

Alexey Nesvizhskii received his Ph.D. from the University of Washington in 2001 for his studies on theoretical solid state physics. After joining the laboratory of Ruedi Aebersold at the Institute for Systems Biology in Seattle, his research interests focused on the emerging fields of mass spectrometry-based proteomics and proteome bioinformatics. He established his own laboratory (www.nesvilab.org) in 2005 at the University of Michigan, Ann Arbor, where he is Professor in the Departments of Pathology and Computational Medicine & Bioinformatics. Dr. Nesvizhskii's research contributions include the development of concepts and computational methods implemented in many widely used bioinformatics tools, including PeptideProphet and ProteinProtein, CRAPome, SAINT, DIA-Umpire, MSFragger, and Philosopher. His lab actively collaborates with technology developers, biologists, and clinical scientists. He has served on the Board of Directors for the American Society of Mass Spectrometry (ASMS), US HUPO, and on the Scientific Advisory Board for Swiss Institute of Bioinformatics. At the University of Michigan (UM), Dr. Nesvizhskii directs the NCI-funded T32 Proteome Informatics of Cancer Training Program and the Proteogenomics Data Analysis Center (UM-PGDAC; part of the Clinical Proteomic Tumor Analysis Consortium initiative). He also Directs the Proteomics Resource Facility which provides cutting-edge proteomics capabilities to UM investigators, and the Michigan Compound Identification Development Cores project which focuses on the identification of previously unknown metabolites.

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Software (GitHub): <https://github.com/Nesvilab>