MOLECULAR ENGINEERING

Partial ordered polypeptides

Roberts, S. et al. *Nat. Mater.* https://doi.org/10.1038/s41563-018-0182-6 (2018).

There is growing interest in understanding the molecular and physical principles behind protein phase separation, because of its critical role in cellular functions. Roberts et al. explored the phase behaviors of intrinsically disordered polypeptides containing ordered protein domains. They recombinantly synthesized partial ordered polypeptides (POPs) that integrate disordered, thermoresponsive elastin-like polypeptides (ELPs) with ordered polyalanine helices. The integration of ordered domains alters the ELPs' phase behavior, in which the newly synthesized POPs exhibit thermal hysteresis, the difference between transition temperatures defined during heating and cooling processes. This reversible thermal hysteresis is correlated with the amount of polymer helicity in POPs and can be tuned through changes in the ratio of ordered to disordered domains. The temperature-triggered phase separation drives POPs to form porous, physically cross-linked viscoelastic networks that hold potential for wound healing and tissue growth in vivo. *LT*

https://doi.org/10.1038/s41592-018-0249-y

GENOMICS

Protein-based cell barcodes

Wroblewska, A. et al. *Cell* **175**, 1141–1115 (2018).

CRISPR is a versatile tool for gene knockout, activation and repression that has become critical for perturbation screens. Recently, it was shown that it is possible to carry out different perturbations at the single-cell level by using single-cell RNA-seq as a readout, which allows for a dramatic scale-up in the number of targets that can be screened in a single experiment. Phenotyping in these screens has largely been limited to transcriptional profiles. Wroblewska et al. now design protein barcodes (Pro-Codes) consisting of uniquely combined triplet epitopes that are assigned to specific guide RNAs, thus making it possible to use CyTOF mass cytometry to generate multidimensional protein profiles in single-cell pooled CRISPR screens. Each linear epitope can be decoded by a small set of antibodies, which leaves many CyTOF channels available for protein quantification. The authors used Pro-Codes to track tumor cell clonality in mice, and to screen for genes that affect whether breast cancer cells are sensitive to T cell killing. *TN*

https://doi.org/10.1038/s41592-018-0250-5

NEUROSCIENCE

A nonhuman primate imaging resource

Milham, P. L. et al. *Neuron* **100**, 61–74 (2018).

The study of neurobiology in nonhuman primates is crucial for basic science research, giving insights that may be translated into human research and enabling the comparison of neurobiology among species. However, although advances in image acquisition are occurring rapidly, there is a relative dearth of nonhuman primate magnetic resonance imaging (MRI) datasets, largely because of the limited number of centers that house these animals and carry out this type of research. To promote this research community and facilitate efforts to map the nonhuman primate connectome, the PRIMatE Data Exchange (PRIME-DE) has been developed. PRIME-DE is an open science resource that aggregates and shares anatomical, functional, and diffusion MRI datasets. The initial release consists of 25 independent data collections aggregated across 22 sites. *RS*

https://doi.org/10.1038/s41592-018-0251-4

CHEMICAL BIOLOGY

A methionine modification method

Taylor, M. T. et al. *Nature* **562**, 563–568 (2018).

The chemical manipulation of specific amino acids in native proteins is a useful approach for probing protein structure and function. Chemistries exist to modify cysteine, lysine and tyrosine residues, but expansion of this toolbox to other amino acids would be a welcome development. Methionine in particular represents a useful target for modification, because it is rare and its function is mainly to protect against oxidative stress, which means that its modification is unlikely to affect protein function. Taylor et al. report a bioconjugation method for methionine, based on the use of a hypervalent iodine reagent that targets the S-Me group. The reaction is selective, efficient and fast, and can be carried out in a one-pot operation. The researchers applied it to modify several native peptides and proteins, and show that the chemistry is compatible with methods for labeling other residues. *AD*

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