**Lit Review for 8-30-16**

**Indu**

1: Ostrov N, Landon M, Guell M, Kuznetsov G, Teramoto J, Cervantes N, Zhou M,

Singh K, Napolitano MG, Moosburner M, Shrock E, Pruitt BW, Conway N, Goodman DB,

Gardner CL, Tyree G, Gonzales A, Wanner BL, Norville JE, Lajoie MJ, Church GM.

Design, synthesis, and testing toward a 57-codon genome. Science. 2016 Aug

19;353(6301):819-22. doi: 10.1126/science.aaf3639. PubMed PMID: 27540174.

2: Sedaghatmehr M, Mueller-Roeber B, Balazadeh S. The plastid metalloprotease

FtsH6 and small heat shock protein HSP21 jointly regulate thermomemory in

Arabidopsis. Nat Commun. 2016 Aug 26;7:12439. doi: 10.1038/ncomms12439. PubMed

PMID: 27561243.

3: Maikova A, Zalutskaya Z, Lapina T, Ermilova E. The HSP70 chaperone machines of

Chlamydomonas are induced by cold stress. J Plant Physiol. 2016 Jul 25;204:85-91.

doi: 10.1016/j.jplph.2016.07.012. [Epub ahead of print] PubMed PMID: 27543887.

4: Fernandez-Funez P, Sanchez-Garcia J, de Mena L, Zhang Y, Levites Y, Khare S,

Golde TE, Rincon-Limas DE. Holdase activity of secreted Hsp70 masks amyloid-β42

neurotoxicity in Drosophila. Proc Natl Acad Sci U S A. 2016 Aug 16. pii:

201608045. [Epub ahead of print] PubMed PMID: 27531960.

* **Patrick**
* **1. Selective Protein Denitrosylation Activity of Thioredoxin-h5 Modulates Plant Immunity**
* Molecular Cell 56, 153–162, October 2, 2014  
  Sophie Kneeshaw,1 Silve ` re Gelineau,1 Yasuomi Tada,2 Gary J. Loake,1 and Steven H. Spoel1,\*  
  1Institute of Molecular Plant Sciences, School of Biological Sciences, University of Edinburgh, Edinburgh EH9 3JR, UK  
  2The Center for Gene Research, Division of Biological Science, Nagoya University, Nagoya, 464-8602, Japan  
  \*Correspondence: steven.spoel@ed.ac.uk  
  <http://dx.doi.org/10.1016/j.molcel.2014.08.003>
* SUMMARY  
  In eukaryotes, bursts of reactive oxygen and nitrogen species mediate cellular responses to the environment by modifying cysteines of signaling proteins. Cysteine reactivity toward nitric oxide (NO) leads to formation of S-nitrosothiols (SNOs) that play important roles in pathogenesis and immunity. However, it remains poorly understood how SNOs are employed as specific, reversible signaling cues. Here we show that in plant immunity the oxidoreductase Thioredoxin-h5 (TRXh5) reverses SNO modifications by acting as a selective protein-SNO reductase. While TRXh5 failed to restore immunity in gsnor1 mutants that display excessive accumulation of the NO donor S-nitrosoglutathione, it rescued immunity in nox1 mutants that exhibit elevated levels of free NO. Rescue by TRXh5 was conferred through selective denitrosylation of excessive protein-SNO, which reinstated signaling by the immune hormone salicylic acid. Our data indicate that TRXh5 discriminates between protein-SNO substrates to provide previously unrecognized specificity and reversibility to proteinSNO signaling in plant immunity.
* **2. Heat-Shock and Redox-Dependent Functional Switching of an h-Type Arabidopsis Thioredoxin from a Disulfide Reductase to a Molecular Chaperone**
* Plant Physiology, June 2009, Vol. 150, pp. 552–561
* Soo Kwon Park2, Young Jun Jung2, Jung Ro Lee2, Young Mee Lee, Ho Hee Jang, Seung Sik Lee, Jin Ho Park, Sun Young Kim, Jeong Chan Moon, Sun Yong Lee, Ho Byoung Chae, Mi Rim Shin, Ji Hyun Jung, Min Gab Kim, Woe Yeon Kim, Dae-Jin Yun, Kyun Oh Lee, and Sang Yeol Lee\* Environmental Biotechnology National Core Research Center, Plant Molecular Biology and Biotechnology Research Center (S.K.P., Y.J.J., J.R.L., Y.M.L., H.H.J., S.S.L., J.H.P., S.Y.K., J.C.M., S.Y.L., H.B.C., M.R.S., J.H.J., W.Y.K., D.-J.Y., K.O.L., S.Y.L.), and Division of Applied Life Science (BK21 program; S.K.P., Y.J.J., J.R.L., Y.M.L., S.S.L., J.H.P., S.Y.K., J.C.M., S.Y.L., H.B.C., M.R.S., J.H.J., D.-J.Y., K.O.L., S.Y.L.), Gyeongsang National University, Jinju 660–701, Korea; Lee Gil Ya Cancer and Diabetes Institute, Gachon University of Medicine and Science, Incheon 406–840, Korea (H.H.J.); Department of Functional Crop, National Institute of Crop Science, Rural Development Administration, Milyang 627–130, Korea (S.K.P.); and Bio-crops Development Division, National Academy of Agricultural Science, Rural Development Administration, 224 Suin-ro, Suwon 441–857, Korea (M.G.K.)
* **Abstract**
* A large number of thioredoxins (Trxs), small redox proteins, have been identified from all living organisms. However, many of the physiological roles played by these proteins remain to be elucidated. We isolated a high Mr (HMW) form of h-type Trx from the heat-treated cytosolic extracts of Arabidopsis (Arabidopsis thaliana) suspension cells and designated it as AtTrx-h3. Using bacterially expressed recombinant AtTrx-h3, we find that it forms various protein structures ranging from low and oligomeric protein species to HMW complexes. And the AtTrx-h3 performs dual functions, acting as a disulfide reductase and as a molecular chaperone, which are closely associated with its molecular structures. The disulfide reductase function is observed predominantly in the low Mr forms, whereas the chaperone function predominates in the HMW complexes. The multimeric structures of AtTrx-h3 are regulated not only by heat shock but also by redox status. Two active cysteine residues in AtTrx-h3 are required for disulfide reductase activity, but not for chaperone function. AtTrx-h3 confers enhanced heat-shock tolerance in Arabidopsis, primarily through its chaperone function.
* **3. The multigenic family of thioredoxin *h* in *Arabidopsis thaliana*: specific  
  expression and stress response**
* Jean-Philippe Reichheld \*, Dominique Mestres-Ortega, Christophe Laloi, Yves Meyer  
  *Laboratoire génome et développement des plantes, université de Perpignan (CNRS, UMR 5096), 52, avenue de Villeneuve, 66000 Perpignan, France*  
  Plant Physiol. Biochem. 40 (2002) 685–690
* **Abstract**  
  In the model plant *Arabidopsis thaliana*, cytosolic thioredoxins *h* (TRXh) are encoded by a multigenic family of eight genes. Genomic studies have revealed that a number of these genes are duplicated genes originating from a common ancestor. This multiplicity of thioredoxin *h* genes raises questions of the specificity of plant thioredoxins and the function of such a large multigenic family in plant. The results from studies using northern blots, semi-quantitative RT-PCR and transgenic promoter–*GUS* fusions provide strong evidence that the members of the *AtTRXh* gene family show expression levels that vary among different plant organs. Moreover, distinct *AtTRXh* genes are induced in response to pathogenic elicitors. Together, our data suggest that the members of the multigenic family of *AtTRXh* may not have redundant functions.

**Ian**

A Novel Method for Assessing the Chaperone Activity of Proteins.Nevena Hristozova,Peter Tompa,Denes Kovacs Published: August 26, 2016. <http://dx.doi.org/10.1371/journal.pone.0161970>

**Minsoo**

**1. Mol Cell. 2016 Aug 18;63(4):553-66. doi: 10.1016/j.molcel.2016.07.019.**

**Cysteine Sulfenylation Directs IRE-1 to Activate the SKN-1/Nrf2 Antioxidant**

**Response.**

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Emerging evidence suggests that many proteins may be regulated through cysteine

modification, but the extent and functions of this signaling remain largely

unclear. The endoplasmic reticulum (ER) transmembrane protein IRE-1 maintains ER

homeostasis by initiating the unfolded protein response (UPR(ER)). Here we show

in C. elegans and human cells that IRE-1 has a distinct redox-regulated function

in cytoplasmic homeostasis. Reactive oxygen species (ROS) that are generated at

the ER or by mitochondria sulfenylate a cysteine within the IRE-1 kinase

activation loop. This inhibits the IRE-1-mediated UPR(ER) and initiates the

p38/SKN-1(Nrf2) antioxidant response, thereby increasing stress resistance and

lifespan. Many AGC-family kinases (AKT, p70S6K, PKC, ROCK1) seem to be regulated

similarly. The data reveal that IRE-1 has an ancient function as a cytoplasmic

sentinel that activates p38 and SKN-1(Nrf2) and indicate that cysteine

modifications induced by ROS signals can direct proteins to adopt unexpected

functions and may coordinate many cellular processes.

**2. Mol Cell. 2016 Aug 18;63(4):621-32. doi: 10.1016/j.molcel.2016.06.033. Epub 2016**

**Aug 4.**

**Mitochondrial Protein Interaction Mapping Identifies Regulators of Respiratory**

**Chain Function.**

Floyd BJ(1), Wilkerson EM(2), Veling MT(1), Minogue CE(2), Xia C(3), Beebe ET(4),

Wrobel RL(4), Cho H(1), Kremer LS(5), Alston CL(6), Gromek KA(4), Dolan BK(4),

Ulbrich A(2), Stefely JA(1), Bohl SL(1), Werner KM(4), Jochem A(7), Westphall

MS(8), Rensvold JW(7), Taylor RW(6), Prokisch H(5), Kim JJ(3), Coon JJ(9),

Pagliarini DJ(10).

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University of Wisconsin-Madison, Madison, WI 53706, USA; Genome Center of

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Mitochondria are essential for numerous cellular processes, yet hundreds of their

proteins lack robust functional annotation. To reveal functions for these

proteins (termed MXPs), we assessed condition-specific protein-protein

interactions for 50 select MXPs using affinity enrichment mass spectrometry. Our

data connect MXPs to diverse mitochondrial processes, including multiple aspects

of respiratory chain function. Building upon these observations, we validated

C17orf89 as a complex I (CI) assembly factor. Disruption of C17orf89 markedly

reduced CI activity, and its depletion is found in an unresolved case of CI

deficiency. We likewise discovered that LYRM5 interacts with and deflavinates the

electron-transferring flavoprotein that shuttles electrons to coenzyme Q (CoQ).

Finally, we identified a dynamic human CoQ biosynthetic complex involving

multiple MXPs whose topology we map using purified components. Collectively, our

data lend mechanistic insight into respiratory chain-related activities and

prioritize hundreds of additional interactions for further exploration of

mitochondrial protein function.

**3. Plant Cell. 2016 Aug 19. pii: tpc.00540.2016. [Epub ahead of print]**

**Mitochondrial Defects Confer Tolerance against Cellulose Deficiency.**

Hu Z(1), Vanderhaeghen R(1), Cools T(2), Wang Y(3), De Clercq I(4), Leroux O(5),

Nguyen L(1), Belt K(6), Millar AH(7), Audenaert D(1), Hilson P(8), Small ID(9),

Mouille G(10), Vernhettes S(11), Van Breusegem F(1), Whelan J(12), Höfte H(10),

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(8)Institut Jean-Pierre Bourgin, UMR1318 INRA-AgroParisTech CITY: Versailles

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Because the plant cell wall provides the first line of defence against biotic and

abiotic assaults, its functional integrity needs to be maintained under stress

conditions. Through a phenotype-based compound screening approach we identified a

novel cellulose synthase inhibitor, designated C17. C17 administration depletes

cellulose synthase complexes (CSCs) from the plasma membrane in Arabidopsis

thaliana, resulting in anisotropic cell elongation and a weak cell wall.

Surprisingly, in addition to mutations in CELLULOSE SYNTHASE 1 (CESA1) and

CELLULOSE SYNTHASE 3 (CESA3), a forward genetic screen identified two independent

defective genes encoding pentatricopeptide repeat (PPR)-like proteins [CELL WALL

MAINTAINER 1 (CWM1) and 2 (CWM2)] as conferring tolerance to C17. Functional

analysis revealed that mutations in these PPR proteins resulted in defective

cytochrome c maturation and activation of mitochondrial retrograde signalling, as

evidenced by the induction of an alternative oxidase. These mitochondrial

perturbations increased tolerance to cell wall damage induced by cellulose

deficiency. Likewise, administration of antimycin A, an inhibitor of

mitochondrial complex III, and constitutive activation of mitochondrial

retrograde signalling resulted in tolerance towards C17. The C17 tolerance of

cwm2 was partially lost upon depletion of the mitochondrial retrograde regulator

ANAC017, demonstrating that ANAC017 links mitochondrial dysfunction with the cell

wall. In view of mitochondria being a major target of a variety of stresses, our

data indicate that plant cells might modulate mitochondrial activity to maintain

a functional cell wall when subjected to stresses.

**Keith**

**The plastid metalloprotease FtsH6 and small heat shock protein HSP21 jointly regulate thermomemory in Arabidopsis.**

Nat Commun. 2016 Aug 26;7:12439. doi: 10.1038/ncomms12439.

[Sedaghatmehr M](http://www.ncbi.nlm.nih.gov/pubmed/?term=Sedaghatmehr%20M%5BAuthor%5D&cauthor=true&cauthor_uid=27561243)1,2, [Mueller-Roeber B](http://www.ncbi.nlm.nih.gov/pubmed/?term=Mueller-Roeber%20B%5BAuthor%5D&cauthor=true&cauthor_uid=27561243)1,2, [Balazadeh S](http://www.ncbi.nlm.nih.gov/pubmed/?term=Balazadeh%20S%5BAuthor%5D&cauthor=true&cauthor_uid=27561243)1,2.

1University of Potsdam, Institute of Biochemistry and Biology, Karl-Liebknecht-Straße 24-25, Haus 20, 14476 Potsdam-Golm, Germany. 2Max Planck Institute of Molecular Plant Physiology, Cooperative Research Group, Am Mühlenberg 1, 14476 Potsdam-Golm, Germany.

Acquired tolerance to heat stress is an increased resistance to elevated temperature following a prior exposure to heat. The maintenance of acquired thermotolerance in the absence of intervening stress is called 'thermomemory' but the mechanistic basis for this memory is not well defined. Here we show that Arabidopsis HSP21, a plastidial small heat shock protein that rapidly accumulates after heat stress and remains abundant during the thermomemory phase, is a crucial component of thermomemory. Sustained memory requires that HSP21 levels remain high. Through pharmacological interrogation and transcriptome profiling, we show that the plastid-localized metalloprotease FtsH6 regulates HSP21 abundance. Lack of a functional FtsH6 protein promotes HSP21 accumulation during the later stages of thermomemory and increases thermomemory capacity. Our results thus reveal the presence of a plastidial FtsH6-HSP21 control module for thermomemory in plants.

**Selective killing of cancer cells by small molecules targeting heat shock stress response.**

Biochem Biophys Res Commun. 2016 Aug 20.

[Zhang D](http://www.ncbi.nlm.nih.gov/pubmed/?term=Zhang%20D%5BAuthor%5D&cauthor=true&cauthor_uid=27553278)1, [Zhang B](http://www.ncbi.nlm.nih.gov/pubmed/?term=Zhang%20B%5BAuthor%5D&cauthor=true&cauthor_uid=27553278)2.

1Department of Biology, Alpine Therapeutics, Inc., 13350 Camino Del Sur, No. 8, San Diego, CA 92129, USA.

2Department of Biology, Alpine Therapeutics, Inc., 13350 Camino Del Sur, No. 8, San Diego, CA 92129, USA. Electronic address: [bzhang418@gmail.com](mailto:bzhang418@gmail.com).

HSF1 **heat shock** response has emerged as a valuable non-oncogenetic intervention point in targeted cancer therapy. Current reporter based high throughput screening has led to the discovery of several compounds or chemotypes that are effective in the growth inhibition of multiple cancer cell lines and relevant animal tumor models. However, some intrinsic limitations of reporter based assays can potentially lead to biased results. Using a previously validated high content image based assay, we performed a phenotypic screen targeting HSF1 **heat shock** pathway with a chemically diversified library of over 100,000 compounds. Several novel functional inhibitors of HSF1 pathway were identified with different chemotypes. Western blot analysis confirmed that selective compounds inhibit phosphorylation of HSF1, followed by reduced expression of HSP **proteins**. Moreover, HeLa cells stably transfected with HSF1 shRNA were more resistant to the compound treatment under lethal temperature than cells containing HSF1, validating HSF1 dependent mechanism of action. These compounds demonstrate nanomolar potency toward multiple cancer cell lines with relatively low cytotoxicity to normal cells. Further SAR and target identification study will pave the way for the potential development of next generation anticancer drugs.

**Small Heat Shock Proteins and the postharvest chilling tolerance of tomato fruit.**

Physiol Plant. 2016 Aug 22.

[Ré MD](http://www.ncbi.nlm.nih.gov/pubmed/?term=R%C3%A9%20MD%5BAuthor%5D&cauthor=true&cauthor_uid=27545651)1, [Gonzalez C](http://www.ncbi.nlm.nih.gov/pubmed/?term=Gonzalez%20C%5BAuthor%5D&cauthor=true&cauthor_uid=27545651)1, [Escobar MR](http://www.ncbi.nlm.nih.gov/pubmed/?term=Escobar%20MR%5BAuthor%5D&cauthor=true&cauthor_uid=27545651)1, [Sossi ML](http://www.ncbi.nlm.nih.gov/pubmed/?term=Sossi%20ML%5BAuthor%5D&cauthor=true&cauthor_uid=27545651)1, [Valle EM](http://www.ncbi.nlm.nih.gov/pubmed/?term=Valle%20EM%5BAuthor%5D&cauthor=true&cauthor_uid=27545651)1, [Boggio SB](http://www.ncbi.nlm.nih.gov/pubmed/?term=Boggio%20SB%5BAuthor%5D&cauthor=true&cauthor_uid=27545651)1.

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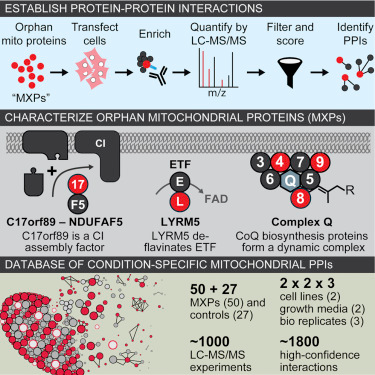
Plants have the largest number of **small** **heat shock proteins** (sHsps) (15-42 kDa) among eukaryotes, but little is known about their function in vivo. They accumulate in response to different stresses, and specific sHsps are also expressed during developmental processes such as seed development, germination, and ripening. The presence of organelle-specific sHsps appears to be unique to plants. The sHsps expression is regulated by **heat** stress transcription factors (Hsfs). In this work, it was explored the role of sHsps in the chilling injury of tomato fruit. The level of transcripts and **proteins** of cytoplasmic and organellar sHsps was monitored in fruit during ripening and after cold storage (four weeks at 4°C). Expression of HsfA1, HsfA2, HsfA3 and HsfB1 was also examined. Two cultivars of tomato (Solanum lycopersicum) contrasting in chilling tolerance were assayed: Micro-Tom (chilling-tolerant) and Minitomato (chilling-sensitive). Results showed that sHsps were induced during ripening in fruit from both cultivars. However, sHsps were induced in Micro-Tom fruit but not in Minitomato fruit after storage at a low temperature. In particular, sHsp 17.4-CII and sHsp 23.8-M transcripts strongly accumulated in Micro-Tom fruit and HsfA3 transcript diminished after cold storage. These data suggest that sHsps may be involved in the protection mechanisms against chilling stress and substantiate the hypothesis that sHsps may participate in the mechanism of tomato genotype chilling tolerance.

Elizabeth:

**August 30**

Molecular Cell: Alert 13 August-19 August

[Mitochondrial Protein Interaction Mapping Identifies Regulators of Respiratory Chain Function](http://www.sciencedirect.com/science?_ob=GatewayURL&_method=citationSearch&_urlVersion=4&_origin=SDVIALERTHTML&_version=1&_piikey=S1097-2765%2816%2930291-X&md5=da7f4c60ae93bcf4ce254e7f9dd4a643&graphAbs=y)   Original Research Article *Pages 621-632*



**The Plant Journal Content Alert (New Articles)**

[**ERIL1, the Plant Homologue of ERI-1 is Involved in the Processing of Chloroplastic rRNAs**](http://onlinelibrary.wiley.com/doi/10.1111/tpj.13304/abstract?campaign=wolacceptedarticle)  
Glykeria Mermigka, Jutta Maria Helm, Ioannis Vlatakis, Heiko Tobias Schumacher, Evgenia Vamvaka and Kriton Kalantidis  
Accepted manuscript online: 17 AUG 2016 04:30AM EST | DOI: 10.1111/tpj.13304

**eLife 10.7554/eLife.13664 (2016).**

Artemisinin, which is critical in defense against malaria, was originally found in tiny hairs on the surface of leaves of the plant Artemisia annua. But this source plant does not support a sufficiently stable supply of artemisinin for worldwide use. Fuentes et al. have developed a synthetic biology approach termed COSTREL (combinatorial supertransformation of transplastomic recipient lines) that produces the immediate precursor of artemisinin, artemisinic acid, in widely cultivated tobacco (Nicotiana tabacum cv. Petit Havana). The first stage of COSTREL involves transformation of tobacco chloroplasts with genes encoding the core enzymes of the artemisinin biosynthetic pathway. With that pathway established, the second stage involves combinatorial nuclear transformation to superimpose genes that regulate flux through the biosynthetic pathway. A transformation mix supports selection of the most optimal gene combination. The resulting tobacco plants produce artemisinic acid at up to ~4.8 kg per acre.

Krsticevic FJ, Arce DP, Ezpeleta J, Tapia E.

Tandem Duplication Events in the Expansion of the Small Heat Shock Protein Gene Family in Solanum lycopersicum (cv. Heinz 1706).

G3 (Bethesda). 2016 Aug 26;. PMID: 27565886 [PubMed - as supplied by publisher]

Hristozova N, Tompa P, Kovacs D.

A Novel Method for Assessing the Chaperone Activity of Proteins.

PLoS One. 2016;11(8):e0161970. PMID: 27564234 [PubMed - as supplied by publisher]

Sedaghatmehr M, Mueller-Roeber B, Balazadeh S.

The plastid metalloprotease FtsH6 and small heat shock protein HSP21 jointly regulate thermomemory in Arabidopsis.

Nat Commun. 2016 Aug 26;7:12439. PMID: 27561243 [PubMed - in process]

RÃ¶th S, Mirus O, Bublak D, Klaus-Dieter S, Schleiff E.

DNA-binding and repressor function are prerequisite for the turnover of the tomato heat stress transcription factor HsfB1.

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Vahid S, Thaper D, Gibson KF, Bishop JL, Zoubeidi A.

Molecular chaperone Hsp27 regulates the Hippo tumor suppressor pathway in cancer.

Sci Rep. 2016 Aug 24;6:31842. PMID: 27555231 [PubMed - in process]

Dubnikov T, Ben-Gedalya T, Reiner R, Hoepfner D, Cabral WA, Marini JC, Cohen E.

PrP-containing aggresomes are cytosolic components of an endoplasmic reticulum quality control mechanism.

J Cell Sci. 2016 Aug 22;. PMID: 27550517 [PubMed - as supplied by publisher]

Behnke J, Mann MJ, Scruggs FL, Feige MJ, Hendershot LM.

Members of the Hsp70 Family Recognize Distinct Types of Sequences to Execute ER Quality Control.

Mol Cell. 2016 Aug 17;.PMID: 27546788 [PubMed - as supplied by publisher]

RÃ© MD, Gonzalez C, Escobar MR, Sossi ML, Valle EM, Boggio SB.

Small Heat Shock Proteins and the postharvest chilling tolerance of tomato fruit.

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Li L, Xing Y, Chang D, Fang S, Cui B, Li Q, Wang X, Guo S, Yang X, Men S, Shen Y.

CaM/BAG5/Hsc70 signaling complex dynamically regulates leaf senescence.

Sci Rep. 2016 Aug 19;6:31889. PMID: 27539741 [PubMed - in process]

Peng R, Bian Z, Zhou L, Cheng W, Hai N, Yang C, Yang T, Wang X, Wang C.

Hydrogen sulfide enhances nitricÂ oxide-induced tolerance of hypoxia in maize (Zea mays L.).

Plant Cell Rep. 2016 Aug 11;. PMID: 27516180 [PubMed - as supplied by publisher]

Lange S, Franks WT, Rajagopalan N, DÃ¶ring K, Geiger MA, Linden A, van Rossum BJ, Kramer G, Bukau B, Oschkinat H.

Structural analysis of a signal peptide inside the ribosome tunnel by DNP MAS NMR.

Sci Adv. 2016 Aug;2(8):e1600379. PMID: 27551685 [PubMed - in process]

Vincent BM, Langlois JB, Srinivas R, Lancaster AK, Scherz-Shouval R, Whitesell L, Tidor B, Buchwald SL, Lindquist S.

A Fungal-Selective Cytochrome bc&lt;sub&gt;1&lt;/sub&gt; Inhibitor Impairs Virulence and Prevents the Evolution of Drug Resistance.

Cell Chem Biol. 2016 Aug 6;.PMID: 27524297 [PubMed - as supplied by publisher]

Chen J, Yu F, Liu Y, Du C, Li X, Zhu S, Wang X, Lan W, Rodriguez PL, Liu X, Li D, Chen L, Luan S.

FERONIA interacts with ABI2-type phosphatases to facilitate signaling cross-talk between abscisic acid and RALF peptide in Arabidopsis.

Proc Natl Acad Sci U S A. 2016 Aug 26;. PMID: 27566404 [PubMed - as supplied by publisher]

Ohtsuki T, Kanzaki S, Nishimura S, Kunihiro Y, Sisido M, Watanabe K.

Phototriggered protein syntheses by using (7-diethylaminocoumarin-4-yl)methoxycarbonyl-caged aminoacyl tRNAs.

Nat Commun. 2016 Aug 17;7:12501. PMID: 27530762 [PubMed - in process]

Sharma H, Adio S, Senyushkina T, Belardinelli R, Peske F, Rodnina MV.

Kinetics of Spontaneous and EF-G-Accelerated Rotation of Ribosomal Subunits.

Cell Rep. 2016 Aug 23;16(8):2187-96. PMID: 27524615 [PubMed - in process]

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Nat Commun. 2016 Apr 4;7:11194. PMID: 27041671

[Methods in Enzymology](http://www.sciencedirect.com/science/journal/00766879) [Volume 579 ,  Pages 2-445, 2016](http://www.sciencedirect.com/science/journal/00766879/579)   
**The Resolution Revolution: Recent Advances In cryoEM** Edited by R.A. Crowther

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