



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:58 PM UTC

PDB ID : 8BG1 / pdb_00008bg1
Title : Crystal structure of the SARS-CoV-2 S RBD in complex with pT1511 scFV
Authors : Hansen, G.; Ssebyatika, G.L.; Krey, T.
Deposited on : 2022-10-27
Resolution : 2.88 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

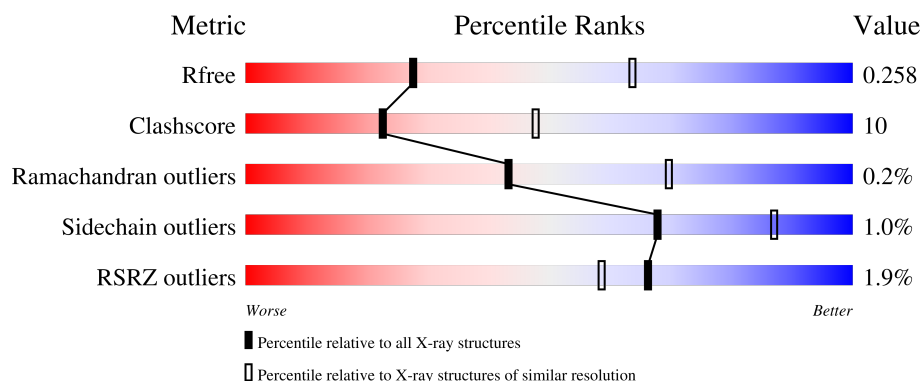
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

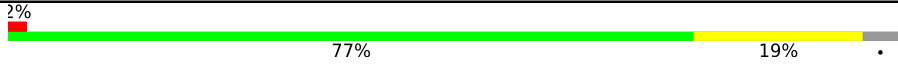
The reported resolution of this entry is 2.88 Å.

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	3557 (2.90-2.86)
Clashscore	190562	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)
RSRZ outliers	180081	3558 (2.90-2.86)

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	237	
1	D	237	
1	G	237	
1	J	237	
2	B	218	

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Mol	Chain	Length	Quality of chain
2	E	218	
2	H	218	
2	K	218	
3	C	199	
3	F	199	
3	I	199	
3	L	199	
4	M	3	
5	N	2	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 19641 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 pT1511 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	227	Total	C	N	O	S	0	0	0
			1710	1080	290	335	5			
1	D	227	Total	C	N	O	S	0	0	0
			1710	1080	290	335	5			
1	G	221	Total	C	N	O	S	0	0	0
			1672	1059	283	325	5			
1	J	220	Total	C	N	O	S	0	0	0
			1663	1053	281	324	5			

- Molecule 2 is a protein called pT1511 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	0	0
			1656	1037	282	331	6			
2	E	215	Total	C	N	O	S	0	0	0
			1656	1037	282	331	6			
2	H	215	Total	C	N	O	S	0	0	0
			1656	1037	282	331	6			
2	K	215	Total	C	N	O	S	0	0	0
			1656	1037	282	331	6			

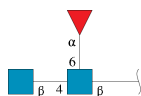
- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	195	Total	C	N	O	S	0	0	0
			1544	989	257	290	8			
3	F	195	Total	C	N	O	S	0	0	0
			1544	989	257	290	8			
3	I	195	Total	C	N	O	S	0	0	0
			1544	989	257	290	8			
3	L	194	Total	C	N	O	S	0	0	0
			1536	985	255	288	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	528	ASP	-	expression tag	UNP P0DTC2
C	529	ASP	-	expression tag	UNP P0DTC2
C	530	ASP	-	expression tag	UNP P0DTC2
C	531	ASP	-	expression tag	UNP P0DTC2
C	532	LYS	-	expression tag	UNP P0DTC2
F	528	ASP	-	expression tag	UNP P0DTC2
F	529	ASP	-	expression tag	UNP P0DTC2
F	530	ASP	-	expression tag	UNP P0DTC2
F	531	ASP	-	expression tag	UNP P0DTC2
F	532	LYS	-	expression tag	UNP P0DTC2
I	528	ASP	-	expression tag	UNP P0DTC2
I	529	ASP	-	expression tag	UNP P0DTC2
I	530	ASP	-	expression tag	UNP P0DTC2
I	531	ASP	-	expression tag	UNP P0DTC2
I	532	LYS	-	expression tag	UNP P0DTC2
L	528	ASP	-	expression tag	UNP P0DTC2
L	529	ASP	-	expression tag	UNP P0DTC2
L	530	ASP	-	expression tag	UNP P0DTC2
L	531	ASP	-	expression tag	UNP P0DTC2
L	532	LYS	-	expression tag	UNP P0DTC2

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



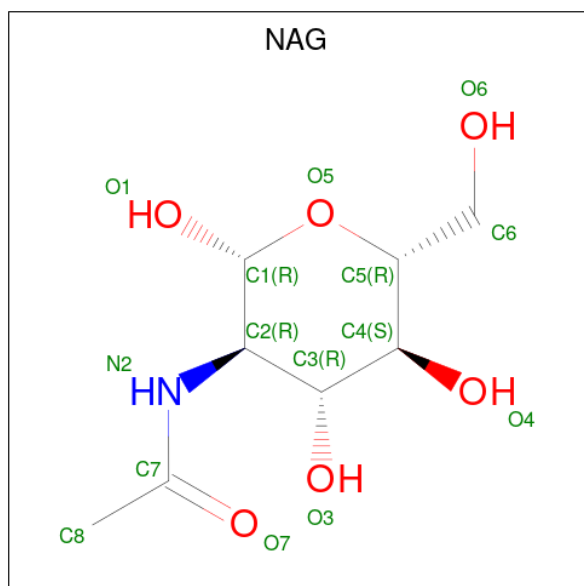
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	M	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 5 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
5	N	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

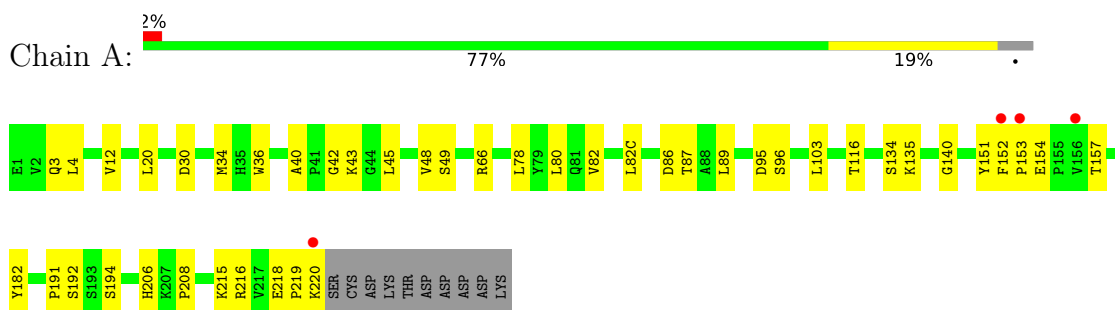


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	I	1	Total	C	N	O	0	0
			14	8	1	5		
6	L	1	Total	C	N	O	0	0
			14	8	1	5		

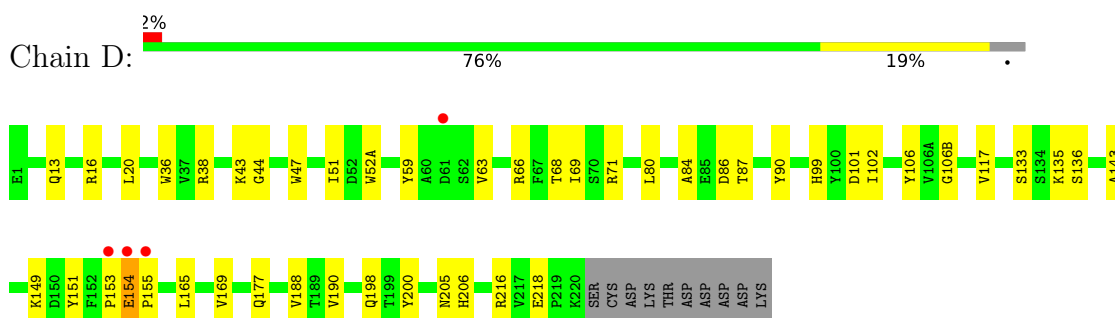
3 Residue-property plots [i](#)

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.

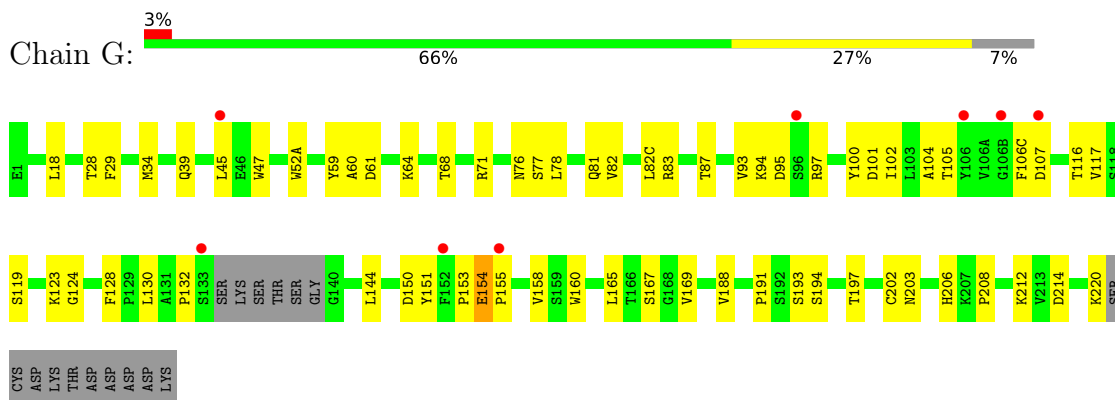
- Molecule 1: pT1511 Fab heavy chain



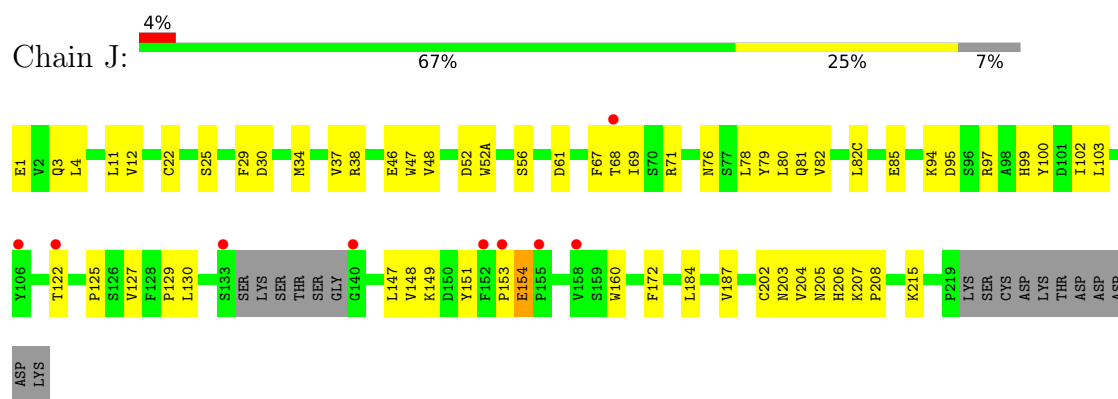
- Molecule 1: pT1511 Fab heavy chain



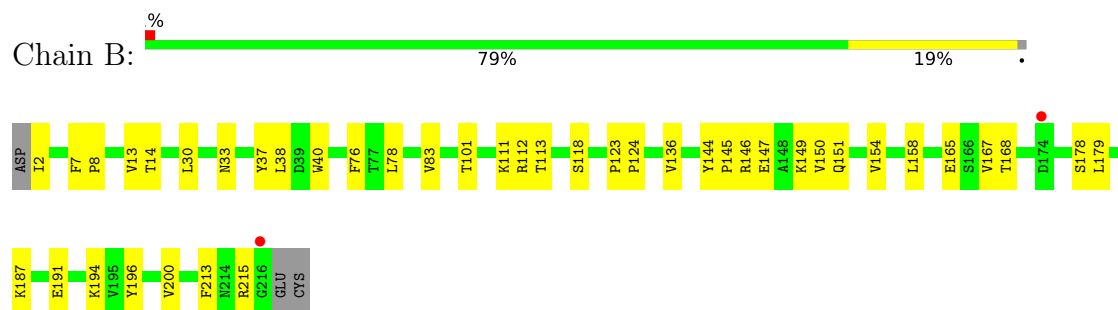
- Molecule 1: pT1511 Fab heavy chain



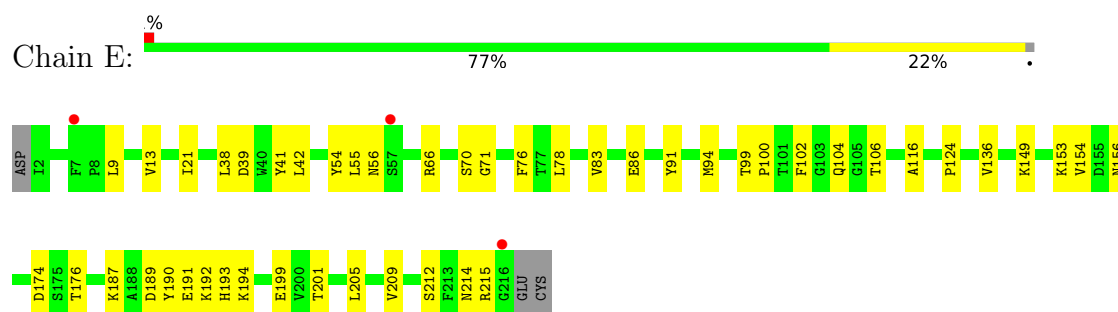
- Molecule 1: pT1511 Fab heavy chain



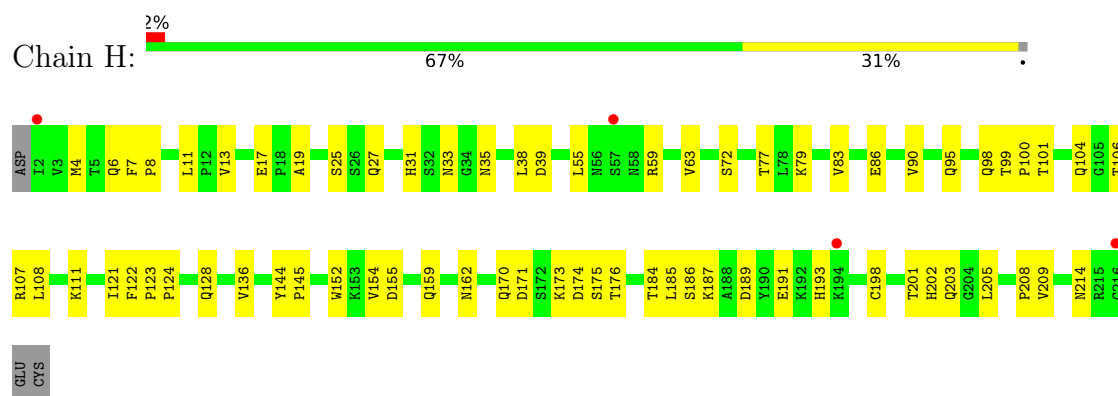
- Molecule 2: pT1511 Fab light chain



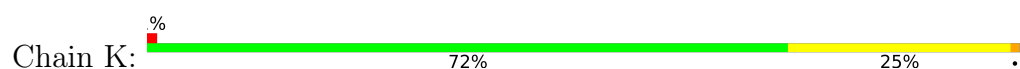
- Molecule 2: pT1511 Fab light chain

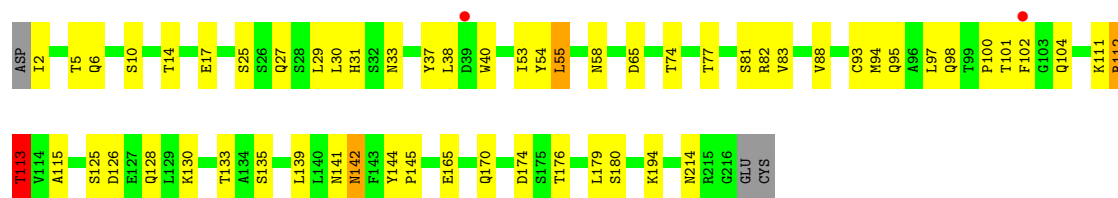


- Molecule 2: pT1511 Fab light chain

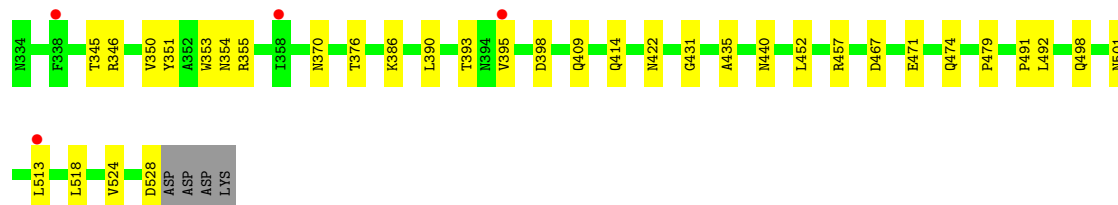
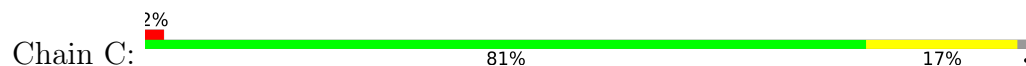


- Molecule 2: pT1511 Fab light chain

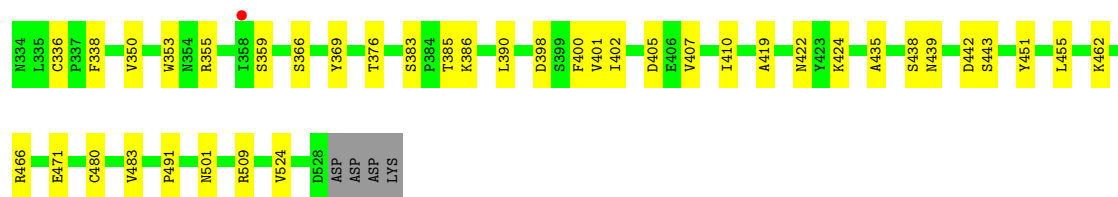
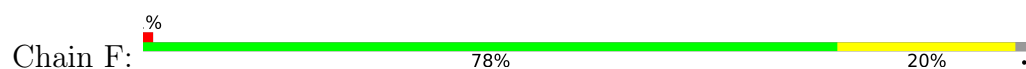




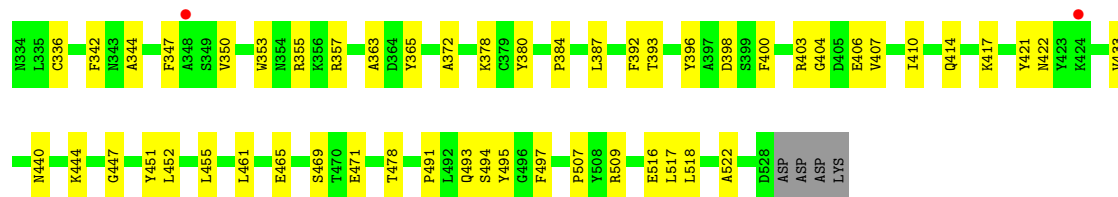
• Molecule 3: Spike protein S1



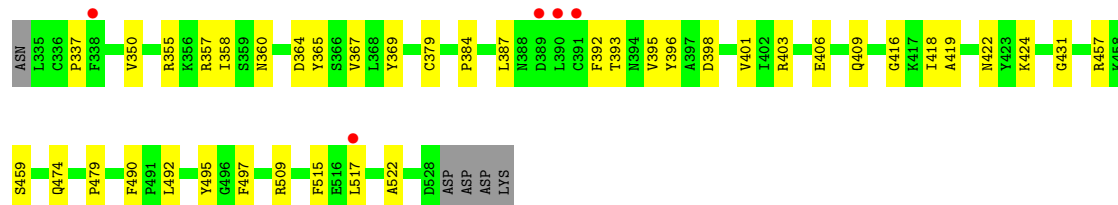
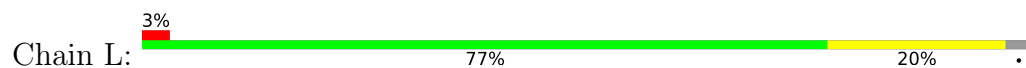
• Molecule 3: Spike protein S1



• Molecule 3: Spike protein S1



• Molecule 3: Spike protein S1



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose

Chain M:  33% 67%

MAG1
MAG2
FUC3

- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain N:  100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	345.27Å 54.37Å 214.69Å 90.00° 105.88° 90.00°	Depositor
Resolution (Å)	48.83 – 2.88 48.83 – 2.88	Depositor EDS
% Data completeness (in resolution range)	97.0 (48.83-2.88) 97.0 (48.83-2.88)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.202 , 0.244 0.217 , 0.258	Depositor DCC
R_{free} test set	4288 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	95.2	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 68.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19641	wwPDB-VP
Average B, all atoms (Å ²)	105.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.64 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.6865e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: FUC, 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	0.16	0/1752	0.38	0/2388
1	D	0.17	0/1752	0.41	0/2388
1	G	0.25	0/1713	0.50	0/2335
1	J	0.18	0/1704	0.44	0/2324
2	B	0.16	0/1692	0.39	0/2299
2	E	0.19	0/1692	0.42	0/2299
2	H	0.17	0/1692	0.41	0/2299
2	K	0.24	0/1692	0.51	3/2299 (0.1%)
3	C	0.16	0/1588	0.34	0/2162
3	F	0.15	0/1588	0.34	0/2162
3	I	0.15	0/1588	0.36	0/2162
3	L	0.18	0/1580	0.38	0/2151
All	All	0.18	0/20033	0.41	3/27268 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	112	ARG	CA-CB-CG	6.94	127.98	114.10
2	K	113	THR	CA-C-N	-5.08	116.89	123.19
2	K	113	THR	C-N-CA	-5.08	116.89	123.19

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	1710	0	1666	25	0
1	D	1710	0	1666	35	0
1	G	1672	0	1627	43	0
1	J	1663	0	1614	55	0
2	B	1656	0	1615	24	0
2	E	1656	0	1615	34	0
2	H	1656	0	1615	50	0
2	K	1656	0	1615	48	0
3	C	1544	0	1456	21	0
3	F	1544	0	1456	25	0
3	I	1544	0	1456	39	0
3	L	1536	0	1450	29	0
4	M	38	0	34	0	0
5	N	28	0	25	1	0
6	I	14	0	13	1	0
6	L	14	0	13	0	0
All	All	19641	0	18936	404	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 10.

The worst 5 of 404 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)
2:K:126:ASP:O	2:K:130:LYS:NZ	1.91	1.04
2:K:112:ARG:NH1	2:K:113:THR:OG1	1.98	0.93
2:E:194:LYS:HE2	2:E:214:ASN:HB3	1.60	0.82
2:K:174:ASP:HB3	2:K:176:THR:HG23	1.62	0.80
1:J:151:TYR:HE1	1:J:154:GLU:HA	1.49	0.77

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	225/237 (95%)	219 (97%)	6 (3%)	0	100	100
1	D	225/237 (95%)	219 (97%)	5 (2%)	1 (0%)	30	56
1	G	217/237 (92%)	208 (96%)	8 (4%)	1 (0%)	24	51
1	J	216/237 (91%)	208 (96%)	7 (3%)	1 (0%)	24	51
2	B	213/218 (98%)	201 (94%)	12 (6%)	0	100	100
2	E	213/218 (98%)	204 (96%)	9 (4%)	0	100	100
2	H	213/218 (98%)	206 (97%)	7 (3%)	0	100	100
2	K	213/218 (98%)	208 (98%)	3 (1%)	2 (1%)	14	38
3	C	193/199 (97%)	186 (96%)	7 (4%)	0	100	100
3	F	193/199 (97%)	183 (95%)	10 (5%)	0	100	100
3	I	193/199 (97%)	185 (96%)	8 (4%)	0	100	100
3	L	192/199 (96%)	182 (95%)	10 (5%)	0	100	100
All	All	2506/2616 (96%)	2409 (96%)	92 (4%)	5 (0%)	43	70

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	154	GLU
1	G	154	GLU
1	J	154	GLU
2	K	113	THR
2	K	142	ASN

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	189/199 (95%)	185 (98%)	4 (2%)	47	75
1	D	189/199 (95%)	189 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	184/199 (92%)	180 (98%)	4 (2%)	45	75
1	J	183/199 (92%)	182 (100%)	1 (0%)	81	93
2	B	190/193 (98%)	187 (98%)	3 (2%)	55	81
2	E	190/193 (98%)	189 (100%)	1 (0%)	81	93
2	H	190/193 (98%)	187 (98%)	3 (2%)	55	81
2	K	190/193 (98%)	187 (98%)	3 (2%)	55	81
3	C	168/172 (98%)	168 (100%)	0	100	100
3	F	168/172 (98%)	167 (99%)	1 (1%)	78	92
3	I	168/172 (98%)	166 (99%)	2 (1%)	63	84
3	L	167/172 (97%)	167 (100%)	0	100	100
All	All	2176/2256 (96%)	2154 (99%)	22 (1%)	68	87

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	198	CYS
3	I	478	THR
3	I	469	SER
1	J	203	ASN
2	B	118	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
2	K	141	ASN
2	K	142	ASN
3	L	388	ASN
3	F	493	GLN
3	F	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 ⓘ

5 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	M	1	3,4	14,14,15	0.32	0	17,19,21	0.58	0
4	NAG	M	2	4	14,14,15	0.67	1 (7%)	17,19,21	0.60	0
4	FUC	M	3	4	10,10,11	0.99	0	14,14,16	0.90	1 (7%)
5	NAG	N	1	3,5	14,14,15	0.35	0	17,19,21	0.40	0
5	NAG	N	2	5	14,14,15	0.36	0	17,19,21	0.52	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
4	NAG	M	1	3,4	-	0/6/23/26	0/1/1/1
4	NAG	M	2	4	-	2/6/23/26	0/1/1/1
4	FUC	M	3	4	-	-	0/1/1/1
5	NAG	N	1	3,5	-	2/6/23/26	0/1/1/1
5	NAG	N	2	5	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	2	NAG	C1-C2	2.00	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
4	M	3	FUC	O5-C5-C4	2.08	113.31	109.55

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

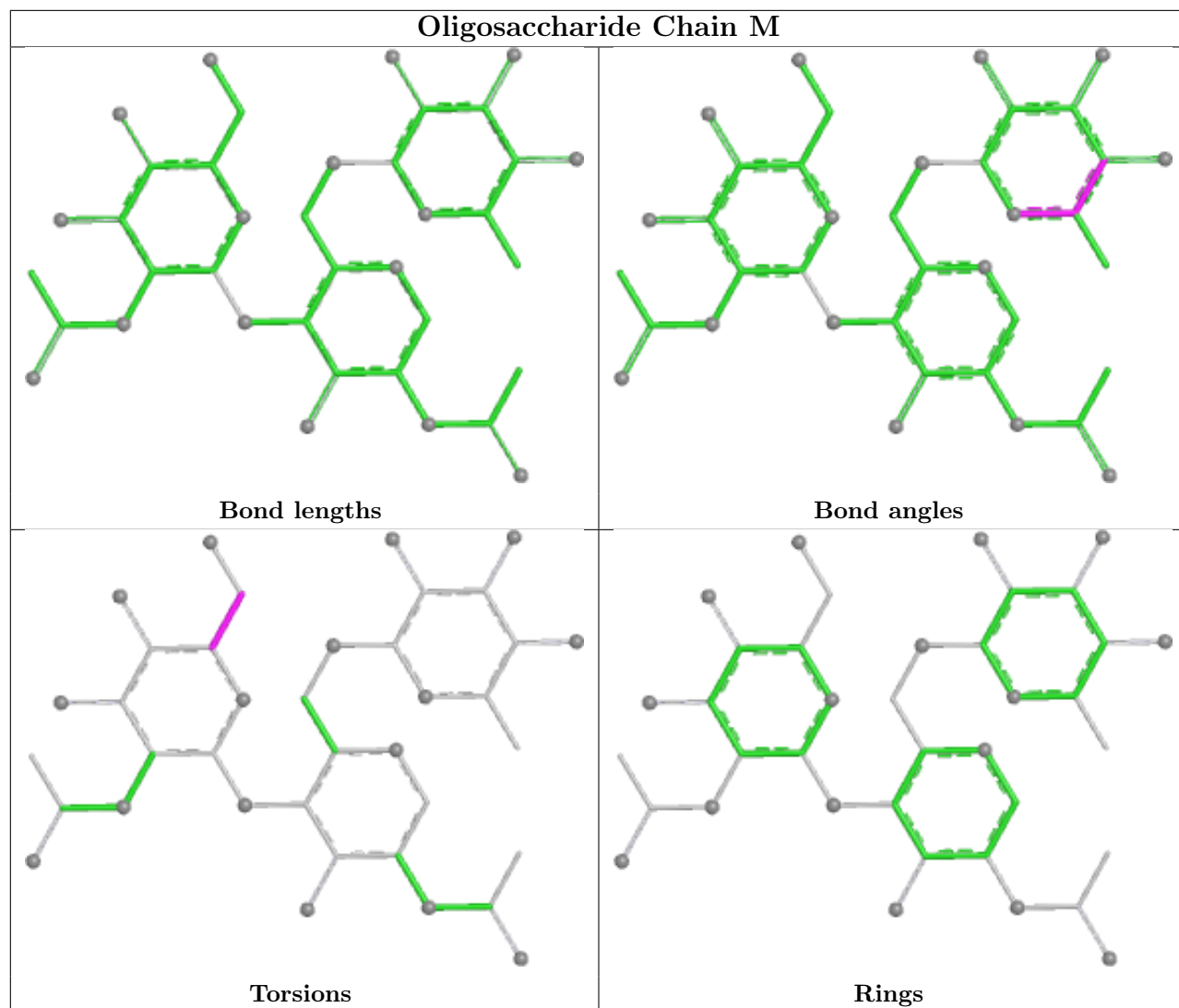
Mol	Chain	Res	Type	Atoms
4	M	2	NAG	C4-C5-C6-O6
5	N	1	NAG	O5-C5-C6-O6
5	N	2	NAG	O5-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6
5	N	2	NAG	C4-C5-C6-O6

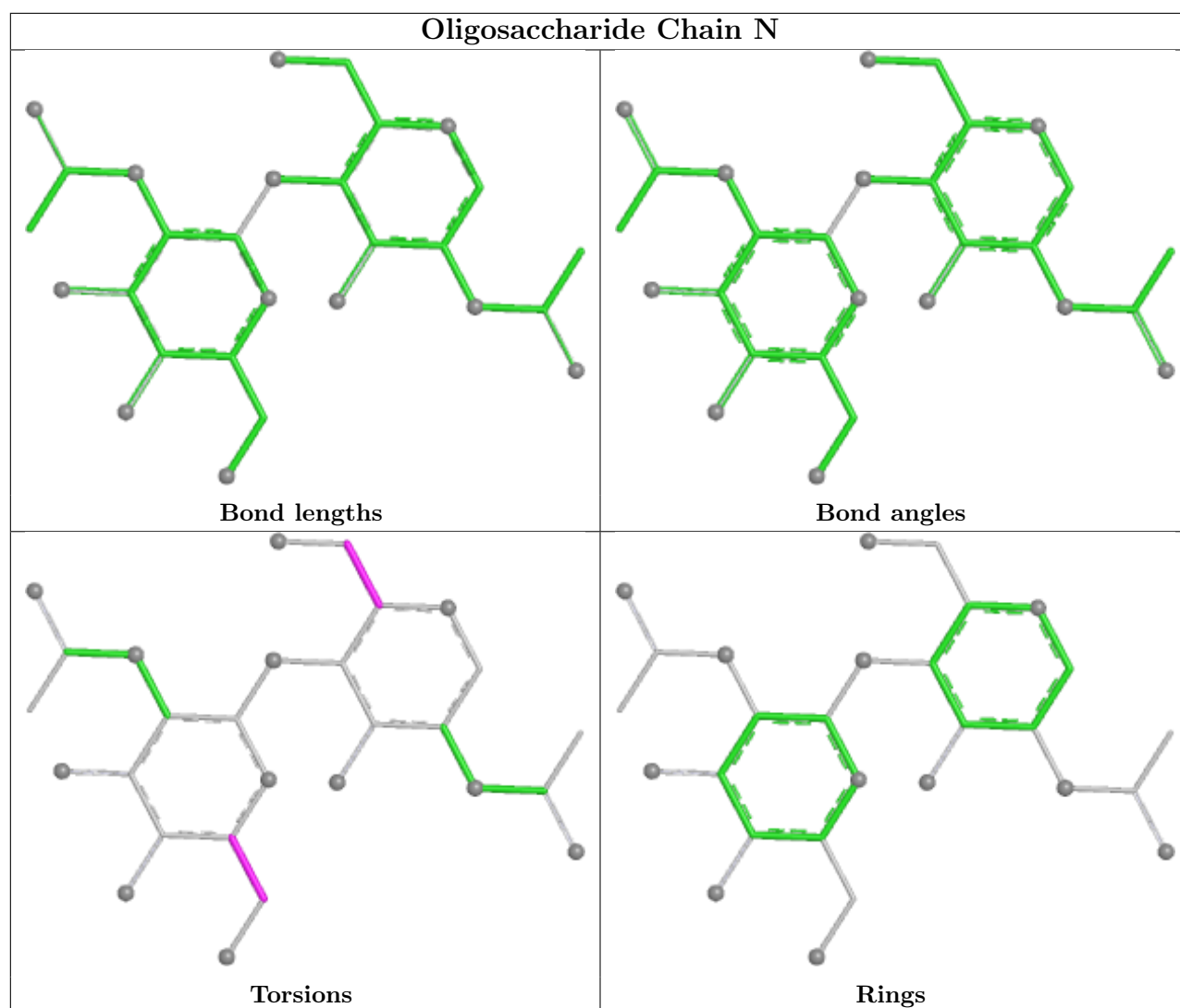
There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	N	2	NAG	1	0
5	N	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](#)

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	$\# Z > 2$
6	NAG	L	601	3	14,14,15	0.40	0	17,19,21	0.58	0
6	NAG	I	601	3	14,14,15	0.49	0	17,19,21	0.64	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
6	NAG	L	601	3	-	2/6/23/26	0/1/1/1
6	NAG	I	601	3	-	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(°)
6	I	601	NAG	C1-O5-C5	2.21	115.15	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	601	NAG	C4-C5-C6-O6
6	L	601	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	I	601	NAG	1	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	227/237 (95%)	-0.16	4 (1%) 67 60	61, 88, 107, 132	0
1	D	227/237 (95%)	-0.05	4 (1%) 67 60	69, 86, 106, 129	0
1	G	221/237 (93%)	0.20	8 (3%) 46 38	90, 119, 152, 172	0
1	J	220/237 (92%)	0.26	9 (4%) 41 33	91, 121, 156, 190	0
2	B	215/218 (98%)	0.02	2 (0%) 81 75	72, 97, 123, 147	0
2	E	215/218 (98%)	-0.10	3 (1%) 73 66	71, 90, 111, 150	0
2	H	215/218 (98%)	0.26	4 (1%) 66 58	90, 114, 143, 177	0
2	K	215/218 (98%)	0.24	2 (0%) 81 75	89, 116, 147, 206	0
3	C	195/199 (97%)	-0.04	4 (2%) 63 55	68, 91, 121, 134	0
3	F	195/199 (97%)	0.00	1 (0%) 87 83	70, 95, 122, 138	0
3	I	195/199 (97%)	0.12	2 (1%) 79 73	88, 110, 150, 190	0
3	L	194/199 (97%)	0.13	5 (2%) 57 48	87, 110, 152, 214	0
All	All	2534/2616 (96%)	0.07	48 (1%) 66 58	61, 102, 142, 214	0

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	216	GLY	3.8
2	K	39	ASP	3.7
1	G	133	SER	3.5
2	K	102	PHE	3.4
1	D	154	GLU	3.3

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](#)

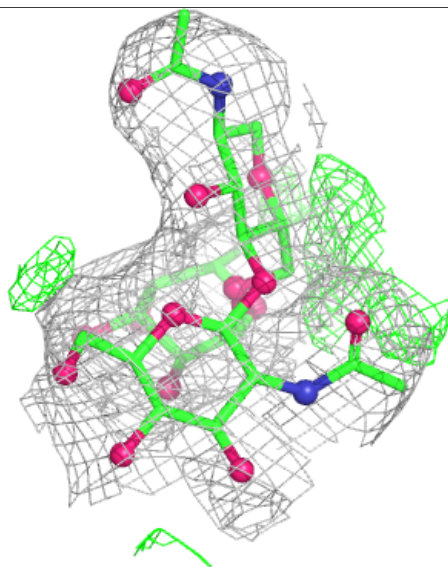
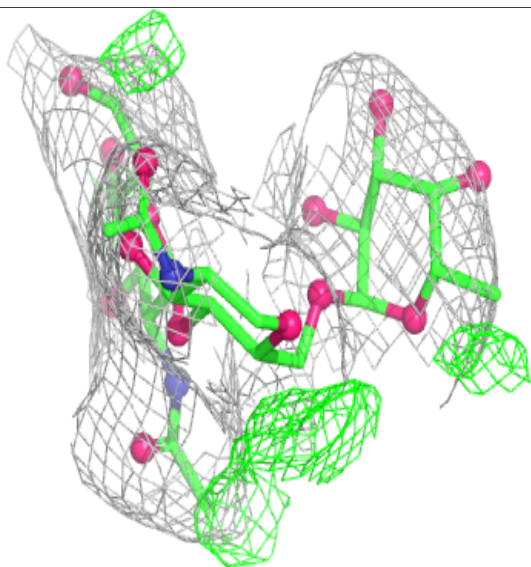
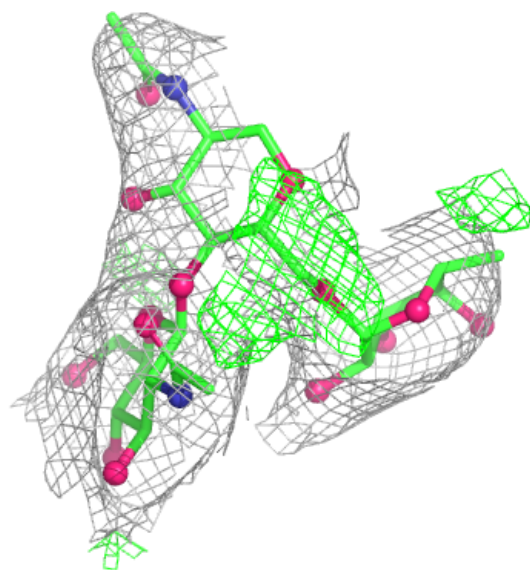
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

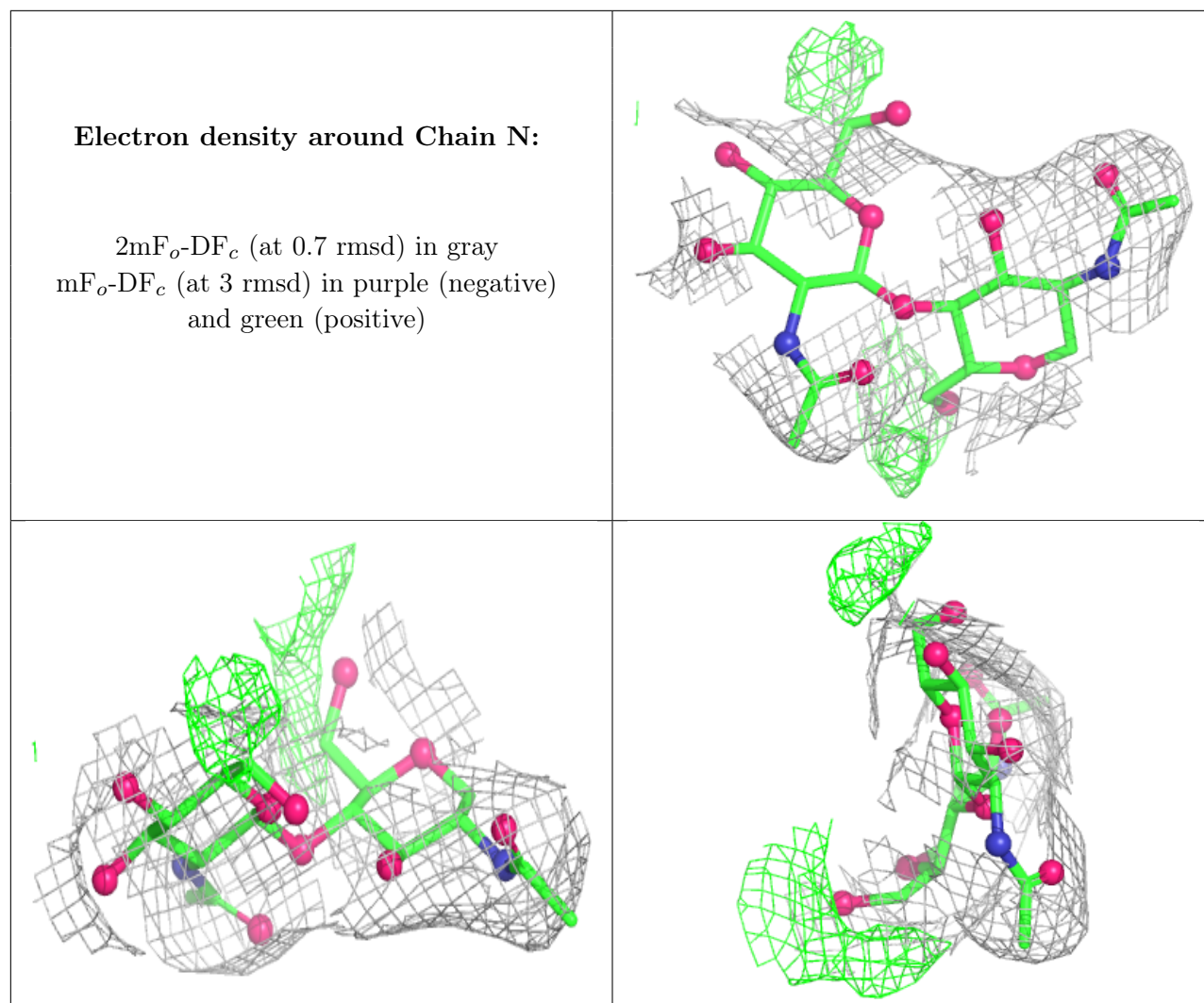
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	FUC	M	3	10/11	0.61	0.14	119,133,141,143	0
5	NAG	N	2	14/15	0.70	0.12	117,136,147,149	0
4	NAG	M	2	14/15	0.74	0.12	107,121,133,137	0
5	NAG	N	1	14/15	0.88	0.09	101,110,127,129	0
4	NAG	M	1	14/15	0.89	0.11	82,109,127,139	0

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 M:

$2mF_o-DF_c$ (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
6	NAG	L	601	14/15	0.77	0.12	113,128,138,143	0
6	NAG	I	601	14/15	0.85	0.10	116,127,136,137	0

6.5 Other polymers [i](#)

There are no such residues in this entry.