Box C/D snoRNPs: solid-state NMR fingerprint of an early-stage 50 kDa assembly intermediate involved in ribosome biogenesis

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Résumé

Many cellular functions rely on stable protein-only or protein-RNA complexes. Deciphering their assembly mechanism is a key question in cell biology. We here focus on box C/D snoRNPs (Ribo Nucleo Proteins), involved in ribosome biogenesis and present in archaea, yeast and humans. Despite their relatively simple composition – one snoRNA and 4 core proteins – these particles don't self-assemble and their formation requires a large number of other proteins, called assembly factors.
We use solid-state NMR to extend previous solution NMR studies and get atomic-scale information on the early part of *Saccharomyces cerevisiae* box C/D snoRNP assembly pathway, through carbon-13 and nitrogen-15 solid-state NMR assignment of yeast 126-residue core protein Snu13 in the context of its 50 kDa pre-complex with assembly factors Rsa1p:Hit1p.

Secondary structure analysis indicates that the overall conformation of Snu13p is retained in the context of the complex. Chemical shift perturbations and dynamics data are analyzed to evaluate Snu13p conformational changes and interaction interface upon binding to its partner proteins. We describe the role of some Snu13p N-terminal and C-terminal residues, not identified in previous structural studies.
Besides structural and conformational details, we could obtain the spectroscopic fingerprint of this complex, setting the basis for further studies, which will involve other partners of Snu13p:Rsa1p:Hit1p, as snoRNA.

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