

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	<ul style="list-style-type: none"> - Nup170: chain(s) 0, Y (1502 residues) - Nup157: chain(s) 1, Z (1391 residues) - Nsp1: chain(s) A, D, G, J (823 residues) - Nup57: chain(s) B, E, H, K (541 residues) - Nup49: chain(s) C, F, I, L (472 residues) - Nup192: chain(s) M, O (1683 residues) - Nup188: chain(s) N, P (1655 residues) - Nic96: chain(s) Q, R, S, T (839 residues) - Nup53: chain(s) U, W (475 residues) - Nup59: chain(s) V, X (528 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Crosslinking-MS data, Zenodo: 10.5281/zenodo.5662389 - 3DEM volume, EMDB: EMD-24232 - Experimental model, PDB: 7N85
2. Representation	
Number of representations	1
Scale	Coarse-grained: 1 residue(s) per bead
Number of <i>rigid</i> and <i>flexible</i> segments	28, 0
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique CrossLinkRestraint: DSS, 114 crosslinks
4. Validation	
Number of ensembles	1
Number of models in ensembles	10
Number of deposited models	10
Model precision (uncertainty of models)	Not available
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	Satisfaction of crosslinks: 50.00-100.00%

<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. <i>Name</i>	Production sampling
<i>Method</i>	Enumeration
<i>Number of computed models</i>	1200
<i>Software</i>	<ul style="list-style-type: none"> - PSIPRED (version 4.0) - Integrative Modeling Platform (IMP) (version 2.2)