



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:21 PM GMT

PDB ID : 4RNT  
Title : HIS 92 ALA MUTATION IN RIBONUCLEASE T1 INDUCES SEGMENTAL FLEXIBILITY. AN X-RAY STUDY  
Authors : Saenger, W.; Koellner, G.  
Deposited on : 1990-02-13  
Resolution : 2.20 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

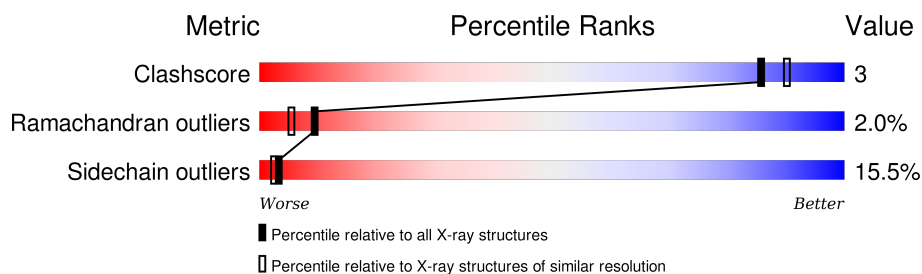
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	104	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 846 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 T1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	104	Total	C	N	O	S	0	0	0
			776	477	125	170	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	LYS	GLN	CONFLICT	UNP P00651
A	92	ALA	HIS	CONFLICT	UNP P00651

- Molecule 2 is water.

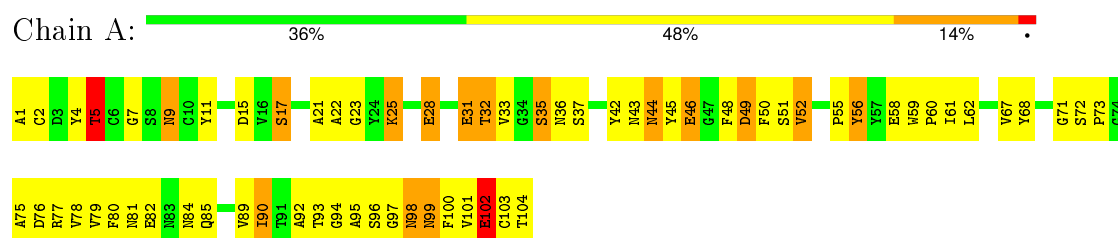
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	70	Total	O	0	0
			70	70		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

#### • Molecule 1: RIBONUCLEASE T1



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	31.04Å 62.31Å 43.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.20)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROFFT	Depositor
R, $R_{free}$	0.162 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	846	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	14.0	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	1.61	4/796 (0.5%)	3.23	106/1084 (9.8%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	31	GLU	CD-OE1	-6.08	1.19	1.25
1	A	58	GLU	CD-OE1	-6.04	1.19	1.25
1	A	59	TRP	NE1-CE2	5.31	1.44	1.37
1	A	36	ASN	C-O	-5.26	1.13	1.23

All (106) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	49	ASP	CB-CG-OD1	23.17	139.15	118.30
1	A	56	TYR	CB-CG-CD1	17.87	131.72	121.00
1	A	77	ARG	NE-CZ-NH1	17.11	128.85	120.30
1	A	56	TYR	CB-CG-CD2	-14.92	112.05	121.00
1	A	99	ASN	CB-CA-C	14.65	139.71	110.40
1	A	77	ARG	NE-CZ-NH2	-12.48	114.06	120.30
1	A	102	GLU	CA-CB-CG	11.89	139.56	113.40
1	A	49	ASP	CB-CG-OD2	-11.57	107.89	118.30
1	A	58	GLU	OE1-CD-OE2	11.49	137.09	123.30
1	A	98	ASN	CA-CB-CG	11.46	138.62	113.40
1	A	46	GLU	CB-CG-CD	11.32	144.78	114.20
1	A	99	ASN	O-C-N	-10.78	105.45	122.70
1	A	100	PHE	N-CA-CB	10.12	128.82	110.60
1	A	9	ASN	C-N-CA	9.77	146.12	121.70
1	A	94	GLY	CA-C-O	-9.68	103.18	120.60
1	A	28	GLU	OE1-CD-OE2	-8.65	112.91	123.30
1	A	77	ARG	CA-CB-CG	8.47	132.03	113.40
1	A	80	PHE	CB-CG-CD2	8.39	126.68	120.80
1	A	48	PHE	CG-CD1-CE1	8.36	130.00	120.80
1	A	84	ASN	OD1-CG-ND2	8.36	141.12	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	43	ASN	CA-C-N	8.28	135.41	117.20
1	A	4	TYR	CZ-CE2-CD2	8.24	127.22	119.80
1	A	46	GLU	OE1-CD-OE2	-8.23	113.42	123.30
1	A	98	ASN	N-CA-CB	8.21	125.38	110.60
1	A	55	PRO	O-C-N	8.10	135.66	122.70
1	A	9	ASN	O-C-N	-8.09	109.76	122.70
1	A	82	GLU	CA-CB-CG	-8.07	95.65	113.40
1	A	99	ASN	OD1-CG-ND2	-8.06	103.37	121.90
1	A	95	ALA	N-CA-CB	-8.00	98.90	110.10
1	A	99	ASN	CA-CB-CG	7.87	130.71	113.40
1	A	25	LYS	CD-CE-NZ	7.86	129.77	111.70
1	A	50	PHE	CB-CG-CD1	7.83	126.28	120.80
1	A	22	ALA	C-N-CA	7.58	138.22	122.30
1	A	99	ASN	CA-C-O	7.57	135.99	120.10
1	A	84	ASN	CB-CG-ND2	-7.55	98.58	116.70
1	A	28	GLU	CA-CB-CG	7.52	129.94	113.40
1	A	25	LYS	CA-CB-CG	7.39	129.66	113.40
1	A	93	THR	N-CA-CB	7.35	124.26	110.30
1	A	22	ALA	CA-C-O	7.33	135.50	120.10
1	A	1	ALA	CB-CA-C	7.29	121.03	110.10
1	A	100	PHE	N-CA-C	-7.23	91.49	111.00
1	A	35	SER	CB-CA-C	-7.07	96.67	110.10
1	A	71	GLY	O-C-N	7.00	133.91	122.70
1	A	95	ALA	CA-C-O	-6.98	105.45	120.10
1	A	61	ILE	O-C-N	6.91	133.75	122.70
1	A	94	GLY	CA-C-N	6.84	132.26	117.20
1	A	42	TYR	CG-CD2-CE2	-6.83	115.84	121.30
1	A	101	VAL	N-CA-CB	6.80	126.46	111.50
1	A	25	LYS	CG-CD-CE	6.63	131.80	111.90
1	A	104	THR	CA-CB-CG2	6.61	121.65	112.40
1	A	103	CYS	CA-CB-SG	-6.58	102.16	114.00
1	A	32	THR	OG1-CB-CG2	6.58	125.12	110.00
1	A	2	CYS	CB-CA-C	-6.57	97.26	110.40
1	A	32	THR	N-CA-CB	-6.54	97.88	110.30
1	A	95	ALA	CB-CA-C	-6.38	100.53	110.10
1	A	67	VAL	CA-CB-CG1	6.31	120.37	110.90
1	A	15	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	93	THR	CA-C-O	6.24	133.20	120.10
1	A	5	THR	CA-CB-CG2	6.22	121.11	112.40
1	A	44	ASN	N-CA-CB	6.21	121.77	110.60
1	A	96	SER	O-C-N	-6.20	112.66	123.20
1	A	68	TYR	O-C-N	6.17	132.57	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	51	SER	O-C-N	6.04	132.36	122.70
1	A	75	ALA	CB-CA-C	-6.00	101.10	110.10
1	A	72	SER	N-CA-CB	-5.94	101.59	110.50
1	A	58	GLU	O-C-N	5.92	132.17	122.70
1	A	89	VAL	CA-CB-CG1	-5.87	102.09	110.90
1	A	61	ILE	N-CA-CB	5.87	124.30	110.80
1	A	49	ASP	CB-CA-C	5.78	121.96	110.40
1	A	9	ASN	CA-C-O	5.75	132.17	120.10
1	A	99	ASN	N-CA-CB	-5.74	100.27	110.60
1	A	43	ASN	OD1-CG-ND2	-5.71	108.77	121.90
1	A	78	VAL	CB-CA-C	5.71	122.25	111.40
1	A	100	PHE	CA-C-N	-5.70	104.65	117.20
1	A	98	ASN	OD1-CG-ND2	-5.64	108.92	121.90
1	A	43	ASN	CB-CA-C	5.62	121.64	110.40
1	A	31	GLU	OE1-CD-OE2	5.62	130.04	123.30
1	A	43	ASN	CA-C-O	-5.61	108.33	120.10
1	A	97	GLY	C-N-CA	5.55	135.58	121.70
1	A	28	GLU	CB-CA-C	-5.53	99.34	110.40
1	A	17	SER	CB-CA-C	5.50	120.54	110.10
1	A	49	ASP	OD1-CG-OD2	-5.48	112.88	123.30
1	A	59	TRP	CD1-NE1-CE2	-5.40	104.14	109.00
1	A	21	ALA	CB-CA-C	-5.37	102.05	110.10
1	A	52	VAL	CA-CB-CG1	5.36	118.95	110.90
1	A	22	ALA	CA-C-N	-5.33	105.55	116.20
1	A	43	ASN	CB-CG-ND2	5.32	129.47	116.70
1	A	44	ASN	CA-C-N	-5.30	105.53	117.20
1	A	23	GLY	N-CA-C	-5.27	99.91	113.10
1	A	76	ASP	N-CA-CB	-5.27	101.12	110.60
1	A	90	ILE	O-C-N	-5.24	114.33	122.70
1	A	45	TYR	CB-CG-CD2	-5.22	117.87	121.00
1	A	11	TYR	CG-CD1-CE1	-5.22	117.13	121.30
1	A	73	PRO	C-N-CA	-5.18	111.42	122.30
1	A	96	SER	N-CA-CB	-5.13	102.80	110.50
1	A	60	PRO	N-CD-CG	-5.12	95.51	103.20
1	A	89	VAL	CB-CA-C	5.11	121.11	111.40
1	A	48	PHE	CB-CG-CD1	5.08	124.36	120.80
1	A	77	ARG	O-C-N	5.08	130.83	122.70
1	A	62	LEU	N-CA-CB	-5.03	100.34	110.40
1	A	49	ASP	O-C-N	-5.03	114.66	122.70
1	A	36	ASN	CB-CG-ND2	-5.02	104.66	116.70
1	A	92	ALA	C-N-CA	5.01	134.23	121.70
1	A	7	GLY	O-C-N	5.01	130.72	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	33	VAL	O-C-N	5.01	131.71	123.20
1	A	100	PHE	CB-CG-CD1	-5.00	117.30	120.80

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	776	0	675	4	0
2	A	70	0	0	0	0
All	All	846	0	675	4	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 3.

All (4) 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:81:ASN:HD21	1:A:85:GLN:HE21	1.57	0.50
1:A:5:THR:HA	1:A:9:ASN:O	2.19	0.43
1:A:56:TYR:HB3	1:A:79:VAL:CG1	2.50	0.41
1:A:90:ILE:HG22	1:A:102:GLU:HA	2.02	0.41

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	102/104 (98%)	97 (95%)	3 (3%)	2 (2%)	9 5

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	SER
1	A	44	ASN

### 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	84/84 (100%)	71 (84%)	13 (16%)	3 2

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	17	SER
1	A	25	LYS
1	A	28	GLU
1	A	31	GLU
1	A	32	THR
1	A	35	SER
1	A	46	GLU
1	A	49	ASP
1	A	52	VAL
1	A	98	ASN
1	A	99	ASN
1	A	102	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	83	ASN
1	A	85	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 carbohydrates 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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.