TOOLS IN BRIEF

BIOPHYSICS

High-throughput optical trapping

Optical trapping is a powerful approach for making single-molecule biophysical measurements. These laser-based tools are limited, however, to manipulating one molecule at a time. Soltani *et al.* describe a new platform that allows high-throughput optical trapping on a chip, based on a nanophotonic standing-wave array. In a fluidic trapping region of the chip, exposed waveguides form stable optical traps at the antinodes of a standing-wave evanescent field. This configuration allows the laser beam to be recycled, forming an array of optical traps, without increasing laser power. An integrated electric microheater enables controlled trapping array repositioning. The researchers demonstrated their platform by sorting single DNA molecules suspended between two trapped beads, showing promise towards high-throughput analysis of single biochemical reactions.

Soltani, M. *et al. Nat. Nanotechnol.* **9**, 448–452 (2014).

SYSTEMS BIOLOGY

A plant membrane–linked interactome

A large subset of the interactome—the set of all physical interactions between proteins—remains unknown for most species. Identifying potential interactors of membrane proteins is particularly challenging. Jones *et al.* now use the established yeast split-ubiquitin assay to screen for the interactions of more than 3,000 membrane proteins from *Arabidopsis*, between one another and between the membrane proteins and over 1,000 cytosolic signaling factors. The 30,000 interactions identified, which constitute less than 1% of all tested pairs, were further validated in a secondary screen, yielding a set of about 12,000 interactions termed the Membrane-linked Interactome Database version 1 (MIND1). This data set contains many previously unknown interactions and should prove a useful resource for the study of membrane-protein function in *Arabidopsis*.

Jones, A.M. *et al. Science* **344**, 711–716 (2014).

STRUCTURAL BIOLOGY

Displaying membrane proteins for cryo-EM

Membrane proteins are tricky for structural biologists to handle because they typically require laborious and expensive solubilization, purification and reconstitution approaches that usually result in very low protein yields and may compromise protein function. Zeev-Ben-Mordehai *et al.* used a simple yet elegant approach to display a membrane protein on cell-derived membrane vesicles in the topologically correct orientation. Overexpressing the target resulted in the accumulation of target-enriched, membrane-derived extracellular vesicles. The vesicles could then be isolated by differential centrifugation and were immediately ready for three-dimensional structural analysis by cryo-electron microscopy (cryo-EM). The approach enabled the researchers to determine a cryo-EM three-dimensional structure for a *Caenorhabditis elegans* cell-cell fusion protein, epithelial fusion failure 1 (EFF-1), and led them to propose a model for EFF-1–mediated fusion.

Zeev-Ben-Mordehai, T. *et al. Nat. Commun.* **5**, 3912 (2014).

PROTEOMICS

Cell-of-origin proteomics

To understand cell-cell communication, methods for detecting cell-specific protein signaling in coculture are needed. Gauthier *et al.* solved this in part with their cell type–specific labeling with amino acid precursors (CTAP) method, in which non-native amino acid biosynthesis enzymes (diaminopimelate decarboxylase (DDC) and lysine racemase (Lyr)) are expressed in cocultured, auxotrophic cells to produce differentially isotope-labeled L-lysine from their differentially labeled precursors. This enables the proteome cell of origin to be determined using mass spectrometry. Tape *et al.* have now improved the CTAP method by engineering optimized DDC and Lyr enzymes to address specific limitations of each. The optimized DDC allows the CTAP method to be expanded to more cell types, and both optimized DDC and Lyr contain retention sequences to anchor them to the endoplasmic reticulum to prevent their secretion. The new developments enable continuous cell-cell communication studies.

Gauthier, N.P. *et al. Nat. Methods* **10**, 768–773 (2013).

Tape, C.J. *et al. Mol. Cell. Proteomics* doi:10.1074/mcp.0113.037119 (12 May 2014).

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