CCAAT/enhancer binding proteins (C/EBPs) are a family of transcription factors that participate in many different cellular functions that include metabolism, reproduction, immunity, senescence and the development of neoplasms. In a Point-of-View article, Leutz et al. discuss the roles of arginine and lysine side chain methylation in the regulation of C/EBPs diverse activities.

**Interfering with Transcription**

pp. 9–14

Transcriptional interference occurs when transcription of one locus suppresses a different transcriptional process in cis. Palmer et al. discuss the process of interference between transcriptional events and propose that interference may be generated by the dislodgement of slow-to-assemble pre-initiation complexes and transcription factors and prolonged occlusion by paused RNA polymerases.

**Modulation of RNA Polymerase in Mycobacteria**

pp. 15–8

Mycobacteria CarD is an essential RNA polymerase-binding protein that modulates many transcripts and has functions in genomic integrity and cell survival. Stallings and Glickman review the physiological roles and molecular features of CarD in mycobacteria, comparing its functions with those of other RNA polymerase-binding proteins in *E. coli*.

MITF is a master regulator of melanocyte development, proliferation and survival. This transcription factor regulates both the expression of pigmentation genes that are only expressed in melanocytes and of other genes that are expressed in multiple cell lineages. Levy and Fisher discuss how MITF in melanocytes can be used as a model system to study lineage restricted transcription factor activation of both tissue-specific and ubiquitously expressed genes.

**Tools for the Discovery of Regulatory Elements**

pp. 23–7

Numerous putative regulatory elements that control gene expression have been discovered thanks to the use of modern genomics tools. In an enlightening Point-of-View, Ott and Harris describe how these tools helped in the identification of functional elements within the human cystic fibrosis transmembrane conductance regulator gene (*CFTR*) locus. While several critical elements activating *CFTR* are found within the promoter region, they do not confer the cell-type specific expression pattern of the gene. The authors therefore reason that regulatory elements likely exist within the locus outside of the promoter, within intergenic and intronic regions.

A complete understanding of how stalled RNA polymerase II (Pol II) complexes are regulated is lacking, but many of the main players have been identified. The human Mediator (a 1.2 MDa multi-subunit complex that provides a physical and functional link between transcription factors and the Pol II machinery) appears to play a crucial role. Knuesel and Taatjes discuss recent data that suggest that activator-induced structural shifts within Mediator trigger activation of stalled Pol II. The authors also present recent findings regarding post-recruitment regulation of Pol II.

**Putting an End to Mitochondrial Transcription**

pp. 32–6

Our understanding of the mechanisms controlling transcriptional regulation in the mitochondria is relatively poor. The recent publication of a 2.2-Angstrom structure of the human mitochondrial transcription termination factor (MTERF1) provides insight into the mechanisms of mitochondrial transcription termination. Byrnes and Garcia-Diaz now describe the possible implications of this structure on our understanding of transcriptional regulation in mitochondria and discuss how this information influences our views on the mechanism of mitochondrial transcription termination in the context of other termination systems. The authors also review new data that link defects in MTERF1 function with the pathogenesis of mitochondrial diseases.
NusA is a transcription elongation factor associated with all elongating RNA polymerases that functions in transcription termination and antitermination. Cohen and Walker review their recent results that implicate that NusA is involved in the recruitment of DNA repair and damage tolerance mechanisms to sites of stalled transcription complexes.

Active polymerases engaged in transcription are usually depicted moving along their templates. Papantonis and Cook review the alternative model that postulates that active enzymes are instead immobilized in “transcription factories” and discuss recent evidence that supports the idea that the DNA, not the polymerase, moves. This model also highlights alternative explanations of how regulatory motifs like enhancers and silencers work.

In mice, B2 RNA binds RNA polymerase II (Pol II) and represses transcription during the cellular heat shock response. B2 RNA enters transcriptional complexes at promoters, preventing Pol II from engaging the DNA. An original research paper by Yakovchuk et al. shows that the promoter of the mouse actin gene displays a decrease in the phosphorylation of Ser5 in the carboxy terminal domain (CTD) of Pol II after heat shock, despite the continued presence of Cdk7 and cyclin H kinases. Biochemical assays revealed that B2 RNA, when present with Pol II in promoter-bound complexes, specifically represses CTD phosphorylation by TFIIH.