1154-55-1794 **Robert H Stolz*** (rstolz@ucdavis.edu). *Modeling pathways of DNA unlinking by site-specific recombination.*

In Escherichia Coli, replication of circular chromosomes yields topologically linked DNA molecules. Topo IV, one of the type-II topoisomerases in E. coli, plays a major role in the decatenation of the newly replicated chromosomes. It has been shown that in the absence of Topo IV, site-specific recombinases XerC/D, in cooperation with the translocase FtsK, can also unlink the replication links in a stepwise manner. However, the topological pathways preferred by this enzyme complex are unknown. We use computational methods to model the recombination pathways as topological reconnection events in the simple cubic lattice and measure transition probabilities between relevant knotted and linked topologies of up to ten crossings. Our results give strong support to the stepwise unlinking pathway explored in previous studies and demonstrate the application of computational knot theory to address complex biological problems. (Received September 16, 2019)