



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 10:27 AM BST

PDB ID : 5HJR
Title : Murine endoplasmic reticulum alpha-glucosidase II with bound covalent intermediate
Authors : Caputo, A.T.; Roversi, P.; Alonzi, D.S.; Kiappes, J.L.; Zitzmann, N.
Deposited on : 2016-01-13
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

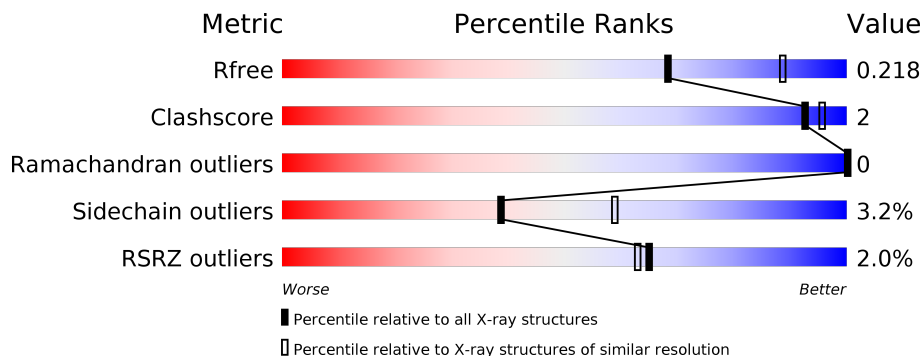
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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

Mol	Chain	Length	Quality of chain
1	A	857	<p>2% 94% 5% •</p>
1	C	857	<p>1% 93% 6% •</p>
2	B	83	<p>11% 94% 5% •</p>
2	D	83	<p>5% 96% ••</p>
3	E	4	<p>100%</p>
4	F	5	<p>80% 20%</p>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EDO	A	1006	-	-	-	X
5	EDO	C	1007	-	-	X	-
6	FMT	A	1012	-	-	-	X
6	FMT	A	1014	-	-	-	X
6	FMT	A	1019	-	-	-	X
6	FMT	C	1017	-	-	-	X
6	FMT	C	1018	-	-	-	X
8	P6G	A	1023	-	-	-	X
8	P6G	C	1024	-	-	-	X

2 Entry composition i

There are 12 unique types of molecules in this entry. The entry contains 30463 atoms, of which 14634 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 Neutral alpha-glucosidase AB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	855	13555	4430	6637	1201	1259	28	0	3	0
1	C	854	13567	4430	6653	1198	1258	28	1	4	0

There are 198 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	VAL	deletion	UNP Q8BHN3
A	?	-	PRO	deletion	UNP Q8BHN3
A	?	-	PHE	deletion	UNP Q8BHN3
A	?	-	SER	deletion	UNP Q8BHN3
A	?	-	ASP	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	VAL	deletion	UNP Q8BHN3
A	?	-	SER	deletion	UNP Q8BHN3
A	?	-	LEU	deletion	UNP Q8BHN3
A	?	-	ALA	deletion	UNP Q8BHN3
A	?	-	LEU	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	SER	deletion	UNP Q8BHN3
A	?	-	VAL	deletion	UNP Q8BHN3
A	?	-	TRP	deletion	UNP Q8BHN3
A	?	-	ASP	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	ILE	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	ASN	deletion	UNP Q8BHN3
A	?	-	LEU	deletion	UNP Q8BHN3
A	?	-	PHE	deletion	UNP Q8BHN3
A	?	-	SER	deletion	UNP Q8BHN3
A	?	-	ARG	deletion	UNP Q8BHN3
A	?	-	GLN	deletion	UNP Q8BHN3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP Q8BHN3
A	?	-	SER	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	ASP	deletion	UNP Q8BHN3
A	?	-	PRO	deletion	UNP Q8BHN3
A	?	-	ALA	deletion	UNP Q8BHN3
A	?	-	GLU	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	ASN	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	ALA	deletion	UNP Q8BHN3
A	?	-	GLN	deletion	UNP Q8BHN3
A	?	-	PRO	deletion	UNP Q8BHN3
A	?	-	GLU	deletion	UNP Q8BHN3
A	?	-	ALA	deletion	UNP Q8BHN3
A	?	-	THR	deletion	UNP Q8BHN3
A	?	-	PRO	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	ASP	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	ASP	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	PRO	deletion	UNP Q8BHN3
A	?	-	GLU	deletion	UNP Q8BHN3
A	?	-	GLU	deletion	UNP Q8BHN3
A	?	-	THR	deletion	UNP Q8BHN3
A	?	-	GLN	deletion	UNP Q8BHN3
A	?	-	GLU	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	ALA	deletion	UNP Q8BHN3
A	?	-	GLU	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	ASP	deletion	UNP Q8BHN3
A	?	-	THR	deletion	UNP Q8BHN3
A	?	-	ALA	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3
A	?	-	THR	deletion	UNP Q8BHN3
A	?	-	LEU	deletion	UNP Q8BHN3
A	?	-	PHE	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	LYS	deletion	UNP Q8BHN3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	MET	deletion	UNP Q8BHN3
A	?	-	LEU	deletion	UNP Q8BHN3
A	?	-	ASP	deletion	UNP Q8BHN3
A	?	-	TYR	deletion	UNP Q8BHN3
A	?	-	LEU	deletion	UNP Q8BHN3
A	?	-	GLN	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	SER	deletion	UNP Q8BHN3
A	?	-	GLY	deletion	UNP Q8BHN3
A	?	-	GLU	deletion	UNP Q8BHN3
A	945	THR	-	expression tag	UNP Q8BHN3
A	946	SER	-	expression tag	UNP Q8BHN3
A	947	VAL	-	expression tag	UNP Q8BHN3
A	948	LEU	-	expression tag	UNP Q8BHN3
A	949	ILE	-	expression tag	UNP Q8BHN3
A	950	LEU	-	expression tag	UNP Q8BHN3
A	951	ARG	-	expression tag	UNP Q8BHN3
A	952	LYS	-	expression tag	UNP Q8BHN3
A	953	PRO	-	expression tag	UNP Q8BHN3
A	954	GLY	-	expression tag	UNP Q8BHN3
A	955	VAL	-	expression tag	UNP Q8BHN3
A	956	SER	-	expression tag	UNP Q8BHN3
A	957	VAL	-	expression tag	UNP Q8BHN3
A	958	ALA	-	expression tag	UNP Q8BHN3
A	959	SER	-	expression tag	UNP Q8BHN3
A	960	ASP	-	expression tag	UNP Q8BHN3
A	961	TRP	-	expression tag	UNP Q8BHN3
A	962	SER	-	expression tag	UNP Q8BHN3
A	963	ILE	-	expression tag	UNP Q8BHN3
A	964	HIS	-	expression tag	UNP Q8BHN3
A	965	LEU	-	expression tag	UNP Q8BHN3
A	966	ARG	-	expression tag	UNP Q8BHN3
C	?	-	VAL	deletion	UNP Q8BHN3
C	?	-	PRO	deletion	UNP Q8BHN3
C	?	-	PHE	deletion	UNP Q8BHN3
C	?	-	SER	deletion	UNP Q8BHN3
C	?	-	ASP	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	VAL	deletion	UNP Q8BHN3
C	?	-	SER	deletion	UNP Q8BHN3
C	?	-	LEU	deletion	UNP Q8BHN3
C	?	-	ALA	deletion	UNP Q8BHN3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	LEU	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	SER	deletion	UNP Q8BHN3
C	?	-	VAL	deletion	UNP Q8BHN3
C	?	-	TRP	deletion	UNP Q8BHN3
C	?	-	ASP	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	ILE	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	ASN	deletion	UNP Q8BHN3
C	?	-	LEU	deletion	UNP Q8BHN3
C	?	-	PHE	deletion	UNP Q8BHN3
C	?	-	SER	deletion	UNP Q8BHN3
C	?	-	ARG	deletion	UNP Q8BHN3
C	?	-	GLN	deletion	UNP Q8BHN3
C	?	-	GLU	deletion	UNP Q8BHN3
C	?	-	SER	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	ASP	deletion	UNP Q8BHN3
C	?	-	PRO	deletion	UNP Q8BHN3
C	?	-	ALA	deletion	UNP Q8BHN3
C	?	-	GLU	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	ASN	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	ALA	deletion	UNP Q8BHN3
C	?	-	GLN	deletion	UNP Q8BHN3
C	?	-	PRO	deletion	UNP Q8BHN3
C	?	-	GLU	deletion	UNP Q8BHN3
C	?	-	ALA	deletion	UNP Q8BHN3
C	?	-	THR	deletion	UNP Q8BHN3
C	?	-	PRO	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	ASP	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	ASP	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	PRO	deletion	UNP Q8BHN3
C	?	-	GLU	deletion	UNP Q8BHN3
C	?	-	GLU	deletion	UNP Q8BHN3
C	?	-	THR	deletion	UNP Q8BHN3
C	?	-	GLN	deletion	UNP Q8BHN3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	GLU	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	ALA	deletion	UNP Q8BHN3
C	?	-	GLU	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	ASP	deletion	UNP Q8BHN3
C	?	-	THR	deletion	UNP Q8BHN3
C	?	-	ALA	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	THR	deletion	UNP Q8BHN3
C	?	-	LEU	deletion	UNP Q8BHN3
C	?	-	PHE	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	LYS	deletion	UNP Q8BHN3
C	?	-	MET	deletion	UNP Q8BHN3
C	?	-	LEU	deletion	UNP Q8BHN3
C	?	-	ASP	deletion	UNP Q8BHN3
C	?	-	TYR	deletion	UNP Q8BHN3
C	?	-	LEU	deletion	UNP Q8BHN3
C	?	-	GLN	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	SER	deletion	UNP Q8BHN3
C	?	-	GLY	deletion	UNP Q8BHN3
C	?	-	GLU	deletion	UNP Q8BHN3
C	945	THR	-	expression tag	UNP Q8BHN3
C	946	SER	-	expression tag	UNP Q8BHN3
C	947	VAL	-	expression tag	UNP Q8BHN3
C	948	LEU	-	expression tag	UNP Q8BHN3
C	949	ILE	-	expression tag	UNP Q8BHN3
C	950	LEU	-	expression tag	UNP Q8BHN3
C	951	ARG	-	expression tag	UNP Q8BHN3
C	952	LYS	-	expression tag	UNP Q8BHN3
C	953	PRO	-	expression tag	UNP Q8BHN3
C	954	GLY	-	expression tag	UNP Q8BHN3
C	955	VAL	-	expression tag	UNP Q8BHN3
C	956	SER	-	expression tag	UNP Q8BHN3
C	957	VAL	-	expression tag	UNP Q8BHN3
C	958	ALA	-	expression tag	UNP Q8BHN3
C	959	SER	-	expression tag	UNP Q8BHN3
C	960	ASP	-	expression tag	UNP Q8BHN3
C	961	TRP	-	expression tag	UNP Q8BHN3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	962	SER	-	expression tag	UNP Q8BHN3
C	963	ILE	-	expression tag	UNP Q8BHN3
C	964	HIS	-	expression tag	UNP Q8BHN3
C	965	LEU	-	expression tag	UNP Q8BHN3
C	966	ARG	-	expression tag	UNP Q8BHN3

- Molecule 2 is a protein called Glucosidase 2 subunit beta.

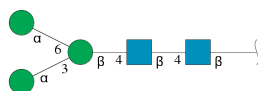
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
2	B	83	Total	C	H	N	O	S	0	0	0
			1151	368	535	101	137	10			
2	D	83	Total	C	H	N	O	S	0	0	0
			1149	368	533	101	137	10			

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



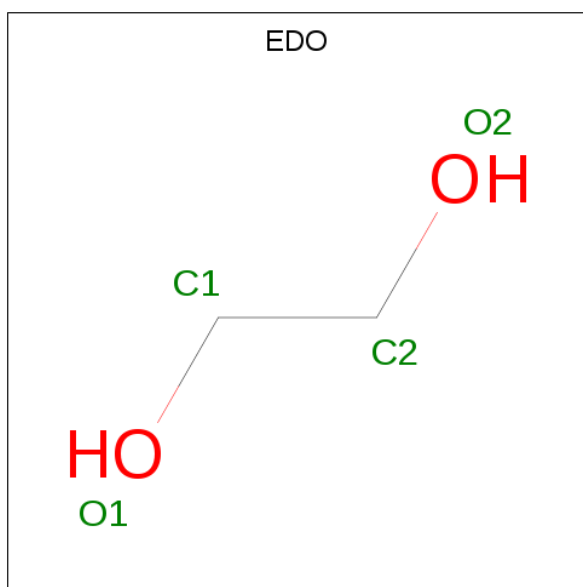
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
3	E	4	Total	C	H	N	O	0	0	0
			93	28	43	2	20			

- Molecule 4 is an oligosaccharide called 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.



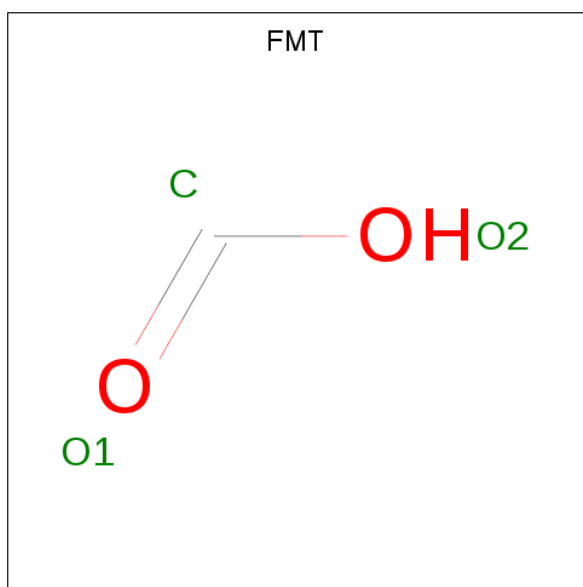
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	H	N	O			
4	F	5	Total	C	H	N	O	0	0	0
			113	34	52	2	25			

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	A	1	10	2	6	2	0	0
5	A	1	10	2	6	2	0	0
5	A	1	10	2	6	2	0	0
5	C	1	10	2	6	2	0	0
5	C	1	10	2	6	2	0	0
5	C	1	10	2	6	2	0	0
5	C	1	10	2	6	2	0	0

- Molecule 6 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



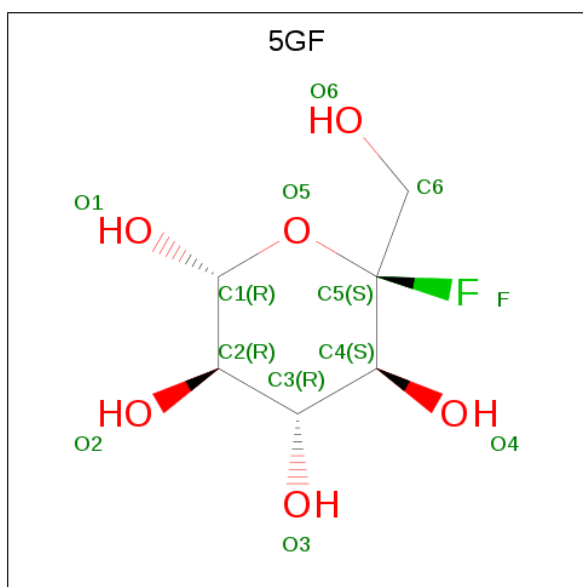
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			5	1	2	2		
6	A	1	Total	C	H	O	0	0
			4	1	1	2		
6	A	1	Total	C	H	O	0	0
			5	1	2	2		
6	A	1	Total	C	H	O	0	0
			5	1	2	2		
6	A	1	Total	C	H	O	0	0
			4	1	1	2		
6	A	1	Total	C	H	O	0	0
			5	1	2	2		
6	A	1	Total	C	H	O	0	0
			4	1	1	2		
6	A	1	Total	C	H	O	0	0
			5	1	2	2		
6	A	1	Total	C	H	O	0	0
			4	1	1	2		
6	A	1	Total	C	H	O	0	0
			4	1	1	2		
6	A	1	Total	C	H	O	0	0
			5	1	2	2		

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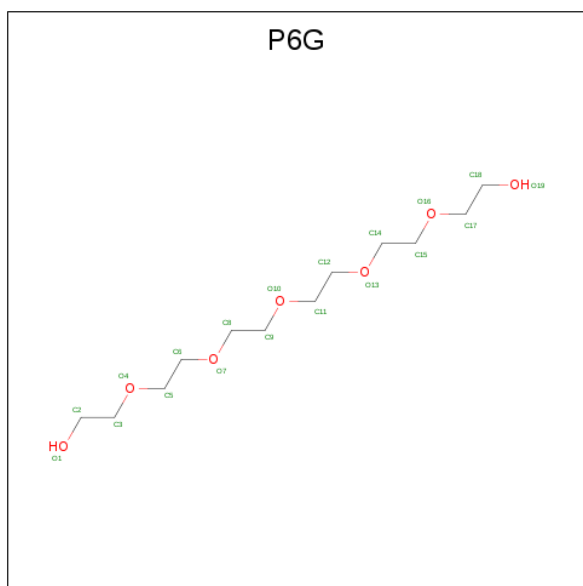
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total 5	C 1	H 2	O 2	0	0
6	A	1	Total 5	C 1	H 2	O 2	0	0
6	B	1	Total 4	C 1	H 1	O 2	0	0
6	C	1	Total 5	C 1	H 2	O 2	0	0
6	C	1	Total 5	C 1	H 2	O 2	0	0
6	C	1	Total 4	C 1	H 1	O 2	0	0
6	C	1	Total 4	C 1	H 1	O 2	0	0
6	C	1	Total 5	C 1	H 2	O 2	0	0
6	C	1	Total 5	C 1	H 2	O 2	0	0
6	C	1	Total 4	C 1	H 1	O 2	0	0
6	C	1	Total 4	C 1	H 1	O 2	0	0
6	C	1	Total 5	C 1	H 2	O 2	0	0
6	C	1	Total 4	C 1	H 1	O 2	0	0
6	C	1	Total 4	C 1	H 1	O 2	0	0
6	C	1	Total 5	C 1	H 2	O 2	0	0
6	C	1	Total 5	C 1	H 2	O 2	0	0
6	D	1	Total 4	C 1	H 1	O 2	0	0

- Molecule 7 is 5-fluoro-beta-D-glucopyranose (three-letter code: 5GF) (formula: C₆H₁₁FO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
7	A	1	Total	C	F	H	O	0	0
			22	6	1	10	5		
7	C	1	Total	C	F	H	O	0	0
			22	6	1	10	5		

- Molecule 8 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



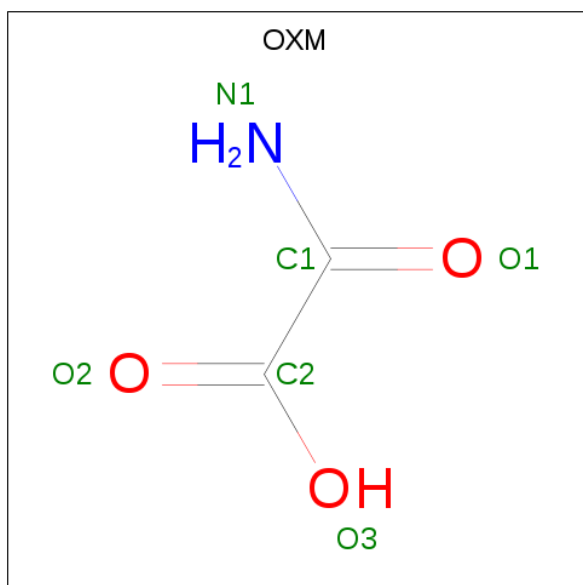
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	H	O	0	0
			26	7	15	4		
8	A	1	Total	C	H	O	0	0
			30	9	16	5		

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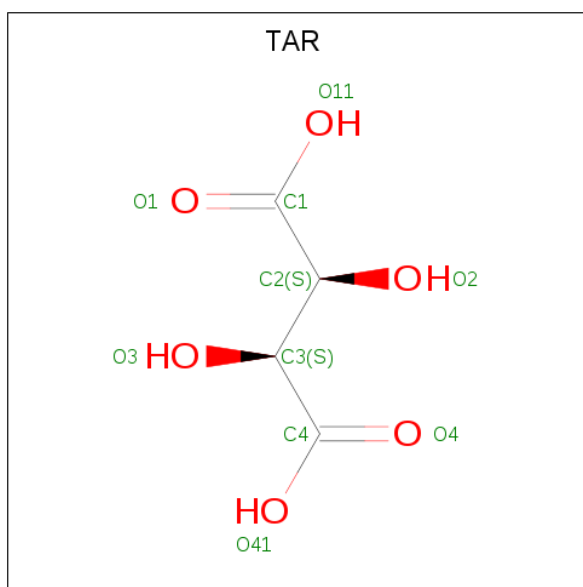
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	C	1	Total	C	H	O	0	0
			30	9	16	5		
8	C	1	Total	C	H	O	0	0
			26	7	15	4		

- Molecule 9 is OXAMIC ACID (three-letter code: OXM) (formula: C₂H₃NO₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	A	1	Total	C	H	N	O	0	0
			8	2	2	1	3		
9	C	1	Total	C	H	N	O	0	0
			8	2	2	1	3		
9	C	1	Total	C	H	N	O	0	0
			8	2	2	1	3		

- Molecule 10 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	H	O	0	0
			14	4	4	6		

- Molecule 11 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	2	Total	Ca	0	0
			2	2		
11	D	2	Total	Ca	0	0
			2	2		

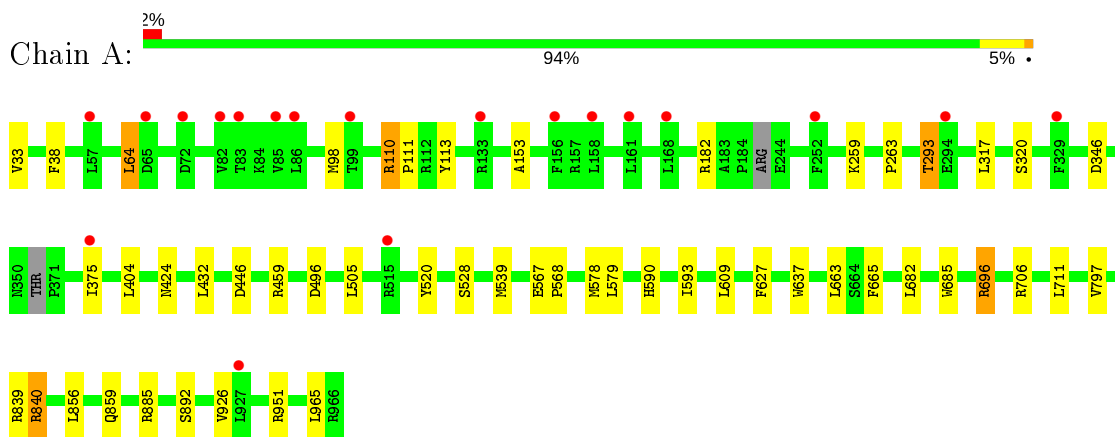
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	178	Total	O	0	0
			178	178		
12	B	13	Total	O	0	0
			13	13		
12	C	223	Total	O	0	0
			223	223		
12	D	10	Total	O	0	0
			10	10		

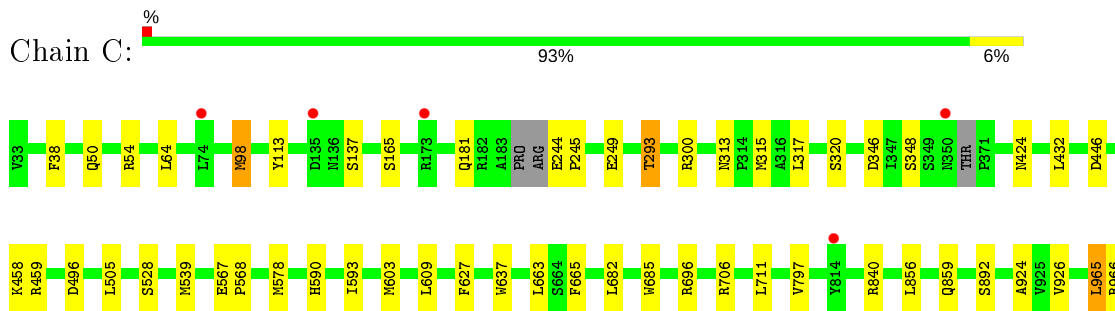
3 Residue-property plots [i](#)

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.

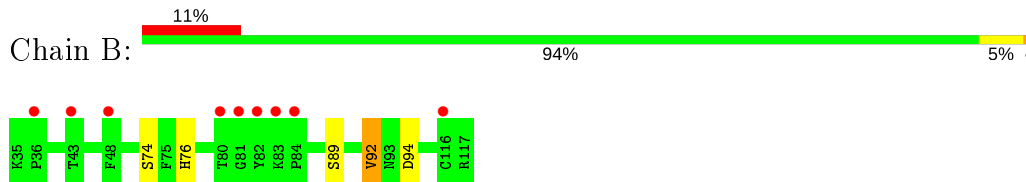
- Molecule 1: Neutral alpha-glucosidase AB



- Molecule 1: Neutral alpha-glucosidase AB

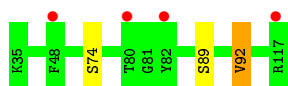


- Molecule 2: Glucosidase 2 subunit beta



- Molecule 2: Glucosidase 2 subunit beta







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

Chain E:  100%



- Molecule 4: 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 F:  80%  20%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.51Å 174.66Å 63.71Å 90.00° 91.31° 90.00°	Depositor
Resolution (Å)	103.48 – 2.40 103.48 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.9 (103.48-2.40) 98.9 (103.48-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.25	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.40Å)	Xtrriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.177 , 0.202 0.192 , 0.218	Depositor DCC
R_{free} test set	4409 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	46.7	Xtrriage
Anisotropy	0.332	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.044 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	30463	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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: BMA, NAG, TAR, FMT, EDO, 5GF, OXM, P6G, CA, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.47	1/7139 (0.0%)	0.72	5/9715 (0.1%)
1	C	0.52	2/7140 (0.0%)	0.70	0/9717
2	B	0.48	0/628	0.76	0/854
2	D	0.52	0/628	0.69	0/854
All	All	0.50	3/15535 (0.0%)	0.71	5/21140 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	603	MET	SD-CE	-7.67	1.34	1.77
1	C	98	MET	SD-CE	-5.36	1.47	1.77
1	A	375	ILE	CG1-CD1	-5.19	1.14	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	696	ARG	CG-CD-NE	10.51	133.87	111.80
1	A	840	ARG	CG-CD-NE	10.38	133.60	111.80
1	A	885	ARG	CG-CD-NE	10.22	133.27	111.80
1	A	951	ARG	CD-NE-CZ	5.30	131.01	123.60
1	A	839	ARG	CD-NE-CZ	5.20	130.88	123.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	76	HIS	Sidechain

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	6918	6637	6672	24	0
1	C	6914	6653	6659	20	0
2	B	616	535	533	2	0
2	D	616	533	533	1	0
3	E	50	43	43	0	0
4	F	61	52	52	0	0
5	A	12	18	18	2	0
5	C	16	24	24	6	0
6	A	48	24	25	0	0
6	B	3	1	2	0	0
6	C	42	21	22	0	0
6	D	3	1	1	0	0
7	A	12	10	9	0	0
7	C	12	10	9	0	0
8	A	25	31	29	0	0
8	C	25	31	29	0	0
9	A	6	2	2	0	0
9	C	12	4	4	0	0
10	A	10	4	4	0	0
11	B	2	0	0	0	0
11	D	2	0	0	0	0
12	A	178	0	0	0	0
12	B	13	0	0	0	0
12	C	223	0	0	0	0
12	D	10	0	0	0	0
All	All	15829	14634	14670	46	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.

All (46) 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:C:505:LEU:HD22	1:C:539:MET:HE1	1.69	0.74
1:A:98:MET:HE3	1:A:404:LEU:HD11	1.69	0.72
1:C:313:ASN:OD1	5:C:1009:EDO:H12	1.90	0.72
1:A:505:LEU:HD22	1:A:539:MET:HE1	1.73	0.70
1:A:293:THR:CG2	1:A:346:ASP:OD1	2.40	0.70
1:C:317:LEU:HD21	5:C:1009:EDO:H21	1.75	0.69
1:C:293:THR:CG2	1:C:346:ASP:OD1	2.41	0.68
1:A:840:ARG:NH1	2:B:94:ASP:OD2	2.29	0.66
1:A:520:TYR:HE2	1:A:579:LEU:HG	1.64	0.62
1:A:98:MET:CE	1:A:404:LEU:HD11	2.29	0.61
1:C:315:MET:HB3	5:C:1007:EDO:H12	1.84	0.60
2:B:89:SER:O	2:B:92:VAL:HG13	2.06	0.56
2:D:89:SER:O	2:D:92:VAL:HG13	2.06	0.55
1:A:64:LEU:HD21	1:A:153:ALA:HB2	1.88	0.55
1:A:110:ARG:HD2	1:A:111:PRO:O	2.08	0.54
1:A:505:LEU:HD22	1:A:539:MET:CE	2.37	0.53
1:C:505:LEU:HD22	1:C:539:MET:CE	2.36	0.53
1:C:293:THR:HG21	1:C:346:ASP:HA	1.91	0.52
1:A:293:THR:HG21	1:A:346:ASP:HA	1.92	0.52
1:A:182:ARG:HG3	1:A:182:ARG:HH11	1.76	0.50
1:C:300:ARG:HH11	5:C:1007:EDO:C2	2.25	0.50
1:A:459:ARG:NH1	1:A:496:ASP:OD2	2.44	0.50
1:C:924:ALA:O	1:C:966:ARG:HA	2.13	0.48
1:A:682:LEU:HD23	1:A:711:LEU:HD11	1.96	0.48
1:C:459:ARG:NH1	1:C:496:ASP:OD2	2.47	0.47
1:C:567:GLU:N	1:C:568:PRO:HA	2.31	0.47
1:C:682:LEU:HD23	1:C:711:LEU:HD11	1.96	0.47
1:A:520:TYR:CE2	1:A:579:LEU:HG	2.48	0.46
1:C:113:TYR:CZ	1:C:593:ILE:HG22	2.51	0.46
1:A:320:SER:O	1:A:627:PHE:HA	2.16	0.46
1:C:315:MET:HB3	5:C:1007:EDO:C1	2.46	0.45
1:C:320:SER:O	1:C:627:PHE:HA	2.16	0.45
1:C:293:THR:HG21	1:C:346:ASP:OD1	2.15	0.45
1:A:182:ARG:NH1	1:A:263:PRO:HG2	2.33	0.44
1:A:113:TYR:CZ	1:A:593:ILE:HG22	2.52	0.44
1:A:293:THR:HG21	1:A:346:ASP:OD1	2.14	0.44
1:A:567:GLU:N	1:A:568:PRO:HA	2.31	0.44
1:A:182:ARG:HG3	1:A:182:ARG:NH1	2.32	0.44
1:A:317:LEU:HD11	5:A:1006:EDO:H21	2.00	0.43
1:C:578:MET:HE3	1:C:590:HIS:ND1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:892:SER:HB3	1:C:965:LEU:O	2.18	0.43
1:A:38:PHE:HB3	5:A:1005:EDO:H12	2.00	0.42
1:A:578:MET:HE3	1:A:590:HIS:ND1	2.35	0.42
1:A:892:SER:O	1:A:965:LEU:HD22	2.20	0.41
1:C:244:GLU:HB2	1:C:245:PRO:CD	2.50	0.41
1:C:38:PHE:HB3	5:C:1007:EDO:H22	2.02	0.41

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	852/857 (99%)	830 (97%)	22 (3%)	0	100	100
1	C	852/857 (99%)	829 (97%)	23 (3%)	0	100	100
2	B	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
2	D	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
All	All	1866/1880 (99%)	1818 (97%)	48 (3%)	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	749/748 (100%)	729 (97%)	20 (3%)	44	65
1	C	748/748 (100%)	720 (96%)	28 (4%)	34	53
2	B	72/72 (100%)	70 (97%)	2 (3%)	43	63
2	D	72/72 (100%)	70 (97%)	2 (3%)	43	63
All	All	1641/1640 (100%)	1589 (97%)	52 (3%)	39	59

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	VAL
1	A	64	LEU
1	A	110	ARG
1	A	259	LYS
1	A	293	THR
1	A	424	ASN
1	A	432	LEU
1	A	446	ASP
1	A	528	SER
1	A	609	LEU
1	A	637	TRP
1	A	663	LEU
1	A	665	PHE
1	A	685	TRP
1	A	696	ARG
1	A	706	ARG
1	A	797	VAL
1	A	856	LEU
1	A	859	GLN
1	A	926	VAL
2	B	74	SER
2	B	92	VAL
1	C	50	GLN
1	C	54	ARG
1	C	64	LEU
1	C	98	MET
1	C	137	SER
1	C	165	SER
1	C	181	GLN
1	C	249	GLU
1	C	293	THR
1	C	348	SER
1	C	424	ASN

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Mol	Chain	Res	Type
1	C	432	LEU
1	C	446	ASP
1	C	458	LYS
1	C	528	SER
1	C	609	LEU
1	C	637	TRP
1	C	663	LEU
1	C	665	PHE
1	C	685	TRP
1	C	696	ARG
1	C	706	ARG
1	C	797	VAL
1	C	840	ARG
1	C	856	LEU
1	C	859	GLN
1	C	926	VAL
1	C	965	LEU
2	D	74	SER
2	D	92	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	928	GLN
1	C	964	HIS

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](#)

9 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
3	NAG	E	1	1,3	14,14,15	0.28	0	17,19,21	0.72	0
3	NAG	E	2	3	14,14,15	0.33	0	17,19,21	0.58	0
3	BMA	E	3	3	11,11,12	0.29	0	15,15,17	0.62	0
3	MAN	E	4	3	11,11,12	0.30	0	15,15,17	0.64	0
4	NAG	F	1	1,4	14,14,15	0.27	0	17,19,21	0.69	0
4	NAG	F	2	4	14,14,15	0.31	0	17,19,21	0.57	0
4	BMA	F	3	4	11,11,12	0.27	0	15,15,17	0.63	0
4	MAN	F	4	4	11,11,12	0.30	0	15,15,17	0.66	0
4	MAN	F	5	4	11,11,12	0.43	0	15,15,17	0.87	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
3	NAG	E	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	0/1/1/1
4	NAG	F	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1
4	BMA	F	3	4	-	0/2/19/22	0/1/1/1
4	MAN	F	4	4	-	0/2/19/22	0/1/1/1
4	MAN	F	5	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	5	MAN	C1-O5-C5	2.84	116.03	112.19

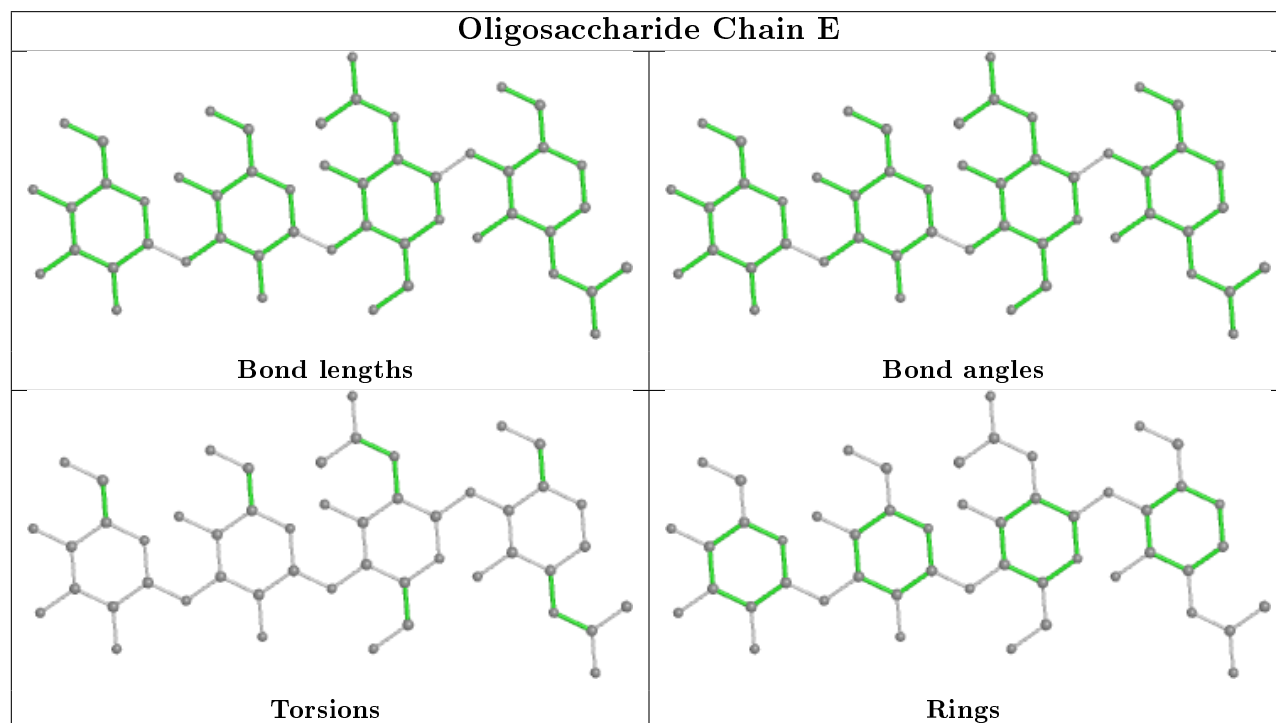
There are no chirality outliers.

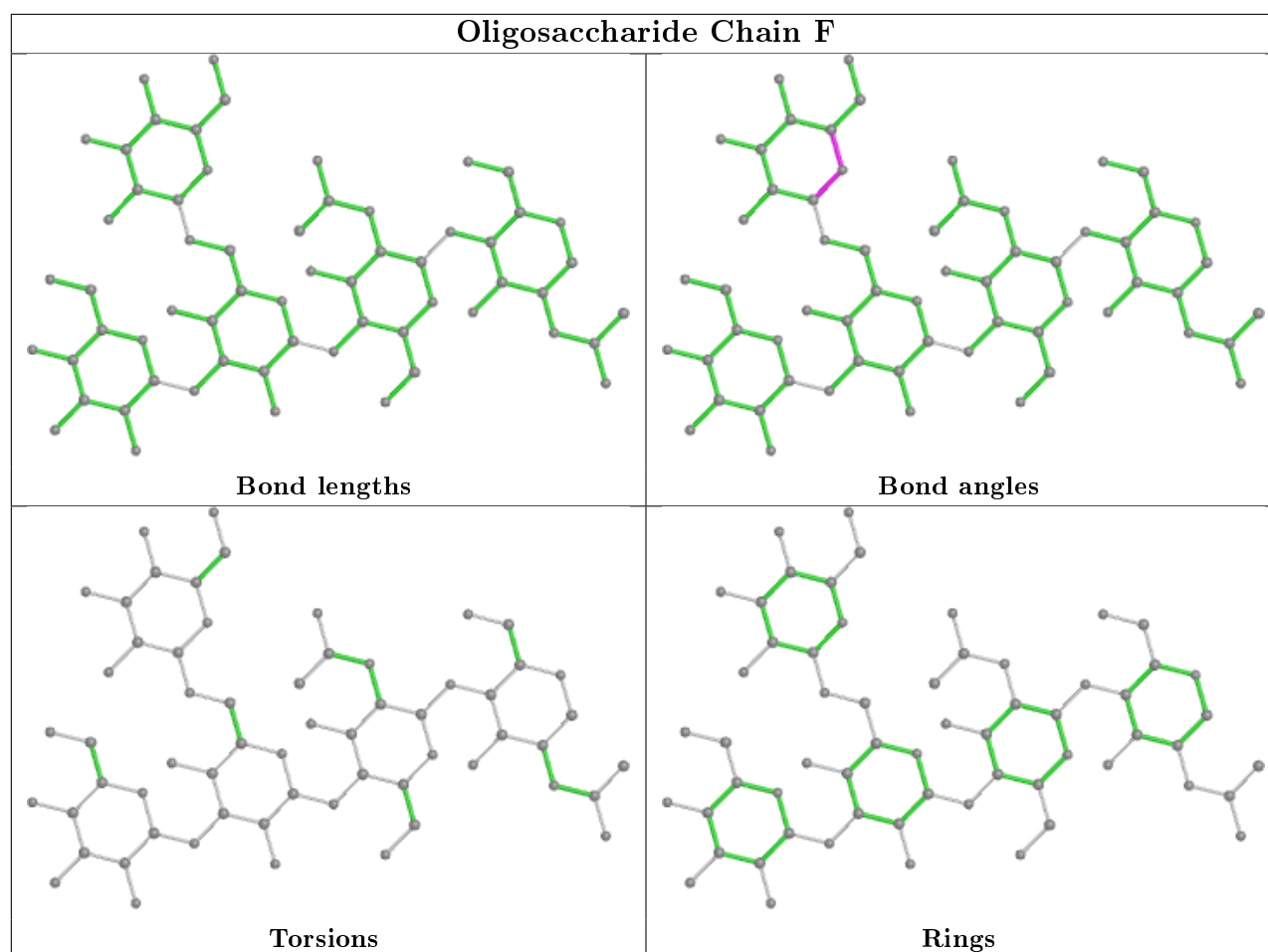
There are no torsion outliers.

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.





5.6 Ligand geometry [i](#)

Of 53 ligands modelled in this entry, 4 are monoatomic - leaving 49 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	$\# Z > 2$
9	OXM	C	1028	-	2,5,5	0.63	0	2,6,6	0.36	0
6	FMT	C	1017	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1007	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1017	-	0,2,2	0.00	-	0,1,1	0.00	-
5	EDO	A	1006	-	3,3,3	0.31	0	2,2,2	0.44	0
6	FMT	A	1008	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1012	-	0,2,2	0.00	-	0,1,1	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	5GF	C	1023	1	9,12,13	0.71	0	14,18,20	2.28	3 (21%)
6	FMT	C	1011	-	0,2,2	0.00	-	0,1,1	0.00	-
9	OXM	A	1024	-	2,5,5	0.41	0	2,6,6	0.50	0
5	EDO	A	1026	-	3,3,3	0.77	0	2,2,2	0.09	0
5	EDO	A	1005	-	3,3,3	0.54	0	2,2,2	0.22	0
6	FMT	A	1010	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1010	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1013	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1027	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1020	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1012	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1016	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1020	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1016	-	0,2,2	0.00	-	0,1,1	0.00	-
8	P6G	C	1024	-	13,13,18	0.25	0	12,12,17	0.40	0
6	FMT	A	1009	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1015	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1011	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1019	-	0,2,2	0.00	-	0,1,1	0.00	-
8	P6G	A	1028	-	13,13,18	0.28	0	12,12,17	0.36	0
7	5GF	A	1021	-	9,12,13	1.11	1 (11%)	14,18,20	2.17	6 (42%)
6	FMT	A	1014	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1022	-	0,2,2	0.00	-	0,1,1	0.00	-
5	EDO	C	1007	-	3,3,3	0.55	0	2,2,2	0.18	0
5	EDO	C	1008	-	3,3,3	0.63	0	2,2,2	0.43	0
9	OXM	C	1025	-	2,5,5	0.58	0	2,6,6	0.40	0
10	TAR	A	1025	-	3,9,9	0.29	0	6,12,12	0.69	0
6	FMT	C	1001	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1015	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1018	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1021	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	B	201	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	D	201	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1022	-	0,2,2	0.00	-	0,1,1	0.00	-
5	EDO	C	1009	-	3,3,3	0.89	0	2,2,2	0.37	0
6	FMT	A	1019	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	C	1014	-	0,2,2	0.00	-	0,1,1	0.00	-
6	FMT	A	1013	-	0,2,2	0.00	-	0,1,1	0.00	-
8	P6G	A	1023	-	10,10,18	0.37	0	9,9,17	0.62	0
6	FMT	C	1018	-	0,2,2	0.00	-	0,1,1	0.00	-
5	EDO	C	1026	-	3,3,3	0.53	0	2,2,2	0.41	0
8	P6G	C	1027	-	10,10,18	0.29	0	9,9,17	0.29	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
5	EDO	A	1026	-	-	0/1/1/1	-
9	OXM	C	1028	-	-	0/0/4/4	-
8	P6G	A	1028	-	-	5/11/11/16	-
5	EDO	C	1009	-	-	1/1/1/1	-
10	TAR	A	1025	-	-	4/4/12/12	-
7	5GF	A	1021	-	-	0/2/23/26	0/1/1/1
5	EDO	C	1007	-	-	0/1/1/1	-
5	EDO	C	1008	-	-	0/1/1/1	-
9	OXM	C	1025	-	-	0/0/4/4	-
5	EDO	A	1006	-	-	1/1/1/1	-
5	EDO	A	1005	-	-	1/1/1/1	-
8	P6G	C	1027	-	-	2/8/8/16	-
5	EDO	C	1026	-	-	1/1/1/1	-
7	5GF	C	1023	1	-	0/2/23/26	0/1/1/1
8	P6G	A	1023	-	-	4/8/8/16	-
8	P6G	C	1024	-	-	2/11/11/16	-
9	OXM	A	1024	-	-	0/0/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1021	5GF	O5-C5	2.69	1.43	1.37

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	1023	5GF	C1-O5-C5	6.16	125.41	113.73
7	A	1021	5GF	C1-O5-C5	5.63	124.40	113.73
7	C	1023	5GF	C1-C2-C3	3.14	113.53	109.67
7	C	1023	5GF	C6-C5-C4	2.89	117.41	112.02
7	A	1021	5GF	O5-C5-C4	-2.68	107.02	110.17
7	A	1021	5GF	O6-C6-C5	-2.45	103.43	111.66
7	A	1021	5GF	C6-C5-C4	2.22	116.17	112.02
7	A	1021	5GF	F-C5-C4	2.22	112.79	108.59
7	A	1021	5GF	C1-C2-C3	2.17	112.33	109.67

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	1025	TAR	C1-C2-C3-O3
10	A	1025	TAR	C1-C2-C3-C4
10	A	1025	TAR	O2-C2-C3-O3
10	A	1025	TAR	O2-C2-C3-C4
8	A	1028	P6G	O10-C11-C12-O13
8	A	1023	P6G	O10-C11-C12-O13
8	A	1023	P6G	O13-C14-C15-O16
5	A	1006	EDO	O1-C1-C2-O2
5	C	1026	EDO	O1-C1-C2-O2
8	C	1024	P6G	O7-C8-C9-O10
5	A	1005	EDO	O1-C1-C2-O2
8	A	1028	P6G	O4-C5-C6-O7
8	C	1024	P6G	C15-C14-O13-C12
8	C	1027	P6G	C12-C11-O10-C9
5	C	1009	EDO	O1-C1-C2-O2
8	A	1028	P6G	O13-C14-C15-O16
8	A	1023	P6G	C12-C11-O10-C9
8	A	1023	P6G	C18-C17-O16-C15
8	A	1028	P6G	C8-C9-O10-C11
8	C	1027	P6G	O16-C17-C18-O19
8	A	1028	P6G	C9-C8-O7-C6

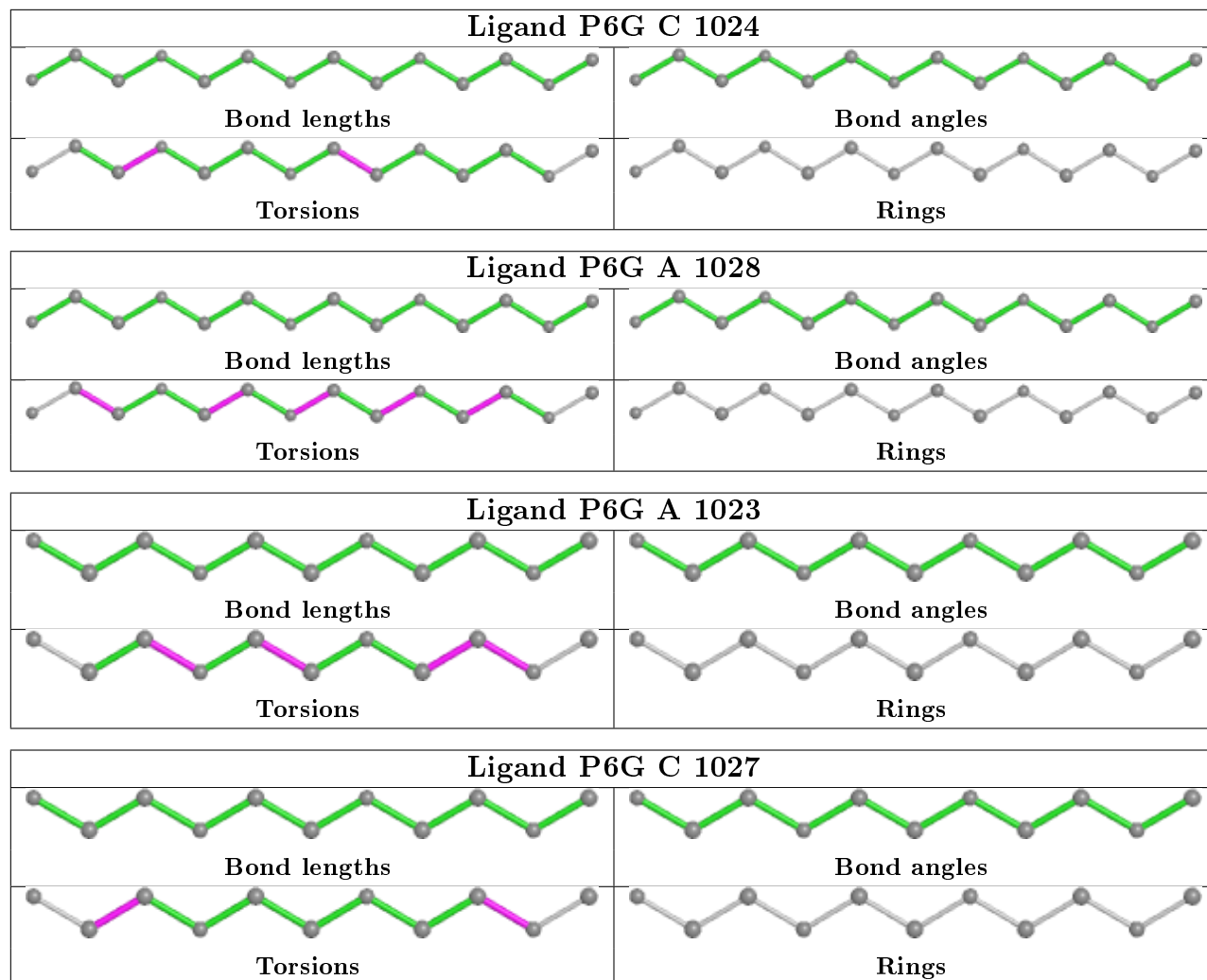
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1006	EDO	1	0
5	A	1005	EDO	1	0
5	C	1007	EDO	4	0
5	C	1009	EDO	2	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

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	855/857 (99%)	0.21	19 (2%) 62 60	37, 55, 100, 126	0
1	C	854/857 (99%)	0.07	5 (0%) 89 88	33, 50, 83, 103	0
2	B	83/83 (100%)	0.61	9 (10%) 5 5	43, 72, 114, 124	0
2	D	83/83 (100%)	0.11	4 (4%) 30 29	42, 68, 101, 122	0
All	All	1875/1880 (99%)	0.16	37 (1%) 65 63	33, 54, 95, 126	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	43	THR	7.7
2	B	81	GLY	5.5
2	D	80	THR	4.1
2	B	80	THR	3.9
1	A	72	ASP	3.8
2	B	36	PRO	3.6
1	C	814	TYR	3.6
1	A	86	LEU	3.4
2	B	82	TYR	3.3
1	A	294	GLU	3.0
1	A	82	VAL	2.9
1	A	83	THR	2.9
2	B	48	PHE	2.9
1	A	133	ARG	2.8
1	A	515	ARG	2.8
1	A	375	ILE	2.7
1	A	85	VAL	2.6
1	A	65	ASP	2.6
2	D	117	ARG	2.4
2	B	83	LYS	2.4
1	A	252	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	161	LEU	2.3
1	A	57	LEU	2.3
2	D	82	TYR	2.3
1	C	135	ASP	2.3
1	A	99	THR	2.3
2	B	116	CYS	2.2
1	C	74	LEU	2.2
1	C	173	ARG	2.2
2	D	48	PHE	2.2
1	A	168	LEU	2.2
1	A	156	PHE	2.1
2	B	84	PRO	2.1
1	A	927	LEU	2.1
1	A	329	PHE	2.1
1	A	158	LEU	2.0
1	C	350	ASN	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](#)

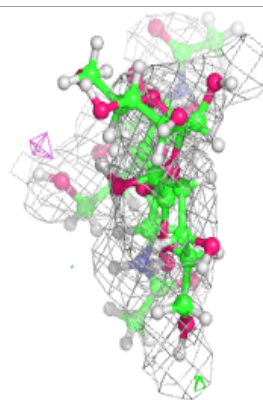
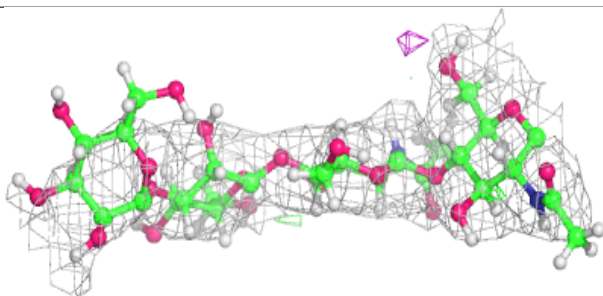
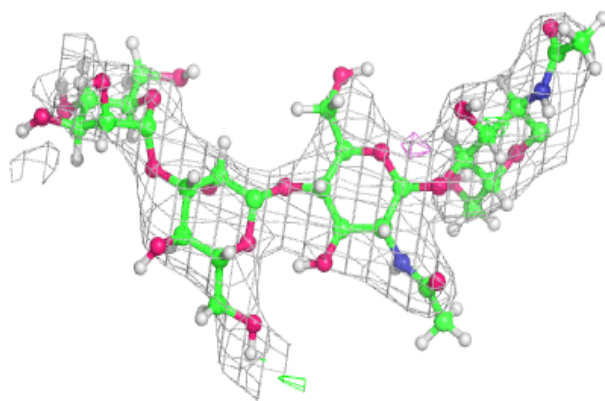
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MAN	F	5	11/12	0.62	0.28	114,118,120,121	0
3	MAN	E	4	11/12	0.70	0.28	129,133,134,134	0
4	MAN	F	4	11/12	0.75	0.16	117,120,121,122	0
3	BMA	E	3	11/12	0.78	0.14	114,118,120,125	0
4	BMA	F	3	11/12	0.84	0.12	101,111,115,117	0
3	NAG	E	2	14/15	0.92	0.17	84,96,99,107	0
3	NAG	E	1	14/15	0.94	0.18	66,72,79,80	0
4	NAG	F	2	14/15	0.95	0.14	67,72,82,92	0
4	NAG	F	1	14/15	0.96	0.16	46,53,60,64	0

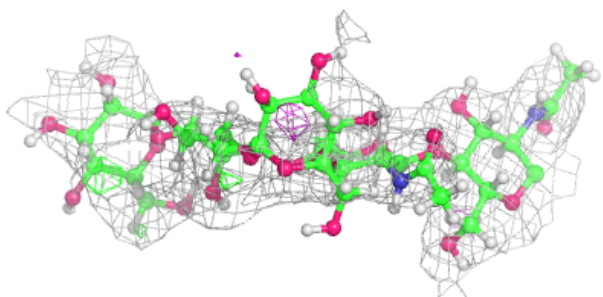
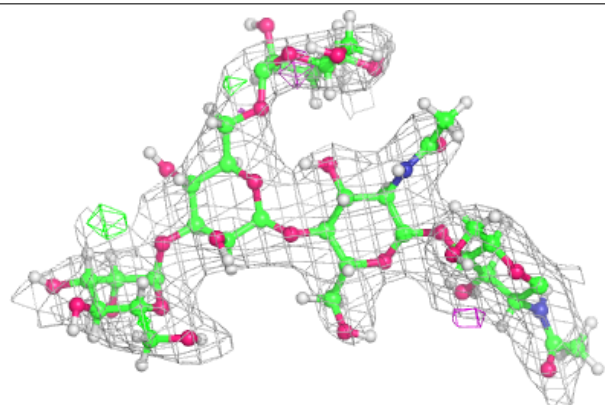
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain E:

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

**Electron density around Chain F:**

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



6.4 Ligands i

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.

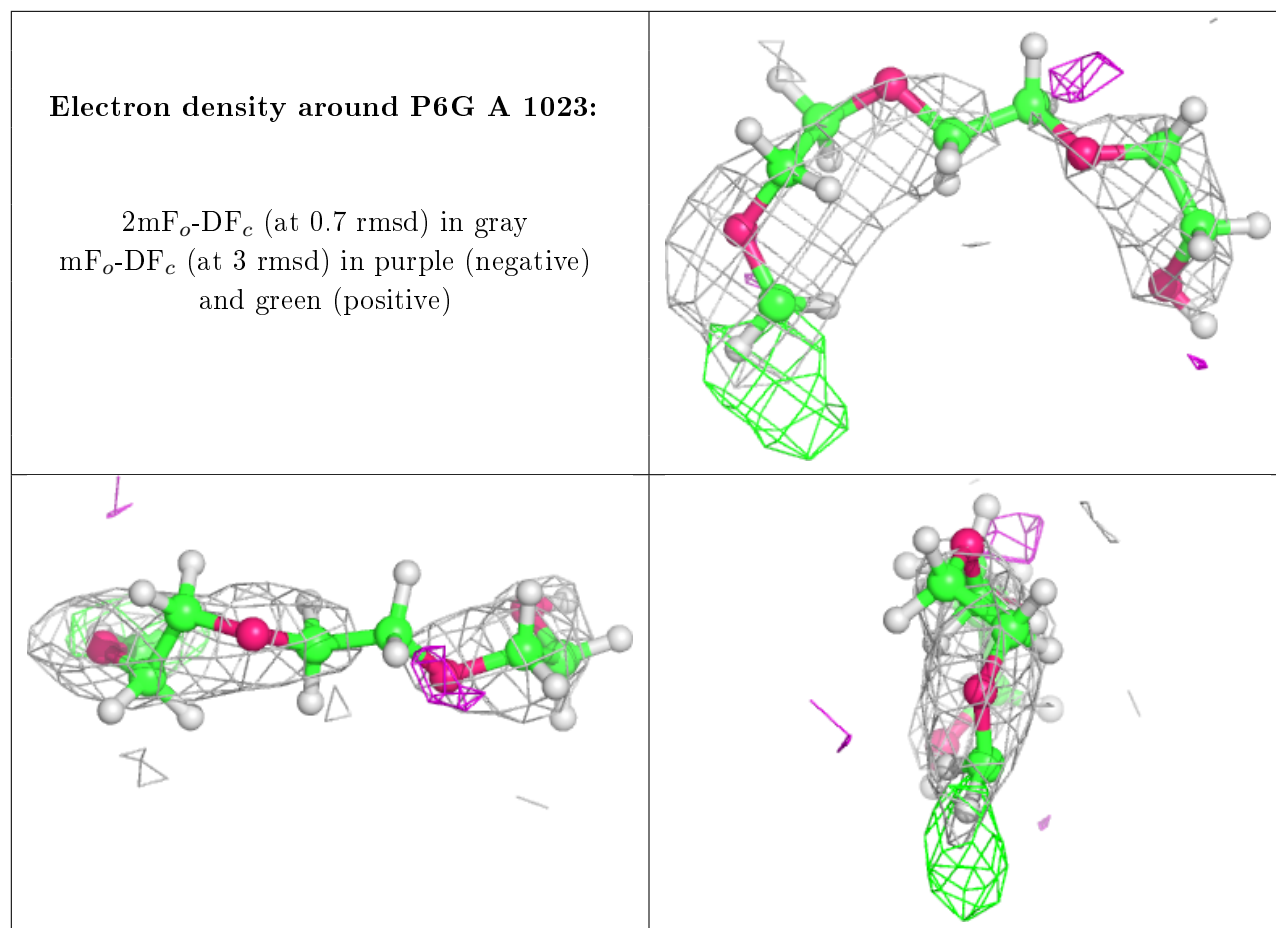
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	FMT	A	1019	3/3	0.43	0.45	78,80,80,80	0
6	FMT	A	1013	3/3	0.50	0.28	89,91,91,92	0
6	FMT	A	1014	3/3	0.56	0.54	78,79,85,87	0
6	FMT	C	1017	3/3	0.59	0.69	85,85,88,88	0
6	FMT	C	1018	3/3	0.60	0.59	88,88,89,89	0
8	P6G	A	1023	11/19	0.66	0.42	73,85,89,89	0
8	P6G	C	1024	14/19	0.67	0.64	85,103,114,114	0
6	FMT	A	1017	3/3	0.69	0.24	91,93,93,94	0
6	FMT	A	1012	3/3	0.71	0.47	106,107,108,109	0
6	FMT	A	1016	3/3	0.71	0.37	78,81,81,81	0
6	FMT	C	1016	3/3	0.72	0.32	77,78,78,78	0
6	FMT	C	1014	3/3	0.73	0.25	75,75,78,79	0
5	EDO	A	1006	4/4	0.73	0.47	59,68,70,70	0
9	OXM	A	1024	6/6	0.75	0.39	85,86,87,87	0
6	FMT	A	1009	3/3	0.75	0.22	81,82,85,86	0
10	TAR	A	1025	10/10	0.76	0.23	97,102,105,105	0
5	EDO	C	1009	4/4	0.76	0.33	47,51,59,60	0
9	OXM	C	1028	6/6	0.78	0.28	74,83,86,89	0
6	FMT	A	1011	3/3	0.78	0.28	89,89,90,90	0
6	FMT	B	201	3/3	0.79	0.22	75,75,76,76	0
6	FMT	C	1020	3/3	0.79	0.31	82,84,85,86	0
6	FMT	D	201	3/3	0.80	0.24	82,85,85,85	0
6	FMT	A	1008	3/3	0.81	0.24	73,73,74,74	0
5	EDO	C	1007	4/4	0.82	0.35	54,59,61,61	0
5	EDO	C	1008	4/4	0.82	0.28	79,82,90,90	0
6	FMT	A	1022	3/3	0.83	0.13	80,80,82,83	0
6	FMT	C	1015	3/3	0.83	0.19	79,79,79,80	0
9	OXM	C	1025	6/6	0.84	0.20	59,67,70,74	0
6	FMT	A	1027	3/3	0.84	0.98	91,91,95,96	0
6	FMT	C	1013	3/3	0.85	0.34	92,92,93,93	0
5	EDO	A	1005	4/4	0.85	0.62	65,68,71,72	0
6	FMT	C	1019	3/3	0.88	0.12	65,65,65,66	0
6	FMT	A	1020	3/3	0.88	0.18	68,68,74,76	0
6	FMT	C	1012	3/3	0.88	0.33	65,67,68,73	0
8	P6G	A	1028	14/19	0.89	0.18	61,66,82,82	0
6	FMT	A	1018	3/3	0.89	0.17	63,64,65,65	0

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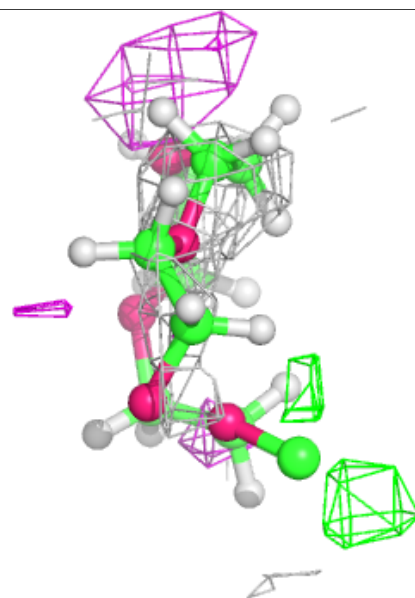
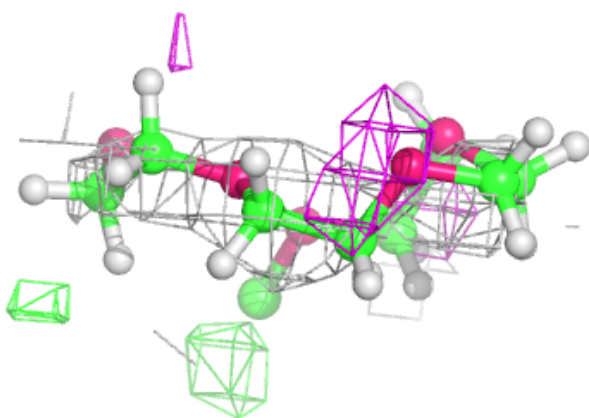
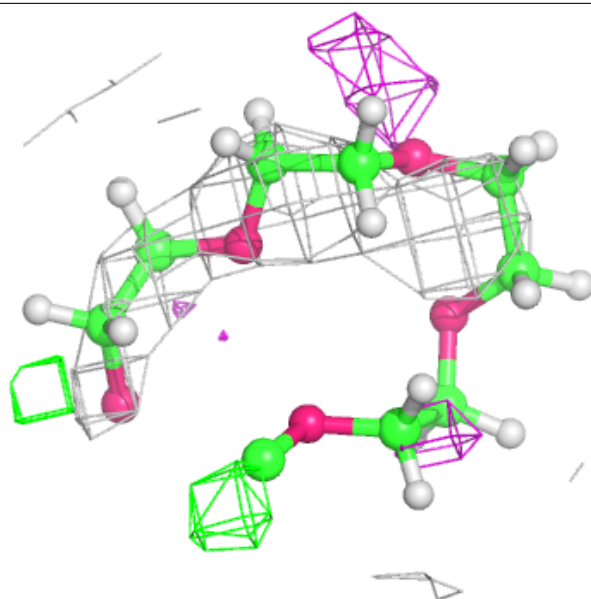
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	FMT	C	1022	3/3	0.90	0.25	69,70,75,79	0
6	FMT	C	1011	3/3	0.91	0.20	68,68,69,71	0
5	EDO	A	1026	4/4	0.91	0.16	61,63,69,69	0
8	P6G	C	1027	11/19	0.91	0.20	70,73,77,77	0
6	FMT	A	1010	3/3	0.92	0.14	63,66,71,71	0
6	FMT	A	1015	3/3	0.92	0.10	62,62,63,63	0
5	EDO	C	1026	4/4	0.94	0.14	64,64,67,67	0
6	FMT	C	1001	3/3	0.94	0.12	72,72,74,74	0
6	FMT	A	1007	3/3	0.96	0.17	74,75,75,76	0
6	FMT	C	1021	3/3	0.96	0.19	62,63,64,64	0
6	FMT	C	1010	3/3	0.96	0.14	47,49,53,54	0
7	5GF	A	1021	12/13	0.97	0.15	40,48,60,67	0
7	5GF	C	1023	12/13	0.97	0.12	40,48,54,55	0
11	CA	B	202	1/1	0.98	0.20	56,56,56,56	0
11	CA	B	203	1/1	0.98	0.18	47,47,47,47	0
11	CA	D	202	1/1	0.99	0.14	51,51,51,51	0
11	CA	D	203	1/1	0.99	0.16	44,44,44,44	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.



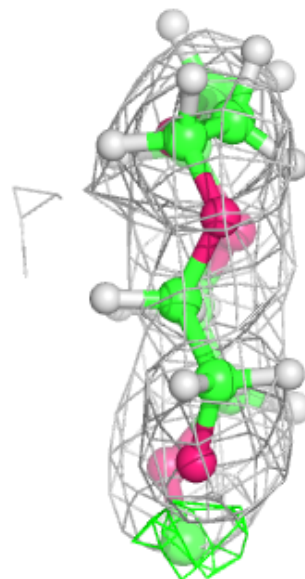
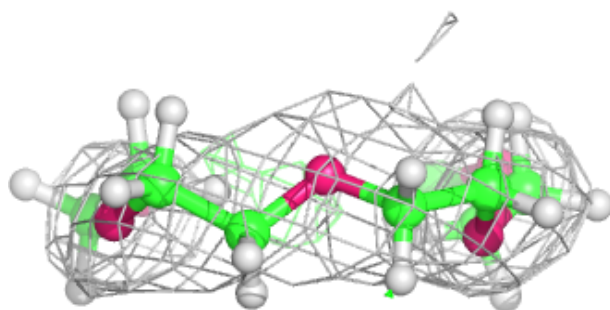
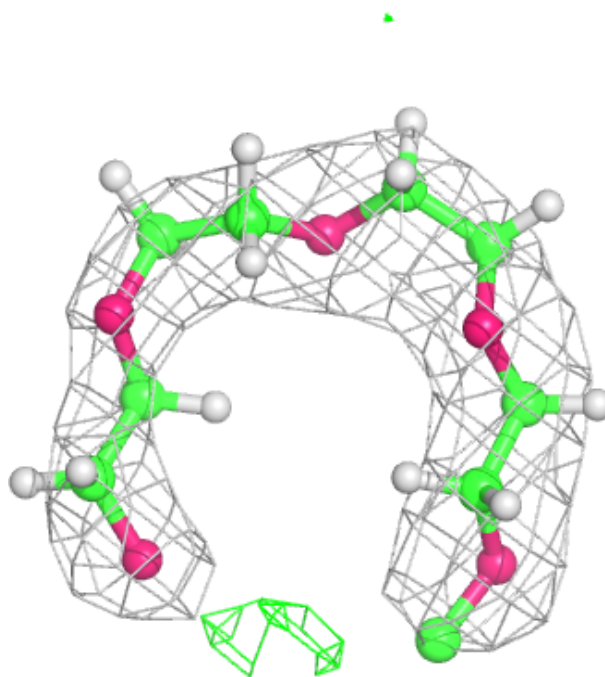
Electron density around P6G C 1024:

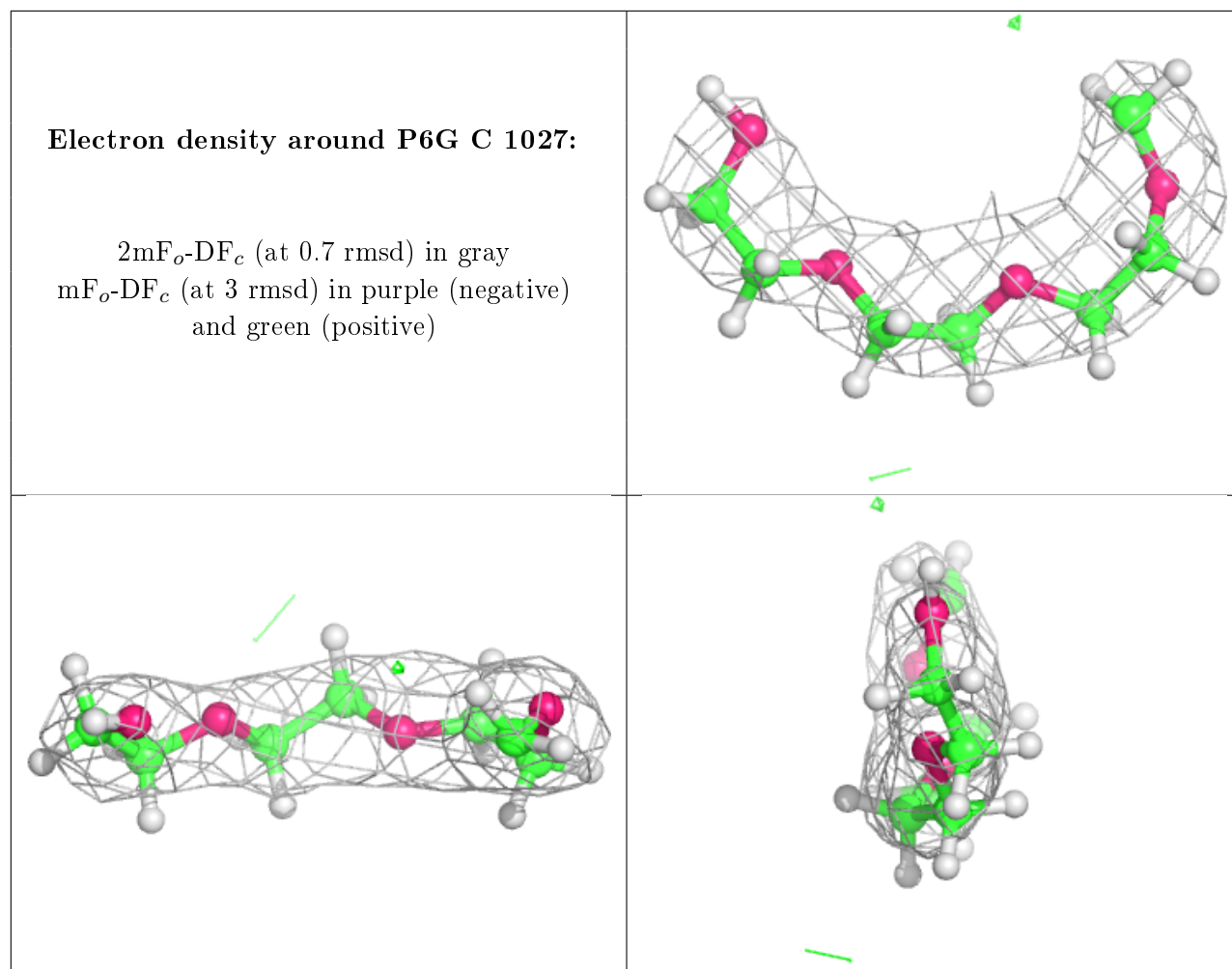
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around P6G A 1028:

$2mF_o-DF_c$ (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.