

IN BRIEF

TECHNOLOGY**Stop-and-go acrobatics through nanopores**

Nanopore devices for DNA sequencing involve passing a DNA strand through a membrane-embedded nanometre-scale pore and detecting the accompanying changes in electrical current that are characteristic of each nucleotide. Using computer simulations, researchers show they can control the speed of DNA going through a nanopore in a graphene membrane by applying an electrical charge to the graphene. The graphene forces DNA into conformations depending on the nucleotides in the pore and their modifications, such as DNA methylation, which could be exploited to provide insights into epigenetics.

ORIGINAL RESEARCH PAPER Shankla, M. & Aksimentiev, A. Conformational transitions and stop-and-go nanopore transport of single-stranded DNA on charged graphene. *Nature Commun.* **5**, 5171 (2014)

DISEASE GENETICS**Zebrafish models ultra-rare X-linked disease**

By combining next-generation sequencing and model organism research, researchers have pinpointed the pathogenic variant responsible for an extremely rare neurodevelopmental X-linked disorder that causes small head size (microcephaly) and growth retardation in three affected males of one family. After locating the candidate mutation in the X-chromosomal *RPL10* gene, which encodes the 60S ribosomal protein L10, the team found that suppression of *rpl10* expression in zebrafish recapitulated the human phenotype of microcephaly owing to reduced translation and increased apoptosis in the brain.

ORIGINAL RESEARCH PAPER Brooks, S. S. *et al.* A novel ribosomopathy caused by dysfunction of RPL10 disrupts neurodevelopment and causes X-linked microcephaly in humans. *Genetics* **198**, 723–733 (2014)

MICROBIAL GENETICS**Selective killing using programmable Cas9**

Bikard *et al.* have developed sequence-specific antimicrobials based on the bacterial CRISPR–Cas immune system. The reprogrammed Cas9 nuclease, guided by small RNAs to specific virulence gene loci where it mediates DNA cleavage, was able to selectively kill virulent *Staphylococcus aureus* while leaving other members of the community (including avirulent strains of the same species) intact, which could then colonize the niche and limit the growth of pathogenic bacteria. This approach could be adapted to target plasmid-borne antibiotic resistance genes, thus preventing the spread of resistance in complex bacterial populations.

ORIGINAL RESEARCH PAPER Bikard, D. *et al.* Exploiting CRISPR–Cas nucleases to produce sequence-specific antimicrobials. *Nature Biotech.* <http://dx.doi.org/10.1038/nbt.3043> (2014)

PLANT GENOMICS**High-throughput phenotyping of rice growth traits**

A high-throughput phenotyping tool enables the study of rice traits during the growth period and after harvest. Yang *et al.* combined imaging techniques with a yield traits scorer to automatically screen for 15 agronomic traits, including two newly defined traits — plant compactness and grain-projected area — that cannot be identified by manual measurement. Together with genome-wide association studies, this tool has the potential to dissect the genetic architecture of complex traits, thus providing insights into crop breeding.

ORIGINAL RESEARCH PAPER Yang, W. *et al.* Combining high-throughput phenotyping and genome-wide association studies to reveal natural genetic variation in rice. *Nature Commun.* **5**, 5087 (2014)