



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:34 AM GMT

PDB ID : 3IXG  
Title : X-ray crystal structure of the extended-spectrum AmpC T70I mutant beta-lactamase with and without benzo(b)thiophene-2-boronic acid bound at 2.14 Angstrom resolution  
Authors : Shoichet, B.K.; Thomas, V.L.  
Deposited on : 2009-09-04  
Resolution : 2.14 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

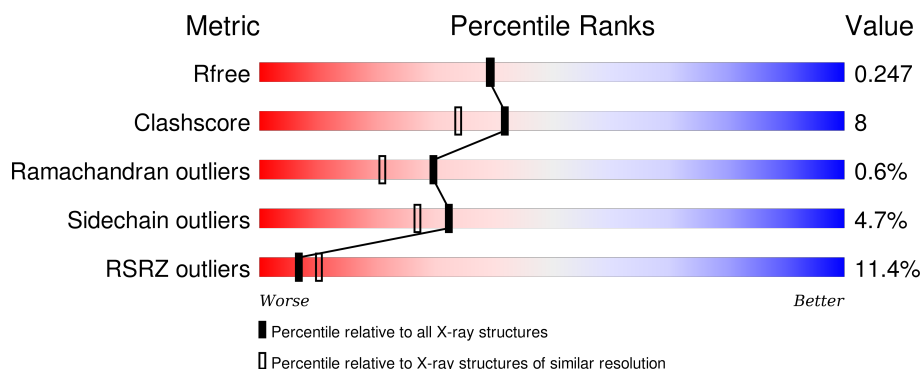
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.14 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))
$R_{free}$	91344	1693 (2.16-2.12)
Clashscore	102246	1824 (2.16-2.12)
Ramachandran outliers	100387	1798 (2.16-2.12)
Sidechain outliers	100360	1798 (2.16-2.12)
RSRZ outliers	91569	1699 (2.16-2.12)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	
1	B	358	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5524 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.

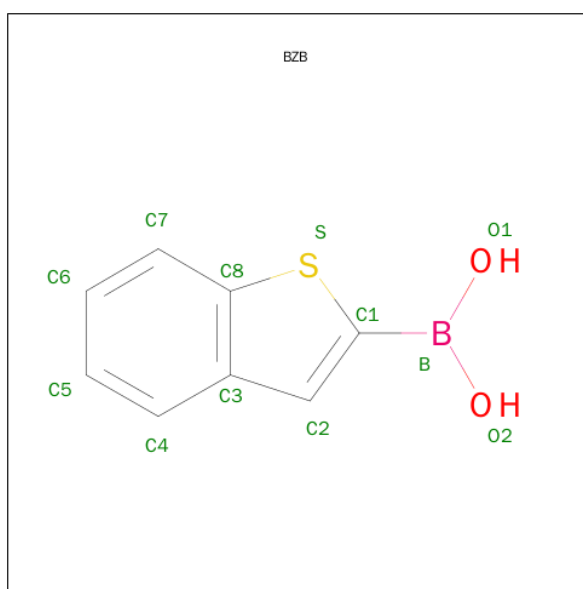
- Molecule 1 is a protein called Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	0
			2491	1616	422	447	6			
1	B	358	Total	C	N	O	S	0	0	0
			2801	1806	476	513	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	70	ILE	THR	ENGINEERED	UNP P00811
B	70	ILE	THR	ENGINEERED	UNP P00811

- Molecule 2 is BENZO[B]THIOPHENE-2-BORONIC ACID (three-letter code: BZB) (formula: C<sub>8</sub>H<sub>7</sub>BO<sub>2</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	B	C	O	S	0	0
			12	1	8	2	1		

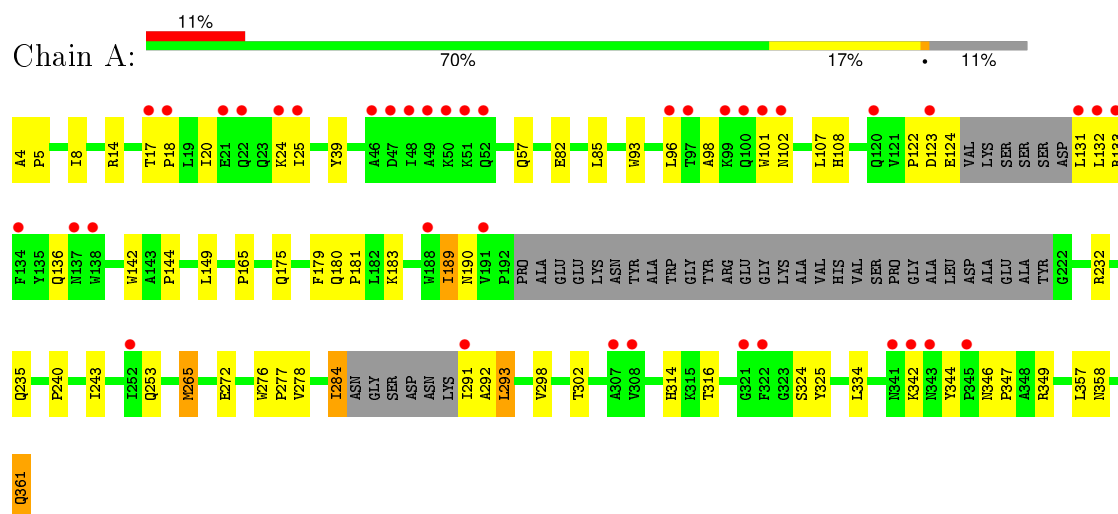
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	110	Total 110	O 110	0	0
3	B	110	Total 110	O 110	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ( $\text{RSRZ} > 2$ ). 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



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.16Å 77.36Å 91.75Å 90.00° 122.12° 90.00°	Depositor
Resolution (Å)	30.00 – 2.14 57.91 – 2.14	Depositor EDS
% Data completeness (in resolution range)	98.4 (30.00-2.14) 98.4 (57.91-2.14)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.22 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, $R_{free}$	0.197 , 0.245 0.202 , 0.247	Depositor DCC
$R_{free}$ test set	1843 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.1	Xtriage
Anisotropy	0.494	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.43 , 63.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 36831 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5524	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: BZB

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	0.49	0/2560	0.60	0/3494
1	B	0.56	0/2881	0.64	1/3934 (0.0%)
All	All	0.53	0/5441	0.62	1/7428 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	288	ASP	CB-CG-OD2	5.23	123.01	118.30

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	2491	0	2497	41	0
1	B	2801	0	2782	47	0
2	B	12	0	7	1	0
3	A	110	0	0	7	0
3	B	110	0	0	4	0
All	All	5524	0	5286	87	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 8.

All (87) 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:308:VAL:HG22	1:B:309:ARG:HG2	1.61	0.81
1:A:149:LEU:HD11	1:A:293:LEU:HG	1.66	0.77
1:B:262:THR:CG2	1:B:298:VAL:HG12	2.15	0.77
1:B:120:GLN:HG2	2:B:362:BZB:HC51	1.69	0.74
1:B:262:THR:HG22	1:B:298:VAL:HG12	1.68	0.73
1:B:290:LYS:HD3	1:B:294:ALA:HB2	1.69	0.72
3:A:471:HOH:O	1:B:250:GLN:HG2	1.90	0.72
1:B:100:GLN:NE2	3:B:405:HOH:O	2.25	0.69
1:A:132:LEU:HG	3:A:389:HOH:O	1.92	0.69
1:A:334:LEU:HG	1:A:357:LEU:HD22	1.75	0.69
1:B:288:ASP:O	1:B:289:ASN:HB2	1.95	0.66
1:A:5:PRO:HG2	1:A:8:ILE:HD12	1.80	0.63
1:B:122:PRO:HB2	1:B:125:VAL:HG23	1.79	0.63
1:B:290:LYS:HD3	1:B:294:ALA:CB	2.28	0.63
1:A:14:ARG:NH2	3:A:398:HOH:O	2.31	0.62
1:B:56:GLN:NE2	1:B:228:GLU:OE2	2.32	0.62
1:B:57:GLN:HA	1:B:57:GLN:HE21	1.66	0.61
1:A:316:THR:HG22	1:A:325:TYR:CE1	2.38	0.59
1:B:189:ILE:HD13	1:B:223:VAL:HG22	1.84	0.58
1:B:276:TRP:CD2	1:B:277:PRO:HA	2.37	0.58
1:B:284:ILE:HG23	1:B:288:ASP:OD2	2.04	0.57
1:B:334:LEU:HG	1:B:357:LEU:HD22	1.86	0.56
1:A:240:PRO:HG2	1:A:253:GLN:HE21	1.72	0.54
1:A:17:THR:HB	1:A:18:PRO:HD3	1.89	0.54
1:A:316:THR:HG21	1:A:346:ASN:HD21	1.73	0.54
1:B:59:LEU:HB2	1:B:199:TYR:HA	1.89	0.54
1:A:232:ARG:HA	1:A:235:GLN:HG2	1.90	0.53
1:B:243:ILE:HD13	1:B:252:ILE:HD12	1.91	0.52
1:B:289:ASN:C	1:B:291:ILE:H	2.12	0.52
1:B:280:PRO:HD3	1:B:354:TRP:CE2	2.44	0.52
1:A:20:ILE:HA	1:A:25:ILE:HD12	1.93	0.51
1:B:128:SER:HA	1:B:131:LEU:HD12	1.92	0.50
1:A:232:ARG:O	1:A:235:GLN:HG2	2.12	0.50
1:B:102:ASN:HA	3:B:484:HOH:O	2.12	0.50
1:A:136:GLN:HG3	3:A:389:HOH:O	2.12	0.50
1:A:131:LEU:N	3:A:475:HOH:O	2.45	0.49
1:B:89:THR:HG22	1:B:96:LEU:HD23	1.94	0.49
1:B:33:ILE:HD12	1:B:33:ILE:N	2.27	0.49

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:THR:CG2	1:B:96:LEU:HD23	2.44	0.48
1:A:180:GLN:HB2	1:A:181:PRO:HD3	1.95	0.47
1:A:82:GLU:HB3	1:A:165:PRO:HB2	1.97	0.47
1:B:89:THR:HG23	1:B:161:LEU:CD1	2.45	0.47
1:A:107:LEU:HD22	1:B:302:THR:HG21	1.97	0.47
1:A:344:TYR:CZ	1:A:349:ARG:HG2	2.50	0.46
1:B:289:ASN:O	1:B:291:ILE:N	2.49	0.46
1:A:324:SER:HB3	3:A:468:HOH:O	2.14	0.46
1:B:8:ILE:O	1:B:12:VAL:HG23	2.16	0.46
1:A:302:THR:HG22	3:B:424:HOH:O	2.16	0.46
1:B:316:THR:HG22	1:B:325:TYR:CD1	2.51	0.46
1:A:276:TRP:CD2	1:A:277:PRO:HA	2.51	0.45
1:B:284:ILE:O	1:B:288:ASP:HB2	2.17	0.45
1:B:288:ASP:O	1:B:289:ASN:CB	2.64	0.45
1:B:288:ASP:OD1	1:B:346:ASN:HB3	2.16	0.45
1:A:175:GLN:HG3	1:A:189:ILE:HD11	1.98	0.45
1:A:179:PHE:HE2	1:A:189:ILE:HG13	1.81	0.45
1:B:243:ILE:CD1	1:B:252:ILE:HD12	2.47	0.45
1:A:316:THR:HG22	1:A:325:TYR:HE1	1.79	0.45
1:B:275:ASP:O	1:B:278:VAL:HG22	2.17	0.44
1:A:316:THR:HG22	1:A:325:TYR:CD1	2.53	0.44
1:B:80:ARG:HH21	1:B:177:ARG:HG2	1.83	0.44
1:A:5:PRO:HD2	1:A:39:TYR:CE2	2.53	0.44
1:A:284:ILE:HG21	1:A:347:PRO:HA	2.00	0.44
1:B:159:GLY:HA3	1:B:170:PHE:CZ	2.53	0.43
1:B:99:LYS:O	1:B:102:ASN:HB2	2.18	0.43
1:A:24:LYS:HB2	1:A:342:LYS:NZ	2.32	0.43
1:A:122:PRO:HB2	1:A:124:GLU:HG2	2.01	0.43
1:B:13:HIS:O	1:B:17:THR:HB	2.19	0.43
1:B:240:PRO:HA	1:B:243:ILE:HD12	2.01	0.43
1:A:175:GLN:NE2	3:A:402:HOH:O	2.53	0.42
1:B:37:LYS:HG3	1:B:38:PRO:HD2	2.01	0.42
1:A:183:LYS:HD2	1:A:232:ARG:NH2	2.35	0.42
1:B:243:ILE:HD13	1:B:252:ILE:CD1	2.49	0.42
1:B:262:THR:HG22	1:B:298:VAL:CG1	2.44	0.41
1:A:358:ASN:HA	1:A:361:GLN:HE21	1.85	0.41
1:A:240:PRO:HA	1:A:243:ILE:HD13	2.01	0.41
1:B:112:TYR:HB3	1:B:149:LEU:O	2.20	0.41
1:A:98:ALA:HB3	1:A:101:TRP:HD1	1.84	0.41
1:A:265:MET:HE1	1:A:272:GLU:OE1	2.21	0.41
1:A:292:ALA:O	1:A:293:LEU:C	2.59	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:288:ASP:OD1	1:B:346:ASN:CB	2.69	0.41
1:B:230:MET:HB3	1:B:337:VAL:HG11	2.02	0.41
1:A:93:TRP:CE3	1:A:96:LEU:HD22	2.56	0.41
1:A:85:LEU:HA	1:A:85:LEU:HD23	1.88	0.41
1:A:108:HIS:CE1	1:A:144:PRO:HB2	2.56	0.41
1:B:224:LYS:HE2	3:B:396:HOH:O	2.19	0.41
1:A:284:ILE:HG12	1:A:284:ILE:H	1.70	0.40
1:A:4:ALA:HA	1:A:5:PRO:HD2	1.94	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	309/358 (86%)	300 (97%)	8 (3%)	1 (0%)	46	41
1	B	356/358 (99%)	344 (97%)	9 (2%)	3 (1%)	24	14
All	All	665/716 (93%)	644 (97%)	17 (3%)	4 (1%)	30	21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	289	ASN
1	A	293	LEU
1	B	213	PRO
1	B	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	261/292 (89%)	247 (95%)	14 (5%)	27	21
1	B	292/292 (100%)	280 (96%)	12 (4%)	37	34
All	All	553/584 (95%)	527 (95%)	26 (5%)	32	27

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	102	ASN
1	A	123	ASP
1	A	133	ARG
1	A	142	TRP
1	A	189	ILE
1	A	190	ASN
1	A	265	MET
1	A	278	VAL
1	A	284	ILE
1	A	291	ILE
1	A	298	VAL
1	A	314	HIS
1	A	361	GLN
1	B	6	GLN
1	B	57	GLN
1	B	139	GLN
1	B	170	PHE
1	B	204	ARG
1	B	209	VAL
1	B	273	MET
1	B	278	VAL
1	B	290	LYS
1	B	293	LEU
1	B	308	VAL
1	B	314	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	35	GLN
1	A	102	ASN
1	A	137	ASN
1	A	190	ASN
1	A	253	GLN
1	A	341	ASN
1	A	358	ASN
1	A	361	GLN
1	B	7	GLN
1	B	9	ASN
1	B	23	GLN
1	B	35	GLN
1	B	56	GLN
1	B	57	GLN
1	B	102	ASN
1	B	120	GLN
1	B	180	GLN
1	B	261	GLN
1	B	285	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	$\# Z  > 2$
2	BZB	B	362	-	11,13,13	4.69	3 (27%)	11,18,18	1.82	3 (27%)

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	BZB	B	362	-	-	0/0/4/4	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	362	BZB	B-C1	-2.33	1.55	1.57
2	B	362	BZB	B-O1	10.30	1.53	1.36
2	B	362	BZB	B-O2	10.85	1.54	1.36

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	362	BZB	C4-C3-C8	-2.76	116.00	119.88
2	B	362	BZB	O2-B-C1	-2.17	114.01	120.50
2	B	362	BZB	C2-C3-C8	3.92	114.80	107.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	362	BZB	1	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	317/358 (88%)	0.87	39 (12%) 5 8	13, 26, 50, 61	12 (3%)
1	B	358/358 (100%)	0.66	38 (10%) 8 12	12, 25, 44, 49	14 (3%)
All	All	675/716 (94%)	0.76	77 (11%) 7 10	12, 26, 46, 61	26 (3%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	49	ALA	8.1
1	A	49	ALA	7.5
1	B	288	ASP	7.4
1	A	48	ILE	6.9
1	A	50	LYS	5.9
1	B	214	GLY	5.9
1	A	131	LEU	5.7
1	A	99	LYS	5.6
1	B	201	TRP	5.5
1	A	137	ASN	5.5
1	A	188	TRP	5.4
1	B	102	ASN	5.4
1	A	291	ILE	5.1
1	A	123	ASP	5.1
1	B	289	ASN	5.0
1	B	290	LYS	5.0
1	A	96	LEU	4.8
1	A	100	GLN	4.7
1	A	133	ARG	4.7
1	A	342	LYS	4.6
1	A	132	LEU	4.6
1	A	97	THR	4.5
1	A	21	GLU	4.4
1	A	321	GLY	4.4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	192	PRO	4.4
1	B	212	SER	4.3
1	B	204	ARG	4.3
1	B	209	VAL	4.3
1	A	25	ILE	4.0
1	B	203	TYR	3.8
1	B	188	TRP	3.8
1	B	206	GLY	3.7
1	A	46	ALA	3.6
1	B	293	LEU	3.4
1	B	211	VAL	3.4
1	B	205	GLU	3.2
1	B	210	HIS	3.2
1	A	345	PRO	3.2
1	A	51	LYS	3.1
1	A	47	ASP	3.0
1	B	130	ASP	2.9
1	A	18	PRO	2.9
1	A	138	TRP	2.9
1	B	125	VAL	2.9
1	B	213	PRO	2.9
1	B	48	ILE	2.8
1	B	291	ILE	2.8
1	A	22	GLN	2.7
1	A	17	THR	2.7
1	B	24	LYS	2.7
1	B	207	LYS	2.7
1	B	6	GLN	2.7
1	B	123	ASP	2.7
1	A	307	ALA	2.7
1	A	191	VAL	2.6
1	B	25	ILE	2.6
1	B	50	LYS	2.6
1	A	308	VAL	2.6
1	A	134	PHE	2.5
1	A	101	TRP	2.5
1	B	4	ALA	2.5
1	B	126	LYS	2.5
1	A	120	GLN	2.5
1	A	102	ASN	2.5
1	B	127	SER	2.4
1	A	322	PHE	2.4

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	208	ALA	2.4
1	A	24	LYS	2.4
1	A	343	ASN	2.4
1	A	341	ASN	2.2
1	B	124	GLU	2.2
1	B	129	SER	2.1
1	A	252	ILE	2.1
1	B	321	GLY	2.1
1	B	292	ALA	2.1
1	A	52	GLN	2.0
1	B	97	THR	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	BZB	B	362	12/12	0.84	0.16	1.11	24,34,35,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.