



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 26, 2026 – 05:22 PM JST

PDB ID : 9XAR / pdb_00009xar
Title : Structure of the SARS-CoV-2 Spike N-terminal domain(NTD) in complex with the C1624 Fab
Authors : Zhou, J.J.; Gao, G.F.
Deposited on : 2025-10-23
Resolution : 2.77 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

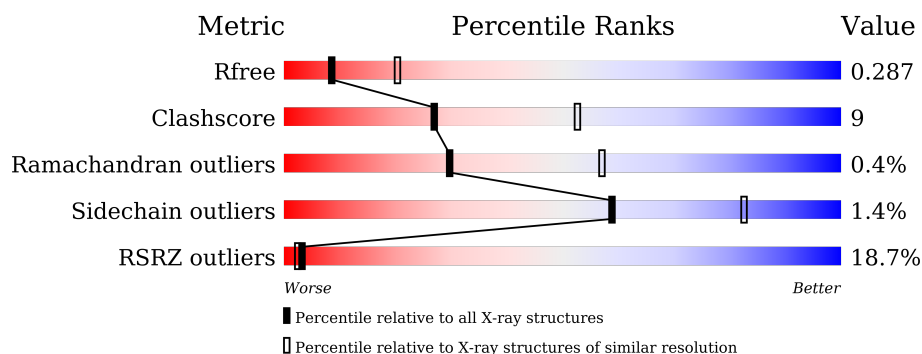
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.77 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



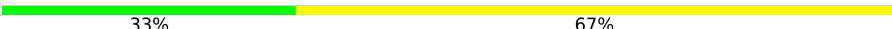
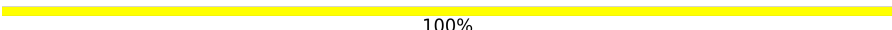
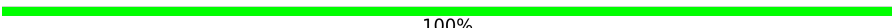
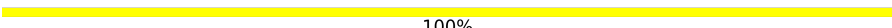
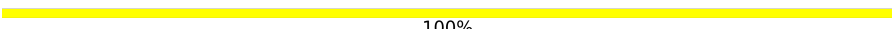
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5248 (2.80-2.76)
Clashscore	190562	5693 (2.80-2.76)
Ramachandran outliers	187476	5590 (2.80-2.76)
Sidechain outliers	187428	5592 (2.80-2.76)
RSRZ outliers	180081	5251 (2.80-2.76)

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

Mol	Chain	Length	Quality of chain
1	A	298	13% 80% 16% ..
1	D	298	14% 82% 12% ..
2	B	236	16% 75% 19% ..
2	E	236	24% 64% 25% 9%
3	C	218	15% 78% 21%
3	F	218	28% 69% 25% 5%

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Mol	Chain	Length	Quality of chain
4	G	3	 33% 67%
4	J	3	 67% 33%
4	M	3	 67% 33%
4	Q	3	 33% 67%
5	H	2	 100%
5	K	2	 50% 50%
5	N	2	 50% 50%
5	R	2	 100%
6	I	4	 100%
6	P	4	 100%
7	L	3	 33% 67%
7	O	3	 67% 33%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11802 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2321	1499	383	431	8			
1	D	285	Total	C	N	O	S	0	0	0
			2291	1481	379	423	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	306	HIS	-	expression tag	UNP P0DTC2
A	307	HIS	-	expression tag	UNP P0DTC2
A	308	HIS	-	expression tag	UNP P0DTC2
A	309	HIS	-	expression tag	UNP P0DTC2
A	310	HIS	-	expression tag	UNP P0DTC2
A	311	HIS	-	expression tag	UNP P0DTC2
D	306	HIS	-	expression tag	UNP P0DTC2
D	307	HIS	-	expression tag	UNP P0DTC2
D	308	HIS	-	expression tag	UNP P0DTC2
D	309	HIS	-	expression tag	UNP P0DTC2
D	310	HIS	-	expression tag	UNP P0DTC2
D	311	HIS	-	expression tag	UNP P0DTC2

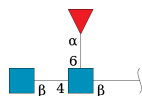
- Molecule 2 is a protein called C1624 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	228	Total	C	N	O	S	0	0	0
			1727	1087	292	341	7			
2	E	214	Total	C	N	O	S	0	0	0
			1635	1032	278	320	5			

- Molecule 3 is a protein called C1624 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	217	Total	C	N	O	S	0	0	0
			1663	1041	284	333	5			
3	F	208	Total	C	N	O	S	0	0	0
			1588	986	275	322	5			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



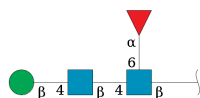
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	3	Total	C	N	O	0	0	0
			38	22	2	14			
4	J	3	Total	C	N	O	0	0	0
			38	22	2	14			
4	M	3	Total	C	N	O	0	0	0
			38	22	2	14			
4	Q	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 5 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
5	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	K	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	N	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	R	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



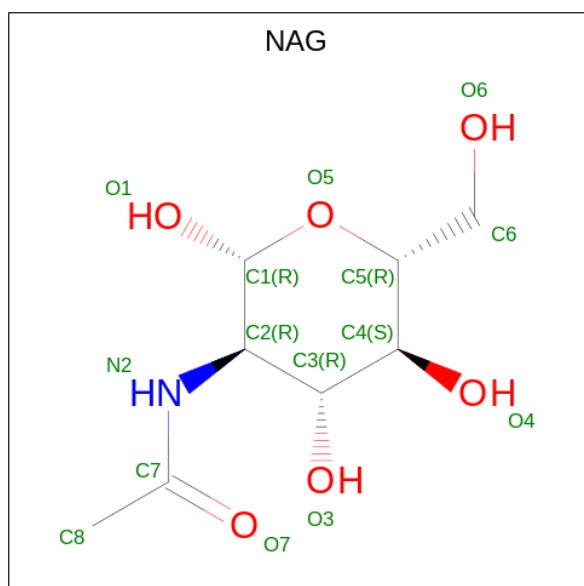
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	I	4	Total	C	N	O	0	0	0
			49	28	2	19			
6	P	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 7 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
7	L	3	Total	C	N	O	0	0	0
			39	22	2	15			
7	O	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

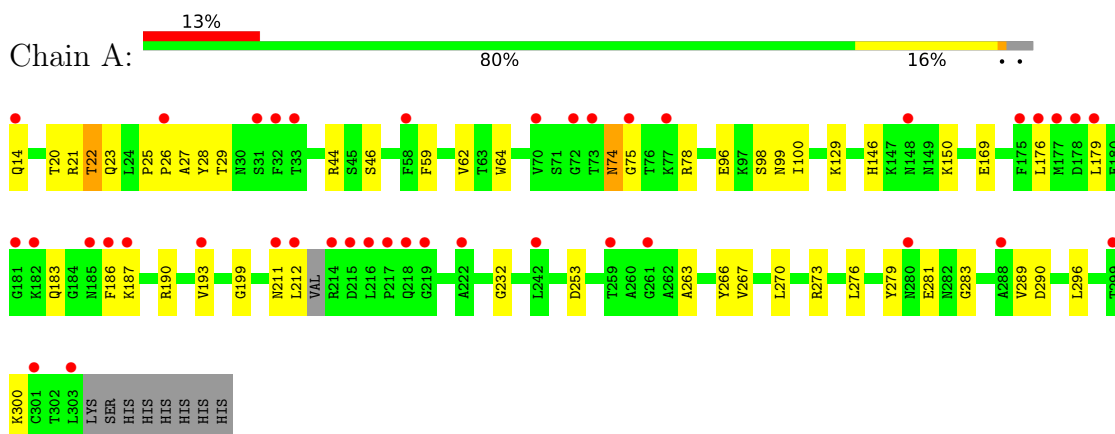
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	19	Total O 19 19	0	0
9	B	6	Total O 6 6	0	0
9	C	20	Total O 20 20	0	0
9	E	6	Total O 6 6	0	0
9	F	11	Total O 11 11	0	0
9	D	19	Total O 19 19	0	0

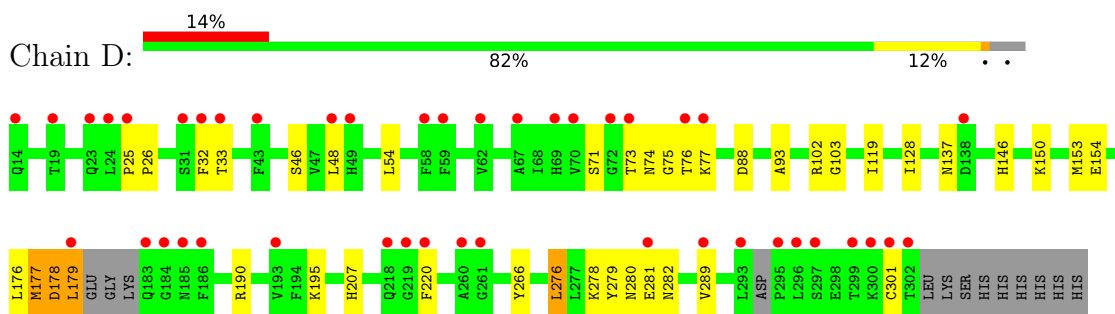
3 Residue-property plots [i](#)

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.

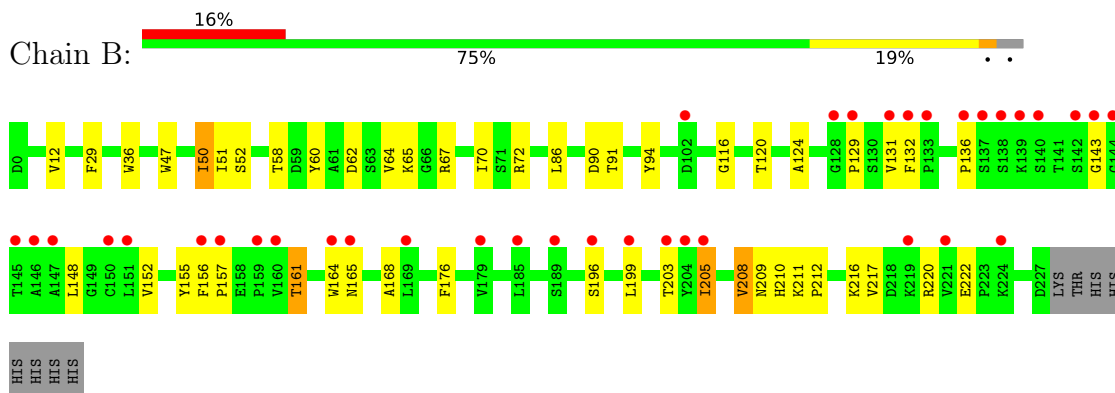
- Molecule 1: Spike protein S1



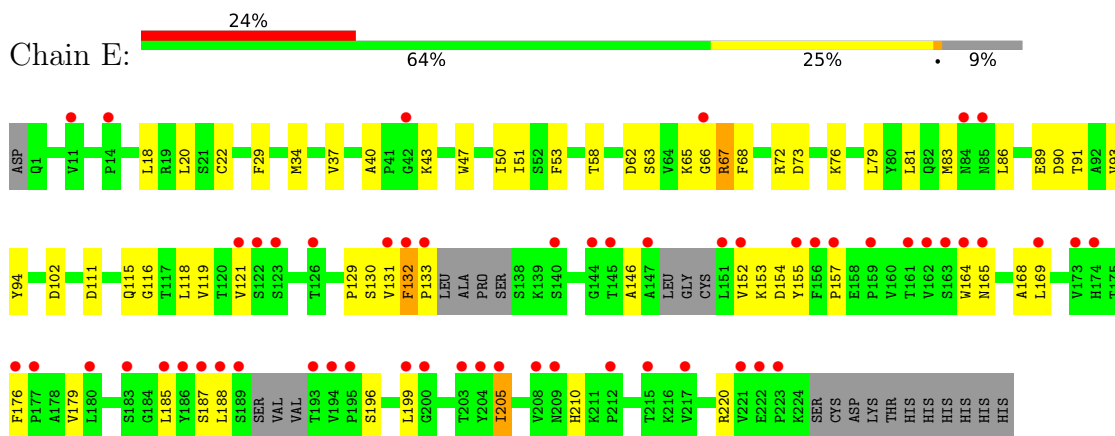
- Molecule 1: Spike protein S1



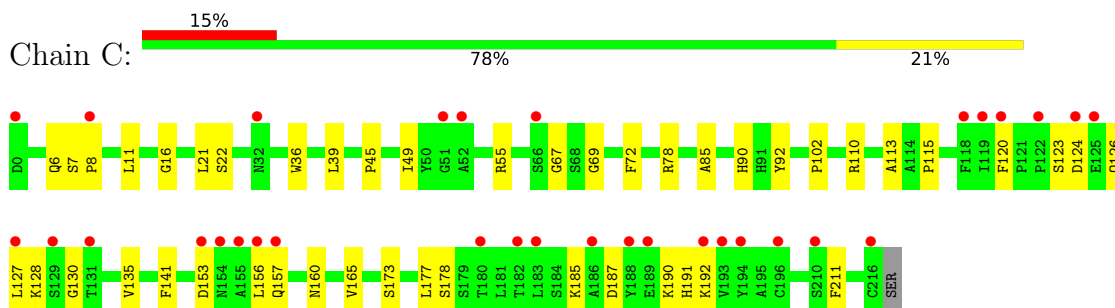
- Molecule 2: C1624 heavy chain



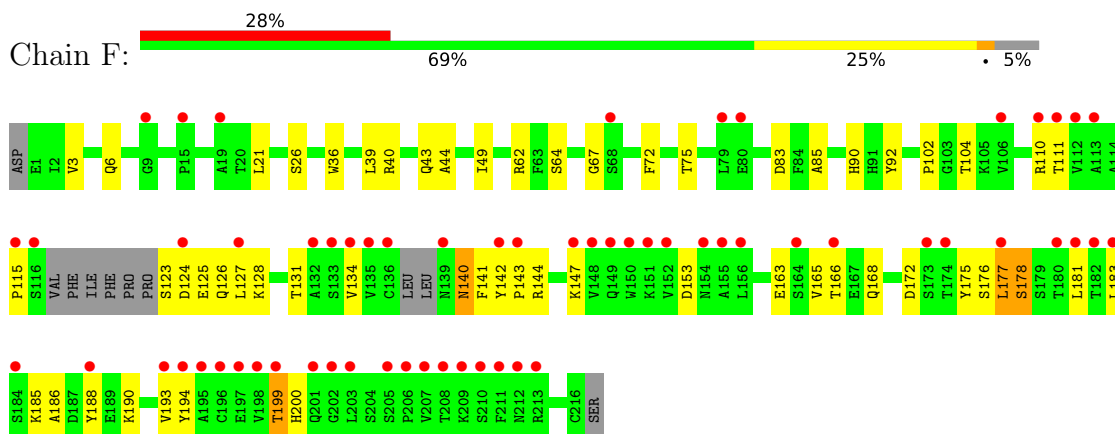
- Molecule 2: C1624 heavy chain



- Molecule 3: C1624 light chain



- Molecule 3: C1624 light chain



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



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

Chain J:  67% 33%



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

Chain M:  67% 33%



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

Chain Q:  33% 67%



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

Chain H:  100%



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

Chain K:  50% 50%



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

Chain N:  50% 50%

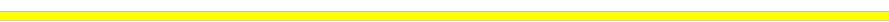


- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain R:  100%

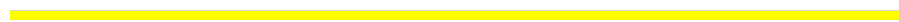


- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%

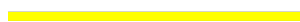
NAG1
NAG2
BMA3
FUC4

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

Chain P:  100%

NAG1
NAG2
BMA3
FUC4

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain L:  33%  67%

NAG1
NAG2
BMA3

- Molecule 7: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:  67%  33%

NAG1
NAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.61Å 116.03Å 137.00Å 90.00° 104.98° 90.00°	Depositor
Resolution (Å)	36.17 – 2.77 36.17 – 2.77	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.17-2.77) 99.8 (36.17-2.77)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.240 , 0.288 0.241 , 0.287	Depositor DCC
R_{free} test set	2790 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	64.4	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11802	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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

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	0.10	0/2386	0.31	0/3247
1	D	0.11	0/2355	0.32	0/3205
2	B	0.11	0/1770	0.31	0/2410
2	E	0.11	0/1674	0.34	0/2273
3	C	0.13	0/1702	0.32	0/2314
3	F	0.22	0/1621	0.39	0/2198
All	All	0.13	0/11508	0.33	0/15647

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

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	2321	0	2236	37	0
1	D	2291	0	2209	32	0
2	B	1727	0	1665	37	0
2	E	1635	0	1576	43	0
3	C	1663	0	1610	30	0
3	F	1588	0	1530	36	0
4	G	38	0	34	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	J	38	0	34	0	0
4	M	38	0	34	0	0
4	Q	38	0	34	0	0
5	H	28	0	25	2	0
5	K	28	0	25	0	0
5	N	28	0	25	0	0
5	R	28	0	25	0	0
6	I	49	0	43	0	0
6	P	49	0	43	0	0
7	L	39	0	34	2	0
7	O	39	0	34	4	0
8	A	28	0	26	0	0
8	D	28	0	26	0	0
9	A	19	0	0	2	0
9	B	6	0	0	0	0
9	C	20	0	0	0	0
9	D	19	0	0	1	0
9	E	6	0	0	0	0
9	F	11	0	0	0	0
All	All	11802	0	11268	211	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 9.

The worst 5 of 211 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:165:ASN:HB2	2:E:169:LEU:HG	1.71	0.72
2:E:89:GLU:N	2:E:89:GLU:OE1	2.20	0.72
3:C:39:LEU:HD21	3:C:45:PRO:HG3	1.70	0.72
3:F:163:GLU:HB2	3:F:177:LEU:HD21	1.72	0.70
2:E:165:ASN:HB3	2:E:168:ALA:HB3	1.72	0.70

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	285/298 (96%)	276 (97%)	9 (3%)	0	100	100
1	D	279/298 (94%)	264 (95%)	13 (5%)	2 (1%)	18	44
2	B	226/236 (96%)	218 (96%)	8 (4%)	0	100	100
2	E	206/236 (87%)	194 (94%)	11 (5%)	1 (0%)	24	52
3	C	215/218 (99%)	203 (94%)	11 (5%)	1 (0%)	24	52
3	F	202/218 (93%)	191 (95%)	9 (4%)	2 (1%)	12	35
All	All	1413/1504 (94%)	1346 (95%)	61 (4%)	6 (0%)	30	57

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	140	ASN
2	E	67	ARG
1	D	178	ASP
3	C	69	GLY
3	F	178	SER

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	258/268 (96%)	255 (99%)	3 (1%)	63	84
1	D	256/268 (96%)	253 (99%)	3 (1%)	63	84
2	B	194/202 (96%)	189 (97%)	5 (3%)	40	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	182/202 (90%)	180 (99%)	2 (1%)	65	85
3	C	187/188 (100%)	187 (100%)	0	100	100
3	F	178/188 (95%)	173 (97%)	5 (3%)	38	70
All	All	1255/1316 (95%)	1237 (99%)	18 (1%)	59	82

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	199	THR
1	D	276	LEU
1	D	179	LEU
2	E	132	PHE
3	F	183	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	43	GLN
1	D	23	GLN
3	F	162	GLN
1	D	52	GLN
2	B	57	ASN

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 ⓘ

34 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	G	1	1,4	14,14,15	0.73	0	17,19,21	1.41	2 (11%)
4	NAG	G	2	4	14,14,15	0.72	0	17,19,21	0.86	0
4	FUC	G	3	4	10,10,11	0.80	0	14,14,16	0.94	0
5	NAG	H	1	1,5	14,14,15	0.78	0	17,19,21	1.55	3 (17%)
5	NAG	H	2	5	14,14,15	0.76	0	17,19,21	0.87	0
6	NAG	I	1	1,6	14,14,15	0.69	0	17,19,21	0.93	1 (5%)
6	NAG	I	2	6	14,14,15	0.71	0	17,19,21	1.05	2 (11%)
6	BMA	I	3	6	11,11,12	0.84	0	15,15,17	1.94	3 (20%)
6	FUC	I	4	6	10,10,11	0.72	0	14,14,16	1.14	1 (7%)
4	NAG	J	1	1,4	14,14,15	0.70	0	17,19,21	1.03	0
4	NAG	J	2	4	14,14,15	0.69	0	17,19,21	1.25	2 (11%)
4	FUC	J	3	4	10,10,11	0.81	0	14,14,16	0.98	0
5	NAG	K	1	1,5	14,14,15	0.74	0	17,19,21	0.98	0
5	NAG	K	2	5	14,14,15	0.69	0	17,19,21	0.93	1 (5%)
7	NAG	L	1	1,7	14,14,15	0.76	0	17,19,21	1.17	2 (11%)
7	NAG	L	2	7	14,14,15	0.77	0	17,19,21	1.21	1 (5%)
7	BMA	L	3	7	11,11,12	0.89	0	15,15,17	2.67	5 (33%)
4	NAG	M	1	1,4	14,14,15	0.71	0	17,19,21	1.33	3 (17%)
4	NAG	M	2	4	14,14,15	0.70	0	17,19,21	0.82	0
4	FUC	M	3	4	10,10,11	0.81	0	14,14,16	0.95	0
5	NAG	N	1	1,5	14,14,15	0.70	0	17,19,21	1.32	1 (5%)
5	NAG	N	2	5	14,14,15	0.74	0	17,19,21	0.89	0
7	NAG	O	1	1,7	14,14,15	0.81	0	17,19,21	1.50	3 (17%)
7	NAG	O	2	7	14,14,15	0.79	0	17,19,21	1.40	3 (17%)
7	BMA	O	3	7	11,11,12	0.86	0	15,15,17	2.00	3 (20%)
6	NAG	P	1	1,6	14,14,15	0.67	0	17,19,21	0.95	1 (5%)
6	NAG	P	2	6	14,14,15	0.72	0	17,19,21	1.13	2 (11%)
6	BMA	P	3	6	11,11,12	0.84	0	15,15,17	1.89	3 (20%)
6	FUC	P	4	6	10,10,11	0.73	0	14,14,16	1.17	1 (7%)
4	NAG	Q	1	1,4	14,14,15	0.74	0	17,19,21	1.14	2 (11%)
4	NAG	Q	2	4	14,14,15	0.68	0	17,19,21	1.23	2 (11%)
4	FUC	Q	3	4	10,10,11	0.82	0	14,14,16	0.93	0
5	NAG	R	1	1,5	14,14,15	0.74	0	17,19,21	0.96	0
5	NAG	R	2	5	14,14,15	0.70	0	17,19,21	0.88	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	G	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	G	2	4	-	0/6/23/26	0/1/1/1
4	FUC	G	3	4	-	-	0/1/1/1
5	NAG	H	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	H	2	5	-	0/6/23/26	0/1/1/1
6	NAG	I	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	I	2	6	-	0/6/23/26	0/1/1/1
6	BMA	I	3	6	-	0/2/19/22	0/1/1/1
6	FUC	I	4	6	-	-	0/1/1/1
4	NAG	J	1	1,4	-	4/6/23/26	0/1/1/1
4	NAG	J	2	4	-	2/6/23/26	0/1/1/1
4	FUC	J	3	4	-	-	0/1/1/1
5	NAG	K	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	K	2	5	-	2/6/23/26	0/1/1/1
7	NAG	L	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	L	2	7	-	1/6/23/26	0/1/1/1
7	BMA	L	3	7	-	1/2/19/22	0/1/1/1
4	NAG	M	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	M	2	4	-	0/6/23/26	0/1/1/1
4	FUC	M	3	4	-	-	0/1/1/1
5	NAG	N	1	1,5	-	4/6/23/26	0/1/1/1
5	NAG	N	2	5	-	0/6/23/26	0/1/1/1
7	NAG	O	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	O	2	7	-	3/6/23/26	0/1/1/1
7	BMA	O	3	7	-	2/2/19/22	0/1/1/1
6	NAG	P	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	P	2	6	-	2/6/23/26	0/1/1/1
6	BMA	P	3	6	-	0/2/19/22	0/1/1/1
6	FUC	P	4	6	-	-	0/1/1/1
4	NAG	Q	1	1,4	-	4/6/23/26	0/1/1/1
4	NAG	Q	2	4	-	2/6/23/26	0/1/1/1
4	FUC	Q	3	4	-	-	0/1/1/1
5	NAG	R	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	R	2	5	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	3	BMA	C1-O5-C5	7.57	122.45	112.19
7	O	3	BMA	C1-O5-C5	5.59	119.77	112.19
6	I	3	BMA	C1-O5-C5	5.30	119.37	112.19
6	P	3	BMA	C1-O5-C5	4.98	118.94	112.19
5	H	1	NAG	O5-C1-C2	-4.19	104.68	111.29

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

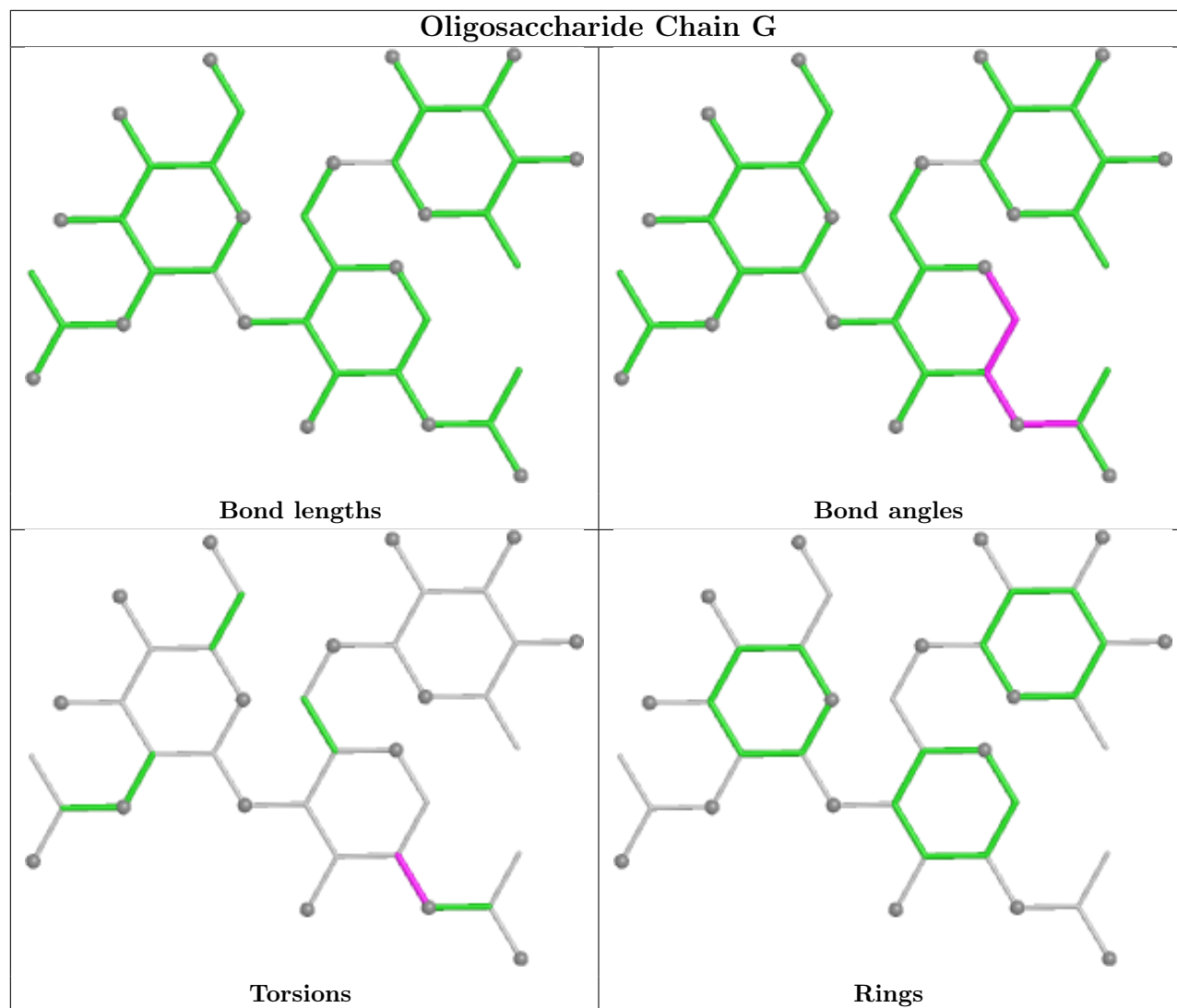
Mol	Chain	Res	Type	Atoms
4	J	1	NAG	O5-C5-C6-O6
4	J	1	NAG	C4-C5-C6-O6
7	O	3	BMA	C4-C5-C6-O6
4	Q	1	NAG	O5-C5-C6-O6
4	J	1	NAG	C8-C7-N2-C2

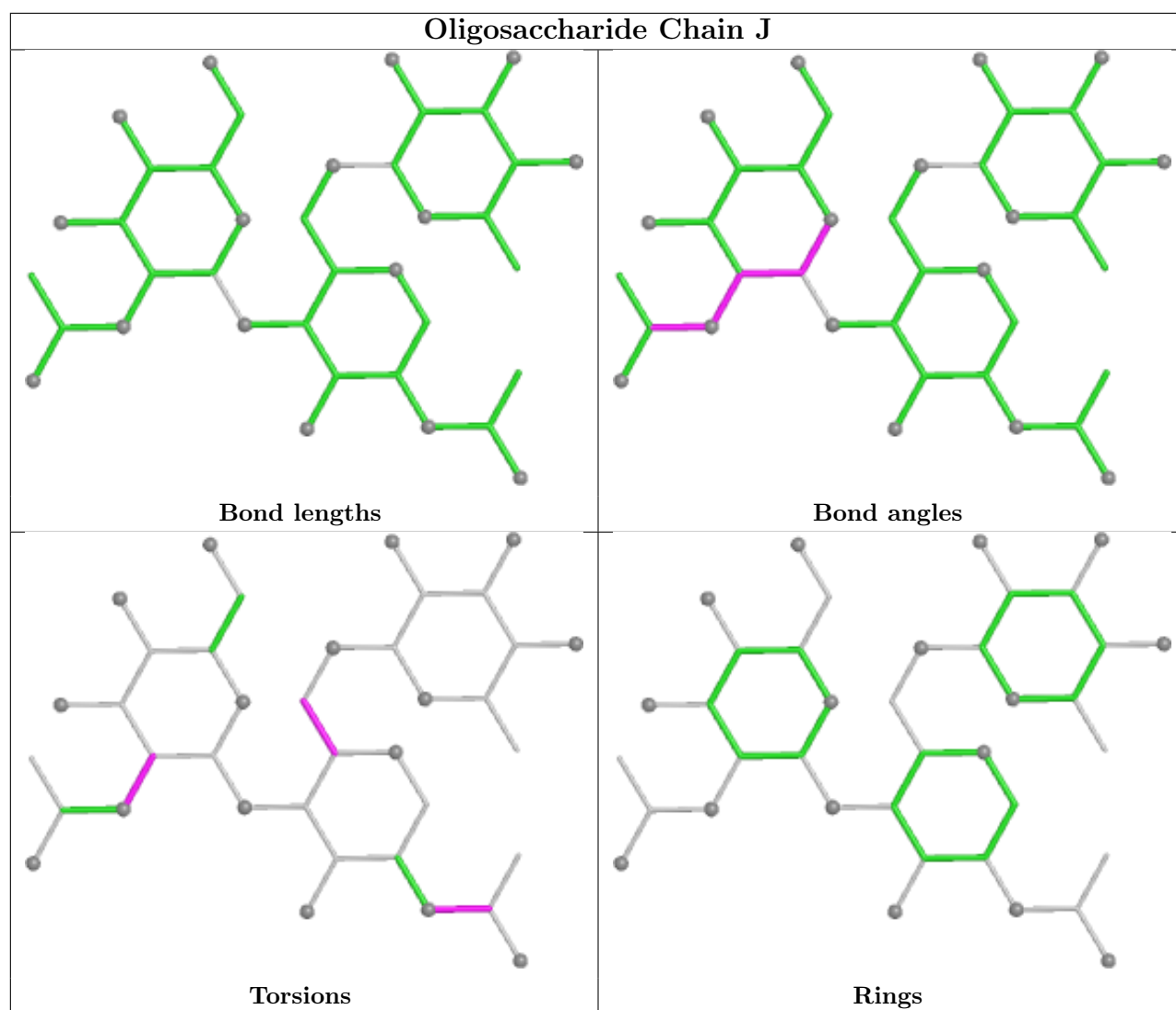
There are no ring outliers.

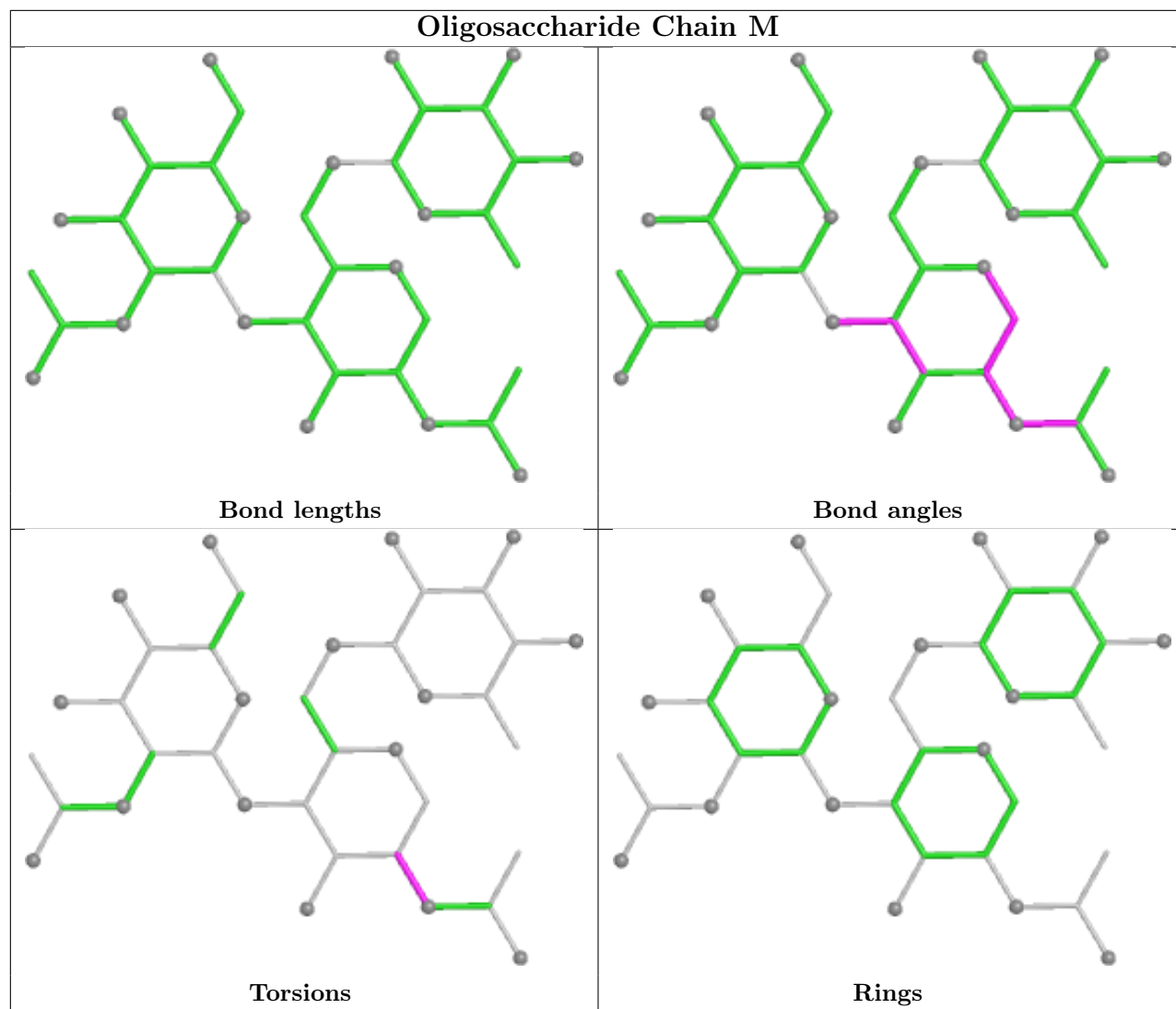
5 monomers are involved in 10 short contacts:

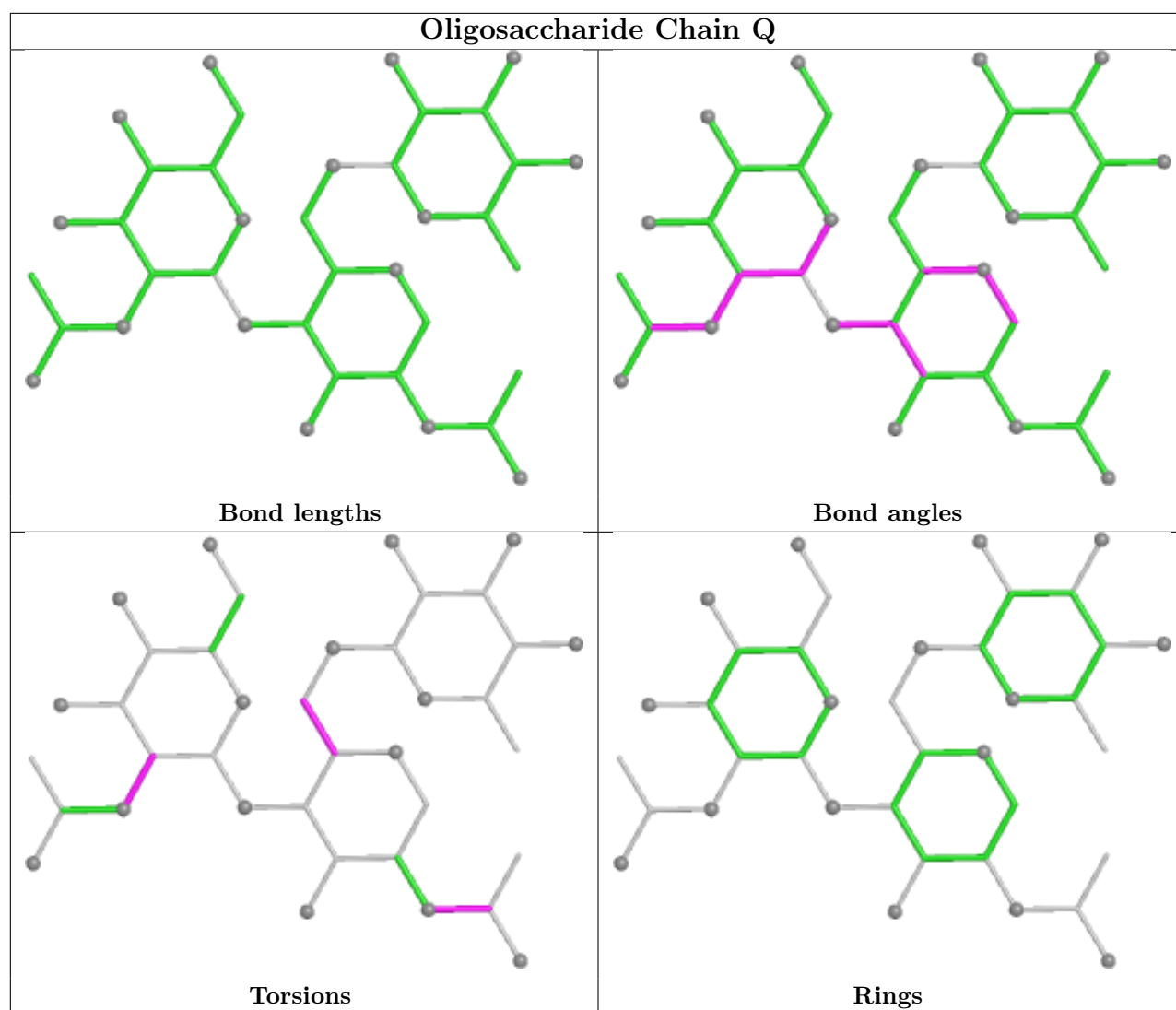
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	2	NAG	1	0
7	L	1	NAG	2	0
5	H	2	NAG	2	0
4	G	3	FUC	2	0
7	O	1	NAG	4	0

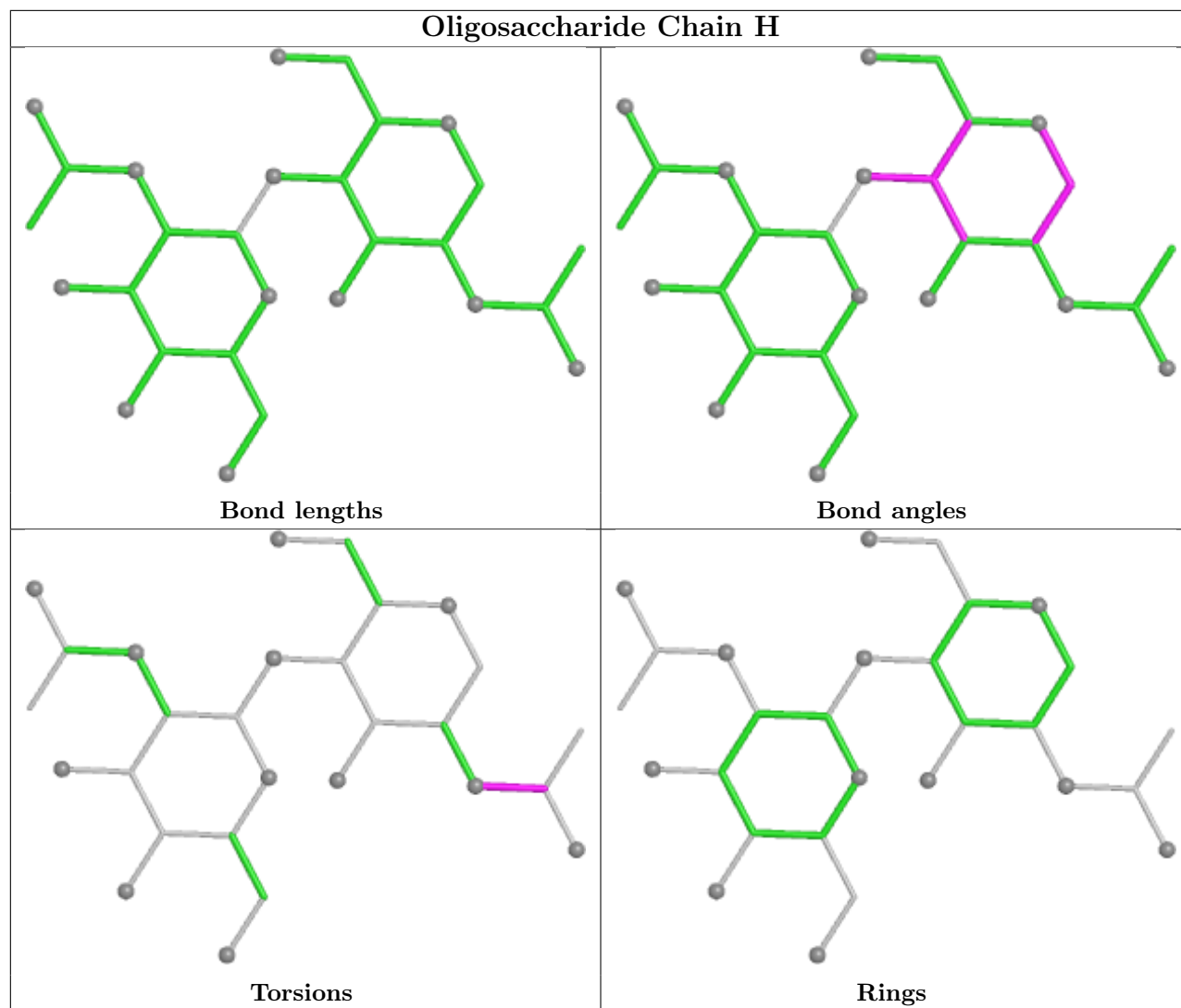
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

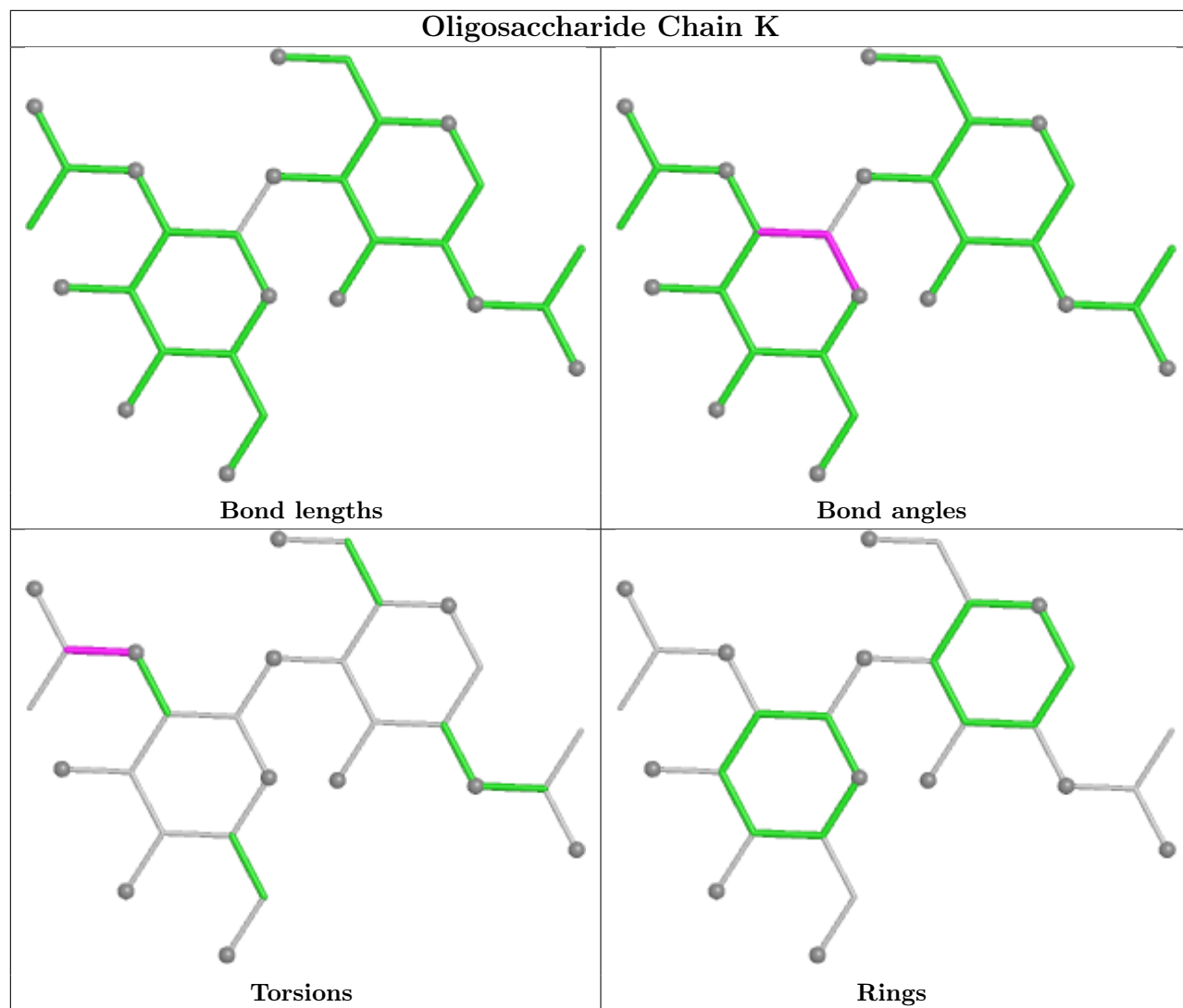


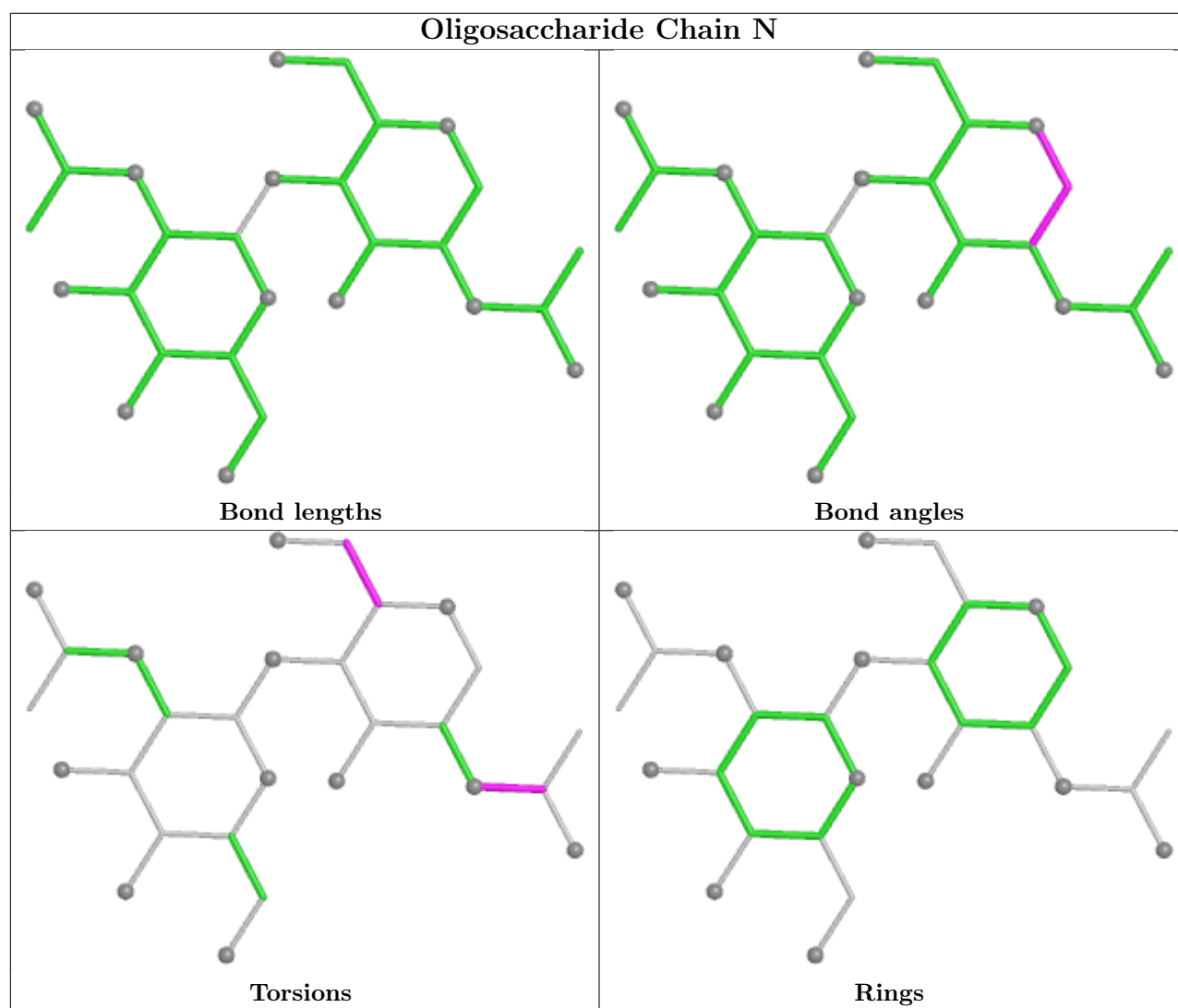


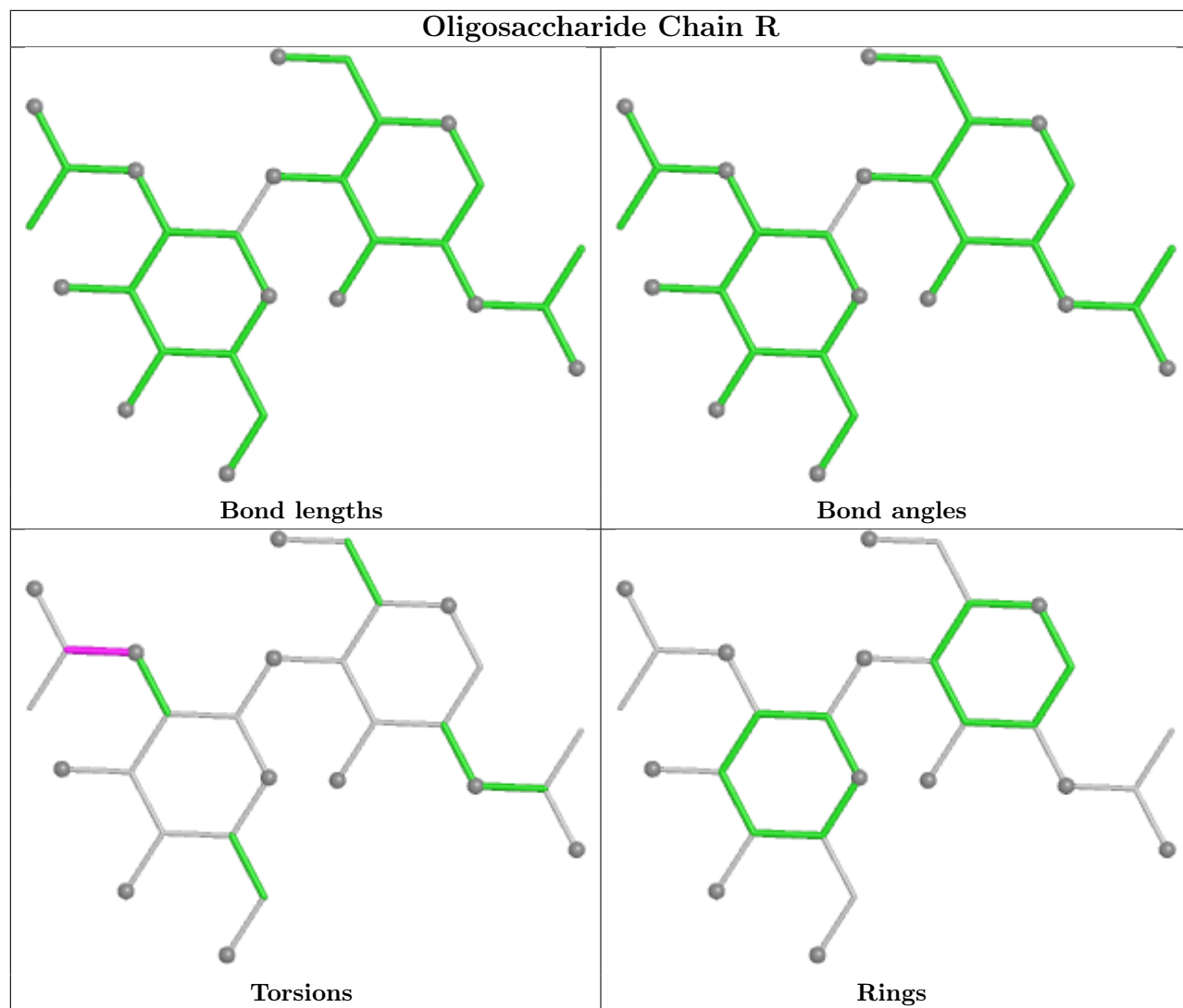


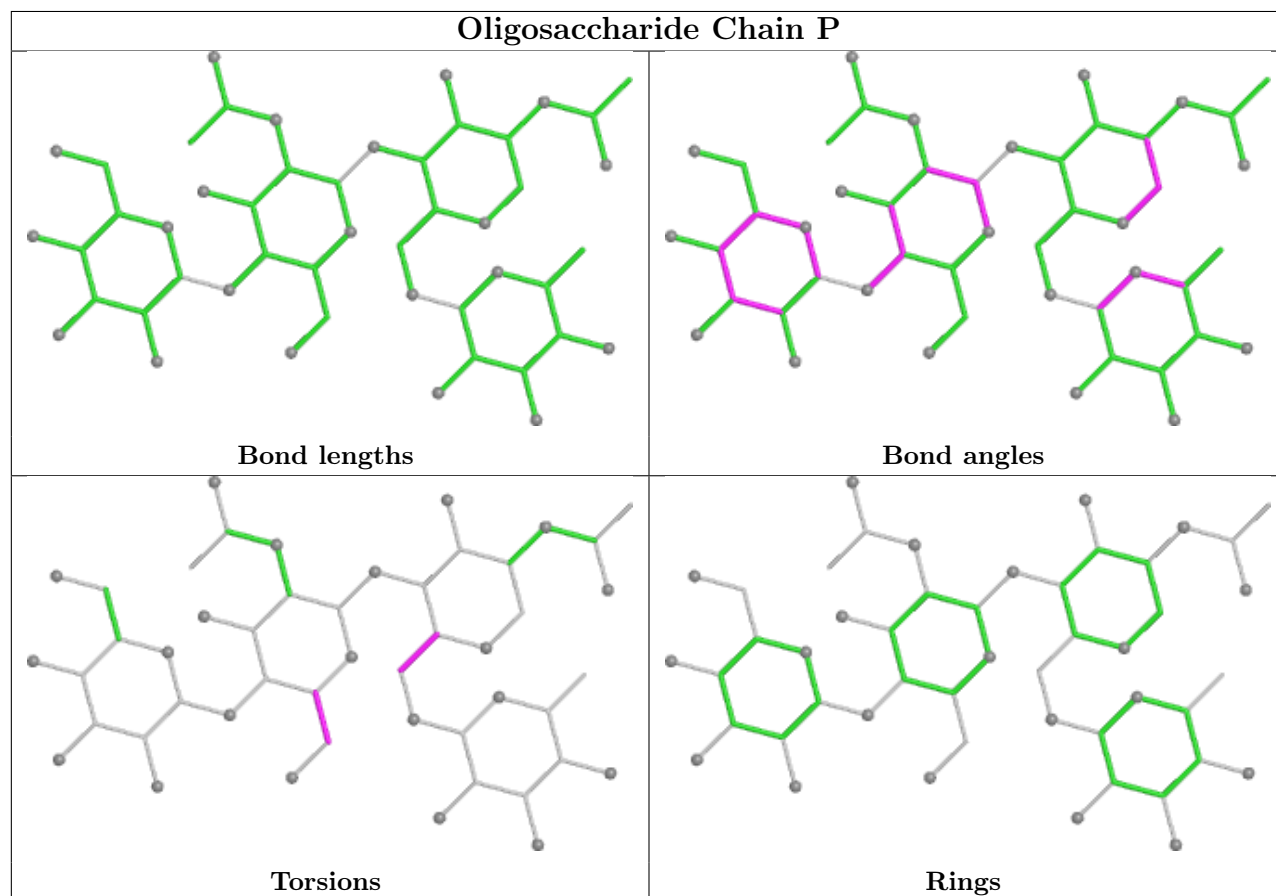
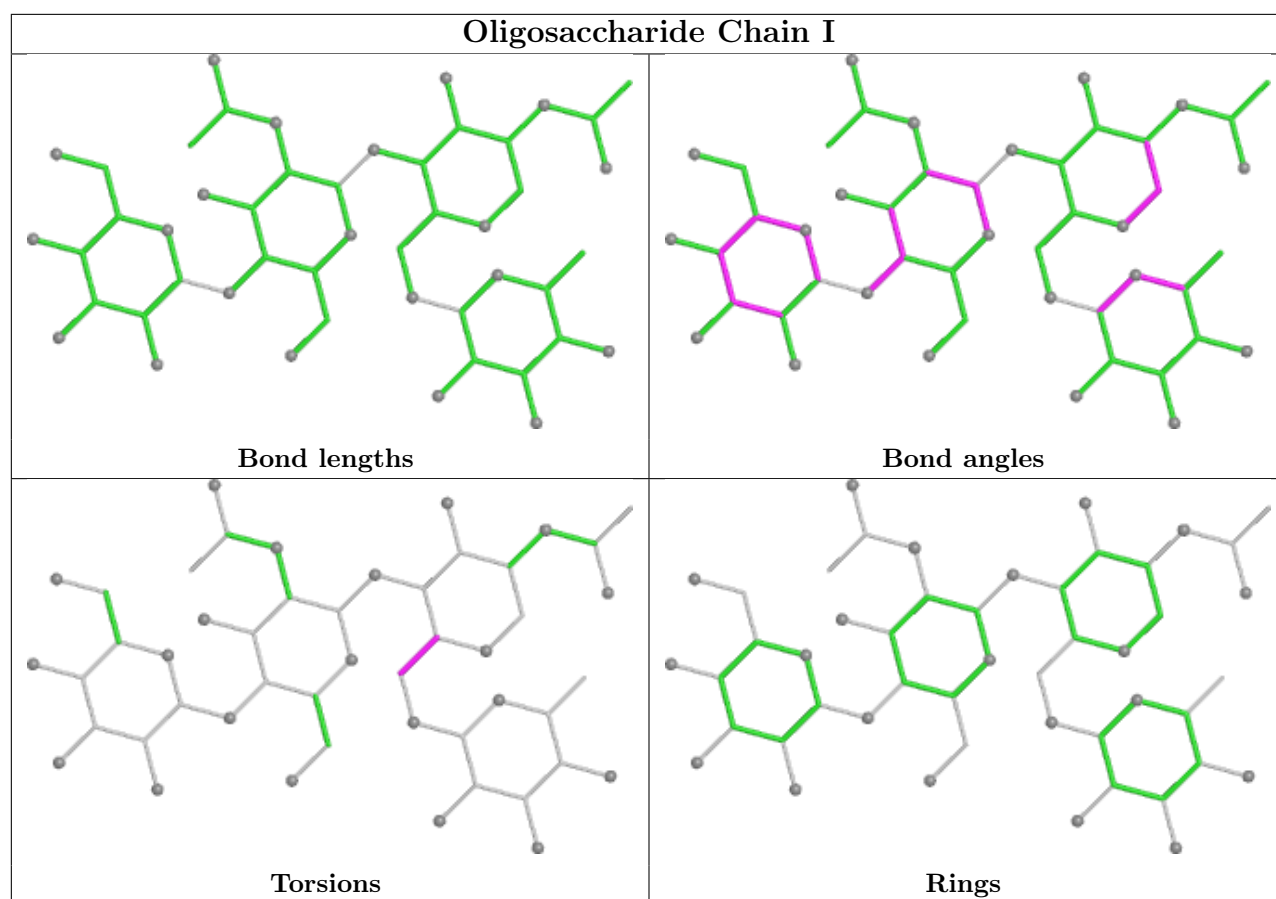


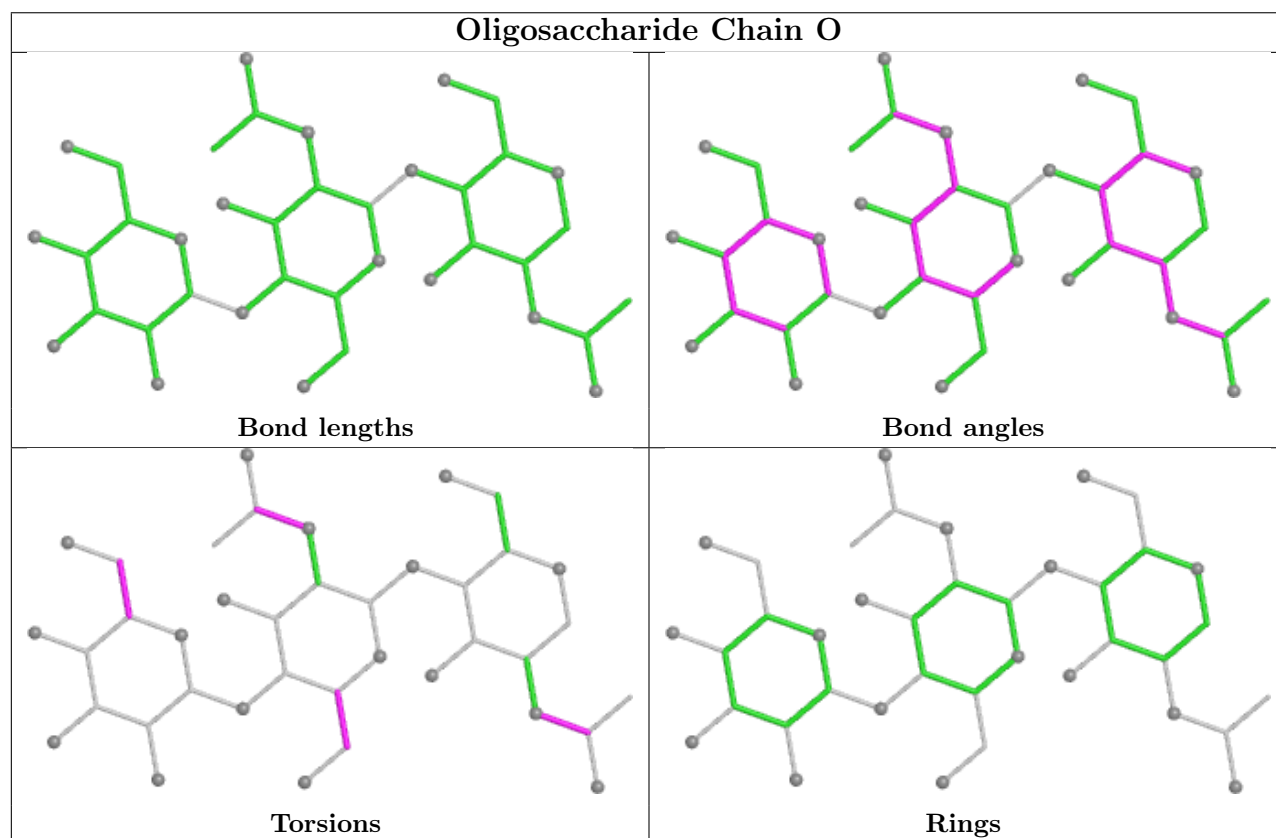
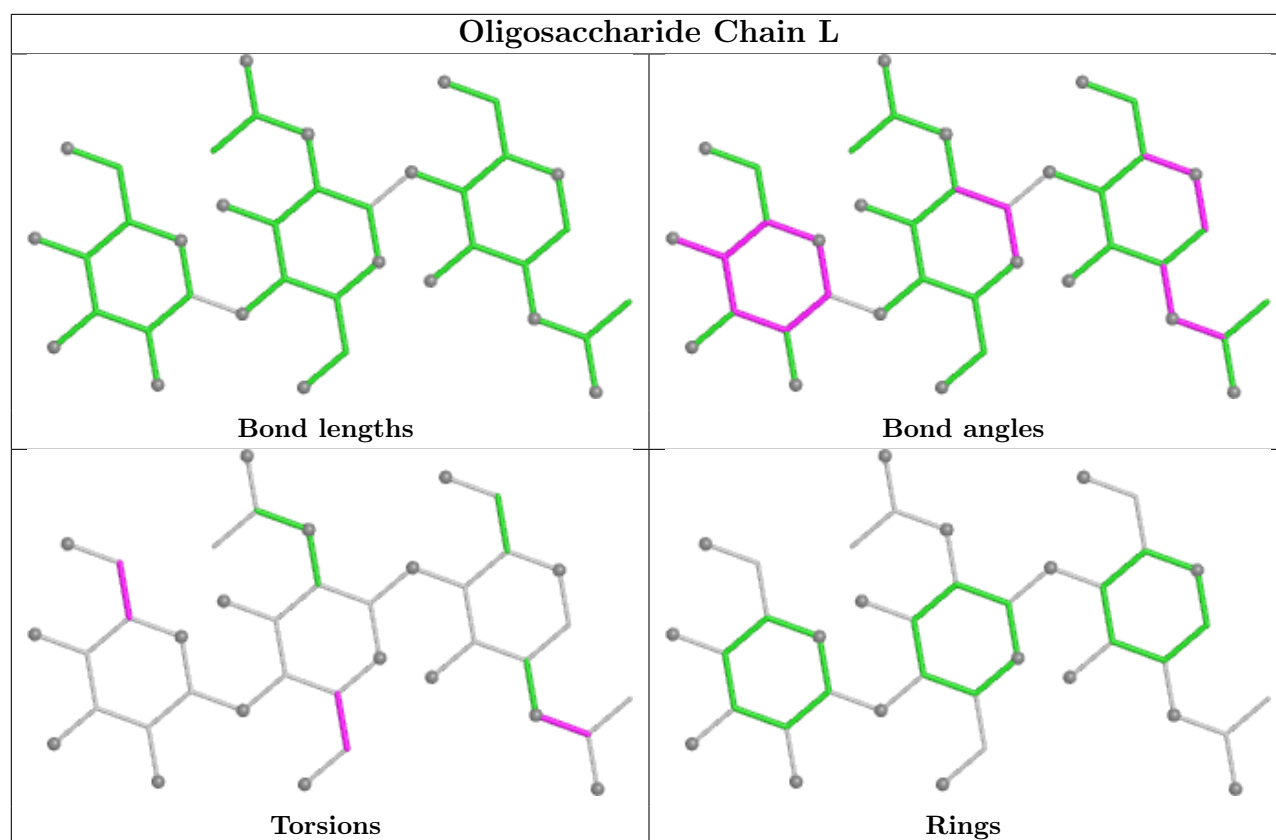












5.6 Ligand geometry

4 ligands 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
8	NAG	D	401	1	14,14,15	0.70	0	17,19,21	0.84	0
8	NAG	D	402	1	14,14,15	0.80	0	17,19,21	1.55	4 (23%)
8	NAG	A	401	1	14,14,15	0.70	0	17,19,21	0.83	0
8	NAG	A	402	1	14,14,15	0.77	0	17,19,21	1.91	4 (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
8	NAG	D	401	1	-	0/6/23/26	0/1/1/1
8	NAG	D	402	1	-	1/6/23/26	0/1/1/1
8	NAG	A	401	1	-	0/6/23/26	0/1/1/1
8	NAG	A	402	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	402	NAG	C1-O5-C5	4.58	118.39	112.19
8	D	402	NAG	C1-O5-C5	3.41	116.82	112.19
8	A	402	NAG	O5-C1-C2	3.28	116.47	111.29
8	A	402	NAG	C3-C4-C5	-3.21	104.51	110.24
8	A	402	NAG	C2-N2-C7	2.85	126.97	122.90

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
8	A	402	NAG	C3-C2-N2-C7
8	D	402	NAG	C3-C2-N2-C7

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](#)

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	289/298 (96%)	0.85	40 (13%) 6 5	41, 65, 126, 177	0
1	D	285/298 (95%)	0.86	43 (15%) 5 4	39, 66, 140, 181	0
2	B	228/236 (96%)	0.99	37 (16%) 4 4	44, 70, 127, 152	0
2	E	214/236 (90%)	1.39	56 (26%) 1 1	50, 82, 133, 148	0
3	C	217/218 (99%)	0.88	32 (14%) 6 5	44, 66, 117, 146	0
3	F	208/218 (95%)	1.57	62 (29%) 1 1	56, 93, 140, 155	0
All	All	1441/1504 (95%)	1.06	270 (18%) 3 2	39, 71, 134, 181	0

The worst 5 of 270 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	164	TRP	5.0
3	C	52	ALA	4.9
2	E	176	PHE	4.9
3	F	135	VAL	4.9
2	B	205	ILE	4.8

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](#)

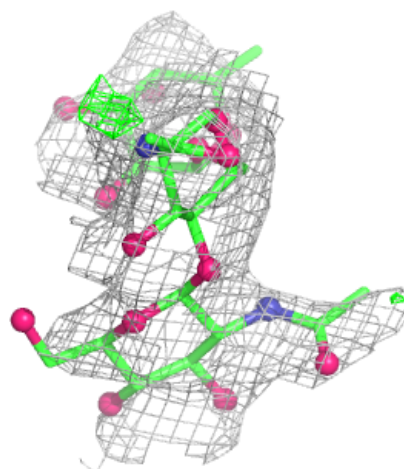
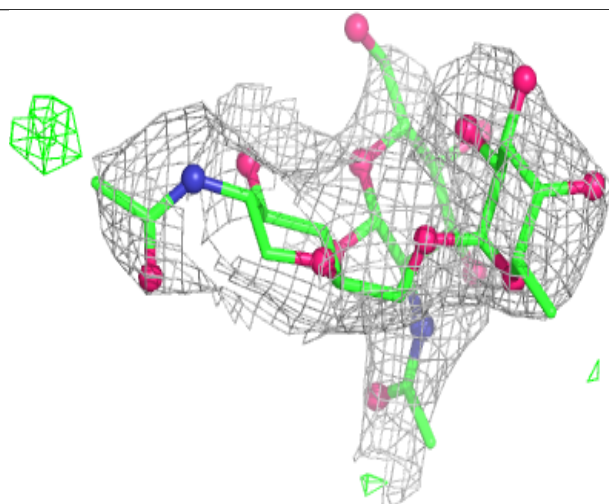
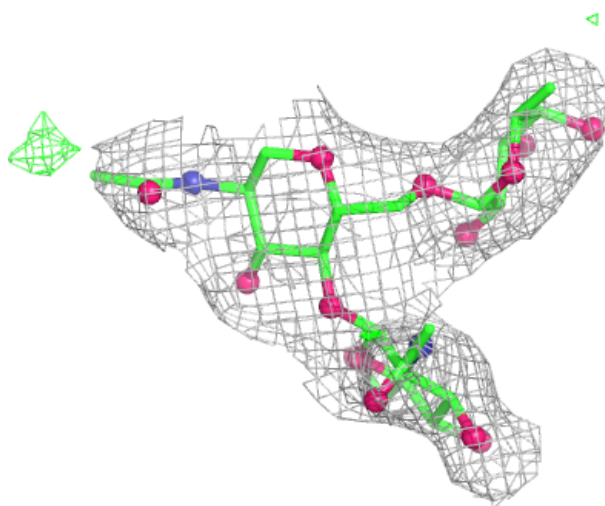
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	NAG	O	2	14/15	-0.14	0.19	176,203,216,219	0
7	NAG	O	1	14/15	-0.03	0.17	161,186,194,195	0
7	BMA	O	3	11/12	0.10	0.20	192,216,219,227	0
7	NAG	L	1	14/15	0.15	0.16	166,186,200,220	0
5	NAG	R	2	14/15	0.26	0.16	122,145,157,158	0
6	BMA	I	3	11/12	0.26	0.17	135,143,148,152	0
5	NAG	N	2	14/15	0.28	0.20	119,127,134,154	0
4	FUC	M	3	10/11	0.29	0.20	141,159,165,168	0
7	BMA	L	3	11/12	0.30	0.14	199,206,216,216	0
6	BMA	P	3	11/12	0.35	0.17	118,130,136,138	0
7	NAG	L	2	14/15	0.35	0.17	186,207,212,215	0
4	NAG	M	2	14/15	0.36	0.17	160,178,186,186	0
5	NAG	H	1	14/15	0.39	0.16	113,131,139,142	0
5	NAG	K	2	14/15	0.42	0.15	129,134,139,143	0
5	NAG	H	2	14/15	0.43	0.17	137,149,152,153	0
4	FUC	J	3	10/11	0.43	0.19	127,139,149,152	0
4	NAG	M	1	14/15	0.45	0.16	117,148,177,179	0
4	NAG	G	2	14/15	0.52	0.14	121,129,137,137	0
4	NAG	J	1	14/15	0.56	0.14	105,121,137,140	0
4	FUC	Q	3	10/11	0.56	0.19	142,150,152,153	0
5	NAG	R	1	14/15	0.56	0.17	99,109,138,144	0
4	NAG	Q	2	14/15	0.58	0.15	157,163,170,173	0
4	NAG	J	2	14/15	0.61	0.14	115,136,145,155	0
5	NAG	N	1	14/15	0.63	0.16	94,104,109,115	0
4	FUC	G	3	10/11	0.65	0.15	119,122,127,129	0
5	NAG	K	1	14/15	0.68	0.14	94,109,127,131	0
4	NAG	G	1	14/15	0.70	0.12	101,110,121,126	0
4	NAG	Q	1	14/15	0.71	0.14	125,141,151,159	0
6	FUC	P	4	10/11	0.75	0.17	75,93,104,106	0
6	NAG	P	2	14/15	0.79	0.14	79,103,116,140	0
6	FUC	I	4	10/11	0.80	0.25	91,98,104,105	0
6	NAG	I	2	14/15	0.84	0.13	87,114,132,154	0
6	NAG	I	1	14/15	0.91	0.12	69,81,90,91	0
6	NAG	P	1	14/15	0.93	0.11	58,69,76,78	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.

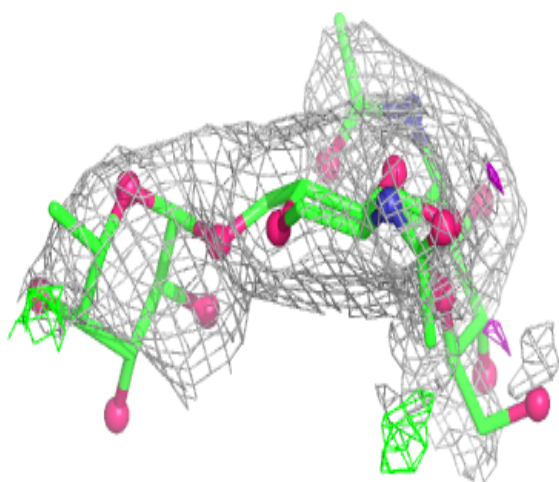
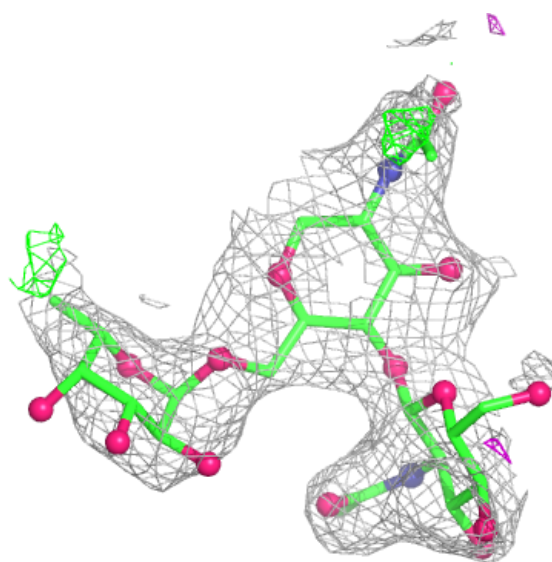
Electron density around Chain G:

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



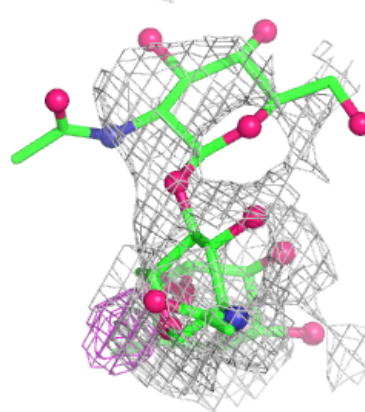
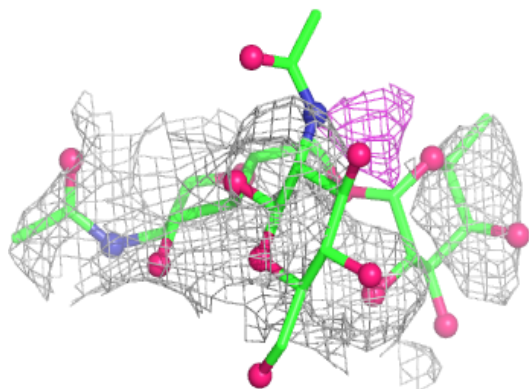
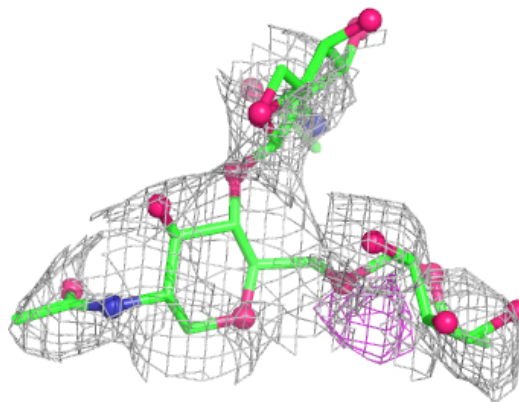
Electron density around Chain J:

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



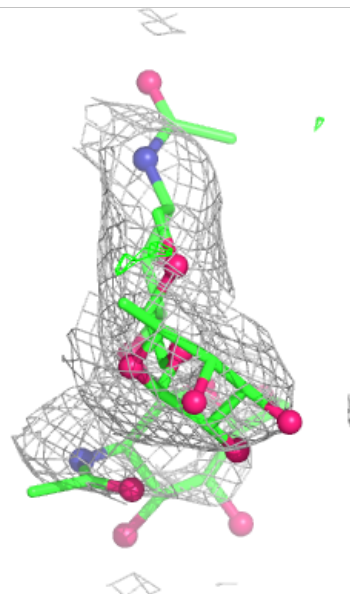
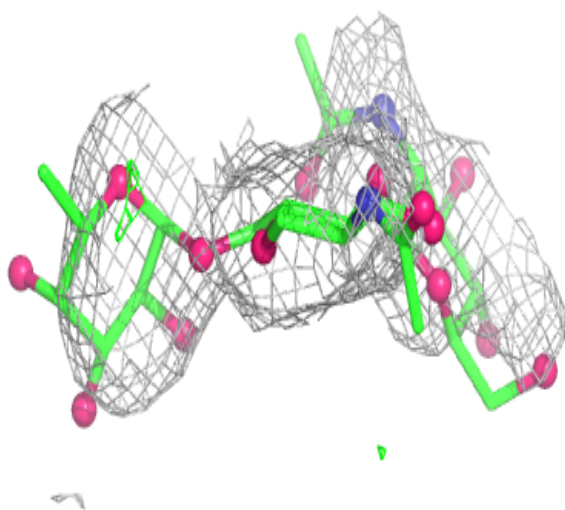
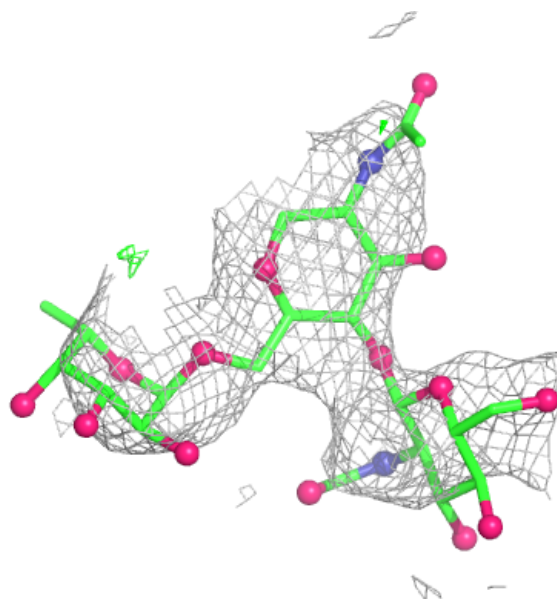
Electron density around Chain M:

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



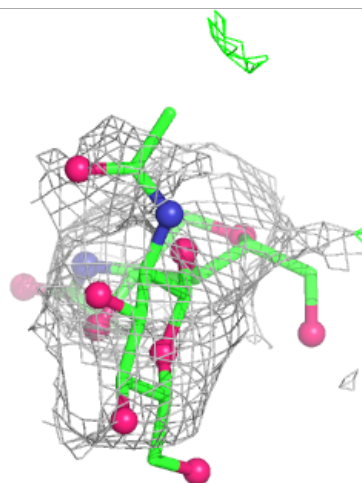
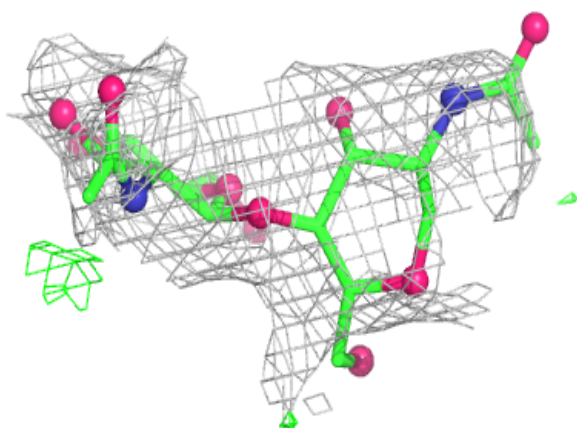
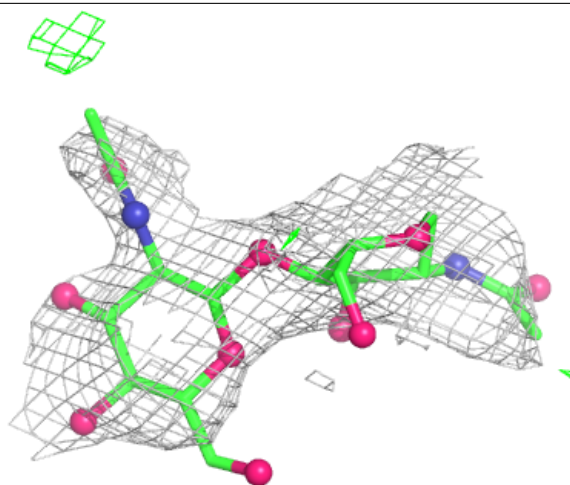
Electron density around Chain Q:

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



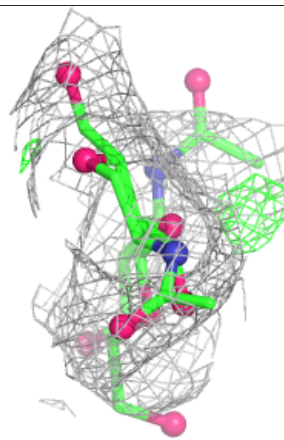
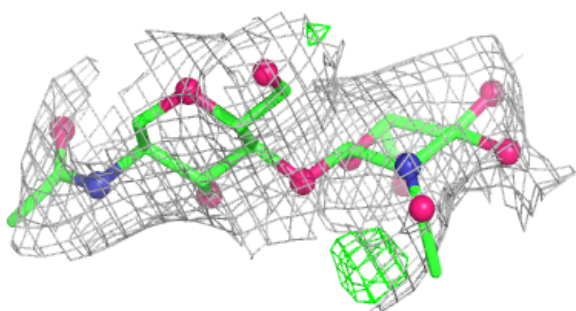
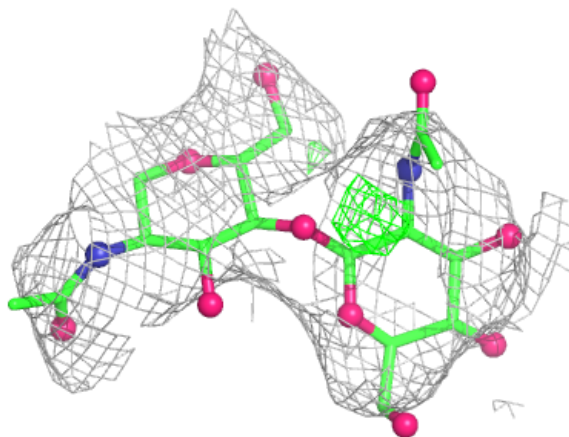
Electron density around Chain H:

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



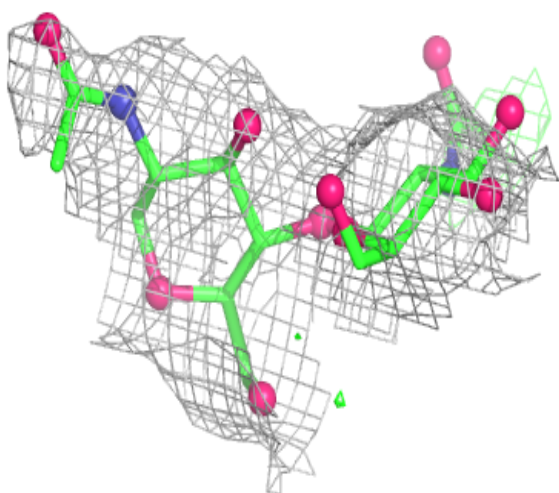
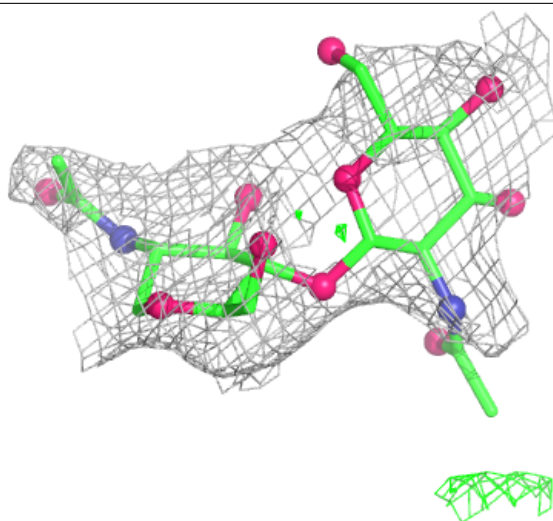
Electron density around Chain K:

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



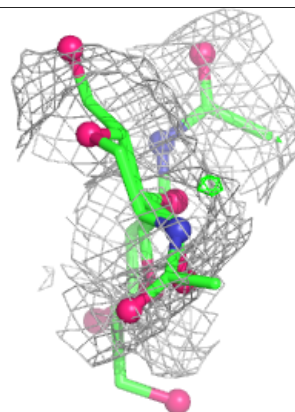
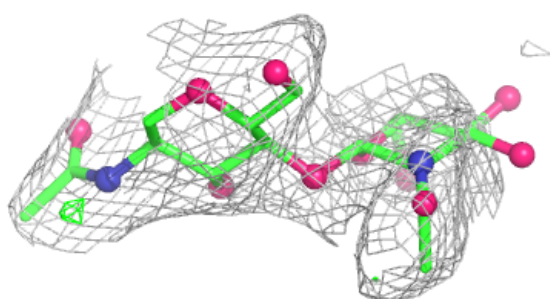
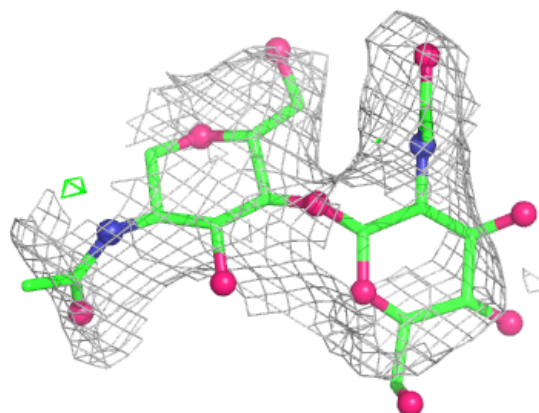
Electron density around Chain N:

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

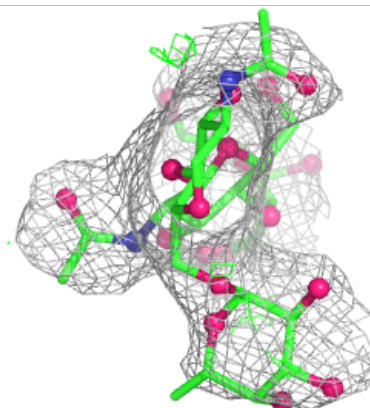
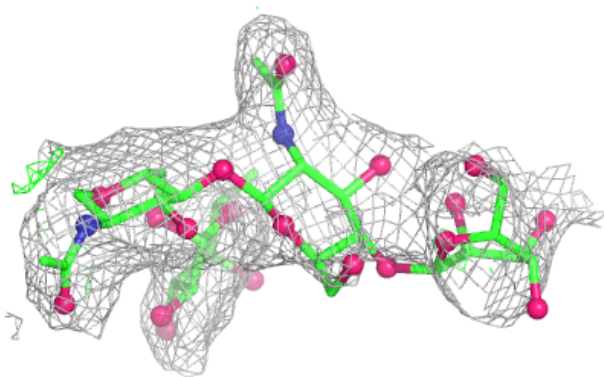
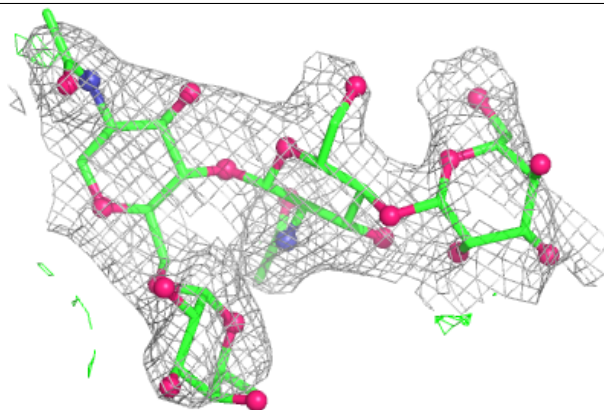


Electron density around Chain R:

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

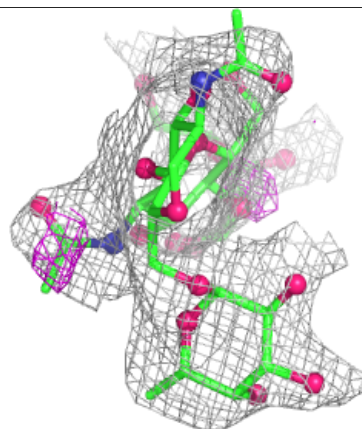
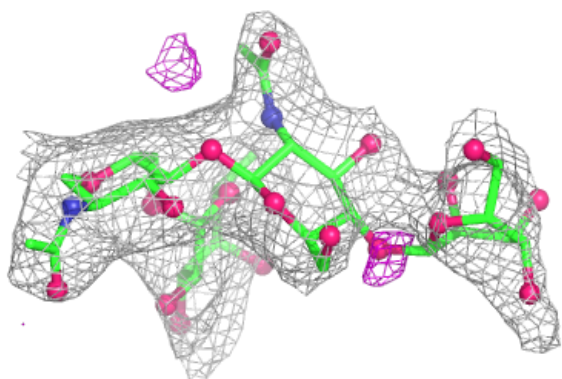
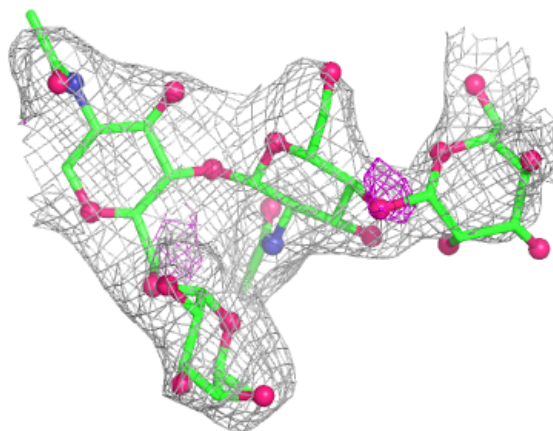
**Electron density around Chain I:**

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



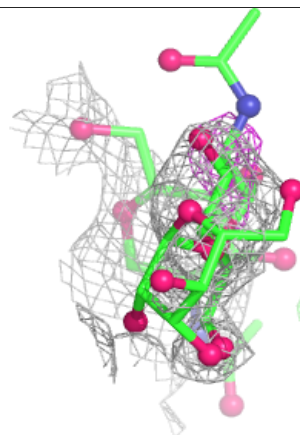
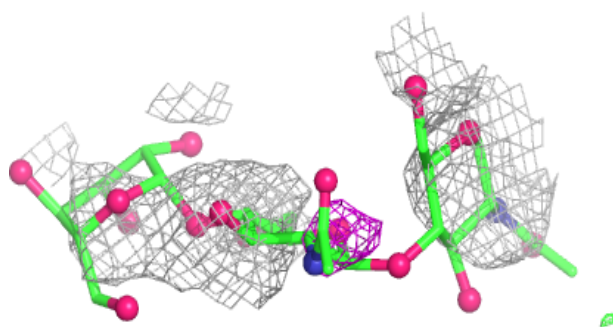
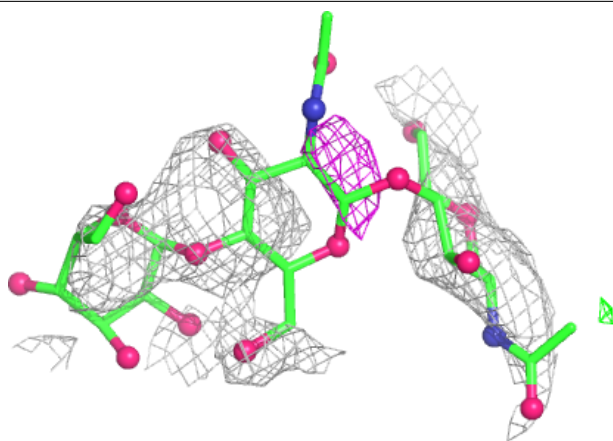
Electron density around Chain P:

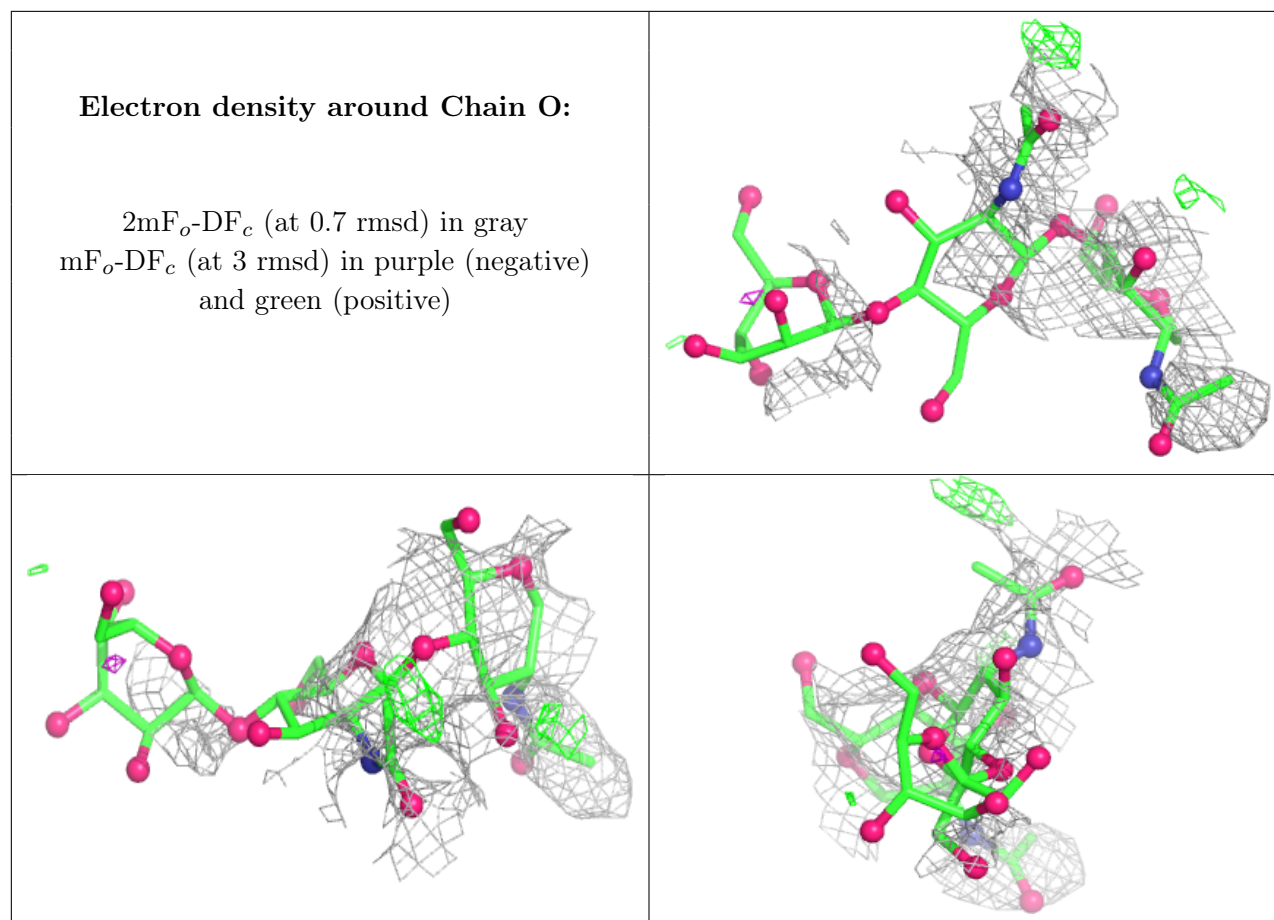
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain L:

$2mF_o - DF_c$ (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
8	NAG	D	401	14/15	0.07	0.20	117,136,143,143	0
8	NAG	A	401	14/15	0.31	0.16	139,156,159,160	0
8	NAG	A	402	14/15	0.35	0.19	121,131,138,139	0
8	NAG	D	402	14/15	0.47	0.16	139,147,151,156	0

6.5 Other polymers [i](#)

There are no such residues in this entry.