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## Integrative structural modeling of the human nuclear pore complex

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**Abstract:** The nuclear pore complexes (NPCs) are huge 110-megadalton protein complexes that mediate transport into and out of the cell nucleus. The NPC adopts a channel-like structure formed by a protein scaffold, which perforates the nuclear membrane, and several structurally flexible subunits, which attach to the scaffold and form the selective transport barrier of the NPC. Determining this structure at the atomic level would help to understand the nucleocytoplasmic transport and many other processes, such as virus invasion through the NPCs. However, due to the huge size and flexibility of the NPC, its structure could not yet be determined by a single technique such as X-ray crystallography or electron microscopy.

I will present how we determined the near-atomic structure of the human NPC scaffold by integrating several complementary techniques, such as structural modeling, cryo-electron tomography, X-ray crystallography, and crosslinking mass spectrometry. The structure shows how the entire scaffold of the NPC is organized. In particular, it reveals that seemingly very complex structure of the NPC is built from reoccurring interaction motifs and simple architectural principles. It also serves as a starting point for modeling the subunits that form the transport barrier of the NPC.

To build the model of the NPC, we created an automated methodology for structural modeling based on electron microscopy maps and other spatial restraints. I will describe this methodology alongside current efforts to make it generically applicable to other biological systems.

*References:*

1. Kosinski, J. et al. *Molecular architecture of the inner ring scaffold of the human nuclear pore complex*. *Science* 352, 363–5 (2016).
2. von Appen, A. et al. *In situ structural analysis of the human nuclear pore complex*. *Nature* 526, 140–3 (2015).

