Full wwPDB X-ray Structure Validation Report (i)

Jan 27, 2022 – 09:16 pm GMT

PDB ID	:	7Q20
Title	:	Ruminococcus gnavus ATC29149 endo-beta-1,4-galactosidase (RgGH98) in complex with blood group A trisaccharide
Authors	:	Owen, C.D.; Wu, H.; Crost, E.H.; van Bakel, W.; Gascuena, A.M.; Latousakis, D.; Hicks, T.; Walpole, S.; Urbanowicz, P.A.; Ndeh, D.; Monaco, S.; Salom, L.S.; Griffiths, R.; Colvile, A.; Spencer, D.I.R.; Walsh, M.A.; Angulo, J.; Juge, N.
Deposited on	:	2021-10-22
Resolution	:	1.95 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

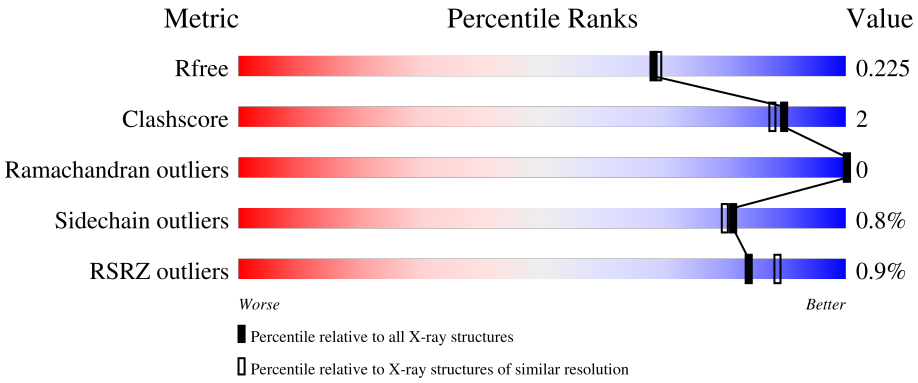
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.26
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

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 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 <=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	846	2% 96% .
1	G	846	95% .
2	E	3	67% 33%
2	H	3	100%

2 Entry composition (i)

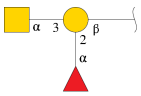
There are 6 unique types of molecules in this entry. The entry contains 14264 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Ruminococcus gnavus endogalactosidase GH98.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	845	Total	C	N	O	S	0	1	0
			6679	4220	1101	1333	25			
1	G	845	Total	C	N	O	S	0	0	0
			6672	4216	1100	1331	25			

- Molecule 2 is an oligosaccharide called alpha-L-fucopyranose-(1-2)-[2-acetamido-2-deoxy-alpha-D-galactopyranose-(1-3)]beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	H	3	Total	C	N	O	0	0	0
			36	20	1	15			
2	E	3	Total	C	N	O	0	0	0
			36	20	1	15			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Ca	0	0
			3	3		
3	G	1	Total	Ca	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

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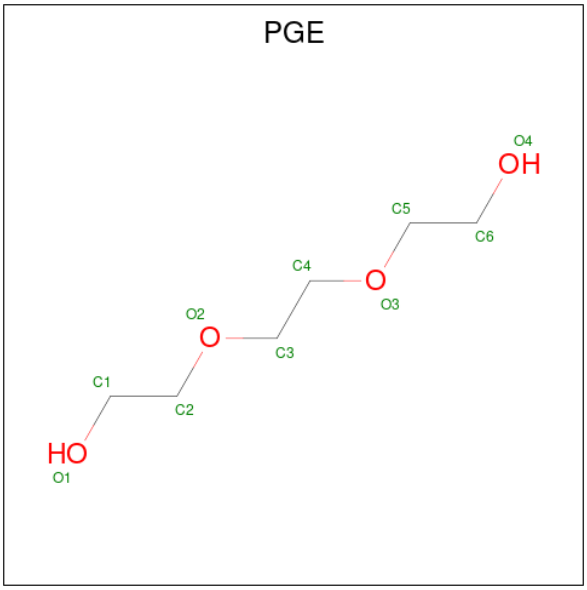
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	3	Total Mg 3 3	0	0

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	G	1	Total C O 10 6 4	0	0

- Molecule 6 is water.

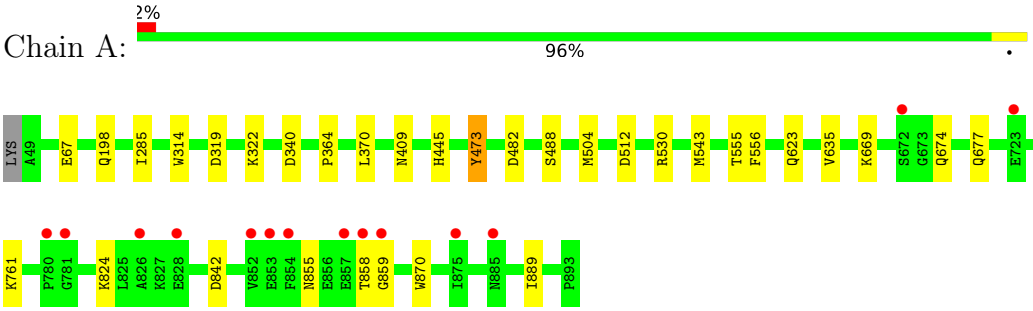
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	368	Total O 368 368	0	0
6	G	455	Total O 455 455	0	0

3 Residue-property plots (i)

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

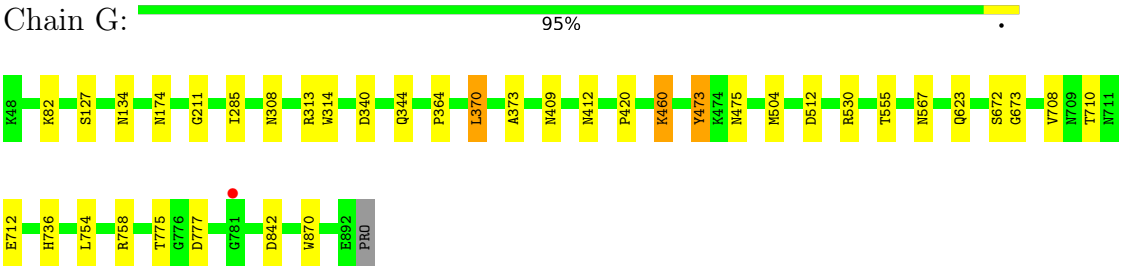
• Molecule 1: Ruminococcus gnavus endogalactosidase GH98

Chain A:



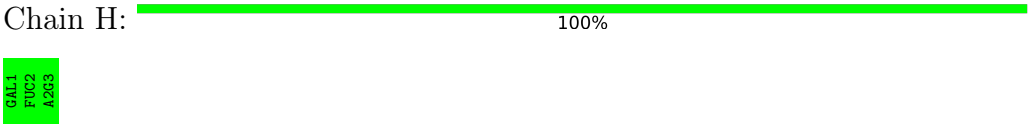
• Molecule 1: Ruminococcus gnavus endogalactosidase GH98

Chain G:



• Molecule 2: alpha-L-fucopyranose-(1-2)-[2-acetamido-2-deoxy-alpha-D-galactopyranose-(1-3)]beta-D-galactopyranose

Chain H:



• Molecule 2: alpha-L-fucopyranose-(1-2)-[2-acetamido-2-deoxy-alpha-D-galactopyranose-(1-3)]beta-D-galactopyranose

Chain E:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	107.59Å 86.95Å 110.20Å 90.00° 100.33° 90.00°	Depositor
Resolution (Å)	108.41 – 1.95 108.41 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.7 (108.41-1.95) 98.9 (108.41-1.95)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.30 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.185 , 0.219 0.192 , 0.225	Depositor DCC
R_{free} test set	7321 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	31.7	Xtriage
Anisotropy	0.448	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.017 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	14264	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GAL, A2G, MG, PGE, CA, FUC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.48	1/6841 (0.0%)	0.66	0/9292
1	G	0.51	1/6833 (0.0%)	0.66	0/9279
All	All	0.49	2/13674 (0.0%)	0.66	0/18571

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	842	ASP	CB-CG	6.29	1.65	1.51
1	G	842	ASP	CB-CG	5.67	1.63	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6679	0	6351	19	0
1	G	6672	0	6350	27	0
2	E	36	0	32	0	0
2	H	36	0	32	0	0
3	A	3	0	0	0	0
3	G	1	0	0	0	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	3	0	0	0	0
5	G	10	0	14	0	0
6	A	368	0	0	1	0
6	G	455	0	0	0	0
All	All	14264	0	12779	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:A:824:LYS:HG3	1:A:859:GLY:HA3	1.54	0.88
1:G:373:ALA:H	1:G:412:ASN:HD22	1.22	0.87
1:G:775:THR:OG1	1:G:777:ASP:OD1	2.05	0.74
1:G:475:ASN:HB3	1:G:623:GLN:HE21	1.53	0.74
1:G:736:HIS:HD2	1:G:758:ARG:HH11	1.36	0.73
1:G:708:VAL:O	1:G:736:HIS:HE1	1.81	0.63
1:A:445:HIS:HD2	1:A:482:ASP:OD2	1.84	0.61
1:A:824:LYS:CG	1:A:859:GLY:HA3	2.30	0.58
1:G:370:LEU:HD21	1:G:420:PRO:HA	1.87	0.57
1:G:308:ASN:ND2	1:G:567:ASN:H	2.01	0.57
1:G:82:LYS:NZ	1:G:134:ASN:HD21	2.04	0.55
1:A:512:ASP:HA	1:A:530:ARG:HB3	1.92	0.52
1:A:824:LYS:HG3	1:A:859:GLY:CA	2.33	0.50
1:A:319:ASP:OD1	1:A:322:LYS:HE2	2.11	0.50
1:G:512:ASP:HA	1:G:530:ARG:HB3	1.94	0.50
1:G:308:ASN:HD22	1:G:567:ASN:H	1.61	0.49
1:G:82:LYS:HZ2	1:G:134:ASN:HD21	1.61	0.49
1:G:736:HIS:CD2	1:G:758:ARG:HH11	2.23	0.49
1:G:285:ILE:HB	1:G:555:THR:HB	1.95	0.48
1:G:373:ALA:H	1:G:412:ASN:ND2	2.01	0.48
1:A:314:TRP:CH2	1:A:364:PRO:HD2	2.50	0.46
1:A:285:ILE:HB	1:A:555:THR:HB	1.96	0.46
1:A:889:ILE:HD12	1:A:889:ILE:N	2.30	0.46
1:A:488:SER:HB3	1:A:635:VAL:HG23	1.98	0.45
1:G:754:LEU:HD12	1:G:754:LEU:C	2.37	0.45
1:G:127:SER:OG	1:G:174:ASN:ND2	2.50	0.45
1:G:708:VAL:O	1:G:736:HIS:CE1	2.68	0.45
1:A:677:GLN:HE21	1:A:677:GLN:HB3	1.65	0.45
1:G:314:TRP:CH2	1:G:364:PRO:HD2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:710:THR:HG22	1:G:712:GLU:HG3	1.99	0.43
1:G:373:ALA:N	1:G:412:ASN:HD22	2.02	0.43
1:A:543:MET:HG3	1:A:556:PHE:HZ	1.82	0.43
1:A:754:LEU:O	1:A:870:TRP:HA	2.19	0.43
1:G:409:ASN:OD1	1:G:409:ASN:C	2.57	0.43
1:G:211:GLY:CA	1:G:344:GLN:HE22	2.32	0.43
1:A:754:LEU:C	1:A:754:LEU:HD12	2.38	0.42
1:G:473:TYR:CZ	1:G:504:MET:HB2	2.54	0.42
1:G:460:LYS:HE3	1:G:460:LYS:HA	2.01	0.42
1:A:761:LYS:NZ	6:A:1011:HOH:O	2.48	0.42
1:G:308:ASN:ND2	1:G:313:ARG:HH11	2.17	0.42
1:A:473:TYR:CZ	1:A:504:MET:HB2	2.55	0.42
1:A:409:ASN:OD1	1:A:409:ASN:C	2.57	0.42
1:G:754:LEU:O	1:G:870:TRP:HA	2.20	0.41
1:G:672:SER:O	1:G:673:GLY:C	2.60	0.40
1:A:855:ASN:O	1:A:858:THR:O	2.39	0.40
1:A:543:MET:CG	1:A:556:PHE:HZ	2.35	0.40

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	844/846 (100%)	826 (98%)	18 (2%)	0	100	100
1	G	843/846 (100%)	825 (98%)	18 (2%)	0	100	100
All	All	1687/1692 (100%)	1651 (98%)	36 (2%)	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	713/713 (100%)	705 (99%)	8 (1%)	73	71
1	G	712/713 (100%)	708 (99%)	4 (1%)	86	85
All	All	1425/1426 (100%)	1413 (99%)	12 (1%)	81	80

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	GLU
1	A	198	GLN
1	A	340	ASP
1	A	370	LEU
1	A	473	TYR
1	A	623	GLN
1	A	669	LYS
1	A	674	GLN
1	G	340	ASP
1	G	370	LEU
1	G	460	LYS
1	G	473	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	ASN
1	A	86	GLN
1	A	100	ASN
1	A	198	GLN
1	A	315	ASN
1	A	445	HIS
1	A	677	GLN
1	A	802	ASN
1	G	68	ASN
1	G	134	ASN

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Mol	Chain	Res	Type
1	G	174	ASN
1	G	268	GLN
1	G	305	GLN
1	G	308	ASN
1	G	315	ASN
1	G	333	ASN
1	G	344	GLN
1	G	412	ASN
1	G	526	ASN
1	G	623	GLN
1	G	736	HIS
1	G	786	ASN

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)

6 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	GAL	E	1	2	12,12,12	0.57	0	17,17,17	0.75	0
2	FUC	E	2	2	10,10,11	0.53	0	14,14,16	0.62	0
2	A2G	E	3	2	14,14,15	0.38	0	17,19,21	0.66	1 (5%)
2	GAL	H	1	2	12,12,12	0.46	0	17,17,17	0.61	0
2	FUC	H	2	2	10,10,11	0.40	0	14,14,16	0.51	0
2	A2G	H	3	2	14,14,15	0.43	0	17,19,21	0.44	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
2	GAL	E	1	2	-	0/2/22/22	0/1/1/1
2	FUC	E	2	2	-	-	0/1/1/1
2	A2G	E	3	2	-	0/6/23/26	0/1/1/1
2	GAL	H	1	2	-	0/2/22/22	0/1/1/1
2	FUC	H	2	2	-	-	0/1/1/1
2	A2G	H	3	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	3	A2G	O5-C1-C2	-2.24	107.76	111.29

There are no chirality outliers.

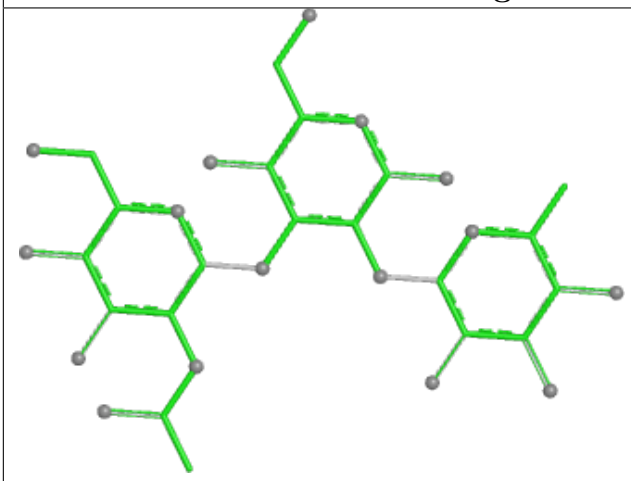
There are no torsion outliers.

There are no ring outliers.

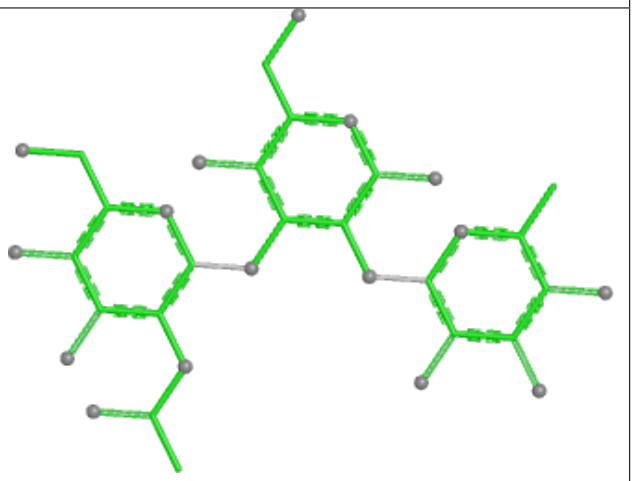
No monomer is involved in short contacts.

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

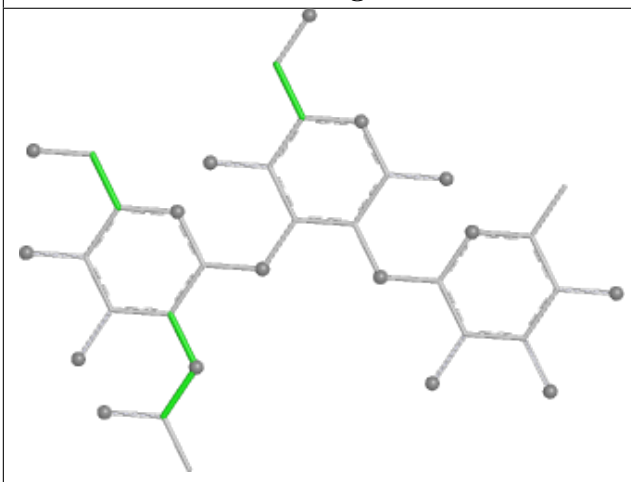
Oligosaccharide Chain H



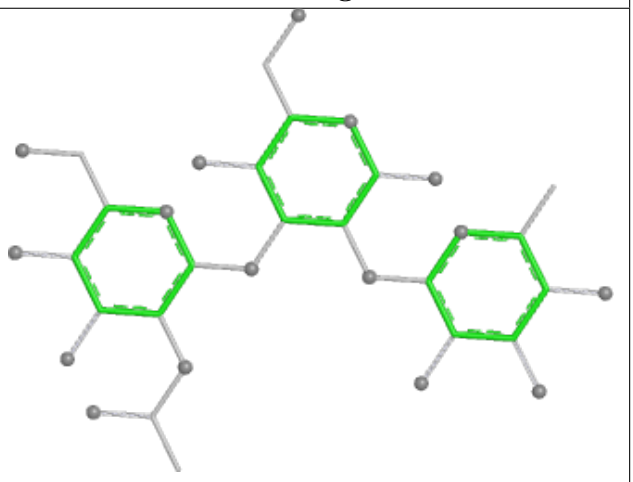
Bond lengths



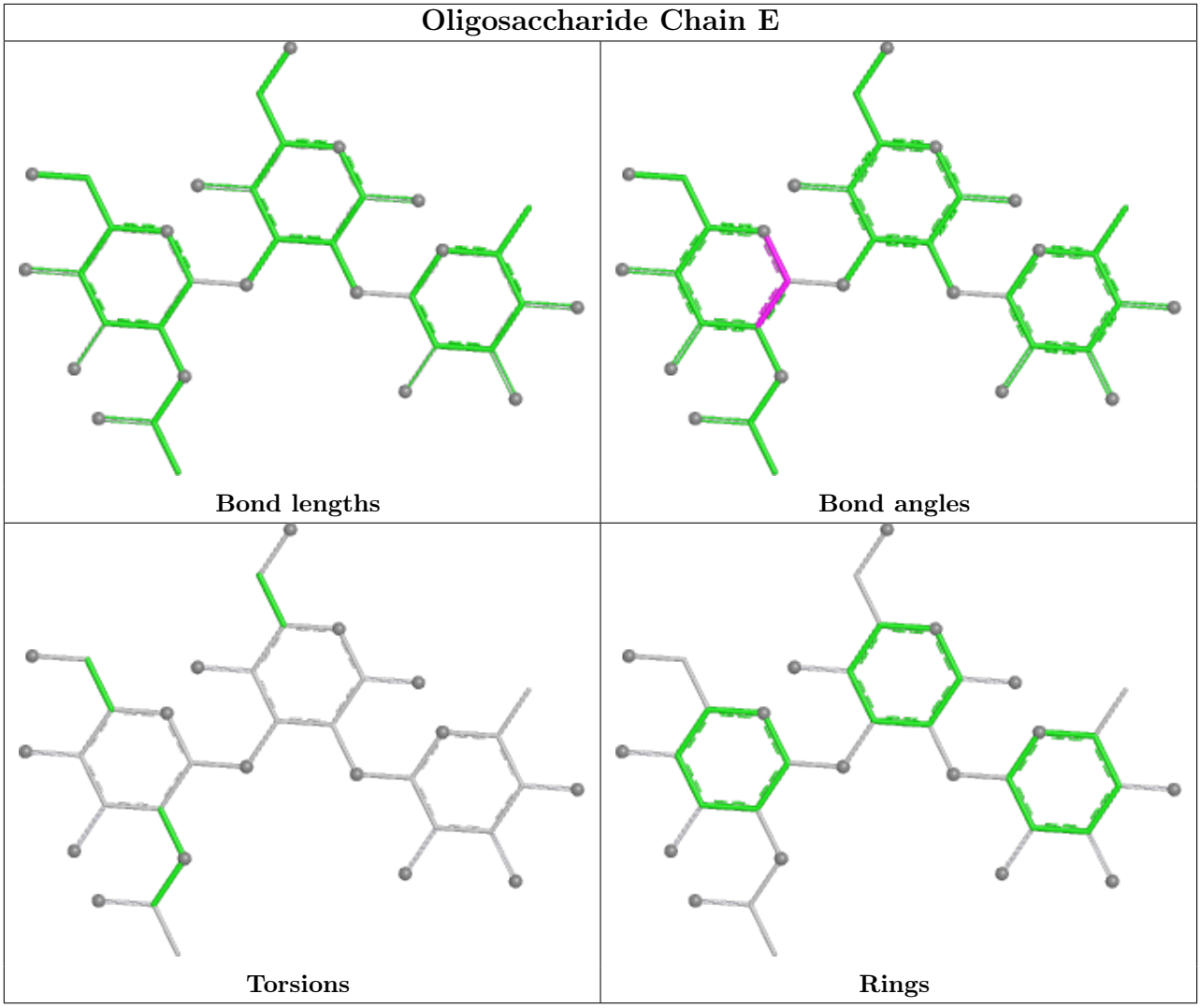
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 8 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
5	PGE	G	901	-	9,9,9	0.22	0	8,8,8	0.09	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	PGE	G	901	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	901	PGE	O2-C3-C4-O3
5	G	901	PGE	O1-C1-C2-O2
5	G	901	PGE	C3-C4-O3-C5
5	G	901	PGE	C4-C3-O2-C2
5	G	901	PGE	O3-C5-C6-O4

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95^{th} 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	845/846 (99%)	-0.02	15 (1%) 68 76	28, 43, 74, 105	0
1	G	845/846 (99%)	-0.12	1 (0%) 95 97	22, 37, 63, 85	0
All	All	1690/1692 (99%)	-0.07	16 (0%) 84 89	22, 40, 70, 105	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	854	PHE	5.0
1	A	826	ALA	4.2
1	A	781	GLY	3.3
1	G	781	GLY	2.9
1	A	723	GLU	2.7
1	A	859	GLY	2.7
1	A	857	GLU	2.7
1	A	875	ILE	2.4
1	A	828	GLU	2.3
1	A	780	PRO	2.2
1	A	852	VAL	2.2
1	A	885	ASN	2.1
1	A	745	GLY	2.1
1	A	853	GLU	2.1
1	A	858	THR	2.0
1	A	672	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates (i)

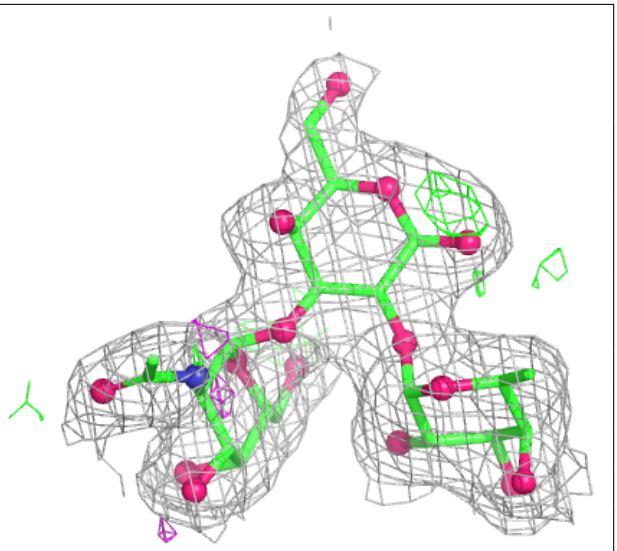
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

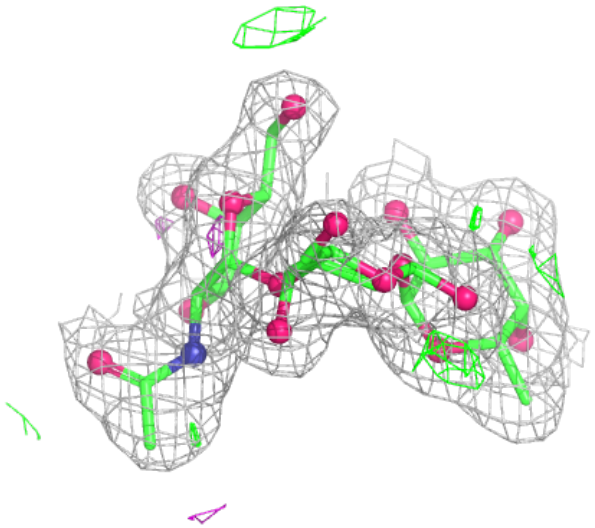
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GAL	H	1	12/12	0.91	0.12	40,43,51,53	0
2	FUC	E	2	10/11	0.92	0.09	30,33,36,37	0
2	A2G	H	3	14/15	0.94	0.10	32,41,45,47	0
2	GAL	E	1	12/12	0.94	0.08	33,38,41,41	0
2	FUC	H	2	10/11	0.94	0.10	35,35,36,38	0
2	A2G	E	3	14/15	0.96	0.09	28,34,39,43	0

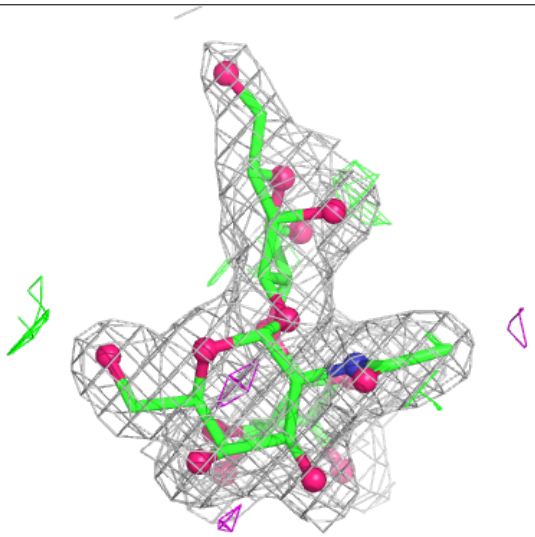
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain H:

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

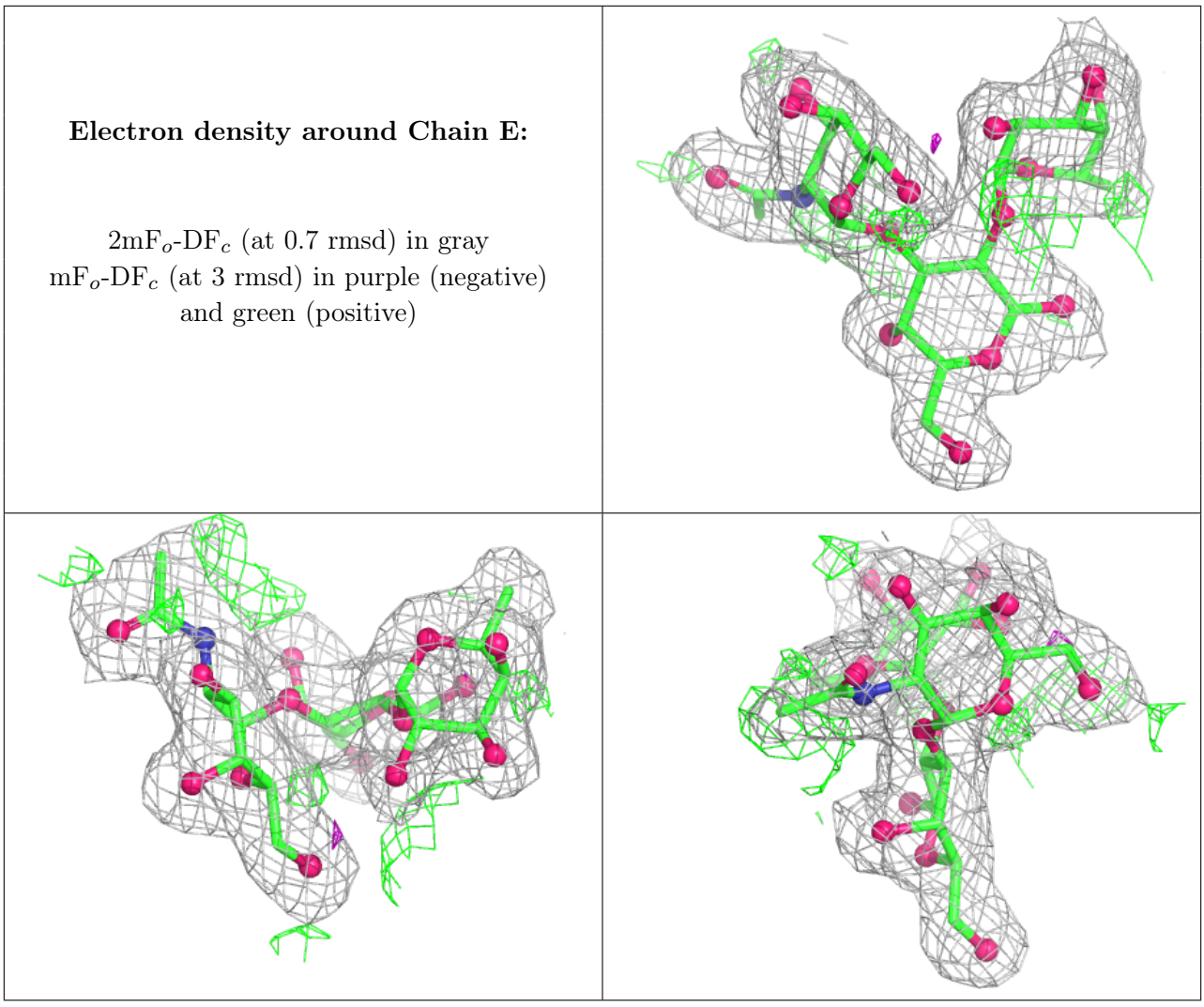






Electron density around Chain E:

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



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, 95^{th} 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
5	PGE	G	901	10/10	0.58	0.16	70,76,79,81	0
3	CA	A	901	1/1	0.88	0.08	56,56,56,56	0
3	CA	A	903	1/1	0.91	0.16	58,58,58,58	0
4	MG	G	905	1/1	0.92	0.15	38,38,38,38	0
4	MG	A	904	1/1	0.93	0.06	54,54,54,54	0
4	MG	G	903	1/1	0.94	0.07	31,31,31,31	0
4	MG	G	904	1/1	0.95	0.16	30,30,30,30	0
3	CA	G	902	1/1	0.96	0.09	34,34,34,34	0
3	CA	A	902	1/1	0.97	0.08	32,32,32,32	0

6.5 Other polymers (i)

There are no such residues in this entry.