



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 9, 2025 – 07:22 pm BST

PDB ID : 9FYS / pdb\_00009fys  
Title : D11 mAbs bound to alpha-Bungarotoxin  
Authors : Wade, J.; Bohn, M.F.; Laustsen, A.H.; Morth, J.P.  
Deposited on : 2024-07-03  
Resolution : 1.32 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.

The types of validation reports are described at

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

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

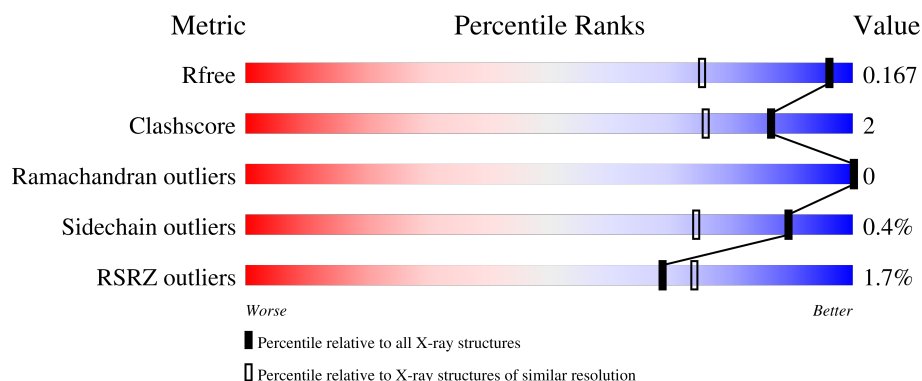
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.32 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))
$R_{free}$	164625	2202 (1.34-1.30)
Clashscore	180529	2378 (1.34-1.30)
Ramachandran outliers	177936	2325 (1.34-1.30)
Sidechain outliers	177891	2325 (1.34-1.30)
RSRZ outliers	164620	2199 (1.34-1.30)

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	C	121	<div> <div>2%</div> <div>97%</div> <div>..</div> </div>
1	M	121	<div> <div>%</div> <div>96%</div> <div>...</div> </div>
2	X	95	<div> <div>%</div> <div>68%</div> <div>6%</div> <div>24%</div> </div>
2	Z	95	<div> <div>%</div> <div>73%</div> <div>5%</div> <div>22%</div> </div>
3	B	144	<div> <div>%</div> <div>88%</div> <div>5%</div> <div>8%</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	I	144	<div><div></div><div>3%</div><div>87%</div><div>6%</div><div>8%</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10693 atoms, of which 4767 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 heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	119	Total	C	H	N	O	S	0	6	0
			1794	569	866	157	197	5			
1	M	120	Total	C	H	N	O	S	11	6	0
			1810	574	870	160	201	5			

- Molecule 2 is a protein called Alpha-bungarotoxin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	X	72	Total	C	H	N	O	S	0	1	0
			1067	333	525	95	103	11			
2	Z	74	Total	C	H	N	O	S	0	0	0
			1081	338	530	97	105	11			

- Molecule 3 is a protein called D11 mAbs Light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	I	133	Total	C	H	N	O	S	0	4	0
			1998	645	971	171	203	8			
3	B	133	Total	C	H	N	O	S	0	10	0
			2041	657	992	173	211	8			

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula:  $C_6H_{13}NO_4S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	Z	1	Total	C	H	N	O	S	
			25	6	13	1	4	1	
								0	0

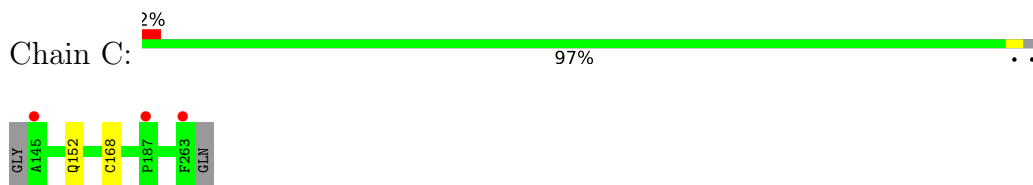
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	147	Total	O		
			147	147	0	0
5	X	93	Total	O		
			93	93	0	0
5	Z	87	Total	O		
			87	87	0	0
5	I	167	Total	O		
			167	167	0	0
5	M	185	Total	O		
			185	185	0	0
5	B	198	Total	O		
			198	198	0	0

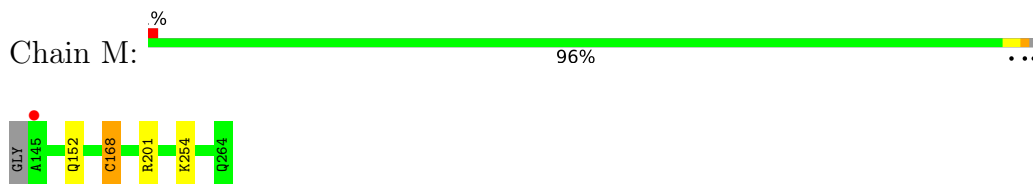
### 3 Residue-property plots [i](#)

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.

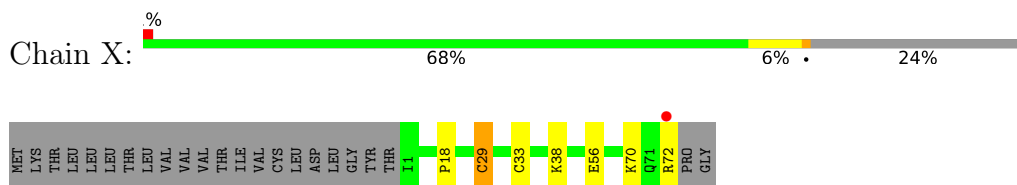
- Molecule 1: heavy chain



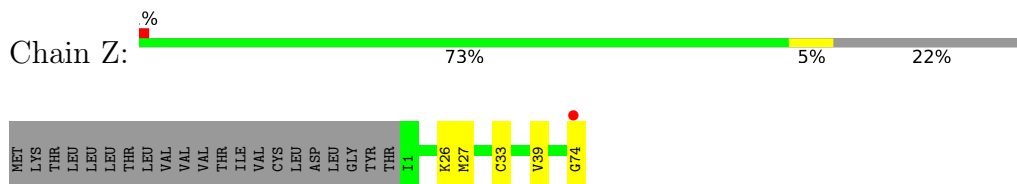
- Molecule 1: heavy chain



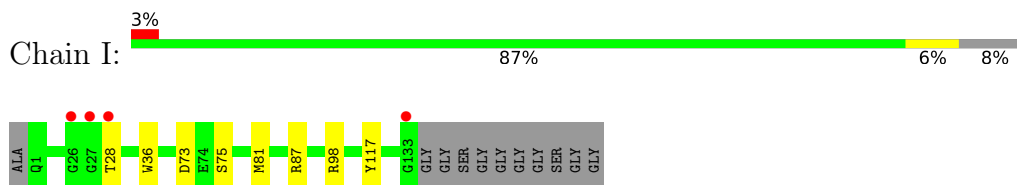
- Molecule 2: Alpha-bungarotoxin



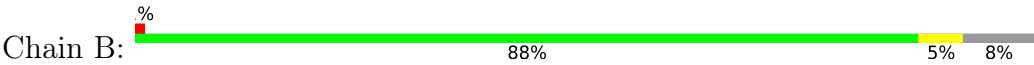
- Molecule 2: Alpha-bungarotoxin



- Molecule 3: D11 mAbs Light chain



- Molecule 3: D11 mAbs Light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.85Å 83.80Å 102.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.17 – 1.32 25.17 – 1.32	Depositor EDS
% Data completeness (in resolution range)	95.2 (25.17-1.32) 95.4 (25.17-1.32)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.97 (at 1.32Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.167 , 0.192 0.167 , 0.167	Depositor DCC
$R_{free}$ test set	10973 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.6	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.42 , 44.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.020 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	10693	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8412e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MES

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	C	0.81	0/973	0.82	0/1321
1	M	0.87	0/984	0.84	0/1334
2	X	0.89	0/558	0.97	2/758 (0.3%)
2	Z	0.86	0/565	0.93	0/767
3	B	0.88	1/1117 (0.1%)	0.90	0/1512
3	I	0.92	1/1067 (0.1%)	0.93	0/1444
All	All	0.87	2/5264 (0.0%)	0.89	2/7136 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	I	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	12	LYS	CE-NZ	5.24	1.65	1.49
3	I	117	TYR	CE1-CZ	-5.08	1.26	1.38

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	29	CYS	N-CA-C	5.22	118.45	110.20
2	X	18	PRO	N-CD-CG	-5.05	95.62	103.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	I	87	ARG	Sidechain

## 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	C	928	866	843	2	0
1	M	940	870	841	4	0
2	X	542	525	527	4	0
2	Z	551	530	532	3	0
3	B	1049	992	951	5	0
3	I	1027	971	966	3	0
4	Z	12	13	13	0	0
5	B	198	0	0	1	0
5	C	147	0	0	0	0
5	I	167	0	0	0	0
5	M	185	0	0	2	0
5	X	93	0	0	0	0
5	Z	87	0	0	2	0
All	All	5926	4767	4673	20	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 2.

All (20) 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:C:152:GLN:HG2	1:C:168[B]:CYS:SG	2.09	0.92
2:Z:74:GLY:OXT	5:Z:201:HOH:O	1.99	0.78
3:I:28:THR:O	3:I:98[B]:ARG:NH2	2.37	0.57
1:C:152:GLN:CG	1:C:168[B]:CYS:SG	2.93	0.52
2:X:70:LYS:HD3	3:B:113:TYR:CZ	2.45	0.52
1:M:152:GLN:CG	1:M:168[A]:CYS:SG	2.99	0.50
2:X:38:LYS:NZ	2:X:56:GLU:OE2	2.44	0.50
1:M:152:GLN:HG2	1:M:168[A]:CYS:SG	2.52	0.49
1:M:254:LYS:NZ	5:M:305:HOH:O	2.45	0.48
3:I:36:TRP:CE2	3:I:81[A]:MET:HB2	2.50	0.47

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:26:LYS:NZ	5:Z:203:HOH:O	2.46	0.46
3:B:15:GLY:HA2	3:B:87:ARG:NH2	2.30	0.46
3:I:73:ASP:OD1	3:I:75:SER:OG	2.27	0.45
3:B:15:GLY:HA2	3:B:87:ARG:HH21	1.85	0.42
2:X:72:ARG:HH11	2:X:72:ARG:HG3	1.84	0.42
2:Z:27:MET:HA	2:Z:39:VAL:O	2.19	0.42
3:B:36:TRP:CE2	3:B:81[A]:MET:HB2	2.55	0.42
2:X:29:CYS:HB3	2:X:33:CYS:HB2	1.92	0.41
1:M:201:ARG:NH1	5:M:311:HOH:O	2.53	0.41
3:B:46[A]:GLU:HG3	5:B:229:HOH:O	2.19	0.41

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	C	123/121 (102%)	119 (97%)	4 (3%)	0	100	100
1	M	124/121 (102%)	120 (97%)	4 (3%)	0	100	100
2	X	71/95 (75%)	69 (97%)	2 (3%)	0	100	100
2	Z	72/95 (76%)	72 (100%)	0	0	100	100
3	B	141/144 (98%)	137 (97%)	4 (3%)	0	100	100
3	I	135/144 (94%)	133 (98%)	2 (2%)	0	100	100
All	All	666/720 (92%)	650 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	C	112/107 (105%)	112 (100%)	0	100	100
1	M	113/107 (106%)	111 (98%)	2 (2%)	54	19
2	X	65/85 (76%)	65 (100%)	0	100	100
2	Z	65/85 (76%)	64 (98%)	1 (2%)	60	27
3	B	115/108 (106%)	115 (100%)	0	100	100
3	I	110/108 (102%)	110 (100%)	0	100	100
All	All	580/600 (97%)	577 (100%)	3 (0%)	89	67

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Z	33	CYS
1	M	168[A]	CYS
1	M	168[B]	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	184	GLN
1	C	185	GLN
3	I	39	GLN
1	M	185	GLN
1	M	200	GLN
3	B	39	GLN
3	B	65	GLN
3	B	100	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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	MES	Z	101	-	12,12,12	1.43	1 (8%)	14,16,16	1.75	3 (21%)

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	MES	Z	101	-	-	5/6/14/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Z	101	MES	C8-S	-4.55	1.71	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	Z	101	MES	O2S-S-C8	3.87	111.58	106.92
4	Z	101	MES	C5-N4-C3	3.20	116.03	108.83
4	Z	101	MES	O3S-S-C8	2.91	110.47	105.77

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	Z	101	MES	C8-C7-N4-C5
4	Z	101	MES	C7-C8-S-O3S
4	Z	101	MES	C8-C7-N4-C3
4	Z	101	MES	C7-C8-S-O1S
4	Z	101	MES	C7-C8-S-O2S

There are no ring outliers.

No monomer is involved in short contacts.

## 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	C	119/121 (98%)	0.04	3 (2%) 58 64	10, 28, 44, 73	3 (2%)
1	M	119/121 (98%)	-0.15	1 (0%) 82 86	11, 25, 39, 50	2 (1%)
2	X	72/95 (75%)	-0.14	1 (1%) 73 78	12, 24, 43, 72	1 (1%)
2	Z	74/95 (77%)	-0.17	1 (1%) 73 78	17, 24, 39, 58	0
3	B	133/144 (92%)	-0.40	1 (0%) 82 86	9, 21, 32, 76	5 (3%)
3	I	133/144 (92%)	0.03	4 (3%) 52 58	11, 25, 50, 86	2 (1%)
All	All	650/720 (90%)	-0.13	11 (1%) 69 74	9, 25, 44, 86	13 (2%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	133	GLY	6.6
1	C	263	PHE	4.9
1	M	145	ALA	4.8
1	C	145	ALA	4.7
2	Z	74	GLY	3.9
3	I	133	GLY	3.4
2	X	72	ARG	3.1
3	I	28	THR	3.1
3	I	27	GLY	2.3
1	C	187	PRO	2.1
3	I	26	GLY	2.1

### 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	MES	Z	101	12/12	0.82	0.14	35,63,82,93	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.