Full wwPDB X-ray Structure Validation Report ⓘ

Aug 16, 2020 – 06:58 PM BST

PDB ID	:	6ZJT
Title	:	Cold-adapted beta-D-galactosidase from Arthrobacter sp. 32cB mutant E441Q in complex with lactulose
Authors	:	Rutkiewicz, M.; Bujacz, A.; Bujacz, G.
Deposited on	:	2020-06-29
Resolution	:	1.97 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:

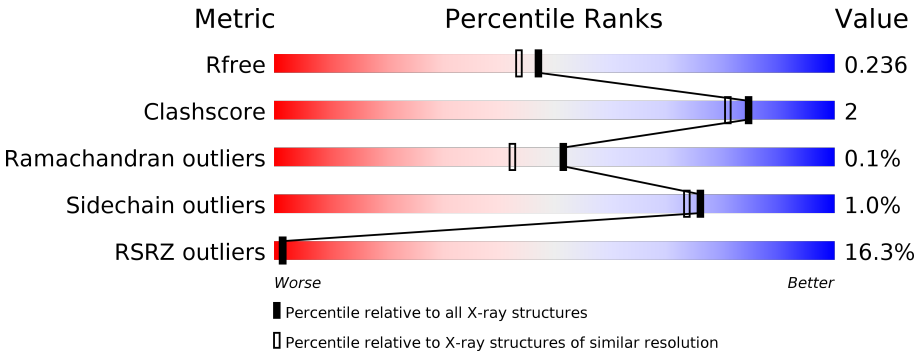
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh &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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.97 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	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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 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 <=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	1010	16%, 93%
2	B	2	50%, 50%
2	C	2	50%, 50%

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
2	FRU	C	1	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8032 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.

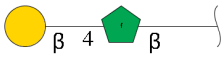
- Molecule 1 is a protein called Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	989	Total	C	N	O	S	0	1	0
			7615	4791	1361	1444	19			

There is a discrepancy between the modelled and reference sequences:

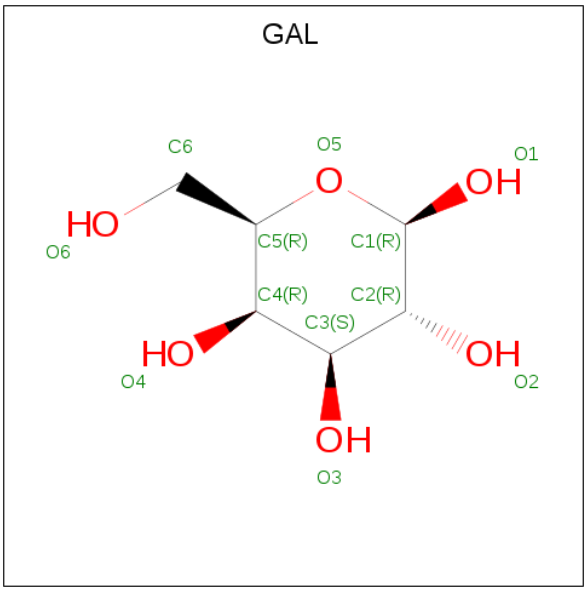
Chain	Residue	Modelled	Actual	Comment	Reference
A	441	GLN	GLU	engineered mutation	UNP A0A023UGN9

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-4)-beta-D-fructofuranose.



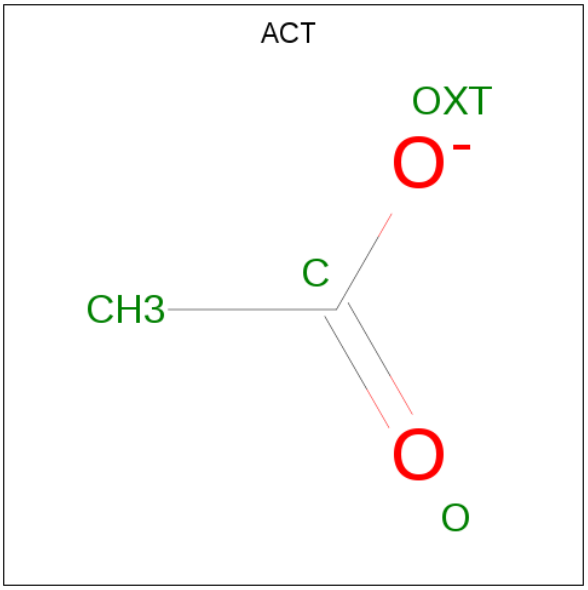
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	O		0	0	0
			23	12	11				
2	C	2	Total	C	O		0	0	0
			23	12	11				

- Molecule 3 is beta-D-galactopyranose (three-letter code: GAL) (formula: $C_6H_{12}O_6$) (labeled as "Ligand of Interest" by author).



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

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	2	Total Na 2 2	0	0

- Molecule 6 is water.

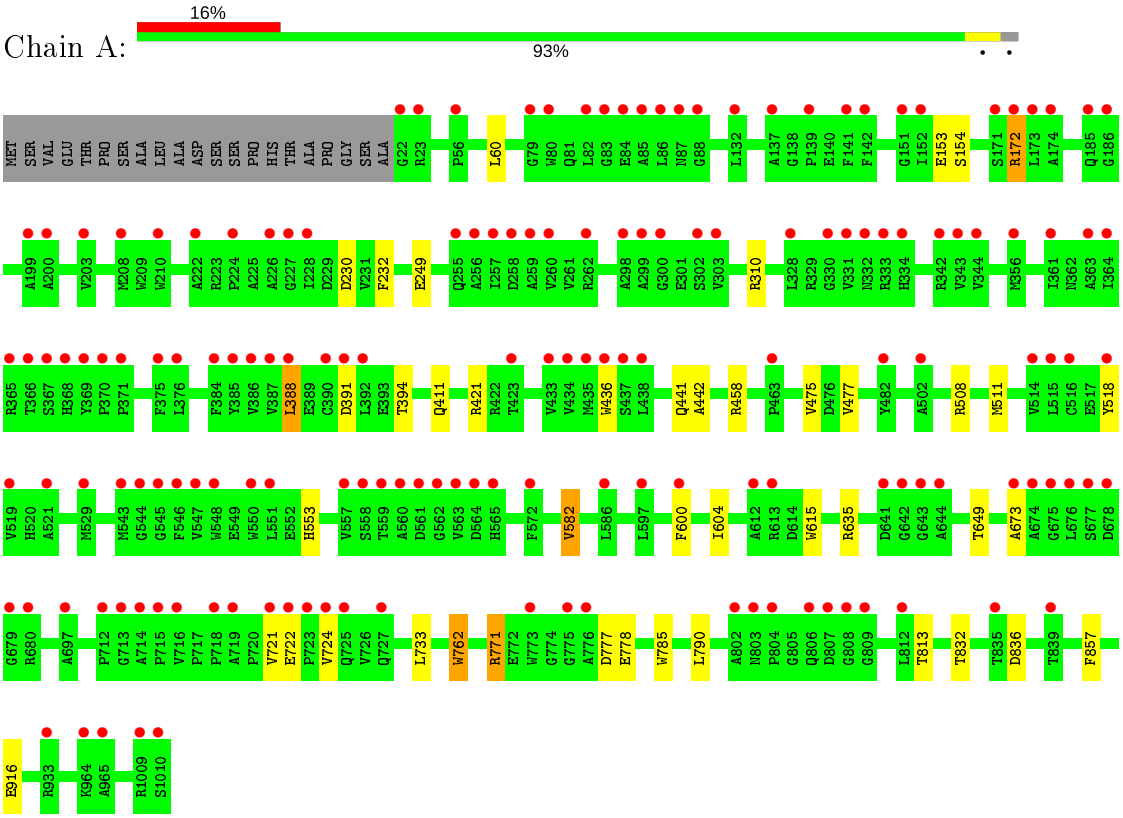
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	337	Total O 337 337	0	0

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: Beta-galactosidase

Chain A:



- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-fructofuranose

Chain B:

- Molecule 2: beta-D-galactopyranose-(1-4)-beta-D-fructofuranose

Chain C:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	138.97Å 138.97Å 127.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.79 – 1.97 47.02 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.79-1.97) 99.7 (47.02-1.97)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.10 (at 1.97Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.195 , 0.226 0.210 , 0.236	Depositor DCC
R_{free} test set	2099 reflections (2.09%)	wwPDB-VP
Wilson B-factor (Å^2)	44.4	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 52.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8032	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.08% 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: NA, GAL, FRU, ACT

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	0/7814	0.61	0/10652

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7615	0	7307	33	0
2	B	23	0	21	1	0
2	C	23	0	21	5	0
3	A	24	0	24	0	0
4	A	8	0	6	0	0
5	A	2	0	0	0	0
6	A	337	0	0	3	0
All	All	8032	0	7379	35	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 (35) 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:724:VAL:HG22	1:A:733:LEU:HD13	1.42	0.97
6:A:1459:HOH:O	2:C:1:FRU:H62	1.70	0.91
1:A:458:ARG:HH12	2:C:2:GAL:H3	1.51	0.74
1:A:724:VAL:CG2	1:A:733:LEU:HD13	2.17	0.73
1:A:635:ARG:HD3	1:A:649:THR:HG22	1.73	0.69
1:A:553:HIS:HB2	1:A:582:VAL:HG22	1.75	0.69
1:A:721:VAL:CG2	1:A:836:ASP:HA	2.32	0.59
1:A:771:ARG:HG3	1:A:778:GLU:O	2.02	0.59
1:A:230:ASP:OD2	2:C:2:GAL:H62	2.07	0.55
2:C:1:FRU:H5	2:C:2:GAL:O2	2.08	0.53
1:A:172:ARG:HD2	1:A:391:ASP:OD2	2.09	0.51
1:A:721:VAL:HG22	1:A:836:ASP:HA	1.95	0.48
1:A:600:PHE:O	1:A:604:ILE:HG12	2.15	0.47
1:A:60:LEU:N	1:A:60:LEU:HD12	2.30	0.47
1:A:421:ARG:NH2	6:A:1212:HOH:O	2.45	0.47
1:A:508:ARG:HA	1:A:511[A]:MET:SD	2.55	0.46
1:A:721:VAL:HG23	1:A:836:ASP:HA	1.97	0.46
1:A:172:ARG:HD2	1:A:172:ARG:N	2.31	0.45
1:A:249:GLU:OE1	2:C:2:GAL:O3	2.34	0.45
1:A:777:ASP:HB2	1:A:857:PHE:CE1	2.50	0.45
1:A:441:GLN:OE1	2:B:2:GAL:H2	2.16	0.45
1:A:813:THR:OG1	1:A:832:THR:HG22	2.16	0.45
1:A:411:GLN:NE2	6:A:1204:HOH:O	2.35	0.45
1:A:477:VAL:C	1:A:511[A]:MET:HE2	2.37	0.45
1:A:553:HIS:CB	1:A:582:VAL:HG22	2.45	0.44
1:A:394:THR:OG1	1:A:442:ALA:HA	2.18	0.44
1:A:475:VAL:HG23	1:A:511[A]:MET:HE3	1.99	0.43
1:A:777:ASP:HB2	1:A:857:PHE:CD1	2.53	0.43
1:A:388:LEU:HD22	1:A:436:TRP:HZ3	1.83	0.43
1:A:153:GLU:HA	1:A:154:SER:HA	1.73	0.43
1:A:785:TRP:CD1	1:A:790:LEU:HD22	2.54	0.43
1:A:553:HIS:CG	1:A:582:VAL:HG22	2.55	0.42
1:A:553:HIS:HB2	1:A:582:VAL:CG2	2.48	0.42
1:A:615:TRP:CE3	1:A:673:ALA:HB2	2.55	0.41
1:A:762:TRP:CD2	1:A:916:GLU:HG2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	988/1010 (98%)	958 (97%)	29 (3%)	1 (0%)	51 42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	722	GLU

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	777/793 (98%)	769 (99%)	8 (1%)	76 73

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	172	ARG
1	A	232	PHE
1	A	310	ARG
1	A	388	LEU
1	A	518	TYR
1	A	582	VAL
1	A	762	TRP
1	A	771	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	121	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)

4 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	FRU	B	1	2	11,12,12	0.44	0	10,18,18	0.51	0
2	GAL	B	2	2	11,11,12	0.59	0	15,15,17	1.63	1 (6%)
2	FRU	C	1	2	11,12,12	0.53	0	10,18,18	0.50	0
2	GAL	C	2	2	11,11,12	0.72	0	15,15,17	0.97	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FRU	B	1	2	-	0/5/24/24	0/1/1/1
2	GAL	B	2	2	-	1/2/19/22	0/1/1/1
2	FRU	C	1	2	-	0/5/24/24	0/1/1/1
2	GAL	C	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2	GAL	C1-O5-C5	5.92	120.22	112.19
2	C	2	GAL	C1-O5-C5	-2.50	108.81	112.19

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	GAL	O5-C5-C6-O6

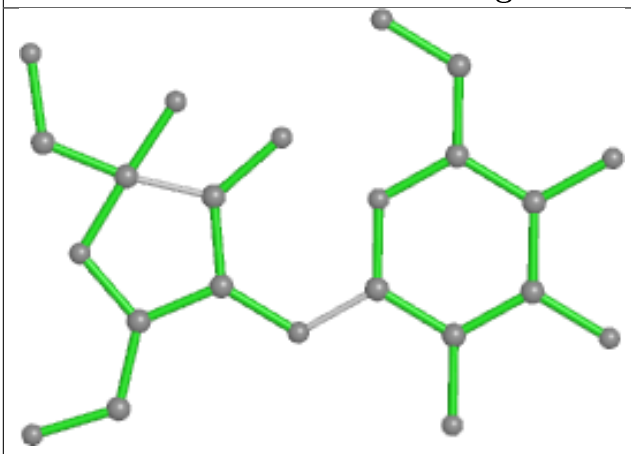
There are no ring outliers.

3 monomers are involved in 6 short contacts:

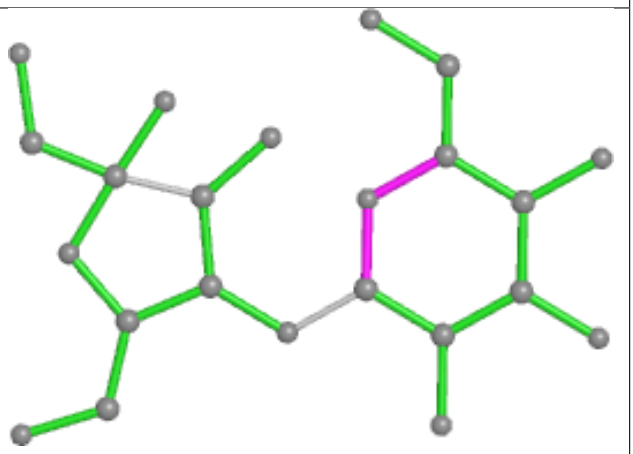
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	GAL	4	0
2	C	1	FRU	2	0
2	B	2	GAL	1	0

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

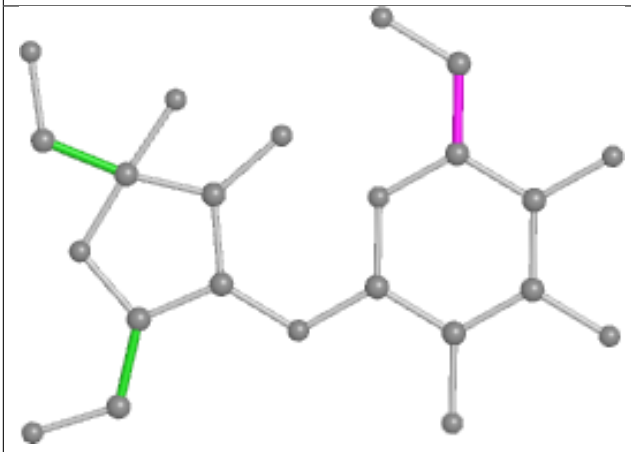
Oligosaccharide Chain B



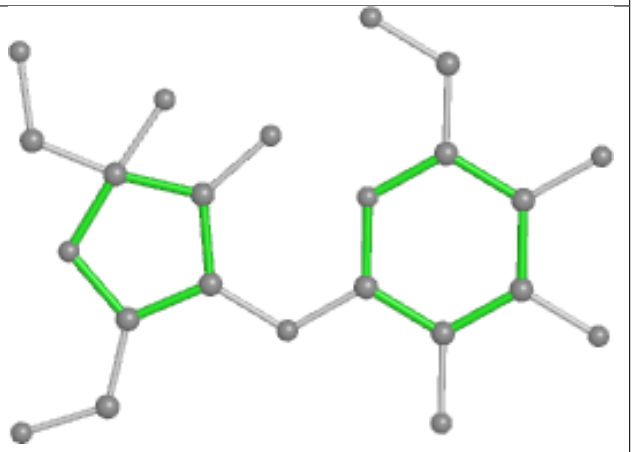
Bond lengths



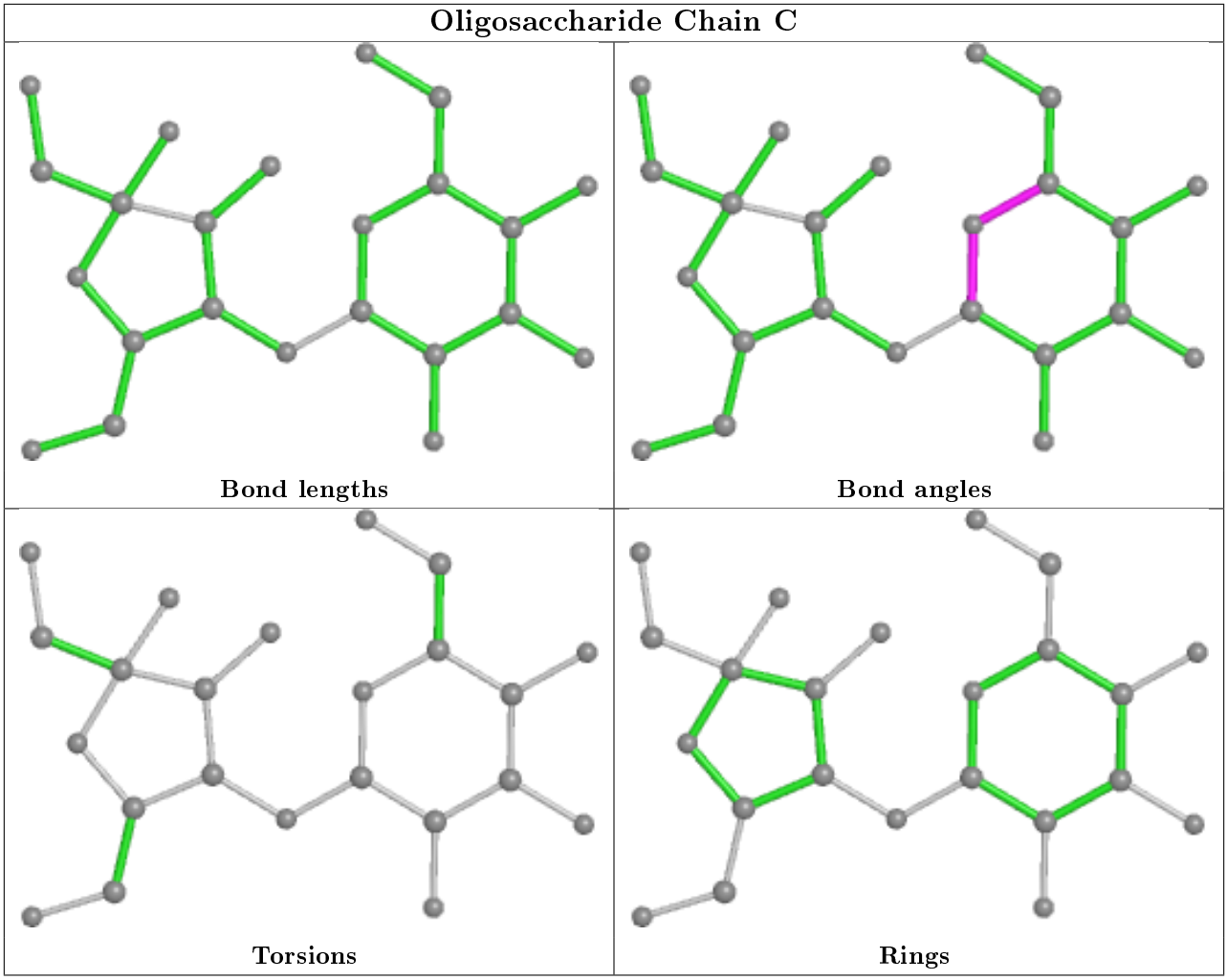
Bond angles



Torsions



Rings



5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
4	ACT	A	1105	-	1,3,3	7.33	1 (100%)	0,3,3	0.00	-
3	GAL	A	1104	-	12,12,12	0.91	0	17,17,17	0.92	1 (5%)
4	ACT	A	1106	-	1,3,3	7.71	1 (100%)	0,3,3	0.00	-
3	GAL	A	1103	-	12,12,12	0.63	0	17,17,17	1.74	3 (17%)

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	GAL	A	1104	-	-	0/2/22/22	0/1/1/1
3	GAL	A	1103	-	-	2/2/22/22	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1106	ACT	CH3-C	7.71	1.58	1.48
4	A	1105	ACT	CH3-C	7.33	1.58	1.48

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1103	GAL	O3-C3-C2	-3.81	101.54	110.35
3	A	1103	GAL	C4-C3-C2	3.73	117.33	110.82
3	A	1104	GAL	O5-C5-C4	2.46	114.15	109.69
3	A	1103	GAL	C3-C4-C5	2.43	114.57	110.24

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1103	GAL	O5-C5-C6-O6
3	A	1103	GAL	C4-C5-C6-O6

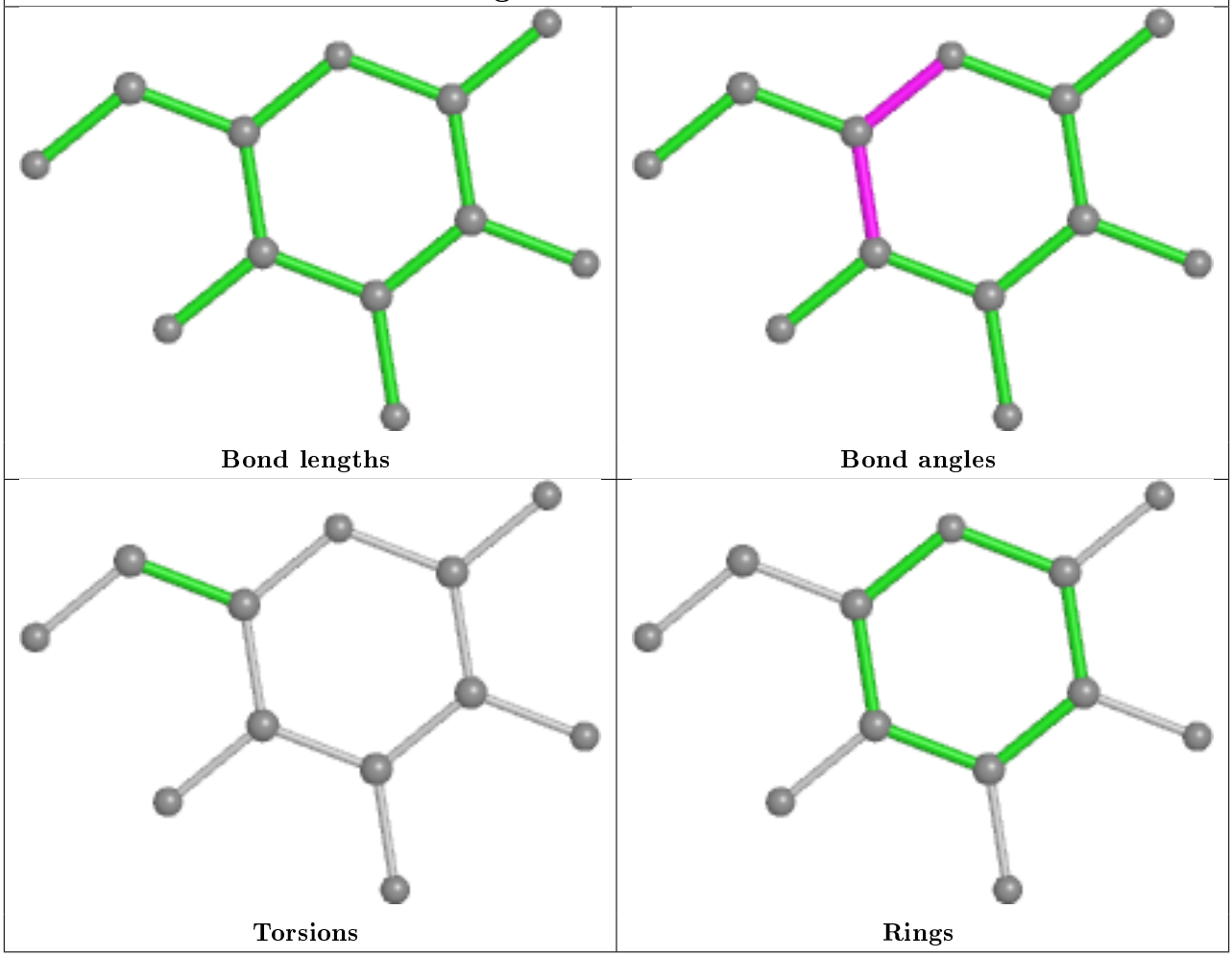
There are no ring outliers.

No monomer is involved in short contacts.

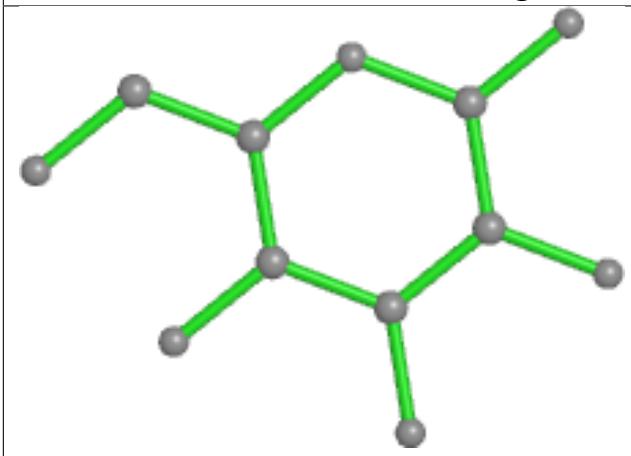
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

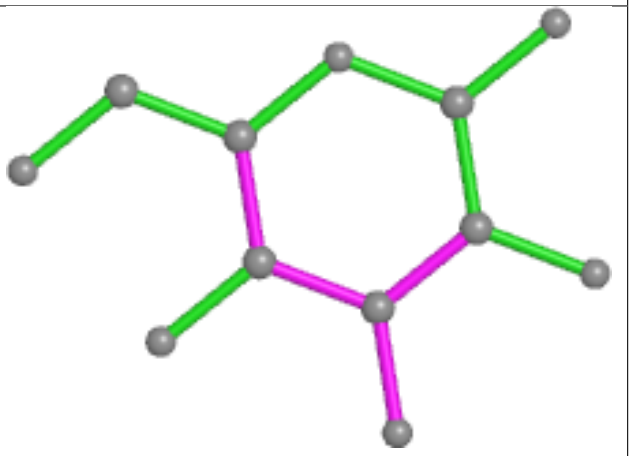
Ligand GAL A 1104



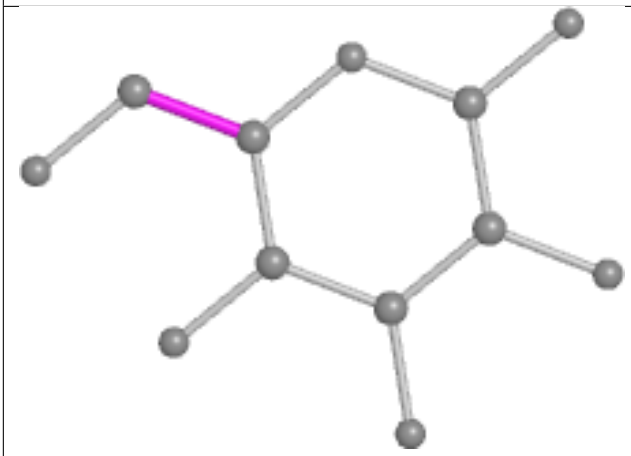
Ligand GAL A 1103



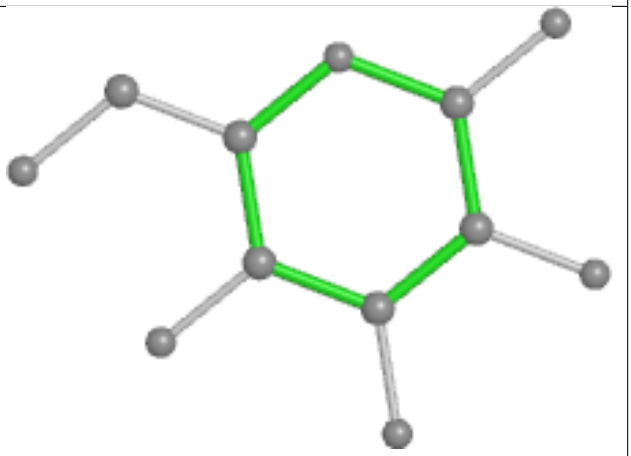
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	989/1010 (97%)	0.88	161 (16%) 1 1	38, 59, 95, 143	0

All (161) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	563	VAL	10.3
1	A	561	ASP	9.7
1	A	559	THR	8.9
1	A	560	ALA	8.7
1	A	562	GLY	8.3
1	A	723	PRO	8.1
1	A	716	VAL	6.8
1	A	713	GLY	6.6
1	A	141	PHE	6.2
1	A	22	GLY	6.1
1	A	558	SER	6.0
1	A	808	GLY	5.9
1	A	86	LEU	5.6
1	A	298	ALA	5.5
1	A	387	VAL	5.3
1	A	83	GLY	5.3
1	A	547	VAL	5.2
1	A	676	LEU	5.1
1	A	331	VAL	5.1
1	A	516	CYS	5.1
1	A	364	ILE	5.1
1	A	557	VAL	5.1
1	A	386	VAL	5.0
1	A	714	ALA	5.0
1	A	299	ALA	4.9
1	A	678	ASP	4.8
1	A	390	CYS	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	673	ALA	4.7
1	A	85	ALA	4.5
1	A	186	GLY	4.5
1	A	328	LEU	4.5
1	A	226	ALA	4.5
1	A	586	LEU	4.4
1	A	388	LEU	4.4
1	A	546	PHE	4.4
1	A	23	ARG	4.4
1	A	721	VAL	4.3
1	A	642	GLY	4.3
1	A	722	GLU	4.3
1	A	87	ASN	4.3
1	A	1010	SER	4.1
1	A	803	ASN	4.1
1	A	775	GLY	4.1
1	A	82	LEU	4.0
1	A	392	LEU	4.0
1	A	677	SER	4.0
1	A	804	PRO	3.9
1	A	203	VAL	3.9
1	A	330	GLY	3.9
1	A	369	TYR	3.9
1	A	88	GLY	3.8
1	A	806	GLN	3.8
1	A	173	LEU	3.7
1	A	514	VAL	3.7
1	A	371	PRO	3.6
1	A	434	VAL	3.6
1	A	519	VAL	3.6
1	A	366	THR	3.6
1	A	137	ALA	3.6
1	A	433	VAL	3.5
1	A	132	LEU	3.5
1	A	365	ARG	3.5
1	A	548	TRP	3.4
1	A	376	LEU	3.4
1	A	545	GLY	3.4
1	A	515	LEU	3.4
1	A	773	TRP	3.3
1	A	363	ALA	3.3
1	A	715	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	375	PHE	3.2
1	A	334	HIS	3.2
1	A	437	SER	3.2
1	A	227	GLY	3.2
1	A	333	ARG	3.2
1	A	84	GLU	3.2
1	A	809	GLY	3.2
1	A	812	LEU	3.1
1	A	257	ILE	3.1
1	A	80	TRP	3.1
1	A	258	ASP	3.1
1	A	564	ASP	3.1
1	A	712	PRO	3.0
1	A	172	ARG	3.0
1	A	185	GLN	3.0
1	A	674	ALA	3.0
1	A	572	PHE	3.0
1	A	255	GLN	3.0
1	A	643	GLY	3.0
1	A	807	ASP	3.0
1	A	171	SER	2.9
1	A	260	VAL	2.9
1	A	550	TRP	2.9
1	A	551	LEU	2.9
1	A	675	GLY	2.8
1	A	367	SER	2.8
1	A	438	LEU	2.8
1	A	719	ALA	2.8
1	A	964	LYS	2.7
1	A	332	ASN	2.7
1	A	600	PHE	2.7
1	A	776	ALA	2.7
1	A	482	TYR	2.7
1	A	303	VAL	2.7
1	A	385	TYR	2.7
1	A	361	ILE	2.6
1	A	435	MET	2.6
1	A	370	PRO	2.6
1	A	613	ARG	2.6
1	A	222	ALA	2.6
1	A	343	VAL	2.6
1	A	502	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	965	ALA	2.5
1	A	208	MET	2.5
1	A	725	GLN	2.5
1	A	391	ASP	2.5
1	A	679	GLY	2.5
1	A	384	PHE	2.5
1	A	302	SER	2.5
1	A	151	GLY	2.5
1	A	518	TYR	2.5
1	A	224	PRO	2.5
1	A	521	ALA	2.5
1	A	644	ALA	2.5
1	A	368	HIS	2.5
1	A	835	THR	2.5
1	A	724	VAL	2.4
1	A	300	GLY	2.4
1	A	210	TRP	2.4
1	A	79	GLY	2.4
1	A	543	MET	2.4
1	A	262	ARG	2.4
1	A	565	HIS	2.4
1	A	56	PRO	2.4
1	A	463	PRO	2.4
1	A	142	PHE	2.4
1	A	199	ALA	2.4
1	A	436	TRP	2.4
1	A	1009	ARG	2.3
1	A	259	ALA	2.3
1	A	228	ILE	2.3
1	A	597	LEU	2.3
1	A	641	ASP	2.3
1	A	152	ILE	2.2
1	A	544	GLY	2.2
1	A	727	GLN	2.2
1	A	839	THR	2.2
1	A	933	ARG	2.2
1	A	344	VAL	2.2
1	A	423	THR	2.1
1	A	256	ALA	2.1
1	A	342	ARG	2.1
1	A	356	MET	2.1
1	A	529	MET	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	802	ALA	2.1
1	A	139	PRO	2.1
1	A	174	ALA	2.0
1	A	200	ALA	2.0
1	A	612	ALA	2.0
1	A	697	ALA	2.0
1	A	718	PRO	2.0
1	A	680	ARG	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)

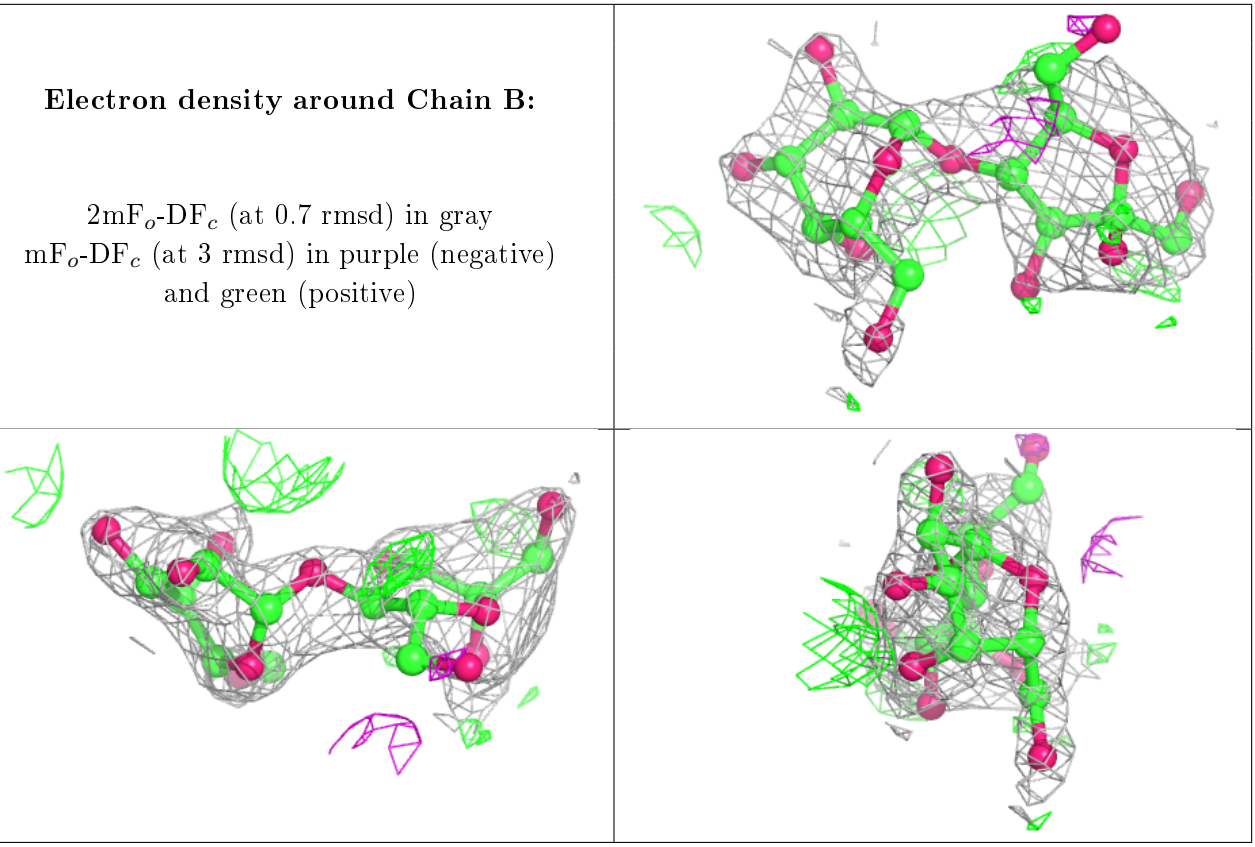
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	FRU	C	1	12/12	0.60	0.68	20,20,20,20	0
2	GAL	C	2	11/12	0.79	0.34	20,20,20,20	0
2	FRU	B	1	12/12	0.85	0.24	53,55,57,58	12
2	GAL	B	2	11/12	0.85	0.29	51,53,54,55	11

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.

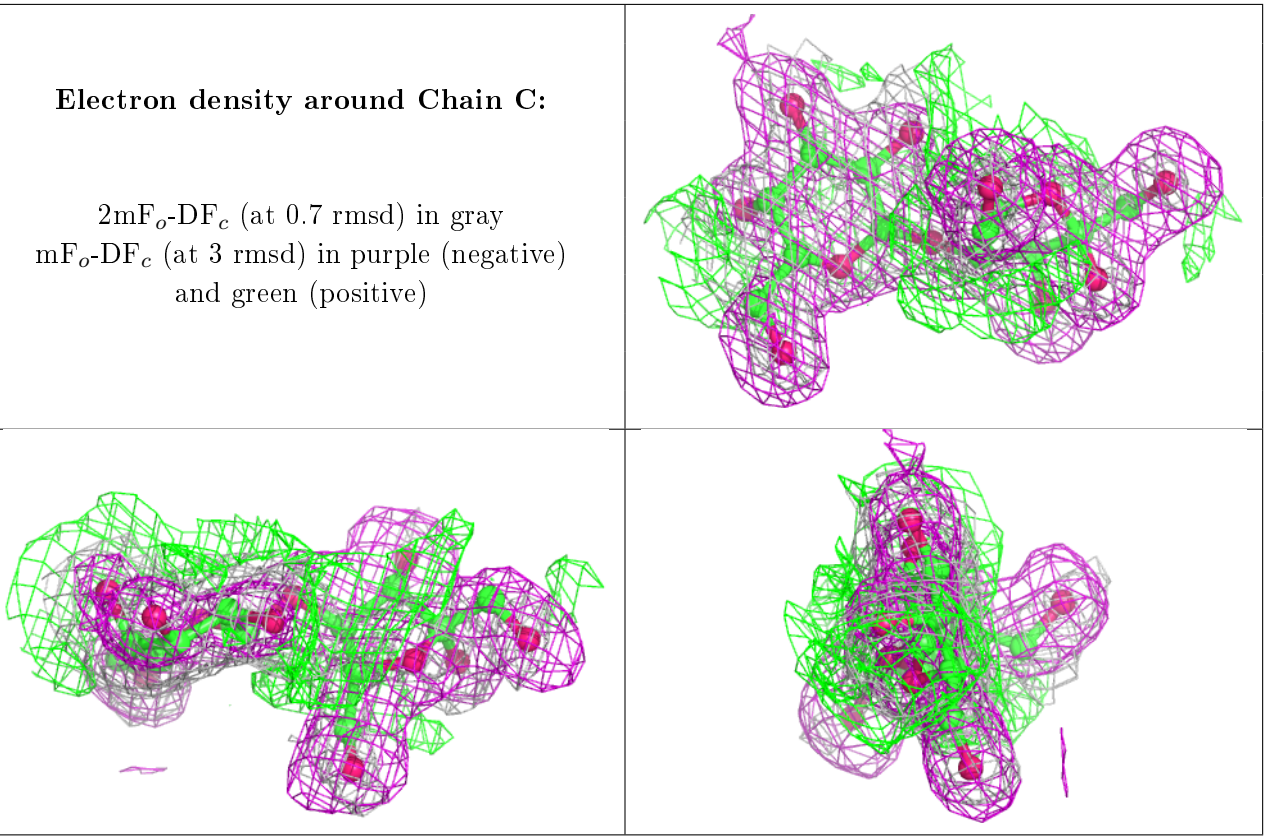
Electron density around Chain B:

$2mF_o$-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 C:

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



6.4 Ligands

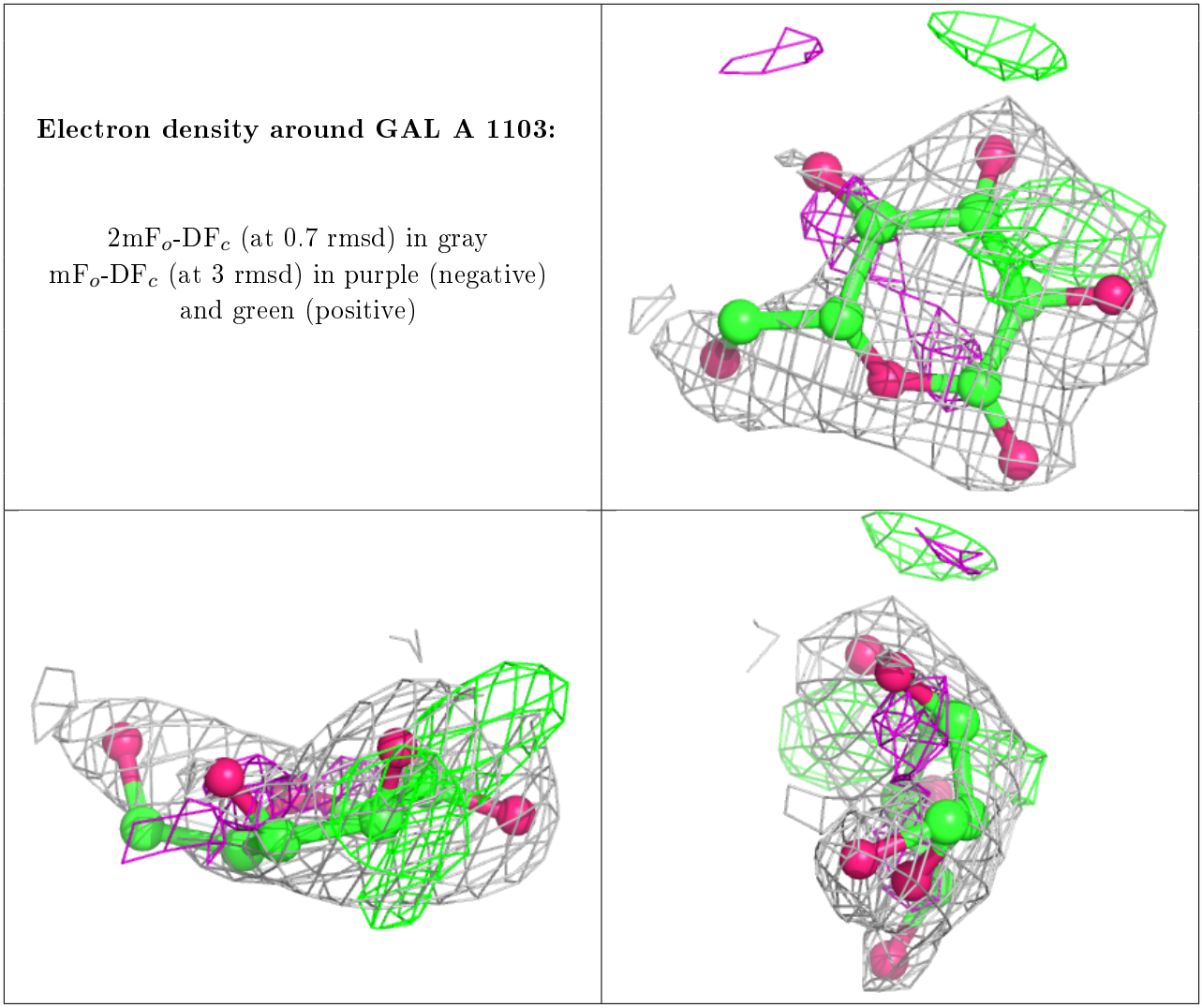
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
3	GAL	A	1103	12/12	0.65	0.27	57,62,66,67	12
3	GAL	A	1104	12/12	0.77	0.32	112,113,116,117	0
4	ACT	A	1106	4/4	0.79	0.36	73,74,74,75	0
4	ACT	A	1105	4/4	0.87	0.21	97,97,98,98	0
5	NA	A	1108	1/1	0.89	0.13	42,42,42,42	0
5	NA	A	1107	1/1	0.92	0.15	67,67,67,67	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.

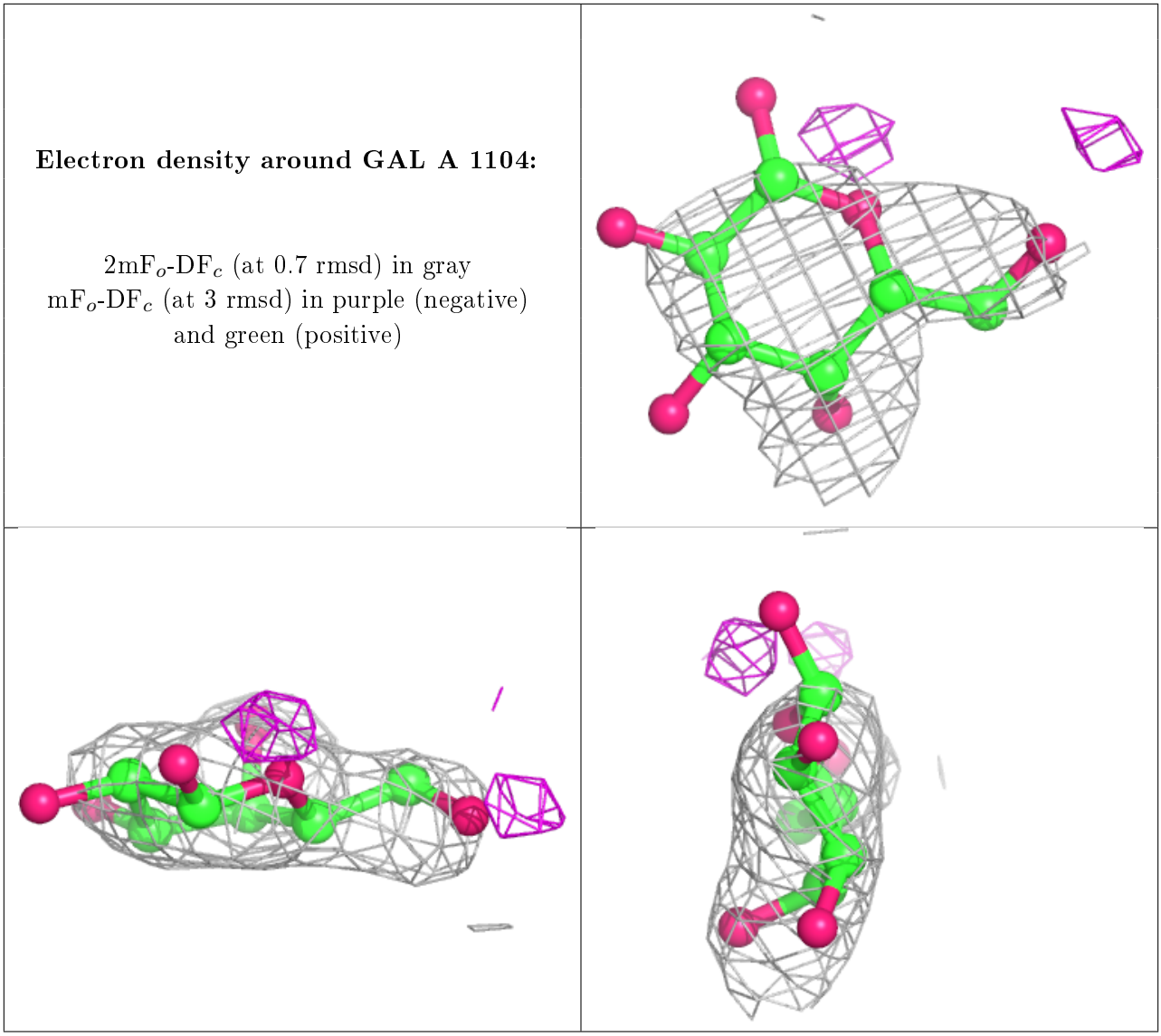
Electron density around GAL A 1103:

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



Electron density around GAL A 1104:

$2mF_o$-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

There are no such residues in this entry.