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Makley LN, McMenimen KA, DeVree BT, Goldman JW, McGlasson BN, Rajagopal P, Dunyak BM, McQuade TJ, Thompson AD, Sunahara R, Klevit RE, Andley UP, Gestwicki JE.
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Lin Z, Eaves DJ, Sanchez-Moran E, Franklin FC, Franklin-Tong VE.

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PMID: 26542573 [PubMed - in process]

Keith

Defining Hsp70 Subnetworks in Dengue Virus Replication Reveals Key Vulnerability in Flavivirus Infection

Cell. 2015 Nov 11. pii: S0092-8674(15)01402-6. doi: 10.1016/j.cell.2015.10.046. [Epub ahead of print]

Taguwa S1, Maringer K2, Li X3, Bernal-Rubio D4, Rauch JN3, Gestwicki JE3, Andino R5, Fernandez-Sesma A4, Frydman J6.

Viral protein homeostasis depends entirely on the machinery of the infected cell. Accordingly, viruses can illuminate the interplay between cellular proteostasis components and their distinct substrates. Here, we define how the Hsp70 chaperone network mediates the dengue virus life cycle. Cytosolic Hsp70 isoforms are required at distinct steps of the viral cycle, including entry, RNA replication, and virion biogenesis. Hsp70 function at each step is specified by nine distinct DNAJ cofactors. Of these, DnaJB11 relocalizes to virus-induced replication complexes to promote RNA synthesis, while DnaJB6 associates with capsid protein and facilitates virion biogenesis. Importantly, an allosteric Hsp70 inhibitor, JG40, potently blocks infection of different dengue serotypes in human primary blood cells without eliciting viral resistance or exerting toxicity to the host cells. JG40 also blocks replication of other medically-important flaviviruses including yellow fever, West Nile and Japanese encephalitis viruses. Thus, targeting host Hsp70 subnetworks provides a path for broad-spectrum antivirals.

Fionn

Cell Stress and Chaperones

Characterization of 5′UTR of rice ClpB-C/Hsp100 gene: evidence
of its involvement in post-transcriptional regulation
Ratnesh Chandra Mishra1 & Richa1 & Amanjot Singh1 & Lalit Dev Tiwari1 & Anil Grover1

Abstract Rice (Oryza sativa) ClpB-C (OsClpB-C) protein is

expressed upon heat stress in vegetative tissues and constitutively in seeds. We produced stably transformed Arabidopsis plants carrying β-glucuronidase (Gus) reporter gene downstream to 1-kb OsClpB-C promoter (1kbPro plants). In the 1kbPro plants, expression of Gus transcript and protein followed the expression pattern of OsClpB-C gene in rice plants, i.e., heat induced in vegetative tissues and constitutive in seeds. Next, we produced transgenic Arabidopsis plants containing Gus downstream to 862-bp fragment of OsClpBC promoter [lacking 138 nucleotides from 3′ end of the 5′ untranslated region (5′UTR); ΔUTR plants). In ΔUTR plants, Gus transcript was expressed in heat-inducible manner, but strikingly, Gus protein levels were negligible after heat treatment. However, Gus protein was expressed in ΔUTR seedlings at levels comparable to 1kbPro seedlings when recovery treatment of 22 °C/2 h was given post heat stress (38 °C/ 15 min). This suggests that 5′UTR of OsClpB-C gene is involved in its post-transcriptional regulation and is an obligate requirement for protein expression during persistent heat stress. Furthermore, the Gus transcript levels were higher in the polysomal RNA fraction in heat-stressed seedlings of 1kbPro plants as compared to ΔUTR plants, indicating that 5′UTR aids in assembly of ribosomes onto the Gus transcript during heat stress. Unlike the case of seedlings, Gus protein was formed constitutively in ΔUTR seeds at levels comparable to 1kbPro seeds. Hence, the function of 5′UTR of OsClpBC is dispensable for expression in seeds.

Plant Cell and environment

 Dissecting the proteome dynamics of the early heat stress response leading to plant survival or death in Arabidopsis Echevarría-Zomeño Sira1*, Fernández-Calvino Lourdes1*, Castro-Sanz Ana B.1, López Juan Antonio2, Vázquez Jesús 2 and Castellano M. Mar1§

Abstract In many plant species, an exposure to a sublethal temperature triggers an adaptative response called acclimation. This response involves an extensive molecular reprogramming that allows the plant to further survive to an otherwise lethal increase of temperature. A related response is also launched under an abrupt and lethal heat stress that, in this case, is unable to successfully promote thermotolerance and therefore ends up in plant death. Although these molecular programs are expected to have common players, the overlapping degree and the specific regulators of each process are currently unknown. We have carried out a high-throughput comparative proteomics analysis during acclimation and during the early stages of the plant response to a severe heat stress that lead Arabidopsis seedlings either to survival or death. This analysis dissects these

responses, unravels the common players and identifies the specific proteins associated with these different fates. Thermotolerance assays of mutants in genes with an uncharacterized role in heat stress demonstrate the relevance of this study to uncover both positive and negative heat regulators and pinpoint a pivotal role of JR1 and BAG6 in heat tolerance.

Nature

Discovery of long-sought biological compass claimed
Protein complex offers explanation for how animals sense Earth's magnetic pull.

Mary

Prion aggregate structure in yeast cells is determined by the Hsp104-Hsp110 disaggregase machinery.
O'Driscoll J1, Clare D1, Saibil H2.

Abstract
Prions consist of misfolded proteins that have adopted an infectious amyloid conformation. In vivo, prion biogenesis is intimately associated with the protein quality control machinery. Using electron tomography, we probed the effects of the heat shock protein Hsp70 chaperone system on the structure of a model yeast [PSI+] prion in situ. Individual Hsp70 deletions shift the balance between fibril assembly and disassembly, resulting in a variable shell of nonfibrillar, but still immobile, aggregates at the surface of the [PSI+] prion deposits. Both Hsp104 (an Hsp100 disaggregase) and Sse1 (the major yeast form of Hsp110) were localized to this surface shell of [PSI+] deposits in the deletion mutants. Elevation of Hsp104 expression promoted the appearance of this novel, nonfibrillar form of the prion aggregate. Moreover, Sse1 was found to regulate prion fibril length. Our studies reveal a key role for Sse1 (Hsp110), in cooperation with Hsp104, in regulating the length and assembly state of [PSI+] prion fibrils in vivo.

Minsoo

1. Plant Physiol. 2015 Nov 4. pii: pp.01591.2015. [Epub ahead of print]

**The MTL1 Pentatricopeptide Repeat Protein is Required for Both Translation and
Splicing of the mitochondrial NADH Dehydrogenase Subunit 7 mRNA in Arabidopsis.**

Nawel H(1), Nadège A(2), Martine Q(1), Planchard N(1), Nathalie V(1), Jennifer D(3), Colas des Francs-Small C(4), Mireau H(5).

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Mitochondrial translation involves a complex interplay of ancient bacterial-like features and host-derived functionalities. Although the basic components of the mitochondrial translation apparatus have been recognized, **very few protein factors aiding in recruiting ribosomes on mitochondria-encoded mRNAs have been identified in higher plants.** In this study, we describe the identification of the Arabidopsis MITOCHONDRIAL TRANSLATION FACTOR 1 (MTL1) protein - a new member of the PentatricoPeptide Repeat family - and show **that it is essential for the translation of the mitochondrial nad7 mRNA.** We demonstrate that mtl1 mutant plants fail to accumulate the Nad7 protein, even though the nad7 mature mRNA is produced and bears the same 5' and 3' extremities as in wild-type plants. We next observed that **polysome association of nad7 mature mRNA is specifically disrupted in mtl1 mutants, indicating that the absence of Nad7 results from a lack of translation of nad7 mRNA**. These findings illustrate that mitochondrial translation requires the intervention of gene-specific nuclear-encoded PPR trans-factors and that their action does not necessarily involve the 5' processing of their target mRNA as previously observed. Interestingly, a partial decrease in nad7 intron 2 splicing was also detected in mtl1 mutants suggesting that MTL1 is also involved in group II intron splicing. However, this second function appears less essential for nad7 expression than its role in translation. MTL1 will be instrumental to understand the multi-functionality of PPR proteins and the mechanisms governing mRNA translation and intron splicing in plant mitochondria.

2. Plant Cell. 2015 Nov 3. pii: tpc.15.00509. [Epub ahead of print]

The EF-Hand Ca2+ Binding Protein MICU Choreographs Mitochondrial Ca2+ Dynamics in Arabidopsis.

Wagner S(1), Behera S(2), De Bortoli S(3), Logan DC(4), Fuchs P(1), Carraretto L(3), Teardo E(3), Cendron L(3), Nietzel T(1), Füßl M(5), Doccula FG(2), Navazio L(3), Fricker MD(6), Van Aken O(7), Finkemeier I(8), Meyer AJ(9), Szabò I(3), Costa A(10), Schwarzländer M(11).

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(5)Plant Proteomics Group, Max-Planck-Institute for Plant Breeding Research, 50829 Cologne, Germany. (6)Department of Plant Sciences, University of Oxford, Oxford OX1 3RB, United Kingdom. (7)ARC Centre of Excellence in Plant Energy Biology, University of Western Australia, Crawley, WA 6009, Australia. (8)Plant Proteomics Group, Max-Planck-Institute for Plant Breeding Research, 50829 Cologne, Germany Institute for Plant Biology and Biotechnology, University of Münster, 48149 Münster, Germany. (9)Department Chemical Signalling, Institute of Crop Science and Resource Conservation, University of Bonn, 53113 Bonn, Germany. (10)Department of Biosciences, University of Milan, 20133 Milan, Italy Institute of Biophysics, Consiglio Nazionale delle Ricerche, 20133 Milan, Italy. (11)Plant Energy Biology Lab, Institute of Crop Science and Resource Conservation, University of Bonn, 53113 Bonn, Germany markus.schwarzlander@uni-bonn.de.

Plant organelle function must constantly adjust to environmental conditions, which requires dynamic coordination. Ca(2+) signaling may play a central role in this process. Free Ca(2+) dynamics are tightly regulated and differ markedly between the cytosol, plastid stroma, and mitochondrial matrix. The mechanistic basis of compartment-specific Ca(2+) dynamics is poorly understood. Here, we studied **the function of At-MICU, an EF-hand protein of Arabidopsis thaliana with homology to constituents of the mitochondrial Ca(2+) uniporter machinery in mammals.** MICU binds Ca(2+) and localizes to the mitochondria in Arabidopsis. In vivo imaging of roots expressing a genetically encoded Ca(2+) sensor in the mitochondrial matrix revealed that lack of MICU increased resting concentrations of free Ca(2+) in the matrix. Furthermore, **Ca(2+) elevations triggered by auxin and extracellular ATP occurred more rapidly and reached higher maximal concentrations in the mitochondria of micu mutants**, whereas cytosolic Ca(2+) signatures remained unchanged. These findings support the idea that a conserved uniporter system, with composition and regulation distinct from the mammalian machinery, mediates mitochondrial Ca(2+) uptake in plants under in vivo conditions. They further suggest that **MICU acts as a throttle that controls Ca(2+) uptake by moderating influx, thereby shaping Ca(2+) signatures in the matrix and preserving mitochondrial homeostasis.** Our results open the door to genetic dissection of mitochondrial Ca(2+) signaling in plants.

3. J Biol Chem. 2015 Nov 13;290(46):27644-59. doi: 10.1074/jbc.M115.654129. Epub 2015 Oct 2.

Subcellular Distribution of NAD+ between Cytosol and Mitochondria Determines the Metabolic Profile of Human Cells.

VanLinden MR(1), Dölle C(2), Pettersen IK(3), Kulikova VA(4), Niere M(1), Agrimi G(5), Dyrstad SE(3), Palmieri F(6), Nikiforov AA(7), Tronstad KJ(3), Ziegler M(1).

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(1)From the Departments of Molecular Biology and. (2)From the Departments of Molecular Biology and Christian.Doelle@uib.no. (3)Biomedicine, University of Bergen, 5020 Bergen, Norway. (4)the Institute of Nanobiotechnologies, Peter the Great St. Petersburg Polytechnic University, 195251 St. Petersburg, Russia. (5)the Department of Biosciences, Biotechnologies and Biopharmaceutics and. (6)the Department of Biosciences, Biotechnologies and Biopharmaceutics and the Center of Excellence in Comparative Genomics, University of Bari, 70125 Bari, Italy, and. (7)the Institute of Nanobiotechnologies, Peter the Great St. Petersburg Polytechnic University, 195251 St. Petersburg, Russia, the Institute of Cytology, Russian Academy of Sciences, 194064 St. Petersburg, Russia.

The mitochondrial NAD pool is particularly important for the maintenance of vital cellular functions. **Although at least in some fungi and plants, mitochondrial NAD
is imported from the cytosol by carrier proteins, in mammals, the mechanism of
how this organellar pool is generated has remained obscure.** A transporter mediating NAD import into mammalian mitochondria has not been identified. In contrast, human recombinant NMNAT3 localizes to the mitochondrial matrix and is able to catalyze NAD(+) biosynthesis in vitro. However, whether the endogenous NMNAT3 protein is functionally effective at generating NAD(+) in mitochondria of intact human cells still remains to be demonstrated**. To modulate mitochondrial NAD(+) content, we have expressed plant and yeast mitochondrial NAD(+) carriers
in human cells and observed a profound increase in mitochondrial NAD(+).** None of
the closest human homologs of these carriers had any detectable effect on mitochondrial NAD(+) content. Surprisingly, **constitutive redistribution of NAD(+)
from the cytosol to the mitochondria by stable expression of the Arabidopsis thaliana mitochondrial NAD(+) transporter NDT2 in HEK293 cells resulted in dramatic growth retardation and a metabolic shift from oxidative phosphorylation
to glycolysis, despite the elevated mitochondrial NAD(+) levels.** These results suggest that a mitochondrial NAD(+) transporter, similar to the known one from A. thaliana, is likely absent and could even be harmful in human cells. We provide further support for the **alternative possibility, namely intramitochondrial NAD(+)
synthesis, by demonstrating the presence of endogenous NMNAT3 in the mitochondria
of human cells.**

Elizabeth

Cell: Alert 31 October-6 November
Modifications on Translation Initiation *Pages 796-798* Sarah F. Mitchell, Roy Parker
The LC Domain of hnRNPA2 Adopts Similar Conformations in Hydrogel Polymers, Liquid-like Droplets, and Nuclei Original Research Article *Pages 829-839*
Siheng Xiang, Masato Kato, Leeju C. Wu, Yi Lin, Ming Ding, Yajie Zhang, Yonghao Yu, Steven L. McKnight
5′ UTR m6A Promotes Cap-Independent Translation Original Research Article *Pages 999-1010*
Kate D. Meyer, Deepak P. Patil, Jun Zhou, Alexandra Zinoviev, Maxim A. Skabkin, Olivier Elemento, Tatyana V. Pestova, Shu-Bing Qian, Samie R. Jaffrey
Discovery of a Unique Clp Component, ClpF, in Chloroplasts: A Proposed Binary ClpF-ClpS1 Adaptor Complex Functions in Substrate Recognition and Delivery
Kenji Nishimura, Janina Apitz, Giulia Friso, Jitae Kim, Lalit Ponnala, Bernhard Grimm, and Klaas J. van Wijk
Plant Cell 2015 27: 2677-2691. First Published on September 29, 2015; doi:10.1105/tpc.15.00574 **OPEN**
http://www.plantcell.org/content/27/10/2677.abstract
Discovery of a multimeric adaptor system for the chloroplast Clp protease machinery suggests a complex mechanism regulates substrate recognition and delivery in chloroplasts.

Arabidopsis CBP1 Is a Novel Regulator of Transcription Initiation in Central Cell-Mediated Pollen Tube Guidance
Hong-Ju Li, Shan-Shan Zhu, Meng-Xia Zhang, Tong Wang, Liang Liang, Yong Xue, Dong-Qiao Shi, Jie Liu, and Wei-Cai Yang
Plant Cell 2015 27: 2880-2893. First Published on October 13, 2015; doi:10.1105/tpc.15.00370 **OPEN**
http://www.plantcell.org/content/27/10/2880.abstract
A novel regulator of transcription initiation in the central cell mediates pollen tube attraction in a non-cell-autonomous manner.

The RECG1 DNA Translocase Is a Key Factor in Recombination Surveillance, Repair, and Segregation of the Mitochondrial DNA in Arabidopsis
Clémentine Wallet, Monique Le Ret, Marc Bergdoll, Marc Bichara, André Dietrich, and José M. Gualberto
Plant Cell 2015 27: 2907-2925. First Published on October 13, 2015; doi:10.1105/tpc.15.00680 **OPEN**
http://www.plantcell.org/content/27/10/2907.abstract
Arabidopsis RECG1 acts in mtDNA repair in the suppression of ectopic recombination and in the segregation of alternative mitotypes.

Dissecting the proteome dynamics of the early heat stress response leading to plant survival or death in Arabidopsis
Sira Echevarría-Zomeño, Lourdes Fernández-Calvino, Ana B. Castro-Sanz, Juan

Antonio López, Jesús Vázquez and M. Mar Castellano
Accepted manuscript online: 18 NOV 2015 07:03PM EST | DOI: 10.1111/pce.12664
Nature Chemical Biology

Focus on Frontiers in chemical biology
XFELs open a new era in structural chemical biology - pp895 – 899 Petra Fromme

doi:10.1038/nchembio.1968

X-ray crystallography, the workhorse of structural biology, has been revolutionized by the advent of serial femtosecond crystallography using X-ray free electron lasers. Here, the fast pace and history of discoveries are discussed together with current challenges and the method's great potential to make new structural discoveries, such as the ability to generate molecular movies of biomolecules at work.

Cell

Plasticity of an Ultrafast Interaction between Nucleoporins and Nuclear Transport Receptors Volume 163, Issue 3, 22 October 2015, Pages 734–745
•Integrative structural biology reveals the basis of rapid nuclear transport
•Transient binding of disordered nucleoporins leaves their plasticity unaffected
•Multiple minimalistic low-affinity binding motifs create a polyvalent complex
•A highly reactive and dynamic surface permits an ultrafast binding mechanism
Sigrid Milles, Davide Mercadante[2, 3, 8], Iker Valle Aramburu[1, 8], Malene Ringkjøbing Jensen[4, 5, 6], Niccolò Banterle[1], Christine Koehler[1], Swati Tyagi[1], Jane Clarke[7], Sarah L. Shammas[7], Martin Blackledge[4, 5, 6,], Frauke Gräter[2, 3,], Edward A. Lemke[1,]

Nature Reviews Molecular Cell Biology 13, 168-182 (March 2012) | doi:10.1038/nrm3286

Designer proteins: applications of genetic code expansion in cell biology
Lloyd Davis[1] & Jason W. Chin[1]

Designer amino acids, beyond the canonical 20 that are normally used by cells, can now be site-specifically encoded into proteins in cells and organisms. This is achieved using 'orthogonal' aminoacyl-tRNA synthetase–tRNA pairs that direct amino acid incorporation in response to an amber stop codon (UAG) placed in a gene of interest. Using this approach, it is now possible to study biology in vitro and in vivo with an increased level of molecular precision. This has allowed new biological insights into protein conformational changes, protein interactions, elementary processes in signal transduction and the role of post-translational modifications.

Nature Chemical Biology

A chemocentric view of the natural product inventory - pp620 - 624
Christopher T Walsh doi:10.1038/nchembio.1894
As the identification of previously undetected microbial biosynthetic pathways burgeons, there arises the question of how much new chemistry is yet to be found. This, in turn, devolves to: what kinds of biosynthetic enzymatic transformations are yet to be characterized?

Layers of structure and function in protein aggregation - pp373 - 377
Motomasa Tanaka & Yusuke Komi doi:10.1038/nchembio.1818
Protein aggregation is a central hallmark of many neurodegenerative disorders, but the relationship of aggregate structural diversity to the resultant cellular cytotoxicity and phenotypic diversity has remained obscure. Recent advances in understanding the mechanisms of protein aggregation and their physiological consequences have been achieved through chemical biology approaches, such as rationally designed protein modifications and chemical probes, providing crucial mechanistic insights and promise for therapeutic strategies for brain disorders.

Nature Chemical Biology | Article
Mechanism of photoprotection in the cyanobacterial ancestor of plant antenna proteins
Hristina Staleva, Josef Komenda, Mahendra K Shukla, Václav Šlouf, Radek Kaňa, Tomáš Polívka & Roman Sobotka
Nature Chemical Biology 11,287–291 (2015) doi:10.1038/nchembio.1755
Plants collect light for photosynthesis using light-harvesting complexes (LHCs)—an array of chlorophyll proteins that are able to reversibly switch from harvesting to energy-dissipation mode to prevent damage of the photosynthetic apparatus. LHC antennae as well as other members of the LHC superfamily evolved from cyanobacterial ancestors called high light–inducible proteins (Hlips). Here, we characterized a purified Hlip family member HliD isolated from the cyanobacterium *Synechocystis* sp. PCC 6803. We found that the HliD binds chlorophyll-*a* (Chl-*a*) and β-carotene and exhibits an energy-dissipative conformation. Using femtosecond spectroscopy, we demonstrated that the energy dissipation is achieved via direct energy transfer from a Chl-*a* Q_y state to the β-carotene S_1 state. We did not detect any cation of β-carotene that would accompany Chl-*a* quenching. These results provide proof of principle that this quenching mechanism operates in the LHC superfamily and also shed light on the photoprotective role of Hlips and the evolution of LHC antennae.

A cytosolic network suppressing mitochondria-mediated proteostatic stress and cell death
Xiaowen Wang & Xin Jie Chen
Nature 524, 481–484 (27 August 2015) doi:10.1038/nature14859

Matsushita K, Azuma Y, Kosaka T, Yakushi T, Hoshida H, Akada R, Yamada M.
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The RING Finger Ubiquitin E3 Ligase OsHTAS Enhances Heat Tolerance by Promoting H2O2-Induced Stomatal Closure in Rice.
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Mechanisms of nitric oxide crosstalk with reactive oxygen species scavenging enzymes during abiotic stress tolerance in plants.
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Plant Cell Advance Publication
Chemical Modifications Mark Alternatively Spliced and Uncapped Messenger RNAs in Arabidopsis
Lee E. Vandivier, Rafael Campos, Pavel P. Kuksa, Ian M. Silverman, Li-San Wang, and Brian D. Gregory
Plant Cell 2015 tpc.15.00591; Advance Publication November 11, 2015; doi:10.1105/tpc.15.00591 OPEN
http://www.plantcell.org/content/early/2015/11/11/tpc.15.00591.abstract
Global identification of RNA modifications that affect the Watson-Crick base-pairing edge across the Arabidopsis transcriptome provides insights into the many functions of these important additions.

The Plant Journal Content Alert: 84, 4 (November 2015)
A phosphopantetheinyl transferase that is essential for mitochondrial fatty acid biosynthesis (pages 718–732)
Xin Guan, Hui Chen, Alex Abramson, Huimin Man, Jinxia Wu, Oliver Yu and Basil J. Nikolau
Article first published online: 13 NOV 2015 | DOI: 10.1111/tpj.13034
The catalytic functions of all Type II fatty acid synthases require

phosphopantetheinylation of apo-acyl carrier proteins. Here we identify the enzyme responsible for this protein modification in mitochondria.

Current Opinion in Structural Biology: Alert 3 November-9 November
Mitochondrial machineries for insertion of membrane proteins Review Article
Pages 92-102
Maria Bohnert, Nikolaus Pfanner, Martin van der Laan
Gaining mass: the structure of respiratory complex I — from bacterial towards mitochondrial versions Review Article
Pages 135-145 James A Letts, Leonid A Sazanov

Novosylna O, Jurewicz E, Pydiura N, Goral A, Filipek A, Negrutskii B, El'skaya A.
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Pharmacological chaperone for Î±-crystallin partially restores transparency in cataract models.
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A dynamic RNA loop in an IRES affects multiple steps of elongation factor-mediated translation initiation.
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Plants Release Precursors of Histone Deacetylase Inhibitors to Suppress Growth of Competitors
Sascha Venturelli, Regina G. Belz, Andreas Kämper, Alexander Berger, Kyra von Horn, André Wegner, Alexander Böcker, Gérald Zabulon, Tobias Langenecker, Oliver Kohlbacher, Fredy Barneche, Detlef Weigel, Ulrich M. Lauer, Michael Bitzer, and Claude Becker
Plant Cell 2015 tpc.15.00585; Advance Publication November 3, 2015; doi:10.1105/tpc.15.00585 OPEN
http://www.plantcell.org/content/early/2015/11/03/tpc.15.00585.abstract
Chemical compounds in plant root exudates influence the growth of neighboring plants by interfering with their chromatin configuration and gene expression.

The EF-Hand Ca^{2+} Binding Protein MICU Choreographs Mitochondrial Ca^{2+} Dynamics in Arabidopsis
Stephan Wagner, Smrutisanjita Behera, Sara De Bortoli, David C. Logan, Philippe Fuchs, Luca Carraretto, Enrico Teardo, Laura Cendron, Thomas Nietzel, Magdalena Füßl, Fabrizio G. Doccula, Lorella Navazio, Mark D. Fricker, Olivier Van Aken, Iris Finkemeier, Andreas J. Meyer, Ildikò Szabò, Alex Costa, and Markus Schwarzländer
Plant Cell 2015 tpc.15.00509; Advance Publication November 3, 2015; doi:10.1105/tpc.15.00509 OPEN
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The mitochondrial Ca2+ uptake protein At-MICU shapes mitochondrial Ca2+ dynamics, providing molecular in vivo evidence for the existence and function of a mitochondrial uniporter complex in plants.

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