



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:53 PM UTC

PDB ID : 2RFK / pdb\_00002rfk  
Title : Substrate RNA Positioning in the Archaeal H/ACA Ribonucleoprotein Complex  
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Deposited on : 2007-09-30  
Resolution : 2.87 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](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
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

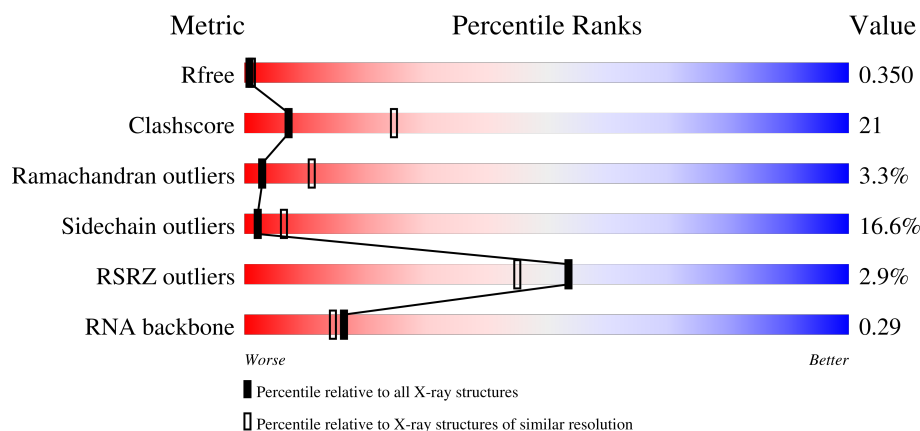
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.87 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	3557 (2.90-2.86)
Clashscore	190562	3801 (2.90-2.86)
Ramachandran outliers	187476	3699 (2.90-2.86)
Sidechain outliers	187428	3702 (2.90-2.86)
RSRZ outliers	180081	3558 (2.90-2.86)
RNA backbone	3983	1174 (3.10-2.66)

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	D	21	
2	E	26	
3	F	14	
4	A	334	

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Mol	Chain	Length	Quality of chain
5	B	53	<div><div></div><div>2%</div><div>55%</div><div>40%</div><div>6%</div></div>
6	C	74	<div><div></div><div>4%</div><div>39%</div><div>47%</div><div>12%</div><div></div></div>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5005 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 RNA chain called guide RNA 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	21	Total	C	N	O	P	0	0	0
			450	201	86	143	20			

- Molecule 2 is a RNA chain called guide RNA 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	26	Total	C	N	O	P	0	0	0
			543	244	94	180	25			

- Molecule 3 is a RNA chain called target RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	14	Total	C	N	O	P	0	0	0
			300	134	54	99	13			

- Molecule 4 is a protein called Probable tRNA pseudouridine synthase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	334	Total	C	N	O	S	0	0	0
			2665	1716	466	473	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	85	ALA	ASP	engineered mutation	UNP Q7LWY0

- Molecule 5 is a protein called Ribosome biogenesis protein Nop10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	53	Total	C	N	O	S	0	0	0
			445	283	86	72	4			

- Molecule 6 is a protein called Small nucleolar rnp similar to gar1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	C	74	Total	C	N	O	S	0	0	0
			601	396	102	101	2			

- Molecule 7 is ZINC ION (CCD ID: ZN) (formula: Zn).

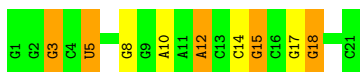
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Zn	0	0
			1	1		

### 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.

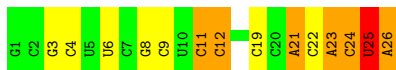
- Molecule 1: guide RNA 1

Chain D: 



- Molecule 2: guide RNA 2

Chain E: 



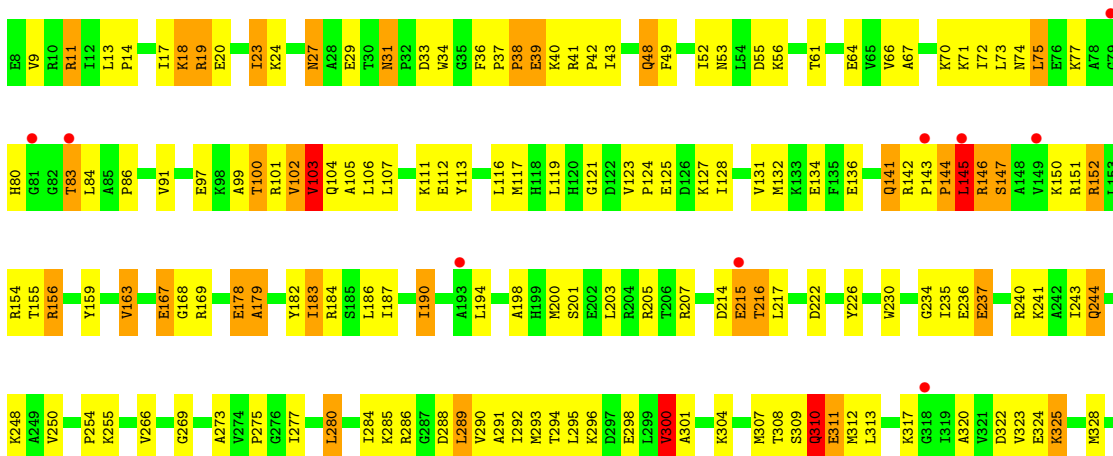
- Molecule 3: target RNA

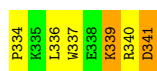
Chain F: 



- Molecule 4: Probable tRNA pseudouridine synthase B

Chain A: 

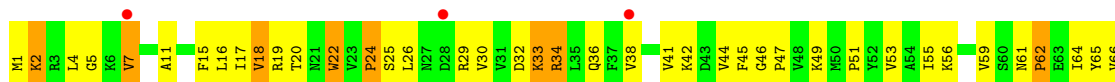




- Molecule 5: Ribosome biogenesis protein Nop10



- Molecule 6: Small nucleolar rnp similar to gar1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.56Å 96.56Å 240.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.52 – 2.87 42.52 – 2.87	Depositor EDS
% Data completeness (in resolution range)	80.0 (42.52-2.87) 79.9 (42.52-2.87)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.10 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.248 , 0.300 0.314 , 0.350	Depositor DCC
$R_{free}$ test set	1175 reflections (4.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	67.0	Xtriage
Anisotropy	0.717	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 4.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	5005	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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

### 5.1 Standard geometry

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

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	D	0.53	0/503	1.09	2/784 (0.3%)
2	E	0.60	0/604	1.20	4/938 (0.4%)
3	F	0.72	0/335	1.17	1/522 (0.2%)
4	A	0.73	3/2725 (0.1%)	0.99	4/3684 (0.1%)
5	B	0.64	0/458	1.06	0/613
6	C	1.00	3/615 (0.5%)	0.95	2/831 (0.2%)
All	All	0.73	6/5240 (0.1%)	1.05	13/7372 (0.2%)

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	145	LEU	C-N	13.45	1.46	1.32
6	C	74	GLU	CD-OE1	12.68	1.49	1.25
6	C	74	GLU	CD-OE2	12.31	1.48	1.25
4	A	143	PRO	CA-C	6.54	1.56	1.52
6	C	36	GLN	CD-OE1	6.38	1.35	1.23

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	147	SER	N-CA-C	-7.12	103.57	112.90
4	A	183	ILE	N-CA-C	6.74	118.72	111.58
1	D	5	U	P-O5'-C5'	-6.09	111.77	120.90
1	D	5	U	C3'-C2'-C1'	-5.98	95.32	101.30
2	E	25	U	O4'-C1'-C2'	-5.80	101.80	107.60

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-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 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	D	450	0	232	7	0
2	E	543	0	284	15	0
3	F	300	0	152	9	0
4	A	2665	0	2750	123	0
5	B	445	0	451	20	0
6	C	601	0	637	36	0
7	B	1	0	0	0	0
All	All	5005	0	4506	195	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 21.

The worst 5 of 195 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)
5:B:20:CYS:HB3	5:B:23:CYS:HB3	1.32	1.08
4:A:284:ILE:HB	4:A:309:SER:HB3	1.46	0.95
3:F:10:U:H4'	3:F:11:G:O5'	1.66	0.92
4:A:19:ARG:HH12	4:A:254:PRO:HB3	1.36	0.88
4:A:41:ARG:O	4:A:240:ARG:NH2	2.09	0.86

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	
4	A	332/334 (99%)	281 (85%)	40 (12%)	11 (3%)	3	11
5	B	51/53 (96%)	43 (84%)	7 (14%)	1 (2%)	6	20
6	C	72/74 (97%)	60 (83%)	9 (12%)	3 (4%)	2	7
All	All	455/461 (99%)	384 (84%)	56 (12%)	15 (3%)	3	11

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	38	PRO
4	A	103	VAL
4	A	152	ARG
4	A	179	ALA
4	A	39	GLU

### 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	
4	A	283/283 (100%)	237 (84%)	46 (16%)	2	7
5	B	48/48 (100%)	43 (90%)	5 (10%)	7	20
6	C	67/67 (100%)	52 (78%)	15 (22%)	1	2
All	All	398/398 (100%)	332 (83%)	66 (17%)	2	6

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	C	29	ARG
6	C	34	ARG
6	C	74	GLU
4	A	156	ARG
4	A	155	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
4	A	268	HIS
4	A	310	GLN
6	C	36	GLN
6	C	27	ASN
4	A	80	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	D	20/21 (95%)	7 (35%)	0
2	E	25/26 (96%)	9 (36%)	1 (4%)
3	F	14/14 (100%)	5 (35%)	2 (14%)
All	All	59/61 (96%)	21 (35%)	3 (5%)

5 of 21 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	D	3	G
1	D	5	U
1	D	8	G
1	D	10	A
1	D	12	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	E	23	A
3	F	4	G
3	F	10	U

## 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 1 ligands modelled in this entry, 1 is 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

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, 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	D	21/21 (100%)	-0.11	0 100 100	32, 51, 84, 87	0
2	E	26/26 (100%)	-0.05	0 100 100	41, 49, 73, 74	0
3	F	14/14 (100%)	0.55	2 (14%) 6 5	52, 83, 106, 117	0
4	A	334/334 (100%)	0.50	9 (2%) 56 47	24, 43, 58, 90	0
5	B	53/53 (100%)	0.47	1 (1%) 66 58	32, 46, 53, 56	0
6	C	74/74 (100%)	0.62	3 (4%) 41 33	29, 35, 40, 41	0
All	All	522/522 (100%)	0.47	15 (2%) 53 45	24, 43, 73, 117	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	A	318	GLY	5.0
5	B	25	GLU	3.5
4	A	215	GLU	3.4
4	A	145	LEU	3.1
4	A	143	PRO	2.9

### 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
7	ZN	B	1	1/1	0.89	0.22	56,56,56,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.