



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2017 – 03:10 AM EDT

PDB ID : 3I32  
Title : Dimeric structure of a Hera helicase fragment including the C-terminal RecA domain, the dimerization domain, and the RNA binding domain  
Authors : Rudolph, M.G.; Klostermeier, D.  
Deposited on : unknown  
Resolution : 2.80 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030345

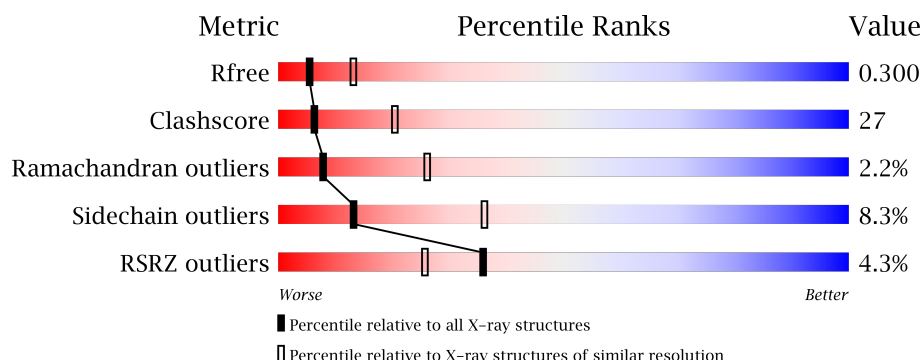
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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	300	<div> <div>4%</div> <div>49%</div> <div>39%</div> <div>•</div> <div>8%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2164 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 Heat resistant RNA dependent ATPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2162	1359	409	390	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	272	MET	LEU	ENGINEERED	UNP Q72GF3
A	281	MET	LEU	ENGINEERED	UNP Q72GF3
A	315	MET	LEU	ENGINEERED	UNP Q72GF3

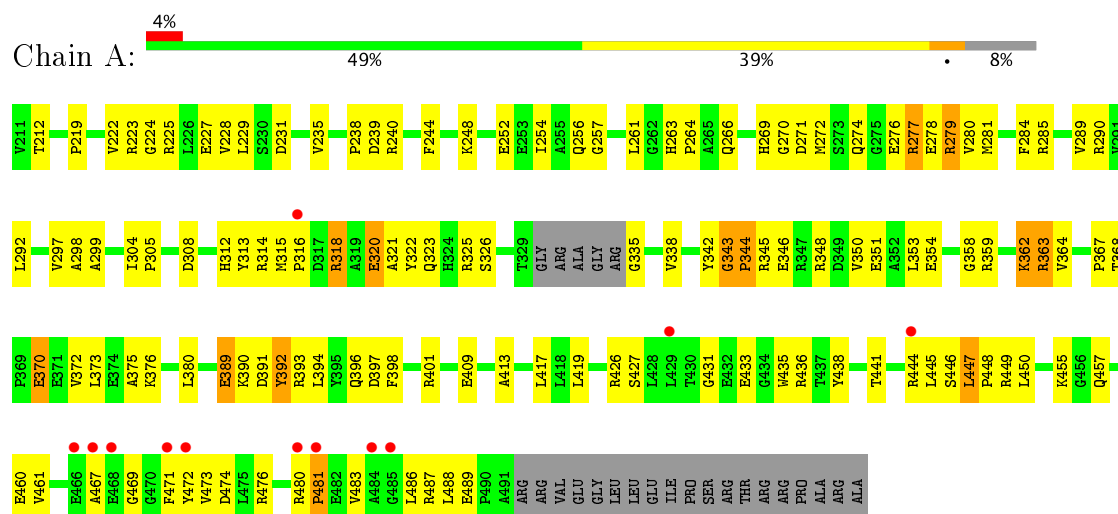
- Molecule 2 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Br	0	0
			2	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 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: Heat resistant RNA dependent ATPase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.96 Å 64.96 Å 153.56 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.42 – 2.80 39.42 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.1 (39.42-2.80) 96.5 (39.42-2.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.92 (at 2.51 Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.253 , 0.292 0.264 , 0.300	Depositor DCC
$R_{free}$ test set	411 reflections (4.80%)	DCC
Wilson B-factor (Å <sup>2</sup> )	89.2	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 81.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2164	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.26% 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: BR

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	0/2201	0.61	0/2977

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	2162	0	2199	117	0
2	A	2	0	0	1	0
All	All	2164	0	2199	117	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 27.

All (117) 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:252:GLU:O	1:A:256:GLN:HG2	1.66	0.94
1:A:389:GLU:HG2	1:A:393:ARG:HD3	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:354:GLU:HB3	1:A:359:ARG:O	1.84	0.77
1:A:276:GLU:HB3	1:A:279:ARG:NH2	1.99	0.77
1:A:240:ARG:HH21	1:A:285:ARG:HA	1.49	0.77
1:A:316:PRO:HG3	1:A:322:TYR:HB2	1.66	0.76
1:A:392:TYR:HE1	1:A:396:GLN:HE21	1.34	0.75
1:A:269:HIS:CE1	1:A:271:ASP:HB2	2.21	0.75
1:A:343:GLY:O	1:A:345:ARG:N	2.20	0.73
1:A:224:GLY:O	1:A:228:VAL:HG23	1.90	0.72
1:A:342:TYR:OH	1:A:363:ARG:HD3	1.90	0.71
1:A:447:LEU:HD23	2:A:512:BR:BR	2.46	0.70
1:A:274:GLN:O	1:A:278:GLU:HG3	1.92	0.68
1:A:348:ARG:HG3	1:A:348:ARG:HH11	1.58	0.68
1:A:231:ASP:O	1:A:235:VAL:HG23	1.94	0.68
1:A:266:GLN:HG3	1:A:289:VAL:HG21	1.74	0.68
1:A:222:VAL:HB	1:A:344:PRO:CG	2.26	0.65
1:A:380:LEU:HD22	1:A:419:LEU:HD21	1.78	0.65
1:A:373:LEU:HD23	1:A:376:LYS:HD2	1.79	0.64
1:A:351:GLU:HA	1:A:354:GLU:HG3	1.79	0.64
1:A:248:LYS:HG3	1:A:269:HIS:HB2	1.78	0.64
1:A:481:PRO:HB2	1:A:488:LEU:HD13	1.79	0.64
1:A:318:ARG:HG3	1:A:320:GLU:H	1.64	0.62
1:A:343:GLY:C	1:A:345:ARG:H	2.03	0.62
1:A:254:ILE:HD11	1:A:314:ARG:HH12	1.66	0.61
1:A:318:ARG:CZ	1:A:318:ARG:HB3	2.29	0.61
1:A:473:VAL:HG13	1:A:473:VAL:O	2.00	0.60
1:A:391:ASP:O	1:A:394:LEU:HB2	2.01	0.60
1:A:238:PRO:O	1:A:290:ARG:HD3	2.01	0.60
1:A:285:ARG:HG2	1:A:305:PRO:HG3	1.84	0.60
1:A:272:MET:HE3	1:A:276:GLU:O	2.03	0.59
1:A:409:GLU:H	1:A:409:GLU:CD	2.05	0.59
1:A:393:ARG:HA	1:A:396:GLN:CG	2.33	0.59
1:A:460:GLU:HG2	1:A:476:ARG:HE	1.66	0.59
1:A:315:MET:HE1	1:A:350:VAL:HA	1.85	0.58
1:A:427:SER:HB2	1:A:435:TRP:HB2	1.86	0.57
1:A:239:ASP:O	1:A:290:ARG:HG2	2.04	0.57
1:A:222:VAL:HB	1:A:344:PRO:HG2	1.87	0.57
1:A:368:THR:OG1	1:A:370:GLU:HG2	2.05	0.56
1:A:392:TYR:HE1	1:A:396:GLN:NE2	2.03	0.55
1:A:446:SER:OG	1:A:448:PRO:HD2	2.07	0.54
1:A:326:SER:OG	1:A:338:VAL:HG11	2.06	0.54
1:A:393:ARG:HA	1:A:396:GLN:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:GLN:HG3	1:A:483:VAL:HG22	1.90	0.53
1:A:390:LYS:HG3	1:A:391:ASP:H	1.73	0.53
1:A:316:PRO:HG2	1:A:353:LEU:HD21	1.90	0.52
1:A:389:GLU:HG2	1:A:393:ARG:CD	2.39	0.52
1:A:254:ILE:HD11	1:A:314:ARG:NH1	2.25	0.52
1:A:398:PHE:CE1	1:A:401:ARG:NH2	2.78	0.52
1:A:342:TYR:HA	1:A:346:GLU:OE1	2.10	0.51
1:A:321:ALA:O	1:A:325:ARG:HG3	2.12	0.50
1:A:392:TYR:CE1	1:A:396:GLN:NE2	2.75	0.50
1:A:389:GLU:HA	1:A:392:TYR:CE2	2.46	0.50
1:A:390:LYS:HG3	1:A:391:ASP:N	2.27	0.50
1:A:455:LYS:HD3	1:A:461:VAL:HG23	1.94	0.50
1:A:326:SER:HB3	1:A:338:VAL:HG21	1.92	0.50
1:A:269:HIS:HE1	1:A:271:ASP:HB2	1.75	0.49
1:A:441:THR:HG22	1:A:469:GLY:O	2.11	0.49
1:A:467:ALA:HB2	1:A:472:TYR:CD2	2.47	0.49
1:A:450:LEU:HD13	1:A:486:LEU:HD21	1.94	0.49
1:A:350:VAL:O	1:A:354:GLU:HG3	2.12	0.49
1:A:389:GLU:O	1:A:393:ARG:HB2	2.12	0.49
1:A:393:ARG:HA	1:A:396:GLN:HG2	1.96	0.48
1:A:235:VAL:HG21	1:A:367:PRO:CB	2.44	0.48
1:A:284:PHE:CD2	1:A:292:LEU:HD22	2.49	0.48
1:A:447:LEU:HD12	1:A:471:PHE:CE2	2.49	0.48
1:A:248:LYS:HG3	1:A:269:HIS:CB	2.44	0.47
1:A:398:PHE:HA	1:A:401:ARG:HG3	1.97	0.47
1:A:284:PHE:HD1	1:A:289:VAL:O	1.98	0.47
1:A:354:GLU:O	1:A:358:GLY:N	2.47	0.47
1:A:447:LEU:HB3	1:A:448:PRO:HD3	1.97	0.47
1:A:436:ARG:O	1:A:438:TYR:CD1	2.67	0.47
1:A:244:PHE:HE2	1:A:299:ALA:HB2	1.81	0.46
1:A:315:MET:HB2	1:A:316:PRO:HD2	1.98	0.46
1:A:299:ALA:O	1:A:304:ILE:HG13	2.15	0.46
1:A:481:PRO:CB	1:A:488:LEU:HD13	2.46	0.46
1:A:368:THR:O	1:A:372:VAL:HG23	2.16	0.46
1:A:269:HIS:CD2	1:A:269:HIS:N	2.83	0.45
1:A:297:VAL:C	1:A:299:ALA:H	2.20	0.45
1:A:285:ARG:CG	1:A:305:PRO:HG3	2.46	0.45
1:A:315:MET:CB	1:A:316:PRO:HD2	2.47	0.45
1:A:263:HIS:HA	1:A:264:PRO:HD3	1.80	0.45
1:A:277:ARG:HH21	1:A:304:ILE:HD11	1.81	0.45
1:A:389:GLU:CD	1:A:390:LYS:N	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:ARG:HB2	1:A:431:GLY:HA3	1.99	0.44
1:A:313:TYR:HD2	1:A:314:ARG:HG3	1.82	0.44
1:A:281:MET:O	1:A:285:ARG:HG3	2.17	0.44
1:A:312:HIS:CE1	1:A:325:ARG:HD3	2.51	0.44
1:A:285:ARG:HG2	1:A:305:PRO:CG	2.47	0.44
1:A:445:LEU:HD12	1:A:449:ARG:HG2	2.00	0.44
1:A:315:MET:HE2	1:A:353:LEU:HD12	2.00	0.44
1:A:320:GLU:HA	1:A:320:GLU:OE2	2.17	0.44
1:A:426:ARG:NH1	1:A:431:GLY:O	2.41	0.44
1:A:318:ARG:HG2	1:A:318:ARG:HH21	1.84	0.43
1:A:427:SER:HB2	1:A:435:TRP:CB	2.49	0.42
1:A:219:PRO:HD3	1:A:364:VAL:O	2.20	0.42
1:A:312:HIS:ND1	1:A:325:ARG:HD3	2.34	0.42
1:A:480:ARG:HA	1:A:481:PRO:HD3	1.65	0.42
1:A:285:ARG:HD3	1:A:305:PRO:HG3	2.02	0.42
1:A:413:ALA:O	1:A:417:LEU:HD13	2.20	0.42
1:A:240:ARG:NH2	1:A:285:ARG:HA	2.27	0.42
1:A:343:GLY:C	1:A:345:ARG:N	2.69	0.42
1:A:398:PHE:HE1	1:A:401:ARG:NH2	2.17	0.42
1:A:450:LEU:CD1	1:A:486:LEU:HD21	2.50	0.42
1:A:224:GLY:HA2	1:A:227:GLU:OE1	2.20	0.41
1:A:235:VAL:HG21	1:A:367:PRO:HB3	2.01	0.41
1:A:436:ARG:O	1:A:438:TYR:HD1	2.04	0.41
1:A:212:THR:O	1:A:335:GLY:HA3	2.21	0.41
1:A:362:LYS:HG2	1:A:364:VAL:HG23	2.02	0.41
1:A:270:GLY:C	1:A:272:MET:H	2.24	0.41
1:A:373:LEU:HD23	1:A:373:LEU:HA	1.94	0.41
1:A:264:PRO:HB2	1:A:290:ARG:H	1.86	0.41
1:A:344:PRO:O	1:A:345:ARG:HB2	2.21	0.40
1:A:348:ARG:CG	1:A:348:ARG:HH11	2.28	0.40
1:A:257:GLY:O	1:A:261:LEU:HD12	2.21	0.40
1:A:372:VAL:O	1:A:375:ALA:HB3	2.21	0.40
1:A:435:TRP:CE3	1:A:474:ASP:HB3	2.56	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	272/300 (91%)	242 (89%)	24 (9%)	6 (2%)	8	26

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	GLY
1	A	344	PRO
1	A	298	ALA
1	A	444	ARG
1	A	481	PRO
1	A	280	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	217/235 (92%)	199 (92%)	18 (8%)	13	36

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	ARG
1	A	229	LEU
1	A	277	ARG
1	A	279	ARG
1	A	308	ASP

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Mol	Chain	Res	Type
1	A	318	ARG
1	A	320	GLU
1	A	323	GLN
1	A	362	LYS
1	A	363	ARG
1	A	370	GLU
1	A	389	GLU
1	A	392	TYR
1	A	397	ASP
1	A	433	GLU
1	A	447	LEU
1	A	487	ARG
1	A	489	GLU

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

Mol	Chain	Res	Type
1	A	256	GLN
1	A	306	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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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

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 [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	276/300 (92%)	0.34	12 (4%) 36 26	65, 113, 177, 203	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	481	PRO	6.3
1	A	444	ARG	5.3
1	A	471	PHE	5.1
1	A	466	GLU	4.9
1	A	480	ARG	4.6
1	A	472	TYR	3.9
1	A	485	GLY	3.0
1	A	484	ALA	3.0
1	A	467	ALA	2.7
1	A	429	LEU	2.6
1	A	468	GLU	2.4
1	A	316	PRO	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( $\text{\AA}^2$ )	Q<0.9
2	BR	A	512	1/1	0.94	0.17	-2.08	106,106,106,106	0
2	BR	A	511	1/1	0.94	0.26	-	111,111,111,111	0

## 6.5 Other polymers

There are no such residues in this entry.