

IN BRIEF

DNA METHYLATION**Plant immune system uses demethylation**

This study provides evidence that DNA methylation is a part of the immune response that plants mount against bacterial pathogens. Studying infection of *Arabidopsis thaliana* by *Pseudomonas syringae* and responses to a bacterial peptide, the authors found demethylation and transcriptional activation of some transposable elements and immune-response genes as a part of the antibacterial response. The demethylaton limits bacterial infection in leaves and seems to result from a combination of repression of transcriptional gene silencing factors and active demethylation.

ORIGINAL RESEARCH PAPER Yu, A. *et al.* Dynamics and biological relevance of DNA demethylation in *Arabidopsis* antibacterial defense. *Proc. Natl Acad. Sci. USA* 18 Jan 2013 (doi:10.1073/pnas.1211757110)

SYNTHETIC BIOLOGY**Small RNAs improve metabolic engineering**

These authors show how synthetic small RNAs (sRNAs) can be used to improve bacterial metabolic engineering. First, they developed an efficient approach to identifying target genes for which downregulation increases the production of a desired compound. They designed synthetic sRNAs against candidate genes and used these to identify combinations of strains and repressed targets with the highest levels of production. They also showed that engineered sRNAs can be used to fine-tune, rather than to knock out, target gene expression to generate better-performing strains.

ORIGINAL RESEARCH PAPER Na, D. *et al.* Metabolic engineering of *Escherichia coli* using synthetic small regulatory RNAs. *Nature Biotech.* 20 Jan 2013 (doi:10.1038/nbt.2461)

GENE EXPRESSION**Complete proteome for quantitative trait analysis**

Using mass spectrometry, Picotti *et al.* have generated an almost complete reference map of the proteome of *Saccharomyces cerevisiae*. They generated two complementary versions of the map: one that supports targeted measurements and another that supports discovery-based experiments. The authors applied this resource to yeast protein quantitative trait locus (pQTL) analysis, which has previously been limited by the difficulties of consistently detecting peptides across samples. Their analysis revealed novel pQTLs and also provided evidence of epistatic interactions and of co-inheritance of several genetic variants that influence the abundance of related proteins.

ORIGINAL RESEARCH PAPER Picotti, P. *et al.* A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. *Nature* 20 Jan 2013 (doi:10.1038/nature11835)

DISEASE GENETICS**Rare inherited mutations in autism**

The contribution of inherited deleterious mutations to the architecture of autism spectrum disorders (ASDs) has been unclear. Two new studies, using exome sequencing, have investigated this topic. Between them, they identify ASD-associated rare variants that are autosomal homozygous, autosomal compound heterozygous or hemizygous (on the X chromosomes of males). Some of the affected genes have not previously been implicated in ASDs, potentially providing new biological insights.

ORIGINAL RESEARCH PAPERS Lim, E. T. *et al.* Rare complete knockouts in humans: population distribution and significant role in autism spectrum disorders. *Neuron* **77**, 235–242 (2013) | Yu, T. W. *et al.* Using whole-exome sequencing to identify inherited causes of autism. *Neuron* **77**, 259–273 (2013)