



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2024 – 04:37 PM EDT

PDB ID : 9RAT
Title : EFFECTS OF TEMPERATURE ON PROTEIN STRUCTURE AND DYNAMICS: X-RAY CRYSTALLOGRAPHIC STUDIES OF THE PROTEIN RIBONUCLEASE-A AT NINE DIFFERENT TEMPERATURES FROM 98 TO 320 K
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Deposited on : 1991-08-13
Resolution : 1.50 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	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

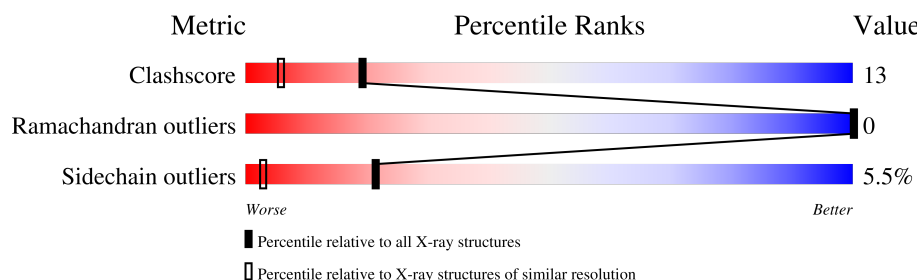
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	124	<div> <div></div> <div>45%</div> <div>47%</div> <div>8%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 951 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 RIBONUCLEASE A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	124	951	575	171	193	12	0	0	0

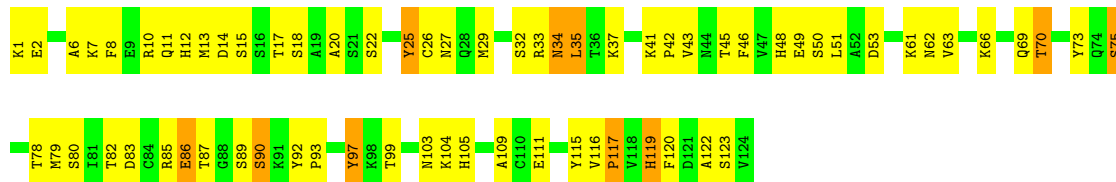
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

• Molecule 1: RIBONUCLEASE A

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	30.40 Å 38.30 Å 53.30 Å 90.00° 106.90° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.191 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	951	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	1.88	20/967 (2.1%)	2.36	57/1304 (4.4%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	117	PRO	N-CD	7.77	1.58	1.47
1	A	15	SER	CB-OG	7.66	1.52	1.42
1	A	12	HIS	CE1-NE2	7.42	1.49	1.32
1	A	2	GLU	CD-OE2	7.22	1.33	1.25
1	A	90	SER	CB-OG	7.00	1.51	1.42
1	A	10	ARG	CD-NE	-5.94	1.36	1.46
1	A	49	GLU	CD-OE2	-5.93	1.19	1.25
1	A	97	TYR	CB-CG	5.79	1.60	1.51
1	A	50	SER	CA-CB	5.66	1.61	1.52
1	A	8	PHE	CG-CD2	5.63	1.47	1.38
1	A	97	TYR	CZ-OH	5.46	1.47	1.37
1	A	49	GLU	C-O	5.43	1.33	1.23
1	A	123	SER	CA-CB	-5.37	1.44	1.52
1	A	90	SER	CA-CB	-5.34	1.45	1.52
1	A	32	SER	C-O	5.26	1.33	1.23
1	A	7	LYS	CA-CB	-5.22	1.42	1.53
1	A	75	SER	CA-CB	-5.17	1.45	1.52
1	A	73	TYR	CG-CD1	5.09	1.45	1.39
1	A	111	GLU	CD-OE1	5.07	1.31	1.25
1	A	15	SER	CA-CB	5.07	1.60	1.52

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	97	TYR	CB-CG-CD2	-13.44	112.93	121.00
1	A	73	TYR	CB-CG-CD2	12.76	128.66	121.00
1	A	10	ARG	NE-CZ-NH2	11.55	126.08	120.30
1	A	86	GLU	OE1-CD-OE2	10.39	135.77	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	TYR	CB-CG-CD2	-10.23	114.86	121.00
1	A	73	TYR	CB-CG-CD1	-9.68	115.19	121.00
1	A	46	PHE	CB-CG-CD1	-8.95	114.53	120.80
1	A	33	ARG	NE-CZ-NH1	8.65	124.62	120.30
1	A	80	SER	O-C-N	8.38	136.10	122.70
1	A	53	ASP	CB-CG-OD2	-8.27	110.86	118.30
1	A	6	ALA	O-C-N	8.11	135.68	122.70
1	A	20	ALA	N-CA-CB	-7.76	99.24	110.10
1	A	120	PHE	CB-CG-CD2	-7.71	115.40	120.80
1	A	73	TYR	CG-CD2-CE2	7.54	127.33	121.30
1	A	14	ASP	CB-CG-OD1	7.41	124.97	118.30
1	A	97	TYR	O-C-N	7.36	134.47	122.70
1	A	53	ASP	CB-CG-OD1	7.35	124.91	118.30
1	A	8	PHE	CB-CG-CD2	-6.94	115.94	120.80
1	A	93	PRO	O-C-N	6.91	133.76	122.70
1	A	17	THR	CA-CB-CG2	-6.87	102.78	112.40
1	A	123	SER	N-CA-CB	6.66	120.50	110.50
1	A	20	ALA	CB-CA-C	6.64	120.07	110.10
1	A	97	TYR	CA-C-N	-6.53	102.84	117.20
1	A	10	ARG	CD-NE-CZ	6.45	132.63	123.60
1	A	97	TYR	CG-CD2-CE2	-6.40	116.18	121.30
1	A	35	LEU	CA-CB-CG	-6.38	100.64	115.30
1	A	10	ARG	NE-CZ-NH1	-6.25	117.17	120.30
1	A	97	TYR	N-CA-CB	6.22	121.80	110.60
1	A	97	TYR	CD1-CG-CD2	6.16	124.68	117.90
1	A	80	SER	N-CA-CB	6.13	119.69	110.50
1	A	70	THR	N-CA-CB	-6.10	98.71	110.30
1	A	115	TYR	O-C-N	6.10	132.46	122.70
1	A	25	TYR	CD1-CG-CD2	6.03	124.53	117.90
1	A	90	SER	O-C-N	5.87	132.09	122.70
1	A	27	ASN	O-C-N	5.78	131.96	122.70
1	A	25	TYR	CG-CD1-CE1	-5.78	116.68	121.30
1	A	104	LYS	CA-CB-CG	-5.69	100.89	113.40
1	A	97	TYR	CG-CD1-CE1	-5.55	116.86	121.30
1	A	35	LEU	O-C-N	5.54	131.56	122.70
1	A	46	PHE	CG-CD1-CE1	-5.52	114.73	120.80
1	A	15	SER	CA-CB-OG	-5.46	96.45	111.20
1	A	119	HIS	O-C-N	5.45	131.42	122.70
1	A	97	TYR	CA-CB-CG	-5.44	103.07	113.40
1	A	13	MET	CA-C-O	5.43	131.50	120.10
1	A	25	TYR	CG-CD2-CE2	-5.38	117.00	121.30
1	A	18	SER	O-C-N	5.27	131.13	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	A	69	GLN	O-C-N	5.23	131.07	122.70
1	A	123	SER	N-CA-C	-5.21	96.94	111.00
1	A	45	THR	OG1-CB-CG2	5.19	121.94	110.00
1	A	92	TYR	CG-CD1-CE1	-5.18	117.16	121.30
1	A	78	THR	CA-CB-OG1	-5.14	98.20	109.00
1	A	92	TYR	CB-CG-CD2	-5.14	117.92	121.00
1	A	42	PRO	N-CA-CB	5.12	109.44	103.30
1	A	48	HIS	CG-ND1-CE1	-5.09	99.08	105.70
1	A	46	PHE	N-CA-CB	5.06	119.70	110.60
1	A	61	LYS	O-C-N	5.03	130.75	122.70

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	A	951	0	905	24	0
All	All	951	0	905	24	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 13.

All (24) 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:87:THR:HG22	1:A:89:SER:H	1.31	0.94
1:A:66:LYS:HE3	1:A:122:ALA:HB2	1.55	0.89
1:A:34:ASN:ND2	1:A:37:LYS:HD2	1.98	0.78
1:A:34:ASN:HD21	1:A:37:LYS:HD2	1.58	0.69
1:A:41:LYS:HE2	1:A:43:VAL:O	1.93	0.67
1:A:26:CYS:HB3	1:A:97:TYR:HB2	1.78	0.65
1:A:109:ALA:HB3	1:A:119:HIS:HB3	1.78	0.65
1:A:11:GLN:HG2	1:A:35:LEU:HD21	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:VAL:HB	1:A:117:PRO:HD2	1.86	0.56
1:A:34:ASN:HD21	1:A:37:LYS:CD	2.19	0.55
1:A:66:LYS:HE3	1:A:122:ALA:CB	2.34	0.55
1:A:116:VAL:HB	1:A:117:PRO:CD	2.37	0.54
1:A:25:TYR:CD2	1:A:82:THR:HG21	2.43	0.54
1:A:75:SER:O	1:A:105:HIS:HD2	1.91	0.51
1:A:25:TYR:CZ	1:A:29:MET:HG3	2.44	0.51
1:A:11:GLN:HG2	1:A:35:LEU:CD2	2.43	0.47
1:A:86:GLU:HG2	1:A:90:SER:CB	2.45	0.46
1:A:26:CYS:HB2	1:A:99:THR:OG1	2.16	0.45
1:A:34:ASN:HD21	1:A:37:LYS:NZ	2.17	0.42
1:A:79:MET:O	1:A:103:ASN:HA	2.19	0.42
1:A:86:GLU:CG	1:A:90:SER:CB	2.98	0.42
1:A:86:GLU:OE2	1:A:90:SER:OG	2.29	0.41
1:A:62:ASN:C	1:A:63:VAL:HG13	2.40	0.41
1:A:26:CYS:CB	1:A:99:THR:HG1	2.32	0.41

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	122/124 (98%)	119 (98%)	3 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	109/109 (100%)	103 (94%)	6 (6%)	21 3

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	LYS
1	A	22	SER
1	A	34	ASN
1	A	51	LEU
1	A	70	THR
1	A	83	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN
1	A	105	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.