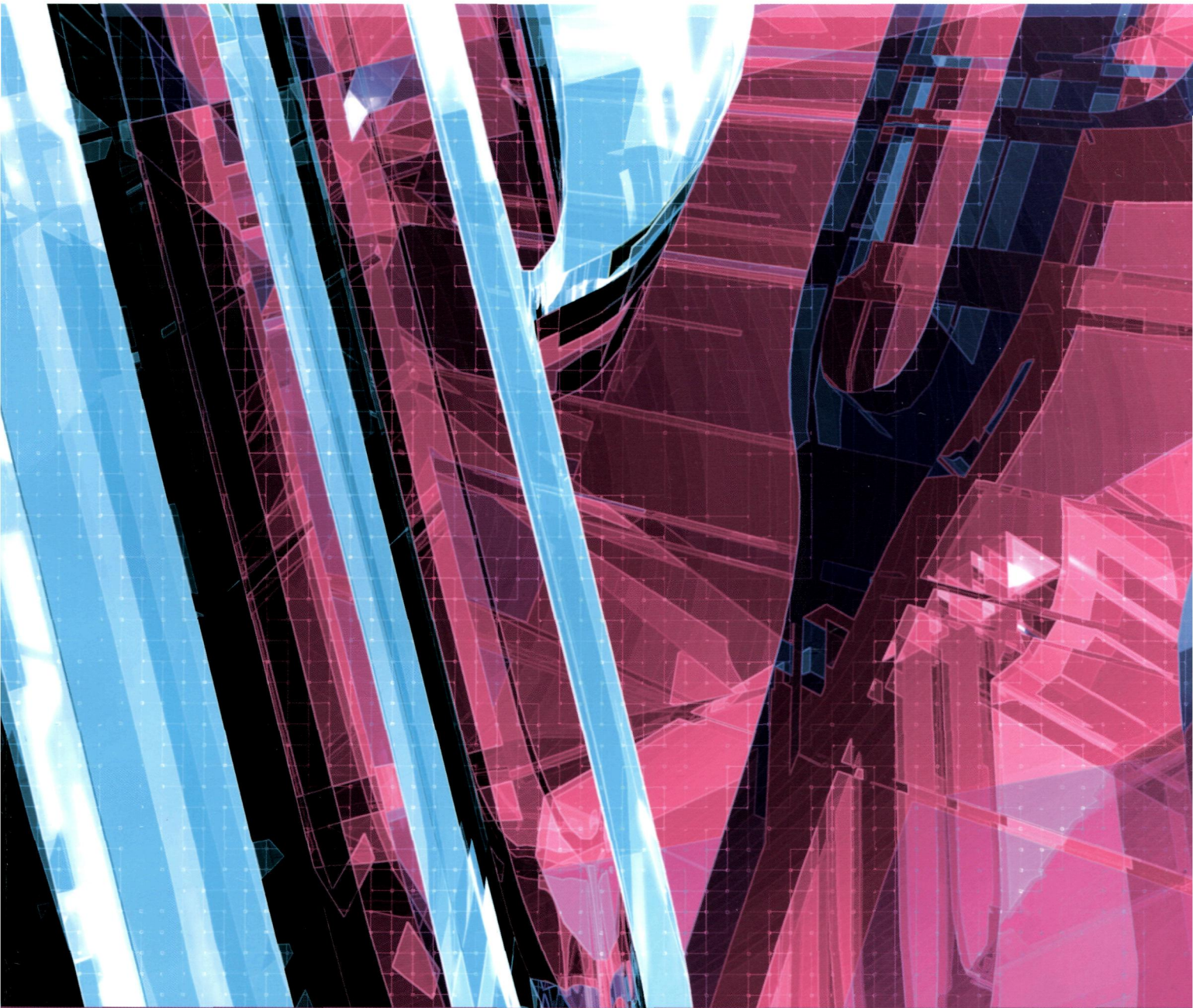


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REVIEWS

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GENETICS



SMALL BUT MEANINGFUL

Functional coding roles for short open reading frames

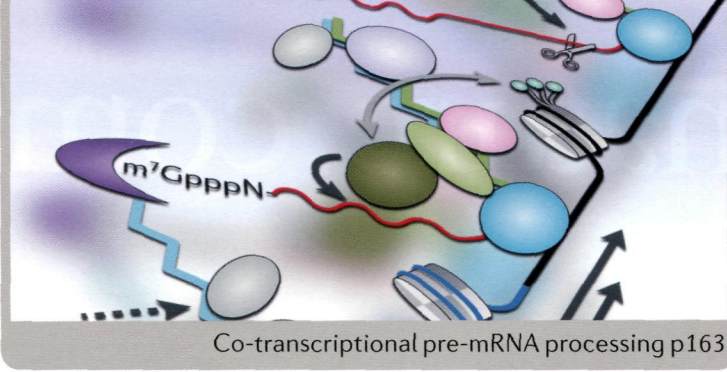
Human population history

Insights from whole-genome sequencing

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Co-transcriptional pre-mRNA processing p163

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The impact of whole-genome sequencing on the reconstruction of human population history

Krishna R. Veeramah and Michael F. Hammer

There continues to be active debate about the timings, locations and details of various events in human population history. This Review describes how whole-genome sequencing of modern and ancient humans has complemented more traditional methods to provide valuable historical insights.

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Coupling mRNA processing with transcription in time and space

David L. Bentley

The cellular transcription, mRNA processing and export machineries seem to have co-evolved to allow spatiotemporal coupling of these processes. Here, the author reviews recent insights into the relative amount of co-transcriptional and post-transcriptional processing, the relationship between mRNA elongation and processing, and the regulating role of the carboxy-terminal domain of RNA polymerase II.

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Genomics and the origin of species

Ole Seehausen, Roger K. Butlin, Irene Keller, Catherine E. Wagner, Janette W. Boughman, Paul A. Hohenlohe, Catherine L. Peichel and Glenn-Peter Saetre et al.

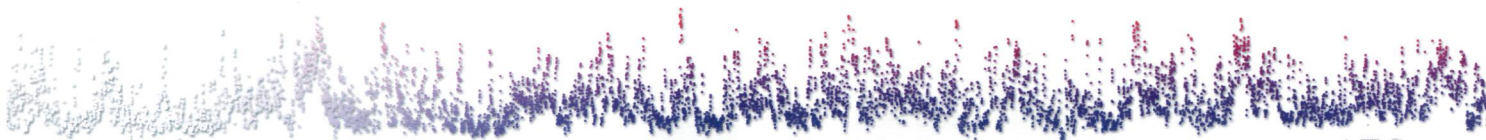
Genomic approaches are an increasingly important aspect of speciation research. The authors review recent insights from speciation genomics and propose a roadmap for this field, which is aimed at addressing both long-standing and emerging questions about speciation.

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Emerging evidence for functional peptides encoded by short open reading frames

Shea J. Andrews and Joseph A. Rothnagel

Recent advances in bioinformatics, proteomics and high-throughput analyses of translation have begun to uncover short open reading frames (sORFs) with coding potential. This Review considers unifying characteristics of these sORFs, methods to identify them and potential functions of the resultant short peptides.



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► **COVER:** 'Amassment' by Patrick Morgan, inspired by the Review on p149.

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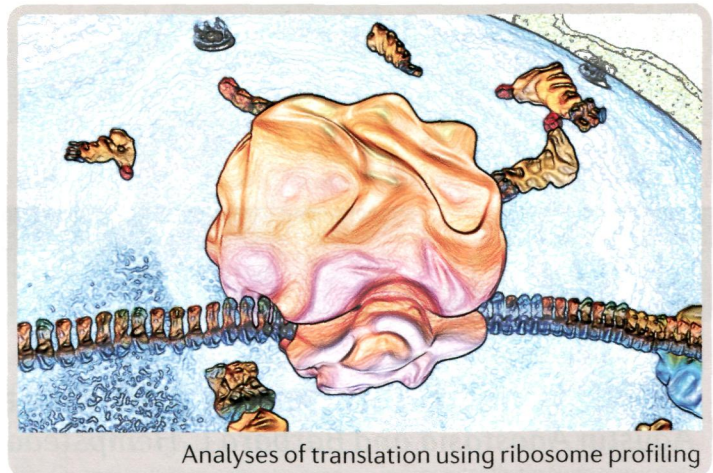
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ARTICLE

Ribosome profiling: new views of translation, from single codons to genome scale

Nicholas T. Ingolia

Ribosome profiling is a recently developed technique that uses deep sequencing to study translation *in vivo*. This approach has provided new insights into the identities and amounts of proteins produced by cells, as well as into the mechanism of protein synthesis itself.



Analyses of translation using ribosome profiling

Arktrek Studios/NPC

P. Morgan/NPC



Research Highlight on the pervasiveness of parent-of-origin effects p145

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HANNAH STOWER



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