



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 04:44 AM UTC

PDB ID : 6DRU / pdb_00006dru
Title : Xylosidase from *Aspergillus niger*
Authors : Cao, H.; Xu, W.; Betancourt, M.; Walton, J.D.; Brumm, P.; Phillips Jr., G.N.;
Enzyme Discovery for Natural Product Biosynthesis (NatPro)
Deposited on : 2018-06-13
Resolution : 2.70 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

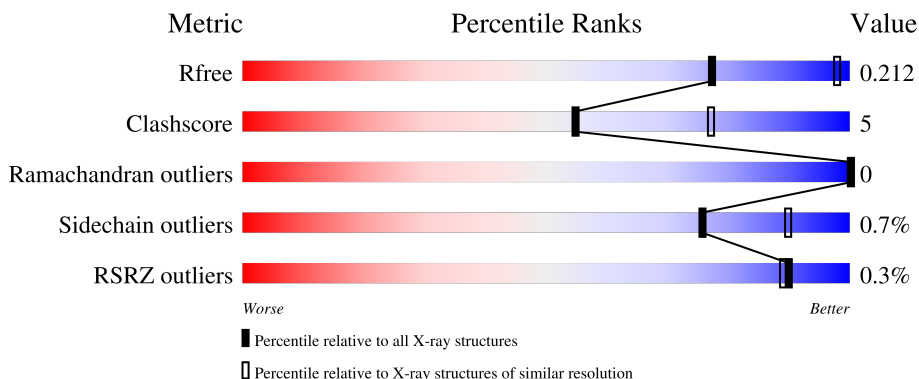
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.







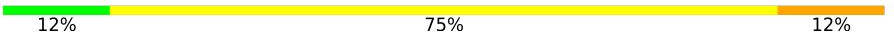
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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 $\leq 5\%$. 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	718	 89% 11%
1	B	718	 88% 11%
2	C	6	 33% 50% 17%
3	D	9	 78% 22%
4	E	10	 10% 90%

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Mol	Chain	Length	Quality of chain
4	I	10	 10% 90%
5	F	5	 20% 80%
5	J	5	 20% 80%
6	G	4	 50% 50%
7	H	8	 12% 75% 12%

2 Entry composition i

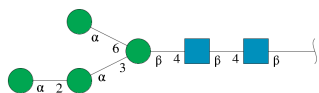
There are 11 unique types of molecules in this entry. The entry contains 12553 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycosyl hydrolases family 31 family protein.

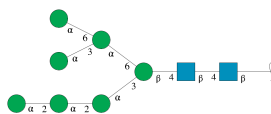
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	718	Total 5724	C 3659	N 961	O 1084	S 20	0	1	0
1	B	717	Total 5718	C 3654	N 960	O 1084	S 20	0	1	0

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	6	Total 72	C 40	N 2	O 30	0	0	0

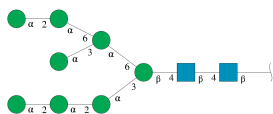
- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	D	9	Total 105	C 58	N 2	O 45	0	0	0

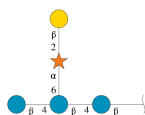
- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-2)-alpha-D-mannopyra

nose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



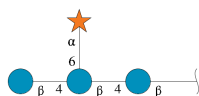
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	E	10	116	64	2	50	0	0	0
4	I	10	116	64	2	50	0	0	0

- Molecule 5 is an oligosaccharide called beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)-[beta-D-glucopyranose-(1-4)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.



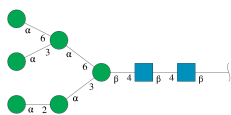
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
5	F	5	54	29	25	0	0	0
5	J	5	54	29	25	0	0	0

- Molecule 6 is an oligosaccharide called beta-D-glucopyranose-(1-4)-[alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
6	G	4	43	23	20	0	0	0

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
7	H	8	94	52	2	40	0	0	0

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



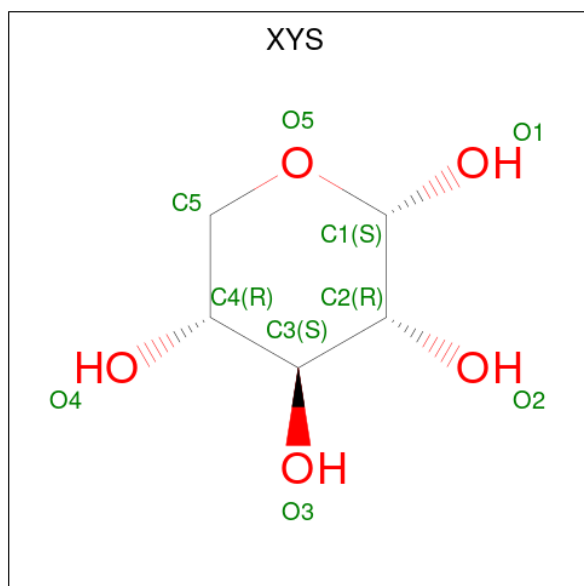
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
8	A	1	14	8	1	5	0	0
8	A	1	14	8	1	5	0	0
8	A	1	14	8	1	5	0	0
8	A	1	14	8	1	5	0	0
8	B	1	14	8	1	5	0	0
8	B	1	14	8	1	5	0	0
8	B	1	14	8	1	5	0	0
8	B	1	14	8	1	5	0	0

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

- Molecule 9 is alpha-D-xylopyranose (CCD ID: XYS) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
9	A	1	10	5	5	0	0
9	B	1	10	5	5	0	0

- Molecule 10 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C O 6 3 3	0	0
10	B	1	Total C O 6 3 3	0	0
10	B	1	Total C O 6 3 3	0	0

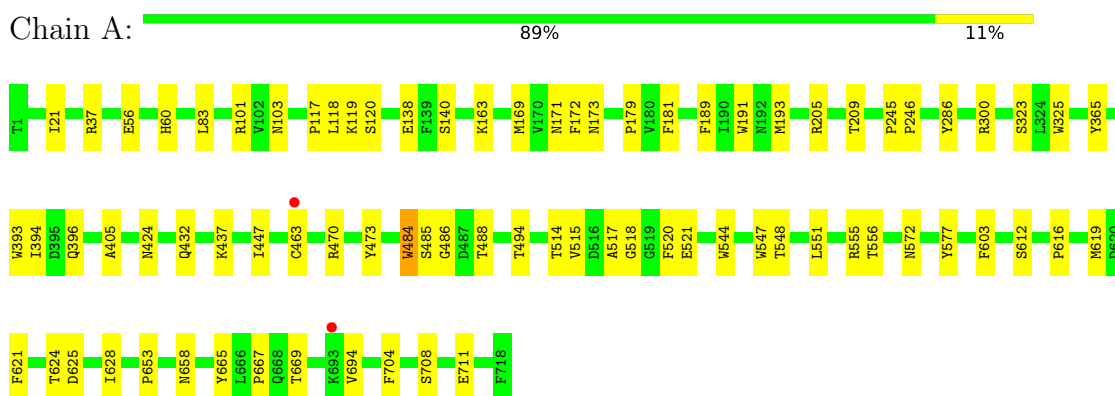
- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	153	Total O 153 153	0	0
11	B	140	Total O 140 140	0	0

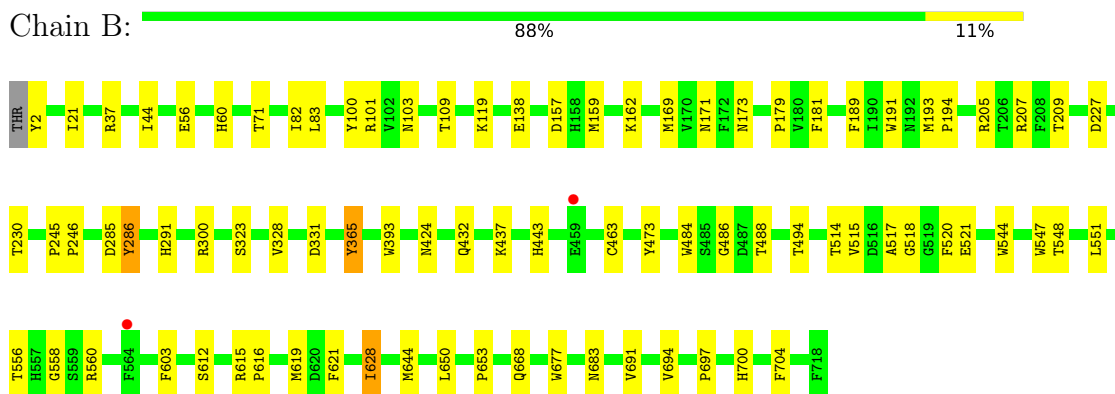
3 Residue-property plots [i](#)

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: Glycosyl hydrolases family 31 family protein



- Molecule 1: Glycosyl hydrolases family 31 family protein




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



- Molecule 3: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-

(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  78% 22%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9

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

Chain E:  10% 90%

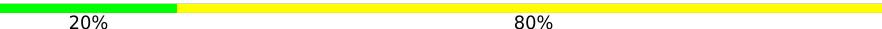
MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10

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

Chain I:  10% 90%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10

- Molecule 5: beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)-[beta-D-glucopyranose-(1-4)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain F:  20% 80%

BGC1
BGC2
XYS3
GAL4
BGC5

- Molecule 5: beta-D-galactopyranose-(1-2)-alpha-D-xylopyranose-(1-6)-[beta-D-glucopyranose-(1-4)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain J:  20% 80%

BGC1
BGC2
XYS3
GAL4
BGC5

- Molecule 6: beta-D-glucopyranose-(1-4)-[alpha-D-xylopyranose-(1-6)]beta-D-glucopyranose-(1-4)-beta-D-glucopyranose

Chain G:  50% 50%

BGC1
BGC2
BGC3
XYS4

- Molecule 7: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:  12% 75% 12%

MAG1	MAG2	MAG3	MAN4	MAN5	MAN6	MAN7	MAN8
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4 Data and refinement statistics i

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	146.13Å 146.13Å 220.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.91 – 2.70 47.91 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.91-2.70) 84.2 (47.91-2.70)	Depositor EDS
R_{merge}	0.53	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.25 (at 2.69Å)	Xtrriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.181 , 0.212 0.181 , 0.212	Depositor DCC
R_{free} test set	1992 reflections (2.65%)	wwPDB-VP
Wilson B-factor (Å ²)	51.2	Xtrriage
Anisotropy	0.352	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12553	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.09% 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, XYS, GAL, MAN, BGC, GOL

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	0/5906	0.30	0/8073
1	B	0.11	0/5900	0.31	0/8064
All	All	0.11	0/11806	0.31	0/16137

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	5724	0	5401	54	0
1	B	5718	0	5386	59	0
2	C	72	0	61	2	0
3	D	105	0	88	3	0
4	E	116	0	97	0	0
4	I	116	0	97	0	0
5	F	54	0	46	0	0
5	J	54	0	46	0	0
6	G	43	0	37	0	0
7	H	94	0	79	1	0
8	A	56	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	70	0	65	1	0
9	A	10	0	10	0	0
9	B	10	0	10	0	0
10	A	6	0	8	0	0
10	B	12	0	16	1	0
11	A	153	0	0	6	0
11	B	140	0	0	3	0
All	All	12553	0	11499	113	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 113 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:396:GLN:HE21	1:A:470:ARG:HH12	1.18	0.90
1:A:101:ARG:NH1	1:A:103:ASN:OD1	2.08	0.86
1:B:101:ARG:NH1	1:B:103:ASN:OD1	2.18	0.76
1:B:103:ASN:HD21	1:B:109:THR:HG23	1.54	0.70
1:A:171:ASN:OD1	1:A:437:LYS:NZ	2.25	0.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	717/718 (100%)	688 (96%)	29 (4%)	0	100	100
1	B	716/718 (100%)	686 (96%)	30 (4%)	0	100	100
All	All	1433/1436 (100%)	1374 (96%)	59 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	607/606 (100%)	604 (100%)	3 (0%)	81	92
1	B	606/606 (100%)	601 (99%)	5 (1%)	73	88
All	All	1213/1212 (100%)	1205 (99%)	8 (1%)	76	90

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	691	VAL
1	B	628	ILE
1	B	328	VAL
1	B	286	TYR
1	B	365	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	339	GLN
1	B	156	GLN
1	A	445	GLN
1	A	426	ASN
1	A	605	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

57 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	1.19	2 (14%)	17,19,21	1.12	1 (5%)
2	NAG	C	2	2	14,14,15	1.22	2 (14%)	17,19,21	1.08	2 (11%)
2	BMA	C	3	2	11,11,12	0.56	0	15,15,17	0.65	0
2	MAN	C	4	2	11,11,12	0.74	0	15,15,17	0.89	1 (6%)
2	MAN	C	5	2	11,11,12	0.69	0	15,15,17	0.83	0
2	MAN	C	6	2	11,11,12	0.72	0	15,15,17	0.93	1 (6%)
3	NAG	D	1	3,1	14,14,15	1.21	2 (14%)	17,19,21	1.09	1 (5%)
3	NAG	D	2	3	14,14,15	1.21	2 (14%)	17,19,21	1.05	1 (5%)
3	BMA	D	3	3	11,11,12	0.57	0	15,15,17	0.65	0
3	MAN	D	4	3	11,11,12	0.76	0	15,15,17	1.02	1 (6%)
3	MAN	D	5	3	11,11,12	0.73	0	15,15,17	1.12	1 (6%)
3	MAN	D	6	3	11,11,12	0.75	0	15,15,17	0.94	1 (6%)
3	MAN	D	7	3	11,11,12	0.74	0	15,15,17	1.05	1 (6%)
3	MAN	D	8	3	11,11,12	0.78	0	15,15,17	1.03	1 (6%)
3	MAN	D	9	3	11,11,12	0.76	0	15,15,17	1.09	1 (6%)
4	NAG	E	1	1,4	14,14,15	1.20	2 (14%)	17,19,21	1.15	2 (11%)
4	MAN	E	10	4	11,11,12	0.77	0	15,15,17	1.02	1 (6%)
4	NAG	E	2	4	14,14,15	1.21	2 (14%)	17,19,21	1.04	1 (5%)
4	BMA	E	3	4	11,11,12	0.57	0	15,15,17	0.72	0
4	MAN	E	4	4	11,11,12	0.75	0	15,15,17	0.90	1 (6%)
4	MAN	E	5	4	11,11,12	0.81	0	15,15,17	1.24	1 (6%)
4	MAN	E	6	4	11,11,12	0.74	0	15,15,17	0.92	1 (6%)
4	MAN	E	7	4	11,11,12	0.74	0	15,15,17	0.93	1 (6%)
4	MAN	E	8	4	11,11,12	0.75	0	15,15,17	0.98	1 (6%)
4	MAN	E	9	4	11,11,12	0.74	0	15,15,17	0.98	1 (6%)
5	BGC	F	1	5	12,12,12	0.82	0	17,17,17	0.87	1 (5%)
5	BGC	F	2	5	11,11,12	1.01	1 (9%)	15,15,17	0.94	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	XYS	F	3	5	9,9,10	0.69	0	10,12,14	0.70	0
5	GAL	F	4	5	11,11,12	2.64	1 (9%)	15,15,17	2.07	3 (20%)
5	BGC	F	5	5	11,11,12	1.00	1 (9%)	15,15,17	0.89	1 (6%)
6	BGC	G	1	6	12,12,12	0.81	0	17,17,17	0.93	1 (5%)
6	BGC	G	2	6	11,11,12	0.27	0	15,15,17	0.52	0
6	BGC	G	3	6	11,11,12	0.95	0	15,15,17	0.89	1 (6%)
6	XYS	G	4	6	9,9,10	0.21	0	10,12,14	0.47	0
7	NAG	H	1	1,7	14,14,15	1.21	2 (14%)	17,19,21	1.00	1 (5%)
7	NAG	H	2	7	14,14,15	1.21	2 (14%)	17,19,21	1.04	1 (5%)
7	BMA	H	3	7	11,11,12	0.57	0	15,15,17	0.72	0
7	MAN	H	4	7	11,11,12	0.73	0	15,15,17	0.95	1 (6%)
7	MAN	H	5	7	11,11,12	0.73	0	15,15,17	0.97	1 (6%)
7	MAN	H	6	7	11,11,12	0.75	0	15,15,17	1.09	1 (6%)
7	MAN	H	7	7	11,11,12	0.78	0	15,15,17	1.02	1 (6%)
7	MAN	H	8	7	11,11,12	0.74	0	15,15,17	1.00	1 (6%)
4	NAG	I	1	1,4	14,14,15	1.19	2 (14%)	17,19,21	1.12	2 (11%)
4	MAN	I	10	4	11,11,12	0.76	0	15,15,17	0.92	1 (6%)
4	NAG	I	2	4	14,14,15	1.24	2 (14%)	17,19,21	1.19	2 (11%)
4	BMA	I	3	4	11,11,12	0.57	0	15,15,17	0.70	0
4	MAN	I	4	4	11,11,12	0.74	0	15,15,17	0.90	1 (6%)
4	MAN	I	5	4	11,11,12	0.80	0	15,15,17	1.06	1 (6%)
4	MAN	I	6	4	11,11,12	0.77	0	15,15,17	1.04	1 (6%)
4	MAN	I	7	4	11,11,12	0.77	0	15,15,17	0.92	1 (6%)
4	MAN	I	8	4	11,11,12	0.76	0	15,15,17	1.01	1 (6%)
4	MAN	I	9	4	11,11,12	0.74	0	15,15,17	1.01	1 (6%)
5	BGC	J	1	5	12,12,12	0.81	0	17,17,17	0.82	1 (5%)
5	BGC	J	2	5	11,11,12	0.96	0	15,15,17	0.83	1 (6%)
5	XYS	J	3	5	9,9,10	0.71	0	10,12,14	0.67	0
5	GAL	J	4	5	11,11,12	2.68	1 (9%)	15,15,17	1.93	3 (20%)
5	BGC	J	5	5	11,11,12	0.97	1 (9%)	15,15,17	0.88	1 (6%)

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	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	1/6/23/26	0/1/1/1
2	BMA	C	3	2	-	2/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	MAN	C	5	2	-	2/2/19/22	0/1/1/1
2	MAN	C	6	2	-	1/2/19/22	0/1/1/1
3	NAG	D	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	D	2	3	-	2/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	MAN	D	4	3	-	0/2/19/22	0/1/1/1
3	MAN	D	5	3	-	2/2/19/22	0/1/1/1
3	MAN	D	6	3	-	2/2/19/22	0/1/1/1
3	MAN	D	7	3	-	2/2/19/22	0/1/1/1
3	MAN	D	8	3	-	2/2/19/22	0/1/1/1
3	MAN	D	9	3	-	1/2/19/22	0/1/1/1
4	NAG	E	1	1,4	-	2/6/23/26	0/1/1/1
4	MAN	E	10	4	-	2/2/19/22	0/1/1/1
4	NAG	E	2	4	-	0/6/23/26	0/1/1/1
4	BMA	E	3	4	-	0/2/19/22	0/1/1/1
4	MAN	E	4	4	-	0/2/19/22	0/1/1/1
4	MAN	E	5	4	-	2/2/19/22	0/1/1/1
4	MAN	E	6	4	-	1/2/19/22	0/1/1/1
4	MAN	E	7	4	-	0/2/19/22	0/1/1/1
4	MAN	E	8	4	-	2/2/19/22	0/1/1/1
4	MAN	E	9	4	-	2/2/19/22	0/1/1/1
5	BGC	F	1	5	-	2/2/22/22	0/1/1/1
5	BGC	F	2	5	-	0/2/19/22	0/1/1/1
5	XYS	F	3	5	-	-	0/1/1/1
5	GAL	F	4	5	-	0/2/19/22	0/1/1/1
5	BGC	F	5	5	-	1/2/19/22	0/1/1/1
6	BGC	G	1	6	-	2/2/22/22	0/1/1/1
6	BGC	G	2	6	-	2/2/19/22	0/1/1/1
6	BGC	G	3	6	-	2/2/19/22	0/1/1/1
6	XYS	G	4	6	-	-	0/1/1/1
7	NAG	H	1	1,7	-	2/6/23/26	0/1/1/1
7	NAG	H	2	7	-	2/6/23/26	0/1/1/1
7	BMA	H	3	7	-	1/2/19/22	0/1/1/1
7	MAN	H	4	7	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	MAN	H	5	7	-	2/2/19/22	0/1/1/1
7	MAN	H	6	7	-	2/2/19/22	0/1/1/1
7	MAN	H	7	7	-	0/2/19/22	0/1/1/1
7	MAN	H	8	7	-	2/2/19/22	0/1/1/1
4	NAG	I	1	1,4	-	0/6/23/26	0/1/1/1
4	MAN	I	10	4	-	2/2/19/22	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1
4	BMA	I	3	4	-	0/2/19/22	0/1/1/1
4	MAN	I	4	4	-	0/2/19/22	0/1/1/1
4	MAN	I	5	4	-	2/2/19/22	0/1/1/1
4	MAN	I	6	4	-	2/2/19/22	0/1/1/1
4	MAN	I	7	4	-	0/2/19/22	0/1/1/1
4	MAN	I	8	4	-	2/2/19/22	0/1/1/1
4	MAN	I	9	4	-	0/2/19/22	0/1/1/1
5	BGC	J	1	5	-	0/2/22/22	0/1/1/1
5	BGC	J	2	5	-	0/2/19/22	0/1/1/1
5	XYS	J	3	5	-	-	0/1/1/1
5	GAL	J	4	5	-	0/2/19/22	0/1/1/1
5	BGC	J	5	5	-	1/2/19/22	0/1/1/1

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	4	GAL	C2-C3	-8.59	1.39	1.52
5	F	4	GAL	C2-C3	-8.45	1.39	1.52
7	H	2	NAG	C7-N2	2.54	1.42	1.34
7	H	1	NAG	C7-N2	2.53	1.42	1.34
3	D	2	NAG	C7-N2	2.50	1.42	1.34

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	4	GAL	C1-C2-C3	6.54	119.16	109.64
5	J	4	GAL	C1-C2-C3	5.76	118.03	109.64
4	E	5	MAN	C1-O5-C5	-3.96	106.88	112.19
3	D	5	MAN	C1-O5-C5	-3.61	107.35	112.19
3	D	9	MAN	C1-O5-C5	-3.56	107.41	112.19

There are no chirality outliers.

5 of 66 torsion outliers are listed below:

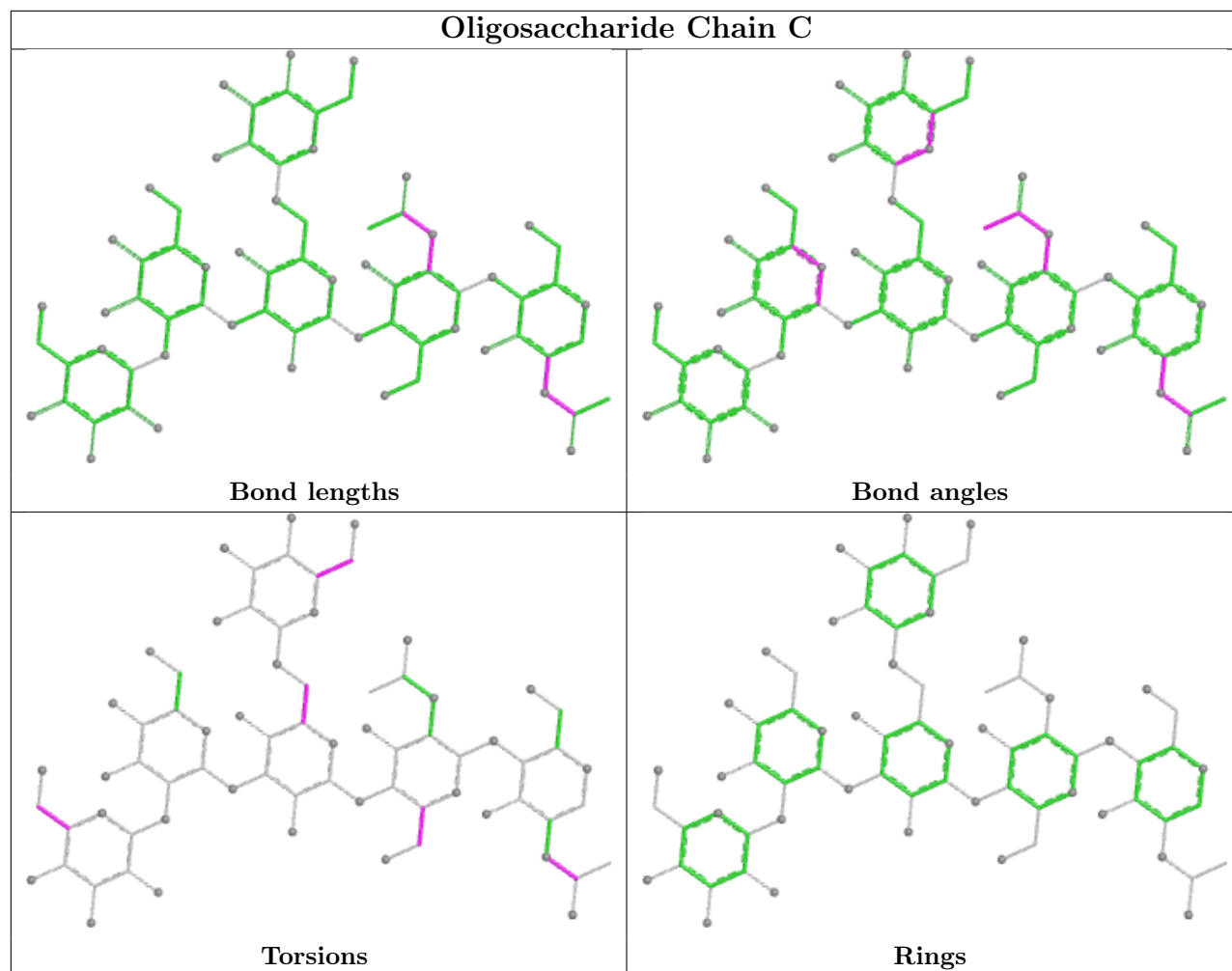
Mol	Chain	Res	Type	Atoms
3	D	8	MAN	C4-C5-C6-O6
3	D	6	MAN	O5-C5-C6-O6
4	E	1	NAG	O5-C5-C6-O6
7	H	2	NAG	O5-C5-C6-O6
7	H	5	MAN	O5-C5-C6-O6

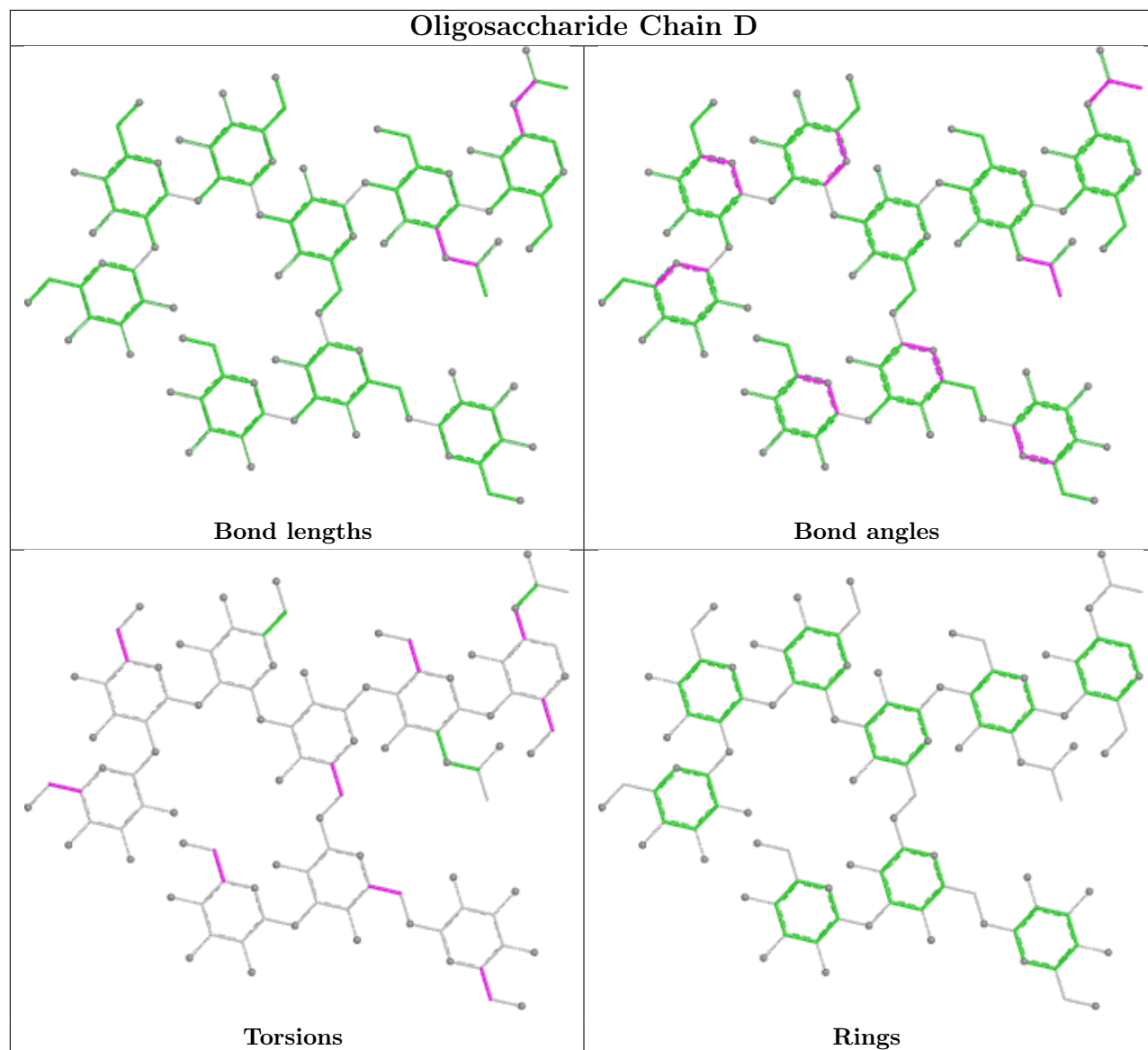
There are no ring outliers.

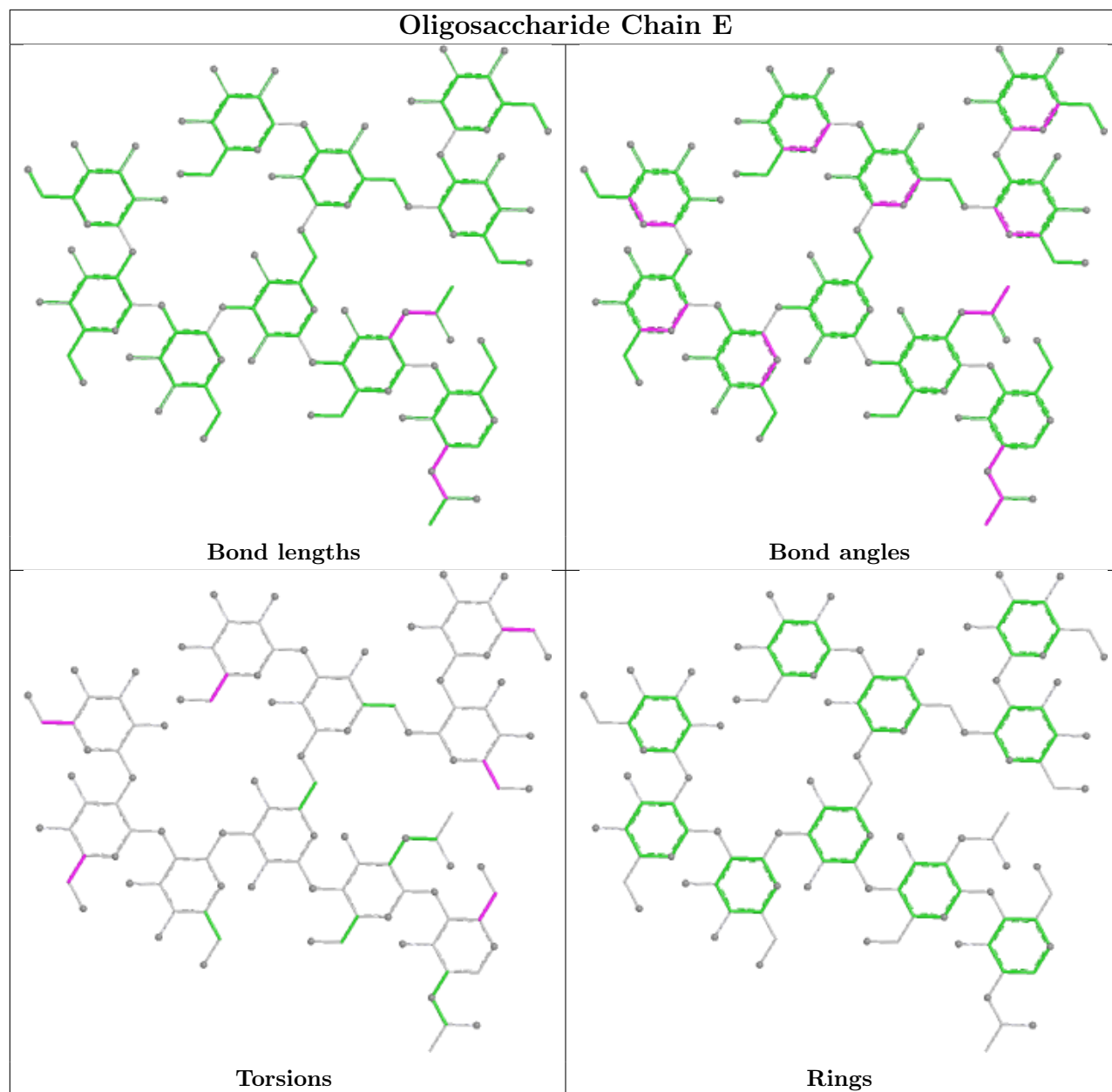
5 monomers are involved in 4 short contacts:

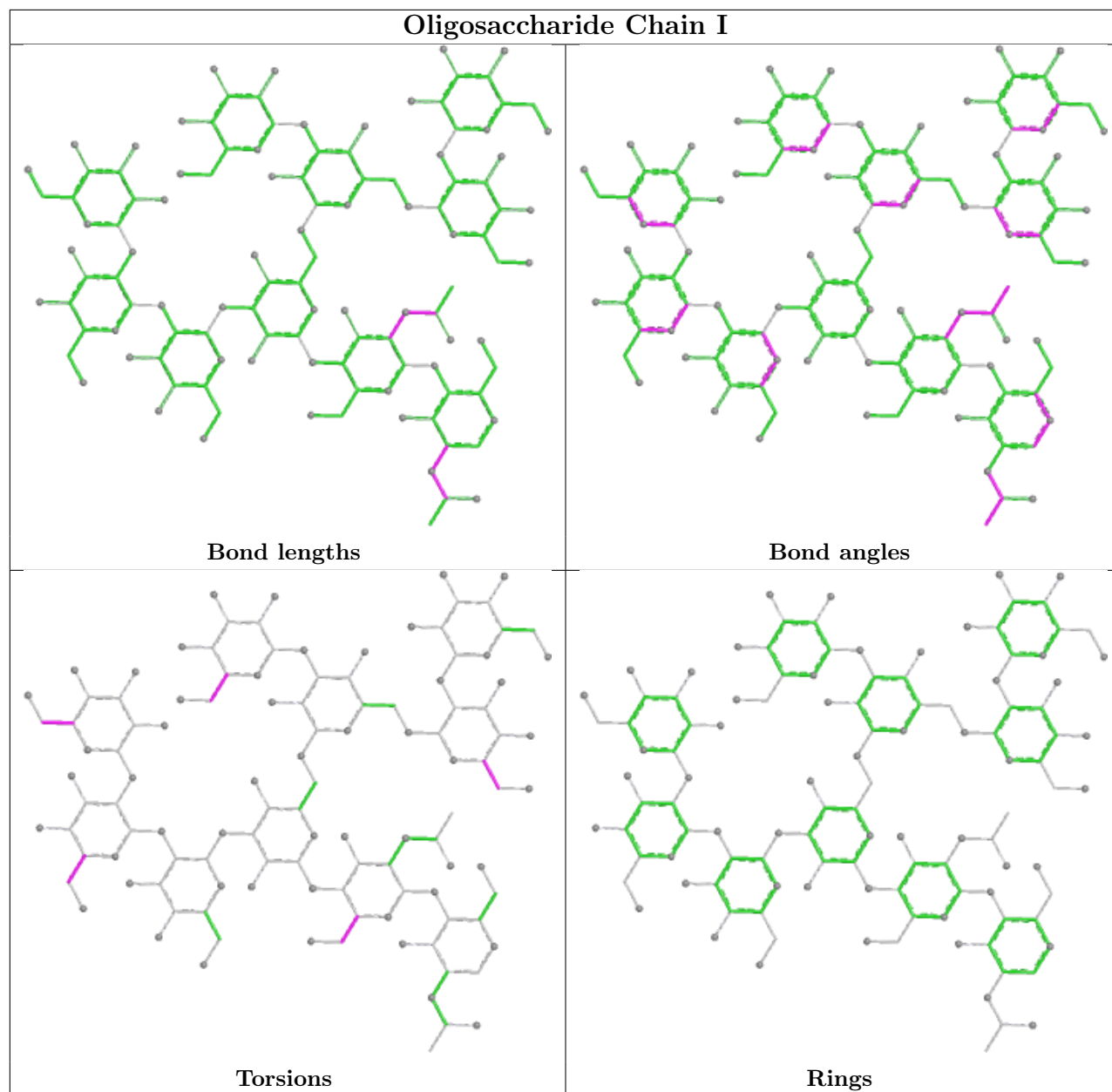
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2	NAG	1	0
7	H	2	NAG	1	0
3	D	4	MAN	1	0
2	C	1	NAG	2	0
3	D	3	BMA	1	0

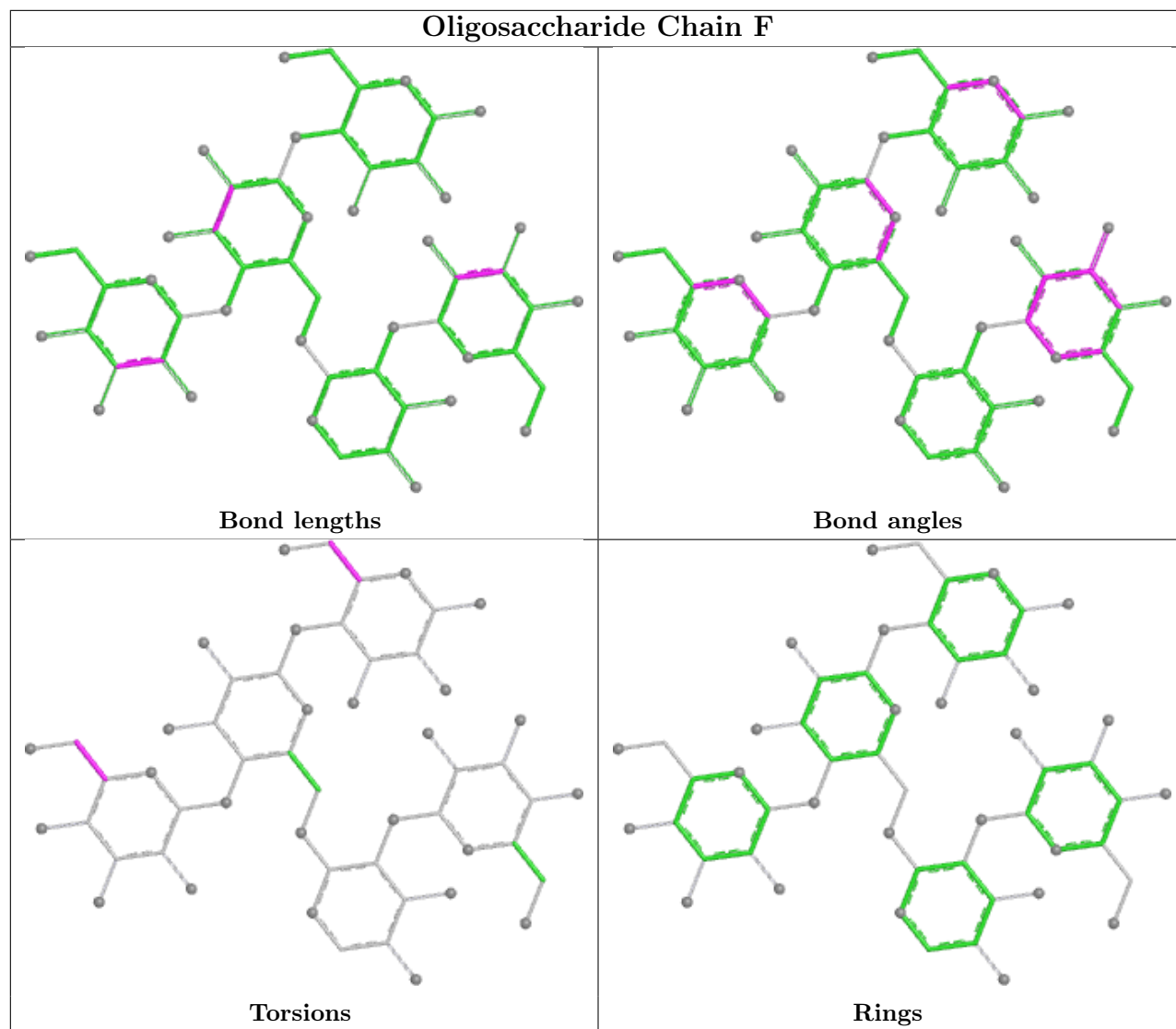
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

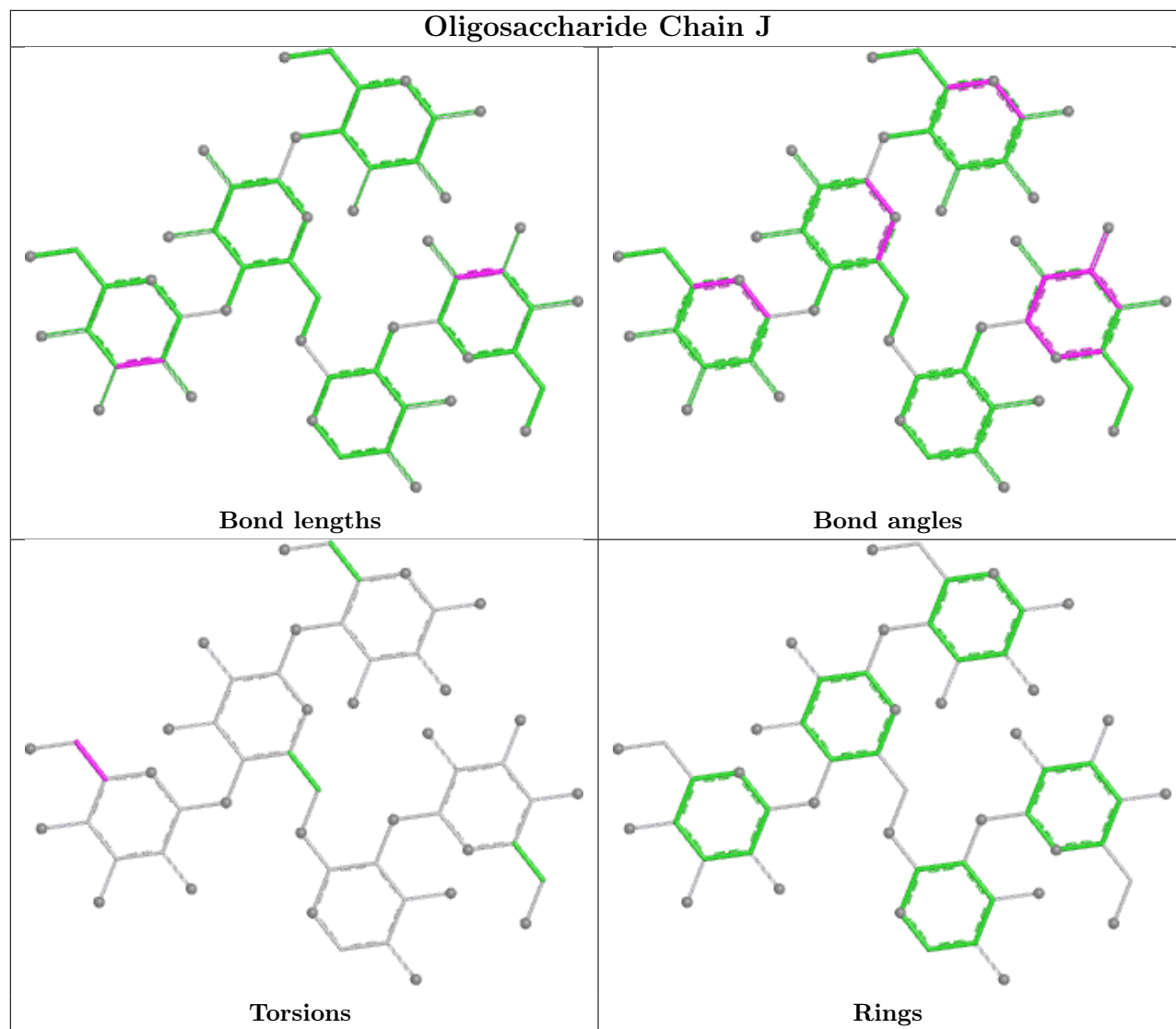


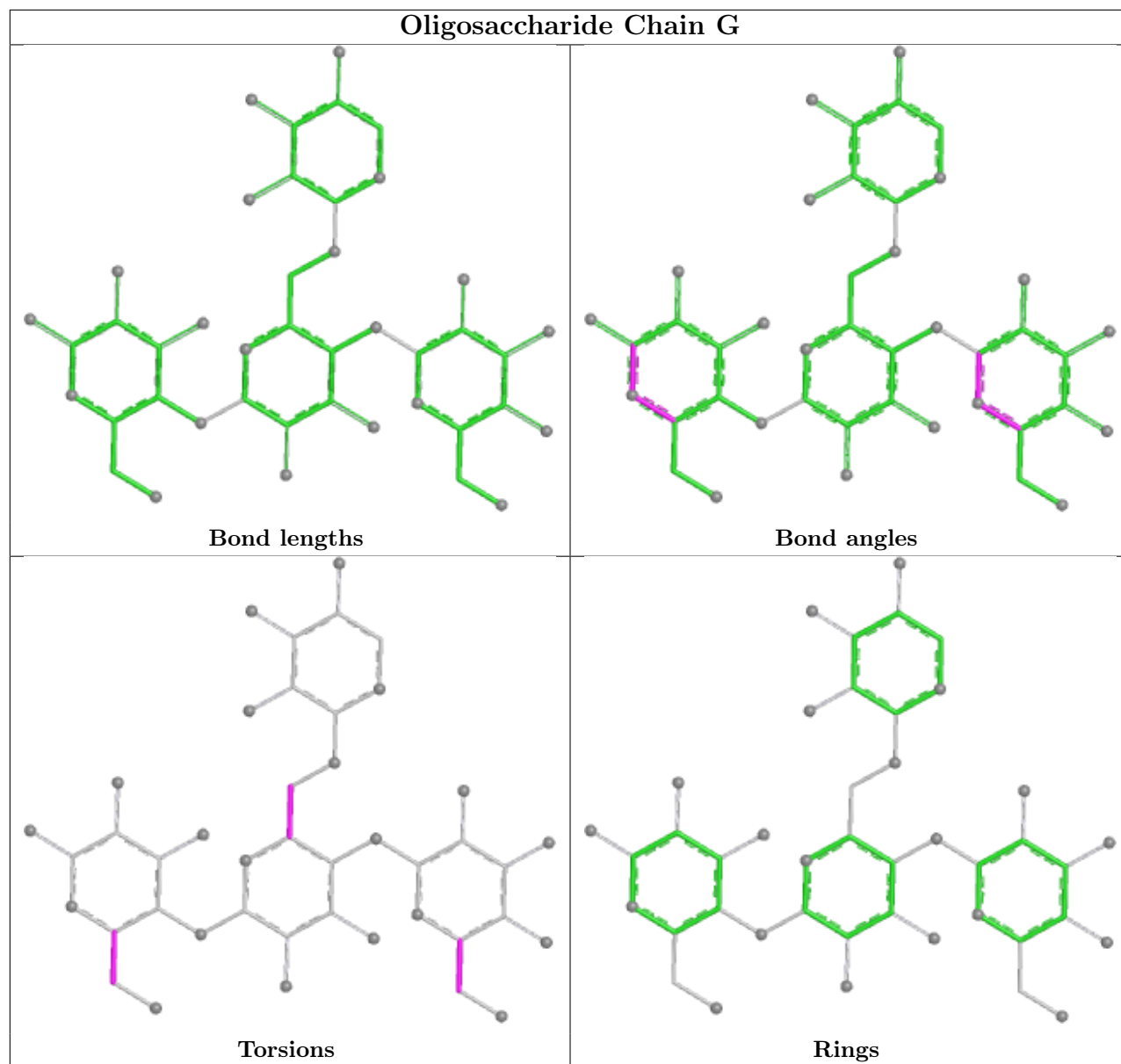


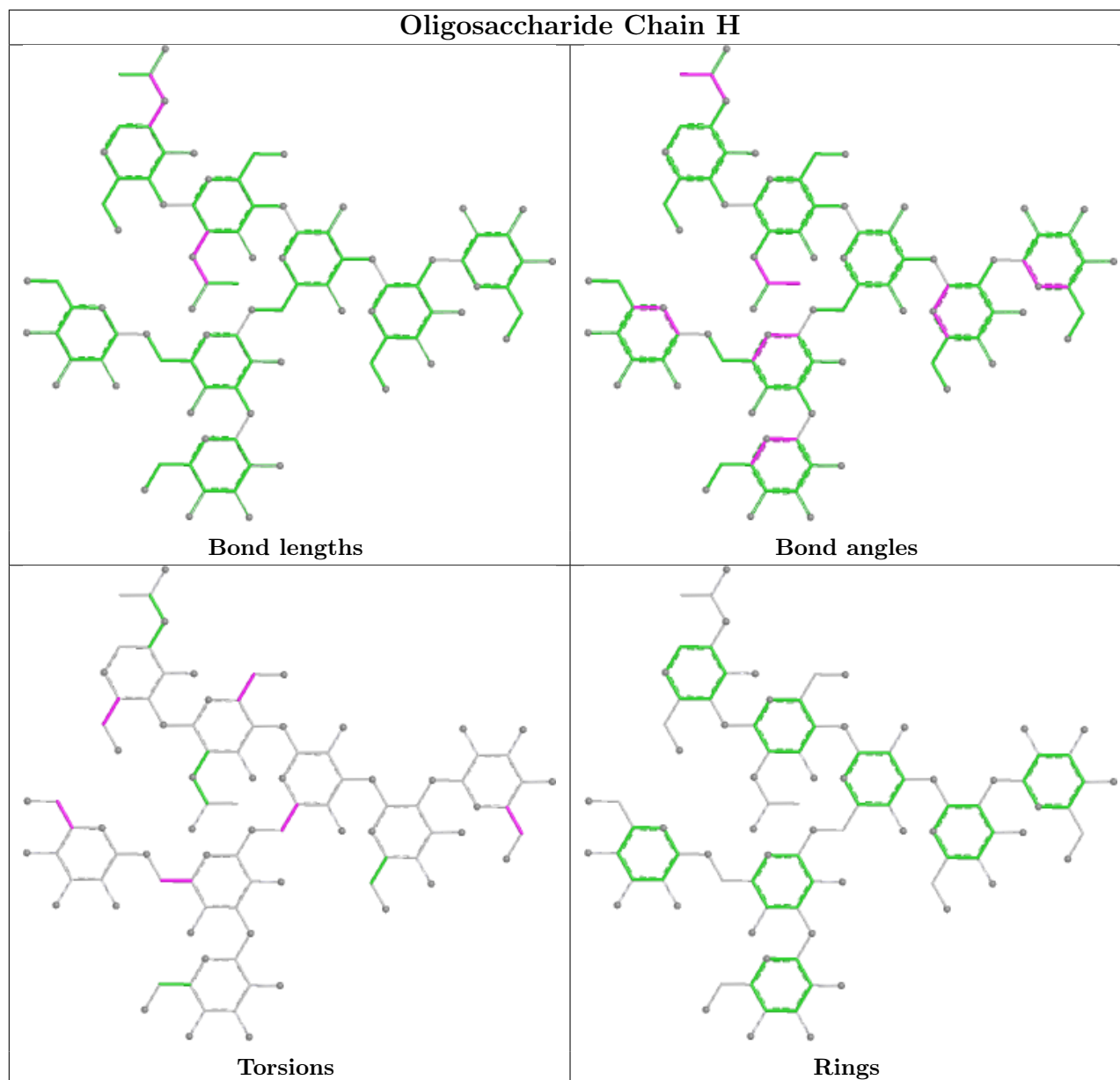












5.6 Ligand geometry [i](#)

14 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
10	GOL	B	830	-	5,5,5	0.90	0	5,5,5	1.09	0
10	GOL	A	840	-	5,5,5	0.90	0	5,5,5	1.08	0
8	NAG	A	826	1	14,14,15	1.22	2 (14%)	17,19,21	1.11	2 (11%)
8	NAG	B	829	1	14,14,15	1.18	2 (14%)	17,19,21	1.38	4 (23%)
8	NAG	A	827	1	14,14,15	1.18	2 (14%)	17,19,21	1.09	2 (11%)
8	NAG	B	821	1	14,14,15	1.19	2 (14%)	17,19,21	1.04	1 (5%)
8	NAG	B	822	1	14,14,15	1.23	2 (14%)	17,19,21	1.09	1 (5%)
8	NAG	A	828	1	14,14,15	1.16	1 (7%)	17,19,21	0.92	0
8	NAG	B	820	1	14,14,15	1.22	2 (14%)	17,19,21	1.16	1 (5%)
9	XYS	A	834	-	10,10,10	0.75	0	14,14,14	0.59	0
10	GOL	B	831	-	5,5,5	0.92	0	5,5,5	1.11	0
8	NAG	B	801	1	14,14,15	1.18	2 (14%)	17,19,21	1.26	3 (17%)
8	NAG	A	835	1	14,14,15	0.29	0	17,19,21	0.56	0
9	XYS	B	828	-	10,10,10	0.75	0	14,14,14	0.72	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
10	GOL	B	830	-	-	2/4/4/4	-
10	GOL	A	840	-	-	2/4/4/4	-
8	NAG	A	826	1	-	2/6/23/26	0/1/1/1
8	NAG	B	829	1	-	1/6/23/26	0/1/1/1
8	NAG	A	827	1	-	2/6/23/26	0/1/1/1
8	NAG	B	821	1	-	2/6/23/26	0/1/1/1
8	NAG	B	822	1	-	4/6/23/26	0/1/1/1
8	NAG	A	828	1	-	2/6/23/26	0/1/1/1
8	NAG	B	820	1	-	3/6/23/26	0/1/1/1
9	XYS	A	834	-	-	-	0/1/1/1
10	GOL	B	831	-	-	2/4/4/4	-
8	NAG	B	801	1	-	0/6/23/26	0/1/1/1
8	NAG	A	835	1	-	0/6/23/26	0/1/1/1
9	XYS	B	828	-	-	-	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	828	NAG	C7-N2	2.71	1.43	1.34
8	B	820	NAG	C7-N2	2.55	1.42	1.34
8	B	829	NAG	C7-N2	2.55	1.42	1.34
8	B	821	NAG	C7-N2	2.53	1.42	1.34
8	B	822	NAG	C7-N2	2.50	1.42	1.34

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	822	NAG	C8-C7-N2	2.84	120.83	116.12
8	B	829	NAG	C1-O5-C5	2.77	115.90	112.19
8	B	820	NAG	C8-C7-N2	2.76	120.70	116.12
8	B	801	NAG	C2-N2-C7	-2.66	119.33	122.90
8	B	801	NAG	C8-C7-N2	2.59	120.41	116.12

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	B	830	GOL	O1-C1-C2-C3
8	B	822	NAG	O5-C5-C6-O6
8	B	822	NAG	C4-C5-C6-O6
8	B	821	NAG	O5-C5-C6-O6
8	A	826	NAG	C8-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	830	GOL	1	0
8	B	820	NAG	1	0

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	718/718 (100%)	-0.17	2 (0%) 90 89	29, 63, 84, 142	1 (0%)
1	B	717/718 (99%)	-0.20	2 (0%) 90 89	32, 63, 85, 137	1 (0%)
All	All	1435/1436 (99%)	-0.18	4 (0%) 90 89	29, 63, 84, 142	2 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	463	CYS	2.5
1	B	564	PHE	2.4
1	A	693	LYS	2.2
1	B	459	GLU	2.0

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

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

6.3 Carbohydrates [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	XYS	G	4	9/10	0.55	0.16	93,110,124,124	0
2	MAN	C	5	11/12	0.56	0.13	81,118,131,137	0
7	MAN	H	8	11/12	0.57	0.13	109,123,135,139	0
7	MAN	H	5	11/12	0.68	0.12	107,115,126,127	0
5	GAL	J	4	11/12	0.68	0.14	78,111,127,128	0

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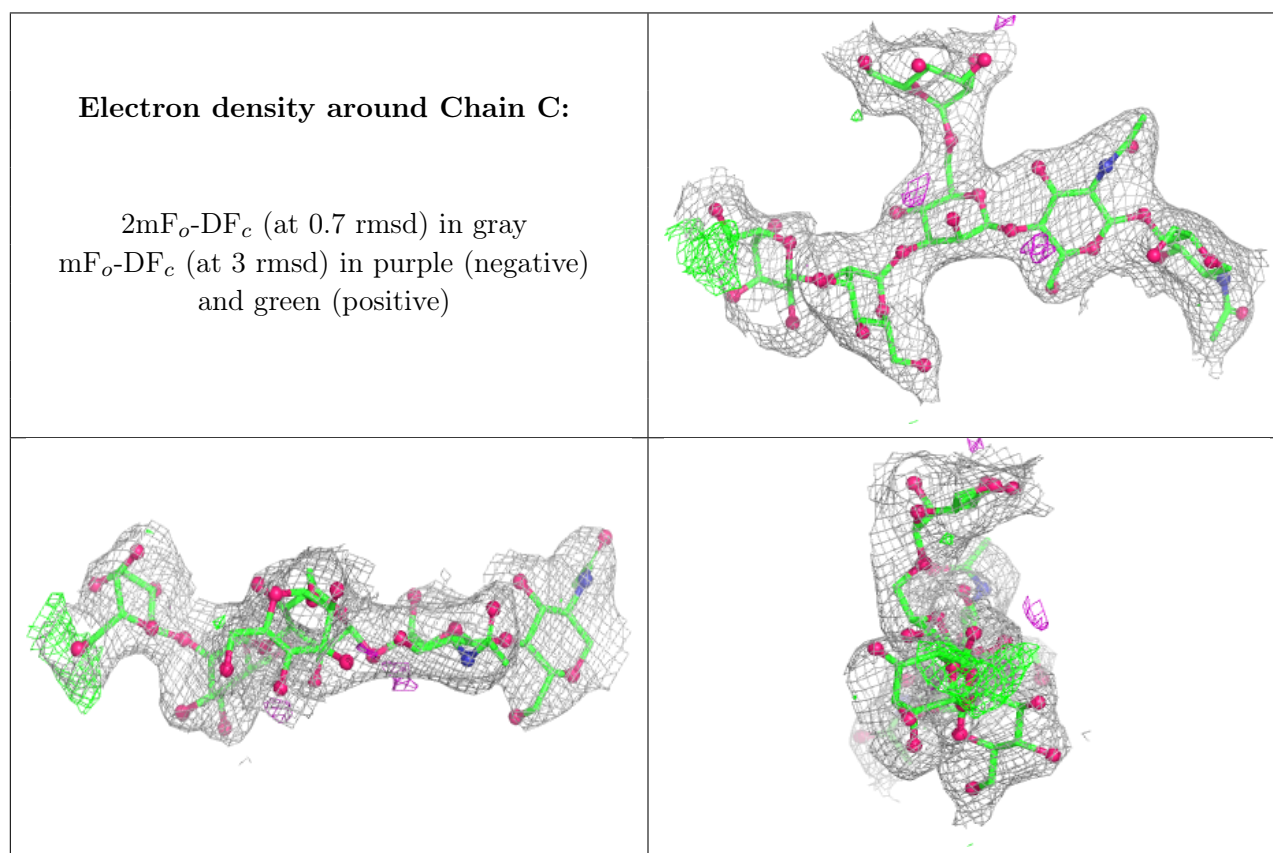
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MAN	E	6	11/12	0.69	0.11	94,111,122,123	0
5	GAL	F	4	11/12	0.69	0.14	92,118,127,132	0
3	MAN	D	9	11/12	0.70	0.11	93,101,123,130	0
3	MAN	D	6	11/12	0.72	0.15	118,138,144,153	0
2	MAN	C	6	11/12	0.74	0.12	99,112,125,136	0
6	BGC	G	3	11/12	0.75	0.11	90,114,119,127	0
3	MAN	D	5	11/12	0.82	0.10	103,110,127,138	0
6	BGC	G	2	11/12	0.83	0.14	97,103,109,114	0
6	BGC	G	1	12/12	0.86	0.16	102,111,131,135	0
4	MAN	I	6	11/12	0.86	0.11	87,101,108,111	0
7	MAN	H	6	11/12	0.89	0.09	71,81,97,111	0
5	XYS	J	3	9/10	0.89	0.12	96,100,106,114	0
5	BGC	F	1	12/12	0.90	0.09	82,91,99,102	0
4	MAN	E	5	11/12	0.91	0.08	73,80,92,93	0
2	MAN	C	4	11/12	0.92	0.08	81,87,96,110	0
4	MAN	I	9	11/12	0.92	0.08	82,87,95,97	0
7	MAN	H	7	11/12	0.92	0.09	73,79,84,88	0
7	NAG	H	1	14/15	0.92	0.10	66,78,84,97	0
4	MAN	I	5	11/12	0.93	0.09	69,78,83,89	0
3	MAN	D	7	11/12	0.93	0.07	63,77,97,108	0
2	BMA	C	3	11/12	0.93	0.07	66,74,83,91	0
4	MAN	E	9	11/12	0.93	0.08	81,86,91,92	0
5	XYS	F	3	9/10	0.94	0.09	88,93,100,107	0
4	MAN	E	4	11/12	0.94	0.08	65,67,72,74	0
5	BGC	J	1	12/12	0.94	0.08	84,95,100,105	0
4	MAN	E	7	11/12	0.94	0.08	61,67,74,77	0
4	MAN	I	8	11/12	0.94	0.07	65,71,77,79	0
4	NAG	E	1	14/15	0.94	0.08	63,68,74,83	0
4	MAN	E	10	11/12	0.94	0.08	56,65,71,72	0
3	BMA	D	3	11/12	0.95	0.07	63,70,75,77	0
2	NAG	C	1	14/15	0.95	0.09	60,70,78,82	0
4	BMA	E	3	11/12	0.95	0.07	54,60,69,71	0
2	NAG	C	2	14/15	0.95	0.07	49,73,80,84	0
5	BGC	F	2	11/12	0.95	0.08	74,79,81,88	0
4	NAG	I	2	14/15	0.95	0.07	61,67,80,85	0
7	NAG	H	2	14/15	0.95	0.08	61,74,76,98	0
7	BMA	H	3	11/12	0.95	0.07	66,74,77,80	0
7	MAN	H	4	11/12	0.95	0.06	71,84,91,95	0
4	BMA	I	3	11/12	0.95	0.07	54,60,69,69	0
5	BGC	F	5	11/12	0.95	0.08	61,73,79,83	0
4	MAN	I	4	11/12	0.95	0.08	54,66,72,73	0
3	NAG	D	2	14/15	0.95	0.08	61,70,78,88	0

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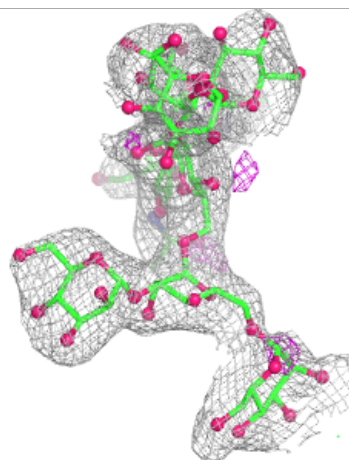
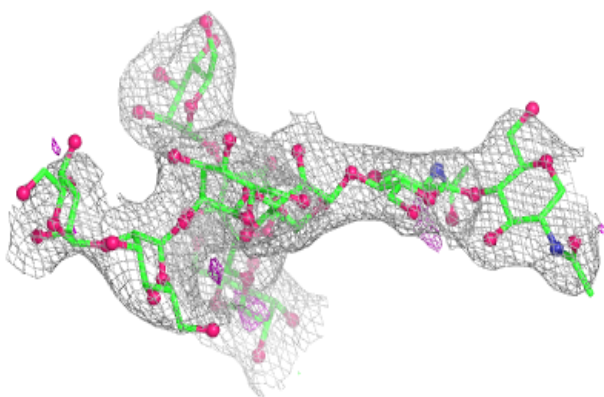
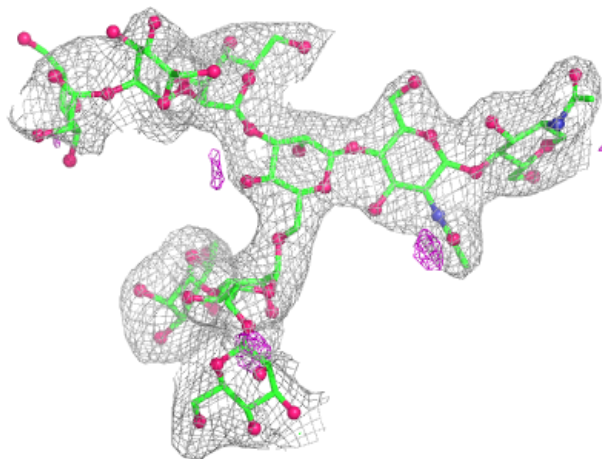
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	BGC	J	2	11/12	0.96	0.09	73,79,87,95	0
3	NAG	D	1	14/15	0.96	0.07	58,64,70,86	0
3	MAN	D	8	11/12	0.96	0.07	66,68,76,78	0
5	BGC	J	5	11/12	0.96	0.07	62,67,76,78	0
4	NAG	I	1	14/15	0.96	0.07	47,65,70,74	0
4	MAN	I	7	11/12	0.96	0.06	61,66,72,73	0
3	MAN	D	4	11/12	0.96	0.06	66,69,81,85	0
4	MAN	E	8	11/12	0.96	0.06	66,72,76,78	0
4	NAG	E	2	14/15	0.97	0.06	64,70,83,97	0
4	MAN	I	10	11/12	0.97	0.05	61,64,69,70	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.



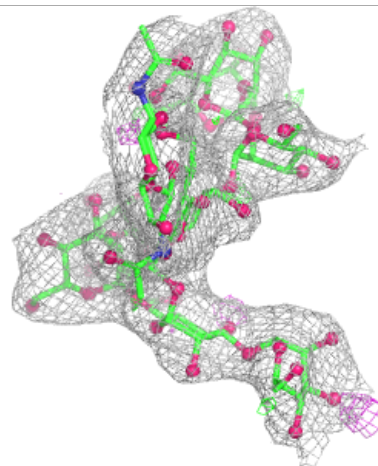
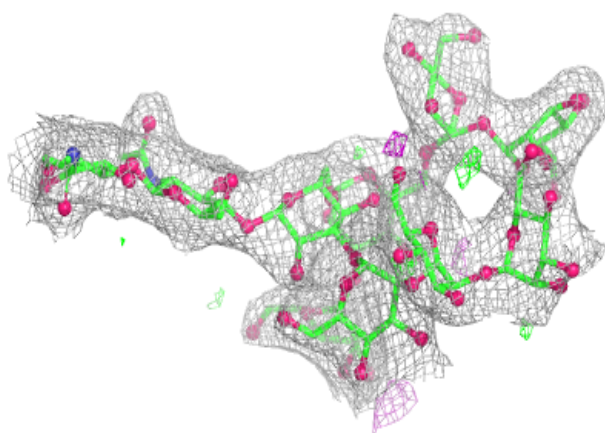
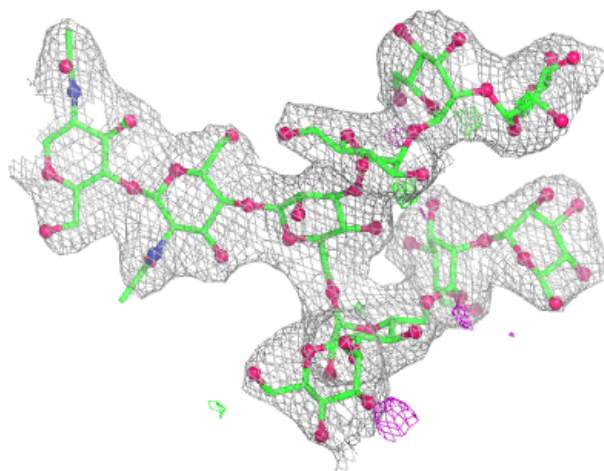
Electron density around Chain D:

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



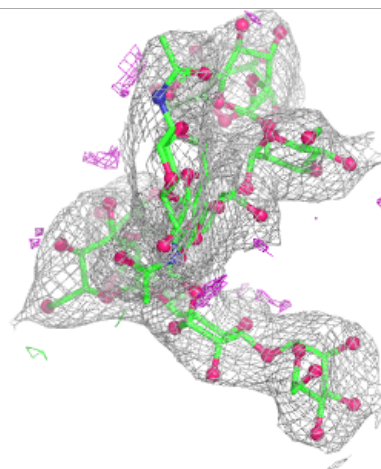
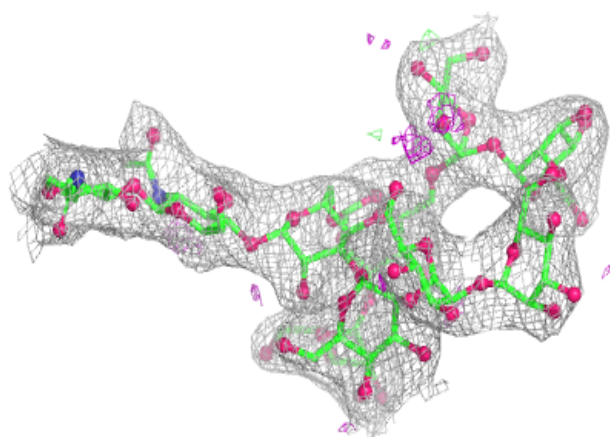
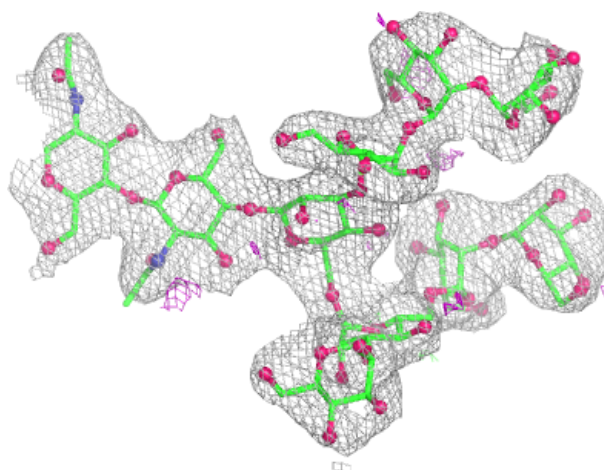
Electron density around Chain E:

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



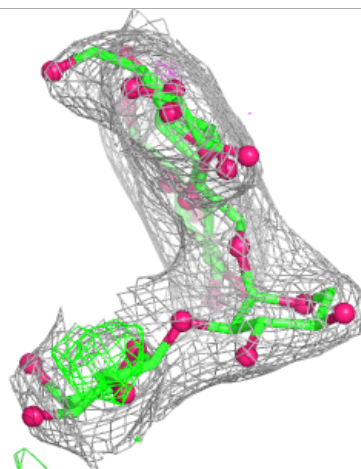
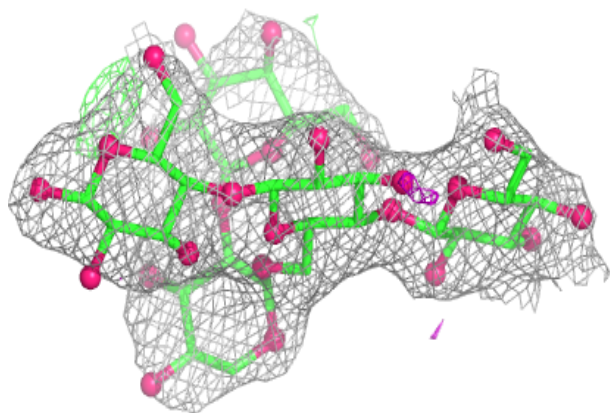
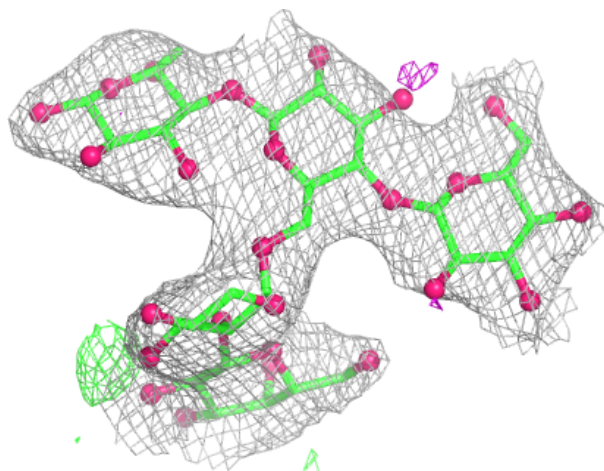
Electron density around Chain I:

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



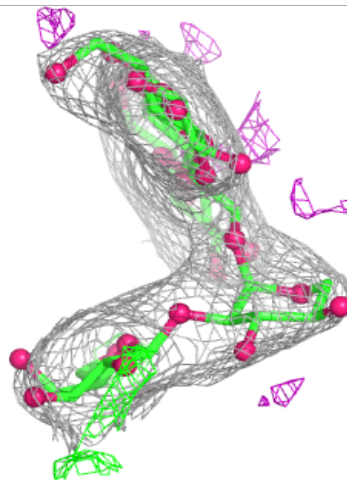
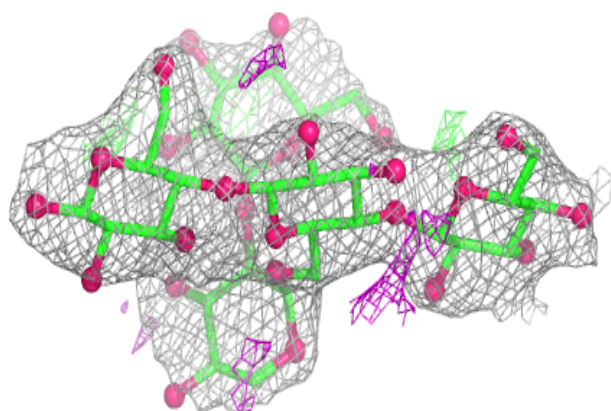
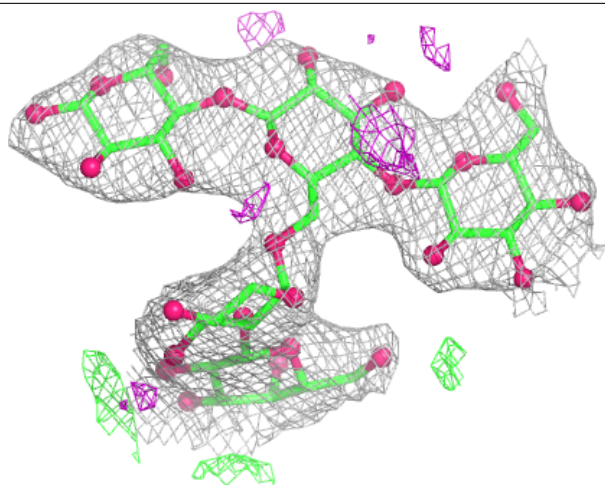
Electron density around Chain F:

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



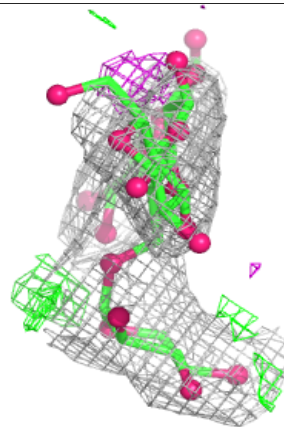
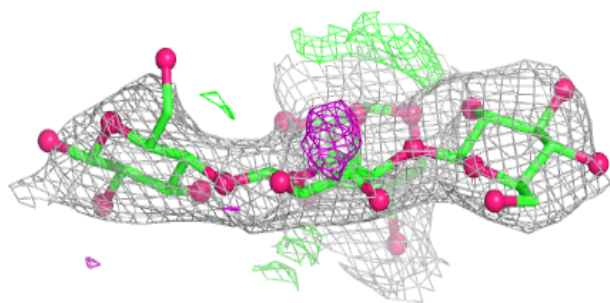
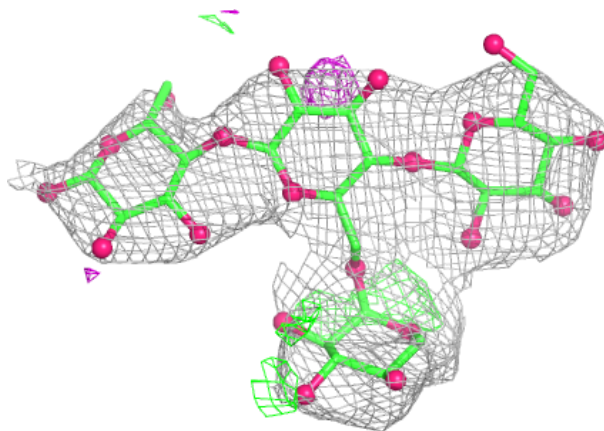
Electron density around Chain J:

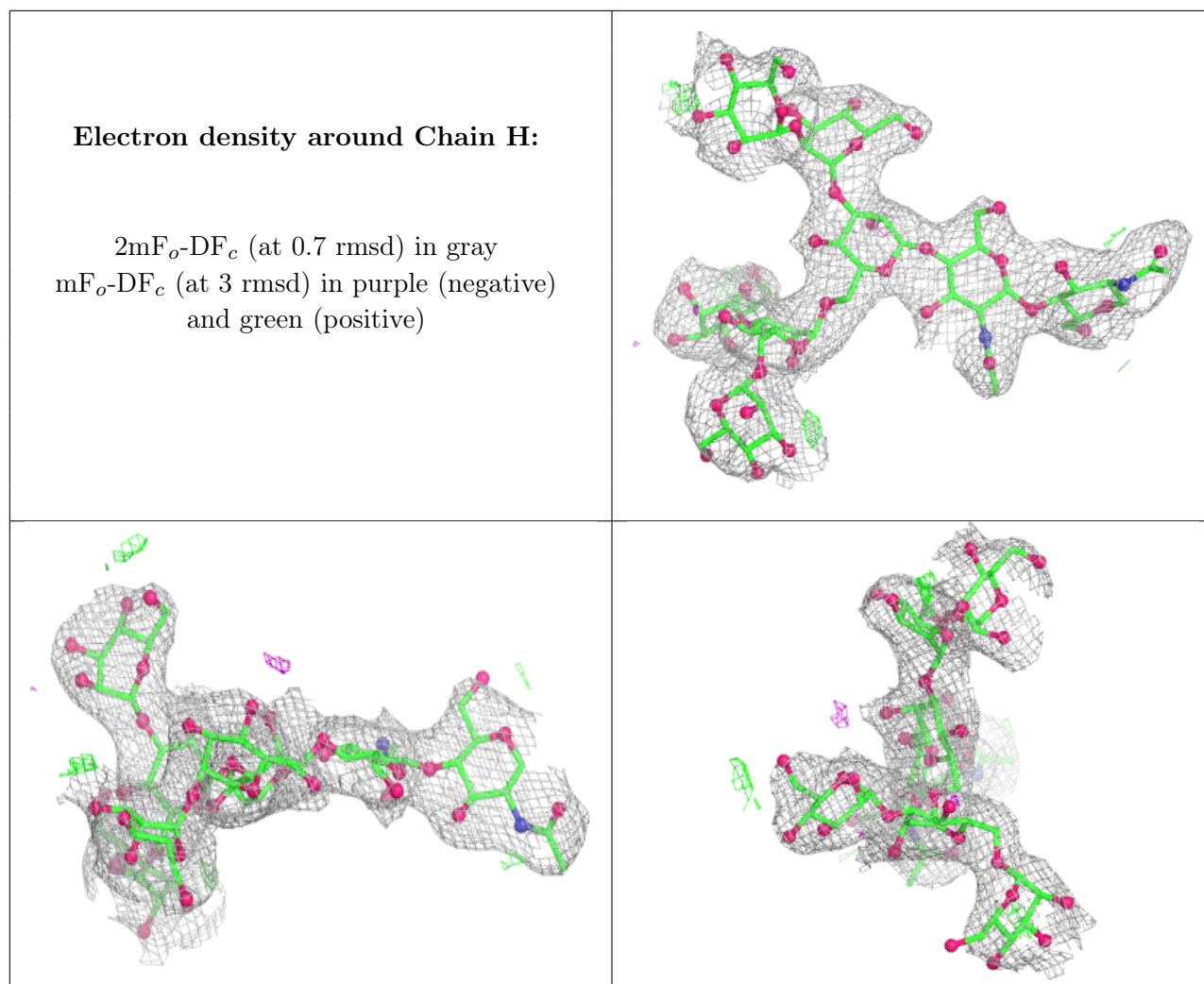
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain 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 [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	B	822	14/15	0.45	0.16	114,126,133,135	14
8	NAG	A	828	14/15	0.59	0.13	107,128,133,136	0
8	NAG	A	835	14/15	0.62	0.12	88,124,137,142	0
8	NAG	B	829	14/15	0.67	0.15	94,114,129,135	0
8	NAG	B	821	14/15	0.75	0.15	106,122,132,137	0
10	GOL	B	830	6/6	0.79	0.16	84,92,96,104	0
10	GOL	A	840	6/6	0.81	0.19	51,72,79,84	0
8	NAG	A	827	14/15	0.81	0.12	86,114,128,130	0
10	GOL	B	831	6/6	0.82	0.21	60,81,89,98	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	NAG	A	826	14/15	0.84	0.11	76,82,85,86	0
8	NAG	B	820	14/15	0.85	0.10	65,77,90,92	0
8	NAG	B	801	14/15	0.92	0.09	53,69,81,82	0
9	XYS	B	828	10/10	0.95	0.08	54,62,73,75	0
9	XYS	A	834	10/10	0.96	0.08	63,72,74,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.