

P011 Molecular mechanisms of transcription elongation
in archaea

Angela Hirtreiter and Finn Werner

*UCL Structural and Molecular Biology, Darwin Building,
London WC1E 6BT*

Archaeal RNA polymerases mirror eukaryotic RNAPII in subunit composition and regulation by basal transcription factors. RNAP subunits F/E form a heterodimeric module that (i) reversibly associates with RNAP, (ii) binds RNA *in vitro* and (iii) is involved in DNA melting during transcription initiation. **Spt4/5** is a universally conserved transcription elongation factor present in both *Eukarya* and *Archaea* (Spt4/5) and *Bacteria* (NusG, homologous to Spt5). Spt4/5-like factors reversibly associate with their cognate RNAP and stimulate transcription elongation through an unknown mechanism. In this study we investigated the molecular mechanisms of transcription elongation. We have characterised the functional contributions of individual RNAP subunits and Spt4/5. Our results demonstrate that the F/E module, in addition to its role during transcription initiation, strongly stimulates transcription elongation. This effect of F/E is due to an allosteric modulation of RNAP rather than the intrinsic RNA binding activity of F/E. The stimulatory activity of F/E is highly reminiscent of the transcription factor Spt4/5. We performed a domain deletion analysis of Spt4/5 and identified the N-terminal domain of Spt5 (Spt5N) as the minimal functional domain of Spt4/5 for elongation. Interestingly, Spt5N also harbours an RNA binding motif that is masked by the C-terminal domain of Spt5 (Spt5C), and Spt5N mediates the complex formation with its interaction partner Spt4.