METHODS IN BRIEF

GENOMICS

Finding noncoding RNA partners

RNA has evolved to play many roles in the cell, and RNA antisense purification (RAP) has been used to probe its interactions with DNA. Engreitz *et al.* now perform a combination of *in vivo* cross-linking, pulldown with biotinylated antisense oligonucleotides and RNA sequencing to map intermolecular RNA interactions in a method they call RAP-RNA. The method uses a psoralen cross-linker to capture only direct RNA-RNA interactions, formaldehyde to capture indirect RNA-RNA interactions via protein intermediates, or a combination of formaldehyde and the strong protein cross-linker disuccinimidyl glutarate to capture very indirect interactions. High-resolution maps of interactions at cross-link sites indicated that U1 small nuclear RNA, a spliceosome factor, binds new transcripts at 5′ splice-site motifs and that the RNA Malat1, found in nuclear speckles, binds to mRNA via RNA-binding proteins.

Engreitz, J.M. *et al. Cell* **159**, 188–199 (2014).

NEUROSCIENCE

Electrophysiology in a virtual world

Visually guided animal behaviors and their underlying neural representations are ideally studied in an environment that is as close to reality as possible. Aronov and Tank describe a complete virtual reality system for rats that allows the animals to rotate and walk on a treadmill in any direction while at the same time allowing the researchers to perform extracellular recording of the neural activity in these animals. With this system, the researchers recorded the activity from thousands of neurons while the rats explored their environment or pursued sites with a visible or hidden reward. In principle, it will be feasible to analyze the response of neurons even to stimuli that are not possible in the real world.

Aronov, D. & Tank, D.W. *Neuron* **84**, 442–456 (2014).

PROTEOMICS

Profiling the N-myristoylated proteome

Little is known about the extent of N-myristoylation in the human proteome. This co- and post-translational modification, which has been implicated in diseases ranging from bacterial infection to epilepsy to cancer, is catalyzed by the N-myristoyltransferase enzyme that transfers myristate to the N-terminal glycine residue of a substrate protein. Thinon *et al.* now report a chemical proteomic approach that is highly specific for detecting this modification. They used an alkyne-tagged myristate analog that is metabolically incorporated by cells, enabling N-myristoylated proteins to be enriched via affinity purification for mass spectrometry analysis. By treating one population of myristate analog–labeled human cells with increasing concentrations of an N-myristoyltransferase inhibitor and performing a quantitative proteomic analysis, they could determine which putative N-myristoylated proteins were true N-myristoyltransferase substrates.

Thinon, E. *et al. Nat. Commun.* **5**, 4919 (2014).

SYNTHETIC BIOLOGY

Bow ties for mammalian cells

Many biological systems are based on 'bow-tie' architectures that integrate multiple inputs, synthesize them with a much smaller number of processes (the knot of the bow tie) and result in highly diverse outputs. This structure allows for an efficient use of resources and a trade-off between robustness and complexity. Prochazka *et al.* now apply a synthetic bow tie to mammalian cells to report on microRNA levels. In a reversible configuration, the bow tie uses the input signal of up- or downregulated microRNAs to control the expression of an activator that in turn regulates the expression of two output reporter genes. In a second configuration, the bow tie permanently records the microRNA inputs by having the activator control a recombinase that permanently switches on reporter expression. The components of bow ties are modular and can be scaled to accommodate additional inputs and outputs.

Prochazka, L. *et al. Nat. Commun.* **5**, 4729 (2014).