RESEARCH HIGHLIGHTS

TOOLS IN BRIEF

PROTEOMICS

Cell-specific proteomics with SORT-E

In order to effectively study differentiated cell and tissue function, it is necessary to use approaches that target specific cell types. Elliott *et al.* describe stochastic orthogonal recoding of translation with enrichment (SORT-E), a method for cotranslationally tagging specific, genetically targeted cell proteomes using a cyclopropene-containing unnatural amino acid that is incorporated in response to diverse codons. A tetrazine–biotin probe is covalently conjugated to the cyclopropene-based amino acid, enabling the enrichment of tagged proteins via streptavidin affinity resin, which is then followed by mass spectrometry analysis for protein identification. The authors applied the method to identify newly synthesized proteins in *Drosophila melanogaster* ovary germ cells. The approach should be particularly useful for following cell-specific proteomes during development or disease progression.

Elliott, T.S. *et al. Cell Chem. Biol.* **23**, 805–815 (2016).

NEUROSCIENCE

An expression atlas of the developing macaque brain

The intricacies of brain development are impossible to study in humans, but nonhuman primates such as macaques can serve as proxies. Bakken *et al.* undertook a detailed study of monkey brain development at the transcriptome level. The researchers combined magnetic resonance imaging, histology, *in situ* hybridization of select marker genes, and microarray-based transcriptional profiling of laser-captured single cells to assemble a transcriptional atlas of the macaque brain from embryonic and postnatal development to early adulthood. This resource can serve as a reference for *in vitro* studies of neural development or for studies into brain dysfunction. Technological advances in single-cell studies are expected to further enrich this resource.

Bakken, T.E. *et al. Nature* **535**, 367–375 (2016).

GENOME EDITING

Showdown between Cas9 and Cpf1

Most genome editing with the CRISPR system to date has been carried out with the type II nuclease Cas9 from *Streptococcus pyogenes*. Recently, another type II nuclease, Cpf1, was introduced with features that SpCas9 is lacking. Cpf1 requires only a 42-nt short CRISPR RNA (crRNA) to find its target, instead of the ~100-nt guide RNA for SpCas9, and it recognizes a protospacer-adjacent motif (PAM) that is 5′ instead of 3′ of the target site. Kleinstiver *et al.* have now compared the two nucleases and found Cpf1 to be efficient and highly specific in human cells, with rare off-target cleavage. Systematically introducing mutations into the crRNA showed that mismatches at the 5′ end are not tolerated, whereas mismatches at the very 3′ end of the crRNA have less of an effect on cleavage. This high specificity makes Cpf1 a candidate for therapeutic applications down the line.

Kleinstiver, B.P. *et al. Nat. Biotechnol.* **34**, 869–874 (2016).

MICROSCOPY

Super-resolution imaging in live fly larvae with RESOLFT

RESOLFT nanoscopy is a super-resolution technology that requires only low levels of light, making it particularly suitable for live imaging. Schnorrenberg *et al.* applied the technology for the first time in live animals to visualize microtubules. The researchers generated transgenic flies expressing an rsEGFP2–α-tubulin fusion and imaged labeled microtubules in a variety of different cell types and at different depths. As expected, images acquired with RESOLFT nanoscopy were superior to images obtained with standard confocal microscopy. Because of the relatively low light levels required for RESOLFT nanoscopy, the researchers were able to acquire time-lapse recordings, thereby visualizing the dynamic changes of the microtubule cytoskeleton in larval body wall muscles, but without inducing apparent phototoxicity.

Schnorrenberg, S. *et al. Elife* **5**, e15567 (2016).