Structural insights into mRNP formation.

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Gene expression regulation is the mechanism by which a particular organism adapts its protein expression profile as a response to environmental or developmental signals. Primarily, the regulation of gene expression correlates with the transcription activation or repression of genes at chromatin level. However, altering the mRNA levels is not always necessary to induce a response and we are beginning to understand that post-transcriptional processes can also dramatically alter the protein expression makeup. In this sense, the concept of RNA operons represents the ultimate revolution in our current understanding about how protein expression is ultimately regulated and coordinated [1]. An RNA operon can be defined as an association of different mRNAs with RNA binding proteins and small non-coding RNAs, forming particles known as mRNPs. A key concept within the RNA operon theory is that a particular mRNA might be distributed between different mRNPs that may be associated with different functions (i.e. synthesis of mitochondrial proteins, ribosomal proteins, etc.). Hence the same mRNA could form different protein-RNA or RNA-RNA interactions within different mRNPs. Studying the molecular basis underlying the structure and dynamics of these interactions would represent a step forward towards a more comprehensive knowledge about how RNA operons work. Here we present a NMR study of protein-protein and protein-RNA interactions involving several proteins that are part of mRNPs. The results highlight the importance for the intermolecular recognition of regions outside the canonical RNA-binding domains, including intrinsically unstructured ones. The existence of these flexible regions and the importance of transient interactions make the NMR an ideal technique to study the biophysical aspects behind the formation of mRNPs**.**

[1] Keene, J. D.., *Nat. Rev. Gen.*, **2007**, *8*, 533-543.