



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:08 PM UTC

PDB ID : 3L0O / pdb_00003l0o
Title : Structure of RNA-free Rho transcription termination factor from *Thermotoga maritima*
Authors : Canals, A.; Uson, I.; Coll, M.
Deposited on : 2009-12-10
Resolution : 2.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

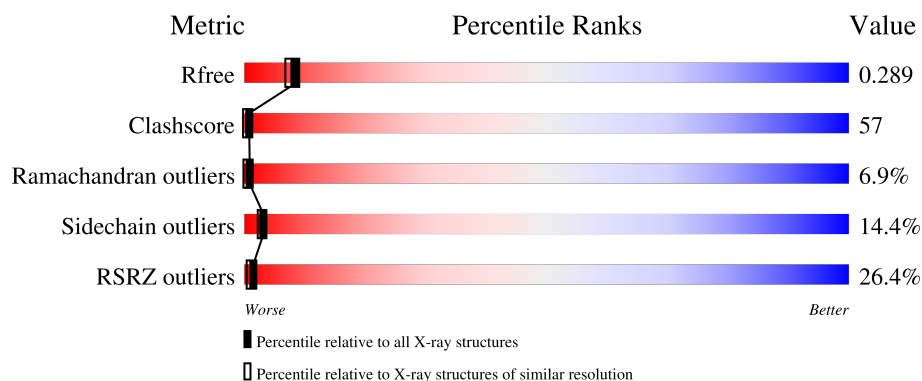
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	427	
1	B	427	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	432	-	-	X	-
3	SO4	B	434	-	-	X	-
3	SO4	B	435	-	-	X	-

2 Entry composition [i](#)

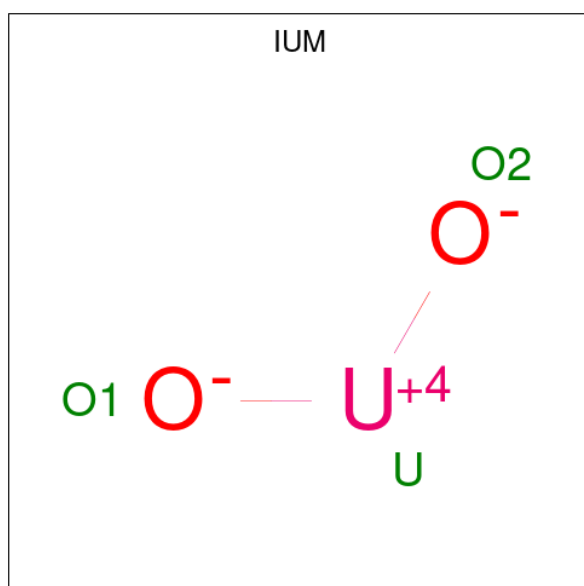
There are 5 unique types of molecules in this entry. The entry contains 6194 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Transcription termination factor rho.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	413	Total	C	N	O	S	1	0	0
			3283	2101	556	616	10			
1	B	347	Total	C	N	O	S	3	0	0
			2737	1749	466	514	8			

- Molecule 2 is URANYL (VI) ION (CCD ID: IUM) (formula: O₂U).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	U	0	0
			3	2	1		
2	A	1	Total	O	U	0	0
			3	2	1		
2	A	1	Total	O	U	0	0
			3	2	1		
2	B	1	Total	O	U	0	0
			3	2	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	U	0	0
			3	2	1		
2	B	1	Total	O	U	0	0
			3	2	1		
2	B	1	Total	O	U	0	0
			3	2	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Na	0	0
			2	2		

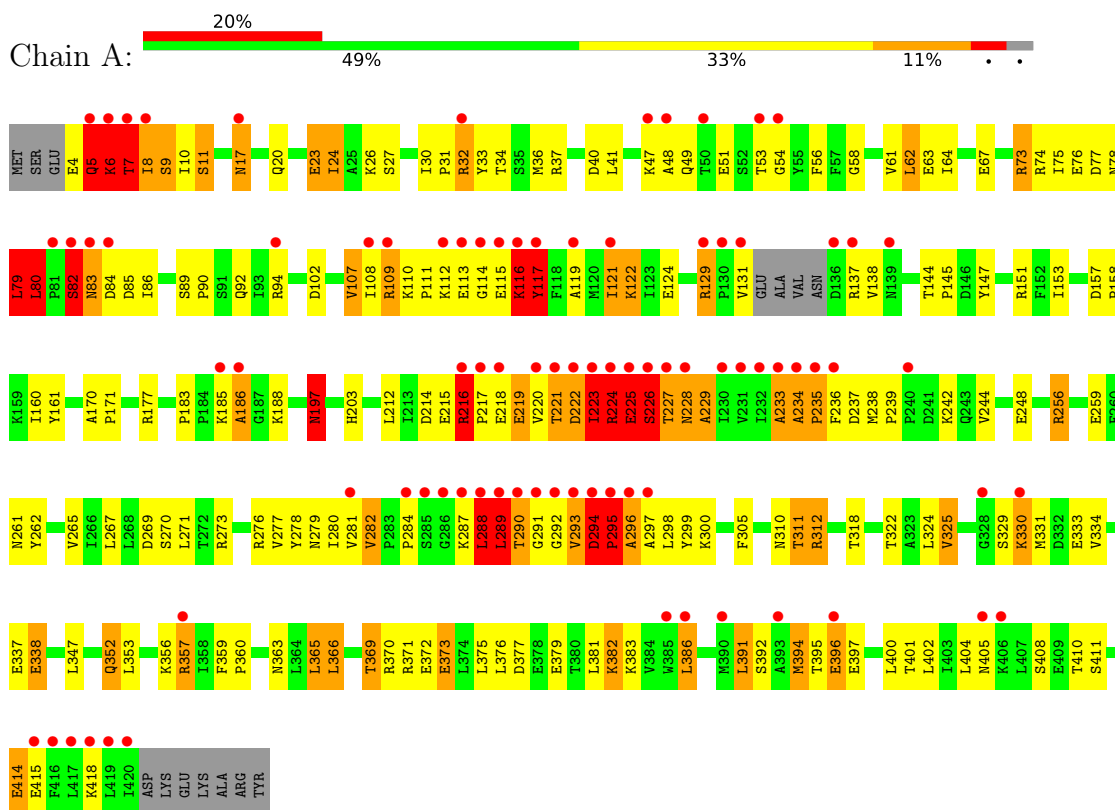
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	70	Total	O	0	0
			70	70		
5	B	36	Total	O	0	0
			36	36		

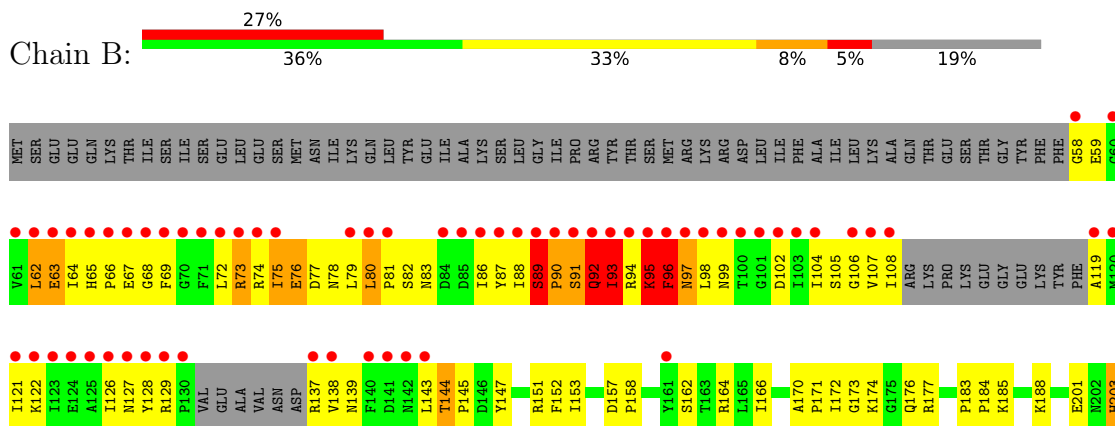
3 Residue-property plots

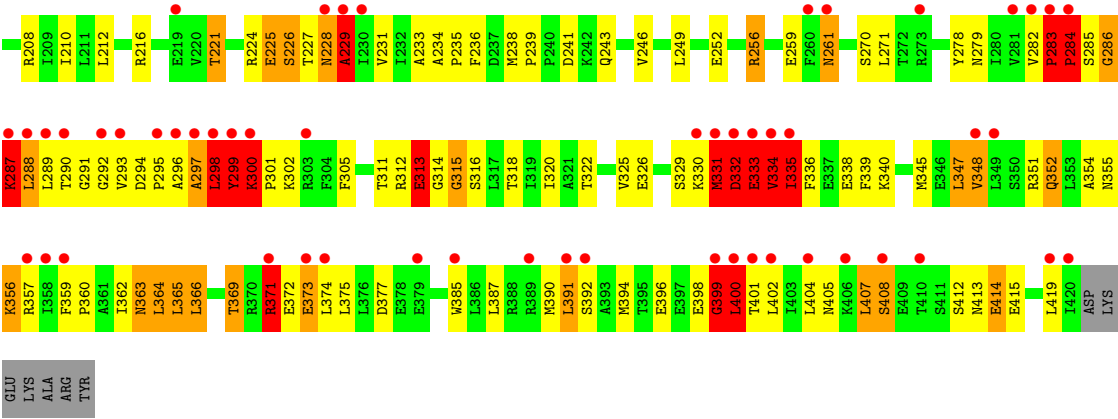
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Transcription termination factor rho



• Molecule 1: Transcription termination factor rho





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	139.00Å 139.00Å 150.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.55 – 2.35 38.55 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.4 (38.55-2.35) 99.4 (38.55-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.68 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.268 , 0.297 0.264 , 0.289	Depositor DCC
R_{free} test set	4886 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6194	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% 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: SO4, IUM, NA

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	0.93	0/3336	1.26	27/4504 (0.6%)
1	B	0.75	0/2779	1.20	31/3758 (0.8%)
All	All	0.85	0/6115	1.23	58/8262 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
1	B	0	7
All	All	0	13

There are no bond length outliers.

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	80	LEU	CA-C-N	12.63	133.47	119.83
1	A	80	LEU	C-N-CA	12.63	133.47	119.83
1	B	300	LYS	CA-C-N	10.73	130.97	119.05
1	B	300	LYS	C-N-CA	10.73	130.97	119.05
1	A	221	THR	N-CA-C	10.13	124.15	111.69

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	ARG	Peptide

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	234	ALA	Peptide
1	A	294	ASP	Peptide
1	A	79	LEU	Peptide
1	A	82	SER	Peptide

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	3283	0	3400	393	0
1	B	2737	0	2835	316	0
2	A	9	0	0	0	0
2	B	12	0	0	3	0
3	A	25	0	0	3	0
3	B	20	0	0	7	0
4	B	2	0	0	0	0
5	A	70	0	0	6	0
5	B	36	0	0	0	0
All	All	6194	0	6235	703	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 57.

The worst 5 of 703 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:B:93:ILE:HG22	1:B:94:ARG:CA	1.33	1.57
1:B:93:ILE:CG2	1:B:94:ARG:HA	1.30	1.52
1:B:228:ASN:CA	1:B:229:ALA:HB2	1.27	1.52
1:B:333:GLU:CA	1:B:334:VAL:HG23	1.41	1.48
1:A:297:ALA:CB	1:A:299:TYR:N	1.82	1.42

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	409/427 (96%)	363 (89%)	23 (6%)	23 (6%)	1	0
1	B	341/427 (80%)	284 (83%)	28 (8%)	29 (8%)	0	0
All	All	750/854 (88%)	647 (86%)	51 (7%)	52 (7%)	1	0

5 of 52 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	6	LYS
1	A	9	SER
1	A	117	TYR
1	A	186	ALA

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	363/375 (97%)	306 (84%)	57 (16%)	2	2
1	B	303/375 (81%)	264 (87%)	39 (13%)	4	4
All	All	666/750 (89%)	570 (86%)	96 (14%)	3	3

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	62	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	241	ASP
1	B	73	ARG
1	B	95	LYS
1	B	298	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	176	GLN
1	B	405	ASN
1	B	203	HIS
1	B	413	ASN
1	B	279	ASN

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](#)

Of 18 ligands modelled in this entry, 2 are monoatomic - leaving 16 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
2	IUM	A	429	1	0,2,2	-	-	-		
2	IUM	A	430	5,1	0,2,2	-	-	-		
3	SO4	B	435	-	4,4,4	0.28	0	6,6,6	0.09	0
2	IUM	B	428	1	0,2,2	-	-	-		
3	SO4	B	433	-	4,4,4	0.26	0	6,6,6	0.12	0
2	IUM	A	428	1	0,2,2	-	-	-		
3	SO4	A	435	-	4,4,4	0.25	0	6,6,6	0.13	0
3	SO4	B	434	-	4,4,4	0.21	0	6,6,6	0.11	0
3	SO4	A	433	-	4,4,4	0.24	0	6,6,6	0.12	0
3	SO4	A	434	-	4,4,4	0.23	0	6,6,6	0.25	0
3	SO4	A	431	-	4,4,4	0.27	0	6,6,6	0.25	0
3	SO4	A	432	-	4,4,4	0.22	0	6,6,6	0.09	0
2	IUM	B	429	5,1	0,2,2	-	-	-		
2	IUM	B	431	1	0,2,2	-	-	-		
3	SO4	B	432	4	4,4,4	0.23	0	6,6,6	0.11	0
2	IUM	B	430	1	0,2,2	-	-	-		

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.

9 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	435	SO4	2	0
3	A	435	SO4	1	0
3	B	434	SO4	2	0
3	A	433	SO4	1	0
3	A	432	SO4	1	0
2	B	429	IUM	1	0
2	B	431	IUM	1	0
3	B	432	SO4	3	0
2	B	430	IUM	1	0

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, 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	413/427 (96%)	1.11	85 (20%) 2 2	23, 43, 77, 92	6 (1%)
1	B	347/427 (81%)	1.67	116 (33%) 1 0	30, 54, 98, 108	4 (1%)
All	All	760/854 (88%)	1.36	201 (26%) 1 1	23, 48, 92, 108	10 (1%)

The worst 5 of 201 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	5	GLN	12.4
1	A	6	LYS	9.9
1	B	119	ALA	8.9
1	B	121	ILE	8.5
1	B	130	PRO	7.1

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
3	SO4	A	435	5/5	0.59	0.30	73,129,189,459	0
2	IUM	A	429	3/3	0.61	0.28	432,432,500,500	0
2	IUM	B	428	3/3	0.68	0.27	56,56,176,328	3
2	IUM	B	430	3/3	0.70	0.30	211,211,480,480	3
3	SO4	A	434	5/5	0.75	0.27	59,62,442,444	0
3	SO4	B	432	5/5	0.84	0.27	84,115,192,461	0
3	SO4	B	434	5/5	0.84	0.35	42,122,458,458	0
4	NA	B	437	1/1	0.84	0.27	66,66,66,66	0
3	SO4	A	432	5/5	0.86	0.24	63,64,239,448	0
4	NA	B	436	1/1	0.91	0.26	49,49,49,49	0
3	SO4	A	431	5/5	0.92	0.14	54,66,113,145	0
2	IUM	B	431	3/3	0.92	0.13	53,53,120,139	3
3	SO4	B	433	5/5	0.94	0.20	36,40,137,413	0
3	SO4	A	433	5/5	0.95	0.12	39,40,58,80	0
3	SO4	B	435	5/5	0.97	0.09	52,57,98,106	0
2	IUM	B	429	3/3	0.99	0.19	63,63,74,145	0
2	IUM	A	430	3/3	1.00	0.06	25,25,36,39	0
2	IUM	A	428	3/3	1.00	0.11	58,58,79,91	0

6.5 Other polymers ⓘ

There are no such residues in this entry.