

Complete nucleotide sequence of an archaeal (*Pyrococcus woesei*) gene encoding a homolog of eukaryotic transcription factor IIB (TFIIB)

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We have previously reported the sequence of the streptomycin (*str*) operon-equivalent of the archaeum *Pyrococcus woesei* (1). Subsequently, Ouzounis and Sander found that a partial ORF located downstream (and on the complementary strand) of the *P. woesei str*-operon-equivalent cluster, encodes the C-terminal 152 amino acids of a polypeptide that shares significant similarity with the eukaryotic transcription factor TFIIB (2). We have now sequenced the *P. woesei* DNA region encompassing the missing (N-terminal) portion of the TFIIB gene and the upstream 296 nucleotides (EMBL Data Bank accession number X70668). The archeal gene is preceded (at -73) by a consensus promoter.

The structural similarities between the *P. woesei* and the eukaryotic TFIIB are shown in Figure 1. The archaeal sequence (300 amino acids) is 27.5% - 33.8% identical with that of eukarya and exhibits unique structural motifs characteristic of eukaryotic TFIIB (4-6) such as (i) an imperfect amino acid repeat (encompassing residues 136-182 and 232-278) with 38.3% identity and 63.8% similarity between the N-terminal and the C-terminal repeats (ii) an intervening sequence characteristically rich (32%) in basic amino acids between repeats (iii) Zn(II)-finger motif (Cys-X₂-Cys-X₁₅-Cys-X₂-Cys) located in close proximity

to the N-terminus and (iv) a predicted amphipatic α -helix situated at the end of the N-terminal repeat (residues 167-184, *P. woesei* numbering). On the whole, the distinguishing structural motifs of TFIIB appear to predate the phylogenetic divergence of archaea and eukarya and have been stringently conserved upon ensuing evolution.

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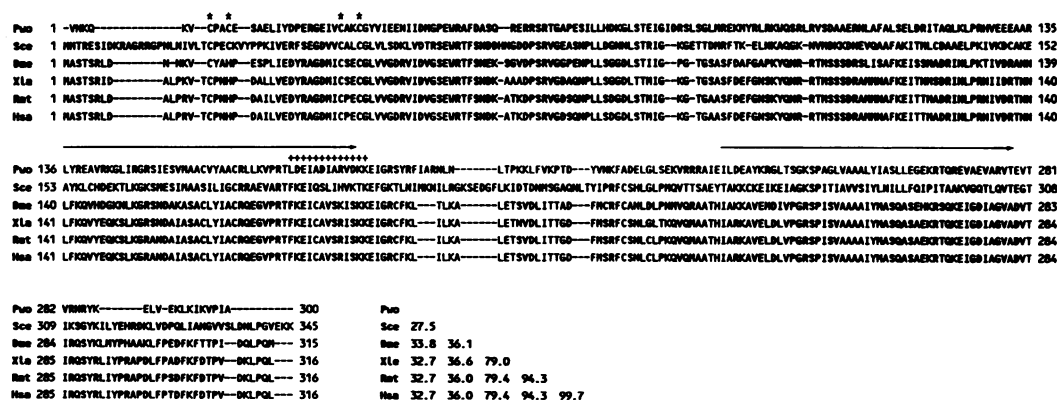


Figure 1. Alignment of the *P. woesei* TFIIB sequence with those from *Saccharomyces cerevisiae* (Sce) (5), *Drosophila melanogaster* (Dme) (7), *Xenopus laevis* (Xla) (8), *Homo sapiens* (Hsa) (6) and rat (9). Asterisks identify the Zn finger motifs. Arrows indicate the N-terminal and the C-terminal elements of the direct repeat; plus symbols identify the putative amphipatic α -helix of the *P. woesei* TFIIB sequence. Pairwise identities (percent) between all sequences are shown in a matrix form.

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