

# wwPDB X-ray Structure Validation Summary Report (i)

Aug 9, 2021 – 02:03 pm BST

PDB ID	:	7OR9
$\operatorname{Title}$	:	Crystal structure of the receptor binding domain of SARS-CoV-2 Spike glyco-
		protein in complex with COVOX-222 and COVOX-278 Fabs
Authors	:	Zhou, D.; Ren, J.; Stuart, D.I.
Deposited on		
Resolution	:	2.34  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:

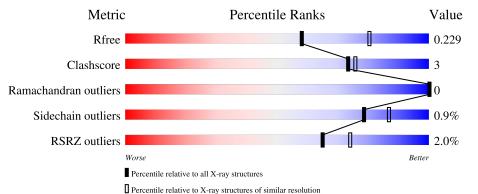
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.23.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
$\rm CCP4$	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.1

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	$2096 \ (2.36-2.32)$
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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	
	_		7%	
1	Е	205	83%	12% 5%
_			<u>%</u>	
2	A	224	88%	8% •
			.% ■	
3	В	214	88%	11%
4	Н	228	87%	9% •
	-		.% ■	
5	L	215	94%	6%



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Mol	Chain	Length		Quality of chain	
6	С	3	33%	67%	



# 2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 8282 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

• Molecule 1 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Е	195	Total 1545	C 990	N 258	O 289	S 8	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	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
Е	527	LYS	PRO	$\operatorname{conflict}$	UNP P0DTC2

• Molecule 2 is a protein called COVOX-222 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	215	Total 1587	C 1001	N 265	0 315	S 6	0	0	0

• Molecule 3 is a protein called COVOX-222 Fab light chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
3	В	213	Total 1640	C 1025	N 279	O 330	S 6	0	2	0

• Molecule 4 is a protein called COVOX-278 Fab heavy chain.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	Н	220	Total	С	Ν	Ο	$\mathbf{S}$	0	0	0
1			1652	1044	277	324	7		0	0

• Molecule 5 is a protein called COVOX-278 Fab light chain.

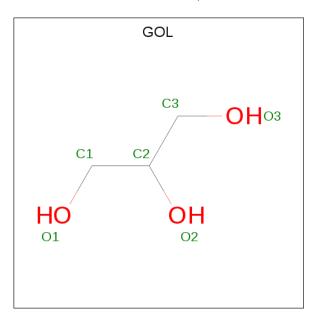
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	L	214	Total 1642	C 1025	N 275	O 336	S 6	0	2	0

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



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

• Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



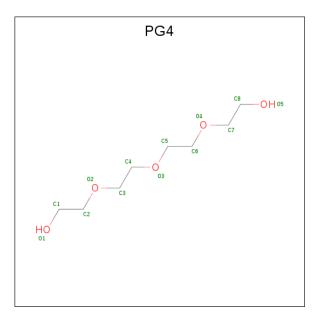
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	Е	1	$\begin{array}{ccc} {\rm Total} & {\rm C} & {\rm O} \\ 6 & 3 & 3 \end{array}$	0	0
7	В	1	$\begin{array}{ccc} \text{Total}  \text{C}  \text{O} \\ 6  3  3 \end{array}$	0	0



• Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	Е	2	$\begin{array}{cc} \text{Total} & \text{Cl} \\ 2 & 2 \end{array}$	0	0
8	А	1	Total Cl 1 1	0	0
8	В	1	Total Cl 1 1	0	0

• Molecule 9 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula:  $C_8H_{18}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	Н	1	Total 13	C 8	O 5	0	0

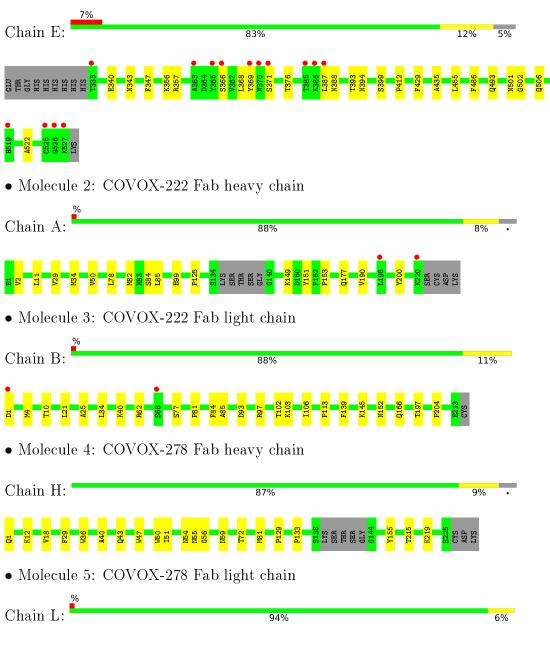
• Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	Ε	40	$\begin{array}{cc} \text{Total} & \text{O} \\ 40 & 40 \end{array}$	0	0
10	А	42	$\begin{array}{cc} \text{Total} & \text{O} \\ 42 & 42 \end{array}$	0	0
10	В	13	Total         O           13         13	0	0
10	Н	21	TotalO2121	0	0
10	L	33	Total O 33 33	0	0



# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.



• Molecule 1: Spike protein S1



#### 

Chain C: 33% 67%

NAG 1 NAG 2 FUC3



# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	70.73Å 114.47Å 177.93Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	57.23 - 2.34	Depositor
Resolution (A)	70.24 - 2.34	EDS
% Data completeness	86.1 (57.23-2.34)	Depositor
(in resolution range)	86.1(70.24-2.34)	EDS
R <sub>merge</sub>	0.10	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.24 (at 2.34 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
B B.	0.194 , $0.230$	Depositor
$R, R_{free}$	0.194 , $0.229$	DCC
$R_{free}$ test set	2655 reflections $(4.99%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	52.9	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.31, $33.3$	EDS
L-test for twinning <sup>2</sup>	$ \langle L  \rangle = 0.50, \langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8282	wwPDB-VP
Average B, all atoms $(Å^2)$	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical 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.



<sup>&</sup>lt;sup>1</sup>Intensities 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: FUC, CL, NAG, GOL, PG4  $\,$ 

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
	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	Е	0.26	0/1588	0.48	0/2160
2	А	0.25	0/1625	0.50	0/2215
3	В	0.26	0/1683	0.51	0/2287
4	Н	0.25	0/1691	0.50	0/2305
5	L	0.26	0/1679	0.50	0/2279
All	All	0.25	0/8266	0.50	0/11246

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	Ε	1545	0	1465	14	0
2	А	1587	0	1550	9	0
3	В	1640	0	1594	12	0
4	Н	1652	0	1615	13	0
5	L	1642	0	1600	6	0
6	С	38	0	34	1	0
7	В	6	0	8	0	0
7	Е	6	0	8	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	А	1	0	0	0	0
8	В	1	0	0	0	0
8	Ε	2	0	0	0	0
9	Н	13	0	18	1	0
10	А	42	0	0	0	0
10	В	13	0	0	0	0
10	Ε	40	0	0	1	0
10	Η	21	0	0	0	0
10	Ĺ	33	0	0	1	0
All	All	8282	0	7892	52	0

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The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

The worst 5 of 52 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic}\\ {\rm distance}~({\rm \AA}) \end{array}$	Clash overlap (Å)
3:B:81:PRO:HA	3:B:106:ILE:HD13	1.75	0.68
5:L:37:GLN:HB2	5:L:47:LEU:HD11	1.76	0.67
5:L:18:ARG:NH2	10:L:301:HOH:O	2.30	0.65
3:B:10:THR:HG22	3:B:103:LYS:HB3	1.81	0.62
2:A:29:VAL:HG13	2:A:34:MET:HG3	1.83	0.61

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	Ε	193/205~(94%)	182 (94%)	11 (6%)	0	100	100
2	А	211/224~(94%)	206 (98%)	5 (2%)	0	100	100



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	$\mathbf{n}$ tiles
3	В	213/214~(100%)	204~(96%)	9 (4%)	0	100	100
4	Н	216/228~(95%)	210~(97%)	6 (3%)	0	100	100
5	L	214/215~(100%)	204~(95%)	10~(5%)	0	100	100
All	All	1047/1086~(96%)	1006 (96%)	41 (4%)	0	100	100

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There are no Ramachandran outliers to report.

#### 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	Ε	168/177~(95%)	167~(99%)	1 (1%)	86 92
2	А	178/186~(96%)	177~(99%)	1 (1%)	86 92
3	В	186/185~(100%)	183~(98%)	3 (2%)	62 74
4	Η	183/191~(96%)	183~(100%)	0	100 100
5	L	189/188~(100%)	186~(98%)	3(2%)	62 74
All	All	904/927~(98%)	896~(99%)	8 (1%)	78 87

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	$\mathbf{Res}$	Type
5	L	214	GLU
5	L	55	GLN
3	В	152	ASN
3	В	93	ASP
5	L	22	THR

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)

3 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	Tune	Chain	Chain Res Link Bond lengths			Bond angles				
	Type	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	NAG	С	1	1,6	14, 14, 15	0.56	0	17,19,21	0.52	0
6	NAG	С	2	6	14, 14, 15	0.29	0	17,19,21	0.43	0
6	FUC	С	3	6	10, 10, 11	0.91	1 (10%)	14,14,16	0.68	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
6	NAG	С	1	1,6	-	2/6/23/26	0/1/1/1
6	NAG	С	2	6	-	2/6/23/26	0/1/1/1
6	FUC	С	3	6	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
6	C	3	FUC	O5-C1	-2.07	1.40	1.43

There are no bond angle outliers.

There are no chirality outliers.



Mol	Chain	Res	Type	Atoms
6	С	2	NAG	O5-C5-C6-O6
6	С	2	NAG	C4-C5-C6-O6
6	С	1	NAG	O5-C5-C6-O6
6	С	1	NAG	C4-C5-C6-O6

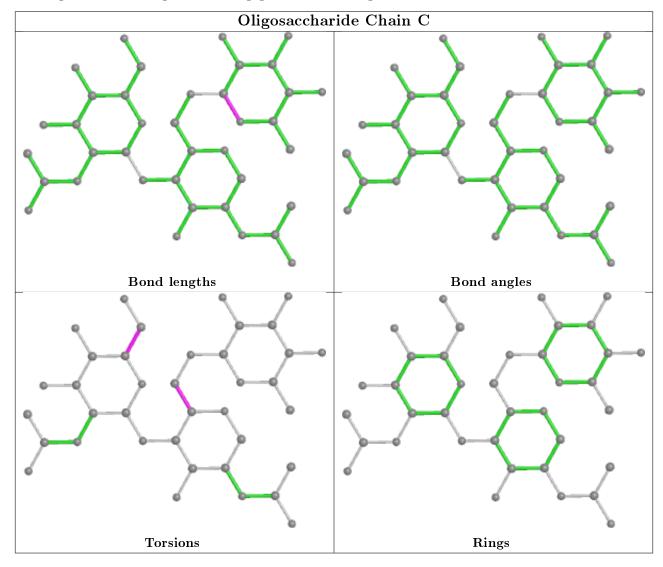
All (4) torsion outliers are listed below:

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	$\mathbf{Res}$	Type	Clashes	Symm-Clashes
6	С	1	NAG	1	0

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





### 5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 for Mogul analysis.

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	Tune	Chain	Res	Link	Bo	ond leng	$\mathbf{ths}$	В	ond ang	les
	Type	Chain	nes		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	GOL	Е	901	-	$5,\!5,\!5$	0.91	0	5, 5, 5	0.98	0
7	GOL	В	301	-	$5,\!5,\!5$	0.93	0	5, 5, 5	1.00	0
9	PG4	Н	301	-	12,12,12	0.16	0	11,11,11	0.63	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	$\mathbf{Res}$	Link	Chirals	Torsions	Rings
7	GOL	Ε	901	-	-	2/4/4/4	-
7	GOL	В	301	-	-	0/4/4/4	-
9	PG4	Η	301	-	_	4/10/10/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	Ε	901	GOL	O1-C1-C2-C3
9	Н	301	PG4	O1-C1-C2-O2
9	Н	301	PG4	O2-C3-C4-O3
7	Е	901	GOL	O1-C1-C2-O2
9	Н	301	PG4	C5-C6-O4-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	Н	301	PG4	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,  $95^{th}$  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	$<$ RSRZ $>$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{A}^2)$	$Q{<}0.9$
1	Ε	195/205~(95%)	0.51	15 (7%) 13 20	37, 53, 114, 141	0
2	А	215/224~(95%)	0.21	2 (0%) 84 89	39, 55, 94, 112	0
3	В	213/214~(99%)	0.18	2 (0%) 84 89	47, 63, 91, 139	0
4	Н	220/228~(96%)	0.13	0 100 100	43, 63, 87, 100	0
5	L	214/215~(99%)	0.26	2 (0%) 84 89	40, 55, 79, 103	0
All	All	1057/1086~(97%)	0.25	21 (1%) 65 74	37, 58, 92, 141	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Ε	527	LYS	6.4
3	В	1	ASP	5.9
1	Е	519	HIS	4.5
2	А	195	LEU	4.2
1	Е	333	THR	4.1

### 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.

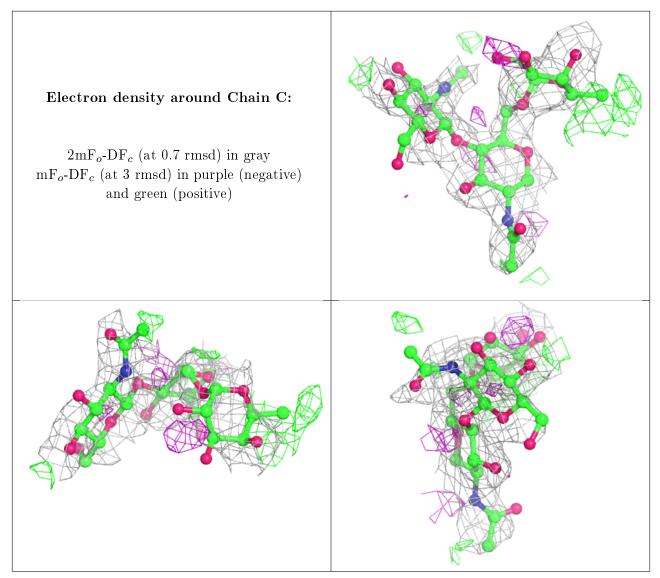
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
6	NAG	С	2	14/15	0.64	0.36	$117,\!127,\!133,\!135$	0



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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
6	FUC	С	3	10/11	0.69	0.35	$119,\!132,\!136,\!136$	0
6	NAG	С	1	14/15	0.80	0.28	$77,\!111,\!129,\!130$	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.



### 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,  $95^{th}$  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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
7	GOL	В	301	6/6	0.67	0.23	$61,\!68,\!78,\!81$	0
9	PG4	Н	301	13/13	0.81	0.19	$50,\!66,\!78,\!79$	0
7	GOL	Е	901	6/6	0.83	0.23	$58,\!68,\!71,\!75$	0
8	CL	В	302	1/1	0.92	0.14	83,83,83,83	0
8	CL	Е	902	1/1	0.93	0.13	80,80,80,80	0
8	CL	Е	903	1/1	0.96	0.08	67,67,67,67	0
8	CL	А	301	1/1	0.98	0.08	59, 59, 59, 59, 59	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

