Table S1: Summary of Integrative Structure Determination of Structure of the S. cerevisiae nuclear pore complex cytoplasmic mRNA export platform, Nup82 (PDBDEV00000020)

1. Model Composition	
Entry composition	- Dyn2: Chain A (92 residues) - Dyn2: Chain B (92 residues) - Nup82: Chain C (713 residues) - Nup82: Chain D (713 residues) - Nup159: Chain E (1460 residues) - Nup159: Chain F (1460 residues) - Nsp1: Chain G (823 residues) - Nsp1: Chain H (823 residues) - Nup116: Chain I (1113 residues) - Nup116: Chain J (1113 residues)
Datasets used for modeling	- Experimental model, PDB ID: 4DS1 - Experimental model, PDB ID: 3PBP - Experimental model, PDB ID: 5CWS - 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 - Experimental model, PDB ID: 1XIP - CX-MS data, Linker name: D, Number of cross-links: S - CX-MS data, Linker name: D, Number of cross-links: S - CX-MS data, Linker name: E, Number of cross-links: D - 2DEM class average, EMDB ID: Not listed - SAS data, Not listed - SAS data, Not listed - SAS data, Not listed
2. Representation	

Atomic structural coverage	37%
Number of rigid bodies, flexible units	38, 42
Rigid regions	- A: 7-92:Experimental model/4DS1. - B: 7-92:Experimental model/4DS1. - C: 7-16:Experimental model/3PBP, 23-120:Experimental model/3PBP, 123-452:Experimental model/3PBP, 522-612:Comparative model/None, 625-669:Comparative model/None, 678-713:Comparative model/None. - D: 7-16:Experimental model/3PBP, 23-120:Experimental model/3PBP, 123-452:Experimental model/3PBP, 522-612:Comparative model/None, 625-669:Comparative model/None, 678-713:Comparative model/None. - E: 2-347:Experimental model/1XIP, 362-381:Experimental model/1XIP, 1117-1126:Experimental model/4DS1, 1211-1239:Comparative model/None, 1266-1321:Comparative model/None, 1332-1372:Comparative model/None, 1382-1412:Comparative model/None, 1429-1456:Experimental model/3PBP. - F: 2-347:Experimental model/1XIP, 362-381:Experimental model/1XIP, 1117-1126:Experimental model/4DS1, 1211-1239:Comparative model/None, 1266-1321:Comparative model/None, 1332-1372:Comparative model/None, 1382-1412:Comparative model/None, 1429-1456:Experimental model/3PBP. - G: 637-727:Comparative model/None, 742-778:Comparative model/None, 788-823:Comparative model/None. - H: 637-727:Comparative model/None, 742-778:Comparative model/None, 788-823:Comparative model/None. - I: 966-1111:Experimental model/3PBP. - J: 966-1111:Experimental model/3PBP.
Flexible units	- A: 1-6. - B: 1-6. - C: 1-6, 17-22, 121-122, 453-521, 613-624, 670-677. - D: 1-6, 17-22, 121-122, 453-521, 613-624, 670-677. - E: 1-1, 348-361, 382-1116, 1127-1210, 1240-1265, 1322-1331, 1373-1381, 1413-1428, 1457-1460. - F: 1-1, 348-361, 382-1116, 1127-1210, 1240-1265, 1322-1331, 1373-1381, 1413-1428, 1457-1460. - G: 1-636, 728-741, 779-787. - H: 1-636, 728-741, 779-787. - I: 1-965, 1112-1113. - J: 1-965, 1112-1113.
Resolution	Rigid bodies: 1 residue per bead. Flexible regions: 50 residues per bead.
3. Restraints	

Physical principles	Excluded volume and Sequence connectivity.
Experimental data	- 1 unique CrossLinkRestraint: DSS, 240 cross-links - 1 unique CrossLinkRestraint: DSS, 109 cross-links - 1 unique CrossLinkRestraint: EDC, 81 cross-links - 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	
Sampling validation	1. Information related to sampling validation has not been provided
Clustering algorithm ,clustering feature	distance threshold-based clustering, dRMSD
Number of ensembles	1
Number of models in ensembles	370
Model precision (uncertainty of models)	9.0Å
Quality of data	1. Quality of input data has not be assessed
Assessment of atomic regions	Not applicable
Assessment of excluded volume	1. Model-1: Number of violations-8455.0
Fit of the model to information used to compute it	1. Fit of model to information used to compute it has not been determined
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) - HHpred (version 2.0.16) - PSIPRED (version 4.0) - DISOPRED (version 3) - DomPred (version None) - COILS/PCOILS (version None) - Multicoil2 (version None) - MODELLER (version 9.15) - No location specified