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Structural basis of transposon end recognition explains central features of Tn7 transposition systems

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Marcin Nowotny

International Institute of Molecular and Cell Biology in Warsaw (IIMCB)

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Tn7 is among the most wide-spread bacterial transposons and uses TnsA, TnsB, TnsC proteins to catalyze its mobility. TnsB is the transposase, which cuts one of the DNA strands at the end of the transposon and catalyzes its joining to the target DNA site. Certain class of Tn7 elements has recently been shown to act together with partner CRISPR systems which guide the site of insertion. We determined the cryo-EM structure of TnsB from canonical E. coli Tn7 element interacting with the transposon end. It showed that the TnsB adopts beads-on-the-string architecture with two DNA-binding domains and a catalytic domain with RNase H fold. In the complex with the DNA the domains are arranged in a tiled fashion which enforces the formation of the nucleoprotein filament at the end of the transposon. TnsB forms very few base-specific contacts with DNA and shows preference rather than strict specificity for the DNA sequence present at the transposon end. We also prepared a model of the synaptic complex in which the catalytic domain is in a position enabling it to catalyze transposon mobility.