

Poster Presentation

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Structural Characterization of Transcription Factor C/EBPbeta

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The basic region:leucine zipper (bZIP) DNA-binding protein, C/EBPbeta, plays a central role in many vital cellular processes, but is also implicated in tumorigenesis, tumor progression, as well as viral replication within cells. C/EBPbeta binds to specific DNA sites as homo- or hetero-dimers and interacts with other transcription factors to control the transcription of a number of eukaryotic genes. C/EBPbeta is an intrinsically repressed protein that is activated in response to growth factors. This study employs a variety of techniques such as sequence analysis, molecular modeling, X-ray crystallography, and mutagenesis to provide structural insights into the mechanisms that modulate the biological activities of C/EBPbeta. Analysis of the primary structure indicates that C/EBPbeta is a largely disordered protein that consists of unstructured regions that have the potential to fold upon binding to molecular partners as well as regions that retain irregular conformations regardless of their environment. Here, a model of the auto-inhibited form of C/EBPbeta is presented as well as the structural basis of its specific dimerization, DNA-binding, and interactions with the p300 transcriptional co-activator.

Keywords: disordered protein, unstructured regions, transcription factor