

# Leading Edge

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## POSITIONS AVAILABLE

On the cover: Human cells contain two genomes—one housed in the nucleus and the other in the mitochondria. The circular mitochondrial genome encodes rRNAs, tRNAs, and mRNAs and is transcribed in its entirety, expressing long polycistronic transcripts that are cleaved at intervening tRNA sequences to liberate individual mRNAs. Mercer et al. (pp. 645–658) use a variety of approaches to survey the complex transcriptional landscape of human mitochondria, uncovering noncoding transcripts, protein-binding sites across the genome, and the hierarchy of processing events that fashion common polycistronic precursors into the mature mitochondrial transcriptome. The cover image represents maps of the multilayered data sets used in this analysis. Original cover design by Tim Mercer, using Circos (<http://circos.ca>).

