



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2026 – 08:54 PM UTC

PDB ID : 5F96 / pdb\_00005f96  
Title : Crystal structure of broadly neutralizing VH1-46 germline-derived CD4-binding site-directed antibody CH235.12 in complex with HIV-1 clade A/E 93TH057 gp120  
Authors : Zhou, T.; Kwong, P.D.  
Deposited on : 2015-12-09  
Resolution : 2.24 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

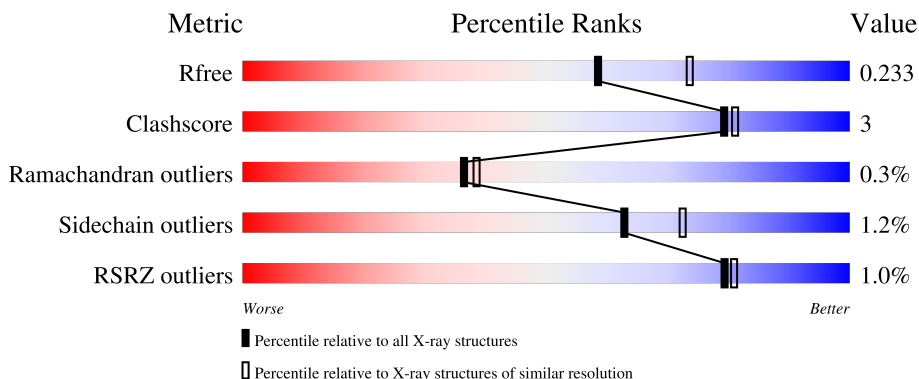
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.24 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))
$R_{free}$	180053	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	G	353	 2% 85% 10% .
2	H	225	 91% 6% .
3	L	213	 93% 6% .

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6385 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 clade A/E 93TH057 HIV-1 gp120 core.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	G	339	2656	1668	461	505	22	0	0	0

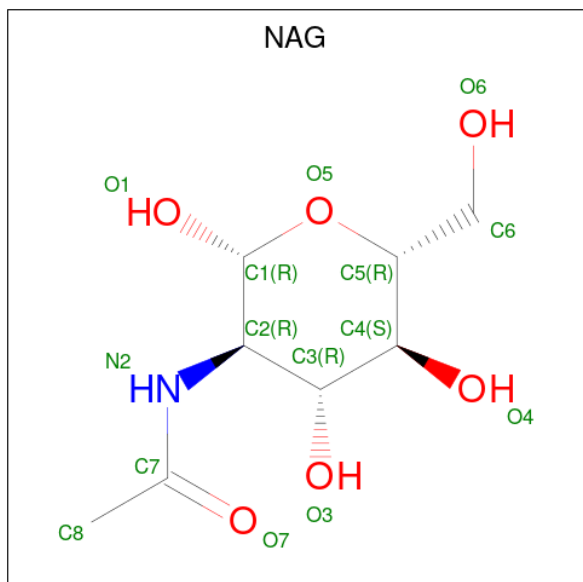
- Molecule 2 is a protein called HEAVY CHAIN OF ANTIBODY CH235.12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	H	220	1685	1066	290	320	9	0	1	0

- Molecule 3 is a protein called LIGHT CHAIN OF ANTIBODY CH235.12.

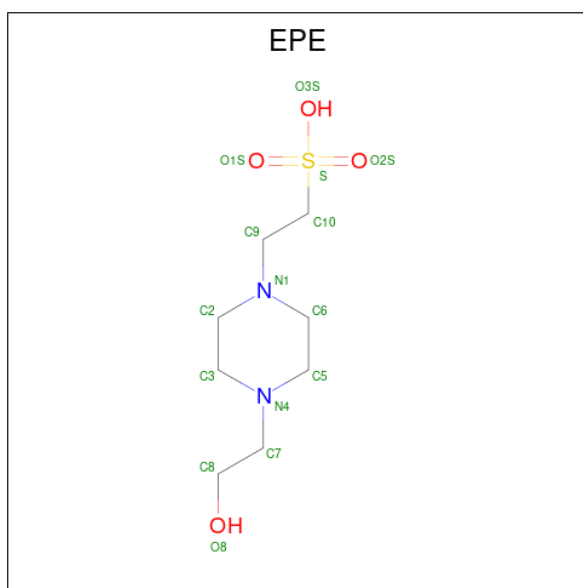
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	L	211	1635	1022	285	324	4	0	0	0

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



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

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C<sub>8</sub>H<sub>18</sub>N<sub>2</sub>O<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	G	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	G	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	L	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

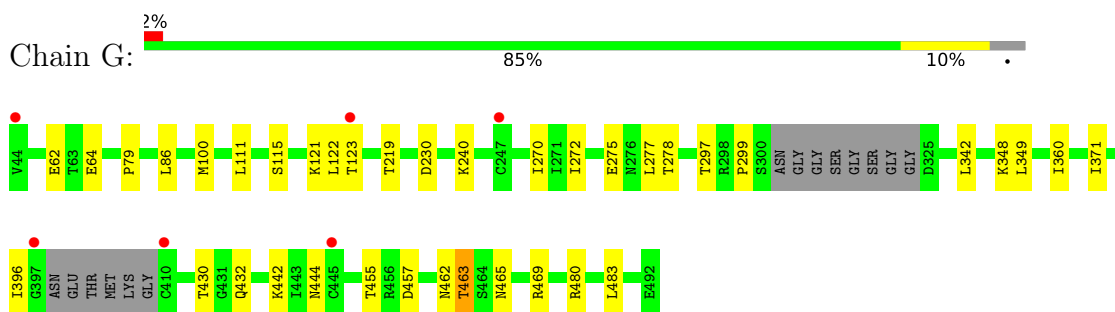
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	75	Total	O	0	0
			75	75		
6	H	60	Total	O	0	0
			60	60		
6	L	61	Total	O	0	0
			61	61		

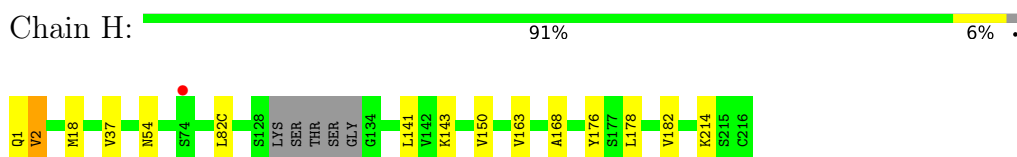
### 3 Residue-property plots [i](#)

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.

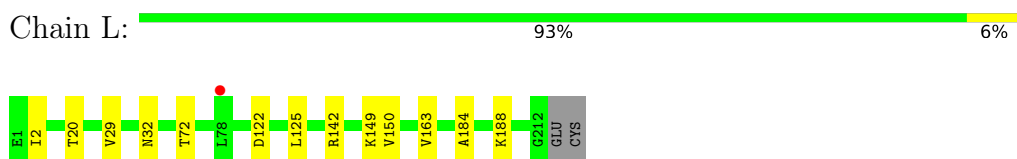
- Molecule 1: clade A/E 93TH057 HIV-1 gp120 core



- Molecule 2: HEAVY CHAIN OF ANTIBODY CH235.12



- Molecule 3: LIGHT CHAIN OF ANTIBODY CH235.12



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.66Å 69.87Å 127.27Å 90.00° 94.61° 90.00°	Depositor
Resolution (Å)	34.55 – 2.24 34.55 – 2.24	Depositor EDS
% Data completeness (in resolution range)	97.0 (34.55-2.24) 93.2 (34.55-2.24)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.10 (at 2.24Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.190 , 0.233 0.192 , 0.233	Depositor DCC
$R_{free}$ test set	1986 reflections (4.52%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	50.1	Xtrriage
Anisotropy	0.123	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 44.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6385	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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, EPE

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	G	0.34	0/2712	0.50	0/3682
2	H	0.35	0/1731	0.54	0/2356
3	L	0.35	0/1671	0.54	0/2272
All	All	0.34	0/6114	0.53	0/8310

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 [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	G	2656	0	2587	19	0
2	H	1685	0	1645	9	0
3	L	1635	0	1585	7	0
4	G	168	0	156	1	0
5	G	30	0	34	0	0
5	L	15	0	17	0	0
6	G	75	0	0	1	0
6	H	60	0	0	3	0
6	L	61	0	0	0	0
All	All	6385	0	6024	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 3.

The worst 5 of 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:G:299:PRO:HA	1:G:442:LYS:HD3	1.80	0.63
3:L:20:THR:HG23	3:L:72:THR:HG23	1.83	0.59
3:L:142:ARG:NH2	3:L:163:VAL:HG21	2.18	0.59
1:G:360:ILE:HD11	1:G:465:ASN:HD22	1.68	0.58
1:G:230:ASP:OD2	1:G:240:LYS:NZ	2.35	0.56

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	G	333/353 (94%)	319 (96%)	12 (4%)	2 (1%)	21	20
2	H	217/225 (96%)	210 (97%)	7 (3%)	0	100	100
3	L	209/213 (98%)	203 (97%)	6 (3%)	0	100	100
All	All	759/791 (96%)	732 (96%)	25 (3%)	2 (0%)	36	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	463	THR
1	G	79	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	G	303/311 (97%)	300 (99%)	3 (1%)	68	76
2	H	185/188 (98%)	182 (98%)	3 (2%)	55	65
3	L	182/184 (99%)	180 (99%)	2 (1%)	65	74
All	All	670/683 (98%)	662 (99%)	8 (1%)	63	72

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	150	VAL
3	L	149	LYS
2	H	37	VAL
2	H	2	VAL
2	H	150	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	137	ASN
3	L	152	ASN
3	L	32	ASN
3	L	92	ASN
3	L	100	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 oligosaccharides in this entry.

## 5.6 Ligand geometry

15 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	G	508	1	14,14,15	0.62	0	17,19,21	1.30	1 (5%)
4	NAG	G	509	1	14,14,15	0.42	0	17,19,21	0.45	0
5	EPE	G	513	-	15,15,15	0.88	1 (6%)	19,20,20	1.64	4 (21%)
4	NAG	G	504	1	14,14,15	0.82	2 (14%)	17,19,21	0.47	0
4	NAG	G	511	1	14,14,15	0.70	1 (7%)	17,19,21	0.88	1 (5%)
4	NAG	G	510	1	14,14,15	0.63	1 (7%)	17,19,21	0.68	1 (5%)
4	NAG	G	501	1	14,14,15	0.50	0	17,19,21	0.47	0
4	NAG	G	502	1	14,14,15	0.30	0	17,19,21	0.42	0
4	NAG	G	507	1	14,14,15	0.25	0	17,19,21	0.54	0
4	NAG	G	506	1	14,14,15	0.47	0	17,19,21	0.40	0
5	EPE	G	514	-	15,15,15	0.73	1 (6%)	19,20,20	1.65	5 (26%)
4	NAG	G	512	1	14,14,15	0.34	0	17,19,21	0.60	0
4	NAG	G	505	1	14,14,15	0.64	1 (7%)	17,19,21	0.76	1 (5%)
5	EPE	L	301	-	15,15,15	0.93	1 (6%)	19,20,20	1.67	5 (26%)
4	NAG	G	503	1	14,14,15	0.35	0	17,19,21	0.65	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	G	508	1	-	6/6/23/26	0/1/1/1
4	NAG	G	509	1	-	0/6/23/26	0/1/1/1
5	EPE	G	513	-	-	6/9/19/19	0/1/1/1
4	NAG	G	504	1	-	2/6/23/26	0/1/1/1
4	NAG	G	511	1	-	3/6/23/26	0/1/1/1
4	NAG	G	510	1	-	1/6/23/26	0/1/1/1
4	NAG	G	501	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	G	502	1	-	4/6/23/26	0/1/1/1
4	NAG	G	507	1	-	2/6/23/26	0/1/1/1
4	NAG	G	506	1	-	1/6/23/26	0/1/1/1
5	EPE	G	514	-	-	8/9/19/19	0/1/1/1
4	NAG	G	512	1	-	2/6/23/26	0/1/1/1
4	NAG	G	505	1	-	4/6/23/26	0/1/1/1
5	EPE	L	301	-	-	4/9/19/19	0/1/1/1
4	NAG	G	503	1	-	2/6/23/26	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	L	301	EPE	C10-S	3.21	1.82	1.77
5	G	513	EPE	C10-S	2.96	1.81	1.77
5	G	514	EPE	C10-S	2.42	1.81	1.77
4	G	504	NAG	O5-C1	2.25	1.47	1.43
4	G	511	NAG	O5-C1	2.12	1.47	1.43

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	508	NAG	C2-N2-C7	4.62	129.09	122.90
5	G	513	EPE	C5-N4-C3	4.53	118.60	108.84
5	G	514	EPE	C5-N4-C3	4.50	118.53	108.84
5	L	301	EPE	C5-N4-C3	3.86	117.16	108.84
5	G	513	EPE	C7-N4-C3	3.05	119.37	111.24

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	513	EPE	C8-C7-N4-C3
5	G	514	EPE	C9-C10-S-O1S
5	L	301	EPE	S-C10-C9-N1
4	G	508	NAG	O5-C5-C6-O6
4	G	508	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	508	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	G	339/353 (96%)	0.26	6 (1%) 67 69	42, 62, 106, 137	0
2	H	220/225 (97%)	0.06	1 (0%) 87 88	22, 57, 88, 130	1 (0%)
3	L	211/213 (99%)	0.12	1 (0%) 87 88	36, 61, 88, 105	0
All	All	770/791 (97%)	0.17	8 (1%) 79 81	22, 60, 97, 137	1 (0%)

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	397	GLY	3.8
1	G	44	VAL	3.5
1	G	410	CYS	3.1
1	G	445	CYS	2.5
1	G	247	CYS	2.5

### 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 oligosaccharides 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
4	NAG	G	511	14/15	0.28	0.15	93,110,117,117	0
4	NAG	G	508	14/15	0.46	0.17	88,98,101,102	0
4	NAG	G	512	14/15	0.49	0.14	101,117,120,121	0
4	NAG	G	501	14/15	0.52	0.14	91,109,112,113	0
4	NAG	G	505	14/15	0.66	0.16	89,102,104,105	0
4	NAG	G	502	14/15	0.67	0.16	92,106,119,120	0
4	NAG	G	503	14/15	0.68	0.14	72,87,92,93	0
5	EPE	L	301	15/15	0.71	0.21	127,130,152,154	0
4	NAG	G	509	14/15	0.72	0.18	91,104,111,114	0
5	EPE	G	514	15/15	0.80	0.22	135,137,142,143	0
4	NAG	G	507	14/15	0.81	0.12	72,81,87,90	0
4	NAG	G	510	14/15	0.87	0.10	58,72,76,81	0
4	NAG	G	506	14/15	0.91	0.09	49,59,63,69	0
4	NAG	G	504	14/15	0.92	0.08	48,54,62,64	0
5	EPE	G	513	15/15	0.95	0.10	59,60,69,74	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.