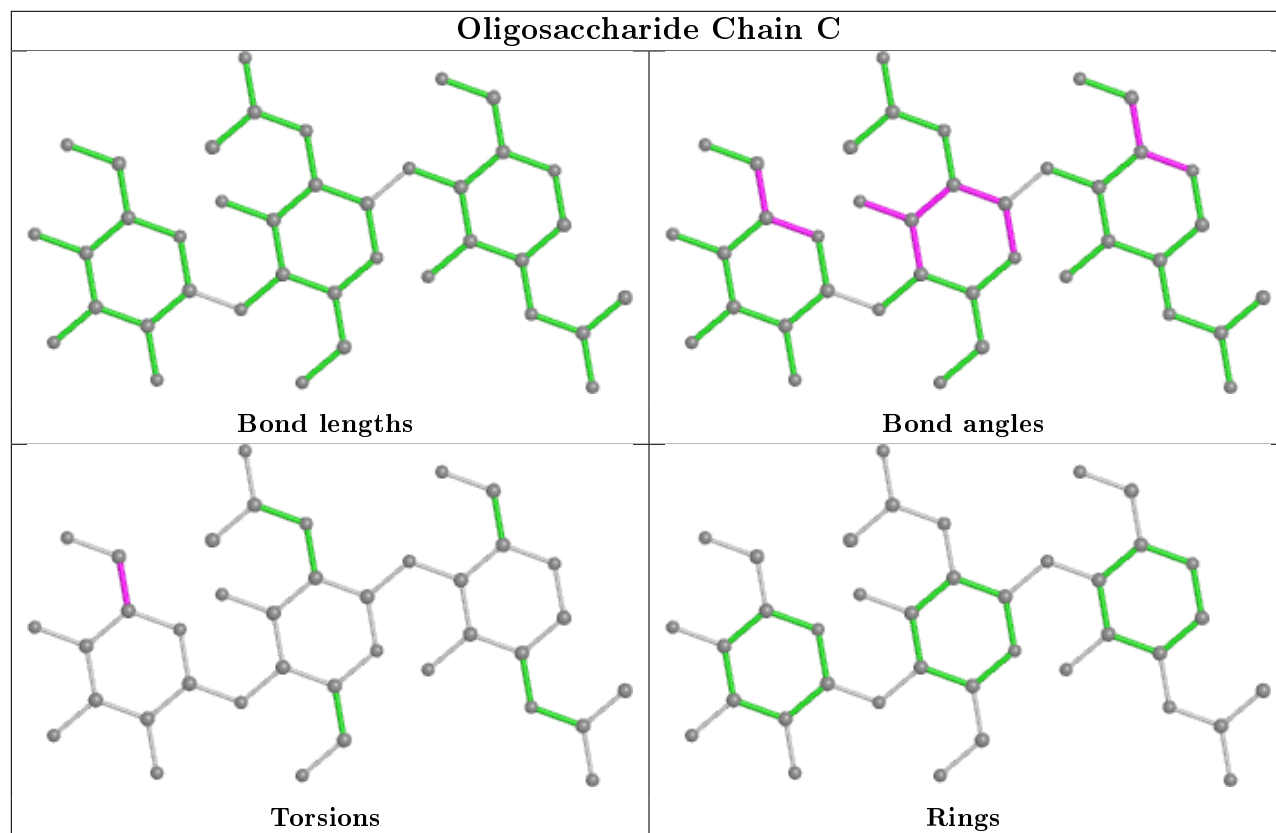
Mol	Chain	Res	Type	Atoms
3	G	1	NAG	C4-C5-C6-O6
2	C	3	BMA	O5-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6

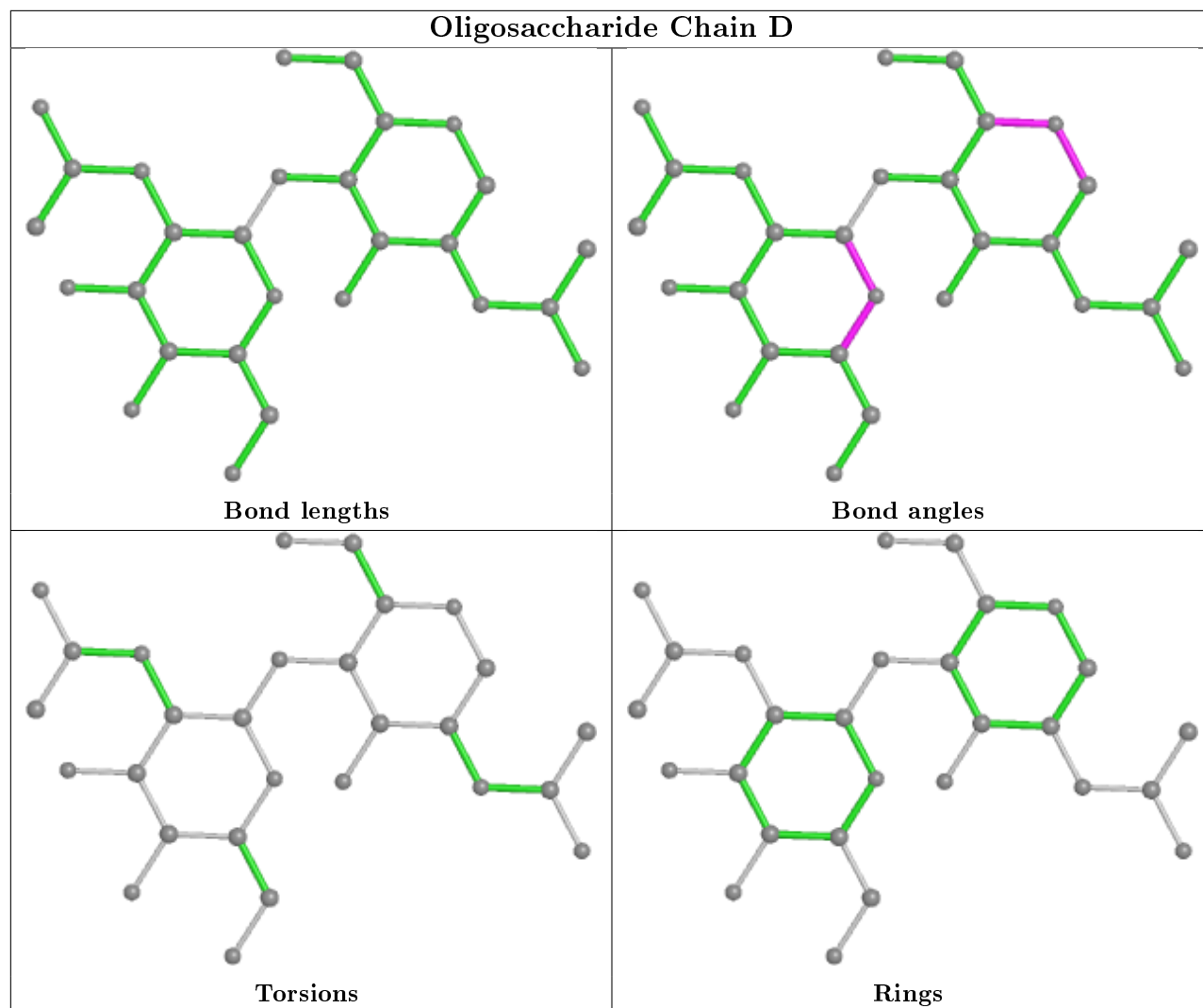
There are no ring outliers.

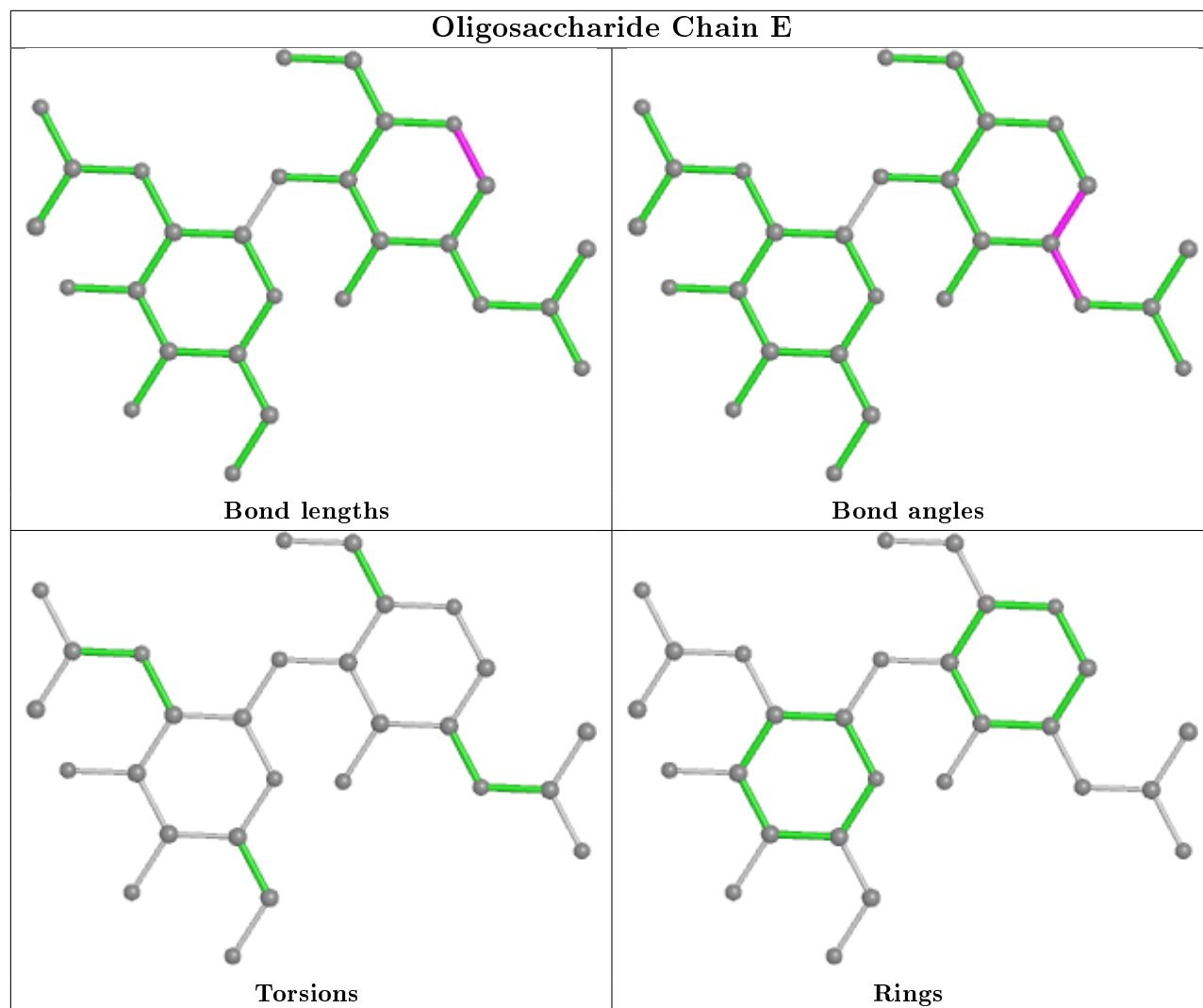
3 monomers are involved in 2 short contacts:

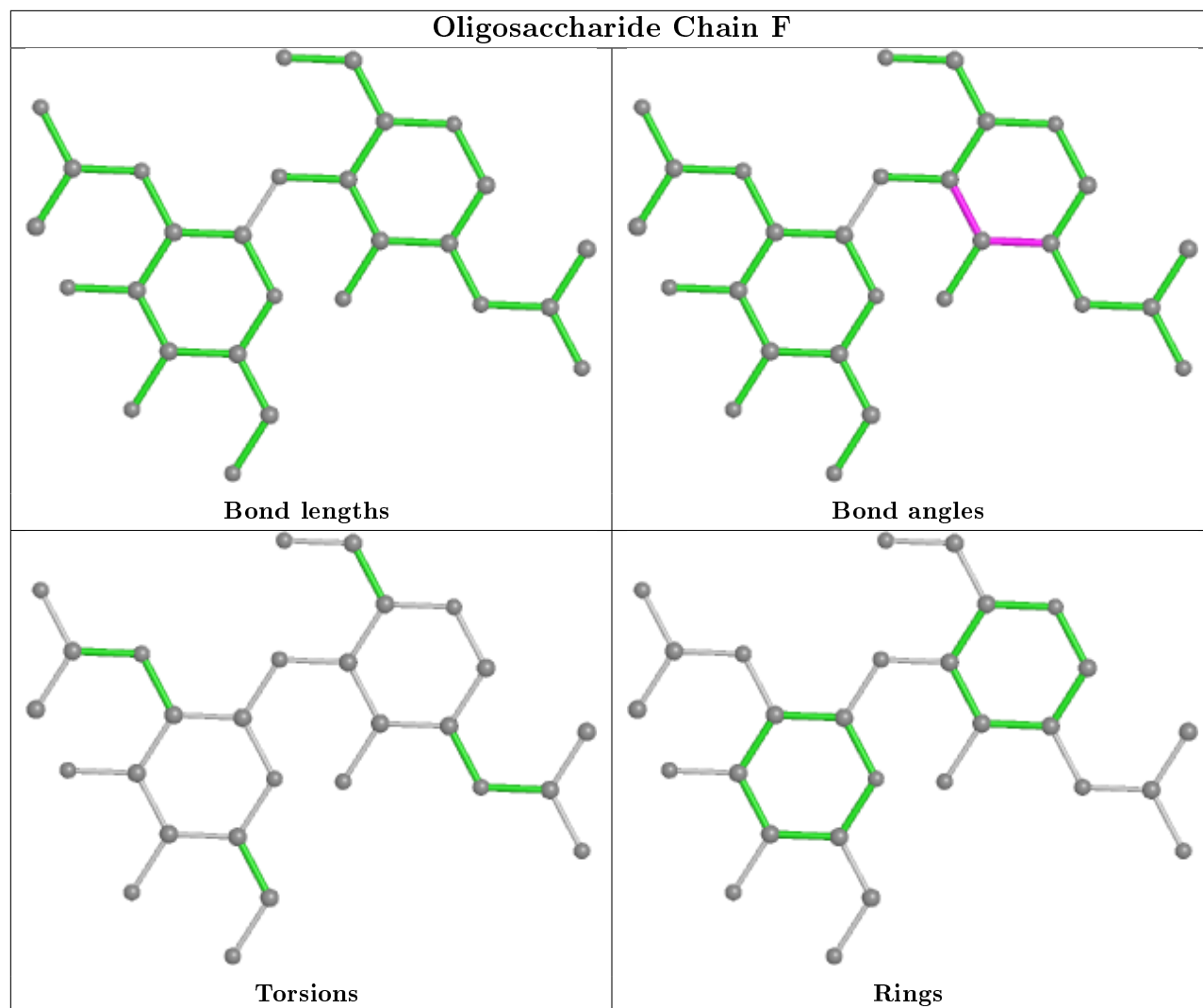
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3	BMA	1	0
3	H	1	NAG	1	0
2	C	2	NAG	1	0

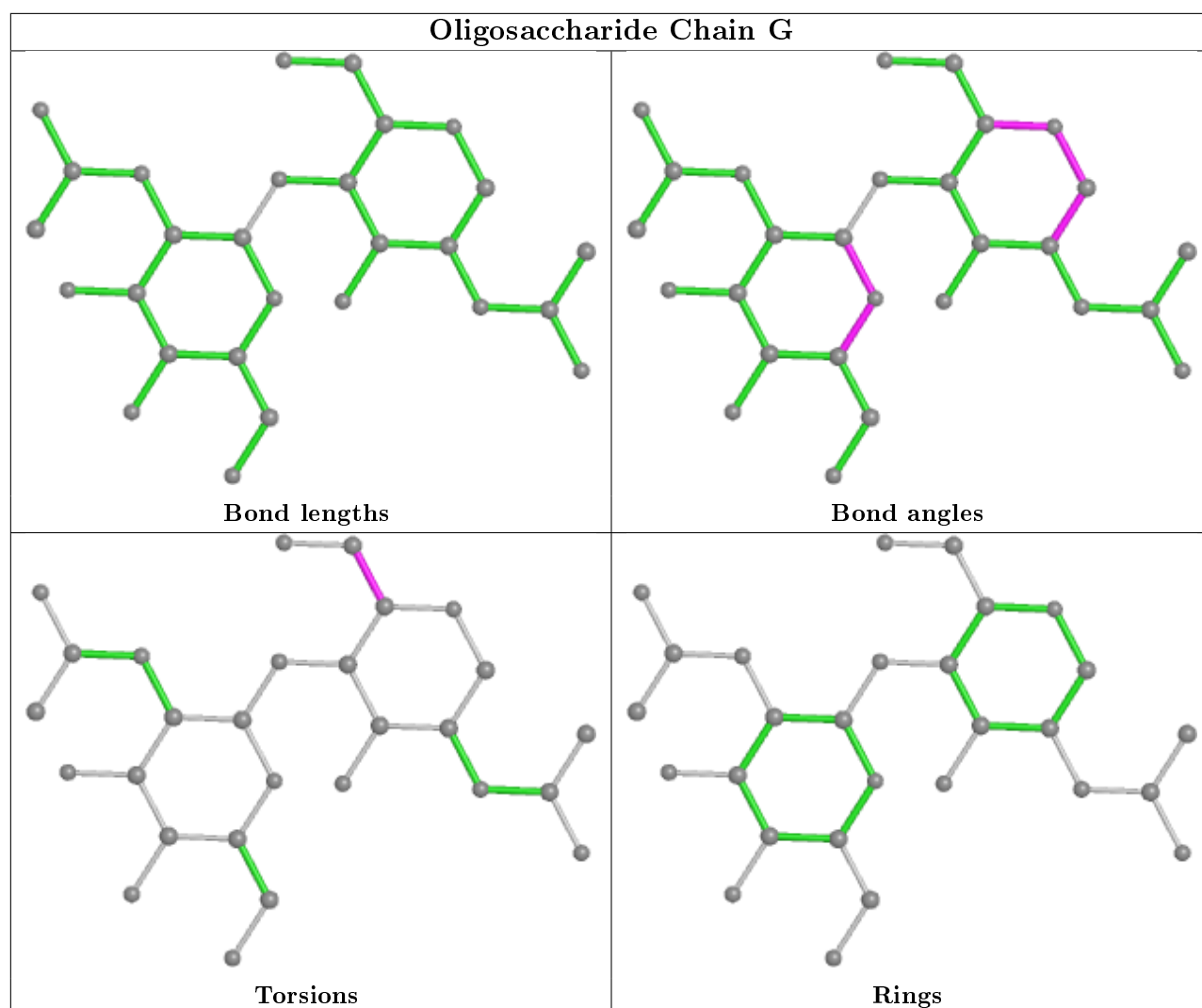
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

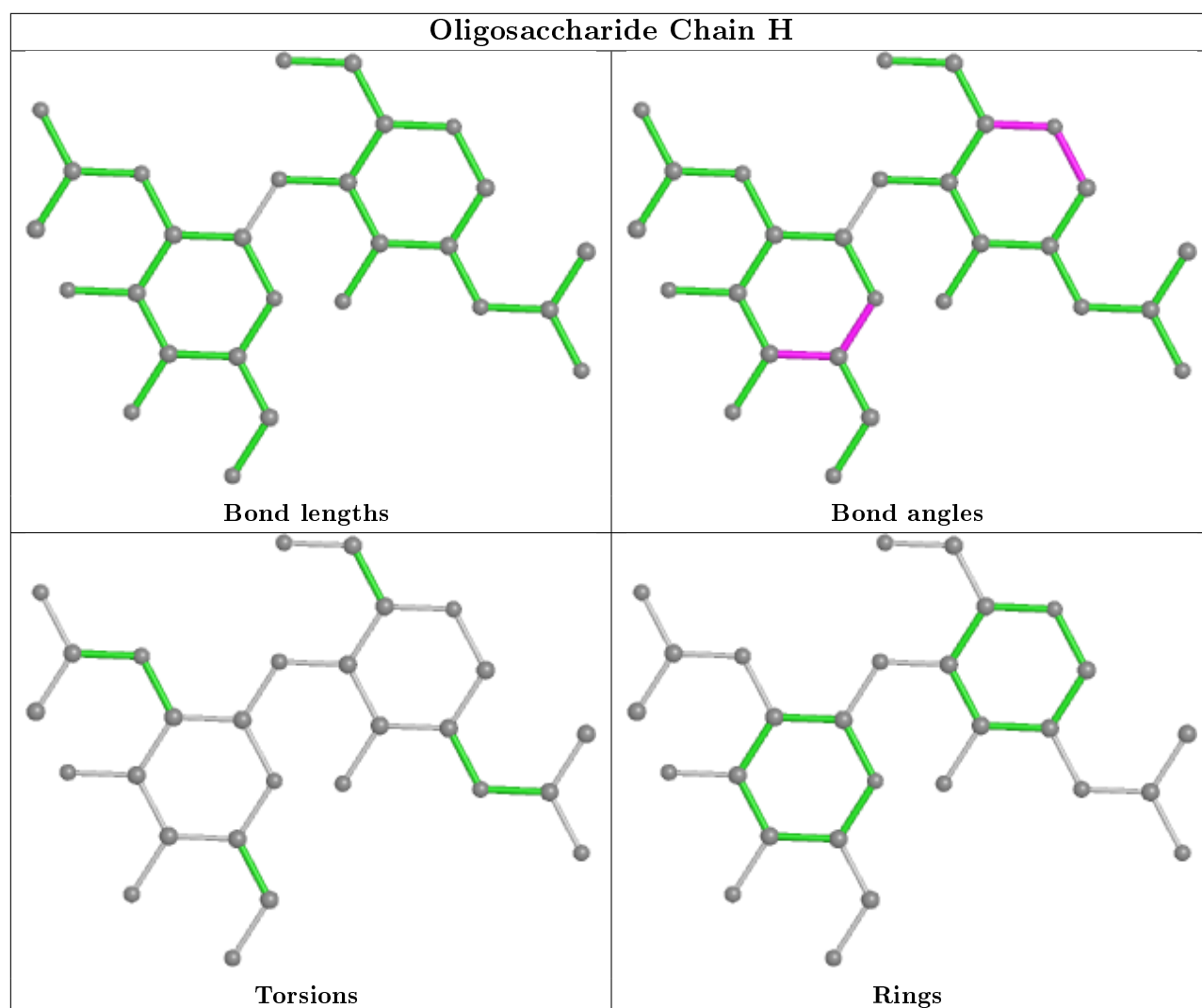












5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	713/731 (97%)	-0.19	17 (2%) 59 63	6, 15, 29, 43	1 (0%)
1	B	709/731 (96%)	-0.17	16 (2%) 60 64	7, 16, 28, 36	1 (0%)
All	All	1422/1462 (97%)	-0.18	33 (2%) 60 64	6, 16, 29, 43	2 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	278	GLU	4.7
1	B	721	ASN	4.1
1	B	28	ARG	3.9
1	A	266	PRO	3.8
1	A	721	ASN	3.6
1	A	267	LEU	3.6
1	B	279	PRO	3.1
1	A	720	ASP	3.1
1	B	130	PRO	2.8
1	A	28	ARG	2.8
1	B	132	PRO	2.7
1	B	720	ASP	2.6
1	A	257	GLU	2.5
1	A	107	GLU	2.5
1	A	572	LYS	2.4
1	B	722	GLY	2.4
1	B	571	ARG	2.4
1	A	256	GLY	2.4
1	A	571	ARG	2.4
1	B	30	ALA	2.4
1	B	80	TYR	2.3
1	B	723	PRO	2.2
1	A	738	MET	2.2
1	A	123	CYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	92	HIS	2.2
1	A	88	LYS	2.1
1	A	600	MET	2.1
1	B	572	LYS	2.1
1	B	751	VAL	2.1
1	B	49	TRP	2.1
1	A	278	GLU	2.1
1	A	255	ASP	2.0
1	B	62	THR	2.0

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	AGQ	B	461	18/19	0.89	0.23	12,20,24,24	13
1	AGQ	A	461	18/19	0.90	0.19	14,19,22,22	13

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.

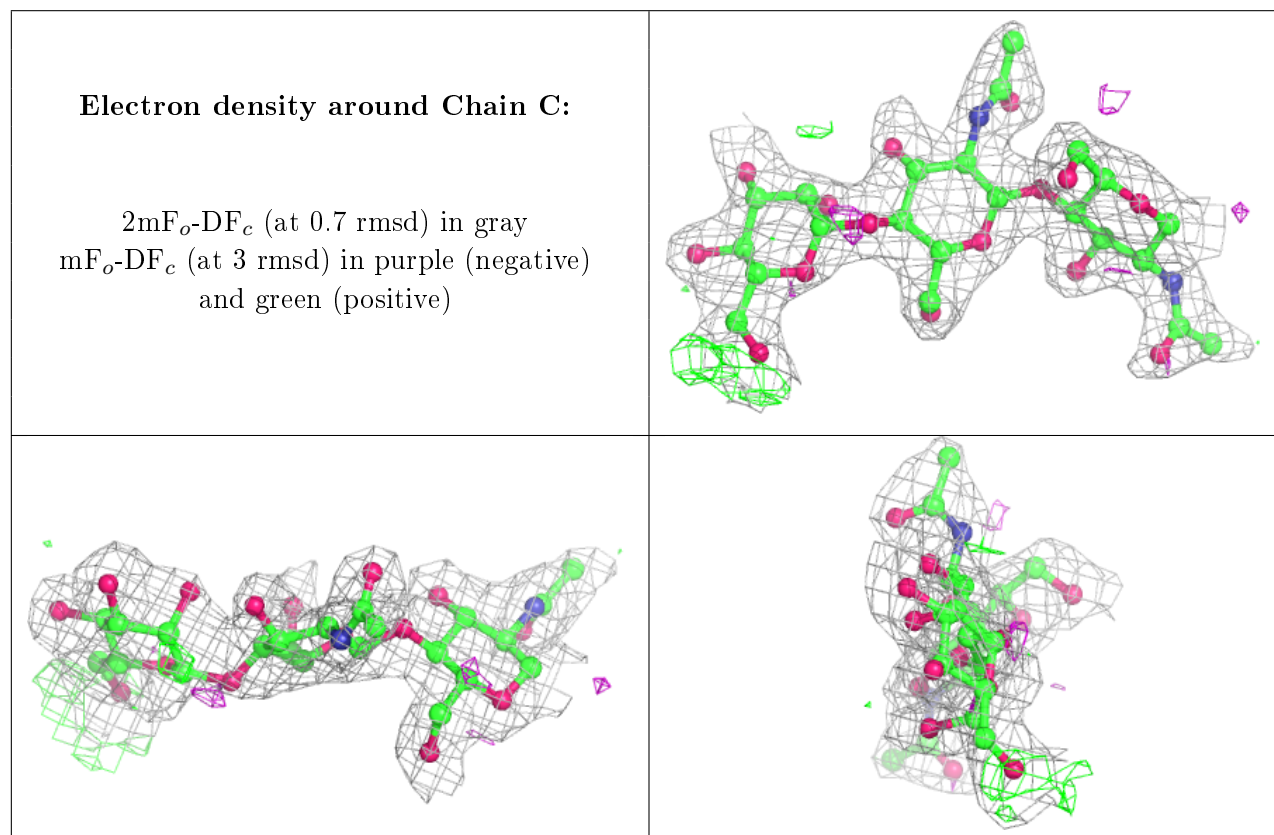
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	H	2	14/15	0.70	0.28	31,35,35,35	14
3	NAG	E	2	14/15	0.76	0.40	45,48,49,50	0
2	BMA	C	3	11/12	0.78	0.21	37,38,39,39	0
3	NAG	E	1	14/15	0.86	0.21	30,35,38,41	0
3	NAG	H	1	14/15	0.86	0.21	29,32,35,36	0
3	NAG	F	2	14/15	0.87	0.20	32,34,37,38	0
2	NAG	C	2	14/15	0.89	0.17	32,34,36,39	0
3	NAG	D	2	14/15	0.89	0.27	38,41,42,43	0
3	NAG	G	1	14/15	0.90	0.17	26,28,32,34	0
3	NAG	G	2	14/15	0.90	0.36	38,39,42,43	0
3	NAG	F	1	14/15	0.91	0.13	24,27,31,33	0
3	NAG	D	1	14/15	0.93	0.17	18,27,30,35	0

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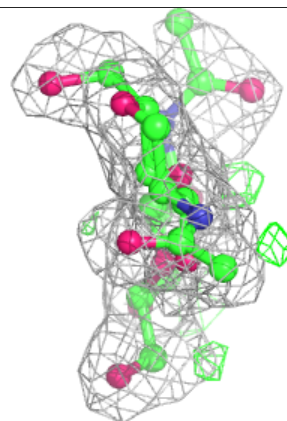
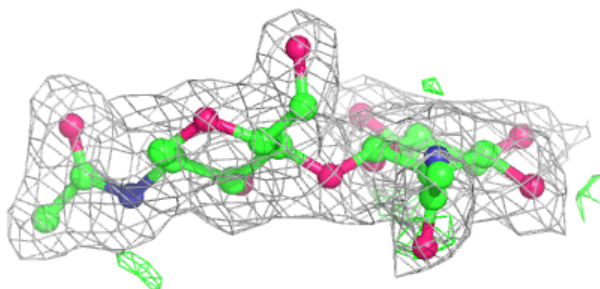
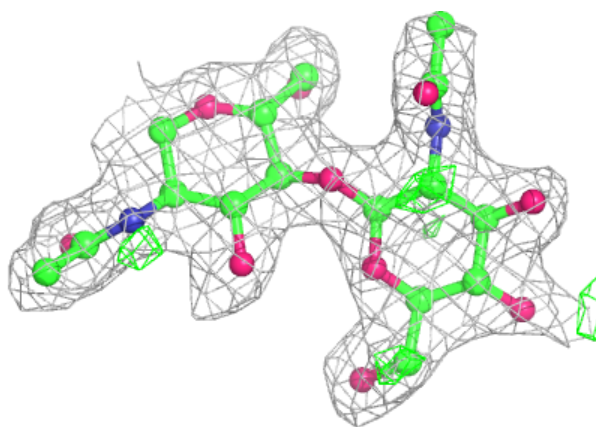
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	C	1	14/15	0.95	0.13	22,24,26,29	0

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.



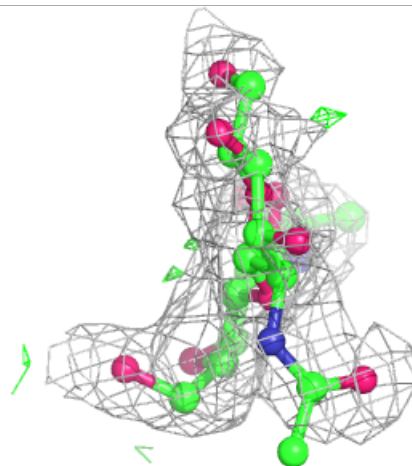
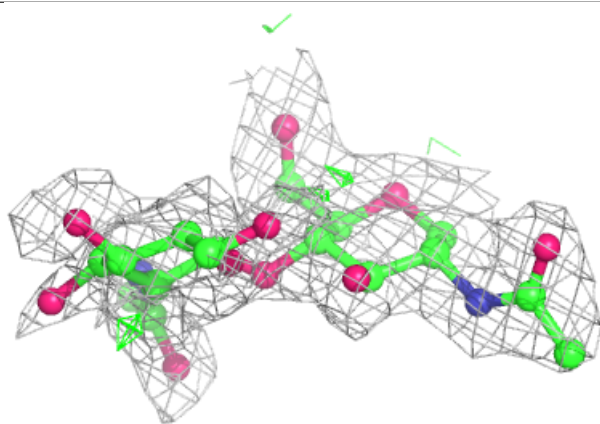
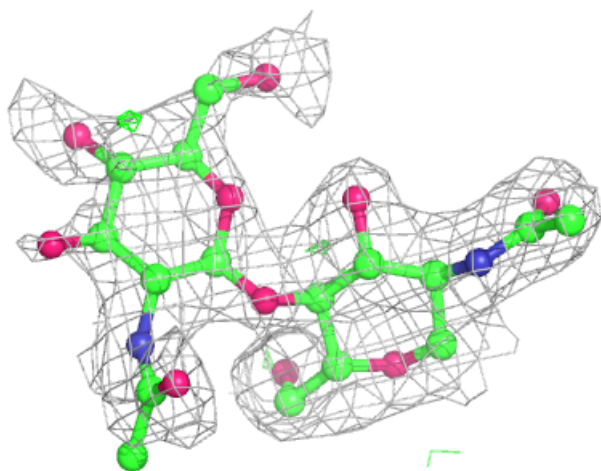
Electron density around Chain D:

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



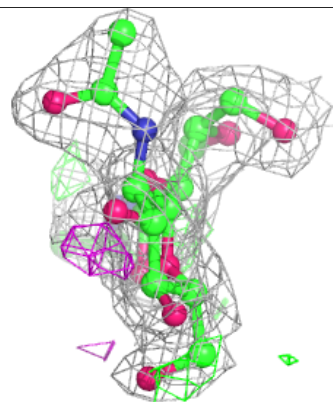
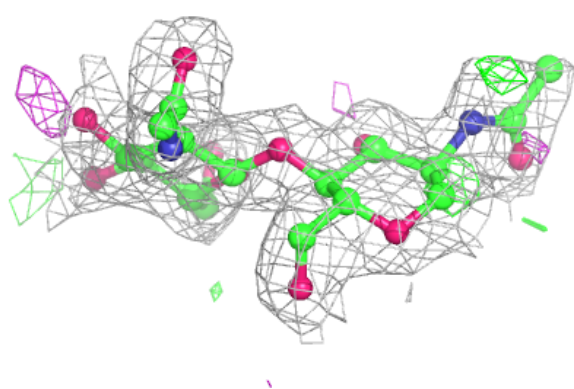
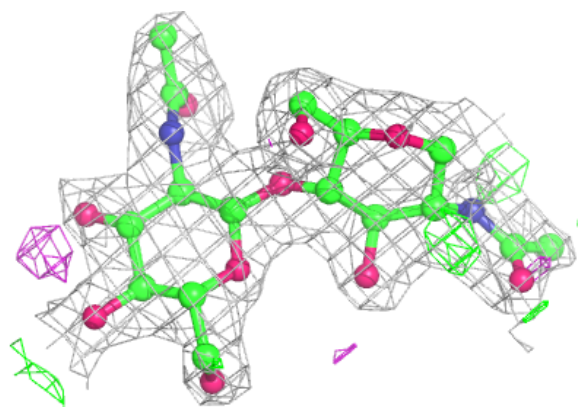
Electron density around Chain E:

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

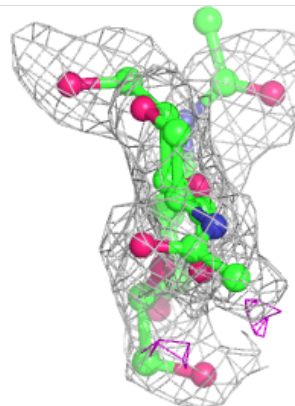
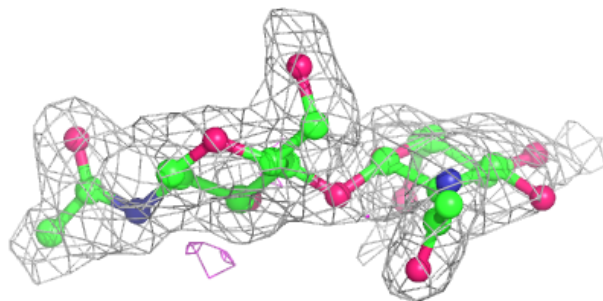
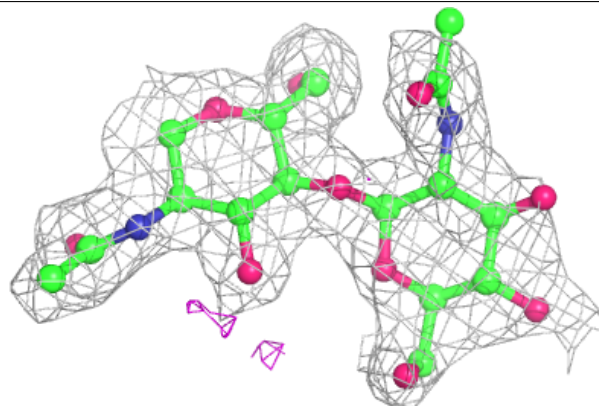


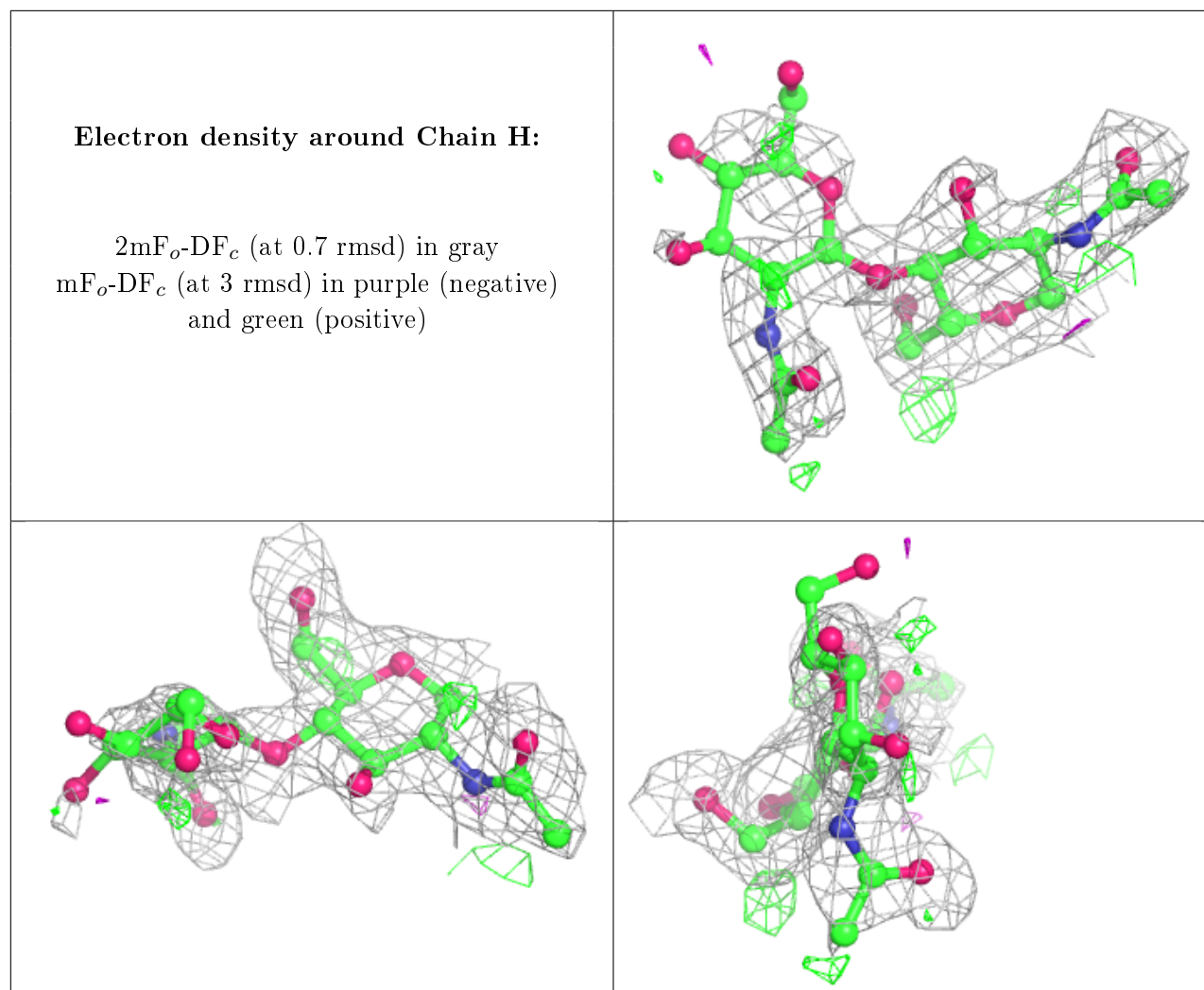
Electron density around Chain F:

$2mF_o - DF_c$ (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)





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(\AA^2)	Q<0.9
5	CA	B	802	1/1	0.99	0.08	13,13,13,13	0
5	CA	B	803	1/1	0.99	0.04	18,18,18,18	0
4	CU	A	801	1/1	1.00	0.03	14,14,14,14	0
5	CA	A	802	1/1	1.00	0.05	9,9,9,9	0
4	CU	B	801	1/1	1.00	0.04	14,14,14,14	0
5	CA	A	803	1/1	1.00	0.05	10,10,10,10	0

6.5 Other polymers [i](#)

There are no such residues in this entry.