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The polyadenylation code: a unified model for the regulation of mRNA alternative polyadenylation

Key words: mRNA 3’ processing, post-transcriptional gene regulation, genomics

The majority of eukaryotic genes produce multiple mRNA isoforms with distinct 3' ends through a process called mRNA alternative polyadenylation (APA). Recent studies have demonstrated that APA is dynamically regulated during development and in response to environmental stimuli. A number of mechanisms have been described for APA regulation. In this review, we attempt to integrate all the known mechanisms into a unified model. This model not only explains most of previous results, but also provides testable predictions that will improve our understanding of the mechanistic details of APA regulation. Finally we briefly discuss the known and putative functions of APA regulation.

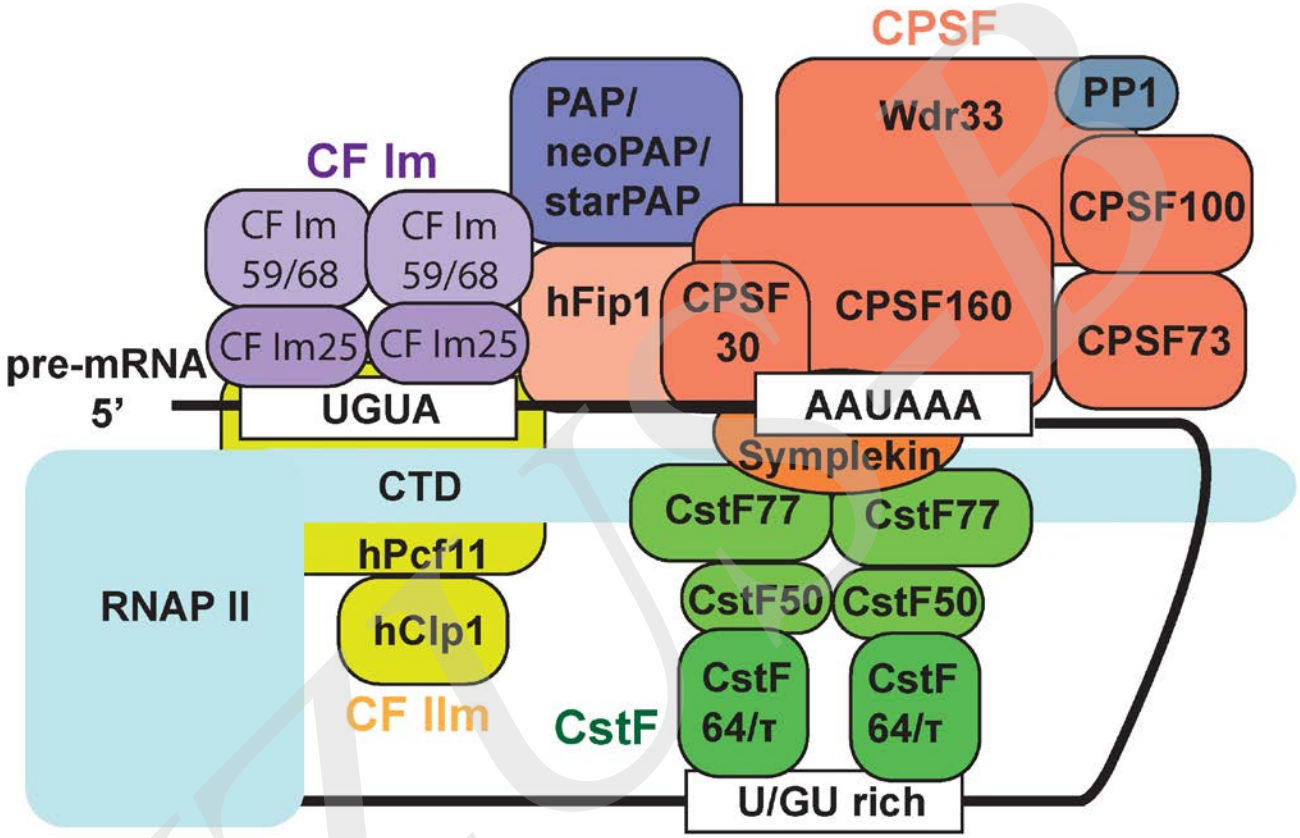
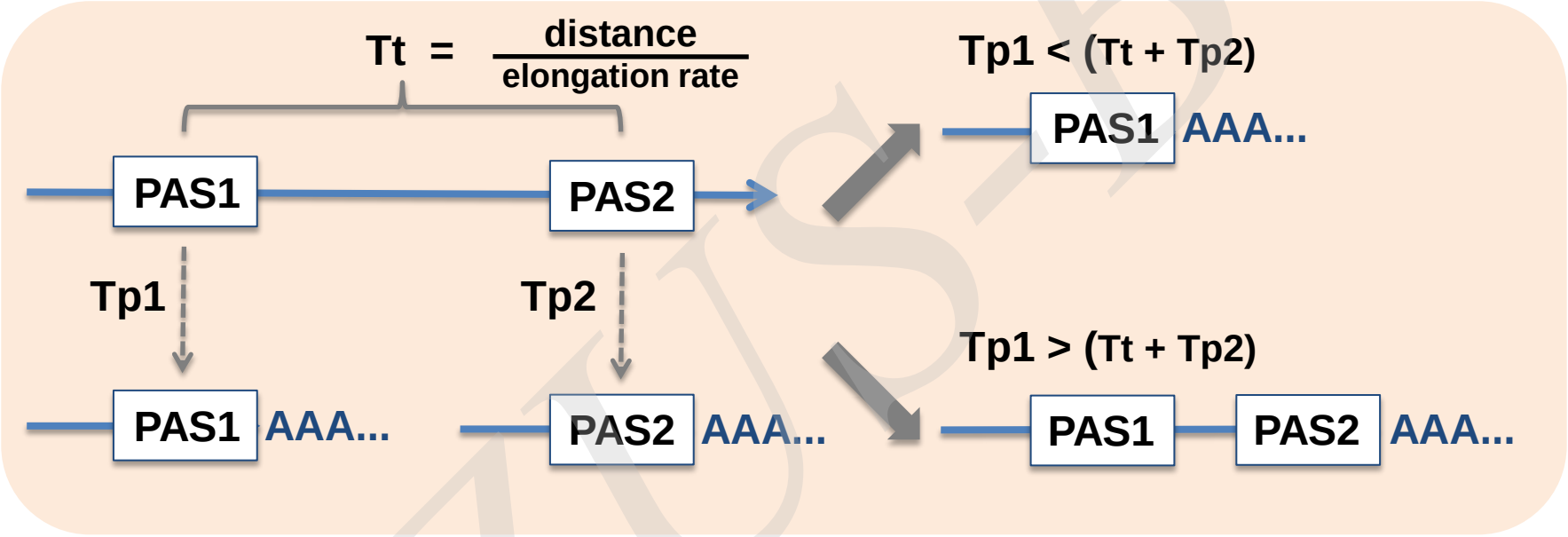


Fig. 1 A model for the mammalian mRNA 3' processing complex.



Tt: the time it takes to transcribe the region between PAS1 and PAS2.
Tp1: the time it takes for cleavage/polyadenylation at PAS1.
Tp2: the time it takes for cleavage/polyadenylation at PAS2.

Fig. 2 A unified model for the regulation of mRNA alternative polyadenylation.