



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 04:41 PM BST

PDB ID : 6BKC
Title : Structure of Hepatitis C Virus Envelope Glycoprotein E2 core from genotype 6a bound to broadly neutralizing antibody AR3B
Authors : Tzarum, N.; Wilson, I.A.; Law, M.
Deposited on : 2017-11-08
Resolution : 2.60 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

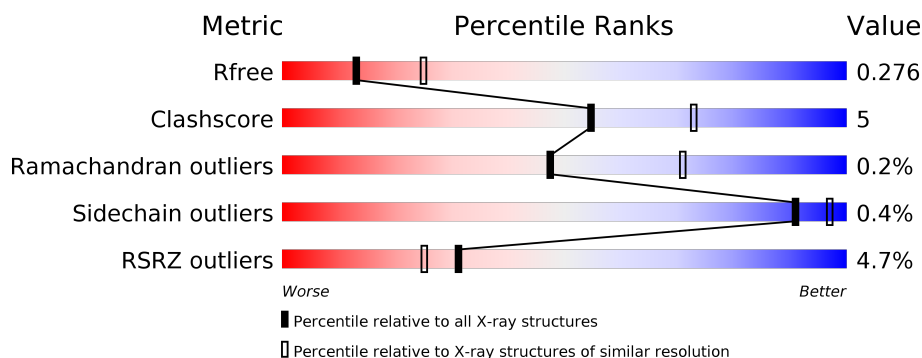
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 ≥ 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	230	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>18%</div> <div>5%</div> </div> </div>
2	L	215	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>10%</div> </div> </div>
3	E	189	<div> <div>10%</div> <div> <div></div> <div>67%</div> <div>9%</div> <div>24%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4473 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 AR3B heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	219	Total	C	N	O	S	0	0	0
			1617	1029	268	314	6			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	108	GLN	LEU	conflict	UNP P0DOX5
H	217	GLY	-	expression tag	UNP P0DOX5
H	218	SER	-	expression tag	UNP P0DOX5

- Molecule 2 is a protein called Fab AR3B light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	0	0
			1640	1022	278	336	4			

- Molecule 3 is a protein called Polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	143	Total	C	N	O	S	0	0	0
			1113	712	189	200	12			

There are 11 discrepancies between the modelled and reference sequences:

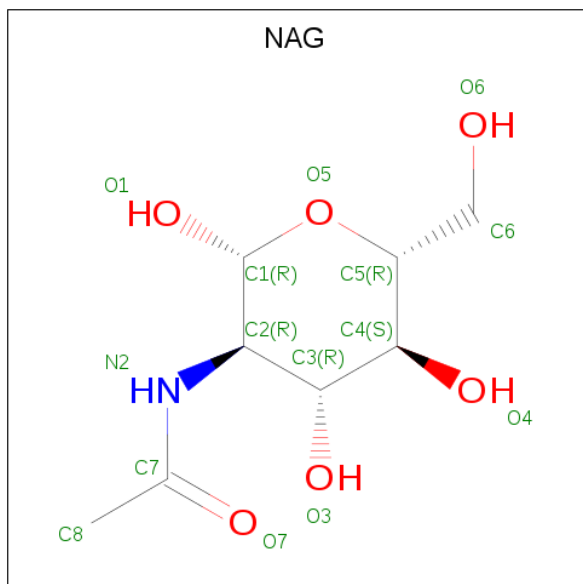
Chain	Residue	Modelled	Actual	Comment	Reference
E	470	ASP	ASN	engineered mutation	UNP B9V0E2
E	482	GLY	-	linker	UNP B9V0E2
E	483	SER	-	linker	UNP B9V0E2
E	484	SER	-	linker	UNP B9V0E2
E	485	GLY	-	linker	UNP B9V0E2
E	586	GLY	-	linker	UNP B9V0E2
E	587	GLY	-	linker	UNP B9V0E2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	588	PRO	-	linker	UNP B9V0E2
E	589	THR	-	linker	UNP B9V0E2
E	590	ASP	-	linker	UNP B9V0E2
E	591	GLY	-	linker	UNP B9V0E2

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

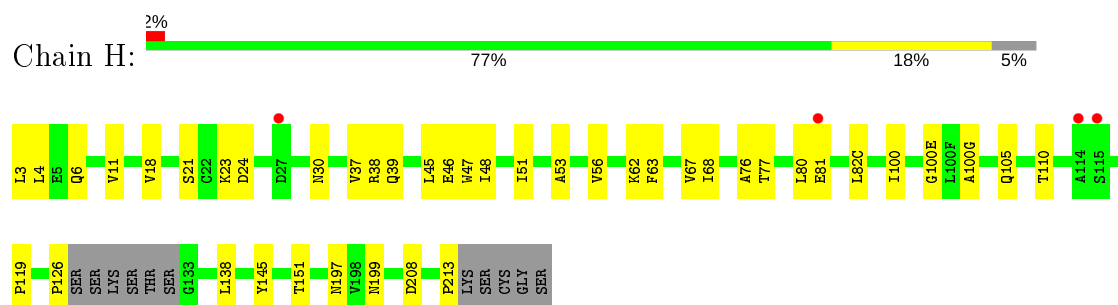
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	12	Total	O	0	0
			12	12		
5	L	31	Total	O	0	0
			31	31		
5	E	4	Total	O	0	0
			4	4		

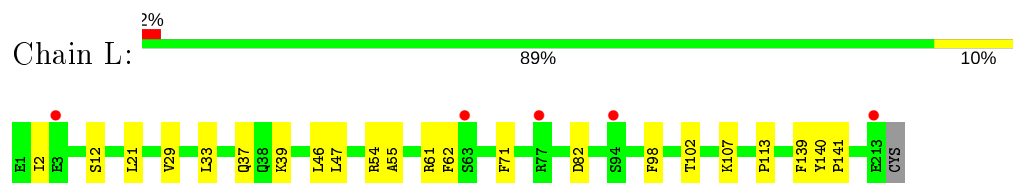
3 Residue-property plots [i](#)

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.

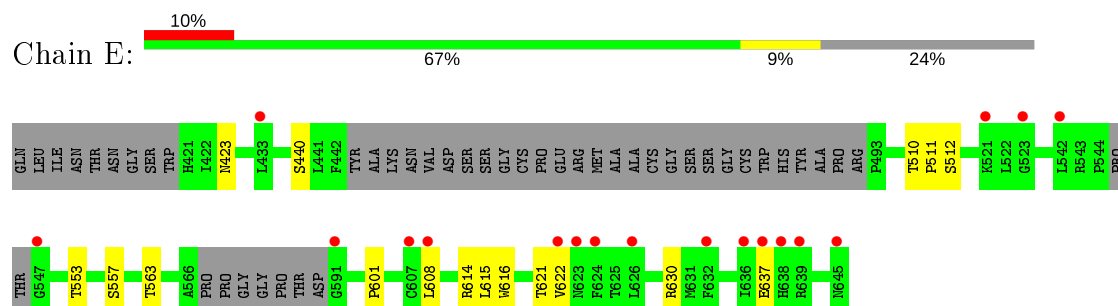
- Molecule 1: Fab AR3B heavy chain



- Molecule 2: Fab AR3B light chain



- Molecule 3: Polyprotein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	36.45Å 59.44Å 143.92Å 90.00° 90.29° 90.00°	Depositor
Resolution (Å)	32.58 – 2.60 32.58 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.8 (32.58-2.60) 94.8 (32.58-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.12_2829)	Depositor
R, R_{free}	0.231 , 0.276 0.231 , 0.276	Depositor DCC
R_{free} test set	915 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	47.9	Xtriage
Anisotropy	0.274	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.046 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4473	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

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	0.25	0/1655	0.46	0/2258
2	L	0.25	0/1675	0.45	0/2273
3	E	0.25	0/1147	0.44	0/1563
All	All	0.25	0/4477	0.45	0/6094

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1617	0	1610	23	0
2	L	1640	0	1587	13	0
3	E	1113	0	1044	10	0
4	E	56	0	52	2	0
5	E	4	0	0	0	0
5	H	12	0	0	0	0
5	L	31	0	0	1	0
All	All	4473	0	4293	45	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 5.

All (45) 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:L:61:ARG:NH1	2:L:82:ASP:OD2	2.24	0.71
3:E:553:THR:HG22	3:E:563:THR:HG22	1.75	0.69
1:H:197:ASN:ND2	1:H:208:ASP:OD2	2.24	0.69
1:H:18:VAL:HG13	1:H:82(C):LEU:HD11	1.80	0.62
1:H:126:PRO:HG2	1:H:213:PRO:HB3	1.84	0.59
3:E:510:THR:O	3:E:512:SER:N	2.36	0.58
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.85	0.57
3:E:440:SER:HB2	3:E:616:TRP:CD1	2.39	0.57
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.87	0.56
1:H:68:ILE:HG23	1:H:81:GLU:HB2	1.89	0.55
3:E:630:ARG:NE	3:E:637:GLU:OE2	2.40	0.54
1:H:37:VAL:HG22	1:H:47:TRP:HA	1.91	0.53
1:H:100:ILE:HD11	1:H:100(G):ALA:HB1	1.91	0.53
1:H:23:LYS:HG3	1:H:76:ALA:HB3	1.90	0.52
1:H:39:GLN:HB2	1:H:45:LEU:HD23	1.92	0.52
2:L:46:LEU:HD23	2:L:55:ALA:HB2	1.90	0.52
1:H:56:VAL:HG11	1:H:100(E):GLY:HA3	1.93	0.51
1:H:11:VAL:HG22	1:H:110:THR:HB	1.93	0.50
1:H:30:ASN:HB3	1:H:53:ALA:HB2	1.94	0.50
3:E:615:LEU:HD22	3:E:622:VAL:HG12	1.94	0.49
1:H:126:PRO:HD3	1:H:138:LEU:HB3	1.94	0.48
3:E:553:THR:HG21	3:E:601:PRO:HD3	1.96	0.48
3:E:608:LEU:HD13	3:E:621:THR:HG21	1.95	0.48
2:L:12:SER:HB3	2:L:107:LYS:HG3	1.97	0.47
2:L:54:ARG:HD3	2:L:62:PHE:O	2.15	0.47
1:H:4:LEU:HD22	1:H:24:ASP:HB3	1.97	0.46
1:H:38:ARG:HB3	1:H:48:ILE:HD11	1.97	0.46
2:L:21:LEU:HD22	2:L:102:THR:HG21	1.98	0.46
3:E:614:ARG:NH1	3:E:621:THR:O	2.49	0.45
2:L:33:LEU:HD22	2:L:71:PHE:CG	2.53	0.44
2:L:39:LYS:NZ	5:L:308:HOH:O	2.50	0.44
1:H:51:ILE:HA	1:H:56:VAL:O	2.18	0.44
1:H:151:THR:OG1	1:H:199:ASN:HB3	2.18	0.43
1:H:46:GLU:OE2	1:H:62:LYS:NZ	2.31	0.43
1:H:21:SER:HB2	1:H:77:THR:HG21	2.00	0.43
2:L:113:PRO:HB3	2:L:139:PHE:CD2	2.54	0.43
1:H:6:GLN:H	1:H:105:GLN:HE22	1.67	0.43
1:H:62:LYS:HE2	1:H:62:LYS:HB3	1.80	0.42
2:L:33:LEU:HD22	2:L:71:PHE:CD1	2.55	0.42
2:L:2:ILE:HD13	2:L:29:VAL:HG12	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:423:ASN:HD22	4:E:704:NAG:H83	1.86	0.41
1:H:45:LEU:HB2	2:L:98:PHE:CG	2.55	0.41
3:E:557:SER:HB2	4:E:702:NAG:H82	2.02	0.41
2:L:140:TYR:CG	2:L:141:PRO:HA	2.55	0.41
1:H:63:PHE:O	1:H:67:VAL:HG12	2.20	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	215/230 (94%)	209 (97%)	6 (3%)	0	100	100
2	L	212/215 (99%)	205 (97%)	7 (3%)	0	100	100
3	E	135/189 (71%)	127 (94%)	7 (5%)	1 (1%)	22	43
All	All	562/634 (89%)	541 (96%)	20 (4%)	1 (0%)	47	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	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	180/190 (95%)	178 (99%)	2 (1%)	73	88
2	L	185/186 (100%)	185 (100%)	0	100	100
3	E	123/159 (77%)	123 (100%)	0	100	100
All	All	488/535 (91%)	486 (100%)	2 (0%)	91	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	3	LEU
1	H	80	LEU

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

Mol	Chain	Res	Type
1	H	39	GLN
2	L	38	GLN

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](#)

4 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	E	701	3	14,14,15	0.32	0	17,19,21	0.46	0
4	NAG	E	702	3	14,14,15	0.30	0	17,19,21	0.51	0
4	NAG	E	703	3	14,14,15	0.32	0	17,19,21	0.53	0
4	NAG	E	704	3	14,14,15	0.25	0	17,19,21	0.37	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	E	701	3	-	0/6/23/26	0/1/1/1
4	NAG	E	702	3	-	2/6/23/26	0/1/1/1
4	NAG	E	703	3	-	3/6/23/26	0/1/1/1
4	NAG	E	704	3	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	702	NAG	C4-C5-C6-O6
4	E	704	NAG	O5-C5-C6-O6
4	E	702	NAG	O5-C5-C6-O6
4	E	704	NAG	C8-C7-N2-C2
4	E	704	NAG	O7-C7-N2-C2
4	E	703	NAG	O5-C5-C6-O6
4	E	704	NAG	C4-C5-C6-O6
4	E	703	NAG	C4-C5-C6-O6
4	E	703	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	702	NAG	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	704	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 ⓘ

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, 95th 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 ²)	Q<0.9
1	H	219/230 (95%)	0.22	4 (1%) 68 64	32, 45, 60, 89	0
2	L	214/215 (99%)	0.13	5 (2%) 60 54	30, 43, 56, 66	0
3	E	143/189 (75%)	0.81	18 (12%) 3 2	41, 59, 79, 90	0
All	All	576/634 (90%)	0.33	27 (4%) 31 25	30, 46, 73, 90	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	645	ASN	5.1
3	E	591	GLY	5.1
3	E	542	LEU	4.3
2	L	94	SER	4.0
3	E	636	ILE	3.8
3	E	607	CYS	3.8
1	H	27	ASP	3.7
1	H	115	SER	3.5
2	L	213	GLU	3.4
3	E	608	LEU	3.2
3	E	624	PHE	3.1
3	E	523	GLY	3.0
3	E	521	LYS	2.9
3	E	632	PHE	2.8
1	H	114	ALA	2.7
2	L	77	ARG	2.5
3	E	622	VAL	2.5
3	E	638	HIS	2.4
3	E	433	LEU	2.3
3	E	639	ARG	2.3
3	E	637	GLU	2.2
2	L	3	GLU	2.2
3	E	547	GLY	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	L	63	SER	2.2
3	E	623	ASN	2.1
1	H	81	GLU	2.0
3	E	626	LEU	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](#)

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, 95th 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(\AA^2)	Q<0.9
4	NAG	E	704	14/15	0.75	0.23	54,66,77,81	0
4	NAG	E	703	14/15	0.78	0.23	58,60,63,65	0
4	NAG	E	701	14/15	0.81	0.26	59,72,89,104	0
4	NAG	E	702	14/15	0.90	0.33	60,64,69,82	0

6.5 Other polymers [i](#)

There are no such residues in this entry.