Structure and Function of RNase E and the RNA Degradosome Assembly

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The essential enzyme RNase E is critical to RNA processing and decay regulation in *Escherichia coli*. The activity of RNase E affects the balance and composition of the transcript population, and the enzyme serves as the scaffold for a multi-component assembly known as the RNA degradosome. RNase E belongs to a widely occurring family of ribonucleases that cleave RNA internally, but whose catalytic power is determined by the 5'-terminus of the substrate, even if this lies at a distance from the cutting site. We report crystal structures of the catalytic domain of RNase E as trapped allosteric intermediates with RNA substrates. The structures explain why a tetrameric quaternary structure is required for activity, and how the recognition of the 5' terminus of the substrate triggers a conformational transition to initiate catalysis. The structure also sheds light on the question of how RNase E might selectively process, rather than destroy, specific RNA precursors. We have also solved the crystal structures of two other components of the degradosome (enolase and polynucleotide phosphorylase), and the cognate complex of enolase with a recognition site from RNase E. These structural data are used to propose a model for the organization and function of the RNA degradosome.

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