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Ternary Structure of *E. Coli* Alpha CTD with DNA and CAP

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Introduction: The catabolite activator protein (CAP) activates transcription at P_{lac} and other promoters through interactions with the RNA polymerase α subunit C-terminal domain (α CTD). We have determined the crystallographic structure of the CAP- α CTD-DNA complex at 3.2 Å resolution. The crystallographic structure establishes that CAP makes direct protein-protein interactions with α CTD [involving residues 157-164 of CAP (“activating region 1” of CAP), and residues 285-290 of α CTD (the “287 determinant” of α CTD)], and that α CTD makes direct protein-DNA interactions with the DNA segment adjacent to the DNA site for CAP [involving the DNA minor groove 6-11 bp from the DNA site for CAP and residues 265-268 and 294-299 of α CTD (the “265 determinant” of α CTD)]. This crystallographic structure is the first high-resolution structure of a complex between a transcriptional activator and a functional target within the general transcription machinery.

Methods and Materials: Catabolite gene activator Protein (wt), DNA, and alpha CTD (wt). Cryo-freezing.

Results: Current resolution 3.2 Å