PROMOTION RECOMMENDATION
THE UNIVERSITY OF MICHIGAN
MEDICAL SCHOOL
DEPARTMENT OF PATHOLOGY
DEPARTMENT OF COMPUTATIONAL MEDICINE AND BIOINFORMATICS

Alexey I. Nesvizhskii, Ph.D., associate professor of pathology, with tenure, Department of Pathology, and associate professor of computational medicine and bioinformatics, without tenure, Department of Computational Medicine and Bioinformatics, Medical School, is recommended for promotion to professor of pathology, with tenure, Department of Pathology, and professor of computational medicine and bioinformatics, without tenure, Department of Computational Medicine and Bioinformatics, Medical School.

Academic Degrees:

Ph.D.	2001	University of Washington
M.S.	1995	St. Petersburg State Technical University, St. Petersburg, Russian Federation

Professional Record:

2011-present	Associate Professor of Pathology, University of Michigan
2011-present	Associate Professor of Computational Medicine and Bioinformatics, University of Michigan
2007-2011	Assistant Professor of Computational Medicine and Bioinformatics, University of Michigan
2005-2011	Assistant Professor of Pathology, University of Michigan
2003-2005	Research Scientist, Institute for Systems Biology, Seattle, WA

Summary of Evaluation:
Teaching: Dr. Nesvizhskii has participated in teaching at multiple levels, including didactic, research, administrative, and mentoring of students' and post-doctoral careers. Dr. Nesvizhskii has participated in multiple courses with didactic contributions that have been focused in bioinformatics. His role as a mentor has been quite extensive with multiple undergraduate, graduate, and post-graduate fellows that have participated in research. He has also participated on multiple dissertation committees for graduate students. Finally, Dr. Nesvizhskii participates extensively in clinical teaching of residents and fellows as an important portion of his role on the diagnostic genitourinary pathology service. Attesting to Dr. Nesvizhskii's teaching acumen were his awards that include a Basic Sciences Teaching Award in 2010, induction into the League of Educational Excellence, and the Endowment for Basic Sciences Teaching Award.

Research: Dr. Nesvizhskii's research interests are in the fields of bioinformatics and proteomics, with a focus on the development of computational methods and tools for complex biological datasets. His focus in computational and statistical methods for mass spectrometry-based proteomics, interactome analysis using affinity purification mass spectrometry (AP-MS) technology, proteogenomics, and multi-omics data integration for reconstruction of pathways deregulated in cancer. Protein expression and function are regulated at transcriptional, post-transcriptional, translational, and post-translational (protein-protein interaction and chemical modifications) stages. While genomic technologies capture the first two, the latter can only be characterized by proteomic technology. Dr. Nesvizhskii is internationally recognized for the development of several key algorithms and computational tools enabling proteomics research. The manuscripts describing these methods and tools are among the most cited manuscripts in the field of proteomics, and the computational tools themselves are used by hundreds of laboratories worldwide.

Dr. Nesvizhskii's laboratory remains at the forefront of proteomics and bioinformatics research and continues leading the field by developing new computational algorithms and resources for new and emerging proteomics technologies and applications. His success and importance to the field have resulted in outstanding scholarship, impressive funding, and extensive numbers of speaker opportunities around the world.

Recent and Significant Publications:

Choi H, Larsen B, Lin ZY, Breitkreutz A, Mellacheruvu D, Fermin D, Qin ZS, Tyers M, Gingras C, Nesvizhskii AI: SAINT: probabilistic scoring of affinity purification-mass spectrometry data. *Nat Methods* 8:70-73, 2011.

Mellacheruvu D, Wright Z, Couzens AL, Lambert JP, St-Denis NA, Li T, Miteva YV, Hauri S, Sardiu ME, Low TY, Halim VA, Bagshaw RD, Hubner NC, Al-Hakim A, Bouchard A, Faubert D, Fermin D, Dunham WH, Goudreault M, Lin ZY, Badillo BG, Pawson T, Durocher D, Coulombe B, Aebersold R, Superti-Furga G, Colinge J, Heck AJ, Choi H, Gstaiger M, Mohammed S, Cristea IM, Bennett KL, Washburn MP, Raught B, Ewing RM, Gingras AC, Nesvizhskii AI: The CRAPome: A contaminant repository for affinity purification-mass spectrometry data. *Nat Methods* 10:730-736, 2013.

Nesvizhskii AI: Proteogenomics: concepts, applications and computational strategies. *Nat Methods* 11:1114-1125, 2014.

Tsou CC, Avtonomov D, Larsen B, Tucholska M, Choi H, Gingras AC, Nesvizhskii AI: DIA-Umpire: comprehensive computational framework for data-independent acquisition proteomics. *Nat Methods* 12:258-264, 7 p following 264, 2015.

Balbin OA, Malik R, Dhanasekaran SM, Prensner JR, Cao X, Wu YM, Robinson D, Wang R, Chen G, Beer DG, Nesvizhskii AI, Chinnaiyan AM: The landscape of antisense gene expression in human cancers. *Genome Res* 25:1068-1079, 2015.

Service: Dr. Nesvizhskii has been very active in service for the University of Michigan and for national and international societies. His local service includes Executive Committee for the Center for Computational Medicine and Bioinformatics and graduate student committees (Admission, Curriculum). His national and international service includes program and organizing committees for multiple conferences, membership on the Human Proteome Project, and meeting session organizer. In addition, Dr. Nesvizhskii has participated extensively on grant review panels, on editorial boards for scientific journals, and as a journal reviewer for a large number of journals. He is also currently the principal investigator of the Proteomics Informatics of Cancer training grant that is housed in the Department of Computational Medicine and Bioinformatics. This training grant is funded by the National Cancer Institute and supports students performing graduate cancer-related research and provides training for proteome informatics research.

External Reviewers:

Reviewer A: "Since moving to Ann Arbor, Dr. Nesvizhskii has become one of the most recognized and respected investigators in the field of computational proteomics....he has become well known for developing sophisticated mathematical models, incorporating them into user friendly computational tools, and making them widely accessible to others. Achieving accuracy in protein identification and quantitation are now very simple to do, thanks to Dr. Nesvizhskii and a handful of other labs. The proteomics field has evolved tremendously in the past 15 years, and Dr. Nesvizhskii has been at the forefront of every major new application, developing computational tools to meet the demands of each new technological advance

as it occurs....The field of computational proteomics has benefited enormously from Dr. Nesvizhskii's rigorous work and he is widely regarded as a proteomics pioneer and leader."

Reviewer B: "He is arguably the single most recognizable name in statistical analysis of mass spectrometry data. Going just by the numbers, his work is published in over 120 publications in all of the top journals...His Google scholar h-index is 50, which is not surprising given the impact and importance of his work....I think he should be on the short list of many universities that seek to develop proteomics as a core facility..."

Reviewer C: "I have followed his work with great interest. Not only does he provide real world solutions to the community, but having known him as an individual also I consider him to be someone of the highest integrity....Alexey must be in the top 1-5%."

Reviewer D: "Dr. Nesvizhskii is an outstanding scientist and innovator, a leader in systems biology and bioinformatics, a brilliant and critical thinker, a reliable collaborator, a gentle and thoughtful colleague, and a quiet leader....My feeling is that Alexey could have a transformative impact on our campus. I am sure that he has been a major driver on yours, enabling advanced proteomics to spread across many labs."

Reviewer E: "Any institution in North America would welcome Dr. Nesvizhskii with open arms and considerable support and count themselves lucky....Dr. Nesvizhskii is using analytical bioinformatics and data base mining of proteomics data sets to decipher biological functions. These are notoriously difficult studies to undertake yet his methods lead to results that are incisive. This too is reflected by a large number of international invited talks that further reflect his prestige and standing in the field and incredibly high funding and grant success rate."

Summary of Recommendation:
Dr. Nesvizhskii is an outstanding researcher and computational biologist with many years of expertise in not only proteomics research but in developing new tools and software to analyze and better understand seminal findings. His already outstanding career not only entails top tier scholarship in research, but also includes outstanding mentorship, teaching and service to the University of Michigan and research community. I am pleased to recommend Alexey I. Nesvizhskii, Ph.D. for promotion to professor of pathology, with tenure, Department of Pathology, and professor of computational medicine and bioinformatics, without tenure, Department of Computational Medicine and Bioinformatics, Medical School.

Marschall S. Runge, M.D., Ph.D.
Executive Vice President for Medical Affairs
Dean, Medical School

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