



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:06 PM UTC

PDB ID : 9N8E / pdb_00009n8e
Title : Crystal structure of EBOV glycoprotein with modified HR1c (L579P) and HR2 stalk
Authors : Lee, Y.Z.; Stanfield, R.L.; Wilson, I.A.; Zhu, J.
Deposited on : 2025-02-08
Resolution : 3.20 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

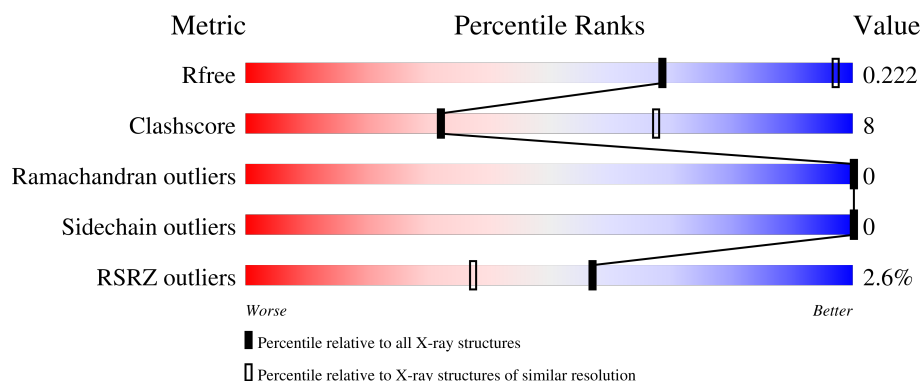
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

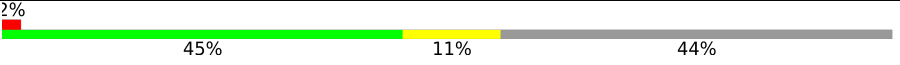
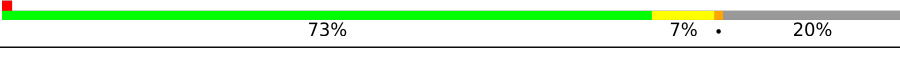
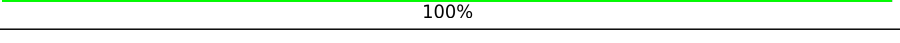
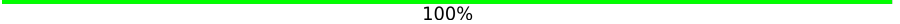
The reported resolution of this entry is 3.20 Å.

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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	475	 2% 45% 11% 44%
2	B	165	 73% 7% 20%
3	C	2	 100%
4	D	6	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3247 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 Envelope glycoprotein GP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2077	1326	350	396	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	ALA	THR	conflict	UNP Q05320

- Molecule 2 is a protein called Envelope glycoprotein GP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	132	Total	C	N	O	S	0	0	0
			1042	663	180	193	6			

There are 31 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	579	PRO	LEU	engineered mutation	UNP Q05320
B	615	LEU	TRP	conflict	UNP Q05320
B	638	ALA	-	expression tag	UNP Q05320
B	639	SER	-	expression tag	UNP Q05320
B	640	GLY	-	expression tag	UNP Q05320
B	641	TYR	-	expression tag	UNP Q05320
B	642	ILE	-	expression tag	UNP Q05320
B	643	PRO	-	expression tag	UNP Q05320
B	644	GLU	-	expression tag	UNP Q05320
B	645	ALA	-	expression tag	UNP Q05320
B	646	PRO	-	expression tag	UNP Q05320
B	647	ARG	-	expression tag	UNP Q05320
B	648	ASP	-	expression tag	UNP Q05320
B	649	GLY	-	expression tag	UNP Q05320
B	650	GLN	-	expression tag	UNP Q05320

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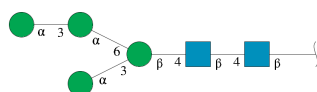
Chain	Residue	Modelled	Actual	Comment	Reference
B	651	ALA	-	expression tag	UNP Q05320
B	652	TYR	-	expression tag	UNP Q05320
B	653	VAL	-	expression tag	UNP Q05320
B	654	ARG	-	expression tag	UNP Q05320
B	655	LYS	-	expression tag	UNP Q05320
B	656	ASP	-	expression tag	UNP Q05320
B	657	GLY	-	expression tag	UNP Q05320
B	658	GLU	-	expression tag	UNP Q05320
B	659	TRP	-	expression tag	UNP Q05320
B	660	VAL	-	expression tag	UNP Q05320
B	661	LEU	-	expression tag	UNP Q05320
B	662	LEU	-	expression tag	UNP Q05320
B	663	SER	-	expression tag	UNP Q05320
B	664	THR	-	expression tag	UNP Q05320
B	665	PHE	-	expression tag	UNP Q05320
B	666	LEU	-	expression tag	UNP Q05320

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



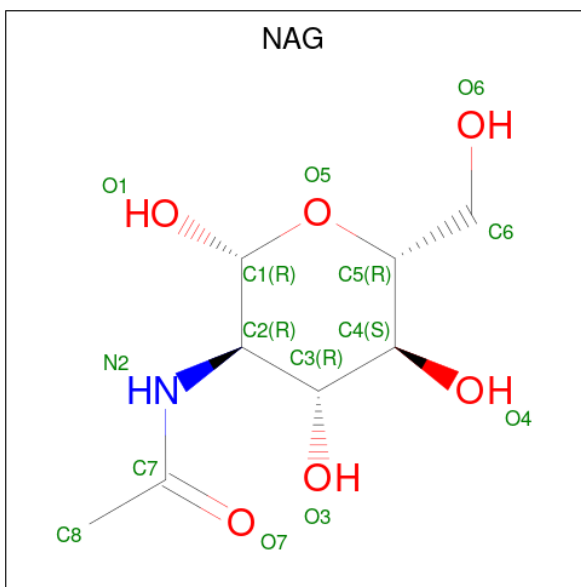
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



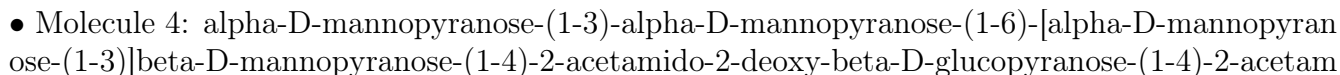
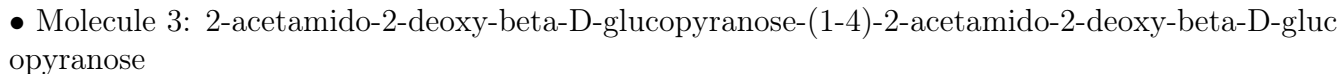
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

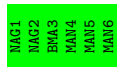
- Molecule 1: Envelope glycoprotein GP1



ido-2-deoxy-beta-D-glucopyranose

Chain D:

100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	114.47Å 114.47Å 133.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.57 – 3.20 40.57 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (40.57-3.20) 99.5 (40.57-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 3.18Å)	Xtriage
Refinement program	PHENIX 1.21rc1_5127	Depositor
R, R_{free}	0.215 , 0.221 0.215 , 0.222	Depositor DCC
R_{free} test set	1675 reflections (9.74%)	wwPDB-VP
Wilson B-factor (Å ²)	113.9	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 73.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.031 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3247	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.27% 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: MAN, BMA, NAG

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	0.55	0/2098	0.89	1/2849 (0.0%)
2	B	0.60	0/1067	0.93	1/1453 (0.1%)
All	All	0.57	0/3165	0.90	2/4302 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	554	LEU	CA-CB-CG	6.00	137.32	116.30
1	A	184	LEU	CA-CB-CG	5.14	134.28	116.30

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	2077	0	1990	47	0
2	B	1042	0	1012	11	0
3	C	28	0	25	0	0
4	D	72	0	61	0	0
5	A	14	0	13	2	0
5	B	14	0	13	0	0
All	All	3247	0	3114	51	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 8.

All (51) 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:51:LEU:HD23	2:B:596:ARG:HH22	1.33	0.91
2:B:623:ILE:HA	2:B:627:ILE:HB	1.55	0.86
1:A:247:ARG:HG3	1:A:283:THR:HG23	1.62	0.81
1:A:127:ASP:O	2:B:580:ARG:NH2	2.14	0.80
1:A:240:THR:C	1:A:241:TYR:HD1	2.00	0.70
1:A:63:LEU:HB3	2:B:585:LEU:HD22	1.75	0.68
1:A:115:LYS:HE3	1:A:146:PRO:O	1.94	0.67
1:A:228:ASN:HD22	5:A:401:NAG:H83	1.62	0.65
1:A:106:GLU:HG3	1:A:290:PHE:CD1	2.31	0.65
1:A:51:LEU:HG	1:A:52:VAL:H	1.63	0.62
1:A:307:SER:HB3	1:A:361:UNK:HA	1.84	0.59
1:A:61:ASN:O	1:A:64:ARG:NH1	2.32	0.59
2:B:623:ILE:O	2:B:628:HIS:HB2	2.02	0.58
1:A:247:ARG:HG3	1:A:283:THR:CG2	2.35	0.56
1:A:71:GLU:HG3	1:A:290:PHE:HE2	1.69	0.56
1:A:237:ASP:OD1	1:A:240:THR:N	2.39	0.55
1:A:221:GLN:HG3	1:A:241:TYR:CE2	2.43	0.53
1:A:89:ARG:NH1	1:A:90:SER:O	2.42	0.52
2:B:551:GLN:O	2:B:554:LEU:HD12	2.08	0.52
1:A:106:GLU:HG3	1:A:290:PHE:CG	2.47	0.51
1:A:120:GLU:HG2	1:A:172:ARG:NE	2.26	0.50
1:A:51:LEU:HD23	2:B:596:ARG:NH2	2.15	0.49
1:A:233:LEU:HD13	1:A:241:TYR:HD2	1.77	0.49
1:A:307:SER:CB	1:A:361:UNK:HA	2.43	0.48
1:A:242:VAL:HG21	1:A:256:LEU:HD21	1.96	0.47
1:A:104:TRP:CD2	2:B:516:HIS:CD2	3.03	0.47
1:A:120:GLU:HG2	1:A:172:ARG:CZ	2.45	0.47
1:A:234:PHE:CD2	1:A:253:LEU:HD22	2.51	0.46
1:A:125:ALA:HB2	1:A:174:THR:HG21	1.98	0.46
1:A:185:ILE:HD13	1:A:185:ILE:HG21	1.69	0.45
1:A:129:ILE:HD13	1:A:165:LEU:HD13	1.99	0.45
1:A:241:TYR:CE2	1:A:272:LYS:HE3	2.52	0.45
1:A:51:LEU:HA	1:A:51:LEU:HD12	1.63	0.45
1:A:357:UNK:O	1:A:359:UNK:N	2.49	0.44
1:A:302:ARG:HG3	1:A:303:SER:H	1.83	0.44
1:A:83:THR:HG22	1:A:86:TRP:CZ3	2.53	0.44
2:B:506:ASN:HA	2:B:560:GLN:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:VAL:HG12	1:A:185:ILE:HB	1.99	0.43
1:A:129:ILE:HD13	1:A:165:LEU:CD1	2.49	0.43
1:A:248:PHE:CD1	1:A:283:THR:HG21	2.54	0.43
1:A:240:THR:C	1:A:241:TYR:CD1	2.90	0.43
1:A:151:PHE:HB2	1:A:153:PHE:CE1	2.54	0.42
1:A:80:PRO:O	1:A:84:LYS:HG2	2.18	0.42
1:A:104:TRP:CG	2:B:516:HIS:CD2	3.07	0.42
1:A:234:PHE:CD1	1:A:234:PHE:C	2.98	0.42
1:A:90:SER:OG	1:A:150:ASP:N	2.47	0.42
1:A:187:PRO:HG2	1:A:190:LYS:HB2	2.02	0.42
1:A:86:TRP:CD1	1:A:86:TRP:N	2.88	0.41
1:A:247:ARG:NH1	1:A:283:THR:HG22	2.35	0.41
1:A:163:ASP:OD1	2:B:543:TYR:OH	2.30	0.40
1:A:228:ASN:HD22	5:A:401:NAG:C8	2.30	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	254/475 (54%)	244 (96%)	10 (4%)	0	100	100
2	B	130/165 (79%)	125 (96%)	5 (4%)	0	100	100
All	All	384/640 (60%)	369 (96%)	15 (4%)	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	222/398 (56%)	222 (100%)	0	100	100
2	B	111/138 (80%)	111 (100%)	0	100	100
All	All	333/536 (62%)	333 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	69	ASN
1	A	73	ASN
1	A	107	ASN
1	A	188	GLN
2	B	551	GLN
2	B	595	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 ⓘ

8 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
3	NAG	C	1	3,1	14,14,15	0.49	0	17,19,21	0.61	0
3	NAG	C	2	3	14,14,15	0.57	0	17,19,21	0.46	0
4	NAG	D	1	2,4	14,14,15	0.53	0	17,19,21	1.21	0
4	NAG	D	2	4	14,14,15	0.37	0	17,19,21	0.75	0
4	BMA	D	3	4	11,11,12	0.26	0	15,15,17	0.63	0
4	MAN	D	4	4	11,11,12	0.22	0	15,15,17	0.59	0
4	MAN	D	5	4	11,11,12	0.20	0	15,15,17	0.55	0
4	MAN	D	6	4	11,11,12	0.20	0	15,15,17	0.60	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	NAG	C	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	C	2	3	-	3/6/23/26	0/1/1/1
4	NAG	D	1	2,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	BMA	D	3	4	-	1/2/19/22	0/1/1/1
4	MAN	D	4	4	-	0/2/19/22	0/1/1/1
4	MAN	D	5	4	-	0/2/19/22	0/1/1/1
4	MAN	D	6	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

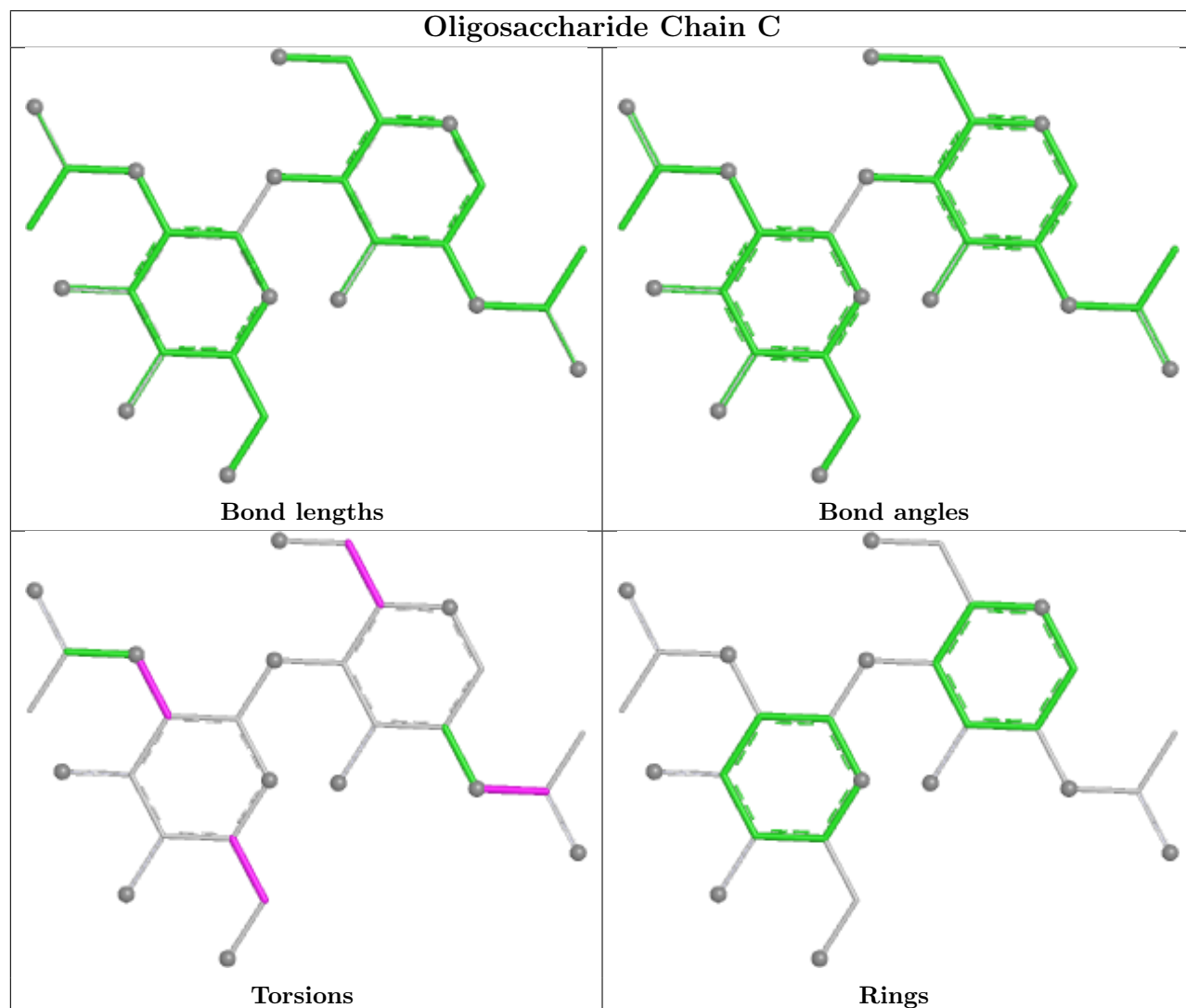
All (8) torsion outliers are listed below:

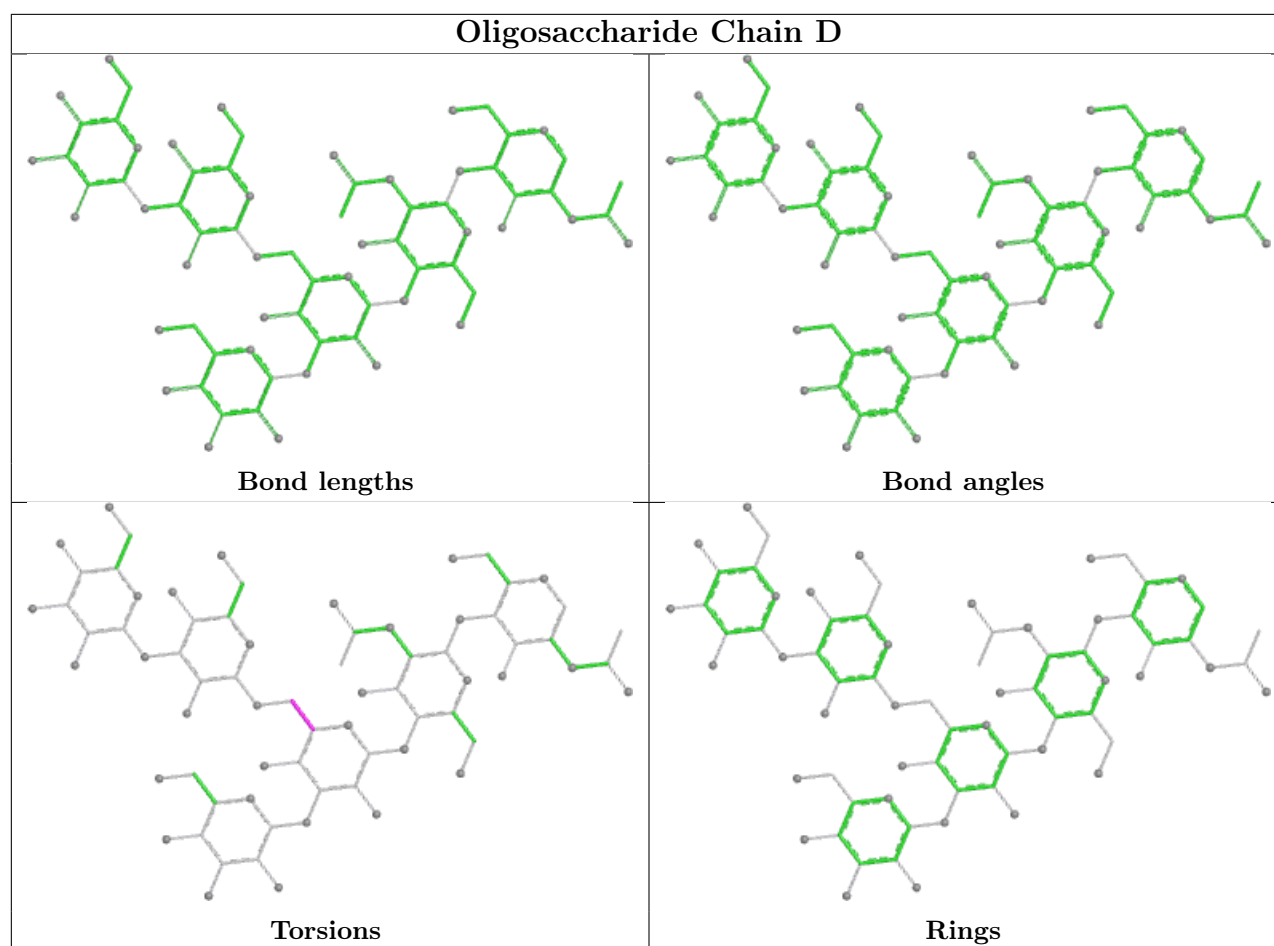
Mol	Chain	Res	Type	Atoms
3	C	1	NAG	C8-C7-N2-C2
3	C	1	NAG	O7-C7-N2-C2
3	C	2	NAG	C4-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
3	C	2	NAG	C1-C2-N2-C7
4	D	3	BMA	O5-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6

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](#)

2 ligands 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	$\# Z > 2$
5	NAG	B	701	2	14,14,15	0.56	0	17,19,21	0.64	0
5	NAG	A	401	1	14,14,15	0.24	0	17,19,21	0.49	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	B	701	2	-	0/6/23/26	0/1/1/1
5	NAG	A	401	1	-	2/6/23/26	0/1/1/1

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
5	A	401	NAG	C8-C7-N2-C2
5	A	401	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	401	NAG	2	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	260/475 (54%)	0.15	8 (3%) 51 32	78, 114, 183, 202	0
2	B	132/165 (80%)	-0.10	2 (1%) 72 52	76, 97, 198, 207	0
All	All	392/640 (61%)	0.06	10 (2%) 57 37	76, 107, 186, 207	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	627	ILE	4.4
1	A	310	VAL	3.8
2	B	626	ILE	3.7
1	A	285	ILE	3.6
1	A	284	THR	3.2
1	A	309	THR	2.8
1	A	306	LEU	2.7
1	A	199	LEU	2.5
1	A	51	LEU	2.1
1	A	308	PHE	2.1

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

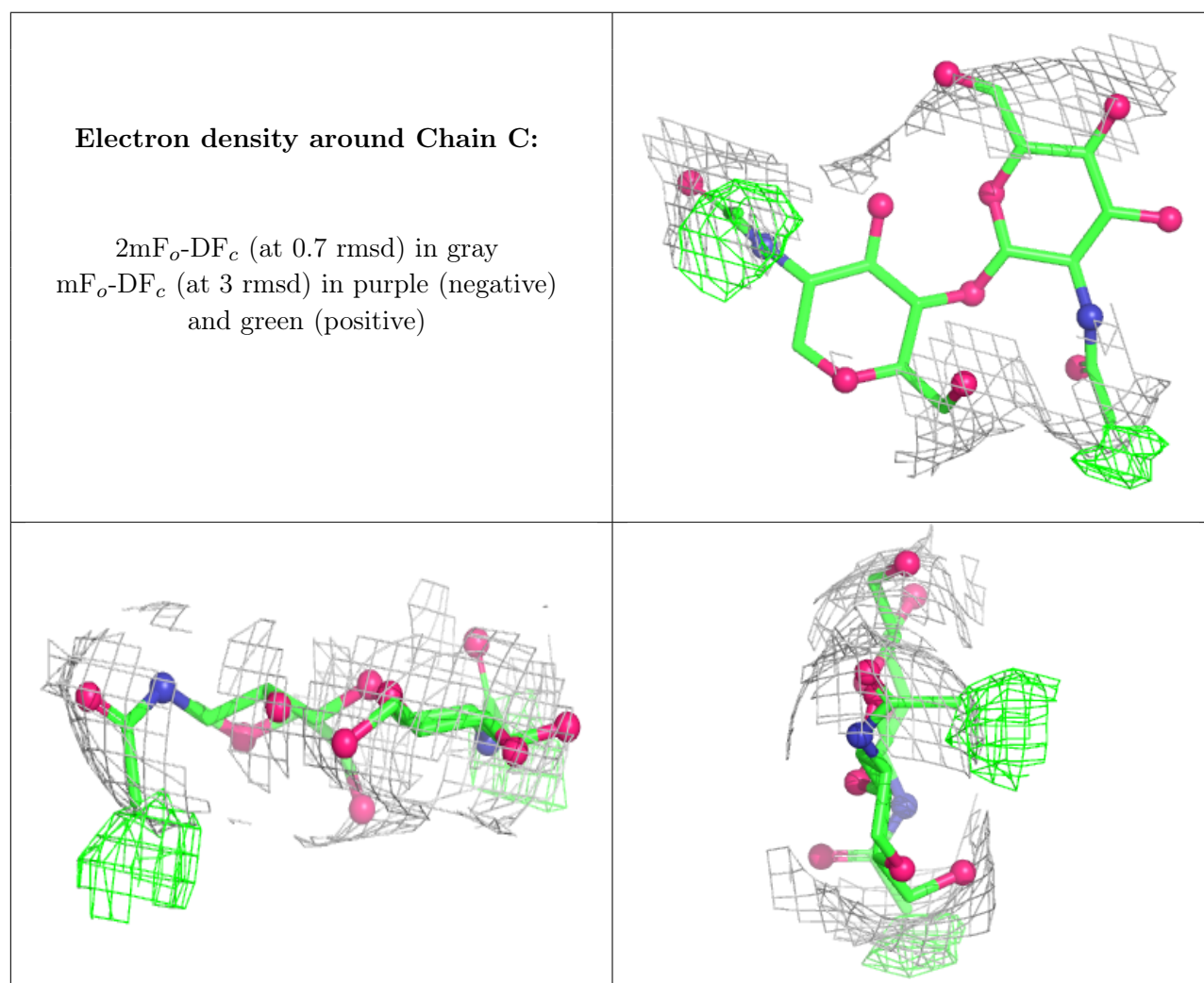
There are no non-standard protein/DNA/RNA residues in this entry.

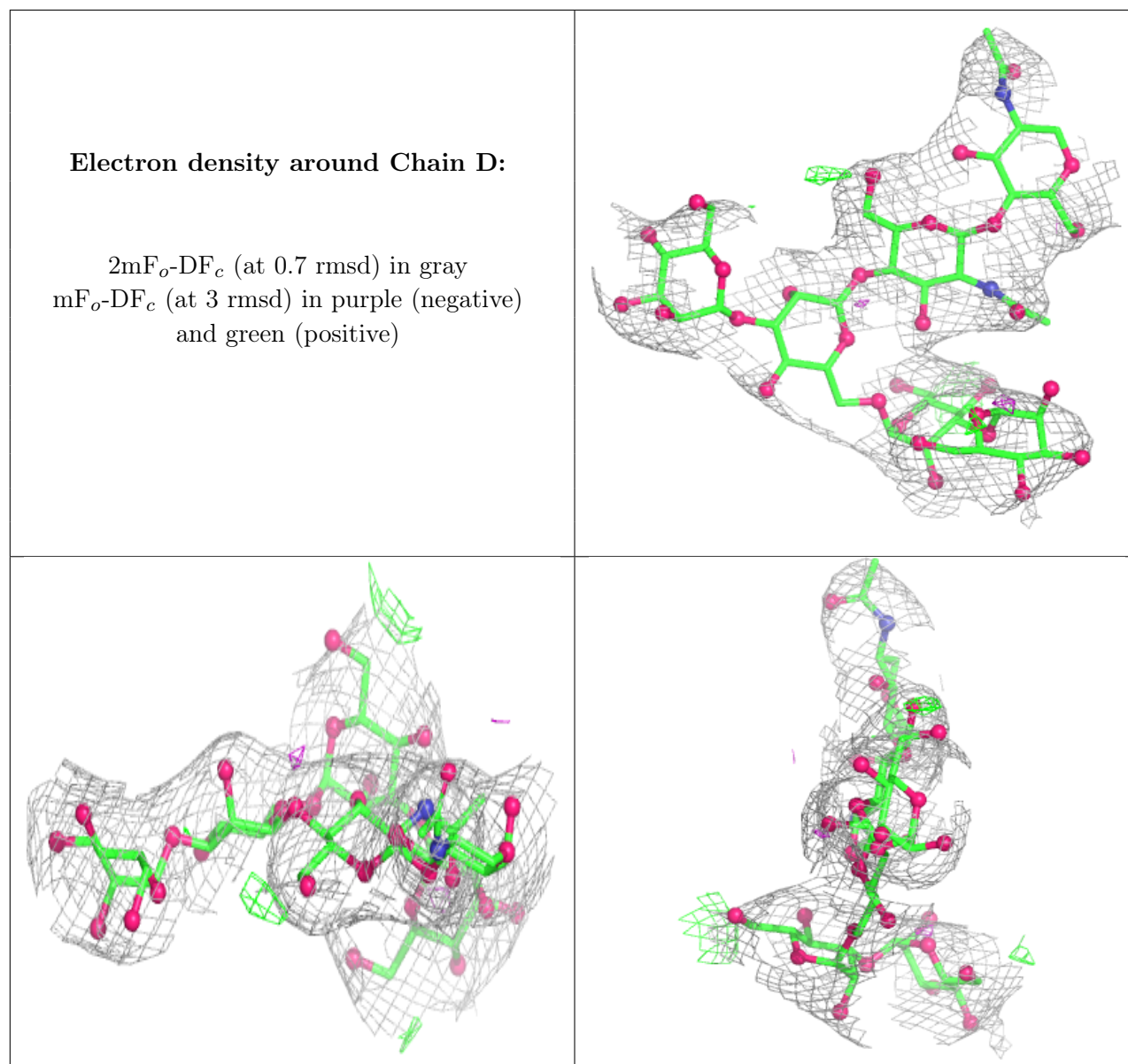
6.3 Carbohydrates [i](#)

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
4	MAN	D	5	11/12	0.35	0.14	157,178,184,191	0
4	MAN	D	4	11/12	0.61	0.11	148,157,162,166	0
3	NAG	C	2	14/15	0.64	0.10	155,168,173,174	0
4	BMA	D	3	11/12	0.75	0.09	143,145,153,153	0
4	MAN	D	6	11/12	0.82	0.11	139,152,158,160	0
3	NAG	C	1	14/15	0.85	0.09	144,153,161,163	0
4	NAG	D	2	14/15	0.87	0.11	108,122,137,137	0
4	NAG	D	1	14/15	0.96	0.09	87,93,106,111	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 [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(Å ²)	Q<0.9
5	NAG	A	401	14/15	0.56	0.11	175,179,182,183	0
5	NAG	B	701	14/15	0.63	0.13	169,177,184,185	0

6.5 Other polymers ⓘ

There are no such residues in this entry.