

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

### Oct 9, 2023 – 02:16 PM EDT

PDB ID	:	7KEI
Title	:	DQA1*01:02/DQB1*06:02 in complex with a hemagglutinin peptide from the
		H1N1 pandemic flu virus.
Authors	:	Birtley, J.R.; Stern, L.J.; Mellins, E.D.; Jiang, W.
Deposited on		
Resolution	:	1.75  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 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:

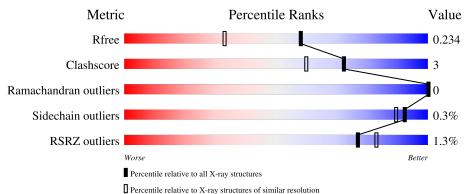
MolProbity	:	4.02b-467 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)		
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

# 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 1.75 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	130704	2340(1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	А	206	% • 83%	5% 12%
2	В	210	% 78%	8% 14%
3	С	25	76%	• 20%
4	D	4	75%	25%
5	Н	2	50%	50%



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	BMA	D	3	-	-	-	Х
5	NAG	Н	2	-	-	-	Х



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# 2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 6770 atoms, of which 3009 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 MHC class II HLA-DQ-alpha chain.

Mol	Chain	Residues			Atom	IS	ZeroOcc	AltConf	Trace		
1	Δ	182	Total	С	Н	Ν	Ο	$\mathbf{S}$	0	5	0
1	11	102	2882	950	1405	239	283	5	0	5	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	196	GLY	-	expression tag	UNP Q30066
А	197	GLY	-	expression tag	UNP Q30066
A	198	GLY	-	expression tag	UNP Q30066
А	199	GLY	-	expression tag	UNP Q30066
А	200	SER	-	expression tag	UNP Q30066
A	201	LEU	-	expression tag	UNP Q30066
A	202	GLU	-	expression tag	UNP Q30066
А	203	VAL	-	expression tag	UNP Q30066
A	204	LEU	-	expression tag	UNP Q30066
A	205	PHE	-	expression tag	UNP Q30066
А	206	GLN	-	expression tag	UNP Q30066

• Molecule 2 is a protein called HLA class II histocompatibility antigen, DQ beta 1 chain.

Mol	Chain	Residues			Atom	S	ZeroOcc	AltConf	Trace		
2	В	180	Total 2922	C 942	Н 1429	N 263	0 281	S 7	0	4	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	2	GLY	-	expression tag	UNP Q5SU54
В	199	GLY	-	expression tag	UNP Q5SU54
В	200	THR	-	expression tag	UNP Q5SU54
В	201	GLY	-	expression tag	UNP Q5SU54
В	202	GLY	-	expression tag	UNP $Q5SU54$



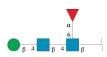
Continu	Continuea from previous page										
Chain	Residue	Modelled	Actual	Comment	Reference						
В	203	GLY	-	expression tag	UNP Q5SU54						
В	204	GLY	-	expression tag	UNP Q5SU54						
В	205	SER	-	expression tag	UNP Q5SU54						
В	206	LEU	-	expression tag	UNP Q5SU54						
В	207	GLU	-	expression tag	UNP Q5SU54						
В	208	VAL	-	expression tag	UNP Q5SU54						
В	209	LEU	-	expression tag	UNP Q5SU54						
В	210	PHE	-	expression tag	UNP Q5SU54						
В	211	GLN	-	expression tag	UNP Q5SU54						

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• Molecule 3 is a protein called HA peptide from 2009 H1N1 pandemic flu virus..

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	С	20	Total 247	C 75	Н 122	N 24	O 26	0	0	0

• Molecule 4 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-b eta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopy ranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
4	Л	4	Total	С	Η	N	0	0	0	0
4	D	4	78	28	29	2	19	0	0	0

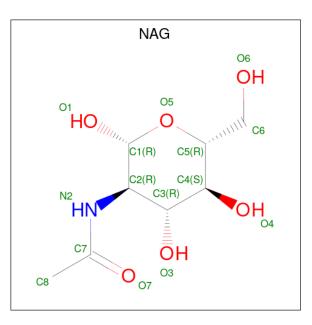
• Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a cetamido-2-deoxy-beta-D-glucopyranose.



Mo	l C	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
5		Н	2	Total 44	C 16	Н 16	N 2	O 10	0	0	0

• Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
6	D	1	Total	С	Η	Ν	0	0	0
0	D	1	22	8	8	1	5	0	0

• Molecule 7 is water.

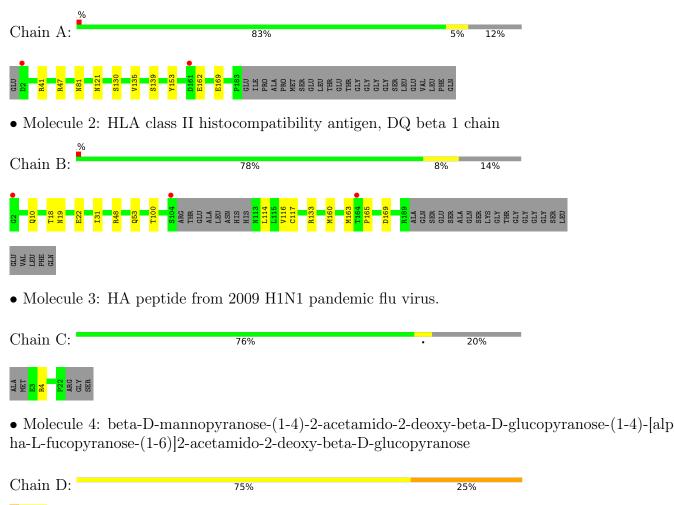
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	272	Total O 272 272	0	0
7	В	267	Total O 267 267	0	0
7	С	36	Total O 36 36	0	0



# 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: MHC class II HLA-DQ-alpha chain



#### NAG1 NAG2 BMA3 FUC4

• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-gluc opyranose

Chain H: 50% 50%







# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	59.31Å $58.26$ Å $67.51$ Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $96.08^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	27.93 - 1.75	Depositor
Resolution (A)	41.45 - 1.52	EDS
% Data completeness	99.5 (27.93-1.75)	Depositor
(in resolution range)	99.5(41.45 - 1.52)	EDS
R <sub>merge</sub>	0.08	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.32 (at 1.52 Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
D D	0.203 , $0.233$	Depositor
$R, R_{free}$	0.204 , $0.234$	DCC
$R_{free}$ test set	3556 reflections $(5.08%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	13.7	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.42 , $41.7$	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	6770	wwPDB-VP
Average B, all atoms $(Å^2)$	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.90% 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: NAG, BMA, 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	Bo	nd lengths	Bond angles		
	Unam	RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.66	0/1533	0.64	0/2092	
2	В	0.68	1/1548~(0.1%)	0.61	0/2104	
3	С	0.46	0/125	0.62	0/167	
All	All	0.67	1/3206~(0.0%)	0.63	0/4363	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
2	В	117	CYS	CB-SG	-5.14	1.73	1.81

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	А	1477	1405	1395	8	1
2	В	1493	1429	1405	12	1
3	С	125	122	122	1	0
4	D	49	29	43	3	0
5	Н	28	16	25	2	0
6	В	14	8	13	4	0
7	А	272	0	0	1	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 3.

The worst 5 of 21 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:19:ASN:HD21	6:B:301:NAG:C1	1.88	0.84
1:A:41:ARG:NH2	7:A:301:HOH:O	2.13	0.79
1:A:47:ARG:NH1	1:A:139[B]:SER:OG	2.30	0.65
1:A:121:ASN:OD1	5:H:1:NAG:H2	1.97	0.65
1:A:81:ASN:OD1	4:D:1:NAG:H2	1.98	0.64

All (1) 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 distance (Å)	Clash overlap (Å)
1:A:162:GLU:OE2	2:B:48:ARG:HH22[1_655]	1.49	0.11

### 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	А	185/206~(90%)	183~(99%)	2(1%)	0	100	100
2	В	180/210~(86%)	174 (97%)	6 (3%)	0	100	100
3	С	18/25~(72%)	18 (100%)	0	0	100	100
All	All	383/441 (87%)	375~(98%)	8 (2%)	0	100	100



Chain Non-H H(model) H(added) Clashes Symm-Clashes Mol В 7 2670 0 0 1 7  $\overline{\mathbf{C}}$ 0 1 0 36 0 All All 3761 3009 3003 211

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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 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.

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	А	166/181~(92%)	165~(99%)	1 (1%)	86 79		
2	В	167/185~(90%)	167~(100%)	0	100 100		
3	С	12/16~(75%)	12 (100%)	0	100 100		
All	All	345/382~(90%)	344 (100%)	1 (0%)	92 89		

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type	
1	А	130	SER	

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	175	GLN
2	В	19	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)

6 monosaccharides are modelled in this entry.



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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	Bond angles		
MIOI	Type	Ullaili	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
4	NAG	D	1	1,4	14,14,15	1.25	2 (14%)	17,19,21	1.02	2 (11%)
4	NAG	D	2	4	14,14,15	0.44	0	17,19,21	0.66	1 (5%)
4	BMA	D	3	4	11,11,12	0.73	0	$15,\!15,\!17$	1.09	1 (6%)
4	FUC	D	4	4	10,10,11	1.03	1 (10%)	14,14,16	0.94	1 (7%)
5	NAG	Н	1	1,5	14,14,15	1.20	2 (14%)	17,19,21	0.85	1 (5%)
5	NAG	Н	2	5	14,14,15	0.55	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	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	BMA	D	3	4	-	0/2/19/22	0/1/1/1
4	FUC	D	4	4	-	-	0/1/1/1
5	NAG	Н	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	Н	2	5	-	0/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
4	D	1	NAG	O5-C1	3.67	1.49	1.43
5	Н	1	NAG	O5-C1	3.18	1.48	1.43
5	Н	1	NAG	C1-C2	2.61	1.56	1.52
4	D	1	NAG	C1-C2	2.34	1.55	1.52
4	D	4	FUC	O5-C1	-2.02	1.40	1.43

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

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	D	4	FUC	O2-C2-C1	2.56	114.40	109.15



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	D	1	NAG	C1-O5-C5	2.37	115.41	112.19
5	Н	1	NAG	C1-O5-C5	2.34	115.37	112.19
4	D	2	NAG	C1-O5-C5	2.30	115.31	112.19
4	D	1	NAG	O5-C1-C2	-2.10	107.97	111.29

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There are no chirality outliers.

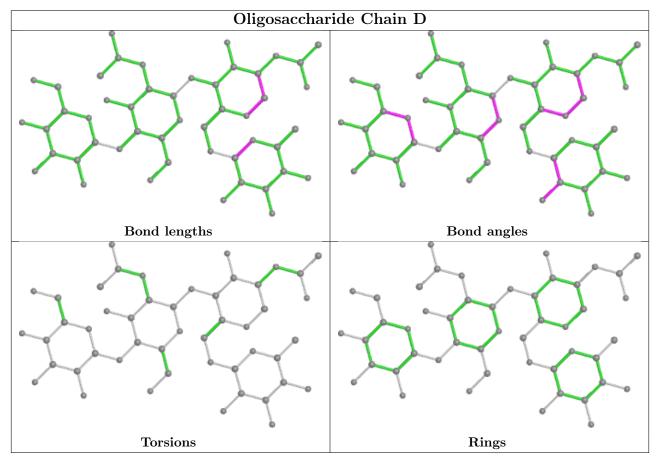
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

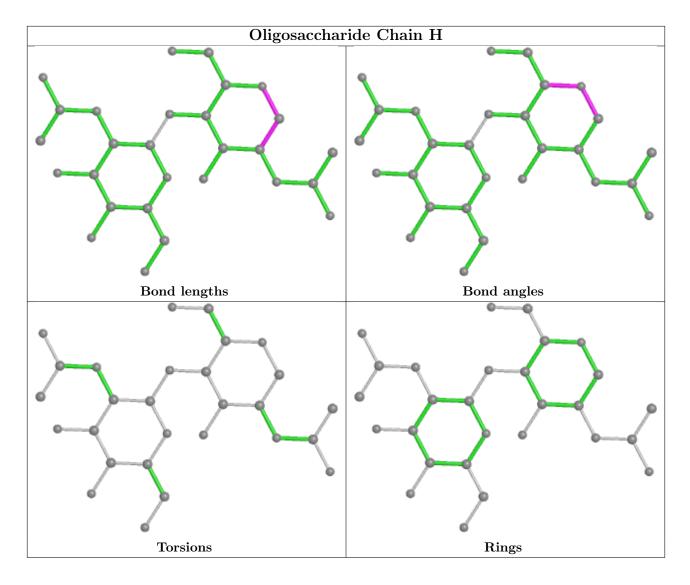
I	Mol	Chain	Res	Type	Clashes	Symm-Clashes
	4	D	1	NAG	3	0
	5	Н	1	NAG	2	0

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)

1 ligand is 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	Bo	ond leng	$\mathbf{ths}$	Bond angles		
WIOI	туре	Unam	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
6	NAG	В	301	-	14,14,15	1.00	1 (7%)	17,19,21	0.70	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	В	301	-	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	В	301	NAG	O5-C1	-3.41	1.38	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	В	301	NAG	O5-C5-C6-O6

There are no ring outliers.

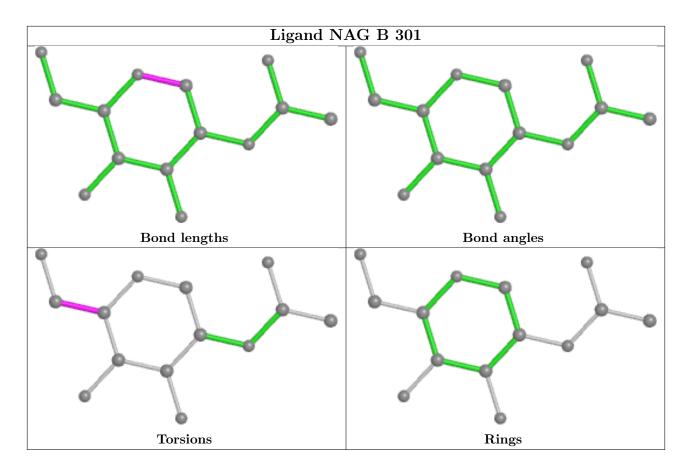
1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	В	301	NAG	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







# 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	А	182/206~(88%)	0.04	2 (1%) 80 86	8, 16, 34, 70	0
2	В	180/210~(85%)	-0.05	3 (1%) 70 77	9, 18, 40, 52	0
3	С	20/25~(80%)	-0.02	0 100 100	10, 19, 35, 39	0
All	All	382/441~(86%)	-0.01	5 (1%) 77 83	8, 17, 38, 70	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	2	GLY	5.8
2	В	104	SER	3.1
2	В	164	THR	2.8
1	А	161	ASP	2.5
1	А	2	ASP	2.2

### 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.

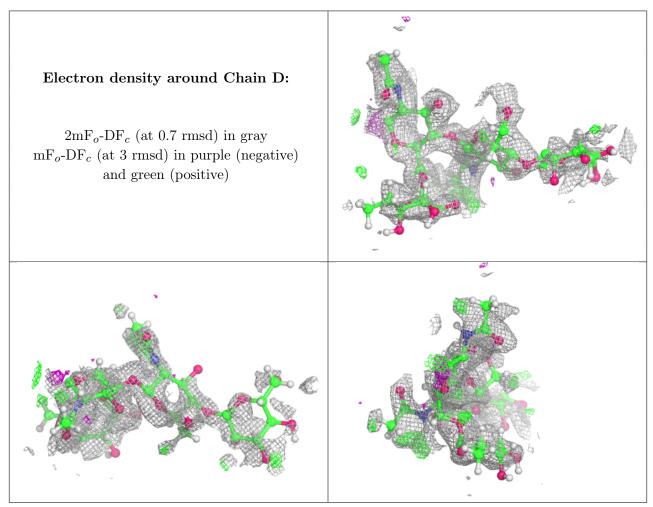
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
5	NAG	Н	2	14/15	0.36	0.41	67, 71, 91, 94	0
4	NAG	D	1	14/15	0.47	0.23	35,47,65,66	0
4	NAG	D	2	14/15	0.53	0.29	53,64,78,80	0



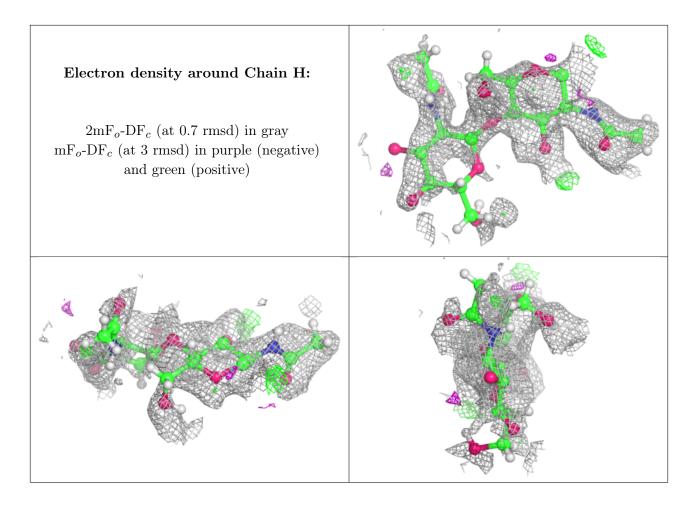
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q < 0.9
4	BMA	D	3	11/12	0.58	0.40	76,81,101,101	0
4	FUC	D	4	10/11	0.72	0.32	59,67,81,88	0
5	NAG	Н	1	14/15	0.74	0.17	24,47,69,69	0

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.







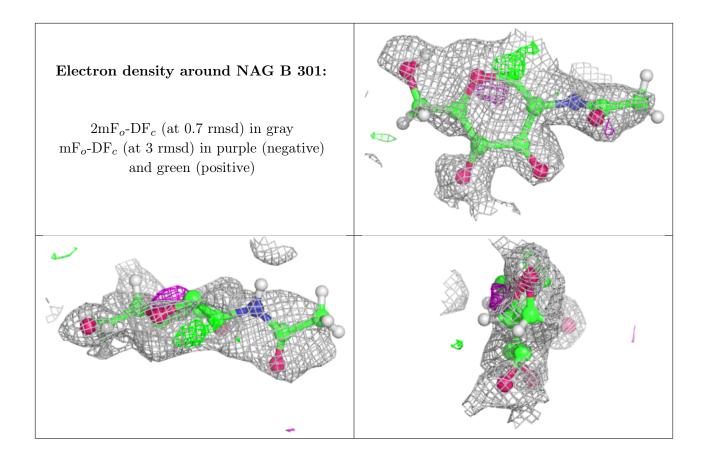
## 6.4 Ligands (i)

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	$\mathbf{B} ext{-factors}(\mathbf{\AA}^2)$	Q<0.9
6	NAG	В	301	14/15	0.61	0.23	41,49,63,63	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





# 6.5 Other polymers (i)

There are no such residues in this entry.

