TOOLS IN BRIEF

CELL BIOLOGY

Finding more ribozymes

To understand evolution, it is important to have a comprehensive understanding of the possible catalytic roles RNA can play, roles that have been largely taken over by proteins. Only 11 classes of ribozymes have been validated to date, and only a few members of the six classes that show self-cleaving activity have known biological functions. To expand the known repertoire of ribozymes, Weinberg *et al.* devised a computational strategy that takes advantage of the fact that known self-cleaving ribozymes are located close to each other and to certain protein-coding genes. Looking for conserved secondary structures in these genomic locations led the researchers to identify new variants of the hammerhead and hepatitis delta virus ribozymes as well as entirely new classes of ribozymes, which they named twister sister, hatchet and pistol.

Weinberg, Z. *et al. Nat. Chem. Biol.* **11**, 606–610 (2015).

SENSORS AND PROBES

Fluorescent proteins for diverse environments

Fluorescent proteins are widely used to label intracellular targets, but their performance can be affected by subcellular conditions. The oxidizing environment of the mammalian endoplasmic reticulum is particularly challenging because it promotes disulfide-bond formation between cysteines present in fluorescent proteins. Costantini *et al.* address this issue by engineering versions of blue, cyan, yellow and green fluorescent proteins that lack native cysteine residues. These changes were not straightforward; for example, cysteine-to-serine substitutions rendered the fluorescent proteins dark. Interestingly, the team found that cysteine-to-valine substitutions, along with additional mutations, led to fluorescent proteins that fold well in the lumen of the endoplasmic reticulum and retain much of the brightness of the parent proteins. These tools will be useful for multicolor studies of proteins in oxidizing environments.

Costantini L.M. *et al. Nat. Commun.* **6**, 7670 (2015).

CELL BIOLOGY

A light switch for microtubule dynamics

Mitosis, motility and transport processes in the cell all rely on microtubule growth and shrinkage. The drugs paclitaxel and colchicine are popular tools for studying microtubule dynamics, but their actions are not immediately reversible and cannot be spatially confined to individual cells within a tissue or culture. Borowiak *et al.* have overcome these drawbacks by creating photoswitchable compounds that inhibit microtubule polymerization. When illuminated with ultraviolet or violet light, these photostatins are active and inhibit microtubule dynamics, and they can be switched off with green light exposure. By targeting light to the cells of interest, the researchers could spatially confine drug action. They demonstrated that these photostatins can cause mitotic arrest in cell culture and in *Caenorhabditis elegans* embryos.

Borowiak, M. *et al. Cell* **162**, 403–411 (2015).

PROTEOMICS

Introducing the BioPlex network

Proteins carry out their functions by interacting with other proteins in the cell. Affinity purification–mass spectrometry (AP-MS) has proven to be a valuable technique for detecting such interactions. As part of an effort to profile the entire collection of human open reading frames, Huttlin *et al.* performed a large-scale systematic AP-MS analysis of 2,594 human protein 'baits', detecting 23,744 interactions between 7,668 proteins in HEK293T cells. The resulting interactome network, which the authors term BioPlex, can be explored via a graphical viewer. They showed that the BioPlex network had nearly perfect overlap with protein complexes annotated in the CORUM mammalian protein database but also detected thousands of new interactions. BioPlex can be used to predict subcellular localization; to characterize the function of 'orphan' proteins, which do not belong to a known network; and to validate interaction subnetworks.

Huttlin, E.L. *et al. Cell* **162**, 425–440 (2015).