

# Full wwPDB Integrative Structure Validation Report

September 06, 2019 -- 04:22 PM

PDB ID	PDBDEV00000014
Molecule Name	Structure of 16S rRNA complexed with methyltransferase A small subunit
Title	Integrative Modeling of Biomolecular Complexes: HADDOCKing with Cryo-Electron Microscopy Data.
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The following softwares were used in the production of this report:

*Integrative Modeling Package : Version XX*  
*Molprobit : Version XX*  
*Phenix : Version XX*  
*Integrative Modeling Validation Package : Version XX*

## 1. Overall quality at a glance

## 2. Entry composition

There are 3 unique types of models in this entry. Models have 2,1,1 chains respectively.

Model ID	Subunit Name	Chain ID	Total Residues
1	16Srna	A	1530
1	ksga	B	252
2	16Srna	A	1530
3	ksga	B	252

There are 2 software packages reported in this entry.

ID	Software Name	Software Version	Software Classification
1	HADDOCK	2.3	molecular docking
2	POWERFIT	2.0	em fitter

There are 4 unique datasets used to build the model in this entry.

ID	Dataset Type	Database Name	Data Access Code
1	Experimental model	PDB	4ADV

2	Mutagenesis data	Not Listed	None
3	3DEM volume	EMDB	EMD-2017
4	unspecified	Not Listed	None

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### 3. Data quality

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### 4. Model quality

#### 4.1 Too-close contacts

#### 4.2 Torsion angles

##### 4.2.1 Protein backbone

##### 4.2.2 Protein sidechains

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### 5. Fit of model and data

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### 6. Uncertainty of model

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