

Lit Review – 9-20-16

Mary

Blondel M, Soubigou F, Evrard J, Nguyen PH, Hasin N, ChÃ©din S, Gillet R, Contesse MA, Friocourt G, Stahl G, Jones GW, Voisset C.

Protein Folding Activity of the Ribosome is involved in Yeast Prion Propagation. Sci Rep. 2016 Sep 16;6:32117. PMID: 27633137 [PubMed - in process]

6AP and GA are potent inhibitors of yeast and mammalian prions and also specific inhibitors of PFAR, the protein-folding activity borne by domain V of the large rRNA of the large subunit of the ribosome. We therefore explored the link between PFAR and yeast prion [*PSI+*] using both PFAR-enriched mutants and site-directed methylation. We demonstrate that PFAR is involved in propagation and *de novo* formation of [*PSI+*]. PFAR and the yeast heat-shock protein Hsp104 partially compensate each other for [*PSI+*] propagation. Our data also provide insight into new functions for the ribosome in basal thermotolerance and heat-shocked protein refolding. PFAR is thus an evolutionarily conserved cell component implicated in the prion life cycle, and we propose that it could be a potential therapeutic target for human protein misfolding diseases.

Ian

S-Nitrosylation Induces Structural and Dynamical Changes in a Rhodanese Family Protein, Cédric Eichmann, Christos Tzitzilonis, Tomohiro Nakamura, Witek Kwiatkowski, Innokentiy Maslennikov, Senyon Choe, Stuart A. Lipton, Roland Riek, Journal of Molecular Biology, Volume 428, Issue 19, 25 September 2016, Pages 3737-3751, ISSN 0022-2836

Indu

- 1 The plant lipidome in human and environmental health.

Horn PJ, Benning C.

Science. 2016 Sep 16;353(6305):1228-32. doi: 10.1126/science.aaf6206. Review. PMID: 27634522 [PubMed - in process]

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PMID: 27634523 [PubMed - in process]

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PMID: 27634521 [PubMed - in process]

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8 The new harvest.

Hines PJ, Travis J.
Science. 2016 Sep 16;353(6305):1218-9. doi: 10.1126/science.353.6305.1218. No abstract available.
PMID: 27634518 [PubMed - in process]

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Leslie M.
Science. 2016 Sep 16;353(6305):1198-201. doi: 10.1126/science.353.6305.1198. No abstract available.
PMID: 27634508 [PubMed - in process]

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1 Continuous genetic recording with self-targeting CRISPR-Cas in human cells.

0

Perli SD, Cui CH, Lu TK.
Science. 2016 Sep 9;353(6304). pii: aag0511. doi: 10.1126/science.aag0511. Epub 2016 Aug 18.
PMID: 27540006 [PubMed - in process]

Similar articles

Minsoo

1. Mol Cell. 2016 Sep 15;63(6):951-64. doi: 10.1016/j.molcel.2016.07.022. Epub 2016 Aug 25.

Soluble Oligomers of PolyQ-Expanded Huntingtin Target a Multiplicity of Key Cellular Factors.

Kim YE(1), Hosp F(2), Frottin F(1), Ge H(3), Mann M(2), Hayer-Hartl M(4), Hartl FU(5).

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Huntington's disease is one of several neurodegenerative disorders characterized by the aggregation of polyglutamine (polyQ)-expanded mutant protein. How polyQ aggregation leads to cellular dysfunction is not well understood. Here, we analyzed aberrant protein interactions of soluble oligomers and insoluble inclusions of mutant huntingtin using in-cell single molecule fluorescence spectroscopy and quantitative proteomics. We find that the interactome of soluble oligomers is highly complex, with an enrichment of RNA-binding proteins as well as proteins functioning in ribosome biogenesis, translation, transcription, and vesicle transport. The oligomers frequently target proteins containing extended low-complexity sequences, potentially interfering with key cellular pathways. In contrast, the insoluble inclusions are less interactive and associate strongly with protein quality control components, such as Hsp40 chaperones and factors of the ubiquitin-proteasome system. Our results suggest a "multiple hit" model for the pathogenic effects of mutant huntingtin, with soluble forms engaging more extensively in detrimental interactions than insoluble aggregates.

2. J Exp Bot. 2016 Sep 3. pii: erw327. [Epub ahead of print]

RPOTmp, an RNA polymerase from Arabidopsis with dual targeting, plays an important role in mitochondria, but not in chloroplasts.

Tarasenko VI(1), Katyshev AI(1), Yakovleva TV(1), Garnik EY(1), Chernikova VV(1), Konstantinov YM(2), Koulintchenko MV(3).

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In a number of dicotyledonous plants, including *Arabidopsis*, the transcription of organellar genes is performed by three nuclear-encoded RNA polymerases, RPOTm, RPOTmp, and RPOTp. RPOTmp is a protein with a dual targeting, which is presumably involved in the control of gene expression in both mitochondria and chloroplasts. A previous study of the *Arabidopsis* insertion *rpotmp* mutant showed that it has retarded growth and development, altered leaf morphology, changed expression of mitochondrial and probably some chloroplast genes, and decreased activities of the mitochondrial respiratory complexes. To date, there is no clear evidence as to which of these disorders are associated with a lack of RPOTmp in each of the two organelles. The aim of this study was to elucidate the role that this RNA polymerase specifically plays in mitochondria and chloroplasts. Two sets of *Arabidopsis* transgenic lines with complementation of RPOTmp function in either mitochondria or chloroplasts were obtained. It was found that the recovery of RPOTmp RNA polymerase activity in chloroplasts, although restoring the transcription from the RPOTmp-specific PC promoter, did not lead to compensation of the mutant growth defects. In contrast, the *rpotmp* plants expressing RPOTmp with mitochondrial targeting restored the level of mitochondrial transcripts and exhibit a phenotype resembling that of the wild-type plants. We conclude that despite its localization in two cell compartments, *Arabidopsis* RPOTmp plays an important role in mitochondria, but not in chloroplasts.

3. *J Cell Sci.* 2016 Sep 8. pii: jcs.190975. [Epub ahead of print]

Plant mitochondria contain the protein translocase subunits TatB and TatC.

Carrie C(1), Weißenberger S(2), Soll J(3).

Author information:

(1)Department of Biology I, Botany, Ludwig-Maximilians-Universität München, Großhaderner Strasse 2-4, D-82152, Planegg-Martinsried, Germany christopher.carrie@lmu.de. (2)Department of Biology I, Botany, Ludwig-Maximilians-Universität München, Großhaderner Strasse 2-4, D-82152, Planegg-Martinsried, Germany. (3)Department of Biology I, Botany, Ludwig-Maximilians-Universität München, Großhaderner Strasse 2-4, D-82152,

Planegg-Martinsried, Germany Munich Center for Integrated Protein Science, CiPSM, Ludwig-Maximilians-Universität München, Feodor-Lynen-Strasse 25, D-81377, Munich, Germany.

Twin-arginine translocation pathways have been well characterized in bacteria and chloroplasts. However, genes encoding for a TatC protein are found in almost all plant mitochondrial genomes. For the first time it could be demonstrated that this mitochondrial encoded TatC is a functional gene which is translated into a protein in the model plant *Arabidopsis thaliana*. An inner membrane localized TatB like subunit was also identified, which is nuclear encoded, and is essential for plant growth and development. Indicating that plants potentially require a Tat pathway for mitochondrial biogenesis.

Jesse

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), De Veylder L(13).

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.

Alyssa

Heat Shock Proteins Promote Cancer: It's a Protection Racket
Stuart K. Calderwood, Jianlin Gong

Abstract: Heat shock proteins (HSP) are expressed at high levels in cancer and form a fostering environment that is essential for tumor development. Here, we review the recent data in this area, concentrating mainly on Hsp27, Hsp70, and Hsp90. The overriding role of HSPs in cancer is to stabilize the active functions of overexpressed and mutated cancer genes. Thus, elevated HSPs are required for many of the traits that underlie the morbidity of cancer, including increased growth, survival, and formation of secondary cancers. In addition, HSPs participate in the evolution of cancer treatment resistance. HSPs are also released from cancer cells and influence malignant properties by receptor-mediated signaling. Current data strongly support efforts to target HSPs in cancer treatment.

Patrick

1. The Ever-Closer Union of Signals: Propagating Waves of Calcium and ROS Are Inextricably Linked

Plant Physiology, September 2016, Vol. 172, pp. 3–4,

Edgar Peiter, Plant Nutrition Laboratory, Institute of Agricultural and Nutritional Sciences (IAEW), Faculty of Natural Sciences III, Martin Luther University Halle-Wittenberg, D-06099 Halle (Saale), Germany

2. Promoting Roles of Melatonin in Adventitious Root Development of *Solanum lycopersicum* L. by Regulating Auxin and Nitric Oxide Signaling

Dan Wen †, Biao Gong †, Shasha Sun, Shiqi Liu, Xiufeng Wang, Min Wei, Fengjuan Yang, Yan Li and Qinghua Shi*

State Key Laboratory of Crop Biology, Key Laboratory of Biology and Genetic Improvement of Horticultural Crops (Huanghuai Region, Ministry of Agriculture), College of Horticulture Science and Engineering, Shandong Agricultural University, Taian, China

Abstract:

Melatonin (MT) plays integral roles in regulating several biological processes including plant growth, seed germination, flowering, senescence, and stress responses. This study investigated the effects of MT on adventitious root formation (ARF) of de-rooted tomato seedlings. Exogenous MT positively or negatively influenced ARF, which was dependent on the concentration of MT application. In the present experiment, 50 μ M MT showed the best effect on inducing ARF. Interestingly, exogenous MT promoted the accumulation of endogenous nitric oxide (NO) by down-regulating the expression of *S*-nitrosoglutathione reductase (*GSNOR*). To determine the interaction of MT and NO in ARF, MT synthesis inhibitor *p*-chlorophenylalanine, NO scavenger 2-(4-carboxyphenyl)-4,4,5,5-tetramethylimidazole-1-oxyl-3-oxide potassium salt as well as *GSNOR*-overexpression plants with low NO levels were used. The function of MT was removed by NO scavenger or *GSNOR*-overexpression plants. However, application of MT synthesis inhibitor did little to abolish the function of NO. These results indicate that NO, as a downstream signal, was involved in the MT-induced ARF. Concentrations of indole-3-acetic acid and indole-3-butyric acid, as well as the expression of several genes related to the auxin signaling pathway (*PIN1*, *PIN3*, *PIN7*, *IAA19*, and *IAA24*), showed that MT influenced auxin transport and signal transduction as well as auxin accumulation through the NO signaling pathway. Collectively, these strongly suggest that elevated NO levels resulting from inhibited *GSNOR* activity and auxin signaling were involved in the MT-induced ARF in tomato plants. This can be applied in basic research and breeding.

3. A Robust CRISPR/Cas9 System for Convenient, High-Efficiency Multiplex Genome Editing in Monocot and Dicot Plants

Xingliang Ma^{1,4}, Qunyu Zhang^{1,2,4}, Qinlong Zhu^{2,4}, Wei Liu^{1,2,4}, Yan Chen⁵, Rong Qiu^{1,2,4}, Bin Wang^{1,2,4}, Zhongfang Yang^{1,2,4}, Heying Li^{1,2,4}, Yuru Lin^{1,2,4}, Yongyao Xie^{1,2,4}, Rongxin Shen^{1,2,4}, Shuifu Chen^{1,2,4}, Zhi Wang⁴, Yuanling Chen^{1,2,4}, Jingxin Guo^{1,2,4}, Letian Chen^{1,2,3,4}, Xiucui Zhao^{1,2,4}, Zhicheng Dong⁵ and Yao-Guang Liu^{1,2,4,*}
1State Key Laboratory for Conservation and Utilization of Subtropical Agro-Bioresources, Guangzhou 510642, China
2Key Laboratory of Plant Functional Genomics and Biotechnology of Guangdong Provincial Higher Education Institutions, Guangzhou 510642, China
3Guangdong Provincial Key Laboratory of Protein Function and Regulation in Agricultural Organisms, Guangzhou 510642, China
4College of Life Sciences, South China Agricultural University, Guangzhou 510642, China
5Key Laboratory of South China Agriculture Plant Molecular Analysis and Genetic Improvement, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650, China

ABSTRACT

CRISPR/Cas9 genome targeting systems have been applied to a variety of species. However, most CRISPR/Cas9 systems reported for plants can only modify one or a few target sites. Here, we report

a robust CRISPR/Cas9 vector system, utilizing a plant codon optimized Cas9 gene, for convenient and high efficiency multiplex genome editing in monocot and dicot plants. We designed PCR-based procedures to rapidly generate multiple sgRNA expression cassettes, which can be assembled into the binary CRISPR/

Cas9 vectors in one round of cloning by Golden Gate ligation or Gibson Assembly. With this system, we edited 46 target sites in rice with an average 85.4% rate of mutation, mostly in biallelic and homozygous status.

We reasoned that about 16% of the homozygous mutations in rice were generated through the non-homologous end-joining mechanism followed by homologous recombination-based repair. We also obtained uniform biallelic, heterozygous, homozygous, and chimeric mutations in Arabidopsis T1 plants. The targeted mutations in both rice and Arabidopsis were heritable. We provide examples of loss-of-function gene mutations in T0 rice and T1 Arabidopsis plants by simultaneous targeting of multiple (up to eight) members of a gene family, multiple genes in a biosynthetic pathway, or multiple sites in a single gene. This system has provided a versatile toolbox for studying functions of multiple genes and gene families in plants for basic research and genetic improvement.

Keith

Small Heat Shock Proteins Prevent Alpha-Synuclein Aggregation via Transient Interactions and their Efficacy is Affected by the Rate of Aggregation

J Biol Chem. 2016 Sep 1. pii: jbc.M116.739250. [Epub ahead of print]

Cox D1, Selig E2, Griffin MD2, Carver JA3, Ecroyd H4.

1University of Wollongong, Australia;

2University of Melbourne, Australia;

3Australian National University, Australia.

4University of Wollongong, Australia.

The aggregation of α -synuclein (α -syn) into amyloid fibrils is associated with neurodegenerative diseases, collectively referred to as the α -synucleinopathies. In vivo, molecular chaperones, such as the small heat-shock proteins (sHsps), normally act to prevent protein aggregation; however, it remains to be determined how aggregation-prone α -syn evades sHsp chaperone action leading to its disease-associated deposition. This work examines the molecular mechanism by which two canonical sHsps, α B-crystallin (α B-c) and Hsp27, interact with aggregation-prone α -syn to prevent its aggregation in vitro. Both sHsps are very effective inhibitors of α -syn aggregation, but no stable complex between the sHsps and α -syn was detected, indicating that the sHsps inhibit α -syn aggregation via transient interactions. Moreover, the ability of these sHsps to prevent α -syn aggregation was dependent on the kinetics of aggregation; the faster the rate of aggregation (shorter the lag phase), the less effective the sHsps were at inhibiting fibril formation of α -syn. Thus, these findings indicate that the rate at which α -syn aggregates in cells may be a significant factor in how it evades sHsp chaperone action in the α -synucleinopathies.

Interaction of a Novel Chaperone PhLP2A with the Heat Shock Protein Hsp90

J Cell Biochem. 2016 Aug 6. doi: 10.1002/jcb.25669. [Epub ahead of print]

Krzemień-Ojak Ł1, Góral A2, Joachimiak E1, Filipek A2, Fabczak H1.

1Laboratory of Cytoskeleton and Cilia Biology, Nencki Institute of Experimental Biology, Polish Academy of Sciences, 3 Pasteur Str., 02-093, Warsaw, Poland.

2Laboratory of Calcium Binding Proteins, Nencki Institute of Experimental Biology, Polish Academy of Sciences, 3 Pasteur Str., 02-093, Warsaw, Poland.

PhLP2 is a small cytosolic protein that belongs to the highly conserved phosphatidylethanolamine-binding protein-like family of proteins. In amniote genomes there are two PhLP2 homologs, PhLP2A and PhLP2B. It has been shown that mammalian PhLP2A modulates the CCT/TRiC chaperonin activity during folding of cytoskeletal proteins. In order to better understand the function of PhLP2A in cellular protein quality control system, in the present study we have searched for its protein targets. Applying immunoprecipitation followed by mass spectrometry analysis we have identified Hsp90 as a partner of PhLP2A. With pull down experiments we have confirmed this interaction in protein lysate and using purified proteins we have shown that PhLP2A interacts directly with Hsp90. Furthermore, the

proximity ligation assay (PLA) performed on mIMCD-3 cells has shown that PhLP2A forms complexes with Hsp90 which are mainly localized in the cytoplasm of these cells. Further analysis has indicated that the level of PhLP2A increases after heat shock or radicicol treatment, similarly as the level of Hsp90, and that expression of PhLP2A after heat shock is regulated at the transcriptional level. Moreover, using recombinant luciferase we have shown that PhLP2A stabilizes this enzyme in a folding competent state and prevents its denaturation and aggregation. In addition, overexpression of PhLP2A in HEK-293 cells leads to increased heat stress resistance. Altogether, our results have shown that PhLP2A interacts with Hsp90 and exhibits molecular chaperone activity toward denatured proteins.

Protein Cross-Linking Capillary Electrophoresis for Protein-Protein Interaction Analysis.

Anal Chem. 2016 Aug 16;88(16):8272-8. doi: 10.1021/acs.analchem.6b02126. Epub 2016 Jul 28

Ouimet CM1, Shao H2, Rauch JN2, Dawod M1, Nordhues B3, Dickey CA3, Gestwicki JE2, Kennedy RT1,4.

1Department of Chemistry, University of Michigan , 930 N. University Ave., Ann Arbor, Michigan 48109, United States.

2Department of Pharmaceutical Chemistry and the Institute for Neurodegenerative Disease, University of California at San Francisco , 675 Nelson Rising Ln., San Francisco, California 94158, United States.

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4Department of Pharmacology, University of Michigan , 1150 W. Medical Center Dr., Ann Arbor, Michigan 48109, United States.

Capillary electrophoresis (CE) has been identified as a useful platform for detecting, quantifying, and screening for modulators of protein-protein interactions (PPIs). In this method, one protein binding partner is labeled with a fluorophore, the protein binding partners are mixed, and then, the complex is separated from free protein to allow direct determination of bound to free ratios. Although it possesses many advantages for PPI studies, the method is limited by the need to have separation conditions that both prevent protein adsorption to capillary and maintain protein interactions during the separation. In this work, we use protein cross-linking capillary electrophoresis (PXCE) to overcome this limitation. In PXCE, the proteins are cross-linked under binding conditions and then separated. This approach eliminates the need to maintain noncovalent interactions during electrophoresis and facilitates method development. We report PXCE methods for an antibody-antigen interaction and heterodimer and homodimer heat shock protein complexes. Complexes are cross-linked by short treatments with formaldehyde after reaching binding equilibrium. Cross-linked complexes are separated by electrophoretic mobility using free solution CE or by size using sieving electrophoresis of SDS complexes. The method gives good quantitative results; e.g., a lysozyme-antibody interaction was found to have $K_d = 24 \pm 3$ nM by

PXCE and $K_d = 17 \pm 2$ nM using isothermal calorimetry (ITC). Heat shock protein 70 (Hsp70) in complex with bcl2 associated athanogene 3 (Bag3) was found to have $K_d = 25 \pm 5$ nM by PXCE which agrees with K_d values reported without cross-linking. Hsp70-Bag3 binding site mutants and small molecule inhibitors of Hsp70-Bag3 were characterized by PXCE with good agreement to inhibitory constants and IC50 values obtained by a bead-based flow cytometry protein interaction assay (FCPIA). PXCE allows rapid method development for quantitative analysis of PPIs.

Elizabeth

September 19, 2016

Ortega-Atienza S, Rubis B, McCarthy C, Zhitkovich A.

Formaldehyde Is a Potent Proteotoxic Stressor Causing Rapid Heat Shock Factor Protein 1 Activation and Lys48-Linked Polyubiquitination of Proteins.

Am J Pathol. 2016 Sep 14;. PMID: 27639166 [PubMed - as supplied by publisher]

Blondel M, Soubigou F, Evrard J, Nguyen PH, Hasin N, ChÃ©din S, Gillet R, Contesse MA, Friocourt G, Stahl G, Jones GW, Voisset C.

Protein Folding Activity of the Ribosome is involved in Yeast Prion Propagation.

Sci Rep. 2016 Sep 16;6:32117. PMID: 27633137 [PubMed - in process]

Jung KW, So YS, Bahn YS.

Unique roles of the unfolded protein response pathway in fungal development and differentiation.

Sci Rep. 2016 Sep 15;6:33413. PMID: 27629591 [PubMed - in process]

Yang F, Chen TY, KrzemiÅ„ski Å„, Santiago AG, Jung W, Chen P.

Single-Molecule Dynamics of the Molecular Chaperone Trigger Factor in Living Cells.

Mol Microbiol. 2016 Sep 14;PMID: 27626893

Zhang S, He D, Yang Y, Lin S, Zhang M, Dai S, Chen PR.

Comparative proteomics reveal distinct chaperone-client interactions in supporting bacterial acid resistance.

Proc Natl Acad Sci U S A. 2016 Sep 12;. PMID: 27621474 [PubMed - as supplied by publisher]

Kummer E, Szlachcic A, Franke KB, Ungelenk S, Bukau B, Mogk A.

Bacterial and yeast AAA+ disaggregases ClpB and Hsp104 operate through conserved mechanism involving cooperation with Hsp70.

J Mol Biol. 2016 Sep 8;. PMID: 27616763 [PubMed - as supplied by publisher]

Wolmarans A, Lee B, Spyropoulos L, LaPointe P.

The Mechanism of Hsp90 ATPase Stimulation by Aha1.

Sci Rep. 2016 Sep 12;6:33179. PMID: 27615124 [PubMed - in process]

Narayanan A, Pullepu D, Kabir MA.

The interactome of CCT complex - A computational analysis.

Comput Biol Chem. 2016 Sep 6;64:396-402. PMID: 27614400 [PubMed - as supplied by publisher]

Zhou YH, Zhang ZW, Zheng C, Yuan S, He Y.

Nitrogen regulates CRY1 phosphorylation and circadian clock input pathways.

Plant Signal Behav. 2016 Sep;11(9):e1219830.PMID: 27617369 [PubMed - in process]

Hachiya T, Ueda N, Kitagawa M, Hanke G, Suzuki A, Hase T, Sakakibara H.
Arabidopsis Root-Type Ferredoxin:NADP(H) Oxidoreductase 2 Is Involved in Detoxification of Nitrite in Roots.

Plant Cell Physiol. 2016 Sep 11;. PMID: 27615794 [PubMed - as supplied by publisher]

Gerashchenko MV, Gladyshev VN.

Ribonuclease selection for ribosome profiling.

Nucleic Acids Res. 2016 Sep 15;. PMID: 27638886 [PubMed - as supplied by publisher]

De Laurentiis EI, Mercier E, Wieden HJ.

The C-terminal helix of Pseudomonas aeruginosa Elongation Factor Ts tunes EF-Tu dynamics to modulate nucleotide exchange.

J Biol Chem. 2016 Sep 13;. PMID: 27624934 [PubMed - as supplied by publisher]

Yifat Geffen, Alon Appleboim, Richard G. Gardner, Nir Friedman, Ronen Sadeh, Tommer Ravid

[Mapping the Landscape of a Eukaryotic Degronome](#)

Molecular Cell, Volume 63, Issue 6, 15 September 2016, Pages 1055-1065

[PDF \(2799 K\)](#)

[Supplementary content](#)

Proteasome degradation is essential, but the intrinsic features of a protein that signals its destruction remain incompletely understood. In this issue of *Molecular Cell*, [Geffen et al. \(2016\)](#) report an unbiased and proteome-wide method that provided insights into the protein destruction signals and pathways.

Molecular Cell, Volume [63, Issue 6](#), 15 September 2016, Pages 918–925

Minireview

[Eyes on Translation](#)

[Marina Chekulaeva](#)^{1,2},

[Markus Landthaler](#)¹

Translation is a fundamental biological process by which ribosomes decode genetic information into proteins. The regulation of this process plays a key role in tuning protein levels, allowing cells to respond rapidly to changes in the environment and to synthesize proteins with precise timing and at specific subcellular locations. Despite detailed biochemical and structural insight into the mechanism of protein synthesis, translational dynamics and localization in a cellular context are less well understood. Here, we summarize recent efforts to quantify and visualize translation, focusing on four publications ([Morisaki et al., 2016](#), [Wang et al., 2016](#), [Wu et al., 2016](#) and [Yan et al., 2016](#)) describing novel approaches to imaging in real time the synthesis of nascent peptides from individual mRNAs in living cells.

Molecular Cell: Alert 10 September-16 September

[Soluble Oligomers of PolyQ-Expanded Huntingtin Target a Multiplicity of Key Cellular Factors](#) Original Research Article

Pages 951-964

Yujin E. Kim, Fabian Hosp, Frédéric Frottin, Hui Ge, Matthias Mann, Manajit Hayer-Hartl, F. Ulrich Hartl

Antioxidants & Redox Signaling Vol. 25, No. 9, September 2016 is now available online

Synthetic Sensors for Reactive Oxygen Species Detection and Quantification: A Critical Review of Current Methods

Anne-Cécile Ribou

Antioxidants & Redox Signaling, Vol. 25, No. 9, September 2016: 520-533.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(659 KB\)](#) | [Full Text PDF with Links \(573 KB\)](#)

Mitochondrial Flash: Integrative Reactive Oxygen Species and pH Signals in Cell and Organelle Biology

Wang Wang, Guohua Gong, Xianhua Wang, Lan Wei-LaPierre, Heping Cheng, Robert Dirksen, and Shey-Shing Sheu

Antioxidants & Redox Signaling, Vol. 25, No. 9, September 2016: 534-549.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(845 KB\)](#) | [Full Text PDF with Links \(548 KB\)](#)

Mitochondrial Flashes: Dump Superoxide and Dance with Protons Now

Nicolas Demaurex and Markus Schwarzländer

Antioxidants & Redox Signaling, Vol. 25, No. 9, September 2016: 550-551.

[Abstract](#) | [Full Text HTML](#) | [Full Text PDF \(123 KB\)](#) | [Full Text PDF with Links \(126 KB\)](#)

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 tpc.16.00408; Advance Publication September 8, 2016;

doi:10.1105/tpc.16.00408

<http://www.plantcell.org/content/early/2016/09/07/tpc.16.00408.abstract>

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.

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Journal of Agronomy and Crop Scienc... Content Alert: 202, 5 (October 2016)

Heat Stress Effects are Stronger on Spikelets Than on Flag Leaves in Rice Due to

Differences in Dissipation Capacity (pages 394–408)

C. X. Zhang, G. F. Fu, X. Q. Yang, Y. J. Yang, X. Zhao, T. T. Chen, X. F. Zhang, Q. Y. Jin and L. X. Tao

Version of Record online: 28 JUL 2015 | DOI: 10.1111/jac.12138

Archives of Biochemistry and Biophysics: Alert 4 September-10 September

[Mitochondrial nitric oxide production supported by reverse electron transfer](#) Original Research Article

Pages 8-19

Silvina S. Bombicino, Darío E. Iglesias, Tamara Zaobornyj, Alberto Boveris, Laura B. Valdez



Mapping-by-sequencing in complex polyploid genomes using genic sequence capture: a case study to map yellow rust resistance in hexaploid wheat (pages 403–419)

Laura-Jayne Gardiner, Pauline Bansept-Basler, Lisa Olohan, Ryan Joynson, Rachel Brenchley, Neil Hall, Donal M. O'Sullivan and Anthony Hall

Version of Record online: 18 JUL 2016 | DOI: 10.1111/tpj.13204

Significance Statement

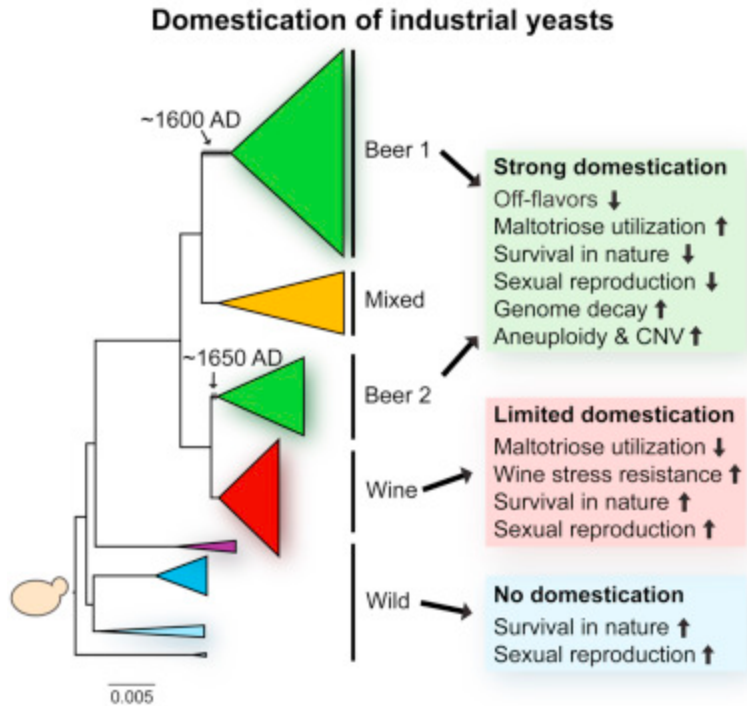
It is challenging to apply mapping-by-sequencing pipelines to large polyploid genomes such as hexaploid wheat. Here we present a method for the rapid mapping of genes responsible for a phenotype, and demonstrate its utility by mapping a disease resistance gene. We show that our bespoke mapping-by-sequencing pipeline, available on iPlant, can be applied to poorly defined polyploid genomes.

Cell: Alert 3 September-9 September

[Domestication and Divergence of *Saccharomyces cerevisiae* Beer Yeasts](#) Original Research Article

Pages 1397-1410.e16

Brigida Gallone



[Lipid Biosynthesis Coordinates a Mitochondrial-to-Cytosolic Stress Response](#) Original

Research Article

Pages 1539-1552.e16

Hyun-Eui Kim, Ana Rodrigues Grant, Milos S. Simic, Rebecca A. Kohnz, Daniel K. Nomura, Jenni Durieux, Celine E. Riera, Melissa Sanchez, Erik Kapernick, Suzanne Wolff, Andrew Dillin

[Neuroendocrine Coordination of Mitochondrial Stress Signaling and Proteostasis](#) Original

Research Article

Pages 1553-1563.e10

Kristen M. Berendzen, Jenni Durieux, Li-Wa Shao, Ye Tian, Hyun-eui Kim, Suzanne Wolff, Ying Liu, Andrew Dillin

[Development of a Comprehensive Genotype-to-Fitness Map of Adaptation-Driving Mutations in Yeast](#) Original Research Article

Pages 1585-1596.e22

Sandeep Venkataram, Barbara Dunn, Yuping Li, Atish Agarwala, Jessica Chang, Emily R. Ebel, Kerry Geiler-Samerotte, Lucas Hérissant, Jamie R. Blundell, Sasha F. Levy, Daniel S. Fisher, Gavin Sherlock, Dmitri A. Petrov

Nature Biotechnology Contents: Volume 34 pp 891 - 996

[Containment of transgenic trees by suppression of *LEAFY*](#) pp918 - 922

Amy L Klocko, Amy M Brunner, Jian Huang, Richard Meilan, Haiwei Lu *et al.*

doi:10.1038/nbt.3636

[Applications of CRISPR technologies in research and beyond](#) - pp933 - 941

Rodolphe Barrangou & Jennifer A Doudna

doi:10.1038/nbt.3659

The unique capabilities of CRISPR technologies have enabled a broad range of applications in biomedicine and agriculture.

Genetic improvement of tomato by targeted control of fruit softening - pp950 - 952

Selman Uluisik, Natalie H Chapman, Rebecca Smith, Mervin Poole, Gary Adams, Richard B Gillis, Tabot M D Besong, Judith Sheldon, Suzy Stiegelmeier, Laura Perez, Nurul Samsulrizal, Duoduo Wang, Ian D Fisk, Ni Yang, Charles Baxter, Daniel Rickett, Rupert Fray, Barbara Blanco-Ulate, Ann L T Powell, Stephen E Harding, Jim Craigon, Jocelyn K C Rose, Eric A Fich, Li Sun, David S Domozych, Paul D Fraser, Gregory A Tucker, Don Grierson & Graham B Seymour

doi:10.1038/nbt.3602

Softening in tomatoes is uncoupled from ripening by silencing a pectate lyase, thereby identifying a route to engineering (or breeding) tomatoes with better shelf life and flavor.

Human SRMATlas: a resource of targeted assays to quantify the complete human proteome

[Kusebauch, U. *et al.* *Cell* **166**, 766–778 \(2016\)](#)

Highlights

Human SRMATlas: 166,174 proteotypic peptides representing the human proteome

Resource of verified high-resolution spectra and multiplexed SRM assays

Supports proteome-scale quantification as well as hypothesis-driven research

Web database with free unlimited access

Summary

The ability to reliably and reproducibly measure any protein of the human proteome in any tissue or cell type would be transformative for understanding systems-level properties as well as specific pathways in physiology and disease. Here, we describe the generation and verification of a compendium of highly specific assays that enable quantification of 99.7% of the 20,277 annotated human proteins by the widely accessible, sensitive, and robust targeted mass spectrometric method selected reaction monitoring, SRM. This human SRMATlas provides definitive coordinates that conclusively identify the respective peptide in biological samples. We report data on 166,174 proteotypic peptides providing multiple, independent assays to quantify any human protein and numerous spliced variants, non-synonymous mutations, and post-translational modifications. The data are freely accessible as a resource at <http://www.srmatlas.org/>, and we demonstrate its utility by examining the network response to inhibition of cholesterol synthesis in liver cells and to docetaxel in prostate cancer lines.

The FEBS Journal

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[Volume 283, Issue 17 Pages 3157 - 3263, September 2016](#)

Special Issue: CRISPR/Cas9 Gene Editing

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