



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:59 AM UTC

PDB ID : 7PS4 / pdb_00007ps4
Title : Crystal structure of the receptor binding domain of SARS-CoV-2 beta variant spike glycoprotein in complex with Beta-38
Authors : Zhou, D.; Ren, J.; Stuart, D.I.
Deposited on : 2021-09-22
Resolution : 1.94 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

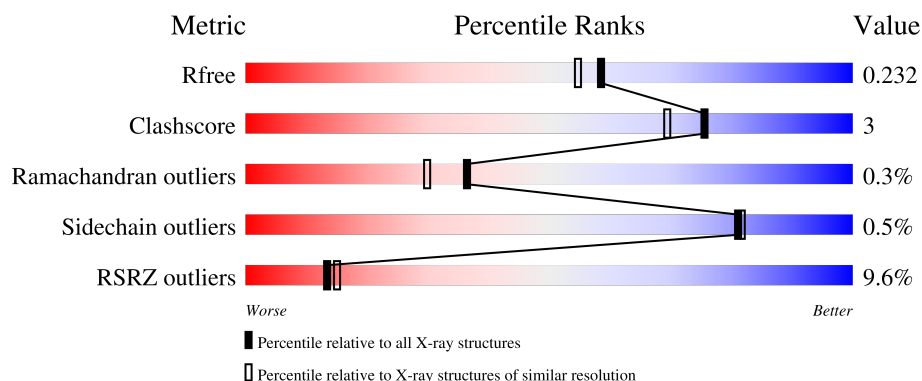
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	210	8% 84% 9% 7%
1	E	210	13% 84% 9% 8%
2	B	230	20% 93% 6% .
2	H	230	3% 92% 5% .
3	C	216	10% 90% 8% .

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Mol	Chain	Length	Quality of chain
3	L	216	% 89% 9%
4	D	2	100%
4	F	2	50% 50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10153 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	194	Total	C	N	O	S	0	1	0
			1544	991	257	288	8			
1	A	195	Total	C	N	O	S	0	1	0
			1549	994	258	289	8			

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	319	MET	-	initiating methionine	UNP P0DTC2
E	320	GLY	-	expression tag	UNP P0DTC2
E	321	CYS	-	expression tag	UNP P0DTC2
E	322	VAL	-	expression tag	UNP P0DTC2
E	323	ALA	-	expression tag	UNP P0DTC2
E	324	GLU	-	expression tag	UNP P0DTC2
E	325	THR	-	expression tag	UNP P0DTC2
E	326	GLY	-	expression tag	UNP P0DTC2
E	327	HIS	-	expression tag	UNP P0DTC2
E	328	HIS	-	expression tag	UNP P0DTC2
E	329	HIS	-	expression tag	UNP P0DTC2
E	330	HIS	-	expression tag	UNP P0DTC2
E	331	HIS	-	expression tag	UNP P0DTC2
E	332	HIS	-	expression tag	UNP P0DTC2
E	417	ASN	LYS	variant	UNP P0DTC2
E	484	LYS	GLU	variant	UNP P0DTC2
E	501	TYR	ASN	variant	UNP P0DTC2
E	527	LYS	-	expression tag	UNP P0DTC2
E	528	LYS	-	expression tag	UNP P0DTC2
A	319	MET	-	initiating methionine	UNP P0DTC2
A	320	GLY	-	expression tag	UNP P0DTC2
A	321	CYS	-	expression tag	UNP P0DTC2
A	322	VAL	-	expression tag	UNP P0DTC2
A	323	ALA	-	expression tag	UNP P0DTC2
A	324	GLU	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	325	THR	-	expression tag	UNP P0DTC2
A	326	GLY	-	expression tag	UNP P0DTC2
A	327	HIS	-	expression tag	UNP P0DTC2
A	328	HIS	-	expression tag	UNP P0DTC2
A	329	HIS	-	expression tag	UNP P0DTC2
A	330	HIS	-	expression tag	UNP P0DTC2
A	331	HIS	-	expression tag	UNP P0DTC2
A	332	HIS	-	expression tag	UNP P0DTC2
A	417	ASN	LYS	variant	UNP P0DTC2
A	484	LYS	GLU	variant	UNP P0DTC2
A	501	TYR	ASN	variant	UNP P0DTC2
A	527	LYS	-	expression tag	UNP P0DTC2
A	528	LYS	-	expression tag	UNP P0DTC2

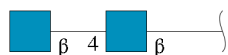
- Molecule 2 is a protein called Beta-38 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	223	Total	C	N	O	S	0	0	0
			1674	1063	275	328	8			
2	B	228	Total	C	N	O	S	0	1	0
			1708	1081	280	338	9			

- Molecule 3 is a protein called Beta-38 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	1	0
			1573	978	265	326	4			
3	C	213	Total	C	N	O	S	0	1	0
			1577	980	265	328	4			

- Molecule 4 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
4	D	2	Total	C	N	O		0	0	0
			28	16	2	10				
4	F	2	Total	C	N	O		0	0	0
			28	16	2	10				

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total 1	Cl 1	0	0
5	B	1	Total 1	Cl 1	0	0

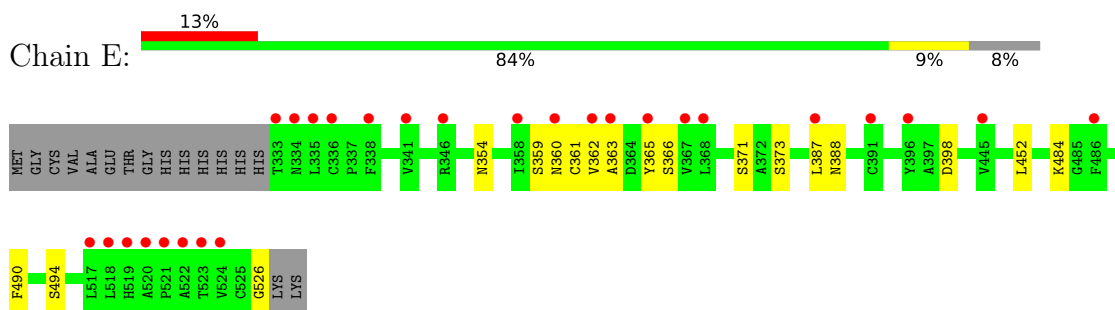
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	81	Total 81	O 81	0	0
6	H	161	Total 161	O 161	0	0
6	L	79	Total 79	O 79	0	0
6	A	90	Total 90	O 90	0	0
6	B	35	Total 35	O 35	0	0
6	C	24	Total 24	O 24	0	0

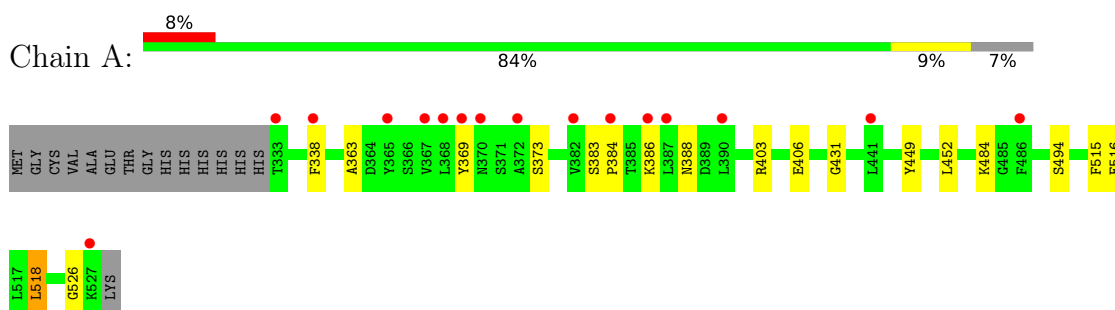
3 Residue-property plots [i](#)

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.

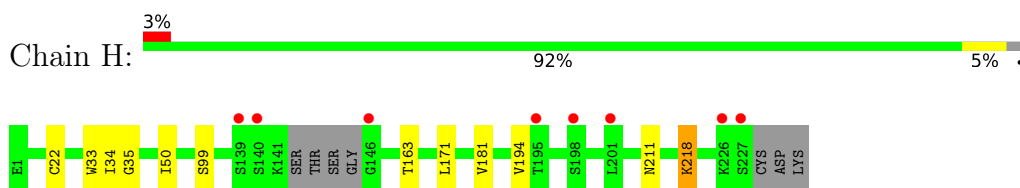
- Molecule 1: Spike protein S1



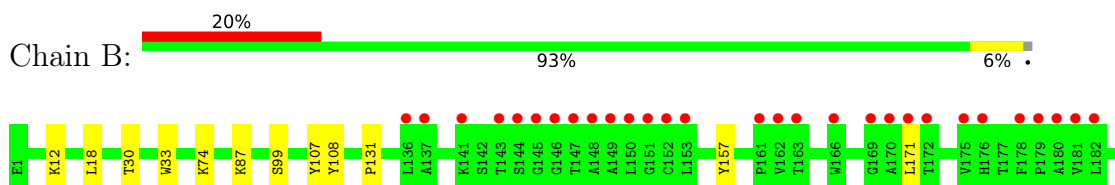
- Molecule 1: Spike protein S1

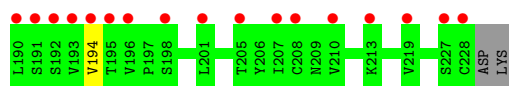


- Molecule 2: Beta-38 Fab heavy chain

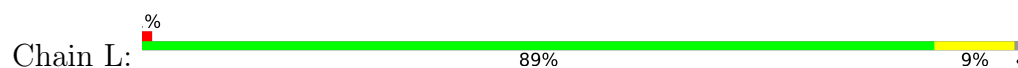


- Molecule 2: Beta-38 Fab heavy chain

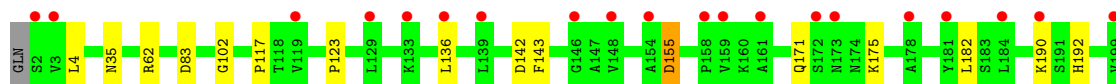
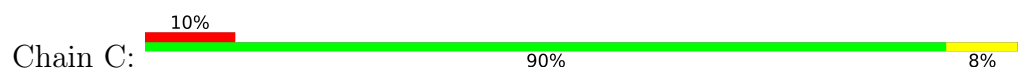




- Molecule 3: Beta-38 Fab light chain



- Molecule 3: Beta-38 Fab light chain



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.07Å 118.49Å 109.27Å 90.00° 93.47° 90.00°	Depositor
Resolution (Å)	54.53 – 1.94 54.53 – 1.94	Depositor EDS
% Data completeness (in resolution range)	97.5 (54.53-1.94) 97.6 (54.53-1.94)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 1.94Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.203 , 0.231 0.204 , 0.232	Depositor DCC
R_{free} test set	5059 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	43.8	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.4	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	0.96	EDS
Total number of atoms	10153	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: CL, 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	0.23	0/1596	0.44	0/2173
1	E	0.23	0/1591	0.45	0/2166
2	B	0.16	0/1756	0.37	0/2392
2	H	0.24	0/1718	0.45	0/2339
3	C	0.15	0/1618	0.37	0/2214
3	L	0.21	0/1614	0.42	0/2209
All	All	0.20	0/9893	0.42	0/13493

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	1549	0	1463	10	0
1	E	1544	0	1461	10	0
2	B	1708	0	1655	9	0
2	H	1674	0	1625	8	0
3	C	1577	0	1522	9	0
3	L	1573	0	1521	14	0
4	D	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	28	0	25	1	0
5	B	1	0	0	0	0
5	H	1	0	0	0	0
6	A	90	0	0	0	0
6	B	35	0	0	0	0
6	C	24	0	0	0	0
6	E	81	0	0	0	0
6	H	161	0	0	1	0
6	L	79	0	0	2	0
All	All	10153	0	9297	56	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 (56) 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)
3:L:131:ALA:O	6:L:301:HOH:O	2.09	0.71
3:L:97:ASN:OD1	6:L:302:HOH:O	2.12	0.68
1:E:388:ASN:HA	1:E:526:GLY:HA3	1.79	0.64
1:A:388:ASN:HA	1:A:526:GLY:HA3	1.79	0.64
3:C:136:LEU:HD12	3:C:182:LEU:HD23	1.82	0.61
3:C:142:ASP:OD1	3:C:171:GLN:NE2	2.34	0.61
3:C:4:LEU:HB2	3:C:102:GLY:HA2	1.83	0.59
2:B:171:LEU:HD21	2:B:194:VAL:HG21	1.84	0.59
3:L:142:ASP:OD1	3:L:171:GLN:NE2	2.34	0.58
1:A:449:TYR:O	2:B:107:TYR:OH	2.17	0.57
1:A:369:TYR:OH	1:A:384:PRO:O	2.13	0.57
2:B:12:LYS:HE3	2:B:18:LEU:HD13	1.88	0.55
3:C:117:PRO:HB3	3:C:143:PHE:HB3	1.91	0.53
3:L:4:LEU:HB2	3:L:102:GLY:HA2	1.90	0.53
3:L:136:LEU:HD12	3:L:182:LEU:HD23	1.89	0.53
2:H:171:LEU:HD21	2:H:194:VAL:HG21	1.92	0.49
2:B:131:PRO:HB3	2:B:157:TYR:HB3	1.93	0.49
3:C:190:LYS:NZ	3:C:212:PRO:HB2	2.28	0.49
1:E:359:SER:O	1:E:361:CYS:N	2.46	0.49
1:A:383:SER:HB2	1:A:386:LYS:HB2	1.95	0.49
3:L:171:GLN:HG2	3:L:175:LYS:O	2.12	0.48
1:A:516:GLU:HG2	1:A:518:LEU:HD13	1.95	0.48
2:H:35:GLY:HA3	2:H:50:ILE:HG22	1.94	0.48
1:A:431:GLY:HA2	1:A:515:PHE:CD2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:155:ASP:OD2	3:C:192:HIS:HD2	1.97	0.48
2:H:22:CYS:SG	2:H:34:ILE:HD11	2.55	0.47
1:E:354:ASN:O	1:E:398:ASP:HA	2.15	0.47
3:L:117:PRO:HB3	3:L:143:PHE:HB3	1.97	0.47
3:L:123:PRO:HA	3:L:136:LEU:HD23	1.97	0.47
2:B:30:THR:HG22	2:B:74:LYS:HD2	1.97	0.47
1:E:484:LYS:HD3	1:E:490:PHE:HB2	1.97	0.46
2:H:181:VAL:HG12	3:L:166:THR:HG23	1.96	0.46
2:H:33:TRP:HB2	2:H:99:SER:HB2	1.96	0.46
2:H:211:ASN:ND2	6:H:410:HOH:O	2.49	0.46
1:A:452:LEU:HD23	1:A:494:SER:HA	1.98	0.45
2:B:30:THR:CG2	2:B:74:LYS:HD2	2.47	0.45
3:C:62:ARG:NH1	3:C:83:ASP:OD2	2.43	0.45
1:E:366:SER:OG	1:E:388:ASN:OD1	2.25	0.45
3:C:123:PRO:HA	3:C:136:LEU:HD23	1.99	0.44
2:H:163:THR:OG1	2:H:211:ASN:HB2	2.18	0.44
1:A:484:LYS:HE2	2:B:108:TYR:CD2	2.53	0.43
1:A:338:PHE:HE2	1:A:363:ALA:HB1	1.83	0.43
1:E:371:SER:OG	1:E:373:SER:OG	2.34	0.43
3:L:171:GLN:HG3	3:L:173:ASN:OD1	2.18	0.43
1:E:484:LYS:HE3	3:L:92:TRP:CD1	2.54	0.43
4:F:1:NAG:H61	4:F:2:NAG:N2	2.34	0.43
1:A:403:ARG:HG2	1:A:406:GLU:CD	2.43	0.42
1:E:452:LEU:HD23	1:E:494:SER:HA	2.00	0.42
1:E:363:ALA:O	1:E:526:GLY:HA2	2.19	0.42
1:E:365:TYR:CD2	1:E:387:LEU:HB3	2.54	0.41
2:B:33:TRP:HB2	2:B:99:SER:HB2	2.01	0.41
2:H:211:ASN:OD1	2:H:218:LYS:HG2	2.20	0.41
3:L:145:PRO:O	3:L:201:HIS:HE1	2.03	0.41
3:L:155:ASP:OD1	3:L:193:ARG:HG2	2.20	0.41
3:L:160:LYS:HE2	2:B:87:LYS:HD3	2.02	0.41
3:C:171:GLN:HG2	3:C:175:LYS:O	2.21	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	194/210 (92%)	188 (97%)	6 (3%)	0	100	100
1	E	193/210 (92%)	183 (95%)	8 (4%)	2 (1%)	12	5
2	B	227/230 (99%)	221 (97%)	6 (3%)	0	100	100
2	H	219/230 (95%)	216 (99%)	3 (1%)	0	100	100
3	C	212/216 (98%)	206 (97%)	5 (2%)	1 (0%)	24	15
3	L	212/216 (98%)	204 (96%)	7 (3%)	1 (0%)	24	15
All	All	1257/1312 (96%)	1218 (97%)	35 (3%)	4 (0%)	36	30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	360	ASN
3	L	155	ASP
3	C	155	ASP
1	E	362	VAL

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	168/180 (93%)	166 (99%)	2 (1%)	63	57
1	E	168/180 (93%)	168 (100%)	0	100	100
2	B	190/193 (98%)	190 (100%)	0	100	100
2	H	185/193 (96%)	184 (100%)	1 (0%)	81	82
3	C	180/182 (99%)	178 (99%)	2 (1%)	65	60
3	L	179/182 (98%)	179 (100%)	0	100	100
All	All	1070/1110 (96%)	1065 (100%)	5 (0%)	81	82

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

Mol	Chain	Res	Type
2	H	218	LYS
1	A	373	SER
1	A	518	LEU
3	C	35	ASN
3	C	213	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	334	ASN
1	E	360	ASN
1	E	460	ASN
1	E	481	ASN
1	A	360	ASN
1	A	460	ASN
1	A	474	GLN
1	A	481	ASN

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
4	NAG	D	1	4,1	14,14,15	0.43	0	17,19,21	0.61	0
4	NAG	D	2	4	14,14,15	0.21	0	17,19,21	0.54	0
4	NAG	F	1	4,1	14,14,15	0.31	0	17,19,21	0.54	0
4	NAG	F	2	4	14,14,15	0.51	0	17,19,21	0.68	1 (5%)

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	D	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	2	NAG	C1-O5-C5	2.35	115.33	112.19

There are no chirality outliers.

All (6) torsion outliers are listed below:

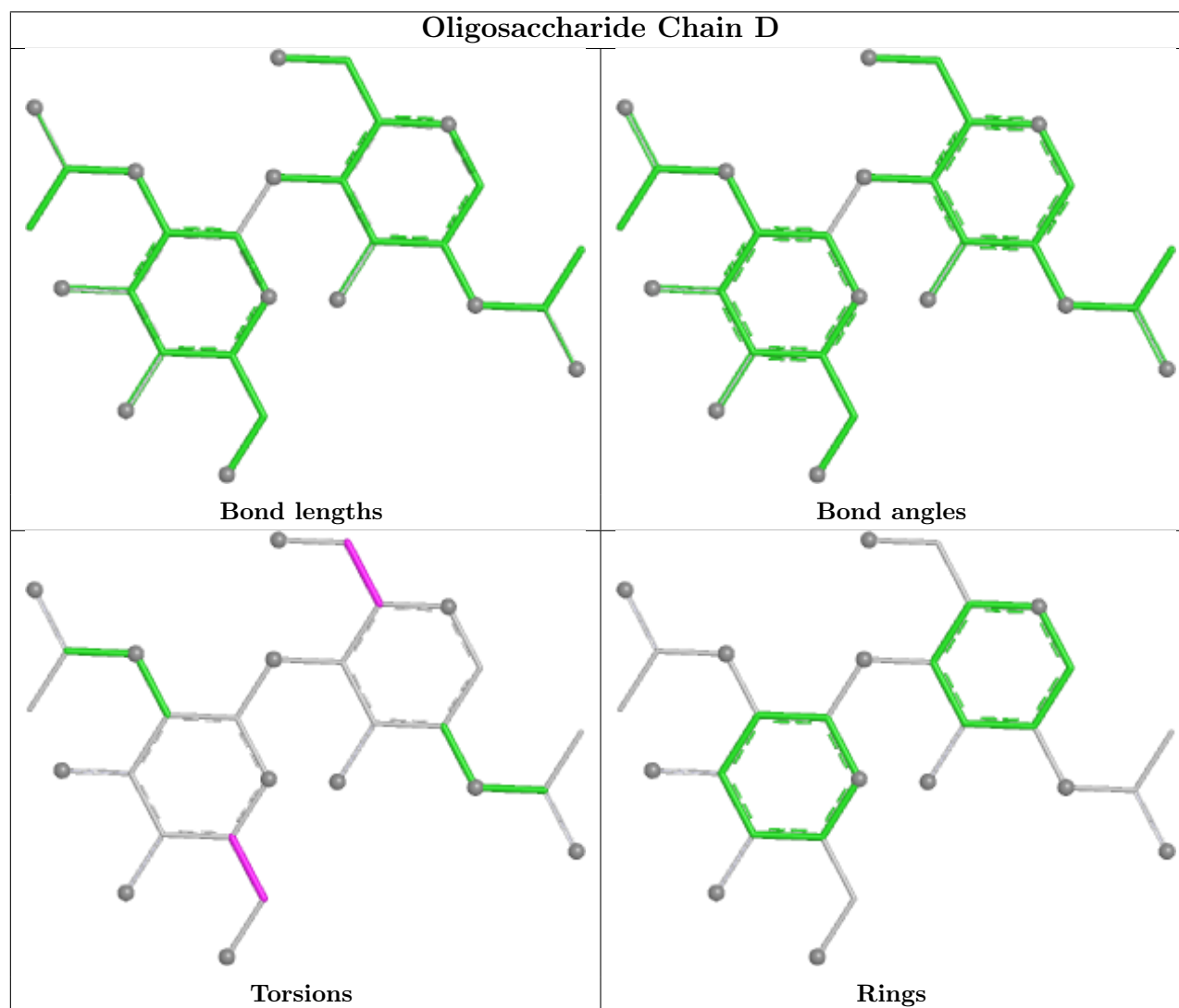
Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O5-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
4	D	1	NAG	C4-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6

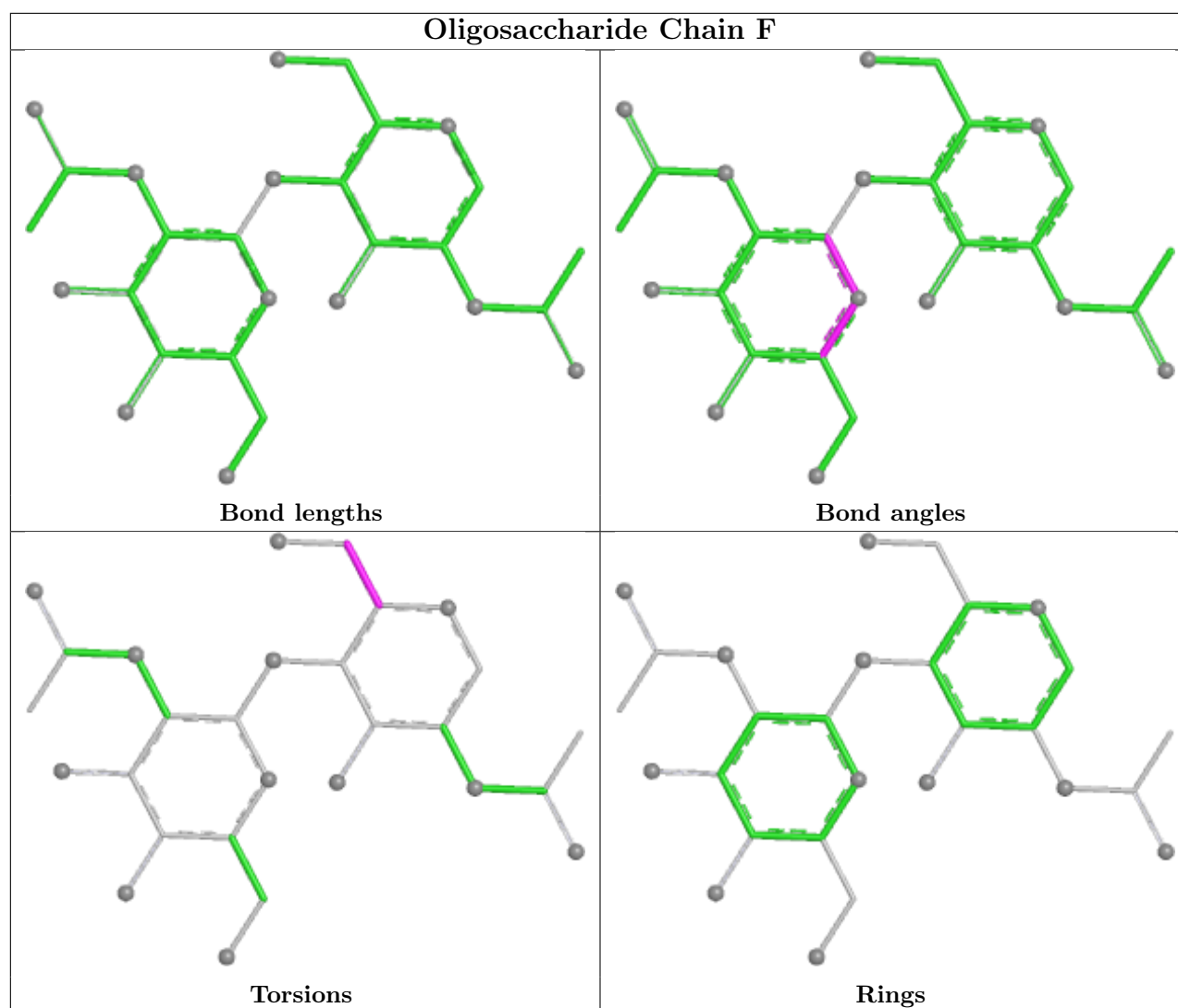
There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	2	NAG	1	0
4	F	1	NAG	1	0

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, 2 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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	195/210 (92%)	0.52	16 (8%) 17 19	23, 52, 92, 122	1 (0%)
1	E	194/210 (92%)	0.73	27 (13%) 6 7	24, 52, 124, 154	1 (0%)
2	B	228/230 (99%)	1.12	46 (20%) 3 3	33, 75, 155, 177	1 (0%)
2	H	223/230 (96%)	0.17	8 (3%) 46 52	32, 45, 74, 129	0
3	C	213/216 (98%)	0.96	22 (10%) 12 13	46, 84, 118, 132	1 (0%)
3	L	213/216 (98%)	0.33	2 (0%) 81 85	34, 56, 94, 118	1 (0%)
All	All	1266/1312 (96%)	0.64	121 (9%) 13 15	23, 58, 128, 177	5 (0%)

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	362	VAL	5.3
2	B	201	LEU	4.6
1	E	365	TYR	4.4
2	B	144	SER	4.2
3	C	159	VAL	4.1
1	A	372	ALA	3.9
2	B	145	GLY	3.9
2	B	191	SER	3.6
1	E	368	LEU	3.6
2	B	148	ALA	3.5
3	L	213	THR	3.5
2	B	170	ALA	3.5
1	E	518	LEU	3.5
2	B	180	ALA	3.5
2	H	146	GLY	3.4
2	H	201	LEU	3.4
1	E	335	LEU	3.3
1	A	368	LEU	3.3
1	E	517	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
2	B	150	LEU	3.3
3	C	2	SER	3.3
2	B	147	THR	3.2
1	E	363	ALA	3.2
2	B	149	ALA	3.2
1	E	333	THR	3.2
1	E	486	PHE	3.2
2	H	227	SER	3.2
1	A	486	PHE	3.2
1	E	524	VAL	3.1
2	B	181	VAL	3.1
2	B	195	THR	3.1
2	B	171	LEU	3.1
1	A	527	LYS	3.1
1	E	360	ASN	3.1
1	E	358	ILE	3.1
3	C	146	GLY	3.1
2	B	193	VAL	3.1
1	A	370	ASN	3.1
3	C	213	THR	3.1
2	B	207	ILE	3.0
1	A	333	THR	3.0
2	B	153	LEU	2.9
2	B	210	VAL	2.9
2	B	169	GLY	2.9
1	E	522	ALA	2.9
2	B	143	THR	2.9
1	E	523	THR	2.8
2	B	163	THR	2.8
1	A	382	VAL	2.8
2	B	194	VAL	2.8
1	A	369	TYR	2.7
1	E	520	ALA	2.7
1	A	441	LEU	2.7
3	C	3	VAL	2.7
2	B	137	ALA	2.7
2	B	178	PHE	2.7
2	B	179	PRO	2.7
1	E	346	ARG	2.7
2	B	151	GLY	2.7
2	B	205	THR	2.7
1	A	387	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	146	GLY	2.6
3	C	154	ALA	2.6
1	E	521	PRO	2.6
1	A	367	VAL	2.6
2	B	219	VAL	2.6
1	E	338	PHE	2.5
3	C	129	LEU	2.5
2	B	141	LYS	2.5
2	B	192	SER	2.5
3	C	204	SER	2.5
2	B	175	VAL	2.5
3	C	139	LEU	2.5
3	C	172	SER	2.5
3	C	161	ALA	2.5
2	H	195	THR	2.5
1	E	396	TYR	2.5
1	E	336	CYS	2.4
3	C	178	ALA	2.4
2	B	161	PRO	2.4
2	B	162	VAL	2.4
3	C	148	VAL	2.4
1	E	519	HIS	2.4
3	C	190	LYS	2.4
2	H	140	SER	2.4
3	C	181	TYR	2.4
1	A	338	PHE	2.4
2	B	227	SER	2.4
2	B	190	LEU	2.3
2	B	172	THR	2.3
1	E	334	ASN	2.3
1	E	387	LEU	2.3
1	A	390	LEU	2.3
3	C	133	LYS	2.3
2	B	213	LYS	2.3
2	B	196	VAL	2.2
1	A	386	LYS	2.2
1	E	391	CYS	2.2
2	B	136	LEU	2.2
2	B	166	TRP	2.2
1	E	341	VAL	2.2
2	B	228	CYS	2.2
3	C	136	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	445	VAL	2.1
3	C	199	VAL	2.1
2	B	198	SER	2.1
2	B	182	LEU	2.1
2	B	208	CYS	2.1
1	A	365	TYR	2.1
2	H	139	SER	2.1
2	B	176	HIS	2.1
1	E	367	VAL	2.1
3	C	158	PRO	2.1
2	B	152	CYS	2.1
3	C	184	LEU	2.1
3	C	173	ASN	2.0
1	A	384	PRO	2.0
2	H	226	LYS	2.0
2	H	198	SER	2.0
3	L	206	VAL	2.0
3	C	119	VAL	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](#)

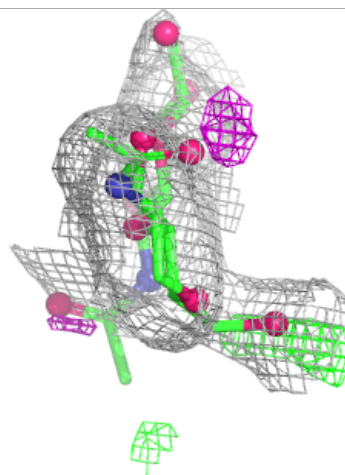
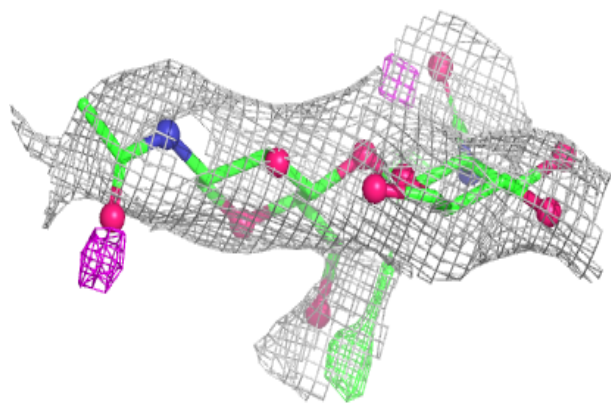
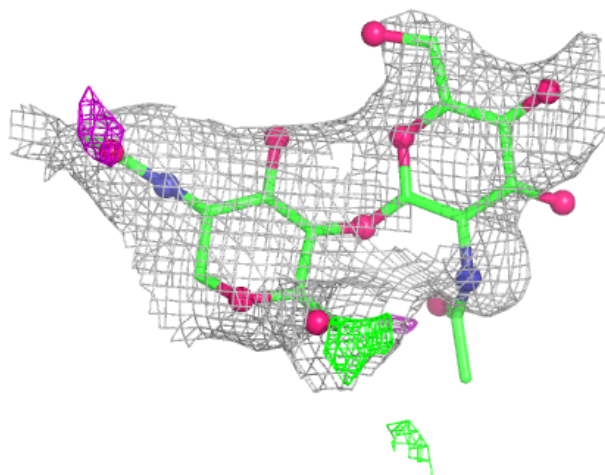
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

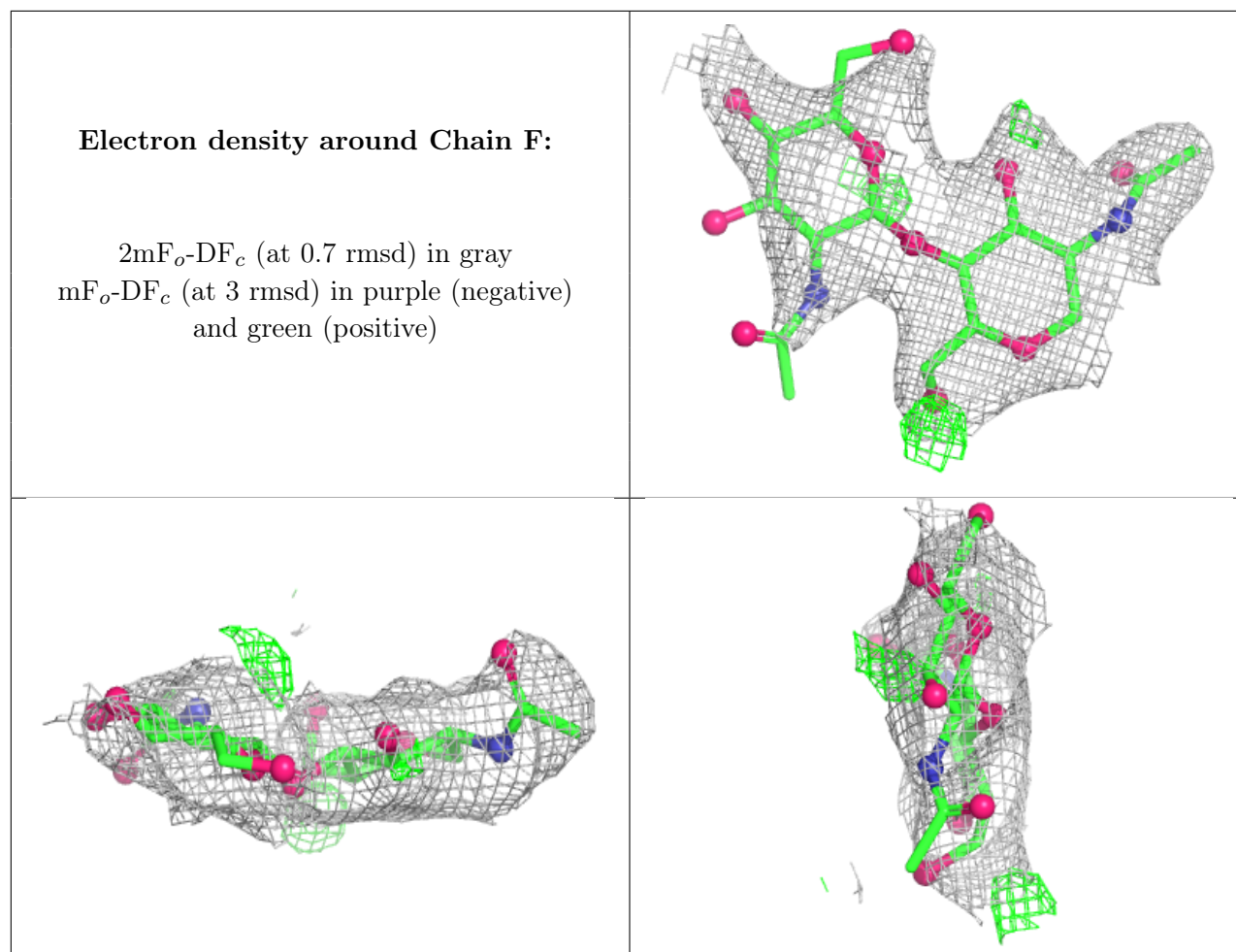
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	D	1	14/15	-	-	88,105,117,118	0
4	NAG	D	2	14/15	-	-	121,129,132,134	0
4	NAG	F	1	14/15	-	-	77,93,105,112	0
4	NAG	F	2	14/15	-	-	114,121,125,128	0

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 D:

$2mF_o-DF_c$ (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(Å ²)	Q<0.9
5	CL	H	301	1/1	0.97	0.13	46,46,46,46	0
5	CL	B	301	1/1	0.97	0.16	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.