



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 16, 2023 – 02:51 PM EDT

PDB ID : 2AEQ  
Title : An epidemiologically significant epitope of a 1998 influenza virus neuraminidase forms a highly hydrated interface in the NA-antibody complex.  
Authors : Venkatramani, L.; Bochkarev, A.; Air, G.M.  
Deposited on : 2005-07-23  
Resolution : 3.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
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

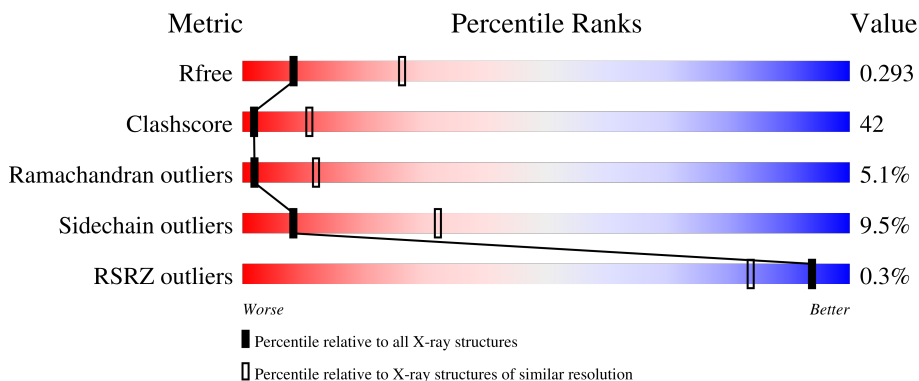
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	395	
2	L	214	
3	H	217	

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	NAG	A	1	-	-	-	X
4	NAG	L	215	-	-	X	-
4	NAG	L	216	-	-	X	-
5	MAN	H	218	-	-	X	-
5	MAN	H	219	-	-	X	-
5	MAN	L	217	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4900 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 neuraminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	388	3018	1876	537	583	22	0	0	0

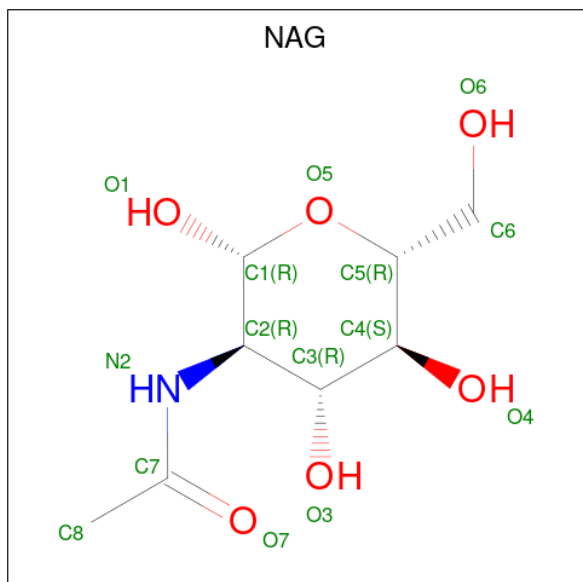
- Molecule 2 is a protein called FAB light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	L	107	832	523	139	166	4	0	0	0

- Molecule 3 is a protein called FAB heavy chain.

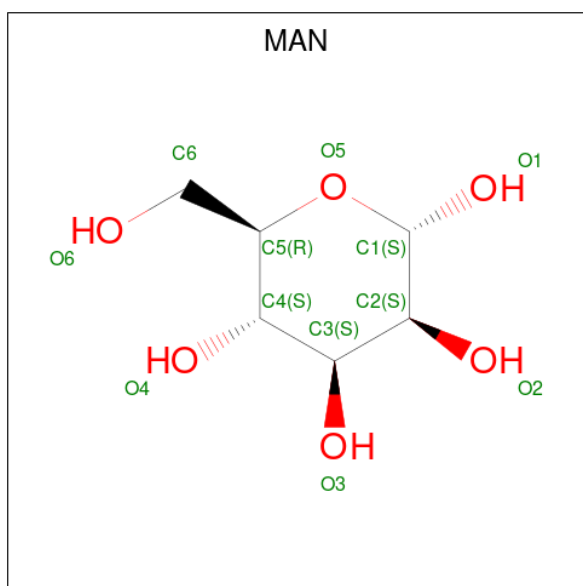
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	H	116	908	577	149	177	5	0	0	0

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 5 is alpha-D-mannopyranose (three-letter code: MAN) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>6</sub>).

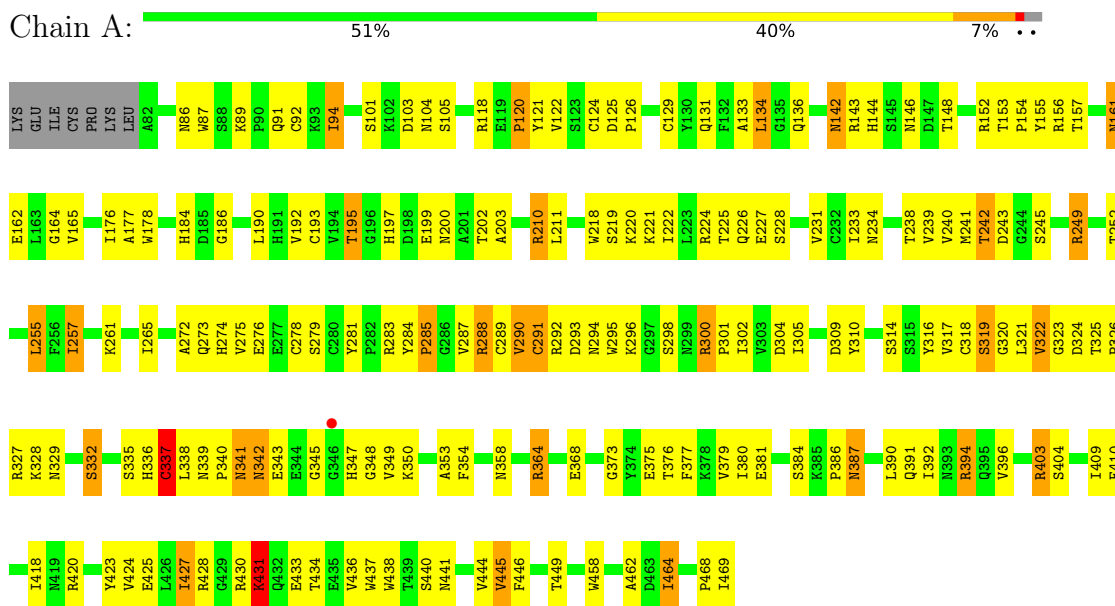


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	L	1	Total	C	O	0	0
			11	6	5		
5	L	1	Total	C	O	0	0
			11	6	5		
5	H	1	Total	C	O	0	0
			11	6	5		
5	H	1	Total	C	O	0	0
			11	6	5		

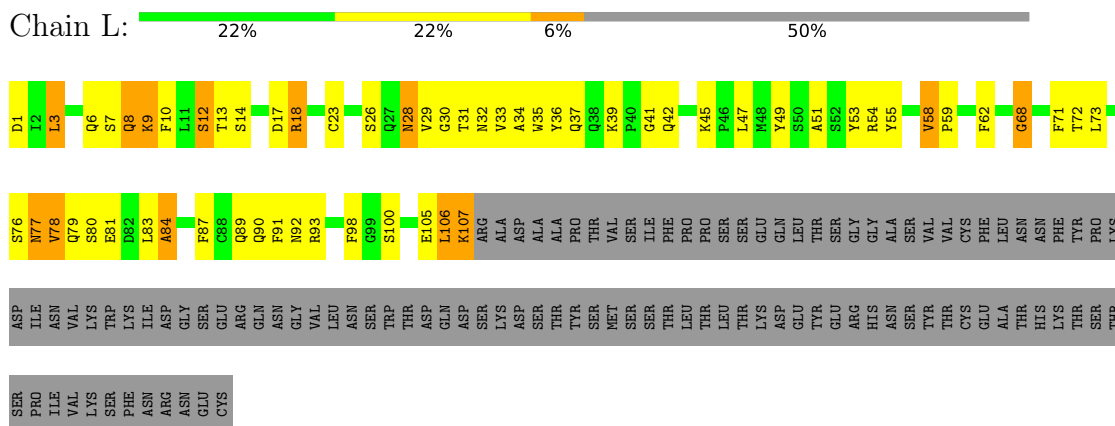
### 3 Residue-property plots

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: neuraminidase

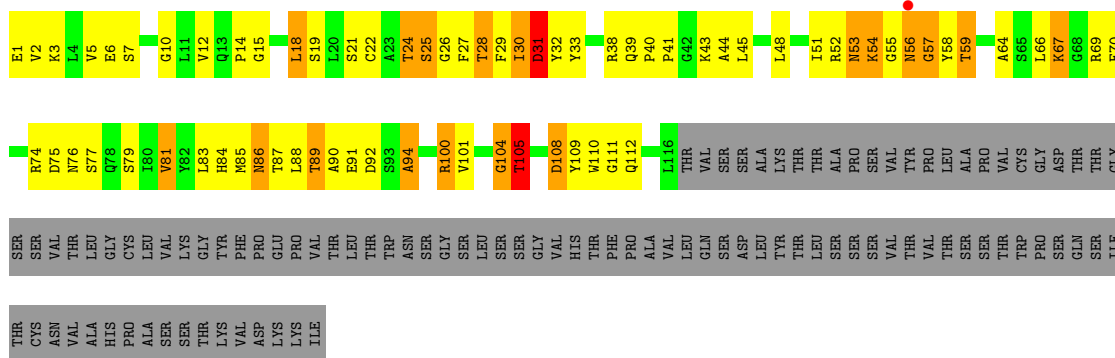


- Molecule 2: FAB light chain



- Molecule 3: FAB heavy chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	159.75Å 159.75Å 104.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.82 – 3.00 20.02 – 2.91	Depositor EDS
% Data completeness (in resolution range)	84.6 (19.82-3.00) 85.9 (20.02-2.91)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.58 (at 2.93Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.267 , 0.312 0.284 , 0.293	Depositor DCC
$R_{free}$ test set	2757 reflections (9.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.4	Xtrriage
Anisotropy	0.159	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 13.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.84	EDS
Total number of atoms	4900	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: 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	0.44	0/3091	0.73	2/4189 (0.0%)
2	L	0.50	0/850	0.67	0/1150
3	H	0.48	0/931	0.77	0/1262
All	All	0.46	0/4872	0.73	2/6601 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	431	LYS	N-CA-C	-5.69	95.64	111.00
1	A	290	VAL	N-CA-C	-5.21	96.94	111.00

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	A	3018	0	2870	195	0
2	L	832	0	805	65	0
3	H	908	0	862	132	0
4	A	70	0	65	11	0
4	L	28	0	26	18	0
5	H	22	0	20	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	L	22	0	20	9	0
All	All	4900	0	4668	402	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 42.

The worst 5 of 402 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)
1:A:176:ILE:HG22	1:A:195:THR:HG21	1.30	1.06
1:A:146:ASN:HD21	4:A:501:NAG:H2	1.18	1.05
3:H:31:ASP:N	3:H:54:LYS:HG3	1.73	1.03
1:A:249:ARG:HH11	1:A:249:ARG:HB2	1.25	1.00
3:H:31:ASP:H	3:H:54:LYS:HE3	1.29	0.98

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	386/395 (98%)	329 (85%)	46 (12%)	11 (3%)	5	25
2	L	105/214 (49%)	89 (85%)	10 (10%)	6 (6%)	1	10
3	H	114/217 (52%)	83 (73%)	17 (15%)	14 (12%)	0	1
All	All	605/826 (73%)	501 (83%)	73 (12%)	31 (5%)	2	12

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	ASN
1	A	322	VAL

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Mol	Chain	Res	Type
1	A	431	LYS
2	L	8	GLN
2	L	9	LYS

### 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	337/344 (98%)	307 (91%)	30 (9%)	9	35
2	L	94/192 (49%)	85 (90%)	9 (10%)	8	32
3	H	96/185 (52%)	85 (88%)	11 (12%)	5	24
All	All	527/721 (73%)	477 (90%)	50 (10%)	8	32

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	445	VAL
2	L	58	VAL
3	H	105	THR
1	A	464	ILE
2	L	12	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	42	GLN
3	H	78	GLN
3	H	112	GLN
3	H	53	ASN
1	A	342	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](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

11 ligands 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
4	NAG	A	501	-	14,14,15	0.62	0	17,19,21	0.65	0
5	MAN	H	218	-	11,11,12	0.51	0	15,15,17	0.48	0
4	NAG	L	216	-	14,14,15	0.56	0	17,19,21	0.70	0
4	NAG	A	502	-	14,14,15	0.62	0	17,19,21	1.19	3 (17%)
4	NAG	A	1	-	14,14,15	0.88	0	17,19,21	0.62	0
5	MAN	H	219	-	11,11,12	0.58	0	15,15,17	0.47	0
5	MAN	L	218	-	11,11,12	0.76	0	15,15,17	0.68	0
5	MAN	L	217	-	11,11,12	0.83	0	15,15,17	0.33	0
4	NAG	L	215	-	14,14,15	0.47	0	17,19,21	0.77	0
4	NAG	A	503	-	14,14,15	0.87	0	17,19,21	0.69	0
4	NAG	A	2	-	14,14,15	0.81	0	17,19,21	0.78	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	501	-	-	4/6/23/26	0/1/1/1
5	MAN	H	218	-	-	0/2/19/22	0/1/1/1
4	NAG	L	216	-	-	5/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	502	-	-	4/6/23/26	0/1/1/1
4	NAG	A	1	-	-	2/6/23/26	0/1/1/1
5	MAN	H	219	-	-	0/2/19/22	0/1/1/1
5	MAN	L	218	-	-	2/2/19/22	0/1/1/1
5	MAN	L	217	-	-	0/2/19/22	0/1/1/1
4	NAG	L	215	-	-	2/6/23/26	0/1/1/1
4	NAG	A	503	-	-	4/6/23/26	0/1/1/1
4	NAG	A	2	-	-	5/6/23/26	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(°)
4	A	502	NAG	C2-N2-C7	-2.42	119.46	122.90
4	A	502	NAG	C6-C5-C4	-2.35	107.51	113.00
4	A	502	NAG	C4-C3-C2	-2.14	107.89	111.02

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	NAG	C8-C7-N2-C2
4	A	501	NAG	O7-C7-N2-C2
4	A	1	NAG	C8-C7-N2-C2
4	A	1	NAG	O7-C7-N2-C2
4	A	2	NAG	C8-C7-N2-C2

There are no ring outliers.

10 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	NAG	3	0
5	H	218	MAN	7	0
4	L	216	NAG	14	0
4	A	502	NAG	2	0
4	A	1	NAG	6	0
5	H	219	MAN	6	0
5	L	217	MAN	9	0
4	L	215	NAG	9	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	NAG	1	0
4	A	2	NAG	2	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	388/395 (98%)	-0.45	1 (0%) 94 84	33, 33, 33, 33	0
2	L	107/214 (50%)	-0.33	0 100 100	33, 33, 33, 33	0
3	H	116/217 (53%)	-0.20	1 (0%) 84 63	33, 33, 33, 33	0
All	All	611/826 (73%)	-0.38	2 (0%) 94 84	33, 33, 33, 33	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	56	ASN	3.0
1	A	346	GLY	2.3

### 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](#)

There are no monosaccharides in this entry.

### 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<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	B-factors(Å <sup>2</sup> )	Q<0.9
5	MAN	L	218	11/12	0.66	0.34	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	A	1	14/15	0.72	0.56	32,32,32,32	0
4	NAG	A	501	14/15	0.75	0.32	32,32,32,32	0
4	NAG	A	2	14/15	0.83	0.40	32,32,32,32	0
5	MAN	H	219	11/12	0.83	0.34	32,32,32,32	0
4	NAG	A	503	14/15	0.86	0.47	32,32,32,32	0
4	NAG	A	502	14/15	0.88	0.33	32,32,32,32	0
5	MAN	H	218	11/12	0.88	0.20	32,32,32,32	0
5	MAN	L	217	11/12	0.88	0.17	32,32,32,32	0
4	NAG	L	216	14/15	0.91	0.19	32,32,32,32	0
4	NAG	L	215	14/15	0.92	0.20	32,32,32,32	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.