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PLASMA PROTEOME PROFILES ASSOCIATED WITH CANCERS. Gilbert S. Omenn, M.D., Ph.D., University of Michigan, Ann Arbor, MI, 48109-0656, USA.

Proteomics can generate important applications for cancer research and cancer care by (1) profiling tumor specimens for diagnosis and for prognosis with particular therapies; (2) discovering and validating circulating plasma or serum proteins, including auto-antibodies, as biomarkers for early diagnosis; and (3) applying such biomarkers to monitoring of patients for responses to treatment and recurrence of tumors. Proteins are much closer to the pathophysiologic changes and molecular targets for drugs than are mRNAs; changes in mRNAs and corresponding proteins often are not highly correlated. Plasma proteomics must overcome the challenges of enormous complexity, huge dynamic range, in vivo and ex vivo degradation, lack of standardized procedures for sample handling and analysis, inherently incomplete sampling by mass spectrometry, and redundancy, incompleteness, and evolution of databases. Rapidly emerging advances in fractionation of complex protein mixtures, identification and quantitation of peptides and proteins, and quality of curated databases of proteins will accelerate the development of biomarker profiles for specific cancers and cancer mechanisms. The construction of a knowledge base of circulating proteins from the HUPO Plasma Proteome Project will be highlighted. Reported findings for various cancers will be reviewed. [Supported by MTTC GR 687 for Proteomics Alliance for Cancer Research, NCI/SAIC contract on Mouse Models of Human Cancers, and NIH U54DA021519 grant for National Center for Integrative Biomedical Informatics.]