

IN BRIEF

SMALL RNAS**MicroRNAs are trimmed by Nibbler**

Two studies have shown that the 3' ends of more than 25% of microRNAs (miRNAs) in *Drosophila melanogaster* undergo an extra processing step after loading into Argonaute 1 (AGO1). They found that a 3'-to-5' exonuclease called Nibbler trims miRNAs. This processing explains the 3' heterogeneity that was previously observed in miRNAs and reveals that the miRNA repertoire depends on proteins in addition to the known processing proteins Dicer and Drosha.

ORIGINAL RESEARCH PAPERS Han, B. W. *et al.* The 3'-to-5' exoribonuclease Nibbler shapes the 3' ends of microRNAs bound to *Drosophila* Argonaute1. *Curr. Biol.* 3 Nov 2011 (doi:10.1016/j.cub.2011.09.034) | Liu, N. *et al.* The exoribonuclease Nibbler controls 3' end processing of microRNAs in *Drosophila*. *Curr. Biol.* 3 Nov 2011 (doi:10.1016/j.cub.2011.10.006)

GENOME ORGANISATION**Bacterial three-dimensional genome architecture**

Using a combination of chromosome conformation capture carbon copy (5C), three-dimensional modelling and live cell imaging, the authors were able to resolve the three-dimensional architecture of the *Caulobacter crescentus* bacterial genome. They show the genome to be ellipsoidal with periodically arranged chromosome arms. The location of *parS* sequence elements dictated the subcellular location of the genome; however, artificially altering this location had little effect on large-scale gene expression.

ORIGINAL RESEARCH PAPER Umbarger, M. A. *et al.* The three-dimensional architecture of a bacterial genome and its alteration by genetic perturbation. *Mol. Cell* 44, 252–264 (2011)

DISEASE GENETICS**Harnessing electronic medical records**

Using electronic medical records (EMRs) as a source of phenotypic information is a potentially cost-effective way of identifying disease-associated genetic variants. These authors developed an algorithm to identify cases and controls from the EMRs of different institutions and applied this to a genome-wide association study for hypothyroidism. They identified significant associations with variants in forkhead box E1 (*FOXE1*). A phenome-wide association study also identified other conditions associated with the same locus.

ORIGINAL RESEARCH PAPER Denny, J. C. *et al.* Variants near *FOXE1* are associated with hypothyroidism and other thyroid conditions: using electronic medical records for genome- and phenome-wide studies. *Am. J. Hum. Genet.* 89, 529–542 (2011)

GENE EXPRESSION**Uncovering proteome complexity**

This study provides new insights into proteome complexity and translational dynamics. The authors combined a modified ribosome-profiling technique with the use of a drug that stalls ribosomes precisely at translation initiation sites. Working in mouse embryonic stem cells, they identified large numbers of previously unannotated translation products, uncovered extensive ribosome pausing and defined a new class of short RNAs that are translated to produce small proteins.

ORIGINAL RESEARCH PAPER Ingolia, N. T. *et al.* Ribosome profiling of mouse embryonic stem cells reveals the complexity and dynamics of mammalian proteomes. *Cell* 11 Nov 2011 (doi:10.1016/j.cell.2011.10.002)