Summary of integrative structure determination of Structure of the Nup84 sub-complex of the Nuclear Pore Complex (PDB ID: 8ZZ1, PDB-Dev ID: PDBDEV_00000001)

1. Model Composition	
Entry composition	- Sec13: Chain G (297 residues) - Nup85: Chain B (744 residues) - Nup84: Chain A (726 residues) - Nup133: Chain D (1157 residues) - Seh1: Chain F (349 residues) - Nup120: Chain C (1037 residues) - Nup145c: Chain E (712 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 available - Experimental model, PDB ID: 3CQC - Comparative model, template PDB ID: Not available - Experimental model, PDB ID: 4LCT - Experimental model, PDB ID: 2QX5 - Experimental model, PDB ID: 3EWE - Comparative model, template PDB ID: Not available - Experimental model, PDB ID: 3F7F - Experimental model, PDB ID: 3HXR - Experimental model, PDB ID: 4FHN - Comparative model, template PDB ID: Not available - Experimental model, PDB ID: 4Q9T - Comparative model, template PDB ID: Not available - Experimental model, PDB ID: 3I4R - Experimental model, PDB ID: 3KFO - Comparative model, template PDB ID: Not available - Experimental model, PDB ID: 3BG1 - Experimental model, PDB ID: 3BG0 - Comparative model, template PDB ID: Not available - Experimental model, PDB ID: 3F3F - Experimental model, PDB ID: 2PM7 - Crosslinking-MS data, Linker name and number of cross-links: DSS, 164 cross-links - Crosslinking-MS data, Linker name and number of cross-links: EDC, 127 cross-links - EM raw micrographs, File: 10.5281/zenodo.58025 - 2DEM class average, File: 10.5281/zenodo.1218053
2. Representation	
Resolution	Coarse-grained: 1, 2, 3, 4, 7, 8 residue(s) per bead
Number of rigid bodies, flexible units	40, 42

IM Summary Table

Rigid bodies	- A: 7-20, 27-80, 96-126, 136-364, 372-483, 506-562, 575-726 - B: 67-122, 135-427, 461-529, 533-602, 620-671, 680-743 - C: 1-29, 53-212, 221-305, 311-429, 440-710, 711-712, 727-781, 805-892, 903-910, 921-1010, 1023-1037 - D: 56-78, 86-125, 133-144, 162-184, 193-200, 206-249, 258-480, 490-763, 772-1155 - E: 126-144, 151-175, 182-553 - F: 1-248, 288-346 - G: 2-158, 166-296
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
Structural coverage (rigid bodies)	84%
3. Restraints	
Physical principles	Information about physical principles was not provided
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	
Number of ensembles	2
Number of models in ensembles	1257, 1010
Number of deposited models	2
Model precision (uncertainty of models)	15.4, Å, 12.7, Å
Data quality	Data quality has not been assessed
Model quality: assessment of excluded volume	Satisfaction: 99.88-99.88%
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
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. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	500
2. Method	Sampling
Name	Replica exchange monte carlo
Number of computed models	5000
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)

1. Method