Integrative Structural Analysis of Human Nuclear Pore Complex

Shyamal Mosalaganti^{1,2,3†}, Agnieszka Obarska-Kosinska^{1,4†}, Marc Siggel^{4,5,6†}, Reiya Taniguchi^{1,2}, ¹²Beata Turoňová^{1,2}, Christian E. Zimmerli^{1,2}, Katarzyna Buczak^{2‡}, Florian H. Schmidt^{2§}, Erica Margiotta^{1,2}, Marie-Therese Mackmull^{2¶}, Wim J. H. Hagen², Gerhard Hummer^{5,7}*, Jan Kosinski^{2,4,6}*, Martin Beck^{1,2}*

¹ Department of Molecular Sociology, Max Planck Institute of Biophysics, Max-von-Laue-Straße 3, 60438 Frankfurt am Main, Germany.

² Structural and Computational Biology Unit, European Molecular Biology Laboratory, Meyerhofstraße 1, 69117, Heidelberg, Germany.

³ Life Sciences Institute, Department of Cell & Developmental Biology, University of Michigan, Ann Arbor, MI 48109, USA.

⁴ European Molecular Biology Laboratory Hamburg, Notkestraße 85, 22607, Hamburg, Germany.

⁵ Department of Theoretical Biophysics, Max Planck Institute of Biophysics, Max-von-Laue-Straße 3, 60438 Frankfurt am Main, Germany.

⁶ Centre for Structural Systems Biology (CSSB), Notkestraße 85, 22607, Hamburg, Germany.

⁷ Institute of Biophysics, Goethe University Frankfurt, 60438 Frankfurt am Main, Germany.

*Corresponding authors Email: Email: jan.kosinski@embl.de, gerhard.hummer@biophys.mpg.de, martin.beck@biophys.mpg.de.

[†] These authors contributed equally to this work

‡ Present address: Proteomics Core Facility, Biozentrum, University of Basel, Spitalstrasse 41, CH-4056 Basel / Switzerland.

§ Present address: Institute of Science and Technology Austria, Am Campus 1, 3400 Klosterneuburg, Austria.

¶ Present address: Institute of Molecular Systems Biology, Department of Biology, ETH Zurich, Zurich, Switzerland.

Nuclear pore complexes (NPCs) mediate nucleocytoplasmic transport. Their intricate 120 MDa architecture remains incompletely understood. Here, we report a 70 MDa model of the human NPC scaffold with explicit membrane and in multiple conformational states. We combined AI-based structure prediction with in situ and in cellulo cryo-electron tomography and integrative modeling. We show that linker Nups spatially organize the scaffold within and across subcomplexes to establish the higher-order structure. Microsecond-long molecular dynamics simulations suggest that the scaffold is not required to stabilize the inner and outer nuclear membrane fusion, but rather widens the central pore. Our work exemplifies how AI-based modeling can be integrated with in situ structural biology to understand subcellular architecture across spatial organization levels.

