



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:49 PM GMT

PDB ID : 4G9R  
Title : B-Raf V600E Kinase Domain Bound to a Type II Dihydroquinazoline Inhibitor  
Authors : Voegtli, W.C.; Sturgis, H.L.  
Deposited on : 2012-07-24  
Resolution : 3.20 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.

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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 : 1.7 (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

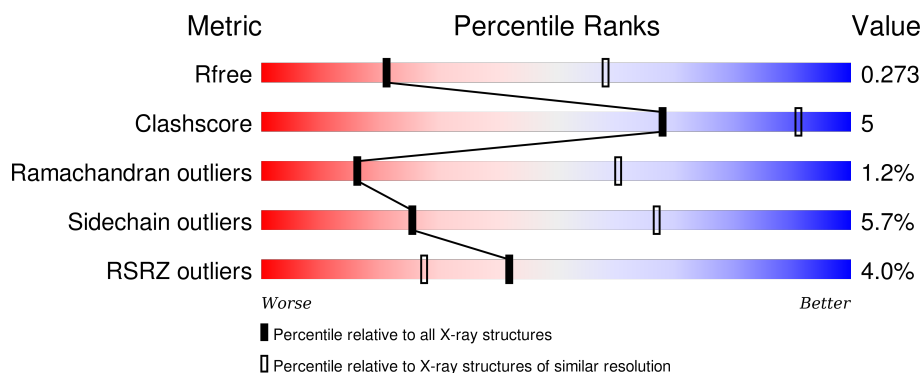
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	307	
1	B	307	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4242 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 Serine/threonine-protein kinase B-raf.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			2090	1338	363	376	13			
1	B	261	Total	C	N	O	S	0	0	0
			2084	1335	362	374	13			

There are 26 discrepancies between the modelled and reference sequences:

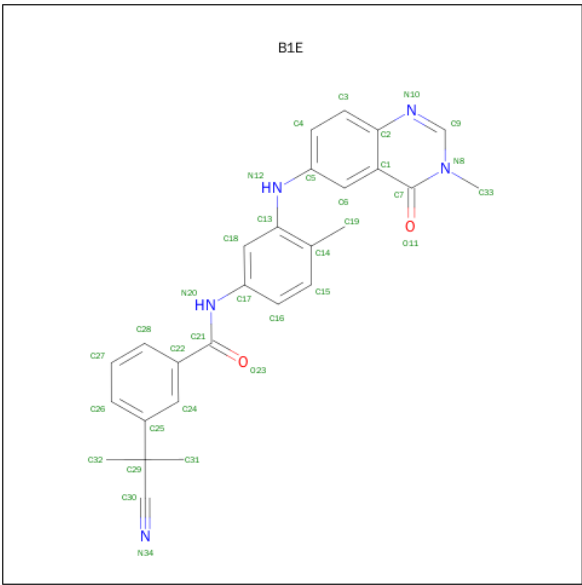
Chain	Residue	Modelled	Actual	Comment	Reference
A	420	MET	-	EXPRESSION TAG	UNP P15056
A	421	ASP	-	EXPRESSION TAG	UNP P15056
A	422	ARG	-	EXPRESSION TAG	UNP P15056
A	423	GLY	-	EXPRESSION TAG	UNP P15056
A	424	SER	-	EXPRESSION TAG	UNP P15056
A	425	HIS	-	EXPRESSION TAG	UNP P15056
A	426	HIS	-	EXPRESSION TAG	UNP P15056
A	427	HIS	-	EXPRESSION TAG	UNP P15056
A	428	HIS	-	EXPRESSION TAG	UNP P15056
A	429	HIS	-	EXPRESSION TAG	UNP P15056
A	430	HIS	-	EXPRESSION TAG	UNP P15056
A	431	GLY	-	EXPRESSION TAG	UNP P15056
A	600	GLU	VAL	ENGINEERED MUTATION	UNP P15056
B	420	MET	-	EXPRESSION TAG	UNP P15056
B	421	ASP	-	EXPRESSION TAG	UNP P15056
B	422	ARG	-	EXPRESSION TAG	UNP P15056
B	423	GLY	-	EXPRESSION TAG	UNP P15056
B	424	SER	-	EXPRESSION TAG	UNP P15056
B	425	HIS	-	EXPRESSION TAG	UNP P15056
B	426	HIS	-	EXPRESSION TAG	UNP P15056
B	427	HIS	-	EXPRESSION TAG	UNP P15056
B	428	HIS	-	EXPRESSION TAG	UNP P15056
B	429	HIS	-	EXPRESSION TAG	UNP P15056
B	430	HIS	-	EXPRESSION TAG	UNP P15056
B	431	GLY	-	EXPRESSION TAG	UNP P15056

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Chain	Residue	Modelled	Actual	Comment	Reference
B	600	GLU	VAL	ENGINEERED MUTATION	UNP P15056

- Molecule 2 is 3-(2-CYANOPROPAN-2-YL)-N-{4-METHYL-3-[(3-METHYL-4-OXO-3,4-DIHYDROQUINAZOLIN-6-YL)AMINO]PHENYL}BENZAMIDE (three-letter code: B1E) (formula: C<sub>27</sub>H<sub>25</sub>N<sub>5</sub>O<sub>2</sub>).

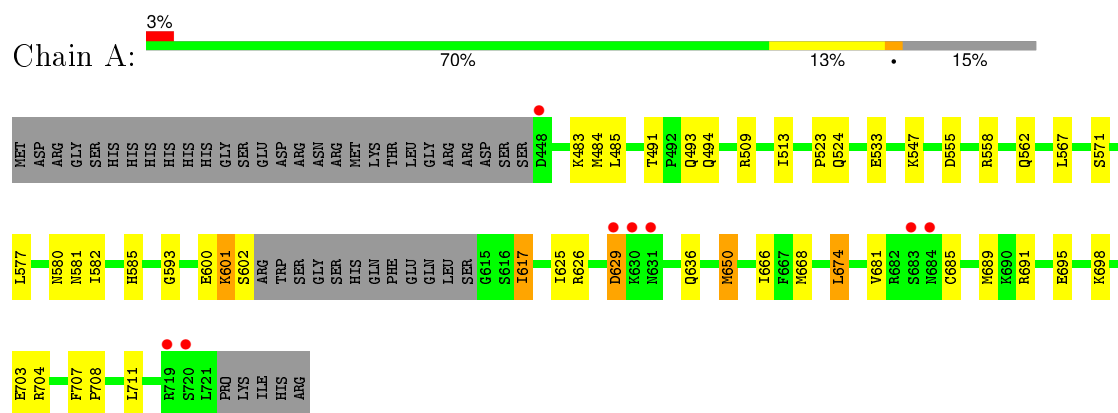


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			34	27	5	2		
2	B	1	Total	C	N	O	0	0
			34	27	5	2		

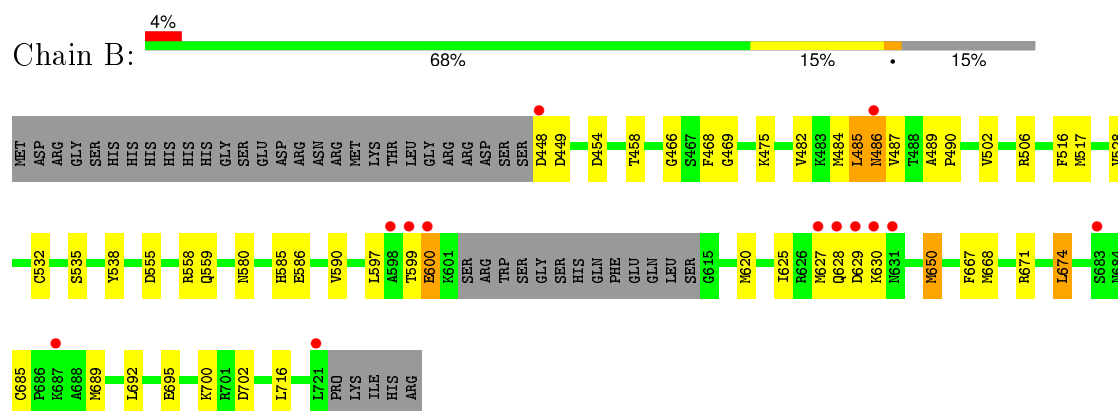
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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: Serine/threonine-protein kinase B-raf



- Molecule 1: Serine/threonine-protein kinase B-raf



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.82Å 96.82Å 168.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.24 – 3.20 29.24 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.24-3.20) 98.9 (29.24-3.20)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.91 (at 3.18Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.226 , 0.277 0.224 , 0.273	Depositor DCC
$R_{free}$ test set	678 reflections (5.21%)	DCC
Wilson B-factor (Å <sup>2</sup> )	43.2	Xtrriage
Anisotropy	0.439	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 12.8	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Outliers	1 of 13681 reflections (0.007%)	Xtrriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4242	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.30 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.2185e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: B1E

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	0.35	0/2134	0.50	0/2880
1	B	0.33	0/2128	0.53	1/2872 (0.0%)
All	All	0.34	0/4262	0.51	1/5752 (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	486	ASN	N-CA-C	5.16	124.92	111.00

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	2090	0	2119	21	0
1	B	2084	0	2114	20	0
2	A	34	0	25	0	0
2	B	34	0	25	0	0
All	All	4242	0	4283	40	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 5.

All (40) 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:469:GLY:HA2	1:B:485:LEU:HA	1.76	0.66
1:A:509:ARG:HD3	1:B:516:PHE:O	1.96	0.66
1:A:650:MET:HE2	1:A:689:MET:HG2	1.80	0.63
1:A:617:ILE:HG12	1:A:666:ILE:HG12	1.82	0.61
1:B:458:THR:HB	1:B:475:LYS:HB2	1.85	0.58
1:B:466:GLY:HA3	1:B:597:LEU:HB3	1.86	0.57
1:A:491:THR:HG22	1:A:493:GLN:H	1.70	0.56
1:A:650:MET:HG3	1:A:685:CYS:SG	2.45	0.56
1:B:650:MET:HE2	1:B:689:MET:HG2	1.87	0.56
1:A:668:MET:HB3	1:A:674:LEU:HB2	1.88	0.55
1:A:562:GLN:HE22	1:A:711:LEU:HD21	1.73	0.54
1:B:532:CYS:HA	1:B:585:HIS:HD2	1.73	0.53
1:B:559:GLN:HB3	1:B:590:VAL:HB	1.91	0.53
1:A:600:GLU:O	1:A:602:SER:N	2.42	0.52
1:B:650:MET:HG3	1:B:685:CYS:SG	2.49	0.52
1:A:483:LYS:HE2	1:A:485:LEU:HD21	1.91	0.51
1:A:581:ASN:HB3	1:A:593:GLY:O	2.10	0.51
1:A:555:ASP:OD1	1:A:558:ARG:NH1	2.44	0.50
1:A:636:GLN:HB3	1:A:704:ARG:HE	1.76	0.49
1:B:538:TYR:HB3	1:B:580:ASN:HD22	1.77	0.49
1:B:620:MET:HB2	1:B:625:ILE:HG13	1.93	0.48
1:B:667:PHE:O	1:B:671:ARG:HG2	2.13	0.48
1:B:532:CYS:HA	1:B:585:HIS:CD2	2.49	0.47
1:B:628:GLN:HG2	1:B:629:ASP:H	1.79	0.47
1:A:577:LEU:HD11	1:A:582:ILE:HD11	1.97	0.47
1:B:502:VAL:O	1:B:506:ARG:HG2	2.14	0.46
1:B:668:MET:HB3	1:B:674:LEU:HB2	1.98	0.46
1:B:482:VAL:HG22	1:B:528:VAL:HG22	1.97	0.45
1:A:691:ARG:O	1:A:695:GLU:HG2	2.16	0.45
1:B:468:PHE:CZ	1:B:600:GLU:HG2	2.52	0.45
1:A:650:MET:HB3	1:A:681:VAL:HG12	2.00	0.43
1:B:489:ALA:HA	1:B:490:PRO:HD3	1.85	0.42
1:A:707:PHE:N	1:A:708:PRO:HD2	2.35	0.42
1:A:698:LYS:HD3	1:A:703:GLU:HB3	2.03	0.41
1:B:692:LEU:O	1:B:695:GLU:HB2	2.21	0.41
1:A:513:ILE:HG12	1:A:567:LEU:HD21	2.03	0.40
1:A:491:THR:HB	1:A:494:GLN:HG3	2.03	0.40
1:A:523:PRO:HG2	1:A:524:GLN:HE21	1.86	0.40
1:A:533:GLU:H	1:A:585:HIS:HD2	1.69	0.40
1:B:555:ASP:OD1	1:B:558:ARG:NH1	2.49	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	258/307 (84%)	243 (94%)	12 (5%)	3 (1%)	16	60
1	B	257/307 (84%)	242 (94%)	12 (5%)	3 (1%)	16	60
All	All	515/614 (84%)	485 (94%)	24 (5%)	6 (1%)	16	60

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	601	LYS
1	A	629	ASP
1	B	486	ASN
1	B	630	LYS
1	A	626	ARG
1	B	487	VAL

### 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	229/271 (84%)	219 (96%)	10 (4%)	35	74
1	B	228/271 (84%)	212 (93%)	16 (7%)	19	58
All	All	457/542 (84%)	431 (94%)	26 (6%)	25	67

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

Mol	Chain	Res	Type
1	A	484	MET
1	A	547	LYS
1	A	571	SER
1	A	580	ASN
1	A	601	LYS
1	A	617	ILE
1	A	625	ILE
1	A	629	ASP
1	A	650	MET
1	A	674	LEU
1	B	448	ASP
1	B	449	ASP
1	B	454	ASP
1	B	484	MET
1	B	485	LEU
1	B	517	MET
1	B	535	SER
1	B	586	GLU
1	B	599	THR
1	B	600	GLU
1	B	627	MET
1	B	650	MET
1	B	674	LEU
1	B	700	LYS
1	B	702	ASP
1	B	716	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	524	GLN
1	A	562	GLN
1	A	585	HIS
1	B	512	ASN
1	B	580	ASN
1	B	585	HIS

### 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 ⓘ

2 ligands are 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	B1E	A	801	-	36,37,37	1.54	4 (11%)	41,54,54	1.10	4 (9%)
2	B1E	B	801	-	36,37,37	1.50	3 (8%)	41,54,54	1.11	4 (9%)

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	B1E	A	801	-	-	0/18/21/21	0/4/4/4
2	B1E	B	801	-	-	0/18/21/21	0/4/4/4

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	B1E	C5-N12	-2.37	1.35	1.40
2	A	801	B1E	C5-N12	-2.32	1.35	1.40
2	A	801	B1E	C2-N10	2.01	1.41	1.37
2	A	801	B1E	C3-C4	2.39	1.41	1.36
2	B	801	B1E	C3-C4	2.40	1.41	1.36
2	B	801	B1E	C7-C1	5.39	1.50	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	B1E	C7-C1	5.68	1.51	1.41

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	B1E	C5-N12-C13	2.06	132.38	126.60
2	A	801	B1E	C5-N12-C13	2.10	132.49	126.60
2	A	801	B1E	C6-C1-C2	2.11	120.65	118.14
2	B	801	B1E	C6-C1-C2	2.19	120.76	118.14
2	B	801	B1E	C9-N10-C2	2.86	118.80	116.46
2	A	801	B1E	C9-N10-C2	3.01	118.92	116.46
2	B	801	B1E	C15-C14-C13	3.30	119.98	117.39
2	A	801	B1E	C15-C14-C13	3.60	120.22	117.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	262/307 (85%)	-0.12	8 (3%) 52 38	21, 33, 47, 62	0
1	B	261/307 (85%)	-0.02	13 (4%) 32 19	27, 38, 52, 61	0
All	All	523/614 (85%)	-0.07	21 (4%) 42 27	21, 35, 51, 62	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	630	LYS	5.6
1	A	629	ASP	5.4
1	A	448	ASP	4.7
1	B	629	ASP	4.4
1	A	630	LYS	4.1
1	A	683	SER	3.3
1	B	448	ASP	3.2
1	B	721	LEU	3.0
1	A	719	ARG	2.9
1	B	627	MET	2.8
1	B	631	ASN	2.7
1	A	631	ASN	2.5
1	A	684	ASN	2.4
1	B	598	ALA	2.3
1	B	628	GLN	2.3
1	B	486	ASN	2.3
1	A	720	SER	2.2
1	B	683	SER	2.2
1	B	600	GLU	2.1
1	B	687	LYS	2.1
1	B	599	THR	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 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( $\text{\AA}^2$ )	Q<0.9
2	B1E	B	801	34/34	0.92	0.22	0.07	26,28,29,29	0
2	B1E	A	801	34/34	0.96	0.17	-0.39	29,30,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.