Sept 20
The Plant Journal

Subdiffraction-resolution live-cell imaging for visualizing thylakoid membranes

Masakazu Iwai, Melissa S. Roth, Krishna K. Niyogi   First Published: 07 July 2018

A key to understanding the dynamic mechanisms of photosynthesis and photoprotection in chloroplast thylakoid membranes is to examine the processes *in vivo*. However, technical limitations regarding spatial resolution have prevented *in vivo* observations of thylakoid membrane dynamics. Here we use live-cell three-dimensional structured illumination microscopy to investigate such dynamic processes occurring within chloroplasts at unprecedented spatiotemporal scales.

The UPF1 interactome reveals interaction networks between RNA degradation and translation repression factors in Arabidopsis

Clara Chicois, Hélène Scheer, Shahïnez Garcia, Hélène Zuber, Jérôme Mutterer, Johana Chicher, Philippe Hammann, Dominique Gagliardi, Damien Garcia   First Published: 07 July 2018

Nonsense-mediated decay is an essential process involved in development, hormone and pathogen response through the repression of gene expression by the RNA helicase UPF1. Despite its major functions, this process is still poorly understood in plants compared with mammals. By an unbiased strategy we identified protein partners of UPF1, and discovered unappreciated associations between factors involved in RNA decay and translation regulation, allowing the identification of hitherto unknown P-body components with potential function in these processes.

PlantSEED enables automated annotation and reconstruction of plant primary metabolism with improved compartmentalization and comparative consistency

Samuel M. D. Seaver, Claudia Lerma-Ortiz, Neal Conrad, Arman Mikaili, Avinash Sreedasyam, Andrew D. Hanson, Christopher S. Henry   First Published: 20 June 2018

An improved version of the PlantSEED resource is released with numerous enhancements: improved assignment of metabolic pathways to subcellular compartments; refined annotation of primary metabolism for 39 reference genomes from Phytozome; a pipeline for automated annotation and modeling of user-uploaded plant sequences; and an upgraded website (http://modelseed.org). PlantSEED provides highly consistent reconstructions and simulations of primary metabolism for any newly sequenced plant species, simplifying the process for comparison of omics data across different species.

These new articles for Physiologia Plantarum are available online.

Enhancing the abiotic stress tolerance of plants: From chemical treatment to biotechnological approaches

Hoang Chinh Nguyen, Kung-Huan Lin, Shin-Lon Ho, Chih-Ming Chiang, Chi-Ming Yang
First Published: 28 July 2018

DNA repair in plant mitochondria – A complete base excision repair pathway in potato tuber mitochondria

Beatriz Ferrando, Ana Luiza Dorigan de Matos Furlanetto, Ricardo Gredilla, Jesper F. Havelund, Kim H. Hebelstrup, Ian Max Møller, Tinna Stevnsner
First Published: 23 July 2018

Short-term high temperature treatment reduces viability and inhibits respiration and DNA repair enzymes in Araucaria angustifolia cells

Ana Luiza Dorigan de Matos Furlanetto, Silvia Maria Suter Correia Cadena, Glaucia Regina Martinez, Beatriz Ferrando, Tinna Stevnsner, Ian Max Møller
First Published: 27 June 2018

Physiological response of tomatoes at drought, heat and their combination followed by recovery

Rong Zhou, Lingpeng Kong, Zhen Wu, Eva Rosenqvist, Yinlei Wang, Liping Zhao, Tongmin Zhao, Carl-Otto Ottosen
First Published: 17 May 2018
These new articles for Plant, Cell & Environment are available online.

Autophagy and its role in plant abiotic stress management

Tamar Avin-Wittenberg
First Published: 11 July 2018

Plants are regularly exposed to changing environmental conditions, among which various types of abiotic stress, damaging plant performance and yield. One of the outcomes of abiotic stress is the need to degrade and recycle damaged proteins and organelles. Autophagy is a conserved eukaryotic mechanism functioning in the degradation of proteins, protein aggregates, and whole organelles. The review describes the current knowledge regarding the involvement of autophagy in plant abiotic stress response, mechanisms functioning in autophagy induction during stress, and possible directions for future research.

Chromatin-based mechanisms of temperature memory in plants

Thomas Friedrich, Léa Faivre, Isabel Bäurle, Daniel Schubert

First Published: 19 June 2018

Plants are constantly exposed to a changing environment, which challenges growth and survival. Therefore, plants can store information from a previous stressful event to become more resistant to subsequent stresses. Here, we review recent progress on chromatin-mediated memory of high and low temperatures.

BRUSHY1/TONSOKU/MGOUN3 is required for heat stress memory

Krzysztof Brzezinka, Simone Altmann, Isabel Bäurle

First Published: 08 June 2018

Plants can be primed by a heat stress exposure to deal more efficiently with a future heat stress incident that occurs after a lag phase at normal growth temperatures. Studying the molecular basis of priming and memory in response to heat stress, we show here that the chromatin protein BRUSHY1 is required for heat stress memory and that it acts through sustaining the activation of heat stress-memory related gene expression during the lag phase. Our findings suggest a model where heat stress memory is mediated through the epigenetic inheritance of chromatin states across cell divisions.

Respiratory burst oxidase homologue-dependent H2O2 and chloroplast H2O2 are essential for the maintenance of acquired thermotolerance during recovery after acclimation

Mintao Sun, Fangling Jiang, Benjian Cen, Junqin Wen, Yanzhao Zhou, Zhen Wu

First Published: 31 May 2018

Thermotolerance is improved by heat stress acclimation, and the level of thermotolerance is "remembered" by plants. However, the underlying signalling mechanisms remain largely unknown. Our results suggest that tomato seedlings increase their maintenance of acquired thermotolerance by enhancing NADPH oxidase-mediated H_2O_2 content and controlling chloroplast-H_2O_2 production during recovery, which enhances the expression of heat stress-responsive genes and balances programmed cell death levels, respectively.

These new articles for Plant Breeding are available online.

Other Crop species moving forward!

Cowpea (Vigna unguiculata): Genetics, genomics and breeding

Ousmane Boukar, Nouhoun Belko, Siva Chamarthi, Abou Togola, Joseph Batieno, Emmanuel Owusu, Mohammed Haruna, Sory Diallo, Muhammed Lawan Umar, Olusoji Olufajo, Christian Fatokun

First Published: 09 May 2018

Open Access

Genomics, genetics and breeding of tropical legumes for better livelihoods of smallholder farmers

Chris Ojiewo, Emmanuel Monyo, Haile Desmae, Ousmane Boukar, Clare Mukankusi-Mugisha, Mahendar Thudi, Manish K. Pandey, Rachit K. Saxena, Pooran M. Gaur, Sushil K. Chaturvedi, Asnake Fikre, NPVR Ganga Rao, CV SameerKumar, Patrick Okori, Pasupuleti Janila, Jean Claude Rubyogo, Chigeza Godfree, Essegbemon Akpo, Lucky Omoigui, Stanley Nkalubo, Berhanu Fenta, Papias Binagwa, Michael Kilango, Magdalena Williams, Omari Mponda, David Okello, Mekasha Chichaybelu, Amos Miningou, Joseph Bationo, Dramane Sako, Sory Diallo, Candidus Echekwu, Muhammad Lawan Umar, Richard Oteng-Frimpong, Haruna Mohammed, Rajeev K. Varshney

First Published: 17 April 2018

Open Access

Genomics, genetics and breeding of common bean in Africa: A review of tropical legume project

Clare Mukankusi, Bodo Raatz, Stanley Nkalubo, Fenta Berhanu, Papias Binagwa, Michael Kilango, Magdalena Williams, Katungi Enid, Rowland Chirwa, Steve Beebe

First Published: 17 April 2018

Current Biology: Alert 14 August-21 August
Chloroplast Biogenesis Controlled by DELLA-TOC159 Interaction in Early Plant Development
Pages 2616-2623.e5
Venkatasalam Shanmugabalaji, Hicham Chahtane, Sonia Accossato, Michèle Rahire, Guillaume Gouzerh, Luis Lopez-Molina, Felix Kessler
Decoupling Yeast Cell Division and Stress Defense Implicates mRNA Repression in Translational Reallocation during Stress
Pages 2673-2680.e4
Yi-Hsuan Ho, Evgenia Shishkova, James Hose, Joshua J. Coon, Audrey P. Gasch
Journal of Plant Physiology: Alert 14 August-21 August
Phytohormones as targets for improving plant productivity and stress tolerance   Review Article
Pages 32-40
Joanna Ciura, Jerzy Kruk
Nature Structural & Molecular Biology
UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites
Vyacheslav Akimov, …..Blagoy Blagoev
vol 25, pages631–640 (2018)

Plant, Cell & Environment Content Alert: 41, 8 (August 2018)
REVIEW

Singlet oxygen-triggered chloroplast-to-nucleus retrograde signalling pathways: An emerging perspective (pages 1727–1738)
Vivek Dogra, Jean-David Rochaix and Chanhong Kim
Version of Record online: 8 JUN 2018 | DOI: 10.1111/pce.13332
Chloroplasts act as environmental sensors translating the perceived information into various forms of signals that eventually alter the expression of nuclear-encoded genes. Among these distinct signals, singlet oxygen generated by photosystem II under photo-oxidative stress conditions has been implicated in photo-damage and in signalling. Therefore, understanding the precise mode of action of singlet oxygen is crucial for improving crop production. As such, this review covers how singlet oxygen is generated and the associated photo-damage, detoxification, and signalling pathways with emerging questions regarding the place where $^1O_2$ is produced and two distinct $^1O_2$-signalling pathways.

HOP family plays a major role in long-term acquired thermotolerance in Arabidopsis (pages 1852–1869)
Nuria Fernández-Bautista, Lourdes Fernández-Calvino, Alfonso Muñoz, René Toribio, Hans P. Mock and M. Mar Castellano Version of Record online: 28 MAY 2018 | DOI: 10.1111/pce.13326
Heat is one of the environmental stresses that most drastically impact on plant growth, development and yield. This article describes for the first time that HOPs (HSP70-1152 HSP90 organizing proteins) play a main role in long term acquired thermotolerance, affecting different aspects of this complex response

Plant Cell
Response to Persistent ER Stress in Plants: A Multiphasic Process That Transitions Cells from Prosurvival Activities to Cell Death
Renu Srivastava, Zhaoxia Li, Giulia Russo, Jie Tang, Ran Bi, Usha Muppirala, Sivanandan Chudalayandi, Andrew Severin, Mingze He, Samuel I. Vaitkevicius, Carolyn J. Lawrence-Dill, Peng Liu, Ann E. Stapleton, Diane C. Bassham, Federica Brandizzi and Stephen H. Howell
Plant Cell 2018 30: 1220-1242. First Published on May 25, 2018; doi:10.1105/tpc.18.00153 **OPEN**
http://www.plantcell.org/content/30/6/1220.abstract
Persistent ER stress in maize activates a gene expression program interwoven among cellular events that transition from cell survival to cell death.
Thylakoid-Bound Polysomes and a Dynamin-Related Protein, FZL, Mediate Critical Stages of the Linear Chloroplast Biogenesis Program in Greening Arabidopsis Cotyledons
Zizhen Liang, Ning Zhu, Keith K Mai, Zhongyuan Liu, David T. W. Tzeng, Katherine W. Osteryoung, Silin Zhong, Andrew Staehelin and Byung-Ho Kang
Plant Cell 2018 tpc.17.00972; Advance Publication June 7, 2018; doi:10.1105/tpc.17.00972 **OPEN**
http://www.plantcell.org/content/early/2018/06/25/tpc.17.00972.abstract

Joret C, Capeyrou R, Belhabich-Baumas K, Plisson-Chastang C, Ghandour R, Humbert O, Fribourg S, Leulliot N, Lebaron S, Henras AK, Henry Y.
The Npa1p complex chaperones the assembly of the earliest eukaryotic large ribosomal subunit precursor.
PLoS Genet. 2018 Aug 31;14(8):e1007597. [Epub ahead of print]
PMID: 30169518 [PubMed - as supplied by publisher]

Park AM, Tsunoda I, Yoshie O.
Heat shock protein 27 promotes cell cycle progression by down-regulating E2F transcription factor 4 and retinoblastoma family protein p130.
J Biol Chem. 2018 Aug 30;. [Epub ahead of print]
PMID: 30166342 [PubMed - as supplied by publisher]

Shiber A, DÃ¶ring K, Friedrich U, Klann K, Merker D, Zedan M, Tippmann F, Kramer G, Bukau B.
Cotranslational assembly of protein complexes in eukaryotes revealed by ribosome profiling.
Nature. 2018 Aug 29;. [Epub ahead of print]
PMID: 30158700 [PubMed - as supplied by publisher]

Agozzino L, Dill KA.
Protein evolution speed depends on its stability and abundance and on chaperone concentrations.
Proc Natl Acad Sci U S A. 2018 Aug 27;. [Epub ahead of print]
PMID: 30150386 [PubMed - as supplied by publisher]

Ekanger LA, Oyala PH, Moradian A, Sweredoski MJ, Barton JK.
Nitric Oxide Modulates Endonuclease III Redox Activity by a 800 mV Negative Shift upon [Fe<sub>4</sub>S<sub>4</sub>] Cluster Nitrosylation.
J Am Chem Soc. 2018 Aug 26;. [Epub ahead of print]
PMID: 30145881 [PubMed - as supplied by publisher]

Ji Z.
Rfoot: Transcriptome-Scale Identification of RNA-Protein Complexes from Ribosome Profiling Data.
Curr Protoc Mol Biol. 2018 Aug 31;:e66. [Epub ahead of print]
PMID: 30168907 [PubMed - as supplied by publisher]

Kaikkonen MU, Adelman K.
Emerging Roles of Non-Coding RNA Transcription.
Trends Biochem Sci. 2018 Sep;43(9):654-667.
PMID: 30145998 [PubMed - in process]

Klassen R, Schaffrath R.
Collaboration of tRNA modifications and elongation factor eEF1A in decoding and nonsense suppression.
Sci Rep. 2018 Aug 24;8(1):12749.
PMID: 30143741 [PubMed - in process]

Jakobsson ME, MaÅ‚ecki JM, Halabelian L, Nilges BS, Pinto R, Kudithipudi S, Munk S, Davydova E, Zuhairi FR, Arrowsmith CH, Jeltsch A, Leidel SA, Olsen JV, Falnes PÃ˜.
The dual methyltransferase METTL13 targets N terminus and Lys55 of eEF1A and modulates codon-specific translation rates.
Nat Commun. 2018 Aug 24;9(1):3411.
PMID: 30143613 [PubMed - in process]

Jee B, Singh Y, Yadav R, Lang F.
Small Heat Shock Protein16.3 of Mycobacterium tuberculosis: After Two Decades of Functional Characterization.
Cell Physiol Biochem. 2018 Aug 23;49(1):368-380. [Epub ahead of print]
PMID: 30138912 [PubMed - as supplied by publisher]

Sedaghatmehr M, Thirumalaikumar VP, Kamranfar I, Marmagne A, Masclaux-Daubresse C, Balazadeh S.

A regulatory role of autophagy for resetting the memory of heat stress in plants.
Plant Cell Environ. 2018 Aug 22;. [Epub ahead of print]
PMID: 30136402 [PubMed - as supplied by publisher]

Kourtis N, Tavernarakis N.
Small heat shock proteins and neurodegeneration: recent developments.
Biomol Concepts. 2018 Aug 20;9(1):94-102.
PMID: 30133417 [PubMed - in process]

Yoo N, Dogra S, Meinen BA, Tse E, Haefliger J, Southworth DR, Gray MJ, Dahl JU, Jakob U.
Polyphosphate Stabilizes Protein Unfolding Intermediates as Soluble Amyloid-like Oligomers.
J Mol Biol. 2018 Aug 18;. [Epub ahead of print]
PMID: 30130556 [PubMed - as supplied by publisher]

Qureshi NS, Bains JK, Sreeramulu S, Schwalbe H, FÃ¼rtig B.
Conformational switch in the ribosomal protein S1 guides unfolding of structured RNAs for translation initiation.
Nucleic Acids Res. 2018 Aug 16;. [Epub ahead of print]
PMID: 30124944 [PubMed - as supplied by publisher]

Vidal A, Cantabella D, Bernal-Vicente A, DÃaz-Vivancos P, HernÃ¡ndez JA.
Nitrate- and nitric oxide-induced plant growth in pea seedlings is linked to antioxidative metabolism and the ABA/GA balance.
J Plant Physiol. 2018 Aug 16;230:13-20. [Epub ahead of print]
PMID: 30138843 [PubMed - as supplied by publisher]

Phillips K, Majola A, Gokul A, Keyster M, Ludidi N, Egbichi I.
Inhibition of NOS- like activity in maize alters the expression of genes involved in H<sub>2</sub>O<sub>2</sub> scavenging and glycine betaine biosynthesis.
Sci Rep. 2018 Aug 22;8(1):12628.
PMID: 30135488 [PubMed - in process]

Wang T, Hou L, Jian H, Di F, Li J, Liu L.
Combined QTL mapping, physiological and transcriptomic analyses to identify candidate genes involved in Brassica napus seed aging.
Mol Genet Genomics. 2018 Jul 4;. [Epub ahead of print]
PMID: 29974306 [PubMed - as supplied by publisher]

Meriin AB, Narayanan A, Meng L, Alexandrov I, Varelas X, CissÃ© II, Sherman MY.
Hsp70-Bag3 complex is a hub for proteotoxicity-induced signaling that controls protein aggregation.
Proc Natl Acad Sci U S A. 2018 Jul 9;. [Epub ahead of print]
PMID: 29987014 [PubMed - as supplied by publisher]

Hanson G, Alhusaini N, Morris N, Sweet T, Coller J.
Translation elongation and mRNA stability are coupled through the ribosomal A-site.
RNA. 2018 Jul 11;. [Epub ahead of print]
PMID: 29997263 [PubMed - as supplied by publisher]

Clark AR, Egberts WV, Kondrat FDL, Hilton GR, Ray NJ, Cole AR, Carver JA, Benesch JLP, Keep NH, Boelens WC, Slingsby C.
Terminal regions confer plasticity to the tetrameric assembly of human HspB2 and HspB3.
J Mol Biol. 2018 Jun 30;. [Epub ahead of print]
PMID: 29969581 [PubMed - as supplied by publisher]

Natesh R, Clare DK, Farr GW, Horwich AL, Saibil HR.
A two-domain folding intermediate of RuBisCO in complex with the GroEL chaperonin.
Int J Biol Macromol. 2018 Jun 26;. [Epub ahead of print]

PMID: 29959019 [PubMed - as supplied by publisher]

Fraisse D, Degerine-Roussel A, Bred A, Ndoye SF, Vivier M, Felgines C, Senejoux F.
A Novel HPLC Method for Direct Detection of Nitric Oxide Scavengers from Complex Plant Matrices and Its Application to <i>Aloysia triphylla</i> Leaves.
Molecules. 2018 Jun 28;23(7).
PMID: 29958472 [PubMed - in process]

Tunney R, McGlincy NJ, Graham ME, Naddaf N, Pachter L, Lareau LF.
Accurate design of translational output by a neural network model of ribosome distribution.
Nat Struct Mol Biol. 2018 Jul 2;. [Epub ahead of print]
PMID: 29967537 [PubMed - as supplied by publisher]

Molecular Cell : Volume 71, Issue 6
Architectural Proteins and Pluripotency Factors Cooperate to Orchestrate the Transcriptional Response of hESCs to Temperature Stress
Pages 940-955.e7
Available Online 2018-08-16
Xiaowen Lyu, M. Jordan Rowley, Victor G. Corces

Cells respond to temperature stress via up- and downregulation of hundreds of genes. This process is thought to be regulated by the heat shock factor HSF1, which controls the release of RNAPII from promoter-proximal pausing. Here, we analyze the events taking place in hESCs upstream of RNAPII release. We find that temperature stress results in the activation or decommissioning of thousands of enhancers. This process involves alterations in the occupancy of transcription factors HSF1, AP-1, NANOG, KLF4, and OCT4 accompanied by nucleosome remodeling by BRG1 and changes in H3K27ac. Furthermore, redistribution of RAD21 and CTCF results in the formation and disassembly of interactions mediated by these two proteins. These alterations tether and untether enhancers to their cognate promoters or refashion insulated neighborhoods, thus transforming the landscape of enhancer-promoter interactions. Details of the 3D interactome remodeling process support loop extrusion initiating at random sites as a mechanism for the establishment of CTCF/cohesin loops.

α-Proteobacterial RNA Degradosomes Assemble Liquid-Liquid Phase-Separated RNP Bodies
Pages 1027-1039.e14
Available Online 2018-09-06
Nadra Al-Husini, Dylan T. Tomares, Obaidah Bitar, W. Seth Childers, Jared M. SchraderRibonucleoprotein (RNP) granules play an important role in organizing eukaryotic mRNA metabolism via liquid-liquid phase separation (LLPS) of mRNA decay factors into membrane-less organelles in the cytoplasm. Here we show that the bacterium *Caulobacter crescentus* Ribonuclease (RNase) E assembles RNP LLPS condensates that we term bacterial RNP-bodies (BR-bodies), similar to eukaryotic P-bodies and stress granules. RNase E requires RNA to assemble a BR-body, and disassembly requires RNA cleavage, suggesting BR-bodies provide localized sites of RNA degradation. The unstructured C-terminal domain of RNase E is both necessary and sufficient to assemble the core of the BR-body, is functionally conserved in related α-proteobacteria, and influences mRNA degradation. BR-bodies are rapidly induced under cellular stresses and provide enhanced cell growth under stress. To our knowledge, *Caulobacter* RNase E is the first bacterial protein identified that forms LLPS condensates, providing an effective strategy for subcellular organization in cells lacking membrane-bound compartments.

Hansen KG, Aviram N, Laborenz J, Bibi C, Meyer M, Spang A, Schuldiner M, Herrmann JM.
An ER surface retrieval pathway safeguards the import of mitochondrial membrane proteins in yeast.
Science. 2018 Sep 14;361(6407):1118-1122.
PMID: 30213914 [PubMed - in process]

Gestwicki JE, Shao H.
Inhibitors and chemical probes for molecular chaperone networks.
J Biol Chem. 2018 Sep 13;. [Epub ahead of print]
PMID: 30213856 [PubMed - as supplied by publisher]

White KI, Zhao M, Choi UB, Pfuetzner RA, Brunger AT.

Structural principles of SNARE complex recognition by the AAA+ protein NSF.
Elife. 2018 Sep 10;7. [Epub ahead of print]
PMID: 30198481 [PubMed - as supplied by publisher]

Haddad R, Heidari-Japelaghi R, Eslami-Bojnourdi N.
Isolation and functional characterization of two thioredoxin h isoforms from grape.
Int J Biol Macromol. 2018 Sep 5;. [Epub ahead of print]
PMID: 30195001 [PubMed - as supplied by publisher]

Rizzolo K, Houry WA.
Multiple functionalities of molecular chaperones revealed through systematic mapping of their interaction networks.
J Biol Chem. 2018 Sep 7;. [Epub ahead of print]
PMID: 30194284 [PubMed - as supplied by publisher]

SjÃ¶gren L, Floris M, Barghetti A, VÃ¶llmy F, Linding R, Brodersen P.
Farnesylated Heat Shock Protein 40 is a component of membrane-bound RISC in Arabidopsis.
J Biol Chem. 2018 Sep 7;. [Epub ahead of print]
PMID: 30194279 [PubMed - as supplied by publisher]

Yang X, Liu YB.
Nitric oxide fumigation for postharvest pest control on lettuce.
Pest Manag Sci. 2018 Jun 19;. [Epub ahead of print]
PMID: 29920930 [PubMed - as supplied by publisher]

Samir P, Brown CM, Rahul R, Sun M, Shen B, Li W, Frank J, Link AJ.
Identification of Changing Ribosome Protein Compositions using Mass Spectrometry.
Proteomics. 2018 Sep 13;:e1800217. [Epub ahead of print]
PMID: 30211483 [PubMed - as supplied by publisher]

Wang YJ, Vaidyanathan PP, Rojas-Duran MF, Udeshi ND, Bartoli KM, Carr SA, Gilbert WV.
Lso2 is a conserved ribosome-bound protein required for translational recovery in yeast.
PLoS Biol. 2018 Sep;16(9):e2005903.
PMID: 30208026 [PubMed - in process]

Lauwers E, Wang YC, Gallardo R, Van der Kant R, Michiels E, Swerts J, Baatsen P, Zaiter SS, McAlpine SR, Gounko NV, Rousseau F, Schymkowitz J, Verstreken P.
Hsp90 Mediates Membrane Deformation and Exosome Release.
Mol Cell. 2018 Sep 6;71(5):689-702.e9.
PMID: 30193096 [PubMed - in process]

Chen J, Gao T, Wan S, Zhang Y, Yang J, Yu Y, Wang W.
Genome-Wide Identification, Classification and Expression Analysis of the
HSP Gene Superfamily in Tea Plant (<i>Camellia sinensis</i>).
Int J Mol Sci. 2018 Sep 5;19(9).
PMID: 30189657 [PubMed - in process]

Fragkostefanakis S, Simm S, El-Shershaby A, Hu Y, Bublak D, Mesihovic A, Darm K, Mishra SK, Tschiersch B, Theres K, Scharf C, Schleiff E, Scharf KD.
The repressor and co-activator HsfB1 regulates the major heat stress transcription factors in tomato.
Plant Cell Environ. 2018 Sep 6;. [Epub ahead of print]
PMID: 30187931 [PubMed - as supplied by publisher]

Xu H.
Cochaperones enable Hsp70 to use ATP energy to stabilize native proteins out of the folding equilibrium.
Sci Rep. 2018 Sep 4;8(1):13213.
PMID: 30181618 [PubMed - in process]

Duran EC, Lucius AL.
ATP hydrolysis inactivating Walker B mutation perturbs E. coli ClpA self-assembly energetics in the absence of nucleotide.
Biophys Chem. 2018 Aug 27;242:6-14. [Epub ahead of print]
PMID: 30173103 [PubMed - as supplied by publisher]

Hillen HS, Temiakov D, Cramer P.
Structural basis of mitochondrial transcription.
Nat Struct Mol Biol. 2018 Sep;25(9):754-765.
PMID: 30190598 [PubMed - in process]

Mondal D, Warshel A.
EF-Tu and EF-G are activated by allosteric effects.
Proc Natl Acad Sci U S A. 2018 Mar 12;. [Epub ahead of print]
PMID: 29531062 [PubMed - as supplied by publisher]