



Full wwPDB X-ray Structure Validation Report ⓘ

May 18, 2026 – 08:11 PM JST

PDB ID : 22HI / pdb_000022hi
Title : Beta-1,2-glucan-binding protein complexed with cyclic beta-1,2-glucoheptaose
Authors : Hirayama, R.; Nakajima, M.
Deposited on : 2026-01-11
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 ⓘ 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
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

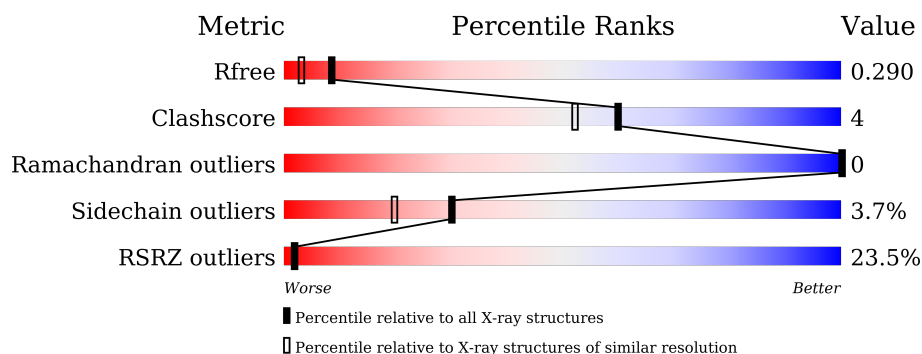
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	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	474	<div> <div>21%</div> <div>77%</div> <div>11%</div> <div>11%</div> </div>
2	B	17	<div> <div>71%</div> <div>29%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3655 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.

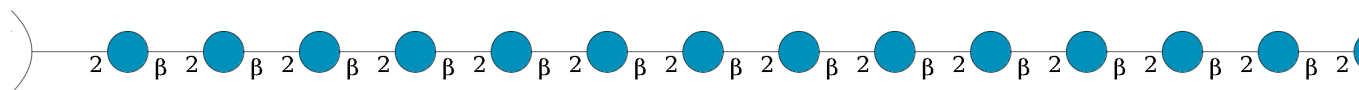
- Molecule 1 is a protein called Extracellular solute-binding protein family 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	421	Total	C	N	O	S	0	0	0
			3358	2157	551	633	17			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	initiating methionine	UNP A9WCS2
A	487	LEU	-	expression tag	UNP A9WCS2
A	488	GLU	-	expression tag	UNP A9WCS2
A	489	HIS	-	expression tag	UNP A9WCS2
A	490	HIS	-	expression tag	UNP A9WCS2
A	491	HIS	-	expression tag	UNP A9WCS2
A	492	HIS	-	expression tag	UNP A9WCS2
A	493	HIS	-	expression tag	UNP A9WCS2
A	494	HIS	-	expression tag	UNP A9WCS2

- Molecule 2 is an oligosaccharide called Cycloheptadecakis-(1-2)-(beta-D-glucopyranose).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	B	17	Total	C	O	0	0	0
			187	102	85			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	104	Total	O	0	0
			104	104		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.39Å 82.91Å 94.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.18 – 1.95 47.18 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.9 (47.18-1.95) 97.9 (47.18-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0430	Depositor
R, R_{free}	0.247 , 0.284 0.253 , 0.290	Depositor DCC
R_{free} test set	1975 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	27.8	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3655	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, BGC

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	0.56	0/3451	1.06	3/4698 (0.1%)

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
1	A	0	2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	440	ASP	CB-CA-C	5.66	119.83	110.78
1	A	353	PHE	CA-CB-CG	-5.42	108.38	113.80
1	A	322	ASP	CA-CB-CG	5.02	117.62	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	121	ARG	Sidechain
1	A	355	ARG	Sidechain

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	3358	0	3202	30	0
2	B	187	0	153	0	0
3	A	6	0	8	0	0
4	A	104	0	0	1	0
All	All	3655	0	3363	30	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 4.

All (30) 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:171:ARG:CB	1:A:173:MET:HE3	2.17	0.74
1:A:171:ARG:HB2	1:A:173:MET:HE3	1.77	0.66
1:A:171:ARG:HB3	1:A:173:MET:HE3	1.84	0.58
1:A:228:MET:HB3	1:A:267:VAL:HG13	1.86	0.57
1:A:228:MET:HE2	1:A:276:GLN:HG2	1.86	0.57
1:A:171:ARG:HB3	1:A:173:MET:CE	2.36	0.56
1:A:451:ARG:HD3	1:A:454:ASP:OD2	2.05	0.56
1:A:155:TRP:HB3	1:A:156:PRO:HD3	1.89	0.54
1:A:191:TYR:CZ	1:A:215:LEU:HD22	2.44	0.53
1:A:133:MET:HB2	1:A:134:PRO:HD3	1.92	0.52
1:A:271:LYS:N	1:A:272:PRO:CD	2.73	0.51
1:A:133:MET:SD	1:A:339:VAL:HG11	2.52	0.50
1:A:112:ASP:OD1	1:A:136:TYR:OH	2.22	0.49
1:A:391:GLN:O	1:A:395:GLN:HG3	2.13	0.49
1:A:179:GLN:HB2	1:A:333:ILE:HD11	1.95	0.49
1:A:160:GLU:HG3	1:A:163:ARG:NH1	2.28	0.49
1:A:298:GLN:HA	4:A:634:HOH:O	2.15	0.46
1:A:268:ALA:HB2	1:A:453:ALA:HB1	1.98	0.46
1:A:235:TYR:O	1:A:238:VAL:HG22	2.15	0.46
1:A:98:HIS:NE2	1:A:349:GLU:OE2	2.34	0.45
1:A:144:ASP:CG	1:A:173:MET:HE1	2.41	0.45
1:A:187:ASN:OD1	1:A:187:ASN:C	2.60	0.45
1:A:142:LEU:O	1:A:342:LYS:HE3	2.18	0.44
1:A:230:PHE:CD2	1:A:304:TRP:HB3	2.52	0.44
1:A:160:GLU:HG3	1:A:163:ARG:HH12	1.84	0.42
1:A:172:VAL:C	1:A:173:MET:HE2	2.44	0.42
1:A:236:PRO:HD3	1:A:263:THR:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:TYR:CE1	1:A:215:LEU:HD22	2.54	0.41
1:A:255:TYR:HB3	1:A:459:TYR:OH	2.21	0.41
1:A:108:GLY:C	1:A:114:MET:HE3	2.47	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	419/474 (88%)	403 (96%)	16 (4%)	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	348/389 (90%)	335 (96%)	13 (4%)	30	20

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	ARG
1	A	134	PRO
1	A	138	LYS

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Mol	Chain	Res	Type
1	A	161	VAL
1	A	203	PHE
1	A	238	VAL
1	A	333	ILE
1	A	345	PRO
1	A	348	GLU
1	A	439	GLU
1	A	458	LYS
1	A	485	LEU
1	A	486	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	139	ASN
1	A	316	ASN
1	A	352	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 ⓘ

17 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	11,11,12	0.39	0	15,15,17	0.75	1 (6%)
2	BGC	B	10	2	11,11,12	0.38	0	15,15,17	0.64	0
2	BGC	B	11	2	11,11,12	0.24	0	15,15,17	0.49	0
2	BGC	B	12	2	11,11,12	0.21	0	15,15,17	0.63	0
2	BGC	B	13	2	11,11,12	0.22	0	15,15,17	0.73	0
2	BGC	B	14	2	11,11,12	0.30	0	15,15,17	0.47	0
2	BGC	B	15	2	11,11,12	0.32	0	15,15,17	0.89	1 (6%)
2	BGC	B	16	2	11,11,12	0.24	0	15,15,17	0.69	1 (6%)
2	BGC	B	17	2	11,11,12	0.37	0	15,15,17	0.77	0
2	BGC	B	2	2	11,11,12	0.45	0	15,15,17	0.62	0
2	BGC	B	3	2	11,11,12	0.47	0	15,15,17	0.80	1 (6%)
2	BGC	B	4	2	11,11,12	0.23	0	15,15,17	0.81	0
2	BGC	B	5	2	11,11,12	0.38	0	15,15,17	0.53	0
2	BGC	B	6	2	11,11,12	0.53	0	15,15,17	0.59	0
2	BGC	B	7	2	11,11,12	0.54	0	15,15,17	1.26	2 (13%)
2	BGC	B	8	2	11,11,12	0.43	0	15,15,17	0.73	0
2	BGC	B	9	2	11,11,12	0.28	0	15,15,17	0.48	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	BGC	B	1	2	-	0/2/19/22	0/1/1/1
2	BGC	B	10	2	-	0/2/19/22	0/1/1/1
2	BGC	B	11	2	-	0/2/19/22	0/1/1/1
2	BGC	B	12	2	-	0/2/19/22	0/1/1/1
2	BGC	B	13	2	-	0/2/19/22	0/1/1/1
2	BGC	B	14	2	-	0/2/19/22	0/1/1/1
2	BGC	B	15	2	-	0/2/19/22	0/1/1/1
2	BGC	B	16	2	-	0/2/19/22	0/1/1/1
2	BGC	B	17	2	-	2/2/19/22	0/1/1/1
2	BGC	B	2	2	-	1/2/19/22	0/1/1/1
2	BGC	B	3	2	-	0/2/19/22	0/1/1/1
2	BGC	B	4	2	-	0/2/19/22	0/1/1/1
2	BGC	B	5	2	-	0/2/19/22	0/1/1/1
2	BGC	B	6	2	-	0/2/19/22	0/1/1/1
2	BGC	B	7	2	-	1/2/19/22	0/1/1/1
2	BGC	B	8	2	-	2/2/19/22	0/1/1/1
2	BGC	B	9	2	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	7	BGC	C1-C2-C3	3.07	113.44	109.67
2	B	15	BGC	C1-C2-C3	2.62	112.89	109.67
2	B	3	BGC	C1-O5-C5	2.34	115.36	112.19
2	B	7	BGC	C2-C3-C4	2.12	114.56	110.89
2	B	16	BGC	C1-C2-C3	2.06	112.20	109.67
2	B	1	BGC	C1-C2-C3	2.01	112.13	109.67

There are no chirality outliers.

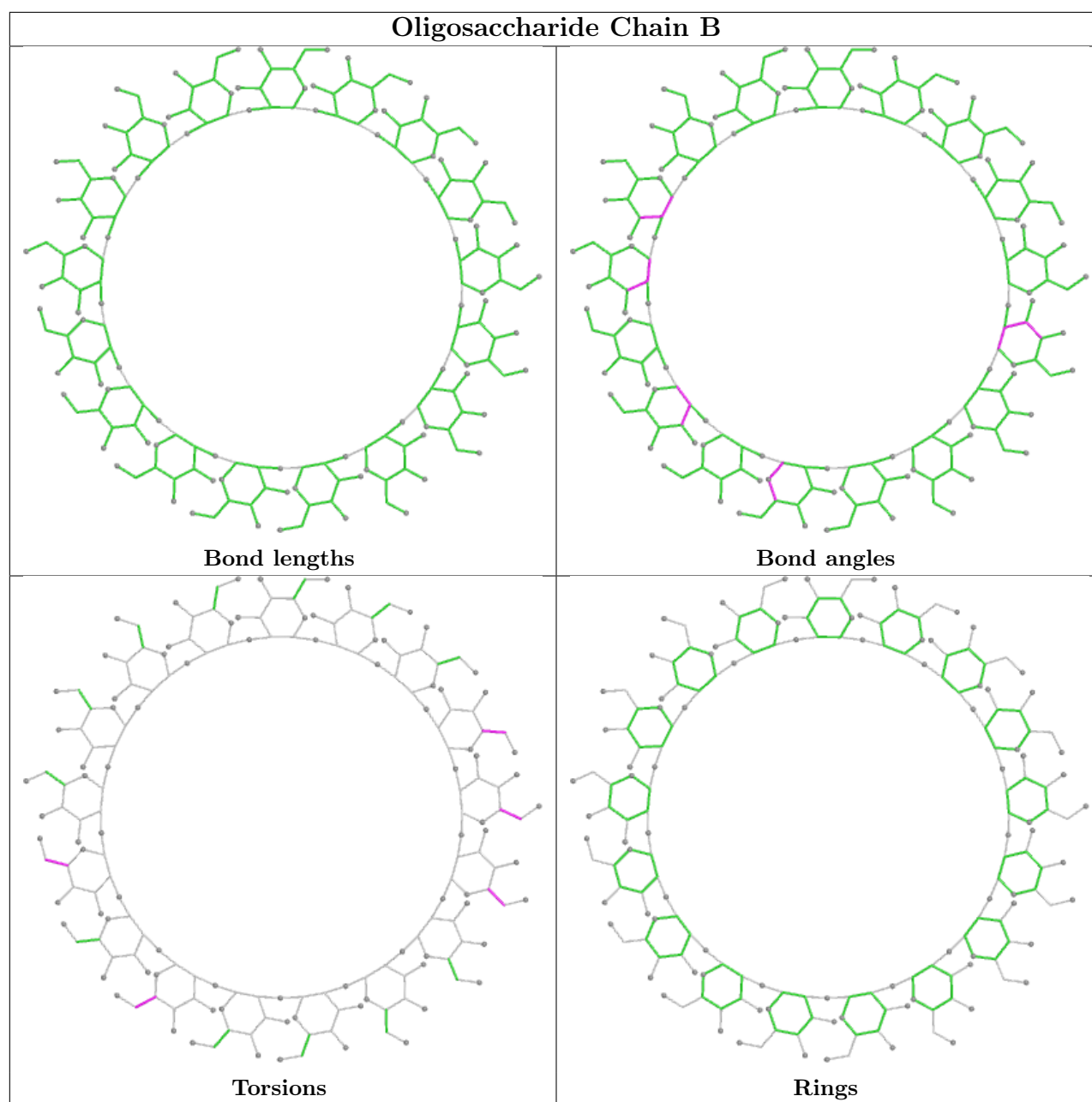
All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	9	BGC	C4-C5-C6-O6
2	B	8	BGC	C4-C5-C6-O6
2	B	9	BGC	O5-C5-C6-O6
2	B	8	BGC	O5-C5-C6-O6
2	B	7	BGC	O5-C5-C6-O6
2	B	17	BGC	C4-C5-C6-O6
2	B	2	BGC	C4-C5-C6-O6
2	B	17	BGC	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 ⓘ

1 ligand is 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	GOL	A	501	-	5,5,5	0.15	0	5,5,5	0.43	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
3	GOL	A	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	GOL	O1-C1-C2-O2
3	A	501	GOL	O1-C1-C2-C3

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, 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	421/474 (88%)	1.45	99 (23%) 2 2	22, 31, 44, 59	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	66	PRO	4.5
1	A	486	LYS	4.2
1	A	437	ILE	4.0
1	A	95	LEU	4.0
1	A	442	ASP	3.8
1	A	435	ILE	3.8
1	A	458	LYS	3.7
1	A	439	GLU	3.6
1	A	80	GLU	3.6
1	A	460	GLU	3.5
1	A	343	THR	3.4
1	A	456	ILE	3.4
1	A	161	VAL	3.4
1	A	239	LEU	3.4
1	A	292	TRP	3.3
1	A	434	GLY	3.3
1	A	115	LEU	3.1
1	A	318	THR	3.1
1	A	464	ALA	3.1
1	A	438	GLY	3.1
1	A	194	ALA	3.0
1	A	190	LEU	3.0
1	A	67	VAL	2.9
1	A	168	TYR	2.9
1	A	406	LEU	2.9
1	A	455	GLY	2.9
1	A	78	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	97	PRO	2.8
1	A	443	VAL	2.8
1	A	241	ASN	2.8
1	A	410	ASP	2.8
1	A	459	TYR	2.8
1	A	295	PHE	2.8
1	A	436	ASP	2.7
1	A	324	VAL	2.7
1	A	451	ARG	2.7
1	A	409	LEU	2.7
1	A	370	LEU	2.7
1	A	398	ASP	2.6
1	A	433	PRO	2.6
1	A	289	ALA	2.6
1	A	457	TYR	2.6
1	A	148	LEU	2.6
1	A	441	LYS	2.6
1	A	108	GLY	2.5
1	A	198	ALA	2.5
1	A	414	VAL	2.5
1	A	347	LEU	2.5
1	A	156	PRO	2.5
1	A	201	TYR	2.4
1	A	160	GLU	2.4
1	A	119	ALA	2.4
1	A	348	GLU	2.4
1	A	472	ASN	2.4
1	A	155	TRP	2.4
1	A	68	THR	2.3
1	A	453	ALA	2.3
1	A	94	GLU	2.3
1	A	473	LEU	2.3
1	A	462	TYR	2.3
1	A	90	LYS	2.3
1	A	143	ALA	2.3
1	A	84	ILE	2.3
1	A	264	VAL	2.3
1	A	300	VAL	2.3
1	A	235	TYR	2.2
1	A	452	ALA	2.2
1	A	340	VAL	2.2
1	A	400	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	337	ILE	2.2
1	A	390	ILE	2.2
1	A	411	ASN	2.2
1	A	215	LEU	2.2
1	A	193	ALA	2.2
1	A	407	ALA	2.2
1	A	333	ILE	2.2
1	A	402	ILE	2.2
1	A	446	TRP	2.2
1	A	137	VAL	2.2
1	A	210	THR	2.2
1	A	111	TRP	2.1
1	A	197	ASP	2.1
1	A	147	SER	2.1
1	A	162	LEU	2.1
1	A	317	ALA	2.1
1	A	346	ASN	2.1
1	A	280	ASP	2.1
1	A	345	PRO	2.1
1	A	319	PHE	2.1
1	A	171	ARG	2.1
1	A	297	ASN	2.1
1	A	421	VAL	2.1
1	A	315	GLN	2.1
1	A	430	GLU	2.0
1	A	214	SER	2.0
1	A	316	ASN	2.0
1	A	76	LEU	2.0
1	A	157	LEU	2.0
1	A	196	LEU	2.0

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

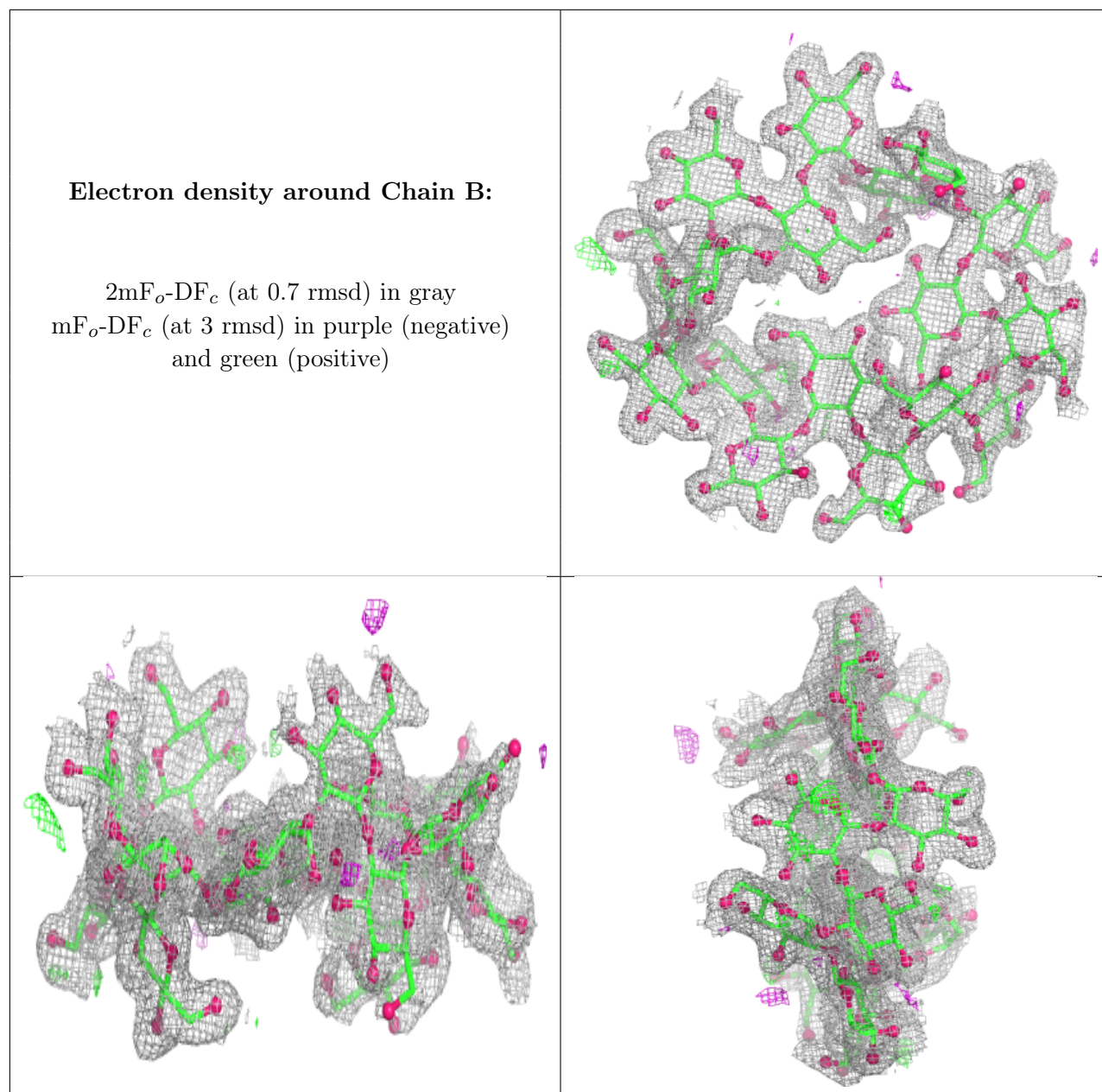
There are no non-standard protein/DNA/RNA residues in this entry.

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(\AA^2)	Q<0.9
2	BGC	B	2	11/12	0.53	0.22	61,64,72,73	0
2	BGC	B	5	11/12	0.63	0.17	54,57,59,61	0
2	BGC	B	7	11/12	0.63	0.22	49,51,53,56	0
2	BGC	B	8	11/12	0.77	0.20	39,46,52,57	0
2	BGC	B	3	11/12	0.80	0.18	38,45,58,61	0
2	BGC	B	4	11/12	0.81	0.16	51,52,61,62	0
2	BGC	B	9	11/12	0.82	0.17	34,41,46,46	0
2	BGC	B	15	11/12	0.82	0.13	30,32,35,36	0
2	BGC	B	17	11/12	0.84	0.12	29,33,37,43	0
2	BGC	B	10	11/12	0.85	0.12	28,33,36,41	0
2	BGC	B	1	11/12	0.87	0.11	35,39,41,44	0
2	BGC	B	16	11/12	0.87	0.10	29,32,34,35	0
2	BGC	B	11	11/12	0.87	0.12	27,30,32,35	0
2	BGC	B	14	11/12	0.89	0.10	25,28,31,32	0
2	BGC	B	6	11/12	0.89	0.12	31,36,40,42	0
2	BGC	B	13	11/12	0.91	0.08	23,25,28,29	0
2	BGC	B	12	11/12	0.93	0.08	23,27,30,30	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
3	GOL	A	501	6/6	0.82	0.21	36,37,39,41	0

6.5 Other polymers ⓘ

There are no such residues in this entry.