



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 02:44 AM UTC

PDB ID : 9I0V / pdb\_00009i0v  
Title : Crystal structure of DasR in complex with a synthetic DasR-binding RNA aptamer  
Authors : Muller, Y.A.; Suess, B.  
Deposited on : 2025-01-15  
Resolution : 2.02 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)

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<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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

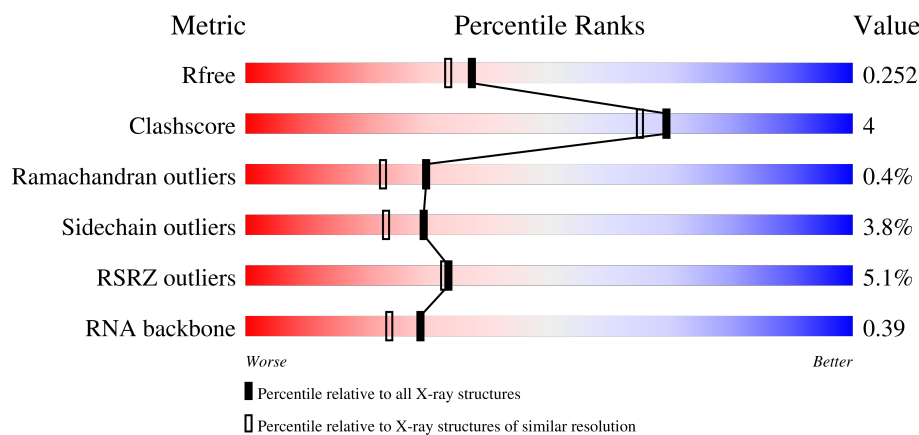
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.02 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))
$R_{free}$	180053	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)
RNA backbone	3983	1000 (2.38-1.66)

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	254	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>9%</div> <div>7%</div> </div> </div>
1	B	254	<div> <div>6%</div> <div> <div></div> <div>80%</div> <div>12%</div> <div>7%</div> </div> </div>
2	C	32	<div> <div></div> <div> <div>66%</div> <div>28%</div> <div>6%</div> </div> </div>
2	D	32	<div> <div>3%</div> <div> <div></div> <div>66%</div> <div>28%</div> <div>6%</div> </div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9696 atoms, of which 4518 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 HTH-type transcriptional repressor DasR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	235	Total	C	H	N	O	S	0	0	0
			3766	1164	1910	340	346	6			
1	B	235	Total	C	H	N	O	S	0	0	0
			3766	1164	1910	340	346	6			

- Molecule 2 is a RNA chain called A SELEX-derived artificial RNA aptamer.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	32	Total	C	H	N	O	P	0	0	0
			1030	303	349	122	224	32			
2	D	32	Total	C	H	N	O	P	0	0	0
			1030	303	349	122	224	32			

- Molecule 3 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Br	0	0
			1	1		
3	B	2	Total	Br	0	0
			2	2		
3	C	1	Total	Br	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	46	Total	O	0	0
			46	46		
4	B	48	Total	O	0	0
			48	48		
4	C	4	Total	O	0	0
			4	4		

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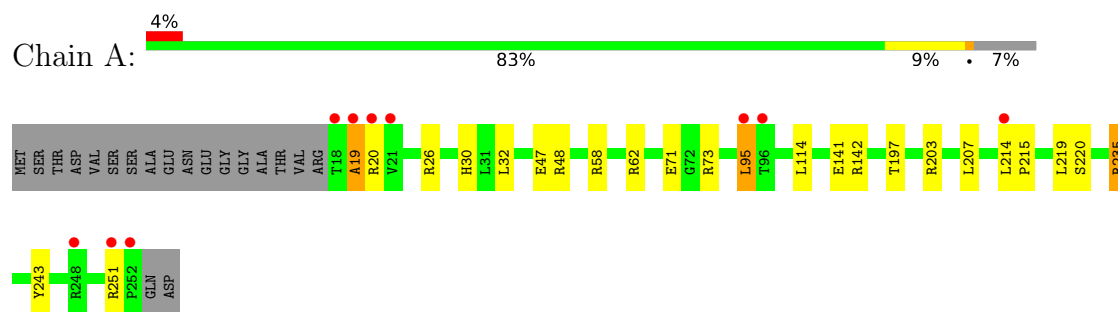
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	2	Total	O	0	0
			2	2		

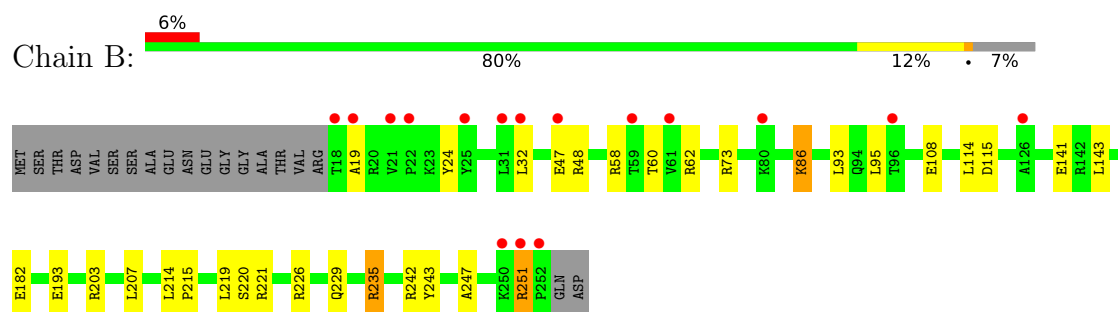
### 3 Residue-property plots [i](#)

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.

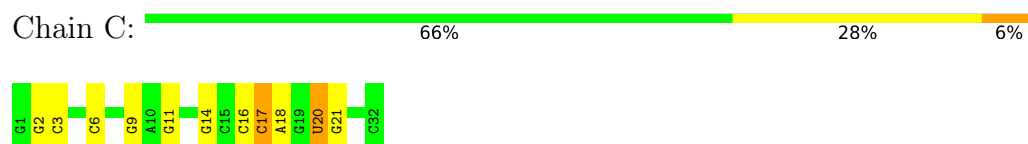
- Molecule 1: HTH-type transcriptional repressor DasR



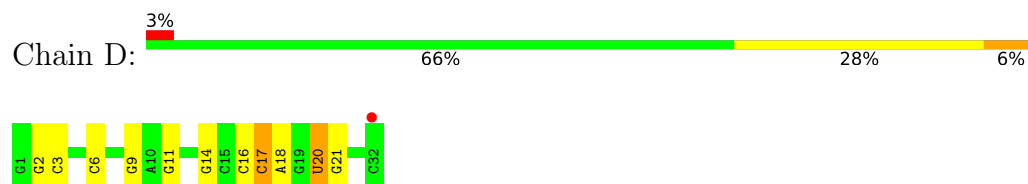
- Molecule 1: HTH-type transcriptional repressor DasR



- Molecule 2: A SELEX-derived artificial RNA aptamer



- Molecule 2: A SELEX-derived artificial RNA aptamer



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.94Å 51.33Å 116.40Å 90.00° 108.73° 90.00°	Depositor
Resolution (Å)	42.31 – 2.02 42.31 – 2.02	Depositor EDS
% Data completeness (in resolution range)	54.3 (42.31-2.02) 54.3 (42.31-2.02)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.09 (at 2.03Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, $R_{free}$	0.204 , 0.254 0.203 , 0.252	Depositor DCC
$R_{free}$ test set	2023 reflections (6.41%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.7	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 41.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9696	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.87% 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](#)

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	0.22	0/1887	0.35	0/2555
1	B	0.22	0/1887	0.34	0/2555
2	C	0.19	0/759	0.37	0/1179
2	D	0.19	0/759	0.36	0/1179
All	All	0.21	0/5292	0.35	0/7468

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	1856	1910	1910	16	1
1	B	1856	1910	1910	17	1
2	C	681	349	349	5	0
2	D	681	349	349	5	0
3	A	1	0	0	0	0
3	B	2	0	0	1	0
3	C	1	0	0	0	0
4	A	46	0	0	1	0
4	B	48	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	4	0	0	0	0
4	D	2	0	0	0	0
All	All	5178	4518	4518	34	1

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 4.

All (34) 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)
2:C:16:C:O2'	2:C:17:C:O4'	2.01	0.78
1:B:58:ARG:NH2	2:D:11:G:O6	2.19	0.76
1:B:93:LEU:HD12	1:B:247:ALA:HB2	1.69	0.74
1:B:32:LEU:HD23	1:B:73:ARG:NH1	2.10	0.67
1:B:47:GLU:OE1	1:B:58:ARG:NH1	2.30	0.63
1:A:47:GLU:OE1	1:A:58:ARG:NH1	2.33	0.62
2:D:16:C:O2'	2:D:17:C:O4'	2.19	0.61
1:A:48:ARG:NH2	2:C:9:G:N7	2.51	0.58
1:A:32:LEU:HD23	1:A:73:ARG:NH1	2.18	0.58
1:A:141:GLU:OE2	1:A:203:ARG:NH2	2.37	0.57
1:A:220:SER:OG	1:A:235:ARG:NH1	2.38	0.55
1:A:58:ARG:NH2	2:C:11:G:O6	2.39	0.55
1:B:48:ARG:NH2	2:D:9:G:N7	2.60	0.50
1:A:197:THR:HG21	1:B:215:PRO:HB2	1.94	0.48
2:D:20:U:O2	2:D:20:U:O4'	2.31	0.47
1:B:141:GLU:OE2	1:B:203:ARG:NH2	2.47	0.47
1:B:226:ARG:HD2	3:B:301:BR:BR	2.70	0.47
1:B:193:GLU:OE2	1:B:221:ARG:NH1	2.49	0.46
1:A:71:GLU:OE1	4:A:401:HOH:O	2.21	0.46
2:C:20:U:O2	2:C:20:U:O4'	2.33	0.46
1:B:220:SER:OG	1:B:235:ARG:NH1	2.48	0.46
1:B:86:LYS:HD2	1:B:242:ARG:CZ	2.46	0.45
1:A:62:ARG:NH2	2:C:14:G:O6	2.49	0.45
1:A:214:LEU:HD12	1:A:215:PRO:HD2	1.99	0.45
1:B:62:ARG:NH2	2:D:14:G:O6	2.49	0.45
1:A:19:ALA:O	1:A:20:ARG:HB2	2.17	0.44
1:B:114:LEU:HD11	1:B:143:LEU:HB2	1.98	0.44
1:A:95:LEU:HD23	1:B:251:ARG:NH1	2.34	0.42
1:A:20:ARG:HD3	1:B:115:ASP:OD1	2.19	0.42
1:B:24:TYR:HB3	1:B:60:THR:HG23	2.02	0.41
1:A:26:ARG:HD2	1:A:30:HIS:CD2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:LEU:HD12	1:A:95:LEU:HA	1.93	0.40
1:B:214:LEU:HD12	1:B:215:PRO:HD2	2.02	0.40
1:A:114:LEU:HB2	1:A:141:GLU:HG2	2.03	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:ARG:HH22	1:B:108:GLU:OE2[1_565]	1.56	0.04

## 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	233/254 (92%)	227 (97%)	5 (2%)	1 (0%)	30	22
1	B	233/254 (92%)	229 (98%)	3 (1%)	1 (0%)	30	22
All	All	466/508 (92%)	456 (98%)	8 (2%)	2 (0%)	30	22

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ALA
1	B	19	ALA

### 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	199/214 (93%)	193 (97%)	6 (3%)	36	32
1	B	199/214 (93%)	190 (96%)	9 (4%)	24	17
All	All	398/428 (93%)	383 (96%)	15 (4%)	29	23

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	LEU
1	A	207	LEU
1	A	219	LEU
1	A	235	ARG
1	A	243	TYR
1	A	251	ARG
1	B	86	LYS
1	B	95	LEU
1	B	182	GLU
1	B	207	LEU
1	B	219	LEU
1	B	229	GLN
1	B	235	ARG
1	B	243	TYR
1	B	251	ARG

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

Mol	Chain	Res	Type
1	A	38	GLN
1	B	63	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	31/32 (96%)	7 (22%)	0
2	D	31/32 (96%)	7 (22%)	0
All	All	62/64 (96%)	14 (22%)	0

All (14) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	2	G
2	C	3	C
2	C	6	C
2	C	17	C
2	C	18	A
2	C	20	U
2	C	21	G
2	D	2	G
2	D	3	C
2	D	6	C
2	D	17	C
2	D	18	A
2	D	20	U
2	D	21	G

There are no RNA pucker outliers to report.

## 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 4 ligands modelled in this entry, 4 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 [i](#)

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	235/254 (92%)	0.31	10 (4%) 40 39	37, 53, 78, 111	0
1	B	235/254 (92%)	0.51	16 (6%) 23 22	36, 55, 97, 144	0
2	C	32/32 (100%)	-0.24	0 100 100	53, 75, 128, 143	0
2	D	32/32 (100%)	0.44	1 (3%) 51 51	71, 108, 184, 206	0
All	All	534/572 (93%)	0.37	27 (5%) 33 33	36, 55, 110, 206	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	18	THR	6.3
1	B	21	VAL	5.7
1	B	19	ALA	5.7
1	B	252	PRO	4.3
1	A	252	PRO	4.2
1	A	19	ALA	3.7
1	B	251	ARG	3.5
1	A	18	THR	3.2
1	A	21	VAL	3.1
1	B	61	VAL	3.1
1	B	22	PRO	3.0
1	B	250	LYS	3.0
1	B	96	THR	2.6
1	B	47	GLU	2.6
1	A	248	ARG	2.6
1	A	96	THR	2.5
1	B	32	LEU	2.5
1	A	214	LEU	2.5
1	A	251	ARG	2.4
1	B	59	THR	2.4
1	B	80	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	31	LEU	2.3
1	A	20	ARG	2.2
2	D	32	C	2.1
1	A	95	LEU	2.1
1	B	126	ALA	2.0
1	B	25	TYR	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 oligosaccharides 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
3	BR	B	302	1/1	0.60	0.35	178,178,178,178	0
3	BR	C	101	1/1	0.93	0.28	100,100,100,100	0
3	BR	B	301	1/1	0.96	0.07	77,77,77,77	0
3	BR	A	301	1/1	0.97	0.09	86,86,86,86	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.