

**Summary of integrative structure determination of Integrative model of Nup116 knockout (at 37C) yeast nuclear pore complex (PDB ID: 9A0H, PDB-Dev ID: PDBDEV\_0000053)**

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- Nic96: chain(s) A1 (839 residues)</li> <li>- Nup188: chain(s) B1 (1655 residues)</li> <li>- Nup157: chain(s) D1 (1391 residues)</li> <li>- Nup133: chain(s) K1 (1157 residues)</li> <li>- Nup84: chain(s) L1 (726 residues)</li> <li>- Nup145c: chain(s) M1 (712 residues)</li> <li>- Sec13: chain(s) N1 (297 residues)</li> <li>- Seh1: chain(s) O1 (349 residues)</li> <li>- Nup85: chain(s) P1 (744 residues)</li> <li>- Nup120: chain(s) R1 (1037 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- 3DEM volume, EMD: <a href="#">EMD-10661</a></li> <li>- 3DEM volume, Zenodo: <a href="#">10.5281/zenodo.3820319</a></li> <li>- 3DEM volume, Zenodo: <a href="#">10.5281/zenodo.3820319</a></li> <li>- Integrative model, PDB: <a href="#">9A0F</a></li> <li>- Integrative model, PDB: <a href="#">9A0F</a></li> <li>- Other, Not available: <a href="https://doi.org/10.1038/nsmb1194">https://doi.org/10.1038/nsmb1194</a></li> <li>- Other, Not available: <a href="https://doi.org/10.1038/nature26003">https://doi.org/10.1038/nature26003</a></li> </ul>
<b>2. Representation</b>	
<a href="#">Number of representations</a>	1
<a href="#">Scale</a>	Atomic
Number of <a href="#">rigid</a> and <a href="#">flexible</a> segments	0, 10
<b>3. Restraints</b>	
<a href="#">Physical principles</a>	Information about physical principles was not provided
<a href="#">Experimental data</a>	- 1 unique InnerSurfaceGeometricRestraint: None
<b>4. Validation</b>	
<a href="#">Number of ensembles</a>	0
<a href="#">Number of models in ensembles</a>	Not applicable
<a href="#">Number of deposited models</a>	1
<a href="#">Model precision (uncertainty of models)</a>	Not available
<a href="#">Data quality</a>	Data quality has not been assessed

<a href="#"><i>Model quality: assessment of atomic segments</i></a>	<ul style="list-style-type: none"><li>- Clashscore: 0.00</li><li>- Ramachandran outliers: 264</li><li>- Sidechain outliers: 399</li></ul>
<a href="#"><i>Fit to data used for modeling</i></a>	Fit of model to information used to compute it has not been determined
<a href="#"><i>Fit to data used for validation</i></a>	Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
1. <a href="#"><i>Name</i></a>	Monte Carlo simulated annealing optimization of multiple rigid bodies with IMP
<a href="#"><i>Software</i></a>	<a href="#">Integrative Modeling Platform (IMP)</a> (version 2.9.0)