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Plant, Cell & Environment

Thioredoxin *h2* contributes to the redox regulation of mitochondrial photorespiratory metabolism

Paula da Fonseca-Pereira, Paulo V.L. Souza, Liang-Yu Hou, Saskia Schwab, Peter Geigenberger, Adriano Nunes-Nesi, Stefan Timm, Alisdair R. Fernie, Ina Thormählen, Wagner L. Araújo, Danilo M. Daloso

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News & Views | 29 July 2019

Nature Plants

The missing link in jasmonic acid biosynthesis

Claus Wasternack & Bettina Hause

Nature Plants **5**, doi:10.1038/s41477-019-0492-y

Review Article | 15 July 2019

The emerging and uncultivated potential of CRISPR technology in plant science

Yingxiao Zhang, Aimee A. Malzahn, Simon Sretenovic & Yiping Qi

Nature Plants **5**, doi:10.1038/s41477-019-0461-5

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JBC

Sulfation pathways from red to green

Süleyman Günal, Rebecca Hardman, Stanislav Kopriva and Jonathan Wolf Mueller

[Large-Scale Analyses of Human Microbiomes Reveal Thousands of Small, Novel Genes](#)

Pages 1245-1259.e14

Hila Sberro, Brayon J. Fremin, Soumaya Zlitni, Fredrik Edfors, Nicholas Greenfield, Michael P. Snyder, Georgios A. Pavlopoulos, Nikos C. Kyrpides, Ami S. Bhatt
Cell : Volume 178, Issue 5

[Tiny Hidden Genes within Our Microbiome](#)

Pages 1034-1035

Karin Mittelman, David Burstein

The human body is teeming with microorganisms that protect us from pathogenic infections, train our immune system, and play a major role in our digestive tract. To understand these complex microbial communities, it is crucial to elucidate the functions encoded by the genomes of these microbes. This is no trivial task: even the initial step of identifying coding genes from metagenomic sequences can be challenging, especially when searching for particularly small genes (15–150 nucleotides). Most standard prediction tools discard such genes, as they are harder to detect without inflating the number of false-positive predictions ([Housman and Ulitsky, 2016](#), [Makarewich and Olson, 2017](#), [Saghatelian and Couso, 2015](#)). Nevertheless, the significance of small proteins should not be understated, as they take part in key processes in all clades of the tree of life, from phages to mammals. In bacteria, their functions encompass spore formation, quorum sensing, mediation of the stress response, regulation of signaling pathways, antimicrobial activity, and protein translation ([Baumgartner et al., 2016](#), [Miravet-Verde et al., 2019](#), [Weaver et al., 2019](#)). In this issue of *Cell*, [Sberro et al. \(2019\)](#) performed a large-scale study seeking small protein-coding genes encoded by the human microbiome. By considering conservation, phylogenetic distribution, signature sequences, and genomic context, they reveal thousands of small protein families. Most of these proteins have never been described before and could have far-reaching effects on our microbiome.

[A Species-Wide Inventory of NLR Genes and Alleles in *Arabidopsis thaliana*](#)

Pages 1260-1272.e14

Anna-Lena Van de Weyer, Freddy Monteiro, Oliver J. Furzer, Marc T. Nishimura, Volkan Cevik, Kamil Witek, Jonathan D.G. Jones, Jeffery L. Dangl, Detlef Weigel, Felix Bemm

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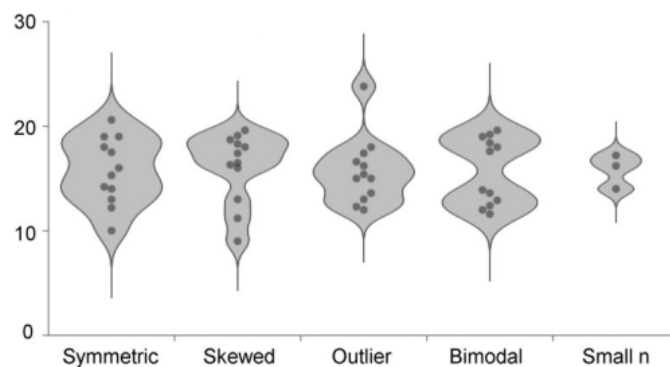
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Ribosome-associated chloroplast SRP54 enables efficient co-translational membrane insertion of key photosynthetic proteins.

Plant Cell. 2019 Aug 23;. [Epub ahead of print] PMID: 31444312 [PubMed - as supplied by publisher]

From JBC – Bar graphs are no longer accepted by many journals. They want more information.

[Data visualization, bar naked: A free tool for creating interactive graphics](#)

Tracey L. Weissgerber, Marko Savic, Stacey J. Winham, Dejana Stanisavljevic, Vesna D. Garovic and Natasa M. Milic



This web-based tool allows authors to create customized interactive graphics that describe their data in an open and transparent manner and helps researchers move away from bar graphs that can hide true data distributions and impede scientific progress.

Plant Cell

Developmental timing is everything (part II): gating of high temperature responses by the circadian clock

Patrice A Salomé

Plant Cell 2019 tpc.19.00632; Advance Publication August 22, 2019; doi:10.1105/tpc.19.00632 **OPEN**

<http://www.plantcell.org/content/early/2019/08/22/tpc.19.00632>

Promoting production: UPL3 promoter variation modulates seed size and crop yields

Estee E-Ling Tee

Plant Cell 2019 tpc.19.00613; Advance Publication August 22, 2019; doi:10.1105/tpc.19.00613 **OPEN**

<http://www.plantcell.org/content/early/2019/08/22/tpc.19.00613>

Variation in expression of the HECT E3 ligase UPL3 modulates LEC2 levels, seed size and crop yield in Brassica napus. Charlotte Miller, Rachel Wells, Neil McKenzie, Martin Trick, Joshua Ball, Abdelhak Fatihi, Bertrand Dubreucq, Thierry Chardot, Loic Lepiniec and Michael W Bevan

Plant Cell 2019 tpc.18.00577; Advance Publication August 22, 2019; doi:10.1105/tpc.18.00577 **OPEN**

<http://www.plantcell.org/content/early/2019/08/22/tpc.18.00577.abstract>

Transcriptome Analyses of FY Mutants Reveal its Role in mRNA Alternative Polyadenylation

Zhibo Yu, Juncheng Lin and Qingshun Quinn Li

Plant Cell 2019 tpc.18.00545; Advance Publication August 19, 2019; doi:10.1105/tpc.18.00545

<http://www.plantcell.org/content/early/2019/08/19/tpc.18.00545.abstract>