



## wwPDB EM Validation Summary Report ⓘ

Oct 5, 2025 – 12:13 AM JST

PDB ID : 9VKU / pdb\_00009vku  
EMDB ID : EMD-65143  
Title : Cryo-EM structure of DRT9 tetramer complex  
Authors : Zhang, H.; Zhang, S.  
Deposited on : 2025-06-23  
Resolution : 3.49 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis	: <b>FAILED</b>
MolProbity	: 4-5-2 with Phenix2.0
Percentile statistics	: 20231227.v01 (using entries in the PDB archive December 27th 2023)
EM percentile statistics	: <b>NOT EXECUTED</b>
MapQ	: <b>FAILED</b>
Ideal geometry (proteins)	: Engh & Huber (2001)
Ideal geometry (DNA, RNA)	: Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	: 2.46

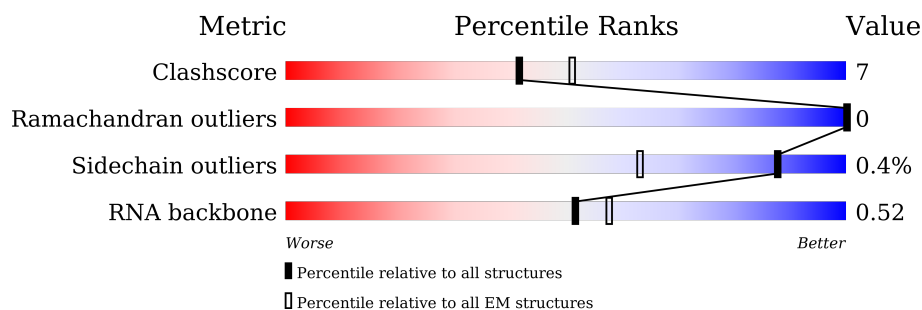
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.49 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)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	499	90% 10%
1	B	499	88% 10% .
1	C	499	86% 12% .
1	D	499	84% 14% ..
2	E	188	49% 24% 13% 13%
2	F	188	46% 28% 13% 13%
2	G	188	50% 24% 13% 13%
2	H	188	47% 29% 11% 13%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 30120 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 RNA-dependent DNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	499	Total	C	N	O	S	0	0
			4117	2649	716	743	9		
1	B	494	Total	C	N	O	S	0	0
			4068	2618	710	731	9		
1	C	492	Total	C	N	O	S	0	0
			4054	2609	708	728	9		
1	D	492	Total	C	N	O	S	0	0
			4054	2609	708	728	9		

- Molecule 2 is a RNA chain called RNA (188-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	163	Total	C	N	O	P	0	0
			3455	1543	584	1165	163		
2	F	163	Total	C	N	O	P	0	0
			3455	1543	584	1165	163		
2	G	163	Total	C	N	O	P	0	0
			3455	1543	584	1165	163		
2	H	163	Total	C	N	O	P	0	0
			3455	1543	584	1165	163		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Mg	0
			1	1	
3	B	1	Total	Mg	0
			1	1	
3	D	1	Total	Mg	0
			1	1	
3	E	1	Total	Mg	0
			1	1	
3	F	1	Total	Mg	0
			1	1	

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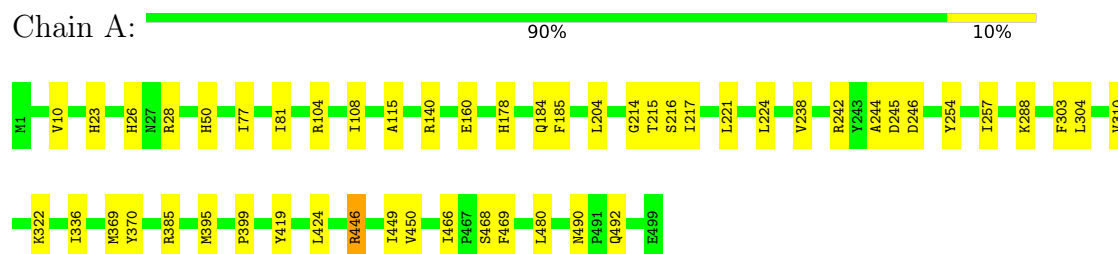
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Mol	Chain	Residues	Atoms		AltConf
3	G	1	Total 1	Mg 1	0
3	H	1	Total 1	Mg 1	0

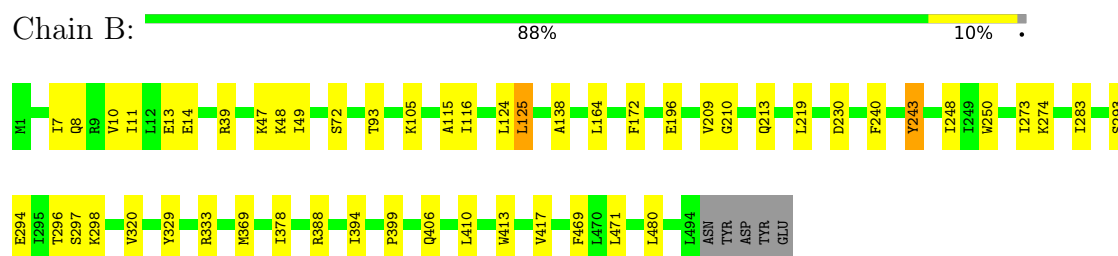
### 3 Residue-property plots

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.

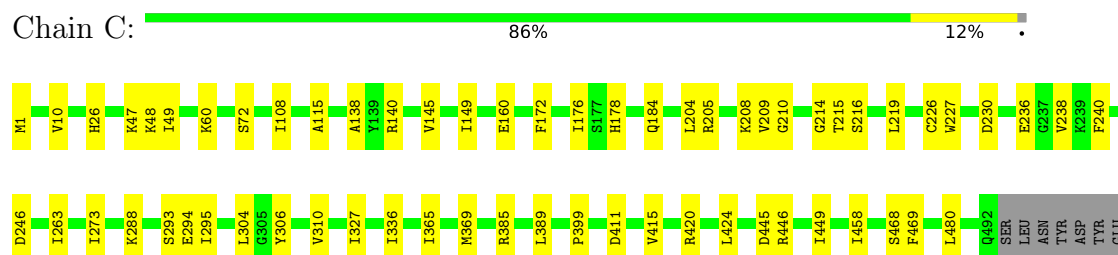
#### • Molecule 1: RNA-dependent DNA polymerase



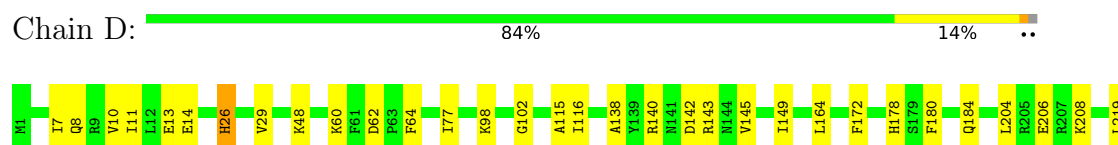
#### • Molecule 1: RNA-dependent DNA polymerase

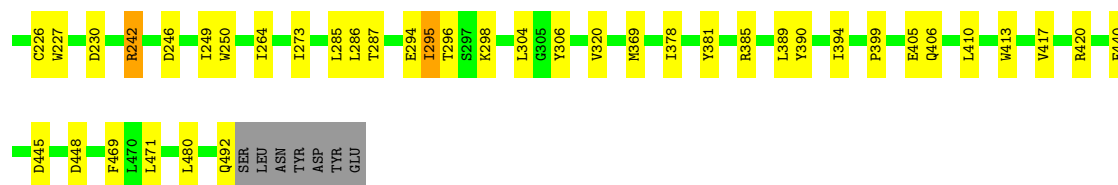


#### • Molecule 1: RNA-dependent DNA polymerase

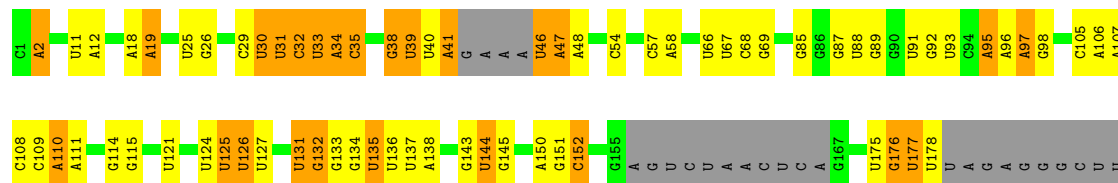


#### • Molecule 1: RNA-dependent DNA polymerase

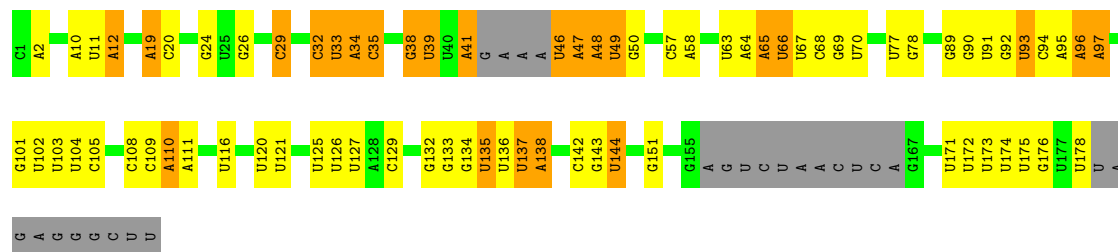




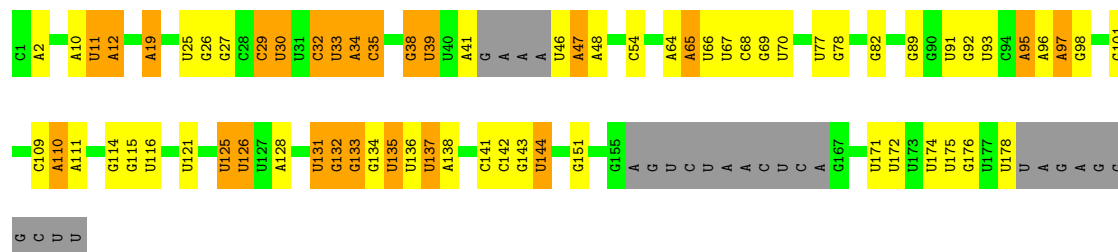
• Molecule 2: RNA (188-MER)



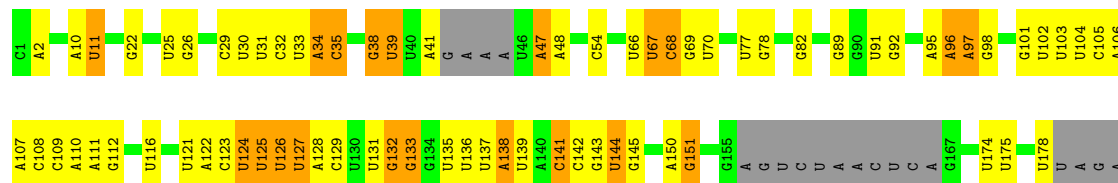
• Molecule 2: RNA (188-MER)



• Molecule 2: RNA (188-MER)



• Molecule 2: RNA (188-MER)



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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	210060	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor



## 5 Model quality

### 5.1 Standard geometry

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

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	0.27	1/4208 (0.0%)	0.45	0/5656
1	B	0.22	0/4157	0.39	0/5586
1	C	0.23	1/4143 (0.0%)	0.40	0/5567
1	D	0.23	0/4143	0.41	0/5567
2	E	0.13	0/3854	0.29	0/5996
2	F	0.23	0/3854	0.38	0/5996
2	G	0.19	0/3854	0.33	0/5996
2	H	0.22	0/3854	0.39	0/5996
All	All	0.22	2/32067 (0.0%)	0.38	0/46360

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	2
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	242	ARG	C-N	6.38	1.40	1.33
1	C	445	ASP	C-N	-5.25	1.26	1.33

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	28	ARG	Sidechain
1	A	446	ARG	Sidechain
1	B	388	ARG	Sidechain
1	C	446	ARG	Sidechain
1	D	242	ARG	Sidechain

## 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	4117	0	4184	47	0
1	B	4068	0	4150	38	0
1	C	4054	0	4134	46	0
1	D	4054	0	4134	48	0
2	E	3455	0	1739	44	0
2	F	3455	0	1739	48	0
2	G	3455	0	1739	43	0
2	H	3455	0	1739	50	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
All	All	30120	0	23558	341	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 7.

The worst 5 of 341 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:446:ARG:HA	1:A:449:ILE:CD1	1.73	1.18
1:B:296:THR:CG2	1:B:298:LYS:HG3	1.76	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:ARG:HA	1:A:449:ILE:HD12	1.25	1.14
1:B:296:THR:HG22	1:B:298:LYS:HG3	1.17	1.11
2:H:96:A:O2'	2:H:97:A:OP1	1.84	0.94

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 PDB entries followed by that with respect to all EM entries.

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	497/499 (100%)	481 (97%)	16 (3%)	0	100	100
1	B	492/499 (99%)	474 (96%)	18 (4%)	0	100	100
1	C	490/499 (98%)	478 (98%)	12 (2%)	0	100	100
1	D	490/499 (98%)	481 (98%)	9 (2%)	0	100	100
All	All	1969/1996 (99%)	1914 (97%)	55 (3%)	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 PDB entries followed by that with respect to all EM entries.

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	456/456 (100%)	455 (100%)	1 (0%)	92	97
1	B	451/456 (99%)	449 (100%)	2 (0%)	89	95

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	449/456 (98%)	449 (100%)	0	100	100
1	D	449/456 (98%)	445 (99%)	4 (1%)	75	86
All	All	1805/1824 (99%)	1798 (100%)	7 (0%)	88	95

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	26	HIS
1	D	29	VAL
1	D	295	ILE
1	D	242	ARG
1	B	243	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	69	ASN
1	C	182	ASN
1	D	490	ASN
1	D	30	HIS
1	D	182	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	161/188 (85%)	36 (22%)	6 (3%)
2	F	161/188 (85%)	39 (24%)	6 (3%)
2	G	161/188 (85%)	38 (23%)	6 (3%)
2	H	160/188 (85%)	36 (22%)	8 (5%)
All	All	643/752 (85%)	149 (23%)	26 (4%)

5 of 149 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	2	A
2	E	11	U
2	E	12	A
2	E	19	A
2	E	30	U

5 of 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	G	38	G
2	G	131	U
2	H	125	U
2	G	67	U
2	H	34	A

## 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](#)

Of 7 ligands modelled in this entry, 7 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.