

Summary of integrative structure determination of Integrative model of the nuclear pore complex in constricted conformation from Schizosaccharomyces pombe (PDB ID: 9A1O, PDB-Dev ID: PDBDEV_00000096)

<i>1. Model Composition</i>	
------------------------------------	--

[Entry composition](#)

- Nup184: chain(s) B, B1, B2, B3, B4, B5, B6, B7, B8, B9, B10, B11, B12, B13, B14, B15 (1564 residues)

- Nup186: chain(s) C, C1, C2, C3, C4, C5, C6, C7, C8, C9, C10, C11, C12, C13, C14, C15 (1647 residues)

- Nup155: chain(s) D, D1, D2, D3, D4, D5, D6, D7, D8, D9, D10, D11, D12, D13, D14, D15, D16, D17, D18, D19, D20, D21, D22, D23, D24, D25, D26, D27, D28, D29, D30, D31 (1315 residues)

- Nup44: chain(s) H, H1, H2, H3, H4, H5, H6, H7, H8, H9, H10, H11, H12, H13, H14, H15, H16, H17, H18, H19, H20, H21, H22, H23, H24, H25, H26, H27, H28, H29, H30, H31 (403 residues)

- Nup45: chain(s) I, I1, I2, I3, I4, I5, I6, I7, I8, I9, I10, I11, I12, I13, I14, I15, I16, I17, I18, I19, I20, I21, I22, I23, I24, I25, I26, I27, I28, I29, I30, I31 (425 residues)

- Nsp1: chain(s) J, J1, J2, J3, J4, J5, J6, J7, J8, J9, J10, J11, J12, J13, J14, J15, J16, J17, J18, J19, J20, J21, J22, J23, J24, J25, J26, J27, J28, J29, J30, J31 (598 residues)

- Nup107: chain(s) L, L1, L2, L3, L4, L5, L6, L7, L8, L9, L10, L11, L12, L13, L14, L15 (813 residues)

- Nup189c: chain(s) M, M1, M2, M3, M4, M5, M6, M7, M8, M9, M10, M11, M12, M13, M14, M15, M16, M17, M18, M19, M20, M21, M22, M23 (844 residues)

- Sec13: chain(s) N, N1, N2, N3, N4, N5, N6, N7, N8, N9, N10, N11, N12, N13, N14, N15, N16, N17, N18, N19, N20, N21, N22, N23 (297 residues)

- Seh1: chain(s) O, O1, O2, O3, O4, O5, O6, O7, O8, O9, O10, O11, O12, O13, O14, O15, O16, O17, O18, O19, O20, O21, O22, O23 (339 residues)

- Nup85: chain(s) P, P1, P2, P3, P4, P5, P6, P7, P8, P9, P10, P11, P12, P13, P14, P15, P16, P17, P18, P19, P20, P21, P22, P23 (675 residues)

- Nup132: chain(s) Q, Q1, Q2, Q3, Q4, Q5, Q6, Q7, Q8, Q9, Q10, Q11, Q12, Q13, Q14, Q15 (1162 residues)

- Nup120: chain(s) R, R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R13, R14, R15, R16, R17, R18, R19, R20, R21, R22, R23 (1136 residues)

- Nup37: chain(s) S, S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23 (391 residues)

- Ely5: chain(s) T, T1, T2, T3, T4, T5, T6, T7, T8, T9, T10, T11, T12, T13, T14, T15, T16, T17, T18, T19, T20, T21, T22, T23 (298 residues)

- Nup97: chain(s) Y, Y1, Y2, Y3, Y4, Y5, Y6, Y7, Y8, Y9, Y10, Y11, Y12, Y13, Y14, Y15, Y16, Y17, Y18, Y19, Y20, Y21, Y22, Y23, Y24, Y25, Y26, Y27, Y28, Y29, Y30, Y31 (851 residues)

<i>Datasets used for modeling</i>	<ul style="list-style-type: none"> - 3DEM volume, EMDB: EMD-11375 - 3DEM volume, Zenodo: 10.5281/zenodo.5585949 - Integrative model, PDB: 9A1M - Other, Not available: https://doi.org/10.1038/nsmb1194 - Other, Not available: https://doi.org/10.1038/nature15381
2. Representation	
<i>Number of representations</i>	1
<i>Scale</i>	Atomic
<i>Number of rigid and flexible segments</i>	392, 0
3. Restraints	
<i>Physical principles</i>	Information about physical principles was not provided
<i>Experimental data</i>	
4. Validation	
<i>Number of ensembles</i>	0
<i>Number of models in ensembles</i>	Not applicable
<i>Number of deposited models</i>	1
<i>Model precision (uncertainty of models)</i>	Not available
<i>Data quality</i>	Data quality has not been assessed
<i>Model quality: assessment of atomic segments</i>	<ul style="list-style-type: none"> - Clashscore: 0.00 - Ramachandran outliers: 4824 - Sidechain outliers: 12723
<i>Fit to data used for modeling</i>	Fit of model to information used to compute it has not been determined
<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	
<i>1. Name</i>	Modeling the full nuclear pore complex at constricted diameter based on the model of the pore with the normal diameter
<i>Software</i>	<ul style="list-style-type: none"> - Assembliner (version 0.99beta) - Integrative Modeling Platform (IMP) (version 2.15.0) - UCSF Chimera (version 1.14)