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Letter to the Editor

NMR assignment of the Cyclin T-binding domain of human Hexim1

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Hexim1 is a protein found in higher eukaryotes where it regulates the elongation of gene transcription. Hexim1 together with the small nuclear RNA 7SK binds and thereby inactivates the positive transcription elongation factor b (P-TEFb). The active form of P-TEFb consists of the cyclin-dependent kinase 9 (Cdk9) and its regulatory subunit Cyclin T. Recently, it was found that residues 255–359 of human Hexim1 form a stable domain that is sufficient to bind Cyclin T1 (Schulte et al., 2005). This 12 kDa domain, referred to as Cyclin T-binding domain (TBD), was found to be homodimeric and bound the cyclin box repeat domain of Cyclin T1 in the low micromolar range. In order to study the structure of the TBD and its interaction with Cyclin T1, the ^{1}H, ^{15}N, and ^{13}C chemical shift resonances of human Hexim1 (255–359, G256A) were assigned using multidimensional heteronuclear NMR experiments. 98% of the backbone and 96% of the side chain ^{1}H, ^{15}N and ^{13}C resonances could be assigned. Chemical shift values have been deposited in the BioMagResBank under accession number 6985.

Reference: Schulte et al. (2005) *J. Biol. Chem.*, **280**, 24968–24977.

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