

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

#### Oct 31, 2023 – 01:55 PM JST

PDB ID : 5F1B

Title: Structural basis of Ebola virus entry: viral glycoprotein bound to its endosomal

receptor Niemann-Pick C1

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Deposited on : 2015-11-30

Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

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)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

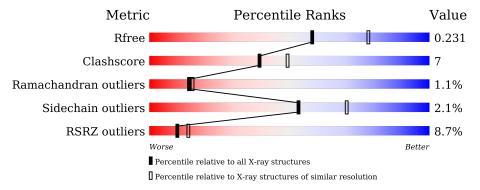
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.30 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 $(\# \mathrm{Entries})$	Similar resolution $(\#\text{Entries, resolution range}(\text{Å}))$		
$R_{free}$	130704	5042 (2.30-2.30)		
Clashscore	141614	5643 (2.30-2.30)		
Ramachandran outliers	138981	5575 (2.30-2.30)		
Sidechain outliers	138945	5575 (2.30-2.30)		
RSRZ outliers	127900	4938 (2.30-2.30)		

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	A	158	12% 85%		13%	<del>.</del>			
2	В	130	56% 9% •	33%		_			
3	С	256	71% 11%	•	16%	_			
4	D	2	50% 50%						



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 3828 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 GP1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Δ	158	Total	С	N	О	S	0	0	0
1	Λ	190	1194	757	209	223	5		U	U

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference	
A	31	ARG	-	expression tag	UNP P87666	
A	42	VAL	THR	engineered mutation	UNP P87666	

• Molecule 2 is a protein called GP2.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	87	Total 687	C 441	N 121	O 122	S 3	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	633	HIS	-	expression tag	UNP P87666
В	634	HIS	-	expression tag	UNP P87666
В	635	HIS	-	expression tag	UNP P87666
В	636	HIS	_	expression tag	UNP P87666
В	637	HIS	-	expression tag	UNP P87666
В	638	HIS	-	expression tag	UNP P87666

• Molecule 3 is a protein called Niemann-Pick C1 protein.

M	ol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3		С	215	Total 1748	C 1134	N 281	O 329	S 4	0	0	0

There are 9 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
С	1	MET	-	expression tag	UNP O15118
С	249	LEU	-	expression tag	UNP O15118
С	250	GLU	-	expression tag	UNP O15118
С	251	HIS	-	expression tag	UNP O15118
С	252	HIS	-	expression tag	UNP O15118
С	253	HIS	-	expression tag	UNP O15118
С	254	HIS	-	expression tag	UNP O15118
С	255	HIS	-	expression tag	UNP O15118
С	256	HIS	-	expression tag	UNP O15118

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	2	Total 28	C 16	N 2	O 10	0	0	0

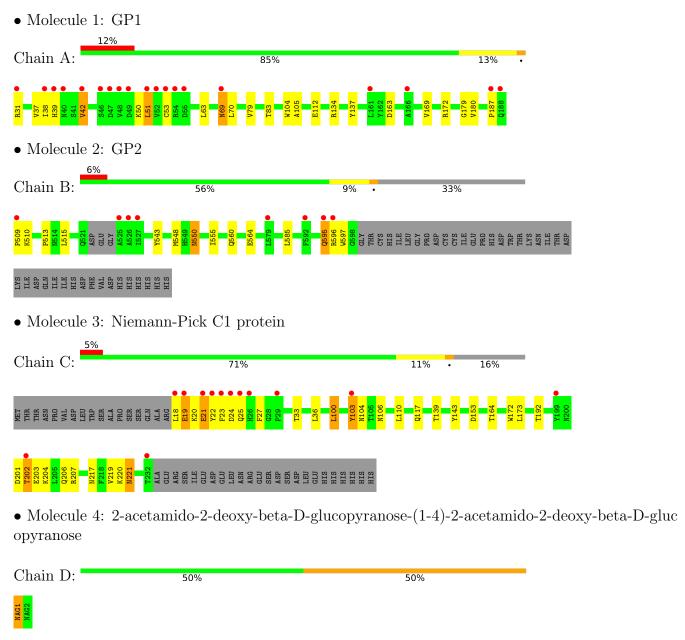
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	77	Total O 77 77	0	0
5	В	31	Total O 31 31	0	0
5	С	63	Total O 63 63	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.





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants	107.26Å 107.26Å 93.78Å	Domositon
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	41.86 - 2.30	Depositor
Resolution (A)	41.86 - 2.30	EDS
% Data completeness	100.0 (41.86-2.30)	Depositor
(in resolution range)	100.0 (41.86-2.30)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.70 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
D D	0.181 , 0.230	Depositor
$R, R_{free}$	0.184 , $0.231$	DCC
$R_{free}$ test set	1369 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.5	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.32 , 41.0	EDS
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.046 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3828	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.77% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  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: 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	Clasica	Bond	lengths	Bond angles		
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.42	0/1223	0.59	1/1664 (0.1%)	
2	В	0.42	0/702	0.62	0/952	
3	С	0.39	0/1803	0.55	0/2469	
All	All	0.40	0/3728	0.58	1/5085 (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	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

$\mathbf{Mol}$	Chain	$\operatorname{Res}$	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^{o})$	$\mathbf{Ideal}(^o)$
1	A	42	VAL	CA-CB-CG2	5.22	118.73	110.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

ľ	Mol	Chain	Res	Type	Group
	1	A	69	ASN	Sidechain

### 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	$\mathbf{H}(\mathbf{model})$	H(added)	Clashes	Symm-Clashes
1	A	1194	0	1153	18	1
2	В	687	0	679	13	1
3	С	1748	0	1656	24	1
4	D	28	0	25	1	0
5	A	77	0	0	1	1
5	В	31	0	0	1	1
5	C	63	0	0	2	1
All	All	3828	0	3513	53	3

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.

All (53) 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:B:510:LYS:NZ	4:D:1:NAG:O6	1.86	1.08
2:B:595:GLN:HE21	2:B:595:GLN:HA	1.25	0.98
1:A:39:HIS:HB2	1:A:42:VAL:HG22	1.60	0.83
2:B:595:GLN:HA	2:B:595:GLN:NE2	1.92	0.82
3:C:21:GLU:O	3:C:25:GLN:HG2	1.79	0.82
3:C:220:LYS:HG3	3:C:221:ASN:OD1	1.78	0.82
3:C:203:GLU:HG3	3:C:207:ARG:HH12	1.51	0.75
1:A:70:LEU:HD13	1:A:179:GLY:HA2	1.70	0.72
2:B:564:GLU:O	5:B:801:HOH:O	2.08	0.71
1:A:39:HIS:HD2	1:A:42:VAL:HG21	1.58	0.68
2:B:595:GLN:HE21	2:B:595:GLN:CA	2.05	0.67
2:B:509:PRO:HB2	2:B:510:LYS:HG3	1.77	0.67
3:C:201:ASP:OD2	3:C:204:LYS:HD3	1.97	0.65
3:C:117:GLN:NE2	5:C:301:HOH:O	2.20	0.58
1:A:39:HIS:CD2	1:A:42:VAL:HG21	2.38	0.57
1:A:31:ARG:N	5:A:203:HOH:O	2.38	0.55
1:A:112:GLU:OE2	1:A:172:ARG:HG3	2.07	0.55
1:A:69:ASN:HD21	1:A:105:ALA:HB2	1.72	0.54
3:C:106:ASN:HB3	3:C:164:THR:HG23	1.88	0.54
1:A:39:HIS:CD2	1:A:42:VAL:CG2	2.92	0.53
3:C:19:GLU:HG3	3:C:23:PHE:CE2	2.44	0.52
3:C:19:GLU:HG3	3:C:23:PHE:HE2	1.75	0.52
3:C:203:GLU:HG3	3:C:207:ARG:NH1	2.22	0.52
2:B:595:GLN:HG3	2:B:596:ARG:NH1	2.25	0.51

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Continued from prec		Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \ (\mathring{\rm A})$	overlap (Å)
1:A:69:ASN:ND2	1:A:105:ALA:HB2	2.25	0.51
1:A:163:ASP:OD1	2:B:543:TYR:OH	2.24	0.50
2:B:515:LEU:HB3	2:B:548:MET:HB2	1.93	0.50
2:B:595:GLN:NE2	2:B:595:GLN:CA	2.72	0.49
3:C:221:ASN:OD1	3:C:221:ASN:N	2.44	0.49
3:C:23:PHE:CD1	3:C:33:THR:HG21	2.48	0.48
3:C:23:PHE:HD1	3:C:27:PHE:HD2	1.60	0.48
1:A:38:ILE:HG13	1:A:187:PRO:HD3	1.95	0.48
3:C:100:LEU:HB3	3:C:104:ASN:HB3	1.95	0.48
1:A:104:TRP:CZ2	1:A:134:ARG:HD2	2.50	0.47
3:C:110:LEU:HB2	3:C:192:THR:HB	1.97	0.47
2:B:560:GLN:O	2:B:564:GLU:HG3	2.16	0.45
3:C:36:LEU:HD22	3:C:219:VAL:HG11	1.98	0.45
1:A:37:VAL:HG21	1:A:51:LEU:HD11	1.97	0.45
3:C:202:THR:O	3:C:206:GLN:HG2	2.16	0.45
3:C:20:LYS:O	3:C:24:ASP:OD2	2.33	0.45
1:A:79:VAL:O	1:A:83:THR:HG23	2.17	0.44
1:A:51:LEU:HD12	1:A:51:LEU:HA	1.68	0.44
1:A:70:LEU:HD11	1:A:180:VAL:HG22	2.00	0.44
3:C:22:TYR:CD1	3:C:173:LEU:HD11	2.52	0.44
3:C:143:TYR:CE2	3:C:153:ASP:HA	2.53	0.42
1:A:39:HIS:CB	1:A:42:VAL:HG22	2.40	0.42
3:C:100:LEU:O	3:C:103:TYR:HB3	2.20	0.42
3:C:22:TYR:HE2	3:C:27:PHE:CZ	2.37	0.42
1:A:63:LEU:HB3	2:B:585:LEU:HD22	2.01	0.41
3:C:23:PHE:HE1	3:C:192:THR:HG21	1.84	0.41
3:C:139:THR:OG1	5:C:302:HOH:O	2.21	0.41
2:B:513:PRO:O	2:B:555:ILE:HD13	2.21	0.41
3:C:18:LEU:HD13	3:C:172:TRP:CD1	2.57	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic	Clash
		${f distance}({ m \AA})$	overlap (Å)
5:A:251:HOH:O	5:B:815:HOH:O[3_655]	2.00	0.20
2:B:550:ASN:ND2	5:C:329:HOH:O[5_555]	2.07	0.13
1:A:137:TYR:OH	3:C:217:ASN:ND2[5_555]	2.19	0.01



### 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	156/158 (99%)	142 (91%)	12 (8%)	2 (1%)	12 12
2	В	83/130 (64%)	77 (93%)	4 (5%)	2 (2%)	6 4
3	С	213/256 (83%)	204 (96%)	8 (4%)	1 (0%)	29 35
All	All	452/544 (83%)	423 (94%)	24 (5%)	5 (1%)	14 15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	С	103	TYR
1	A	50	LYS
1	A	51	LEU
2	В	597	TRP
2	В	550	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	126/130 (97%)	124 (98%)	2 (2%)	62 78
2	В	70/111 (63%)	69 (99%)	1 (1%)	67 81
3	С	194/232 (84%)	189 (97%)	5 (3%)	46 63
All	All	390/473 (82%)	382 (98%)	8 (2%)	53 70

All (8) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	53	CYS
1	A	169	VAL
2	В	595	GLN
3	С	19	GLU
3	С	21	GLU
3	С	100	LEU
3	С	202	THR
3	С	221	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	HIS
2	В	595	GLN
3	С	25	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)

2 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).

Mal	True	Chain	Dag	T inle	Bond lengths			Bond angles		
Mol	Type	Chain	Res	Link	Counts	RMSZ	# Z  > 2	Counts	Counts $\mid \text{RMSZ} \mid \# \mid Z$	# Z  > 2
4	NAG	D	1	4,2	14,14,15	0.70	0	17,19,21	0.99	1 (5%)
4	NAG	D	2	4	14,14,15	0.29	0	17,19,21	0.55	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	D	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

	Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
ſ	4	D	1	NAG	O5-C1-C2	-3.04	106.49	111.29

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	2	NAG	C8-C7-N2-C2
4	D	2	NAG	O7-C7-N2-C2
4	D	2	NAG	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6

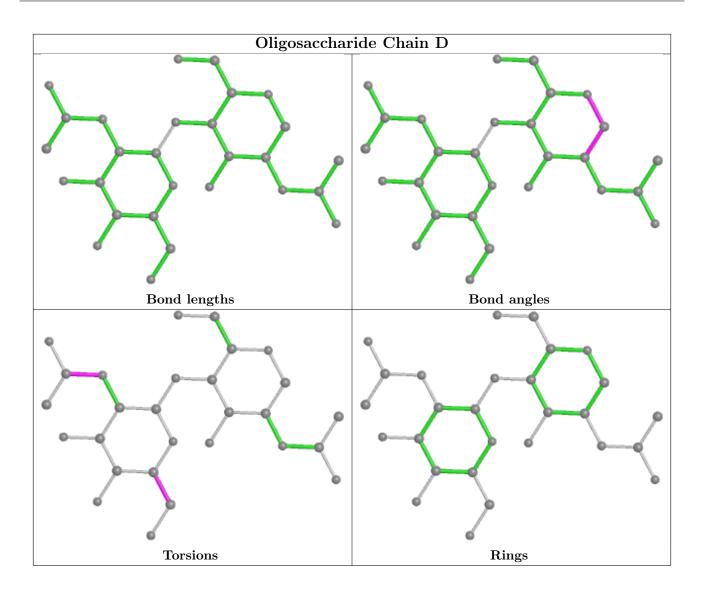
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	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)

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	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(Å^2)$	Q<0.9
1	A	158/158 (100%)	0.46	19 (12%) 4 6	25, 37, 123, 157	0
2	В	87/130 (66%)	0.48	8 (9%) 9 12	31, 48, 98, 143	0
3	С	215/256~(83%)	0.07	13 (6%) 21 28	31, 43, 111, 188	0
All	All	460/544 (84%)	0.28	40 (8%) 10 14	25, 41, 117, 188	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	525	ALA	12.5
3	С	21	GLU	11.2
3	С	18	LEU	9.7
3	С	25	GLN	7.2
1	A	53	CYS	6.4
3	С	24	ASP	6.3
2	В	526	ALA	6.1
2	В	527	ILE	6.1
3	С	26	HIS	5.3
3	С	22	TYR	5.1
1	A	51	LEU	4.8
1	A	54	ARG	4.7
3	С	103	TYR	4.6
2	В	509	PRO	4.5
1	A	49	ASP	4.2
1	A	39	HIS	4.0
3	С	232	THR	3.8
1	A	48	VAL	3.7
1	A	47	ASP	3.3
3	С	199	TYR	3.2
1	A	31	ARG	2.9
3	С	23	PHE	2.9
2	В	596	ARG	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	38	ILE	2.8
1	A	55	ASP	2.6
1	A	187	PRO	2.6
1	A	40	ASN	2.6
1	A	46	SER	2.6
3	С	202	THR	2.5
1	A	42	VAL	2.5
3	С	19	GLU	2.5
1	A	161	LEU	2.5
1	A	52	VAL	2.4
2	В	592	PHE	2.3
2	В	579	LEU	2.2
2	В	595	GLN	2.2
1	A	166	ALA	2.1
3	С	29	PRO	2.1
1	A	69	ASN	2.1
1	A	188	GLN	2.1

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

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

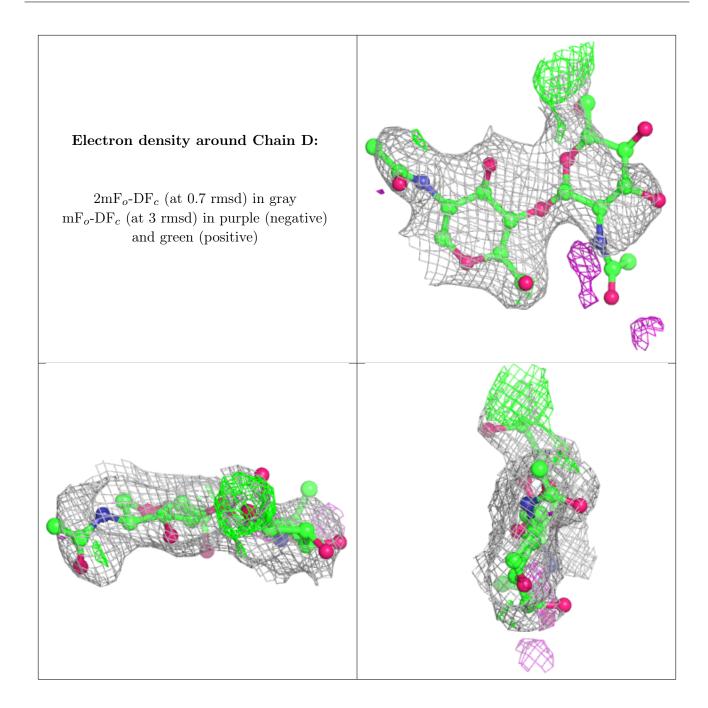
### 6.3 Carbohydrates (i)

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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
4	NAG	D	2	14/15	0.65	0.39	124,133,140,140	0
4	NAG	D	1	14/15	0.80	0.17	61,92,104,111	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)

There are no ligands in this entry.

# 6.5 Other polymers (i)

There are no such residues in this entry.

