Near-atomic resolution visualization of human transcription promoter opening

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In eukaryotic transcription initiation a large pre-initiation complex (PIC) assembles at the core promoter and is required for the opening of the duplex DNA and the positioning of the start site at the active site of Pol II. We have used cryo-EM to generate near atomic models of the human PIC in a close state (engaged with duplex DNA), an open state (engaged with a transcription bubble), and an initially transcribing complex (containing six base pairs of DNA-RNA hybrid). Our studies provide models for previously uncharacterized components of the PIC, such as TFIIE and TFIIH, and segments of TFIIA, TFIIB and TFIIF. Comparison of the different structures has allowed us to describe the sequential conformational changes that accompany the transitions from one state to the other throughout the transcription initiation process.