## IN BRIEF

MICROBIOLOGY

### Diet influences microbe–host interaction

Kovatcheva-Datchary, P. et al. *Cell Rep.* **26**, 3772–3783 (2019).

The gut microbiota plays a critical role in human metabolism through, for example, the production of short-chain fatty acids. Yet it is still a challenge to decipher microbe–diet–host interplay owing to the lack of fully characterized microorganisms and the lack of understanding regarding bacterial interactions with complex food networks. To ease the complexity, Kovatcheva-Datchary et al. developed a mouse model that is colonized with a simplified intestinal microbiota (SIM) containing ten known bacterial strains from the human gut microbiome. They fed the SIM mice different diets including high fiber, high fat/high sucrose, or zero fat/high sucrose. They observed a reduced abundance of fiber-degrading bacteria when dietary fiber was limited. Using RNA sequencing, they were able to annotate the altered genes associated with metabolism that are induced by a change in diet. In addition, the simplified mouse model allows researchers to assess how dietary interventions affect circulating metabolites through metabolomic analysis of the plasma. *LT*

https://doi.org/10.1038/s41592-019-0413-z

SENSORS AND PROBES

### Bright probes for EM

Prigozhin, M. B. et al. *Nat. Nanotechnol.* https://doi.org/10.1038/s41565-019-0395-0 (2019).

Electron microscopy (EM) is a powerful approach for imaging biological structures. However, the ability to label specific targets, such as proteins of interest, is limited owing to the relatively small number of tags that are suitable for single-molecule imaging or compatible with multiplexed imaging of multiple targets. One exciting possibility for multiplexed imaging comes in the form of cathodoluminescent probes, which emit light after excitation by an electron beam. Prigozhin et al. have developed lanthanide-based cathodoluminescent nanoparticles suitable for multiplexed EM. The researchers developed optimized synthesis protocols to develop sub-20-nm particles that use different lanthanides to emit in nine different colors with sharp emission spectra. They showed proof-of-principle multiplexed imaging experiments for their nanoparticles on a silicon substrate. These probes could find myriad uses in biological imaging applications. *RS*

https://doi.org/10.1038/s41592-019-0417-8

MOLECULAR BIOLOGY

### Imaging chromatin and RNA in embryos

Mateo, L. J. et al. *Nature* https://doi.org/10.1038/s41586-019-1035-4 (2019).

The 3D organization of the genome and how it relates to gene expression are fundamental questions in biology. This regulation may be especially important in embryos, where the timing and nature of gene expression are crucial for proper development. Mateo et al. have developed optical reconstruction of chromatin architecture (ORCA), a method that uses Oligopaint probes to label the genome with resolution reaching two kilobases. The probes are tiled over the genome sequentially to enable 3D reconstruction of genomic organization. The method can be combined with single-molecule RNA fluorescence in situ hybridization to examine gene expression in the same cells. The researchers used ORCA to study genome organization in *Drosophila* embryos, where they observed Polycomb-independent borders between active and Polycomb-repressed DNA, the deletion of which led to aberrant gene expression and developmental defects. *RS*

https://doi.org/10.1038/s41592-019-0414-y

CELL BIOLOGY

### Mitochondrial barcodes

Ludwig, L. S. et al. *Cell* **176**, 1325–1339 (2019).

We all start life as a zygote, and if we could follow each cell's divisions and fate decisions, we would understand a lot more about the development of complex tissues in vertebrates. One option is to genetically tag cells early in development, but this is not feasible in humans. Ludwig et al. instead use sequence variations in the transcriptome of mitochondrial DNA as natural barcodes to infer clonal relationships and draw lineage trees. In combination with single-cell ATAC-seq data, the researchers can use this approach to correlate clonal dynamics and gene expression with chromatin accessibility. These natural barcodes allowed them to define the subclonal structure in colorectal tumors and to follow clones of chronic myelogenous leukemia in patients from the time of diagnosis to the sixth month of therapy. The approach holds promise for elucidating the clonal evolution of cancer and the development of drug resistance. *NR*

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