

Sequencing and bioinformatics analyses of ciliate eRF1s toward understanding stop codon recognition

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Eukaryotic release factor 1 (eRF1) is believed to play an important role in the stop codon reassignment in ciliates. To clarify the specificity of stop codon recognition in ciliate eRF1s, we have sequenced eRF1 genes from four ciliate species. Phylogenetic and structure-based analyses of eRF1s have been carried out. We have statistically analyzed protein-RNA complexes available in a structure database (Protein Data Bank) and obtained a propensity for each amino acid residue being located in the RNA-binding sites. Using the RNA-binding propensity, we have suggested areas on the protein surface that are important for stop codon recognition in ciliate eRF1s.