

**P017** Multiple transcription factors (TFBs) in the archaeal transcription of the hyperthermophilic Crenarchaeon *Thermoproteus tenax*  
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The minimal archaeal transcriptional machinery consists of a eukaryal like -RNA polymerase II, eukaryal like-TATA-box binding protein (TBP) and transcription factor B (TFB) similar to eukaryal TFBII. Multiplicity of general transcription factors TBP and TFB is commonly found in Archaea. It is suggested that multiple TBPs and TFBs function similar as bacterial sigma-factors, which regulate transcription in response to environmental changes. The classical TFBs show a conserved domain structure, containing a zinc-ribbon, a B-finger, and two TFB-repeats, consisting of five  $\alpha$ -helices each.

In the genome sequence of *T. tenax*, one TBP and four TFB homologues (*Ttx*-TFB1–4) were identified, which surprisingly show peculiarities in their domain structure. Whereas homologues of *Ttx*-TFB1, *Ttx*-TFB2 and *Ttx*-TFB3 are found in several crenarchaeal species, and *Ttx*-TFB4 seems to be organism-specific. In this study, *Ttx*-TBP and the multiple *Ttx*-TFBs have been heterologously expressed in *E. coli* and purified. Using radioactive electrophoretic mobility shift assay (rEMSA) the DNA- interaction with *Ttx*-TFBs homologues and *Ttx*-TBP has been studied. The presence of TBP stabilizes *Ttx*-TFB1 – DNA complex as a typical transcription factor. Interestingly *Ttx*-TFB2 seem to bind DNA in a TBP independent way.