METHODS IN BRIEF

CELL BIOLOGY

Improved RNA interactomes

RNA molecules, often part of larger protein networks, regulate many cellular processes such as the alteration of chromatin structure, transcription and DNA damage responses. To characterize such networks, Conrad *et al.* modified the established RNA interactome capture technique (IC), which relies on cross-linking of RNAs and their protein targets by UV light followed by poly-A capture of the RNA and identification of the bound proteins by mass spectrometry. The modification to serial IC adds a second purification step during which contaminating DNA and DNA-binding proteins are removed and non-cross-linked interactions are eliminated. The authors characterized the nuclear RNA interactome of human cells and found that only 48% of proteins contained classical RNA-binding domains. They identified proteins with dual specificity for DNA and RNA and investigated their role in transcriptional regulation, splicing and DNA repair.

Conrad, T. *et al. Nat. Commun.* **7**, 11212 (2016).

NANOBIOTECHNOLOGY

Nanopores for multiplexed protein sensing

Nanopores are proving to be useful tools not only for DNA sequencing, but also for protein analysis. Globular proteins present an analytical challenge because different proteins show hardly any differences in current modulation when passing through a nanopore. Chemical selectivity must therefore be imparted in some way in order for globular proteins to be distinguishable. Bell and Keyser report a promising solution: they used DNA nanotechnology to construct long DNA molecules with a series of attached 'dumbbell' hairpins in unique barcoded designs. Each barcoded DNA was modified with a unique antigen specific for one of four different antibodies of the same isotype. The DNA thus carried the bound antibody through the nanopore, and the barcode was read by its distinct current blockade signal, demonstrating the potential for multiplexed protein sensing.

Bell, N.A.W. & Keyser, U.F. *Nat. Nanotechnol.* http://dx.doi.org/10.1038/nnano.2016.50 (2016).

GENOMICS

Variants that change transcription factor binding

It is straightforward to find the genome-wide binding sites of transcription factors (TFs) using chromatin immunoprecipitation (ChIP), but it remains somewhat difficult to predict how single-nucleotide variants (SNVs) affect such binding. Tehranchi *et al.* devised a pooling-based ChIP-seq approach to find binding quantitative trait loci (bQTLs). Comparing allele frequency in the pool before and after ChIP allowed the researchers to identify alleles with high or low affinity for a TF. Looking at five TFs in a pool of 60 human cell lines, they identified 3% of SNVs as bQTLs. Some bQTLs change the binding of pioneer factors, such as CTCF, which regulates chromatin structure, and thus these bQTLs also affect the recruitment of other TFs as well as long-range chromatin interactions.

Tehranchi, A.K. *et al. Cell* **165**, 1–12 (2016).

IMAGING

Open-source software for structured illumination

Structured illumination microscopy (SIM) is a super-resolution imaging approach that roughly doubles the resolution that can be achieved using diffraction-limited microscopes. In SIM, samples are imaged with a special illumination pattern. After acquisition, the images are processed with an algorithm that allows super-resolution information to be extracted from the individual images. Although software exists for commercial SIM instruments, few software tools are available for users who build their own. To make SIM more broadly accessible, Müller *et al.* developed fairSIM (free analysis and interactive reconstruction for structured illumination microscopy). The fairSIM reconstruction software is free and open-source, and it works within ImageJ or FIJI for easy integration into existing image acquisition and analysis methods.

Müller, M. *et al. Nat. Commun.* **7**, 10980 (2016).