

## IN BRIEF

## GENOMICS

**A pan-cancer atlas**Hoadley, K. A. et al. *Cell* **173**, 291–304 (2018).

The Cancer Genome Atlas (TCGA), a program funded by the US National Institutes of Health (NIH), has ended over a decade after its inception. The ambitious project coordinated the multi-omic sequencing and clinical annotation of approximately 10,000 tumors across 33 cancer types. The resulting resource, publicly available through the NIH Genomic Data Commons (<https://gdc.cancer.gov/>), includes data on DNA sequence, DNA methylation, RNA and microRNA expression, and reverse-phase protein array binding, and makes it possible to rigorously characterize the molecular features of cancers. A set of 27 analysis papers associated with the final data release (<https://www.cell.com/consortium/pancanceratlas>) organize our current understanding by cell-of-origin patterns, oncogenic processes and signaling pathways. A flagship paper by Hoadley et al. shows that tumors cluster by histology, tissue type and anatomic origin when classified on the basis of nearly any data type. Integrated data analysis by iCluster defines various pan-cancer groupings of similar tumor types, which will help to orient future work on diagnostics and therapeutic development. *TN*

<https://doi.org/10.1038/s41592-018-0020-4>

## NEUROSCIENCE

**Analyzing *Drosophila* activity**Cichewicz, K. & Hirsh, J. *Commun. Biol.* **1**, 25 (2018).

Circadian rhythms, sleep and activity of fruit flies can be recorded in the *Drosophila* Activity Monitor (DAM) system. In this device, individual flies walk around in glass tubes with food at one end, and breaks in an infrared beam that crosses the glass tube are recorded as fly activity. Several options for data analysis are available, but they rely on software that requires commercial licenses or that might not be straightforward to install or use. Cichewicz and Hirsh developed a web-based solution called ShinyR-DAM, which is easy to use and can handle standard experimental designs as well as multiple genotypes and conditions. ShinyR-DAM accepts output files from the DAM system and generates plots of individual and population activity, as well as summary graphs. A useful feature is the automated exclusion of data from dead flies. The analysis can be customized for sleep, circadian rhythm or general activity studies in *Drosophila*. *NV*

<https://doi.org/10.1038/s41592-018-0021-3>

## STEM CELLS

**What hPSCs need**Yilmaz, A. et al. *Nat. Cell Biol.* **20**, 610–619 (2018).

To discover how much something is needed, it is a good strategy to try going without it. Yilmaz et al. applied this approach to characterize genes essential for the maintenance of human pluripotent stem cells (PSCs). They combined two previously characterized tools: a haploid human PSC line and CRISPR-based knockout screening. Along with Cas9, the researchers delivered a library of single guide RNAs (sgRNAs) targeting 18,000 genes with 10 sgRNAs per gene to the cells and assessed cell survival and growth rate, as well as the abundance of sgRNAs over time. This study uncovered essential and growth-restricting genes. Looking at the cellular distribution of the proteins encoded by the essential genes, they found high proportions in nuclear and mitochondrial compartments. The definition of what the authors call the essentialome goes far beyond the known transcription factors and highlights, for example, the role of cell-cycle regulators and DNA-repair genes in PSC growth and identity. *NR*

<https://doi.org/10.1038/s41592-018-0022-2>

## MICROSCOPY

**Hessian structured illumination microscopy**Huang, X. et al. *Nat. Biotechnol.* **36**, 451–459 (2018).

Structured illumination microscopy (SIM) offers twice the resolving power of diffraction-limited microscopy with relatively low doses of light compared with those required for other super-resolution modes, which makes it useful for live imaging. However, SIM involves image reconstruction that is prone to artifacts. Huang et al. have developed an approach called Hessian-SIM to reduce artifacts in SIM image reconstruction for improved fast live-cell super-resolution imaging. Hessian-SIM uses a deconvolution algorithm based on Hessian matrices that makes use of a priori knowledge of an imaged structure to guide image reconstruction. This deconvolution algorithm outperforms current algorithms at low signal intensities and allows imaging at a fraction of the photon dose of conventional SIM. Using their approach, the researchers carried out hour-long time-lapse imaging of actin filaments in live cells and were able to image never-before-observed structures involved in endocytosis. *RS*

<https://doi.org/10.1038/s41592-018-0023-1>

**Premium labware for research and discovery****CryoPure Storage System**

- Certified tubes, racks and boxes for cryogenic storage
- Volumes from 1.2 to 5.0 ml
- Skirted bases and QuickSeal caps for ergonomic handling
- 6 cap and insert colors for up to 36 color coding options



FREE samples!



[www.sarstedt.com](http://www.sarstedt.com)

[customerservice@sarstedt.us](mailto:customerservice@sarstedt.us)