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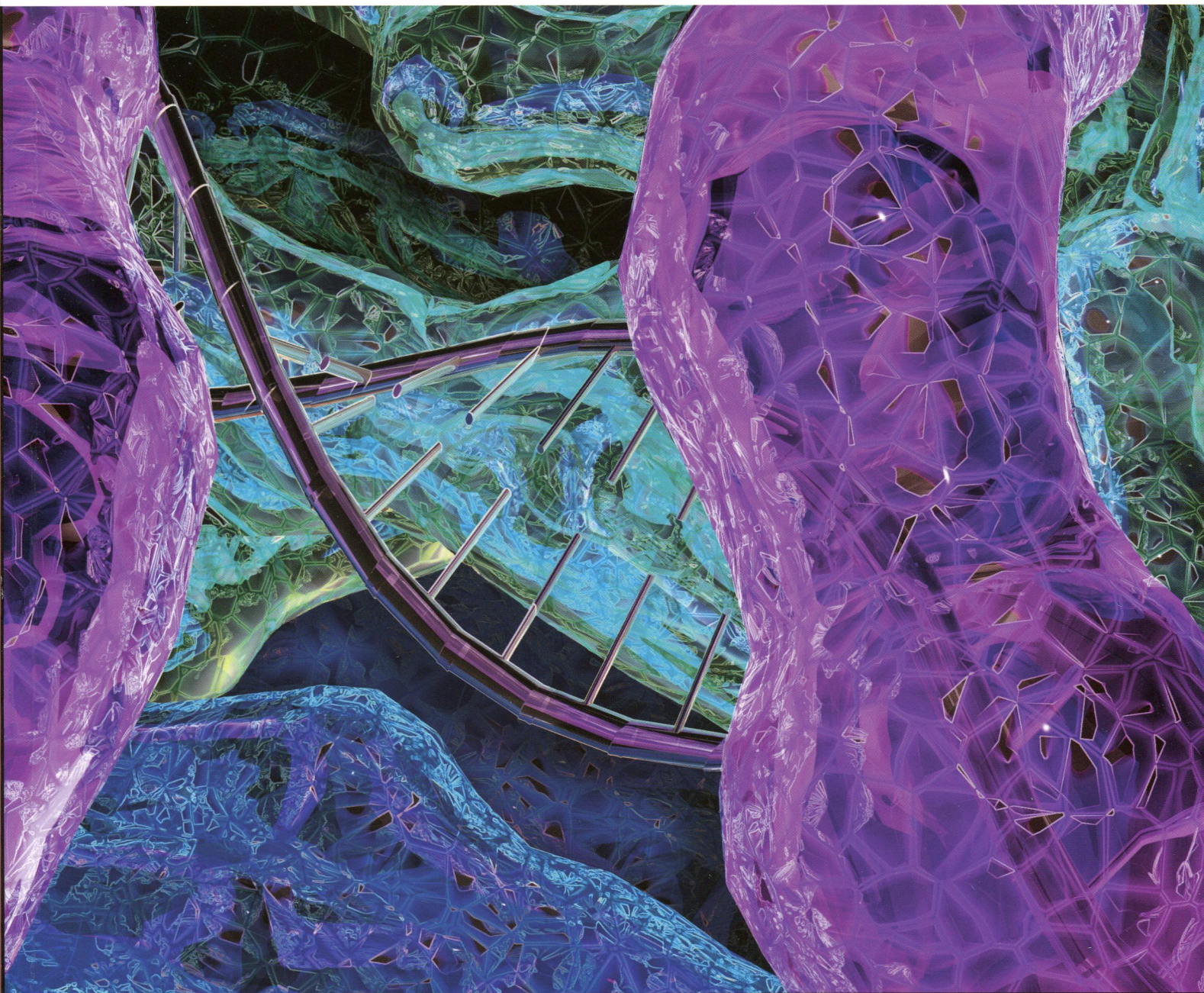
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# REVIEWS

may 2014 volume 15 no. 5  
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# GENETICS

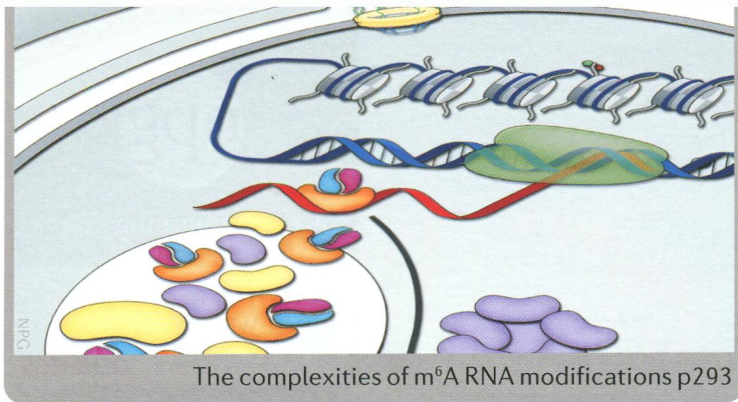


## GENOME EDITING OPTIONS

User's guide for ZFNs, TALENs and CRISPR tools

## Primate genomics

Evolutionary and functional insights from genome comparisons



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## REVIEWS

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ARTICLE

### Gene expression regulation mediated through reversible m<sup>6</sup>A RNA methylation

Ye Fu, Dan Dominissini, Gideon Rechavi and Chuan He

Diverse types of RNA in various species are modified by methylation to form N<sup>6</sup>-methyladenosine (m<sup>6</sup>A). This Review describes how progress in the characterization of m<sup>6</sup>A distributions and of proteins that 'write', 'erase' and 'read' this mark is revealing roles for reversible m<sup>6</sup>A methylation in dynamic gene expression control.

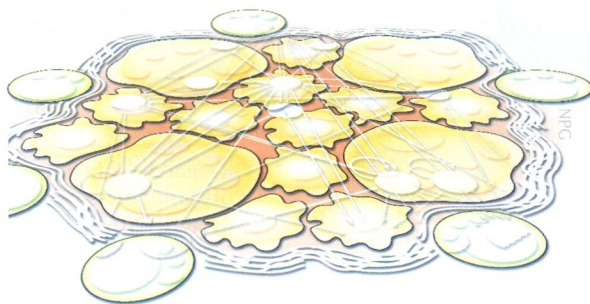
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### Genomic insights into tuberculosis

James E. Galagan

This Review describes how genomic technologies are providing novel insights into *Mycobacterium tuberculosis*, which is the causative agent of human tuberculosis. There has been progress in understanding the ancient evolutionary history of human-adapted *M. tuberculosis*, mutations underlying strain diversity and drug resistance, and the host-pathogen molecular interactions.



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### A guide to genome engineering with programmable nucleases

Hyongbum Kim and Jin-Soo Kim

Programmable nucleases — including ZFNs, TALENs and RGENs derived from the prokaryotic CRISPR-Cas system — enable targeted high-precision genome engineering. This Review summarizes current knowledge of nuclease-specific features, individual pros and cons, and approaches to improve the efficiency of these enzymes to help researchers to choose the most appropriate tool for various genome editing experiments and applications.

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### Statistical power and significance testing in large-scale genetic studies

Pak C. Sham and Shaun M. Purcell

This Review discusses the principles and applications of significance testing and power calculation, including recently proposed gene-based tests for rare variants.

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### Comparative primate genomics: emerging patterns of genome content and dynamics

Jeffrey Rogers and Richard A. Gibbs

Whole-genome assemblies of humans and non-human primates are yielding data on the evolutionary origins of the human genome, as well as insights into genetic similarities and differences between species used as models for disease-related research. This Review discusses current knowledge and opportunities for comparative primate genomics created by recent advances in genome sequencing technologies.

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Kevin V. Morris and John S. Mattick

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Xinxian Deng, Joel B. Berletch, Di K. Nguyen and Christine M. Disteche

RNA-directed DNA methylation: an epigenetic pathway of increasing complexity

Marjori A. Matzke and Rebecca A. Moshier

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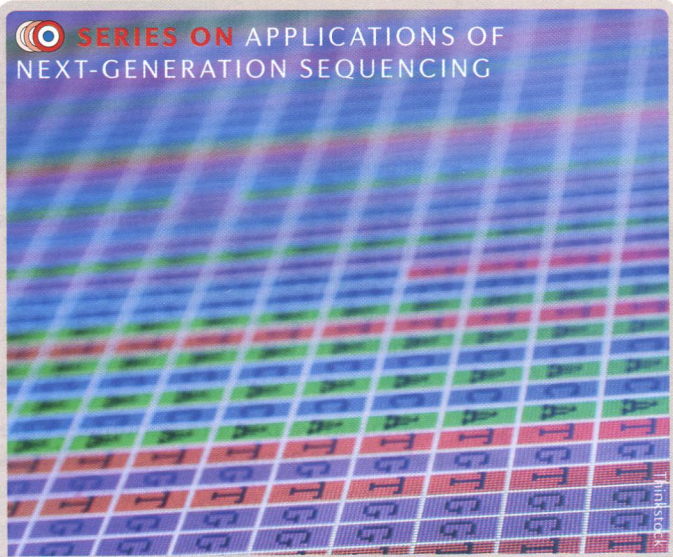
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Research Highlight on the loss of plastid genomes during plant evolution p288

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