X-ray Structure of Recombinant Core 8D of the Nuclear Chaperone Nucleoplasmin

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The efficient assembly of histone complexes and nucleosomes involves the participation of molecular chaperones. The histone chaperone nucleoplasmin represents the most abundant protein in the *Xenopus* oocyte nucleus. It mediates nucleosome assembly by removing basic proteins from sperm chromatin and exchanging them with histones. This function is modulated by phosphorylation of nucleoplasmin at multiple sites.

The nucleoplasmin core domain structure forms a pentameric arrangement where each monomer consists of two domains: a core, that forms a stable ring-like pentamer, and a tail, which holds a polyglutamic tract and the nuclear localization signal. The lacking of the poly-Glu region, a putative binding site for basic proteins, does not affect its capacity for the binding of the sperm basic proteins and the chromatin decondensation. This activity has been reproduced artificially in a recombinant core domain through mutation of putative phosphorylation sites to aspartate, thus mimicking the charge effect of phosphorylation. The crystallographic studies of this recombinant domain (called CORE8D) at 2.5 **Å** resolution show the presence of these mutations which do not affect the folding of the monomer and so the formation of the pentameric structure, even though they are located in exposed flexible regions. The crystal packing has revealed the formation of a nucleoplasmin-core decamer that could represent its normal biological oligomerisation state. This decamer has localized negative charges near the interface (interactions between the Asp58 and Lys82 from all the opposite monomers), with a network of hydrogen bond waters which serve to maintain together the opposite pentamers.

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