



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 06:27 PM EDT

PDB ID : 6AR7  
Title : Crystal structure of a putative uncharacterized protein from Burkholderia thailandensis  
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)  
Deposited on : 2017-08-21  
Resolution : 2.10 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>.

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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	:	2.37.1
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)	:	2.37.1

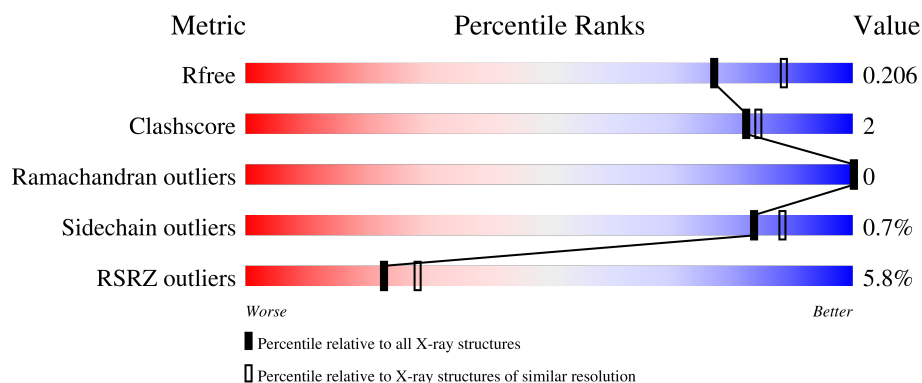
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	A	227	<div> <div>4%</div> <div>83%</div> <div>7%</div> <div>10%</div> </div>
1	B	227	<div> <div>5%</div> <div>86%</div> <div>•</div> <div>9%</div> </div>
1	C	227	<div> <div>5%</div> <div>87%</div> <div>•</div> <div>9%</div> </div>
1	D	227	<div> <div>6%</div> <div>85%</div> <div>•</div> <div>11%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7093 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	Se	0	7	0
			1645	1008	324	296	4	13			
1	B	206	Total	C	N	O	S	Se	0	7	0
			1659	1016	323	303	4	13			
1	C	207	Total	C	N	O	S	Se	0	5	0
			1624	998	315	294	4	13			
1	D	203	Total	C	N	O	S	Se	0	4	0
			1593	978	304	294	4	13			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	MSE	-	expression tag	UNP Q2T081
A	13	ALA	-	expression tag	UNP Q2T081
A	14	HIS	-	expression tag	UNP Q2T081
A	15	HIS	-	expression tag	UNP Q2T081
A	16	HIS	-	expression tag	UNP Q2T081
A	17	HIS	-	expression tag	UNP Q2T081
A	18	HIS	-	expression tag	UNP Q2T081
A	19	HIS	-	expression tag	UNP Q2T081
A	20	MSE	-	expression tag	UNP Q2T081
A	21	GLY	-	expression tag	UNP Q2T081
A	22	THR	-	expression tag	UNP Q2T081
A	23	LEU	-	expression tag	UNP Q2T081
A	24	GLU	-	expression tag	UNP Q2T081
A	25	ALA	-	expression tag	UNP Q2T081
A	26	GLN	-	expression tag	UNP Q2T081
A	27	THR	-	expression tag	UNP Q2T081
A	28	GLN	-	expression tag	UNP Q2T081
A	29	GLY	-	expression tag	UNP Q2T081
A	30	PRO	-	expression tag	UNP Q2T081
A	31	GLY	-	expression tag	UNP Q2T081
A	32	SER	-	expression tag	UNP Q2T081

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Chain	Residue	Modelled	Actual	Comment	Reference
A	33	MSE	-	expression tag	UNP Q2T081
A	34	ALA	-	expression tag	UNP Q2T081
B	12	MSE	-	expression tag	UNP Q2T081
B	13	ALA	-	expression tag	UNP Q2T081
B	14	HIS	-	expression tag	UNP Q2T081
B	15	HIS	-	expression tag	UNP Q2T081
B	16	HIS	-	expression tag	UNP Q2T081
B	17	HIS	-	expression tag	UNP Q2T081
B	18	HIS	-	expression tag	UNP Q2T081
B	19	HIS	-	expression tag	UNP Q2T081
B	20	MSE	-	expression tag	UNP Q2T081
B	21	GLY	-	expression tag	UNP Q2T081
B	22	THR	-	expression tag	UNP Q2T081
B	23	LEU	-	expression tag	UNP Q2T081
B	24	GLU	-	expression tag	UNP Q2T081
B	25	ALA	-	expression tag	UNP Q2T081
B	26	GLN	-	expression tag	UNP Q2T081
B	27	THR	-	expression tag	UNP Q2T081
B	28	GLN	-	expression tag	UNP Q2T081
B	29	GLY	-	expression tag	UNP Q2T081
B	30	PRO	-	expression tag	UNP Q2T081
B	31	GLY	-	expression tag	UNP Q2T081
B	32	SER	-	expression tag	UNP Q2T081
B	33	MSE	-	expression tag	UNP Q2T081
B	34	ALA	-	expression tag	UNP Q2T081
C	12	MSE	-	expression tag	UNP Q2T081
C	13	ALA	-	expression tag	UNP Q2T081
C	14	HIS	-	expression tag	UNP Q2T081
C	15	HIS	-	expression tag	UNP Q2T081
C	16	HIS	-	expression tag	UNP Q2T081
C	17	HIS	-	expression tag	UNP Q2T081
C	18	HIS	-	expression tag	UNP Q2T081
C	19	HIS	-	expression tag	UNP Q2T081
C	20	MSE	-	expression tag	UNP Q2T081
C	21	GLY	-	expression tag	UNP Q2T081
C	22	THR	-	expression tag	UNP Q2T081
C	23	LEU	-	expression tag	UNP Q2T081
C	24	GLU	-	expression tag	UNP Q2T081
C	25	ALA	-	expression tag	UNP Q2T081
C	26	GLN	-	expression tag	UNP Q2T081
C	27	THR	-	expression tag	UNP Q2T081
C	28	GLN	-	expression tag	UNP Q2T081

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Chain	Residue	Modelled	Actual	Comment	Reference
C	29	GLY	-	expression tag	UNP Q2T081
C	30	PRO	-	expression tag	UNP Q2T081
C	31	GLY	-	expression tag	UNP Q2T081
C	32	SER	-	expression tag	UNP Q2T081
C	33	MSE	-	expression tag	UNP Q2T081
C	34	ALA	-	expression tag	UNP Q2T081
D	12	MSE	-	expression tag	UNP Q2T081
D	13	ALA	-	expression tag	UNP Q2T081
D	14	HIS	-	expression tag	UNP Q2T081
D	15	HIS	-	expression tag	UNP Q2T081
D	16	HIS	-	expression tag	UNP Q2T081
D	17	HIS	-	expression tag	UNP Q2T081
D	18	HIS	-	expression tag	UNP Q2T081
D	19	HIS	-	expression tag	UNP Q2T081
D	20	MSE	-	expression tag	UNP Q2T081
D	21	GLY	-	expression tag	UNP Q2T081
D	22	THR	-	expression tag	UNP Q2T081
D	23	LEU	-	expression tag	UNP Q2T081
D	24	GLU	-	expression tag	UNP Q2T081
D	25	ALA	-	expression tag	UNP Q2T081
D	26	GLN	-	expression tag	UNP Q2T081
D	27	THR	-	expression tag	UNP Q2T081
D	28	GLN	-	expression tag	UNP Q2T081
D	29	GLY	-	expression tag	UNP Q2T081
D	30	PRO	-	expression tag	UNP Q2T081
D	31	GLY	-	expression tag	UNP Q2T081
D	32	SER	-	expression tag	UNP Q2T081
D	33	MSE	-	expression tag	UNP Q2T081
D	34	ALA	-	expression tag	UNP Q2T081

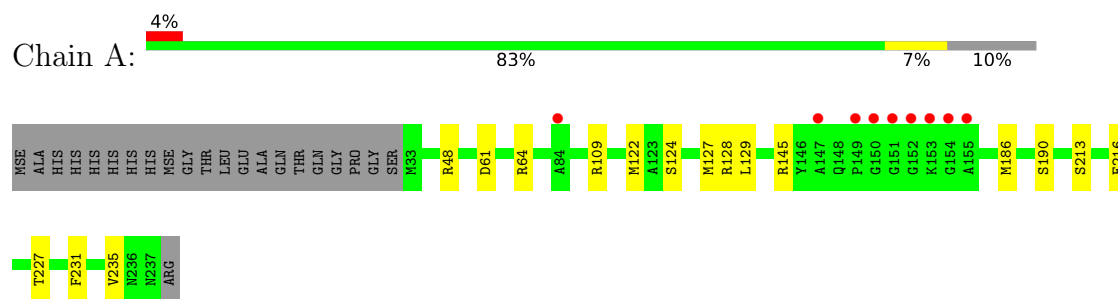
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	155	Total O 157 157	0	2
2	B	169	Total O 169 169	0	0
2	C	129	Total O 131 131	0	2
2	D	115	Total O 115 115	0	0

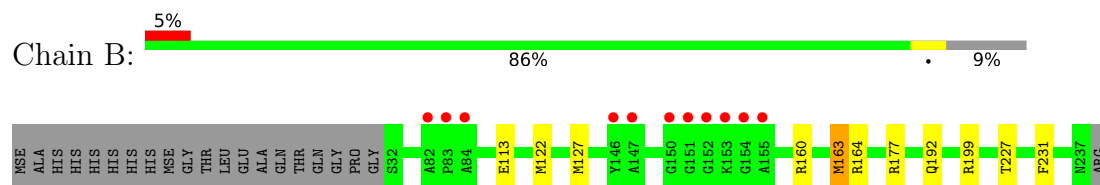
### 3 Residue-property plots

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.

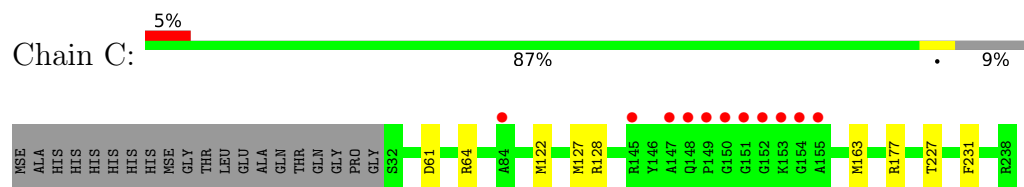
- Molecule 1: Uncharacterized protein



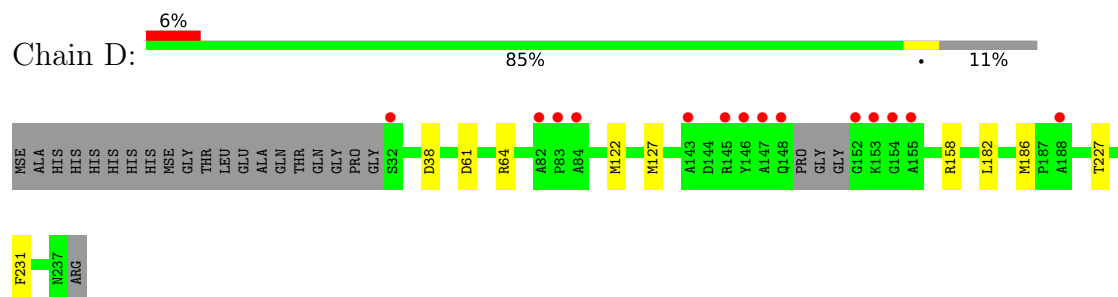
- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



- Molecule 1: Uncharacterized protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.69Å 77.58Å 80.86Å 65.46° 90.03° 83.51°	Depositor
Resolution (Å)	48.31 – 2.10 48.31 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.1 (48.31-2.10) 98.2 (48.31-2.10)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.10Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.171 , 0.206 0.171 , 0.206	Depositor DCC
$R_{free}$ test set	1964 reflections (3.21%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.0	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 43.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7093	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.39% 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](#)

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	0.38	0/1685	0.55	0/2257
1	B	0.40	0/1698	0.54	0/2272
1	C	0.38	0/1657	0.52	0/2221
1	D	0.37	0/1621	0.52	0/2173
All	All	0.39	0/6661	0.53	0/8923

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	A	1645	0	1612	12	0
1	B	1659	0	1624	9	0
1	C	1624	0	1573	7	0
1	D	1593	0	1528	6	0
2	A	157	0	0	4	0
2	B	169	0	0	4	0
2	C	131	0	0	2	0
2	D	115	0	0	1	0
All	All	7093	0	6337	32	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 (32) 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:127[B]:MSE:HE1	1:B:227:THR:HG23	1.57	0.86
1:A:127[B]:MSE:HE1	1:A:227:THR:HG23	1.58	0.85
1:D:127[B]:MSE:HE1	1:D:227:THR:HG23	1.60	0.83
1:C:127[B]:MSE:HE1	1:C:227:THR:HG23	1.62	0.81
1:D:61[B]:ASP:OD1	1:D:64:ARG:NH1	2.16	0.78
1:A:216:GLU:OE1	2:A:301:HOH:O	2.07	0.72
1:B:113[A]:GLU:OE2	2:B:301:HOH:O	2.06	0.72
1:B:199:ARG:NH1	2:B:302:HOH:O	2.18	0.64
1:C:61[B]:ASP:OD1	1:C:64:ARG:NH1	2.30	0.64
1:A:48[A]:ARG:NH1	2:A:303:HOH:O	2.37	0.57
1:A:122[B]:MSE:HE2	1:D:122[B]:MSE:HE2	1.88	0.56
1:A:127[B]:MSE:SE	1:A:231:PHE:CE1	3.09	0.56
1:A:61[B]:ASP:OD1	1:A:64:ARG:NH1	2.42	0.53
1:D:182:LEU:O	1:D:186:MSE:HG3	2.09	0.53
1:B:122[A]:MSE:HG3	1:C:122[A]:MSE:HE3	1.93	0.49
1:B:127[B]:MSE:SE	1:B:231:PHE:CE1	3.15	0.49
1:B:177:ARG:NH2	2:B:309:HOH:O	2.42	0.47
1:C:127[B]:MSE:SE	1:C:231:PHE:CE1	3.17	0.47
1:A:128[B]:ARG:NH1	2:A:311:HOH:O	2.50	0.44
1:A:109:ARG:HD3	2:A:413:HOH:O	2.18	0.43
1:B:192:GLN:NE2	2:B:303:HOH:O	2.23	0.43
1:C:128:ARG:HD3	2:C:321:HOH:O	2.18	0.43
1:C:177:ARG:NH2	2:C:306:HOH:O	2.47	0.42
1:A:186:MSE:HG2	1:A:235:VAL:HG21	2.02	0.42
1:B:163[A]:MSE:HE2	1:B:163[A]:MSE:HB2	1.94	0.42
1:D:38:ASP:OD2	2:D:302:HOH:O	2.22	0.42
1:D:127[B]:MSE:SE	1:D:231:PHE:CE1	3.22	0.42
1:A:213:SER:OG	1:A:216:GLU:HG3	2.21	0.41
1:B:160:ARG:HB3	1:B:164:ARG:HD3	2.03	0.41
1:A:124:SER:OG	1:A:128[B]:ARG:NH2	2.54	0.40
1:A:64:ARG:HG3	1:A:129:LEU:HA	2.02	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	210/227 (92%)	210 (100%)	0	0	100	100
1	B	211/227 (93%)	211 (100%)	0	0	100	100
1	C	210/227 (92%)	209 (100%)	1 (0%)	0	100	100
1	D	203/227 (89%)	203 (100%)	0	0	100	100
All	All	834/908 (92%)	833 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains

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	161/165 (98%)	158 (98%)	3 (2%)	57	63
1	B	164/165 (99%)	162 (99%)	2 (1%)	71	77
1	C	156/165 (94%)	156 (100%)	0	100	100
1	D	154/165 (93%)	153 (99%)	1 (1%)	86	90
All	All	635/660 (96%)	629 (99%)	6 (1%)	84	84

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	145[A]	ARG
1	A	145[B]	ARG

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Mol	Chain	Res	Type
1	A	190	SER
1	B	163[A]	MSE
1	B	163[B]	MSE
1	D	158	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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<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	A	195/227 (85%)	-0.01	9 (4%) 32 38	23, 37, 76, 102	0
1	B	196/227 (86%)	-0.04	11 (5%) 24 29	23, 36, 77, 99	0
1	C	197/227 (86%)	-0.06	11 (5%) 24 29	22, 40, 82, 109	0
1	D	193/227 (85%)	-0.01	14 (7%) 15 19	26, 43, 86, 111	0
All	All	781/908 (86%)	-0.03	45 (5%) 23 28	22, 39, 82, 111	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	151	GLY	6.2
1	A	151	GLY	5.4
1	D	147	ALA	5.4
1	B	151	GLY	5.1
1	C	152	GLY	5.0
1	C	149	PRO	4.6
1	C	147	ALA	4.6
1	B	154	GLY	4.4
1	C	154	GLY	4.1
1	D	152	GLY	4.0
1	A	150	GLY	4.0
1	D	146	TYR	3.8
1	D	155	ALA	3.8
1	B	150	GLY	3.6
1	A	154	GLY	3.6
1	B	147	ALA	3.5
1	B	152	GLY	3.4
1	A	147	ALA	3.2
1	D	84	ALA	3.2
1	A	153	LYS	3.2
1	B	155	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	152	GLY	3.2
1	A	155	ALA	3.0
1	C	84	ALA	3.0
1	D	148	GLN	2.9
1	B	84	ALA	2.9
1	D	154	GLY	2.9
1	C	155	ALA	2.9
1	D	143	ALA	2.8
1	D	188	ALA	2.8
1	A	149	PRO	2.7
1	A	84	ALA	2.7
1	D	153	LYS	2.6
1	B	146	TYR	2.6
1	B	82	ALA	2.5
1	D	82	ALA	2.4
1	D	83	PRO	2.4
1	B	83	PRO	2.2
1	B	153	LYS	2.2
1	C	153	LYS	2.2
1	C	150	GLY	2.2
1	D	32	SER	2.2
1	C	145	ARG	2.2
1	D	145	ARG	2.1
1	C	148	GLN	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.