# IN BRIEF

## MICROBIAL GENETICS

### Horizontal gene transfer of antibacterial genes

Horizontally transferred genes with wide-ranging antibacterial properties may prove useful as new sources of antibiotic drugs, a study in *eLife* suggests. Metcalf *et al.* identified a bacterial lysozyme gene family with an unprecedented spread through horizontal gene transfer across the tree of life and diverse ecological contexts: the gene encoding glycosyl hydrolase 25 muramidase was found in a number of bacterial species, in eukaryotes (specifically in several fungal species, a plant and an insect) and in archaea (specifically in a single-cell microbe that lives in hot, deep-sea vents). Recombinant archaeal lysozyme exhibited broad-spectrum, dose-dependent antibacterial action. Moreover, when co-cultured with bacteria, lysozyme gene transcription was increased in the archaeon. This finding lends further support to the hypothesis that the transferred muramidase functions as a potent antibacterial molecule.

**ORIGINAL RESEARCH PAPER** Metcalf, J. A. *et al.* Antibacterial gene transfer across the tree of life. *eLife* **3**, e04266 (2014)

## TECHNOLOGY

### DNase Hi-C — pitch-perfect chromatin mapping?

Researchers at the University of Washington have developed a new high-throughput method to map chromatin interactions genome-wide. Named DNase Hi-C, this methodology uses DNase I for chromatin fragmentation, thus overcoming limitations on efficiency and resolution imposed on previous methods such as conventional Hi-C, which uses restriction enzymes for fragmentation. Among other experiments, the team validated their approach in two human cell lines by coupling DNase Hi-C with a targeted DNA sequence capture technology to map fine-scale three-dimensional chromatin architecture of 998 promoters of genes encoding long intergenic non-coding RNAs. Expression of lincRNAs was found to be tightly controlled via super-enhancers and Polycomb repressive complex 2.

**ORIGINAL RESEARCH PAPER** Ma, W. *et al.* Fine-scale chromatin interaction maps reveal the *cis*-regulatory landscape of human lincRNA genes. *Nature Methods* http://dx.doi.org/10.1038/nmeth.3205 (2014)

## DEVELOPMENT

### Cell fate decisions in mammalian embryogenesis

Using single-cell RNA sequencing, researchers have analysed global gene expression in mouse embryos at multiple defined stages of development. In support of the 'asymmetric hypothesis', Biase *et al.* found that the individual cells in two-cell and four-cell embryos are not equivalent and that non-trivial, reproducible differences between them influence cell fate decisions. The researchers identified several protein-coding genes with bimodal expression in cells from the same embryo, including some encoding proteins in the WNT signalling pathway, which has a role in cell–cell communication. In a second study, Huang *et al.* support these findings using a bioinformatic approach: a model for time-variant clustering was used to analyse single-cell gene expression data from mouse pre-implantation embryos. In contrast to the 'equivalence hypothesis', which states that there are no quantitative differences between individual cells of an embryo before the 8-cell stage, the computational analysis suggests that decisions on cell lineage are made as early as the 4-cell stage in mice.

**ORIGINAL RESEARCH PAPERS** Biase, F. H. *et al.* Cell fate inclination within 2-cell and 4-cell mouse embryos revealed by single-cell RNA sequencing. *Genome Res.* **24**, 1787–1796 (2014) | Huang, W. *et al.* Time-variant clustering model for understanding cell fate decisions. *Proc. Natl Acad. Sci. USA* **111**, E4797–E4806 (2014)