NEUROSCIENCE

A comparative atlas of the brain

Sjöstedt, E. et al. *Science* **367**, eaay5947 (2020).

Several large-scale projects have mapped protein expression in the brains of various species. Sjöstedt et al. worked with data from multiple sources, such as from the Allen Institute, the GTEx consortium and the FANTOM consortium, and supplemented them with their own mapping efforts. The researchers integrated RNA-seq data, in situ hybridizations and immunofluorescence stainings in three species: human, pig and mouse. In comparative analyses, the researchers observe large overlaps in expression profiles across the three species, but there are also substantial differences, in particular for genes involved in neurotransmission. The data are available via the Human Protein Atlas portal at http://www.proteinatlas.org. *NV*

https://doi.org/10.1038/s41592-020-0842-8

IMMUNOLOGY

Paired TCR discovery in high throughput

Spindler, M. J. et al. *Nat. Biotechnol.* https://doi.org/10.1038/s41587-020-0438-y (2020).

T cell receptors (TCRs) consist of α and β chains, which together mediate antigen specificity. However, high-throughput methods for analyzing the pairing of α and β chains have been elusive. Spindler et al. have removed this bottleneck by developing a droplet microfluidics-based system that maintains physical linkage between α and β TCR chains. TCR mRNA transcripts from individual T cells undergo reverse transcription into cDNA and subsequent amplification. Short linker DNA constructs attached to the amplification primers fuse the two TCR chains to ensure native pairing. αβ cDNA TCR libraries are then subcloned into lentiviral constructs for expression in Jurkat cells. This approach could elicit up to 100-fold more paired TCRs than previously described single-cell methods. The researchers generated multiple Jurkat libraries from donor peripheral blood samples, which allowed them to identify rare high-avidity antigen-specific TCR clonotypes in the context of cancer and viral infections. This method of high-resolution, high-throughput TCR repertoire analysis enhances our understanding of the dynamics of human αβ TCR repertoires and may facilitate the rapid discovery of rare TCRs for the development of efficient adoptive cell therapies. *MM*

https://doi.org/10.1038/s41592-020-0845-5

SENSORS AND PROBES

Mining bacteria for biosensors

Grazon, C. et al. *Nat. Commun.* **11**, 1276 (2020).

Förster resonance energy transfer (FRET)-based biosensors are widely used in biomedical research. One challenge that is often associated with making FRET-based sensors is identifying proteins that are suitable for sensing molecules at relevant concentrations. Grazon et al. have developed a strategy to identify bacterial allosteric transcription factors that recognize a target analyte for subsequent development into biosensors. The researchers were interested in developing a progesterone sensor. For this, they turned to *Pimelobacter simplex*, which is known to use steroids as an energy source. They treated the bacteria with various steroids to identify upregulated gene clusters. Within the gene cluster, they identified three uncharacterized putative transcription factors and went on to validate one, a protein called SRTF1, by showing that it binds progesterone. They then used SRTF1 to develop a highly sensitive quantum-dot-based FRET reporter of progesterone. *RS*

https://doi.org/10.1038/s41592-020-0843-7

PROTEOMICS

A pan-plant protein complex map

McWhite, C. D. et al. *Cell* https://doi.org/10.1016/j.cell.2020.02.049 (2020).

Large-scale discovery of protein complexes in plants has been limited because methods used for similar analyses in humans and pathogens don't work well in plants owing to genomic complexity, high transformation rate and the commonness of polyploidy. McWhite et al. have used cofractionation mass spectrometry (CF-MS), which chromatographically separates native protein extracts, to develop a pan-plant protein complex map using 2 million protein association measurements made across 13 plant species spanning 1.1 billion years of green plant evolution. Coeluting proteins have a high probability of physical contact, and observation of repeated coelution across species adds further validation for such measurements. The resuwlts provide an extensive map of high-confidence protein–protein interactions of high resource value with agronomic, evolutionary and biochemical importance. *AS*

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