



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 03:09 PM GMT

PDB ID : 2FJV  
Title : RT29 Bound to D(CTTAATTCGAATTAAG) in complex with MMLV RT  
Catalytic Fragment  
Authors : Goodwin, K.D.; Georgiadis, M.M.  
Deposited on : 2006-01-03  
Resolution : 2.05 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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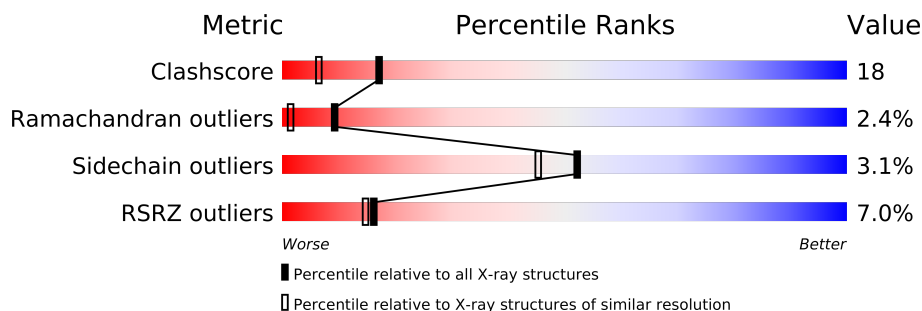
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.05 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))
Clashscore	79885	1577 (2.06-2.02)
Ramachandran outliers	78287	1565 (2.06-2.02)
Sidechain outliers	78261	1565 (2.06-2.02)
RSRZ outliers	66119	1381 (2.06-2.02)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	B	8	
2	G	8	
3	A	255	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	HXL	G	301	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2616 atoms, of which 0 are hydrogen and 0 are deuterium.

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 DNA chain called 5'-D(\*CP\*TP\*TP\*AP\*AP\*TP\*TP\*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	8	Total	C	N	O	P	0	0	0
			157	78	24	48	7			

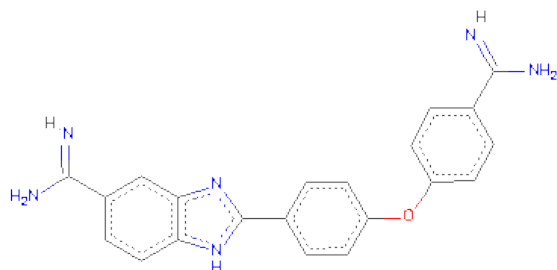
- Molecule 2 is a DNA chain called 5'-D(P\*GP\*AP\*AP\*TP\*TP\*AP\*AP\*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	8	Total	C	N	O	P	0	0	0
			168	80	34	46	8			

- Molecule 3 is a protein called Reverse transcriptase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	255	Total	C	N	O	S	0	0	0
			2041	1311	356	367	7			

- Molecule 4 is 2-(4-(4-CARBAMIMIDOYLPHENOXY)PHENYL)-1H-BENZO[D]IMIDAZOLE-6-CARBOXIMIDAMIDE (three-letter code: HXL) (formula: C<sub>21</sub>H<sub>18</sub>N<sub>6</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	G	1	Total	C	N	O	0	0
			28	21	6	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	209	Total	O	0	0
			209	209		
5	B	4	Total	O	0	0
			4	4		
5	G	9	Total	O	0	0
			9	9		

### 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 (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: 5'-D(\*CP\*TP\*TP\*AP\*AP\*TP\*TP\*C)-3'

Chain B:

- Molecule 2: 5'-D(P\*GP\*AP\*AP\*TP\*TP\*AP\*AP\*G)-3'

Chain G:

- Molecule 3: Reverse transcriptase

Chain A:

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.55Å 145.65Å 46.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.05 30.29 – 2.05	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.05) 93.1 (30.29-2.05)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.48 (at 2.05Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.228 , 0.280 0.247 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	27.1	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 36.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 23344 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2616	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.78% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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

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	B	0.31	0/174	0.71	0/266
2	G	0.30	0/189	0.70	0/290
3	A	0.33	0/2097	0.64	1/2858 (0.0%)
All	All	0.32	0/2460	0.65	1/3414 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	202	ALA	N-CA-C	-5.38	96.47	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	157	0	94	7	1
2	G	168	0	91	5	1
3	A	2041	0	2056	71	0
4	G	28	0	17	0	0
5	A	209	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	4	0	0	0	0
5	G	9	0	0	0	0
All	All	2616	0	2258	82	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 18.

All (82) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:103:LYS:HB2	3:A:104:PRO:HD3	1.38	1.05
3:A:74:ILE:HG23	3:A:111:PRO:HG3	1.43	1.00
3:A:61:ILE:HD11	3:A:117:GLU:HG3	1.59	0.84
3:A:174:ASP:HB3	3:A:178:GLY:HA3	1.58	0.82
3:A:274:LYS:HG2	3:A:275:GLU:HG3	1.62	0.81
3:A:265:GLN:HE21	3:A:274:LYS:HD2	1.46	0.81
3:A:179:ILE:HD13	3:A:183:LEU:HD21	1.72	0.71
3:A:272:LEU:H	3:A:278:ARG:HH11	1.40	0.70
3:A:62:LYS:HE3	3:A:62:LYS:HA	1.75	0.68
3:A:103:LYS:HB2	3:A:104:PRO:CD	2.21	0.67
3:A:102:LYS:HD3	3:A:102:LYS:N	2.11	0.66
3:A:104:PRO:HB2	3:A:107:ASN:HD21	1.61	0.66
3:A:62:LYS:CE	3:A:62:LYS:HA	2.27	0.65
2:G:16:DG:C2	3:A:99:LEU:HD11	2.35	0.62
3:A:64:TYR:HE2	3:A:99:LEU:HD23	1.64	0.61
3:A:110:ARG:NH1	3:A:110:ARG:HB2	2.15	0.61
3:A:161:HIS:CD2	3:A:163:THR:H	2.19	0.61
3:A:161:HIS:HD2	3:A:163:THR:H	1.49	0.60
3:A:268:TYR:HB3	3:A:273:LEU:HD21	1.82	0.60
3:A:266:VAL:HG23	3:A:273:LEU:HD23	1.85	0.58
3:A:75:LYS:HB3	3:A:76:PRO:HD3	1.88	0.56
3:A:173:ARG:HH12	3:A:181:GLY:HA2	1.71	0.55
3:A:101:VAL:C	3:A:102:LYS:HD3	2.27	0.55
3:A:174:ASP:HB3	3:A:178:GLY:CA	2.34	0.55
3:A:277:GLN:O	3:A:278:ARG:HB2	2.07	0.55
3:A:62:LYS:HE3	3:A:63:GLN:H	1.72	0.55
3:A:202:ALA:O	3:A:203:LEU:HB3	2.07	0.54
3:A:104:PRO:CB	3:A:107:ASN:HD21	2.20	0.54
3:A:110:ARG:CB	3:A:110:ARG:HH11	2.20	0.54
3:A:172:TRP:HD1	3:A:179:ILE:HD12	1.73	0.53
3:A:206:ASP:HB3	3:A:250:LEU:HD13	1.91	0.52
3:A:248:GLY:HA3	5:A:355:HOH:O	2.09	0.52
3:A:174:ASP:CB	3:A:178:GLY:HA3	2.33	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:227:LEU:HD13	3:A:227:LEU:C	2.30	0.52
3:A:273:LEU:N	3:A:273:LEU:HD22	2.25	0.52
3:A:126:HIS:HB2	5:A:421:HOH:O	2.08	0.52
1:B:6:DT:H2''	1:B:7:DT:C5'	2.40	0.51
3:A:57:THR:HG22	5:A:398:HOH:O	2.10	0.51
3:A:24:THR:HB	3:A:27:SER:OG	2.11	0.50
3:A:110:ARG:HB2	3:A:110:ARG:HH11	1.76	0.50
3:A:202:ALA:O	3:A:203:LEU:CB	2.58	0.50
3:A:62:LYS:CA	3:A:62:LYS:HE3	2.43	0.49
3:A:104:PRO:CG	3:A:107:ASN:HD21	2.25	0.49
3:A:49:ILE:O	3:A:51:PRO:HD3	2.13	0.48
3:A:104:PRO:HB2	3:A:107:ASN:ND2	2.27	0.48
3:A:218:ILE:HB	3:A:229:ALA:HB3	1.95	0.48
1:B:6:DT:H2''	1:B:7:DT:H5''	1.97	0.47
1:B:7:DT:H5'	1:B:7:DT:H6	1.80	0.47
3:A:148:VAL:HG22	3:A:227:LEU:HD23	1.98	0.46
3:A:237:GLN:NE2	5:A:451:HOH:O	2.49	0.46
3:A:165:GLN:HG2	3:A:185:TRP:O	2.16	0.46
1:B:6:DT:C2'	1:B:7:DT:H5''	2.46	0.46
3:A:138:GLY:O	3:A:140:PRO:HD3	2.15	0.46
1:B:4:DA:H2''	1:B:5:DA:OP2	2.15	0.45
3:A:172:TRP:CD1	3:A:179:ILE:HD12	2.49	0.45
2:G:12:DT:H2''	2:G:13:DT:C5'	2.47	0.45
3:A:174:ASP:O	3:A:176:GLU:N	2.49	0.45
1:B:6:DT:H1'	1:B:7:DT:H5''	1.99	0.44
3:A:199:PHE:O	3:A:202:ALA:O	2.35	0.44
2:G:12:DT:H2''	2:G:13:DT:H5''	2.00	0.44
3:A:173:ARG:HH11	3:A:173:ARG:HG2	1.82	0.44
3:A:274:LYS:HE2	3:A:275:GLU:OE1	2.18	0.43
3:A:98:LEU:HD12	3:A:98:LEU:HA	1.87	0.43
3:A:203:LEU:HD23	5:A:295:HOH:O	2.18	0.43
3:A:68:GLN:HG2	3:A:72:LEU:HD22	2.00	0.43
3:A:110:ARG:CB	3:A:110:ARG:NH1	2.81	0.43
3:A:139:LEU:HD22	5:A:484:HOH:O	2.19	0.43
3:A:107:ASN:O	3:A:108:ASP:C	2.57	0.42
3:A:104:PRO:HG2	3:A:107:ASN:HD21	1.84	0.42
2:G:13:DT:H5'	2:G:13:DT:H6	1.84	0.42
3:A:104:PRO:HD2	3:A:107:ASN:OD1	2.18	0.42
3:A:126:HIS:HA	3:A:127:PRO:HD3	1.93	0.42
3:A:237:GLN:O	3:A:241:ARG:HG3	2.20	0.42
3:A:72:LEU:HA	3:A:72:LEU:HD12	1.93	0.42
3:A:278:ARG:NH2	5:A:426:HOH:O	2.52	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:A:214:HIS:HB3	3:A:217:LEU:HD12	2.02	0.41
3:A:273:LEU:HD22	3:A:273:LEU:H	1.86	0.41
3:A:70:ALA:HA	3:A:109:TYR:CE2	2.56	0.41
2:G:12:DT:C2'	2:G:13:DT:H5''	2.50	0.40
3:A:99:LEU:HA	3:A:100:PRO:HD3	1.79	0.40
1:B:1:DC:C6	1:B:2:DT:H72	2.57	0.40
3:A:156:PHE:O	3:A:187:ARG:NH1	2.43	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	Distance(Å)	Clash(Å)
1:B:8:DC:O3'	2:G:9:DG:P[2.765]	1.60	0.60

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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
3	A	253/255 (99%)	234 (92%)	13 (5%)	6 (2%)	9 1

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	104	PRO
3	A	103	LYS
3	A	223	VAL
3	A	175	PRO
3	A	108	ASP
3	A	181	GLY

### 5.3.2 Protein sidechains ⓘ

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
3	A	224/224 (100%)	217 (97%)	7 (3%)	52 45

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	28	ASP
3	A	57	THR
3	A	62	LYS
3	A	64	TYR
3	A	72	LEU
3	A	102	LYS
3	A	139	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	84	GLN
3	A	134	ASN
3	A	144	GLN
3	A	161	HIS
3	A	237	GLN
3	A	238	GLN
3	A	263	GLN
3	A	265	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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$
4	HXL	G	301	-	31,31,31	6.37	26 (83%)	44,44,44	1.73	5 (11%)

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
4	HXL	G	301	-	-	0/16/16/16	0/2/4/4

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	301	HXL	C19-C18	10.08	1.56	1.39
4	G	301	HXL	C8-C2	9.71	1.56	1.39
4	G	301	HXL	C9-C5	9.38	1.59	1.47
4	G	301	HXL	C3-C2	9.27	1.53	1.37
4	G	301	HXL	C20-C19	9.18	1.56	1.38
4	G	301	HXL	C3-C4	9.17	1.52	1.41
4	G	301	HXL	C7-C8	8.92	1.55	1.36
4	G	301	HXL	C14-C13	8.84	1.55	1.38
4	G	301	HXL	C13-C12	8.03	1.55	1.38
4	G	301	HXL	C20-C15	7.78	1.55	1.38
4	G	301	HXL	C11-C12	7.54	1.54	1.38
4	G	301	HXL	C7-C6	6.63	1.55	1.40
4	G	301	HXL	C14-C9	6.47	1.53	1.39
4	G	301	HXL	C16-C15	6.46	1.52	1.38
4	G	301	HXL	C17-C18	6.44	1.50	1.39
4	G	301	HXL	C11-C10	5.93	1.50	1.38
4	G	301	HXL	C17-C16	5.82	1.50	1.38
4	G	301	HXL	C18-C21	5.81	1.55	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	301	HXL	C10-C9	4.70	1.49	1.39
4	G	301	HXL	C2-C1	4.56	1.53	1.49
4	G	301	HXL	O1-C12	4.55	1.50	1.39
4	G	301	HXL	O1-C15	4.31	1.49	1.39
4	G	301	HXL	C21-N5	2.55	1.35	1.27
4	G	301	HXL	C6-C4	2.44	1.49	1.42
4	G	301	HXL	C4-N3	-2.15	1.31	1.38
4	G	301	HXL	C1-N1	2.05	1.33	1.27

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	301	HXL	C15-O1-C12	7.50	137.68	118.76
4	G	301	HXL	C5-N3-C4	3.18	109.28	103.70
4	G	301	HXL	C9-C5-N4	2.68	126.03	121.22
4	G	301	HXL	C13-C12-C11	-2.33	116.22	120.21
4	G	301	HXL	C17-C16-C15	2.10	122.57	119.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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(Å²)	Q<0.9	
1	B	8/8 (100%)	0.19	0	100	100	44, 50, 58, 58	0
2	G	8/8 (100%)	0.12	0	100	100	29, 49, 53, 58	0
3	A	255/255 (100%)	0.35	19 (7%)	14	13	13, 26, 64, 92	0
All	All	271/271 (100%)	0.33	19 (7%)	16	15	13, 27, 62, 92	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	106	THR	10.1
3	A	105	GLY	8.6
3	A	179	ILE	8.2
3	A	177	MET	6.9
3	A	178	GLY	5.4
3	A	104	PRO	5.2
3	A	180	SER	5.2
3	A	101	VAL	3.7
3	A	108	ASP	3.4
3	A	100	PRO	3.3
3	A	107	ASN	3.0
3	A	174	ASP	3.0
3	A	202	ALA	2.9
3	A	176	GLU	2.8
3	A	103	LYS	2.8
3	A	275	GLU	2.8
3	A	175	PRO	2.8
3	A	173	ARG	2.6
3	A	99	LEU	2.5

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

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	HXL	G	301	28/28	0.31	5.34	71,72,74,75	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.