

John A. Lynch Lecture Series

Genotypic Variability and the Quantitative Proteotype



FRIDAY, APRIL 8, 1:00 PM

DEBARTOLO HALL, ROOM 141

Ruedi Aebersold

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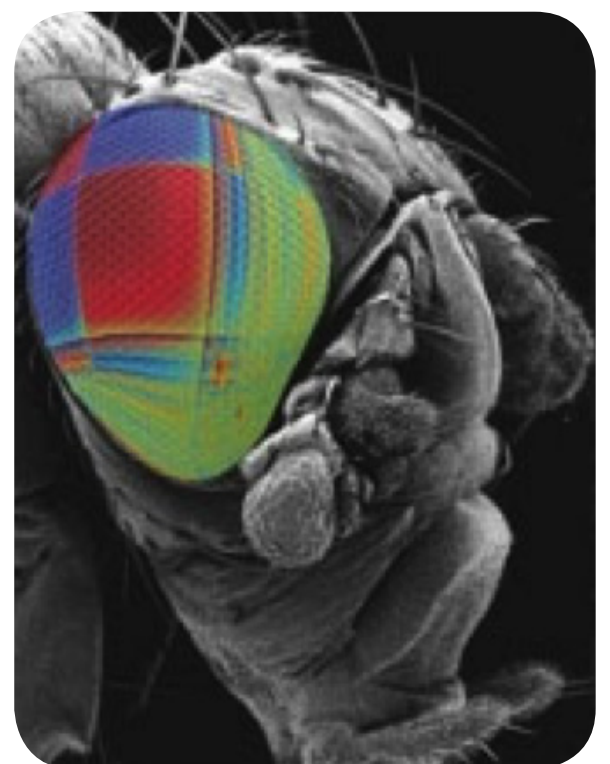
Aebersold is a native of Switzerland and earned his Ph.D. in Cellular Biology at the Biocenter of the University of Basel in 1983. He was a faculty member at the University of Washington and the University of British Columbia until 2000 when he co-founded the Institute for Systems Biology in Seattle. In 2004, he accepted a position as full professor at the Institute of Biotechnology at the Swiss Federal Institute of Technology (ETH) in Zurich, where in 2005 his research group became the first integral part of the newly founded Institute of Molecular Systems Biology. He serves on numerous scientific advisory committees and is a member of several editorial boards in the fields of protein science, genomics, and proteomics.

Abstract:

In this presentation we will discuss emerging computational and quantitative proteomic technologies to relate genotypic variation to the proteome. Proteomic data to support such correlations need to be quantitatively accurate, highly reproducible across multiple measurements and samples and generated at high throughput. Ideally, the data also would provide information about spatial arrangement of proteins in the cell. Data with these qualities can now be generated by the targeted proteomic methods selected reaction monitoring (SRM) and, at higher throughput, by SWATH-MS (1).

We will discuss the principles of these mass spectrometric methods, discuss the computational challenges they pose for data analysis and demonstrate with selected applications, using genetic reference strain compendia, their ability to determine the effect of genetic variability on the quantitative proteome, thus functionally connecting the genome to the proteome.

This lecture is organized by the Department of Chemistry and Biochemistry.



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