TOOLS IN BRIEF

STRUCTURAL BIOLOGY

The Protein Contacts Atlas

The adage "a picture is worth a thousand words" certainly applies to protein structure; visualization tools enable researchers from many disciplines to understand how functions are carried out by a protein's unique 3D structure. Though there are many ways of rendering the covalent molecular structure of a protein on a computer screen, noncovalent contacts between atoms—important for folding, stability and function—are challenging to represent. Kayikci *et al.* present the Protein Contacts Atlas (http://www.mrc-lmb.cam.ac.uk/pca/), a visual resource of noncovalent contacts in more than 100,000 protein crystal structures from the Protein Data Bank (PDB). The interactive database offers users many options and plots for visualizing 3D structures at different scales of organization, from an atom to a biological complex, and for visualizing contacts within a single protein or between proteins and ligands.

Kayikci, M. *et al. Nat. Struct. Mol. Biol.* https://dx.doi.org/10.1038/s41594-017-0019-z (2018).

NEUROSCIENCE

A four-armed patch-clamping robot

Neurons are team players, working together in larger ensembles, but monitoring their activity with intracellular recordings is challenging *in vivo*. Kodandaramaiah *et al.* developed a robot that can simultaneously record from up to four neurons at a time. Their multipatcher is an extension of their previously described autopatcher, both of which establish patch-clamp recordings without visual guidance. The multipatcher is equipped with four patch pipettes that independently hunt for neurons. Once a pipette is in close contact with a neuron, all other pipettes cease movement, and the initial pipette is directed to establish a gigaseal. The other pipettes then continue hunting for neurons. When all pipettes have either formed a gigaseal or been inactivated because of clogging, they are instructed to break into the neurons and start recording. The researchers obtained dual or triple recordings in 29% of trials in anesthetized mice and in 18% of trials in awake mice.

Kodandaramaiah, S.B. *et al. eLife* **7**, e24656 (2018).

MICROBIOLOGY

An expanded set of full-length microbial marker genes

Most microbial profiling efforts rely on the amplification and sequencing of the small subunit (SSU) ribosomal RNA gene, a phylogenetic marker that can reveal the taxonomy of different species in a sample. The assignment of taxonomic categories relies on full-length reference SSU sequences, which range from 1.4 to 1.9 kilobases and are thus difficult to capture with traditional short-read sequencing. To help fill gaps in reference databases, Karst *et al.* developed a pipeline that involves RNA size selection to enrich for SSU genes, ligation-based amplification to avoid primer bias, and dual end-tagging and sequence subassembly to reconstruct full-length SSU sequences. The high throughput of short-read sequencing enabled the researchers to generate 1.6 million sequences, thereby adding considerable new diversity to the existing 2 million sequences in public databases.

Karst, S.M. *et al. Nat. Biotechnol.* https://dx.doi.org/10.1038/nbt.4045 (2018).

IMAGING

Tracking nanoparticles by eye

Upconverting nanoparticles convert near-infrared light into visible light. The particles are typically very stable and bleach-resistant and, from this perspective, are good labels for tracking experiments. Wang *et al.* now show that single nanoparticles can be detected within cells by eye, through the microscope eyepiece. They determined the threshold for this detection and show that single nanoparticles can be distinguished from clusters. In post-acquisition analysis, the researchers monitored the diffusion of multiple individual nanoparticles over 21 seconds and inferred the viscosity of the cellular environment on the basis of this movement. Finally, they made use of the excitation power density dependence of upconverting nanoparticle clusters to introduce a new 'channel' for multiplex biological imaging.

Wang, F. *et al. Light Sci. Appl.* **7**, e18007 (2018).