



# wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 15, 2024 – 01:12 AM EST

PDB ID : 2HDU  
Title : AmpC beta-lactamase in complex with 2-acetamidothiophene-3-carboxylic acid  
Authors : Babaoglu, K.; Shoichet, B.K.  
Deposited on : 2006-06-20  
Resolution : 1.49 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

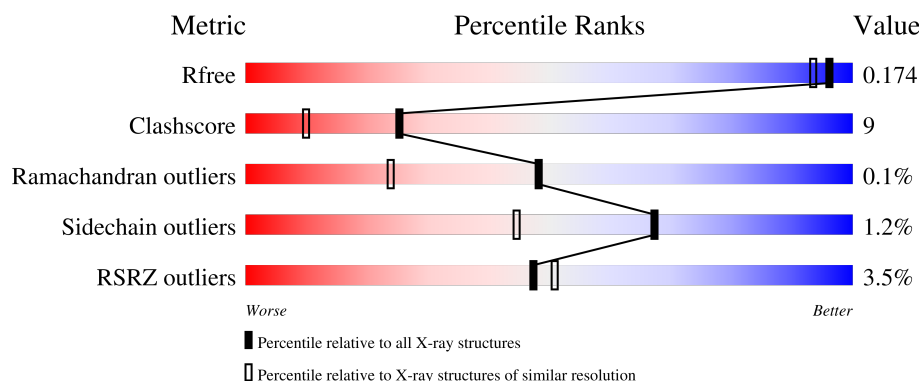
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.49 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	3717 (1.50-1.50)
Clashscore	180529	4048 (1.50-1.50)
Ramachandran outliers	177936	3970 (1.50-1.50)
Sidechain outliers	177891	3967 (1.50-1.50)
RSRZ outliers	164620	3718 (1.50-1.50)

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	358	<div> <div>6%</div> <div>88%</div> <div>10%</div> <div>..</div> </div>
1	B	358	<div> <div>%</div> <div>89%</div> <div>11%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	F12	B	1002[B]	-	-	X	-
2	F12	B	1008	-	-	X	-

## 2 Entry composition [i](#)

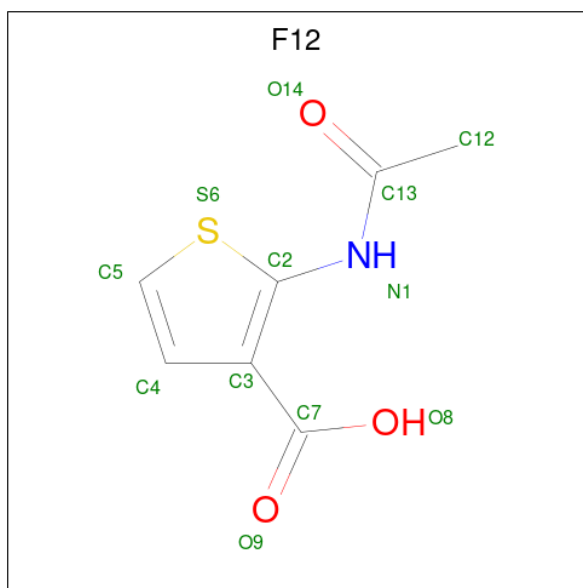
There are 5 unique types of molecules in this entry. The entry contains 6978 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	25	0
			2957	1916	499	535	7			
1	B	358	Total	C	N	O	S	0	25	0
			2940	1905	493	535	7			

- Molecule 2 is 2-(ACETYLAMINO)THIOPHENE-3-CARBOXYLIC ACID (three-letter code: F12) (formula: C<sub>7</sub>H<sub>7</sub>NO<sub>3</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	7	1	3	1		
2	A	1	Total	C	N	O	S	0	0
			12	7	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			12	7	1	3	1		
2	B	1	Total	C	N	O	S	0	1
			24	14	2	6	2		

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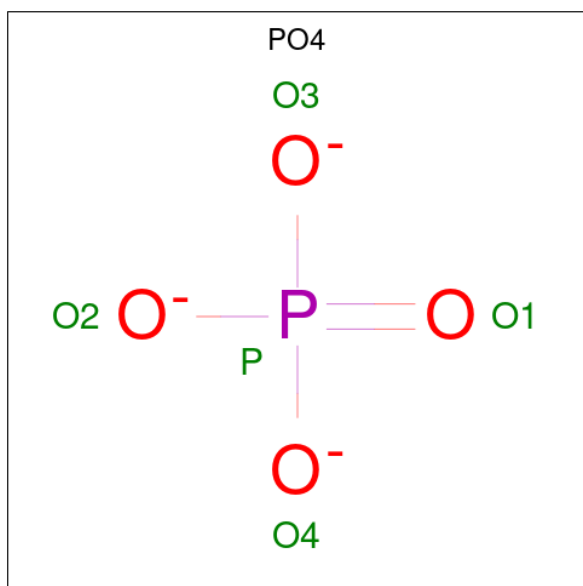
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			12	7	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			12	7	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			12	7	1	3	1		
2	B	1	Total	C	N	O	S	0	0
			12	7	1	3	1		

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	K	0	0
			1	1		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	O P	0	0
			5	4 1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	471	Total	O	0	3
			474	474		

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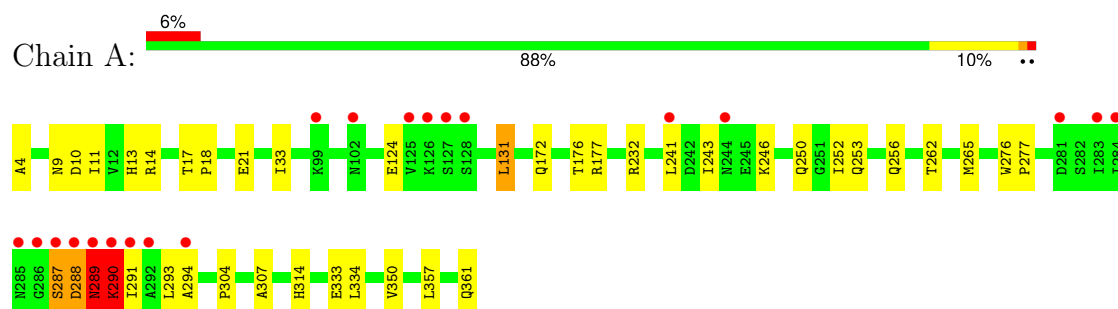
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	491	Total 493	O 493	0	2

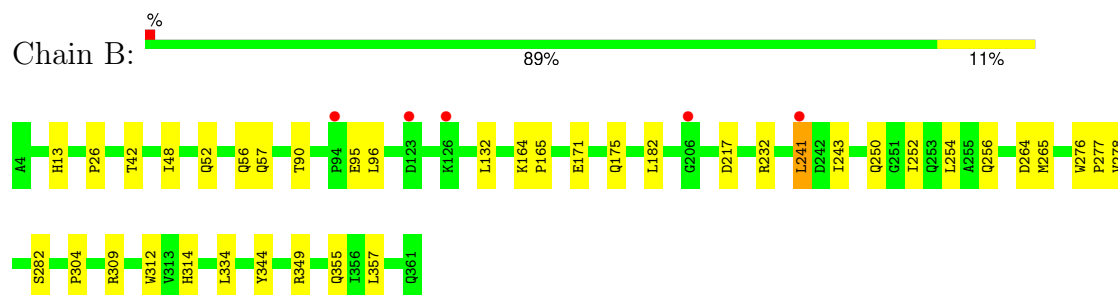
### 3 Residue-property plots

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: Beta-lactamase



#### • Molecule 1: Beta-lactamase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	117.91 Å   77.06 Å   97.52 Å 90.00°   116.86°   90.00°	Depositor
Resolution (Å)	87.04 – 1.49 87.00 – 1.49	Depositor EDS
% Data completeness (in resolution range)	99.5 (87.04-1.49) 99.6 (87.00-1.49)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 1.49 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.135   ,   0.168 0.145   ,   0.174	Depositor DCC
$R_{free}$ test set	6316 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.1	Xtriage
Anisotropy	0.159	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 57.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	6978	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.72% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, F12, K

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	0.70	0/3114	0.80	2/4245 (0.0%)
1	B	0.65	0/3097	0.73	1/4227 (0.0%)
All	All	0.68	0/6211	0.77	3/8472 (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
1	A	1	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	131	LEU	CB-CG-CD2	6.37	121.82	111.00
1	B	217	ASP	CB-CG-OD1	5.81	123.53	118.30
1	A	289	ASN	N-CA-C	5.53	125.92	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	288	ASP	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	287	SER	Peptide

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Mol	Chain	Res	Type	Group
1	A	288	ASP	Peptide
1	A	289	ASN	Peptide

## 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	2957	0	3003	58	0
1	B	2940	0	2984	46	0
2	A	24	0	12	4	0
2	B	84	0	42	21	0
3	B	1	0	0	0	0
4	B	5	0	0	0	0
5	A	474	0	0	19	0
5	B	493	0	0	18	0
All	All	6978	0	6041	114	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 9.

The worst 5 of 114 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:A:289:ASN:HB3	5:A:1066:HOH:O	1.29	1.25
1:B:175[B]:GLN:OE1	5:B:2482:HOH:O	1.57	1.17
1:A:250[B]:GLN:NE2	5:A:1473:HOH:O	1.72	1.16
1:B:250[B]:GLN:NE2	2:B:1002[B]:F12:O8	1.92	1.01
1:A:250[B]:GLN:CD	5:A:1473:HOH:O	1.96	1.01

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	382/358 (107%)	372 (97%)	9 (2%)	1 (0%)	37	17
1	B	382/358 (107%)	376 (98%)	6 (2%)	0	100	100
All	All	764/716 (107%)	748 (98%)	15 (2%)	1 (0%)	48	24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	290	LYS

### 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	317/292 (109%)	311 (98%)	6 (2%)	52	24
1	B	318/292 (109%)	316 (99%)	2 (1%)	84	70
All	All	635/584 (109%)	627 (99%)	8 (1%)	67	41

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

Mol	Chain	Res	Type
1	B	314	HIS
1	B	241	LEU
1	A	314	HIS
1	A	290	LYS
1	A	361	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	137	ASN
1	B	22	GLN
1	B	198	ASN
1	B	137	ASN
1	A	35	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 [i](#)

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 for Mogul analysis.

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	$\# Z  > 2$
2	F12	B	1006	-	11,12,12	1.44	1 (9%)	7,16,16	1.15	1 (14%)
2	F12	A	1004	-	11,12,12	1.33	1 (9%)	7,16,16	0.55	0
2	F12	B	1002[B]	-	11,12,12	1.34	1 (9%)	7,16,16	0.56	0
2	F12	B	1005	-	11,12,12	1.19	1 (9%)	7,16,16	0.89	0
2	F12	B	1002[A]	-	11,12,12	1.34	2 (18%)	7,16,16	0.89	0
4	PO4	B	2002	-	4,4,4	0.80	0	6,6,6	0.80	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	F12	B	1003	-	11,12,12	1.43	1 (9%)	7,16,16	0.97	0
2	F12	B	1008	-	11,12,12	1.12	1 (9%)	7,16,16	1.78	2 (28%)
2	F12	A	1009	-	11,12,12	1.31	1 (9%)	7,16,16	0.87	0
2	F12	B	1001	-	11,12,12	0.99	1 (9%)	7,16,16	0.96	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
2	F12	B	1006	-	-	0/3/8/8	0/1/1/1
2	F12	A	1004	-	-	0/3/8/8	0/1/1/1
2	F12	B	1002[B]	-	-	0/3/8/8	0/1/1/1
2	F12	B	1005	-	-	0/3/8/8	0/1/1/1
2	F12	B	1002[A]	-	-	0/3/8/8	0/1/1/1
2	F12	B	1003	-	-	0/3/8/8	0/1/1/1
2	F12	B	1008	-	-	0/3/8/8	0/1/1/1
2	F12	A	1009	-	-	0/3/8/8	0/1/1/1
2	F12	B	1001	-	-	0/3/8/8	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1006	F12	C3-C2	3.91	1.49	1.41
2	A	1009	F12	C3-C2	3.75	1.49	1.41
2	A	1004	F12	C3-C2	3.70	1.49	1.41
2	B	1003	F12	C3-C2	3.68	1.49	1.41
2	B	1002[B]	F12	C3-C2	3.34	1.48	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1008	F12	O8-C7-O9	3.45	130.78	123.35
2	B	1008	F12	O9-C7-C3	-2.75	115.42	121.97
2	B	1006	F12	O9-C7-C3	-2.38	116.28	121.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1004	F12	1	0
2	B	1002[B]	F12	12	0
2	B	1005	F12	1	0
2	B	1002[A]	F12	1	0
2	B	1008	F12	6	0
2	A	1009	F12	3	0
2	B	1001	F12	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	A	358/358 (100%)	-0.18	20 (5%) 31 33	6, 13, 25, 38	47 (13%)
1	B	358/358 (100%)	-0.37	5 (1%) 73 75	7, 13, 22, 28	34 (9%)
All	All	716/716 (100%)	-0.28	25 (3%) 47 51	6, 13, 24, 38	81 (11%)

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	289	ASN	6.3
1	A	291	ILE	5.1
1	A	287	SER	5.1
1	B	241	LEU	4.9
1	A	283	ILE	4.5

### 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 monosaccharides 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
2	F12	A	1009	12/12	0.75	0.26	30,31,32,33	12
4	PO4	B	2002	5/5	0.85	0.13	33,36,38,39	0
2	F12	B	1008	12/12	0.87	0.13	21,22,24,24	12
2	F12	B	1003	12/12	0.88	0.13	16,18,20,21	12
2	F12	B	1006	12/12	0.88	0.12	19,22,23,24	12
2	F12	A	1004	12/12	0.92	0.12	18,20,21,21	12
2	F12	B	1005	12/12	0.96	0.09	10,13,16,18	12
2	F12	B	1001	12/12	0.98	0.06	12,14,16,18	0
2	F12	B	1002[B]	12/12	0.99	0.04	11,12,13,13	12
2	F12	B	1002[A]	12/12	0.99	0.04	8,9,10,10	12
3	K	B	2001	1/1	1.00	0.08	18,18,18,18	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.