



# Full wwPDB Integrative Structure Validation Report

November 05, 2019 -- 04:07 PM

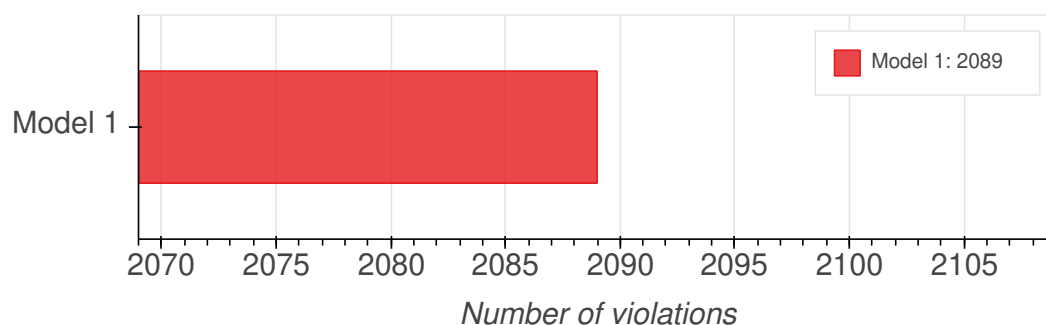
<i>PDB ID</i>	<i>PDBDEV00000017</i>
Molecule Name	Molecular architecture of the major membrane ring component, Pom152, of the yeast nuclear pore complex
Title	Molecular Architecture of the Major Membrane Ring Component of the Nuclear Pore Complex.
Authors	Upla P;Kim SJ;Sampathkumar P;Dutta K;Cahill SM;Chemmama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

The following software were used in the production of this report:

*Integrative Modeling Validation Package : Version 1.0*

## 1. Overall quality at a glance

### Model quality: Excluded Volume Analysis



## 2. Ensemble information

*This entry consists of 1 distinct ensemble.*

<i>Ensemble number</i>	<i>Ensemble name</i>	<i>Model ID</i>	<i>Number of models</i>	<i>Clustering method</i>	<i>Clustering feature</i>	<i>Cluster precision</i>
1	Cluster 0	1	364	None	dRMSD	7.0

### 3. Model composition

#### 3.1 Summary

*This entry consists of 1 unique models, with 1 subunits in each model. A total of 22 datasets or restraints was used to build this entry. Each model is represented by 9 rigid bodies and 9 flexible or non-rigid units.*

#### 3.2 Entry composition

*There is 1 unique type of model in this entry. This model is titled Cluster 0/None respectively.*

<i>Model ID</i>	<i>Subunit number</i>	<i>Subunit ID</i>	<i>Subunit name</i>	<i>Chain ID</i>	<i>Total residues</i>
1	1	1	pom152	A	1337

#### 3.3 Datasets used for modeling

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

<i>ID</i>	<i>Dataset type</i>	<i>Database name</i>	<i>Data access code</i>
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

## 4. Representation

*This entry has only one representation and includes 9 rigid bodies and 9 flexible units.*

<i>Chain ID</i>	<i>Rigid bodies</i>	<i>Non-rigid segments</i>
A	379-472:Comparative model/None, 520-611:Comparative model/None, 616-714:Comparative model/None, 722-818:Comparative model/None, 824-918:Comparative model/None, 931-1026:Comparative model/None, 1036-1141:Comparative model/None, 1150-1229:Comparative model/None, 1244-1337:Comparative model/None.	1-378, 473-519, 612-615, 715-721, 819-823, 919-930, 1027-1035, 1142-1149, 1230-1243.

## 5. Methodology and software

<i>Step number</i>	<i>Protocol ID</i>	<i>Method name</i>	<i>Method type</i>	<i>Number of computed models</i>	<i>Multi state modeling</i>	<i>Multi scale modeling</i>

1	1	Replica exchange monte carlo	Sampling	100000	False	True
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*There are 3 software packages reported in this entry.*

<i><b>ID</b></i>	<i><b>Software name</b></i>	<i><b>Software version</b></i>	<i><b>Software classification</b></i>
1	Integrative Modeling Platform (IMP)	develop-0a5706e202	integrative model building
2	IMP PMI module	67456c0	integrative model building
3	MODELLER	9.13	comparative modeling

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## 6. Data quality

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## 7. Model quality

### 7.1 Excluded volume satisfaction

*Excluded volume satisfaction for the models in the entry are listed below.*

<i><b>Models</b></i>	<i><b>Excluded Volume Satisfaction</b></i>	<i><b>Number of violations</b></i>
1	99.46	2089

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## 8. Fit of model to data used for modeling

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## 9. Fit of model to data not used for modeling

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## 10. Uncertainty of model

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