TFIIF and Transcript Initiation
pp. 156–159
The general transcription factor TFIIF is essential for assembly of RNAP II preinitiation complexes on fully double-stranded templates in vitro. Although existing models assign various tasks to TFIIF during preinitiation complex formation and transcript initiation, recent results suggest that some aspects of those models may need to be revised. In this issue of Transcription, Luse discusses recently published manuscripts that emphasize the significance of the interaction of TFIIF and TFIIB and raise the possibility that a fraction of RNAP II transcription complex assembly proceeds through a pathway that is independent of TFIIF.

σ70 and PhoB Get a Better Grip
pp. 160–164
Canals et al. discuss the recently obtained crystal structure of a bacterial transcription subcomplex comprising the effector domain of factor PhoB, its target DNA and the σ70 domain of the RNA polymerase σ70 subunit. This structure supports the notion that a stronger grip on the promoter-factor complex results in an enhanced RNAP architecture.

Endocrine Resistance in Breast Cancer: Epigenetic Mechanisms
pp. 165–170
The genomics events promoting the dysregulation of gene expression during endocrine resistance in breast cancer are not clearly understood. Multiple cellular mechanisms have been proposed to be involved. Now, Bianco and Gévry review the signaling pathways involved in endocrine resistance in the context of recent epigenetic studies.

HCF-1 and Cell Cycle Regulation
pp. 187–192
Initially discovered as a cofactor in multiprotein DNA complexes that form on Herpex Simplex Virus immediate early gene promoters to activate the transcription of viral genes, HCF-1 is an abundant chromatin-associated protein that also regulates various stages of the cell cycle. Recently, HCF-1 was shown to interact with diverse E2F proteins to induce cell cycle-specific transcription. In this issue of Transcription, Zargar and Tyagi review the diversity of HCF-E2F interactions and the variety of multiprotein complexes it occurs in, to influence the local chromatin landscape at E2F-promoters.

Transcription at Centromeres in Budding Yeast
pp. 193–197
Centromeres are specialized chromosomal loci that are essential for proper chromosome segregation. Recent data show that a certain level of active transcription, regulated by transcription factors Cbf1 and Ste12, makes a direct contribution to centromere function in budding yeast. Ohkuni and Kitagawa now discuss the requirement and function of transcription at centromeres.

Terminating Transcription Between Closely Spaced Genes
pp. 198–212
In this issue of Transcription, Henriques et al. study transcription termination between closely spaced genes of Drosophila, where about 52% of tandem genes are separated by regions of less than 1 kb. The authors show that an intergenic spacing of 168 bp is sufficient for efficient transcription termination between the polo-snap tandem gene pair. For the polo-snap pair, displacement of the poised polymerase from the snap promoter by depletion of the initiation factor TFIIB results in an increase of polo transcriptional read-through, which suggests that poised polymerase is necessary for transcription termination. Interestingly, the authors show that polo forms a TFIIB dependent gene loop between its promoter and terminator regions. In addition, deletion of the polo promoter causes an increase in snap expression, as does deletion of polo poly(A) signals.