

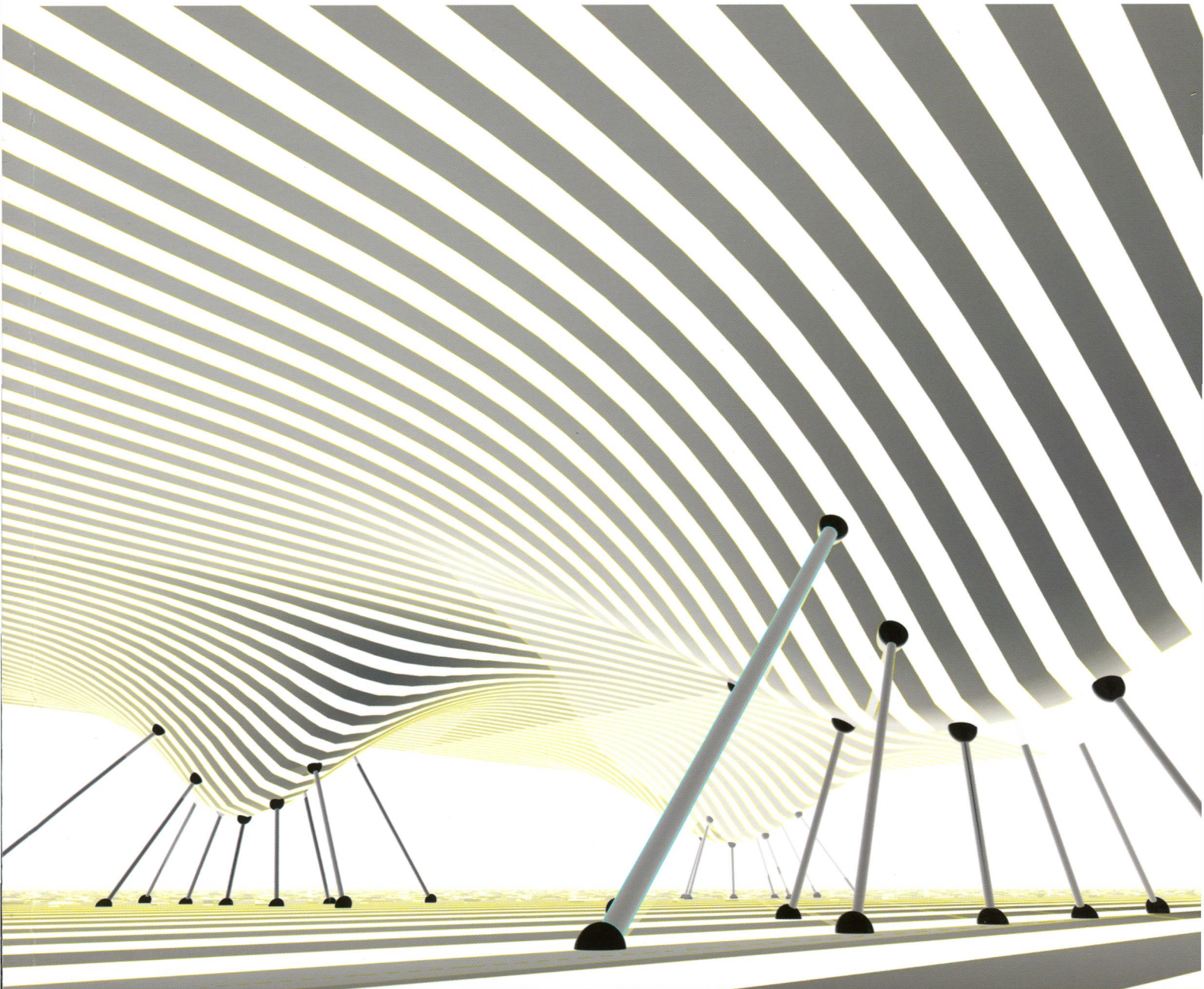
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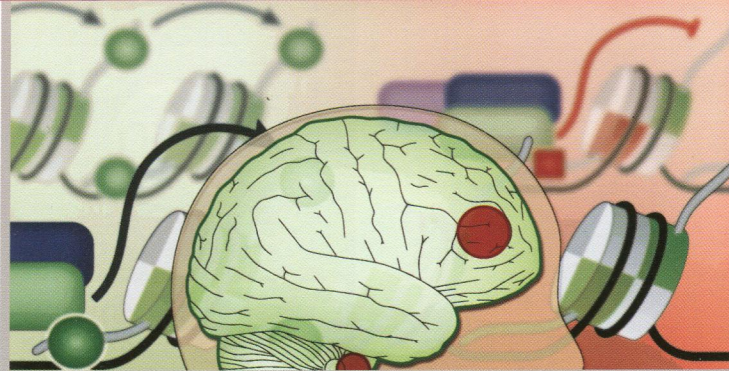
april 2014 volume 15 no. 4
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GENETICS



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Roles for cryptic genetic variation
in evolution

Kept in the loop
A unifying mechanism for CTCF
functions?



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Evolution of transcription factor binding in metazoans — mechanisms and functional implications

Diego Villar, Paul Flicek and Duncan T. Odom

The rate and mechanisms of evolution of transcription factor binding show striking differences across diverse metazoan phyla. This Review highlights insights gained from sequence-based comparisons of genomes and ChIP-seq studies analysing the evolution of transcription factor binding, as well as their conceptual contribution to models of regulatory evolution and gene expression control.

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CTCF: an architectural protein bridging genome topology and function

Chin-Tong Ong and Victor G. Corces

CCCTC-binding factor (CTCF) is a DNA-binding protein that has various, often seemingly contradictory, roles in gene regulation. This Review describes these disparate functions and how the context-dependent looping of DNA regions by CTCF is emerging as a potential unifying mechanism that underpins these diverse roles.

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Cryptic genetic variation: evolution's hidden substrate

Annalise B. Paaby and Matthew V. Rockman

This Review discusses cryptic genetic variation and focuses particularly on empirical support for widespread cryptic genetic variation in natural populations, its potential role in human diseases and its contribution to evolution.

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Every amino acid matters: essential contributions of histone variants to mammalian development and disease

Ian Maze, Kyung-Min Noh, Alexey A. Soshnev and C. David Allis

Increasing evidence suggests crucial functions for histone variants in diverse biological processes. This Review examines the roles of histone variants in mammalian germ cell and embryonic development, as well as the consequences of their aberrant regulation in human disease.

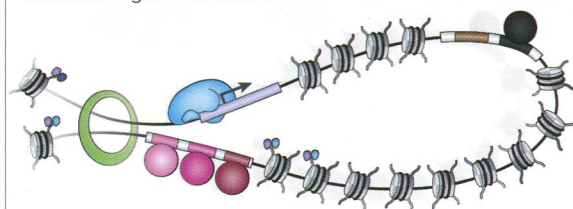
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Transcriptional enhancers: from properties to genome-wide predictions

Daria Shlyueva, Gerald Stampfel and Alexander Stark

Enhancers are DNA elements that are key regulators of gene expression, but their complexities and context dependence makes their identification and characterization challenging. This Review discusses how an improved understanding of the varied properties of enhancers is being used in diverse approaches for the systematic prediction of enhancers genome wide.



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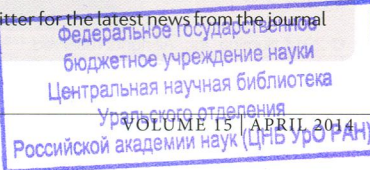
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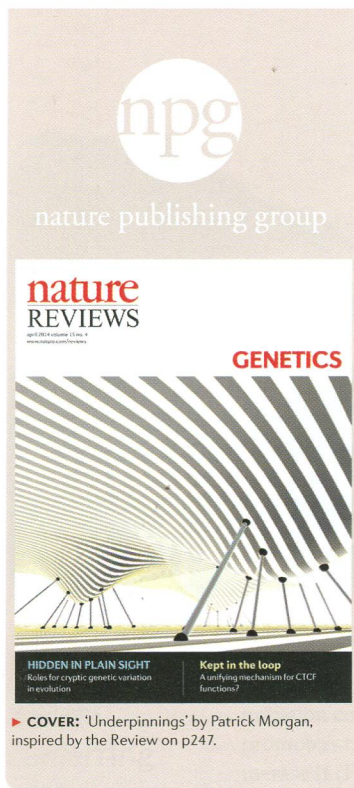
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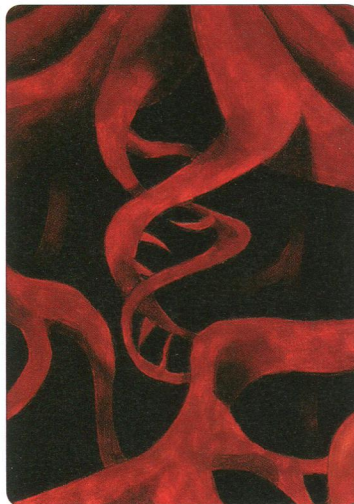
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