



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 21, 2023 – 07:28 AM JST

PDB ID : 7F5R
Title : Crystal structure of SARS-CoV-2 Y453F-RBD bound to mink ACE2
Authors : Wang, X.Q.; Ding, Q.; Lan, J.; Ren, W.L.
Deposited on : 2021-06-22
Resolution : 3.01 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 : 1.8.5 (274361), 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

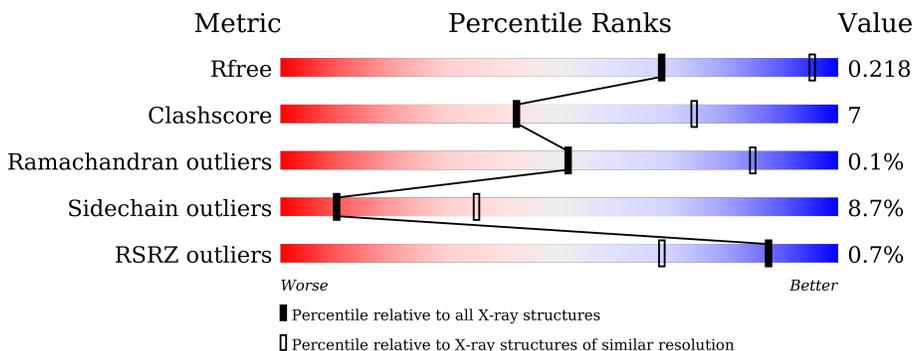
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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.



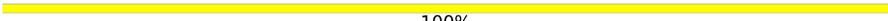
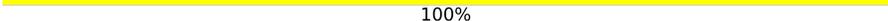
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)
RSRZ outliers	127900	2287 (3.04-3.00)

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	597	 % 78% 19% .
1	B	597	 76% 22% .
1	D	597	 % 77% 20% .
2	C	197	 % 78% 16% . 5%
2	E	197	 3% 70% 22% . 6%
2	F	197	 81% 18% .

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Mol	Chain	Length	Quality of chain
3	G	2	 100%
3	I	2	 50% 50%
4	H	2	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 19386 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 mink ACE2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	596	4904	3132	823	920	29	0	0	0
1	B	596	4904	3132	823	920	29	0	0	0
1	D	596	4904	3132	823	920	29	0	0	0

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	185	1468	942	247	271	8	0	0	0
2	C	187	1483	950	250	275	8	0	0	0
2	F	197	1559	1000	261	290	8	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	332	PRO	-	expression tag	UNP P0DTC2
E	453	PHE	TYR	variant	UNP P0DTC2
E	528	HIS	-	expression tag	UNP P0DTC2
C	332	PRO	-	expression tag	UNP P0DTC2
C	453	PHE	TYR	variant	UNP P0DTC2
C	528	HIS	-	expression tag	UNP P0DTC2
F	332	PRO	-	expression tag	UNP P0DTC2
F	453	PHE	TYR	variant	UNP P0DTC2
F	528	HIS	-	expression tag	UNP P0DTC2

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



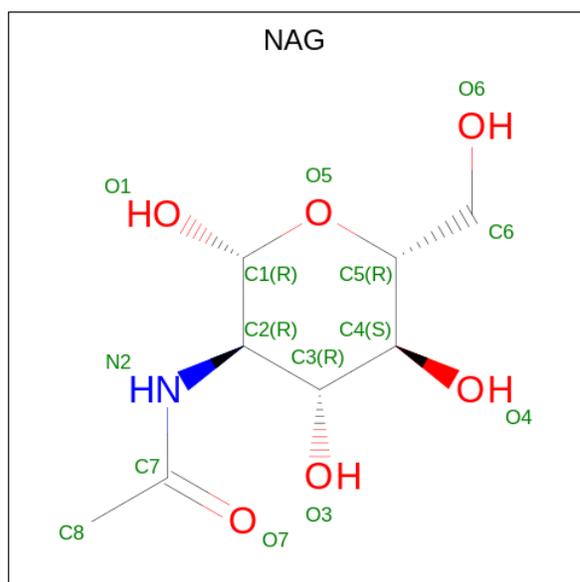
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	H	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).

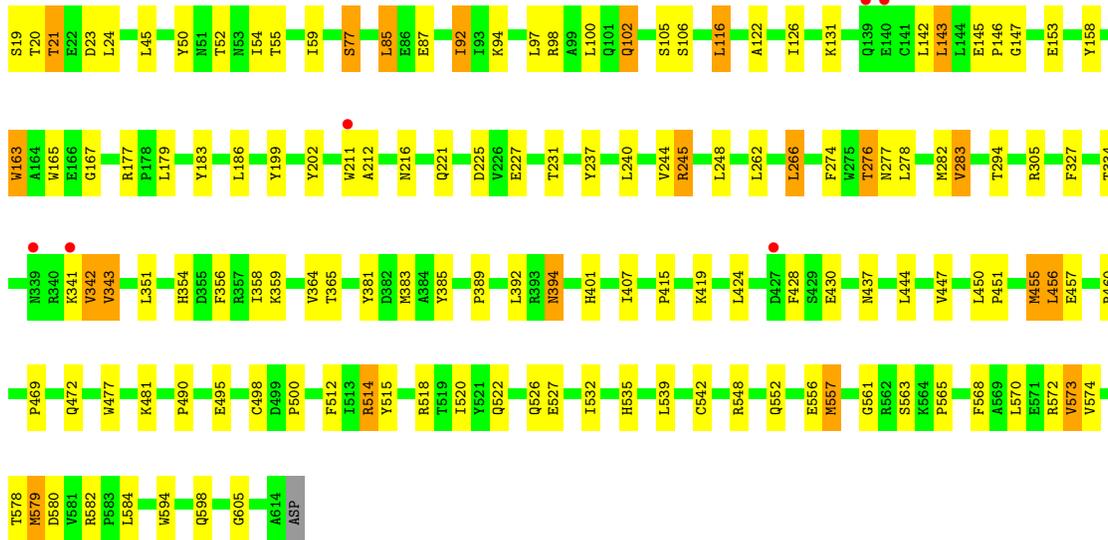
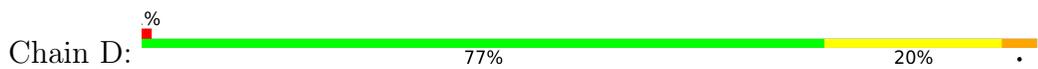


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		

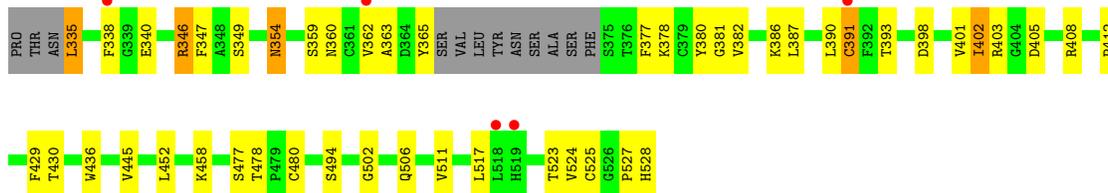
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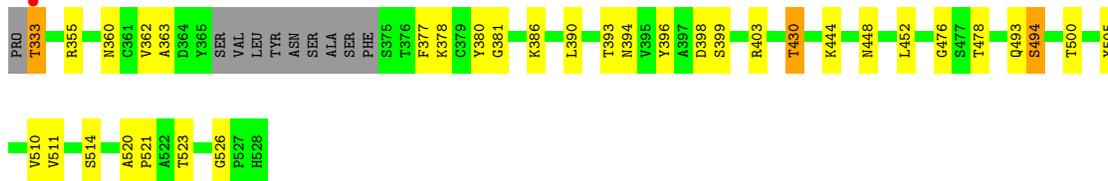
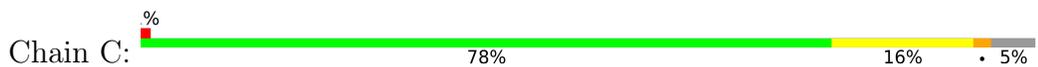
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	E	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		
5	D	1	Total	C	N	O	0	0
			14	8	1	5		



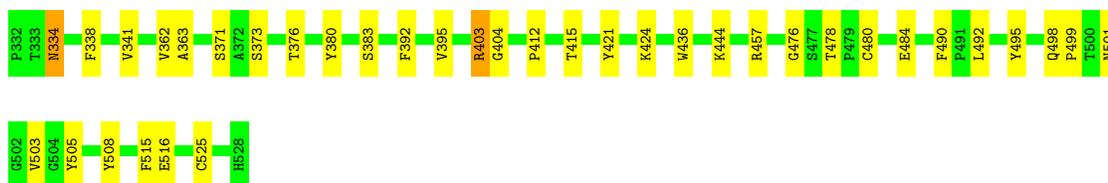
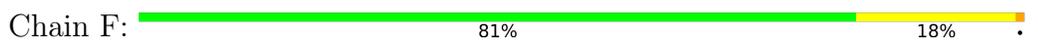
• Molecule 2: Spike protein S1



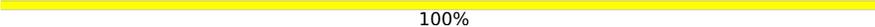
• Molecule 2: Spike protein S1



• Molecule 2: Spike protein S1



- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:  100%

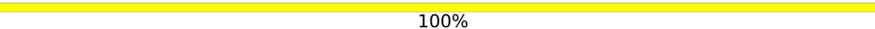
MAG1
MAG2

- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  50% 50%

MAG1
MAG2

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

Chain H:  100%

MAG1
FUC2

4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	290.19Å 130.19Å 136.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.53 – 3.01 43.53 – 3.01	Depositor EDS
% Data completeness (in resolution range)	98.1 (43.53-3.01) 98.1 (43.53-3.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.181 , 0.218 0.181 , 0.218	Depositor DCC
R_{free} test set	5072 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	68.6	Xtrriage
Anisotropy	0.285	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.015 for -h,l,k	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19386	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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: 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	0.52	3/5047 (0.1%)	0.62	0/6855
1	B	0.49	0/5047	0.63	3/6855 (0.0%)
1	D	0.47	0/5047	0.62	2/6855 (0.0%)
2	C	0.51	0/1525	0.66	0/2074
2	E	0.53	0/1510	0.68	1/2053 (0.0%)
2	F	0.57	1/1605 (0.1%)	0.67	0/2185
All	All	0.50	4/19781 (0.0%)	0.63	6/26877 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	74	GLU	CG-CD	6.36	1.61	1.51
1	A	74	GLU	CB-CG	6.29	1.64	1.52
1	A	74	GLU	CD-OE1	5.48	1.31	1.25
2	F	484	GLU	CG-CD	5.36	1.59	1.51

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	584	LEU	CA-CB-CG	7.66	132.92	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	456	LEU	CA-CB-CG	6.94	131.27	115.30
1	B	169	ARG	NE-CZ-NH1	-6.48	117.06	120.30
1	D	584	LEU	CA-CB-CG	6.00	129.09	115.30
2	E	380	TYR	C-N-CA	-5.87	109.98	122.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	52	THR	Peptide
1	D	102	GLN	Peptide

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	4904	0	4657	65	0
1	B	4904	0	4656	71	0
1	D	4904	0	4658	77	0
2	C	1483	0	1402	18	0
2	E	1468	0	1390	18	0
2	F	1559	0	1475	16	0
3	G	28	0	25	0	0
3	I	28	0	25	0	0
4	H	24	0	22	0	0
5	A	14	0	13	0	0
5	B	42	0	39	1	0
5	D	14	0	13	0	0
5	E	14	0	13	0	0
All	All	19386	0	18388	261	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 7.

The worst 5 of 261 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:457:GLU:OE1	1:A:460:ARG:NH1	1.95	0.98
1:B:288:LYS:HB3	1:B:434:THR:HG22	1.50	0.93
2:E:346:ARG:NH1	2:E:347:PHE:O	2.13	0.81
1:A:192:ARG:NH1	1:A:197:GLU:O	2.18	0.77
1:A:23:ASP:O	1:A:27:THR:HG22	1.85	0.76

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	594/597 (100%)	574 (97%)	19 (3%)	1 (0%)	47	81
1	B	594/597 (100%)	574 (97%)	19 (3%)	1 (0%)	47	81
1	D	594/597 (100%)	574 (97%)	20 (3%)	0	100	100
2	C	183/197 (93%)	176 (96%)	7 (4%)	0	100	100
2	E	181/197 (92%)	167 (92%)	14 (8%)	0	100	100
2	F	195/197 (99%)	183 (94%)	12 (6%)	0	100	100
All	All	2341/2382 (98%)	2248 (96%)	91 (4%)	2 (0%)	51	85

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	146	PRO
1	A	146	PRO

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	524/525 (100%)	476 (91%)	48 (9%)	9	32
1	B	524/525 (100%)	478 (91%)	46 (9%)	10	34
1	D	524/525 (100%)	483 (92%)	41 (8%)	12	40
2	C	161/170 (95%)	152 (94%)	9 (6%)	21	54
2	E	159/170 (94%)	136 (86%)	23 (14%)	3	14
2	F	170/170 (100%)	158 (93%)	12 (7%)	14	44
All	All	2062/2085 (99%)	1883 (91%)	179 (9%)	10	35

5 of 179 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	584	LEU
1	D	276	THR
2	C	393	THR
1	D	59	ILE
1	D	354	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	GLN

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](#)

6 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	1	3,1	14,14,15	1.03	1 (7%)	17,19,21	0.86	1 (5%)
3	NAG	G	2	3	14,14,15	0.94	1 (7%)	17,19,21	1.22	2 (11%)
4	NAG	H	1	4,1	14,14,15	1.39	2 (14%)	17,19,21	0.84	1 (5%)
4	FUC	H	2	4	10,10,11	2.50	5 (50%)	14,14,16	1.62	4 (28%)
3	NAG	I	1	3,1	14,14,15	0.38	0	17,19,21	0.63	0
3	NAG	I	2	3	14,14,15	0.30	0	17,19,21	0.94	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
3	NAG	G	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	3/6/23/26	0/1/1/1
4	NAG	H	1	4,1	-	0/6/23/26	0/1/1/1
4	FUC	H	2	4	-	-	0/1/1/1
3	NAG	I	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	3/6/23/26	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	2	FUC	C4-C5	3.86	1.61	1.52
4	H	2	FUC	C4-C3	3.70	1.61	1.52
3	G	1	NAG	O5-C1	3.57	1.49	1.43
4	H	1	NAG	C1-C2	3.52	1.57	1.52
4	H	1	NAG	O5-C1	3.51	1.49	1.43

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	2	NAG	C2-N2-C7	3.41	127.76	122.90
4	H	2	FUC	O5-C5-C4	3.07	115.03	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	2	NAG	C1-C2-N2	2.77	115.22	110.49
3	G	1	NAG	C1-O5-C5	2.58	115.69	112.19
4	H	2	FUC	C1-C2-C3	2.55	112.80	109.67

There are no chirality outliers.

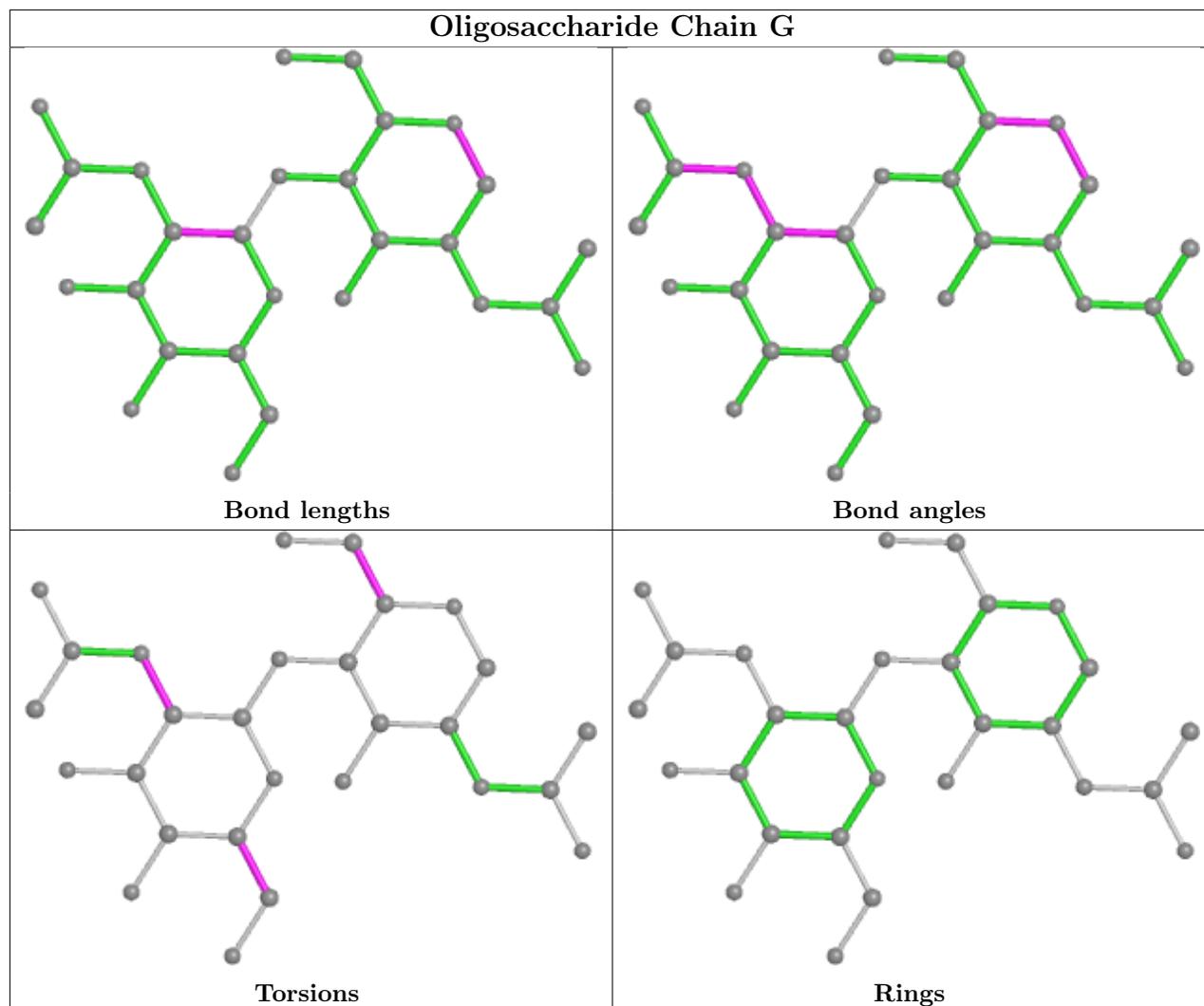
5 of 8 torsion outliers are listed below:

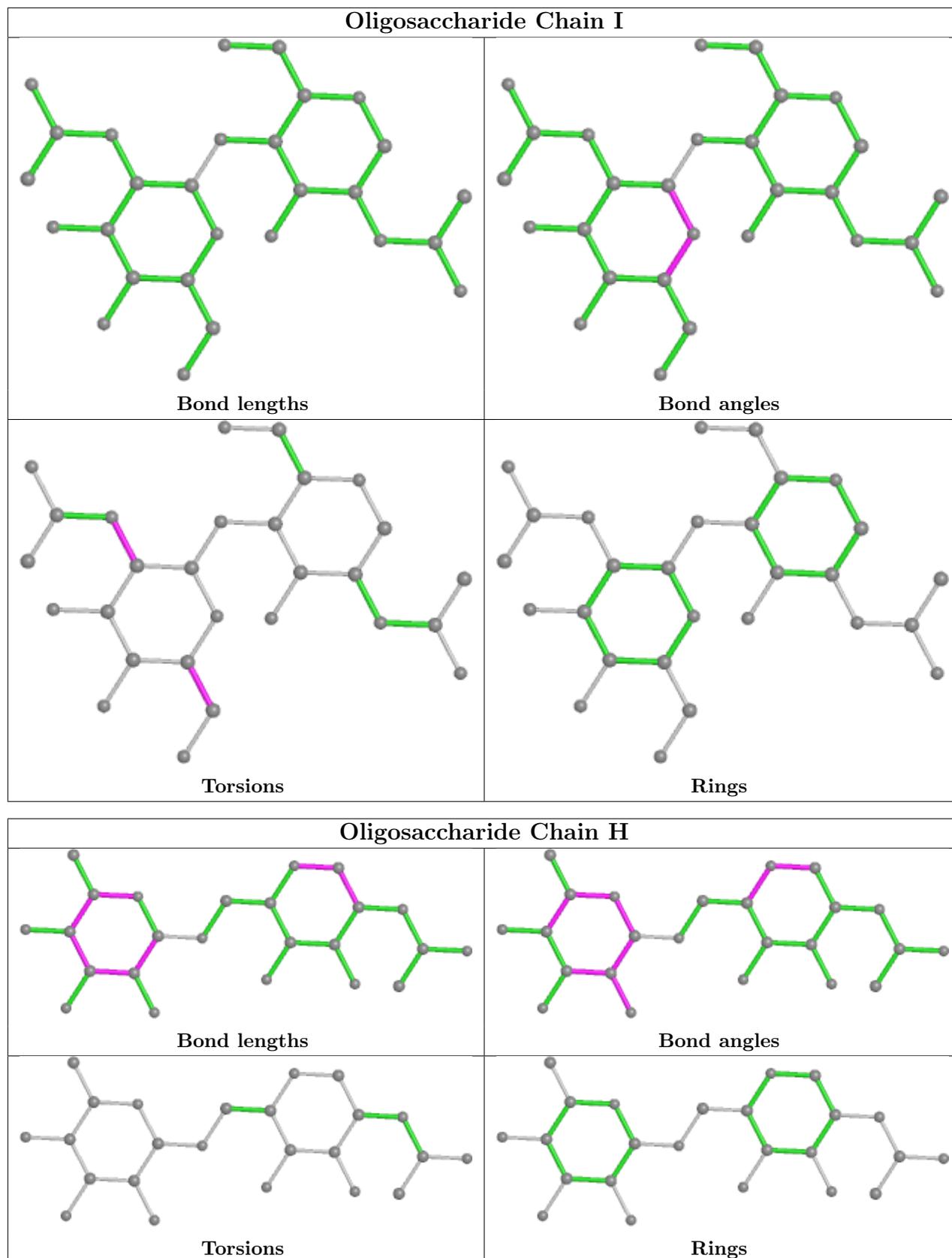
Mol	Chain	Res	Type	Atoms
3	G	2	NAG	O5-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	B	903	1	14,14,15	1.91	2 (14%)	17,19,21	1.26	2 (11%)
5	NAG	E	601	2	14,14,15	1.84	1 (7%)	17,19,21	1.56	4 (23%)
5	NAG	B	905	1	14,14,15	1.96	2 (14%)	17,19,21	0.90	1 (5%)
5	NAG	D	903	1	14,14,15	1.16	2 (14%)	17,19,21	0.58	0
5	NAG	B	904	1	14,14,15	0.55	0	17,19,21	0.95	1 (5%)
5	NAG	A	903	1	14,14,15	0.64	0	17,19,21	1.07	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
5	NAG	B	903	1	-	2/6/23/26	0/1/1/1
5	NAG	E	601	2	-	2/6/23/26	0/1/1/1
5	NAG	B	905	1	-	2/6/23/26	0/1/1/1
5	NAG	D	903	1	-	2/6/23/26	0/1/1/1
5	NAG	B	904	1	-	2/6/23/26	0/1/1/1
5	NAG	A	903	1	-	3/6/23/26	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	601	NAG	O5-C1	6.65	1.54	1.43
5	B	905	NAG	O5-C1	6.29	1.53	1.43
5	B	903	NAG	O5-C1	5.88	1.53	1.43
5	B	903	NAG	C1-C2	3.69	1.57	1.52
5	B	905	NAG	C1-C2	3.46	1.57	1.52

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	601	NAG	C1-O5-C5	3.94	117.53	112.19
5	B	903	NAG	C1-O5-C5	3.69	117.19	112.19
5	B	904	NAG	C1-O5-C5	3.35	116.73	112.19
5	E	601	NAG	C2-N2-C7	2.85	126.96	122.90
5	B	905	NAG	C1-O5-C5	2.69	115.84	112.19

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	903	NAG	O5-C5-C6-O6
5	A	903	NAG	C4-C5-C6-O6
5	D	903	NAG	O5-C5-C6-O6
5	B	904	NAG	O5-C5-C6-O6
5	D	903	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	904	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	596/597 (99%)	-0.34	3 (0%) 91 75	44, 60, 87, 114	0
1	B	596/597 (99%)	-0.35	1 (0%) 95 87	42, 62, 92, 133	0
1	D	596/597 (99%)	-0.31	6 (1%) 82 58	48, 70, 94, 132	0
2	C	187/197 (94%)	-0.34	1 (0%) 91 75	43, 53, 100, 140	0
2	E	185/197 (93%)	-0.27	5 (2%) 54 26	44, 55, 98, 145	0
2	F	197/197 (100%)	-0.41	0 100 100	46, 58, 87, 111	0
All	All	2357/2382 (98%)	-0.34	16 (0%) 87 68	42, 63, 94, 145	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	211	TRP	3.2
1	A	339	ASN	3.0
1	D	339	ASN	3.0
1	B	338	ASP	2.9
1	D	341	LYS	2.7

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

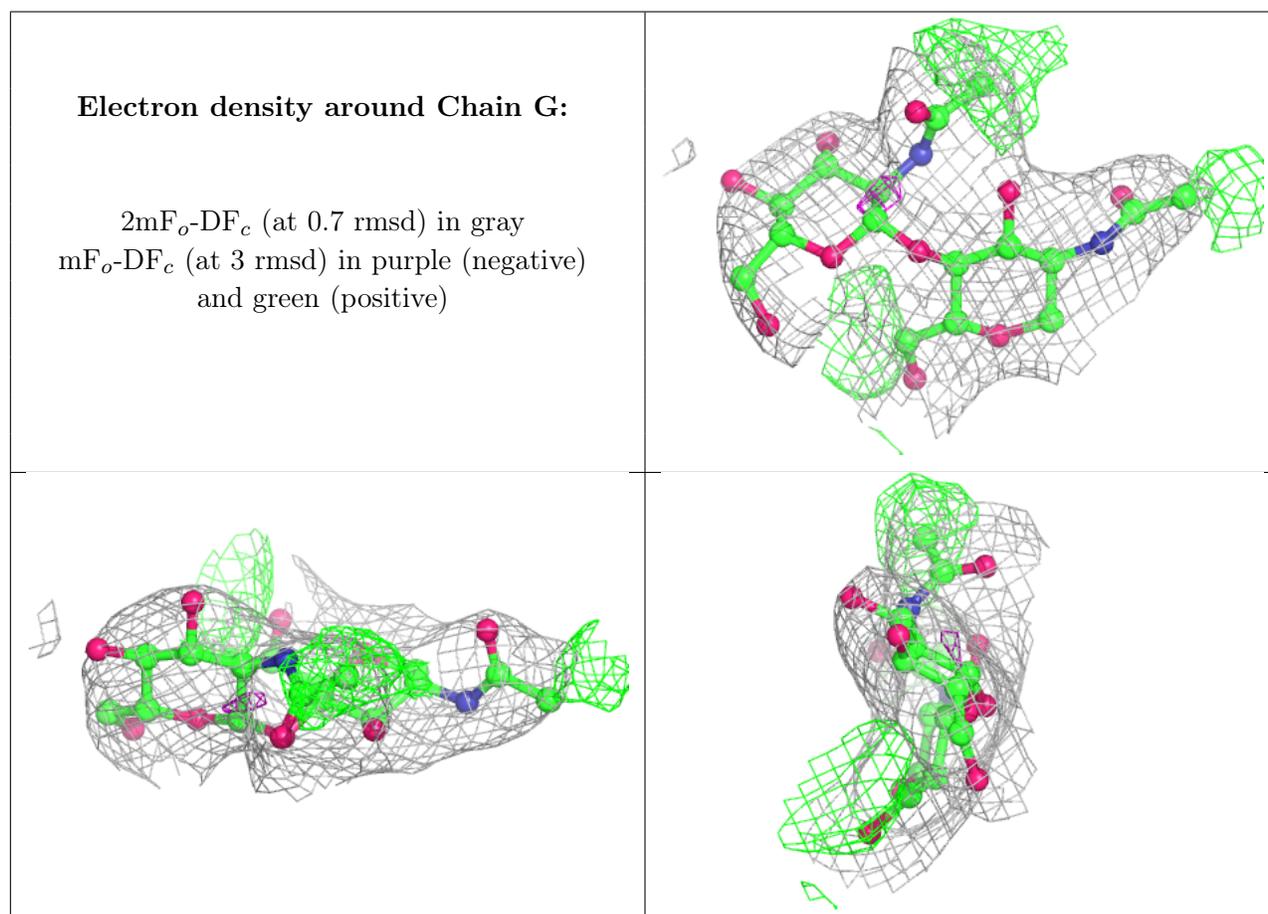
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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

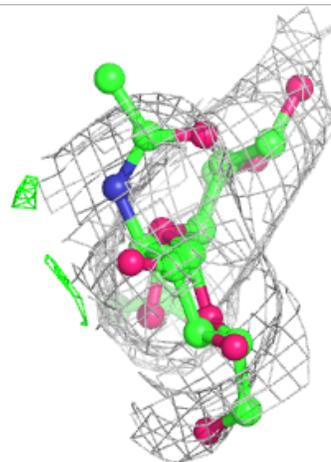
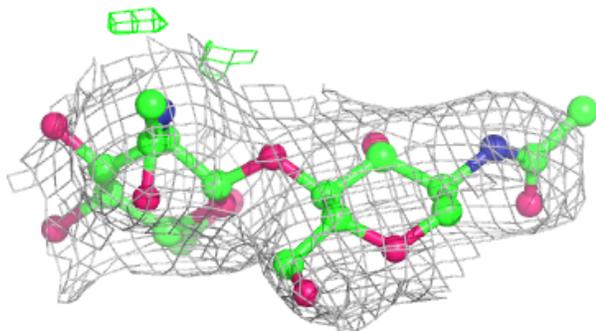
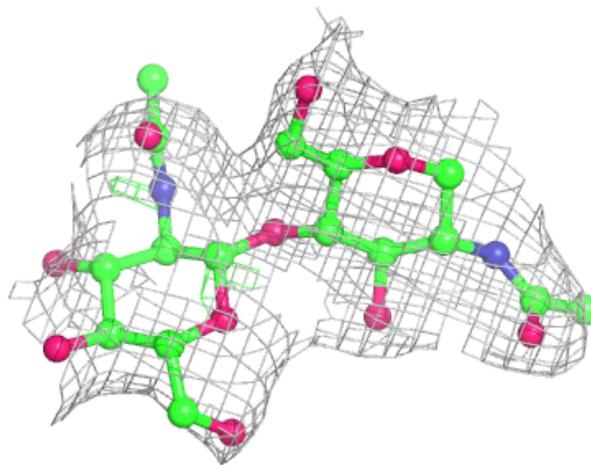
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	I	2	14/15	0.80	0.37	117,126,134,138	0
3	NAG	G	2	14/15	0.82	0.24	87,105,109,110	0
3	NAG	G	1	14/15	0.86	0.16	67,87,98,107	0
4	NAG	H	1	14/15	0.86	0.28	71,85,97,105	0
4	FUC	H	2	10/11	0.93	0.46	86,99,102,102	0
3	NAG	I	1	14/15	0.95	0.35	81,87,104,119	0

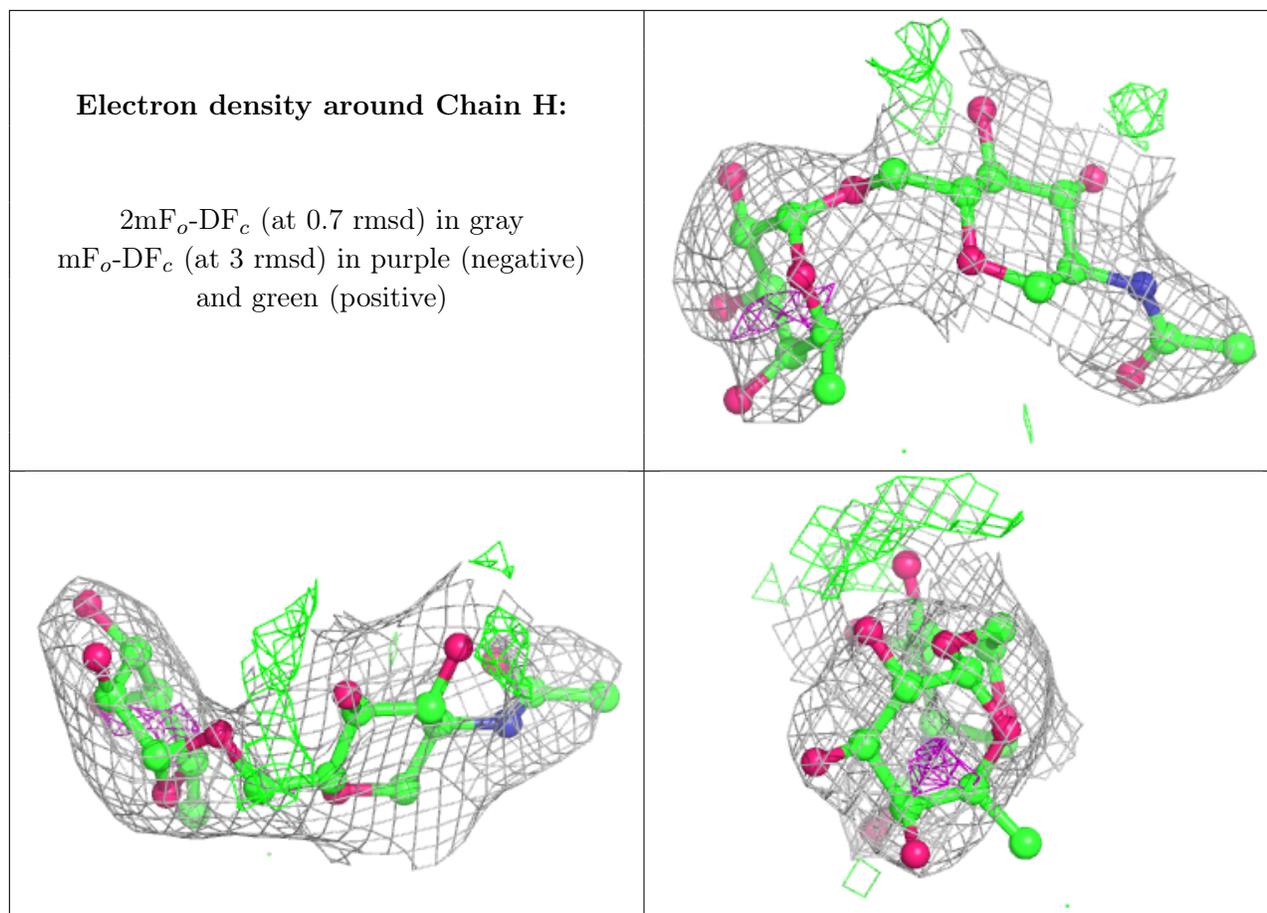
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



Electron density around Chain I:

$2mF_o-DF_c$ (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	NAG	E	601	14/15	0.55	0.31	104,122,127,130	0
5	NAG	B	905	14/15	0.75	0.30	75,89,93,97	0
5	NAG	B	903	14/15	0.78	0.19	56,74,83,83	0
5	NAG	D	903	14/15	0.82	0.30	100,115,118,122	0
5	NAG	B	904	14/15	0.89	0.31	74,78,84,86	0
5	NAG	A	903	14/15	0.92	0.35	72,81,87,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.