TOOLS IN BRIEF

PROTEOMICS

A human tissue proteomic map

Uhlén *et al.* present a near-complete map of the human tissue proteome. This comprehensive map, covering all major organs and tissues in the human body and 90% of all putative protein-coding genes, was constructed using quantitative transcriptome profiling data from RNA sequencing and protein profiling data from tissue microarray–based immunohistochemistry. The analysis revealed that almost half of all protein-coding genes are expressed in all tissues, suggesting that these proteins are responsible for 'housekeeping' functions. The researchers also examined global traits of the secretome, membrane proteome, regulatory proteome, isoform proteome, cancer proteome and druggable proteome. All of the data are available in a free, interactive web resource as part of the Human Protein Atlas (http://www.proteinatlas.org/), which should be a valuable tool for studying both basic human biology and disease.

Uhlén, M. *et al. Science* **347**, 1260419 (2015).

GENOMICS

Inducing CRISPR

Many genetically engineered mouse models have been generated with the CRISPR (clustered, regularly interspaced, short palindromic repeats)-Cas9 system, but embryonic lethality caused by some mutations has prevented the study of their function in adult animals. Dow *et al.* circumvented this bottleneck by expressing a doxycycline-inducible Cas9 nuclease or nickase together with specific guide RNAs in mouse embryonic stem cells (ESCs). Induction of Cas9 expression led to biallelic modifications in almost 50% of the targeted tumor suppressor genes. Mice generated from these ESCs showed hyperplastic lesions in their intestines, recapitulating a phenotype seen with the disruption of tumor suppressor genes in adult animals. This inducible CRISPR system can be multiplexed to up to six guide RNAs and will enable rapid *in vivo* loss-of-function studies.

Dow, L.E. *et al. Nat. Biotechnol.* doi:10.1038/nbt.3155 (18 February 2015).

SENSORS AND PROBES

Stable linear probes for cellular mRNA labeling

Specific labeling of RNAs in living cells can be technically challenging. Asanuma *et al.* describe a new type of linear probe for fluorescent labeling of target mRNAs that is both highly specific and resistant to nuclease activity. This probe consists of nucleobases built on a D-threoninol scaffold that is modified at multiple positions with perylene moieties. In solution, the probe is linear, and the perylene fluorescence is self-quenched. Upon target binding, however, the probe becomes brightly fluorescent. For use in cells, the probe was also modified with an anthraquinone to further quench the perylene. The researchers tested probes targeting DsRed mRNA in live mammalian cells. They observed blue fluorescence of the probe only in cells expressing DsRed, demonstrating that this probe should enable live-cell imaging of mRNA.

Asanuma, H. *et al. Angew. Chem. Int. Ed. Engl.* doi:10.1002/anie.201411000 (17 February 2015).

GENE EXPRESSION

StringTie assembles transcriptomes

Transcriptomes in higher eukaryotes are highly complex, with coding and noncoding transcripts subject to intricate regulation and alternative splicing. High-throughput RNA sequencing (RNA-seq) can rapidly produce short reads that make up a transcriptome, but unambiguous assembly of the correct transcripts is difficult. Pertea *et al.* developed a *de novo* read assembly approach that simultaneously assembles transcripts and assesses their expression level. In a comparison with the popular RNA-seq assembly algorithm Cufflinks, StringTie assembled over 50% more transcripts on data from human blood. The researchers also demonstrated its higher accuracy for assembly and quantitation of transcripts—without loss of sensitivity and precision—relative to the accuracies of competing algorithms.

Pertea, M. *et al. Nat Biotechnol.* **33**, 290–295 (2015).

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