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## research highlights

### IN BRIEF

#### NEUROSCIENCE

### Proteins on the brain

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

The mammalian brain can be divided into 10 major regions. Species-by-species, however, the molecular organization of those regions can differ. To help others compare and contrast, an international team of researchers led by Mathias Uhlén and Jan Mulder of the Karolinska Institutet in Sweden combined transcriptomics, single-cell genomics, in situ hybridization, and antibody protein profiling data to compile a new atlas of protein-coding genes in the human brain and that of two model organisms: the pig and the mouse.

Analysis of the datasets, which classified over 16,000 genes by region, suggests that the three species indeed share similar regional organization and expression profiles. There is however greater variability between man and mouse in a number of respects, such as neurotransmitter receptors, than between man and pig. The datasets for each species can be explored in the [Human Protein Atlas \(HPA\) Brain Atlas](#). *EPN*

<https://doi.org/10.1038/s41684-020-0539-8>

#### NEUROSCIENCE

### Honey bees & brain waves

Popov, T. and Szyszka, P. *Proc. R. Soc. B* <https://doi.org/10.1098/rspb.2020.0115> (2020).

As the honey bees took in different scents, Tzvetan Popov of the University of Heidelberg and Paul Szyszka at the University of Otago were busy observing the local field potentials and neuronal spikes coming from the mushroom bodies of the bees' brains. They saw a spontaneous oscillation move across both hemispheres with the odor stimuli—a wave not unlike the alpha oscillations observed in humans.

Alpha oscillations are brain waves that ripple across the human brain as neurons fire. Detectable by electroencephalogram, these waves have been linked to attention, memory, and other cognitive functions. Though the frequency of human alpha waves is a bit lower than that of bees—10 Hz vs 18 Hz, respectively—and the function of the bee oscillations is still to be determined, Popov and Szyszka suggest the honey bee might serve as a new invertebrate model to study alpha oscillations. *EPN*

<https://doi.org/10.1038/s41684-020-0541-1>

#### GENETICS

### Editing instructions

Vallecillo-Viejo, I.C. et al. *Nucleic Acids Res.* gkaa172 (2020)

In most organisms, RNA produces proteins exactly as DNA dictates. Cephalopods, however, aren't most organisms. Octopuses and squids can edit their messenger RNA, changing the genetic message and altering the resulting protein. This editing has been described in the neurons of several species, but all within the confines of nuclei—before the mRNA is released to its ultimate destination.

A new study led by Joshua Rosenthal's lab at the Marine Biological Laboratory in Woods Hole, MA reveals that changes might be made...anywhere. In the longfin inshore squid, *Doryteuthis pealeii*, the research team detected tens of thousands of potential editing sites along the length of the giant axon. The results suggest that the animals' have the ability to tailor their proteins long after the mRNA has departed the nucleus in order to fine-tune localized cellular physiology. *EPN*

<https://doi.org/10.1038/s41684-020-0540-2>

#### MICROBIOME

### Integrated metagenomics

Lesker, T.R. et al. *Cell Rep.* **30**, 2909–2922 (2020)

What makes up the microbiome of the mouse gut? The level of detail that can be captured often depends on the sequencing approach used and the gene catalogs and databases referenced to determine the microbes present. To help make more complete assemblies of mouse microbiomes, researchers working with Till Strowig's lab at the Helmholtz Centre for Infection Research in Germany present the integrated Mouse Gut Metagenomic Catalog (iMGMC).

The team developed a bioinformatics workflow to combine several existing gene catalogs that included 4.6 million genes and 660 metagenome-assembled genomes. The resource provides high taxonomic resolution, which can be used to help characterize microbiome profiles to species-level in mouse gut samples. [The iMGMC resource can be accessed via github](#). *EPN*

<https://doi.org/10.1038/s41684-020-0542-0>