



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2025 – 12:07 AM JST

PDB ID : 9IIY
EMDB ID : EMD-60609
Title : Cryo-EM Structure of EfPiwi-piRNA-target (25-nt, bilobed)
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Deposited on : 2024-06-21
Resolution : 3.00 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

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>.

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

EMDB validation analysis : **FAILED**
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.2

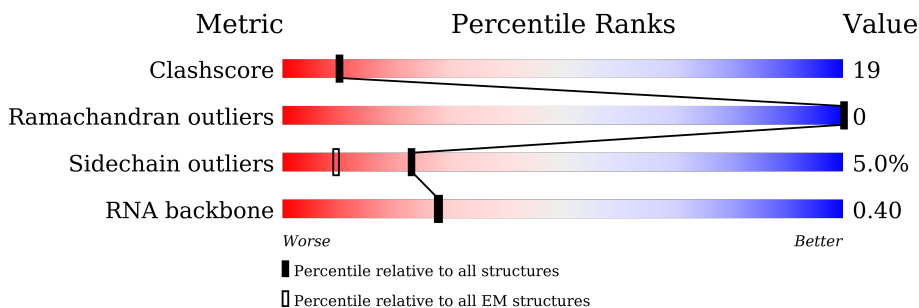
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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 ≥ 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	987	
2	B	22	
3	C	21	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5943 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 Piwi.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	620	Total	C	N	O	S	0	0
			5030	3202	885	914	29		

- Molecule 2 is a RNA chain called RNA (5'-R(P*UP*AP*GP*CP*AP*GP*AP*UP*CP*GP*GP*UP*UP*GP*UP*AP*UP*AP*GP*AP*CP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	22	Total	C	N	O	P	0	0
			474	211	86	155	22		

- Molecule 3 is a RNA chain called RNA (5'-R(P*CP*GP*UP*CP*UP*AP*UP*AP*CP*AP*AP*CP*CP*GP*AP*UP*CP*AP*GP*CP*U)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	21	Total	C	N	O	P	0	0
			439	198	76	144	21		



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	87581	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor

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	0.25	0/5135	0.54	1/6944 (0.0%)
2	B	0.54	1/530 (0.2%)	1.10	4/823 (0.5%)
3	C	0.25	0/489	0.87	0/756
All	All	0.28	1/6154 (0.0%)	0.65	5/8523 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	U	OP3-P	-10.60	1.48	1.61

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	11	G	OP1-P-O3'	-10.99	81.02	105.20
2	B	11	G	OP2-P-O3'	-9.52	84.26	105.20
2	B	12	U	OP1-P-OP2	7.13	130.30	119.60
1	A	335	LEU	CA-CB-CG	5.85	128.76	115.30
2	B	14	G	C4-N9-C1'	5.27	133.34	126.50

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	5030	0	5077	181	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	474	0	237	36	0
3	C	439	0	227	21	0
All	All	5943	0	5541	217	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 19.

The worst 5 of 217 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)
2:B:15:U:H2'	2:B:16:A:H8	1.49	0.76
1:A:734:LEU:HD23	1:A:744:LEU:HD22	1.68	0.75
1:A:744:LEU:H	1:A:784:THR:HB	1.50	0.75
2:B:5:A:N1	3:C:19:G:N3	2.38	0.71
1:A:333:VAL:O	1:A:337:ASN:ND2	2.25	0.69

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	608/987 (62%)	553 (91%)	55 (9%)	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	562/872 (64%)	534 (95%)	28 (5%)	20 53

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	ARG
1	A	986	PHE
1	A	623	TRP
1	A	814	TYR
1	A	539	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	795	GLN
1	A	882	HIS
1	A	909	HIS
1	A	450	ASN
1	A	243	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	21/22 (95%)	8 (38%)	1 (4%)
3	C	20/21 (95%)	8 (40%)	2 (10%)
All	All	41/43 (95%)	16 (39%)	3 (7%)

5 of 16 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	2	A
2	B	3	G
2	B	6	G
2	B	7	A
2	B	11	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	5	A
3	C	8	A
3	C	20	C

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.