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GILBERT S. OMENN, M.D., PH.D.

THE ESSENTIAL ROLE OF BIOINFORMATICS IN EXPLORING THE WORLD OF PROTEINS AND CHARACTERIZING THE HUMAN PROTEOME

FEBRUARY 25, 2016

4:00 P.M.

208 LIGHT HALL

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Upcoming Discovery Lecture:

JOSEPH T. COYLE, M.D.

Eben S. Draper Chair of Psychiatry and Neuroscience, Harvard Medical School

Chief Scientific Officer, McLean Hospital

March 10, 2016

208 Light Hall / 4:00 P.M.

VANDERBILT V UNIVERSITY
MEDICAL CENTER

THE ESSENTIAL ROLE OF BIOINFORMATICS IN EXPLORING THE WORLD OF PROTEINS AND CHARACTERIZING THE HUMAN PROTEOME

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Proteins play numerous crucial roles in the complexity of biological systems, linking the genome to phenotypes in health and disease. It is not possible to predict the concentrations and dynamics of proteins and the variety and functions of their isoforms from the genome or transcriptome. Direct study of the proteome is essential, using mass spectrometry and/or antibody profiling. The Human Proteome Project (HPP) of the international Human Proteome Organization has made major progress in identifying and characterizing protein products from the approximately 20,000 human protein-coding genes (1). One of the key challenges is matching peptide sequences deduced from mass spectrometry to the protein sequences from which the peptides were released by tryptic digestion, while avoiding false-positive identifications and redundant identifications. Research teams around the world analyze proteins coded on each of the 24 chromosomes, plus mitochondria, and another 20 groups focus on a wide array of biology and disease. In the HPP, we utilize PeptideAtlas, Global Protein Machine, Human Protein Atlas, and UniProt/neXtProt as our primary data resources, linked together through the ProteomeXchange created since 2008. The HPP is able to reanalyze with standard pipelines major published studies to facilitate quality assurance and comparisons. High-quality protein data, curated with these resources, now represent 16,741 protein-coding genes, with mRNA data for an additional 2682 genes. Informatics resources for glycoproteins, phosphoproteins, and other post-translational modifications, for sequence variants, and for splice isoforms have been developed. I am particularly interested in the recognition and characterization of differentially-expressed splice isoforms of key proteins in cancer pathways and networks compared with normal tissues. The emergence of alternative splicing at the pre-mRNA stage is one of the most remarkable features of the evolution of multi-cellular organisms with multi-exonic genes. These splice variants are likely to become important as biomarkers and as therapeutic targets.

Gilbert Omenn is the Harold T. Shapiro Distinguished University Professor of Internal Medicine, Human Genetics, and Public Health and founding Director of the Center for Computational Medicine & Bioinformatics at the University of Michigan. He leads the international Human Proteome Project. He was CEO of the University of Michigan Health System from 1997 to 2002. He was Dean of the School of Public Health and Professor of Medicine and Environmental Health at the University of Washington, Seattle, 1982-97. He was Associate Director, Office of Science and Technology Policy and Office of Management and Budget, in the Executive Office of the President in the Carter Administration. He was a Howard Hughes Medical Investigator. And he was a White House Fellow at the U.S. Atomic Energy Commission. His research interests include cancer proteomics, bioinformatics, chemoprevention of cancers, public health genetics, science-based risk analysis, and health policy. He led the beta-Carotene and Retinol Efficacy Trial (CARET) of preventive agents against lung cancers and heart disease and the Center for Health Promotion in Older Adults, and created a university-wide initiative on Public Health Genetics in Ethical, Legal, and Policy Context while at the University of Washington and Fred Hutchinson Cancer Research Center. He is the author of 548 research papers and scientific reviews and author/editor of 18 books. He is an elected member of the National Academy of Medicine, American Academy of Arts and Sciences, Association of American Physicians, and American College of Physicians. In 2013 he received the David E. Rogers Award from the Association of American Medical Colleges "for major contributions to health and health care in America". Omenn received his B.A. summa cum laude from Princeton, M.D. magna cum laude from Harvard Medical School, and Ph.D. in genetics from the University of Washington. He has three children and five grandchildren. He is active in cultural, educational, and public policy organizations, a musician and tennis player.