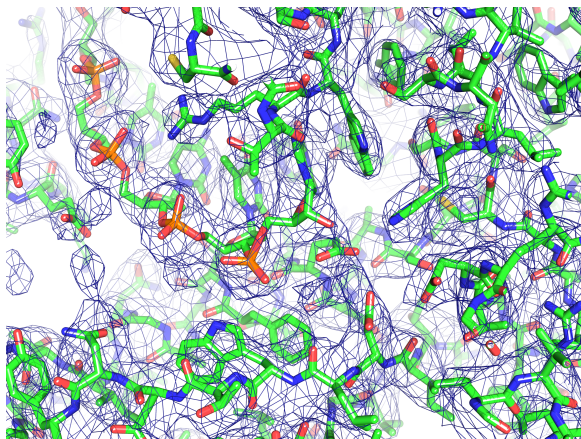
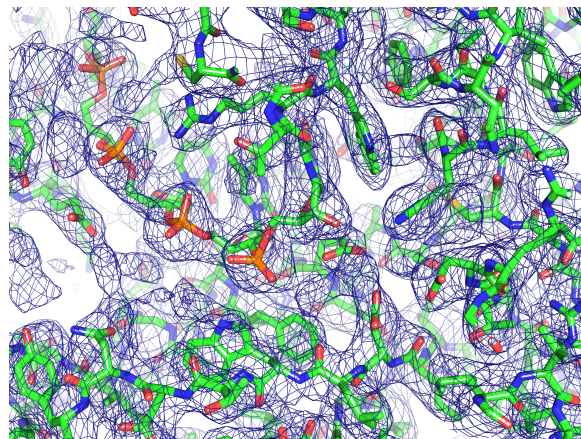


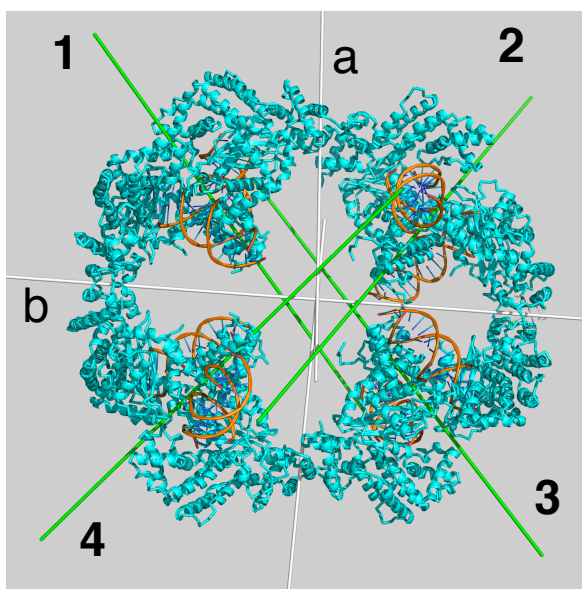
A Experimental:



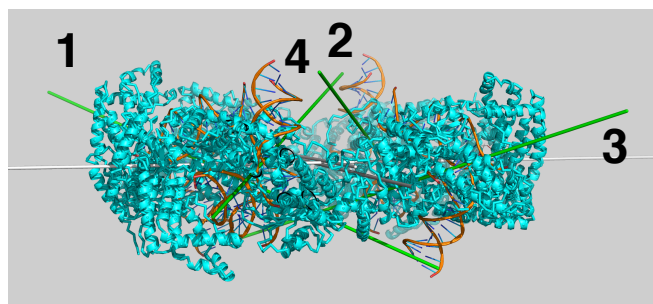
B Simulated anneal omit:



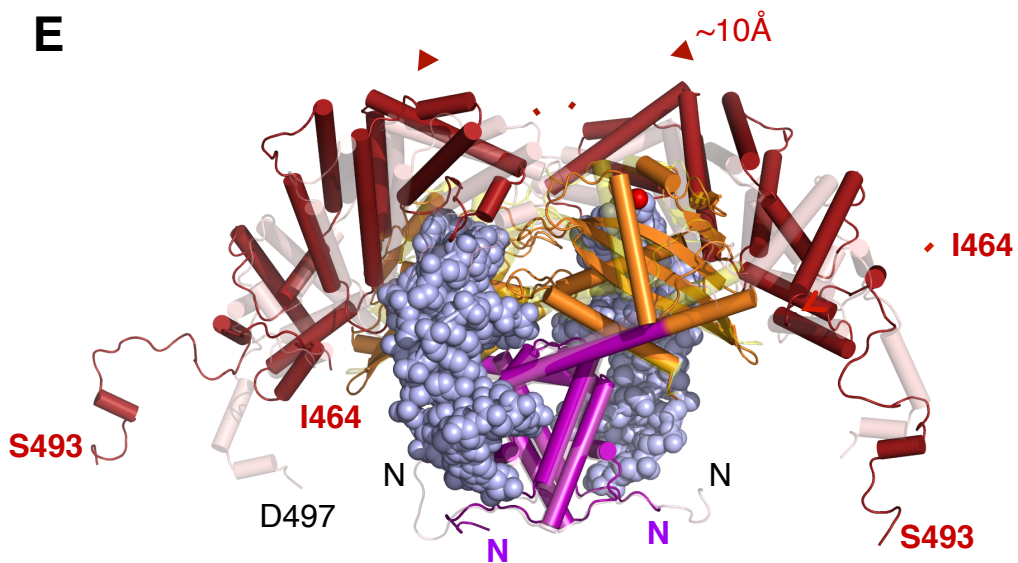
C



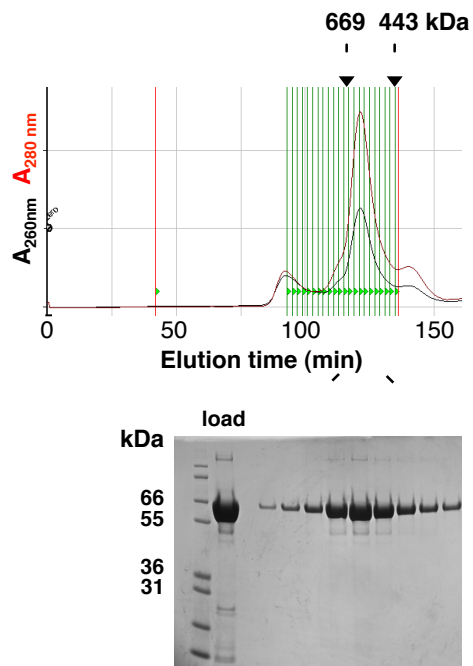
D



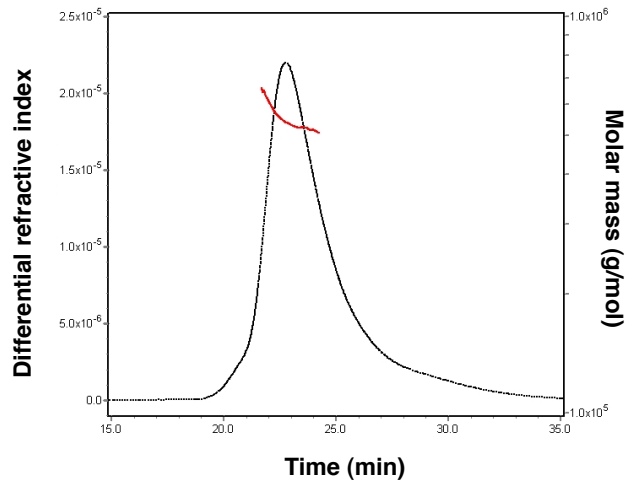
E



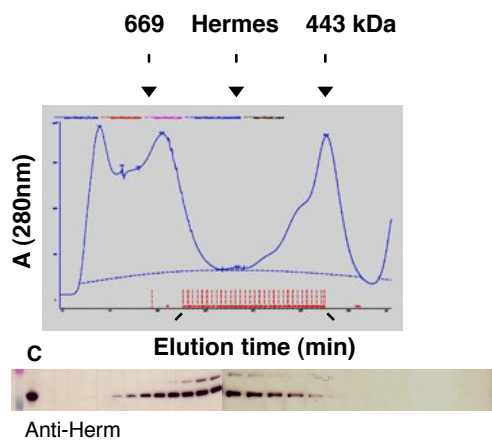
A *E. coli*



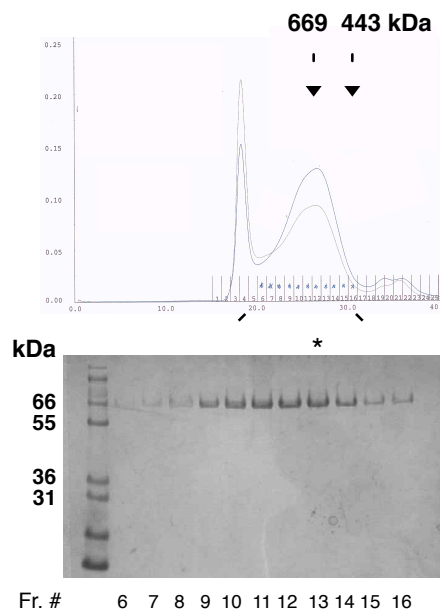
B SEC-MALS

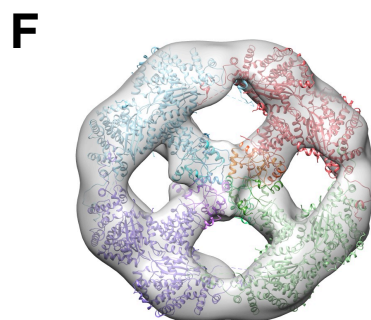
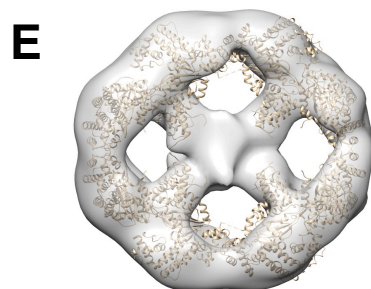
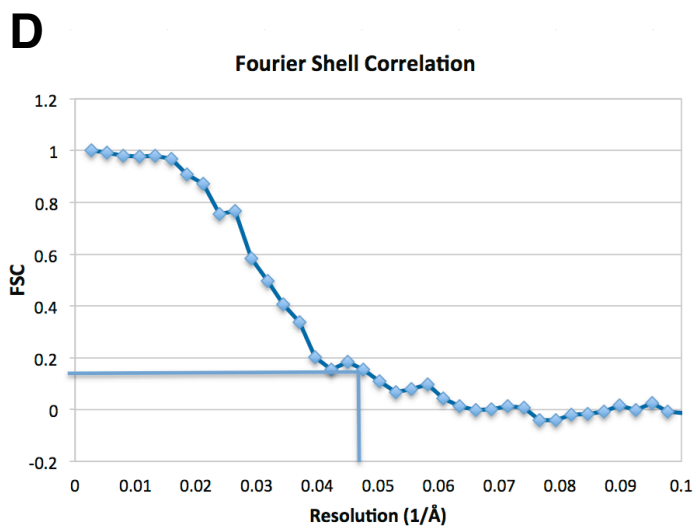
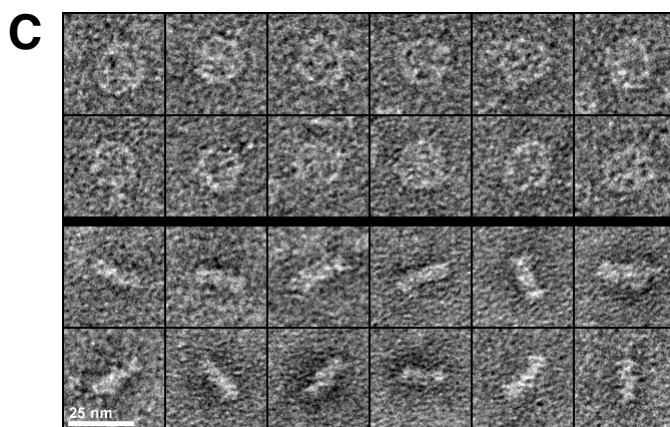
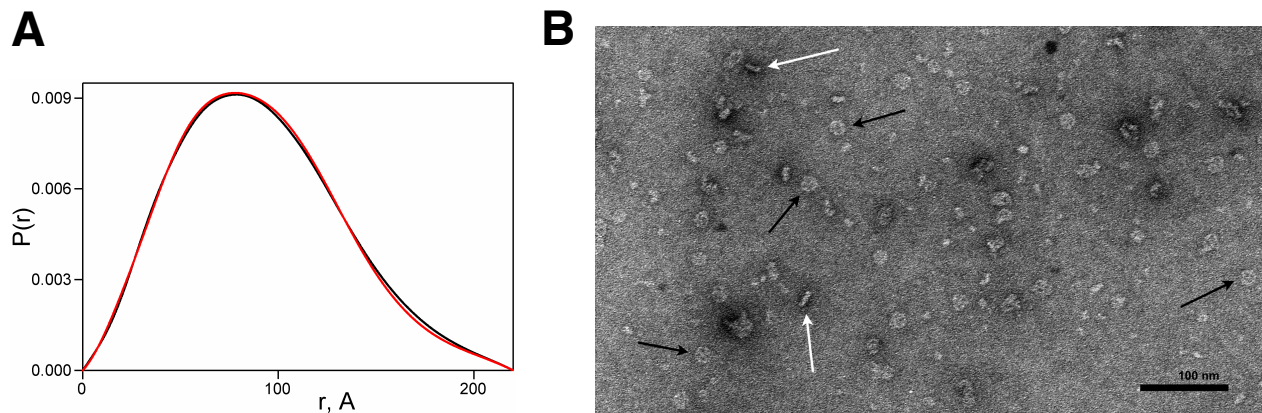


C *S. cerevisiae*

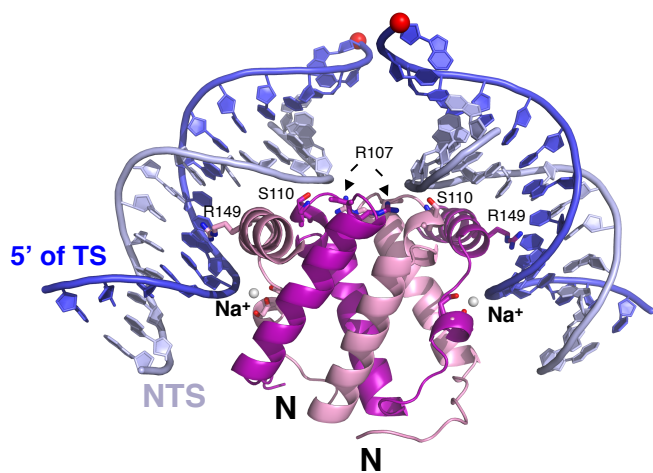


D Sf9 cells

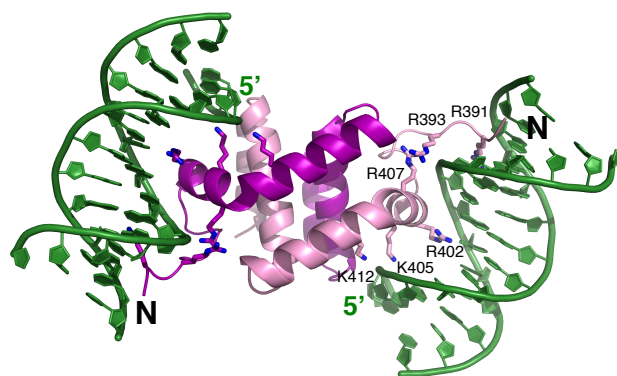


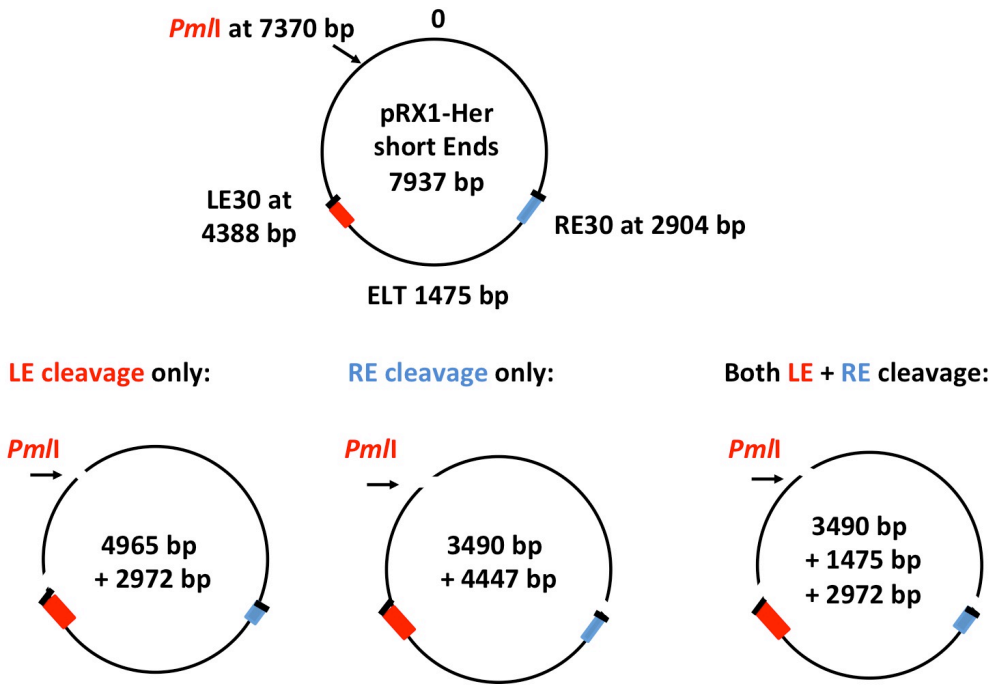


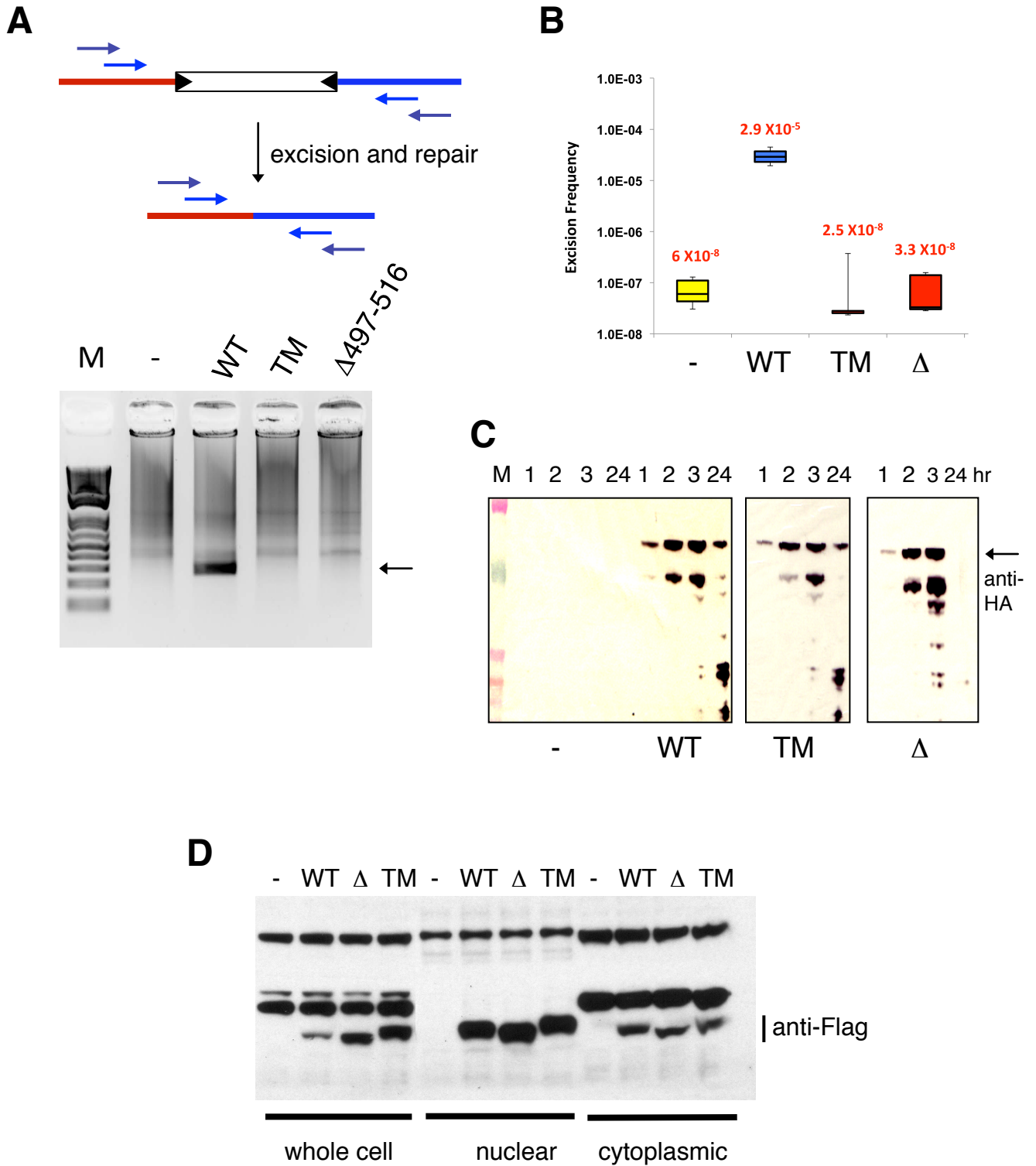
Hermes 79-162

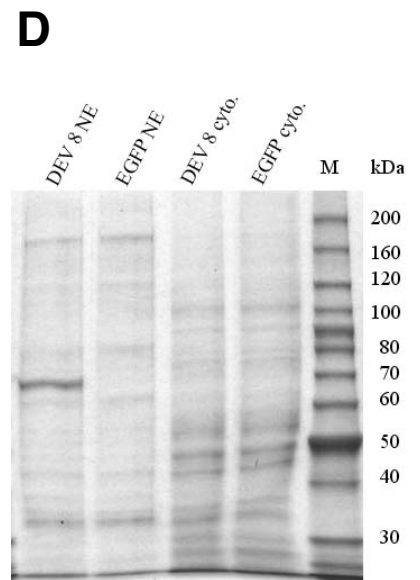
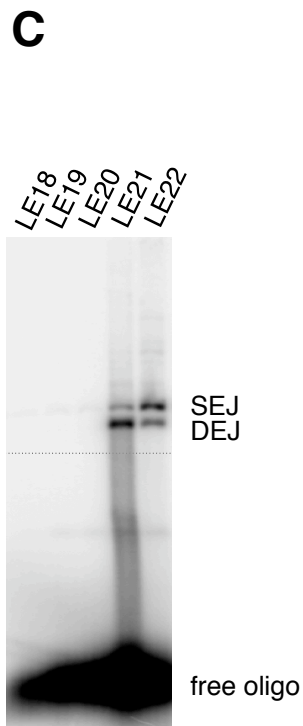
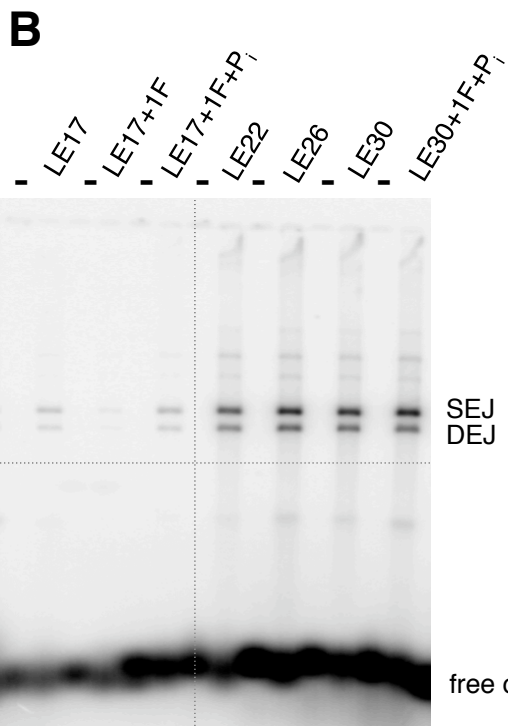
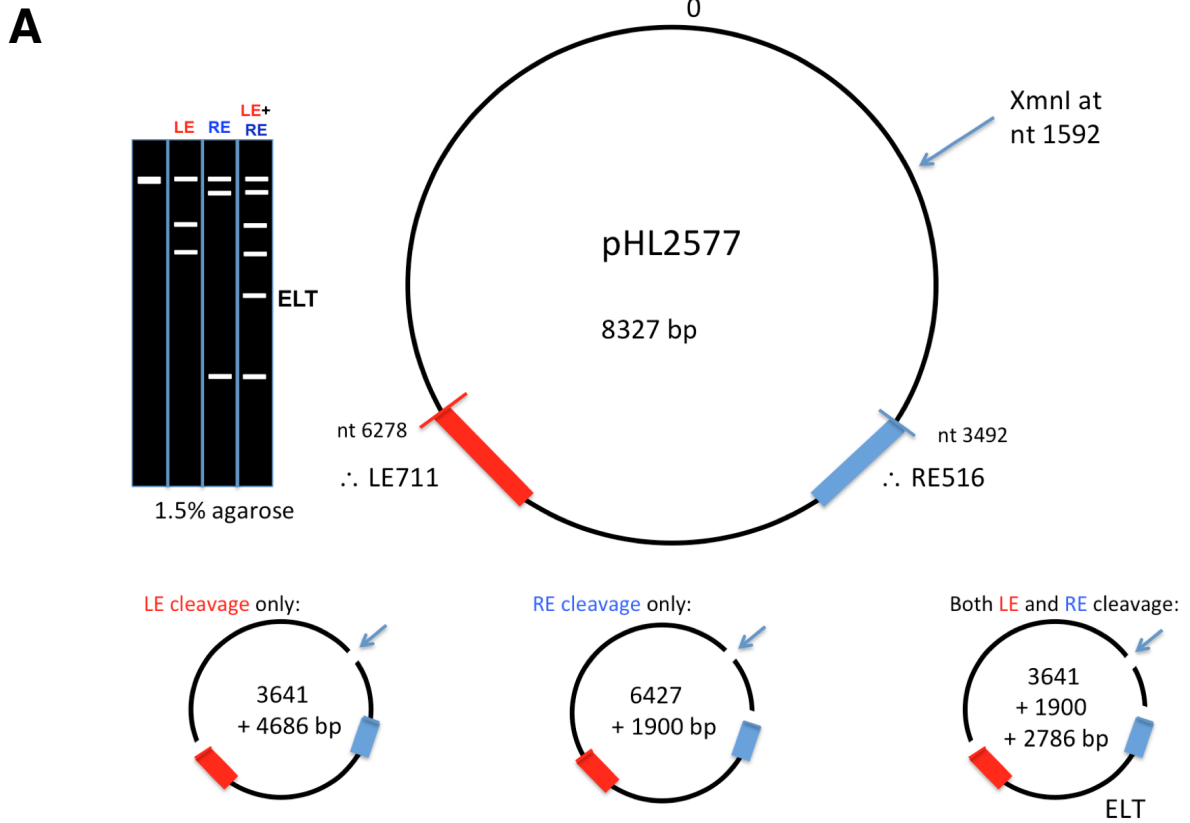


RAG1 389-464 (NBD)









DNA transposons are pieces of DNA that use self-encoded enzymes to move from one genomic location to another. This movement affects genome organization and may be evolutionarily important. The investigation of the structure and properties of a eukaryotic *hAT* transposase bound to transposon ends reveals an unusual octameric ring of subunits. This subunit overabundance provides multiple DNA binding domains to bind repeated sequences within transposon ends. This study also suggests how the transposase might bind to longer ends and its insertion site, and why this family of transposons necessarily have asymmetric ends.

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