



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:48 PM UTC

PDB ID : 3N41 / pdb_00003n41
Title : Crystal structure of the mature envelope glycoprotein complex (spontaneous cleavage) of Chikungunya virus.
Authors : Voss, J.; Vaney, M.C.; Duquerroy, S.; Rey, F.A.
Deposited on : 2010-05-21
Resolution : 3.01 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

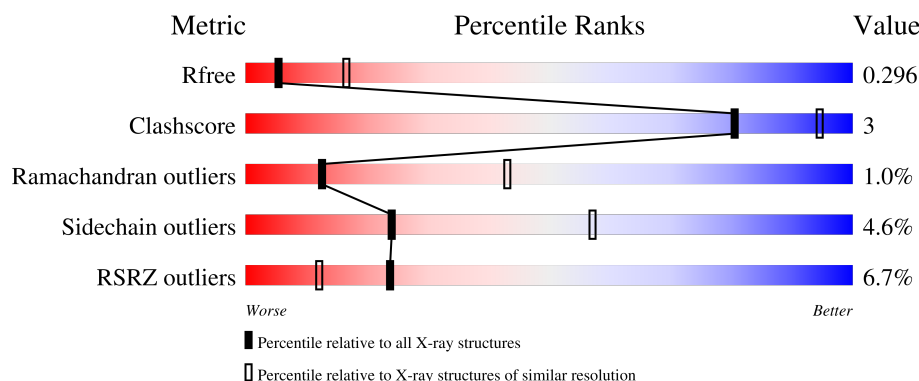
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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	65	6% 66% 15% • 15%
2	B	360	2% 83% 11% 6%
3	F	473	8% 74% 6% • 19%
4	C	2	100%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6070 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 E3 envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	55	Total	C	N	O	S	0	0	0
			427	268	67	83	9			

- Molecule 2 is a protein called E2 envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	338	Total	C	N	O	S	0	1	0
			2669	1666	483	500	20			

- Molecule 3 is a protein called E1 envelope glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	382	Total	C	N	O	S	0	1	0
			2909	1838	487	560	24			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	0	GLY	-	expression tag	UNP Q1H8W5

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



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

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

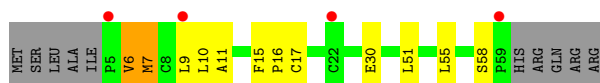


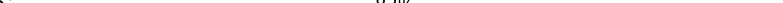
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	F	1	Total	C	N	O	0	0
			14	8	1	5		

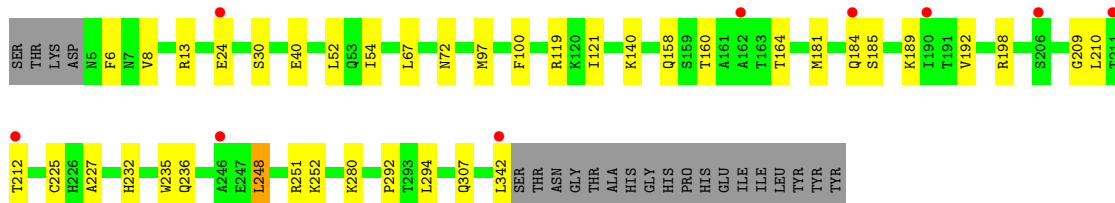
- Molecule 6 is water.

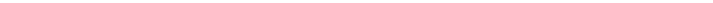
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	7	Total	O	0	0
			7	7		
6	F	16	Total	O	0	0
			16	16		

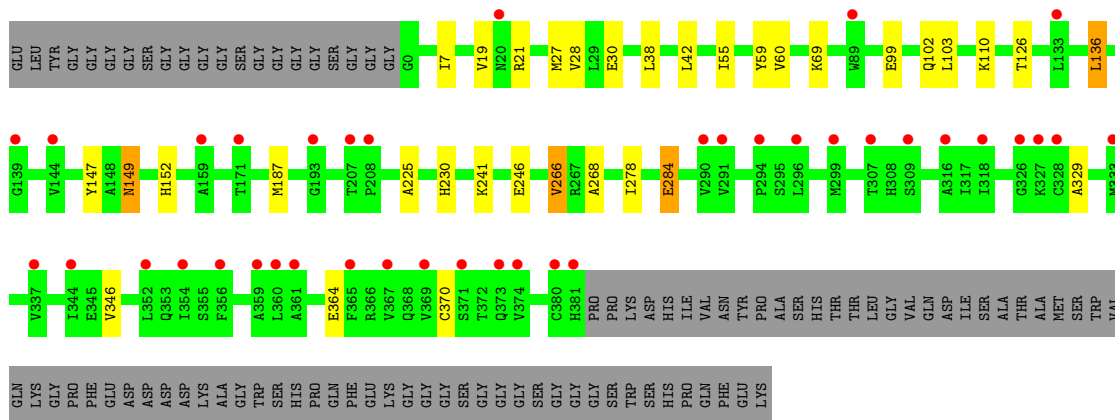
- Molecule 1: E3 envelope glycoprotein



- Chain B: 



- Chain F:  8% 74% 6% 19%



- 

Chain C:  100%

RMG1
RMG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.24Å 99.61Å 107.10Å 90.00° 102.90° 90.00°	Depositor
Resolution (Å)	50.00 – 3.01 50.00 – 3.01	Depositor EDS
% Data completeness (in resolution range)	98.3 (50.00-3.01) 98.3 (50.00-3.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 3.01Å)	Xtriage
Refinement program	BUSTER 2.9.3	Depositor
R, R_{free}	0.252 , 0.275 0.272 , 0.296	Depositor DCC
R_{free} test set	1029 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	70.7	Xtriage
Anisotropy	0.197	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6070	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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: NDG, 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	0.78	0/438	1.31	0/598
2	B	0.73	0/2741	1.17	8/3731 (0.2%)
3	F	0.70	0/2981	1.07	1/4064 (0.0%)
All	All	0.72	0/6160	1.13	9/8393 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	30	SER	N-CA-C	6.08	117.47	109.93
2	B	209	GLY	CA-C-N	5.88	132.28	121.70
2	B	209	GLY	C-N-CA	5.88	132.28	121.70
2	B	6	PHE	CA-CB-CG	5.75	119.55	113.80
2	B	100	PHE	N-CA-C	5.66	118.70	109.59
2	B	209	GLY	CA-C-O	-5.50	118.44	122.23
2	B	252	LYS	CA-C-N	5.32	126.29	121.82
2	B	252	LYS	C-N-CA	5.32	126.29	121.82
3	F	266	VAL	N-CA-CB	5.10	116.58	110.31

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	427	0	410	9	0
2	B	2669	0	2587	11	0
3	F	2909	0	2818	12	0
4	C	28	0	24	0	0
5	F	14	0	13	0	0
6	B	7	0	0	0	0
6	F	16	0	0	0	0
All	All	6070	0	5852	31	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 3.

All (31) 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:6:VAL:HG12	1:A:6:VAL:O	1.71	0.90
1:A:6:VAL:O	1:A:6:VAL:CG1	2.30	0.77
2:B:198:ARG:HA	2:B:210:LEU:H	1.51	0.73
3:F:225:ALA:H	3:F:230:HIS:HE1	1.38	0.72
3:F:42:LEU:HD11	3:F:266:VAL:HG22	1.85	0.58
3:F:21:ARG:HH12	3:F:284:GLU:HG2	1.70	0.56
1:A:7:MET:HE3	1:A:16:PRO:HA	1.91	0.53
3:F:38:LEU:HB2	3:F:268:ALA:HB3	1.90	0.53
2:B:181:MET:HE1	2:B:225:CYS:HB3	1.92	0.52
2:B:248:LEU:HD13	2:B:251:ARG:HB2	1.93	0.51
1:A:6:VAL:HG13	1:A:17:CYS:SG	2.51	0.49
3:F:60:VAL:HG22	3:F:102:GLN:HG3	1.95	0.49
1:A:6:VAL:CG1	1:A:17:CYS:SG	3.01	0.48
1:A:7:MET:HE3	1:A:16:PRO:CA	2.43	0.48
3:F:28:VAL:HG23	3:F:329:ALA:HB1	1.95	0.48
2:B:181:MET:HE3	2:B:227:ALA:HB2	1.96	0.48
3:F:19:VAL:HB	3:F:27:MET:HB3	1.96	0.48
2:B:52:LEU:HD22	2:B:67:LEU:HD21	1.97	0.47
2:B:184:GLN:HG2	2:B:189:LYS:HB2	1.97	0.46
3:F:30:GLU:HB3	3:F:136:LEU:HB2	1.98	0.46
2:B:97:MET:HE3	2:B:160:THR:HG23	1.98	0.44
2:B:184:GLN:HA	2:B:185:SER:HA	1.76	0.42
3:F:59:TYR:HB3	3:F:103:LEU:HB3	2.02	0.42
3:F:147:TYR:H	3:F:152:HIS:HD2	1.68	0.42
3:F:149:ASN:H	3:F:149:ASN:HD22	1.68	0.42
2:B:140:LYS:HB2	2:B:292:PRO:HB2	2.02	0.41
1:A:7:MET:HE3	1:A:15:PHE:C	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:LEU:HD13	2:B:8:VAL:HA	2.02	0.41
2:B:13:ARG:HE	2:B:236:GLN:HE21	1.69	0.41
1:A:7:MET:HE3	1:A:16:PRO:N	2.36	0.40
3:F:7:ILE:HG12	3:F:278:ILE:HD12	2.04	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	53/65 (82%)	50 (94%)	1 (2%)	2 (4%)	2	13
2	B	336/360 (93%)	313 (93%)	19 (6%)	4 (1%)	10	38
3	F	381/473 (80%)	369 (97%)	10 (3%)	2 (0%)	24	59
All	All	770/898 (86%)	732 (95%)	30 (4%)	8 (1%)	12	43

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	121	ILE
3	F	99	GLU
1	A	11	ALA
2	B	72	ASN
2	B	164	THR
3	F	126	THR
2	B	232	HIS
1	A	58	SER

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	52/61 (85%)	46 (88%)	6 (12%)	5	22
2	B	300/319 (94%)	287 (96%)	13 (4%)	26	59
3	F	319/378 (84%)	307 (96%)	12 (4%)	29	62
All	All	671/758 (88%)	640 (95%)	31 (5%)	24	57

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	VAL
1	A	7	MET
1	A	9	LEU
1	A	10	LEU
1	A	30	GLU
1	A	51	LEU
2	B	24	GLU
2	B	40	GLU
2	B	54	ILE
2	B	119	ARG
2	B	158	GLN
2	B	192	VAL
2	B	212	THR
2	B	235	TRP
2	B	248	LEU
2	B	280	LYS
2	B	294	LEU
2	B	307	GLN
2	B	342	LEU
3	F	55	ILE
3	F	69	LYS
3	F	110	LYS
3	F	136	LEU
3	F	149	ASN
3	F	187	MET
3	F	241	LYS

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Mol	Chain	Res	Type
3	F	246	GLU
3	F	284	GLU
3	F	346	VAL
3	F	364	GLU
3	F	370	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
2	B	18	HIS
2	B	184	GLN
2	B	202	ASN
2	B	224	GLN
2	B	236	GLN
2	B	245	ASN
2	B	282	GLN
2	B	307	GLN
3	F	102	GLN
3	F	138	GLN
3	F	152	HIS
3	F	218	GLN
3	F	230	HIS
3	F	331	HIS
3	F	368	GLN
3	F	373	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	$\# Z > 2$
4	NAG	C	1	4,2	14,14,15	1.44	1 (7%)	17,19,21	1.57	3 (17%)
4	NDG	C	2	4	14,14,15	1.31	1 (7%)	17,19,21	1.71	5 (29%)

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
4	NAG	C	1	4,2	-	0/6/23/26	0/1/1/1
4	NDG	C	2	4	-	3/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1	NAG	C1-C2	3.79	1.57	1.52
4	C	2	NDG	C1-C2	2.91	1.56	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1	NAG	C1-O5-C5	3.43	116.78	112.19
4	C	2	NDG	C1-O5-C5	3.29	116.60	112.19
4	C	2	NDG	O5-C5-C4	3.08	118.32	110.83
4	C	1	NAG	O4-C4-C3	3.07	117.61	110.38
4	C	2	NDG	C3-C4-C5	2.56	114.87	110.23
4	C	2	NDG	C2-N2-C7	2.54	126.31	122.90
4	C	2	NDG	C1-C2-N2	2.27	114.01	110.43
4	C	1	NAG	C4-C3-C2	2.14	114.16	111.02

There are no chirality outliers.

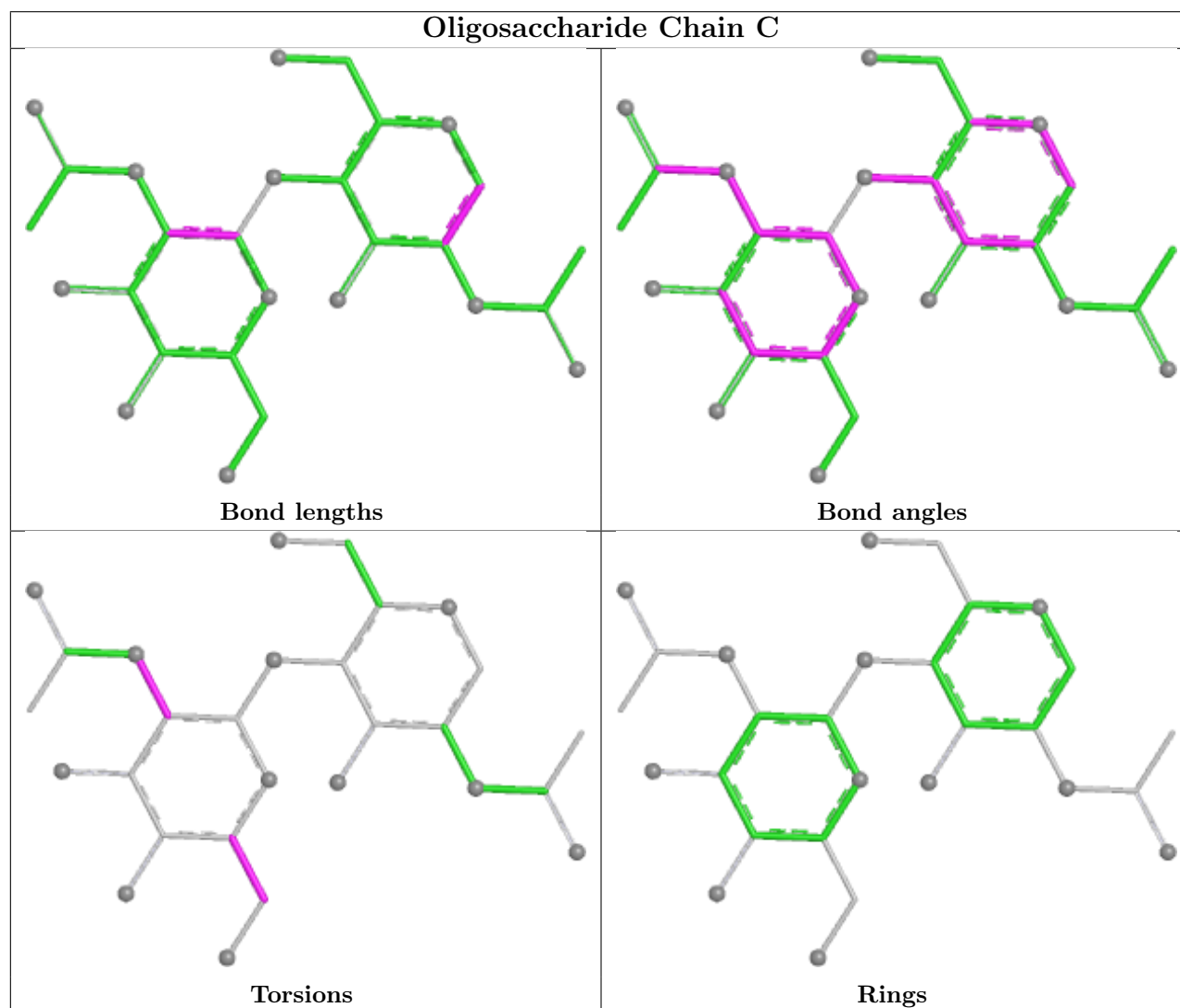
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	2	NDG	C4-C5-C6-O6
4	C	2	NDG	C3-C2-N2-C7
4	C	2	NDG	C1-C2-N2-C7

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](#)

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
5	NAG	F	1001	3	14,14,15	1.35	2 (14%)	17,19,21	1.20	2 (11%)

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	F	1001	3	-	1/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	1001	NAG	C1-C2	3.34	1.56	1.52
5	F	1001	NAG	C3-C2	2.23	1.57	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	1001	NAG	C4-C3-C2	3.18	115.67	111.02
5	F	1001	NAG	C2-N2-C7	2.00	125.58	122.90

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	F	1001	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	55/65 (84%)	0.62	4 (7%) 21 10	63, 81, 92, 101	0
2	B	338/360 (93%)	0.46	9 (2%) 56 33	45, 77, 109, 155	0
3	F	382/473 (80%)	0.82	39 (10%) 12 6	32, 85, 165, 177	1 (0%)
All	All	775/898 (86%)	0.65	52 (6%) 24 12	32, 81, 163, 177	1 (0%)

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	354	ILE	3.9
2	B	212	THR	3.9
3	F	318	ILE	3.8
3	F	290	VAL	3.6
3	F	337	VAL	3.5
3	F	291	VAL	3.4
3	F	328	CYS	3.3
3	F	344	ILE	3.3
3	F	356	PHE	3.2
3	F	144	VAL	3.1
3	F	316	ALA	3.0
3	F	371	SER	3.0
3	F	193	GLY	3.0
3	F	352	LEU	3.0
3	F	296	LEU	2.9
3	F	373	GLN	2.8
3	F	369	VAL	2.8
3	F	365	PHE	2.7
3	F	360	LEU	2.7
1	A	59	PRO	2.6
3	F	327	LYS	2.6
3	F	367	VAL	2.6
2	B	184	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	211	THR	2.6
3	F	361	ALA	2.6
3	F	89	TRP	2.5
3	F	374	VAL	2.4
2	B	162	ALA	2.4
3	F	159	ALA	2.4
2	B	190	ILE	2.3
3	F	307	THR	2.3
2	B	246	ALA	2.2
2	B	206	SER	2.2
1	A	5	PRO	2.2
2	B	342	LEU	2.2
1	A	22	CYS	2.2
3	F	359	ALA	2.2
1	A	9	LEU	2.2
3	F	299	MET	2.2
3	F	333	MET	2.2
3	F	139	GLY	2.2
3	F	208	PRO	2.1
3	F	326	GLY	2.1
3	F	381	HIS	2.1
3	F	171	THR	2.1
3	F	207	THR	2.1
3	F	309	SER	2.1
3	F	20	ASN	2.1
3	F	380	CYS	2.1
3	F	133	LEU	2.0
2	B	24	GLU	2.0
3	F	294	PRO	2.0

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

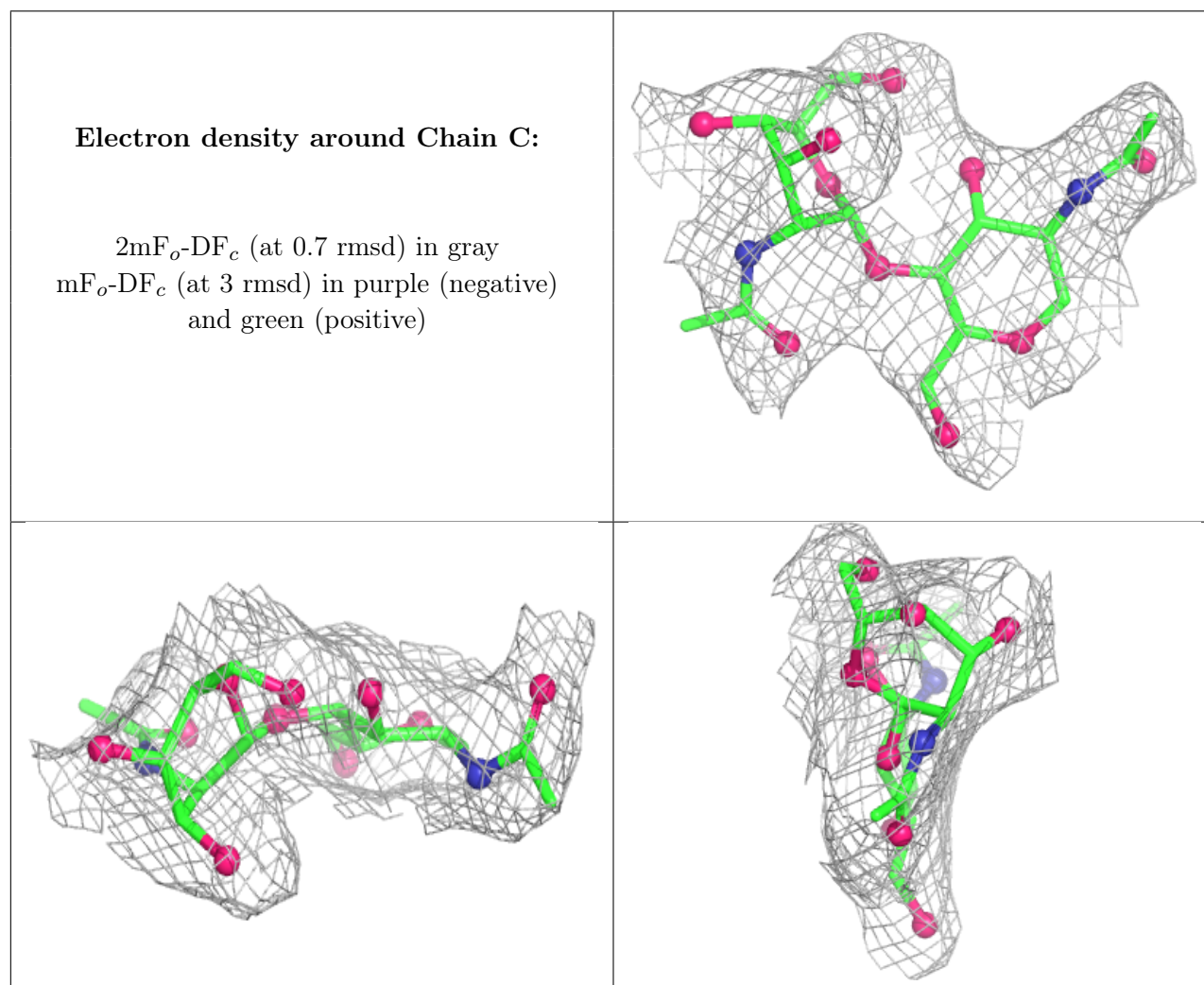
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
4	NAG	C	1	14/15	-	-	78,82,85,85	0
4	NDG	C	2	14/15	-	-	85,89,91,91	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($\text{\AA}^2$)	Q<0.9
5	NAG	F	1001	14/15	0.44	0.19	115,119,121,121	0

6.5 Other polymers ⓘ

There are no such residues in this entry.