



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:13 PM UTC

PDB ID : 8PXV / pdb_00008pxv
Title : Targeting extended blood antigens by Akkermansia muciniphila enzymes unveils a missing link for generating universal donor blood
Authors : Weikum, J.; Jensen, M.; Abou Hachem, M.; Morth, J.P.
Deposited on : 2023-07-24
Resolution : 2.50 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
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

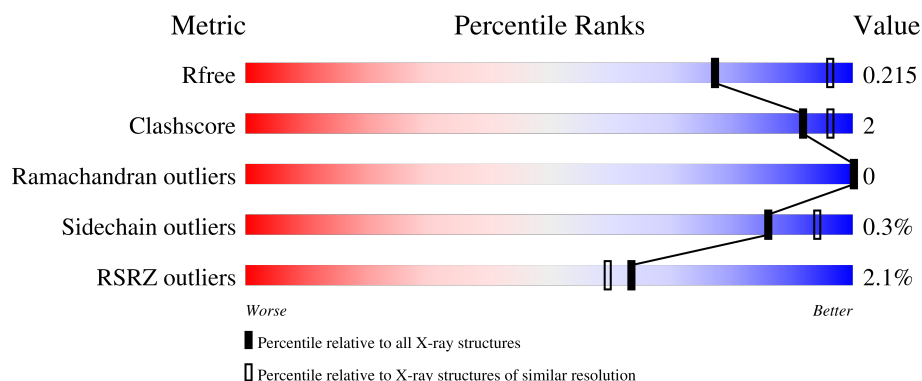
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	655	% 95%
1	B	655	2% 93%
1	C	655	3% 91% 5%
2	E	2	100%
2	F	2	100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 30553 atoms, of which 14963 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-N-acetylhexosaminidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	646	Total	C	H	N	O	S	0	0	0
			10102	3230	5019	891	945	17			
1	B	634	Total	C	H	N	O	S	0	0	0
			9963	3188	4955	875	928	17			
1	C	632	Total	C	H	N	O	S	0	0	0
			9932	3178	4942	872	923	17			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP B2UN02
A	648	LEU	-	expression tag	UNP B2UN02
A	649	GLU	-	expression tag	UNP B2UN02
A	650	HIS	-	expression tag	UNP B2UN02
A	651	HIS	-	expression tag	UNP B2UN02
A	652	HIS	-	expression tag	UNP B2UN02
A	653	HIS	-	expression tag	UNP B2UN02
A	654	HIS	-	expression tag	UNP B2UN02
A	655	HIS	-	expression tag	UNP B2UN02
B	1	MET	-	initiating methionine	UNP B2UN02
B	648	LEU	-	expression tag	UNP B2UN02
B	649	GLU	-	expression tag	UNP B2UN02
B	650	HIS	-	expression tag	UNP B2UN02
B	651	HIS	-	expression tag	UNP B2UN02
B	652	HIS	-	expression tag	UNP B2UN02
B	653	HIS	-	expression tag	UNP B2UN02
B	654	HIS	-	expression tag	UNP B2UN02
B	655	HIS	-	expression tag	UNP B2UN02
C	1	MET	-	initiating methionine	UNP B2UN02
C	648	LEU	-	expression tag	UNP B2UN02
C	649	GLU	-	expression tag	UNP B2UN02
C	650	HIS	-	expression tag	UNP B2UN02
C	651	HIS	-	expression tag	UNP B2UN02

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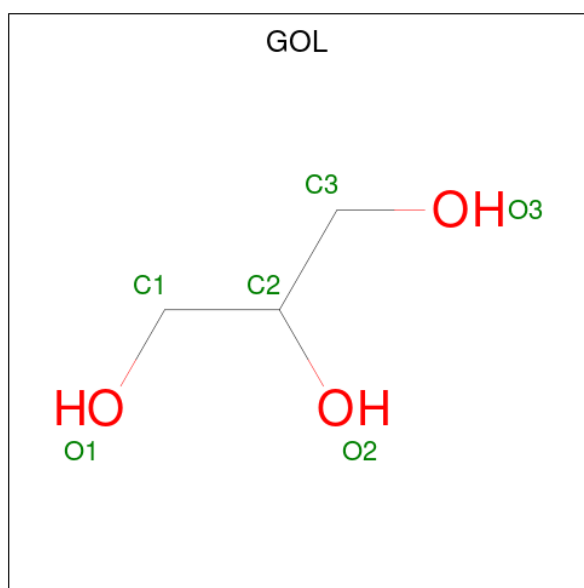
Chain	Residue	Modelled	Actual	Comment	Reference
C	652	HIS	-	expression tag	UNP B2UN02
C	653	HIS	-	expression tag	UNP B2UN02
C	654	HIS	-	expression tag	UNP B2UN02
C	655	HIS	-	expression tag	UNP B2UN02

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	2	Total	C	H	O	0	0	0
			45	12	22	11			
2	F	2	Total	C	H	O	0	0	0
			45	12	22	11			

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



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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total 1	Na 1	0	0

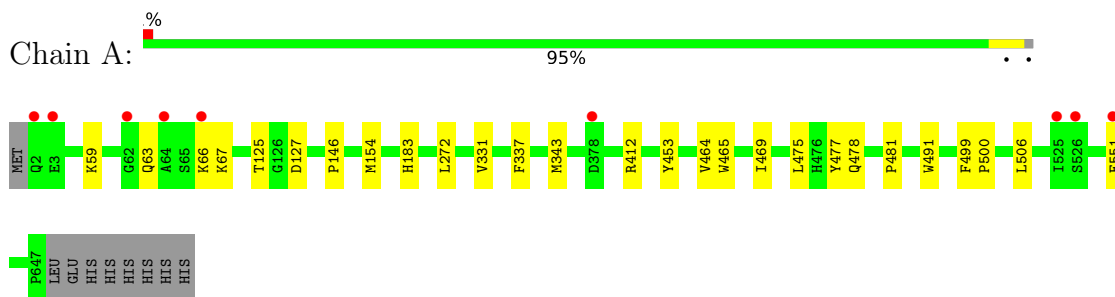
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	165	Total 165	O 165	0	0
5	B	142	Total 142	O 142	0	0
5	C	149	Total 149	O 149	0	0

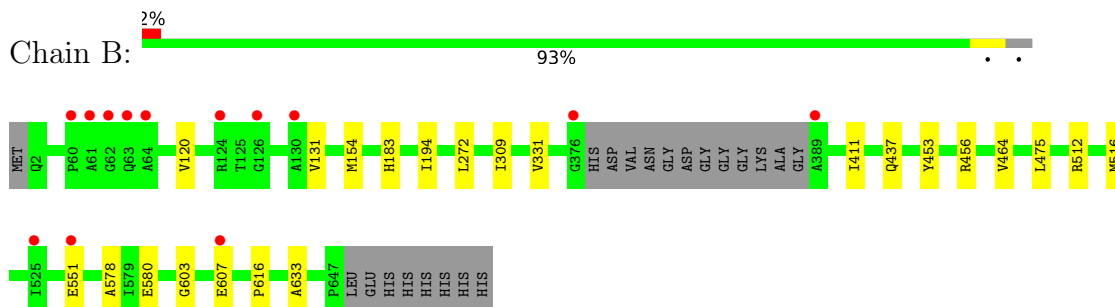
3 Residue-property plots [i](#)

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.

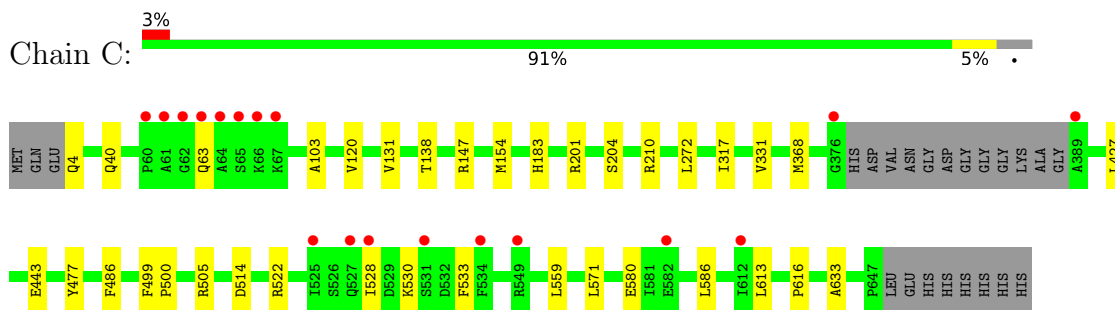
- Molecule 1: Beta-N-acetylhexosaminidase



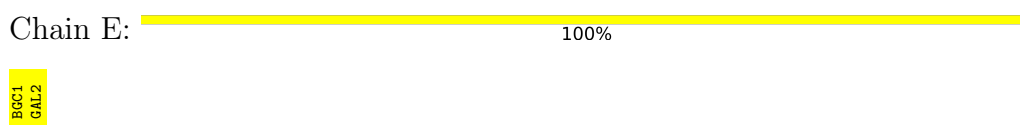
- Molecule 1: Beta-N-acetylhexosaminidase



- Molecule 1: Beta-N-acetylhexosaminidase



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



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

Chain F:

100%

BGL
GAL2

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.26Å 170.42Å 171.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.32 – 2.50 54.32 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.3 (54.32-2.50) 95.3 (54.32-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158, PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.178 , 0.212 0.181 , 0.215	Depositor DCC
R_{free} test set	4659 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	46.0	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 34.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	30553	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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: BGC, GAL, NA, GOL

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	0.13	0/5211	0.36	0/7054
1	B	0.12	0/5134	0.35	0/6950
1	C	0.13	0/5116	0.36	0/6926
All	All	0.13	0/15461	0.35	0/20930

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	5083	5019	5017	18	0
1	B	5008	4955	4953	15	0
1	C	4990	4942	4939	19	0
2	E	23	22	21	0	0
2	F	23	22	21	0	0
3	A	6	3	8	0	0
4	C	1	0	0	0	0
5	A	165	0	0	2	0
5	B	142	0	0	0	0
5	C	149	0	0	0	0
All	All	15590	14963	14959	49	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 (49) 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:B:120:VAL:HG11	1:B:131:VAL:HG21	1.58	0.84
1:B:411:ILE:HG23	1:B:456:ARG:HG3	1.76	0.68
1:A:63:GLN:NE2	5:A:802:HOH:O	2.24	0.66
1:C:120:VAL:HG11	1:C:131:VAL:HG21	1.85	0.58
1:A:272:LEU:HD13	1:A:331:VAL:HG11	1.87	0.57
1:B:194:ILE:HD11	1:B:309:ILE:HD11	1.87	0.54
1:C:272:LEU:HD13	1:C:331:VAL:HG11	1.92	0.52
1:C:530:LYS:HA	1:C:571:LEU:HD21	1.92	0.51
1:B:464:VAL:HG11	1:B:475:LEU:CD1	2.39	0.51
1:B:551:GLU:N	1:B:551:GLU:OE1	2.44	0.51
1:B:607:GLU:O	1:B:607:GLU:HG3	2.10	0.51
1:B:551:GLU:HG2	1:B:551:GLU:O	2.12	0.50
1:A:59:LYS:HA	1:A:59:LYS:HE2	1.94	0.49
1:B:464:VAL:HG11	1:B:475:LEU:HD12	1.95	0.47
1:A:412:ARG:HG2	1:A:453:TYR:CZ	2.49	0.47
1:B:616:PRO:HB3	1:C:477:TYR:CE1	2.49	0.47
1:C:40:GLN:HG3	1:C:103:ALA:HB1	1.97	0.47
1:B:580:GLU:HG3	1:B:633:ALA:HB2	1.97	0.47
1:C:4:GLN:HB2	1:C:505:ARG:HG2	1.97	0.46
1:A:551:GLU:N	1:A:551:GLU:OE1	2.49	0.46
1:C:427:LEU:HD21	1:C:486:PHE:HE2	1.81	0.45
1:C:147:ARG:NH2	1:C:443:GLU:OE2	2.48	0.45
1:A:154:MET:HA	1:A:183:HIS:O	2.17	0.45
1:A:477:TYR:CE1	1:C:616:PRO:HB3	2.52	0.45
1:B:411:ILE:HG21	1:B:453:TYR:HB3	1.99	0.45
1:B:578:ALA:HB2	1:B:603:GLY:HA3	1.99	0.45
1:A:337:PHE:CE2	1:A:343:MET:HE1	2.53	0.44
1:A:337:PHE:CD2	1:A:343:MET:HE1	2.52	0.44
1:B:512:ARG:HB3	1:B:516:MET:HE2	2.00	0.43
1:C:580:GLU:HG3	1:C:633:ALA:HB2	2.01	0.43
1:C:514:ASP:OD1	1:C:522:ARG:NH1	2.49	0.43
1:A:125:THR:HB	1:C:138:THR:HG22	2.00	0.43
1:C:528:ILE:HG23	1:C:533:PHE:CE1	2.54	0.43
1:A:154:MET:HE1	1:A:465:TRP:CD2	2.54	0.43
1:B:272:LEU:HD13	1:B:331:VAL:HG11	2.00	0.42
1:A:154:MET:HE1	1:A:465:TRP:CE3	2.55	0.42
1:A:464:VAL:HG11	1:A:475:LEU:CD1	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:MET:HA	1:B:183:HIS:O	2.19	0.42
1:A:127:ASP:O	5:A:801:HOH:O	2.22	0.41
1:A:469:ILE:HD11	1:A:478:GLN:HG3	2.02	0.41
1:A:481:PRO:HB2	1:A:506:LEU:HD21	2.02	0.41
1:C:154:MET:HG3	1:C:183:HIS:CG	2.56	0.41
1:A:146:PRO:HB3	1:A:491:TRP:CE3	2.56	0.41
1:C:499:PHE:HB3	1:C:500:PRO:HD3	2.02	0.41
1:C:586:LEU:HB2	1:C:613:LEU:HD13	2.03	0.41
1:C:317:ILE:HD13	1:C:368:MET:SD	2.61	0.40
1:C:201:ARG:HA	1:C:204:SER:OG	2.21	0.40
1:A:499:PHE:HB3	1:A:500:PRO:HD3	2.02	0.40
1:C:559:LEU:HD12	1:C:559:LEU:N	2.36	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	644/655 (98%)	630 (98%)	14 (2%)	0	100	100
1	B	630/655 (96%)	617 (98%)	13 (2%)	0	100	100
1	C	628/655 (96%)	611 (97%)	17 (3%)	0	100	100
All	All	1902/1965 (97%)	1858 (98%)	44 (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	533/542 (98%)	531 (100%)	2 (0%)	84	93
1	B	527/542 (97%)	526 (100%)	1 (0%)	87	95
1	C	525/542 (97%)	523 (100%)	2 (0%)	84	93
All	All	1585/1626 (98%)	1580 (100%)	5 (0%)	86	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	LYS
1	A	67	LYS
1	B	437	GLN
1	C	63	GLN
1	C	210	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	377	HIS
1	A	394	ASN
1	A	527	GLN
1	A	610	GLN
1	A	639	HIS
1	B	33	GLN
1	B	173	GLN
1	B	218	ASN
1	B	403	ASN
1	B	409	ASN
1	B	478	GLN
1	B	610	GLN
1	B	639	HIS
1	C	639	HIS

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 ⓘ

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	BGC	E	1	2	12,12,12	0.19	0	17,17,17	1.78	3 (17%)
2	GAL	E	2	2	11,11,12	0.40	0	15,15,17	1.54	2 (13%)
2	BGC	F	1	2	12,12,12	0.15	0	17,17,17	1.79	7 (41%)
2	GAL	F	2	2	11,11,12	0.40	0	15,15,17	1.54	3 (20%)

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	E	1	2	-	2/2/22/22	0/1/1/1
2	GAL	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	F	1	2	-	1/2/22/22	0/1/1/1
2	GAL	F	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	1	BGC	O4-C4-C3	-3.64	101.79	110.38
2	F	1	BGC	O4-C4-C3	-3.43	102.30	110.38
2	E	1	BGC	C4-C3-C2	-2.67	106.14	110.83
2	E	1	BGC	O1-C1-O5	-2.51	102.96	110.41
2	F	1	BGC	O1-C1-O5	-2.27	103.68	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	BGC	O3-C3-C4	-2.26	105.05	110.38
2	F	2	GAL	O3-C3-C2	-2.15	105.66	110.05
2	F	1	BGC	C4-C3-C2	-2.15	107.05	110.83
2	F	2	GAL	O4-C4-C5	-2.11	104.12	109.32
2	E	2	GAL	O3-C3-C2	-2.10	105.76	110.05
2	E	2	GAL	C1-C2-C3	-2.08	106.62	109.64
2	F	1	BGC	O1-C1-C2	-2.07	102.98	108.98
2	F	2	GAL	O2-C2-C3	-2.04	105.93	110.15
2	F	1	BGC	O5-C5-C4	-2.03	106.04	109.70
2	F	1	BGC	O4-C4-C5	-2.03	104.33	109.32

There are no chirality outliers.

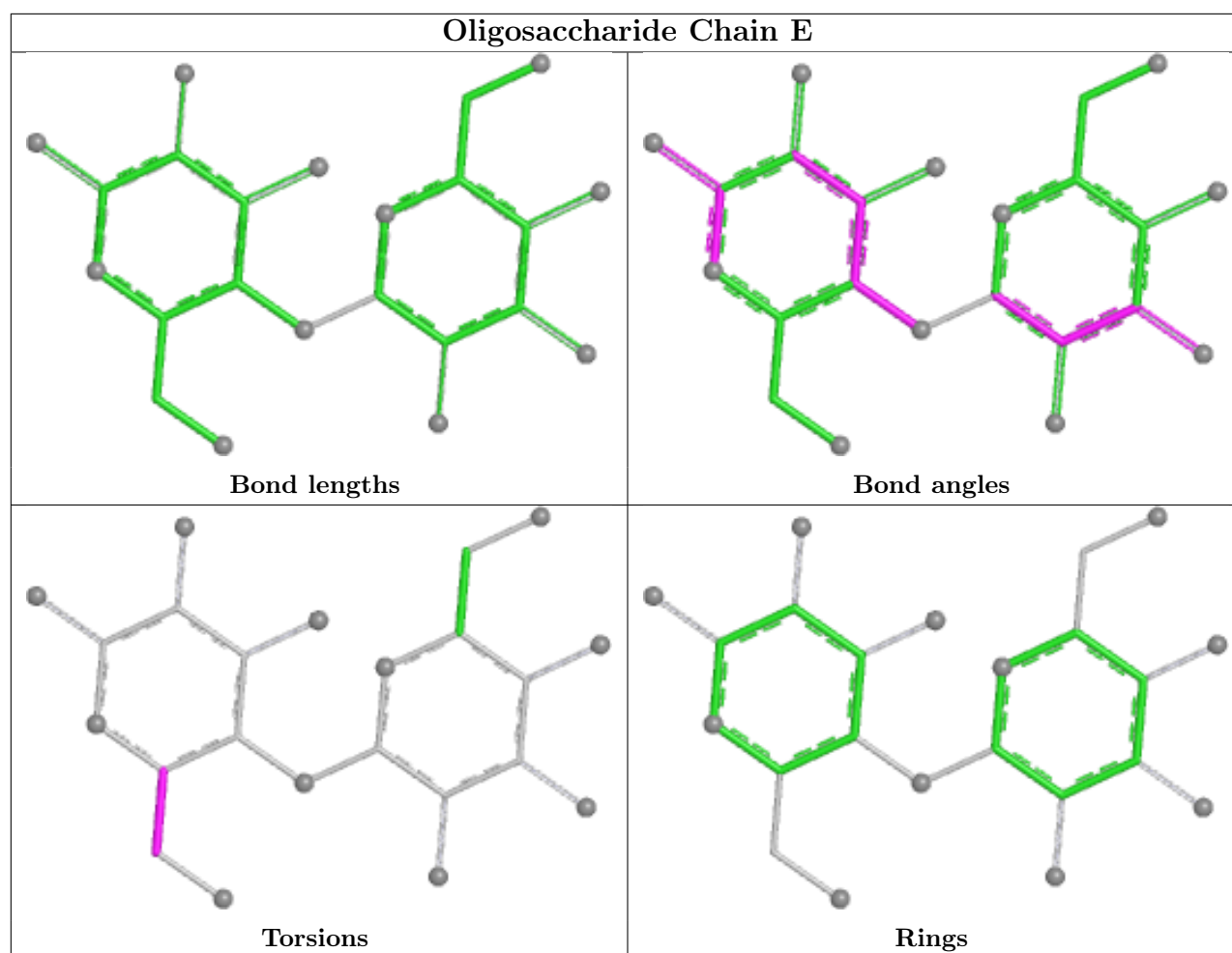
All (3) torsion outliers are listed below:

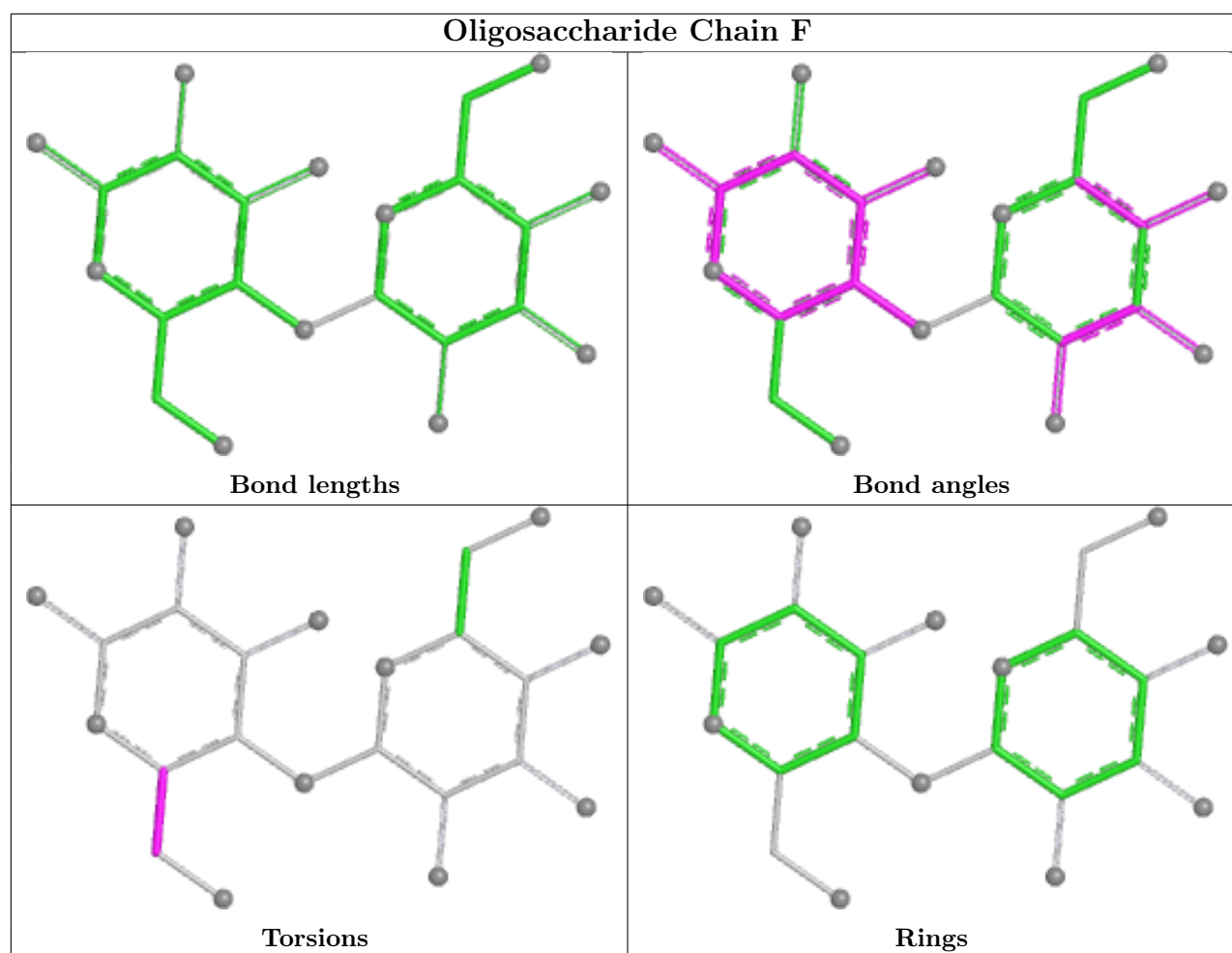
Mol	Chain	Res	Type	Atoms
2	E	1	BGC	O5-C5-C6-O6
2	E	1	BGC	C4-C5-C6-O6
2	F	1	BGC	O5-C5-C6-O6

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 [i](#)

Of 2 ligands modelled in this entry, 1 is 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	$\# Z > 2$
3	GOL	A	701	-	5,5,5	0.98	0	5,5,5	1.06	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	701	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	646/655 (98%)	-0.13	9 (1%) 73 70	38, 54, 79, 114	0
1	B	634/655 (96%)	-0.15	13 (2%) 63 59	37, 52, 92, 157	0
1	C	632/655 (96%)	-0.16	18 (2%) 55 50	37, 51, 84, 151	0
All	All	1912/1965 (97%)	-0.15	40 (2%) 63 59	37, 52, 86, 157	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	64	ALA	5.6
1	B	389	ALA	5.2
1	B	62	GLY	4.7
1	C	389	ALA	4.1
1	B	64	ALA	3.5
1	B	61	ALA	3.4
1	C	527	GLN	3.3
1	C	65	SER	3.2
1	A	551	GLU	3.1
1	C	549	ARG	3.0
1	C	534	PHE	2.9
1	A	62	GLY	2.8
1	B	607	GLU	2.7
1	A	526	SER	2.7
1	C	63	GLN	2.7
1	C	525	ILE	2.7
1	B	130	ALA	2.7
1	B	60	PRO	2.6
1	C	531	SER	2.6
1	C	528	ILE	2.6
1	A	3	GLU	2.6
1	B	124	ARG	2.5
1	B	126	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	376	GLY	2.5
1	C	61	ALA	2.4
1	C	62	GLY	2.4
1	C	66	LYS	2.4
1	C	612	ILE	2.3
1	A	2	GLN	2.3
1	B	525	ILE	2.3
1	A	66	LYS	2.2
1	B	376	GLY	2.2
1	C	60	PRO	2.2
1	A	64	ALA	2.2
1	B	551	GLU	2.2
1	C	67	LYS	2.1
1	C	582	GLU	2.1
1	B	63	GLN	2.1
1	A	525	ILE	2.1
1	A	378	ASP	2.1

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 ⓘ

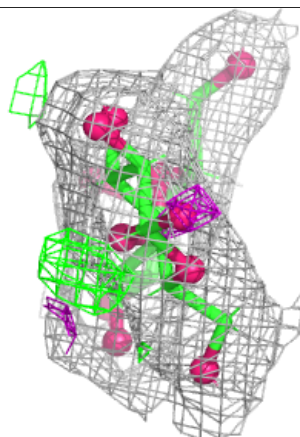
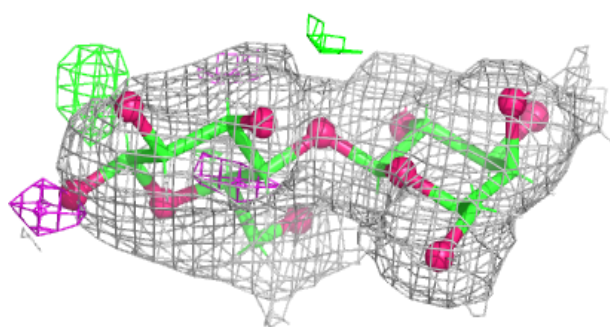
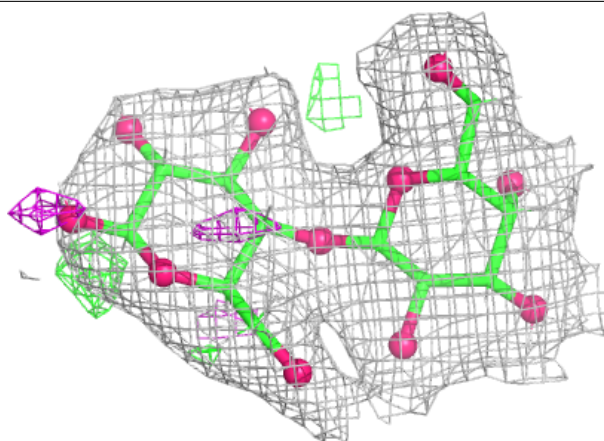
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

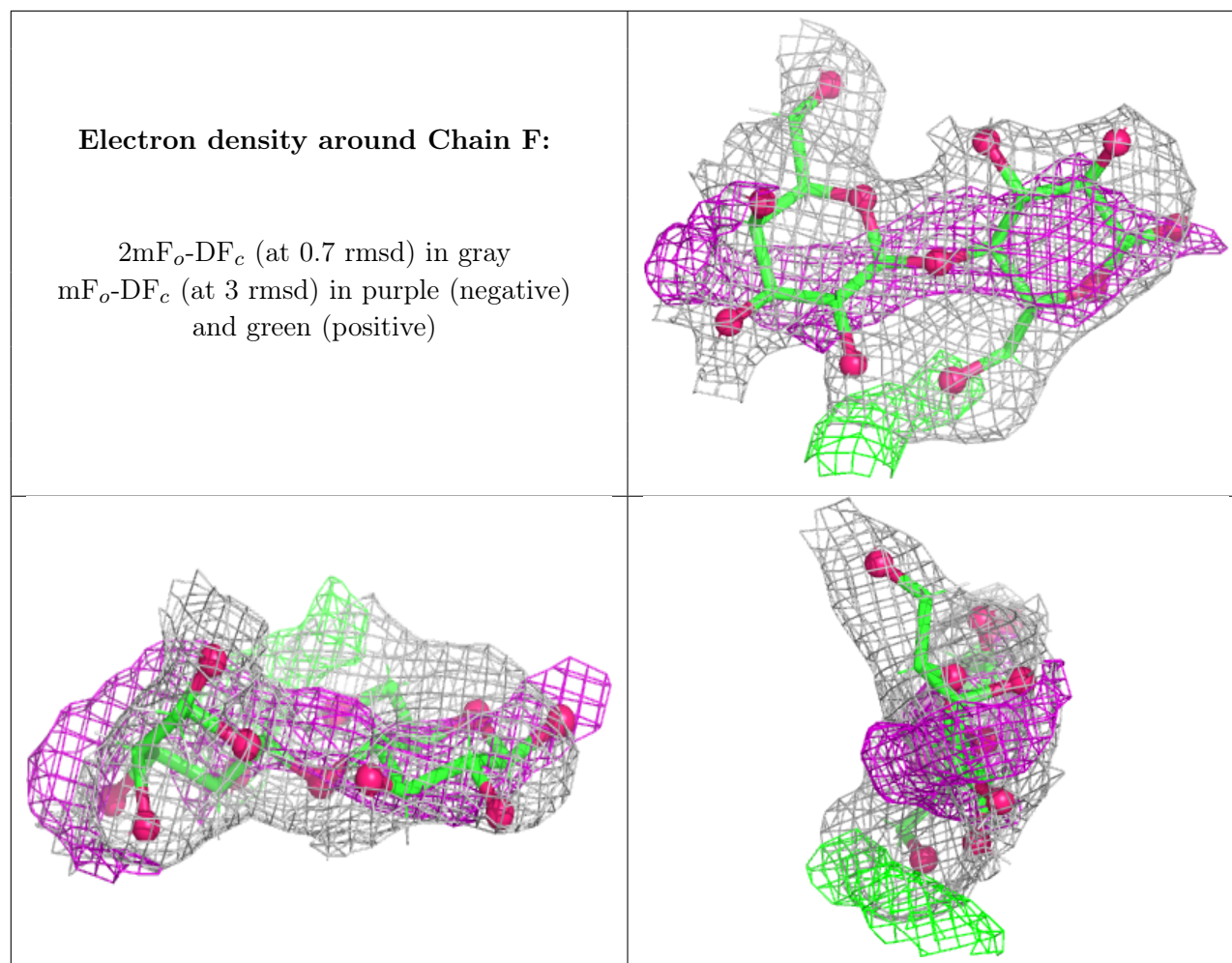
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BGC	E	1	12/12	0.78	0.15	41,50,59,68	0
2	GAL	E	2	11/12	0.85	0.12	33,42,50,55	0
2	BGC	F	1	12/12	-	-	41,61,73,81	0
2	GAL	F	2	11/12	-	-	42,53,62,64	0

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

Electron density around Chain E:

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	A	701	6/6	0.82	0.24	44,53,64,64	0
4	NA	C	701	1/1	0.90	0.14	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.