TOOLS IN BRIEF

GENOMICS

Self-limiting Cas9

It is in the interest of specificity to limit the active time of the nuclease Cas9 when using CRISPR technology for genome editing. The shorter the duration of Cas9 activity, the less likely the enzyme is to cut at sites other than the intended target. Petris *et al.* developed SLiCES (self-limiting Cas9 circuit for enhanced safety and specificity), a genetic circuit in which a guide RNA targeting Cas9 to its intended site is coexpressed with a guide RNA that targets Cas9 itself and thus inactivates it. All components of SLiCES are delivered to cells via a lentiviral vector system and result in a several-fold increase in the specificity of several guide RNAs with known off-target activities. SLiCES can easily be adapted for other Cas species.

Petris, G. *et al. Nat. Commun.* **8**, 15334 (2017).

STEM CELLS

Functional blood progenitors for mouse and man

Blood research and therapeutics for blood disorders would greatly benefit from a ready source of stem and progenitor cells. Although hematopoietic stem cells (HSCs) have been produced by many routes and from many sources, they generally fail to exhibit long-term engraftment in stem-cell-depleted bone marrow or to generate functional immune cells. Sugimura *et al.* screened transcription factors in human pluripotent-stem-cell-derived hemogenic endothelium (a blood-producing fetal tissue) and identified a set of seven that confer HSC-like long-term engraftment in a mouse host. Lis *et al.* started with endothelial cells from adult mice and used a combination of four transcription factors and coculture with an inductive vascular niche to generate HSCs that exhibit long-term engraftment, as well as antigen-dependent adaptive immune function. The two studies bring the greatly anticipated prospect of cultured blood much closer to reality.

Lis, R. *et al. Nature* **545**, 439–445 (2017).

Sugimura, R. *et al. Nature* **545**, 432–438 (2017).

SYSTEMS BIOLOGY

The BioPlex network, 2.0

Most proteins do not act in isolation, but instead carry out their functions by interacting with other proteins in the cell. A key technology for identifying such interactions is affinity purification coupled with mass spectrometry (AP-MS), where a 'bait' protein is affinity-tagged, and, after pulldown, captured 'prey' proteins are identified by MS. In 2015, researchers presented BioPlex, a large-scale, systematic AP-MS analysis that detected nearly 24,000 interactions. Huttlin *et al.* now present BioPlex 2.0, a substantial further effort that reveals more than 56,000 interactions and covers more than 25% of human protein-coding genes. The authors additionally performed several biological analyses, identifying, for example, ~1,300 protein communities that represent diverse cellular activities, and 442 communities associated with disease. The data and a graphical viewer are available to the community.

Huttlin, E.L. *et al. Nature* **545**, 505–509 (2017).

SENSORS AND PROBES

Supramolecular assemblies for NIR II imaging

Imaging in the near-infrared (NIR) II region (1,000–1,700 nm) is potentially useful for deep tissue imaging, as light scattering and autofluoresence are minimized at longer wavelengths. However, probes for such imaging often suffer from poor photophysical properties, such as low quantum yields. Antaris *et al.* built on previous work with donor-acceptor-donor dyes that fluoresce in the NIR range to develop a bright new NIR II probe for *in vivo* imaging. By changing functional groups on a previously developed dye, the group produced the dye CH-4T, which, when mixed with plasma proteins in the blood, spontaneously forms brightly fluorescent supramolecular assemblies. The researchers demonstrate that the probe is useful for vascular imaging and for resolving cardiac cycles in living mice.

Antaris, A.L. *et al. Nat. Commun.* **8**, 15269 (2017).