

wwPDB X-ray Structure Validation Summary Report (i)

Dec 14, 2021 – 12:09 pm GMT

PDB ID	:	7PS5
Title	:	Crystal structure of the receptor binding domain of SARS-CoV-2 beta variant
		spike glycoprotein in complex with Beta-47 Fab
Authors	:	Zhou, D.; Ren, J.; Stuart, D.I.
Deposited on	:	2021-09-22
Resolution	:	3.14 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

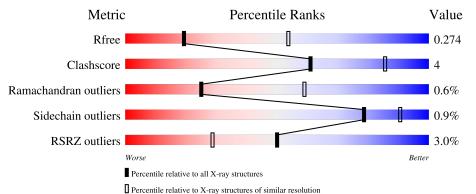
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.24
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.24

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 3.14 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1626 (3.18-3.10)
Clashscore	141614	1735 (3.18-3.10)
Ramachandran outliers	138981	1677 (3.18-3.10)
Sidechain outliers	138945	1677 (3.18-3.10)
RSRZ outliers	127900	1588 (3.18-3.10)

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 <=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	Н	228		86%	13% •
2	L	215	.%	85%	14% •
3	Е	210	8%	82%	9% 8%
4	А	6	33%	33%	33%
5	В	5	60'	%	40%



The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MAN	А	4	-	-	-	Х



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5007 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 Beta-47 Fab heavy chain.

Mol	Chain	Residues		At	oms		ZeroOcc	AltConf	Trace	
1	Н	224	Total	С	Ν	Ο	\mathbf{S}	0	0	0
	11		1675	1046	287	330	12	0	0	

• Molecule 2 is a protein called Beta-47 Fab light chain.

Mol	Chain	Residues		Ate	oms		ZeroOcc	AltConf	Trace	
2	L	215	Total 1666	C 1043	N 285	O 332	S 6	0	2	0

• Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	Е	193	Total 1535	C 986	N 255	0 286	S 8	0	0	0

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Е	319	MET	-	initiating methionine	UNP P0DTC2
Е	320	GLY	-	expression tag	UNP P0DTC2
Е	321	CYS	-	expression tag	UNP P0DTC2
Е	322	VAL	-	expression tag	UNP P0DTC2
Е	323	ALA	-	expression tag	UNP P0DTC2
Е	324	GLU	-	expression tag	UNP P0DTC2
Е	325	THR	-	expression tag	UNP P0DTC2
Е	326	GLY	-	expression tag	UNP P0DTC2
Е	327	HIS	-	expression tag	UNP P0DTC2
Е	328	HIS	-	expression tag	UNP P0DTC2
Е	329	HIS	-	expression tag	UNP P0DTC2
Е	330	HIS	-	expression tag	UNP P0DTC2
Е	331	HIS	-	expression tag	UNP P0DTC2
Е	332	HIS	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
Е	417	ASN	LYS	variant	UNP P0DTC2
Е	484	LYS	GLU	variant	UNP P0DTC2
Е	501	TYR	ASN	variant	UNP P0DTC2
Е	527	LYS	-	expression tag	UNP P0DTC2
Е	528	LYS	-	expression tag	UNP P0DTC2

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• Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-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	А	6	Total 71	C 40	N 2	O 29	0	0	0

• Molecule 5 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-beta-D-mannopyranos e-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acet amido-2-deoxy-beta-D-glucopyranose.

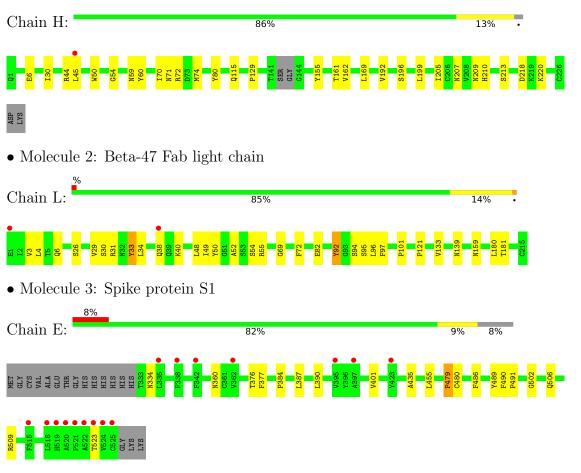


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	В	5	Total 60	C 34	N 2	O 24	0	0	0



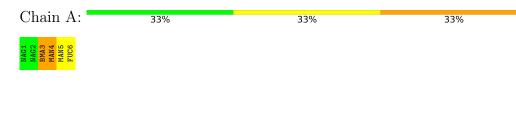
3 Residue-property plots (i)

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: Beta-47 Fab heavy chain

 $\label{eq:mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]} beta-D-mannopyranose-(1-6)] beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)] 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-6)] beta-D-mannopyranose-(1-6)] beta-D-glucopyranose-(1-6)] beta-D-gluco$





 • Molecule 5: alpha-D-mannopyranose-(1-6)-beta-D
-mannopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)] 2-acetamido-2-deoxy-beta-D-glucopyranose e

Chain B: 60%

40%

NAG1 NAG2 BMA3 MAN4 FUC5



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	78.10Å 114.41Å 168.97Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.35 - 3.14	Depositor
Resolution (A)	60.26 - 3.14	EDS
% Data completeness	98.2 (57.35-3.14)	Depositor
(in resolution range)	98.3 (60.26-3.14)	EDS
R _{merge}	0.23	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.00 (at 3.13 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
D D.	0.226 , 0.274	Depositor
R, R_{free}	0.226 , 0.274	DCC
R_{free} test set	1310 reflections (4.91%)	wwPDB-VP
Wilson B-factor $(Å^2)$	114.2	Xtriage
Anisotropy	0.403	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ L > = 0.43, < L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5007	wwPDB-VP
Average B, all atoms $(Å^2)$	129.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.28% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: MAN, BMA, 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).

Mal	Mol Chain		lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	Н	0.26	0/1713	0.50	0/2332	
2	L	0.26	0/1707	0.51	0/2316	
3	Е	0.26	0/1579	0.47	0/2150	
All	All	0.26	0/4999	0.49	0/6798	

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	Н	1675	0	1624	16	0
2	L	1666	0	1629	19	0
3	Е	1535	0	1452	12	0
4	А	71	0	61	1	0
5	В	60	0	52	0	0
All	All	5007	0	4818	44	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 4.

The worst 5 of 44 close contacts within the same asymmetric unit are listed below, sorted by their



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:30:SER:HB2	2:L:94:SER:HB2	1.74	0.70
1:H:210:HIS:HD1	1:H:213:SER:HG	1.38	0.69
2:L:40:LYS:NZ	2:L:82:GLU:O	2.28	0.67
2:L:38:GLN:HB2	2:L:48:LEU:HD11	1.80	0.63
1:H:205:ILE:HG13	1:H:220:LYS:HG2	1.80	0.62

clash magnitude.

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	Perce	ntiles
1	Н	220/228~(96%)	209~(95%)	11 (5%)	0	100	100
2	L	215/215~(100%)	205~(95%)	7(3%)	3 (1%)	11	39
3	Е	191/210 (91%)	176 (92%)	14 (7%)	1 (0%)	29	63
All	All	626/653~(96%)	590 (94%)	32 (5%)	4 (1%)	25	59

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	95	SER
2	L	52	ALA
3	Е	479	PRO
2	L	139	ASN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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.



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	Н	190/195~(97%)	189 (100%)	1 (0%)	88 95
2	L	189/187~(101%)	187~(99%)	2(1%)	73 88
3	Е	167/180~(93%)	165~(99%)	2(1%)	71 87
All	All	546/562~(97%)	541 (99%)	5 (1%)	78 90

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

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

Mol	Chain	Res	Type
1	Н	72	ARG
2	L	33	TYR
2	L	92	TYR
3	Е	480	CYS
3	Е	489	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

11 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	Turne	Chain	Res	Link	Bo	ond leng	ths	В	ond ang	les
	Type	Chain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
4	NAG	А	1	1,4	14,14,15	0.25	0	17,19,21	0.50	0
4	NAG	А	2	4	14,14,15	0.27	0	$17,\!19,\!21$	0.50	0
4	BMA	А	3	4	11,11,12	0.96	0	$15,\!15,\!17$	1.31	2 (13%)
4	MAN	А	4	4	11,11,12	1.16	1 (9%)	$15,\!15,\!17$	0.86	0
4	MAN	А	5	4	11,11,12	0.70	0	$15,\!15,\!17$	1.13	2 (13%)
4	FUC	А	6	4	10,10,11	0.89	1 (10%)	14,14,16	1.10	1 (7%)
5	NAG	В	1	3,5	14,14,15	0.37	0	17,19,21	0.39	0
5	NAG	В	2	5	14,14,15	0.27	0	17,19,21	0.45	0
5	BMA	В	3	5	11,11,12	0.86	0	$15,\!15,\!17$	0.88	0
5	MAN	В	4	5	11,11,12	1.58	3 (27%)	$15,\!15,\!17$	2.01	2 (13%)
5	FUC	В	5	5	10,10,11	1.03	1 (10%)	14,14,16	1.14	2 (14%)

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	А	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	А	2	4	-	0/6/23/26	0/1/1/1
4	BMA	А	3	4	-	2/2/19/22	0/1/1/1
4	MAN	А	4	4	-	0/2/19/22	0/1/1/1
4	MAN	А	5	4	-	0/2/19/22	0/1/1/1
4	FUC	А	6	4	-	-	0/1/1/1
5	NAG	В	1	3,5	-	0/6/23/26	0/1/1/1
5	NAG	В	2	5	-	2/6/23/26	0/1/1/1
5	BMA	В	3	5	-	2/2/19/22	0/1/1/1
5	MAN	В	4	5	-	0/2/19/22	0/1/1/1
5	FUC	В	5	5	-	-	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	В	4	MAN	O5-C1	3.14	1.48	1.43
5	В	4	MAN	C1-C2	3.05	1.59	1.52
4	А	4	MAN	O5-C1	-2.87	1.39	1.43
5	В	4	MAN	O5-C5	2.74	1.49	1.43
5	В	5	FUC	C1-C2	2.50	1.57	1.52

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



Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
5	В	4	MAN	C1-O5-C5	6.79	121.39	112.19
4	А	5	MAN	C1-O5-C5	3.05	116.32	112.19
4	А	6	FUC	C1-O5-C5	2.56	118.59	112.78
5	В	5	FUC	C1-O5-C5	2.45	118.32	112.78
4	А	3	BMA	O3-C3-C4	2.43	115.98	110.35

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	3	BMA	O5-C5-C6-O6
5	В	3	BMA	O5-C5-C6-O6
4	А	3	BMA	C4-C5-C6-O6
5	В	3	BMA	C4-C5-C6-O6
5	В	2	NAG	O5-C5-C6-O6

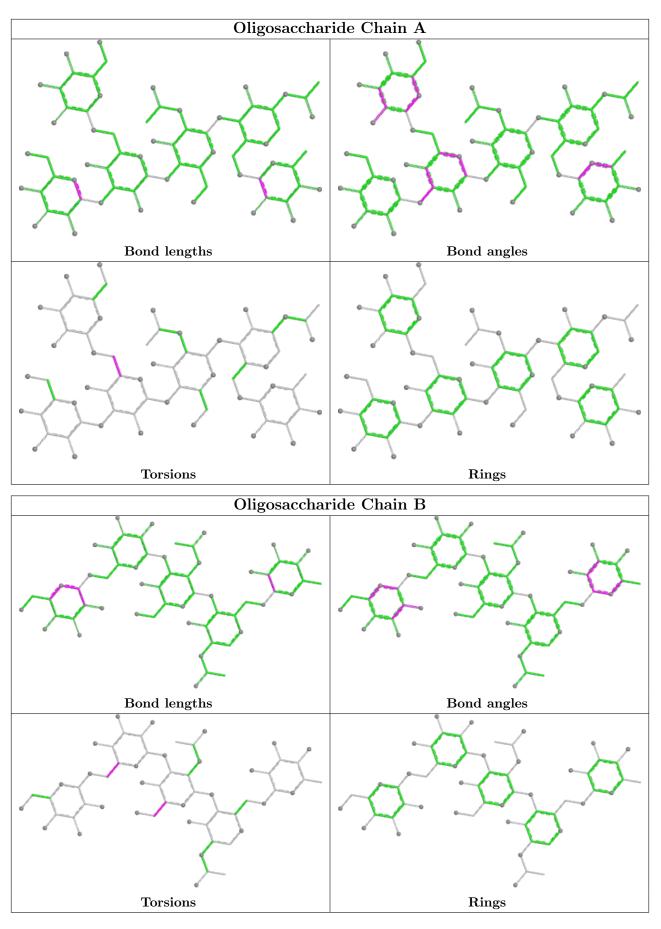
There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	А	3	BMA	1	0
4	А	4	MAN	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)

There are no ligands in this entry.

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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\AA}^2)$	$Q{<}0.9$
1	Н	224/228~(98%)	0.10	1 (0%) 92 86	90, 119, 152, 194	0
2	L	215/215~(100%)	0.21	2 (0%) 84 72	93, 127, 163, 193	0
3	Е	193/210~(91%)	0.57	16 (8%) 11 4	98, 128, 187, 245	0
All	All	632/653~(96%)	0.28	19 (3%) 50 29	90, 124, 171, 245	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	Ε	521	PRO	4.9
3	Е	423	TYR	4.0
3	Е	522	ALA	3.8
3	Е	520	ALA	3.5
3	Е	518	LEU	3.4

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, 95^{th} 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	$\mathbf{B} extsf{-}\mathbf{factors}(\mathbf{A}^2)$	Q<0.9
4	MAN	А	4	11/12	0.49	0.40	181,244,265,270	0
4	BMA	А	3	11/12	0.67	0.23	225,231,249,259	0
5	BMA	В	3	11/12	0.69	0.24	208,234,252,262	0

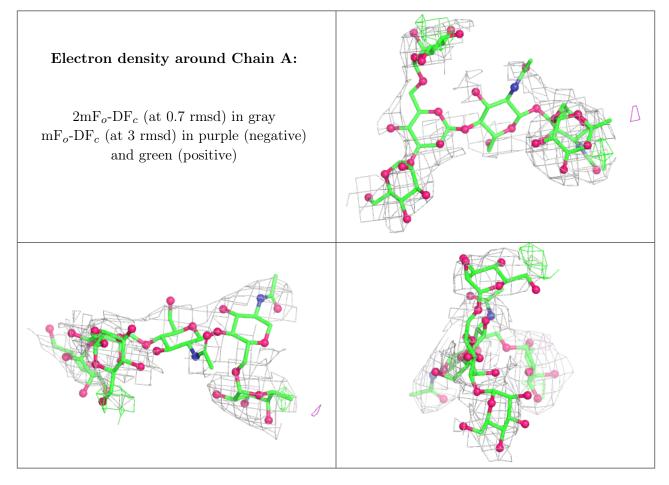
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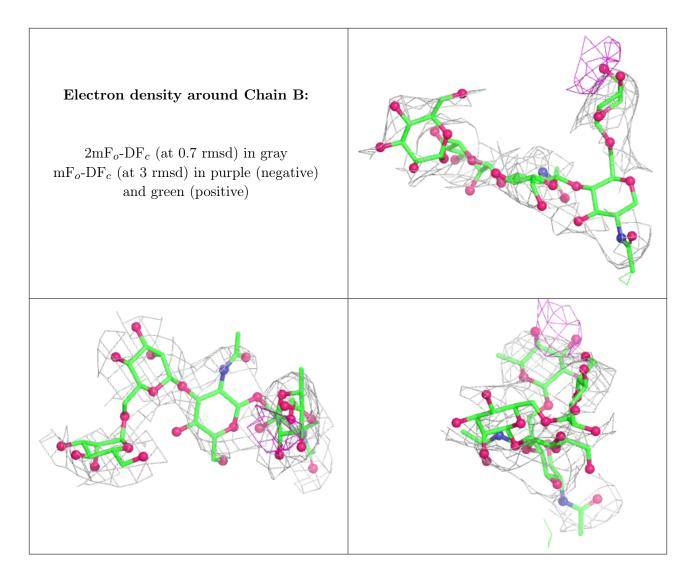
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(A^2)$	Q<0.9
4	MAN	А	5	11/12	0.71	0.27	175,219,229,232	0
5	MAN	В	4	11/12	0.77	0.26	203,227,242,244	0
5	FUC	В	5	10/11	0.85	0.41	138,176,182,194	0
4	FUC	А	6	10/11	0.88	0.22	107,133,143,144	0
5	NAG	В	2	14/15	0.89	0.31	152,197,240,246	0
5	NAG	В	1	14/15	0.90	0.14	127,170,190,196	0
4	NAG	А	2	14/15	0.94	0.14	155,178,203,213	0
4	NAG	А	1	14/15	0.96	0.14	100,126,152,156	0

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







6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

