



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 8, 2020 – 01:24 PM BST

PDB ID : 4R4H  
Title : Crystal structure of non-neutralizing, A32-like antibody 2.2c in complex with HIV-1 Env gp120  
Authors : Mclellan, J.; Acharya, P.; Huang, C.-C.; Kwong, P.D.  
Deposited on : 2014-08-19  
Resolution : 4.28 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.

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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 : 2.13.1  
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) : 2.13.1

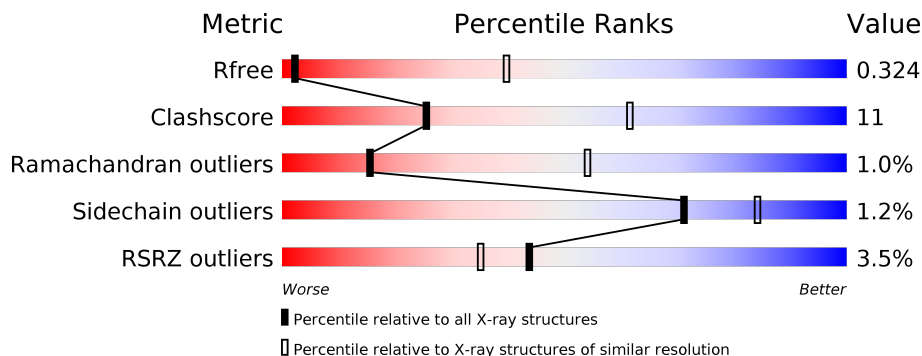
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.28 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	1001 (4.76-3.80)
Clashscore	141614	1063 (4.76-3.80)
Ramachandran outliers	138981	1018 (4.76-3.80)
Sidechain outliers	138945	1002 (4.76-3.80)
RSRZ outliers	127900	1074 (4.84-3.70)

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 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	433	 5% 59% 18% 22%
2	B	178	 10% 83% 16%
3	L	210	 86% 14%
4	H	220	 5% 75% 24%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	A	601	-	-	-	X
5	NAG	A	603	-	-	-	X
5	NAG	A	604	-	-	X	-
5	NAG	A	606	-	-	-	X
5	NAG	A	607	-	-	-	X
5	NAG	H	301	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7415 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 HIV-1 Env gp120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	337	2629	1644	461	503	21	0	0	0

- Molecule 2 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	178	1391	868	243	276	4	0	3	0

- Molecule 3 is a protein called Antibody 2.2c, Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	210	1612	1012	272	323	5	0	0	0

- Molecule 4 is a protein called Antibody 2.2c, Heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	220	1671	1064	283	319	5	0	0	0

- Molecule 5 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>).

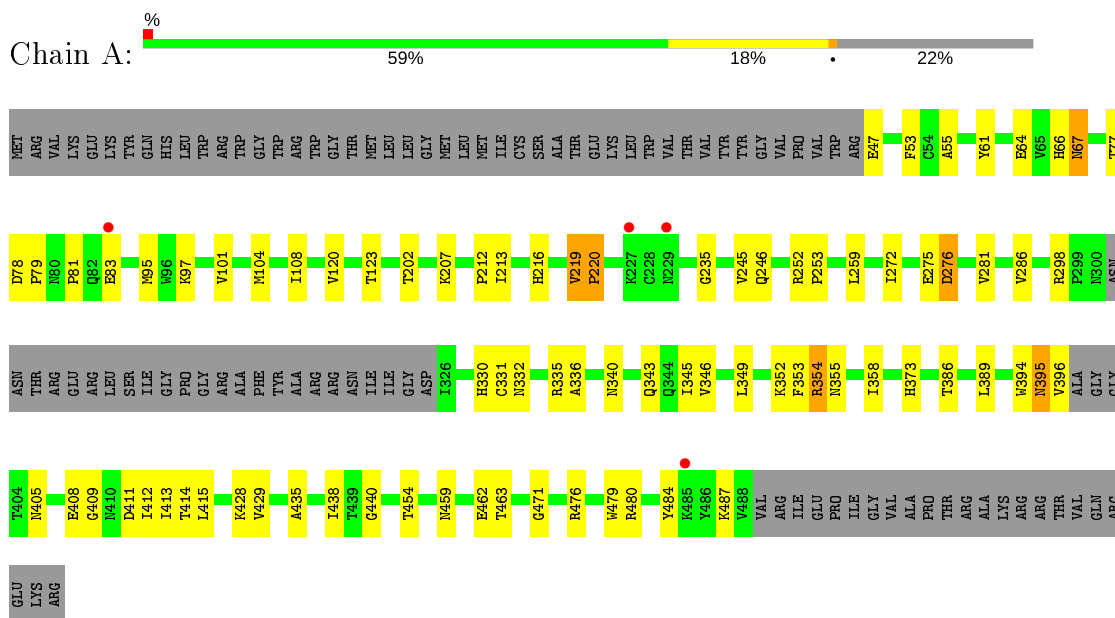


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	Total 14	8	1	5	0	0
5	A	1	Total 14	8	1	5	0	0
5	A	1	Total 14	8	1	5	0	0
5	A	1	Total 14	8	1	5	0	0
5	A	1	Total 14	8	1	5	0	0
5	A	1	Total 14	8	1	5	0	0
5	A	1	Total 14	8	1	5	0	0
5	H	1	Total 14	8	1	5	0	0

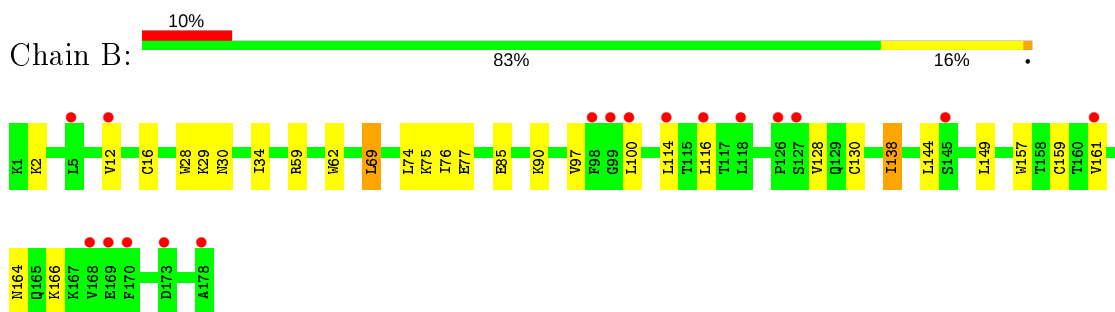
### 3 Residue-property plots [i](#)

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.

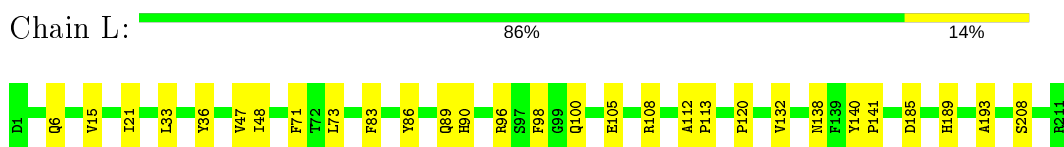
- Molecule 1: HIV-1 Env gp120



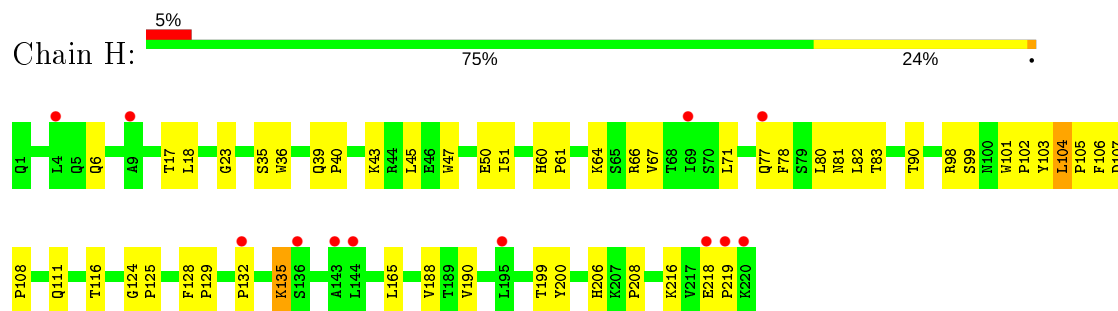
- Molecule 2: T-cell surface glycoprotein CD4



- Molecule 3: Antibody 2.2c, Light chain



- Molecule 4: Antibody 2.2c, Heavy chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.36Å 69.43Å 328.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.73 – 4.28 47.73 – 4.28	Depositor EDS
% Data completeness (in resolution range)	76.8 (47.73-4.28) 68.0 (47.73-4.28)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.13 (at 4.29Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.309 , 0.320 0.314 , 0.324	Depositor DCC
$R_{free}$ test set	424 reflections (5.34%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	120.6	Xtrriage
Anisotropy	0.062	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 133.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	7415	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	166.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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

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	0.29	0/2681	0.45	1/3642 (0.0%)
2	B	0.22	0/1424	0.38	0/1921
3	L	0.22	0/1646	0.37	0/2231
4	H	0.23	0/1720	0.39	0/2352
All	All	0.25	0/7471	0.41	1/10146 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	276	ASP	CB-CG-OD2	5.20	122.98	118.30

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	2629	0	2555	83	0
2	B	1391	0	1417	26	0
3	L	1612	0	1583	18	0
4	H	1671	0	1648	40	0
5	A	98	0	89	20	0
5	H	14	0	13	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7415	0	7305	155	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 11.

The worst 5 of 155 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)
4:H:81:ASN:HD21	5:H:301:NAG:C1	1.32	1.43
4:H:81:ASN:ND2	5:H:301:NAG:O5	1.63	1.30
1:A:332:ASN:HD21	5:A:604:NAG:H2	1.07	1.10
1:A:332:ASN:OD1	5:A:604:NAG:C1	2.06	1.04
1:A:340:ASN:HA	1:A:343:GLN:HG3	1.40	1.03

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	331/433 (76%)	288 (87%)	36 (11%)	7 (2%)	7	39
2	B	179/178 (101%)	170 (95%)	9 (5%)	0	100	100
3	L	208/210 (99%)	196 (94%)	11 (5%)	1 (0%)	29	68
4	H	218/220 (99%)	201 (92%)	16 (7%)	1 (0%)	29	68
All	All	936/1041 (90%)	855 (91%)	72 (8%)	9 (1%)	15	54

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	354	ARG
1	A	395	ASN

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Mol	Chain	Res	Type
1	A	405	ASN
3	L	138	ASN
1	A	97	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	298/379 (79%)	295 (99%)	3 (1%)	76	86
2	B	164/161 (102%)	161 (98%)	3 (2%)	59	77
3	L	183/183 (100%)	181 (99%)	2 (1%)	73	85
4	H	191/191 (100%)	189 (99%)	2 (1%)	76	86
All	All	836/914 (92%)	826 (99%)	10 (1%)	71	84

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	69	LEU
2	B	138	ILE
3	L	108	ARG
2	B	2	LYS
3	L	105	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	82	GLN
1	A	330	HIS
4	H	81	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](#)

8 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
5	NAG	A	604	-	14,14,15	1.09	1 (7%)	17,19,21	0.87	0
5	NAG	A	601	1	14,14,15	0.57	0	17,19,21	0.73	1 (5%)
5	NAG	H	301	4	14,14,15	0.44	0	17,19,21	1.00	0
5	NAG	A	606	1	14,14,15	0.43	0	17,19,21	0.78	0
5	NAG	A	602	1	14,14,15	0.59	0	17,19,21	3.20	1 (5%)
5	NAG	A	605	1	14,14,15	1.84	2 (14%)	17,19,21	2.29	4 (23%)
5	NAG	A	607	1	14,14,15	0.64	0	17,19,21	1.19	1 (5%)
5	NAG	A	603	1	14,14,15	0.53	0	17,19,21	0.50	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
5	NAG	A	604	-	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	601	1	-	0/6/23/26	0/1/1/1
5	NAG	H	301	4	-	2/6/23/26	0/1/1/1
5	NAG	A	606	1	-	2/6/23/26	0/1/1/1
5	NAG	A	602	1	-	5/6/23/26	0/1/1/1
5	NAG	A	605	1	-	2/6/23/26	0/1/1/1
5	NAG	A	607	1	-	1/6/23/26	0/1/1/1
5	NAG	A	603	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	605	NAG	O5-C1	-5.92	1.34	1.43
5	A	604	NAG	O5-C1	-3.44	1.38	1.43
5	A	605	NAG	C1-C2	-2.63	1.48	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	NAG	C2-N2-C7	12.63	140.89	122.90
5	A	605	NAG	C2-N2-C7	6.78	132.56	122.90
5	A	605	NAG	C4-C3-C2	-3.55	105.82	111.02
5	A	605	NAG	C1-C2-N2	-3.46	104.58	110.49
5	A	607	NAG	C4-C3-C2	-2.92	106.73	111.02

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	602	NAG	C8-C7-N2-C2
5	A	602	NAG	O7-C7-N2-C2
5	A	605	NAG	C8-C7-N2-C2
5	A	605	NAG	O7-C7-N2-C2
5	A	602	NAG	C1-C2-N2-C7

There are no ring outliers.

5 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	604	NAG	17	0
5	A	601	NAG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	301	NAG	4	0
5	A	605	NAG	1	0
5	A	607	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	337/433 (77%)	0.12	4 (1%) 79 70	89, 150, 183, 214	0
2	B	178/178 (100%)	0.51	17 (9%) 8 7	135, 180, 273, 288	0
3	L	210/210 (100%)	0.02	0 100 100	138, 171, 213, 232	0
4	H	220/220 (100%)	0.34	12 (5%) 25 22	132, 157, 208, 226	0
All	All	945/1041 (90%)	0.22	33 (3%) 44 35	89, 160, 227, 288	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	118	LEU	4.1
4	H	219	PRO	3.7
2	B	169	GLU	3.7
4	H	132	PRO	3.6
2	B	100	LEU	3.5

### 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( $\text{\AA}^2$ )	Q<0.9
5	NAG	A	603	14/15	0.52	0.60	154,158,162,163	0
5	NAG	H	301	14/15	0.64	0.44	166,171,178,179	0
5	NAG	A	605	14/15	0.68	0.36	175,181,185,187	0
5	NAG	A	607	14/15	0.69	0.45	144,151,156,156	0
5	NAG	A	606	14/15	0.71	0.46	161,164,168,168	0
5	NAG	A	601	14/15	0.75	0.45	135,138,141,141	0
5	NAG	A	602	14/15	0.81	0.32	167,172,178,178	0
5	NAG	A	604	14/15	0.86	0.21	153,163,170,170	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.