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Structural basis for stable DNA complex formation by the caspase-activated DNase

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Abstract

We describe a structural model for DNA binding by the caspase-activated DNase (CAD). Results of a mutational analysis and computational modeling suggest that DNA is bound via a positively charged surface with two functionally distinct regions, one being the active site facing the DNA minor groove and the other comprising distal residues close to or directly from helix α4, which binds DNA in the major groove. This bipartite protein-DNA interaction is present once in the CAD/inhibitor of CAD heterodimer and repeated twice in the active CAD dimer. © 2005 by The American Society for Biochemistry and Molecular Biology, Inc.

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