

Dec 3

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A Proteomics Approach to Profiling  
the Temporal Translational Response  
to Stress and Growth

Daniel A. Rothenberg, J. Matthew Taliaferro, Sabrina M. Huber, Thomas J. Begley, Peter C. Dedon, and Forest M. White  
SUMMARY

To quantify dynamic protein synthesis rates, we developed MITNCAT, a method combining multiplexed isobaric mass tagging with pulsed SILAC (pSILAC) and bio-orthogonal non-canonical amino acid tagging (BONCAT) to label newly synthesized proteins with azidohomoalanine (Aha), thus enabling high temporal resolution across multiple conditions in a single analysis. MITNCAT quantification of protein synthesis rates following induction of the unfolded protein response revealed global down-regulation of protein synthesis, with stronger down-regulation of glycolytic and protein synthesis machinery proteins, but up-regulation of several key chaperones. Waves of temporally distinct protein synthesis were observed in response to epidermal growth factor, with altered synthesis detectable in the first 15 min. Comparison of protein synthesis with mRNA sequencing and ribosome footprinting distinguished protein synthesis driven by increased transcription versus increased translational efficiency. Temporal delays between ribosome occupancy and protein synthesis

**PLOS Genetics Volume 14(11) November 2018**

**[Arabidopsis class I formins control membrane-originated actin polymerization at pollen tube tips](#)**

Yaxian Lan, Xiaonan Liu, Ying Fu, Shanjin Huang

**[A single class of ARF GTPase activated by several pathway-specific ARF-GEFs regulates essential membrane traffic in Arabidopsis](#)**

Manoj K. Singh,..... Peter Pimpl, Gerd Jürgens

**Current Biology**

**[Insights into the Molecular Mechanisms of CO<sub>2</sub>-Mediated Regulation of Stomatal Movements](#)**

Pages R1356-R1363

Available Online 2018-12-03

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## PNAS

### *Global aeroplankton dispersal*

Airborne particulates include large numbers of living organisms, as well as dust, pollutants, and other chemicals. Cáliz *et al.* collected aeroplankton fortnightly for 7 years in the Spanish Pyrenees. High-throughput sequencing of 16S and 18S amplicons identified microbes, including potential pathogens, that had made landfall in rain and snow. Distinct seasonal and climate signals in the data associated with the origin of the air masses. For example, winter microbial fallout originated from as far away as the North American taiga, and summer-occurring organisms contained desert-adapted bacteria from North Africa. Over the collection period, air-mass origins shifted, possibly as a result of climate change. Most atmospheric microbes are cosmopolitan, and it seems the upper atmosphere acts as a global highway for many taxa.

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Questions about Coenzyme Q? A New Genetic/Metabolic Study Has Answers

Jennifer Mach

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