

# Molecular C-clamps start transcription

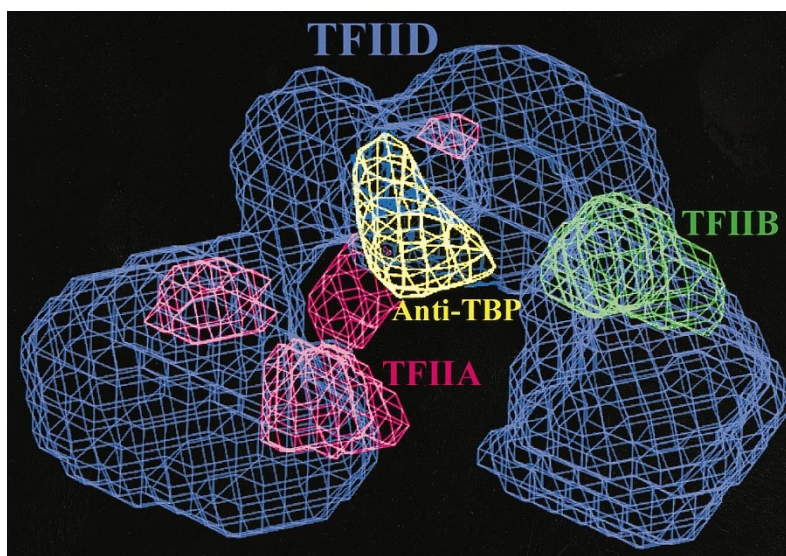
In eukaryotes, accurate and regulated transcription of protein-encoding genes by RNA polymerase II depends on the ordered assembly of transcription factors (TFIIA through I) onto specific promoter elements. TFIID is a multi-component (>5 subunits) transcription factor that recognizes and binds to the promoter. One of its subunits recognizes the TATA element and is thus known as TATA-binding protein or TBP. TFIID also contains several TBP-associated factors (TAFs). Binding of TFIID to the promoter is followed by the assembly of the rest of the transcription factors that include TFIIA and TFIIB to form the core transcription complex.

While X-ray and NMR structures of various parts of TFIIA and TFIIB and of subunits contained within TFIID have been determined, the overall architecture and arrangement of the core initiation complex is unknown. To begin to address this question, two groups in a recent issue of *Science* (286: 2151–2153 and 2153–2156) have used electron microscopy and single-particle image analysis to obtain the structure of TFIID alone or in complex with TFIIA and TFIIB. The three-dimensional reconstruction of TFIID reveals a C-shaped structure with a central cavity and an opening that could readily accommodate double-stranded DNA.

By comparing TFIID alone with the binary (TFIID–TFIIB) and ternary complexes (TFIID–TFIIA–TFIIB), Nogales and coworkers were able to determine the relative positions of all three components. They found that TFIIA (red) and TFIIB (green) bind on opposite sides of the central cavity formed by TFIID (purple). Using anti-TBP antibody (yellow) they found that TBP binds between TFIIA and TFIIB. This finding is consistent with the idea that DNA

binds at the top of the central cavity formed by TFIID. Binding of TFIIA and TFIIB on opposite sides of TFIID could affect the overall shape of the complex by constricting or enlarging the channel opening and in so doing influence DNA binding. Ultimately, cofactors that enhance the levels of transcription initiation (such as activators) can be added to the pot to get a more complete picture of how eukaryotic gene expression gets started.

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Adapted from Ansel *et al.* 1999, courtesy of E. Nogales.