Table S1: Summary of Integrative Structure Determination of Molecular architecture of the major membrane ring component, Pom152, of the yeast nuclear pore complex (PDBDEV00000017)

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 listed - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - Comparative model, template PDB ID: Not listed - 3DEM volume, EMDB ID: EMD-8543 - 3DEM volume, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed - SAS data, SASDBV9 - SAS data, SASDBW9 - SAS data, SASDBX9 - SAS data, SASDBY9 - SAS data, SASDBZ9
2. Representation	
Atomic structural coverage	64%
Number of rigid bodies, flexible units	9, 9
Rigid regions	- 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.
Flexible units	- A: 1-378, 473-519, 612-615, 715-721, 819-823, 919-930, 1027-1035, 1142-1149, 1230-1243.
Resolution	Rigid bodies: 1 residue per bead. Flexible regions: N/A
3. Restraints	
Physical principles	Excluded volume and Sequence connectivity.

Experimental data	- 1 unique EM3DRestraint: Gaussian mixture models, 50 - 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	
Sampling validation	1. Information related to sampling validation has not been provided
Clustering algorithm ,*clustering feature*	Distance threshold-based clustering used if ensembles are deposited, dRMSD
Number of ensembles	1
Number of models in ensembles	364
Model precision (uncertainty of models)	7.0Å
Quality of data	1. SASDBV9: Rg from Gunier is 1.824nm and Rg from p(r) is 1.77nm 2. SASDBW9: Rg from Gunier is 2.787nm and Rg from p(r) is 2.71nm 3. SASDBX9: Rg from Gunier is 2.636nm and Rg from p(r) is 2.78nm 4. SASDBY9: Rg from Gunier is 2.976nm and Rg from p(r) is 2.95nm 5. SASDBZ9: Rg from Gunier is 4.629nm and Rg from p(r) is 4.34nm
Assessment of atomic regions	Not applicable
Assessment of excluded volume	1. Model-1: Number of violations-2089.0
Fit of the model to information used to compute it	1. SASDBV9: Fit 1 with X^2 value 1.28 2. SASDBV9: Fit 2 with X^2 value 1.1 3. SASDBW9: Fit 1 with X^2 value 1.97 4. SASDBX9: Fit 1 with X^2 value 2.86 5. SASDBY9: Fit 1 with X^2 value 2.02 6. SASDBZ9: Fit 1 with X^2 value 1.94
Fit of the model to information not used to compute it	1. Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
Method	Sampling
Name	Replica exchange Monte Carlo
Details	- Method details unspecified

Software	- Integrative Modeling Platform (IMP) (version develop-0a5706e202) - IMP PMI module (version 67456c0) - MODELLER (version 9.13) - No location specified