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Crystallography of RNA Capping and Repair

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T4 polynucleotide kinase, in addition to being an invaluable research tool, exemplifies a family of bifunctional enzymes with 5'-kinase and 3'-phosphatase activities that play key roles in RNA and DNA repair. T4 Pnk is a homotetramer composed of a C-terminal phosphatase domain and an N-terminal kinase domain. The 2.0Å crystal structure of the isolated N-terminal kinase domain highlights a tunnel-like active site through the heart of the enzyme, with an entrance on the 5'-OH acceptor side that can accommodate a single-stranded polynucleotide. The active site is composed of essential side chains that coordinate the β -phosphate of the NTP donor and the 3' phosphate of the 5'-OH acceptor, plus a general acid that activates the 5'-OH. The structure further rationalizes the different specificities of T4 and eukaryotic Pnk and suggests a model for the assembly of the tetramer. *Candida albicans* guanylyltransferase mediates the second step in 5' mRNA cap formation by catalyzing GMP transfer to nascent messenger RNA and by recruiting the capping apparatus to the phosphorylated C-terminal domain of RNA polymerase II. The 2.8Å crystal structure and genetic analysis of a complex between several repeats of phosphorylated CTD and *C. albicans* guanylyltransferase suggests interfaces utilized in its interaction with both RNA triphosphatase and RNA polymerase II. The structure reveals a previously unobserved open conformation for the guanylyltransferase that shows the enzyme in a stabilized intermediate prepared for 5' diphosphate pre-mRNA attack at the enzyme guanylate.