Lit Lunch 2-27-13

Nature Structural and Molecular Biology

February

Characterization of prion-like conformational changes of the neuronal isoform of *Aplysia* CPEB

Bindu L Raveendra, Ansgar B Siemer, Sathyanarayanan V Puthanveettil, Wayne A Hendrickson, Eric R Kandel & Ann E McDermott

Columbia University, New York, New York, USA.

The neuronal isoform of cytoplasmic polyadenylation element–binding protein (CPEB) is a regulator of local protein synthesis at synapses and is critical in maintaining learning-related synaptic plasticity in *Aplysia.* Previous studies indicate that the function of *Aplysia* CPEB can be modulated by conversion to a stable prion-like state, thus contributing to the stabilization of long-term memory on a molecular level. Here, we used biophysical methods to demonstrate that *Aplysia* CPEB, like other prions, undergoes a conformational switch from soluble α-helix–rich oligomer to β-sheet–rich fiber *in vitro*. Solid-state NMR analyses of the fibers indicated a relatively rigid N-terminal prion domain. The fiber form of *Aplysia* CPEB showed enhanced binding to target mRNAs as compared to the soluble form. Consequently, we propose a model for the *Aplysia* CPEB fibers that may have relevance for functional prions in general. Although significant knowledge of cellular and molecular mechanisms underlying the acquisition and early storage of implicit and explicit long-term memory has been gained, the mechanisms by which memories are maintained for long periods of time are still not fully understood1, 2. Because proteins normally have relatively short half-lives, of hours or days, the question remains: How can the change in molecular composition of a synapse be maintained for long periods of time, as is required for long-term memory? We previously found one answer to this conundrum in a work describing a prion-like regulator of local protein synthesis at the synapse in the marine snail *Aplysia californica*: the cytoplasmic polyadenylation element–binding protein *Aplysia* CPEB3, 4. This provided physiological evidence that the prion-like properties of *Aplysia* CPEB might explain the self-sustained, continuous molecular turnover at the synapse5.

J Mol Biol. 2013 Feb 8;425(3):492-505. doi: 10.1016/j.jmb.2012.11.003. Epub 2012 Nov 12.

Amyloid formation in heterogeneous environments: islet amyloid polypeptide glycosaminoglycan interactions.

Wang H, Cao P, Raleigh DP.

Source

Department of Chemistry, State University of New York at Stony Brook, Stony Brook, NY 11794-3400, USA.

Abstract

Amyloid formation plays an important role in a broad range of diseases, and the search for amyloid inhibitors is an active area of research. Amyloid formation takes places in a heterogeneous environment in vivo with the potential for interactions with membranes and with components of the extracellular matrix. Naturally occurring amyloid deposits are associated with sulfated proteoglycans and other factors. However, the vast majority of in vitro assays of amyloid formation and amyloid inhibition are conducted in homogeneous solution where the potential for interactions with membranes or sulfated proteoglycans is lacking and it is possible that different results may be obtained in heterogeneous environments. We show that variants of islet amyloid polypeptide (IAPP), which are non-amyloidogenic in homogeneous solution, can be readily induced to form amyloid in the presence of glycosaminoglycans (GAGs). GAGs are found to be more effective than anionic lipid vesicles at inducing amyloid formation on a per-charge basis. Several known inhibitors of IAPP amyloid formation are shown to be less effective in the presence of GAGs.

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J Mol Biol. 2013 Feb 8;425(3):536-45. doi: 10.1016/j.jmb.2012.11.021. Epub 2012 Nov 23.

Identification of Functionally Conserved Regions in the Structure of the Chaperone/CenH3/H4 Complex.

Hong J, Feng H, Zhou Z, Ghirlando R, Bai Y.

Source

Laboratory of Biochemistry and Molecular Biology, National Cancer Institute, NIH, Bethesda, MD 20892, USA.

Abstract

In eukaryotes, a variant of conventional histone H3 termed CenH3 epigenetically marks the centromere. The conserved CenH3 chaperone specifically recognizes CenH3 and is required for CenH3 deposition at the centromere. Recently, the structures of the chaperone/CenH3/H4 complexes have been determined for Homo sapiens (Hs) and the budding yeasts Saccharomyces cerevisiae (Sc) and Kluyveromyces lactis (Kl). Surprisingly, the three structures are very different, leading to different proposed structural bases for chaperone function. The question of which structural region of CenH3 provides the specificity determinant for the chaperone recognition is not fully answered. Here, we investigated these issues using solution NMR and site-directed mutagenesis. We discovered that, in contrast to previous findings, the structures of the Kl and Sc chaperone/CenH3/H4 complexes are actually very similar. This new finding reveals that both budding yeast and human chaperones use a similar structural region to block DNA from binding to the histones. Our mutational analyses further indicate that the N-terminal region of the CenH3 α2 helix is sufficient for specific recognition by the chaperone for both budding yeast and human. Thus, our studies have identified conserved structural bases of how the chaperones recognize CenH3 and perform the chaperone function.

Published by Elsevier Ltd.

Nature

Seed-patent case in Supreme Court

A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis

Paola Picotti, Mathieu Clément-Ziza, Henry Lam, David S. Campbell, Alexander Schmidt, Eric W. Deutsch, Hannes Röst, Zhi Sun, Oliver Rinner, Lukas Reiter, Qin Shen, Jacob J. Michaelson, Andreas Frei, Simon Alberti, Ulrike Kusebauch, Bernd Wollscheid, Robert L. Moritz, Andreas Beyer & Ruedi Aebersold

Experience from different fields of life sciences suggests that accessible, complete reference maps of the components of the system under study are highly beneficial research tools. Examples of such maps include libraries of the spectroscopic properties of molecules, or databases of drug structures in analytical or forensic chemistry. Such maps, and methods to navigate them, constitute reliable assays to probe any sample for the presence and amount of molecules contained in the map. So far, attempts to generate such maps for any proteome have failed to reach complete proteome coverage1, 2, 3. Here we use a strategy based on high-throughput peptide synthesis and mass spectrometry to generate an almost complete reference map (97% of the genome-predicted proteins) of the Saccharomyces cerevisiae proteome. We generated two versions of this mass-spectrometric map, one supporting discovery-driven (shotgun)3, 4 and the other supporting hypothesis-driven (targeted)5, 6 proteomic measurements. Together, the two versions of the map constitute a complete set of proteomic assays to support most studies performed with contemporary proteomic technologies. To show the utility of the maps, we applied them to a protein quantitative trait locus (QTL) analysis7, which requires precise measurement of the same set of peptides over a large number of samples. Protein measurements over 78 S. cerevisiae strains revealed a complex relationship between independent genetic loci, influencing the levels of related proteins. Our results suggest that selective pressure favours the acquisition of sets of polymorphisms that adapt protein levels but also maintain the stoichiometry of functionally related pathway members.

Cell 152, 859–872, February 14, 2013 ª2013 Elsevier Inc.

Regulation of Transcription through Acetylation of H3K122 on the Lateral Surface of the Histone Octamer

Philipp Tropberger,1,2 Sebastian Pott,3,10 Claudia Keller,4,5 Kinga Kamieniarz-Gdula,1,11 Matthieu Caron,6,7,8

Florian Richter,1 Guohong Li,9 Gerhard Mittler,1 Edison T. Liu,3,12 Marc Bu¨
hler,4,5 Raphael Margueron,6,7,8
and Robert Schneider1,2,*

SUMMARY
Histone modifications are key regulators of chromatinfunction. However, little is known to whatextent histone modifications can directly impact onchromatin. Here, we address how a modificationwithin the globular domain of histones regulateschromatin function. We demonstrate that H3K122accan be sufficient to stimulate transcription and thatmutation of H3K122 impairs transcriptional activation,which we attribute to a direct effect ofH3K122ac on histone-DNA binding. In line with this,we find that H3K122ac defines genome-wide geneticelements and chromatin features associated withactive transcription. Furthermore, H3K122ac is catalyzedby the coactivators p300/CBP and can beinduced by nuclear hormone receptor signaling.Collectively, this suggests that transcriptional regulatorselicit their effects not only via signaling tohistone tails but also via direct structural perturbationof nucleosomes by directing acetylation to theirlateral surface.

352 Cell 152, 352–364, January 17, 2013 ª2013 Elsevier Inc.

Comprehensive Analysis of Silencing
Mutants Reveals Complex Regulation of the Arabidopsis Methylome

Hume Stroud,1 Maxim V.C. Greenberg,1,4 Suhua Feng,1,2,3,4 Yana V.
Bernatavichute,1 and Steven E. Jacobsen1,2,3

SUMMARY
Cytosine methylation is involved in various biologicalprocesses such as silencing of transposable elements(TEs) and imprinting. Multiple pathways regulateDNA methylation in different sequence contexts,but the factors that regulate DNA methylation ata given site in the genome largely remain unknown.Here we have surveyed the methylomes of a comprehensivelist of 86 Arabidopsis gene silencingmutants by generating single-nucleotide resolutionmaps of DNA methylation. We find that DNA methylationis site specifically regulated by different factors.Furthermore, we have identified additional regulatorsof DNA methylation. These data and analyses willserve as a comprehensive community resource forfurther understanding the control of DNA methylationpatterning.

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Molecular Cell Volume 49, Issue 3, 7 February 2013, Pages 511–523

PGRL1 Is the Elusive Ferredoxin-Plastoquinone Reductase in Photosynthetic Cyclic Electron Flow

Alexander P. Hertle[1], Thomas Blunder[1], Tobias Wunder[1], Paolo Pesaresi[3], Mathias Pribil[1, 2], Ute Armbruster[1], Dario Leister[1],

- http://dx.doi.org.silk.library.umass.edu/10.1016/j.molcel.2012.11.030,
- During plant photosynthesis, photosystems I (PSI) and II (PSII), located in the thylakoid membranes of the chloroplast, use light energy to mobilize electron transport. Different modes of electron flow exist. Linear electron flow is driven by both photosystems and generates ATP and NADPH, whereas cyclic electron flow (CEF) is driven by PSI alone and generates ATP only. Two variants of CEF exist in flowering plants, of which one is sensitive to antimycin A (AA) and involves the two thylakoid proteins, PGR5 and PGRL1. However, neither the mechanism nor the site of reinjection of electrons from ferredoxin into the thylakoid electron transport chain during AA-sensitive CEF is known. Here, we show that PGRL1 accepts electrons from ferredoxin in a PGR5-dependent manner and reduces quinones in an AA-sensitive fashion. PGRL1 activity itself requires several redox-active cysteine residues and a Fe-containing cofactor. We therefore propose that PGRL1 is the elusive ferredoxin-plastoquinone reductase (FQR).

Highlights

► PGRL1 is the elusive FQR which has been sought for almost three decades ► PGR5 is required for the transfer of electrons from ferredoxin to PGRL1 ► The six redox-active cysteine residues of PGRL1 can form intra- and intermolecular disulfide bridges ► Thioredoxins destabilize PGRL1 homodimers

J. Biol. Chem., published online 27 November 2012;
doi:10.1074/jbc.M112.424077

The Biochemical Mechanism of Auxin Biosynthesis by an *Arabidopsis* YUCCA Flavin-containing Monooxygenase*

Xinhua Dai[‡,1], Kiyoshi Mashiguchi[‡§,1], Qingguo Chen[‡], Hiroyuki Kasahara[§], Yuji Kamiya[§], Sunil Ojha[¶], Jennifer DuBois[¶], David Ballou[†] and Yunde Zhao[‡,2]

Background: Auxin is essential for plant growth, but its biosynthesis in plants has not been biochemically defined.

Results: Key features of the catalytic mechanism for the YUCCA flavoprotein, the rate-limiting enzyme of auxin biosynthesis, are determined.

Conclusion: YUCs generate an observable though relatively short lived C4a-(hydro)peroxyflavin intermediate for catalysis in auxin biosynthesis.

Significance: This work establishes the previously unknown biochemical mechanism of auxin biosynthesis.

Auxin regulates every aspect of plant growth and development. Previous genetic studies demonstrated that YUCCA (YUC) flavin-containing monooxygenases (FMOs) catalyze a rate-limiting step in auxin biosynthesis and that YUCs are essential for many developmental processes. We proposed that YUCs convert indole-3-pyruvate (IPA) to indole-3-acetate (IAA). However, the exact biochemical mechanism of YUCs has remained elusive. Here we present the biochemical characterization of recombinant *Arabidopsis* YUC6. Expressed in and purified from *Escherichia coli*, YUC6 contains FAD as a cofactor, which has peaks at 448 nm and 376 nm in the UV-visible spectrum. We show that YUC6 uses NADPH and oxygen to convert IPA to IAA. The first step of the YUC6-catalyzed reaction is the reduction of the FAD cofactor to $FADH^-$ by NADPH. Subsequently, $FADH^-$ reacts with oxygen to form a flavin-C4a-(hydro)peroxy intermediate, which we show has a maximum absorbance at 381 nm in its UV-visible spectrum. The final chemical step is the reaction of the C4a-intermediate with IPA to produce IAA. Although the sequences of the YUC enzymes are related to those of the mammalian FMOs, which oxygenate nucleophilic substrates, YUC6 oxygenates an electrophilic substrate (IPA). Nevertheless, both classes of enzymes form quasi-stable C4a-(hydro)peroxyl FAD intermediates. The YUC6 intermediate has a half-life of ~20 s whereas that of some FMOs is >30 min. This work reveals the catalytic mechanism of the first known plant flavin monooxygenase and provides a foundation for further investigating how YUC activities are regulated in plants.

Redox control: A black hole for oxidized glutathione - pp69 - 70

Jakob R Winther & Ursula Jakob

doi:10.1038/nchembio.1161

There is a considerable amount of oxidized glutathione in living cells, yet it is virtually absent from the cytosol. The mystery of where it resides has now been solved. A study in baker's yeast revealed that oxidized glutathione is selectively stashed in vacuoles.

Multiple glutathione disulfide removal pathways mediate cytosolic redox homeostasis - pp119 - 125

Bruce Morgan, Daria Ezeriņa, Theresa N E Amoako, Jan Riemer, Matthias Seedorf & Tobias P Dick

doi:10.1038/nchembio.1142

Quantification of cytosolic glutathione redox potential leads to the discovery that the ABC-C transporter Ycf1 rapidly transports oxidized glutathione (GSSG) into vacuoles and whole-cell GSSG should not be used as a proxy for cytosolic GSSG.

Activation of Hsp70 reduces neurotoxicity by promoting polyglutamine protein degradation - pp112 - 118

Adrienne M Wang, Yoshinari Miyata, Susan Klinedinst, Hwei-Ming Peng, Jason P Chua, Tomoko Komiyama, Xiaokai Li, Yoshihiro Morishima, Diane E Merry, William B Pratt, Yoichi Osawa, Catherine A Collins, Jason E Gestwicki & Andrew P Lieberman

doi:10.1038/nchembio.1140

An allosteric activator of Hsp70 mimics Hip and reduces neurotoxicity in a model for spinobulbar muscular atrophy by promoting ubiquitination and degradation of oligomeric polyglutamine-containing clients.

RNA SHAPE analysis in living cells - pp18 - 20

Robert C Spitale, Pete Crisalli, Ryan A Flynn, Eduardo A Torre, Eric T Kool & Howard Y Chang

doi:10.1038/nchembio.1131

Selective 2′-hydroxyl acylation analyzed by primer extension (SHAPE) is a proven methodology for *in vitro* RNA secondary structure analysis. The identification of a new acylating agent permits the use of SHAPE to probe folded RNAs within living cells.

Nature Reviews Microbiology contents March 2013 Volume 11 Number 3 pp 143-217

Environmental microbiology: Plant bacteria thrive in storm clouds

p146 | doi:10.1038/nrmicro2978

The first comprehensive biogeochemical survey of a storm cloud reveals a selection bias for plant-associated bacteria over soil bacteria, which could influence the global distribution of bacteria.

Article series: Vector-borne diseases

Beyond insecticides: new thinking on an ancient problem

Elizabeth A. McGraw & Scott L. O'Neill

p181 | doi:10.1038/nrmicro2968
In addition to developing vaccines and drugs that target vector-borne diseases, historically the use of insecticides has been the main approach for targeting the vector itself. However, as McGraw and O'Neill describe in this Review, there has been substantial recent progress in developing alternative genetic and biological vector-control strategies.

Methods in Enzymology Volume 523, 2013, Pages 191–212 Methods in Protein Design

Chapter Nine – Using Analyses of Amino Acid Coevolution to Understand Protein Structure and Function

Orr Ashenberg[*,‡], Michael T. Laub[*,‡,]

Department of Biology, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA

Determining which residues of a protein contribute to a specific function is a difficult problem. Analyses of amino acid covariation within a protein family can serve as a useful guide by identifying residues that are functionally coupled. Covariation analyses have been successfully used on several different protein families to identify residues that work together to promote folding, enable protein–protein interactions, or contribute to an enzymatic activity. Covariation is a statistical signal that can be measured in a multiple sequence alignment of homologous proteins. As sequence databases have expanded dramatically, covariation analyses have become easier and more powerful. In this chapter, we describe how functional covariation arises during the evolution of proteins and how this signal can be distinguished from various background signals. We discuss the basic methodology for performing amino acid covariation analysis, using bacterial two-component signal transduction proteins as an example. We provide practical suggestions for each step of the process including assembly of protein sequences, construction of a multiple sequence alignment, measurement of covariation, and analysis of results.

Methods in Enzymology Volume 523, 2013, Pages 237–256

Chapter Eleven – Protein Engineering and Stabilization from Sequence Statistics: Variation and Covariation Analysis

Venuka Durani[*], Thomas J. Magliery[*,] Department of Chemistry, The Ohio State University, Columbus, Ohio, USA

http://dx.doi.org/10.1016/B978-0-12-394292-0.00011-4,

The concepts of consensus and correlation in multiple sequence alignments (MSAs) have been used in the past to understand and engineer proteins. However, there are multiple ways of acquiring MSA databases and also

numerous mathematical metrics that can be applied to calculate each of the parameters. This chapter describes an overall methodology that we have chosen to employ for acquiring and statistically analyzing MSAs. We have provided a step-by-step protocol for calculating relative entropy and mutual information metrics and describe how they can be used to predict mutations that have a high probability of stabilizing a protein. This protocol allows for flexibility for modification of formulae and parameters without using anything more complicated than Microsoft Excel. We have also demonstrated various aspects of data analysis by carrying out a sample analysis on the BPTI-Kunitz family of proteins and identified mutations that would be predicted to stabilize this protein based on consensus and correlation values.

Physiologia Plantarum Content Alert (New Articles)

Whole plant and organ level nitrogen isotope discrimination indicates modification of partitioning of assimilation, fluxes and allocation of nitrogen in knockout lines of *Arabidopsis thaliana*
Lee A. Kalcsits and Robert D. Guy
Accepted manuscript online: 15 FEB 2013 11:28AM EST | DOI: 10.1111/ppl.12038

The Plant Journal Content Alert: 73, 4 (February 2013)
The pollen tube: a soft shell with a hard core (pages 617–627)
Hannes Vogler, Christian Draeger, Alain Weber, Dimitris Felekis, Christof Eichenberger, Anne-Lise Routier-Kierzkowska, Aurélien Boisson-Dernier, Christoph Ringli, Bradley J. Nelson, Richard S. Smith and Ueli Grossniklaus
Article first published online: 10 DEC 2012 | DOI: 10.1111/tpj.12061

The EMBO Journal - Table of Contents alert Volume 32 Issue 4
Running a little late: chloroplast Fe status and the circadian clock
Iron homeostasis is essential for plant growth and survival. Two papers now report that chloroplast Iron levels also regulate the period of the circadian clock, which might confer fitness advantage by linking iron status to daily changes in environmental conditions.
Grandon T Wilson and Erin L Connolly
The EMBO Journal (2013), **32**, 490 - 492; 10.1038/emboj.2013.14
Abstract | Full text | PDF | Related article

ublished online: 01 February 2013
Circadian clock adjustment to plant iron status depends on chloroplast and phytochrome function **EMBO Open**
The circadian clock of Arabidopsis is found to be hardwired to cellular iron levels, with chloroplasts playing a central role in iron sensing.
Patrice A Salomé, Michele Oliva, Detlef Weigel and Ute Krämer
The EMBO Journal (2013), **32**, 511 - 523; 10.1038/emboj.2012.330
Abstract | Full text | PDF | Supp. info. | Review Process File

Current Opinion in Microbiology: Alert 15 February-21 February

Ribosome heterogeneity: another level of complexity in bacterial translation regulation Review
Available online 14 February 2013
Konstantin Byrgazov, Oliver Vesper, Isabella Moll

Highlights

► Bacterial ribosomes have an intrinsic regulatory capacity. ► Ribosomes can vary in their protein and/or rRNA complement. ► Variations in rRNA and r-protein modifications likewise could lead to heterogeneity. ► Heterogeneous ribosomes can exhibit a functional specificity.

Developmental Cell
Volume 24, Issue 2, 28 January 2013, Pages 125–132

A Protodermal miR394 Signal Defines a Region of Stem Cell Competence in the *Arabidopsis* Shoot Meristem

Steffen Knauer[1], Anna L. Holt[1], Ignacio Rubio-Somoza[2], Elise J. Tucker[1, 5], Annika Hinze[1], Melanie Pisch[1], Marie Javelle[3], Marja C. Timmermans[3], Matthew R. Tucker[1, 6], Thomas Laux[1, 4, ,]

http://dx.doi.org/10.1016/j.devcel.2012.12.009, How to Cite or Link Using DOI

Long-standing question in plants and animals is how spatial patterns are maintained within stem cell niches despite ongoing cell divisions. Here we address how, during shoot meristem formation in *Arabidopsis thaliana*, the three apical cell layers acquire stem cell identity. Using a sensitized mutant screen, we identified miR394 as a mobile signal produced by the surface cell layer (the protoderm) that confers stem cell competence to the distal meristem by repressing the F box protein LEAF CURLING RESPONSIVENESS. This repression is required to potentiate signaling from underneath the stem cells by the transcription factor WUSCHEL, maintaining stem cell pluripotency. The interaction of two opposing signaling centers provides a mechanistic framework of how stem cells are localized at the tip of the meristem. Although the constituent cells change, the surface layer provides a stable point of reference in the self-organizing meristem.

Rhee, H.-W. *et al*. Proteomic mapping of mitochondria in living cells via spatially restricted enzymatic tagging. Science 31 January 2013 (doi: 10.1126/science.1230593)

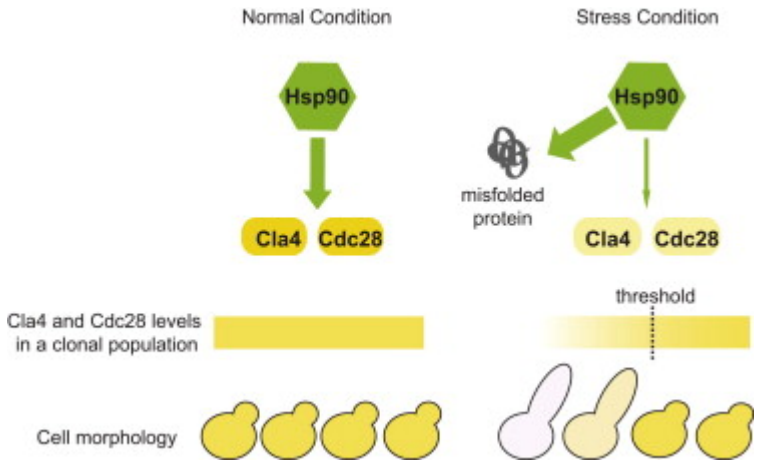
- Article

Ting and colleagues describe a technique that allows spatio-temporal information to be captured by mass spectrometry (MS). The authors used engineered ascorbate peroxidase as a targetable genetic tag to label proteins in live cells. Ascorbate peroxidase biotinylates nearby proteins when biotin-phenol and H_2O_2 are added to tagged cells, allowing them to be captured for MS with streptavidin beads. The authors fused ascorbate peroxidase to a peptide that targeted it to the mitochondrial matrix. This enabled them to identify 495 proteins within the human mitochondrial matrix, 94% of which had previously been associated with mitochondria, and they performed various experiments to verify their results. As well as presenting a technique that can be used to map the proteome of whole organelles from living cells, this paper identifies 31 proteins with a novel mitochondrial matrix association.

1. **Hsp90 Regulates Nongenetic Variation in Response to Environmental Stress** Original Research Article

Available online 21 February 2013
Yu-Ying Hsieh, Po-Hsiang Hung, Jun-Yi Leu

Graphical Abstract



Highlights

► Reducing Hsp90 triggers morphological heterogeneity in a clonal yeast population ► Morphological change is caused by reduced levels of a septin regulator and CDK ► Morphological change is induced by stress and rescued by overexpressing Hsp90 ► Hsp90-dependent morphological heterogeneity is conserved in diverse yeast species

The Coming Age of Complete, Accurate, and Ubiquitous Proteomes Review Article

Pages 583-590
Matthias Mann, Nils A. Kulak, Nagarjuna Nagaraj, Jürgen Cox

High-resolution mass spectrometry (MS)-based proteomics has progressed tremendously over the years. For model organisms like yeast, we can now quantify complete proteomes in just a few hours. Developments discussed in this Perspective will soon enable complete proteome analysis of mammalian cells, as well, with profound impact on biology and biomedicine.

The "Observer Effect" in Genome-wide Surveys of Protein-RNA Interactions Review Article

Pages 601-604
Kasandra J. Riley, Joan A. Steitz

Recent technological advances have spurred genome-wide studies that afford insights into ribonucleoprotein biology and transcript regulation on an unprecedented scale. Here we review techniques currently used to obtain genome-wide profiles of RNA-protein interactions in living cells. We highlight recent studies of the mRNA-bound proteome and address pitfalls inherent in such investigations.

New Insights from Existing Sequence Data: Generating Breakthroughs without a Pipette Review Article

Pages 605-617
Alex M. Plocik, Brenton R. Graveley

With the rapidly declining cost of data generation and the accumulation of massive data sets, molecular biology is entering an era in which incisive analysis of existing data will play an increasingly prominent role in the discovery of new biological phenomena and the elucidation of molecular mechanisms. Here, we discuss resources of publicly available sequencing data most useful for interrogating the mechanisms of gene expression. Existing next-generation sequence data sets, however, come with significant challenges in the form of technical and bioinformatic artifacts, which we discuss in detail. We also recount several breakthroughs made largely through the analysis of existing data, primarily in the RNA field.

Finka A, Goloubinoff P.
Proteomic data from human cell cultures refine mechanisms of chaperone-mediated protein homeostasis.
Cell Stress Chaperones. 2013 Feb 21;. [Epub ahead of print]
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Bogamuwa S, Jang JC.
The Arabidopsis tandem CCCH zinc finger proteins AtTZF4, 5, and 6 are involved in light-, ABA- and GA-mediated regulation of seed germination.
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Quantitative analysis of chaperone network throughput in budding yeast.
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Liu S, Dai X, Cai L, Ma X, Liu J, Jiang S, Liu J, Cui Y.
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Single Nucleotide Polymorphisms in HSP17.8 and Their Association with Agronomic Traits in Barley.
PLoS One. 2013;8(2):e56816.
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Lee JG, Ye Y.
Bag6/Bat3/Scythe: A novel chaperone activity with diverse regulatory functions in protein biogenesis and degradation.
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The regulatory properties of Rubisco activase differ among species and affect photosynthetic induction during light transitions.
Plant Physiol. 2013 Feb 15;. [Epub ahead of print]
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Kummer E, Oguchi Y, Seyffer F, Bukau B, Mogk A.
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The exocyst complex contributes to PIN auxin efflux carrier recycling and polar auxin transport in Arabidopsis (pages 709–719)
Edita Janková Drdová, Lukáš Synek, Tamara Pečenková, Michal Hála, Ivan Kulich, John E. Fowler, Angus S. Murphy and Viktor Žárský
Article first published online: 10 JAN 2013 | DOI: 10.1111/tpj.12074

Current Opinion in Chemical Biology: Alert 19 February-25 February

Advances in characterizing ubiquitylation sites by mass spectrometry Review Article

Pages 49-58
Kathrine B Sylvestersen, Clifford Young, Michael L Nielsen

Highlights

► Ubiquitin is a widely occurring and dynamic post-translational modification. ► Mass spectrometry has emerged as a powerful methodology to characterize ubiquitylation sites. ► Peptide-centric enrichment strategies are currently superior to protein-centric methodologies.

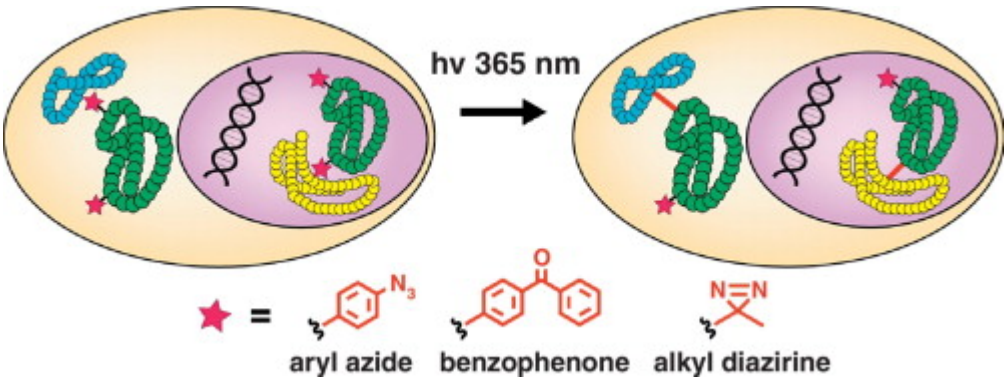
11. **Ubiquitin — omics reveals novel networks and associations with human disease** Review Article

Highlights

► Proteome-wide abundance measurements of ubiquitin components. ► Novel tools to profile protein ubiquitination sites. ► Dynamics of the poly-ubiquitinated protein pool related to human diseases. ► Chemoproteomics in the ubiquitin system.

Photocrosslinking approaches to interactome mapping Review Article

Graphical abstract



Highlights

► Photocrosslinking provides insight into context-dependent interactions. ► Interactome dynamics can be determined by photocrosslinking. ► Use of photocrosslinkers defines specific interaction interfaces within large complexes. ► Crosslinking captures transient interaction complexes containing IDPs and glycoproteins.

Current Opinion in Plant Biology: Alert 18 February-24 February

Regulation of the mitochondrial tricarboxylic acid cycle Review Article

Available online 22 February 2013
Adriano Nunes-Nesi, Wagner L Araújo, Toshihiro Obata, Alisdair R Fernie

Highlights

► The functional roles of the constituent enzymes of the plant TCA cycle are largely clarified. ► By contrast, the regulation of the flux through this vital pathway is currently poorly understood. ► Detailed enzyme kinetic studies alongside gene expression studies hint for a complex regulatory hierarchy. ► Proteomics approaches hint towards at least some conservation of regulatory principals with those characterized in non-plant systems.

Natural variation and genetic constraints on drought tolerance Review Article

Available online 22 February 2013
Thomas E Juenger

Highlights

► Drought is a central abiotic stress for plants. ► Drought tolerance is genetically variable, but we know little about underlying molecular details. ► The genetic and molecular details can matter and determine constraints on evolution. ► Studies linking gene to function for natural alleles are needed. ► A better understanding of pleiotropy and plasticity will provide new avenues for plant improvement.

Proteostasis Modulators with Discriminating Taste

Ville O. Paavilainen[1], Jack Taunton[1,]

- http://dx.doi.org/10.1016/j.chembiol.2013.02.002, How to Cite or Link Using DOI

Krishna Kannan, Nora Vázquez-Laslop, Alexander S. Mankin

Selective Protein Synthesis by Ribosomes with a Drug-Obstructed Exit Tunnel

Cell, Volume 151, Issue 3, 26 October 2012, Pages 508-520

Small molecules that perturb protein homeostasis are used as cancer therapeutics and as antibiotics to treat bacterial infections. In a recent issue of *Cell*, Kannan and colleagues describe an intriguing mechanism that enables ribosome-targeted macrolides to selectively remodel the bacterial proteome. This finding suggests the

exciting possibility of targeting additional proteostasis regulators in a substrate-selective manner.

Current Opinion in Biotechnology

New Articles in Press, 18 February-24 February 2013

Plant metabolic engineering: future prospects and challenges

Available online 20 February 2013
Natalia Dudareva, Dean DellaPenna

Nature Genetics Contents: March 2013 pp 227 - 337

Oomycete pathogens encode RNA silencing suppressors pp330 - 333
Yongli Qiao, Lin Liu, Qin Xiong, Cristina Flores, James Wong, Jinxia Shi, Xianbing Wang, Xigang Liu, Qijun Xiang, Shushu Jiang, Fuchun Zhang, Yuanchao Wang, Howard S Judelson, Xuemei Chen and Wenbo Ma
doi:10.1038/ng.2525
Wenbo Ma and colleagues show that two effectors from the oomycete plant pathogen *Phytophthora sojae* suppress RNA silencing in plants by inhibiting the biogenesis of small RNAs. These findings show that some eukaryotic pathogens, like their prokaryotic and viral counterparts, have evolved virulence proteins that target host RNA silencing processes to promote infection.

Quantitative variation in maize kernel row number is controlled by the *FASCIATED EAR2* locus pp334 - 337
Peter Bommert, Namiko Satoh Nagasawa and David Jackson
doi:10.1038/ng.2534
Domesticated maize make 8-20 rows of kernels, whereas its ancestor teosinte makes 2 rows. David Jackson and colleagues report that variation at the *FEA2* locus in maize influences kernel row number and kernels per ear, which are important crop yield traits.