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Crystal Structure of a Rad51 Filament. Phoebe A. Rice¹, Adam B. Conway¹, Thomas W. Lynch¹, Ying Zhang¹, Gary S. Fortin² and Lorraine Symington², ¹The Univ. of Chicago, Chicago IL, ²Columbia Univ., New York, NY.

The homologous recombinases are central to the repair of double stranded breaks in DNA, catalyzing the invasion of a single-stranded DNA into a DNA duplex of the same or similar sequence. The eubacterial RecA protein is the most well-studied of this class, with the Rad51 protein being its homologue in eukaryotes. While the crystal structure of the RecA protein has been known (Story *et al.*, Nature, 355:318, 1992) and both monomeric and toroidal structures of Rad51 have been more recently solved (Pellegrini *et al.*, Nature, 420:287, 2002; Shin *et al.*, EMBO J., 2003), there have been no crystallographic structures available of a eukaryotic homologous recombinase in its biologically active filament. We have obtained diffracting crystals of a *S. cerevisiae* Rad51 filament. This structure displays substantial differences from the previously observed filament of RecA, showing the ATPase site positioned directly at the filament interface. The effects of site-directed mutations at this new interface will also be presented.