

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	<ul style="list-style-type: none"> - 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	<ul style="list-style-type: none"> - 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: DSS, Number of cross-links: 164 cross-links - CX-MS data, Linker name: EDC, Number of cross-links: 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
	<ul style="list-style-type: none"> - A: 7-20:Comparative model/None, 27-80:Comparative model/None, 96-126:Comparative

<i>Rigid bodies</i>	<p>model/None, 136-364:Comparative model/None, 372-483:Comparative model/None, 506-562:Comparative model/None, 575-726:Comparative model/None.</p> <p>- 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.</p> <p>- 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.</p> <p>- 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.</p> <p>- E: 126-144:Comparative model/None, 151-175:Comparative model/None, 182-553:Comparative model/None.</p> <p>- F: 1-248:Experimental model/3F3F, 288-346:Experimental model/3F3F.</p> <p>- G: 2-158:Experimental model/2PM7, 166-296:Experimental model/2PM7.</p>
<i>— Flexible units</i>	<p>- A: 1-6, 21-26, 81-95, 127-135, 365-371, 484-505, 563-574.</p> <p>- B: 1-66, 123-134, 428-460, 530-532, 603-619, 672-679, 744-744.</p> <p>- C: 30-52, 213-220, 306-310, 430-439, 713-726, 782-804, 893-902, 911-920, 1011-1022.</p> <p>- D: 1-55, 79-85, 126-132, 145-161, 185-192, 201-205, 250-257, 481-489, 764-771, 1156-1157.</p> <p>- E: 1-125, 145-150, 176-181, 554-712.</p> <p>- F: 249-287, 347-349.</p> <p>- G: 1-1, 159-165, 297-297.</p>
Resolution	<p>Rigid bodies: 1 residue per bead.</p> <p>Flexible regions: 10 residues per bead.</p>
3. Restraints	
Physical principles	Excluded volume and Sequence connectivity.
Experimental data	<p>- CrossLinkRestraint: 164 cross-links, DSS</p> <p>- CrossLinkRestraint: 127 cross-links, EDC</p> <p>- EM2DRestraint: Image resolution: 30.0, Number of micrographs: 800</p>

4. Validation	
<i>Sampling validation</i>	
<i>Clustering algorithm ,clustering feature</i>	None, dRMSD
<i>Number of ensembles</i>	2
<i>Number of models in ensembles</i>	1257, 1010
<i>Model precision (uncertainty of models)</i>	15.4Å, 12.7Å
<i>Quality of data</i>	-
<i>Assessment of atomic segments</i>	-
<i>Fit of the model to information used to compute it</i>	
<i>Fit of the model to information not used to compute it</i>	
5. Methodology and Software	
<i>Method</i>	Sampling
<i>Name</i>	Replica exchange Monte Carlo
<i>Details</i>	
<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) - MODELLER (version 9.12)