



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:55 PM UTC

PDB ID : 4EXT / pdb\_00004ext  
Title : Structure of polymerase-interacting domain of human Rev1 in complex with translesional synthesis polymerase zeta  
Authors : Liu, D.N.; Ryu, K.S.; Ko, J.S.; Choi, B.S.  
Deposited on : 2012-05-01  
Resolution : 1.90 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

<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  
Xtrriage (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

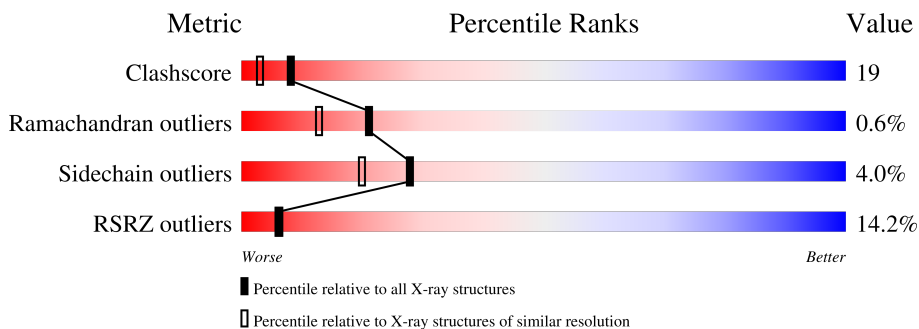
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	96	
2	B	23	
3	C	204	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2685 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 DNA repair protein REV1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	96	778	500	121	152	5	0	0	0

- Molecule 2 is a protein called peptide from DNA polymerase zeta catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	23	178	113	31	32	2	0	0	0

- Molecule 3 is a protein called Mitotic spindle assembly checkpoint protein MAD2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	198	1614	1039	274	291	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	6	THR	-	expression tag	UNP Q9UI95

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	25	Total	O	0	0
			25	25		
4	B	12	Total	O	0	0
			12	12		
4	C	78	Total	O	0	0
			78	78		

### 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.

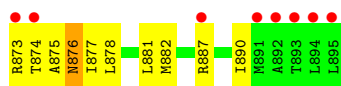
- Molecule 1: DNA repair protein REV1

Chain A: 



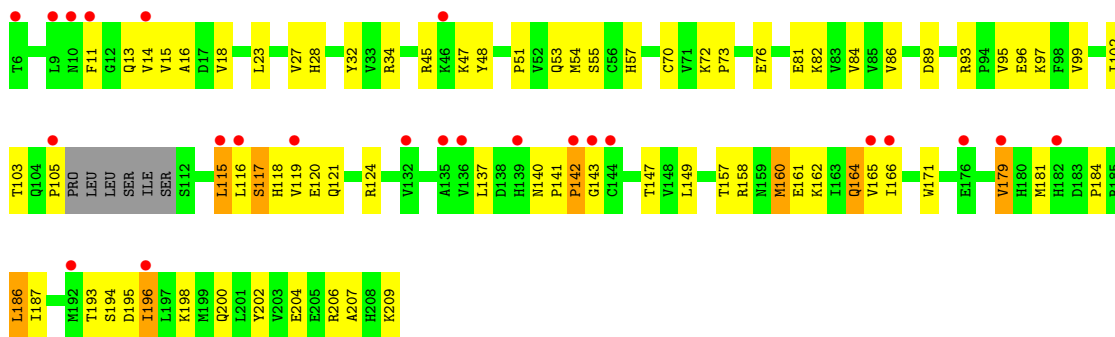
- Molecule 2: peptide from DNA polymerase zeta catalytic subunit

Chain B: 



- Molecule 3: Mitotic spindle assembly checkpoint protein MAD2B

Chain C: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.70Å 71.52Å 84.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90 50.00 – 1.91	Depositor EDS
% Data completeness (in resolution range)	94.4 (50.00-1.90) 95.6 (50.00-1.91)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.80 (at 1.91Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.224 , 0.285 0.242 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.8	Xtrriage
Anisotropy	0.308	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	2685	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.09% 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](#)

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	0.43	0/789	0.87	3/1070 (0.3%)
2	B	0.41	0/180	0.88	0/243
3	C	0.49	2/1648 (0.1%)	0.91	5/2237 (0.2%)
All	All	0.47	2/2617 (0.1%)	0.89	8/3550 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	200	GLN	C-O	-7.88	1.14	1.23
3	C	200	GLN	CA-C	-5.23	1.46	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	179	ILE	N-CA-C	8.01	118.90	111.45
3	C	200	GLN	N-CA-C	7.09	121.12	109.06
3	C	84	VAL	N-CA-C	6.09	116.64	108.11
3	C	102	ILE	N-CA-C	5.80	116.94	108.53
3	C	117	SER	N-CA-C	-5.48	106.55	113.18
1	A	176	ILE	N-CA-C	5.33	116.05	110.62
1	A	216	LEU	N-CA-C	5.17	117.82	111.82
3	C	99	VAL	N-CA-C	5.03	115.33	107.99

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	778	0	789	29	0
2	B	178	0	195	15	0
3	C	1614	0	1644	62	0
4	A	25	0	0	2	0
4	B	12	0	0	0	0
4	C	78	0	0	4	0
All	All	2685	0	2628	101	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 19.

All (101) 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:222:GLU:HG2	1:A:224:VAL:HG12	1.48	0.92
3:C:11:PHE:HB3	3:C:14:VAL:HG13	1.49	0.91
2:B:876:ASN:H	2:B:876:ASN:HD22	1.29	0.80
3:C:195:ASP:O	3:C:196:ILE:HG12	1.82	0.80
1:A:214:LYS:NZ	1:A:218:GLN:HE22	1.80	0.79
1:A:214:LYS:HZ3	1:A:218:GLN:HE22	1.27	0.78
1:A:158:ASN:HD22	1:A:161:GLY:H	1.33	0.77
3:C:28:HIS:HD2	3:C:55:SER:H	1.35	0.74
3:C:103:THR:HB	3:C:198:LYS:HB3	1.74	0.70
3:C:164:GLN:HA	3:C:164:GLN:HE21	1.56	0.69
1:A:209:VAL:HG12	1:A:213:MET:HE2	1.73	0.68
3:C:48:TYR:O	3:C:124:ARG:HD3	1.95	0.67
3:C:116:LEU:O	3:C:119:VAL:HG12	1.94	0.67
3:C:137:LEU:HD23	3:C:187:ILE:HD13	1.75	0.67
3:C:93:ARG:HD2	4:C:319:HOH:O	1.95	0.66
1:A:179:ILE:O	1:A:180:SER:HB2	1.95	0.64
1:A:175:TRP:O	1:A:179:ILE:HD13	1.98	0.63
1:A:164:GLU:HB2	1:A:167:ASP:OD2	2.00	0.62
3:C:72:LYS:O	3:C:76:GLU:HG3	2.01	0.60
2:B:887:ARG:HG3	2:B:887:ARG:HH11	1.66	0.60
3:C:95:VAL:HG12	3:C:206:ARG:NH1	2.17	0.60
1:A:156:ALA:HB3	1:A:157:PRO:HD3	1.84	0.60
3:C:165:VAL:HG13	3:C:166:ILE:HG13	1.82	0.60
3:C:11:PHE:HB3	3:C:14:VAL:CG1	2.30	0.58
2:B:874:THR:O	2:B:874:THR:HG22	2.04	0.58
2:B:874:THR:HG23	2:B:877:ILE:HD12	1.86	0.58
1:A:250:VAL:O	1:A:251:THR:HG23	2.04	0.58
1:A:230:ASP:O	1:A:234:ASP:HB2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:45:ARG:HD3	3:C:54:MET:HG3	1.87	0.56
3:C:95:VAL:HG12	3:C:206:ARG:CZ	2.35	0.56
3:C:32:TYR:CE2	3:C:53:GLN:HG3	2.41	0.56
3:C:115:LEU:O	3:C:118:HIS:HB3	2.06	0.56
3:C:164:GLN:HE22	3:C:171:TRP:H	1.51	0.56
1:A:157:PRO:CG	1:A:200:GLU:HG3	2.37	0.55
2:B:873:ARG:HD3	2:B:875:ALA:HB3	1.89	0.55
3:C:45:ARG:HG2	3:C:45:ARG:HH11	1.71	0.54
1:A:158:ASN:HD22	1:A:161:GLY:N	2.04	0.54
1:A:169:LYS:HG3	1:A:212:TYR:CE2	2.43	0.53
1:A:176:ILE:HG21	1:A:216:LEU:HB3	1.89	0.53
1:A:227:MET:HA	1:A:227:MET:HE2	1.91	0.53
3:C:181:MET:HE1	3:C:204:GLU:C	2.34	0.52
1:A:157:PRO:HG3	1:A:200:GLU:HG3	1.92	0.52
1:A:218:GLN:C	1:A:220:SER:H	2.18	0.52
3:C:14:VAL:O	3:C:18:VAL:HG23	2.09	0.52
3:C:105:PRO:HG2	3:C:196:ILE:N	2.26	0.49
3:C:121:GLN:HG2	3:C:124:ARG:NH2	2.27	0.49
3:C:141:PRO:HB3	3:C:142:PRO:HD2	1.94	0.49
1:A:156:ALA:HB1	4:A:317:HOH:O	2.12	0.49
3:C:70:CYS:SG	3:C:165:VAL:HG12	2.54	0.48
3:C:15:VAL:HG13	3:C:16:ALA:N	2.29	0.48
1:A:175:TRP:HA	1:A:179:ILE:HD13	1.95	0.48
2:B:878:LEU:HD22	3:C:160:MET:HE3	1.97	0.47
3:C:51:PRO:HD3	4:C:356:HOH:O	2.14	0.47
2:B:876:ASN:H	2:B:876:ASN:ND2	2.05	0.47
3:C:73:PRO:HB2	3:C:162:LYS:HE3	1.96	0.47
1:A:158:ASN:ND2	1:A:161:GLY:H	2.06	0.47
1:A:215:ARG:O	1:A:219:GLN:HG2	2.14	0.47
1:A:182:PRO:HB3	1:A:225:TRP:CH2	2.50	0.46
2:B:878:LEU:CD2	3:C:160:MET:HE3	2.44	0.46
1:A:215:ARG:NH2	4:A:325:HOH:O	2.48	0.46
1:A:169:LYS:HG3	1:A:212:TYR:CD2	2.51	0.45
3:C:186:LEU:HD21	3:C:202:TYR:CD2	2.51	0.45
3:C:32:TYR:CD2	3:C:53:GLN:HG3	2.51	0.45
3:C:45:ARG:HB3	3:C:45:ARG:CZ	2.47	0.45
2:B:887:ARG:HG3	2:B:887:ARG:NH1	2.31	0.45
3:C:117:SER:O	3:C:120:GLU:HB3	2.17	0.45
3:C:140:ASN:HD21	3:C:209:LYS:HZ3	1.65	0.45
3:C:34:ARG:NH2	3:C:96:GLU:OE1	2.50	0.44
2:B:881:LEU:HG	2:B:882:MET:CE	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:887:ARG:NH2	3:C:143:GLY:HA2	2.33	0.44
3:C:181:MET:HE1	3:C:204:GLU:O	2.17	0.44
3:C:186:LEU:C	3:C:187:ILE:HG13	2.41	0.44
3:C:160:MET:O	3:C:164:GLN:HG2	2.17	0.44
3:C:193:THR:O	3:C:194:SER:HB3	2.17	0.44
3:C:157:THR:O	3:C:161:GLU:HG3	2.18	0.43
1:A:181:ASP:CG	1:A:181:ASP:O	2.60	0.43
2:B:887:ARG:HH21	3:C:143:GLY:HA2	1.83	0.43
3:C:89:ASP:C	3:C:89:ASP:OD1	2.60	0.43
3:C:207:ALA:HB3	4:C:359:HOH:O	2.18	0.43
3:C:28:HIS:HE1	4:C:308:HOH:O	2.02	0.43
3:C:47:LYS:HE3	3:C:54:MET:HE2	2.00	0.42
2:B:890:ILE:HG23	3:C:57:HIS:CD2	2.55	0.42
3:C:86:VAL:HB	3:C:147:THR:CG2	2.49	0.42
1:A:214:LYS:NZ	1:A:218:GLN:NE2	2.60	0.42
2:B:873:ARG:C	2:B:875:ALA:N	2.76	0.42
3:C:23:LEU:O	3:C:27:VAL:HG23	2.20	0.42
3:C:181:MET:HE2	3:C:184:PRO:HB3	2.02	0.42
3:C:34:ARG:HH21	3:C:140:ASN:ND2	2.16	0.42
1:A:216:LEU:HA	1:A:219:GLN:HG2	2.02	0.41
3:C:140:ASN:HD21	3:C:209:LYS:NZ	2.17	0.41
3:C:140:ASN:ND2	3:C:209:LYS:NZ	2.68	0.41
3:C:81:GLU:HG2	3:C:82:LYS:HG3	2.02	0.41
3:C:72:LYS:N	3:C:73:PRO:HD2	2.35	0.41
3:C:86:VAL:HG22	3:C:97:LYS:HG2	2.02	0.41
3:C:165:VAL:HG22	3:C:165:VAL:O	2.20	0.41
3:C:72:LYS:HB2	3:C:72:LYS:HE3	1.89	0.41
2:B:873:ARG:HG3	2:B:875:ALA:H	1.86	0.40
3:C:149:LEU:HD13	3:C:179:VAL:HG12	2.02	0.40
1:A:179:ILE:N	1:A:179:ILE:HD12	2.36	0.40
3:C:86:VAL:HB	3:C:147:THR:HG22	2.02	0.40
3:C:45:ARG:HH11	3:C:45:ARG:CG	2.35	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	94/96 (98%)	89 (95%)	5 (5%)	0	100	100
2	B	21/23 (91%)	18 (86%)	3 (14%)	0	100	100
3	C	194/204 (95%)	180 (93%)	12 (6%)	2 (1%)	12	5
All	All	309/323 (96%)	287 (93%)	20 (6%)	2 (1%)	21	13

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	142	PRO
3	C	196	ILE

### 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	90/90 (100%)	86 (96%)	4 (4%)	25	17
2	B	21/21 (100%)	20 (95%)	1 (5%)	23	15
3	C	187/193 (97%)	180 (96%)	7 (4%)	30	22
All	All	298/304 (98%)	286 (96%)	12 (4%)	28	20

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	GLU
1	A	216	LEU
1	A	230	ASP
1	A	251	THR
2	B	876	ASN
3	C	13	GLN
3	C	115	LEU

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Mol	Chain	Res	Type
3	C	158	ARG
3	C	160	MET
3	C	164	GLN
3	C	179	VAL
3	C	186	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	ASN
1	A	166	ASN
1	A	218	GLN
1	A	235	ASN
1	A	241	GLN
2	B	876	ASN
3	C	7	GLN
3	C	10	ASN
3	C	13	GLN
3	C	28	HIS
3	C	43	GLN
3	C	53	GLN
3	C	57	HIS
3	C	92	HIS
3	C	140	ASN
3	C	159	ASN
3	C	164	GLN
3	C	177	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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	96/96 (100%)	0.89	13 (13%) <b>7</b> <b>7</b>	21, 35, 53, 62	0
2	B	23/23 (100%)	1.37	8 (34%) <b>1</b> <b>0</b>	24, 42, 81, 83	0
3	C	198/204 (97%)	0.78	24 (12%) <b>8</b> <b>9</b>	18, 37, 65, 87	1 (0%)
All	All	317/323 (98%)	0.86	45 (14%) <b>6</b> <b>6</b>	18, 37, 67, 87	1 (0%)

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	895	LEU	5.0
3	C	144	CYS	4.5
2	B	893	THR	3.7
3	C	142	PRO	3.7
1	A	251	THR	3.7
1	A	179	ILE	3.4
1	A	163	VAL	3.3
3	C	10	ASN	3.1
3	C	116	LEU	3.0
3	C	196	ILE	3.0
1	A	220	SER	2.9
1	A	167	ASP	2.9
3	C	139	HIS	2.8
3	C	135	ALA	2.8
3	C	6	THR	2.7
3	C	11	PHE	2.7
1	A	250	VAL	2.7
1	A	156	ALA	2.6
1	A	219	GLN	2.6
3	C	182	HIS	2.5
1	A	221	VAL	2.5
3	C	165	VAL	2.5
3	C	14	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	105	PRO	2.5
2	B	887	ARG	2.4
2	B	894	LEU	2.4
3	C	143	GLY	2.4
3	C	9	LEU	2.4
1	A	165	PHE	2.4
3	C	166	ILE	2.4
1	A	164	GLU	2.4
3	C	46	LYS	2.4
2	B	874	THR	2.3
3	C	179	VAL	2.3
2	B	873	ARG	2.2
2	B	892	ALA	2.2
2	B	891	MET	2.2
3	C	132	VAL	2.1
1	A	171	LEU	2.1
3	C	115	LEU	2.1
1	A	160	ALA	2.1
3	C	119	VAL	2.1
3	C	136	VAL	2.1
3	C	192	MET	2.0
3	C	176	GLU	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 [\(i\)](#)

There are no ligands in this entry.

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.