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Structures, Mechanism, and Functional Relevance of Filament Formation by SgrAI

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Abstract

SgrAI is a type II Restriction endonuclease (REases) enzyme from the bacterium *Streptomyces griseus*. It has been proposed that SgrAI protects the host DNA from off-target cleavage activity, through a new regulation mechanism via filamentation. Binding of SgrAI to invading phage DNA activates the enzyme leading to DNA sequence specificity expansion from 3 recognition sites to 17 and increased DNA cleavage rate. Like other types of II REases, SgrAI cleaves DNA in a Mg^{2+} dependent manner. But unlike other REases that form homodimers and cleave near their 4-6bp recognition sequence, SgrAI forms a filament when in its active form, and a dimer when found in its inactive form. In its active form, SgrAI exhibits an increased rate of DNA cleavage 200 to 1000-fold faster. The mechanistic underlying these events remain unclear.

We have been investigating the details of SgrAI's structure and cleavage activity on its secondary site DNA sequences to complete our understanding of SgrAI's kinetic pathway and filament formation. In our recent discoveries, we described two new structures of the SgrAI enzyme, one is the Cryo-EM structure of the filamentous form of SgrAI bound to intact primary site DNA, and the other one is a high-resolution x-ray crystal structure of apo SgrAI. These structures help us to understand important conformational changes that could be contributed to the catalytic mechanism of this enzyme.

This is the full abstract presented at the Experimental Biology meeting and is only available in HTML format. There are no additional versions or additional content available for this abstract.