

Summary of integrative structure determination of Integrative model of the wild type yeast nuclear pore complex (PDB ID: 9A0F, PDB-Dev ID: PDBDEV_00000051)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - Dyn2: chain(s) 91, 92 (92 residues) - Nic96: chain(s) A1, A2, A3, A4 (839 residues) - Nup188: chain(s) B1, B2 (1655 residues) - Nup192: chain(s) C1, C2 (1683 residues) - Nup157: chain(s) D1, D2 (1391 residues) - Nup57: chain(s) H1, H2, H3, H4 (541 residues) - Nup49: chain(s) I1, I2, I3, I4 (472 residues) - Nsp1: chain(s) J1, J2, J3, J4, J5, J6 (823 residues) - Nup133: chain(s) K1, K2 (1157 residues) - Nup84: chain(s) L1, L2 (726 residues) - Nup145c: chain(s) M1, M2 (712 residues) - Sec13: chain(s) N1, N2 (297 residues) - Seh1: chain(s) O1, O2 (349 residues) - Nup85: chain(s) P1, P2 (744 residues) - Nup120: chain(s) R1, R2 (1037 residues) - Nup159: chain(s) V1, V2 (1460 residues) - Nup82: chain(s) W1, W2 (713 residues) - Nup170: chain(s) d1, d2 (1502 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - 3DEM volume, EMDB: EMD-10198 - 3DEM volume, Zenodo: 10.5281/zenodo.3820319 - 3DEM volume, Zenodo: 10.5281/zenodo.3820319 - Experimental model, PDB: 4XMM - Comparative model, Zenodo: 10.5281/zenodo.1194547 - Comparative model, Zenodo: 10.5281/zenodo.1194547 - Integrative model, PDB: 8ZZA - Integrative model, PDB: 8ZZA - Integrative model, PDB: 8ZZA - Other, Not available: https://doi.org/10.1038/nsmb1194
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	0, 46
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 1 unique EM3DRestraint: None

4. Validation	
<i>Number of ensembles</i>	0
<i>Number of models in ensembles</i>	Not applicable
<i>Number of deposited models</i>	1
<i>Model precision (uncertainty of models)</i>	Not available
<i>Data quality</i>	Data quality has not been assessed
<i>Model quality: assessment of atomic segments</i>	<ul style="list-style-type: none"> - Clashscore: 0.00 - Ramachandran outliers: 1068 - Sidechain outliers: 1409
<i>Fit to data used for modeling</i>	Fit of model to information used to compute it has not been determined
<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>	Systematic fitting to EM maps with Global search from UCSF Chimera
2. <i>Name</i>	Monte Carlo simulated annealing optimization of multiple rigid bodies with IMP
<i>Software</i>	<ul style="list-style-type: none"> - Integrative Modeling Platform (IMP) (version 2.9.0) - UCSF Chimera (version 1.14)