



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:31 PM UTC

PDB ID : 1DIX / pdb_00001dix
Title : CRYSTAL STRUCTURE OF RNASE LE
Authors : Tanaka, N.; Nakamura, K.T.
Deposited on : 1999-11-30
Resolution : 1.65 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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

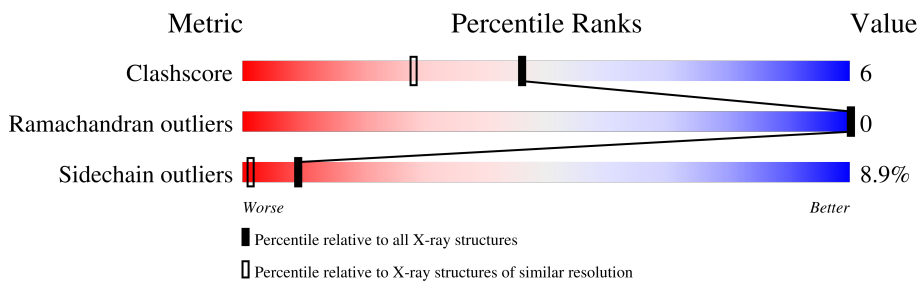
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)

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 ≥ 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	208	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1748 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 EXTRACELLULAR RIBONUCLEASE LE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	208	1612	1017	262	322	11	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1X	ALA	-	cloning artifact	UNP P80022
A	2X	SER	-	cloning artifact	UNP P80022
A	3X	GLY	-	cloning artifact	UNP P80022
A	4X	SER	-	cloning artifact	UNP P80022

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	136	Total	O	0	0
			136	136		

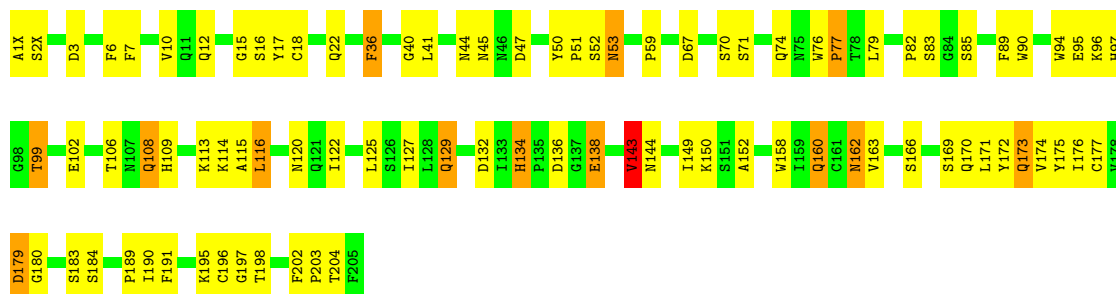
3 Residue-property plots

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: EXTRACELLULAR RIBONUCLEASE LE

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 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.02Å 78.79Å 32.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.65	Depositor
% Data completeness (in resolution range)	(Not available) (40.00-1.65)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.219 , 0.278	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1748	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1.41	16/1662 (1.0%)	2.50	115/2266 (5.1%)

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	1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	44	ASN	CA-C	14.66	1.70	1.52
1	A	158	TRP	CA-C	8.40	1.62	1.52
1	A	174	VAL	N-CA	7.94	1.55	1.46
1	A	173	GLN	CA-C	6.61	1.60	1.52
1	A	7	PHE	N-CA	6.26	1.53	1.45
1	A	41	LEU	N-CA	6.13	1.54	1.46
1	A	18	CYS	C-O	6.08	1.31	1.24
1	A	40	GLY	CA-C	6.02	1.59	1.51
1	A	45	ASN	N-CA	5.97	1.53	1.45
1	A	6	PHE	CA-C	5.95	1.60	1.53
1	A	160	GLN	CA-C	5.80	1.59	1.52
1	A	203	PRO	C-N	5.61	1.40	1.33
1	A	203	PRO	N-CA	5.43	1.53	1.46
1	A	89	PHE	C-N	-5.43	1.26	1.33
1	A	172	TYR	C-N	5.21	1.40	1.33
1	A	150	LYS	N-CA	5.05	1.52	1.46

All (115) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	ASN	O-C-N	22.60	149.01	123.25
1	A	149	ILE	O-C-N	13.01	135.43	121.90
1	A	160	GLN	O-C-N	12.49	139.07	123.21
1	A	173	GLN	O-C-N	11.65	136.50	123.33
1	A	108	GLN	OE1-CD-NE2	10.73	133.33	122.60
1	A	50	TYR	O-C-N	10.38	129.12	121.85
1	A	160	GLN	CA-C-O	-10.35	109.74	120.71
1	A	172	TYR	CA-C-O	9.98	135.03	120.16
1	A	40	GLY	O-C-N	9.76	134.94	123.61
1	A	6	PHE	O-C-N	9.74	133.92	122.72
1	A	44	ASN	CA-C-N	-9.43	106.14	123.03
1	A	44	ASN	C-N-CA	-9.43	106.14	123.03
1	A	44	ASN	CA-C-O	-9.35	111.24	121.33
1	A	158	TRP	O-C-N	9.26	134.32	123.30
1	A	173	GLN	CA-C-N	-9.13	110.46	123.06
1	A	173	GLN	C-N-CA	-9.13	110.46	123.06
1	A	44	ASN	CA-CB-CG	8.90	121.50	112.60
1	A	77	PRO	N-CA-CB	-8.87	94.54	103.15
1	A	172	TYR	O-C-N	-8.52	110.85	121.92
1	A	175	TYR	CB-CG-CD2	8.48	133.53	120.80
1	A	44	ASN	CB-CG-ND2	8.24	128.76	116.40
1	A	191	PHE	CA-CB-CG	8.24	122.04	113.80
1	A	77	PRO	O-C-N	-7.97	113.08	123.13
1	A	202	PHE	O-C-N	7.93	129.99	121.02
1	A	149	ILE	CA-C-O	-7.84	112.35	121.05
1	A	143	VAL	O-C-N	-7.76	114.35	121.87
1	A	162	ASN	CA-C-N	-7.62	112.54	123.06
1	A	162	ASN	C-N-CA	-7.62	112.54	123.06
1	A	190	ILE	CA-C-O	-7.61	114.57	120.96
1	A	173	GLN	CA-C-O	-7.57	112.51	120.99
1	A	36	PHE	O-C-N	7.37	131.88	122.81
1	A	108	GLN	CG-CD-NE2	-7.32	105.41	116.40
1	A	138	GLU	CA-C-O	-7.28	113.42	121.87
1	A	40	GLY	CA-C-N	-7.27	112.48	122.95
1	A	40	GLY	C-N-CA	-7.27	112.48	122.95
1	A	144	ASN	CB-CG-ND2	7.09	127.04	116.40
1	A	190	ILE	O-C-N	7.00	129.06	122.97
1	A	179	ASP	CA-C-N	6.96	128.90	120.13
1	A	179	ASP	C-N-CA	6.96	128.90	120.13
1	A	180	GLY	CA-C-N	6.84	132.15	120.72
1	A	180	GLY	C-N-CA	6.84	132.15	120.72
1	A	175	TYR	CA-C-O	-6.74	113.03	120.38
1	A	17	TYR	O-C-N	6.68	131.29	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	TRP	CA-C-O	-6.58	113.26	120.36
1	A	113	LYS	CA-C-O	-6.56	113.60	120.55
1	A	129	GLN	CA-C-O	6.47	127.41	120.55
1	A	6	PHE	CA-C-N	-6.47	112.65	122.81
1	A	6	PHE	C-N-CA	-6.47	112.65	122.81
1	A	175	TYR	O-C-N	6.47	130.93	123.29
1	A	174	VAL	N-CA-C	-6.46	99.18	108.48
1	A	120	ASN	OD1-CG-ND2	6.45	129.05	122.60
1	A	50	TYR	CA-C-O	-6.41	113.38	119.91
1	A	85	SER	CA-C-O	-6.34	111.45	119.31
1	A	85	SER	O-C-N	6.33	131.20	122.46
1	A	116	LEU	CA-C-O	-6.31	113.73	120.42
1	A	202	PHE	CA-CB-CG	6.24	120.04	113.80
1	A	152	ALA	CA-C-N	-6.20	112.75	121.55
1	A	152	ALA	C-N-CA	-6.20	112.75	121.55
1	A	10	VAL	O-C-N	6.16	129.91	123.26
1	A	12	GLN	CA-C-O	-6.13	113.61	120.66
1	A	115	ALA	CA-C-O	-6.09	113.96	120.42
1	A	77	PRO	CA-C-O	6.08	129.27	121.86
1	A	12	GLN	OE1-CD-NE2	6.08	128.68	122.60
1	A	10	VAL	CA-C-O	-6.06	114.03	120.39
1	A	169	SER	CA-C-O	-6.00	113.53	120.49
1	A	97	HIS	CA-C-N	5.97	126.60	119.98
1	A	97	HIS	C-N-CA	5.97	126.60	119.98
1	A	6	PHE	CA-C-O	-5.89	114.87	121.05
1	A	71	SER	CA-C-N	5.88	128.16	120.28
1	A	71	SER	C-N-CA	5.88	128.16	120.28
1	A	47	ASP	CA-CB-CG	5.83	118.43	112.60
1	A	90	TRP	CA-C-O	-5.74	114.47	120.55
1	A	202	PHE	CA-C-O	-5.72	114.48	120.09
1	A	175	TYR	CA-CB-CG	5.72	124.20	113.90
1	A	138	GLU	O-C-N	5.72	129.31	122.79
1	A	144	ASN	CA-CB-CG	-5.63	106.97	112.60
1	A	90	TRP	N-CA-C	-5.62	105.15	111.28
1	A	149	ILE	CA-C-N	-5.62	112.75	120.28
1	A	149	ILE	C-N-CA	-5.62	112.75	120.28
1	A	144	ASN	OD1-CG-ND2	-5.60	117.00	122.60
1	A	116	LEU	N-CA-C	-5.60	105.26	111.36
1	A	15	GLY	O-C-N	-5.59	116.31	122.24
1	A	53	ASN	CA-C-O	-5.59	115.21	122.14
1	A	99	THR	CA-C-O	-5.57	113.81	120.10
1	A	76	TRP	CA-C-N	-5.54	114.27	120.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	TRP	C-N-CA	-5.54	114.27	120.14
1	A	184	SER	N-CA-C	5.53	117.68	108.99
1	A	99	THR	O-C-N	5.50	128.65	122.22
1	A	74	GLN	OE1-CD-NE2	5.47	128.07	122.60
1	A	170	GLN	OE1-CD-NE2	5.45	128.05	122.60
1	A	7	PHE	CA-C-N	-5.44	114.54	122.65
1	A	7	PHE	C-N-CA	-5.44	114.54	122.65
1	A	95	GLU	CA-CB-CG	-5.40	103.30	114.10
1	A	59	PRO	CA-C-O	5.39	128.69	121.95
1	A	144	ASN	O-C-N	-5.38	116.52	122.07
1	A	169	SER	CA-C-N	5.38	131.04	122.59
1	A	169	SER	C-N-CA	5.38	131.04	122.59
1	A	129	GLN	CA-C-N	5.35	126.83	120.14
1	A	129	GLN	C-N-CA	5.35	126.83	120.14
1	A	204	THR	CA-CB-OG1	-5.31	101.63	109.60
1	A	127	ILE	CB-CA-C	-5.29	105.11	111.88
1	A	177	CYS	CA-C-N	5.29	130.29	122.94
1	A	177	CYS	C-N-CA	5.29	130.29	122.94
1	A	16	SER	N-CA-CB	-5.28	102.36	110.44
1	A	196	CYS	CA-CB-SG	5.22	126.41	114.40
1	A	152	ALA	CA-C-O	-5.21	114.45	120.24
1	A	3	ASP	N-CA-C	5.20	117.85	111.82
1	A	160	GLN	CG-CD-NE2	5.19	124.19	116.40
1	A	2(X)	SER	CA-CB-OG	-5.17	100.76	111.10
1	A	51	PRO	CA-C-O	-5.12	115.77	122.12
1	A	134	HIS	CA-CB-CG	-5.09	108.71	113.80
1	A	172	TYR	CB-CA-C	5.09	118.87	110.83
1	A	1(X)	ALA	CA-C-O	-5.08	112.16	120.80
1	A	17	TYR	CA-C-N	-5.06	114.59	122.73
1	A	17	TYR	C-N-CA	-5.06	114.59	122.73

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	197	GLY	Peptide

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	1612	0	1475	18	0
2	A	136	0	0	6	0
All	All	1748	0	1475	18	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 6.

All (18) 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:36:PHE:HD1	2:A:265:HOH:O	1.68	0.76
1:A:160:GLN:NE2	1:A:173:GLN:HE21	1.87	0.70
1:A:67:ASP:OD2	1:A:109:HIS:HE1	1.80	0.64
1:A:125:LEU:HB2	2:A:265:HOH:O	2.02	0.59
1:A:160:GLN:NE2	1:A:173:GLN:NE2	2.50	0.59
1:A:143:VAL:HG13	2:A:230:HOH:O	2.02	0.58
1:A:99:THR:O	1:A:102:GLU:HG3	2.03	0.58
1:A:132:ASP:OD2	1:A:134:HIS:HE1	1.88	0.55
1:A:109:HIS:HD2	2:A:236:HOH:O	1.91	0.53
1:A:125:LEU:O	1:A:129:GLN:HG2	2.10	0.51
1:A:36:PHE:CD1	2:A:265:HOH:O	2.53	0.48
1:A:94:TRP:CZ2	1:A:108:GLN:HG2	2.50	0.45
1:A:82:PRO:O	1:A:83:SER:C	2.58	0.45
1:A:122:ILE:HD13	1:A:176:ILE:HD13	1.99	0.45
1:A:52:SER:HA	1:A:96:LYS:O	2.17	0.44
1:A:52:SER:O	1:A:53:ASN:C	2.60	0.42
1:A:136:ASP:OD2	1:A:138:GLU:OE2	2.39	0.41
1:A:77:PRO:HD2	2:A:206:HOH:O	2.21	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	206/208 (99%)	202 (98%)	4 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	180/180 (100%)	164 (91%)	16 (9%)	9	1

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	70	SER
1	A	79	LEU
1	A	106	THR
1	A	114	LYS
1	A	116	LEU
1	A	143	VAL
1	A	162	ASN
1	A	163	VAL
1	A	166	SER
1	A	171	LEU
1	A	179	ASP
1	A	183	SER
1	A	189	PRO
1	A	195	LYS
1	A	198	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	62	GLN
1	A	73	GLN
1	A	109	HIS
1	A	129	GLN
1	A	134	HIS
1	A	160	GLN
1	A	162	ASN
1	A	168	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](#)

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.