

BCATS Keynote Speaker

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Biography

Douglas A. Lauffenburger is Uncas & Helen Whitaker Professor of Bioengineering and Head of the Department of Biological Engineering at MIT, and also holds appointments in the Departments of Biology and Chemical Engineering. He is a member of the Biotechnology Process Engineering Center, Center for Biomedical Engineering, Center for Cancer Research, and Center for Environmental Health Sciences, and serves on the Steering Committee of the Computational & Systems Biology Initiative.

Prof. Lauffenburger has served as a consultant or scientific advisory board member for the Burroughs-Wellcome Fund, the Whitaker Foundation, and many biomedical companies. A few of his awards include the Pierre Galletti Award, the W.H. Walker Award, and the Distinguished Lecture Award from BMES. He is a member of the National Academy of Engineering and of the American Academy of Arts & Sciences, and has served as President of the Biomedical Engineering Society.

Dr. Lauffenburger's major research interests are in cell engineering: the fusion of engineering with molecular cell biology. A central focus of his research program is in receptor-mediated cell communication and intracellular signal transduction, with emphasis on development of predictive computational models derived from quantitative experimental studies, for cell cue/signal/response relationships important in pathophysiology with application to drug discovery and development.

Keynote Address

Quantitative multi-pathway analysis of the EGF receptor signaling network and its governance of cell behavior

Cell behavioral functions are controlled by biomolecular networks that translate stimulatory cues (e.g., ligand/receptor binding interactions) into intracellular signals, which in turn regulate transcriptional and post-transcriptional, metabolic, and cytoskeletal processes that effect proximal and ultimate cell responses. While there is a growing body of work enhancing our understanding of how intracellular signals are generated by cue-mediated receptor activation, an exceptionally difficult challenge at the present time is to understand how these signals operate in integrated manner to govern cell phenotypic behavior. We are attempting to address this question via a combination of quantitative, dynamic protein-centric experimental manipulations and measurements with a spectrum of computational mining and modeling approaches. This talk will present an overview of our perspective and approach, along with a specific example vignette describing work aimed at understanding how the Epidermal Growth Factor Receptor signaling network operation helps govern human epithelial cell behaviors.