April/May

Redox-mediated kick-start of mitochondrial energy metabolism drives resource-efficient seed germination
Thomas Nietzel, Jörg Mostertz, Cristina Ruberti, Guillaume Née, View ORCID ProfilePhilippe Fuchs, Stephan Wagner, Anna Moseler, View ORCID ProfileStefanie J. Müller-Schüssele, Abdelilah Benamar, Gernot Poschet, Michael Büttner, Ian Max Møller, Christopher H. Lillig, David Macherel, View ORCID ProfileMarkus Wirtz, Rüdiger Hell, Iris Finkemeier, View ORCID ProfileAndreas J. Meyer, Falko Hochgräfe, and View ORCID ProfileMarkus Schwarzländer
PNAS January 7, 2020 117 (1) 741-751; first published December 23, 2019 https://doi.org/10.1073/pnas.1910501117
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Nature | www.nature.com | 1ArticleA reference map of the human binary protein interactomeKatja LuckCalderwood1,2,3 ✉Global insights into cellular organization and genome function require comprehensive understanding of the interactome networks that mediate genotype–phenotype relationships1,2. Here we present a human 'all-by-all' reference interactome map of human binary protein interactions, or 'HuRI'. With approximately 53,000 protein–protein interactions, HuRI has approximately four times as many such interactions as there are high-quality curated interactions from small-scale studies. The integration of HuRI with genome3, transcriptome4 and proteome5 data enables cellular function to be studied within most physiological or pathological cellular contexts. We demonstrate the utility of HuRI in identifying the specific subcellular roles of protein–protein interactions. Inferred tissue-specific networks reveal general principles for the formation of cellular context-specific functions and elucidate potential molecular mechanisms that might underlie tissue-specific phenotypes of Mendelian diseases. HuRI is a systematic proteome-wide reference that links genomic variation to phenotypic outcomes.The reference human genome sequence has enabled systematic study of genetic6 and expression4 variability at the organism6, tissue4, cell type7 and single-cell level8. Despite advances in sequencing genomes, transcriptomes and proteomes, we still understand little about the cellular mechanisms that mediate phenotypic and tissue or cell type variability. A mechanistic understanding of cellular function and organization emerges from studying how genes and their products, primarily proteins, interact with each other, forming a dynamic inter-actome that drives biological function. Analogous to the reference human genome sequence9,10, a reference map of the human protein interactome, generated systematically and comprehensively, is needed to provide a scaffold for the unbiased proteome-wide study of biologi-cal mechanisms, generally and within specific cellular contexts.It remains infeasible to assemble a reference interactome map by sys-tematically identifying endogenous protein–protein interactions (PPIs) in thousands of physiological and pathological cellular contexts11,12. However, systematic affinity purification of exogenously expressed bait proteins in immortalized-cell contexts13 as well as binary PPI detection assays in cell models2,14 have generated biophysical human protein interactome maps of demonstrated high functional relevance. Specifi-cally, yeast two-hybrid (Y2H) represents the only binary PPI assay that can be operated at sufficient throughput to systematically screen the
https://doi.org/10.1038/s41586-020-2188-xReceived: 19 April 2019Accepted: 14 February 2020Published online: xx xx
Research Article

Horizontal gene transfer of *Fhb7* from fungus underlies *Fusarium* head blight resistance in wheat
Science 09 Apr 2020:
eaba5435
DOI: 10.1126/science.aba5435

Abstract
Fusarium head blight (FHB), a fungal disease caused by *Fusarium* species that produce food toxins, currently devastates wheat production worldwide, yet few resistance resources have been discovered in wheat germplasm. Here, we cloned the FHB resistance gene *Fhb7* based on assembling the genome of *Thinopyrum elongatum*, a species used in wheat distant hybridization breeding. *Fhb7* encodes a glutathione S-transferase (GST) and confers broad resistance to *Fusarium* species by detoxifying trichothecenes via de-epoxidation. *Fhb7* GST homologs are absent in plants, and our evidence supports *Th. elongatum* has gained *Fhb7* via horizontal gene transfer (HGT) from an endophytic *Epichloë* species. *Fhb7* introgressions in wheat confers resistance to both FHB and crown rot in diverse wheat backgrounds without yield penalty, providing a solution for *Fusarium* resistance breeding.

Plant Journal
FLOURY ENDOSPERM11-2 encodes plastid HSP70-2 involved with temperature-dependent chalkiness of rice (*Oryza sativa* L.) grains
Rehenuma Tabassum, Tokinori Dosaka, Hiroyuki Ichida, Ryouhei Morita, Yifan Ding, Tomoko Abe, Tomoyuki Katsube-Tanaka
First Published: 26 March 2020

Plant gene editing through de novo induction of meristems

By:Maher, MF (Maher, Michael F.)[1,2,3]; Nasti, RA (Nasti, Ryan A.)[2,3,4]; Vollbrecht, M (Vollbrecht, Macy)[4]; Starker, CG (Starker, Colby G.)[2,3,4]; Clark, MD (Clark, Matthew D.)[5]; Voytas, DF (Voytas, Daniel F.)[1,2,3,4]
View ResearcherID and ORCID

NATURE BIOTECHNOLOGY
Volume: 38 Issue: 1 Pages: 84-+ DOI: 10.1038/s41587-019-0337-2
Plant gene editing is typically performed by delivering reagents such as Cas9 and single guide RNAs to explants in culture. Edited cells are then induced to differentiate into whole plants by exposure to various hormones. The creation of edited plants through tissue culture is often inefficient, time-consuming, works for only limited species and genotypes, and causes unintended changes to the genome and epigenome. Here we report two methods to generate gene-edited dicotyledonous plants through de novo meristem induction. Developmental regulators and gene-editing reagents are delivered to somatic cells of whole plants. This induces meristems that produce shoots with targeted DNA modifications, and gene edits are transmitted to the next generation. The de novo induction of gene-edited meristems sidesteps the need for tissue culture and promises to overcome a bottleneck in plant gene editing.

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Structural and kinetic basis for the regulation and potentiation of Hsp104 function.
Proc Natl Acad Sci U S A. 2020 Apr 10;. PMID: 32277033 [PubMed - as supplied by publisher]

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The Molecular Chaperone CCT/TRiC: An Essential Component of Proteostasis and a Potential Modulator of Protein Aggregation.
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Small heat-shock proteins and their role in mechanical stress.
Cell Stress Chaperones. 2020 Apr 6;. PMID: 32253742 [PubMed - as supplied by publisher]

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Structural aspects of the human small heat shock proteins related to their functional activities.
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FERONIA controls pectin- and nitric oxide-mediated male-female interaction.
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Arabidopsis thaliana SURFEIT1-like genes link mitochondrial function to early plant development and hormonal growth responses.
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Trends in Plant Science
Towards Engineering Broad-Spectrum Disease-Resistant Crops
Pages 424-427
Jingjing Tian, Guoyong Xu, Meng Yuan

Malate Circulation: Linking Chloroplast Metabolism to Mitochondrial ROS
Pages 446-454
Yannan Zhao, Hong Yu, Jian-Min Zhou, Steven M. Smith, Jiayang Li

Review
The physiology of plant responses to drought

Aditi Gupta, Andrés Rico-Medina, Ana I. Caño-Delgado*

Department of Molecular Genetics, Centre for Research in Agricultural Genomics (CRAG), CSIC-IRTA-UAB-UB, Campus UAB (Cerdanyola del Vallès), 08193 Barcelona, Spain.
Science 17 Apr 2020:
Vol. 368, Issue 6488, pp. 266-269
DOI: 10.1126/science.aaz7614

Drought alone causes more annual loss in crop yield than all pathogens combined. To adapt to moisture gradients in soil, plants alter their physiology, modify root growth and architecture, and close stomata on their aboveground segments. These tissue-specific responses modify the flux of cellular signals, resulting in early flowering or stunted growth and, often, reduced yield. Physiological and molecular analyses of the model plant *Arabidopsis thaliana* have identified phytohormone signaling as key for regulating the response to drought or water insufficiency. Here we discuss how engineering hormone signaling in specific cells and cellular domains can facilitate improved plant responses to drought. We explore current knowledge and future questions central to the quest to produce high-yield, drought-resistant crops.

Harnessing rhizosphere microbiomes for drought-resilient crop production
By Franciska T. de Vries, Rob I. Griffiths, Christopher G. Knight, Oceane Nicolitch, Alex Williams
*Science*17 Apr 2020 : 270-274
PDF

A PAMless base editor

CRISPR-Cas DNA base editing typically requires a specific motif for targeting known as a protospacer-adjacent motif (PAM). This requirement limits the sequences within a genome that can be targeted. Walton *et al.* engineered specific variants of the *Streptococcus pyogenes* Cas9 enzyme named SpG and SpRY that could recognize and edit a wider array of PAMs. Using SpRY, the authors were able to correct previously uneditable mutations associated with human disease. Although off-target effects were observed for these engineered Cas enzymes at levels similar to those of the wild-type enzyme, depending on the context, these engineered enzymes widen the potential applications of precision genome editing.

Science, this issue p. 290
Unconstrained genome targeting with near-PAMless engineered CRISPR-Cas9 variants
Science 17 Apr 2020:
Vol. 368, Issue 6488, pp. 290-296
DOI: 10.1126/science.aba8853

PerspectiveMetabolism
Probing metabolism in time and space
1. Theodore Alexandrov
See all authors and affiliations
Science 17 Apr 2020:
Vol. 368, Issue 6488, pp. 241-242
DOI: 10.1126/science.abb3094

Signs of a metabolon in action
Eukaryotic cells have a heterogeneous cytoplasm, with compartments large and small, membrane bound or not. Enzymes that catalyze the de novo synthesis of purine nucleotides, which are needed in rapidly dividing cells, are known to assemble into loosely associated, multienzyme structures called purinosomes, but the extent to which these structures are metabolically active has been less certain. Pareek *et al.* performed metabolomics to trace how purines are synthesized

within purinosomes and used sophisticated mass spectrometry imaging to directly observe hotspots of metabolic activity within frozen HeLa cells (see the Perspective by Alexandrov). They found evidence for metabolic channeling between enzymes, which limits equilibration of intermediates formed in purinosomes with the bulk cellular metabolite pool. This process occurs specifically within purinosomes associated with mitochondria, because the input metabolites, glycine, aspartate, and formate, come from mitochondrial metabolism. Such channeling may help cells control the ratio and abundance of purine nucleotides.

Science, this issue p. 283; see also p. 241

Metabolomics and mass spectrometry imaging reveal channeled de novo purine synthesis in cells
By Vidhi Pareek, Hua Tian, Nicholas Winograd, Stephen J. Benkovic
*Science*17 Apr 2020 : 283-290
Channeled de novo purine biosynthesis intermediates within an in vivo metabolon are examined.

- Editor's Summary
- Abstract
- Full Text
- PDF
- Supplementary Materials

Coupling translation and mRNA decay
Gene expression requires messenger RNAs (mRNAs)—DNA-derived blueprints of genes—to be translated by protein-producing ribosomes. The levels of mRNAs are tightly regulated, in part by controlling their half-lives. In eukaryotic cells, mRNA half-life is largely linked to translational efficiency, but the mechanism underlying this link has remained elusive. Buschauer *et al.* used cryo–electron microscopy and RNA sequencing to show how a key regulator of mRNA degradation, the Ccr4-Not complex, monitors the ribosome during mRNA translation. They found that the Not5 subunit directly binds to a ribosomal site exposed specifically during inefficient decoding, thereby triggering mRNA degradation. Analysis of mutants revealed the importance of this sensing mechanism for mRNA homeostasis.

Science, this issue p. eaay6912

The Ccr4-Not complex monitors the translating ribosome for codon optimality
By Robert Buschauer, Yoshitaka Matsuo, Takato Sugiyama, Ying-Hsin Chen, Najwa Alhusaini, Thomas Sweet, Ken Ikeuchi, Jingdong Cheng, Yasuko Matsuki, Risa Nobuta, Andrea Gilmozzi, Otto Berninghausen, Petr Tesina, Thomas Becker, Jeff Coller, Toshifumi Inada, Roland Beckmann
*Science*17 Apr 2020
A protein complex binds to ribosomes that lack bound tRNAs, thus connecting translation elongation problems and mRNA decay.

- Editor's Summary
- Abstract
- Full Text
- PDF
- Supplementary Materials

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The Ccr4-Not complex monitors the translating ribosome for codon optimality.
Science. 2020 Apr 17;368(6488).
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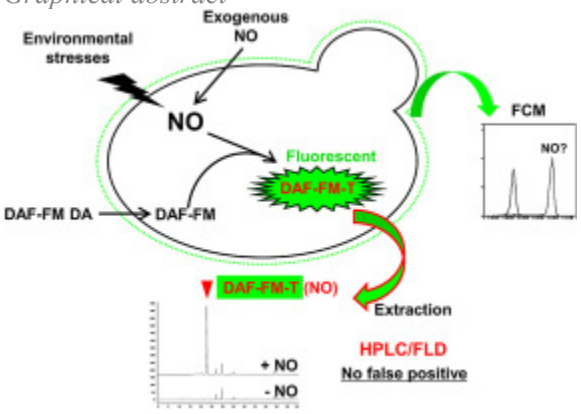
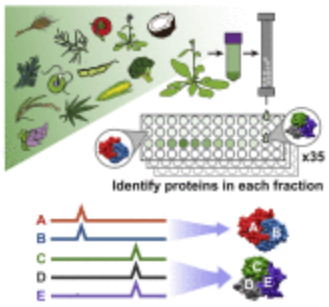
Detection system of the intracellular nitric oxide in yeast by HPLC with a fluorescence detector
Ryo Nasuno, Seiya Shino, Yuki Yoshikawa, Natsuko Yoshioka, ... Hiroshi Takagi

Graphical abstract





A Pan-plant Protein Complex Map Reveals Deep Conservation and Novel Assemblies
Claire D. McWhite,… Edward M. Marcotte

This massive plant proteomics project, using co-fractionation mass spectrometry to measure the amounts and associations of over two million proteins from 13 diverse plant species, reveals stable protein complexes shared across plant cells and provides a framework for interpreting plant genetics and mutant phenotypes. PDF

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Trends in Plant Science
Mass Spectrometry Untangles Plant Membrane Protein Signaling Networks
Available Online 28 April 2020
Yanmei Chen, Wolfram Weckwerth

Structural Proteomics Applied to Plant Membrane Protein Complexes
Available Online 29 April 2020
Pascal Albanese, Sem Tamara, Richard A. Scheltema, Cristina Pagliano

eLIFE
STRUCTURAL BIOLOGY AND MOLECULAR BIOPHYSICS
Multi-state recognition pathway of the intrinsically disordered protein kinase inhibitor by protein kinase A
Cristina Olivieri, Yingjie Wang ... Gianluigi Veglia

COMPUTATIONAL AND SYSTEMS BIOLOGY, EVOLUTIONARY BIOLOGY
Over half a million enzymes share the same minimal core
The origins and evolution of carbohydrate-building enzymes have been traced across the tree of life, uncovering a minimal structural unit of this diverse enzyme family.

Plant,Cell & Environment

Glutathione-dependent denitrosation of GSNOR1 promotes oxidative signalling downstream of H2O2
Tianru Zhang, Mingyue Ma, Tao Chen, Linlin Zhang, Lingling Fan, Wei Zhang, Bo Wei, Shengchun Li, Wei Xuan, Graham Noctor, Yi Han
Pages: 1175-1191 | First Published: 28 January 2020

The present study investigates the roles of GSNOR and glutathione in regulating the SA pathway triggered by photorespiratory H_2O_2 in Arabidopsis. Up-regulation of GSNOR is required for the activation of SA pathway downstream

of H_2O_2. Glutathione-dependent denitrosation is necessary to maintain the up-regulation of GSNOR activities and may coordinate GSNOR activities with protein SNO levels to ensure appropriate signalling strength through the SA pathway in response to H_2O_2.

VIPP2 interacts with VIPP1 and HSP22E/F at chloroplast membranes and modulates a retrograde signal for *HSP22E/F* gene expression

Jasmine Theis, Justus Niemeyer, Stefan Schmollinger, Fabian Ries, Mark Rütgers, Tilak Kumar Gupta, Frederik Sommer, Ligia Segatto Muranaka, Benedikt Venn, Miriam Schulz-Raffelt, Felix Willmund, Benjamin D. Engel, Michael Schroda

Pages: 1212-1229 | First Published: 29 January 2020

The VIPP2 protein from *Chlamydomonas reinhardtii* localizes predominantly to chloroplast membranes under stresses inducing protein mistargeting and misfolding. VIPP2 interacts with VIPP1 as major partner and with HSP22E/F as minor partner and modulates a retrograde signal for HSP22E/F gene expression in high light.

Foundations of ER-phagy regulation

In their study in *Cell* Liang et al. identify 200 regulators of ER-phagy and specifically dissect the role of mitochondrial oxidative metabolism and protein UFMylation in promoting ER-phagy.

The functions of short ORFs and their microproteins

Many ‘non-coding’ RNAs contain different types of coding sequences, which are translated into functional microproteins or peptides.

Eytan Zlotorynski

Research Highlight | 26 March 2020

DNA 6mA in times of mitochondrial stress

A new study in *Molecular Cell* shows that human mitochondrial DNA is enriched for the DNA modification N^6-methyldeoxyadenosine, which can repress mitochondrial gene expression and regulate the transcriptional response to mitochondrial stress.

ELIFE

STRUCTURAL BIOLOGY AND MOLECULAR BIOPHYSICS

Same structure, different mechanisms?

Francis TF Tsai, Christopher P Hill

Two interpretations of similar structures for the same molecular machine illustrate the limits of inferring biochemical mechanism from protein structure.

This is a commentary about AAA+ATPAses.

Current Biology

Selecting for Altered Substrate Specificity Reveals the Evolutionary Flexibility of ATP-Binding Cassette Transporters

Pages 1689-1702.e6 Sriram Srikant, Rachelle Gaudet, Andrew W. Murray

Shatov VM, Gusev NB.

Physico-chemical properties of two point mutants of small heat shock protein HspB6 (Hsp20) with abrogated cardioprotection.

Biochimie. 2020 Apr 27;. [Epub ahead of print]

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