



## wwPDB EM Validation Summary Report ⓘ

Jul 15, 2025 – 07:23 PM JST

PDB ID : 8IN8 / pdb\_00008in8  
EMDB ID : EMD-35592  
Title : Cryo-EM structure of the target ssDNA-bound SIR2-APAZ/Ago-gRNA quaternary complex  
Authors : Zhang, H.; Li, Z.; Yu, G.M.; Li, X.Z.; Wang, X.S.  
Deposited on : 2023-03-08  
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](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 : **FAILED**  
MolProbity : 4-5-2 with Phenix2.0rc1  
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) : 2.44

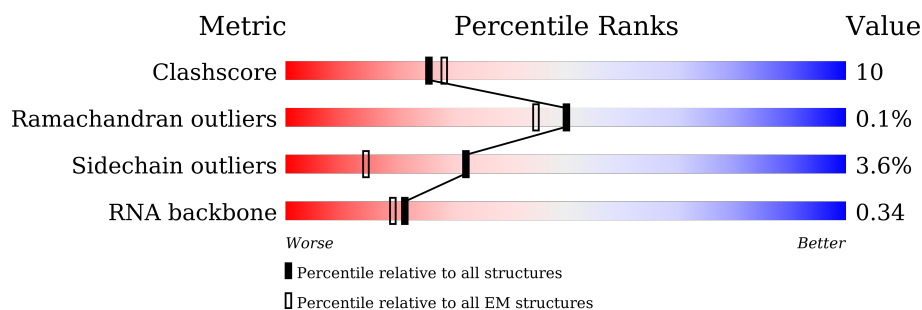
# 1 Overall quality at a glance

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  $\geq 3$ , 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	B	587	
2	C	473	
3	I	24	
4	J	23	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6663 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 Sir2 superfamily protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	254	Total	C	N	O	S	0	0
			2009	1290	347	368	4		

- Molecule 2 is a protein called Piwi domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	470	Total	C	N	O	S	0	0
			3685	2362	624	681	18		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	24	Total	C	N	O	P	0	0
			506	226	81	175	24		

- Molecule 4 is a DNA chain called DNA (5'-D(P\*AP\*AP\*CP\*GP\*AP\*CP\*GP\*TP\*CP\*TP\*AP\*AP\*GP\*AP\*AP\*AP\*CP\*CP\*AP\*TP\*TP\*AP\*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
4	J	23	Total	C	N	O	P	0	0
			462	220	88	131	23		

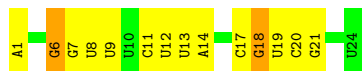
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
5	I	1	Total	Mg	0
			1	1	

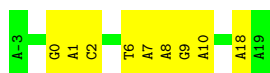




- Molecule 3: RNA (5'-R(P\*AP\*UP\*AP\*AP\*UP\*GP\*GP\*UP\*UP\*UP\*CP\*UP\*UP\*AP\*GP\*AP\*CP\*GP\*UP\*CP\*GP\*UP\*UP\*U)-3')



- Molecule 4: DNA (5'-D(P\*AP\*AP\*CP\*GP\*AP\*CP\*GP\*TP\*CP\*TP\*AP\*AP\*GP\*AP\*AP\*A\*P\*CP\*CP\*AP\*TP\*TP\*AP\*A)-3')



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	380948	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	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 [i](#)

### 5.1 Standard geometry [i](#)

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	B	0.12	0/2049	0.34	0/2768
2	C	0.13	0/3782	0.33	0/5146
3	I	0.12	0/563	0.30	0/872
4	J	0.21	0/519	0.39	0/797
All	All	0.13	0/6913	0.34	0/9583

There are no bond length outliers.

There are no bond angle outliers.

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	B	2009	0	2027	42	0
2	C	3685	0	3598	72	0
3	I	506	0	254	10	0
4	J	462	0	253	9	0
5	I	1	0	0	0	0
All	All	6663	0	6132	129	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 10.

The worst 5 of 129 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:375:THR:HG22	1:B:376:GLU:H	1.54	0.72
1:B:561:CYS:HB3	1:B:569:ALA:HB3	1.73	0.70
1:B:528:ARG:HA	1:B:531:ARG:HG3	1.77	0.67
4:J:9:DG:H2'	4:J:10:DA:C8	2.31	0.65
1:B:409:GLN:N	1:B:409:GLN:OE1	2.30	0.64

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	B	250/587 (43%)	240 (96%)	10 (4%)	0	100	100
2	C	468/473 (99%)	433 (92%)	34 (7%)	1 (0%)	44	77
All	All	718/1060 (68%)	673 (94%)	44 (6%)	1 (0%)	50	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	266	ILE

### 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	B	213/502 (42%)	203 (95%)	10 (5%)	22	56
2	C	393/407 (97%)	381 (97%)	12 (3%)	35	68
All	All	606/909 (67%)	584 (96%)	22 (4%)	32	64

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	260	TYR
2	C	358	SER
2	C	285	SER
2	C	382	VAL
1	B	479	THR

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

Mol	Chain	Res	Type
2	C	11	HIS
2	C	73	ASN
2	C	387	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	I	23/24 (95%)	4 (17%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	I	6	G
3	I	17	C
3	I	18	G
3	I	21	G

There are no RNA pucker outliers to report.

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

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 1 ligands modelled in this entry, 1 is 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.