Structural basis for topological control of serine-family DNA recombinases

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Site-specific DNA recombinases play a variety of biological roles, often related to the dissemination of antibiotic resistance, and are also useful tools for synthetic biology. The simplest site-specific recombination systems will recombine any two cognate sites regardless of context. However, other systems have evolved elaborate mechanisms, that sense DNA topology to ensure that only one of multiple possible recombination products is produced. The closely-related resolvases from the Tn3 and γδ transposons have historically served as paradigms for the topological regulation of recombinase activity. However, despite many proposals, models of the multi-subunit protein-DNA complex (termed the synaptosome) that enforces this regulation have been unsatisfying due to a lack of experimental constraints. Here we present new structural and biochemical data that lead to a new, detailed model of the Tn3 synaptosome. Comparison to our previous model of the synaptosome for a different serine resolvase, Sin, shows interesting conserved features and differences.