

In this issue of *Transcription*

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A Role for DNA Methylation in Splicing pp. 106–109

In a variety of species, the level of 5-mC is higher at exons than at introns, suggesting that intragenic DNA methylation aids the spliceosome in the process of exon definition. In this issue of *Transcription*, Oberdoerffer reviews recent genome-wide associations and direct evidence linking DNA methylation to pre-mRNA alternative splicing.

On the Mediator Tail Module pp. 110–114

Ansari and Morse discuss recent evidence that indicates that the tail module subunits of the Mediator complex are targets of activators, both in yeast and metazoans. The authors discuss studies of tail module specificity for SAGA-dependent, TATA-containing genes (including highly regulated stress response genes) and of the independent recruitment and function of the tail module.

Trigger Loop Substitution in Multi-Subunit RNA Polymerase pp. 115–118

The active center of multi-subunit RNA polymerase contains two modules: the Mg²⁺ module, holding the catalytic Mg²⁺ ion, and a module made of a flexible domain, the Trigger Loop. Yuzenkova et al. discuss results that indicate that the Trigger Loop module can be substituted by alternative modules, thus changing the catalytic properties of the active center.

Regulation of Metabolism by p53 pp. 119–123

The tumor suppressor p53 is intimately linked with the control of cell cycle progression and apoptosis. Now, Sen et al. discuss an emerging role for p53 in the transcriptional regulation of metabolism. This activity is key for p53 tumor suppressor function.

Cdc6: Many Functions and a Role in Carcinogenesis pp. 124–129

The replication licensing factor Cdc6, conserved in all eukaryotes, was initially identified in a genetic screen aimed at finding mutations that arrested the budding yeast cell cycle. Its functions include roles in DNA replication, cell proliferation and, more recently, a role in transcriptional repression linked with human cancer development. Petrakis et al. now summarize all the findings arguing over a role of Cdc6 as a transcriptional repressor and shed light towards new research directions for this field.

Heparanase, H3 Methylation and Transcription pp. 130–145

The methylation of histones is a fundamental epigenetic process regulating gene expression programs in mammalian cells. In this issue of *Transcription*, He et al. report that the invasive extracellular matrix degrading endoglycosidase heparanase

enters the nucleus of activated human T lymphocytes and regulates the transcription of a cohort of inducible immune response genes by controlling histone H3 methylation patterns. The authors found that heparanase is recruited to both the promoter and transcribed regions of transcriptionally active genes. Heparanase seems to influence gene transcription by associating with the demethylase LSD1, preventing recruitment of the methylase MLL and thereby modifying histone H3 methylation patterns. Therefore, in addition to their extra-nuclear function, heparanase appears to play an important role in regulating transcription.

Reconstituting Single Transcription Elongation Complexes pp. 146–153

Single-molecule studies of RNAP II require high yields of transcription elongation complexes with long DNA tethers upstream and downstream of them. Palangat et al. have developed a robust system to reconstitute both yeast and mammalian RNAP II into transcription elongation complexes that elongate with very high efficiency. This method has produced single transcription elongation complexes (both from yeast and mammals) that have been successfully used in an optical-trapping transcription assay capable of applying forces that either assist or hinder transcript elongation.