METHODS IN BRIEF

NEUROSCIENCE

Genome editing in the brain

CRISPR–Cas9-mediated genome editing can occur via either nonhomologous end joining or homology-directed repair (HDR); the latter is preferable in the brain, as HDR introduces fewer errors. However, HDR in postmitotic neurons has been inefficient thus far, which has made the technology difficult to use in the adult brain. Nishiyama *et al.* now show that they can achieve efficient genome editing in the brains of mice at various ages by delivering the guide RNA and the HDR template through infection with adeno-associated viruses (AAVs). The source for Cas9 can either be a transgene or an AAV as well. The researchers apply the technology to introduce tags such as HA or mEGFP into postmitotic neurons with high fidelity.

Nishiyama, J. *et al. Neuron* https://doi.org/10.1016/j.neuron.2017.10.004 (2017).

LAB-ON-A-CHIP

Freestyle fluidics

Microfluidic devices have a broad range of uses in biological experiments, yet they can be complicated to build and operate. Walsh *et al.* develop an approach called 'Freestyle Fluidics' (FF) to overcome some of these difficulties. In FF, microfluidic devices are made with fluid, not solid, walls. Aqueous circuits with a desired pattern are printed on a surface such as a Petri dish and are then overlaid with an immiscible liquid to prevent evaporation, forming walls that can self-heal after liquids have been pipetted through them. The researchers produced a range of functional microfluidic devices using their approach, and they show that the circuits can withstand passive and active flow. They further demonstrate that their devices can be used to study an inflammatory response in human cells as well as bacterial chemotaxis.

Walsh, E.J. *et al. Nat. Commun.* **8**, 816 (2017).

CELL BIOLOGY

Measuring cellular mass with a picobalance

How much does a cell weigh? Determining the mass of single cells is not trivial, as balances that are sensitive in the nanogram range are not readily available. Martínez-Martín *et al.* developed a balance that can measure the mass of a single cell with an accuracy of a few pictograms. This picobalance consists of a cantilever that oscillates at its natural resonance frequency. The researchers then attach a cell to the cantilever, which changes the resonance frequency; and this change allows them to calculate the change in mass. Using this technology, the researchers demonstrate that the mass of HeLa cells or mouse fibroblasts fluctuates by 12–15 picograms, and that these fluctuations depend on physiological processes such as water exchange and ATP levels. The researchers also study how viral infection influences cellular mass.

Martínez-Martín, D. *et al. Nature* **550**, 500–505 (2017).

STRUCTURAL BIOLOGY

Improving the efficiency of cryo-EM

To obtain the highest possible resolution using single-particle cryo-electron microscopy (cryo-EM), protein particles on plunge-frozen sample grids should ideally adopt random orientations. However, many proteins adopt preferred orientations, which limits the achievable resolution. Naydenova and Russo report a statistical metric that they call the 'efficiency', E_{od}, for characterizing particle orientation distribution. This metric can be calculated using a relatively small number of particles; its value is interpreted to indicate whether data collection can proceed to reach a desired resolution, or whether one should first try alternative sample grids or data collection strategies, such as optimizing the sample tilt angle, to achieve higher resolution. The authors demonstrate the use of E_{od} for four previously published data sets with a broad range of particle orientation distributions. An open-source software tool is available.

Naydenova, K. & Russo, C.J. *Nat. Commun.* **8**, 629 (2017).