

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

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - 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)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB: 4DS1 - Experimental model, PDB: 3PBP - Experimental model, PDB: 5CWS - 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: 1XIP - 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 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259 - 2DEM class average, Zenodo: 10.5281/zenodo.1256259

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2. Representation	
Number of representations	1
Scale	Multiscale: Coarse-grained: 1 - 100 residue(s) per bead
Number of rigid and flexible segments	38, 42
3. Restraints	
Physical principles	Information about physical principles was not provided
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	
Number of ensembles	1
Number of models in ensembles	370
Number of deposited models	1
Model precision (uncertainty of models)	9.00, Å
Data quality	
Model quality: assessment of excluded volume	Satisfaction: 99.84%
Fit to data used for modeling	Satisfaction of crosslinks: 69.30%

<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>	Sampling
<i>Method</i>	Replica exchange monte carlo
<i>Number of computed models</i>	1000
2. <i>Name</i>	Sampling
<i>Method</i>	Replica exchange monte carlo
<i>Number of computed models</i>	1350000
3. <i>Name</i>	Sampling
<i>Method</i>	Replica exchange monte carlo
<i>Number of computed models</i>	10000
<i>Software</i>	<ul style="list-style-type: none"> - 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)