



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 16, 2025 – 10:16 PM JST

PDB ID : 9L3O / pdb_00009L3o
Title : Crystal structure of endo-processive xyloglucanase Xeg5A from *Aspergillus oryzae* with XXLG
Authors : Nakamichi, Y.; Shimada, N.; Watanabe, M.; Fujii, T.; Matsuzawa, T.
Deposited on : 2024-12-19
Resolution : 2.00 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:

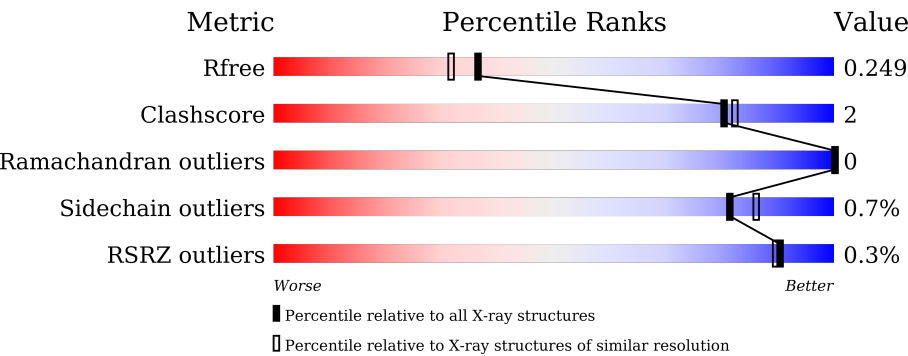
MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.00 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.



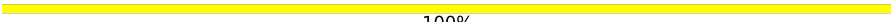


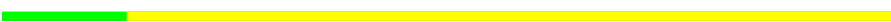
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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	648	<div><div></div><div>78%6%15%</div></div>
1	B	648	<div><div></div><div>79%6%15%</div></div>
2	C	10	<div><div>20%</div><div>80%</div></div>
2	F	10	<div><div>10%</div><div>90%</div></div>
3	D	7	<div><div>100%</div></div>
3	H	7	<div><div>100%</div></div>

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Mol	Chain	Length	Quality of chain
4	E	8	 100%
5	G	3	 33%67%
5	J	3	 100%
6	I	7	 14%86%

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 9964 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 Glycoside hydrolase superfamily.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	550	Total	C	N	O	S	0	0	0
			4315	2748	705	855	7			
1	B	550	Total	C	N	O	S	0	1	0
			4324	2753	706	858	7			

There are 192 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-70	MET	-	initiating methionine	UNP I8IVP5
A	-69	ARG	-	expression tag	UNP I8IVP5
A	-68	PHE	-	expression tag	UNP I8IVP5
A	-67	PRO	-	expression tag	UNP I8IVP5
A	-66	SER	-	expression tag	UNP I8IVP5
A	-65	ILE	-	expression tag	UNP I8IVP5
A	-64	PHE	-	expression tag	UNP I8IVP5
A	-63	THR	-	expression tag	UNP I8IVP5
A	-62	ALA	-	expression tag	UNP I8IVP5
A	-61	VAL	-	expression tag	UNP I8IVP5
A	-60	LEU	-	expression tag	UNP I8IVP5
A	-59	PHE	-	expression tag	UNP I8IVP5
A	-58	ALA	-	expression tag	UNP I8IVP5
A	-57	ALA	-	expression tag	UNP I8IVP5
A	-56	SER	-	expression tag	UNP I8IVP5
A	-55	SER	-	expression tag	UNP I8IVP5
A	-54	ALA	-	expression tag	UNP I8IVP5
A	-53	LEU	-	expression tag	UNP I8IVP5
A	-52	ALA	-	expression tag	UNP I8IVP5
A	-51	ALA	-	expression tag	UNP I8IVP5
A	-50	PRO	-	expression tag	UNP I8IVP5
A	-49	VAL	-	expression tag	UNP I8IVP5
A	-48	ASN	-	expression tag	UNP I8IVP5
A	-47	THR	-	expression tag	UNP I8IVP5
A	-46	THR	-	expression tag	UNP I8IVP5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-45	THR	-	expression tag	UNP I8IVP5
A	-44	GLU	-	expression tag	UNP I8IVP5
A	-43	ASP	-	expression tag	UNP I8IVP5
A	-42	GLU	-	expression tag	UNP I8IVP5
A	-41	THR	-	expression tag	UNP I8IVP5
A	-40	ALA	-	expression tag	UNP I8IVP5
A	-39	GLN	-	expression tag	UNP I8IVP5
A	-38	ILE	-	expression tag	UNP I8IVP5
A	-37	PRO	-	expression tag	UNP I8IVP5
A	-36	ALA	-	expression tag	UNP I8IVP5
A	-35	GLU	-	expression tag	UNP I8IVP5
A	-34	ALA	-	expression tag	UNP I8IVP5
A	-33	VAL	-	expression tag	UNP I8IVP5
A	-32	ILE	-	expression tag	UNP I8IVP5
A	-31	GLY	-	expression tag	UNP I8IVP5
A	-30	TYR	-	expression tag	UNP I8IVP5
A	-29	SER	-	expression tag	UNP I8IVP5
A	-28	ASP	-	expression tag	UNP I8IVP5
A	-27	LEU	-	expression tag	UNP I8IVP5
A	-26	GLU	-	expression tag	UNP I8IVP5
A	-25	GLY	-	expression tag	UNP I8IVP5
A	-24	ASP	-	expression tag	UNP I8IVP5
A	-23	PHE	-	expression tag	UNP I8IVP5
A	-22	ASP	-	expression tag	UNP I8IVP5
A	-21	VAL	-	expression tag	UNP I8IVP5
A	-20	ALA	-	expression tag	UNP I8IVP5
A	-19	VAL	-	expression tag	UNP I8IVP5
A	-18	LEU	-	expression tag	UNP I8IVP5
A	-17	PRO	-	expression tag	UNP I8IVP5
A	-16	PHE	-	expression tag	UNP I8IVP5
A	-15	SER	-	expression tag	UNP I8IVP5
A	-14	ASN	-	expression tag	UNP I8IVP5
A	-13	SER	-	expression tag	UNP I8IVP5
A	-12	THR	-	expression tag	UNP I8IVP5
A	-11	ASN	-	expression tag	UNP I8IVP5
A	-10	ASN	-	expression tag	UNP I8IVP5
A	-9	GLY	-	expression tag	UNP I8IVP5
A	-8	LEU	-	expression tag	UNP I8IVP5
A	-7	LEU	-	expression tag	UNP I8IVP5
A	-6	PHE	-	expression tag	UNP I8IVP5
A	-5	ILE	-	expression tag	UNP I8IVP5
A	-4	ASN	-	expression tag	UNP I8IVP5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	THR	-	expression tag	UNP I8IVP5
A	-2	THR	-	expression tag	UNP I8IVP5
A	-1	ILE	-	expression tag	UNP I8IVP5
A	0	ALA	-	expression tag	UNP I8IVP5
A	1	SER	-	expression tag	UNP I8IVP5
A	2	ILE	-	expression tag	UNP I8IVP5
A	3	ALA	-	expression tag	UNP I8IVP5
A	4	ALA	-	expression tag	UNP I8IVP5
A	5	LYS	-	expression tag	UNP I8IVP5
A	6	GLU	-	expression tag	UNP I8IVP5
A	7	GLU	-	expression tag	UNP I8IVP5
A	8	GLY	-	expression tag	UNP I8IVP5
A	9	VAL	-	expression tag	UNP I8IVP5
A	10	SER	-	expression tag	UNP I8IVP5
A	11	LEU	-	expression tag	UNP I8IVP5
A	12	GLU	-	expression tag	UNP I8IVP5
A	13	LYS	-	expression tag	UNP I8IVP5
A	14	ARG	-	expression tag	UNP I8IVP5
A	15	GLU	-	expression tag	UNP I8IVP5
A	16	ALA	-	expression tag	UNP I8IVP5
A	17	GLU	-	expression tag	UNP I8IVP5
A	570	VAL	-	expression tag	UNP I8IVP5
A	571	ASP	-	expression tag	UNP I8IVP5
A	572	HIS	-	expression tag	UNP I8IVP5
A	573	HIS	-	expression tag	UNP I8IVP5
A	574	HIS	-	expression tag	UNP I8IVP5
A	575	HIS	-	expression tag	UNP I8IVP5
A	576	HIS	-	expression tag	UNP I8IVP5
A	577	HIS	-	expression tag	UNP I8IVP5
B	-70	MET	-	initiating methionine	UNP I8IVP5
B	-69	ARG	-	expression tag	UNP I8IVP5
B	-68	PHE	-	expression tag	UNP I8IVP5
B	-67	PRO	-	expression tag	UNP I8IVP5
B	-66	SER	-	expression tag	UNP I8IVP5
B	-65	ILE	-	expression tag	UNP I8IVP5
B	-64	PHE	-	expression tag	UNP I8IVP5
B	-63	THR	-	expression tag	UNP I8IVP5
B	-62	ALA	-	expression tag	UNP I8IVP5
B	-61	VAL	-	expression tag	UNP I8IVP5
B	-60	LEU	-	expression tag	UNP I8IVP5
B	-59	PHE	-	expression tag	UNP I8IVP5
B	-58	ALA	-	expression tag	UNP I8IVP5

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Chain	Residue	Modelled	Actual	Comment	Reference
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B	-56	SER	-	expression tag	UNP I8IVP5
B	-55	SER	-	expression tag	UNP I8IVP5
B	-54	ALA	-	expression tag	UNP I8IVP5
B	-53	LEU	-	expression tag	UNP I8IVP5
B	-52	ALA	-	expression tag	UNP I8IVP5
B	-51	ALA	-	expression tag	UNP I8IVP5
B	-50	PRO	-	expression tag	UNP I8IVP5
B	-49	VAL	-	expression tag	UNP I8IVP5
B	-48	ASN	-	expression tag	UNP I8IVP5
B	-47	THR	-	expression tag	UNP I8IVP5
B	-46	THR	-	expression tag	UNP I8IVP5
B	-45	THR	-	expression tag	UNP I8IVP5
B	-44	GLU	-	expression tag	UNP I8IVP5
B	-43	ASP	-	expression tag	UNP I8IVP5
B	-42	GLU	-	expression tag	UNP I8IVP5
B	-41	THR	-	expression tag	UNP I8IVP5
B	-40	ALA	-	expression tag	UNP I8IVP5
B	-39	GLN	-	expression tag	UNP I8IVP5
B	-38	ILE	-	expression tag	UNP I8IVP5
B	-37	PRO	-	expression tag	UNP I8IVP5
B	-36	ALA	-	expression tag	UNP I8IVP5
B	-35	GLU	-	expression tag	UNP I8IVP5
B	-34	ALA	-	expression tag	UNP I8IVP5
B	-33	VAL	-	expression tag	UNP I8IVP5
B	-32	ILE	-	expression tag	UNP I8IVP5
B	-31	GLY	-	expression tag	UNP I8IVP5
B	-30	TYR	-	expression tag	UNP I8IVP5
B	-29	SER	-	expression tag	UNP I8IVP5
B	-28	ASP	-	expression tag	UNP I8IVP5
B	-27	LEU	-	expression tag	UNP I8IVP5
B	-26	GLU	-	expression tag	UNP I8IVP5
B	-25	GLY	-	expression tag	UNP I8IVP5
B	-24	ASP	-	expression tag	UNP I8IVP5
B	-23	PHE	-	expression tag	UNP I8IVP5
B	-22	ASP	-	expression tag	UNP I8IVP5
B	-21	VAL	-	expression tag	UNP I8IVP5
B	-20	ALA	-	expression tag	UNP I8IVP5
B	-19	VAL	-	expression tag	UNP I8IVP5
B	-18	LEU	-	expression tag	UNP I8IVP5
B	-17	PRO	-	expression tag	UNP I8IVP5
B	-16	PHE	-	expression tag	UNP I8IVP5

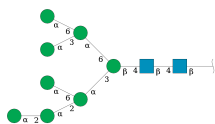
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Chain	Residue	Modelled	Actual	Comment	Reference
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B	-14	ASN	-	expression tag	UNP I8IVP5
B	-13	SER	-	expression tag	UNP I8IVP5
B	-12	THR	-	expression tag	UNP I8IVP5
B	-11	ASN	-	expression tag	UNP I8IVP5
B	-10	ASN	-	expression tag	UNP I8IVP5
B	-9	GLY	-	expression tag	UNP I8IVP5
B	-8	LEU	-	expression tag	UNP I8IVP5
B	-7	LEU	-	expression tag	UNP I8IVP5
B	-6	PHE	-	expression tag	UNP I8IVP5
B	-5	ILE	-	expression tag	UNP I8IVP5
B	-4	ASN	-	expression tag	UNP I8IVP5
B	-3	THR	-	expression tag	UNP I8IVP5
B	-2	THR	-	expression tag	UNP I8IVP5
B	-1	ILE	-	expression tag	UNP I8IVP5
B	0	ALA	-	expression tag	UNP I8IVP5
B	1	SER	-	expression tag	UNP I8IVP5
B	2	ILE	-	expression tag	UNP I8IVP5
B	3	ALA	-	expression tag	UNP I8IVP5
B	4	ALA	-	expression tag	UNP I8IVP5
B	5	LYS	-	expression tag	UNP I8IVP5
B	6	GLU	-	expression tag	UNP I8IVP5
B	7	GLU	-	expression tag	UNP I8IVP5
B	8	GLY	-	expression tag	UNP I8IVP5
B	9	VAL	-	expression tag	UNP I8IVP5
B	10	SER	-	expression tag	UNP I8IVP5
B	11	LEU	-	expression tag	UNP I8IVP5
B	12	GLU	-	expression tag	UNP I8IVP5
B	13	LYS	-	expression tag	UNP I8IVP5
B	14	ARG	-	expression tag	UNP I8IVP5
B	15	GLU	-	expression tag	UNP I8IVP5
B	16	ALA	-	expression tag	UNP I8IVP5
B	17	GLU	-	expression tag	UNP I8IVP5
B	570	VAL	-	expression tag	UNP I8IVP5
B	571	ASP	-	expression tag	UNP I8IVP5
B	572	HIS	-	expression tag	UNP I8IVP5
B	573	HIS	-	expression tag	UNP I8IVP5
B	574	HIS	-	expression tag	UNP I8IVP5
B	575	HIS	-	expression tag	UNP I8IVP5
B	576	HIS	-	expression tag	UNP I8IVP5
B	577	HIS	-	expression tag	UNP I8IVP5

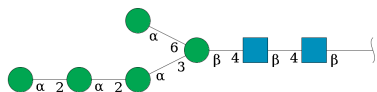
- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-2)-alpha-D-mannopyran

ose-(1-2)-[alpha-D-mannopyranose-(1-6)]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.



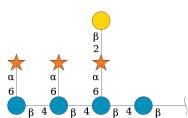
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	0	0
			116	64	2	50			
2	F	10	Total	C	N	O	0	0	0
			116	64	2	50			

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



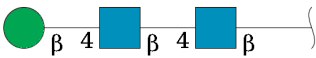
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	7	Total	C	N	O	0	0	0
			83	46	2	35			
3	H	7	Total	C	N	O	0	0	0
			83	46	2	35			

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



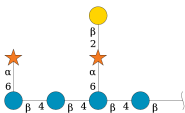
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	E	8	Total	C	O	0	0	0
			83	45	38			

- Molecule 5 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.



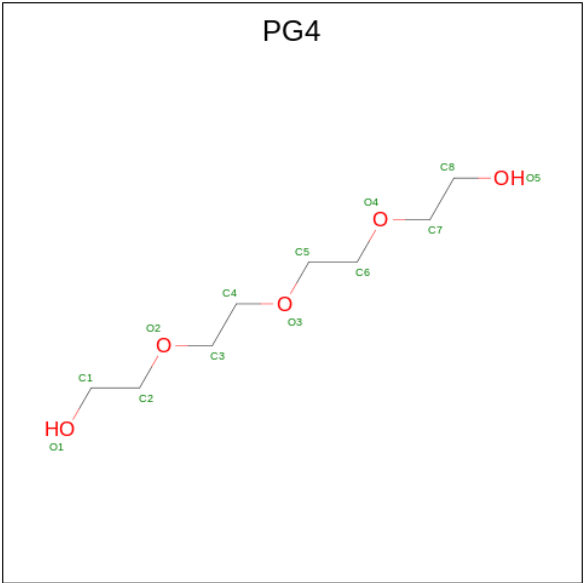
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	G	3	Total	C	N	O	0	0	0
			39	22	2	15			
5	J	3	Total	C	N	O	0	0	0
			39	22	2	15			

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



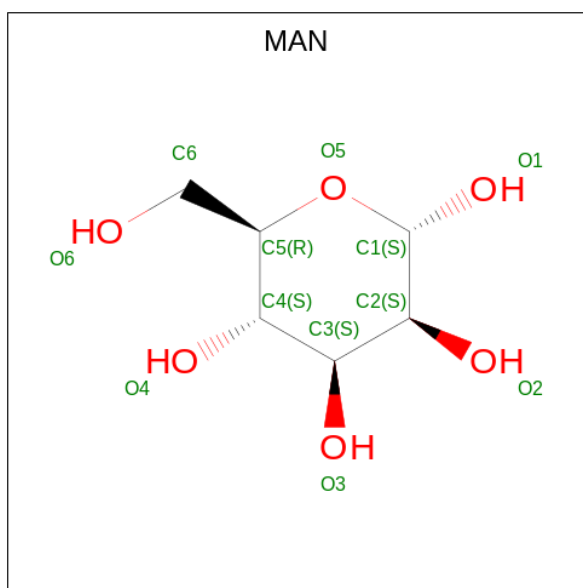
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
6	I	7	Total	C	O	0	0	0
			74	40	34			

- Molecule 7 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



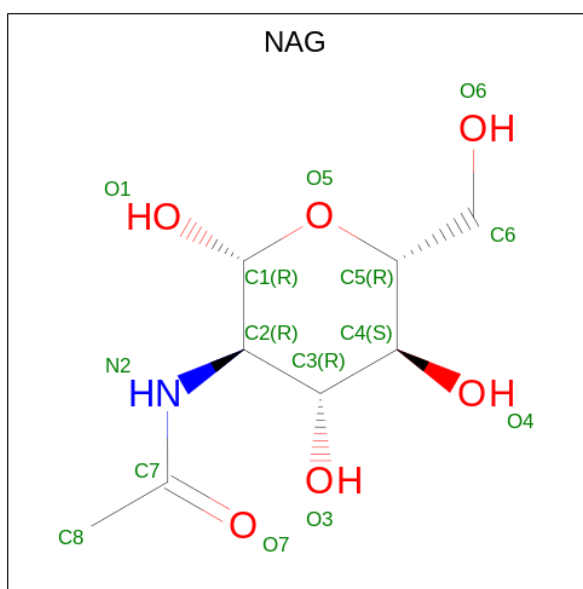
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 8 is alpha-D-mannopyranose (CCD ID: MAN) (formula: $C_6H_{12}O_6$).



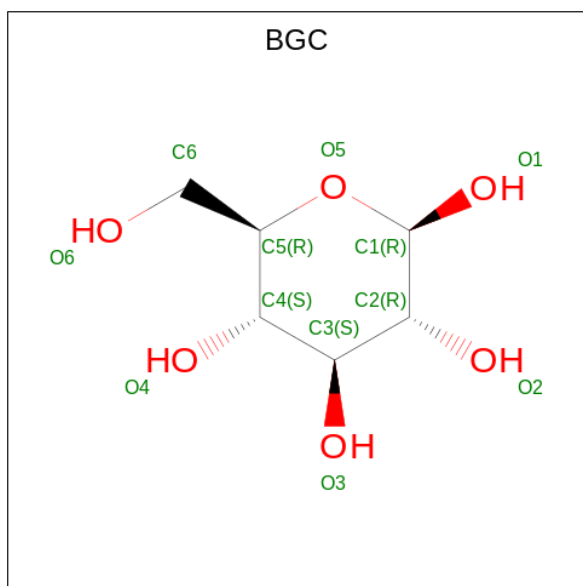
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			11	6	5		
8	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 9 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



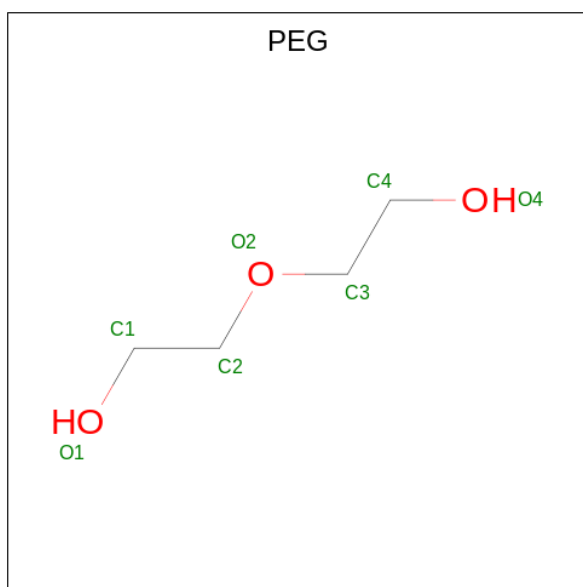
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	A	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is beta-D-glucopyranose (CCD ID: BGC) (formula: C₆H₁₂O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			12	6	6		
10	B	1	Total	C	O	0	0
			12	6	6		

- Molecule 11 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	A	1	Total	C	O	0	0
			7	4	3		
11	B	1	Total	C	O	0	0
			7	4	3		
11	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	1	Total	Mg	0	0
			1	1		
12	B	1	Total	Mg	0	0
			1	1		

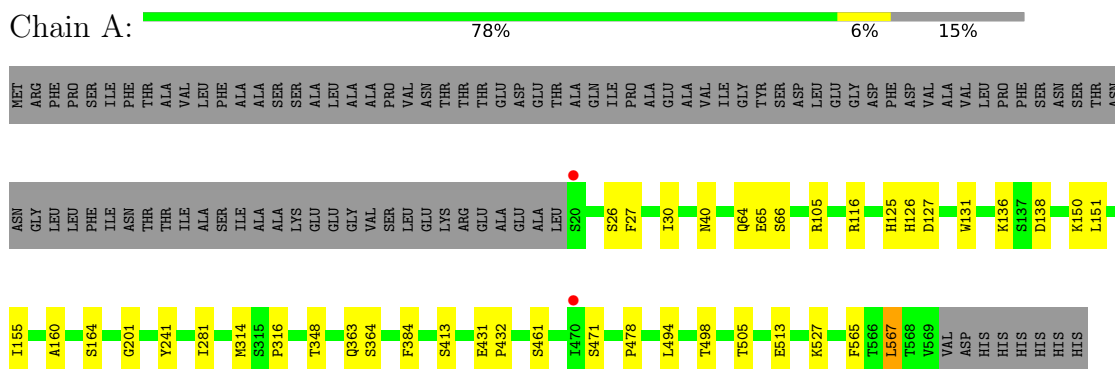
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	245	Total	O	0	0
			245	245		
13	B	267	Total	O	0	0
			267	267		

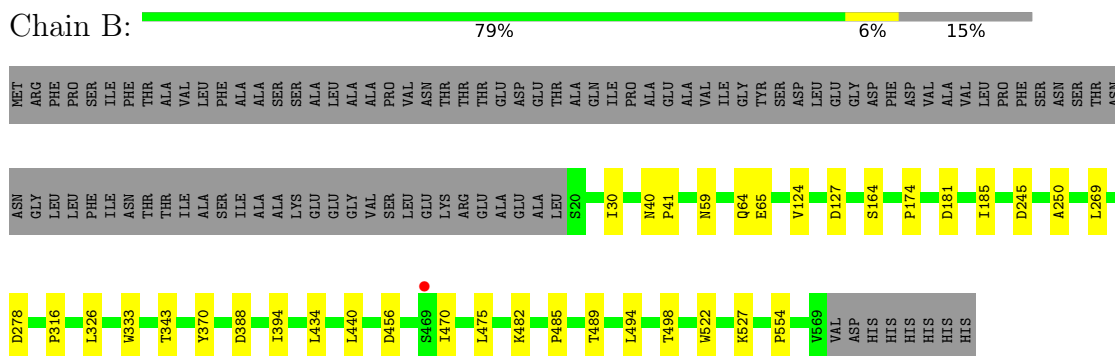
3 Residue-property plots

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

- Molecule 1: Glycoside hydrolase superfamily



- Molecule 1: Glycoside hydrolase superfamily



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



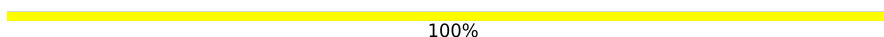
- Molecule 2: alpha-D-mannopyranose-(1-2)-alpha-D-mannopyranose-(1-2)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

(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 F:  10% 90%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7
MAN8
MAN9
MAN10

• Molecule 3: alpha-D-mannopyranose-(1-2)-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

Chain D:  100%

MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7

• Molecule 3: alpha-D-mannopyranose-(1-2)-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

Chain H:  100%

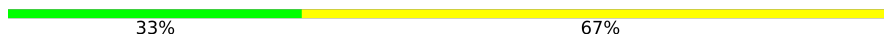
MAG1
MAG2
BMA3
MAN4
MAN5
MAN6
MAN7

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

Chain E:  100%

BGC1
BGC2
BGC3
BGC4
XTS5
XTS6
XTS7
GAL8

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

Chain G:  33% 67%

MAG1
MAG2
BMA3

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

Chain J:  100%

MAG1
MAG2
BMA3

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

Chain I:  14% 86%

BGC1
BGC2
BGC3
BGC4
XYS5
XYS6
GAL7

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.71Å 105.90Å 82.95Å 90.00° 91.60° 90.00°	Depositor
Resolution (Å)	39.84 – 2.00 39.84 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (39.84-2.00) 98.7 (39.84-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.204 , 0.248 0.204 , 0.249	Depositor DCC
R_{free} test set	5488 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.319	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.009 for h,-k,-l 0.168 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9964	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: YYS, GAL, NAG, BGC, MG, BMA, MAN, PG4, PEG

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	0.25	0/4436	0.44	0/6072
1	B	0.24	0/4445	0.44	0/6084
All	All	0.25	0/8881	0.44	0/12156

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4315	0	4103	25	0
1	B	4324	0	4109	21	0
2	C	116	0	97	0	0
2	F	116	0	97	0	0
3	D	83	0	70	0	0
3	H	83	0	70	0	0
4	E	83	0	69	0	0
5	G	39	0	34	0	0
5	J	39	0	34	0	0
6	I	74	0	62	0	0
7	A	13	0	18	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	11	0	10	0	0
8	B	11	0	10	0	0
9	A	56	0	52	0	0
9	B	42	0	39	0	0
10	A	12	0	12	0	0
10	B	12	0	12	1	0
11	A	7	0	10	1	0
11	B	14	0	20	1	0
12	A	1	0	0	0	0
12	B	1	0	0	0	0
13	A	245	0	0	2	0
13	B	267	0	0	1	0
All	All	9964	0	8928	45	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 2.

The worst 5 of 45 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:105:ARG:HH12	1:B:64:GLN:HE22	1.35	0.72
1:A:64:GLN:NE2	1:B:65:GLU:OE1	2.29	0.65
1:A:105:ARG:NH1	1:B:64:GLN:HE22	1.96	0.62
1:A:565:PHE:HE2	1:A:567:LEU:HD13	1.66	0.60
1:B:278:ASP:OD2	1:B:278:ASP:N	2.32	0.59

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	548/648 (85%)	526 (96%)	22 (4%)	0	100	100
1	B	549/648 (85%)	524 (95%)	25 (5%)	0	100	100
All	All	1097/1296 (85%)	1050 (96%)	47 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	482/561 (86%)	477 (99%)	5 (1%)	73	78
1	B	483/561 (86%)	481 (100%)	2 (0%)	89	92
All	All	965/1122 (86%)	958 (99%)	7 (1%)	81	86

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	SER
1	A	567	LEU
1	B	388	ASP
1	B	269	LEU
1	A	364	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	64	GLN
1	B	88	HIS
1	B	237	GLN
1	B	197	ASN
1	B	209	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 ⓘ

55 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	2,1	14,14,15	0.75	0	17,19,21	1.21	1 (5%)
2	MAN	C	10	2	11,11,12	0.76	0	15,15,17	0.95	0
2	NAG	C	2	2	14,14,15	0.74	0	17,19,21	0.85	0
2	BMA	C	3	2	11,11,12	0.89	0	15,15,17	2.35	4 (26%)
2	MAN	C	4	2	11,11,12	0.64	0	15,15,17	1.52	1 (6%)
2	MAN	C	5	2	11,11,12	0.78	1 (9%)	15,15,17	1.15	1 (6%)
2	MAN	C	6	2	11,11,12	0.70	0	15,15,17	1.28	2 (13%)
2	MAN	C	7	2	11,11,12	0.73	0	15,15,17	1.48	2 (13%)
2	MAN	C	8	2	11,11,12	0.80	0	15,15,17	0.99	1 (6%)
2	MAN	C	9	2	11,11,12	0.76	0	15,15,17	0.97	1 (6%)
3	NAG	D	1	1,3	14,14,15	0.78	0	17,19,21	1.47	2 (11%)
3	NAG	D	2	3	14,14,15	0.78	1 (7%)	17,19,21	0.96	1 (5%)
3	BMA	D	3	3	11,11,12	1.05	1 (9%)	15,15,17	1.98	4 (26%)
3	MAN	D	4	3	11,11,12	0.59	0	15,15,17	1.46	1 (6%)
3	MAN	D	5	3	11,11,12	0.71	0	15,15,17	1.48	1 (6%)
3	MAN	D	6	3	11,11,12	0.89	1 (9%)	15,15,17	0.98	2 (13%)
3	MAN	D	7	3	11,11,12	0.65	0	15,15,17	1.44	1 (6%)
4	BGC	E	1	4	12,12,12	0.55	0	17,17,17	1.02	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BGC	E	2	4	11,11,12	0.75	0	15,15,17	0.88	1 (6%)
4	BGC	E	3	4	11,11,12	0.64	0	15,15,17	1.12	1 (6%)
4	BGC	E	4	4,12	11,11,12	0.79	0	15,15,17	1.22	2 (13%)
4	XYS	E	5	4	9,9,10	0.81	0	10,12,14	2.71	1 (10%)
4	XYS	E	6	4	9,9,10	0.88	0	10,12,14	2.33	3 (30%)
4	XYS	E	7	4	9,9,10	0.88	0	10,12,14	2.96	4 (40%)
4	GAL	E	8	4	11,11,12	0.78	0	15,15,17	1.28	1 (6%)
2	NAG	F	1	2,1	14,14,15	0.83	0	17,19,21	1.26	2 (11%)
2	MAN	F	10	2	11,11,12	0.78	0	15,15,17	1.25	1 (6%)
2	NAG	F	2	2	14,14,15	0.70	0	17,19,21	0.74	0
2	BMA	F	3	2	11,11,12	0.94	1 (9%)	15,15,17	2.70	5 (33%)
2	MAN	F	4	2	11,11,12	0.63	0	15,15,17	1.91	1 (6%)
2	MAN	F	5	2	11,11,12	0.93	1 (9%)	15,15,17	0.73	0
2	MAN	F	6	2	11,11,12	0.65	0	15,15,17	1.57	2 (13%)
2	MAN	F	7	2	11,11,12	0.70	0	15,15,17	2.66	4 (26%)
2	MAN	F	8	2	11,11,12	1.01	1 (9%)	15,15,17	1.23	1 (6%)
2	MAN	F	9	2	11,11,12	0.66	0	15,15,17	1.33	1 (6%)
5	NAG	G	1	5,1	14,14,15	0.82	0	17,19,21	1.10	1 (5%)
5	NAG	G	2	5	14,14,15	0.73	0	17,19,21	1.05	0
5	BMA	G	3	5	11,11,12	0.86	0	15,15,17	2.38	4 (26%)
3	NAG	H	1	1,3	14,14,15	0.75	0	17,19,21	1.22	1 (5%)
3	NAG	H	2	3	14,14,15	0.76	0	17,19,21	1.17	1 (5%)
3	BMA	H	3	3	11,11,12	1.03	1 (9%)	15,15,17	2.19	4 (26%)
3	MAN	H	4	3	11,11,12	0.61	0	15,15,17	1.62	1 (6%)
3	MAN	H	5	3	11,11,12	0.66	0	15,15,17	1.84	3 (20%)
3	MAN	H	6	3	11,11,12	0.88	1 (9%)	15,15,17	0.83	0
3	MAN	H	7	3	11,11,12	0.65	0	15,15,17	1.20	1 (6%)
6	BGC	I	1	6	12,12,12	0.54	0	17,17,17	0.97	0
6	BGC	I	2	6	11,11,12	0.75	0	15,15,17	1.02	1 (6%)
6	BGC	I	3	6	11,11,12	0.65	0	15,15,17	1.23	2 (13%)
6	BGC	I	4	6,12	11,11,12	0.77	0	15,15,17	1.18	1 (6%)
6	XYS	I	5	6	9,9,10	0.90	0	10,12,14	2.30	4 (40%)
6	XYS	I	6	6	9,9,10	0.80	0	10,12,14	2.83	3 (30%)
6	GAL	I	7	6	11,11,12	0.69	0	15,15,17	1.37	1 (6%)
5	NAG	J	1	5,1	14,14,15	0.82	0	17,19,21	1.08	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	J	2	5	14,14,15	0.70	0	17,19,21	0.90	1 (5%)
5	BMA	J	3	5	11,11,12	0.90	1 (9%)	15,15,17	2.71	4 (26%)

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	2,1	-	0/6/23/26	0/1/1/1
2	MAN	C	10	2	-	1/2/19/22	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	MAN	C	5	2	-	0/2/19/22	0/1/1/1
2	MAN	C	6	2	-	2/2/19/22	0/1/1/1
2	MAN	C	7	2	-	2/2/19/22	0/1/1/1
2	MAN	C	8	2	-	0/2/19/22	0/1/1/1
2	MAN	C	9	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	1,3	-	2/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	1/2/19/22	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	-	0/2/19/22	0/1/1/1
4	BGC	E	1	4	-	2/2/22/22	0/1/1/1
4	BGC	E	2	4	-	0/2/19/22	0/1/1/1
4	BGC	E	3	4	-	2/2/19/22	0/1/1/1
4	BGC	E	4	4,12	-	0/2/19/22	0/1/1/1
4	XYS	E	5	4	-	-	0/1/1/1
4	XYS	E	6	4	-	-	0/1/1/1
4	XYS	E	7	4	-	-	0/1/1/1
4	GAL	E	8	4	-	0/2/19/22	0/1/1/1
2	NAG	F	1	2,1	-	1/6/23/26	0/1/1/1
2	MAN	F	10	2	-	2/2/19/22	0/1/1/1
2	NAG	F	2	2	-	0/6/23/26	0/1/1/1
2	BMA	F	3	2	-	0/2/19/22	0/1/1/1
2	MAN	F	4	2	-	2/2/19/22	0/1/1/1
2	MAN	F	5	2	-	2/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	F	6	2	-	0/2/19/22	0/1/1/1
2	MAN	F	7	2	-	2/2/19/22	0/1/1/1
2	MAN	F	8	2	-	2/2/19/22	0/1/1/1
2	MAN	F	9	2	-	1/2/19/22	0/1/1/1
5	NAG	G	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	2/6/23/26	0/1/1/1
5	BMA	G	3	5	-	0/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	0/6/23/26	0/1/1/1
3	BMA	H	3	3	-	0/2/19/22	0/1/1/1
3	MAN	H	4	3	-	0/2/19/22	0/1/1/1
3	MAN	H	5	3	-	2/2/19/22	0/1/1/1
3	MAN	H	6	3	-	0/2/19/22	0/1/1/1
3	MAN	H	7	3	-	2/2/19/22	0/1/1/1
6	BGC	I	1	6	-	0/2/22/22	0/1/1/1
6	BGC	I	2	6	-	0/2/19/22	0/1/1/1
6	BGC	I	3	6	-	0/2/19/22	0/1/1/1
6	BGC	I	4	6,12	-	0/2/19/22	0/1/1/1
6	XYS	I	5	6	-	-	0/1/1/1
6	XYS	I	6	6	-	-	0/1/1/1
6	GAL	I	7	6	-	0/2/19/22	0/1/1/1
5	NAG	J	1	5,1	-	0/6/23/26	0/1/1/1
5	NAG	J	2	5	-	2/6/23/26	0/1/1/1
5	BMA	J	3	5	-	2/2/19/22	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	3	BMA	C2-C3	2.65	1.56	1.52
3	D	3	BMA	C2-C3	2.49	1.56	1.52
2	F	8	MAN	O5-C1	-2.46	1.39	1.43
2	F	5	MAN	O5-C1	-2.31	1.40	1.43
2	F	3	BMA	C2-C3	2.28	1.55	1.52

The worst 5 of 90 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	7	MAN	C1-O5-C5	8.96	124.33	112.19
5	J	3	BMA	C1-O5-C5	8.78	124.09	112.19
2	F	3	BMA	C1-O5-C5	8.46	123.65	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	3	BMA	C1-O5-C5	7.65	122.56	112.19
2	C	3	BMA	C1-O5-C5	7.24	122.01	112.19

There are no chirality outliers.

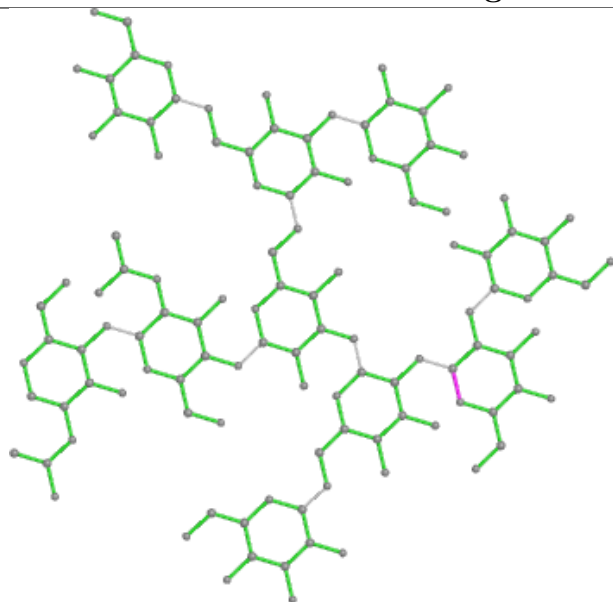
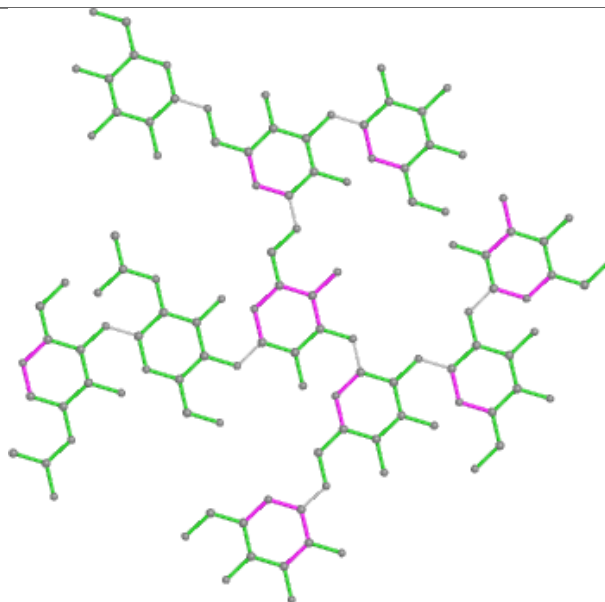
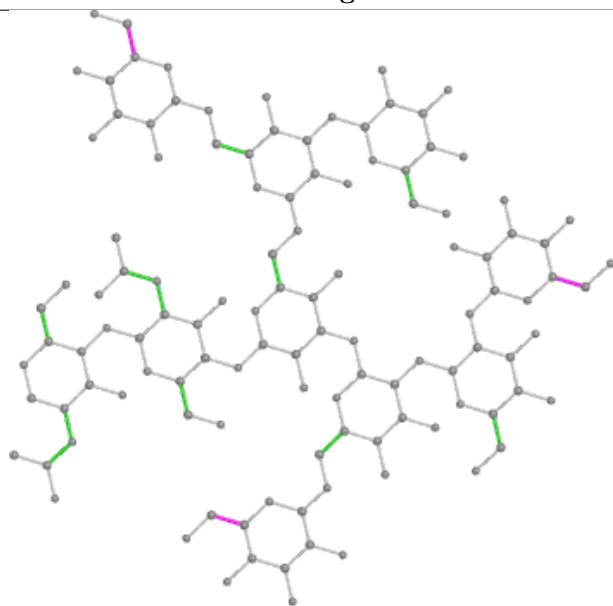
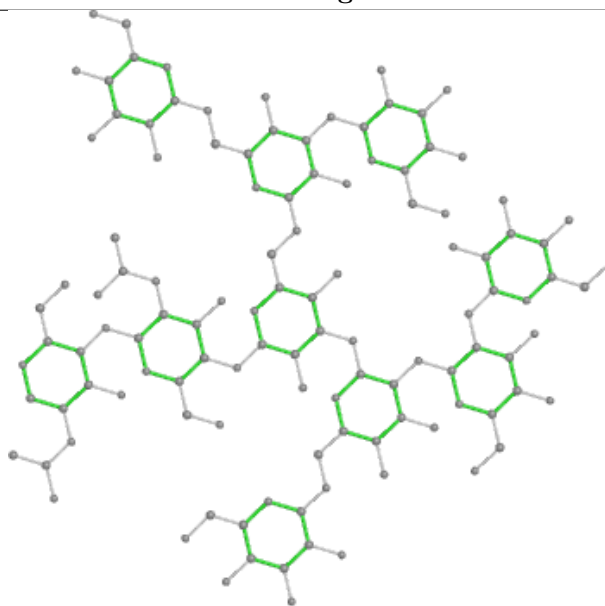
5 of 38 torsion outliers are listed below:

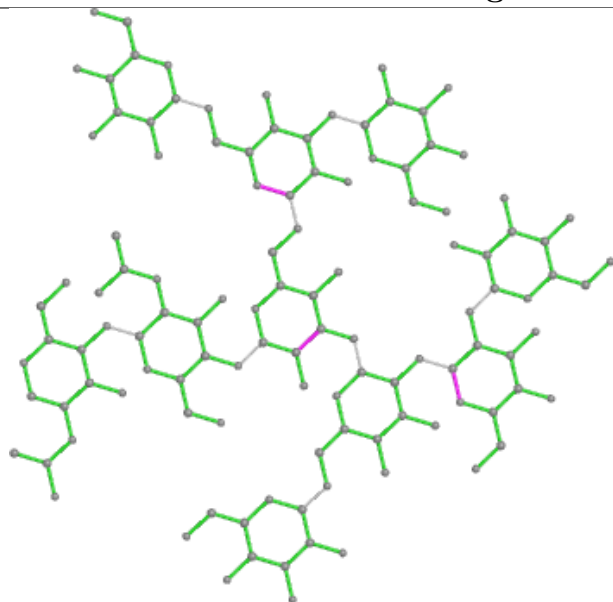
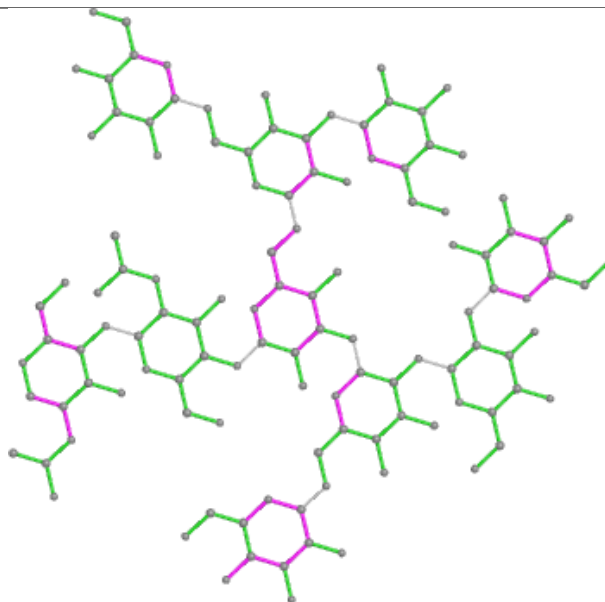
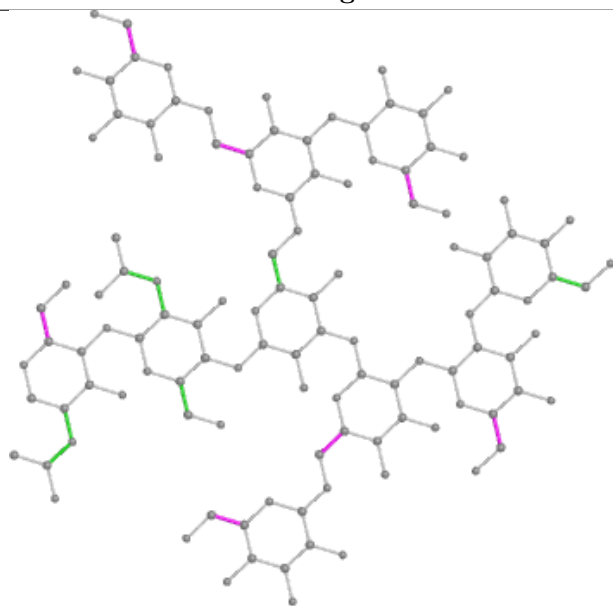
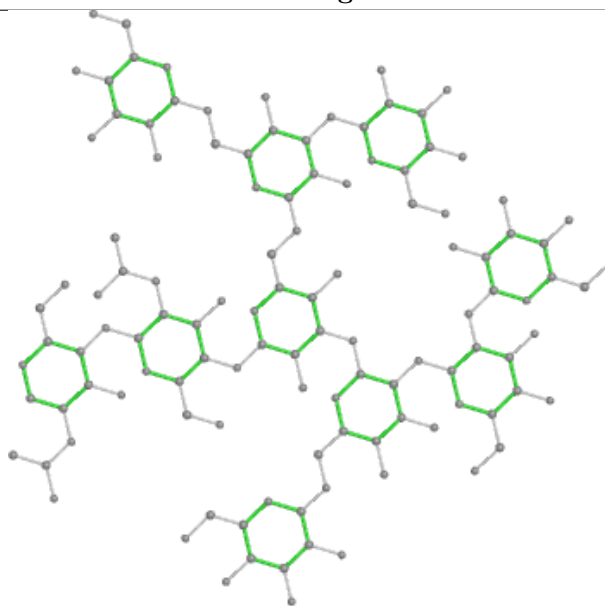
Mol	Chain	Res	Type	Atoms
4	E	1	BGC	O5-C5-C6-O6
5	J	3	BMA	O5-C5-C6-O6
2	F	8	MAN	C4-C5-C6-O6
2	F	7	MAN	O5-C5-C6-O6
2	F	5	MAN	O5-C5-C6-O6

There are no ring outliers.

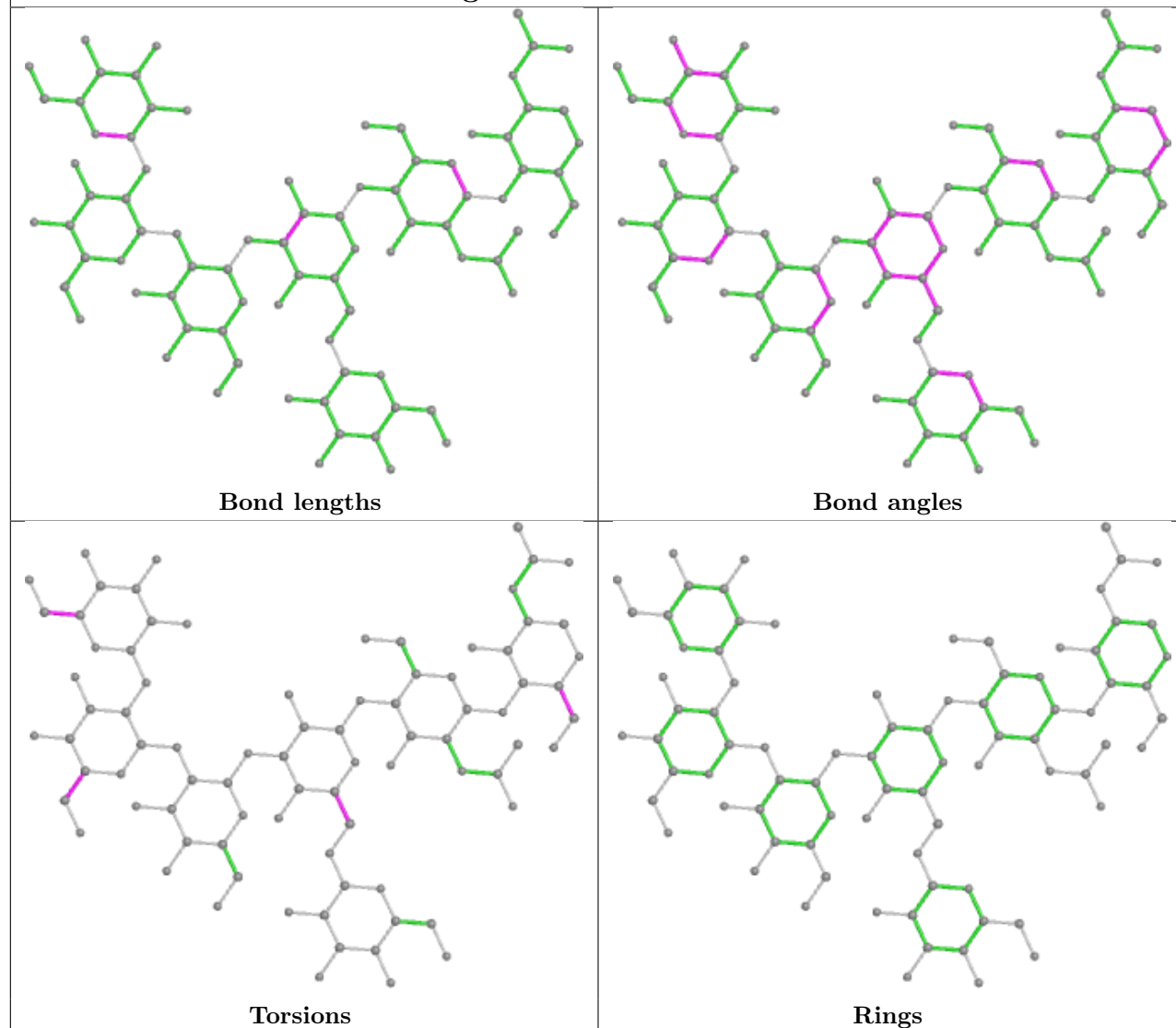
No monomer is involved in short contacts.

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

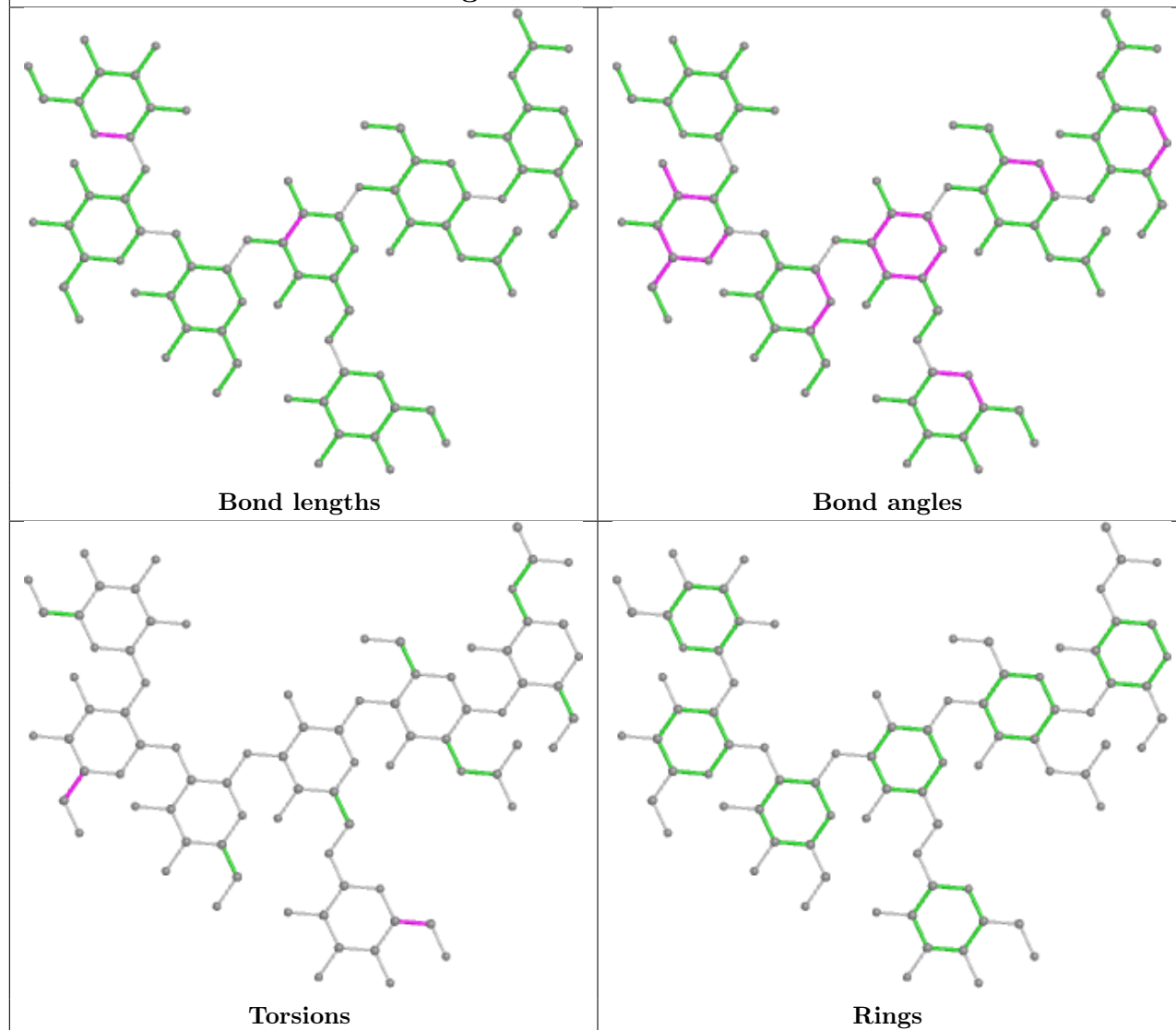
Oligosaccharide Chain C**Bond lengths****Bond angles****Torsions****Rings**

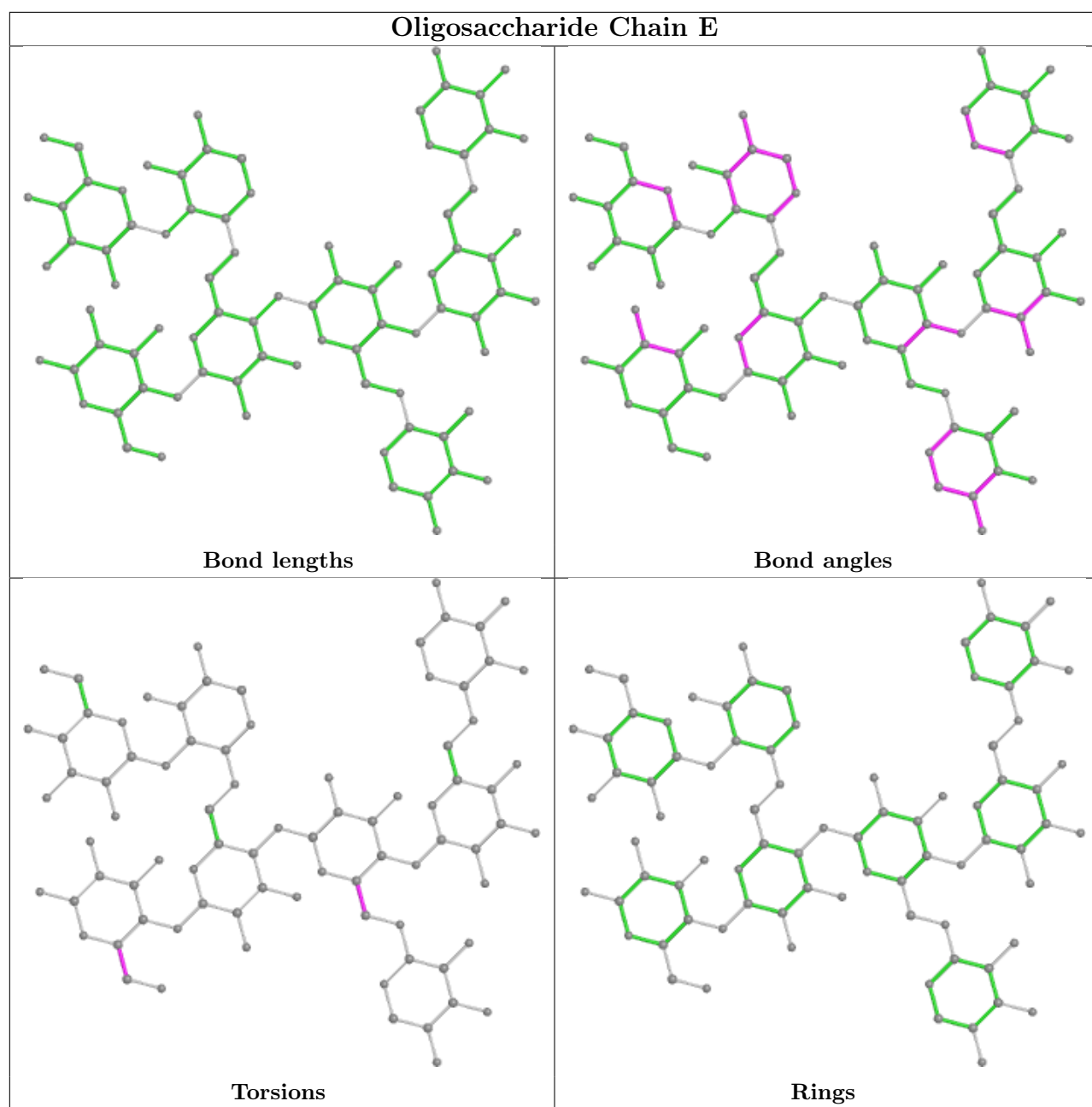
Oligosaccharide Chain F**Bond lengths****Bond angles****Torsions****Rings**

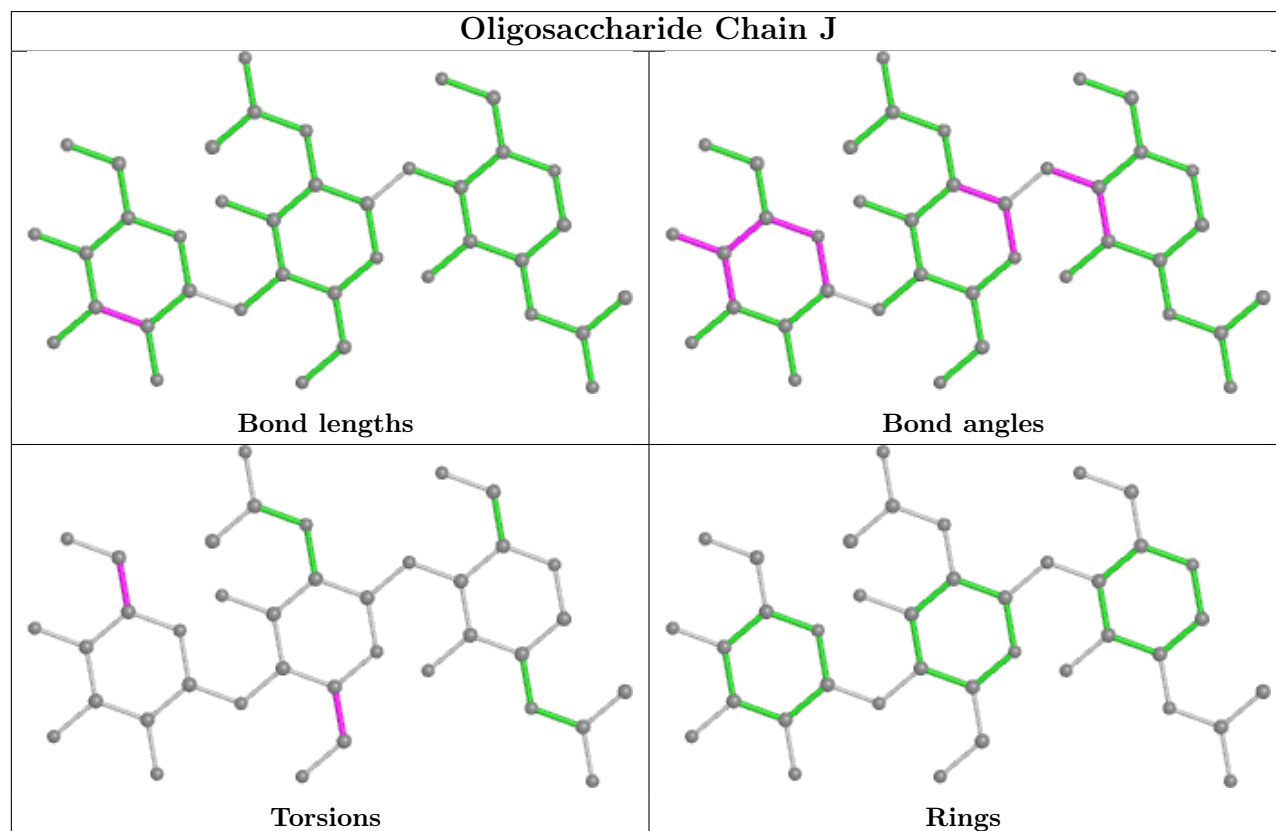
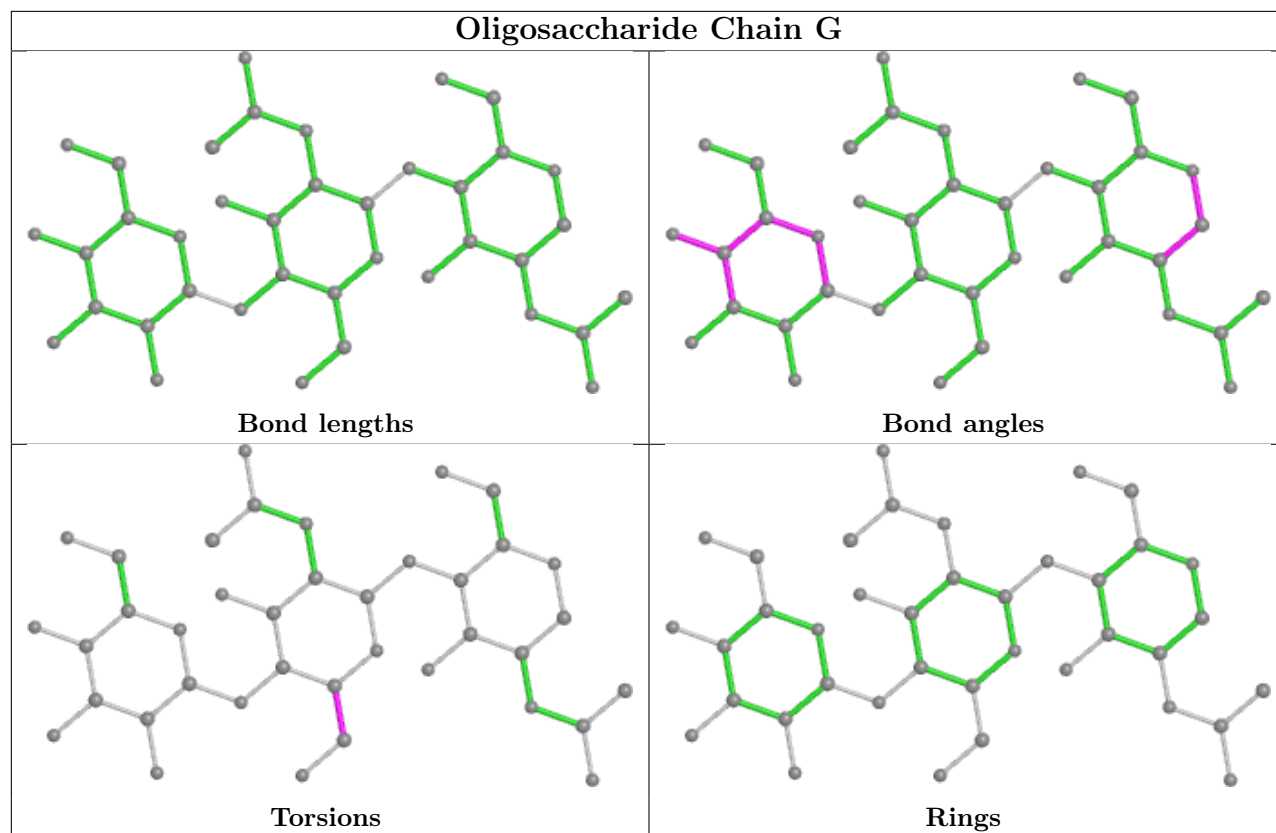
Oligosaccharide Chain D

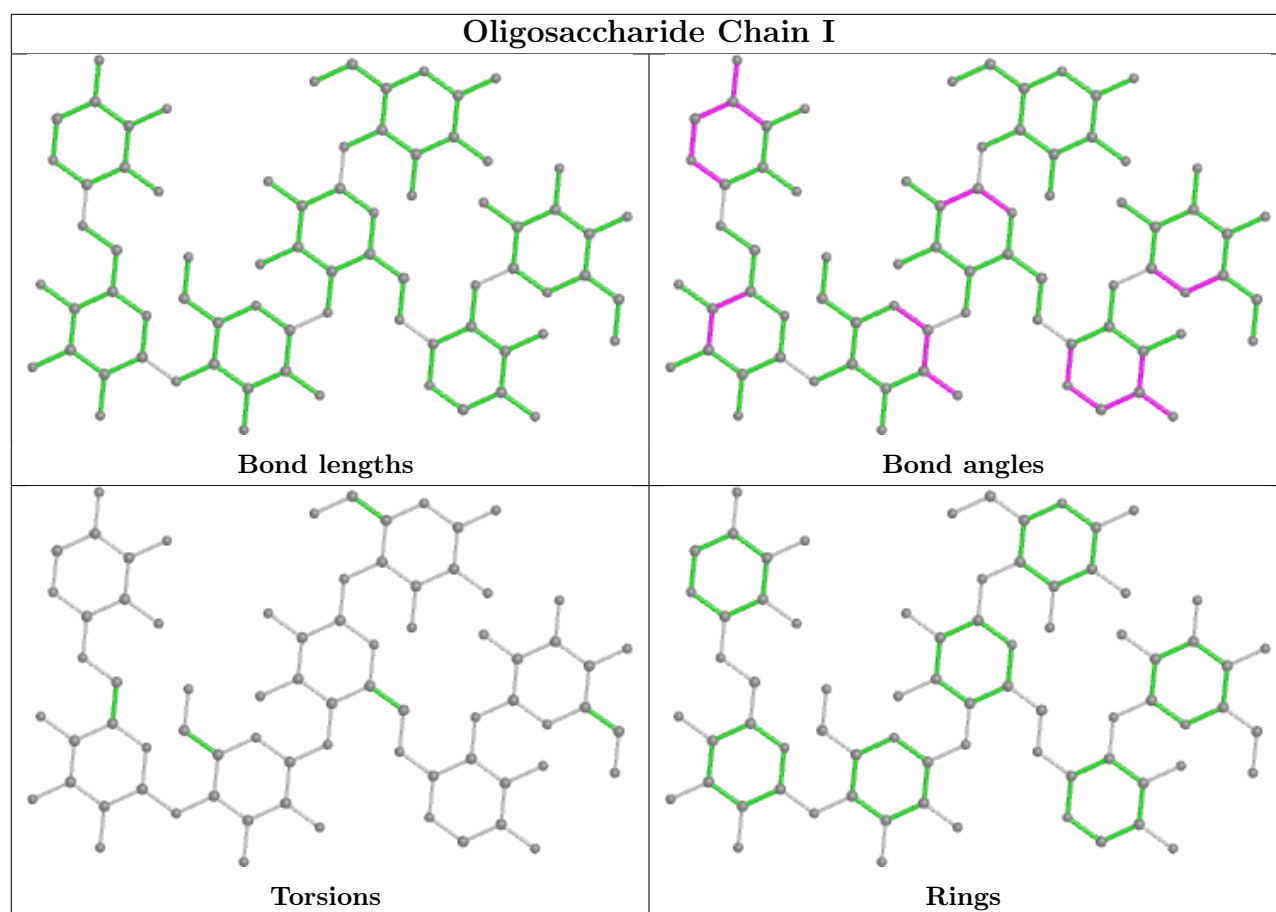


Oligosaccharide Chain H









5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 2 are monoatomic - leaving 15 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
10	BGC	B	605	-	12,12,12	0.54	0	17,17,17	0.93	0
8	MAN	A	602	1	11,11,12	0.68	0	15,15,17	1.84	2 (13%)
9	NAG	B	603	1	14,14,15	0.69	0	17,19,21	0.88	1 (5%)
10	BGC	A	607	-	12,12,12	0.56	0	17,17,17	0.79	0
9	NAG	A	603	1	14,14,15	0.71	0	17,19,21	1.32	2 (11%)
7	PG4	A	601	-	12,12,12	0.29	0	11,11,11	0.26	0
11	PEG	A	608	-	6,6,6	0.26	0	5,5,5	0.17	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
9	NAG	B	602	1	14,14,15	0.72	0	17,19,21	0.74	0
11	PEG	B	606	-	6,6,6	0.23	0	5,5,5	0.29	0
9	NAG	A	605	1	14,14,15	0.67	0	17,19,21	0.88	0
9	NAG	B	604	1	14,14,15	0.72	0	17,19,21	1.11	1 (5%)
9	NAG	A	604	1	14,14,15	0.68	0	17,19,21	1.17	1 (5%)
11	PEG	B	607	12	6,6,6	0.23	0	5,5,5	0.27	0
8	MAN	B	601	1	11,11,12	0.86	1 (9%)	15,15,17	2.07	6 (40%)
9	NAG	A	606	1	14,14,15	0.70	0	17,19,21	0.94	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
10	BGC	B	605	-	-	2/2/22/22	0/1/1/1
8	MAN	A	602	1	-	0/2/19/22	0/1/1/1
9	NAG	B	603	1	-	1/6/23/26	0/1/1/1
10	BGC	A	607	-	-	0/2/22/22	0/1/1/1
9	NAG	A	603	1	-	2/6/23/26	0/1/1/1
7	PG4	A	601	-	-	7/10/10/10	-
11	PEG	A	608	-	-	0/4/4/4	-
9	NAG	B	602	1	-	1/6/23/26	0/1/1/1
11	PEG	B	606	-	-	2/4/4/4	-
9	NAG	A	605	1	-	2/6/23/26	0/1/1/1
9	NAG	B	604	1	-	2/6/23/26	0/1/1/1
9	NAG	A	604	1	-	0/6/23/26	0/1/1/1
11	PEG	B	607	12	-	0/4/4/4	-
8	MAN	B	601	1	-	1/2/19/22	0/1/1/1
9	NAG	A	606	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	601	MAN	O5-C1	-2.14	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	602	MAN	C1-O5-C5	6.31	120.75	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	601	MAN	C1-O5-C5	4.58	118.40	112.19
9	A	603	NAG	C1-O5-C5	4.13	117.79	112.19
9	A	604	NAG	C1-O5-C5	3.65	117.13	112.19
8	B	601	MAN	C3-C4-C5	3.59	116.65	110.24

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

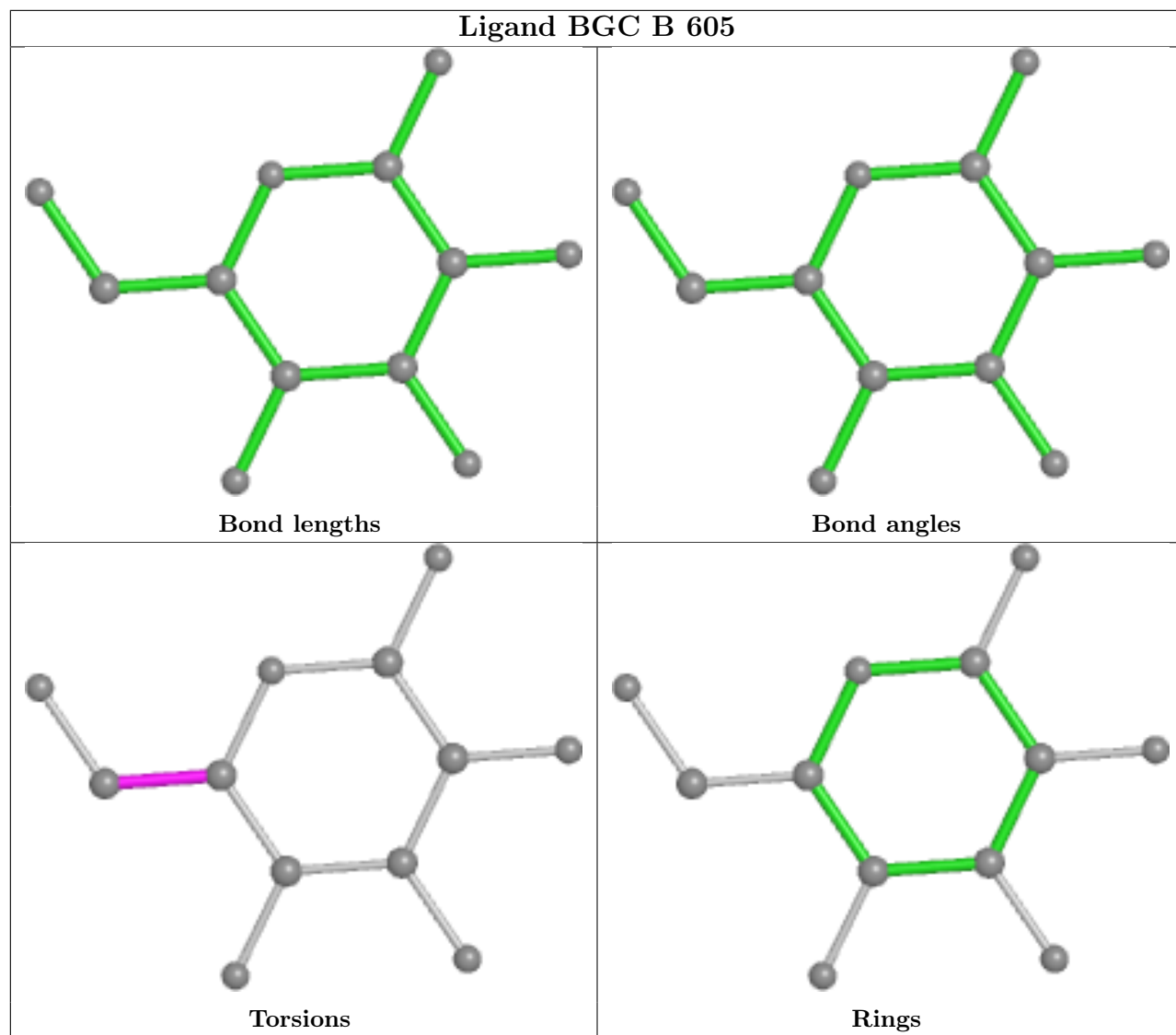
Mol	Chain	Res	Type	Atoms
10	B	605	BGC	O5-C5-C6-O6
10	B	605	BGC	C4-C5-C6-O6
7	A	601	PG4	O3-C5-C6-O4
9	A	605	NAG	O5-C5-C6-O6
9	B	604	NAG	O5-C5-C6-O6

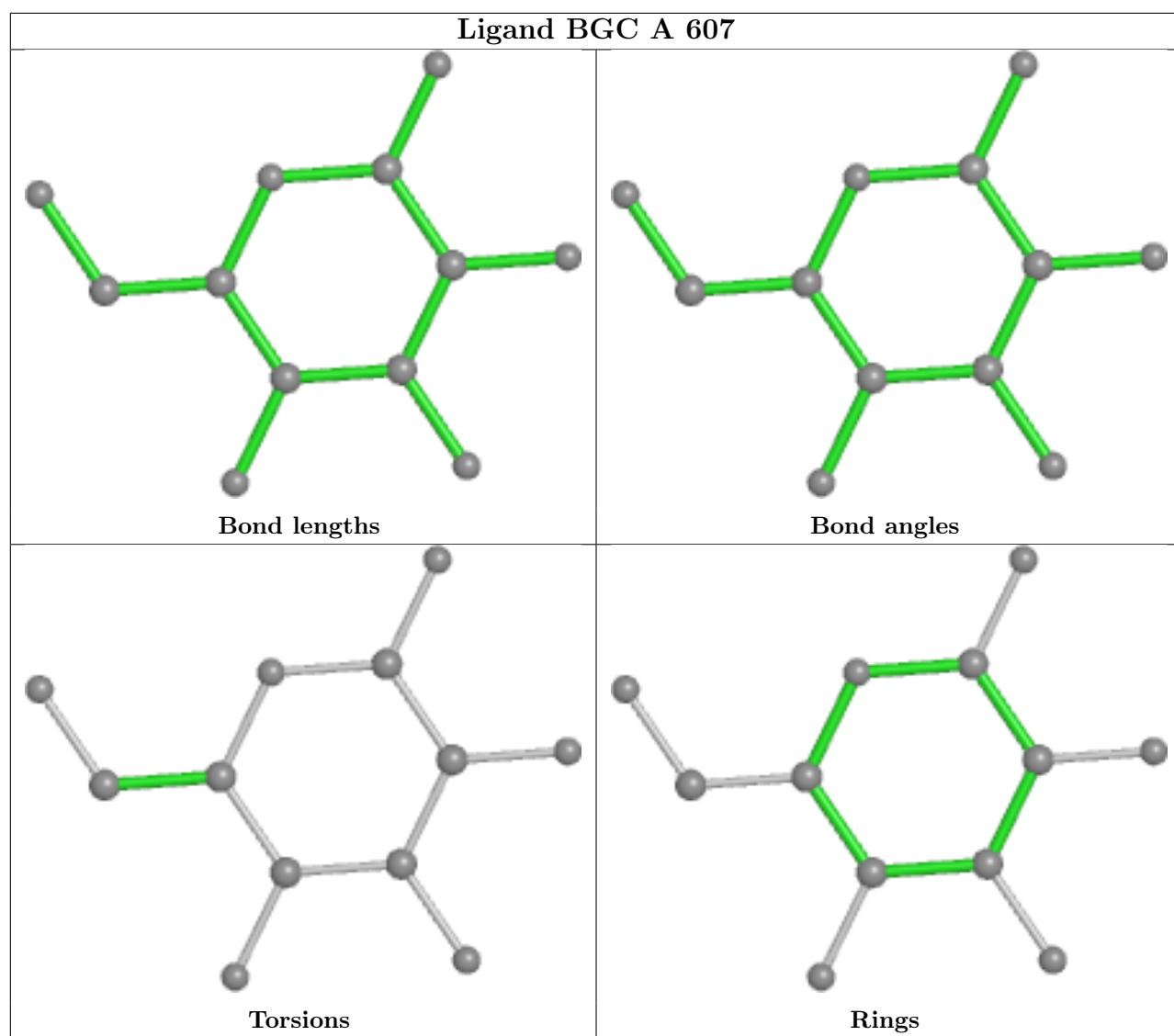
There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	B	605	BGC	1	0
7	A	601	PG4	1	0
11	A	608	PEG	1	0
11	B	607	PEG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	550/648 (84%)	-0.09	2 (0%) 89 88	29, 41, 61, 85	0
1	B	550/648 (84%)	-0.08	1 (0%) 92 91	24, 41, 60, 81	1 (0%)
All	All	1100/1296 (84%)	-0.08	3 (0%) 90 89	24, 41, 60, 85	1 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	20	SER	3.7
1	B	469	SER	2.2
1	A	470	ILE	2.1

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
4	XYX	E	6	9/10	0.44	0.20	67,68,74,78	9
5	BMA	G	3	11/12	0.60	0.13	72,78,83,90	0
3	MAN	D	7	11/12	0.61	0.14	67,71,76,77	0
5	BMA	J	3	11/12	0.63	0.12	70,72,80,80	0
3	MAN	H	7	11/12	0.67	0.12	68,72,76,76	0
2	MAN	F	10	11/12	0.67	0.11	72,75,79,80	0

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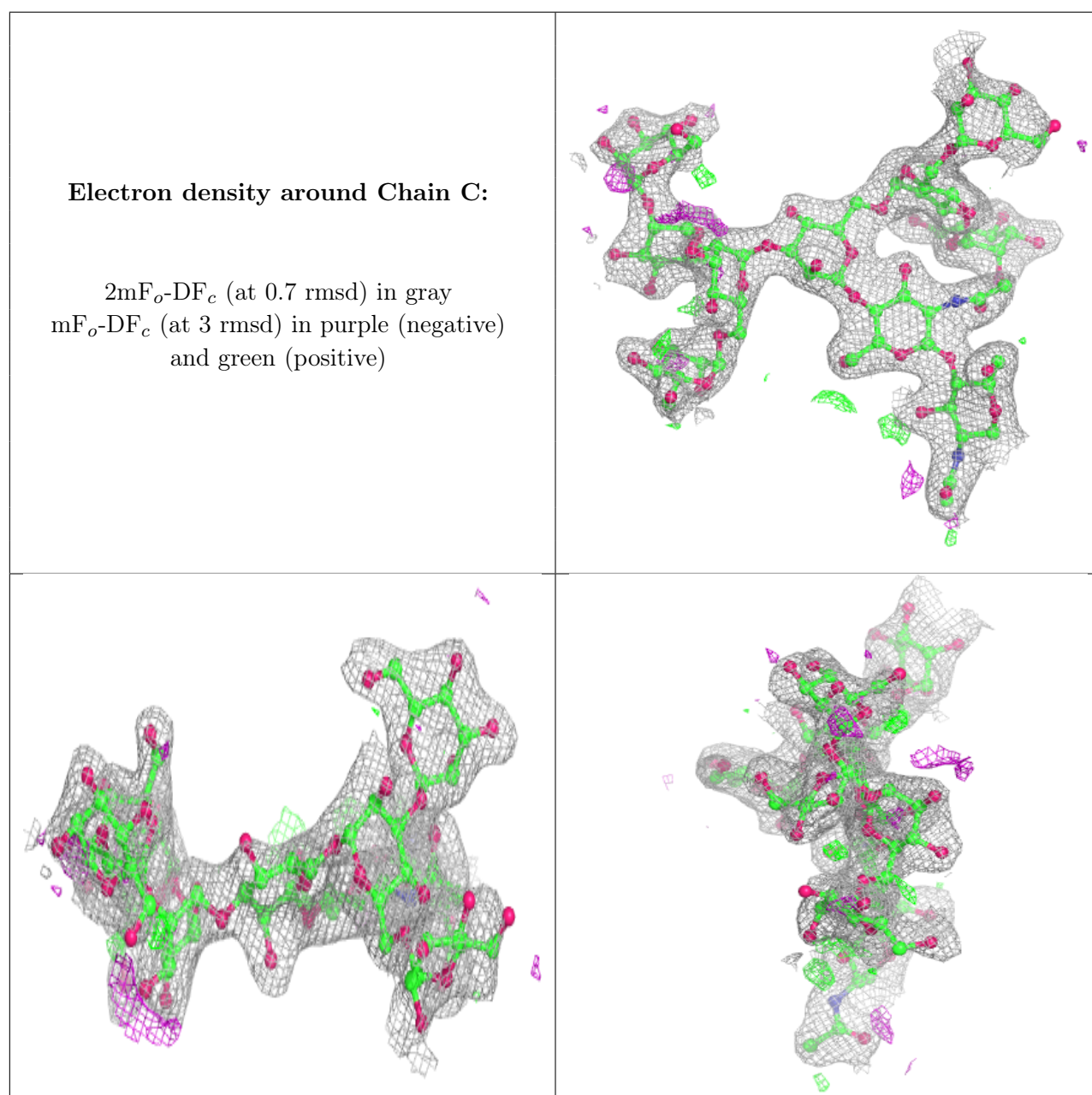
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MAN	C	10	11/12	0.68	0.12	70,76,80,81	0
2	MAN	F	7	11/12	0.68	0.14	54,63,69,74	0
2	MAN	F	6	11/12	0.69	0.15	61,65,75,77	0
2	MAN	C	7	11/12	0.69	0.14	56,65,68,71	0
6	GAL	I	7	11/12	0.72	0.17	40,43,45,47	11
4	GAL	E	8	11/12	0.75	0.16	37,48,49,51	11
2	MAN	C	6	11/12	0.80	0.12	50,59,66,67	0
2	MAN	F	4	11/12	0.80	0.11	49,55,59,65	0
4	BGC	E	3	11/12	0.84	0.10	48,56,65,71	0
2	MAN	C	5	11/12	0.84	0.09	49,59,65,66	0
4	BGC	E	1	12/12	0.84	0.09	54,58,59,67	0
4	BGC	E	4	11/12	0.85	0.11	47,55,61,64	0
6	BGC	I	3	11/12	0.85	0.10	46,51,57,65	0
6	BGC	I	4	11/12	0.85	0.10	42,51,55,55	0
3	NAG	D	1	14/15	0.85	0.09	42,47,55,59	0
4	XYS	E	7	9/10	0.86	0.10	48,55,57,57	0
2	MAN	C	8	11/12	0.86	0.10	48,54,60,68	0
2	MAN	F	5	11/12	0.86	0.09	48,59,64,69	0
5	NAG	J	2	14/15	0.86	0.11	50,57,61,67	0
5	NAG	G	2	14/15	0.87	0.10	43,52,63,63	0
3	MAN	D	5	11/12	0.87	0.10	39,42,48,53	0
3	MAN	D	6	11/12	0.87	0.10	43,46,48,51	0
2	MAN	F	8	11/12	0.87	0.08	49,54,59,68	0
6	BGC	I	1	12/12	0.87	0.08	53,57,63,66	0
3	MAN	H	5	11/12	0.87	0.10	40,44,48,54	0
3	MAN	H	6	11/12	0.87	0.10	44,49,53,55	0
2	MAN	F	9	11/12	0.87	0.09	44,50,53,60	0
2	MAN	C	4	11/12	0.88	0.10	50,57,60,64	0
3	NAG	H	2	14/15	0.88	0.10	45,55,64,65	0
6	XYS	I	6	9/10	0.88	0.10	46,50,55,60	0
6	BGC	I	2	11/12	0.88	0.08	49,52,54,57	0
3	BMA	H	3	11/12	0.89	0.08	41,53,58,61	0
2	MAN	C	9	11/12	0.89	0.09	43,49,51,56	0
4	BGC	E	2	11/12	0.90	0.08	50,54,60,61	0
3	NAG	D	2	14/15	0.90	0.09	47,53,59,60	0
6	XYS	I	5	9/10	0.91	0.09	39,43,48,49	0
2	NAG	C	1	14/15	0.91	0.10	37,41,44,46	0
2	NAG	F	2	14/15	0.91	0.08	39,45,48,50	0
3	MAN	D	4	11/12	0.92	0.07	33,43,47,50	0
2	NAG	C	2	14/15	0.92	0.08	40,45,51,52	0
2	BMA	C	3	11/12	0.92	0.07	43,51,56,57	0
4	XYS	E	5	9/10	0.92	0.08	40,43,51,53	0

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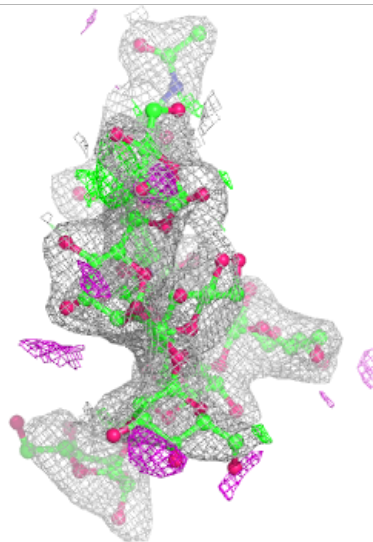
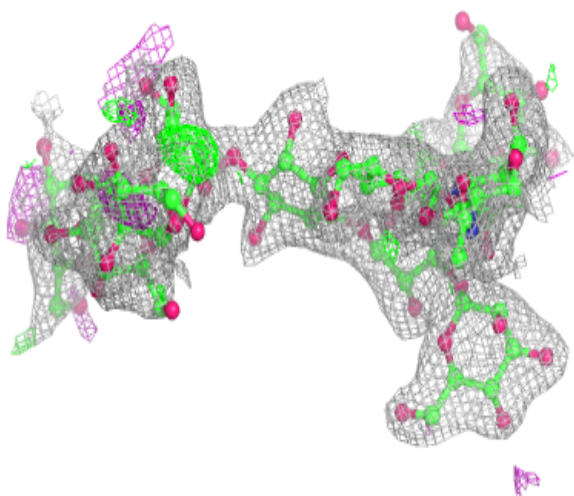
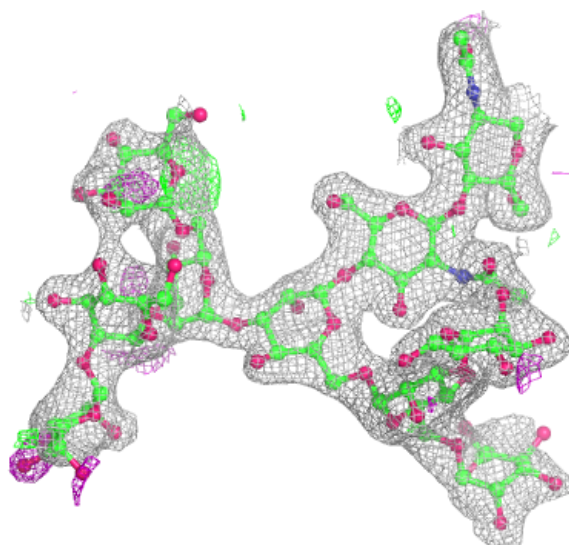
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BMA	F	3	11/12	0.92	0.07	43,52,55,55	0
3	BMA	D	3	11/12	0.92	0.07	41,48,55,59	0
3	NAG	H	1	14/15	0.93	0.07	38,48,51,52	0
3	MAN	H	4	11/12	0.93	0.07	36,45,48,49	0
2	NAG	F	1	14/15	0.94	0.07	34,39,44,45	0
5	NAG	J	1	14/15	0.96	0.06	34,41,44,46	0
5	NAG	G	1	14/15	0.96	0.07	34,40,43,46	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.



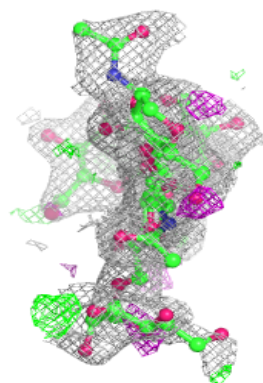
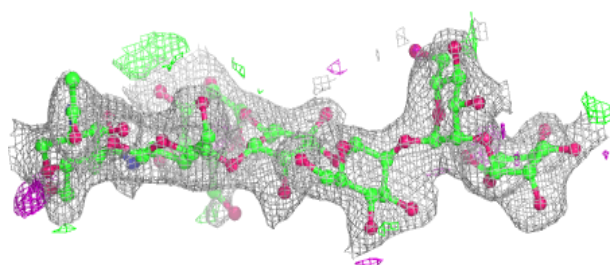
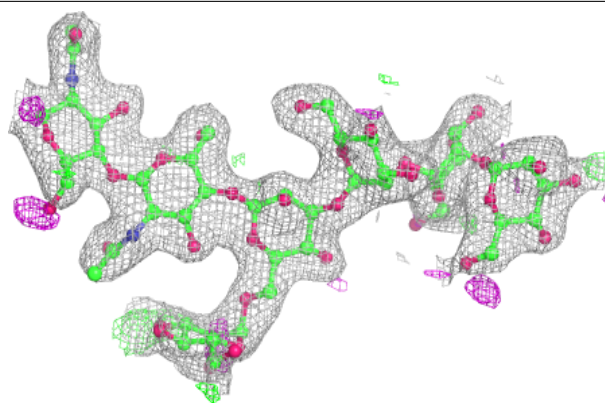
Electron density around Chain F:

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

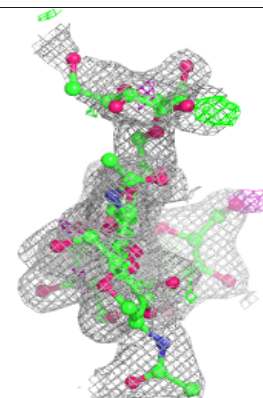
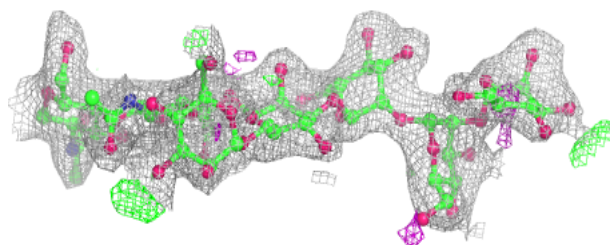
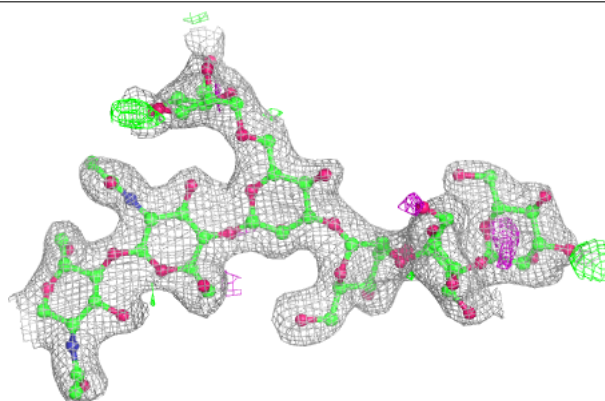


Electron density around Chain D:

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

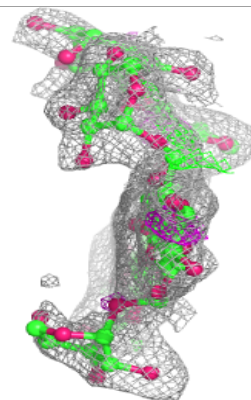
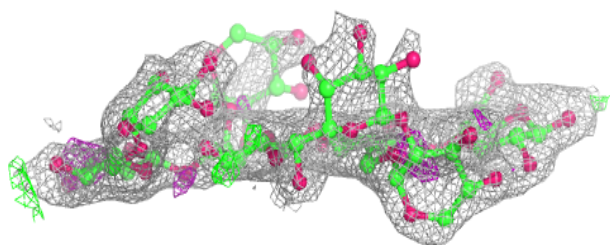
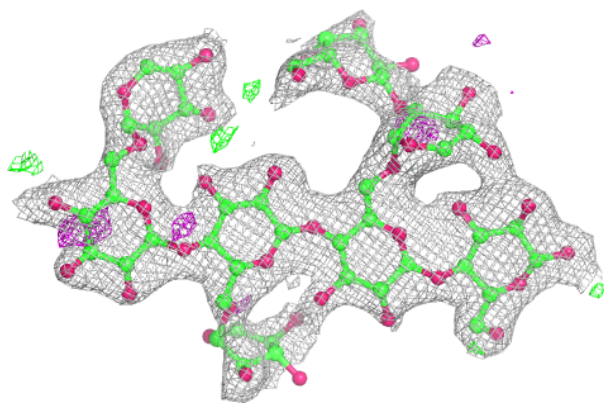
**Electron density around Chain H:**

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

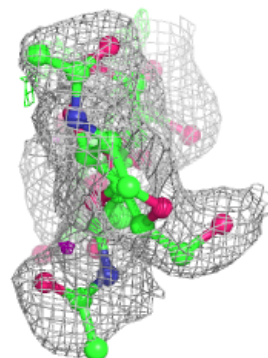
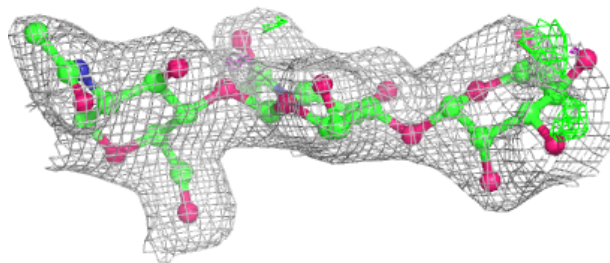
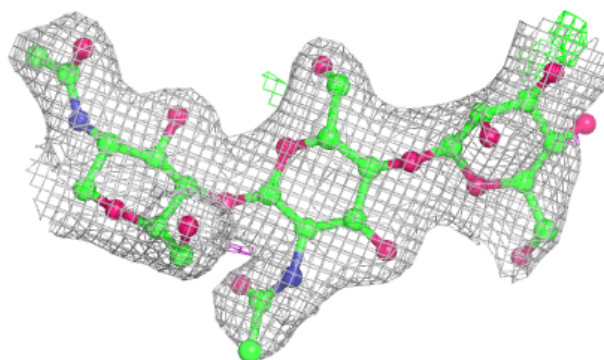


Electron density around Chain E:

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

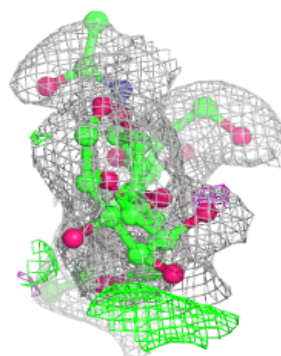
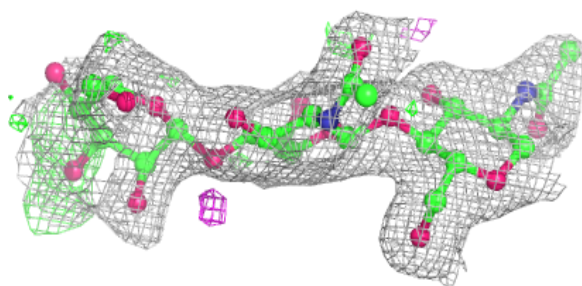
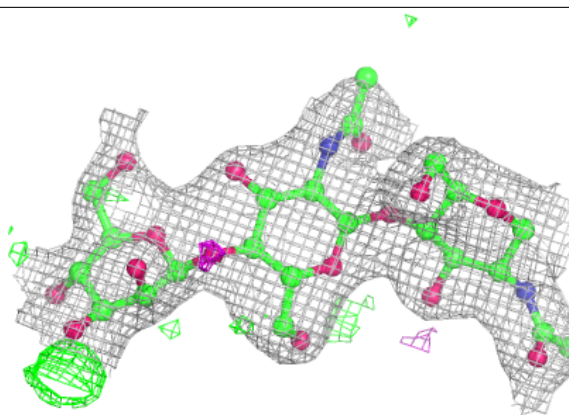
**Electron density around Chain G:**

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

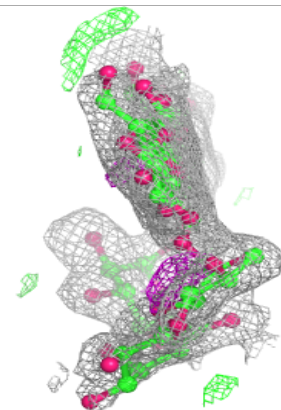
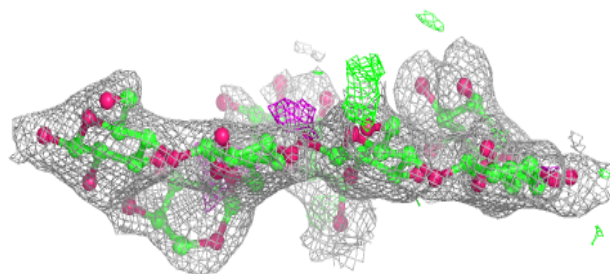
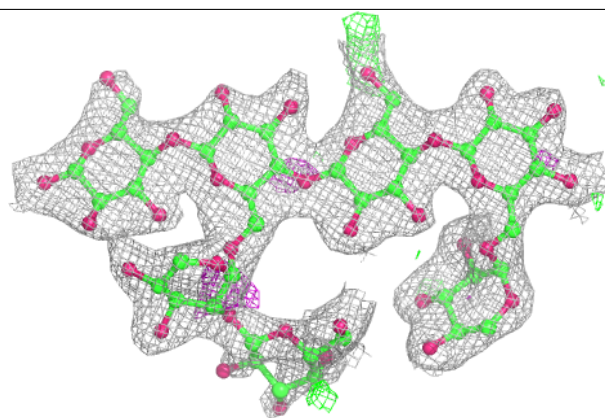


Electron density around Chain J:

$2mF_o-DF_c$ (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)



6.4 Ligands ⓘ

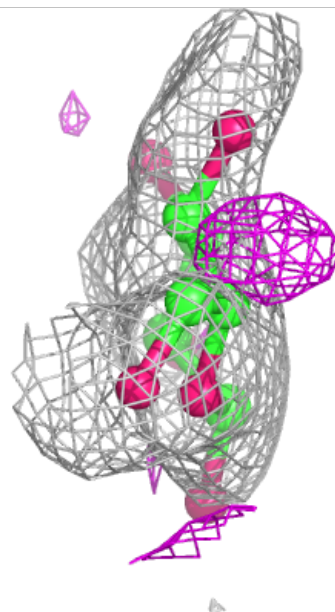
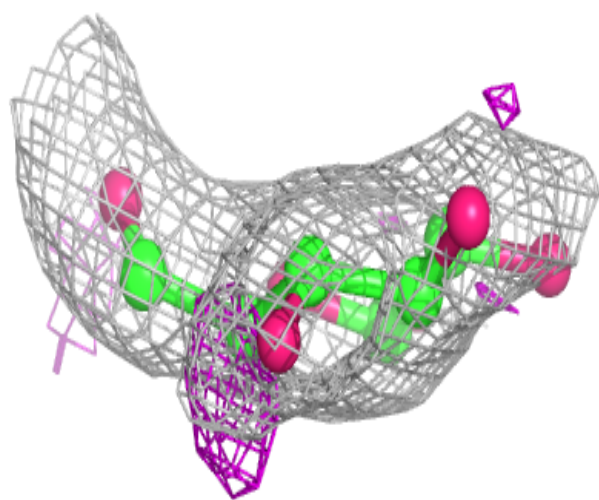
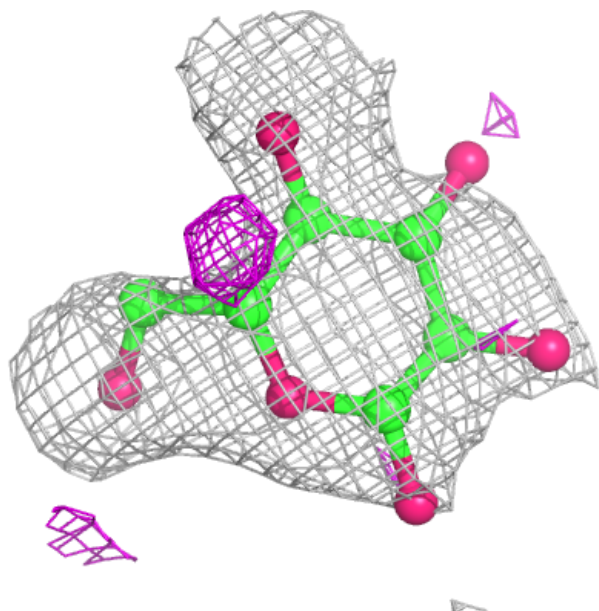
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	MAN	A	602	11/12	0.58	0.15	59,67,70,71	0
8	MAN	B	601	11/12	0.70	0.13	60,67,74,74	0
9	NAG	B	604	14/15	0.70	0.12	64,70,75,76	0
9	NAG	B	602	14/15	0.73	0.12	57,65,73,74	0
9	NAG	A	603	14/15	0.73	0.12	61,71,74,77	0
7	PG4	A	601	13/13	0.74	0.16	50,55,59,59	0
10	BGC	B	605	12/12	0.76	0.13	52,57,60,69	0
9	NAG	A	604	14/15	0.77	0.11	62,74,81,81	0
9	NAG	A	606	14/15	0.78	0.11	64,71,78,82	0
11	PEG	B	607	7/7	0.79	0.14	46,55,59,62	0
11	PEG	B	606	7/7	0.80	0.12	41,44,54,55	0
10	BGC	A	607	12/12	0.81	0.12	50,57,62,65	0
9	NAG	B	603	14/15	0.81	0.10	66,74,81,82	0
9	NAG	A	605	14/15	0.84	0.11	60,63,66,70	0
11	PEG	A	608	7/7	0.86	0.12	37,44,51,53	0
12	MG	A	609	1/1	0.88	0.14	51,51,51,51	0
12	MG	B	608	1/1	0.91	0.13	51,51,51,51	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

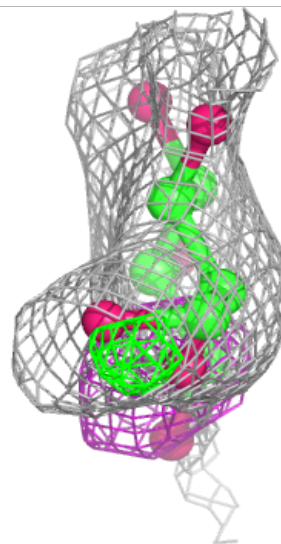
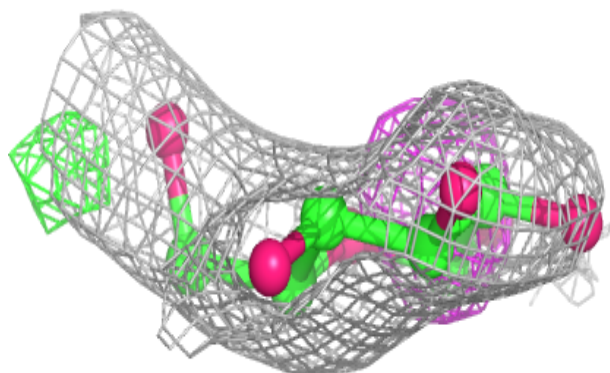
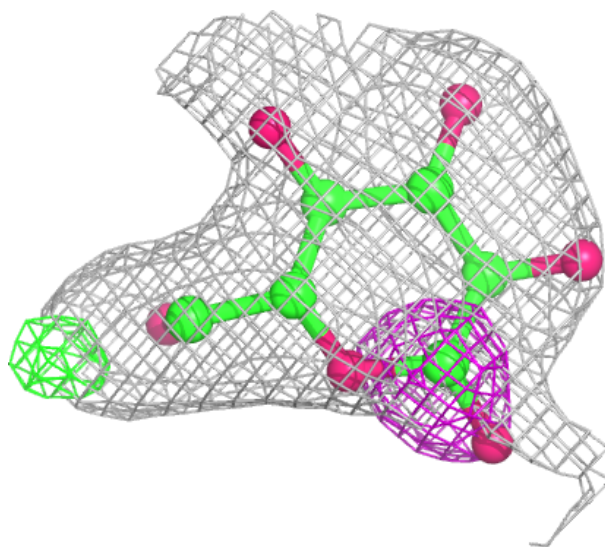
Electron density around BGC B 605:

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



Electron density around BGC A 607:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.