In this issue of *Transcription*

Winged-Helix Domains at the Core of Transcription
pp. 2–7

The winged-helix domain represents a subclass of the helix-turn-helix motif that is found in core components of transcription systems and participates in establishing protein-DNA and protein-protein-interactions. Teichmann et al. discuss possible explanations for the enrichment of this motif in transcription systems.

A Novel Function for a Conserved Splicing Complex
pp. 8–12

During transcription of protein-coding genes by RNAP II, several mRNA-processing factors and mRNA-binding proteins associate with the nascent pre-mRNA to produce a mature messenger ribonucleoprotein particle (mRNP). One of the protein complexes coupling transcription to mRNA export is the TREX complex. The mechanism by which TREX is recruited to genes has remained elusive. Chanarat et al. review their recent work in which the conserved Prp19 complex, known for its function in splicing, was shown to be essential for TREX occupancy at transcribed genes.

Discussing the SAGA Complex
pp. 13–8

The SAGA complex is a conserved, multifunctional co-activator that controls the transcription of many inducible genes in response to environmental changes. Helmlinger reviews recent studies that provide new insights into the functions of one of its subunits, Tra1/TRRAP, and discusses its role in the control of SAGA activity in response to external stimuli.

PPARγ in Adipocytes
pp. 19–24

Schmidt et al. discuss major findings from three recent studies that investigated interspecies retention of binding sites of peroxisome proliferator-activated receptor γ (PPARγ), the master regulator of adipocyte differentiation, between mouse and human adipocytes. The authors propose that retention of binding events is highly context dependent.

Lifting the Roadblock to Differentiation
pp. 25–8

In order to keep cells in an undifferentiated, pluripotent state, many metazoans recur to the inhibition of transcriptional elongation. Recent studies suggest that, in plants, a mechanism for turning on differentiation functions via the lifting of a transcriptional elongation barrier. Sanmartín et al. argue that targeting the elongation phase of transcription may be a solution adopted widely in evolution to allow for the global transcriptional changes needed during cellular differentiation.

RNAP II Need for Speed
pp. 29–34

Mammalian RNAP II transcription elongation rates have been estimated to average between 1 and 4 kilobases per minute. However, recent direct measurements of RNA biogenesis from a single gene exceeded 50 kilobases per minute. Marcello reviews the implications of this unexpected finding, which opens novel and intriguing perspectives on the control of metazoan transcription.

Meeting Report
pp. 35–8

The fourth edition of the “Gene Expression and RNA Processing” symposium took place this year at the Iguazú Falls, bringing together an outstanding array of speakers from all over the world to discuss mechanisms of transcriptional regulation and RNA processing. Highlights from this meeting are presented in this issue.

Stress Responses in Yeast: Controlling mRNA Levels
pp. 39–44

Stress-responding genes in yeast are enriched in cryptic transcripts. The presence of these cryptic transcripts has been proposed as the cause for the differences observed between mRNA amount and RNAP occupancy profiles in these genes. García-Martínez et al. analyze the relationship between the presence of cryptic transcripts in genes and their stress response profiles. The authors found no statistically significant evidence that cryptic transcription is responsible for the differences observed between mRNA and transcription rate profiles.