Summary of integrative structure determination of Comprehensive structure and functional adaptations of the yeast nuclear pore complex (PDB ID: 9A1P, PDB-Dev ID: PDBDEV_00000097)

1. Model Composition	
Entry composition	- Nsp1: Chain A (823 residues) - Nup49: Chain C (472 residues) - Nup57: Chain K (541 residues) - Nup49: Chain I (472 residues) - Nup59: Chain X (528 residues) - Nup188: Chain N (1655 residues) - Nic96: Chain Q (839 residues) - Nsp1: Chain D (823 residues) - Nup170: Chain Y (1502 residues) - Nup157: Chain 1 (1391 residues) - Nic96: Chain S (839 residues) - Nup170: Chain 0 (1502 residues) - Nup49: Chain L (472 residues) - Nup59: Chain V (528 residues) - Nup192: Chain O (1683 residues) - Nsp1: Chain J (823 residues) - Nup53: Chain W (475 residues) - Nic96: Chain R (839 residues) - Nup192: Chain M (1683 residues) - Nup57: Chain E (541 residues) - Nic96: Chain T (839 residues) - Nup49: Chain F (472 residues) - Nup57: Chain B (541 residues) - Nup57: Chain H (541 residues) - Nsp1: Chain G (823 residues) - Nup157: Chain Z (1391 residues) - Nup53: Chain U (475 residues) - Nup188: Chain P (1655 residues)
Datasets used for modeling	- Crosslinking-MS data, Linker name and number of cross-links: DSS, 114 cross-links - 3DEM volume, EMDB: EMDB-24232 - Experimental model, PDB ID: 7N85
2. Representation	
Resolution	Coarse-grained: 1 residue(s) per bead
Number of rigid bodies, flexible units	28, 0

Rigid bodies	- Z: 1-1391 - 1: 1-1391 - Y: 1-1502 - 0: 1-1502 - U: 1-475 - W: 1-475 - V: 1-528 - X: 1-528 - A: 1-823 - D: 1-823 - G: 1-823 - J: 1-823 - B: 1-541 - E: 1-541 - H: 1-541 - K: 1-541 - C: 1-472 - F: 1-472 - I: 1-472 - L: 1-472 - N: 1-1655 - P: 1-1655 - M: 1-1683 - O: 1-1683 - Q: 1-839 - R: 1-839 - S: 1-839 - T: 1-839
Structural coverage (rigid bodies)	100%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSS, 114 cross-links
4. Validation	
Number of ensembles	1
Number of models in ensembles	10
Number of deposited models	10
Model precision (uncertainty of models)	None, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 100.00-100.00%
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	Production sampling
Name	Enumeration
Number of computed models	1200
Software	- PSIPRED (version 4.0) - Integrative Modeling Platform (IMP) (version 2.2)