TOOLS IN BRIEF

SYNTHETIC BIOLOGY

Speaking the same synthetic language

As in other engineering fields, progress in synthetic biology depends on the exchange of parts and designs by researchers and will be most effective if designs adhere to common standards. A group of experimental and computational researchers from many different institutions in several countries, coordinated by Herbert Sauro from the University of Washington, describes such a data standard: the Synthetic Biology Open Language (SBOL). SBOL uses standard graphical notations—for example, for promoters, 5′ untranslated regions, coding sequence and terminators—to describe the structure of genetic designs. Software support allows developers of computational tools to incorporate SBOL. The participants stress the open nature of SBOL: any researcher in the field may join the Developers Group, and all information is freely accessible.

Galdzicki, M. *et al. Nat. Biotechnol.* **32**, 545–550 (2014).

GENE EXPRESSION

An atlas of fruit fly enhancer activity

Gene expression patterns during organismal development are controlled by regulatory sequences in the genome known as enhancers. In recent work, Kvon *et al.* describe a genome-wide study of enhancer activity during fruit fly embryogenesis. They assessed gene expression patterns in developing fly embryos by applying high-throughput *in situ* hybridization to a collection of transgenic fly lines, each bearing a *GAL4* transcriptional reporter under the control of an enhancer candidate (a 2-kilobase fragment of genomic DNA). The collection covers 13–14% of the noncoding and nonrepetitive genome. Almost half the candidate enhancers are active in the embryo, the authors report, and a substantial percentage of them regulate distal genes. The resulting collection of annotated expression patterns and computationally identified *cis*-regulatory motifs are available to other researchers.

Kvon, E.Z. *et al. Nature* doi:10.1038/nature13395 (1 June 2014).

NEUROSCIENCE

A magic wand for optogenetics

To unravel the function of different brain subregions in a neural circuit, spatially selective and user-defined optogenetic control over these subregions is desirable. To achieve this goal, Pisanello *et al.* developed multipoint-emitting optical fibers. The tapered ends of these fibers are gold coated, with the exception of some small windows along the tip of the fiber. The researchers directed light emission to different windows by capitalizing on the behavior of light at reflective surfaces and by simply changing the input angle of a laser beam into the optical fiber. In the mouse striatum or cortex, the optogenetic activation of GABAergic neurons in different subregions led to the activation of different populations of neurons. This tool provides a versatile option for optically manipulating neural circuits.

Pisanello, F. *et al. Neuron* **82**, 1245–1254 (2014).

STRUCTURAL BIOLOGY

A cross-linking reagent for acidic residues

The combination of chemical cross-linking and mass spectrometry is proving useful for helping to elucidate the structure of protein complexes. With mass spectrometry, the locations of cross-linked sites can be unambiguously identified, providing spatial information about the arrangement of subunits in a complex. Current chemical cross-linking reagents typically target the primary amine moieties found on lysine residues. Leitner *et al.* now show that a reaction combining homobifunctional dihydrazide molecules with a coupling reagent can be used to cross-link the acidic residues aspartic acid and glutamic acid. As test cases, they studied the chaperonin TRiC and the 26S proteasome complexes. Not only does the acidic residue cross-linking reaction provide an alternative to lysine cross-linking, it provides orthogonal distance restraints, which expands the amount of structural information that can be obtained.

Leitner, A. *et al. Proc. Natl. Acad. Sci. USA* **111**, 9455–9460 (2014).