Full wwPDB X-ray Structure Validation Report ⓘ

Oct 27, 2023 – 02:39 AM EDT

PDB ID	:	3PL7
Title	:	Crystal structure of Bcl-xL in complex with the BaxBH3 domain
Authors	:	Czabotar, P.E.; Colman, P.M.
Deposited on	:	2010-11-14
Resolution	:	2.61 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 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:

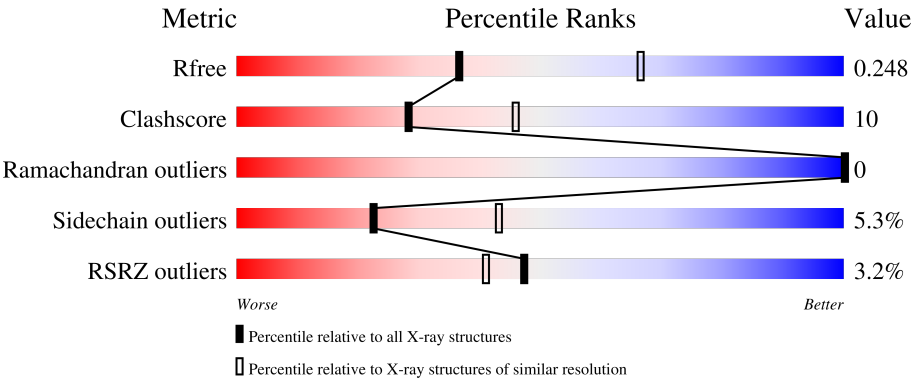
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.61 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	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 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	A	181	3% 61% 14% . 22%
1	B	181	2% 63% 12% . 22%
2	C	34	50% 26% 24%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2540 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 Bcl-2-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	7	0	0
			1149	735	192	219	3			
1	B	141	Total	C	N	O	S	11	0	0
			1148	734	191	220	3			

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	expression tag	UNP Q07817
A	-2	SER	-	expression tag	UNP Q07817
A	-1	MET	-	expression tag	UNP Q07817
A	0	ALA	-	expression tag	UNP Q07817
A	?	-	MET	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ILE	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	TRP	deletion	UNP Q07817
A	?	-	HIS	deletion	UNP Q07817
A	?	-	LEU	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ASP	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	VAL	deletion	UNP Q07817

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASN	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	HIS	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	LEU	deletion	UNP Q07817
A	?	-	ASP	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ARG	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	VAL	deletion	UNP Q07817
A	?	-	ILE	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	MET	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	210	LEU	-	expression tag	UNP Q07817
A	211	GLU	-	expression tag	UNP Q07817
A	212	HIS	-	expression tag	UNP Q07817
A	213	HIS	-	expression tag	UNP Q07817
A	214	HIS	-	expression tag	UNP Q07817
A	215	HIS	-	expression tag	UNP Q07817
A	216	HIS	-	expression tag	UNP Q07817
A	217	HIS	-	expression tag	UNP Q07817
B	-3	MET	-	expression tag	UNP Q07817
B	-2	SER	-	expression tag	UNP Q07817
B	-1	MET	-	expression tag	UNP Q07817
B	0	ALA	-	expression tag	UNP Q07817
B	?	-	MET	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ILE	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	SER	deletion	UNP Q07817
B	?	-	TRP	deletion	UNP Q07817
B	?	-	HIS	deletion	UNP Q07817
B	?	-	LEU	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ASP	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	VAL	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	HIS	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	LEU	deletion	UNP Q07817
B	?	-	ASP	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ARG	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	VAL	deletion	UNP Q07817
B	?	-	ILE	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	MET	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	210	LEU	-	expression tag	UNP Q07817
B	211	GLU	-	expression tag	UNP Q07817
B	212	HIS	-	expression tag	UNP Q07817
B	213	HIS	-	expression tag	UNP Q07817
B	214	HIS	-	expression tag	UNP Q07817
B	215	HIS	-	expression tag	UNP Q07817
B	216	HIS	-	expression tag	UNP Q07817
B	217	HIS	-	expression tag	UNP Q07817

- Molecule 2 is a protein called Apoptosis regulator BAX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	26	Total	C	N	O	S	7	0	0
			205	123	37	42	3			

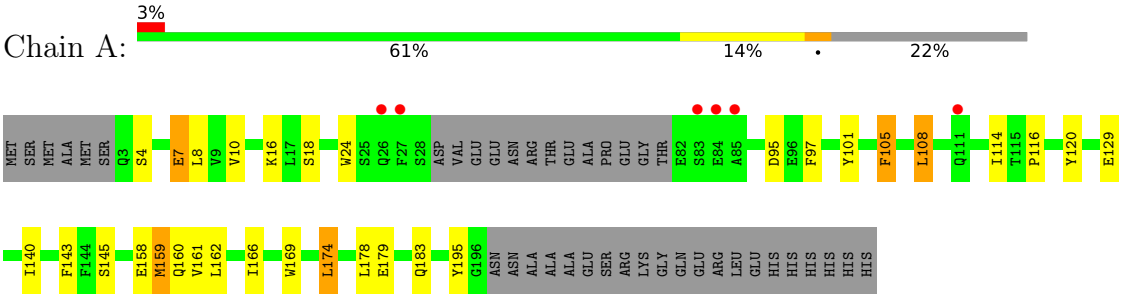
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	14	Total O 14 14	0	0
3	C	6	Total O 6 6	0	0
3	B	18	Total O 18 18	0	0

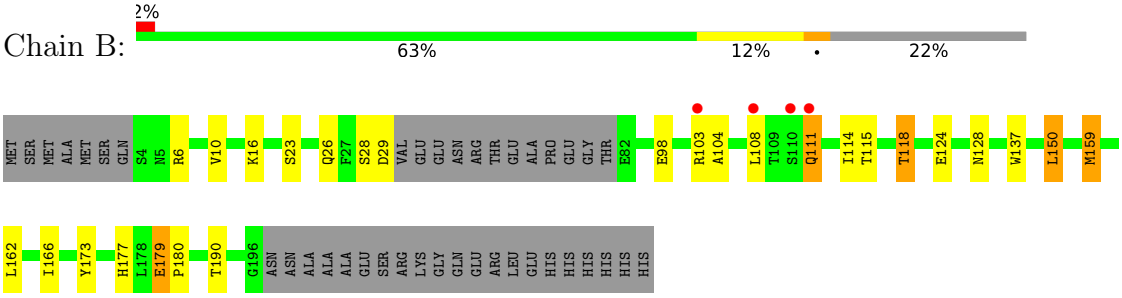
3 Residue-property plots (i)

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.

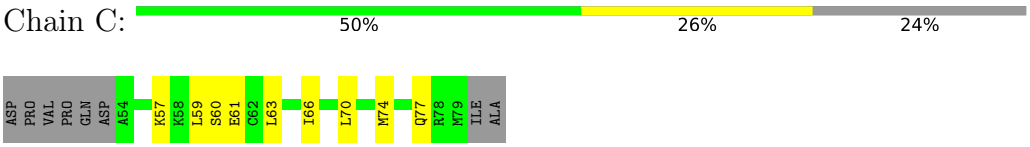
• Molecule 1: Bcl-2-like protein 1



• Molecule 1: Bcl-2-like protein 1



• Molecule 2: Apoptosis regulator BAX



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	70.25Å 99.05Å 113.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.54 – 2.61 33.54 – 2.61	Depositor EDS
% Data completeness (in resolution range)	99.3 (33.54-2.61) 99.3 (33.54-2.61)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.36 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.186 , 0.249 0.184 , 0.248	Depositor DCC
R_{free} test set	587 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	39.0	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 57.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	2540	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.68% 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

5.1 Standard geometry

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	A	0.41	0/1177	0.52	0/1592
1	B	0.42	0/1176	0.53	0/1591
2	C	0.43	0/204	0.58	0/268
All	All	0.42	0/2557	0.53	0/3451

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	A	1149	0	1082	26	0
1	B	1148	0	1078	19	0
2	C	205	0	212	11	0
3	A	14	0	0	0	0
3	B	18	0	0	0	0
3	C	6	0	0	0	0
All	All	2540	0	2372	47	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 (47) 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:B:115:THR:H	1:B:118:THR:HG23	1.37	0.89
1:A:4:SER:HA	1:A:7:GLU:HG3	1.65	0.78
1:B:115:THR:H	1:B:118:THR:CG2	2.00	0.74
1:A:97:PHE:CE2	2:C:66:ILE:HG22	2.27	0.70
2:C:77:GLN:NE2	1:B:103:ARG:HH22	1.90	0.70
1:B:159:MET:HB3	1:B:162:LEU:HD13	1.75	0.68
1:A:158:GLU:HA	1:A:160:GLN:NE2	2.11	0.65
1:B:150:LEU:HB3	1:B:166:ILE:HD13	1.80	0.64
2:C:70:LEU:O	2:C:74:MET:HG2	1.99	0.63
1:B:173:TYR:CE2	1:B:177:HIS:HD2	2.21	0.59
1:A:97:PHE:HE1	1:A:105:PHE:HE2	1.50	0.59
2:C:57:LYS:O	2:C:61:GLU:HG3	2.05	0.57
1:A:105:PHE:CZ	1:A:145:SER:HB3	2.39	0.57
1:A:101:TYR:CD2	2:C:66:ILE:HG23	2.41	0.56
1:B:111:GLN:O	1:B:111:GLN:HG3	2.06	0.55
1:A:140:ILE:O	1:A:143:PHE:HB3	2.07	0.55
1:B:159:MET:CB	1:B:162:LEU:HD13	2.36	0.54
1:B:28:SER:O	1:B:29:ASP:HB2	2.08	0.53
1:A:195:TYR:CE2	2:C:74:MET:HG3	2.44	0.53
1:A:105:PHE:HZ	1:A:145:SER:HB3	1.75	0.52
1:A:129:GLU:HB3	2:C:60:SER:OG	2.09	0.52
1:A:101:TYR:CE2	2:C:66:ILE:HG23	2.44	0.52
1:B:179:GLU:HB3	1:B:180:PRO:HD3	1.92	0.51
1:A:114:ILE:HG22	1:A:159:MET:HE3	1.91	0.50
1:A:97:PHE:CE2	2:C:66:ILE:CG2	2.95	0.49
1:B:137:TRP:HE1	1:B:190:THR:HG22	1.75	0.49
1:A:114:ILE:HG22	1:A:159:MET:CE	2.43	0.49
1:A:97:PHE:CE1	1:A:105:PHE:HE2	2.31	0.48
1:B:114:ILE:HA	1:B:118:THR:HG21	1.96	0.48
1:B:104:ALA:O	1:B:108:LEU:HG	2.15	0.47
1:B:16:LYS:NZ	1:B:98:GLU:OE2	2.46	0.46
1:A:179:GLU:O	1:A:183:GLN:HG2	2.17	0.45
1:A:16:LYS:HD3	1:A:16:LYS:HA	1.73	0.44
1:A:162:LEU:O	1:A:166:ILE:HG13	2.18	0.44
1:B:23:SER:O	1:B:26:GLN:HB3	2.17	0.44
1:A:16:LYS:NZ	1:A:95:ASP:OD1	2.52	0.42
1:A:97:PHE:CE1	1:A:105:PHE:CE2	3.08	0.42
1:B:6:ARG:NH1	1:B:10:VAL:HG21	2.35	0.42
1:A:97:PHE:HE1	1:A:105:PHE:CE2	2.34	0.42
1:A:10:VAL:HG13	1:A:24:TRP:CE2	2.55	0.42
2:C:77:GLN:HE21	1:B:103:ARG:HH22	1.64	0.41
1:B:124:GLU:HG2	1:B:128:ASN:ND2	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:LEU:HD12	1:B:150:LEU:HA	1.80	0.41
1:A:120:TYR:HB2	1:A:169:TRP:CZ2	2.56	0.41
1:A:108:LEU:HD22	2:C:59:LEU:HD11	2.04	0.40
1:A:116:PRO:HA	1:A:162:LEU:HD21	2.02	0.40
1:A:174:LEU:HD23	1:A:178:LEU:HB2	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	A	137/181 (76%)	133 (97%)	4 (3%)	0	100	100
1	B	137/181 (76%)	133 (97%)	4 (3%)	0	100	100
2	C	24/34 (71%)	24 (100%)	0	0	100	100
All	All	298/396 (75%)	290 (97%)	8 (3%)	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	A	121/154 (79%)	113 (93%)	8 (7%)	16	32
1	B	121/154 (79%)	116 (96%)	5 (4%)	30	55

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	C	24/31 (77%)	23 (96%)	1 (4%)	30 53
All	All	266/339 (78%)	252 (95%)	14 (5%)	22 43

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	8	LEU
1	A	18	SER
1	A	105	PHE
1	A	108	LEU
1	A	159	MET
1	A	161	VAL
1	A	174	LEU
2	C	63	LEU
1	B	111	GLN
1	B	118	THR
1	B	150	LEU
1	B	159	MET
1	B	179	GLU

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

Mol	Chain	Res	Type
2	C	77	GLN
1	B	177	HIS

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

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^{th} 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	A	141/181 (77%)	-0.06	6 (4%) 35 29	19, 41, 76, 90	4 (2%)
1	B	141/181 (77%)	-0.19	4 (2%) 53 47	19, 39, 80, 97	6 (4%)
2	C	26/34 (76%)	0.04	0 100 100	24, 37, 69, 92	2 (7%)
All	All	308/396 (77%)	-0.11	10 (3%) 47 41	19, 40, 78, 97	12 (3%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	111	GLN	4.6
1	A	27	PHE	4.4
1	A	83	SER	3.1
1	A	111	GLN	3.0
1	A	84	GLU	2.5
1	B	103	ARG	2.3
1	A	26	GLN	2.2
1	A	85	ALA	2.1
1	B	110	SER	2.1
1	B	108	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.