



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 21, 2020 – 08:56 PM BST

PDB ID : 6WO4  
Title : Structure of Hepatitis C Virus Envelope Glycoprotein E2 core from genotype 6a bound to broadly neutralizing antibody HC11  
Authors : Tzarum, N.; Wilson, I.A.; Law, M.  
Deposited on : 2020-04-24  
Resolution : 2.35 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](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 : 2.14.6  
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) : 2.14.6

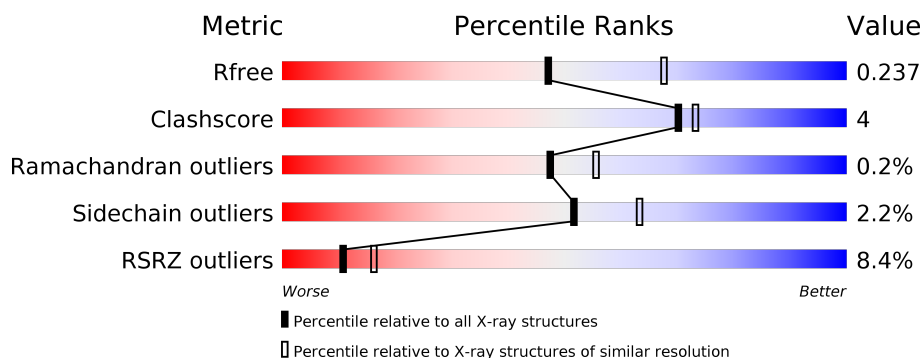
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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	H	231	<div> <div>7%</div> <div>87%</div> <div>10%</div> <div>••</div> </div>
2	E	189	<div> <div>17%</div> <div>78%</div> <div>8%</div> <div>•</div> <div>14%</div> </div>
3	L	235	<div> <div>%</div> <div>83%</div> <div>8%</div> <div>9%</div> </div>
4	A	2	<div> <div>100%</div> </div>
4	B	2	<div> <div>50%</div> <div>50%</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4732 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 Fab HC11 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	228	Total	C	N	O	S	0	0	0
			1671	1058	275	326	12			

- Molecule 2 is a protein called Envelope glycoprotein E2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	163	Total	C	N	O	S	0	0	0
			1253	796	214	230	13			

- Molecule 3 is a protein called Fab HC11 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total	C	N	O	S	0	0	0
			1628	1012	281	329	6			

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



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

- 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
5	E	1	Total	C	N	O	0	0
			14	8	1	5		
5	E	1	Total	C	N	O	0	0
			14	8	1	5		

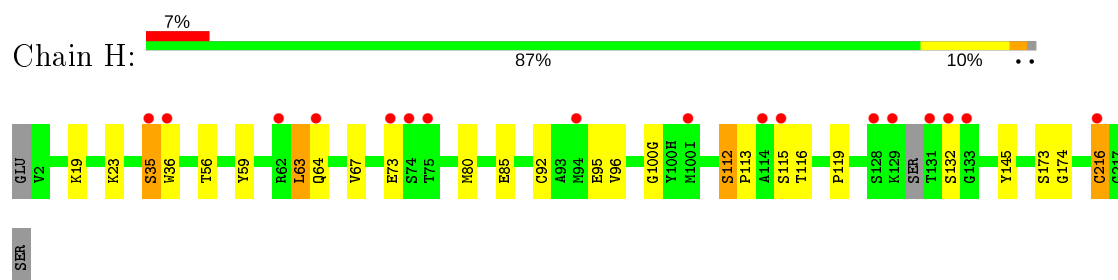
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	H	36	Total	O	0	0
			36	36		
6	E	10	Total	O	0	0
			10	10		
6	L	50	Total	O	0	0
			50	50		

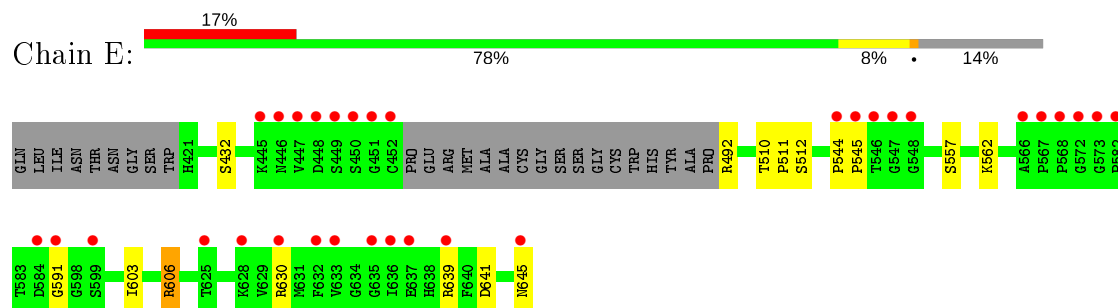
### 3 Residue-property plots [i](#)

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.

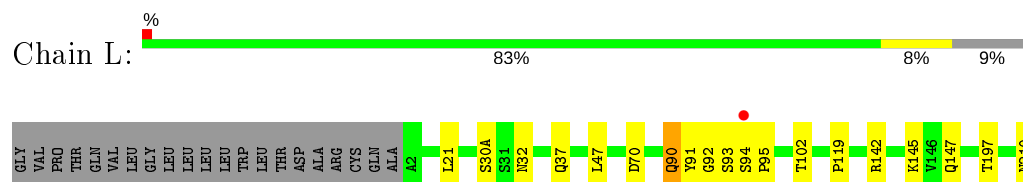
- Molecule 1: Fab HC11 heavy chain



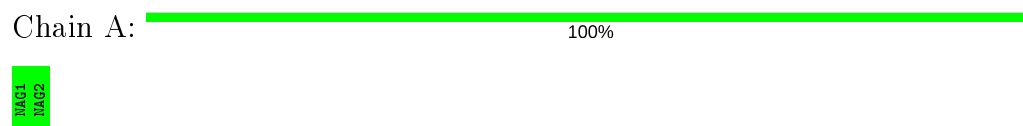
- Molecule 2: Envelope glycoprotein E2



- Molecule 3: Fab HC11 light chain



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	60.71Å 67.11Å 222.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.37 – 2.35 29.37 – 2.35	Depositor EDS
% Data completeness (in resolution range)	94.2 (29.37-2.35) 94.2 (29.37-2.35)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.12 _2829	Depositor
R, $R_{free}$	0.209 , 0.236 0.211 , 0.237	Depositor DCC
$R_{free}$ test set	1770 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.4	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4732	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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	H	0.29	0/1712	0.50	0/2328
2	E	0.28	0/1294	0.53	1/1770 (0.1%)
3	L	0.29	0/1663	0.48	0/2257
All	All	0.29	0/4669	0.50	1/6355 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	492	ARG	NE-CZ-NH1	8.87	124.73	120.30

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	H	1671	0	1645	15	0
2	E	1253	0	1172	8	0
3	L	1628	0	1574	12	0
4	A	28	0	25	0	0
4	B	28	0	25	2	0
5	E	28	0	26	1	0
6	E	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	H	36	0	0	2	0
6	L	50	0	0	1	0
All	All	4732	0	4467	33	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 4.

All (33) 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:H:216:CYS:HB3	3:L:119:PRO:HG2	1.48	0.94
1:H:112:SER:HB2	1:H:174:GLY:HA3	1.68	0.73
3:L:142:ARG:NH1	6:L:301:HOH:O	2.14	0.70
2:E:510:THR:O	2:E:512:SER:N	2.29	0.66
3:L:90:GLN:HE21	3:L:93:SER:H	1.45	0.64
3:L:21:LEU:HD22	3:L:102:THR:HG21	1.82	0.60
2:E:630:ARG:HG2	2:E:639:ARG:HG2	1.84	0.59
1:H:56:THR:HG22	5:E:701:NAG:H62	1.86	0.58
1:H:59:TYR:HB2	1:H:64:GLN:HG3	1.85	0.58
1:H:73:GLU:O	6:H:301:HOH:O	2.17	0.58
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.87	0.56
1:H:115:SER:OG	1:H:116:THR:N	2.38	0.56
3:L:90:GLN:HG2	3:L:92:GLY:H	1.72	0.55
2:E:557:SER:HB2	4:B:1:NAG:H82	1.90	0.54
2:E:562:LYS:NZ	4:B:1:NAG:O5	2.43	0.52
1:H:35:SER:OG	1:H:95:GLU:OE1	2.27	0.52
1:H:112:SER:HB2	1:H:174:GLY:CA	2.40	0.51
3:L:145:LYS:HB3	3:L:197:THR:HB	1.92	0.51
1:H:36:TRP:CE2	1:H:80:MET:HB2	2.46	0.51
3:L:145:LYS:HZ2	3:L:147:GLN:HG3	1.78	0.49
3:L:210:ASN:HB3	3:L:213:GLU:HB3	1.95	0.47
1:H:85:GLU:H	1:H:85:GLU:HG3	1.61	0.44
2:E:606:ARG:NH2	2:E:645:ASN:HB2	2.33	0.44
2:E:432:SER:HA	3:L:30(A):SER:HB2	2.00	0.43
1:H:113:PRO:HD2	1:H:173:SER:O	2.18	0.43
2:E:544:PRO:HA	2:E:545:PRO:HD3	1.94	0.43
3:L:37:GLN:HB2	3:L:47:LEU:HD11	2.02	0.42
3:L:94:SER:OG	3:L:95:PRO:HD3	2.20	0.42
1:H:23:LYS:NZ	6:H:304:HOH:O	2.47	0.42
1:H:96:VAL:O	1:H:100(G):GLY:HA3	2.20	0.41
2:E:591:GLY:HA2	2:E:603:ILE:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:L:32:ASN:HB3	3:L:91:TYR:CD1	2.55	0.41
1:H:63:LEU:HD13	1:H:67:VAL:HG21	2.02	0.40

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	H	224/231 (97%)	219 (98%)	5 (2%)	0	100	100
2	E	159/189 (84%)	149 (94%)	9 (6%)	1 (1%)	25	26
3	L	212/235 (90%)	207 (98%)	5 (2%)	0	100	100
All	All	595/655 (91%)	575 (97%)	19 (3%)	1 (0%)	47	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	511	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	H	188/191 (98%)	181 (96%)	7 (4%)	34	43
2	E	139/159 (87%)	137 (99%)	2 (1%)	67	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	L	183/200 (92%)	181 (99%)	2 (1%)	73	83
All	All	510/550 (93%)	499 (98%)	11 (2%)	52	63

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	19	LYS
1	H	35	SER
1	H	63	LEU
1	H	92	CYS
1	H	112	SER
1	H	132	SER
1	H	216	CYS
2	E	606	ARG
2	E	641	ASP
3	L	70	ASP
3	L	90	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 ⓘ

4 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	A	1	2,4	14,14,15	0.30	0	17,19,21	0.54	0
4	NAG	A	2	4	14,14,15	0.38	0	17,19,21	0.53	0
4	NAG	B	1	2,4	14,14,15	0.20	0	17,19,21	0.55	0
4	NAG	B	2	4	14,14,15	0.24	0	17,19,21	0.47	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	A	1	2,4	-	1/6/23/26	0/1/1/1
4	NAG	A	2	4	-	1/6/23/26	0/1/1/1
4	NAG	B	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	B	2	4	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1	NAG	C4-C5-C6-O6
4	B	1	NAG	O5-C5-C6-O6
4	A	1	NAG	O5-C5-C6-O6
4	A	2	NAG	O5-C5-C6-O6
4	B	2	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1	NAG	2	0

## 5.6 Ligand geometry ⓘ

2 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	E	701	2	14,14,15	0.20	0	17,19,21	0.66	0
5	NAG	E	706	2	14,14,15	0.19	0	17,19,21	0.35	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	E	701	2	-	4/6/23/26	0/1/1/1
5	NAG	E	706	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	701	NAG	C4-C5-C6-O6
5	E	701	NAG	O5-C5-C6-O6
5	E	701	NAG	C1-C2-N2-C7
5	E	701	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	701	NAG	1	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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	H	228/231 (98%)	0.41	17 (7%) 14 21	30, 53, 78, 90	0
2	E	163/189 (86%)	1.20	32 (19%) 1 2	46, 74, 109, 127	0
3	L	214/235 (91%)	0.18	2 (0%) 84 89	35, 49, 70, 92	0
All	All	605/655 (92%)	0.54	51 (8%) 11 16	30, 56, 91, 127	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	450	SER	9.8
2	E	449	SER	8.2
2	E	447	VAL	7.3
2	E	566	ALA	7.1
2	E	452	CYS	6.8
2	E	546	THR	6.7
1	H	115	SER	6.6
2	E	451	GLY	6.6
2	E	567	PRO	6.4
1	H	131	THR	6.0
2	E	448	ASP	5.1
1	H	132	SER	4.8
2	E	547	GLY	4.8
1	H	216	CYS	4.6
1	H	114	ALA	4.3
2	E	568	PRO	4.3
2	E	630	ARG	4.0
2	E	545	PRO	3.9
2	E	639	ARG	3.8
2	E	446	ASN	3.6
2	E	573	GLY	3.4
3	L	94	SER	3.4
2	E	591	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	H	129	LYS	3.4
2	E	632	PHE	3.3
2	E	636	ILE	3.3
2	E	628	LYS	3.2
2	E	599	SER	3.1
1	H	75	THR	3.0
2	E	625	THR	2.6
3	L	214	CYS	2.6
1	H	133	GLY	2.5
2	E	582	PRO	2.4
1	H	100(I)	MET	2.4
2	E	633	VAL	2.4
2	E	637	GLU	2.4
2	E	635	GLY	2.3
1	H	74	SER	2.3
2	E	548	GLY	2.3
1	H	94	MET	2.3
2	E	572	GLY	2.2
2	E	445	LYS	2.2
2	E	584	ASP	2.2
1	H	64	GLN	2.2
1	H	35	SER	2.2
1	H	62	ARG	2.1
2	E	544	PRO	2.1
1	H	73	GLU	2.1
1	H	36	TRP	2.1
1	H	128	SER	2.1
2	E	645	ASN	2.0

## 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<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
4	NAG	A	1	14/15	0.79	0.23	81,85,98,106	0
4	NAG	A	2	14/15	0.85	0.28	88,95,104,107	0
4	NAG	B	2	14/15	0.86	0.38	74,89,107,108	0
4	NAG	B	1	14/15	0.91	0.17	59,71,82,84	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. 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	E	701	14/15	0.84	0.38	84,93,102,102	0
5	NAG	E	706	14/15	0.87	0.48	94,102,111,112	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.