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Integrative multi-omics analysis facilitates discovery and understanding of key biological pathways

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A key step in proteomics research continues to be identification of biologically significant differential proteins using shotgun techniques. An alternative approach will be described that takes advantage of an integrative multi-omics workflow. New pathway analysis and data visualization software facilitate simultaneous, integrated, multi-omics analyses that could include a combination of LC/MS, GC/MS or microarray data. A significant improvement in the metabolomic workflow has been the development of metabolite data mining and identification tools based on pathways which direct discovery and identification of metabolites beyond traditional accurate-mass metabolite database matching. Using the results from this data, a list of proteins of interest in those pathways is exported to other proteomics software tools such as Spectrum Mill or Skyline. This allows the creation of the targeted proteomics experiment. This workflow will be illustrated using a multi-omics experiment where metabolomics and transcriptomics results led to a targeted analysis of specific pathway proteins.

Biography

Steven Fischer received his bachelors in chemistry (1981) and masters in chemistry (1991) at California State University, Hayward. In 1986, he joined Agilent Technologies in Santa Clara (previously part of Hewlett-Packard Company) where he has designed and applied HPLC/MS instrumentation for analytical problems for 20 years. He has over 40 United States issued patents in the field of mass spectrometry. He was the 2007 Bill Hewlett Award recipient for outstanding instrument design innovation. He currently is Marketing Manager responsible for Agilent's world wide metabolomics and proteomics program. This position includes the development of methods and software to facilitate proteomics research.

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