

Full wwPDB Integrative Structure Validation Report

September 06, 2019 -- 02:06 PM

PDB ID	PDBDEV00000017
Molecule Name	Molecular architecture of the major membrane ring component, Pom152, of the yeast nuclear pore complex
Title	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex.
Authors	Upla P;Kim SJ;Sampathkumar P;Dutta K;Cahill SM;Chemmmama IE;Williams R;Bonanno JB;Rice WJ;Stokes DL;Cowburn D;Almo SC;Sali A;Rout MP;Fernandez-Martinez J

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 6 unique types of models in this entry. Models have 1,1,1,1,1,1 chains respectively.

Molecule ID	Molecule Name	Chain ID	Total Residues
1	pom152	A	1337

There are 3 software packages reported in this entry.

ID	Software Name	Software Version	Software Classification
1	Integrative Modeling Platform (IMP)	develop-0a5706e202	integrative model building
2	IMP PMI module	67456c0	integrative model building
3	MODELLER	9.13	comparative modeling

There are 22 unique datasets used to build the model in this entry.

ID	Dataset Type	Database Name	Data Access Code

1	Experimental model	PDB	5TVZ
2	Comparative model	Not Listed	None
3	Comparative model	Not Listed	None
4	Comparative model	Not Listed	None
5	Comparative model	Not Listed	None
6	Comparative model	Not Listed	None
7	Comparative model	Not Listed	None
8	3DEM volume	EMDB	EMD-8543
9	3DEM volume	Not Listed	None
10	2DEM class average	Not Listed	None
11	2DEM class average	Not Listed	None
12	2DEM class average	Not Listed	None
13	2DEM class average	Not Listed	None
14	2DEM class average	Not Listed	None
15	2DEM class average	Not Listed	None
16	2DEM class average	Not Listed	None
17	2DEM class average	Not Listed	None
18	SAS data	SASBDB	SASDBV9
19	SAS data	SASBDB	SASDBW9
20	SAS data	SASBDB	SASDBX9
21	SAS data	SASBDB	SASDBY9
22	SAS data	SASBDB	SASDBZ9

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. Uncertainty of model
