Full wwPDB X-ray Structure Validation Report (i)

Aug 27, 2023 – 12:35 AM EDT

PDB ID	:	3ESV
Title	:	Crystal structure of the engineered neutralizing antibody M18
Authors	:	Monzingo, A.F.; Leysath, C.E.; Barnett, J.; Iverson, B.L.; Georgiou, G.; Robertus, J.D.
Deposited on	:	2008-10-06
Resolution	:	2.00 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 (i) 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 (1)) were used in the production of this report:

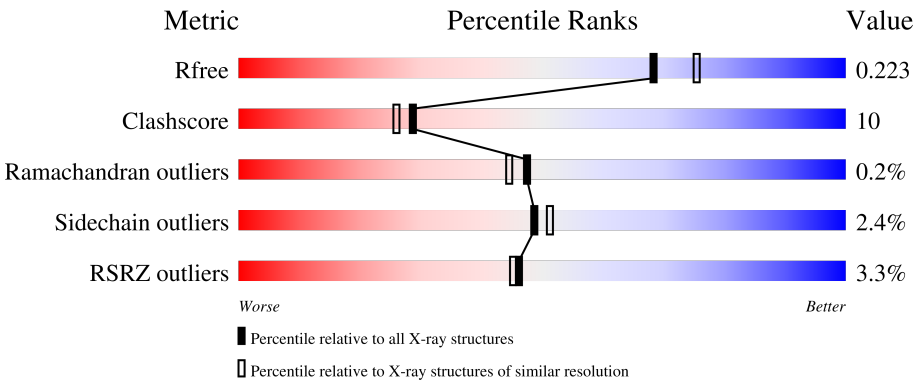
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 >=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 <=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	F	252	3% 73% 16% • 9%
1	G	252	3% 72% 17% • 10%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3807 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 Antibody M18 light chain and antibody M18 heavy chain linked with a synthetic (GGGGS)4 linker.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	F	229	1762	1105	299	350	8	0	0	1
1	G	228	1759	1103	300	348	8	0	0	1

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-4	MET	-	expression tag	PDB 3ESV
F	-3	ALA	-	expression tag	PDB 3ESV
F	-2	ASP	-	expression tag	PDB 3ESV
F	-1	TYR	-	expression tag	PDB 3ESV
F	0	LYS	-	expression tag	PDB 3ESV
F	21	VAL	ILE	engineered mutation	PDB 3ESV
F	46	PHE	LEU	engineered mutation	PDB 3ESV
F	56	PRO	SER	engineered mutation	PDB 3ESV
F	76	ASN	SER	engineered mutation	PDB 3ESV
F	78	LEU	GLN	engineered mutation	PDB 3ESV
F	94	PRO	LEU	engineered mutation	PDB 3ESV
F	109	GLY	-	linker	PDB 3ESV
F	110	GLY	-	linker	PDB 3ESV
F	111	GLY	-	linker	PDB 3ESV
F	112	GLY	-	linker	PDB 3ESV
F	113	SER	-	linker	PDB 3ESV
F	114	GLY	-	linker	PDB 3ESV
F	115	GLY	-	linker	PDB 3ESV
F	116	GLY	-	linker	PDB 3ESV
F	117	GLY	-	linker	PDB 3ESV
F	118	SER	-	linker	PDB 3ESV
F	119	GLY	-	linker	PDB 3ESV
F	120	GLY	-	linker	PDB 3ESV
F	121	GLY	-	linker	PDB 3ESV

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Chain	Residue	Modelled	Actual	Comment	Reference
F	122	GLY	-	linker	PDB 3ESV
F	123	SER	-	linker	PDB 3ESV
F	124	GLY	-	linker	PDB 3ESV
F	125	GLY	-	linker	PDB 3ESV
F	126	GLY	-	linker	PDB 3ESV
F	127	GLY	-	linker	PDB 3ESV
F	128	SER	-	linker	PDB 3ESV
F	1030	ASN	SER	engineered mutation	PDB 3ESV
F	1057	SER	THR	engineered mutation	PDB 3ESV
F	1064	GLU	LYS	engineered mutation	PDB 3ESV
F	1068	ILE	THR	engineered mutation	PDB 3ESV
G	-4	MET	-	expression tag	PDB 3ESV
G	-3	ALA	-	expression tag	PDB 3ESV
G	-2	ASP	-	expression tag	PDB 3ESV
G	-1	TYR	-	expression tag	PDB 3ESV
G	0	LYS	-	expression tag	PDB 3ESV
G	21	VAL	ILE	engineered mutation	PDB 3ESV
G	46	PHE	LEU	engineered mutation	PDB 3ESV
G	56	PRO	SER	engineered mutation	PDB 3ESV
G	76	ASN	SER	engineered mutation	PDB 3ESV
G	78	LEU	GLN	engineered mutation	PDB 3ESV
G	94	PRO	LEU	engineered mutation	PDB 3ESV
G	109	GLY	-	linker	PDB 3ESV
G	110	GLY	-	linker	PDB 3ESV
G	111	GLY	-	linker	PDB 3ESV
G	112	GLY	-	linker	PDB 3ESV
G	113	SER	-	linker	PDB 3ESV
G	114	GLY	-	linker	PDB 3ESV
G	115	GLY	-	linker	PDB 3ESV
G	116	GLY	-	linker	PDB 3ESV
G	117	GLY	-	linker	PDB 3ESV
G	118	SER	-	linker	PDB 3ESV
G	119	GLY	-	linker	PDB 3ESV
G	120	GLY	-	linker	PDB 3ESV
G	121	GLY	-	linker	PDB 3ESV
G	122	GLY	-	linker	PDB 3ESV
G	123	SER	-	linker	PDB 3ESV
G	124	GLY	-	linker	PDB 3ESV
G	125	GLY	-	linker	PDB 3ESV
G	126	GLY	-	linker	PDB 3ESV
G	127	GLY	-	linker	PDB 3ESV
G	128	SER	-	linker	PDB 3ESV

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1030	ASN	SER	engineered mutation	PDB 3ESV
G	1057	SER	THR	engineered mutation	PDB 3ESV
G	1064	GLU	LYS	engineered mutation	PDB 3ESV
G	1068	ILE	THR	engineered mutation	PDB 3ESV

- Molecule 2 is water.

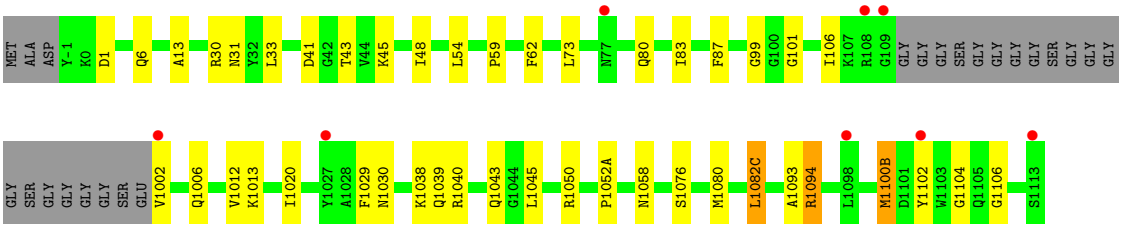
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	F	147	147	147	0	0
			Total	O		
2	G	139	139	139	0	0

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.

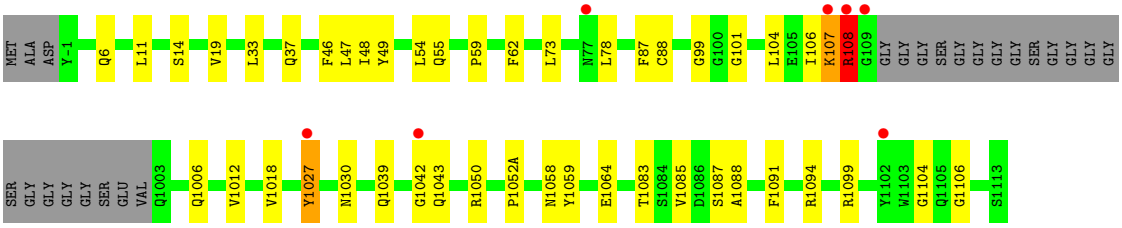
• Molecule 1: Antibody M18 light chain and antibody M18 heavy chain linked with a synthetic (GGGGS)4 linker

Chain F:



• Molecule 1: Antibody M18 light chain and antibody M18 heavy chain linked with a synthetic (GGGGS)4 linker

Chain G:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	36.07Å 54.21Å 61.95Å 71.80° 75.58° 71.25°	Depositor
Resolution (Å)	20.00 – 2.00 31.48 – 2.01	Depositor EDS
% Data completeness (in resolution range)	90.0 (20.00-2.00) 93.3 (31.48-2.01)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.60 (at 2.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.194 , 0.229 0.191 , 0.223	Depositor DCC
R_{free} test set	1321 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	16.1	Xtriage
Anisotropy	0.527	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 54.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.088 for h,h-k,h-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	3807	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.13% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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)

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	F	0.35	0/1802	0.65	0/2440
1	G	0.35	0/1799	0.64	0/2435
All	All	0.35	0/3601	0.64	0/4875

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	F	1762	0	1681	28	0
1	G	1759	0	1684	39	0
2	F	147	0	0	0	0
2	G	139	0	0	0	0
All	All	3807	0	3365	67	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 10.

All (67) 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:55:GLN:HE22	1:G:1099:ARG:HH12	1.14	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1050:ARG:HE	1:F:1058:ASN:HD22	1.26	0.82
1:G:1012:VAL:HG11	1:G:1018:VAL:HG12	1.67	0.75
1:G:1083:THR:OG1	1:G:1085:VAL:HG12	1.88	0.73
1:G:1050:ARG:HE	1:G:1058:ASN:HD22	1.37	0.70
1:F:83:ILE:HD11	1:F:106:ILE:HD11	1.75	0.68
1:G:1027:TYR:HD2	1:G:1027:TYR:H	1.41	0.67
1:G:48:ILE:HG12	1:G:54:LEU:HD23	1.78	0.66
1:F:1030:ASN:HA	1:F:1052(A):PRO:HB2	1.79	0.65
1:F:41:ASP:OD1	1:F:43:THR:HG22	1.96	0.65
1:F:1093:ALA:HB3	1:F:1100(B):MET:HG2	1.79	0.64
1:G:14:SER:HA	1:G:107:LYS:HD2	1.79	0.64
1:G:11:LEU:HD21	1:G:19:VAL:HG13	1.80	0.63
1:F:1050:ARG:HE	1:F:1058:ASN:ND2	1.97	0.62
1:F:1006:GLN:HE21	1:F:1104:GLY:HA3	1.66	0.60
1:G:1012:VAL:HG11	1:G:1018:VAL:CG1	2.32	0.59
1:G:1006:GLN:HE21	1:G:1104:GLY:HA3	1.73	0.54
1:G:106:ILE:HG22	1:G:107:LYS:HD3	1.91	0.53
1:G:1039:GLN:O	1:G:1088:ALA:HB1	2.09	0.53
1:G:1030:ASN:HA	1:G:1052(A):PRO:HB2	1.91	0.52
1:G:55:GLN:NE2	1:G:1099:ARG:HH12	1.95	0.52
1:F:1039:GLN:HB2	1:F:1045:LEU:HD23	1.91	0.52
1:F:1094:ARG:HG2	1:F:1094:ARG:HH11	1.75	0.52
1:G:107:LYS:HE2	1:G:108:ARG:CZ	2.40	0.51
1:F:6:GLN:HE22	1:F:87:PHE:HA	1.75	0.51
1:G:55:GLN:HE22	1:G:1099:ARG:NH1	1.95	0.51
1:F:1040:ARG:HB2	1:F:1043:GLN:HB2	1.93	0.50
1:F:59:PRO:HG2	1:F:62:PHE:CD1	2.47	0.50
1:G:46:PHE:CZ	1:G:49:TYR:HB2	2.47	0.50
1:G:48:ILE:HD12	1:G:73:LEU:HD13	1.93	0.50
1:F:1006:GLN:NE2	1:F:1106:GLY:H	2.10	0.50
1:G:1006:GLN:NE2	1:G:1106:GLY:H	2.11	0.48
1:G:107:LYS:HG2	1:G:108:ARG:CG	2.43	0.48
1:F:1012:VAL:HG21	1:F:1082(C):LEU:HD23	1.95	0.48
1:G:46:PHE:HZ	1:G:49:TYR:HB2	1.77	0.48
1:G:6:GLN:HE21	1:G:99:GLY:HA3	1.79	0.47
1:F:80:GLN:O	1:F:83:ILE:HD13	2.14	0.47
1:F:1:ASP:OD1	1:F:1:ASP:C	2.54	0.46
1:G:6:GLN:HE22	1:G:87:PHE:HA	1.81	0.46
1:G:6:GLN:NE2	1:G:101:GLY:H	2.14	0.46
1:G:59:PRO:HG2	1:G:62:PHE:CD1	2.51	0.45
1:G:14:SER:CA	1:G:107:LYS:HD2	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:78:LEU:HD11	1:G:104:LEU:HD21	1.99	0.45
1:G:1087:SER:O	1:G:1088:ALA:HB2	2.17	0.45
1:F:1002:VAL:HA	1:F:1102:TYR:OH	2.17	0.45
1:G:33:LEU:HD21	1:G:88:CYS:HB2	1.99	0.44
1:F:1038:LYS:HE2	1:F:1040:ARG:HD2	2.00	0.44
1:G:107:LYS:HD3	1:G:107:LYS:N	2.32	0.44
1:F:1029:PHE:CD2	1:F:1076:SER:HA	2.53	0.44
1:F:33:LEU:C	1:F:33:LEU:HD13	2.39	0.43
1:F:48:ILE:HG12	1:F:54:LEU:HD23	2.00	0.43
1:G:107:LYS:HG2	1:G:108:ARG:HG3	2.00	0.43
1:F:1093:ALA:CB	1:F:1100(B):MET:HG2	2.47	0.43
1:F:13:ALA:O	1:F:106:ILE:HA	2.19	0.43
1:G:1006:GLN:HE22	1:G:1091:PHE:HA	1.83	0.43
1:G:107:LYS:C	1:G:108:ARG:HG3	2.40	0.42
1:F:1020:ILE:HD11	1:F:1080:MET:HE2	2.01	0.42
1:G:1027:TYR:CD2	1:G:1027:TYR:N	2.84	0.42
1:F:30:ARG:O	1:F:31:ASN:HB2	2.20	0.42
1:G:1042:GLY:O	1:G:1043:GLN:HB2	2.19	0.42
1:G:37:GLN:HB2	1:G:47:LEU:HD11	2.02	0.41
1:G:107:LYS:O	1:G:108:ARG:HG3	2.19	0.41
1:F:48:ILE:HD12	1:F:73:LEU:HD13	2.01	0.41
1:G:33:LEU:C	1:G:33:LEU:HD13	2.41	0.41
1:G:1059:TYR:HB2	1:G:1064:GLU:HG2	2.03	0.41
1:F:6:GLN:HE21	1:F:99:GLY:HA3	1.85	0.41
1:F:6:GLN:NE2	1:F:101:GLY:H	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	F	225/252 (89%)	223 (99%)	2 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	224/252 (89%)	218 (97%)	5 (2%)	1 (0%)	34	30
All	All	449/504 (89%)	441 (98%)	7 (2%)	1 (0%)	47	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	108	ARG

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	F	191/201 (95%)	186 (97%)	5 (3%)	46	48
1	G	191/201 (95%)	187 (98%)	4 (2%)	53	57
All	All	382/402 (95%)	373 (98%)	9 (2%)	49	51

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	45	LYS
1	F	1013	LYS
1	F	1082(C)	LEU
1	F	1094	ARG
1	F	1100(B)	MET
1	G	107	LYS
1	G	108	ARG
1	G	1027	TYR
1	G	1094	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	6	GLN

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Mol	Chain	Res	Type
1	F	1006	GLN
1	F	1058	ASN
1	G	6	GLN
1	G	31	ASN
1	G	55	GLN
1	G	76	ASN
1	G	80	GLN
1	G	1006	GLN
1	G	1058	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)

There are no ligands in this entry.

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, 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	F	229/252 (90%)	0.13	8 (3%)	44	43	8, 17, 26, 32	0
1	G	228/252 (90%)	0.08	7 (3%)	49	48	9, 16, 25, 36	0
All	All	457/504 (90%)	0.11	15 (3%)	46	45	8, 16, 26, 36	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	109	GLY	7.0
1	F	109	GLY	4.7
1	G	108	ARG	3.9
1	F	108	ARG	3.4
1	F	1027	TYR	3.1
1	G	77	ASN	2.8
1	F	1102	TYR	2.8
1	G	1027	TYR	2.7
1	F	1113	SER	2.6
1	G	1102	TYR	2.5
1	F	77	ASN	2.3
1	G	1042	GLY	2.3
1	F	1002	VAL	2.3
1	G	107	LYS	2.3
1	F	1098	LEU	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 monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.