



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:57 AM UTC

PDB ID : 4XR1 / pdb_00004xr1
Title : Escherichia Coli Replication Terminator Protein (Tus) Complexed With DNA-AG/AT mismatch.
Authors : Oakley, A.J.
Deposited on : 2015-01-20
Resolution : 2.40 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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
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

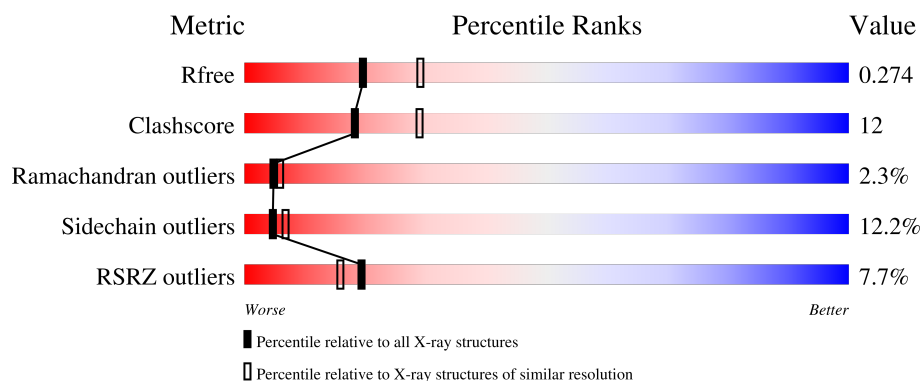
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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 ≥ 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	316	7% 68% 22% 6% ••
2	B	16	12% 44% 38% 6% 12%
3	C	16	12% 75% 19% 6%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3214 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 replication terminus site-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	S	0	3	0
			2530	1605	479	443	3			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP P16525
A	-5	HIS	-	expression tag	UNP P16525
A	-4	HIS	-	expression tag	UNP P16525
A	-3	HIS	-	expression tag	UNP P16525
A	-2	HIS	-	expression tag	UNP P16525
A	-1	HIS	-	expression tag	UNP P16525
A	0	HIS	-	expression tag	UNP P16525

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	P	0	0	0
			285	138	54	80	13			

- Molecule 3 is a DNA chain called DNA (5'-D(*GP*TP*AP*AP*TP*GP*TP*TP*GP*TP*AP*AP*CP*TP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	15	Total	C	N	O	P	0	0	1
			289	139	50	86	14			

- Molecule 4 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	6	Total I 6 6	0	0

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 8 6 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	72	Total O 72 72	0	0
6	B	13	Total O 13 13	0	0
6	C	11	Total O 11 11	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	64.81Å 64.81Å 246.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	62.68 – 2.40 62.68 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.4 (62.68-2.40) 99.4 (62.68-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.03 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.198 , 0.269 0.204 , 0.274	Depositor DCC
R_{free} test set	1092 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3214	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: IOD, MPD

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	1.22	7/2594 (0.3%)	1.33	19/3519 (0.5%)
2	B	0.62	0/320	1.26	4/492 (0.8%)
3	C	0.56	0/323	1.15	1/498 (0.2%)
All	All	1.13	7/3237 (0.2%)	1.30	24/4509 (0.5%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	232	ARG	CA-C	6.29	1.58	1.52
1	A	200	VAL	CA-C	6.00	1.60	1.52
1	A	188	ALA	CA-C	5.88	1.60	1.52
1	A	55	ARG	CZ-NH2	-5.70	1.26	1.33
1	A	120	LEU	CA-C	5.49	1.59	1.52
1	A	179	LYS	CA-C	5.48	1.59	1.52
1	A	302	ARG	CD-NE	-5.13	1.39	1.46

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	299	ILE	CB-CA-C	-10.80	99.13	111.55
1	A	199	SER	N-CA-C	8.89	120.34	108.07
3	C	338	DA	C2'-C3'-O3'	-8.18	99.23	111.50
1	A	247	ASP	N-CA-C	7.71	121.17	109.23
2	B	311	DT	C2'-C3'-O3'	-7.11	100.84	111.50
2	B	323	DA	C1'-O4'-C4'	-7.03	99.16	109.70
2	B	312	DA	C4'-C3'-O3'	-6.98	99.53	110.00
1	A	232	ARG	NE-CZ-NH2	-6.68	113.19	119.20
1	A	219	ILE	N-CA-C	-6.50	104.69	111.58
1	A	189	GLN	CA-CB-CG	6.09	126.28	114.10
1	A	302	ARG	CG-CD-NE	-5.95	98.91	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	SER	CA-C-N	-5.92	112.44	119.84
1	A	196	SER	C-N-CA	-5.92	112.44	119.84
1	A	308	ALA	CA-C-N	5.55	131.68	121.70
1	A	308	ALA	C-N-CA	5.55	131.68	121.70
1	A	145	ARG	N-CA-C	-5.53	105.26	111.28
1	A	200	VAL	N-CA-C	5.51	120.81	109.34
1	A	232	ARG	NE-CZ-NH1	5.47	126.97	121.50
1	A	302	ARG	NE-CZ-NH2	-5.37	114.36	119.20
1	A	218	ASP	N-CA-C	5.23	116.98	111.28
1	A	203	TRP	N-CA-C	5.18	117.89	109.24
1	A	177	ILE	N-CA-CB	5.16	117.33	110.26
1	A	140	PHE	N-CA-C	5.16	117.30	111.11
2	B	315	DT	C2'-C3'-O3'	-5.03	103.95	111.50

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	2530	0	2570	67	0
2	B	285	0	160	3	0
3	C	289	0	161	2	0
4	A	6	0	0	1	0
5	A	8	0	14	3	0
6	A	72	0	0	6	0
6	B	13	0	0	1	0
6	C	11	0	0	2	0
All	All	3214	0	2905	73	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 12.

All (73) 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:199:SER:HB3	1:A:205:ARG:HA	1.20	1.15
1:A:200:VAL:HG13	1:A:201:ALA:H	1.12	1.10
1:A:200:VAL:HG11	1:A:208:TRP:CE3	1.96	0.99
1:A:217:GLN:NE2	6:A:1101:HOH:O	1.90	0.92
1:A:194:LEU:O	1:A:196:SER:N	2.03	0.91
1:A:200:VAL:HG13	1:A:201:ALA:N	1.85	0.91
1:A:80:GLN:H	1:A:80:GLN:NE2	1.73	0.87
1:A:80:GLN:H	1:A:80:GLN:HE21	0.90	0.85
1:A:199:SER:CB	1:A:205:ARG:HA	2.05	0.84
1:A:80:GLN:HE21	1:A:80:GLN:N	1.74	0.84
1:A:199:SER:HB3	1:A:205:ARG:CA	2.08	0.80
1:A:201:ALA:HB1	1:A:202:PRO:HD3	1.67	0.76
1:A:75[A]:ARG:NE	6:A:1162:HOH:O	2.19	0.75
5:A:1007:MPD:H31	6:C:403:HOH:O	1.86	0.75
1:A:211:LYS:HE3	6:A:1169:HOH:O	1.88	0.73
1:A:144:HIS:HE1	1:A:150:LEU:O	1.72	0.72
1:A:228:LEU:HD22	1:A:299:ILE:HD11	1.71	0.72
1:A:201:ALA:CB	1:A:202:PRO:CD	2.68	0.71
1:A:29:GLU:HG3	6:A:1113:HOH:O	1.91	0.71
1:A:201:ALA:CB	1:A:202:PRO:HD3	2.20	0.70
1:A:20:GLU:OE2	1:A:113:HIS:HE1	1.73	0.70
1:A:196:SER:HB2	1:A:197:PRO:HD3	1.74	0.69
1:A:78:PHE:HB3	1:A:80:GLN:NE2	2.08	0.69
1:A:232:ARG:NH2	3:C:333:DG:N7	2.40	0.68
1:A:77:LEU:H	1:A:81:GLN:HE22	1.43	0.66
1:A:31:HIS:HD2	1:A:101:GLN:O	1.80	0.64
2:B:316:DA:OP2	6:B:409:HOH:O	2.15	0.63
5:A:1007:MPD:H11	5:A:1007:MPD:H53	1.80	0.62
1:A:211:LYS:HB3	6:A:1169:HOH:O	1.98	0.62
1:A:12:THR:HG22	1:A:16:GLN:HE21	1.63	0.62
2:B:316:DA:H2''	2:B:317:DC:O5'	2.01	0.60
1:A:37:ARG:HH11	1:A:60:GLN:NE2	2.00	0.59
1:A:39:PHE:HE1	1:A:60:GLN:HE21	1.50	0.59
1:A:141:GLU:O	1:A:141:GLU:HG3	2.03	0.58
1:A:201:ALA:HB3	1:A:202:PRO:CD	2.34	0.57
1:A:228:LEU:CD2	1:A:299:ILE:HD11	2.35	0.56
1:A:15:ARG:HD2	4:A:1006:IOD:I	2.77	0.55
1:A:24:PHE:HB2	1:A:113:HIS:CD2	2.42	0.54
1:A:200:VAL:CG1	1:A:201:ALA:N	2.61	0.54
1:A:200:VAL:CG1	1:A:208:TRP:CE3	2.83	0.54
1:A:36:ALA:O	1:A:62:LEU:HA	2.07	0.54
1:A:210:ARG:HD3	6:A:1166:HOH:O	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ARG:NH1	1:A:60:GLN:NE2	2.55	0.53
1:A:20:GLU:OE2	1:A:113:HIS:CE1	2.59	0.53
1:A:78:PHE:H	1:A:81:GLN:NE2	2.05	0.53
1:A:46:LYS:O	1:A:49:GLU:HB2	2.09	0.52
1:A:208:TRP:NE1	1:A:212:LEU:HD11	2.25	0.52
5:A:1007:MPD:C3	6:C:403:HOH:O	2.51	0.52
1:A:140:PHE:O	1:A:144:HIS:HD2	1.94	0.51
1:A:178:ILE:HA	1:A:230:ILE:O	2.11	0.50
1:A:200:VAL:HG11	1:A:208:TRP:CZ3	2.46	0.50
1:A:144:HIS:CE1	1:A:150:LEU:O	2.61	0.50
1:A:78:PHE:HB3	1:A:80:GLN:HE22	1.75	0.49
1:A:111:VAL:HG21	1:A:163:HIS:HE1	1.76	0.49
1:A:173:ALA:HB2	1:A:239:ILE:HD13	1.95	0.49
1:A:9:ARG:HH21	1:A:131:GLU:CD	2.22	0.48
1:A:76:HIS:CE1	1:A:82:GLN:OE1	2.68	0.47
1:A:77:LEU:H	1:A:81:GLN:NE2	2.11	0.46
1:A:50:HIS:HE1	1:A:89:LYS:NZ	2.13	0.46
1:A:219:ILE:O	1:A:222:LEU:HB2	2.15	0.46
1:A:31:HIS:CD2	1:A:101:GLN:O	2.66	0.45
2:B:322:DT:H2''	2:B:323:DA:H5'	1.99	0.45
1:A:234:VAL:HG13	3:C:334:DT:H72	2.00	0.44
1:A:215:GLU:OE2	1:A:302:ARG:HD3	2.17	0.44
1:A:12:THR:CG2	1:A:16:GLN:HE21	2.31	0.44
1:A:111:VAL:CG2	1:A:163:HIS:HE1	2.30	0.43
1:A:203:TRP:CH2	1:A:211:LYS:HE2	2.53	0.43
1:A:37:ARG:NH1	1:A:60:GLN:HE22	2.16	0.43
1:A:200:VAL:CG1	1:A:201:ALA:H	1.98	0.42
1:A:140:PHE:O	1:A:144:HIS:CD2	2.73	0.42
1:A:198:ARG:NE	1:A:199:SER:H	2.18	0.41
1:A:198:ARG:CD	1:A:199:SER:H	2.34	0.41
1:A:9:ARG:NH2	1:A:131:GLU:OE2	2.54	0.40

There are no symmetry-related clashes.

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
1	A	308/316 (98%)	293 (95%)	8 (3%)	7 (2%)	5 6

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	LYS
1	A	197	PRO
1	A	200	VAL
1	A	201	ALA
1	A	194	LEU
1	A	198	ARG
1	A	196	SER

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
1	A	273/280 (98%)	240 (88%)	33 (12%)	5 7

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	21	LEU
1	A	28	LEU
1	A	32	LYS
1	A	41	LEU
1	A	46	LYS
1	A	53	LEU
1	A	55	ARG
1	A	58	VAL
1	A	71	LEU
1	A	77	LEU
1	A	79	ILE

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Mol	Chain	Res	Type
1	A	80	GLN
1	A	83	SER
1	A	98	LEU
1	A	111	VAL
1	A	112	SER
1	A	119	LYS
1	A	141	GLU
1	A	168	LEU
1	A	177	ILE
1	A	187	LEU
1	A	192	LYS
1	A	198	ARG
1	A	205	ARG
1	A	214	ARG
1	A	222	LEU
1	A	292	GLN
1	A	294	GLN
1	A	297	ARG
1	A	299	ILE
1	A	305	LEU
1	A	307	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	31	HIS
1	A	50	HIS
1	A	51	ASN
1	A	60	GLN
1	A	80	GLN
1	A	81	GLN
1	A	85	ASN
1	A	107	GLN
1	A	113	HIS
1	A	144	HIS
1	A	163	HIS
1	A	287	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
5	MPD	A	1007	-	7,7,7	1.62	2 (28%)	9,10,10	3.02	5 (55%)

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
5	MPD	A	1007	-	-	1/5/5/5	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1007	MPD	C1-C2	2.75	1.60	1.52
5	A	1007	MPD	CM-C2	2.09	1.58	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1007	MPD	O2-C2-CM	-6.01	89.27	107.99
5	A	1007	MPD	O2-C2-C3	-3.89	94.72	109.27
5	A	1007	MPD	CM-C2-C1	3.08	117.52	110.63
5	A	1007	MPD	CM-C2-C3	3.06	123.41	110.20
5	A	1007	MPD	O2-C2-C1	2.62	116.14	107.99

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1007	MPD	O2-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1007	MPD	3	0

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, 95th 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 ²)	Q < 0.9
1	A	307/316 (97%)	0.28	22 (7%)	21 18	35, 60, 103, 139	3 (0%)
2	B	14/16 (87%)	0.61	2 (14%)	6 5	54, 63, 112, 175	0
3	C	15/16 (93%)	0.86	2 (13%)	7 5	50, 60, 95, 108	2 (13%)
All	All	336/348 (96%)	0.32	26 (7%)	19 16	35, 61, 108, 175	5 (1%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	342	DA	8.1
3	C	328	DG	6.3
1	A	3	ARG	4.6
1	A	197	PRO	4.3
2	B	324	DG	3.8
1	A	4	TYR	3.7
1	A	198	ARG	3.5
1	A	200	VAL	3.4
1	A	201	ALA	3.4
1	A	195	LYS	3.3
1	A	192	LYS	3.2
1	A	206	GLU	3.2
1	A	203	TRP	3.0
1	A	292	GLN	2.9
1	A	72[A]	ARG	2.9
1	A	205	ARG	2.8
1	A	196	SER	2.8
1	A	204	THR	2.4
2	B	323	DA	2.4
1	A	84	GLU	2.3
1	A	62	LEU	2.2
1	A	309	ASP	2.1
1	A	209	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	210	ARG	2.1
1	A	8	ASP	2.1
1	A	83	SER	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, 95th 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
5	MPD	A	1007	8/8	0.78	0.25	46,59,71,79	0
4	IOD	A	1004	1/1	0.94	0.10	90,90,90,90	1
4	IOD	A	1006	1/1	0.97	0.10	94,94,94,94	1
4	IOD	A	1003	1/1	0.98	0.07	71,71,71,71	1
4	IOD	A	1005	1/1	0.98	0.07	95,95,95,95	1
4	IOD	A	1002	1/1	0.99	0.04	68,68,68,68	1
4	IOD	A	1001	1/1	1.00	0.01	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.