Patrick

1. **Ferredoxin:NADP(H) Oxidoreductase Abundance and Location Influences Redox Poise and Stress Tolerance**
   Marina Kozuleva, Tatjana Goss, Manuel Twachtmann, Katherina Rudi, Jennifer Trapka, Jennifer Selinski,
   Boris Ivanov, Prashanth Garapati, Heinz-Juergen Steinhoff, Toshiharu Hase, Renate Scheibe,
   Johann P. Klare, and Guy T. Hanke*
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   Department of Plant Physiology (T.G., M.T., J.T., J.S., P.G., R.S., G.T.H.) and Department of Biophysics (K.R.,
   H.-J.S., J.P.K.), Osnabrück University, Osnabrück 49076, Germany; Institute for Protein Research, Osaka
   University, Osaka 565-0871, Japan (T.H.); and School of Biochemistry and Chemistry, Queen Mary University
   of London, London E1 4NS, United Kingdom (G.T.H.)

ABSTRACT:
In linear photosynthetic electron transport, ferredoxin:NADP(H) oxidoreductase (FNR) transfers electrons from ferredoxin (Fd) to NADP+. Both NADPH and reduced Fd (Fdred) are required for reductive assimilation and light/dark activation/deactivation of enzymes. FNR is therefore a hub, connecting photosynthetic electron transport to chloroplast redox metabolism. A correlation between FNR content and tolerance to oxidative stress is well established, although the precise mechanism remains unclear. We investigated the impact of altered FNR content and localization on electron transport and superoxide radical evolution in isolated thylakoids, and probed resulting changes in redox homeostasis, expression of oxidative stress markers, and tolerance to high light in planta. Our data indicate that the ratio of Fdred to FNR is critical, with either too much or too little FNR potentially leading to increased superoxide production, and perception of oxidative stress at the level of gene transcription. In FNR overexpressing plants, which show more NADP(H) and glutathione pools, improved tolerance to high-light stress indicates that disturbance of chloroplast redox poise and increased free radical generation may help “prime” the plant and induce protective mechanisms. In fnr1 knock-outs, the NADP(H) and glutathione pools are more oxidized relative to the wild type, and the photoprotective effect is absent despite perception of oxidative stress at the level of gene transcription.

2. NAD Acts as an Integral Regulator of Multiple Defense Layers

Pierre Pétriacq*, Jurriaan Ton, Oriane Patrit, Guillaume Tcherkez, and Bertrand Gakière
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of Medicine, Biology, and Environment, Australian National University, 2601 Australian Capital Territory,
Australia (G.T.); and Institute of Plant Sciences Paris-Saclay, Unité Mixte de Recherche 9213, Université
Paris-Sud, Bâtiment 630, 91405 Orsay cedex, France (B.G.)

ABSTRACT:
Pyridine nucleotides, such as NAD, are crucial redox carriers and have emerged as important signaling molecules in stress
responses. Previously, we have demonstrated in Arabidopsis (Arabidopsis thaliana) that the inducible NAD-overproducing nadC lines are more resistant to an avirulent strain of Pseudomonas syringae pv tomato (Pst-AvrRpm1), which was associated with salicylic acid-dependent defense. Here, we have further characterized the NAD-dependent immune response in Arabidopsis. Quinolinate-induced stimulation of intracellular NAD in transgenic nadC plants enhanced resistance against a diverse range of (a)virulent pathogens, including Pst-AvrRpt2, Dickeya dadantii, and Botrytis cinerea. Characterization of the redox status demonstrated that elevated NAD levels induce reactive oxygen species (ROS) production and the expression of redox marker genes of the cytosol and mitochondrion. Using pharmacological and reverse genetics approaches, we show that NAD-induced ROS production functions independently of NADPH oxidase activity and light metabolism but depends on mitochondrial respiration, which was increased at higher NAD. We further demonstrate that NAD primes pathogen-induced callose deposition and cell death. Mass spectrometry analysis reveals that NAD simultaneously induces different defense hormones and that the NAD-induced metabolic profiles are similar to those of defense-expressing plants after treatment with pathogen-associated molecular patterns. We thus conclude that NAD triggers metabolic profiles rather similar to that of pathogen-associated molecular patterns and discuss how signaling cross talk between defense hormones, ROS, and NAD explains the observed resistance to pathogens.

Mary

Mashaghi A, Bezrukavnikov S, Minde DP, Wentink AS, Kityk R, Zachmann-Brand B, Mayer MP, Kramer G, Bukau B, Tans SJ.
Alternative modes of client binding enable functional plasticity of Hsp70.
Nature. 2016 Oct 26;.
PMID: 27783598 [PubMed - as supplied by publisher]

Jesse

Dynamic Interactions of Arabidopsis TEN1: Stabilizing Telomeres in Response to Heat Stress

Jung Ro Lee, Xiaoyuan Xie, Kailu Yang, Junji Zhang, Sang Yeol Lee, and Dorothy E. Shippen.

Telomeres are the essential nucleoprotein structures that provide a physical cap for the ends of linear chromosomes. The highly conserved CST (CTC1/STN1/TEN1) protein complex facilitates telomeric DNA replication and promotes telomere stability. Here we report three unexpected properties of Arabidopsis thaliana TEN1 that indicate it possesses functions distinct from other previously characterized telomere proteins. First, we show that telomeres in ten1 mutants are highly sensitive to thermal stress. Heat shock causes abrupt and dramatic loss of telomeric DNA in ten1 plants, likely via deletional recombination. Second, we show that AtTEN1 has the properties of a heat-shock induced molecular chaperone. At elevated temperature, AtTEN1 rapidly assembles into high molecular weight homo-oligomeric complexes that efficiently suppress heat-induced aggregation of model protein substrates in vitro. Finally, we report that AtTEN1 specifically protects CTC1 from heat-induced aggregation in vitro, and from heat-induced protein degradation and loss of telomere association in vivo. Collectively, these observations define Arabidopsis TEN1 as a highly dynamic protein that works in concert with CTC1 to preserve telomere integrity in response to environmental stress.

The Plant Cell September 2016

Alyssa

Spell Checking Nature: Versatility of CRISPR/Cas9 for Developing Treatments for Inherited Disorders

Clustered regularly interspaced short palindromic repeat (CRISPR) has arisen as a frontrunner for efficient genome engineering. How- ever, the potentially broad therapeutic implications are largely unexplored. Here, to investigate the therapeutic potential of CRISPR/ Cas9 in a diverse set of genetic disorders, we establish a pipeline that uses readily obtainable cells from affected individuals. We show that an adapted version of CRISPR/Cas9 increases the amount of utrophin, a known disease modifier in Duchenne muscular dystrophy (DMD). Furthermore, we demonstrate preferential elimination of the dominant-negative FGFR3 c.1138G>A allele in fibroblasts of an individual affected by achondroplasia. Using a previously undescribed approach involving single guide RNA, we successfully removed large genome rearrangement in primary cells of an individual with an X chromosome duplication including MECP2. Moreover, removal of a duplication of DMD exons 18–30 in myotubes of an individual affected by DMD produced full-length dystrophin. Our findings establish the far-reaching therapeutic utility of CRISPR/Cas9, which can be tailored to target numerous inherited disorders.

Keith

The Function of Ile-X-Ile Motif in the Oligomerization and Chaperone-Like Activity of Small Heat Shock Protein AgsA at Room Temperature

Protein J. Nov. 4, 2016

[1]Qiuhu Zhou, 2Xiaodong Shi, [1]Kaiming Zhang, [1]Chao Shi, [1]Lixin Huang, [1]Zhenzhan Chang

1. Department of Biophysics, School of Basic Medical Sciences Peking University Health Science Center Beijing People's Republic of China
2. Jiangsu Province Key Laboratory of Anesthesiology Xuzhou Medical University Xuzhou People's Republic of China

Small heat shock proteins assemble as large oligomers in vitro and exhibit ATP-independent chaperone activities. Ile-X-Ile motif is essential in both the function and oligomer formation. AgsA of *Salmonella enterica* serovar Typhimurium has been demonstrated to adopt large oligomeric structure and possess strong chaperone activity. Size exclusion chromatography, non-denaturing pore gradient PAGE, and negatively stain electron microscopic analysis of the various C-terminal truncated mutants were performed to investigate the role of Ile-X-Ile motif in the oligomer assembly of AgsA. By measuring the ability to prevent insulin from aggregating induced by TCEP, the chaperone-like activity of AgsA and the C-terminal truncated mutants at room temperature were determined. We found that the truncated mutants with Ile-X-Ile motif partially or fully deleted lost the ability to form large oligomers. Contrast to wild type AgsA which displayed weak chaperone-like activity, those mutants shown significantly enhanced activities at room temperature. In summary, biochemical experiment, activity assay and electron microscopic analysis suggested that Ile-X-Ile motif is essential in oligomer assembly of AgsA and might take the role of an inhibitor for its chaperone-like activity at room temperature.

Elizabeth

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Dual Role of a SAS10/C1D Family Protein in Ribosomal RNA Gene Expression and Processing Is Essential for Reproduction in Arabidopsis thaliana.
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Plant Cell

Global Analysis of Truncated RNA Ends Reveals New Insights into Ribosome Stalling in Plants

Cheng-Yu Hou, Wen-Chi Lee, Hsiao-Chun Chou, Ai-Ping Chen, Shu-Jen Chou, and Ho-Ming Chen
Plant Cell 2016 tpc.16.00295; Advance Publication October 14, 2016; doi:10.1105/tpc.16.00295
OPEN
http://www.plantcell.org/content/early/2016/10/20/tpc.16.00295.abstract

The reverse-transcriptase/RNA-maturase protein MatR is required for the splicing of various group II introns in Brassicaceae mitochondria
Laure D Sultan, Daria Mileshina, Felix Grewe, Katarzyna Rolle, Sivan Abudraham, Paweł Głodowicz, Adnan Khan Niazi, Ido keren, Sofia Shevtsov, Liron Klipcan, Jan Barciszewski, Jeffrey P Mower, Andre Dietrich, and Oren Ostersetzer
Plant Cell 2016 tpc.16.00398; Advance Publication October 19, 2016; doi:10.1105/tpc.16.00398
http://www.plantcell.org/content/early/2016/10/19/tpc.16.00398.abstract

In Planta Single-Molecule Pull-Down Reveals Tetrameric Stoichiometry of HD-ZIPIII:LITTLE ZIPPER Complexes
Aman Y. Husbands, Vasudha Aggarwal, Taekjip Ha, and Marja C.P. Timmermans
Plant Cell 2016 28: 1783-1794. First Published on July 6, 2016; doi:10.1105/tpc.16.00289
OPEN
http://www.plantcell.org/content/28/8/1783.abstract

Establishment of single-molecule pull-down in plants allows rapid, sensitive, and quantitative interrogation of protein interactions and reveals tetrameric HD-ZIPIII:ZPR complexes.

The LSM1-7 Complex Differentially Regulates Arabidopsis Tolerance to Abiotic Stress Conditions by Promoting Selective mRNA Decapping
Carlos Perea-Resa, Cristian Carrasco-López, Rafael Catalá, Veronika Turečková, Ondrej Novak, Weiping Zhang, Leslie Sieburth, José Manuel Jiménez-Gómez, and Julio Salinas
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The Arabidopsis NRG2 Protein Mediates Nitrate Signaling and Interacts with and Regulates Key Nitrate Regulators
Na Xu, Rongchen Wang, Lufei Zhao, Chengfei Zhang, Zehui Li, Zhao Lei, Fei Liu, Peizhu Guan, Zhaohui Chu, Nigel M. Crawford, and Yong Wang
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The RNA polymerase II C-terminal domain phosphatase-like protein FIERY2/CPL1 interacts with eIF4AIII and is essential for nonsense-mediated mRNA decay in Arabidopsis
peng cui, Tao Chen, Tao Qin, Feng Ding, Zhenyu Wang, Hao Chen, and Liming Xiong
Plant Cell 2016 tpc.15.00771; Advance Publication February 17, 2016;
doi:10.1105/tpc.15.00771 **OPEN**
http://www.plantcell.org/content/early/2016/02/17/tpc.15.00771.abstract

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 tpc.15.00574; Advance Publication September 29, 2015;
doi:10.1105/tpc.15.00574 **OPEN**
http://www.plantcell.org/content/early/2015/10/21/tpc.15.00574.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 tpc.15.00370; Advance Publication October 13, 2015; doi:10.1105/tpc.15.00370 **OPEN**
http://www.plantcell.org/content/early/2015/10/13/tpc.15.00370.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 tpc.15.00680; Advance Publication October 13, 2015; doi:10.1105/tpc.15.00680 **OPEN**
http://www.plantcell.org/content/early/2015/10/13/tpc.15.00680.abstract
Arabidopsis RECG1 acts in mtDNA repair in the suppression of ectopic recombination and in the segregation of alternative mitotypes.

Genome-Wide Prediction and Validation of Intergenic Enhancers in Arabidopsis Using Open Chromatin Signatures
Bo Zhu, Wenli Zhang, Tao Zhang, Bao Liu, and Jiming Jiang
Plant Cell 2015 27: 2415-2426. First Published on September 15, 2015;
doi:10.1105/tpc.15.00537 **OPEN**
http://www.plantcell.org/content/27/9/2415.abstract
More than 10,000 enhancers located in intergenic regions in Arabidopsis, which regulate gene expression, were predicted using genomic data based on hypersensitivity to DNase I digestion.

The Circadian Clock Modulates Global Daily Cycles of mRNA Ribosome Loading
Anamika Missra, Ben Ernest, Tim Lohoff, Qidong Jia, James Satterlee, Kenneth Ke, and Albrecht G. von Arnim
Plant Cell 2015 27: 2582-2599. First Published on September 21, 2015;
doi:10.1105/tpc.15.00546 **OPEN**
http://www.plantcell.org/content/27/9/2582.abstract

Measurements of mRNA ribosome loading in wild-type and clock-deficient plants show that the circadian clock regulates the translation of Arabidopsis mRNAs in concert with diurnal light-dark changes.

HIGH CHLOROPHYLL FLUORESCENCE145 Binds to and Stabilizes the *psaA* 5′ UTR via a Newly Defined Repeat Motif in Embryophyta
Nikolay Manavski, Salar Torabi, Lina Lezhneva, Muhammad Asif Arif, Wolfgang Frank, and Jörg Meurer
Plant Cell 2015 27: 2600-2615. First Published on August 25, 2015; doi:10.1105/tpc.15.00234
http://www.plantcell.org/content/27/9/2600.abstract
The plastid HCF145 protein, composed of two ligand binding domains followed by a newly defined transcript binding motif repeat (TMR) domain, is essential for plant growth, binds to the 5′ UTR of the plastid tricistronic psaA-psaB-rps14 mRNA, and protects it from degradation.

Streamlined Construction of the Cyanobacterial CO_2-Fixing Organelle via Protein Domain Fusions for Use in Plant Synthetic Biology
C. Raul Gonzalez-Esquer, Tyler B. Shubitowski, and Cheryl A. Kerfeld
Plant Cell 2015 27: 2637-2644. First Published on August 28, 2015; doi:10.1105/tpc.15.00329
http://www.plantcell.org/content/27/9/2637.abstract
A strategy for the design of novel enzymatic cores for bacterial microcompartments was devised and tested in cyanobacteria, which have potential uses as metabolic modules in plants.

Not Throwing Baby Out with the Bathwater
Peter Chien
Plant Cell 2015 tpc.15.00801; Advance Publication September 29, 2015;
doi:10.1105/tpc.15.00801
http://www.plantcell.org/content/early/2015/09/29/tpc.15.00801

Inference of Longevity-Related Genes from a Robust Coexpression Network of Seed Maturation Identifies Regulators Linking Seed Storability to Biotic Defense-Related Pathways
Karima Righetti, Joseph Ly Vu, Sandra Pelletier, Benoit Ly Vu, Enrico Glaab, David Lalanne, Asher Pasha, Rohan V. Patel, Nicholas J. Provart, Jerome Verdier, Olivier Leprince, and Julia Buitink
Plant Cell 2015 tpc.15.00632; Advance Publication September 26, 2015;
doi:10.1105/tpc.15.00632
http://www.plantcell.org/content/early/2015/09/28/tpc.15.00632.abstract
The identification of a gene regulatory network related to seed longevity in both Medicago truncatula and Arabidopsis reveals a role for biotic defense-related genes in acquisition of longevity.

A Time-Calibrated Road Map of Brassicaceae Species Radiation and Evolutionary History
Nora Hohmann, Eva M. Wolf, Martin A. Lysak, and Marcus A. Koch
Plant Cell 2015 tpc.15.00482; Advance Publication September 26, 2015;
doi:10.1105/tpc.15.00482 **OPEN**
http://www.plantcell.org/content/early/2015/09/28/tpc.15.00482.abstract

The time-calibrated evolutionary history of Brassicaceae is characterized by polyploidization and rapid genomic stabilization indicating polyploidization as driver for future diversification.

Reassess the *t* Test: Interact with All Your Data via ANOVA
Siobhan M. Brady, Meike Burow, Wolfgang Busch, Örjan Carlborg, Katherine J. Denby, Jane Glazebrook, Eric S. Hamilton, Stacey L. Harmer, Elizabeth S. Haswell, Julin N. Maloof, Nathan M. Springer, and Daniel J. Kliebenstein
Plant Cell 2015 27: 2088-2094. First Published on July 28, 2015; doi:10.1105/tpc.15.00238
http://www.plantcell.org/content/27/8/2088.abstract
A perspective on how moving away from pairwise t tests towards general linear modelling such as ANOVA will help the plant biology community.

The Plant Peptidome: An Expanding Repertoire of Structural Features and Biological Functions
Patrizia Tavormina, Barbara De Coninck, Natalia Nikonorova, Ive De Smet, and Bruno P.A. Cammue
Plant Cell 2015 27: 2095-2118. First Published on August 14, 2015; doi:10.1105/tpc.15.00440
OPEN
http://www.plantcell.org/content/27/8/2095.abstract
A unifying peptide classification system is proposed, reflecting the huge diversity of plant peptides.

Characteristics of Plant Essential Genes Allow for within- and between-Species Prediction of Lethal Mutant Phenotypes
John P. Lloyd, Alexander E. Seddon, Gaurav D. Moghe, Matthew C. Simenc, and Shin-Han Shiu
Plant Cell 2015 27: 2133-2147. First Published on August 18, 2015; doi:10.1105/tpc.15.00051
OPEN
http://www.plantcell.org/content/27/8/2133.abstract
Essential genes in Arabidopsis thaliana display distinct characteristics that are used to build machine learning models capable of predicting lethal-phenotype genes within and between species.

$SCF^{TIR1/AFB}$-Based Auxin Perception: Mechanism and Role in Plant Growth and Development
Mohammad Salehin, Rammyani Bagchi, and Mark Estelle
Plant Cell 2015 27: 9-19. First Published on January 20, 2015; doi:10.1105/tpc.114.133744
http://www.plantcell.org/content/27/1/9.abstract

PIN-Dependent Auxin Transport: Action, Regulation, and Evolution
Maciek Adamowski and Jiří Friml
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http://www.plantcell.org/content/27/1/20.abstract

The PB1 Domain in Auxin Response Factor and Aux/IAA Proteins: A Versatile Protein Interaction Module in the Auxin Response
Tom J. Guilfoyle
Plant Cell 2015 27: 33-43. First Published on January 20, 2015; doi:10.1105/tpc.114.132753
OPEN

http://www.plantcell.org/content/27/1/33.abstract

The Yin-Yang of Hormones: Cytokinin and Auxin Interactions in Plant Development
G. Eric Schaller, Anthony Bishopp, and Joseph J. Kieber
Plant Cell 2015 27: 44-63. First Published on January 20, 2015; doi:10.1105/tpc.114.133595
http://www.plantcell.org/content/27/1/44.abstract

The Roles of ROS and ABA in Systemic Acquired Acclimation
Ron Mittler and Eduardo Blumwald
Plant Cell 2015 27: 64-70. First Published on January 20, 2015; doi:10.1105/tpc.114.133090
OPEN
http://www.plantcell.org/content/27/1/64.abstract

Understanding the Biochemical Basis of Temperature-Induced Lipid Pathway Adjustments in Plants
Qiang Li, Qian Zheng, Wenyun Shen, Dustin Cram, D. Brian Fowler, Yangdou Wei, and Jitao Zou
Plant Cell 2015 27: 86-103. First Published on January 6, 2015; doi:10.1105/tpc.114.134338
http://www.plantcell.org/content/27/1/86.abstract
Analysis of three plant species with distinct patterns of lipid profiles addresses how glycerolipid pathways in the ER and chloroplast are coordinated under temperature stress at the metabolite and transcript levels.

A Maize Glutaredoxin Gene, *Abphyl2*, Regulates Shoot Meristem Size and Phyllotaxy
Fang Yang, Huyen Thanh Bui, Michael Pautler, Victor Llaca, Robyn Johnston, Byeong-ha Lee, Allison Kolbe, Hajime Sakai, and David Jackson
Plant Cell 2015 27: 121-131. First Published on January 23, 2015; doi:10.1105/tpc.114.130393
OPEN
http://www.plantcell.org/content/27/1/121.abstract
A novel pathway, composed of a glutaredoxin and a TGA transcription factor, regulates shoot apical meristem size independently of CLV-WUS signaling.

MET1 Is a Thylakoid-Associated TPR Protein Involved in Photosystem II Supercomplex Formation and Repair in *Arabidopsis*
Nazmul H. Bhuiyan, Giulia Friso, Anton Poliakov, Lalit Ponnala, and Klaas J. van Wijk
Plant Cell 2015 27: 262-285. First Published on January 13, 2015; doi:10.1105/tpc.114.132787
http://www.plantcell.org/content/27/1/262.abstract
TMET1 is a thylakoid-associated protein that functions in assembly of PSII complexes and interacts with PSII core proteins CP43 and CP47.

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Amyloid precursor protein maintains constitutive and adaptive plasticity of dendritic spines in adult brain by regulating D-serine homeostasis
Chengyu Zou, Sophie Crux, Stephane Marinesco, Elena Montagna, Carmelo Sgobio, Yuan Shi, Song Shi, Kaichuan Zhu, Mario M Dorostkar, Ulrike C Müller, and Jochen Herms

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Loss of APP in the adult brain impairs dendritic spine dynamics and plasticity leading to cognitive deficits.

Codon identity regulates mRNA stability and translation efficiency during the maternal-to-zygotic transition
Ariel A Bazzini, Florencia del Viso, Miguel A Moreno-Mateos, Timothy G Johnstone, Charles E Vejnar, Yidan Qin, Jun Yao, Mustafa K Khokha, and Antonio J Giraldez
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In addition to spelling out protein sequence, mRNA codon triplets contain translation-dependent regulatory information that influences transcript stability and contributes to controlled turnover of maternal mRNAs in frogs, mice, and flies.

NSUN3 and ABH1 modify the wobble position of mt-tRNA^Met to expand codon recognition in mitochondrial translation
Sara Haag, Katherine E Sloan, Namit Ranjan, Ahmed S Warda, Jens Kretschmer, Charlotte Blessing, Benedikt Hübner, Jan Seikowski, Sven Dennerlein, Peter Rehling, Marina V Rodnina, Claudia Höbartner, and Markus T Bohnsack
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RNA methyltransferase NSUN3 acts specifically on mitochondrial tRNA^Met, allowing different codons to be recognised by this single tRNA and offering insight on the consequence of reported disease mutations.

eIF4A moonlights as an off switch for TORC1
Marta M Swierczynska and Michael N Hall
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A new study shows that eIF4A negatively regulates TOR complex 1 activity upon amino acid starvation, revealing a translation-independent function of eIF4A-containing eIF4F complex.

The mitochondrial outer membrane protein MDI promotes local protein synthesis and mtDNA replication
Yi Zhang, Yong Chen, Marjan Gucek, and Hong Xu
Published online 06.04.2016
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MDI recruits translational activator Larp to the outer mitochondrial

membrane to regulate mitochondrial protein expression and mtDNA replication in Drosophila ovaries.

BMC Biology

Molecular insights into substrate recognition and catalytic mechanism of the chaperone and FKBP peptidyl-prolyl isomerase SlyD

Esben M. Quistgaard, Ulrich Weininger, Yonca Ural-Blimke, Kristofer Modig, Pär Nordlund, Mikael Akke and Christian Löw