

April 1

This Week in *Science*

Science 29 Mar 2019:

Vol. 363, Issue 6434, pp. 1411

Precise packing for membrane proteins

Although nonpolar amino acid side chains pack efficiently in membrane proteins, it has been difficult to determine how much this contributes to membrane protein stability. Designed membrane proteins have largely relied on other stabilizing interactions such as metal-ligand interactions and hydrogen bonds. Mravic *et al.* uncovered a steric packing code underlying the folding of the natural protein phospholamban, which they used to design stable membrane proteins with nonpolar interfaces. They suggest that packing of nonpolar residues plays a role in the folding and stability of many membrane proteins. *Science*, this issue p. [1418](#)

The features that stabilize the structures of membrane proteins remain poorly understood. Polar interactions contribute modestly, and the hydrophobic effect contributes little to the energetics of apolar side-chain packing in membranes. Disruption of steric packing can destabilize the native folds of membrane proteins, but is packing alone sufficient to drive folding in lipids? If so, then membrane proteins stabilized by this feature should be readily designed and structurally characterized—yet this has not been achieved. Through simulation of the natural protein phospholamban and redesign of variants, we define a steric packing code underlying its assembly. Synthetic membrane proteins designed using this code and stabilized entirely by apolar side chains conform to the intended fold. Although highly stable, the steric complementarity required for their folding is surprisingly stringent. Structural informatics shows that the designed packing motif recurs across the proteome, emphasizing a prominent role for precise apolar packing in membrane protein folding, stabilization, and evolution.

Gene expression at fine scale

Mapping gene expression at the single-cell level within tissues remains a technical challenge. Rodriques *et al.* developed a method called Slide-seq, whereby RNA was spatially resolved from tissue sections by transfer onto a surface covered with DNA-barcoded beads. Applying Slide-seq to regions of a mouse brain revealed spatial gene expression patterns in the Purkinje layer of the cerebellum and axes of variation across Purkinje cell compartments. The authors used this method to dissect the temporal evolution of cell type-specific responses in a mouse model of traumatic brain injury. *Science*, this issue p. [1463](#)

Speeding up stomatal responses

A plant's cellular metabolism rapidly adjusts to changes in light conditions, but its stomata—pores that allow gas exchange in leaves—are slower to respond. Because of the lagging response, photosynthesis is less efficient, and excess water is lost through the open pores. Papanatsiou *et al.* introduced a blue light-responsive ion channel into stomata of the small mustard plant *Arabidopsis*. The channel increased the rate of stomata opening and closing in response to light. The engineered plants produced more biomass, especially in the fluctuating light conditions typical of outdoor growth. *Science*, this issue p. [1456](#)

How to make an organelle in eukaryotes

A key step in the evolution of complex organisms like eukaryotes was the organization of specific tasks into organelles. Reinkemeier *et al.* designed an artificial, membraneless organelle into mammalian cells to perform orthogonal translation. In response to a specific codon in a selected messenger RNA, ribosomes confined to this organelle were able to introduce chemical functionalities site-specifically, expanding the canonical set of amino acids. This approach opens possibilities in synthetic cell engineering and biomedical research. *Science*, p. [eaaw2644](#)

[Designer membraneless organelles enable codon reassignment of selected mRNAs in eukaryotes](#)

By Christopher D. Reinkemeier, Gemma Estrada Girona, Edward A. Lemke

Science 29 Mar 2019 Full Access

Orthogonal translation of specific proteins is enabled by a phase-separated synthetic organelle in eukaryotic cells.

Physiologia Plantarum, Vol. 165, No. 4, April 2019

Minireview

The role of C2H2 zinc finger proteins in plant responses to abiotic stresses

Ke Wang, Yanfei Ding, Chong Cai, Zhixiang Chen, Cheng Zhu

Pages: 690-700 | First Published: 23 March 2018

Plant Journal

An updated gene atlas for maize reveals organ-specific and stress-induced genes

Genevieve M. Hoopes, John P. Hamilton, Joshua C. Wood, Eddi Esteban, Asher Pasha, Brienne Vaillancourt, Nicholas J. Provart, C. Robin Buell

Pages: 1154-1167 | First Published: 07 December 2018

We developed a comprehensive transcriptome resource for the maize reference genotype B73 based on the AGPv4 long-read assembly using replicated and publicly available RNA-sequencing datasets. Gene expression analyses were performed on a robust B73 developmental and stress gene expression atlas, utilizing core and dispensable genes of the maize pan-genome as a case study to demonstrate the utility of the data.

What to do about those immunoprecipitation blues

[Vivien Marx](#)

Nature Methods volume 16, pages 289–292 (2019) | [Download Citation](#)

ChIP-seq, DIP-seq and related techniques are informative genome-wide assays, but they don't always work as planned.

Marnik EA, Updike DL.

Membraneless organelles: P granules in *C. elegans*.

Traffic. 2019 Mar 29;. PMID: 30924287 [PubMed - as supplied by publisher]

Ye X, Lin J, Mayne L, Shorter J, Englander SW.

Hydrogen exchange reveals Hsp104 architecture, structural dynamics, and energetics in physiological solution.

Proc Natl Acad Sci U S A. 2019 Mar 27;. PMID: 30918129 [PubMed - as supplied by publisher]

Ye X, Lin J, Mayne L, Shorter J, Englander SW.

Hydrogen exchange reveals Hsp104 architecture, structural dynamics, and energetics in physiological solution.

Proc Natl Acad Sci U S A. 2019 Mar 27;. PMID: 30918129 [PubMed - as supplied by publisher]

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The cochaperone CHIP marks Hsp70- and Hsp90-bound substrates for degradation through a very flexible mechanism.

Sci Rep. 2019 Mar 25;9(1):5102.

PMID: 30911017 [PubMed - in process]

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Nitric Oxide. 2019 Mar 19;. PMID: 30902590 [PubMed - as supplied by publisher]

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Nitric oxide and plant mineral nutrition: current knowledge.

J Exp Bot. 2019 Mar 23;. [Epub ahead of print] PMID: 30903155 [PubMed - as supplied by publisher]

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Cycloheximide can distort measurements of mRNA levels and translation efficiency.

Nucleic Acids Res. 2019 Mar 27;. [Epub ahead of print] PMID: 30916348 [PubMed - as supplied by publisher]

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Chloroplast Translation Elongation Factor EF-Tu/SVR11 Is Involved in Ca^{2+} -Mediated Leaf Variegation and Leaf Development in *Arabidopsis*.

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Perli E, Pisano A, Glasgow RIC, Carbo M, Hardy SA, Falkous G, He L, Cerbelli B, Pignataro MG, Zacara E, Re F, Della Monica PL, Morea V, Bonnen PE, Taylor RW, d'Amati G, Giordano C.

Novel compound mutations in the mitochondrial translation elongation factor (TSFM) gene cause severe cardiomyopathy with myocardial fibro-adipose replacement.

Sci Rep. 2019 Mar 25;9(1):5108. PMID: 30911037 [PubMed - in process]

Plant Journal

[Hybrid sequencing reveals insight into heat sensing and signaling of bread wheat](#)

Xiaoming Wang, Siyuan Chen, Xue Shi, Danni Liu, Peng Zhao, Yunze Lu, Yanbing Cheng, Zhenshan Liu, Xiaojun Nie, Weining Song, Qixin Sun, Shengbao Xu, Chuang Ma

First Published: 19 March 2019

[Identification and characterization of a core set of ROS wave-associated transcripts involved in the systemic acquired acclimation response of *Arabidopsis* to excess light](#)

Sara I. Zandalinas, Soham Sengupta, David Burks, Rajeev K. Azad, Ron Mittler

Pages: 126-141 | First Published: 16 December 2018

The reactive oxygen species (ROS) wave is required for a rapid, early and transient systemic transcriptomic response to light stress that includes thousands of transcripts, many of them important for light stress acclimation. A core set of transcripts that includes several transcriptional regulators involved in H_2O_2 signaling is directly associated with the ROS wave and could be associated with systemic responses to many other stresses.

Plant Cell & Environment

[EgRBP42 from oil palm enhances adaptation to stress in *Arabidopsis* through regulation of nucleocytoplasmic transport of stress-responsive mRNAs](#)

Wan-Chin Yeap, Parameswari Namasivayan, Tony Eng Keong Ooi, David Ross Appleton, Harikrishna

Kulaveerasingam, Chai-Ling Ho Version of Record online: 25 January 2019

This study shows that EgRBP42, an RNA-binding protein from oil palm, is involved in plant response to abiotic stress. Overexpression of *EgRBP42* in *Arabidopsis* conferred drought, flood, salinity, and cold tolerance with early flowering. EgRBP42 harbours nucleocytoplasmic shuttling activity, and it interacts directly and is colocalized with stress-responsive mRNAs in response to abiotic stresses, suggesting that EgRBP42 may be involved in intracellular transport of stress-responsive RNAs in response to abiotic stress.

[Can leaf net photosynthesis acclimate to rising and more variable temperatures?](#)

Giulia Vico, Danielle A. Way, Vaughan Hurry, Stefano Manzoni Record online: 22 March 2019

Under future climates, leaf temperatures will be higher and more variable, with effects on the plant carbon balance. This study asks the question: To what extent can leaf net photosynthesis acclimate to buffer leaf carbon gains from rising and increasingly variable leaf temperatures? A probabilistic description of short- and long-term changes in leaf temperature is parameterized by means of a dataset on net photosynthetic responses to these changes, encompassing 75 genera and 111 species. Our results show that (a) the expected increases in leaf temperature variability have always detrimental effects on leaf performance, whereas the effects of higher mean leaf temperatures depend on the species and initial temperature, and (b) acclimation greatly reduces the consequences of leaf warming.

EMBO J.

Extracellular matrix sensing by FERONIA and Leucine-Rich Repeat Extensins controls vacuolar expansion during cellular elongation in *Arabidopsis thaliana*

Kai Dünser, Shibu Gupta, Aline Herger, Mugurel I Feraru, Christoph Ringli and Jürgen Kleine-Vehn

Published online 08.03.2019

<http://EMBOJ.embopress.org/content/38/7/e100353?etoc>

Extracellular Leucine-Rich Repeat Extensin proteins link the plasma membrane receptor-like kinase FERONIA with the cell wall for sensing mechanical constraints affecting vacuolar size and plant cell elongation.

Nature Genetics

A genome-wide algal mutant library and functional screen identifies genes required for eukaryotic photosynthesis

Xiaobo Li,Paul A. Lefebvre, Arthur R. Grossman & Martin C. Jonikas

Nature Genetics Vol 51, pages627–635 (2019)

Photosynthetic organisms provide food and energy for nearly all life on Earth, yet half of their protein-coding genes remain uncharacterized^{1,2}. Characterization of these genes could be greatly accelerated by new genetic resources for unicellular organisms. Here we generated a genome-wide, indexed library of mapped insertion mutants for the unicellular alga *Chlamydomonas reinhardtii*. The 62,389 mutants in the library, covering 83% of nuclear protein-coding genes, are available to the community. Each mutant contains unique DNA barcodes, allowing the collection to be screened as a pool. We performed a genome-wide survey of genes required for photosynthesis, which identified 303 candidate genes. Characterization of one of these genes, the conserved predicted phosphatase-encoding gene *CPL3*, showed that it is important for accumulation of multiple photosynthetic protein complexes. Notably, 21 of the 43 higher-confidence genes are novel, opening new opportunities for advances in understanding of this biogeochemically fundamental process. This library will accelerate the characterization of thousands of genes in algae, plants, and animals.

Plant, Cell & Environment

Predicting dark respiration rates of wheat leaves from hyperspectral reflectance

Onoriode Coast, Shahen Shah, Alexander Ivakov, Oorbessy Gaju, Philippa B. Wilson, Bradley C. Posch, Callum J. Bryant, Anna Clarissa A. Negrini, John R. Evans, Anthony G. Condon, Viridiana Silva-Pérez, Matthew P. Reynolds, Barry J. Pogson, A. Harvey Millar, Robert T. Furbank, Owen K. Atkin

Version of Record online: 28 March 2019

Measuring leaf dark respiration is either slow and cumbersome or rapid and destructive. We used light reflected from wheat leaf surfaces to rapidly and non-destructively estimate wheat respiration. Predictions were largely independent of the relationships between leaf dark respiration and leaf nitrogen or leaf mass per unit area. This finding highlights the potential for rapid non-invasive monitoring of various aspects of leaf energy metabolism in wheat.

Defining the developmental program leading to meiosis in maize

Science 05 Apr 2019:

Vol. 364, Issue 6435, pp. 52-56

Following meiosis in maize

Plants do not set aside a germ-cell lineage from early development as animals do, but instead generate germ cells on demand. Nelms and Walbot, working in maize, took advantage of a size differential between somatic and developing germ cells in the anthers at the top of the maize plant to isolate individual germ cells during the meiotic progression to pollen development. They used single-cell RNA sequencing to study changes in the transcriptome through meiosis. These studies revealed increasing specialization as meiosis progressed, with a reorganization of the transcriptome in a transition during the leptotene stage of meiosis.

Science, this issue p. [52](#)

Abstract

In multicellular organisms, the entry into meiosis is a complex process characterized by increasing meiotic specialization. Using single-cell RNA sequencing, we reconstructed the developmental program into maize male meiosis. A smooth continuum of expression stages before meiosis was followed by a two-step transcriptome reorganization in leptotene, during which 26.7% of transcripts changed in abundance by twofold or more. Analysis of cell-cycle gene expression

indicated that nearly all pregerminal cells proliferate, eliminating a stem-cell model to generate meiotic cells. Mutants defective in somatic differentiation or meiotic commitment expressed transcripts normally present in early meiosis after a delay; thus, the germinal transcriptional program is cell autonomous and can proceed despite meiotic failure.

The plant resistosome comes into focus

Nucleotide-binding, leucine-rich repeat receptors (NLRs) initiate immune responses when they sense a pathogen-associated effector. In animals, oligomerization of NLRs upon binding their effectors is key to downstream activity, but plant systems differ in many ways and their activation mechanisms have been less clear. In two papers, Wang *et al.* studied the composition and structure of an NLR called ZAR1 in the small mustard plant *Arabidopsis* (see the Perspective by Dangl and Jones). They determined cryo-electron microscopy structures that illustrate differences between inactive and intermediate states. The active, intermediate state of ZAR1 forms a wheel-like pentamer, called the resistosome. In this activated complex, a set of helices come together to form a funnel-shaped structure required for immune responsiveness and association with the plasma membrane.

Science, this issue p. [eaav5868](#), p. [eaav5870](#); see also p. [31](#)

[Ligand-triggered allosteric ADP release primes a plant NLR complex](#)

By Jizong Wang, Jia Wang, Meijuan Hu, Shan Wu, Jinfeng Qi, Guoxun Wang, Zhifu Han, Yijun Qi, Ning Gao, Hong-Wei Wang, Jian-Min Zhou, Jijie Chai

Science 05 Apr 2019 Full Access

Structural, biochemical, and functional studies show how a plant immune resistosome complex mediates cell death and disease resistance. [PDF](#)

[Reconstitution and structure of a plant NLR resistosome conferring immunity](#)

By Jizong Wang, Meijuan Hu, Jia Wang, Jinfeng Qi, Zhifu Han, Guoxun Wang, Yijun Qi, Hong-Wei Wang, Jian-Min Zhou, Jijie Chai

Science 05 Apr 2019 Full Access

Structural, biochemical, and functional studies show how a plant immune resistosome complex mediates cell death and disease resistance. [PDF](#)

GTPase clustering in response to a hormone

Some lipid variants that are rare in plasma membranes function as signaling components. Studying root tip cells of the model plant *Arabidopsis*, Platre *et al.* found that phosphatidylserine, which is relatively abundant in plasma membranes, also modulates signaling pathways. Phosphatidylserine is required for the clustering of ROP6, a small guanosine triphosphatase (GTPase), in membranes in response to signals from the plant hormone auxin. Changes in phosphatidylserine concentration altered the clustering of ROP6 and thus the auxin signaling response.

Science, this issue p. [57](#)

Review

[The challenge of antimicrobial resistance: What economics can contribute](#)

By Laurence S. J. Roope, Richard D. Smith, Koen B. Pouwels, James Buchanan, Lucy Abel, Peter Eibich, Christopher C. Butler, Pui San Tan, A. Sarah Walker, Julie V. Robotham, Sarah Wordsworth

Science 05 Apr 2019 Full Access [PDF](#)

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Genome-wide identification and abiotic stress-responsive pattern of heat shock transcription factor family in *Triticum aestivum* L.

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