Summary of integrative structure determination of Molecular architecture of the major membrane ring component, Pom152, of the yeast nuclear pore complex (PDB ID: 8ZZH, PDB-Dev ID: PDBDEV_00000017)

1. Model Composition	
Entry composition	pom152: Chain A (1337 residues)
Datasets used for modeling	- Experimental model, PDB ID: 5TVZ - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - Comparative model, template PDB ID: Not available - 3DEM volume, EMDB: EMD-8543 - 3DEM volume, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - 2DEM class average, File: 10.5281/zenodo.1231518 - SAS data, SASBDB: SASDBV9 - SAS data, SASBDB: SASDBW9 - SAS data, SASBDB: SASDBX9 - SAS data, SASBDB: SASDBY9 - SAS data, SASBDB: SASDBZ9
2. Representation	
Resolution	Coarse-grained: 1, 2, 5, 15 residue(s) per bead
Number of rigid bodies, flexible units	9, 9
Rigid bodies	A: 379-472, 520-611, 616-714, 722-818, 824-918, 931-1026, 1036-1141, 1150-1229, 1244-1337
Flexible units	A: 1-378, 473-519, 612-615, 715-721, 819-823, 919-930, 1027-1035, 1142-1149, 1230-1243
Structural coverage (rigid bodies)	64%

3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique EM3DRestraint: Gaussian mixture models - 6 unique EM2DRestraint: Number of micrographs: None, Image resolution: 50.0 - 2 unique EM2DRestraint: Number of micrographs: None, Image resolution: 60.0 - 5 unique SASRestraint: Assembly name: SAXS subassembly Fitting method: FoXS Multi-state: False
4. Validation	
Number of ensembles	1
Number of models in ensembles	364
Number of deposited models	1
Model precision (uncertainty of models)	7.0, Å
Data quality	- SASDBV9: Rg from Gunier is 1.77nm and Rg from p(r) is 1.82nm - SASDBW9: Rg from Gunier is 2.71nm and Rg from p(r) is 2.79nm - SASDBX9: Rg from Gunier is 2.78nm and Rg from p(r) is 2.64nm - SASDBY9: Rg from Gunier is 2.95nm and Rg from p(r) is 2.98nm - SASDBZ9: Rg from Gunier is 4.34nm and Rg from p(r) is 4.63nm
Model quality: assessment of excluded volume	Satisfaction: 99.46-99.46%
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	100000
Software	- Integrative Modeling Platform (IMP) (version develop-0a5706e202) - IMP PMI module (version 67456c0) - MODELLER (version 9.13)