



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 18, 2023 – 10:24 AM EDT

PDB ID : 2E0M
Title : Mutant Human Ribonuclease 1 (T24L, Q28L, R31L, R32L)
Authors : Yamada, H.; Tamada, T.; Kosaka, M.; Kuroki, R.
Deposited on : 2006-10-10
Resolution : 1.70 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

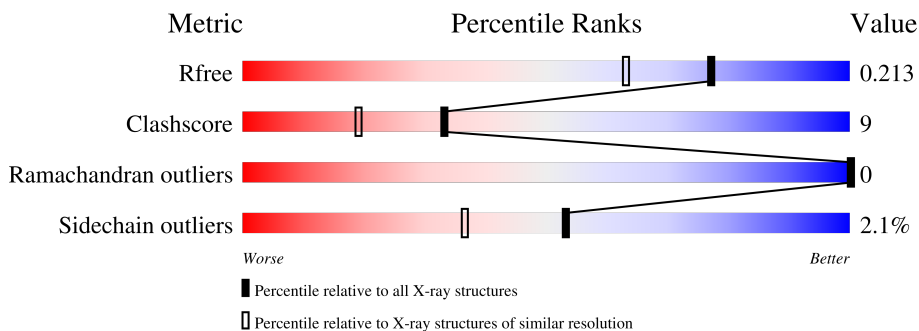
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	129	81% 15% ...
1	B	129	83% 13% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2423 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	128	1007	613	185	196	13	0	0	0
1	B	128	1007	613	185	196	13	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP P07998
A	24	LEU	THR	engineered mutation	UNP P07998
A	28	LEU	GLN	engineered mutation	UNP P07998
A	31	LEU	ARG	engineered mutation	UNP P07998
A	32	LEU	ARG	engineered mutation	UNP P07998
B	0	MET	-	expression tag	UNP P07998
B	24	LEU	THR	engineered mutation	UNP P07998
B	28	LEU	GLN	engineered mutation	UNP P07998
B	31	LEU	ARG	engineered mutation	UNP P07998
B	32	LEU	ARG	engineered mutation	UNP P07998

- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	5	Total	Cd	0	0
			5	5		
2	B	3	Total	Cd	0	0
			3	3		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	Cl	0	0
			6	6		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	5	Total	Cl	0	0
			5	5		


- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	195	Total	O	0	0
			195	195		
4	B	195	Total	O	0	0
			195	195		

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. 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.

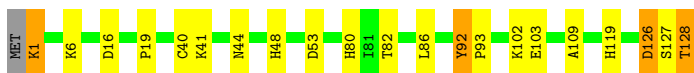
- Molecule 1: Ribonuclease

Chain A:  81% 15% ...



- Molecule 1: Ribonuclease

Chain B:  83% 13% ...



4 Data and refinement statistics i

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	93.51Å 93.51Å 94.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.70 19.97 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-1.70) 99.9 (19.97-1.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.57 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0003	Depositor
R, R_{free}	0.194 , 0.214 0.193 , 0.213	Depositor DCC
R_{free} test set	2242 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.526	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.004 for l,-k,h 0.006 for -l,-k,-h 0.004 for -h,-l,-k 0.002 for -h,l,k 0.487 for -h,k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2423	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.33% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.77	4/1027 (0.4%)	1.00	5/1383 (0.4%)
1	B	0.97	5/1027 (0.5%)	1.15	6/1383 (0.4%)
All	All	0.87	9/2054 (0.4%)	1.08	11/2766 (0.4%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	92	TYR	CG-CD1	13.59	1.56	1.39
1	B	92	TYR	CE1-CZ	11.45	1.53	1.38
1	B	92	TYR	CD1-CE1	8.89	1.52	1.39
1	A	92	TYR	CG-CD1	8.22	1.49	1.39
1	B	92	TYR	CE2-CZ	7.91	1.48	1.38

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	92	TYR	CB-CG-CD2	-21.03	108.38	121.00
1	B	92	TYR	CB-CG-CD1	17.32	131.39	121.00
1	A	92	TYR	CB-CG-CD2	-17.25	110.65	121.00
1	A	92	TYR	CB-CG-CD1	12.85	128.71	121.00
1	B	126	ASP	CB-CG-OD2	12.70	129.73	118.30

There are no chirality outliers.

There are no planarity outliers.

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	1007	0	967	19	0
1	B	1007	0	967	15	0
2	A	5	0	0	0	0
2	B	3	0	0	0	0
3	A	6	0	0	1	0
3	B	5	0	0	0	1
4	A	195	0	0	5	1
4	B	195	0	0	5	0
All	All	2423	0	1934	34	1

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 9.

The worst 5 of 34 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:103:GLU:HG2	4:B:2148:HOH:O	1.75	0.85
1:B:127:SER:O	1:B:128:THR:HB	1.78	0.81
1:A:1:LYS:HB2	4:A:2198:HOH:O	1.87	0.74
1:B:19:PRO:HB3	1:B:80:HIS:CD2	2.23	0.74
1:A:19:PRO:HB3	1:A:80:HIS:CD2	2.23	0.74

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:2008:CL:CL	4:A:2094:HOH:O[4_544]	2.02	0.18

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	126/129 (98%)	123 (98%)	3 (2%)	0	100	100
1	B	126/129 (98%)	124 (98%)	2 (2%)	0	100	100
All	All	252/258 (98%)	247 (98%)	5 (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	119/120 (99%)	116 (98%)	3 (2%)	47	29
1	B	119/120 (99%)	117 (98%)	2 (2%)	60	46
All	All	238/240 (99%)	233 (98%)	5 (2%)	53	36

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	LYS
1	A	91	ARG
1	A	128	THR
1	B	1	LYS
1	B	128	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	34	ASN
1	B	34	ASN
1	B	48	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 19 are 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 [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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.