Summary of integrative structure determination of Structure of the S. cerevisiae nuclear pore complex cytoplasmic mRNA export platform, Nup82 (PDB ID: 8ZZK | pdb_00008zzk, PDB-Dev ID: PDBDEV_00000020)

1. Model Composition	
1.1. Entry composition	- Dyn2: chain(s) A, B (92 residues) - Nup82: chain(s) C, D (713 residues) - Nup159: chain(s) E, F (1460 residues) - Nsp1: chain(s) G, H (823 residues) - Nup116: chain(s) I, J (1113 residues)
1.2. Datasets used for modeling	- Experimental model, PDB: pdb_00004ds1 - Experimental model, PDB: pdb_00003pbp - Experimental model, PDB: pdb_00005cws - Comparative model, Zenodo: 10.5281/zenodo.1256259 - Comparative model, Zenodo: 10.5281/zenodo.1256259 - Comparative model, Zenodo: 10.5281/zenodo.1256259 - Comparative model, Zenodo: 10.5281/zenodo.1256259 - Comparative model, Zenodo: 10.5281/zenodo.1256259 - Comparative model, Zenodo: 10.5281/zenodo.1256259 - Experimental model, PDB: pdb_00001xip - Crosslinking-MS data, Zenodo: 10.5281/zenodo.1256259 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.1256259 - Crosslinking-MS data, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - SAS data, Zenodo: 10.5281/zenodo.1256259 - SAS data, Zenodo: 10.5281/zenodo.1256259 - SAS data, Zenodo: 10.5281/zenodo.1256259
2. Representation	
2.1. Number of representations	1
2.2. Scale	Multiscale: Coarse-grained: 1 - 100 residue(s) per bead

2.3. Number of rigid and flexible segments	38, 42
3. Restraints	
3.1. Physical principles	Information about physical principles was not provided
3.2. Experimental data	- 1 unique CrossLinkRestraint: DSS, 240 crosslinks - 1 unique CrossLinkRestraint: DSS, 109 crosslinks - 1 unique CrossLinkRestraint: EDC, 81 crosslinks - 21 unique EM2DRestraint: Number of micrographs: None, Image resolution: 35.0 - 3 unique SASRestraint: Assembly name: SAXS subassembly Fitting method: FoXS Multi-state: False
4. Validation	
4.2. Number of ensembles	1
4.3. Number of models in ensembles	370
4.4. Number of deposited models	1
4.5. Model precision	9.00, Å
4.6. Data quality	Data quality has not been assessed
4.7. Model quality: assessment of excluded volume	Satisfaction: 99.84%
4.8. Fit to data used for modeling	Satisfaction of crosslinks: 69.30%
4.9. 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. *5.1. Method name*	Sampling
5.2. Method type	Replica exchange monte carlo
5.4. Number of computed models	1000
2. *5.1. Method name*	Sampling
5.2. Method type	Replica exchange monte carlo
5.4. Number of computed models	1350000
3. *5.1. Method name*	Sampling
5.2. Method type	Replica exchange monte carlo
5.4. Number of computed models	10000

5.5. Software	- Integrative Modeling Platform (IMP) (version develop-0a5706e202) - IMP PMI module (version 67456c0) - HHpred (version 2.0.16) - PSIPRED (version 4.0) - DISOPRED (version 3) - DomPred (version Not available) - COILS/PCOILS (version Not available) - Multicoil2 (version Not available) - MODELLER (version 9.15)