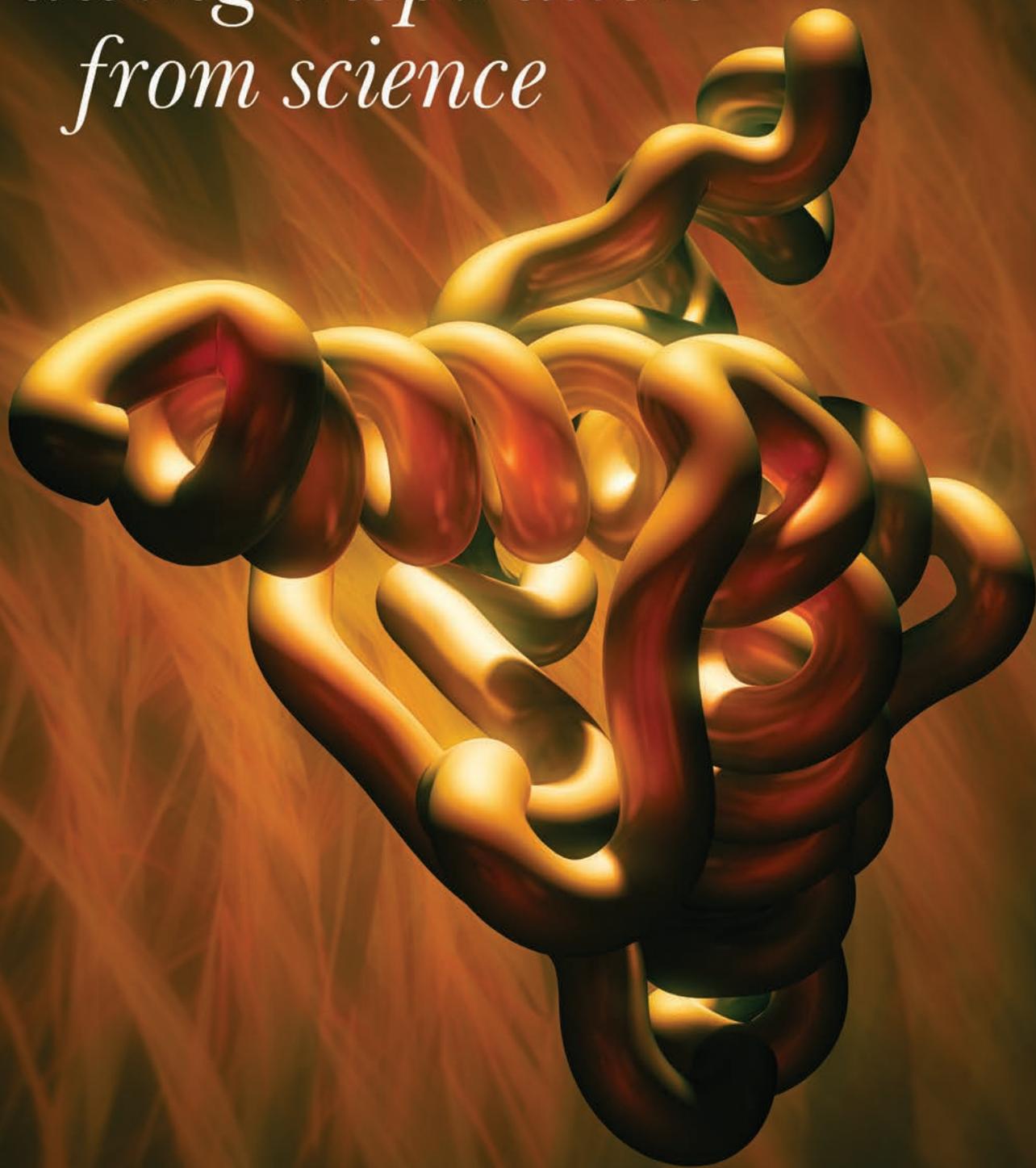


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ASBMB TODAY

THE MEMBER MAGAZINE OF THE AMERICAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY

*Drawing inspiration
from science*



Special symposium: evolution and core processes in gene regulation

Join us at this small, focused meeting in June in St. Louis

By Justin Fay, David Arnosti and Julia Zeitlinger

*“Nothing in biology
makes sense except in the
light of evolution”*

– THEODOSIUS DOBZHANSKY

The American Society for Biochemistry and Molecular Biology will host a special symposium this summer exploring the gap between evolutionary biology and mechanistic gene-expression studies.

The ability to survive and reproduce exerts considerable evolutionary pressure on diverse biological processes, perhaps none more than gene

expression, a central hub of life. Many molecular studies have illustrated ways alterations in cis-regulatory elements play key roles in evolutionary innovations. Such changes are expected to have fewer pleiotropic effects than alterations in transcription factors or even the core transcriptional machinery.

However, the core machinery of gene expression is also subject to evolutionary selection, but less is known about how selection sculpts these complexes. The advent of new technologies has made it increasingly possible, and indeed necessary, to investigate how the central components, including the complex transcriptional, RNA processing and translational machines, experience evolutionary pressure to drive diverse outcomes on population- and species-specific levels.

The symposium seeks to foster cross-fertilization between the disciplines. By bringing together diverse international researchers in a small setting, this focused, four-day meeting will allow extensive informal interac-

tions between participants, help them gain a better understanding of key challenges in the respective areas of study and provoke collaborations.

Speakers will include renowned scientists who have bridged the gap between hard-core mechanistic and evolutionary studies. Other outstanding invited scientists study gene regulation from standpoints of evo-devo, mechanism and genomics, including Trisha Wittkopp, Tracy Johnson and Alex Stark. In all, we will have 27 top speakers from North America and Europe who will present a rich offering of views from gene-expression research at many scales.



Justin Fay (jfay@genetics.wustl.edu) studies evolution of gene regulation at Washington University in St. Louis. David Arnosti (arnosti@msu.edu) studies transcriptional regulation in the context of *Drosophila* development, and leads the Gene Expression in Development and Disease group at Michigan State University. Julia Zeitlinger (jzb@stowers.org) is an associate investigator at the Stowers Institute for Medical Research.



ABOUT THE MEETING

WHEN: June 25 – June 28

WHERE: St. Louis, Mo.

SAMPLING OF SPEAKERS:

- Robert Tjian, a pioneer in biochemical studies of transcription factors and the core transcription machinery, discovered that general transcription factors may not be always general but may function in a tissue-specific fashion and thus may have created tissue diversity in evolution. In addition to biochemistry, he currently is using genomics and imaging approaches to study transcription in stem cells and in differentiating cells.
- Mike Levine always has operated at the interface of transcription, development and evolution. Using *Drosophila* as a model system, his work has been pivotal in understanding the mechanisms by which enhancers control the spatio-temporal expression of genes. He also has established the model organism *Ciona intestinalis* to study the evolutionary origin of body plans.

- Robb Krumlauf, a long-standing investigator of Hox genes, has made key contributions to understanding segmental identity and body plan organization in development and evolution. His laboratory's recent genomic analysis of Hox genes has revealed complex specificity of regulation by Hox transcription factors.

- Rachel Green has provided key insights into the workings of that most ancient RNA enzyme, the ribosome, following early in vitro evolutionary work on self-copying ribozymes with Jack Szostak. Her own laboratory has identified key molecular mechanisms affecting ribosome processivity and control.

DEADLINES:

- **April 15:** Deadline to submit abstract for short talk consideration
- **April 24:** Deadline for discounted registration (save \$100)
- **May 13:** Deadline to submit abstract for poster presentation

MORE INFO: www.asbmb.org/SpecialSymposia/GeneRegulation

LIPID NEWS CONTINUED

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Studies in yeast and mammals established lipins, a family of phosphatidic acid phosphatases, called PAH for short, as key players in triacylglycerol synthesis. Interestingly, Arabidopsis lipin homologs PAH1 and PAH2 are not required for triacylglycerol synthesis in developing seeds, the major lipid-storage organ of plants

(7). However, disruption of lipin homologs in the *tgdl* mutant causes a severe decrease in leaf triacylglycerol accumulation (4), suggesting a conserved role for lipins in triacylglycerol synthesis for yeast, mammals and plant vegetative tissues.

Recent biochemical and genetic analysis has uncovered an intricate interplay between triacylglycerol

metabolism, fatty acid β -oxidation and membrane lipid homeostasis in plants. These studies highlight the similarities of the roles these metabolic events play in plants, yeast and mammalian cells. They also illuminate another potential model system for studying these relationships that may provide important insights for advances in agriculture, drug development and human health.

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