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Mol Cell. 2018 Jan 12. pii: S1097-2765(17)30976-0. doi: 10.1016/j.molcel.2017.12.019. [Epub ahead of print]

Evidence against Stable Protein S-Nitrosylation as a Widespread Mechanism of Post-translational Regulation. Wolhuter  $K^1$ , Whitwell HJ<sup>2</sup>, Switzer CH<sup>1</sup>, Burgoyne JR<sup>1</sup>, Timms JF<sup>2</sup>, Eaton P<sup>3</sup>.

King's College London, School of Cardiovascular Medicine & Sciences, British Heart Foundation Centre of Research Excellence the Rayne Institute, St. Thomas' Hospital, London SE1 7EH, UK.

Institute for Women's Health, University College London, Gower Street, London WC1E 6BT, UK.

King's College London, School of Cardiovascular Medicine & Sciences, British Heart Foundation Centre of Research Excellence the Rayne Institute, St. Thomas' Hospital, London SE1 7EH, UK. Electronic address: philip.eaton@kcl.ac.uk.

S-nitrosation, commonly referred to as S-nitrosylation, is widely regarded as a ubiquitous, stable post-translational modification that directly regulates many proteins. Such a widespread role would appear to be incompatible with the inherent lability of the S-nitroso bond, especially its propensity to rapidly react with thiols to generate disulfide bonds. As anticipated, we observed robust and widespread protein S-nitrosation after exposing cells to nitrosocysteine or lipopolysaccharide. Proteins detected using the ascorbate-dependent biotin switch method are typically interpreted to be directly regulated by S-nitrosation. However, these S-nitrosated proteins are shown to predominantly comprise transient intermediates leading to disulfide bond formation. These disulfides are likely to be the dominant end effectors resulting from elevations in nitrosating cellular nitric oxide species. We propose that S-nitrosation primarily serves as a transient intermediate leading to disulfide formation. Overall, we conclude that the current widely held perception that stable S-nitrosation directly regulates the function of many proteins is significantly incorrect.

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# Bioprotocol

Determining Ribosome Translational Status by Ribo-ELISA

Authors: Amandine Bastide, Jonathan W. Yewdell and Alexandre David

[Abstract] The Ribo-ELISA was originally developed to elucidate the basis for the ribopuromycylation method (RPM)based detection of ribosome bound nascent chains. The Ribo-ELISA enables characterization of the ...

Article identifier: bio-protocol.org/e2670

Easy and Efficient Permeabilization of Cyanobacteria for in vivo Enzyme Assays Using B-PER

Authors: Simon Matthé Erstad and Yumiko Sakuragi

[Abstract] Cyanobacteria are photosynthetic bacteria that thrive in diverse ecosystems and play major roles in the global carbon cycle. The abilities of cyanobacteria to fix atmospheric  $CO_2$  and to allocate the fixed ... *Article identifier: bio-protocol.org/e2667* 

# Cell: Alert 22 January-29 January

Context-Dependent and Disease-Specific Diversity in Protein Interactions within Stress Granules Pages 590-604.e13 Sebastian Markmiller, Sahar Soltanieh, Kari L. Server, Raymond Mak, Wenhao Jin, Mark Y. Fang, En-Ching Luo, Florian Krach, Dejun Yang, Anindya Sen, Amit Fulzele, Jacob M. Wozniak, David J. Gonzalez, Mark W. Kankel, Fen-Biao Gao, Eric J. Bennett, Eric Lécuyer, Gene W. Yeo

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Nature Cell Biology

The MTM1–UBQLN2–HSP complex mediates degradation of misfolded intermediate filaments in skeletal muscle Gavriilidis et al. show that MTM1, which is mutated in X-linked centronuclear myopathy, and UBQLN2 recognize misfolded desmin and vimentin and trigger their degradation to clear misfolded intermediated filaments prior to aggregate formation. Christos Gavriilidis , Leila Laredj [...] & Karim Hnia

EXD2 governs germ stem cell homeostasis and lifespan by promoting mitoribosome integrity and translation

By analysing the exonuclease EXD2, Silva et al. find that it localizes to mitochondria, and that its loss alters metabolism by affecting mitochondrial translation and causes developmental delay and lifespan extension in flies. Joana Silva, , Suvi Aivio[...] & Travis H. Stracker

Physiologia Plantarum Content Alert: 162, 2 (February 2018) <u>Stress response regulation by epigenetic mechanisms: changing of the guards (pages 239–250)</u> Maria Luz Annacondia, Melissa H. Magerøy and German Martinez Version of Record online: 30 NOV 2017 | DOI: 10.1111/ppl.12662

Interaction points in plant stress signaling pathways (pages 191-204)

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Harnessing transcription for bioproduction in cyanobacteria (pages 148–155)

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### Science 19 Jan 2018:

## A global atlas of the dominant bacteria found in soil

Manuel Delgado-Baquerizo<sup>1</sup>, et al

Vol. 359, Issue 6373, pp. 320-325 DOI: 10.1126/science.aap9516

The immense diversity of soil bacterial communities has stymied efforts to characterize individual taxa and document their global distributions. We analyzed soils from 237 locations across six continents and found that only 2% of bacterial phylotypes (~500 phylotypes) consistently accounted for almost half of the soil bacterial communities worldwide. Despite the overwhelming diversity of bacterial communities, relatively few bacterial taxa are abundant in soils globally. We clustered these dominant taxa into ecological groups to build the first global atlas of soil bacterial taxa. Our study narrows down the immense number of bacterial taxa to a "most wanted" list that will be fruitful targets for genomic and cultivation-based efforts aimed at improving our understanding of soil microbes and their contributions to ecosystem functioning.

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**High-Density Proximity Mapping Reveals the Subcellular Organization of mRNA-Associated Granules and Bodies** Molecular Cell, Volume 69, Issue 3, 1 February 2018, Pages 517-532.e11 <u>PDF (8100 K)</u>

Sebastian Markmiller, Sahar Soltanieh, Kari L. Server, Raymond Mak, Wenhao Jin, Mark Y. Fang, En-Ching Luo, Florian Krach, Dejun Yang, Anindya Sen, Amit Fulzele, Jacob M. Wozniak, David J. Gonzalez, Mark W. Kankel, Fen-Biao Gao, Eric J. Bennett, Eric Lécuyer, Gene W. Yeo

<u>Context-Dependent and Disease-Specific Diversity in Protein Interactions within Stress Granules</u> Cell, Volume 172, Issue 3, 25 January 2018, Pages 590-604.e13 <u>PDF (8733 K)</u>

Molecular Cell <u>Advances in CLIP Technologies for Studies of Protein-RNA Interactions</u> Review Article *Pages 354-369* Flora C.Y. Lee, Jernej Ule

Nature Plants

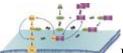
Dynamic thylakoid stacking regulates the balance between linear and cyclic photosynthetic electron transfer

William H. J. Wood, Craig MacGregor-Chatwin, Samuel F. H. Barnett, Guy E. Mayneord, Xia Huang *et al. Nature Plants* **4**, doi:10.1038/s41477-017-0092-7

The FEBS Journal Content Alert: 285, 3 (February 2018)

Bax, Bak and beyond — mitochondrial performance in apoptosis (pages 416-431) Review

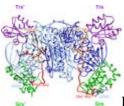
Aida Peña-Blanco and Ana J. García-Sáez Version of Record online: 4 SEP 2017 | DOI: 10.1111/febs.14186



Bax and Bak are members of the Bcl-2 family and core regulators of the intrinsic pathway of apoptosis. Here, we review recent structural and biophysical evidence on how Bax and Bak mediate mitochondrial outer membrane permeabilization. We also discuss the regulation of Bax and Bak by the Bcl-2

Kinetic characterization of wild-type and mutant human thioredoxin glutathione reductase defines its reaction and regulatory mechanisms (pages 542–558)

Christina Brandstaedter, Karin Fritz-Wolf, Stine Weder, Marina Fischer, Beate Hecker, Stefan Rahlfs and Katja Becker Version of Record online: 29 DEC 2017 | DOI: 10.1111/febs.14357



Human thioredoxin glutathione reductase is a multifunctional selenocysteine-containing enzyme composed of a thioredoxin reductase and a monothiol glutaredoxin domain. In our study, we kinetically characterized the full-length protein, the Sec $\rightarrow$ Cys mutant, and the isolated domains mechanistically by using Trx, DTNB, HED, or GSSG as substrates. Furthermore, glutathionylation was identified as a regulatory principle of the enzyme.

The FEBS Journal Content Alert (New Articles)

### <u>Structural mechanisms for the S-nitrosylation-derived protection of mouse galectin-2 from oxidation-induced</u> <u>inactivation revealed by NMR</u>

Masayoshi Sakakura, Mayumi Tamura, Norihiko Fujii, Tomoharu Takeuchi, Tomomi Hatanaka, Seishi Kishimoto, Yoichiro Arata and Hideo Takahashi

Accepted manuscript online: 2 FEB 2018 03:52AM EST | DOI: 10.1111/febs.14397

Current Biology: Alert 30 January-06 February

<u>TOM70 Sustains Cell Bioenergetics by Promoting IP3R3-Mediated ER to Mitochondria Ca<sup>2+</sup> Transfer</u> *Pages 369-382.e6* Riccardo Filadi, Nuno Santos Leal, Bernadette Schreiner, Alice Rossi, Giacomo Dentoni, Catarina Moreira Pinho, Birgitta Wiehager, Domenico Cieri, Tito Calì, Paola Pizzo, Maria Ankarcrona

Nature volume 554, pages 128–132 (01 February 2018)

Mitochondrial translation requires folate-dependent tRNA methylation

Raphael J. Morscher, Gregory S. Ducker, Sophia Hsin-Jung Li, Johannes A. Mayer, Zemer Gitai+ et al.

Mammalian mitochondria use folate-bound one-carbon units generated by the enzyme SHMT2 to methylate tRNA, and this modification is required for mitochondrial translation and thus oxidative phosphorylation.

Nature Structural and Molecular Biology 22 January 2018

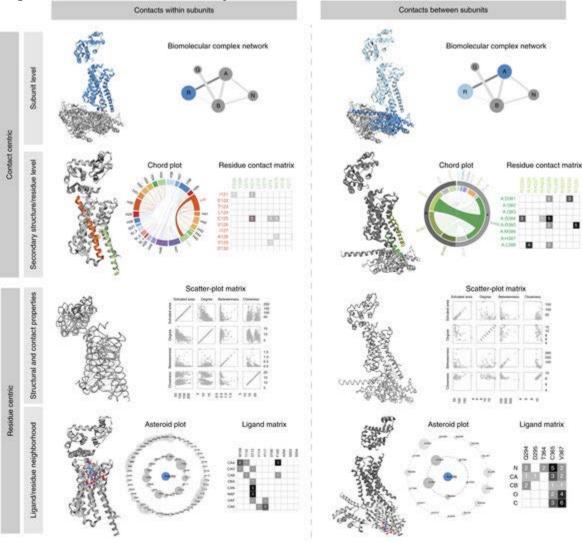
**Structural basis of AAUAAA polyadenylation signal recognition by the human CPSF complex** 

The cryo-EM structure of the human core CPSF complex, containing CPSF160, WDR33, CPSF30 and Fip1 subunits, bound to its RNA target reveals the mechanism of PAS recognition. Marcello Clerici, Marco Faini [...] & Martin Jinek

Visualization and analysis of non-covalent contacts using the Protein Contacts Atlas

The Protein Contacts Atlas is an interactive resource of non-covalent contacts that can generate multiple representations of non-covalent contacts from PDB structures at different scales, from atoms to subunits and entire complexes. Melis Kayikci, A. J. Venkatakrishnan[...] & M. Madan Babu

#### http s://www.mrc-lmb.cam.ac.uk/rajini/index.html



#### Nature contents: 18 January 2018

An extracellular network of Arabidopsis leucine-rich repeat receptor kinases

Elwira Smakowska-Luzan, G. Adam Mott, Katarzyna Parys, Martin Stegmann, Timothy C Howton<u>+ et al.</u> A high-throughput assay is used to analyse 40,000 potential extracellular domain interactions of a large family of plant cell surface receptors (LRR-RKs) and provide a cell surface interaction network for these receptors.

EMBO J. http://EMBOJ.embopress.org/content/37/2/282?etoc

Complete suppression of Htt fibrilization and disaggregation of Htt fibrils by a trimeric chaperone complex

Annika Scior, Alexander Buntru, Kristin Arnsburg, Anne Ast, Manuel Iburg,

Katrin Juenemann, Maria Lucia Pigazzini, Barbara Mlody, Dmytro Puchkov,

Josef Priller, Erich E Wanker, Alessandro Prigione and Janine Kirstein

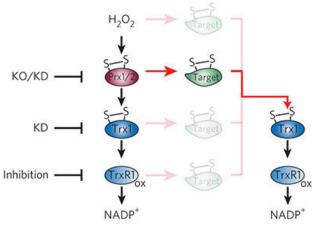
A dynamic chaperone complex of Hsc70, Hsp110 and J-protein dissolves

pathological Huntingtin fibrils in vitro and prevents aggregate formation

in Huntington's disease patient-derived neurons.

Nature Chemical Biology Contents: February 2018, Volume 14 No 2 pp 103 - 186 A role for 2-Cys peroxiredoxins in facilitating cytosolic protein thiol oxidation - pp148 - 155 Sarah Stöcker, Michael Maurer, Thomas Ruppert & Tobias P Dick

doi:10.1038/nchembio.2536



Cytosolic 2-Cys peroxiredoxins can enable, rather than compete with, rapid thiol oxidation by relaying  $H_2O_2$ derived oxidizing equivalents to other proteins, suggesting a broadened role for peroxiredoxins as sensors and transmitters of  $H_2O_2$  signals.

Plant, Cell & Environment Content Alert (New Articles)

<u>Plasticity of photosynthetic heat tolerance in plants adapted to thermally contrasting biomes</u> Lingling Zhu, Keith J. Bloomfield, Charles H. Hocart, John J.G. Egerton, Odhran S. O'Sullivan, Aurore Penillard, Lasantha K. Weerasinghe and Owen K. Atkin Accepted manuscript online: 5 JAN 2018 01:35AM EST | DOI: 10.1111/pce.13133