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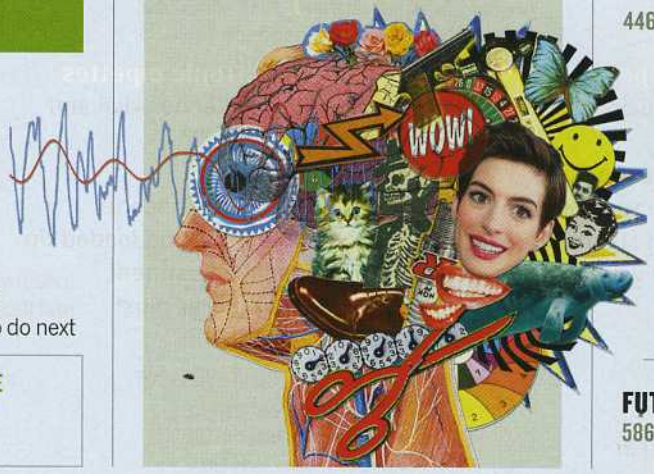

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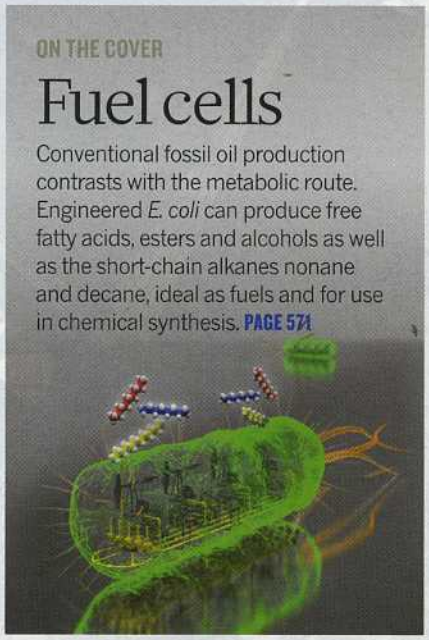

ON THE COVER

Fuel cells

Conventional fossil oil production contrasts with the metabolic route. Engineered *E. coli* can produce free fatty acids, esters and alcohols as well as the short-chain alkanes nonane and decane, ideal as fuels and for use in chemical synthesis. PAGE 571

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524 ASTRONOMY **A galaxy rapidly forming stars 700 million years after the Big Bang at redshift 7.51**
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567 CELL BIOLOGY **αTAT1 catalyses microtubule acetylation at clathrin-coated pits**
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580 CORRIGENDUM **APOBEC3B is an enzymatic source of mutation in breast cancer**
M B Burns et al.

580 CORRIGENDUM **Calving fluxes and basal melt rates of Antarctic ice shelves**
M A Depoorter et al.

580 CORRIGENDUM **Dietary intervention impact on gut microbial gene richness**
A Cotillard et al.

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PLANT DEVELOPMENT

Shoot now

The signals that govern shoot meristem activity in maize. PAGE 555

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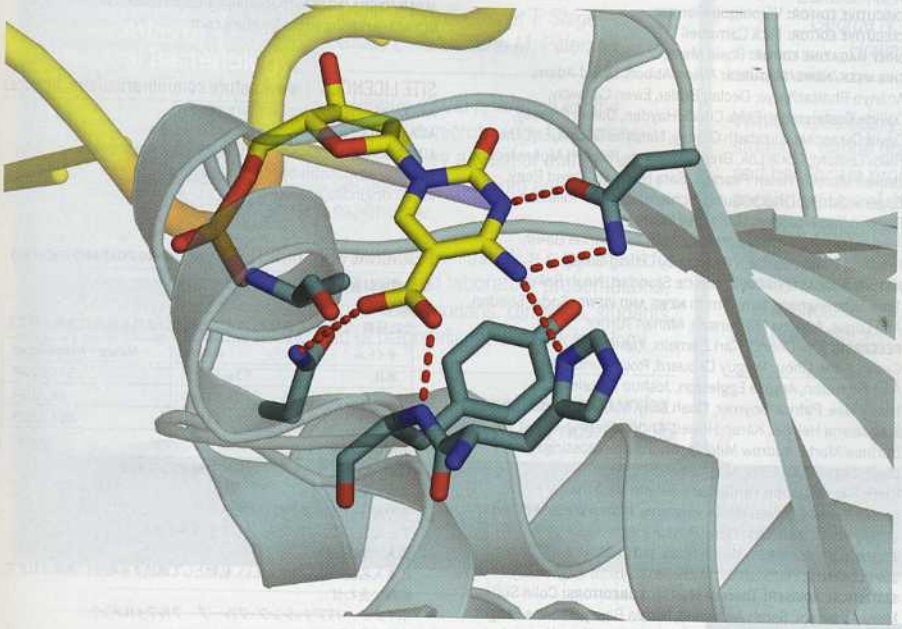
TRANSCRIPTION AND EPIGENETICS

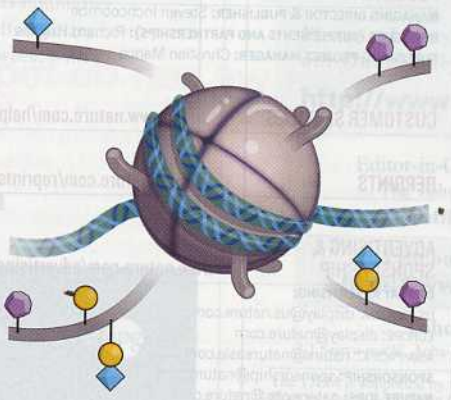


REVIEWS

462 Chromatin dynamics during cellular reprogramming
Reprogramming of somatic cells to pluripotency can be achieved by the combination of four transcription factors — Oct4, Klf4, Sox2 and c-Myc, known as OKSM. Induced pluripotency is an experimentally tractable system to dissect the transcriptional, chromatin and epigenetic mechanisms that underlie this remarkable cell-fate change, as well as the barriers that resist such changes in normal physiological settings. Reprogramming can also be achieved by methods such as somatic-cell nuclear transfer into oocytes and cell–cell fusion, and can be compared with biological processes such as germ-cell maturation and tumorigenesis.
Effie Apostolou & Konrad Hochedlinger

472 TET enzymes, TDG and the dynamics of DNA demethylation
DNA methylation is an epigenetic modification associated with gene silencing, and is thought to help shape cellular transcriptional programs during development. Loss of DNA methylation has been observed in various biological contexts, and we are now beginning to understand the mechanisms behind active DNA demethylation. The TET family enzymes can oxidize 5-methylcytosine to 5-hydroxymethylcytosine, and pathways to complete demethylation are being elucidated. The dynamics of DNA demethylation in various biological settings can now be examined from a fresh perspective.
Rahul M. Kohli & Yi Zhang

480 Chromatin proteins and modifications as drug targets
Post-translational modifications of histones, such as methylation and acetylation, are important in gene regulation, and histone-modifying enzymes are frequently altered in cancer. New small-molecule inhibitors are now being developed that target histone methyltransferases, histone demethylases or the bromodomain-containing proteins that interact with histone acetylation. These inhibitors are showing promise in preclinical research as potential therapeutics for cancer and inflammation.
Kristian Helin & Dashyant Dhanak



489 The nexus of chromatin regulation and intermediary metabolism
Cells and organisms must respond to changes in their environment, such as the availability of nutrients and energy. An emerging model suggests that transcription factors and chromatin regulators integrate environmental inputs to mediate homeostatic transcriptional responses. Most chromatin-modifying enzymes use cofactors or substrates that are metabolites in intermediary metabolism, and so these enzymes may sense metabolites and dynamically adapt transcriptional programs accordingly. Through such mechanisms, metabolites may influence the transcriptional programs involved in pluripotency, cancer and ageing.
Philipp Gut & Eric Verdin

499 Topology of mammalian developmental enhancers and their regulatory landscapes
DNA elements termed enhancers contain binding motifs for transcription factors and act at various distances from their target genes to precisely regulate them during development. Genomics studies have predicted that there are millions of these enhancers, forming complex regulatory landscapes. Chromosome-conformation studies are revealing that higher-order chromosome structures contribute to enhancer function and the physical interactions between enhancers and the promoters of target genes.
Wouter de Laat & Denis Duboule