Indu

1: Lau W, Sattely ES. Six enzymes from mayapple that complete the biosynthetic pathway to the etoposide aglycone. Science. 2015 Sep 11;349(6253):1224-8. doi:10.1126/science.aac7202. PubMed PMID: 26359402.

2: Zanet J, Benrabah E, Li T, Pélissier-Monier A, Chanut-Delalande H, Ronsin B, Bellen HJ, Payre F, Plaza S. Pri sORF peptides induce selective proteasome-mediated protein processing. Science. 2015 Sep 18;349(6254):1356-8.doi: 10.1126/science.aac5677. PubMed PMID: 26383956.

3: Lightowlers RN, Taylor RW, Turnbull DM. Mutations causing mitochondrial disease: What is new and what challenges remain? Science. 2015 Sep 25;349(6255):1494-9. doi: 10.1126/science.aac7516. Epub 2015 Sep 24. Review. PubMed PMID: 26404827.

4: Shiota T, Imai K, Qiu J, Hewitt VL, Tan K, Shen HH, Sakiyama N, Fukasawa Y,Hayat S, Kamiya M, Elofsson A, Tomii K, Horton P, Wiedemann N, Pfanner N, Lithgow T, Endo T. Molecular architecture of the active mitochondrial protein gate.Science. 2015 Sep 25;349(6255):1544-8. doi: 10.1126/science.aac6428. PubMed PMID:26404837.

Fionn

Plant cell

Discovery of a Unique Clp Component, ClpF, in Chloroplasts:
A Proposed Binary ClpF-ClpS1 Adaptor Complex
Functions in Substrate Recognition and Delivery

Kenji Nishimura,a,1 Janina Apitz,c Giulia Friso,a Jitae Kim,a Lalit Ponnala,bBernhard Grimm,c and Klaas J. van Wijka,2

Clp proteases are found in prokaryotes, mitochondria, and plastids where they play crucial roles in maintaining protein
homeostasis (proteostasis). The plant plastid Clp machinery comprises a hetero-oligomeric ClpPRT proteolytic core, ATPdependent
chaperones ClpC and ClpD, and an adaptor protein, ClpS1. ClpS1 selects substrates to the ClpPR protease-ClpC
chaperone complex for degradation, but the underlying substrate recognition and delivery mechanisms are currently unclear.
Here, we characterize a ClpS1-interacting protein in Arabidopsis thaliana, ClpF, which can interact with the Clp substrate

glutamyl-tRNA reductase. ClpF and ClpS1 mutually stimulate their association with ClpC. ClpF, which is only found in
photosynthetic eukaryotes, contains bacterial uvrB/C and YccV protein domains and a unique N-terminal domain. We
propose a testable model in which ClpS1 and ClpF form a binary adaptor for selective substrate recognition and delivery to
ClpC, reflecting an evolutionary adaptation of the Clp system to the plastid proteome.

Nature biotech

Syngenta rebuffs Monsanto, again

Chinese government reaffirms backing for GM products

Nature

Alternative CRISPR system could improve genome editing

Smaller enzyme may make process simpler and more exact.

Heidi Ledford

Structure of mammalian eIF3 in the context of the 43S preinitiation complex
Amedee des Georges, Vidya Dhote, Lauriane Kuhn, Christopher U. T. Hellen, Tatyana V. Pestova+ et al.
The cryo-electron microscopy structure of the eukaryotic initiation factor 3 (eIF3) within the larger 43S complex is determined; the improved resolution enables visualization of the secondary structures of the subunits, as well as the contacts between eIF3 and both eIF2 and DHX29.

Minsoo

1. Proc Natl Acad Sci U S A. 2015 Oct 6;112(40):12456-61. doi: 10.1073/pnas.1517448112. Epub 2015 Sep 21.

Dialogue between E. coli free radical pathways and the mitochondria of C. elegans.

Govindan JA(1), Jayamani E(2), Zhang X(3), Mylonakis E(4), Ruvkun G(5).

Author information:
(1)Department of Molecular Biology, Massachusetts General Hospital, Boston, MA 02114; Department of Genetics, Harvard Medical School, Boston, MA 02115;
(2)Department of Molecular Biology, Massachusetts General Hospital, Boston, MA 02114; Division of Infectious Diseases, Rhode Island Hospital, Alpert Medical

School of Brown University, Providence, RI 02903. (3)Department of Molecular Biology, Massachusetts General Hospital, Boston, MA 02114; (4)Division of Infectious Diseases, Rhode Island Hospital, Alpert Medical School of Brown University, Providence, RI 02903. (5)Department of Molecular Biology, Massachusetts General Hospital, Boston, MA 02114; Department of Genetics, Harvard
Medical School, Boston, MA 02115; ruvkun@molbio.mgh.harvard.edu.

The microbial world presents a complex palette of opportunities and dangers to animals, which have developed surveillance and response strategies to hints of microbial intent. We show here that the **mitochondrial homeostatic response pathway of the nematode Caenorhabditis elegans responds to Escherichia coli mutations that activate free radical detoxification pathways.** Activation of C. elegans mitochondrial responses could be suppressed by additional mutations in E. coli, suggesting that C. elegans responds to products of E. coli to anticipate challenges to its mitochondrion. Out of 50 C. elegans gene inactivations known to mediate mitochondrial defense, we found that 7 genes were required for C. elegans response to a free radical producing E. coli mutant, including the **bZip transcription factor atfs-1** (activating transcription factor associated with stress). An atfs-1 loss-of-function mutant was partially resistant to the effects of free radical-producing E. coli mutant, but a constitutively active atfs-1 mutant growing on wild-type E. coli inappropriately activated the pattern of mitochondrial responses normally induced by an E. coli free radical pathway mutant. Carbonylated proteins from free radical-producing E. coli mutant may directly activate the ATFS-1/bZIP transcription factor to induce mitochondrial stress response: feeding C. elegans with H2O2-treated E. coli induces the mitochondrial unfolded protein response, and inhibition of a gut peptide transporter partially suppressed C. elegans response to free radical damaged E. coli.

2. Nat Cell Biol. 2015 Jun;17(6):782-92. doi: 10.1038/ncb3170. Epub 2015 May 11.
A nuclear role for the respiratory enzyme CLK-1 in regulating mitochondrial stress responses and longevity.
Monaghan RM, Barnes RG, Fisher K, Andreou T, Rooney N, Poulin GB, Whitmarsh AJ.
Abstract
The coordinated regulation of mitochondrial and nuclear activities is essential for cellular respiration and its disruption leads to mitochondrial dysfunction, a hallmark of ageing. Mitochondria communicate with nuclei through retrograde signalling pathways that modulate nuclear gene expression to maintain mitochondrial homeostasis. **The monooxygenase CLK-1 (human homologue COQ7) was previously reported to be mitochondrial, with a role in respiration and longevity.** We have uncovered a distinct **nuclear form of CLK-1 that independently regulates lifespan.** Nuclear CLK-1 mediates a retrograde signalling pathway that is conserved from Caenorhabditis elegans to humans and is responsive to mitochondrial reactive oxygen species, thus acting as a barometer of oxidative metabolism. We show that, through modulation of gene expression, the

pathway regulates both mitochondrial reactive oxygen species metabolism and the mitochondrial unfolded protein response. Our results demonstrate that **a respiratory enzyme acts in the nucleus to control mitochondrial stress responses and longevity.**

3. Proc Natl Acad Sci U S A. 2015 Sep 29;112(39):12093-8. doi: 10.1073/pnas.1515623112. Epub 2015 Sep 11.

Proteomic mapping in live Drosophila tissues using an engineered ascorbate peroxidase.

Chen CL(1), Hu Y(2), Udeshi ND(3), Lau TY(3), Wirtz-Peitz F(2), He L(2), Ting AY(4), Carr SA(3), Perrimon N(5).

Author information:
(1)Department of Genetics, Harvard Medical School, Boston, MA 02115; clchen@genetics.med.harvard.edu perrimon@receptor.med.harvard.edu. (2)Department
of Genetics, Harvard Medical School, Boston, MA 02115; (3)Broad Institute, Cambridge, MA 02142; (4)Broad Institute, Cambridge, MA 02142; Department of Chemistry, Massachusetts Institute of Technology, Cambridge, MA 02139; (5)Department of Genetics, Harvard Medical School, Boston, MA 02115; Howard Hughes Medical Institute, Boston, MA 02115 clchen@genetics.med.harvard.edu perrimon@receptor.med.harvard.edu.

Characterization of the proteome of organelles and subcellular domains is essential for understanding cellular organization and identifying protein complexes as well as networks of protein interactions**. We established a proteomic
mapping platform in live Drosophila tissues using an engineered ascorbate peroxidase (APEX). Upon activation, the APEX enzyme catalyzes the biotinylation
of neighboring endogenous proteins that can then be isolated and identified by
mass spectrometry.** We demonstrate that APEX labeling functions effectively in multiple fly tissues for different subcellular compartments and maps the mitochondrial matrix proteome of Drosophila muscle to demonstrate the power of APEX for characterizing subcellular proteomes in live cells. Further, we generate "MitoMax," a database that provides an inventory of Drosophila mitochondrial proteins with subcompartmental annotation. Altogether, **APEX labeling in live Drosophila tissues provides an opportunity to characterize the organelle proteome
of specific cell types in different physiological conditions.**

4. Sci Rep. 2015 Sep 2;5:13492. doi: 10.1038/srep13492.

PEA-CLARITY: 3D molecular imaging of whole plant organs.

Palmer WM(1), Martin AP(1), Flynn JR(2), Reed SL(1), White RG(3), Furbank RT(4), Grof CP(1).

Author information:
(1)School of Environmental and Life Sciences, University of Newcastle, Callaghan, NSW, 2308, Australia. (2)School of Biomedical Sciences and Pharmacy, University of Newcastle, Callaghan, NSW 2308, Australia. (3)CSIRO Agriculture, Black Mountain, ACT, 2601, Australia. (4)ARC Centre of Excellence for Translational Photosynthesis, Australian National University, Acton, ACT, 2601, Australia.

Here we report the adaptation of the CLARITY technique to plant tissues with addition of enzymatic degradation to improve optical clearing and facilitate antibody probe penetration. Plant-Enzyme-Assisted (PEA)-CLARITY, has allowed deep
optical visualisation of stains, expressed fluorescent proteins and IgG-antibodies in Tobacco and Arabidopsis leaves. Enzyme treatment enabled penetration of antibodies into whole tissues without the need for any sectioning of the material, thus facilitating protein localisation of intact tissue in 3D whilst retaining cellular structure.

Mary

The network of molecular chaperones: insights in the cellular proteostasis machinery

Marina Ostankovitch[1,] , Johannes Buchner[2,]

Keith

Active-State Structures of a Small Heat-Shock Protein Revealed a Molecular Switch for Chaperone Function

Structure 23, 1–10 November 3, 2015

Liu L[1], Chen JY[2], Yang B[3], Wang FH[4], Wang YH[5], Yun CH[6].

1Institute of Systems Biomedicine, Department of Biophysics, Beijing Key Laboratory of Tumor Systems Biology and Center for Molecular and Translational Medicine, School of Basic Medical Sciences, Peking University Health Science Center, Beijing 100191, P.R. China; School of Bioscience and Bioengineering, South China University of Technology, Guangzhou 510006, P.R. China; Co-first author.
2Institute of Systems Biomedicine, Department of Biophysics, Beijing Key Laboratory of Tumor Systems Biology and Center for Molecular and Translational

Medicine, School of Basic Medical Sciences, Peking University Health Science Center, Beijing 100191, P.R. China; Co-first author.
3School of Bioscience and Bioengineering, South China University of Technology, Guangzhou 510006, P.R. China.
4College of Light Industry and Food Sciences, South China University of Technology, Guangzhou 510641, P.R. China.
5College of Light Industry and Food Sciences, South China University of Technology, Guangzhou 510641, P.R. China. Electronic address: yonghw@scut.edu.cn.
6Institute of Systems Biomedicine, Department of Biophysics, Beijing Key Laboratory of Tumor Systems Biology and Center for Molecular and Translational Medicine, School of Basic Medical Sciences, Peking University Health Science Center, Beijing 100191, P.R. China.

Small heat-shock proteins (sHsps) maintain cellular homeostasis by binding to denatured client proteins to prevent aggregation. Numerous studies indicate that the N-terminal domain (NTD) of sHsps is responsible for binding to client proteins, but the binding mechanism and chaperone activity regulation remain elusive. Here, we report the crystal structures of the wild-type and mutants of an sHsp from Sulfolobus solfataricus representing the inactive and active state of this protein, respectively. All three structures reveal well-defined NTD, but their conformations are remarkably different. The mutant NTDs shows disrupted helices presenting a reformed hydrophobic surface compatible with recognizing client proteins. Our functional data show that mutating key hydrophobic residues in this region drastically altered the chaperone activity of this sHsp. These data suggest a new model in which a molecular switch located in NTD facilitates conformational changes for client protein binding.

Elizabeth

Cell: Alert 3 October-9 October
Andrew P. Bailey, Grielof Koster, Christelle Guillermier, Elizabeth M.A. Hirst, James I. MacRae, Claude P. Lechene, Anthony D. Postle, Alex P. Gould
Antioxidant Role for Lipid Droplets in a Stem Cell Niche of *Drosophila*
Cell, *Volume 163, Issue 2*, *8 October 2015*, *Pages 340-353* PDF (0 K) Supplementary content

Luke E. Berchowitz, Greg Kabachinski, Margaret R. Walker, Thomas M. Carlile, Wendy V. Gilbert, Thomas U. Schwartz, Angelika Amon
Regulated Formation of an Amyloid-like Translational Repressor Governs Gametogenesis
Cell, *Volume 163, Issue 2*, *8 October 2015*, *Pages 406-418* PDF (0 K) Supplementary content
Berchowitz et al. establish that transient amyloid-like forms of Rim4, a yeast RNA-binding protein with a predicted prion domain, translationally repress cyclin *CLB3* in meiosis I, thereby ensuring homologous chromosome segregation. These findings

suggest that prion domains might enable formation of tightly regulated amyloid-like effectors in diverse functional settings.

A Single α Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly Original Research Article *Pages 432-444*
Robert J. Tomko, David W. Taylor, Zhuo A. Chen, Hong-Wei Wang, Juri Rappsilber, Mark Hochstrasser

Highlights

First in vitro reconstitution of RP assembly with completely recombinant components
Electron microscopy and cross-linking reveal massive remodeling of a lid precursor
Remodeling of the lid relieves steric clash with the RP base to promote RP assembly
Lid remodeling can be triggered by a single C-terminal α helix in the Rpn12 subunit
The Plant Journal Content Alert: 84, 2 (October 2015)

Empty pericarp7 encodes a mitochondrial E–subgroup pentatricopeptide repeat protein that is required for _ccmF$_N$_ editing, mitochondrial function and seed development in maize (pages 283–295)

Feng Sun, Xiaomin Wang, Géraldine Bonnard, Yun Shen, Zhihui Xiu, Xiaojie Li, Dahai Gao, Zhonghang Zhang and Bao-Cai Tan
Article first published online: 8 OCT 2015 | DOI: 10.1111/tpj.12993
Significance Statement
Pentatricopeptide repeat (PPR) proteins are important for RNA editing in organelles. Here we show that Emp7 is essential for cytochrome c maturation in mitochondria and consequently for seed development.

Analysis of non-coding transcriptome in rice and maize uncovers roles of conserved lncRNAs associated with agriculture traits (pages 404–416)

Huan Wang, Qi-Wen Niu, Hui-Wen Wu, Jun Liu, Jian Ye, Niu Yu and Nam-Hai Chua
Article first published online: 8 OCT 2015 | DOI: 10.1111/tpj.13018
Significance Statement
Long noncoding RNAs (lncRNAs) play key roles in numerous biological processes. Here we sequenced and characterized lncRNAs from many rice and maize tissues.Hundreds of the lncRNAs have single nucleotide polymorphisms associated with agricultural traits, suggesting that they may play roles in controlling such traits

Non-invasive, whole-plant imaging of chloroplast movement and chlorophyll fluorescence reveals photosynthetic phenotypes independent of chloroplast photorelocation defects in chloroplast division mutants (pages 428–442)

Siddhartha Dutta, Jeffrey A. Cruz, Yuhua Jiao, Jin Chen, David M. Kramer and Katherine W. Osteryoung
Article first published online: 8 OCT 2015 | DOI: 10.1111/tpj.13009
Significance Statement
Here we demonstrate a dual-imaging platform for continuous, high-sensitivity, and non-invasive measurements of chloroplast movement and chlorophyll fluorescence

in whole plants. We further introduce an approach to correct calculations of non-photochemical quenching for interference from chloroplast movement. We use this platform and Arabidopsis mutants with drastically enlarged chloroplasts to show that their photosynthetic phenotypes, induced by high-light stress, are due predominantly to altered chloroplast size and shape rather than to reduced chloroplast movement.

Plant, Cell & Environment Content Alert (New Articles)

The cytochrome ***c*** oxidase biogenesis factor AtCOX17 modulates stress responses in Arabidopsis

Lucila Garcia, Elina Welchen, Uta Gey, Agustín L. Arce, Iris Steinebrunner and Daniel H. Gonzalez

Accepted manuscript online: 5 OCT 2015 12:17PM EST | DOI: 10.1111/pce.12647

Current Biology: Alert 30 September-6 October

The Evolutionary Origin of a Terrestrial Flora Review Article *Pages R899-R910*

Charles Francis Delwiche, Endymion Dante Cooper

Regulation of Chloroplast Protein Import by the Ubiquitin E3 Ligase SP1 Is Important for Stress Tolerance in Plants

Pages 2527-2534 Qihua Ling, Paul Jarvis

An Endophyte Constructs Fungicide-Containing Extracellular Barriers for Its Host Plant

Pages 2570-2576 Sameh S.M. Soliman, John S. Greenwood, Aureliano Bombarely, Lukas A. Mueller, Rong Tsao, Dick D. Mosser, Manish N. Raizada

Elizabeth

Cell: Alert 3 October-9 October

Andrew P. Bailey, Grielof Koster, Christelle Guillermier, Elizabeth M.A. Hirst, James I. MacRae, Claude P. Lechene, Anthony D. Postle, Alex P. Gould

Antioxidant Role for Lipid Droplets in a Stem Cell Niche of *Drosophila*

Cell, *Volume 163*, *Issue 2*, *8 October 2015*, *Pages 340-353* PDF (0 K) Supplementary content

Luke E. Berchowitz, Greg Kabachinski, Margaret R. Walker, Thomas M. Carlile, Wendy V. Gilbert, Thomas U. Schwartz, Angelika Amon

Regulated Formation of an Amyloid-like Translational Repressor Governs Gametogenesis

Cell, *Volume 163*, *Issue 2*, *8 October 2015*, *Pages 406-418* PDF (0 K) Supplementary content

Berchowitz et al. establish that transient amyloid-like forms of Rim4, a yeast RNA-binding protein with a predicted prion domain, translationally repress cyclin *CLB3* in meiosis I, thereby ensuring homologous chromosome segregation. These findings suggest that prion domains might enable formation of tightly regulated amyloid-like effectors in diverse functional settings.

A Single α Helix Drives Extensive Remodeling of the Proteasome Lid and Completion of Regulatory Particle Assembly Original Research Article *Pages 432-444*

Robert J. Tomko, David W. Taylor, Zhuo A. Chen, Hong-Wei Wang, Juri Rappsilber, Mark Hochstrasser

Highlights

First in vitro reconstitution of RP assembly with completely recombinant components

Electron microscopy and cross-linking reveal massive remodeling of a lid precursor

Remodeling of the lid relieves steric clash with the RP base to promote RP assembly

Lid remodeling can be triggered by a single C-terminal α helix in the Rpn12 subunit

The Plant Journal Content Alert: 84, 2 (October 2015)

Empty pericarp7 encodes a mitochondrial E–subgroup pentatricopeptide repeat protein that is required for _ccmF_$_N$ editing, mitochondrial function and seed development in maize (pages 283–295)

Feng Sun, Xiaomin Wang, Géraldine Bonnard, Yun Shen, Zhihui Xiu, Xiaojie Li, Dahai Gao, Zhonghang Zhang and Bao-Cai Tan

Article first published online: 8 OCT 2015 | DOI: 10.1111/tpj.12993

Significance Statement

Pentatricopeptide repeat (PPR) proteins are important for RNA editing in organelles. Here we show that Emp7 is essential for cytochrome c maturation in mitochondria and consequently for seed development.

Analysis of non-coding transcriptome in rice and maize uncovers roles of conserved lncRNAs associated with agriculture traits (pages 404–416)

Huan Wang, Qi-Wen Niu, Hui-Wen Wu, Jun Liu, Jian Ye, Niu Yu and Nam-Hai Chua

Article first published online: 8 OCT 2015 | DOI: 10.1111/tpj.13018

Significance Statement

Long noncoding RNAs (lncRNAs) play key roles in numerous biological processes. Here we sequenced and characterized lncRNAs from many rice and maize tissues.Hundreds of the lncRNAs have single nucleotide polymorphisms associated with agricultural traits, suggesting that they may play roles in controlling such traits

Non-invasive, whole-plant imaging of chloroplast movement and chlorophyll fluorescence reveals photosynthetic phenotypes independent of chloroplast photorelocation defects in chloroplast division mutants (pages 428–442)

Siddhartha Dutta, Jeffrey A. Cruz, Yuhua Jiao, Jin Chen, David M. Kramer and Katherine W. Osteryoung

Article first published online: 8 OCT 2015 | DOI: 10.1111/tpj.13009

Significance Statement

Here we demonstrate a dual-imaging platform for continuous, high-sensitivity, and non-invasive measurements of chloroplast movement and chlorophyll fluorescence in whole plants. We further introduce an approach to correct calculations of non-photochemical quenching for interference from chloroplast movement. We use this platform and Arabidopsis mutants with drastically enlarged chloroplasts to show that their photosynthetic phenotypes, induced by high-light stress, are due predominantly to altered chloroplast size and shape rather than to reduced chloroplast movement.

Plant, Cell & Environment Content Alert (New Articles)

The cytochrome ***c*** oxidase biogenesis factor AtCOX17 modulates stress responses in Arabidopsis

Lucila Garcia, Elina Welchen, Uta Gey, Agustín L. Arce, Iris Steinebrunner and Daniel H. Gonzalez

Accepted manuscript online: 5 OCT 2015 12:17PM EST | DOI: 10.1111/pce.12647

Current Biology: Alert 30 September-6 October

The Evolutionary Origin of a Terrestrial Flora Review Article *Pages R899-R910*
Charles Francis Delwiche, Endymion Dante Cooper

Regulation of Chloroplast Protein Import by the Ubiquitin E3 Ligase SP1 Is Important for Stress Tolerance in Plants

Pages 2527-2534 Qihua Ling, Paul Jarvis

An Endophyte Constructs Fungicide-Containing Extracellular Barriers for Its Host Plant

Pages 2570-2576 Sameh S.M. Soliman, John S. Greenwood, Aureliano Bombarely, Lukas A. Mueller, Rong Tsao, Dick D. Mosser, Manish N. Raizada