



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 30, 2023 – 09:11 am GMT

PDB ID : 8BG1
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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

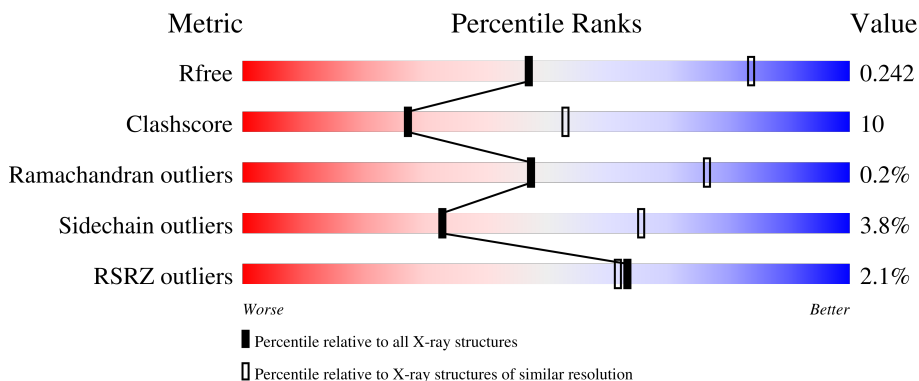
1 Overall quality at a glance

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.







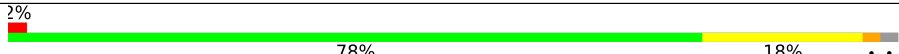
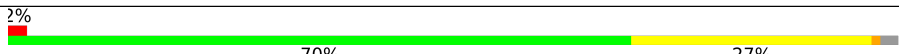
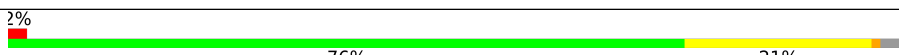
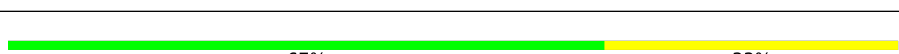
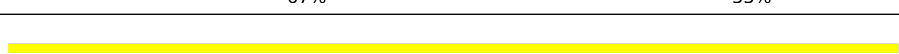
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)

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	 77% 18% . .
1	D	237	 75% 20% . .
1	G	237	 2% 66% 26% . 7%
1	J	237	 6% 66% 24% . 7%
2	B	218	 % 78% 21% .

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Mol	Chain	Length	Quality of chain
2	E	218	 78% 20% ..
2	H	218	 4% 66% 32% ..
2	K	218	 3% 70% 26% ..
3	C	199	 3% 80% 17% ..
3	F	199	 2% 78% 18% ..
3	I	199	 2% 70% 27% ..
3	L	199	 2% 76% 21% ..
4	M	3	 67% 33%
5	N	2	 100%

2 Entry composition [i](#)

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
			Total	C	N	O	S			
1	A	227	Total 1710	C 1080	N 290	O 335	S 5	0	0	0
1	D	227	Total 1710	C 1080	N 290	O 335	S 5	0	0	0
1	G	221	Total 1672	C 1059	N 283	O 325	S 5	0	0	0
1	J	220	Total 1663	C 1053	N 281	O 324	S 5	0	0	0

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

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

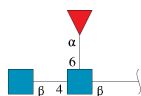
- Molecule 3 is a protein called Spike protein S1.

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

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.



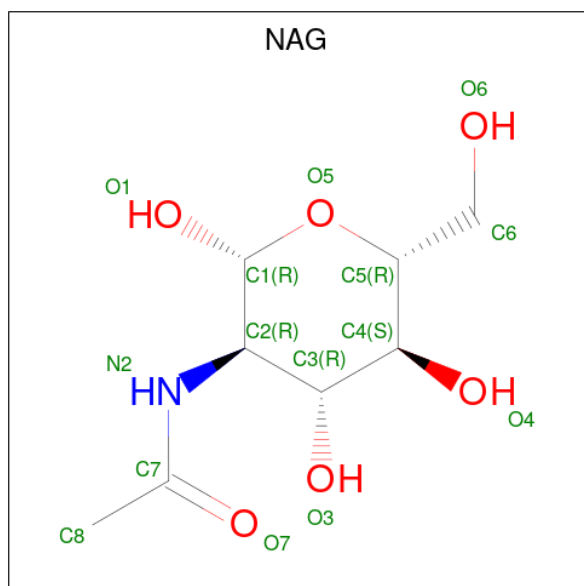
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	M	3	38	22	2	14	0	0	0

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

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

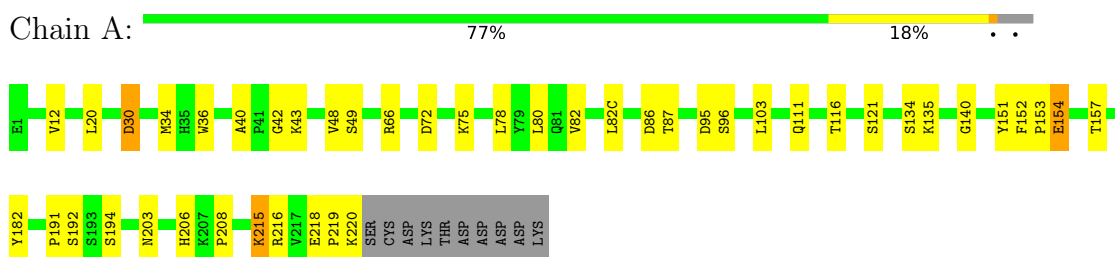


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
6	I	1	14	8	1	5	0	0
6	L	1	14	8	1	5	0	0

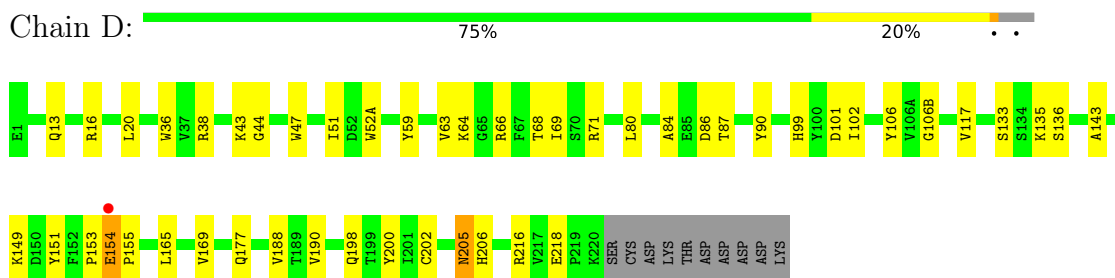
3 Residue-property plots [i](#)

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.

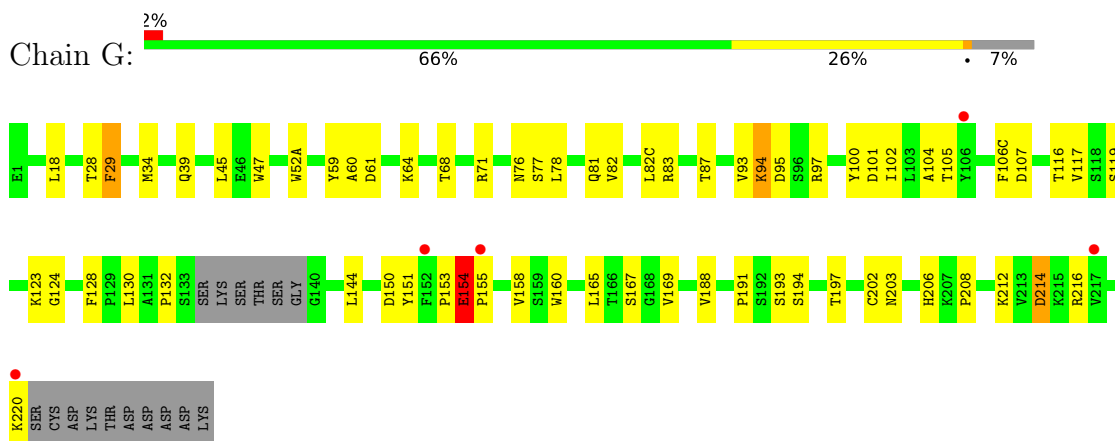
- Molecule 1: pT1511 Fab heavy chain



- Molecule 1: pT1511 Fab heavy chain

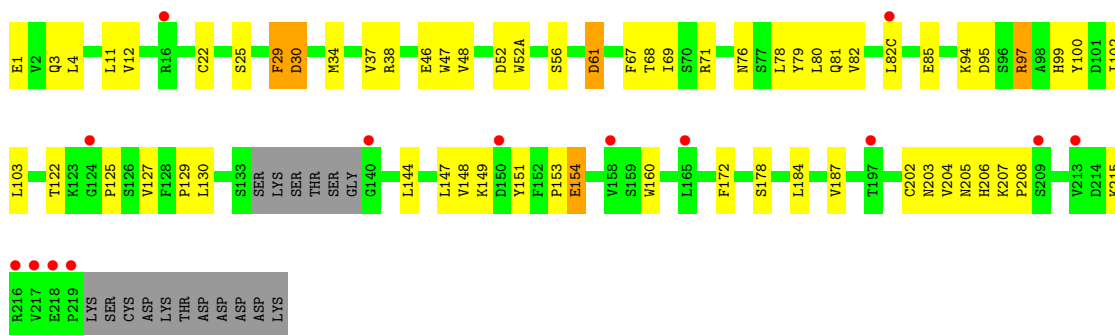


- Molecule 1: pT1511 Fab heavy chain

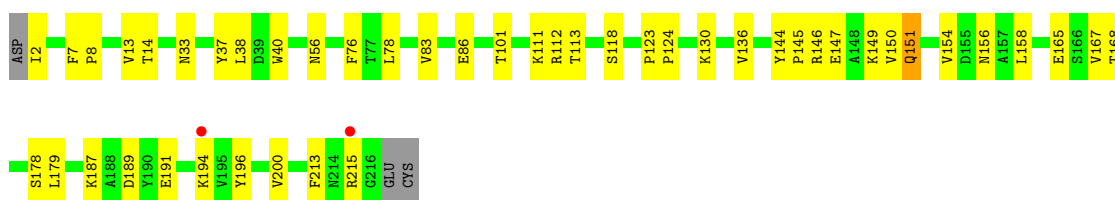
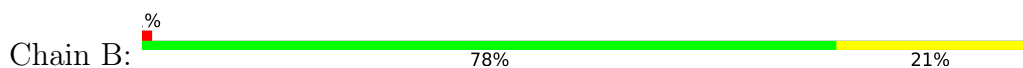


- Molecule 1: pT1511 Fab heavy chain

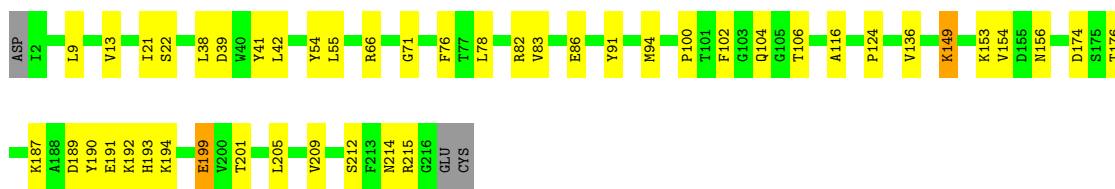
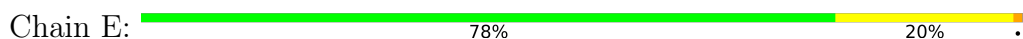




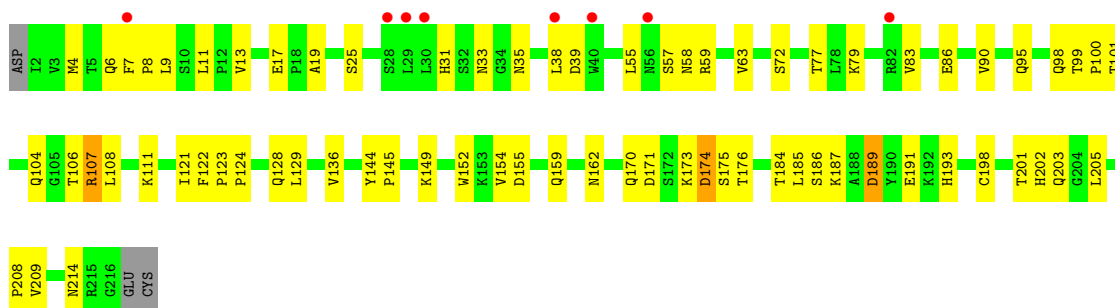
- Molecule 2: pT1511 Fab light chain



- Molecule 2: pT1511 Fab light chain

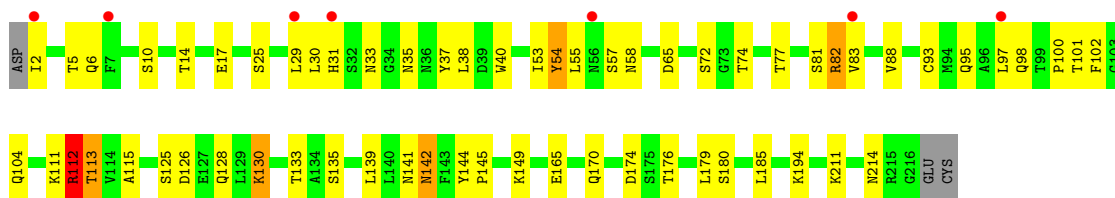


- Molecule 2: pT1511 Fab light chain

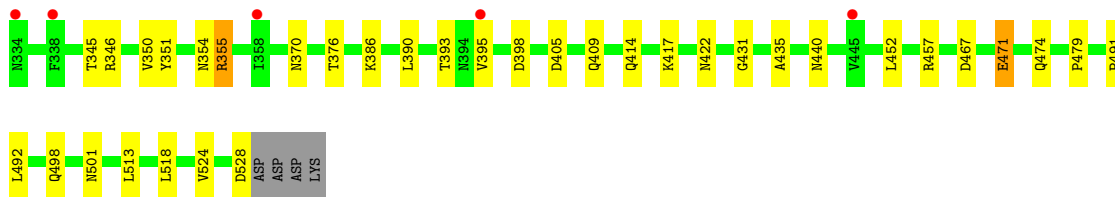
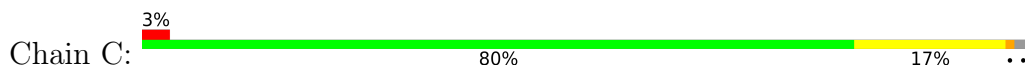


- Molecule 2: pT1511 Fab light chain

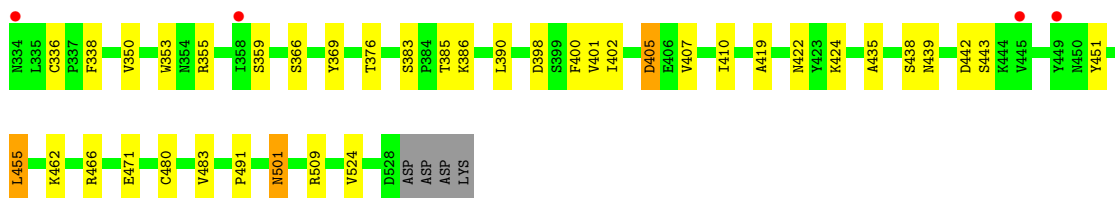
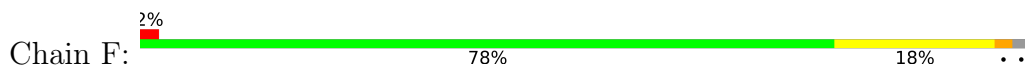




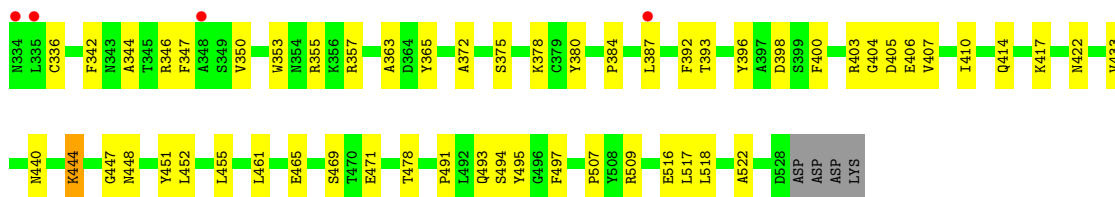
• Molecule 3: Spike protein S1



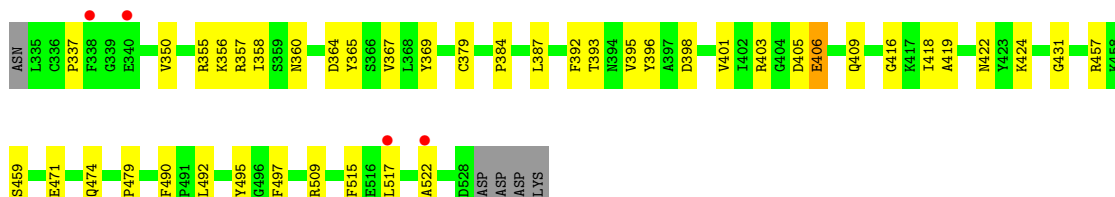
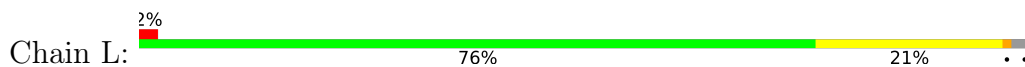
• Molecule 3: Spike protein S1



• 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:  67% 33%

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) 97.1 (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)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.202 , 0.244 0.200 , 0.242	Depositor DCC
R_{free} test set	4264 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	95.2	Xtrriage
Anisotropy	0.347	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 59.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19641	wwPDB-VP
Average B, all atoms (Å ²)	105.0	wwPDB-VP

Xtrriage'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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, FUC

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	0.29	0/1752	0.55	0/2388
1	D	0.29	0/1752	0.56	0/2388
1	G	0.33	0/1713	0.62	0/2335
1	J	0.30	0/1704	0.58	0/2324
2	B	0.30	0/1692	0.55	0/2299
2	E	0.31	0/1692	0.56	0/2299
2	H	0.29	0/1692	0.55	0/2299
2	K	0.33	0/1692	0.60	2/2299 (0.1%)
3	C	0.29	0/1588	0.53	0/2162
3	F	0.29	0/1588	0.52	1/2162 (0.0%)
3	I	0.29	0/1588	0.53	0/2162
3	L	0.30	0/1580	0.54	0/2151
All	All	0.30	0/20033	0.56	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	6.63	127.98	113.40
3	F	455	LEU	CA-CB-CG	5.15	127.14	115.30
2	K	112	ARG	NE-CZ-NH1	-5.01	117.79	120.30

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	1710	0	1666	23	0
1	D	1710	0	1666	35	0
1	G	1672	0	1627	42	0
1	J	1663	0	1614	54	0
2	B	1656	0	1615	24	0
2	E	1656	0	1615	31	0
2	H	1656	0	1615	48	0
2	K	1656	0	1615	45	0
3	C	1544	0	1456	20	0
3	F	1544	0	1456	24	0
3	I	1544	0	1456	37	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	388	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 388 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 [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	225/237 (95%)	219 (97%)	6 (3%)	0	100	100
1	D	225/237 (95%)	219 (97%)	5 (2%)	1 (0%)	34	64
1	G	217/237 (92%)	208 (96%)	8 (4%)	1 (0%)	29	59
1	J	216/237 (91%)	208 (96%)	7 (3%)	1 (0%)	29	59
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%)	17	45
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%)	47	76

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 [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/199 (95%)	179 (95%)	10 (5%)	22	52
1	D	189/199 (95%)	186 (98%)	3 (2%)	62	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	184/199 (92%)	174 (95%)	10 (5%)	22	51
1	J	183/199 (92%)	176 (96%)	7 (4%)	33	65
2	B	190/193 (98%)	182 (96%)	8 (4%)	30	61
2	E	190/193 (98%)	186 (98%)	4 (2%)	53	80
2	H	190/193 (98%)	179 (94%)	11 (6%)	20	48
2	K	190/193 (98%)	178 (94%)	12 (6%)	18	44
3	C	168/172 (98%)	164 (98%)	4 (2%)	49	78
3	F	168/172 (98%)	165 (98%)	3 (2%)	59	83
3	I	168/172 (98%)	161 (96%)	7 (4%)	30	61
3	L	167/172 (97%)	163 (98%)	4 (2%)	49	78
All	All	2176/2256 (96%)	2093 (96%)	83 (4%)	33	65

5 of 83 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	I	448	ASN
2	K	72	SER
3	I	478	THR
1	J	178	SER
2	K	130	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	159	GLN
3	I	448	ASN
3	L	409	GLN
3	I	414	GLN
1	J	205	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

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	4,3	14,14,15	0.31	0	17,19,21	0.57	0
4	NAG	M	2	4	14,14,15	0.64	0	17,19,21	0.58	0
4	FUC	M	3	4	10,10,11	0.99	0	14,14,16	0.96	1 (7%)
5	NAG	N	1	5,3	14,14,15	0.33	0	17,19,21	0.39	0
5	NAG	N	2	5	14,14,15	0.34	0	17,19,21	0.50	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	4,3	-	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	5,3	-	2/6/23/26	0/1/1/1
5	NAG	N	2	5	-	2/6/23/26	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	M	3	FUC	O5-C5-C4	2.11	113.31	109.52

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

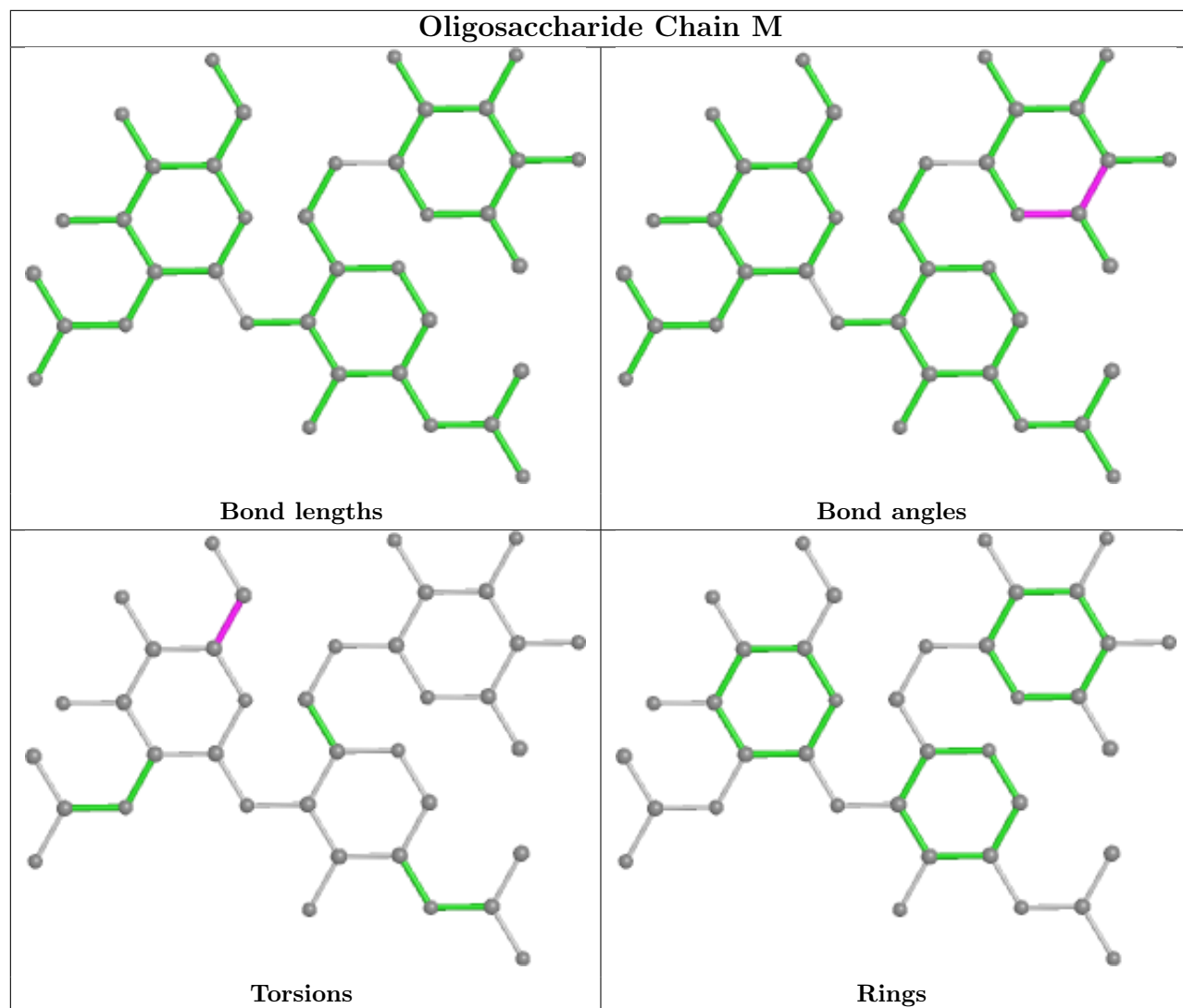
Mol	Chain	Res	Type	Atoms
4	M	2	NAG	C4-C5-C6-O6
5	N	1	NAG	O5-C5-C6-O6
5	N	2	NAG	O5-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6
5	N	2	NAG	C4-C5-C6-O6

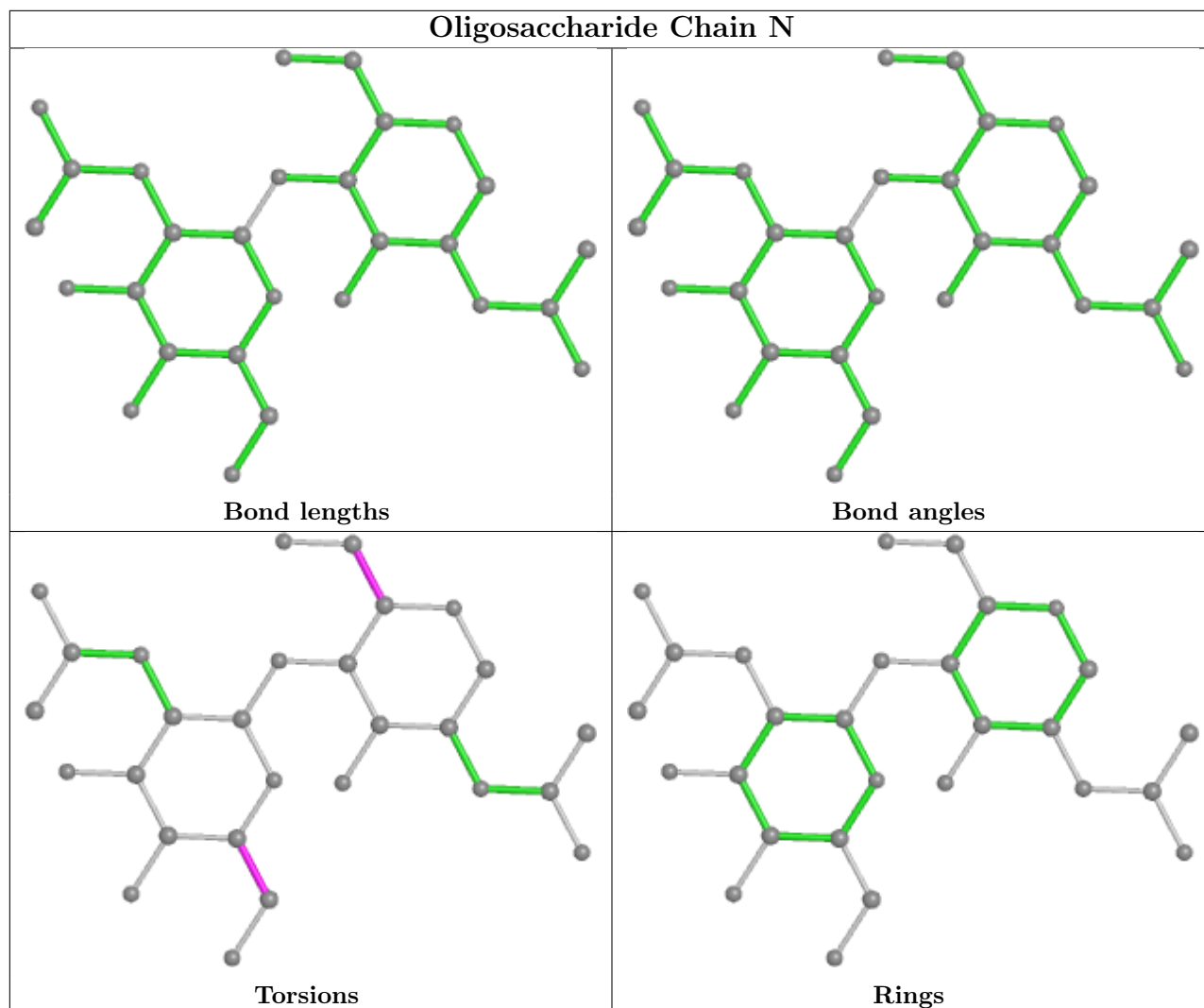
There are no ring outliers.

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	0.39	0	17,19,21	0.57	0
6	NAG	I	601	3	14,14,15	0.48	0	17,19,21	0.62	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($^{\circ}$)	Ideal($^{\circ}$)
6	I	601	NAG	C1-O5-C5	2.19	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%)	0.00	0 100 100	61, 88, 107, 132	0
1	D	227/237 (95%)	0.07	1 (0%) 92 92	69, 86, 106, 129	0
1	G	221/237 (93%)	0.24	5 (2%) 60 59	90, 119, 152, 172	0
1	J	220/237 (92%)	0.38	14 (6%) 19 15	91, 121, 156, 190	0
2	B	215/218 (98%)	0.06	2 (0%) 84 84	72, 97, 123, 147	0
2	E	215/218 (98%)	0.01	0 100 100	71, 90, 111, 150	0
2	H	215/218 (98%)	0.30	8 (3%) 41 37	90, 114, 143, 177	0
2	K	215/218 (98%)	0.36	7 (3%) 46 41	89, 116, 147, 206	0
3	C	195/199 (97%)	0.05	5 (2%) 56 53	68, 91, 121, 134	0
3	F	195/199 (97%)	0.09	4 (2%) 63 62	70, 95, 122, 138	0
3	I	195/199 (97%)	0.13	4 (2%) 63 62	88, 110, 150, 190	0
3	L	194/199 (97%)	0.15	4 (2%) 63 62	87, 110, 152, 214	0
All	All	2534/2616 (96%)	0.15	54 (2%) 63 62	61, 102, 142, 214	0

The worst 5 of 54 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	7	PHE	4.8
1	J	197	THR	4.3
3	I	334	ASN	4.2
1	J	217	VAL	4.2
2	K	7	PHE	3.8

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

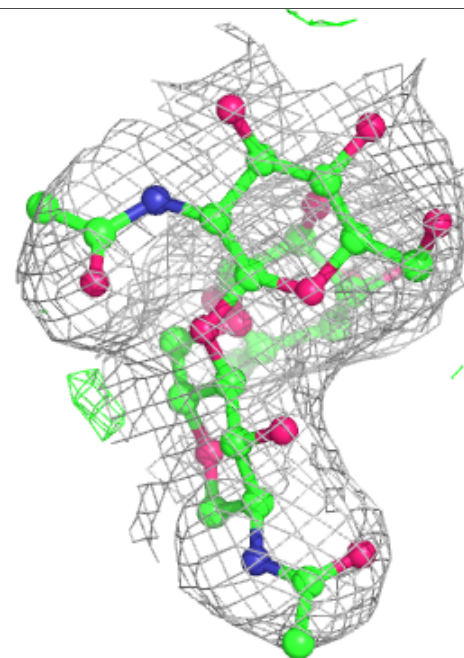
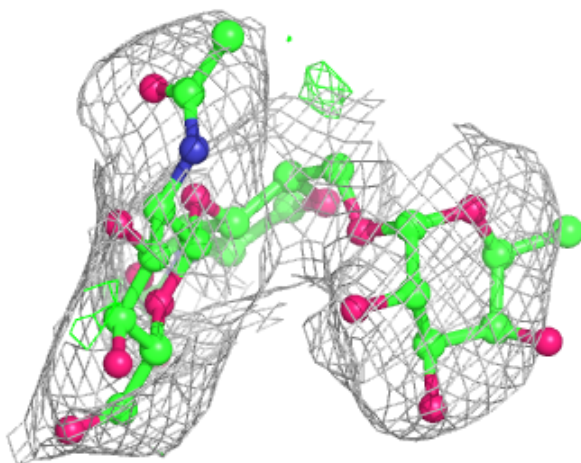
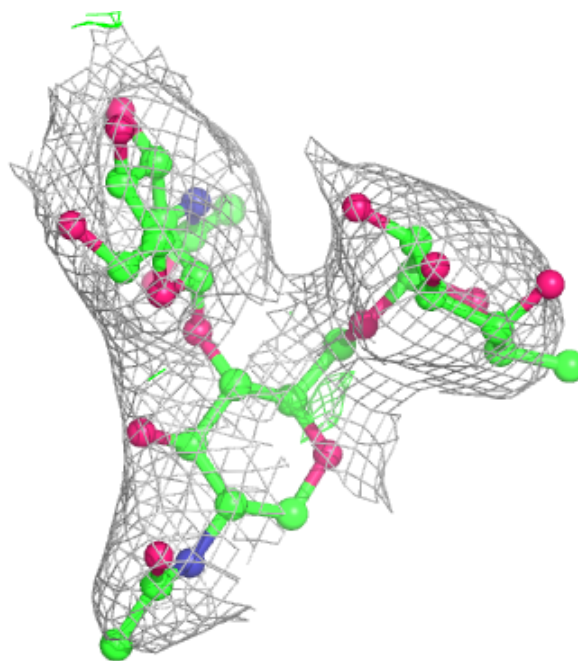
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

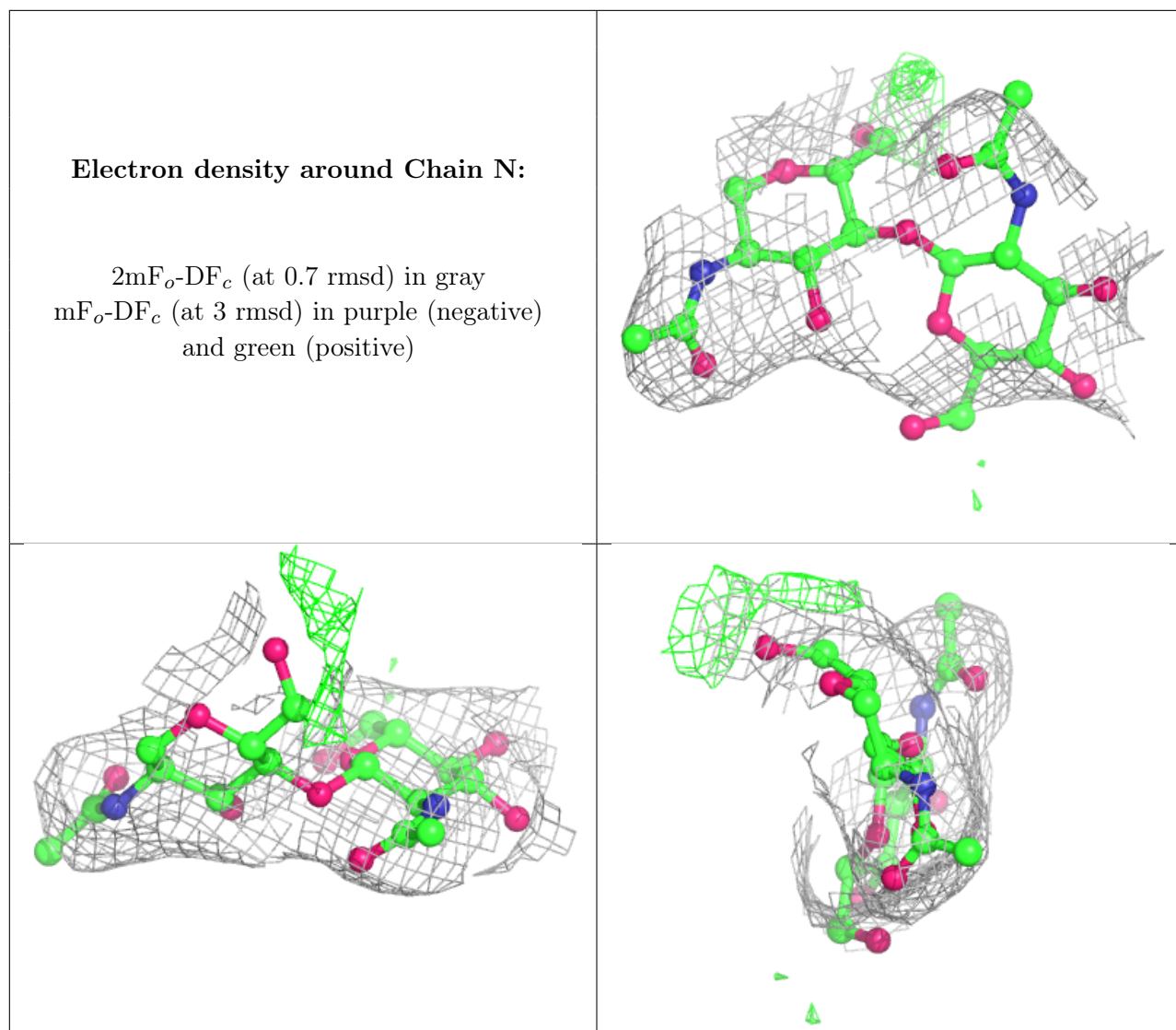
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	N	2	14/15	0.87	0.16	117,136,147,149	0
4	FUC	M	3	10/11	0.90	0.15	119,133,141,143	0
4	NAG	M	1	14/15	0.93	0.16	82,109,127,139	0
4	NAG	M	2	14/15	0.93	0.12	107,121,133,137	0
5	NAG	N	1	14/15	0.94	0.14	101,110,127,129	0

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(Å ²)	Q < 0.9
6	NAG	L	601	14/15	0.83	0.15	113,128,138,143	0
6	NAG	I	601	14/15	0.85	0.12	116,127,136,137	0

6.5 Other polymers [i](#)

There are no such residues in this entry.