

Researchers Identify a Conserved RNA Polymerase Transcription Factor

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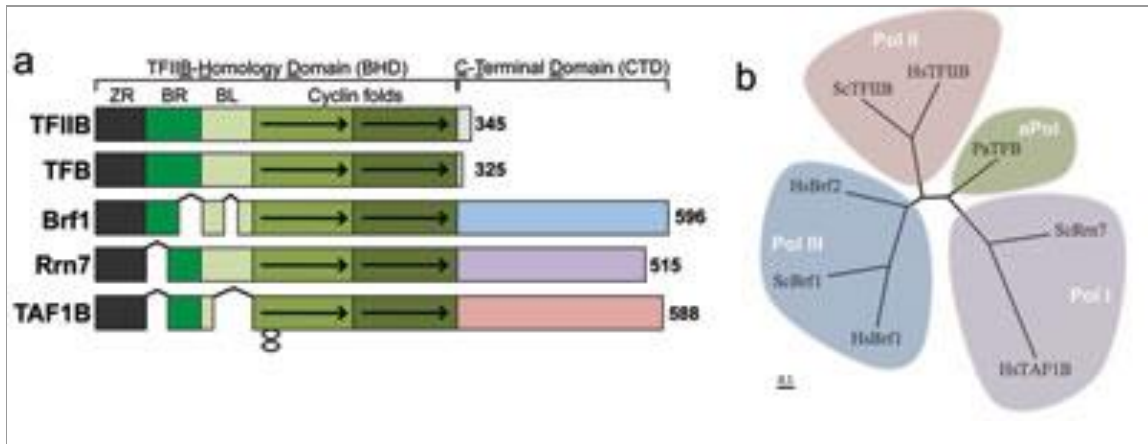
DNA to RNA transcription is mediated by RNA Polymerase (Pol) and assisted by general transcription factors that serve to position Pol at gene promoters, separate DNA strands and release Pol from promoter binding into elongation mode. In bacteria, this process is performed by one Pol, whereas eukaryotes manage genomic transcription with three Pols. Eukaryotic Pols are structurally similar, but target different regions of DNA. Therefore, when general transcription factor (TF) IIB, or TFIIB-like proteins, were found to be an essential and evolutionarily conserved component of Pol II and III transcription pre-initiation complexes, postdoctoral fellow Dr. Bruce Knutson and Basic Science Division member Dr. Steven Hahn, inquired whether a previously undescribed TFIIB-like counterpart was involved in Pol I transcription pre-initiation complexes.

Based on the structural similarity and low protein sequence homology between Pol I and Pol II or III, Knutson and Hahn chose to use a structural homology detection program to identify the counterpart of TFIIB or a TFIIB-like protein among Pol I general transcription factors. They found that Rrn7, a general transcription factor for Pol I in yeast, and TAF1B, a general transcription factor for Pol I in humans, share >75% of their predicted secondary structure and <15% of their protein sequence with TFIIB family members from Pol II and Pol III pre-initiation complexes. In fact, Rrn7 and TAF1B contain four domains that are absolutely conserved among all TFIIB and TFIIB-like proteins.

Knutson and Hahn first confirmed that the region of TFIIB homology in Rrn7 interacts with Pol I. They then swapped each domain of Rrn7 with the corresponding domains from other TFIIB family members and evaluated the functionality of the resulting clones. They observed that all four domains of TAF1B could complement Rrn7 function in yeast, whereas only two domains of Pol III TFIIB-like proteins and only one domain of Pol II TFIIB proteins could complement Rrn7 function. The converse was also true (i.e., only one or two homology domains from the Pol II or Pol III TFIIB family members could be replaced with the corresponding domains of Rrn7 and retain functionality). Taken together, these results are consistent with the degree of secondary structure homology between the different TFIIB family members and suggest that Pol I TFIIB-like proteins are more functionally related to Pol III TFIIB-like proteins. Moreover, the authors' findings underscore the value of structure homology studies for defining gene function.

(N.b., in the same issue of *Science*, Naidu *et al.* reported the structural similarity of TAF1B to TFIIB and TFIIB-like proteins.)

[Knutson BA, Hahn S.](#) 2011. Yeast Rrn7 and human TAF1B are TFIIB-related RNA polymerase I general transcription factors. *Science* 333:1637-40.



Bruce Knutson

A) Conserved structural domains of the TFIIB protein family. B) Genetic tree created by comparing homology domains of TFIIB and TFIIB-like proteins (Sc, *Saccharomyces cerevisiae*; Hs, *Homo sapiens*; Pa, *Pyrococcus abyssi*; aPol, archaeal Pol).