

# **Full wwPDB Integrative Structure Validation Report**

# August 20, 2019 -- 05:25 PM

PDB ID	PDBDEV00000009
Molecule Name	Structure of the human Rev7 dimer
Title	Rev7 dimerization is important for assembly and function of the Rev1/Polζ translesion synthesis complex
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#### The following softwares were used in the production of this report:

Integrative Modeling Package: Version XX
Molprobity: Version XX
Phenix: Version XX
Integrative Modeling Validation Package: Version XX

## 1. Overall quality at a glance

### 2. Entry composition

There are 2 unique types of models in this entry. The entry contains 4 chains.

Molecule ID	Molecule Name	Chain ID	Total Residues
1	Rev7-monomer	Α	212
1	Rev3-RBM2	С	212
1	Rev7-monomer	В	28
1	Rev3-RBM2	D	28

Software packages used for modeling were either not reported or not used.

There are 3 unique datasets used to build the model(s) in this entry.

ID	Dataset Type	Database Name	Data Access Code
1	SAS data	SASBDB	SASDC29
2	Experimental model	PDB	6BC8
3	Mutagenesis data	Not Listed	None

3. Data quality		
4. Model quality		
4.1 Too-close contacts		
4.2 Torsion angles		
4.2.1 Protein backbone		
4.2.2 Protein sidechains		
5. Fit of model and data		
6. Uncertaintiy of model		