Table S1: Summary of Integrative Structure Determination of Structure of the Nup84 sub-complex of the Nuclear Pore Complex (PDBDEV00000001)

1. Model Composition	
Entry composition	- Nup84: Chain A (726 residues) - Nup85: Chain B (744 residues) - Nup120: Chain C (1037 residues) - Nup133: Chain D (1157 residues) - Nup145c: Chain E (712 residues) - Seh1: Chain F (349 residues) - Sec13: Chain G (297 residues) - Nup84: Chain A (726 residues) - Nup85: Chain B (744 residues) - Nup120: Chain C (1037 residues) - Nup133: Chain D (1157 residues) - Nup145c: Chain E (712 residues) - Seh1: Chain F (349 residues) - Sec13: Chain G (297 residues)
Datasets used for modeling	- Experimental model, PDB ID: 3JRO - Experimental model, PDB ID: 3F3F - Experimental model, PDB ID: 3IKO - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 3CQC - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 4LCT - Experimental model, PDB ID: 2QX5 - Experimental model, PDB ID: 3EWE - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 3F7F - Experimental model, PDB ID: 3HXR - Experimental model, PDB ID: 4FHN - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 4Q9T - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 3I4R - Experimental model, PDB ID: 3KFO - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 3BG1 - Experimental model, PDB ID: 3BG0 - Comparative model, template PDB ID: Not listed - Experimental model, PDB ID: 3F3F - Experimental model, PDB ID: 2PM7 - CX-MS data, Linker name and number of cross-links: DSS, 164 cross-links - CX-MS data, Linker name and number of cross-links: EDC, 127 cross-links - EM raw micrographs, EMDB ID: Not listed - 2DEM class average, EMDB ID: Not listed
2. Representation	
Atomic structural coverage	84%
Number of rigid bodies, flexible units	40, 42
	- A: 7-20:Comparative model/None, 27-80:Comparative model/None, 96-126:Comparative

Rigid regions	model/None, 136-364:Comparative model/None, 372-483:Comparative model/None, 506-562:Comparative model/None, 575-726:Comparative model/None. - B: 67-122:Comparative model/None, 135-427:Comparative model/None, 461-529:Comparative model/None, 533-602:Comparative model/None, 620-671:Comparative model/None, 680-743:Comparative model/None. - C: 1-29:Comparative model/None, 53-212:Comparative model/None, 221-305:Comparative model/None, 311-429:Comparative model/None, 440-710:Comparative model/None, 711-712:Comparative model/None, 727-781:Comparative model/None, 805-892:Comparative model/None, 903-910:Comparative model/None, 921-1010:Comparative model/None, 1023-1037:Comparative model/None. - D: 56-78:Comparative model/None, 86-125:Comparative model/None, 133-144:Comparative model/None, 162-184:Comparative model/None, 193-200:Comparative model/None, 206-249:Comparative model/None, 258-480:Comparative model/None, 490-763:Comparative model/None, 772-1155:Comparative model/None. - E: 126-144:Comparative model/None, 151-175:Comparative model/None, 182-553:Comparative model/None. - F: 1-248:Experimental model/3F3F, 288-346:Experimental model/3F3F. - G: 2-158:Experimental model/2PM7, 166-296:Experimental model/2PM7.
Flexible units	- A: 1-6, 21-26, 81-95, 127-135, 365-371, 484-505, 563-574. - B: 1-66, 123-134, 428-460, 530-532, 603-619, 672-679, 744-744. - C: 30-52, 213-220, 306-310, 430-439, 713-726, 782-804, 893-902, 911-920, 1011-1022. - D: 1-55, 79-85, 126-132, 145-161, 185-192, 201-205, 250-257, 481-489, 764-771, 1156-1157. - E: 1-125, 145-150, 176-181, 554-712. - F: 249-287, 347-349. - G: 1-1, 159-165, 297-297.
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, 164 cross-links - 1 unique CrossLinkRestraint: EDC, 127 cross-links - 1 unique EM2DRestraint: Number of micrographs: 800, Image resolution: 30.0

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	2
Number of models in ensembles	1257, 1010
Model precision (uncertainty of models)	15.4Å, 12.7Å
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-10899.0 2. Model-2: Number of violations-10935.0
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) - MODELLER (version 9.12) - No location specified