



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:27 AM GMT

PDB ID : 3LZF  
Title : Crystal Structure of Fab 2D1 in Complex with the 1918 Influenza Virus Hemagglutinin  
Authors : Ekiert, D.C.; Wilson, I.A.  
Deposited on : 2010-03-01  
Resolution : 2.80 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

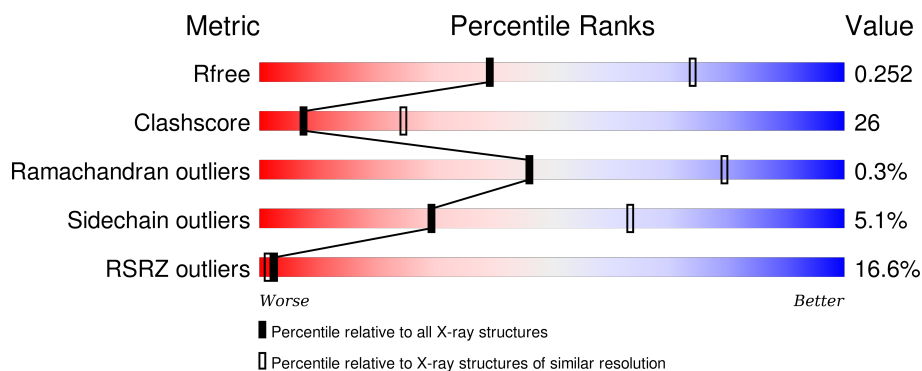
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	331	<div> <div>3%</div> <div>67%</div> <div>28%</div> <div>• •</div> </div>
2	B	179	<div> <div>21%</div> <div>65%</div> <div>28%</div> <div>• •</div> </div>
3	H	230	<div> <div>17%</div> <div>53%</div> <div>38%</div> <div>• 6%</div> </div>
4	L	217	<div> <div>30%</div> <div>66%</div> <div>30%</div> <div>• •</div> </div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7207 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 Hemagglutinin, HA1 Subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2506	1580	430	485	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ALA	-	EXPRESSION TAG	UNP Q9WFX3
A	8	ASP	-	EXPRESSION TAG	UNP Q9WFX3
A	9	PRO	-	EXPRESSION TAG	UNP Q9WFX3
A	10	GLY	-	EXPRESSION TAG	UNP Q9WFX3

- Molecule 2 is a protein called Hemagglutinin, HA2 Subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1391	868	239	278	6			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	SER	-	EXPRESSION TAG	UNP Q9WFX3
B	178	GLY	-	EXPRESSION TAG	UNP Q9WFX3
B	179	ARG	-	EXPRESSION TAG	UNP Q9WFX3

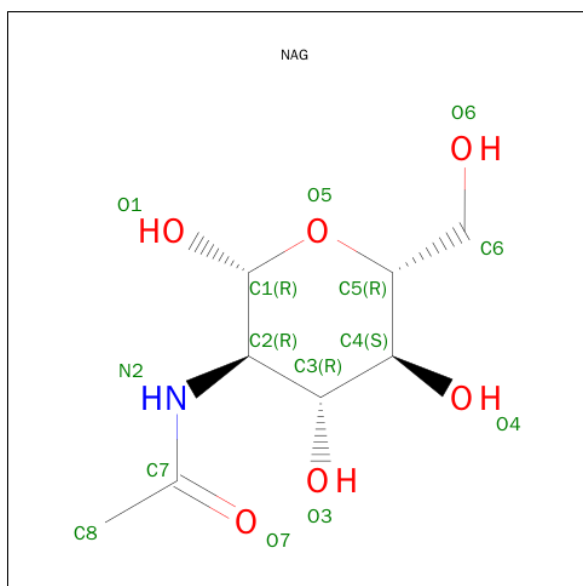
- Molecule 3 is a protein called 2D1 Fab, Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	216	Total	C	N	O	S	0	0	0
			1623	1030	264	322	7			

- Molecule 4 is a protein called 2D1 Fab, Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	212	Total	C	N	O	S	0	0	0
			1567	982	260	321	4			

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 6 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	2	Total	C	N	O	0	0
			28	16	2	10		
6	A	2	Total	C	N	O	0	0
			28	16	2	10		

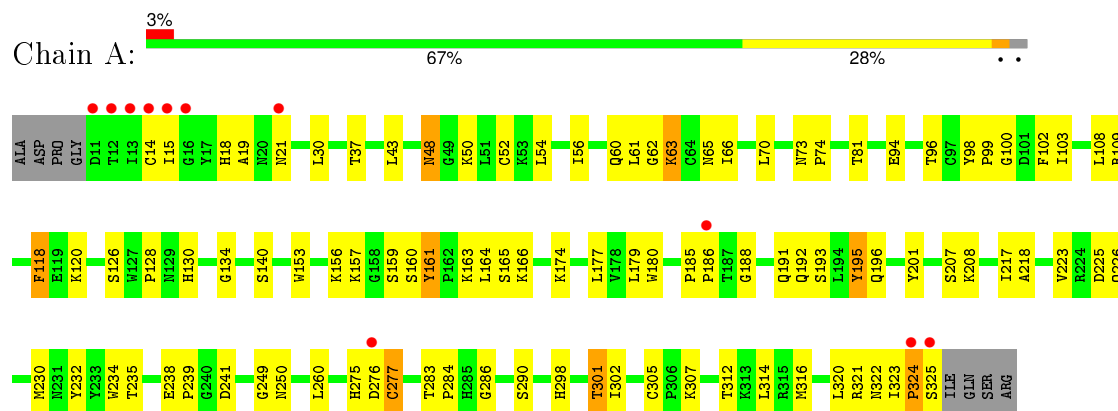
- Molecule 7 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	4	Total	C	N	O	0	0
			50	28	2	20		

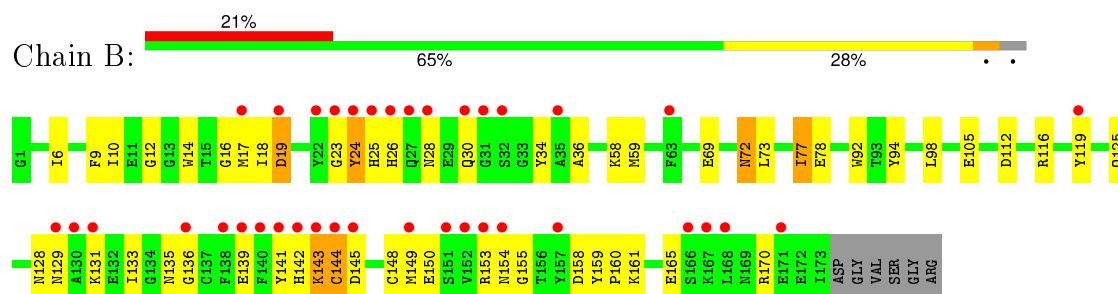
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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.

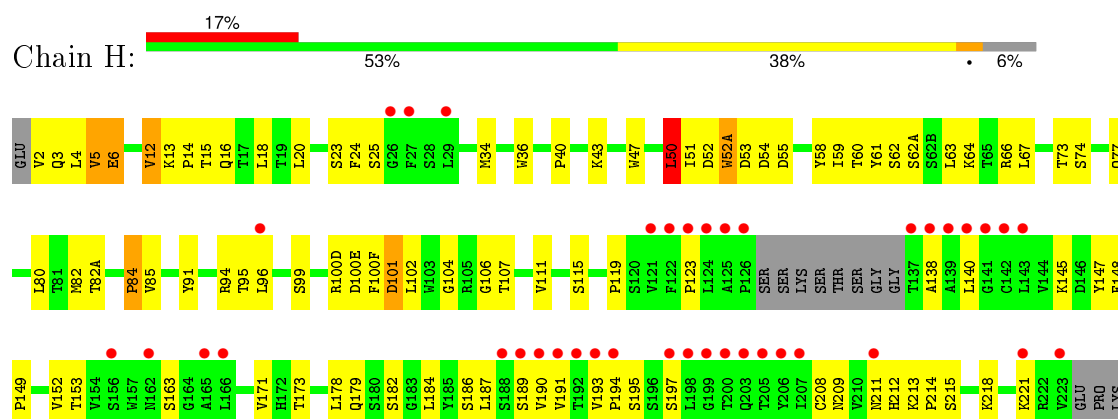
#### • Molecule 1: Hemagglutinin, HA1 Subunit



#### • Molecule 2: Hemagglutinin, HA2 Subunit



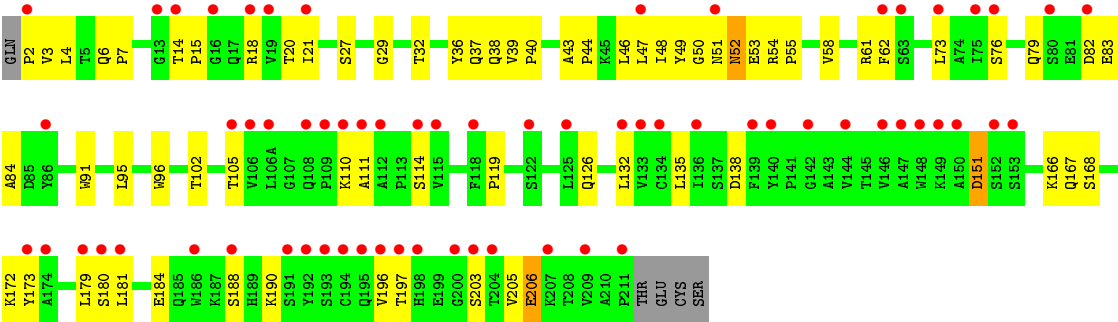
#### • Molecule 3: 2D1 Fab, Heavy Chain



SER

CYS

● Molecule 4: 2D1 Fab, Light Chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	161.75Å 161.75Å 143.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.69 – 2.80 49.67 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.1 (49.69-2.80) 98.1 (49.67-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.52 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.4.0069	Depositor
R, $R_{free}$	0.230 , 0.259 0.226 , 0.252	Depositor DCC
$R_{free}$ test set	2596 reflections (5.18%)	DCC
Wilson B-factor (Å <sup>2</sup> )	75.8	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 96.7	EDS
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 52718 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7207	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: BMA, NAG, MAN

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	0.90	2/2570 (0.1%)	0.93	2/3501 (0.1%)
2	B	0.69	1/1418 (0.1%)	0.74	0/1909
3	H	0.74	1/1660 (0.1%)	0.96	4/2274 (0.2%)
4	L	0.62	2/1608 (0.1%)	0.72	1/2199 (0.0%)
All	All	0.76	6/7256 (0.1%)	0.86	7/9883 (0.1%)

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

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	277	CYS	CB-SG	-9.33	1.66	1.82
1	A	120	LYS	CE-NZ	6.36	1.65	1.49
4	L	91	TRP	CB-CG	-5.49	1.40	1.50
3	H	101	ASP	CB-CG	-5.32	1.40	1.51
2	B	78	GLU	CB-CG	-5.30	1.42	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	101	ASP	CB-CG-OD1	-10.04	109.26	118.30
1	A	120	LYS	CD-CE-NZ	7.23	128.34	111.70
3	H	101	ASP	CB-CG-OD2	5.87	123.59	118.30
3	H	12	VAL	CB-CA-C	-5.35	101.23	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	50	LEU	CB-CG-CD2	5.31	120.03	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	276	ASP	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	2506	0	2427	91	0
2	B	1391	0	1302	87	0
3	H	1623	0	1601	122	0
4	L	1567	0	1511	70	0
5	A	14	0	13	1	0
6	A	56	0	50	0	0
7	A	50	0	43	1	0
All	All	7207	0	6947	360	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 26.

The worst 5 of 360 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:26:HIS:HB2	2:B:149:MET:CE	1.66	1.24
3:H:6:GLU:OE1	3:H:106:GLY:HA2	1.41	1.17
2:B:133:ILE:HD12	2:B:139:GLU:HB2	1.18	1.15
2:B:30:GLN:HE22	2:B:145:ASP:HB2	1.07	1.11
2:B:26:HIS:CB	2:B:149:MET:CE	2.29	1.10

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	321/331 (97%)	292 (91%)	27 (8%)	2 (1%)	30	65
2	B	171/179 (96%)	159 (93%)	12 (7%)	0	100	100
3	H	212/230 (92%)	199 (94%)	13 (6%)	0	100	100
4	L	210/217 (97%)	193 (92%)	16 (8%)	1 (0%)	34	69
All	All	914/957 (96%)	843 (92%)	68 (7%)	3 (0%)	46	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
4	L	52	ASN
1	A	324	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	279/285 (98%)	265 (95%)	14 (5%)	30	64
2	B	147/152 (97%)	140 (95%)	7 (5%)	31	66
3	H	188/204 (92%)	173 (92%)	15 (8%)	15	40
4	L	176/181 (97%)	172 (98%)	4 (2%)	58	88
All	All	790/822 (96%)	750 (95%)	40 (5%)	29	63

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	116	ARG
3	H	6	GLU
4	L	114	SER
2	B	144	CYS
3	H	50	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	42	GLN
2	B	72	ASN
3	H	16	GLN
2	B	28	ASN
2	B	30	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

8 carbohydrates 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	$\# Z  > 2$
6	NAG	A	501	1,6	14,14,15	0.48	0	15,19,21	1.40	4 (26%)
6	NAG	A	502	6	14,14,15	0.63	0	15,19,21	1.47	1 (6%)
7	NAG	A	601	1,7	14,14,15	0.91	1 (7%)	15,19,21	1.57	3 (20%)
7	NAG	A	602	7	14,14,15	0.60	0	15,19,21	2.15	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
7	BMA	A	603	7	11,11,12	0.69	0	14,15,17	1.64	2 (14%)
7	MAN	A	604	7	11,11,12	0.59	0	14,15,17	1.36	1 (7%)
6	NAG	A	701	1,6	14,14,15	0.60	0	15,19,21	1.49	2 (13%)
6	NAG	A	702	6	14,14,15	0.72	1 (7%)	15,19,21	1.28	2 (13%)

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	A	501	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	502	6	-	0/6/23/26	0/1/1/1
7	NAG	A	601	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	602	7	-	0/6/23/26	0/1/1/1
7	BMA	A	603	7	-	0/2/19/22	0/1/1/1
7	MAN	A	604	7	-	0/2/19/22	0/1/1/1
6	NAG	A	701	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	702	6	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	601	NAG	O5-C1	-2.23	1.40	1.43
6	A	702	NAG	C1-C2	2.21	1.55	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	702	NAG	C1-O5-C5	-3.31	108.05	112.25
7	A	601	NAG	O6-C6-C5	-3.08	101.16	111.33
7	A	602	NAG	C2-N2-C7	-2.74	119.52	123.04
7	A	601	NAG	O3-C3-C4	-2.61	104.46	110.34
7	A	604	MAN	C1-C2-C3	-2.52	106.56	109.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	601	NAG	1	0
7	A	602	NAG	1	0

## 5.6 Ligand geometry

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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	NAG	A	401	1	14,14,15	0.61	0	15,19,21	1.64	3 (20%)

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	A	401	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	401	NAG	C4-C3-C2	-3.47	105.83	111.23
5	A	401	NAG	O3-C3-C2	2.21	113.49	109.11
5	A	401	NAG	C1-O5-C5	3.08	116.16	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	401	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	323/331 (97%)	0.61	11 (3%) 49 36	68, 80, 91, 101	0
2	B	173/179 (96%)	1.27	37 (21%) 1 1	68, 82, 92, 105	0
3	H	216/230 (93%)	1.12	39 (18%) 2 1	71, 82, 95, 108	1 (0%)
4	L	212/217 (97%)	1.63	66 (31%) 1 0	71, 83, 90, 97	0
All	All	924/957 (96%)	1.08	153 (16%) 2 1	68, 81, 92, 108	1 (0%)

The worst 5 of 153 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	138	ALA	9.2
4	L	194	CYS	9.1
3	H	198	LEU	8.1
4	L	186	TRP	8.0
3	H	139	ALA	7.7

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
7	NAG	A	601	14/15	0.94	0.24	1.29	70,79,83,89	0
7	NAG	A	602	14/15	0.93	0.25	-	93,96,102,109	0
6	NAG	A	701	14/15	0.70	0.52	-	119,128,130,135	0
7	MAN	A	604	11/12	0.86	0.43	-	128,129,131,131	0
6	NAG	A	502	14/15	0.53	0.54	-	145,147,148,149	0
6	NAG	A	702	14/15	0.73	0.52	-	138,140,141,141	0
6	NAG	A	501	14/15	0.83	0.29	-	122,129,134,140	0
7	BMA	A	603	11/12	0.84	0.31	-	114,116,120,123	0

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	NAG	A	401	14/15	0.64	0.41	-	119,127,132,133	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.