



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:53 AM UTC

PDB ID : 6SE9 / pdb_00006se9
Title : Cold-adapted beta-D-galactosidase from *Arthrobacter* sp. 32cB mutant E441Q
in complex with lactose bound in shallow mode
Authors : Rutkiewicz, M.; Bujacz, A.; Bujacz, G.
Deposited on : 2019-07-29
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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

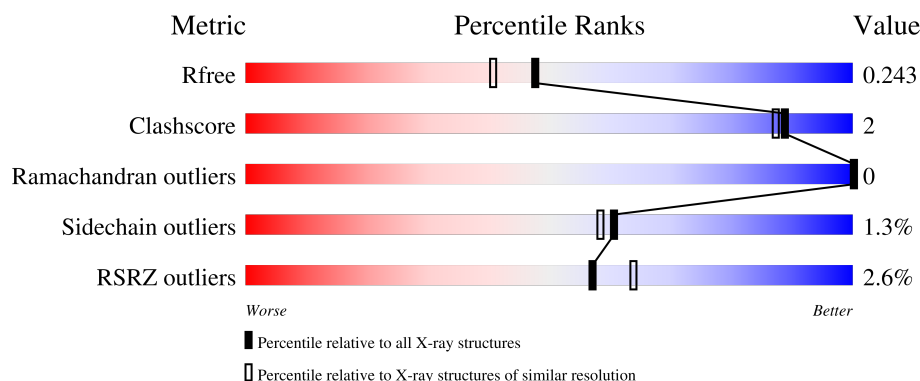
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

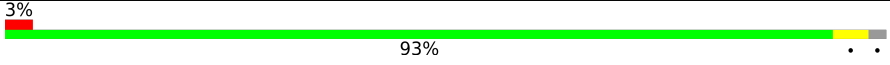
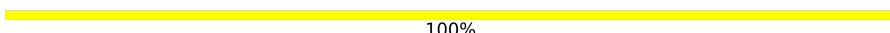
The reported resolution of this entry is 1.97 Å.

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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (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 $\leq 5\%$. 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	1010	 3% 93% . .
2	B	2	 100%

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 8098 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	2	0
			7619	4794	1363	1443	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-glucopyranose.



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

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

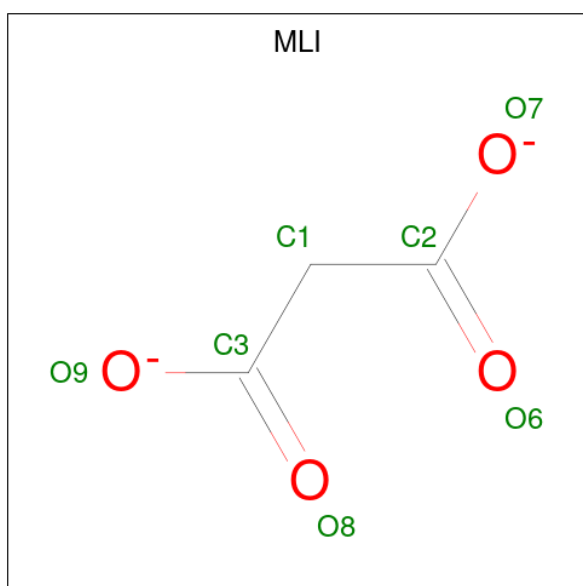
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Na	0	0
			2	2		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



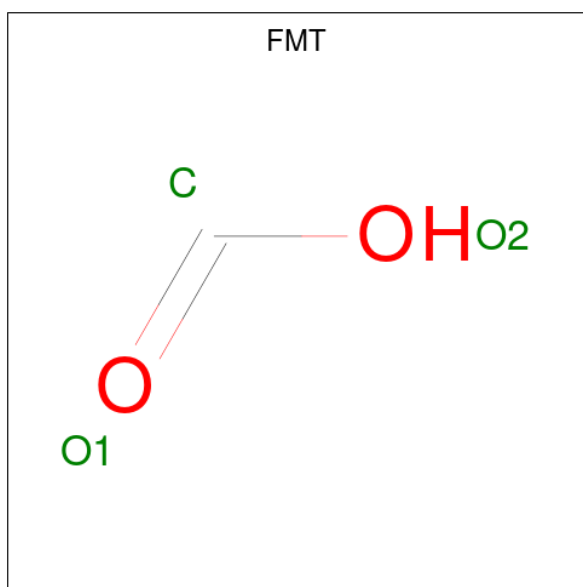
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is MALONATE ION (CCD ID: MLI) (formula: C₃H₂O₄).



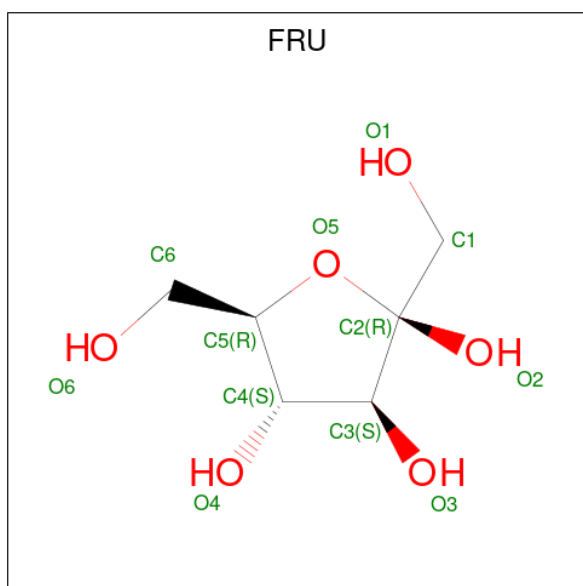
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	3	4		

- Molecule 6 is FORMIC ACID (CCD ID: FMT) (formula: CH₂O₂).



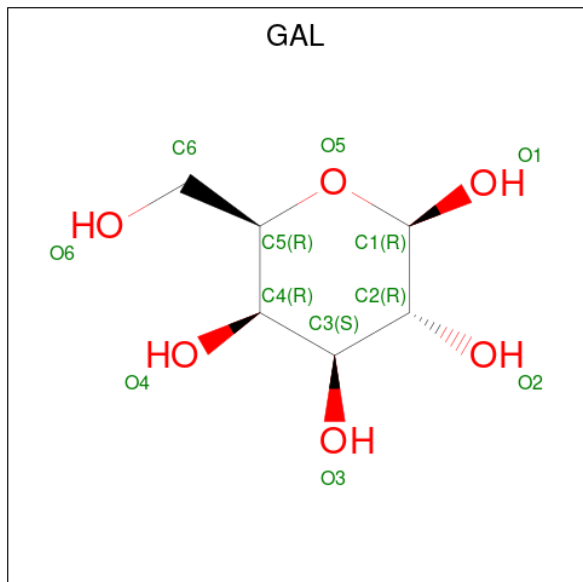
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			3	1	2		

- Molecule 7 is beta-D-fructofuranose (CCD ID: FRU) (formula: $C_6H_{12}O_6$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 8 is beta-D-galactopyranose (CCD ID: GAL) (formula: $C_6H_{12}O_6$) (labeled as "Ligand of Interest" by depositor).



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

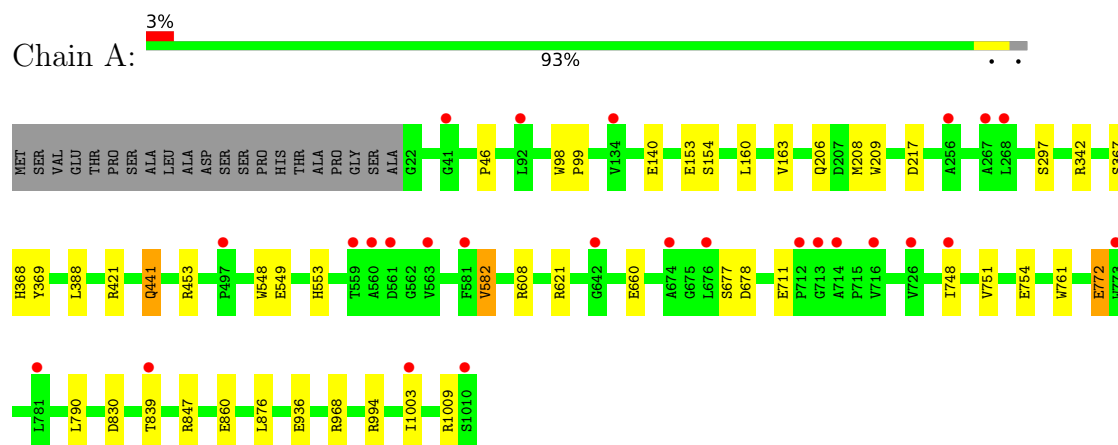
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	400	Total	O	0	0
			400	400		

3 Residue-property plots

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

- Molecule 1: Beta-galactosidase



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.90Å 138.90Å 127.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.04 – 1.97 47.04 – 1.97	Depositor EDS
% Data completeness (in resolution range)	99.0 (47.04-1.97) 99.4 (47.04-1.97)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 1.97Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.202 , 0.238 0.206 , 0.243	Depositor DCC
R_{free} test set	2098 reflections (2.08%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.646	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8098	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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: GAL, BGC, FMT, MLI, FRU, ACT, NA

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	0.14	0/7824	0.33	0/10663

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7619	0	7319	27	0
2	B	23	0	19	0	0
3	A	2	0	0	0	0
4	A	8	0	6	0	0
5	A	7	0	2	0	0
6	A	3	0	1	0	0
7	A	24	0	20	4	0
8	A	12	0	12	0	0
9	A	400	0	0	3	0
All	All	8098	0	7379	29	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 (29) 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)
7:A:1108:FRU:O5	7:A:1108:FRU:C2	1.64	1.21
1:A:830:ASP:OD1	1:A:847:ARG:NH1	2.20	0.74
1:A:860:GLU:OE1	1:A:994:ARG:NH1	2.21	0.73
1:A:208[A]:MET:SD	1:A:342:ARG:NH1	2.70	0.64
1:A:46:PRO:HA	7:A:1109:FRU:O2	2.00	0.62
1:A:772:GLU:OE2	1:A:994:ARG:NH2	2.32	0.62
1:A:206:GLN:HB2	1:A:208[A]:MET:HE3	1.84	0.59
1:A:608:ARG:NH2	1:A:660:GLU:OE2	2.36	0.59
1:A:441:GLN:NE2	9:A:1208:HOH:O	2.38	0.56
1:A:421:ARG:HD2	7:A:1109:FRU:H5	1.88	0.55
1:A:754:GLU:OE1	1:A:968:ARG:NH1	2.42	0.53
1:A:453:ARG:NH2	9:A:1211:HOH:O	2.41	0.50
1:A:208[A]:MET:HE1	1:A:369:TYR:CE2	2.48	0.48
1:A:208[A]:MET:HE1	1:A:369:TYR:HE2	1.80	0.47
1:A:153:GLU:HA	1:A:154:SER:HA	1.77	0.46
1:A:677:SER:O	1:A:678:ASP:HB2	2.16	0.46
1:A:553:HIS:HB2	1:A:582:VAL:HG22	1.99	0.45
7:A:1108:FRU:O1	9:A:1201:HOH:O	2.21	0.45
1:A:160:LEU:O	1:A:163:VAL:HG12	2.17	0.44
1:A:936:GLU:OE2	1:A:1009:ARG:NE	2.49	0.43
1:A:98:TRP:N	1:A:99:PRO:CD	2.82	0.43
1:A:748:ILE:O	1:A:751:VAL:HG22	2.18	0.42
1:A:217:ASP:N	1:A:217:ASP:OD1	2.52	0.42
1:A:936:GLU:OE2	1:A:1009:ARG:NH1	2.50	0.42
1:A:761:TRP:HB2	1:A:790:LEU:HB3	2.03	0.41
1:A:367:SER:HA	1:A:368:HIS:HA	1.83	0.40
1:A:548:TRP:HA	1:A:549:GLU:HA	1.86	0.40
1:A:208[A]:MET:HG3	1:A:209:TRP:N	2.35	0.40
1:A:1003:ILE:N	1:A:1003:ILE:HD12	2.37	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	989/1010 (98%)	957 (97%)	32 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	778/793 (98%)	768 (99%)	10 (1%)	61	58

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	140	GLU
1	A	297	SER
1	A	388	LEU
1	A	441	GLN
1	A	582	VAL
1	A	621	ARG
1	A	711	GLU
1	A	772	GLU
1	A	839	THR
1	A	876	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	103	HIS
1	A	175	HIS
1	A	882	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

2 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	BGC	B	1	2	12,12,12	1.26	1 (8%)	17,17,17	1.02	0
2	GAL	B	2	2,3	11,11,12	1.63	3 (27%)	15,15,17	1.05	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	BGC	B	1	2	-	2/2/22/22	0/1/1/1
2	GAL	B	2	2,3	-	1/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	GAL	O5-C1	3.53	1.49	1.43
2	B	1	BGC	O5-C1	3.12	1.50	1.42
2	B	2	GAL	C2-C3	-2.38	1.48	1.52
2	B	2	GAL	O5-C5	2.06	1.47	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	GAL	C1-C2-C3	2.49	113.27	109.64

There are no chirality outliers.

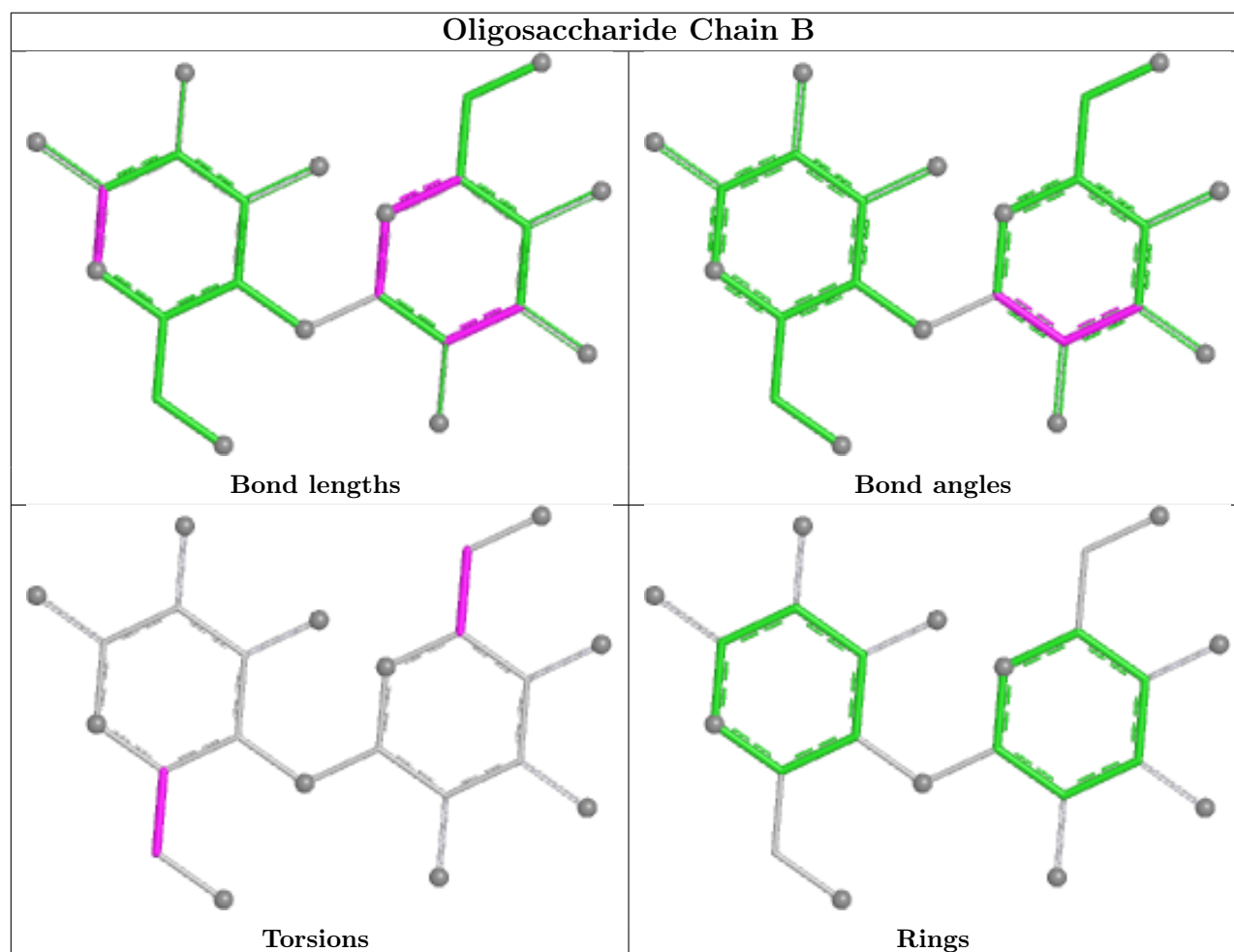
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	BGC	O5-C5-C6-O6
2	B	1	BGC	C4-C5-C6-O6
2	B	2	GAL	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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
7	FRU	A	1109	-	11,12,12	4.67	6 (54%)	10,18,18	1.17	1 (10%)
8	GAL	A	1110	-	12,12,12	0.53	0	17,17,17	0.79	0
6	FMT	A	1107	-	2,2,2	0.73	0	1,1,1	0.44	0
5	MLI	A	1106	-	6,6,6	1.34	0	7,7,7	1.29	0
4	ACT	A	1105	-	3,3,3	0.90	0	3,3,3	0.94	0
4	ACT	A	1104	-	3,3,3	1.03	0	3,3,3	0.75	0
7	FRU	A	1108	-	11,12,12	4.66	6 (54%)	10,18,18	0.82	1 (10%)

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
7	FRU	A	1109	-	-	5/5/24/24	0/1/1/1
7	FRU	A	1108	-	-	3/5/24/24	0/1/1/1
5	MLI	A	1106	-	-	2/4/4/4	-
8	GAL	A	1110	-	-	0/2/22/22	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1109	FRU	O5-C2	13.20	1.64	1.43
7	A	1108	FRU	O5-C2	13.15	1.64	1.43
7	A	1108	FRU	O5-C5	-5.38	1.32	1.43
7	A	1109	FRU	O5-C5	-5.24	1.32	1.43
7	A	1109	FRU	O4-C4	-4.14	1.32	1.43
7	A	1108	FRU	O4-C4	-3.92	1.33	1.43
7	A	1109	FRU	O2-C2	-2.96	1.35	1.40
7	A	1108	FRU	O2-C2	-2.87	1.35	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1108	FRU	C4-C5	2.63	1.59	1.53
7	A	1109	FRU	C4-C5	2.45	1.59	1.53
7	A	1109	FRU	O3-C3	2.31	1.47	1.42
7	A	1108	FRU	O3-C3	2.14	1.47	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1109	FRU	O1-C1-C2	-2.65	105.81	111.67
7	A	1108	FRU	C6-C5-C4	-2.04	110.27	115.10

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1108	FRU	O1-C1-C2-C3
7	A	1108	FRU	O1-C1-C2-O2
7	A	1109	FRU	O1-C1-C2-C3
7	A	1109	FRU	O1-C1-C2-O2
7	A	1109	FRU	O1-C1-C2-O5
7	A	1109	FRU	O5-C5-C6-O6
7	A	1109	FRU	C4-C5-C6-O6
7	A	1108	FRU	O1-C1-C2-O5
5	A	1106	MLI	C3-C1-C2-O7
5	A	1106	MLI	C3-C1-C2-O6

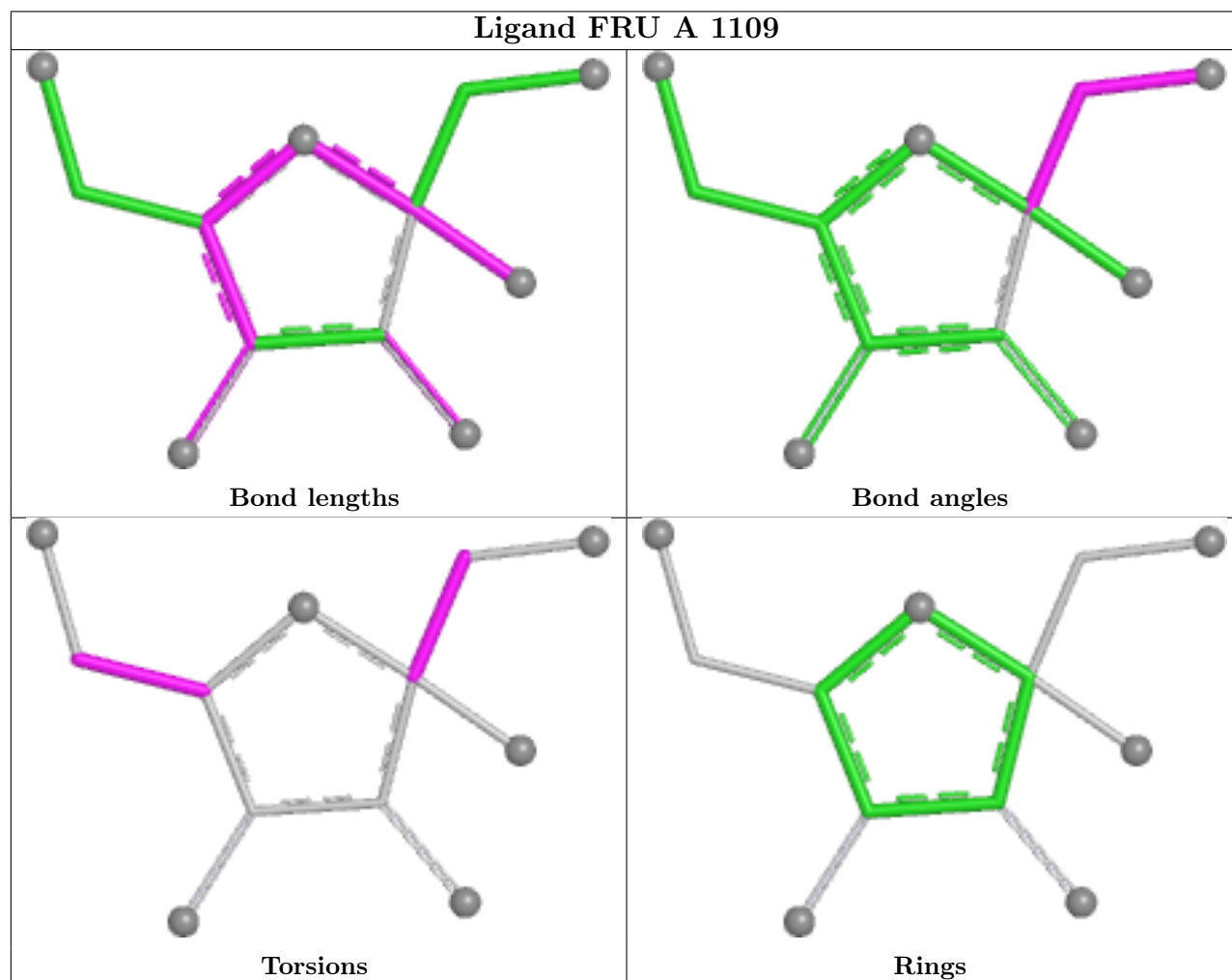
There are no ring outliers.

2 monomers are involved in 4 short contacts:

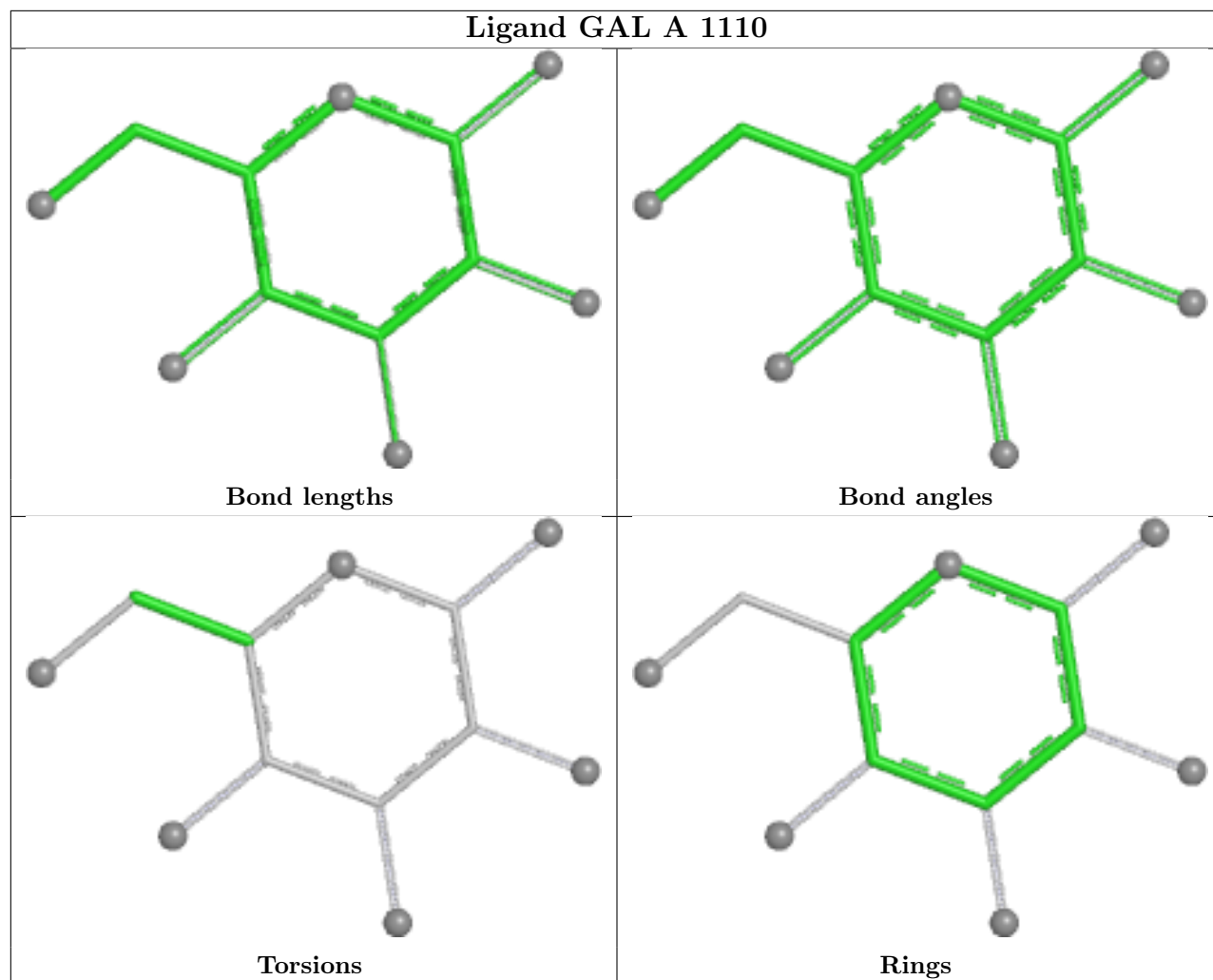
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1109	FRU	2	0
7	A	1108	FRU	2	0

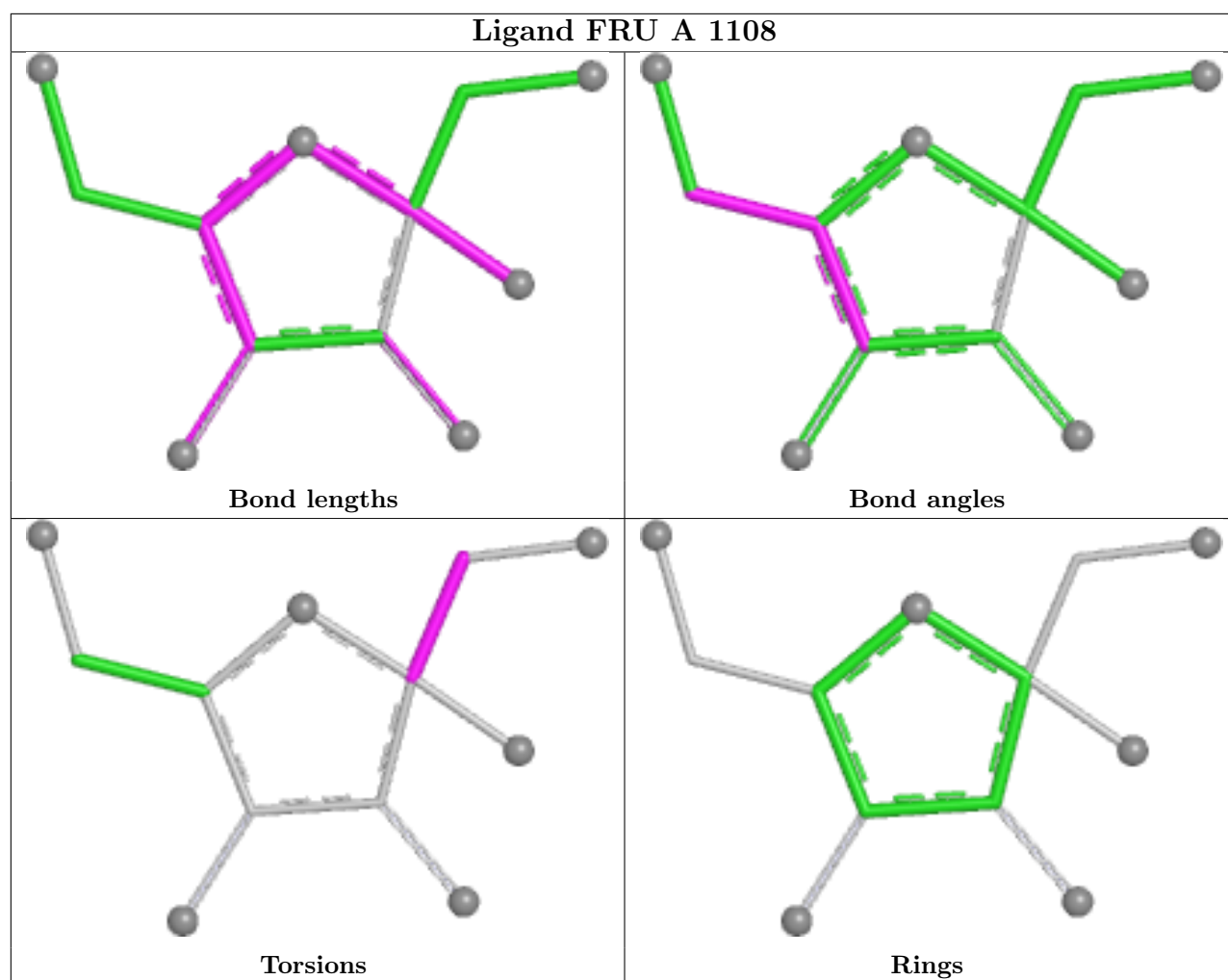
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



Ligand GAL A 1110





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	989/1010 (97%)	0.50	26 (2%) 57 64	33, 69, 105, 157	2 (0%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	716	VAL	3.3
1	A	642	GLY	3.2
1	A	773	TRP	3.0
1	A	676	LEU	2.9
1	A	674	ALA	2.8
1	A	563	VAL	2.7
1	A	560	ALA	2.6
1	A	268	LEU	2.6
1	A	267	ALA	2.6
1	A	748	ILE	2.6
1	A	712	PRO	2.6
1	A	714	ALA	2.5
1	A	92	LEU	2.4
1	A	713	GLY	2.4
1	A	839	THR	2.4
1	A	726	VAL	2.3
1	A	581	PHE	2.3
1	A	134	VAL	2.3
1	A	256	ALA	2.2
1	A	1003	ILE	2.1
1	A	561	ASP	2.1
1	A	559	THR	2.1
1	A	1010	SER	2.1
1	A	41	GLY	2.1
1	A	497	PRO	2.1
1	A	781	LEU	2.0

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

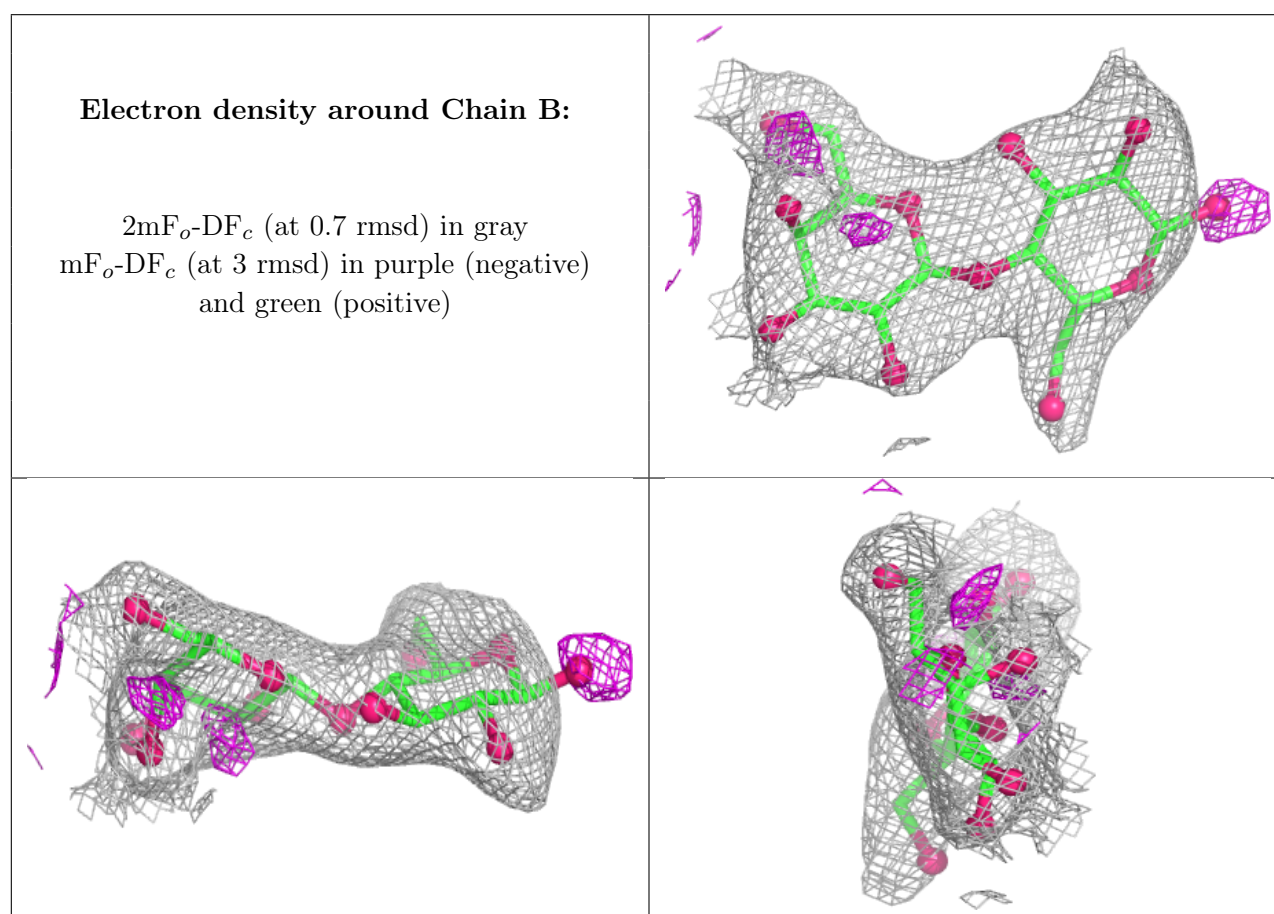
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
2	BGC	B	1	12/12	0.84	0.14	92,99,100,102	0
2	GAL	B	2	11/12	0.94	0.11	77,82,85,87	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.

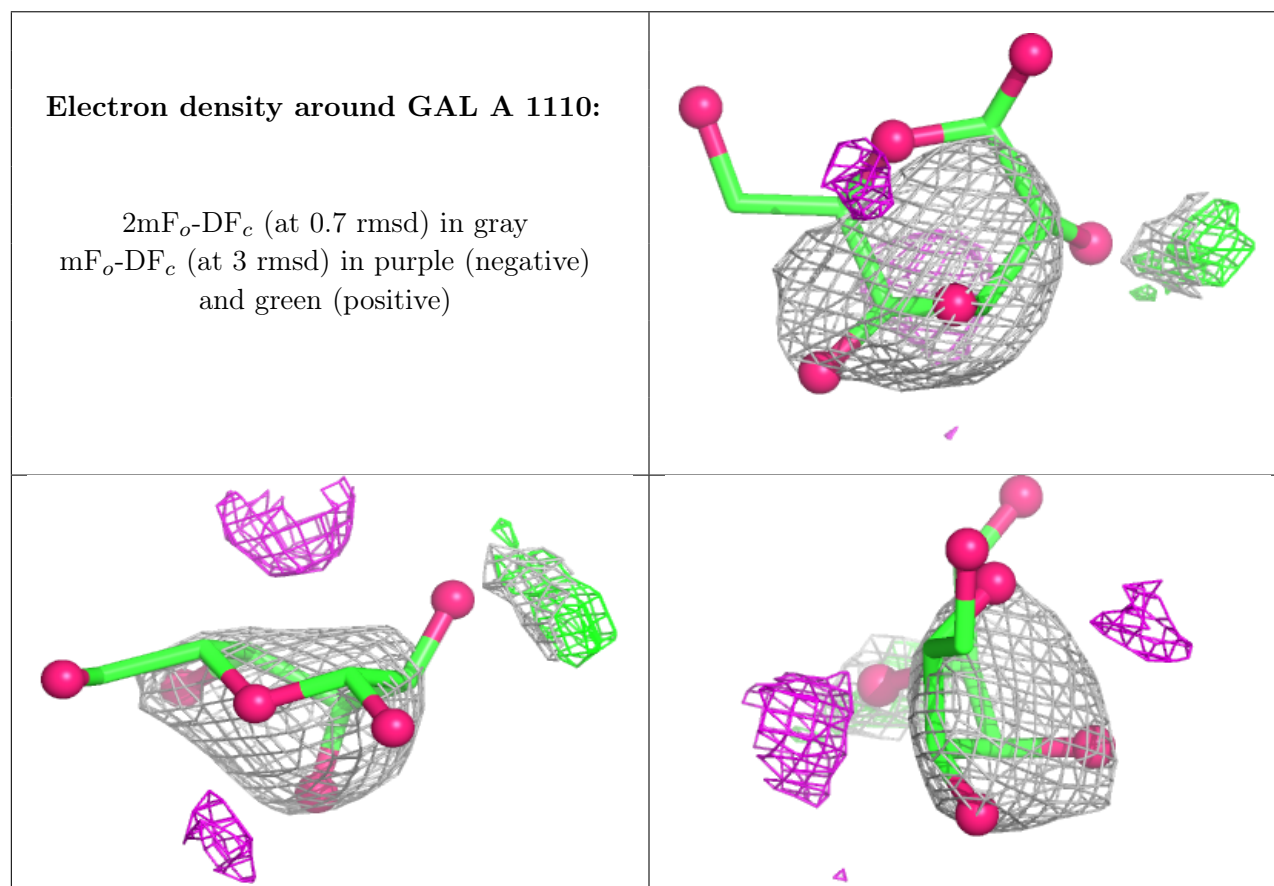


6.4 Ligands ⓘ

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

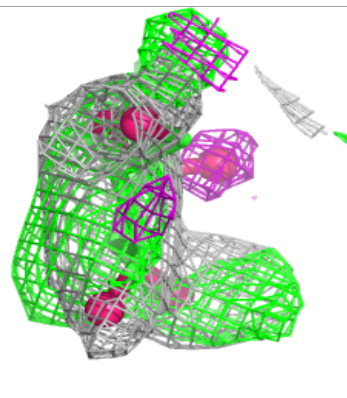
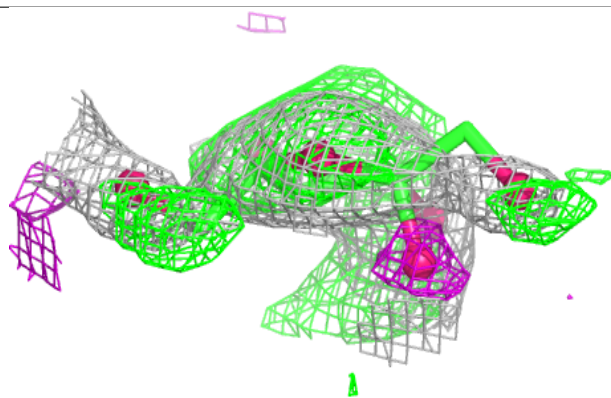
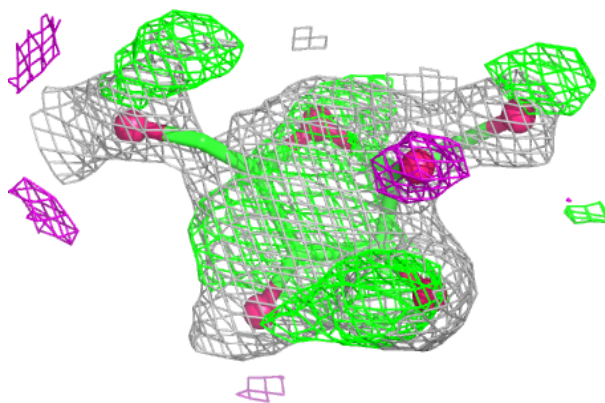
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	GAL	A	1110	12/12	0.42	0.17	168,170,170,171	0
5	MLI	A	1106	7/7	0.59	0.16	100,101,102,102	0
4	ACT	A	1104	4/4	0.63	0.20	94,94,94,94	0
6	FMT	A	1107	3/3	0.74	0.16	83,83,84,84	0
4	ACT	A	1105	4/4	0.82	0.31	129,130,130,130	0
7	FRU	A	1109	12/12	0.83	0.34	54,61,64,65	12
7	FRU	A	1108	12/12	0.87	0.16	86,90,91,92	0
3	NA	A	1102	1/1	0.94	0.20	62,62,62,62	0
3	NA	A	1101	1/1	0.95	0.12	59,59,59,59	0

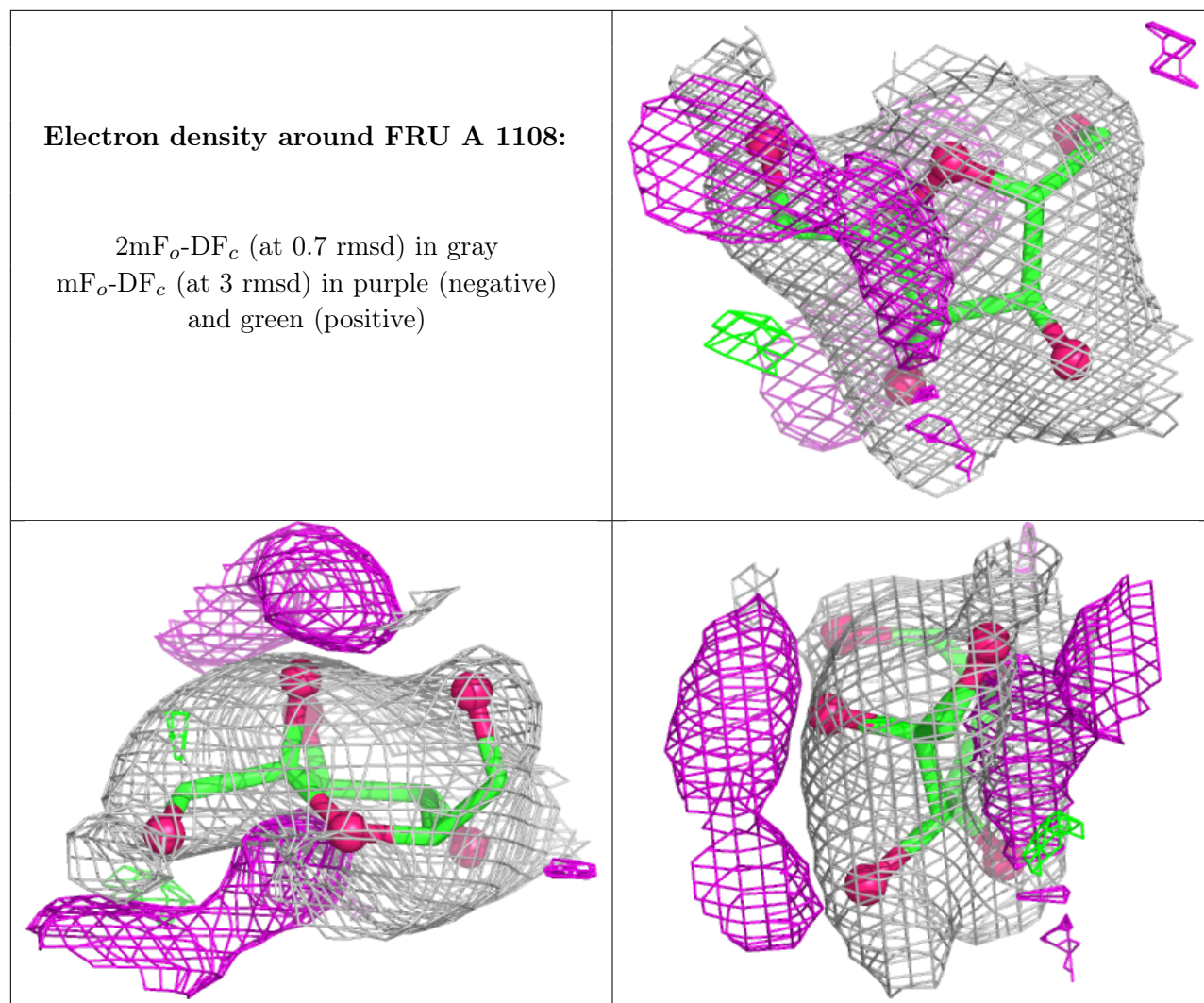
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around FRU A 1109:

$2mF_o-DF_c$ (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.