Ian

Free Radic Biol Med. 2016 Sep 27. pii: S0891-5849(16)30429-4. doi: 10.1016/j.freeradbiomed.2016.09.015. [Epub ahead of print]

Ferriheme catalyzes nitric oxide reaction with glutathione to form S-nitrosoglutathione: A novel mechanism for formation of S-nitrosothiols.

Nagababu E1.

PLoS Genet. 2016 Sep 29;12(9):e1006255. doi: 10.1371/journal.pgen.1006255. eCollection 2016.

Arabidopsis CaM1 and CaM4 Promote Nitric Oxide Production and Salt Resistance by Inhibiting S-Nitrosoglutathione Reductase via Direct Binding.

Zhou S1, Jia L1, Chu H1, Wu D1, Peng X1, Liu X1, Zhang J1, Zhao J1, Chen K2, Zhao L1.

Alyssa

CRISPR-Barcoding for Intratumor Genetic Heterogeneity Modeling and Functional Analysis of Oncogenic Driver Mutations

Intratumor genetic heterogeneity underlies the ability of tumors to evolve and adapt to different environmental conditions. Using CRISPR/Cas9 technology and specific DNA barcodes, we devised a strategy to recapitulate and trace the emergence of subpopulations of cancer cells containing a mutation of interest. We used this approach to model different mechanisms of lung cancer cell resistance to EGFR inhibitors and to assess effects of combined drug therapies. By overcoming intrinsic limitations of current approaches, CRISPR-barcoding also enables investigation of most types of genetic modifications, including repair of oncogenic driver mutations. Finally, we used highly complex barcodes inserted at a specific genome location as a means of simultaneously tracing the fates of many thousands of genetically labeled cancer cells. CRISPR-barcoding is a straightforward and highly flexible method that should greatly facilitate the functional investigation of specific mutations, in a context that closely mimics the complexity of cancer.

Patrick

1. Cytokinin Response Factor 6 Represses Cytokinin-Associated Genes during Oxidative Stress

Paul J. Zwack, Inge De Clercq, Timothy C. Ho
wton, H. Tucker Hallmark, Andrej Hurny,

Erika A. Keshishian, Alyssa M. Parish, Eva Benk
ova, M. Shahid Mukhtar, Frank Van Breusegem, and
Aaron M. Rashotte*
Department of Biological Sciences, Auburn University, Auburn, AL 36849 (P.J.Z., H.T.H., E.A.K., A.M.P., A.M.R.);
Department of Plant Systems Biology, VIB, 9052 Ghent, Belgium (I.D.C., F.V.B.);
Department of Plant
Biotechnology and Bioinformatics, Ghent University, Technologiepark 927, B-9052 Gent,
Belgium (I.D.C., F.V.B.);
Department of Biology, University of Alabama, Birm
ingham, AL 35294 (T.C.H., M.S.M.); and Institute of
Science and Technology Austria (IST Austria), 3400 Klosterneuburg, Austria (A.H., E.B.)

Cytokinin is a phytohormone that is well known for its roles in numerous plant growth and developmental processes, yet it has also been linked to abiotic stress response in a less defined manner. Arabidopsis (Arabidopsis thaliana) Cytokinin Response Factor 6 (CRF6) is a cytokinin-responsive AP2/ERF-family transcription factor that, through the cytokinin signaling pathway, plays a key role in the inhibition of dark-induced senescence. CRF6 expression is also induced by oxidative stress, and here we show a novel function for CRF6 in relation to oxidative stress and identify downstream transcriptional targets of CRF6 that are repressed in response to oxidative stress. Analysis of transcriptomic changes in wild-type and crf6 mutant plants treated with H2O2 identified CRF6-dependent differentially expressed transcripts, many of which were repressed rather than induced. Moreover, many repressed genes also show decreased expression in 35S:CRF6 overexpressing plants. Together, these findings suggest that CRF6 functions largely as a transcriptional repressor. Interestingly, among the H2O2 repressed CRF6-dependent transcripts was a set of five genes associated with cytokinin processes: (signaling) ARR6, ARR9, ARR11, (biosynthesis) LOG7, and (transport) ABCG14. We have examined mutants of these cytokinin-associated target genes to reveal novel connections to oxidative stress. Further examination of CRF6-DNA interactions indicated that CRF6 may regulate its targets both directly and indirectly. Together, this shows that CRF6 functions during oxidative stress as a negative regulator to control this cytokinin-associated module of CRF6- dependent genes and establishes a novel connection between cytokinin and oxidative stress response.

2. Reactive Oxygen Species Tune Root Tropic Responses

Gat Krieger2, Doron Shkolnik2, Gad Miller, and Hillel Fromm*
Department of Molecular Biology and Ecology of Plants, Faculty of Life Sciences, Tel Aviv University, Tel
Aviv 69978, Israel (G.K., D.S., H.F.); and Mina and Everard Goodman Faculty of Life Sciences, Bar-Ilan
University, Ramat-Gan 5290002, Israel (G.M.)

ORCID IDs: 0000-0003-3498-4362 (D.S.); 0000-0002-7196-6529 (G.M.); 0000-0003-1977-1211 (H.F.).

The default growth pattern of primary roots of land plants is directed by gravity. However, roots possess the ability to sense and respond directionally to other chemical and physical stimuli, separately and in combination. Therefore, these root tropic responses must be antagonistic to gravitropism. The role of reactive oxygen species (ROS) in gravitropism of maize and
Arabidopsis (Arabidopsis thaliana) roots has been previously described. However, which cellular signals underlie the
integration of the different environmental stimuli, which lead to an appropriate root tropic response, is currently unknown.
In gravity-responding roots, we observed, by applying the ROS-sensitive fluorescent dye dihydrorhodamine-123 and confocal microscopy, a transient asymmetric ROS distribution, higher at the concave side of the root. The asymmetry, detected at the distal elongation zone, was built in the first 2 h of the gravitropic response and dissipated after another 2 h. In contrast, hydrotropically responding roots show no transient asymmetric distribution of ROS. Decreasing ROS levels by applying the antioxidant ascorbate, or the ROS-generation inhibitor diphenylene iodonium attenuated gravitropism while enhancing hydrotropism. Arabidopsis mutants deficient in Ascorbate Peroxidase 1 showed attenuated hydrotropic root bending. Mutants of the root-expressed NADPH oxidase RBOH C, but not rbohD, showed enhanced hydrotropism and less ROS in their roots apices (tested in tissue extracts with Amplex Red). Finally, hydrostimulation prior to gravistimulation attenuated the gravistimulated asymmetric ROS and auxin signals that are required for gravity-directed curvature. We suggest that ROS, presumably H2O2, function in tuning root tropic responses by promoting gravitropism and negatively regulating hydrotropism.

Keith

Expression of Cataract-linked γ-crystallin Variants in Zebrafish Reveals a Proteostasis Network that Senses Protein Stability.

J Biol Chem. 2016 Oct 21.

Wu SY1, Zou P1, Fuller AW1, Mishra S1, Wang Z1, Schey KL1, Mchaourab HS2.

1,2 Vanderbilt University, United States.

The refractivity and transparency of the ocular lens is dependent on the stability and solubility of the crystallins in the fiber cells. A number of mutations of lens crystallins have been associated with dominant cataracts in humans and mice. Of particular interest were γB- and γD-crystallin mutants linked to dominant cataracts in mouse models. While thermodynamically destabilized and aggregation-prone, these mutants

were found to have weak affinity to the resident chaperone α-crystallin in vitro To better understand the mechanism of the cataract phenotype, we transgenically expressed different γD-crystallin mutants in the zebrafish lens, and observed a range of lens defects that arise primarily from the aggregation of the mutant proteins. Unlike mouse models, a strong correlation was observed between the severity and penetrance of the phenotype and the level of destabilization of the mutant. We interpret this result to reflect the presence of a proteostasis network which can "sense" protein stability. In the more destabilized mutants, the capacity of this network is overwhelmed leading to the observed increase in phenotypic penetrance. Overexpression of αA-crystallin had no significant effects on the penetrance of lens defects suggesting that its chaperone capacity is not limiting. While consistent with the prevailing hypothesis that a chaperone network is required for lens transparency, our results suggest that αA-crystallin may not be efficient to inhibit aggregation of lens γ-crystallin. Our work further implicates additional inputs/factors are involved in this underlying proteostasis network and demonstrates the utility of zebrafish as a platform to delineate mechanisms of cataract.

The preferential heterodimerization of human small heat shock proteins HSPB1 and HSPB6 is dictated by the N-terminal domain.

Arch Biochem Biophys. 2016 Nov 15;610:41-50.

Heirbaut M1, Lermyte F2, Martin EM3, Beelen S1, Verschueren T3, Sobott F3, Strelkov SV4, Weeks SD5.

Small heat shock proteins are ATP-independent molecular chaperones. Their function is to bind partially unfolded proteins under stress conditions. In vivo, members of this chaperone family are known to preferentially assemble together forming large, polydisperse heterooligomers. The exact molecular mechanisms that drive specific heteroassociation are currently unknown. Here we study the oligomers formed between human HSPB1 and HSPB6. Using small-angle X-ray scattering we could characterize two distinct heterooligomeric species present in solution. By employing native mass spectrometry we show that such assemblies are formed purely from heterodimeric building blocks, in line with earlier cross-linking studies. Crucially, a detailed analysis of truncation variants reveals that the preferential association between these two sHSPs is solely mediated by their disordered N-terminal domains.

The small heat shock protein Hsp31 cooperates with Hsp104 to modulate Sup35 prion aggregation.

Prion. 2016 Oct 3

Aslam K1, Tsai CJ1, Hazbun TR1.

1Department of Medicinal Chemistry and Molecular Pharmacology and the Purdue University Center for Cancer Research , Purdue University , West Lafayette , IN 47907 , USA

The yeast homolog of DJ-1, Hsp31, is a multifunctional protein that is involved in several cellular pathways including detoxification of the toxic metabolite methylglyoxal and as a protein deglycase. Prior studies ascribed Hsp31 as a molecular chaperone that can inhibit α-Syn aggregation in vitro and alleviate its toxicity in vivo. It was also shown that Hsp31 inhibits Sup35 aggregate formation in yeast, however, it is unknown if Hsp31 can modulate [PSI+] phenotype and Sup35 prionogenesis. Other small heat shock proteins, Hsp26 and Hsp42 are known to be a part of a synergistic proteostasis network that inhibits Sup35 prion formation and promotes its disaggregation. Here, we establish that Hsp31 inhibits Sup35 [PSI+] prion formation in collaboration with a well-known disaggregase, Hsp104. Hsp31 transiently prevents prion induction but does not suppress induction upon prolonged expression of Sup35 indicating that Hsp31 can be overcome by larger aggregates. In addition, elevated levels of Hsp31 do not cure [PSI+] strains indicating that Hsp31 cannot intervene in a pre-existing prion oligomerization cycle. However, Hsp31 can modulate prion status in cooperation with Hsp104 because it inhibits Sup35 aggregate formation and potentiates [PSI+] prion curing upon overexpression of Hsp104. The absence of Hsp31 reduces [PSI+] prion curing by Hsp104 without influencing its ability to rescue cellular thermotolerance. Hsp31 did not synergize with Hsp42 to modulate the [PSI+] phenotype suggesting that both proteins act on similar stages of the prion cycle. We also showed that Hsp31 physically interacts with Hsp104 and together they prevent Sup35 prion toxicity to greater extent than if they were expressed individually. These results elucidate a mechanism for Hsp31 on prion modulation that suggest it acts at a distinct step early in the Sup35 aggregation process that is different from Hsp104. This is the first demonstration of the modulation of [PSI+] status by the chaperone action of Hsp31. The delineation of Hsp31's role in the chaperone cycle has implications for understanding the role of the DJ-1 superfamily in controlling misfolded proteins in neurodegenerative disease and cancer.

Elizabeth

Oct 16

Plant Cell Table of Contents for September 2016; Vol. 28, No. 9

Lost in Transit: Long-Distance Trafficking and Phloem Unloading of Protein Signals in Arabidopsis Homografts

Danae Simone Genevieve Paultre, Marie-Paule Gustin, Attila Molnar, and Karl J. Oparka

Plant Cell 2016 28: 2016-2025. First Published on September 6, 2016; doi:10.1105/tpc.16.00249

OPEN

http://www.plantcell.org/content/28/9/2016.abstract

In Arabidopsis homografts, proteins carrying organelle-targeting signals move from companion cells to sieve elements and traffic across the graft union to target the correct organelle in the root.

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

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

Plant Cell 2016 28: 2212-2224. First Published on September 8, 2016; doi:10.1105/tpc.16.00408
http://www.plantcell.org/content/28/9/2212.abstract
The Arabidopsis TEN1 telomere protein possesses a molecular chaperone activity that is responsive to heat shock and links environmental stress to genome stability.

Thylakoid Membrane Architecture in *Synechocystis* Depends on CurT, a Homolog of the Granal CURVATURE THYLAKOID1 Proteins
Steffen Heinz, Anna Rast, Lin Shao, Andrian Gutu, Irene L. Gügel, Eiri Heyno, Mathias Labs, Birgit Rengstl, Stefania Viola, Marc M. Nowaczyk, Dario Leister, and Jörg Nickelsen
Plant Cell 2016 28: 2238-2260. First Published on August 19, 2016; doi:10.1105/tpc.16.00491
http://www.plantcell.org/content/28/9/2238.abstract
CurT is required for shaping the thylakoid membrane architecture in *Synechocystis* and mediates osmotic stress responses.

Jones AM, Westwood IM, Osborne JD, Matthews TP, Cheeseman MD, Rowlands MG, Jeganathan F, Burke R, Lee D, Kadi N, Liu M, Richards M, McAndrew C, Yahya N, Dobson SE, Jones K, Workman P, Collins I, van Montfort RL.
A fragment-based approach applied to a highly flexible target: Insights and challenges towards the inhibition of HSP70 isoforms.
Sci Rep. 2016 Oct 6;6:34701. PMID: 27708405 [Unknown status]

Seo JH, Park JH, Lee EJ, Vo TT, Choi H, Kim JY, Jang JK, Wee HJ, Lee HS, Jang SH, Park ZY, Jeong J, Lee KJ, Seok SH, Park JY, Lee BJ, Lee MN, Oh GT, Kim KW.
ARD1-mediated Hsp70 acetylation balances stress-induced protein refolding and degradation.
Nat Commun. 2016 Oct 6;7:12882. PMID: 27708256 [Unknown status]

Fang NN, Zhu M, Rose A, Wu KP, Mayor T.
Deubiquitinase activity is required for the proteasomal degradation of misfolded cytosolic proteins upon heat-stress.
Nat Commun. 2016 Oct 4;7:12907. PMID: 27698423 [Unknown status]

Attar N.
Bacterial physiology: A new chaperone for regulatory sRNAs.
Nat Rev Microbiol. 2016 Oct 3;. PMID: 27694886 [PubMed]

Krapp S, Greiner E, Amin B, Sonnewald U, Krenz B.
The stress granule component G3BP is a novel interaction partner for the nuclear shuttle proteins of the nanovirus pea necrotic yellow dwarf virus and geminivirus abutilon mosaic virus.
Virus Res. 2016 Sep 29;227:6-14. PMID: 27693920 [PubMed]

Aslam K, Tsai CJ, Hazbun TR.
The small heat shock protein Hsp31 cooperates with Hsp104 to modulate Sup35 prion aggregation.
Prion. 2016 Oct 3;:0. PMID: 27690738 [PubMed]

Kumar R, Nawroth PP, Tyedmers J.
Prion Aggregates Are Recruited to the Insoluble Protein Deposit (IPOD) via Myosin 2-Based Vesicular Transport.
PLoS Genet. 2016 Sep;12(9):e1006324. PMID: 27689885 [PubMed - as supplied by publisher]

Floryszak-Wieczorek J, Arasimowicz-Jelonek M.
Contrasting Regulation of NO and ROS in Potato Defense-Associated Metabolism in Response to Pathogens of Different Lifestyles.
PLoS One. 2016 Oct 3;11(10):e0163546. PMID: 27695047 [Unknown status]

Zhou S, Jia L, Chu H, Wu D, Peng X, Liu X, Zhang J, Zhao J, Chen K, Zhao L.
Arabidopsis CaM1 and CaM4 Promote Nitric Oxide Production and Salt Resistance by Inhibiting S-Nitrosoglutathione Reductase via Direct Binding.
PLoS Genet. 2016 Sep;12(9):e1006255. PMID: 27684709 [PubMed - as supplied by publisher]

The FEBS Journal Content Alert: 283, 19 (October 2016)

To deliver or to degrade – an interplay of the ubiquitin–proteasome system, autophagy and vesicular transport in plants (pages 3534–3555)
Katarzyna Zientara-Rytter and Agnieszka Sirko
Version of Reco DOI: 10.1111/febs.13712rd online: 2 APR 2016 |

Autophagy is a catabolic process that involves vesicle formation. Besides the ubiquitin–proteasome system (UPS), it is main the degradation mechanism in cells. It is also an important component of vesicle transport. In this article, we summarize the knowledge on both UPS and autophagy pathways in plants, pointing the interplay between them and discussing the relationships between autophagy and vesicular transport.

Santolini J, AndrÃ© F, Jeandroz S, Wendehenne D.
Nitric oxide synthase in plants: Where do we stand?
Nitric Oxide. 2016 Sep 19;. PMID: 27658319 [PubMed]

Chakrabortee S, Byers JS, Jones S, Garcia DM, Bhullar B, Chang A, She R, Lee L, Fremin B, Lindquist S, Jarosz DF.
Intrinsically Disordered Proteins Drive Emergence and Inheritance of Biological Traits.
Cell. 2016 Oct 6;167(2):369-381.e12. PMID: 27693355 [Unknown status]

Losada A, MuÃ±oz-Alonso MJ, GarcÃa C, SÃ¡nchez-Murcia PA, MartÃnez-Leal JF, DomÃnguez JM, Lillo MP, Gago F, Galmarini CM.
Translation Elongation Factor eEF1A2 is a Novel Anticancer Target for the Marine Natural Product Plitidepsin.
Sci Rep. 2016 Oct 7;6:35100. PMID: 27713531

Lecampion C, Floris M, Fantino JR, Robaglia C, Laloi C.
An Easy Method for Plant Polysome Profiling.
J Vis Exp. 2016 Aug 28;(114). PMID: 27684295 [PubMed - as supplied by publisher]

Mills EW, Wangen J, Green R, Ingolia NT.
Dynamic Regulation of a Ribosome Rescue Pathway in Erythroid Cells and Platelets.
Cell Rep. 2016 Sep 27;17(1):1-10. PMID: 27681415 [PubMed - in process]

Pisani C, Onori A, Gabanella F, Delle Monache F, Borreca A, Ammassari-Teule M, Fanciulli M, Di Certo MG, Passananti C, Corbi N.
eEF1BÎ³ binds the Che-1 and TP53 gene promoters and their transcripts.

J Exp Clin Cancer Res. 2016 Sep 17;35(1):146. PMID: 27639846 [PubMed - in process]

McLoughlin F, Basha E, Fowler ME, Kim M, Bordowitz J, Katiyar-Agarwal S, Vierling E.
Class I and II Small Heat Shock Proteins Together with HSP101 Protect Protein Translation Factors during Heat Stress.
Plant Physiol. 2016 Oct;172(2):1221-1236. PMID: 27474115

Lee KH, Zhang P, Kim HJ, Mitrea DM, Sarkar M, Freibaum BD, Cika J, Coughlin M, Messing J, Molliex A, Maxwell BA, Kim NC, Temirov J, Moore J, Kolaitis RM, Shaw TI, Bai B, Peng J, Kriwacki RW, Taylor JP.
C9orf72 Dipeptide Repeats Impair the Assembly, Dynamics, and Function of Membrane-Less Organelles.
Cell. 2016 Oct 20;167(3):774-788.e17. PMID: 27768896

Economou K, Kotsiliti E, Mintzas AC.
Stage and cell-specific expression and intracellular localization of the small heat shock protein Hsp27 during oogenesis and spermatogenesis in the Mediterranean fruit fly, Ceratitis capitata.
J Insect Physiol. 2016 Oct 15; PMID: 27756555

Sinetova MA, Los DA.
Systemic analysis of stress transcriptomics of Synechocystis reveals common stress genes and their universal triggers.
Mol Biosyst. 2016 Oct 18;12(11):3254-3258. PMID: 27754509

Bar-Lavan Y, Shemesh N, Ben-Zvi A.
Chaperone families and interactions in metazoa.
Essays Biochem. 2016 Oct 15;60(2):237-253. PMID: 27744339

Voos W, Jaworek W, Wilkening A, Bruderek M.
Protein quality control at the mitochondrion.
Essays Biochem. 2016 Oct 15;60(2):213-225. PMID: 27744337

Gamerdinger M.
Protein quality control at the ribosome: focus on RAC, NAC and RQC.
Essays Biochem. 2016 Oct 15;60(2):203-212. PMID: 27744336

Strauch A, Haslbeck M.
The function of small heat-shock proteins and their implication in proteostasis.
Essays Biochem. 2016 Oct 15;60(2):163-172. PMID: 27744332

Scior A, Juenemann K, Kirstein J.
Cellular strategies to cope with protein aggregation.
Essays Biochem. 2016 Oct 15;60(2):153-161. PMID: 27744331

Bett JS.
Proteostasis regulation by the ubiquitin system.
Essays Biochem. 2016 Oct 15;60(2):143-151. PMID: 27744330 [Unknown status]

Diokmetzidou A, Soumaka E, Kloukina I, Tsikitis M, Makridakis M, Varela A, Davos CH, Georgopoulos S, Anesti V, Vlahou A, Capetanaki Y.
Desmin and Î±B-crystallin interplay in the maintenance of mitochondrial homeostasis and cardiomyocyte survival.
J Cell Sci. 2016 Oct 15;129(20):3705-3720. PMID: 27566162 [Unknown status]

Pan J, Wang W, Li D, Shu Z, Ye X, Chang P, Wang Y.
Gene expression profile indicates involvement of NO in Camellia sinensis pollen tube growth at low temperature.
BMC Genomics. 2016 Oct 18;17(1):809. PMID: 27756219 [Unknown status]

Kalous KS, Wynia-Smith SL, Olp MD, Smith BC.
Mechanism of Sirt1 NAD+-dependent Deacetylase Inhibition by Cysteine S-nitrosation.
J Biol Chem. 2016 Oct 18;. PMID: 27756843 [PubMed]

Zollbrecht C, Persson AE, Lundberg JO, Weitzberg E, CarlstrÃ¶m M.
Nitrite-mediated reduction of macrophage NADPH oxidase activity is dependent on xanthine oxidoreductase-derived nitric oxide but independent of S-nitrosation.
Redox Biol. 2016 Sep 28;10:119-127. PMID: 27744114 [PubMed]

Hou CY, Lee WC, Chou HC, Chen AP, Chou SJ, Chen HM.
Global Analysis of Truncated RNA Ends Reveals New Insights into Ribosome Stalling in Plants.
Plant Cell. 2016 Oct 14; PMID: 27742800 [PubMed]

Jan E, Mohr I, Walsh D.
A Cap-to-Tail Guide to mRNA Translation Strategies in Virus-Infected Cells.
Annu Rev Virol. 2016 Sep 29;3(1):283-307. PMID: 27501262 [Unknown status]

Cell: Alert 14 October-21 October

ALKBH1-Mediated tRNA Demethylation Regulates Translation ***Pages 816-828.e16***

Fange Liu, Wesley Clark, Guanzheng Luo, Xiaoyun Wang, Ye Fu, Jiangbo Wei, Xiao Wang, Ziyang Hao, Qing Dai, Guanqun Zheng, Honghui Ma, Dali Han, Molly Evans, Arne Klungland, Tao Pan, Chuan He

PDF (4085 K) Supplementary content

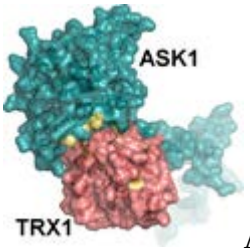
Toxic PR Poly-Dipeptides Encoded by the C9orf72 Repeat Expansion Target LC Domain Polymers
Pages 789-802.e12
Yi Lin, Eiichiro Mori, Masato Kato, Siheng Xiang, Leeju Wu, Ilmin Kwon, Steven L. McKnight
PDF (4503 K) **Supplementary content**

C9orf72 Dipeptide Repeats Impair the Assembly, Dynamics, and Function of Membrane-Less Organelles
Pages 774-788.e17

Kyung-Ha Lee, Peipei Zhang, Hong Joo Kim, Diana M. Mitrea, Mohona Sarkar, Brian D. Freibaum, Jaclyn Cika, Maura Coughlin, James Messing, Amandine Molliex, Brian A. Maxwell, Nam Chul Kim, Jamshid Temirov, Jennifer Moore, Regina-Maria Kolaitis, Timothy I. Shaw, Bing Bai, Junmin Peng, Richard W. Kriwacki, J. Paul Taylor
PDF (14430 K) Supplementary content

Archives of Biochemistry and Biophysics: Alert 14 October-21 October
The preferential heterodimerization of human small heat shock proteins HSPB1 and HSPB6 is dictated by the N-terminal domain *Pages 41-50*
Michelle Heirbaut, Frederik Lermyte, Esther M. Martin, Steven Beelen, Tim Verschueren, Frank Sobott, Sergei V. Strelkov, Stephen D. Weeks

The FEBS Journal Content Alert: 283, 20 (October 2016)
Cysteine residues mediate high-affinity binding of thioredoxin to ASK1 (pages 3821–3838)
Salome Kylarova, Dalibor Kosek, Olivia Petrvalska, Katarina Psenakova, Petr Man, Jaroslav Vecer, Petr Herman, Veronika Obsilova and Tomas Obsil
Version of Record online: 18 SEP 2016 | DOI: 10.1111/febs.13893



Apoptosis signal-regulating kinase 1 (ASK1, MAP3K5) activates p38 and c-Jun kinases in response to proinflammatory and stress signals. ASK1 is inhibited by association with thioredoxin (TRX) which dissociates in response to oxidative stress, thus allowing the ASK1 activation. Here, we investigated the role of cysteine residues on the interaction between TRX1 and ASK1 in both reducing and oxidizing conditions.

The Plant Journal Content Alert (New Articles)
CPR5 modulates salicylic acid and unfolded protein response to manage tradeoffs between plant growth and stress responses Zhe Meng, Cristina Ruberti, Zhizhong Gong and Federica Brandizzi
Accepted manuscript online: 16 OCT 2016 10:45PM EST | DOI: 10.1111/tpj.13397

The RRM protein CP33A is a global ligand of chloroplast mRNAs and is essential for plastid biogenesis and plant development
Marlene Teubner, Janina Fuß, Kristina Kühn, Kirsten Krause and Christian Schmitz-Linneweber
Accepted manuscript online: 15 OCT 2016 03:16AM EST | DOI: 10.1111/tpj.13396

Science 20 October 2016; Vol. 354, No. 6310
Photoactivation and inactivation of *Arabidopsis* cryptochrome 2
By Qin Wang, Zecheng Zuo, Xu Wang, Lianfeng Gu, Takeshi Yoshizumi, Zhaohe Yang, Liang Yang, Qing Liu, Wei Liu, Yun-Jeong Han, Jeong-Il Kim, Bin Liu, James A. Wohlschlegel, Minami Matsui, Yoshito Oka, Chentao Lin
*Science*21 Oct 2016 : 343-347 Full Access

A feedback loop ensures against a runaway response to light in plants.

Li L, Nelson C, Fenske R, TrÃ¶sch J, PruÅ¾inskÃ¡ A, Millar AH, Huang S.
Changes in specific protein degradation rates in Arabidopsis thaliana reveal multiple roles of Lon1 in mitochondrial protein homeostasis.
Plant J. 2016 Oct 11;.PMID: 27726214

Zierer BK, RÃ¼bbelke M, Tippel F, Madl T, Schopf FH, Rutz DA, Richter K, Sattler M, Buchner J.
Importance of cycle timing for the function of the molecular chaperone Hsp90.
Nat Struct Mol Biol. 2016 Oct 10;PMID: 27723736

BÃ¨gue H, Jeandroz S, Blanchard C, Wendehenne D, Rosnoblet C.
Structure and functions of the chaperone-like p97/CDC48 in plants.
Biochim Biophys Acta. 2016 Oct 4; PMID: 27717811

Cerveau D, Kraut A, Stotz HU, Mueller MJ, CoutÃ© Y, Rey P.
Characterization of the Arabidopsis thaliana 2-Cys peroxiredoxin interactome.
Plant Sci. 2016 Nov;252:30-41.

Senthil Kumar R, Shen CH, Wu PY, Suresh Kumar S, Hua MS, Yeh KW.
Nitric oxide participates in plant flowering repression by ascorbate.
Sci Rep. 2016 Oct 12;6:35246. PMID: 27731387

Astuti RI, Nasuno R, Takagi H.
Nitric oxide signaling in yeast.
Appl Microbiol Biotechnol. 2016 Oct 8; PMID: 27722918

Fu ZW, Wang YL, Lu YT, Yuan TT.
Nitric oxide is involved in stomatal development by modulating the expression of stomatal regulator genes in Arabidopsis.
Plant Sci. 2016 Nov;252:282-289. PMID: 27717464

Wynia-Smith SL, Smith BC.
Nitrosothiol formation and S-nitrosation signaling through nitric oxide synthases.
Nitric Oxide. 2016 Oct 5; PMID: 27720836

Lukoszek R, Feist P, Ignatova Z.
Insights into the adaptive response of Arabidopsis thaliana to prolonged thermal stress by ribosomal profiling and RNA-Seq.
BMC Plant Biol. 2016 Oct 10;16(1):221. PMID: 27724872