David Fenyö, PhD: David Fenyö received an M.Sc. in engineering physics in 1987 from Uppsala University in Sweden, and joined the laboratory of Dr. Bo Sundqvist at Uppsala University where he studied the mechanisms of ion-solid interaction both experimentally, and using molecular dynamics and Monte Carlo simulations. After receiving a Ph.D. in Physics in 1991, he joined the laboratory of Dr. Brian Chait at the Rockefeller University, where he developed algorithms to analyze mass-spectrometry based proteomics data. In 1997 he co-founded ProteoMetrics, a bioinformatics startup and served as its president and created several software packages, including a distributed software system for fully automated analysis of large-scale proteomics data. Subsequently, he worked for several companies including GE Healthcare before returning to academia and joining the faculty of NYU School of Medicine in 2010. He is currently Professor of Biochemistry and Molecular Pharmacology, Director for the Ph.D. program in Systems and Computational Biomedicine and the Master's program in Biomedical Informatics, and Associate Director for informatics for the Clinical and Translational Science Institute (CTSI).

Dr. Fenyö has over 30 years of experience with all aspects of biomedical data analysis in both academia and industry and his work has resulted in over 180 scientific publications. During these years, he has laid a statistical foundation to test the significance of protein identification results, he has developed algorithms for identifying proteins by matching mass spectrometry data to databases, detecting retrotransposon insertions using next generation sequencing data, analyzing protein interactions using microscopy data. Dr. Fenyö has extensive experience in software development in academia as well as in small and large biotechnology companies, and he has managed large commercial software projects for customers in the pharmaceutical and biotech industries.

His research focuses on providing a detailed understanding of the dynamics of cellular processes. He applies mathematical, statistical, and computational methods to optimize experimental design, analyze quantitative data, and model biological systems. His efforts to integrate data from multiple technologies—including mass spectrometry, sequencing, and microscopy—have provided a wide array of powerful tools to discover and verify biomarkers and therapeutic targets in cancer.