



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 22, 2025 – 01:51 AM EDT

PDB ID : 6CMI / pdb_00006cmi
Title : Crystal Structure of the Hendra Virus Attachment G Glycoprotein Bound to a Potent Cross-Reactive Neutralizing Human Monoclonal Antibody m102.3
Authors : Xu, K.; Nikolov, D.
Deposited on : 2018-03-05
Resolution : 2.72 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	FAILED
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

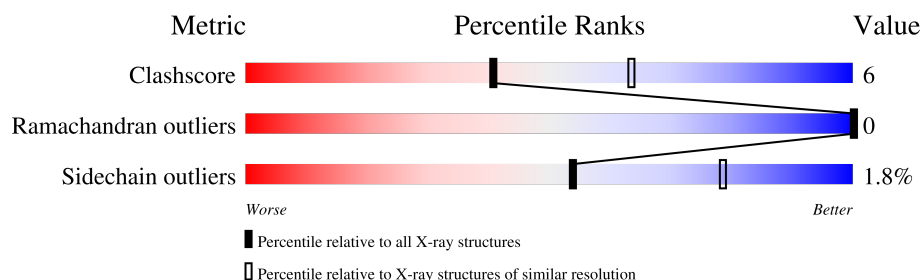
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.72 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))
Clashscore	180529	4439 (2.74-2.70)
Ramachandran outliers	177936	4374 (2.74-2.70)
Sidechain outliers	177891	4375 (2.74-2.70)

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

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	B	428	80% 19% .
2	C	214	86% 13% .
3	D	235	81% 16% .
4	A	2	50% 50%
4	E	2	50% 50%
4	F	2	50% 50%
5	G	6	50% 33% 17%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6955 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 Glycoprotein G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	428	Total	C	N	O	S	0	0	0
			3372	2147	566	640	19			

- Molecule 2 is a protein called m102.3 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	213	Total	C	N	O	S	0	0	0
			1640	1023	282	330	5			

- Molecule 3 is a protein called IgG Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	228	Total	C	N	O	S	0	0	0
			1721	1090	287	337	7			

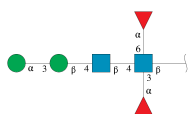
- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

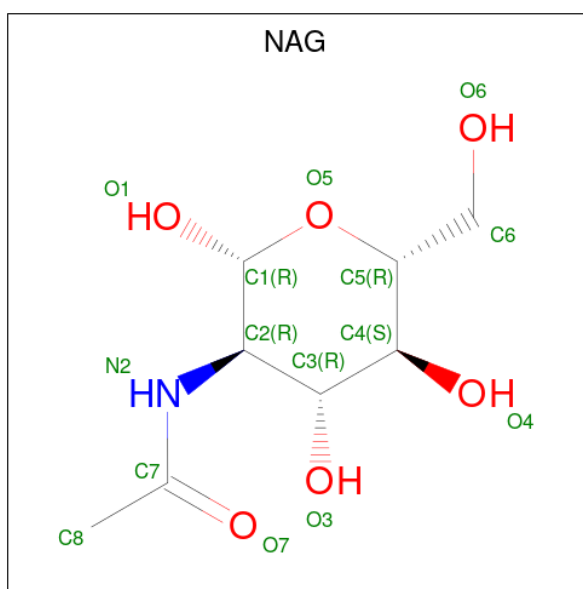
- Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alpha

-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	6	Total	C	N	O	0	0	0
			70	40	2	28			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 7 is water.

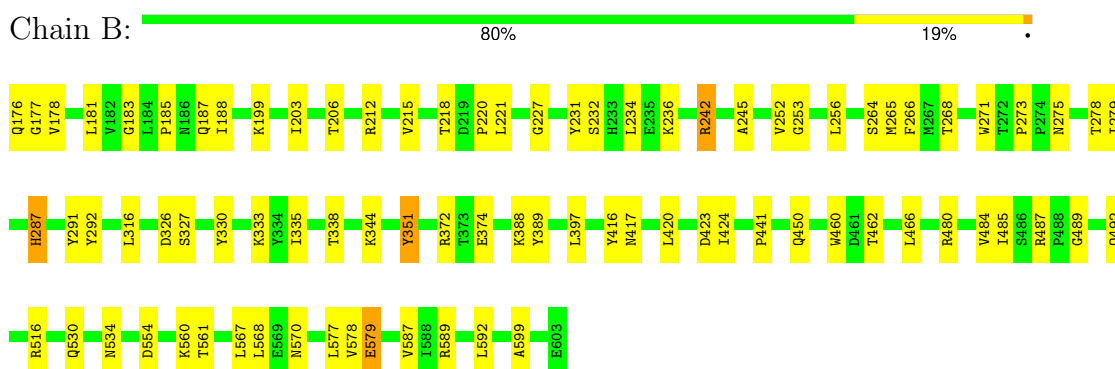
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	25	Total	O	0	0
			25	25		
7	C	10	Total	O	0	0
			10	10		
7	D	19	Total	O	0	0
			19	19		

3 Residue-property plots

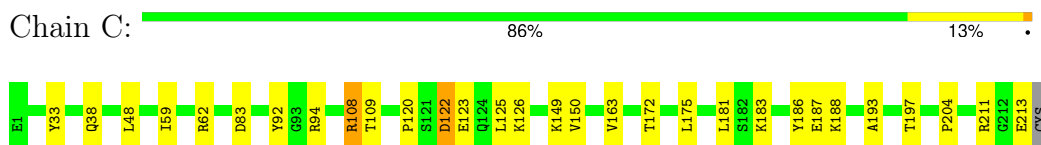
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

Note EDS failed to run properly.

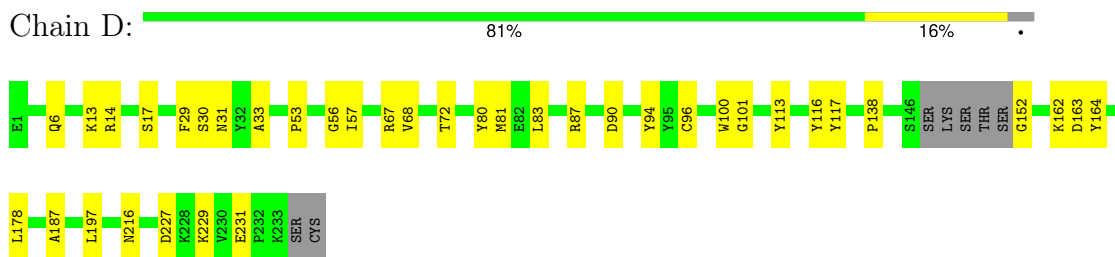
- Molecule 1: Glycoprotein G



- Molecule 2: m102.3 light chain



- Molecule 3: IgG Heavy chain



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



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

Chain E:  50% 50%

 MAG1
MAG2

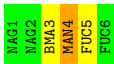
- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  50% 50%

 MAG1
MAG2

- Molecule 5: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-3)][alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  50% 33% 17%

 MAG1
MAG2
BMA3
MAN4
FUC5
FUC6

4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	89.28Å 148.53Å 185.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.99 – 2.72	Depositor
% Data completeness (in resolution range)	99.4 (35.99-2.72)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.72Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.196 , 0.246	Depositor
Wilson B-factor (Å ²)	60.8	Xtriage
Anisotropy	0.350	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6955	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, BMA, FUC, MAN

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	B	0.30	0/3453	0.53	0/4703
2	C	0.27	0/1676	0.53	0/2273
3	D	0.28	0/1764	0.55	0/2403
All	All	0.29	0/6893	0.53	0/9379

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2
3	D	0	2
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	287	HIS	Peptide
1	B	423	ASP	Peptide
3	D	29	PHE	Peptide
3	D	56	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3372	0	3310	48	1
2	C	1640	0	1596	19	0
3	D	1721	0	1680	21	1
4	A	28	0	25	0	0
4	E	28	0	25	0	0
4	F	28	0	25	1	0
5	G	70	0	61	1	0
6	B	14	0	13	0	0
7	B	25	0	0	1	0
7	C	10	0	0	0	0
7	D	19	0	0	2	0
All	All	6955	0	6735	87	1

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 6.

All (87) 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)
3:D:216:ASN:ND2	3:D:227:ASP:OD2	1.85	1.07
1:B:416:TYR:HE1	1:B:424:ILE:HG23	1.33	0.92
2:C:187:GLU:HA	2:C:211:ARG:HH12	1.36	0.91
1:B:178:VAL:HG23	1:B:227:GLY:HA2	1.71	0.72
7:B:801:HOH:O	5:G:4:MAN:O4	2.10	0.70
3:D:152:GLY:O	7:D:301:HOH:O	2.12	0.68
3:D:229:LYS:CE	3:D:231:GLU:HG2	2.24	0.67
1:B:416:TYR:CE1	1:B:424:ILE:HG23	2.23	0.67
1:B:333:LYS:HE3	1:B:335:ILE:HD11	1.76	0.66
1:B:327:SER:HB2	1:B:330:TYR:HB3	1.75	0.66
4:F:2:NAG:H83	4:F:2:NAG:H3	1.80	0.64
3:D:229:LYS:HE3	3:D:231:GLU:HG2	1.82	0.62
1:B:176:GLN:OE1	1:B:177:GLY:N	2.33	0.61
3:D:178:LEU:O	7:D:302:HOH:O	2.16	0.61
1:B:206:THR:HG21	1:B:264:SER:OG	2.01	0.60
1:B:417:ASN:HB3	1:B:420:LEU:HD12	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:108:ARG:HD3	2:C:109:THR:O	2.04	0.57
2:C:122:ASP:O	2:C:126:LYS:HG2	2.05	0.57
2:C:94:ARG:HD3	3:D:113:TYR:HB3	1.87	0.57
1:B:561:THR:HG22	1:B:578:VAL:HG13	1.87	0.56
1:B:178:VAL:HG12	1:B:568:LEU:HD13	1.86	0.56
2:C:123:GLU:OE2	2:C:123:GLU:N	2.29	0.56
2:C:149:LYS:HB2	2:C:193:ALA:HB3	1.87	0.56
1:B:534:ASN:ND2	1:B:554:ASP:O	2.40	0.54
1:B:178:VAL:CG2	1:B:227:GLY:HA2	2.39	0.53
3:D:229:LYS:NZ	3:D:231:GLU:HG2	2.24	0.52
3:D:138:PRO:HB3	3:D:164:TYR:HB3	1.91	0.52
1:B:242:ARG:HD2	3:D:57:ILE:HG12	1.91	0.52
3:D:53:PRO:HG3	3:D:72:THR:HG21	1.93	0.51
2:C:38:GLN:HB2	2:C:48:LEU:HD11	1.92	0.51
2:C:163:VAL:HG22	2:C:175:LEU:HD12	1.92	0.51
1:B:234:LEU:HD21	1:B:236:LYS:HE3	1.92	0.50
2:C:92:TYR:HB2	3:D:116:TYR:O	2.10	0.50
1:B:273:PRO:HG3	1:B:279:ILE:HD13	1.94	0.49
3:D:6:GLN:NE2	3:D:94:TYR:O	2.46	0.49
1:B:587:VAL:HG13	1:B:589:ARG:HG2	1.93	0.49
2:C:33:TYR:HA	2:C:92:TYR:CE1	2.47	0.49
2:C:183:LYS:O	2:C:187:GLU:HG2	2.13	0.49
1:B:203:ILE:HG13	1:B:592:LEU:HD23	1.95	0.49
1:B:287:HIS:HB3	1:B:292:TYR:HE2	1.78	0.49
1:B:561:THR:HA	1:B:577:LEU:O	2.12	0.48
1:B:253:GLY:HA2	1:B:268:THR:HG23	1.94	0.48
1:B:185:PRO:HA	1:B:570:ASN:ND2	2.29	0.48
1:B:292:TYR:HD1	1:B:316:LEU:HD21	1.79	0.47
2:C:120:PRO:HB2	2:C:125:LEU:HD21	1.95	0.47
1:B:188:ILE:HA	1:B:599:ALA:HA	1.95	0.47
1:B:256:LEU:HD12	1:B:266:PHE:HD1	1.80	0.47
3:D:187:ALA:HA	3:D:197:LEU:HB3	1.97	0.47
1:B:203:ILE:O	1:B:206:THR:OG1	2.32	0.47
3:D:33:ALA:HB2	3:D:101:GLY:HA3	1.97	0.46
1:B:181:LEU:HA	1:B:567:LEU:HG	1.97	0.46
1:B:212:ARG:O	1:B:215:VAL:HG22	2.16	0.46
3:D:13:LYS:HD3	3:D:13:LYS:HA	1.75	0.46
1:B:218:THR:HA	1:B:579:GLU:OE1	2.16	0.45
1:B:199:LYS:HD2	1:B:199:LYS:HA	1.71	0.45
1:B:275:ASN:O	1:B:278:THR:OG1	2.34	0.45
2:C:62:ARG:NH1	2:C:83:ASP:OD1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:108:ARG:NH1	2:C:172:THR:HG23	2.31	0.45
3:D:30:SER:OG	3:D:31:ASN:N	2.50	0.45
1:B:252:VAL:HG11	1:B:291:TYR:HB2	1.99	0.44
1:B:221:LEU:O	1:B:231:TYR:HA	2.18	0.44
1:B:351:TYR:CZ	1:B:441:PRO:HD3	2.53	0.44
1:B:466:LEU:O	1:B:480:ARG:HG2	2.17	0.44
1:B:484:VAL:HG23	1:B:485:ILE:HG12	1.99	0.44
1:B:460:TRP:O	1:B:462:THR:HG23	2.18	0.44
1:B:206:THR:HB	1:B:265:MET:O	2.18	0.43
2:C:197:THR:HG22	2:C:204:PRO:HG3	1.99	0.43
3:D:100:TRP:HB2	3:D:117:TYR:HB2	2.00	0.43
3:D:67:ARG:NH2	3:D:90:ASP:OD2	2.52	0.43
1:B:292:TYR:HB3	1:B:316:LEU:HD11	2.00	0.43
1:B:388:LYS:HE2	1:B:389:TYR:CZ	2.53	0.43
2:C:150:VAL:HG23	2:C:150:VAL:O	2.19	0.42
2:C:188:LYS:HG2	2:C:188:LYS:O	2.18	0.42
2:C:59:ILE:HD13	2:C:59:ILE:HA	1.90	0.42
1:B:236:LYS:HG2	1:B:245:ALA:HA	2.01	0.42
1:B:220:PRO:HA	1:B:232:SER:O	2.20	0.42
1:B:344:LYS:NZ	1:B:374:GLU:HB3	2.34	0.42
1:B:187:GLN:HG2	1:B:188:ILE:N	2.35	0.41
1:B:271:TRP:CH2	1:B:273:PRO:HB3	2.55	0.41
1:B:489:GLY:O	1:B:530:GLN:HA	2.20	0.41
1:B:450:GLN:HG2	1:B:516:ARG:CZ	2.50	0.41
2:C:181:LEU:HD12	2:C:186:TYR:HA	2.01	0.41
1:B:372:ARG:NH2	1:B:397:LEU:HA	2.36	0.41
3:D:81:MET:HE3	3:D:81:MET:HB3	1.96	0.41
3:D:162:LYS:NZ	3:D:163:ASP:OD2	2.42	0.40
1:B:183:GLY:O	1:B:185:PRO:HD3	2.21	0.40
3:D:68:VAL:HG22	3:D:83:LEU:HD13	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:338:THR:O	3:D:80:TYR:OH[8_545]	2.16	0.04

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	B	426/428 (100%)	408 (96%)	18 (4%)	0	100	100
2	C	211/214 (99%)	206 (98%)	5 (2%)	0	100	100
3	D	224/235 (95%)	216 (96%)	8 (4%)	0	100	100
All	All	861/877 (98%)	830 (96%)	31 (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	B	383/383 (100%)	376 (98%)	7 (2%)	54	78
2	C	184/185 (100%)	181 (98%)	3 (2%)	58	81
3	D	190/197 (96%)	186 (98%)	4 (2%)	48	75
All	All	757/765 (99%)	743 (98%)	14 (2%)	54	78

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

Mol	Chain	Res	Type
1	B	242	ARG
1	B	326	ASP
1	B	351	TYR
1	B	487	ARG
1	B	492	GLN

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Mol	Chain	Res	Type
1	B	560	LYS
1	B	579	GLU
2	C	108	ARG
2	C	122	ASP
2	C	213	GLU
3	D	14	ARG
3	D	17	SER
3	D	87	ARG
3	D	96	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	3	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

12 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	$\# Z > 2$
4	NAG	A	1	1,4	14,14,15	0.88	1 (7%)	17,19,21	0.73	0
4	NAG	A	2	4	14,14,15	0.16	0	17,19,21	0.51	0
4	NAG	E	1	1,4	14,14,15	0.45	0	17,19,21	0.65	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	E	2	4	14,14,15	0.48	0	17,19,21	0.50	0
4	NAG	F	1	1,4	14,14,15	0.52	0	17,19,21	0.64	0
4	NAG	F	2	4	14,14,15	0.86	1 (7%)	17,19,21	1.23	1 (5%)
5	NAG	G	1	1,5	14,14,15	0.50	0	17,19,21	0.66	0
5	NAG	G	2	5	14,14,15	0.40	0	17,19,21	0.43	0
5	BMA	G	3	5	11,11,12	1.12	2 (18%)	15,15,17	1.29	2 (13%)
5	MAN	G	4	5	11,11,12	0.71	0	15,15,17	1.27	2 (13%)
5	FUC	G	5	5	10,10,11	0.95	0	14,14,16	1.31	1 (7%)
5	FUC	G	6	5	10,10,11	0.71	0	14,14,16	0.82	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
4	NAG	A	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	A	2	4	-	1/6/23/26	0/1/1/1
4	NAG	E	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	NAG	F	1	1,4	-	3/6/23/26	0/1/1/1
4	NAG	F	2	4	-	4/6/23/26	0/1/1/1
5	NAG	G	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	4/6/23/26	0/1/1/1
5	BMA	G	3	5	-	2/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	1/1/1/1
5	FUC	G	5	5	-	-	0/1/1/1
5	FUC	G	6	5	-	-	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1	NAG	C1-C2	2.71	1.56	1.52
4	F	2	NAG	C1-C2	2.47	1.55	1.52
5	G	3	BMA	C4-C5	2.17	1.57	1.53
5	G	3	BMA	O5-C1	-2.06	1.40	1.43

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	2	NAG	C2-N2-C7	4.24	128.58	122.90
5	G	4	MAN	C1-O5-C5	3.67	117.10	112.19
5	G	5	FUC	C1-O5-C5	3.25	120.63	112.97
5	G	3	BMA	C3-C4-C5	3.18	116.00	110.23
5	G	3	BMA	C2-C3-C4	2.59	115.41	110.86
5	G	4	MAN	O2-C2-C3	-2.12	105.77	110.15
4	E	1	NAG	C1-O5-C5	2.08	114.97	112.19

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	3	BMA	O5-C5-C6-O6
5	G	2	NAG	O5-C5-C6-O6
5	G	2	NAG	C4-C5-C6-O6
4	F	2	NAG	C8-C7-N2-C2
4	F	2	NAG	O7-C7-N2-C2
5	G	2	NAG	C8-C7-N2-C2
5	G	2	NAG	O7-C7-N2-C2
4	E	2	NAG	O5-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
4	A	1	NAG	C4-C5-C6-O6
5	G	3	BMA	C4-C5-C6-O6
4	A	1	NAG	O5-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
4	E	1	NAG	C1-C2-N2-C7
4	F	1	NAG	C1-C2-N2-C7
4	F	2	NAG	C1-C2-N2-C7
4	F	2	NAG	C3-C2-N2-C7
4	A	2	NAG	C4-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6

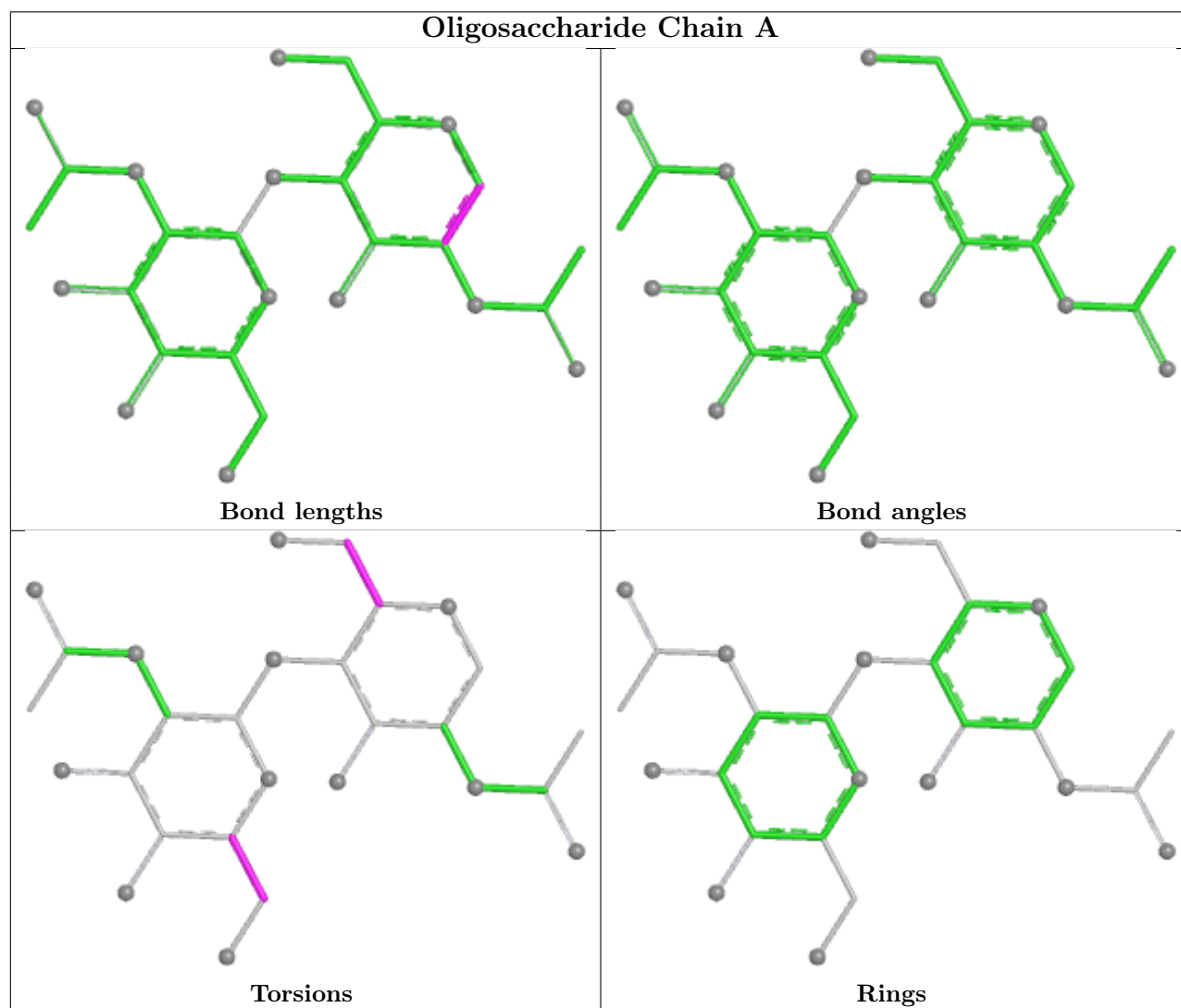
All (1) ring outliers are listed below:

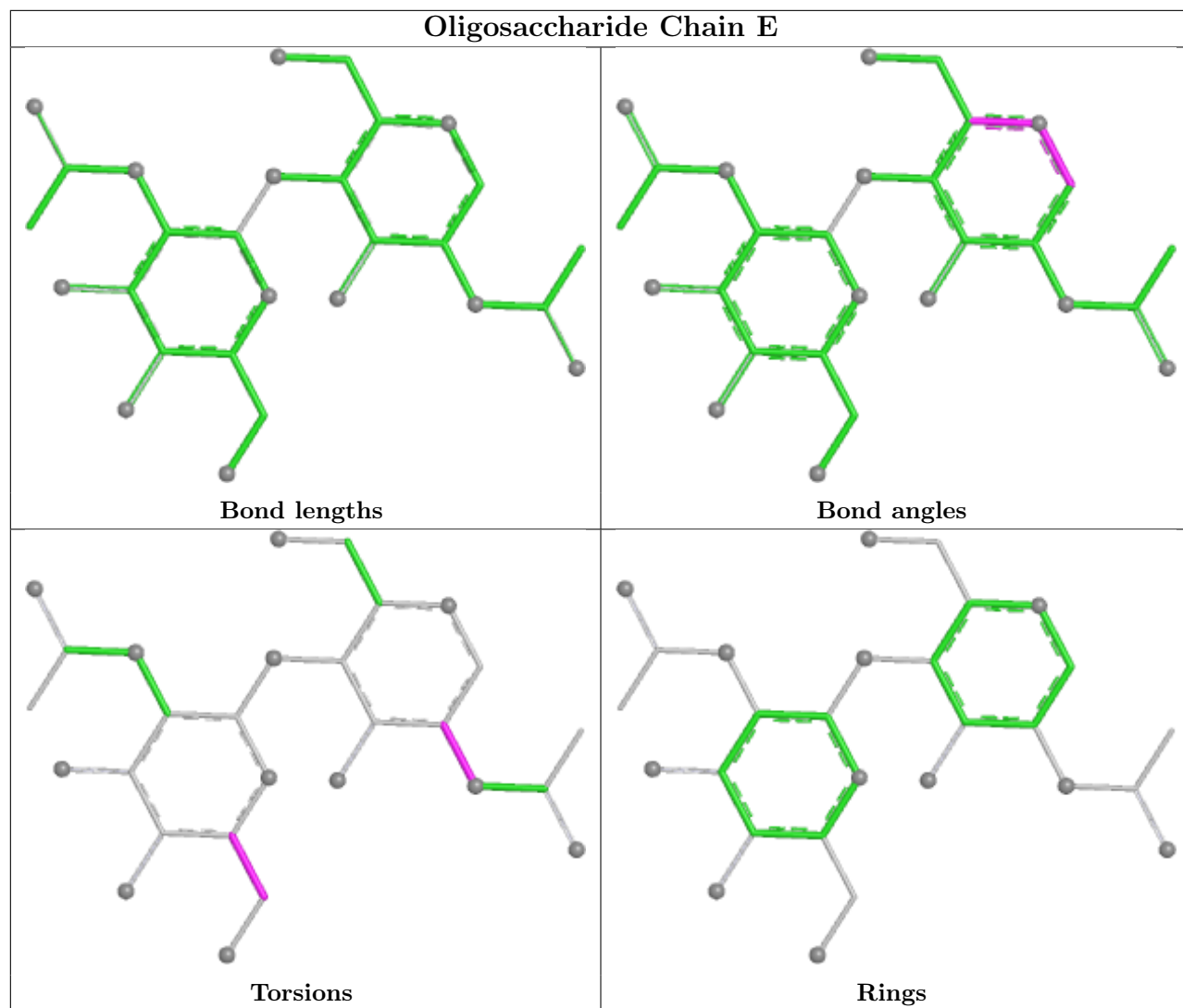
Mol	Chain	Res	Type	Atoms
5	G	4	MAN	C1-C2-C3-C4-C5-O5

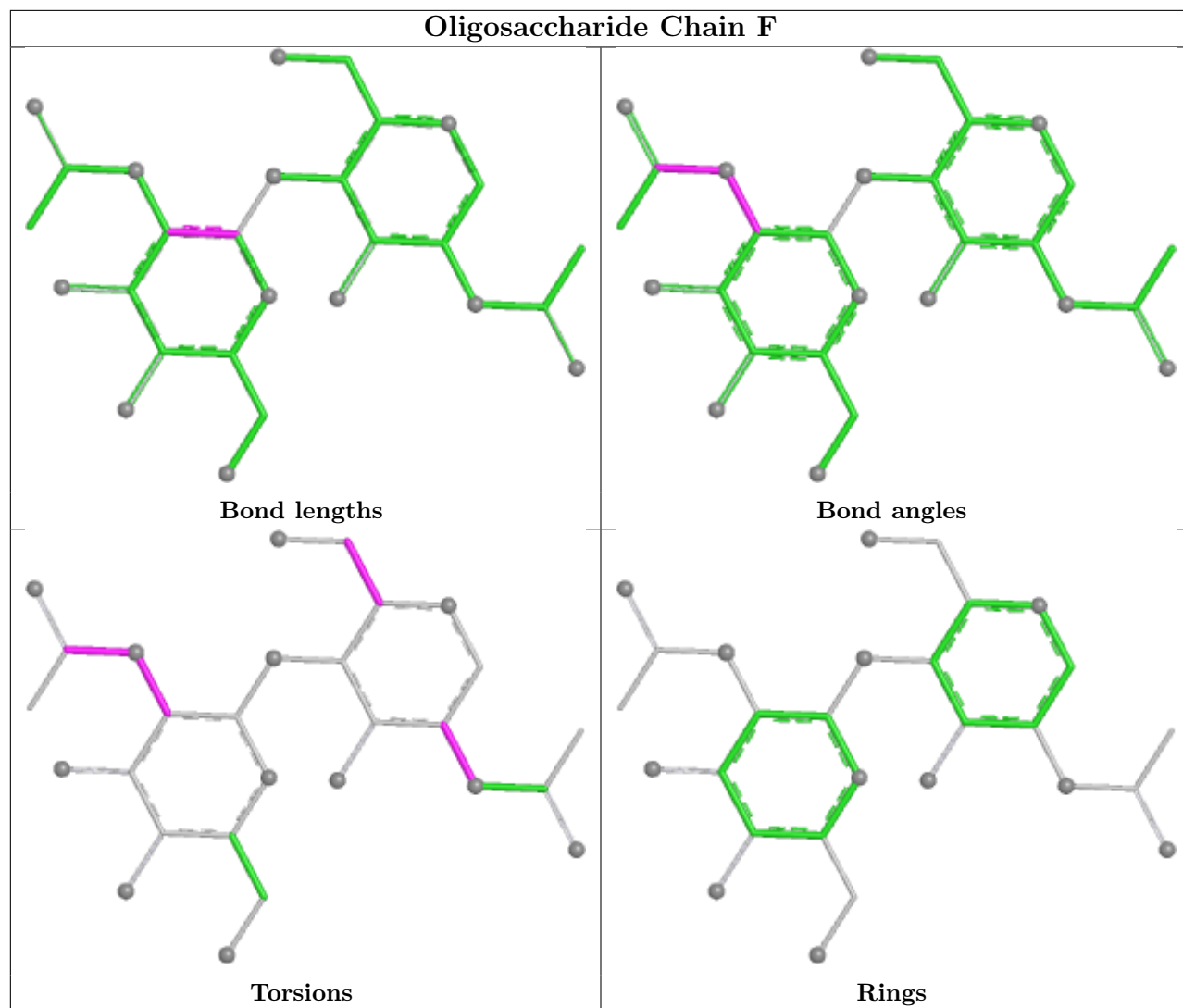
2 monomers are involved in 2 short contacts:

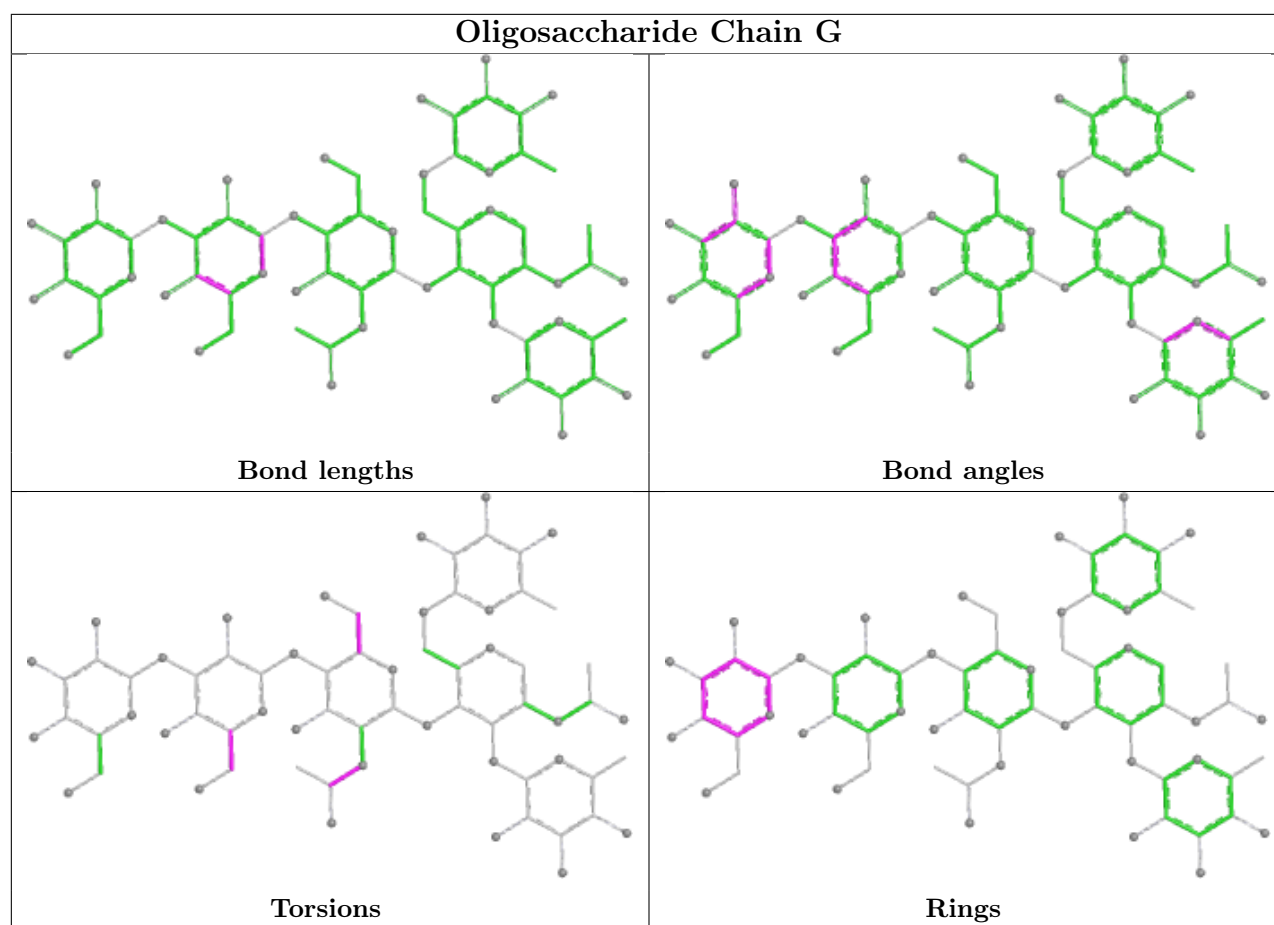
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	2	NAG	1	0
5	G	4	MAN	1	0

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](#)

1 ligand 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	$\# Z > 2$
6	NAG	B	703	1	14,14,15	0.38	0	17,19,21	0.80	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
6	NAG	B	703	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	703	NAG	C1-O5-C5	2.90	116.07	112.19

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 [i](#)

There are no chain breaks in this entry.

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

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

EDS failed to run properly - this section is therefore empty.

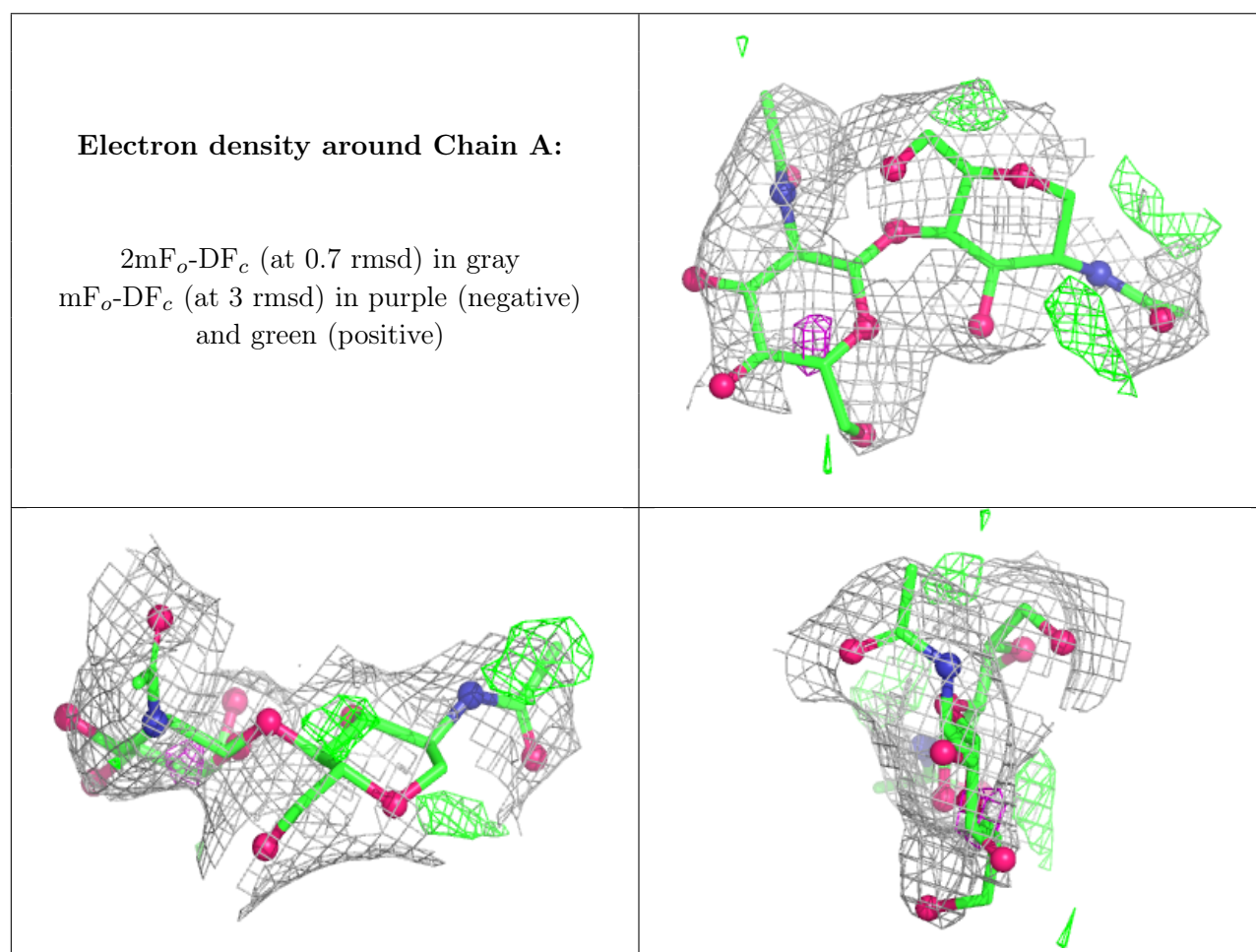
6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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6.3 Carbohydrates [i](#)

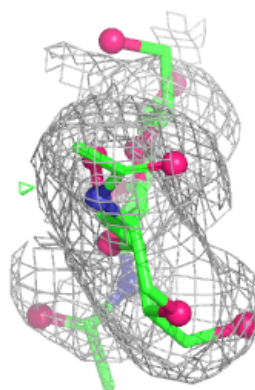
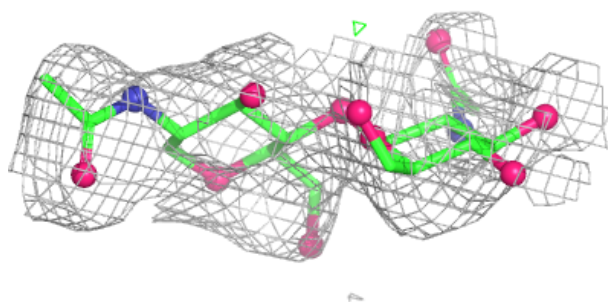
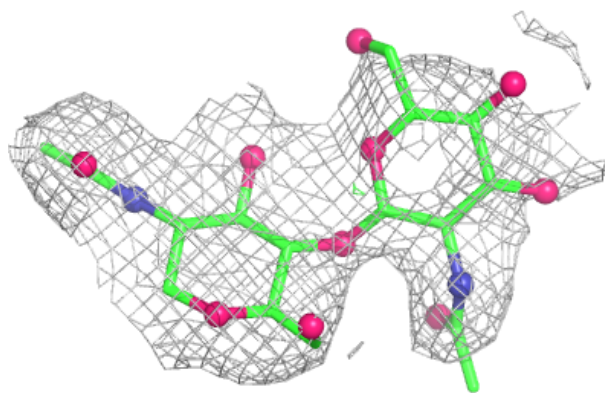
EDS failed to run properly - this section is therefore empty.

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



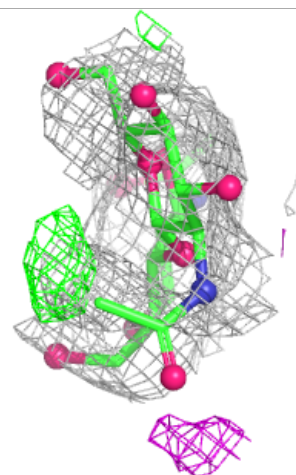
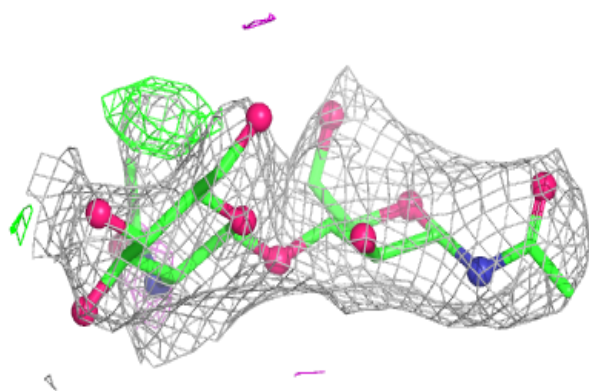
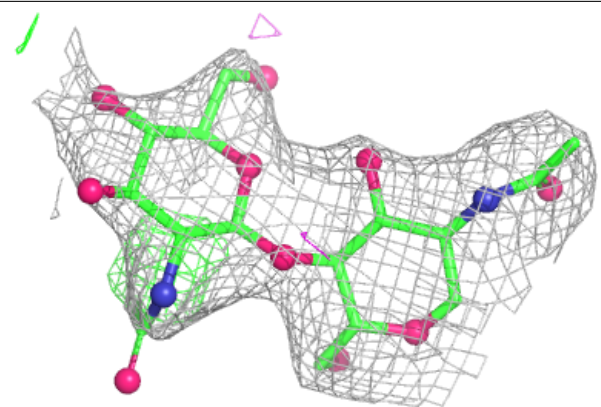
Electron density around Chain E:

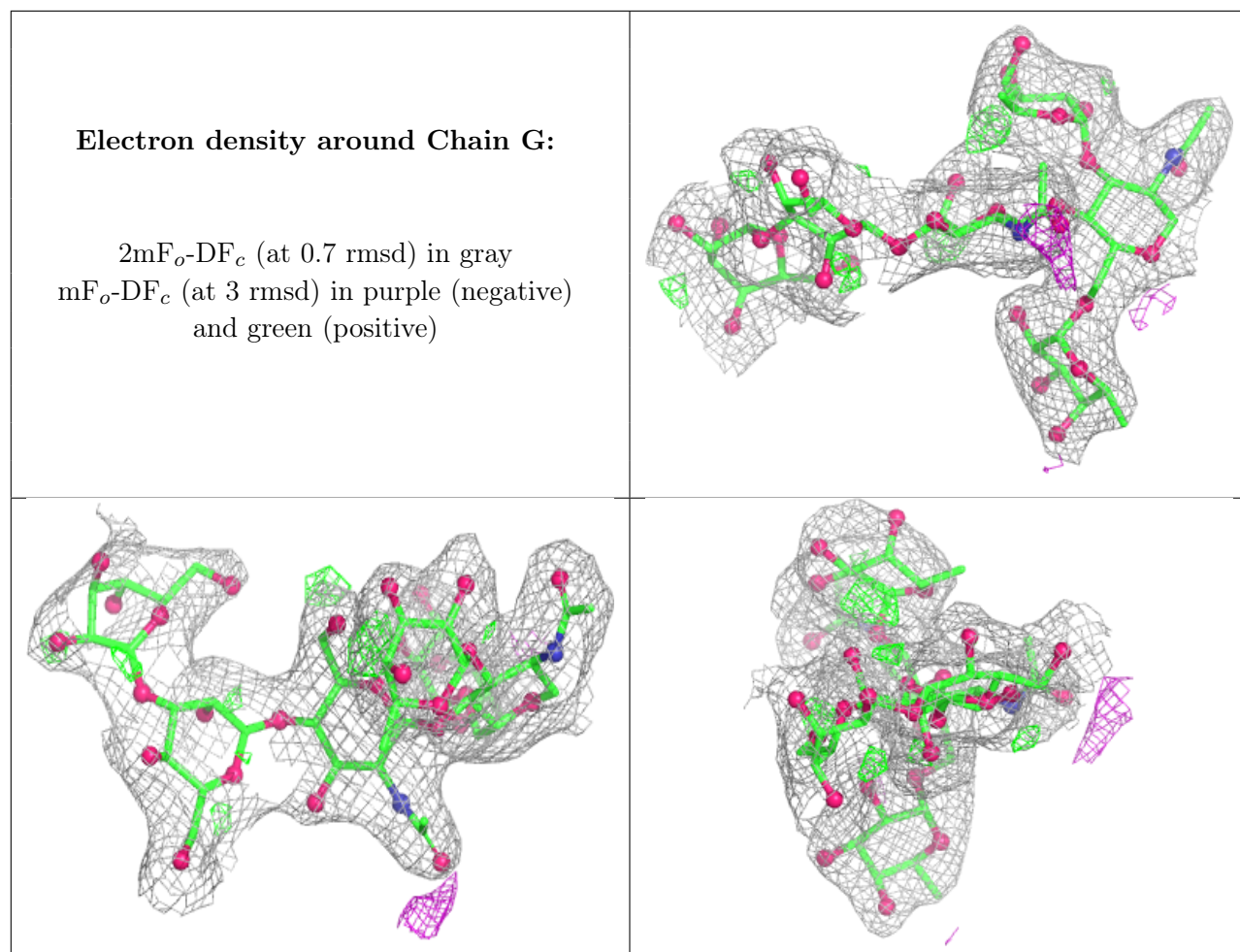
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





6.4 Ligands [i](#)

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers [i](#)

EDS failed to run properly - this section is therefore empty.