IN BRIEF

DEVELOPMENT

Retroviruses as cell fate regulators

The authors used RNA sequencing to identify a transient population of cells that resemble two cell embryos within induced pluripotent stem cell and embryonic stem cell populations. This population is totipotent, which means that it is able to produce cells from both embryonic and extraembryonic tissues, and its transient formation is regulated by histone modifications. Furthermore, many of the activated two-cell-stage transcripts in this transient population have regulatory elements derived from endogenous retroviruses, suggesting that these foreign sequences can be key regulators of cell fate.

ORIGINAL RESEARCH PAPER Macfarlan, T. S. *et al.* Embryonic stem cell potency fluctuates with endogenous retrovirus activity. *Nature* **487**, 57–63 (2012)

MICROBIOLOGY

The Human Microbiome Project

A large project aimed at identifying the baseline of human microbial diversity has published a series of articles with the findings from the profiling of 15–18 different human sites from 242 healthy individuals. The project used a combination of 16S ribosomal sequencing and whole-genome sequencing. The articles published across the *PLoS* journals, *Nature* titles and *Genome Biology* vary from in-depth analyses of species composition and the metabolic pathways used by these microbes at various body sites to the development of new tools for these types of analyses.

ORIGINAL RESEARCH PAPERS The Human Microbiome Project DACC homepage: http://hmpdacc.org/pubs/publications.php

GENETIC INTERACTIONS

Improved yield through interaction studies under different conditions

Most studies of genetic interactions have measured a single phenotypic readout (usually growth rate in the case of *Saccharomyces cerevisiae*) under one set of experimental conditions, but several studies have recently generated networks using different phenotypes and conditions. This paper presents a systematic analysis of such data from *Saccharomyces cerevisiae* to assess the extent to which interaction networks vary. The authors show that using a greater range of conditions will increase insights from interaction studies, and they describe a method for helping to combine the networks that are generated.

ORIGINAL RESEARCH PAPER Michaut, M. & Bader, G. B. Multiple genetic interaction experiments provide complementary information useful for gene function prediction. *PLoS Comput. Biol.* **8**, e1002559 (2012)

GENE REGULATION

Transcription factors slide to find binding sites *in vivo*

In vitro studies have previously shown that transcription factors find their binding sites through a mechanism of 'facilitated' diffusion that combines three-dimensional diffusion with sliding along DNA. Using a single-molecule approach, Hammar *et al.* have now shown that this mechanism also occurs in living bacterial cells. They used a fluoroescently labelled *lac* repressor protein (LacI) and monitored its binding to the *lac* operator. They show that LacI slides on average 45 ± 10 bp, and in most cases it slides over the operator sequence at least once before binding to it. During evolution, transcription factors may need to maintain the ability to slide over non-specific sequences as well as to bind specifically.

ORIGINAL RESEARCH PAPER Hammar, P. *et al.* The *lac* repressor displays facilitated diffusion in living cells. *Science* **336**, 1595–1598 (2012)