

# A comparative sequence analysis system for detecting RNA patterns in mRNAs: application to prion protein mRNAs

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## Résumé

We developed a Structural Pattern Finder (SPF) computer program to detect structured RNAs in mRNAs by measuring folding free energies (FFE). The program was applied to the human prion mRNA, and in particular to the 24-nt repeat region involved in Creutzfeldt-Jakob disease (1). The FFE of the human prion mRNA indicated a biased codon selection and the presence of RNA patterns. Using RNAMOT (2), we developed a descriptor to locate a pseudoknot structure previously reported by Wills in the 24-nt repeat region of the human prion protein gene. Pseudoknots similar to the one predicted were found in all available prion mRNAs, but not those of avians and the red slider turtle. An alignment of these mRNAs and the use of Blast in the repeat region showed low sequence homology, but several covariations used to maintain the pseudoknot pattern were noted. The 3-D structure of the RNA pseudoknot was modeled using MC-SYM (3), and highlights protein and RNA interaction domains suggesting a possible effect in prion protein translation.

## Références

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