

CURRICULUM VITAE

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Alexey I. Nesvizhskii, Ph.D.

Personal Data

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Current Position

Associate Professor
Department of Pathology
Department of Computational Medicine and Bioinformatics
University of Michigan, Ann Arbor, MI

Education

9/1989 - 6/1995 M.S. Department of Physics and Technology, St. Petersburg State
Technical University, Russia (graduated with honors)
9/1996 - 8/2001 Ph.D. Department of Physics, University of Washington, Seattle,
Washington

Postdoctoral Training

10/2001 - 10/2003 Postdoctoral Fellow, Institute for Systems Biology, Seattle, Washington

Academic and Administrative Appointments

10/2003 - 11/2005 Research Scientist, Institute for Systems Biology, Seattle, Washington
11/2005 - 8/2011 Assistant Professor, Department of Pathology, University of Michigan
12/2007 - 8/2011 Assistant Professor, Center for Computational Medicine and
Bioinformatics, University of Michigan
5/2010 - 12/2011 Associate Director, “Advanced Proteome Informatics of Cancer”, NIH
T32 Training Program at the University of Michigan
9/2011 - present Associate Professor, Department of Pathology, University of Michigan
9/2011 - present Associate Professor, Department of Computational Medicine and
Bioinformatics, University of Michigan
1/2012 - present Director, “Advanced Proteome Informatics of Cancer”, NIH T32 Training
Program at the University of Michigan
1/2008 – present Affiliate Faculty, Michigan Center for Translational Pathology

Research Interests

Bioinformatics; computational biology; systems biology; proteomics; integrative analysis of proteomic, genomic, and metabolomics data; mass spectrometry; statistical modeling and algorithm development; databases, data repositories, and data mining; analysis of protein-protein interactions and networks; cancer biology; protein biomarker discovery; pathology informatics

Grants

Present and Active

1. Principal Investigator, "Computational Tools for Mass Spectrometry Based Interactome Data", National Institutes of Health, R01, 30%, \$1,149,745/4 yr total cost, 09/2010 – 08/2014
2. Principal Investigator, Competing Supplement for "Computational Tools for Mass Spectrometry Based Interactome Data", National Institutes of Health (\$184,233/ 2 yr total), 01/2013 – 08/2014
3. Principal Investigator, "Analysis of Measurement Variability in Mass Spectrometry-based Proteomics", Measurement Science and Engineering (HSE) Research Grant Programs 12012-NIST-MSE-01 (National Institute of Standards and technology), 5%, (\$530,914/5 yr total), 10/2012-09/2017
4. Principal Investigator and Director, "Advanced Proteome Informatics of Cancer", NIH T32 Training grant, 5% salary effort, (\$1,845,243/5 yr total), 09/2010-08/2015
5. Co-Investigator, "Targeting the MLL Transcription Complex in Acute Myelogenous Leukemia", Leukemia and Lymphoma Society of America (PI: Licht), 5%, \$50,000/yr total, 01/2007 – 09/2017
6. Co-Investigator, "Proteomic analysis of api2-MALT1 positive gastric MALT lymphoma" (P.I.: K. Elenitoba-Johnson), National Institutes of Health, R01, 5% (\$1,436,205/5 yr total), 06/2009 – 07/2014
7. Co-Investigator, Michigan Regional Comprehensive Metabolomics Resource Core (MRC2) (PI: C. Burant), 10%, 09/2012-8/2017
8. Co-Investigator, American Society of Hematology (PI: JF Rual) Characterization of the MLL and HoxA9-Regulated Enhanceosome Molecular Networks in Acute Leukemia, 0% (Consultant), 07/2012-06/2015

Completed

1. Principal Investigator, "Analysis and Statistical Validation of Proteomic Datasets", National Institutes of Health, R01, 25%, \$1,248,281.00/5 yr total, 09/2006 – 08/2012
2. Co-Investigator, "Proteomic biomarkers of Alk+ lymphoma" (P.I.: Lim), National Institutes of Health, R01, 5% (\$320,588/yr total), 11/2009 – 10/2013
3. Co-Investigator, "Mass spectrometry-driven systems biologic analysis of salivary MALT lymphoma" (P.I.: Elenitoba-Johnson), National Institutes of Health, R01, 10%, \$250,000.00/yr total (\$1,545,000.00/4 yr total), 07/2008 – 06/2012

4. Co-Investigator, "Multiple Myeloma Proteomics Initiative", Multiple Myeloma Research Foundation (MMRF) (P.I.: Jakubowiak) 5%, \$49,675/year to Nesvizhskii lab, 08/2008 – 07/2011
5. Co-Investigator, "Hdl, Atherosclerosis and Chronic Kidney Disease", Duke, Doris, Charitable Foundation (PI: Pennathur), 5%, \$14,854 total cost to Nesvizhskii lab, 07/2009 – 07/2010
6. Co-investigator, "Integrated Proteome Technologies for Pathway Mapping", NCCR/NIH P41 RR018627 (PI: P. Andrews), 5% effort, \$76,076 total cost to Nesvizhskii lab, 09/2007 - 07/2008
7. Principal Investigator, "Computational Analysis and Development of Statistical Methodology for Validation of Mass Spectrometry-based Protein Identifications Derived Using the Product terminal Isotope Coding Strategy", NIH - Subcontracts sourced funding through the Burnham Institute, 15%, \$114,000 total costs to Nesvizhskii lab, 08/2006 – 07/2008
8. Co-investigator, "Detection of Autoantibody Signature and Early Detection Markers of Colon Cancer", NIH - Subcontracts sourced funding through Fred Hutchinson Cancer Research Center (PI: A. Chinnaiyan), \$19,500 total cost, 12/2006 - 03/2007

Honors and Awards

1994	Medal, "Best Student Scientific Work", awarded by the Russian Federation State Committee of Higher Education
1994	Ioffe Institute of Physics and Technology Prize
1994 - 1995	Russian Presidential Fellow
1995 - 1996	Soros Fellow
2007	Rising Young Investigator by Genome Technology magazine
2010	Basic Sciences Teaching Award, University of Michigan Medical School
2012	Inaugural Member of the League of Educational Excellence, University of Michigan Medical School

Membership in Professional Societies

1996 - 2002	American Physical Society (APS)
2002 - present	Human Proteome Organization (HUPO)
2002 - present	International Society for Computational Biology (ISCB)
2002 - present	American Society for Mass Spectrometry (ASMS)
2006 - 2009	Association of Biomolecular Resource Facilities (ABRF)
2007 - present	American Society for Biochemistry and Molecular Biology (ASBMB)

Editorial Positions, Boards, and Peer-Review Service

Editorial Positions and Boards

2006 – 2008	Member, Editorial Board, <i>Practical Proteomics</i> (Wiley)
2008 - 2011	Section Editor, Journal <i>Amino Acid</i> (Springer)
2009 - present	Senior Editor, Journal <i>PROTEOMICS</i> and its sister journal <i>PROTEOMICS: CLINICAL APPLICATIONS</i> (Wiley)
2009 - present	Member, Editorial Board, <i>Molecular and Cellular Proteomics</i>
2011 - present	Section Editor in the area of proteomics, <i>BMC Bioinformatics</i>
2012	Guest Editor, <i>PROTEOMICS</i> Special Issue on Protein Complexes and Interaction Networks (May 2012)
2013 – present	Member, Editorial Advisory Board, Journal of Proteomics Research

Manuscript Peer-Review

2001 - present	Ad hoc journal reviewer: <i>BMC Genomics, BMC Bioinformatics, Bioinformatics, OMICS, Proteomics, Molecular and Cellular Proteomics, Molecular Systems Biology, Journal of Proteome Research, Journal of Mass Spectrometry, Journal of the American Society for Mass Spectrometry, Rapid Communications in Mass Spectrometry, Trends Guide to Proteomics, Analytical Chemistry, Expert Reviews in Proteomics, Drug Discovery Today, Nature, Nature Biotechnology, Nature Methods, Science</i>
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Grant Review

2003	Member, NIH Special Emphasis Review Panel, NIAID Program, “Bioinformatics Resource Centers for Category A-C pathogens and Emerging/Re-Emerging Infectious Disease”
2003	Member, NIH Special Emphasis Review Panel, NIDCR Program “Molecular Anatomy of Head and Neck Cancer: A genomic/Proteomic Approach”
2004, 2005	Grant Reviewer, Dutch Cancer Society
2006	Grant Reviewer, National Sciences and Engineering Research Council of Canada (NSERC), Strategic Project Program
2007	Member, NIH Special Emphasis Panel ZRR1 BT-B, NCRR, Technology Development for Biomedical Applications
2007	Member, Technology Development Competition Review Panel, Genome Canada
2007	Grant Reviewer, National Science Foundation

2010	Member, ZRG1 IMST-14, the NIH Small Business Computational Biology, Image Processing, and Data Mining Study Section
2010	Member, ZRG1 CB-P 90 Special Topics in Cell Biology Grant Review Panel
2010	Grant reviewer, Foundation for Polish Science, Team Programme
2012	Member (mail reviewer), NIH MSFD review panel
2012	Grant reviewer, The Portuguese Foundation for Science and Technology
2012	Proposal reviewer for AAAS (peer review on behalf of the Indo-US Science & Technology Forum)
2013	Reviewer, The Multiple Sclerosis Society of Canada Annual Grant Competition
2013	Member, NIH Special Emphasis Panel ZRG1-BST-N(40), NIGMS, A Proteomics Research Center for Integrative Biology Review
2014	Member, ZEB1 OSR-F (J1) S Training Applications Review Committee
2014	Reviewer, the National Science and Engineering Research Council of Canada, Discovery Grants Program

Committee and Organizational Service

Institutional (University of Michigan)

2006, 2012	Grant Reviewer, Pilot Research Projects, Center for Computational Biology and Medicine
2006 - 2007	Member, Curriculum Development Committee, Bioinformatics Program
2007 - 2009	Member, Student Admission Committee (Bioinformatics Program)
2007 - present	Interviewer, Candidates for Pathology Resident Program
2007 - 2009	Interviewer, Candidates for Pathology and CCMB Faculty Positions
2008	Member, Research Insensitive Compensation Committee, Department of Pathology
2010, 2011	Member, Center for Computational Medicine and Bioinformatics (CCMB) Faculty Requirement Committee
2011 - present	Member of the Executive Committee, Center for Computational Medicine and Bioinformatics

National/International

2002	Member, Proteomics Standards Initiative, Human Proteome Organization (HUPO)
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2004	Member, Organizing Committee, Peptide Fragmentation and identification Workshop, National Institute of Standards Technology, Maryland
2004	Member, Working Group on Publication Guidelines for Peptide and Protein Identification Data, <i>Journal Molecular and Cellular Proteomics</i>
2006	Member, Program Committee, RECOMB Satellite Conferences on Systems Biology and Computational Proteomics, San Diego, California
2006-2008	Member, Proteome Informatics Research Group, the Association of Biomolecular Research Facilities
2007-2008	Member, Organizing Group, Critical Assessment of Mass Spectrometry-based Identifications Competition (CAMSI)
2010, 2012	Member, Program Committee, RECOMB Satellite Conferences on Computational Proteomics, San Diego, California
2011	Chair, Program Committee, RECOMB Satellite Conferences on Computational Proteomics, San Diego, California
2011	Member, Working group on Data Sharing, Data-Enabled Life Sciences Alliance (DELSA) Workshop, Seattle, Washington
2011-present	Member, Mass Spectrometry Pillar Committee, Human Proteome Project (HPP)
2012-present	Member, Management and Awards Committee, CIHR Training Program in Neurodegenerative Lipidomics, University of Ottawa, Ottawa, Canada
2013	Member, Program Committee, ISMB 2013 Conference, Berlin, Germany
2013-present	Member, Board of Directors, US Human Proteome Organization (US HUPO)

Consulting Positions

2008 - 2009	Member, Scientific Advisory Board, Core Facilities for Proteomics and Glycomics, Taiwan National Research Program in Genomic Medicine, Academia Sinica, Taipei, Taiwan
2011 - present	Member, Scientific Advisory Board, Swiss Institute of Bioinformatics, Lausanne, Switzerland

Teaching Activities

Institutional

1996-1997	Teaching Assistant, Department of Physics, University of Washington
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1998-2001 Grading Assistant, Department of Statistics, University of Washington

2006-2007 Lecturer, Bioinformatics 551 course: Proteome Informatics (cross-listed with Chemistry, Biological Chemistry, Chemical and Biomedical Engineering), University of Michigan (2 lectures/course)

2006-2007 Lecturer, Bioinformatics 527 (2 lectures/course)

2007 Lecturer, Seminar in Cancer Biostatistics, Department of Biostatistics (1 lecture)

2008-2012 Course Master and Primary Instructor, Bioinformatics 551: Proteomics and Informatics course (cross-listed with Pathology, Chemistry, Biological Chemistry, Chemical and Biomedical Engineering), University of Michigan. (3 credit course; 27 lectures). Developed the curriculum; prepared and graded homework, exams, and a term project, selected and coordinated guest speakers

2009 Lecturer, MCDB 408 Genomic Biology (2 lectures)

2009, 2010 Primary Instructor, Bioinformatics 662 Bioinformatics Journal Club (weekly). Suggest publications to students for presentation in class, assist students during preparation, provide formal feedback

2010, 2011, 2013 Lecturer, Bioinformatics 527 (2 lectures)

2010 Lecturer, Chemistry 647: Mass Spectrometry (1 lecture)

2011, 2013 Lecturer, Bioinformatics 528 (2 lectures)

National/International

2002-2009 Instructor, Proteomics Informatics Course. A popular 5 day workshop administered semiannually at the NHLBI Proteomics Center at the Institute for Systems Biology, Seattle (role: one of the original course developers; guest lecturer and hand-on tutorial leader, 6 hour workshop)

2007-2010 NHLBI Genomics and Proteomics Hands-On Workshop: From Sample Preparation to Data Analysis, Denver, Colorado. A 10 day workshop offered annually (role: keynote speaker, guest lecturer, hand-on workshop section leader)

2007 Proteomics and Informatics Workshop, Chicago Biomedical Consortium, Chicago, IL (invited tutorial lecture)

2008 Proteomics Workshop, Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan (invited tutorial lecturer)

2010 Instructor, Proteome Informatics Course at the University of New South Wales, Sydney, Australia (role: lecturer and hand-on tutorial leader on PeptideProphet, iProphet, and ProteinProphet, 8 hour), September 15, 2010

- 2011 Instructor, “Bioinformatics for Proteomics” 2-day short course (4 lectures and 2 panel discussions) organized by the American Society for Mass Spectrometry, Denver, Colorado, Jun4-5, 2011
- 2011 Guest lecture, STAT598C: Statistical Bioinformatics, Department of Statistics, Purdue University, West Lafayette, IN
- 2011 Invited lecturer, Fall School on Systems Biology of Neurodegenerative Disease, CIHR Training Program in Neurodegenerative Lipidomics and the Ottawa Institute of Systems Biology, Ottawa, Canada, October 27, 2011
- 2012 Instructor (with Ileana Cristea, Princeton), “Stable and Transient Protein-Protein Interactions: Discovery, Quantification and Validation”, 4 hour short course at US HUPO Conference, San Francisco, CA, March 4, 2012.
- 2012 Instructor (with David Tabb, Vanderbilt; and Nuno Bandeira, UCSD), "Bioinformatics for Proteomics" 2-day short course at the American Society for Mass Spectrometry annual conference, Vancouver, BC, Canada, June 19-20, 2012
- 2012 Instructor, Cold Spring Harbor Laboratory Course on Proteomics. Taught a 5 hour workshop “Computational Analysis of AP-MS Protein-Protein Interaction D”, Cold Spring Harbor, New York, July 19, 2012
- 2012 Invited lecturer, Summer School on Systems Biology of Neurodegenerative Disease, CIHR Training Program in Neurodegenerative Lipidomics and the Ottawa Institute of Systems Biology, Ottawa, Canada, June 21, 2012
- 2013 Instructor (with Ileana Cristea, Princeton), “Stable and Transient Protein-Protein Interactions: Discovery, Quantification and Validation”, 4 hour short course at US HUPO Conference, Baltimore, MD, March 10, 2013.
- 2013 Instructor (with David Tabb, Vanderbilt; and Nuno Bandeira, UCSD), "Bioinformatics for Proteomics" 2-day short course at the American Society for Mass Spectrometry annual conference, Minneapolis, MN, June 8-9, 2013

Postdoctoral fellows and graduate students

Post doctoral fellows:

- a. Xia Cao, 2006-2009
- b. Kang Ning, 2007-2010
- c. Hyungwon Choi, 2009-2010
- d. Ana Rodriguez, 2009-2010 (visiting scientist)
- e. Scott Walmsley, 2011-present
- f. Dmitry Avtonomov, 2013-present

Graduate Students:

- a. Ying Ding, 2006-2007, Biostatistics (Research Assistant)
- b. Hyungwon Choi, Ph.D. in Biostatistics, 2006-2008 (co-mentored with Steve Qin and Debashis Gosh)
- c. Peter Ulintz, Ph.D. in Bioinformatics, 2005-2008 (co-mentored with Phil Andrews)
- d. Alejandro Balbin, 2010-2013, Ph.D. in Bioinformatics (co-mentored with Arul Chinnaiyan)
- e. Lee Sam, 2010-2013, Ph.D. in Bioinformatics (co-mentored with Arul Chinnaiyan)
- f. Datta Mellacheruvu, 2009-present, Bioinformatics
- g. Avinash Shanmugam, 2010-present, Bioinformatics
- h. Thomas Wolfe, M.S. in Bioinformatics, 2012 (co-mentored with Megan Lim)
- i. Andy Kong, 2012-present, Bioinformatics
- j. Chih-Chiang Tsou, 2012-present, Bioinformatics

Rotation Student:

- a. Yu-Hsuan Lin, Winter 2006, Bioinformatics
- b. Chaitanya Bandlamudi, Spring 2008, Bioinformatics

Ph.D. Thesis committee member:

- a. Damian Fermin, Bioinformatics (graduated 2007)
- b. Jayson Falkner, Bioinformatics (graduated 2008)
- c. Stephanie Joe, Pathology (graduated 2011)
- d. Huy Vuong, Bioinformatics (graduated 2011)
- e. Yan Zhang, Bioinformatics (graduated 2012)
- f. Christian A. Shively, Cellular and Molecular Biology
- g. Di Gao, Chemistry (graduated June 2013)
- h. Brendan Veeneman, Bioinformatics

Preliminary examination committee member:

- a. Dai Lai, Bioinformatics
- b. Jing Lu, Bioinformatics

Invited external Ph. D. Examination Committee Member:

- a. Lennart Martens, Ghent University, Belgium

Visiting Professorships, Seminars and Extramural Invited Presentations

1. Invited seminar, "Analysis of x-ray absorption data", National Synchrotron Radiation Research Center, Taiwan, September 1999
2. Invited seminar, "Analysis of x-ray absorption data", Department of Physics, National Changhua University of Education, Taiwan, September 1999
3. Invited speaker, "Statistical models for proteomics", Proteomics Standards Initiative Meeting, European Bioinformatics Institute, Cambridge, England, October 2002

4. Invited seminar, “Statistical models to estimate the accuracy of protein identifications made by MS/MS and database search”, Oxford Glycosciences, Oxford, England, October 2002
5. Invited speaker, “Bioinformatics challenges of high throughput proteomics”, Systems Biology Workshop, National Yang-Ming University, Taipei, Taiwan, September 2002
6. Invited seminar, “Proteome profiling using mass spectrometry”, Academia Sinica, Taipei, Taiwan, September 2002
7. Invited seminar, “Statistical models for high throughput proteomics”, National Center for Biotechnology Information (NCBI), Bethesda, Maryland, August 2002
8. Invited seminar, “Statistical model to estimate the accuracy of protein identifications using MS/MS and database search”, European Molecular Biology Laboratory, Heidelberg, Germany, May 2003
9. Invited speaker, “Computational tools for high throughput proteomics”, University of Tennessee – Oak Ridge National Laboratory Bioinformatics Summit, Falls Creek Falls State Park, Tennessee, March 29, 2003
10. Invited speaker, “Statistical models for identifying peptides and proteins by tandem mass spectrometry”, Department of Computer Science and Engineering, UC - San Diego, California, January 13, 2003
11. Invited speaker, “Statistical Validation of High-throughput mass spectrometric protein identifications”, CHI’s 2nd Pep Talk – The Protein Information Week, San Diego, California, January 14, 2003
12. Invited speaker, “A novel probability-based method to estimate the accuracy of high throughput protein identifications made by MS/MS and database search”, ABRF Meeting: Translating Biology Using Proteomics and Functional Genomics, Denver, Colorado, February 13, 2003
13. Invited speaker, “Protein identification using MS/MS spectra: sequence database searching and validation”, 1st Pacific-Rim International Conference on Protein Science, Yokohama, Japan, April 18, 2004
14. Invited speaker, “Analysis, statistical validation, and dissemination of large scale proteomics datasets”, Peptide Fragmentation and Identification Workshop, Gaithersburg, Maryland, May 4, 2004
15. Invited speaker and round table discussion leader, “Top ten challenges in proteomics: Proteome informatics”, Beyond Genome 2004, San Francisco, California, June 23, 2004
16. Invited seminar, “High throughput proteomics: computational challenges and solutions”, Biogen Idec, Cambridge, Massachusetts, August 2004.
17. Invited seminar, “High throughput proteomics: computational challenges and solutions”, Broad Institute of Harvard and MIT, Boston, Massachusetts, October 2004
18. Invited seminar, “High throughput proteomics: computational challenges and solutions”, Department of Biostatistics, Bioinformatics, and Epidemiology, Medical University of South Carolina, Charleston, South Carolina, October 11, 2004

19. Invited seminar, "Computational challenges of proteomics: from protein identification to biological interpretation", McGill University, Department of Biomedical Engineering, Montreal, Canada, December 14, 2004.
20. Invited speaker, "Statistical validation of database search results", NIH Workshop Standards in Proteomics, Bethesda, Maryland, January 4, 2005
21. Invited speaker, "Analysis and statistical validation of shotgun proteomic datasets", Computational Proteomics and Mass Spectrometry Workshop, Mathematical Biosciences Institute, Ohio State University, Columbus, Ohio, January 13, 2005
22. Invited seminar, "Bioinformatics and applications in proteomics", University of Colorado Health Sciences Center, Denver, Colorado, May 24, 2005
23. Invited seminar, "Computational challenges of proteomics: from protein identification to biological interpretation", University of Southern California, Department of Molecular and Computational Biology, Los Angeles, CA, March 3, 2005
24. Invited speaker, "Computational challenges of proteomics: from protein identification to biological interpretation", Bioinformatics 2005 Conference, Tartu, Estonia, June 12, 2005
25. Invited speaker, "Current protein mixtures and standards in proteomics", Standards, Methods, Assays, Reagents and Technologies (SMART) For Early Cancer Detection and Diagnosis, a National Institute of Standards and Technology (NIST) and the Early Detection Research Network Joint Workshop, NIST, Gaithersburg, Maryland, August, 2005
26. Invited speaker and instructor, "The protein inference with ProteinProphet", Proteomics Software Course at the Institute for Systems Biology, Seattle, WA, February, 2006
27. Invited seminar, "Computational analysis of proteomic data", Faculty of Medicine and Health Sciences, Ghent University, Rommelaere Institute, Ghent, Belgium, June, 2006
28. Invited speaker, "Interpretation of quantitative shotgun proteomic data", Beyond Genome 2006 Conference, San Francisco, CA, June, 2006
29. Invited panel discussant, Measurement Challenges in Proteomics Workshop, organized by the National Institute of Standards and Technology, Boston, MA, March, 2006
30. Invited panel discussant, HUPO Plasma Proteome Initiative Workshop, Long Beach, California, October 29th, 2006
31. Invited speaker and instructor, "The protein inference with ProteinProphet", Proteomics Software Course at the Institute for Systems Biology, Seattle, WA, October 12th 2006; May 7th 2007
32. Invited speaker, "Interpretation of shotgun proteomic data", Protein Biomarkers 2006 Conference, Philadelphia, PA, November 16th, 2006
33. Invited speaker, "Analysis and statistical validation of proteomic datasets", AACR Special Conference in Cancer Research: Advances in Proteomics in Cancer Research, Amelia Island, Florida, March 2, 2007

34. Invited speaker and panel discussant, "Error rates in peptide and protein identification analysis", Statistical Proteomics Workshop, US HUPO Annual Meeting, Seattle, Washington, March 8th, 2007
35. Invited speaker, "Methods for quality assessment of MS/MS spectra", NIH Mouse Proteomic Technologies Initiative and CPTAC Team Meeting, Seattle, Washington, March 9, 2007
36. Invited seminar, "Computational analysis of large scale proteomics datasets", Department of Biochemistry, University of Colorado, Boulder, Colorado, July 25, 2007
37. Invited seminar, "Computational analysis of shotgun proteomic data", Stowers Institute for Medical Research, Kansas City, Missouri, November 13, 2007
38. Invited seminar, "Computational analysis of proteomic data generated using tandem mass spectrometry", Samuel Lunenfeld Research Institute, Toronto, Canada, November 5, 2007
39. Invited speaker, "Assigning confidence to peptide identifications", NCI/NIST Workshop for Next-Generation Methods of Peptide Identification, National Institute of Standards and Technology, Gaithersburg, Maryland, November 15, 2007
40. Invited panel discussant, Statistical Proteomics Workshop, US HUPO Annual Meeting, Bethesda, Maryland, March 17, 2008
41. Invited speaker, "Computational tools and statistical models for proteomic data validation", Proteomics Workshop, Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan, April 17, 2008
42. Invited speaker and instructor, Genomics and Proteomics Hand-on Workshop, University of Colorado Health Sciences Center and National Jewish Medical and Research Center", Denver, Colorado, July 31-August 1, 2008
43. Invited speaker, "Challenges in release and sharing of mass spectrometry data", International Proteomics Data Release and Sharing Policy Summit, Amsterdam, The Netherlands, Aug 14, 2008
44. Invited speaker, "How to analyze data and how to make the data accessible and exchangeable efficiently", Model Organisms Workshop, Human Proteome Initiative (HUPO), Amsterdam, The Netherlands, Aug 16, 2008
45. Invited speaker, "Significance analysis of spectral count data", Protein Biomarkers Conference, Philadelphia, PA, September 29, 2008
46. Invited seminar, "Analysis of protein complexes using label-free mass spectrometry-based proteomics", University of Iowa, Iowa City, December 2, 2008
47. Invited speaker, "Comparison and optimization of mass spectrometric and bioinformatics strategies for phosphopeptide identification", Pittcon Conference, Chicago, March 12, 2009
48. Invited instructor, "Protein inference using ProteinProphet", Proteome Informatics Course, Institute for Systems Biology, Seattle, Washington, April 29, 2009

49. Invited speaker, “Computational tools for AP/MS protein interaction data”, HUPO World Congress, Toronto, Canada, September 30, 2009
50. Invited speaker, “Computational methods for AP/MS protein interaction data”, Understanding Protein Complexes, Networks and the Interactome Workshop, Case Western Reserve University, Cleveland, OH, October 19, 2009
51. Invited speaker, “Analysis and statistical validation of large proteomic datasets”, Quantitative Model Organisms Workshop, University of Zurich, Zurich, Switzerland, October 30, 2009
52. Invited speaker, “Analysis and statistical validation of large proteomic datasets”, Computational Proteomics Workshop, Institute of Molecular and Cell Biology, Biopolis, Singapore, December 2, 2009
53. Invited speaker, “Experimental and computational strategies in quantitative proteomics”, Annual American Society for Mass Spectrometry (ASMS) conference, Salt Lake City, UT, May 25, 2010
54. Invited presenter, Computational Mass Spectrometry/Bioinformatics Interest Group Meeting, Salt Lake City, UT, May 25, 2010
55. Invited lecturer, 2 lectures: “Assessment of peptide level error rates” “Mapping peptides to proteins”. MaxQuant Summer School course on “Computational mass spectrometry-based proteomics – Quantitative proteomics applied to life sciences and systems biology“, Max-Planck-Institute of Biochemistry in Martinsried, Germany, June 13-14 2010
56. Invited speaker, “Mass spectrometry-based label free quantitative proteomics”, Institute of Information Sciences, Academia Sinica, Taipei, Taiwan, September 7, 2010
57. Presenter (together with Hyungwon Choi), Mini-workshop on statistical analysis of AP-MS protein interaction data, Samuel Lunenfeld Research Institute, Toronto, Canada, October 14, 2010
58. Invited speaker, “Analysis of protein complexes and interaction networks using mass spectrometry-based label free quantitative proteomics”, Randolph Cancer Center, West Virginia University, Morgantown, WV, October 27, 2010
59. Invited speaker, “Computational analysis of MS/MS database search results”, 2011 ASMS Sanibel Conference “From Fragmentation Mechanisms to Sequencing: Tandem Mass Spectrometry Based Peptide and Protein Identification”, San Pete Beach, Florida, January 23, 2011
60. Invited speaker, “Computational analysis of AP/MS protein-protein interaction data”, US HUPO Annual Meeting, Raleigh, North Carolina, March 21, 2011
61. Invited speaker, “Probabilistic approaches for integrating peptide identifications from multiple database search engines”, Institute of Information Sciences, Academia Sinica, Taipei, Taiwan, April 26, 2011
62. Invited speaker, “Label-free quantitative proteomics: methods and applications”, 2011 Translational Medicine Conference and Taiwan Proteomics Society Annual Symposium, Taipei, Taiwan, April 28, 2011

63. Invited speaker, “Mass Spectrometry-Based Label-Free Quantitative Proteomics: Methods and Applications”, Department of Biochemistry and Molecular Biology, Indiana University School of Medicine, Indianapolis, May 9, 2011
64. Invited speaker, “Computational analysis of AP/MS protein-protein interaction data”, Bioinformatics Program, University of Kansas, Lawrence, Kansas, September 13, 2011
65. Invited speaker, “Label-free quantitative proteomics: methods and application”, Department of Statistics, Purdue University, West Lafayette, Indiana, October 25, 2011
66. Invited speaker, “Label-free quantitative proteomics: methods and applications”, University of Washington, Seattle, Washington, November 17, 2011
67. Invited speaker, “Analysis of Protein Complexes and Interaction Networks using Label-free Mass Spectrometry-based Proteomics”, Institute for Systems Biology, Seattle, WA, November 18, 2011
68. Invited Speaker, “Proteomic Data Analysis and Data Sharing”, Proteome Exchange Annual Meeting, San Diego, CA, March 15, 2012
69. Invited Speaker, “Computational Analysis and Comparison of Continuous and Count-Based Label-Free Quantitative Proteomic Data”, International Symposium of the Association of the Biomedical Research Facilities (ABRF 2012), Orlando, Florida, March 18, 2012
70. Invited Speaker, “Computational Analysis of Label-free Proteomic Data and Comparison of Different Quantification Strategies”, Mass Spectrometry Special Interest Group, ISMB 2012 Conference, Long Beach, California, July 14, 2012
71. Invited speaker, “Mass spectrometry-based proteomics and its applications in biomedical research”, National Cheng Kung University, Tainan, Taiwan, December 13, 2012
72. Invited speaker, “How to Generate High Quality Protein Interaction Maps”, International Symposium of the Association of the Biomedical Research Facilities (ABRF 2013), Palm Springs, California, March 4, 2013
73. Invited speaker, “Label-free quantitative proteomics and applications in cancer research”, International Symposium Membrane Proteins: Functions, Structures, and Diseases, Academia Sinica, Taipei, Taiwan, May 22, 2013
74. Invited speaker, “Combined proteome and transcriptome analysis: methods and applications, 2013 Taiwan Proteomics Society International Conference: Recent Advances in Translational Medicine, Taipei, Taiwan, May 24, 2013
75. Invited speaker, “Combined proteome and transcriptome analysis: methods and applications”, Scientific Meeting for the Chromosome-centric Human Proteome Project, St. Petersburg, Russia, July 11, 2013
76. Invited speaker, “ Mass spectrometry and bioinformatics”, Fifth International Conference-School “Fundamental issues of mass spectrometry and its analytical application”, St. Petersburg, Russia, July 14, 2013

Conference presentations (contributed oral presentation) and NIH progress report workshops

1. Annual Meeting of the American Physical Society, Minneapolis, MN, March 2000
2. Annual Meeting of the American Physical Society, Seattle, Washington, March 2001
3. 50th ASMS Conference, Orlando, Florida, June 2002
4. HUPO 1st World Congress, Versailles, France, November 2003
5. 2nd NHLBI Proteomics Initiative Investigators Meeting, Gaithersburg, Maryland, 2003
6. 1st Annual Clinical Proteomic Technologies for Cancer Meeting, National Cancer Institute, Washington DC, October 2007
7. 2nd Annual Clinical Proteomic Technologies for Cancer Meeting, National Cancer Institute, Boston, MD, October 2008
8. 3rd Annual Clinical Proteomic Technologies for Cancer Meeting, National Cancer Institute, Washington DC, October 2009
9. “Comparative analysis of different label-free MS-based protein quantification methods”, HUPO 8st World Congress, Sydney, Australia, September 21 2010
10. “Computational methods for modeling AP/MS protein-protein interaction data”, Moscow Conference on Computational Molecular Biology (MCCMB'11), Moscow, Russia, July 23 2011.
11. “QPROT: a computational tool for label-free differential expression analysis using spectral count and intensity data”, Annual ASMS Conference, Vancouver, Canada, May 22, 2012
12. “The utility of prior information such as GPMdb frequency and RNA-Seq transcript abundance for improved protein identification in shotgun proteomics, Annual ASMS Conference, Minneapolis, MN, June 12, 2013

Institutional Invited Presentations

1. “Computational analysis of quantitative mass spectrometry-based proteomic data”, Fall Term 2006 Kick-Off Event, Bioinformatics Program, University of Michigan, Ann Arbor, September 6th, 2006
2. “Mass spectrometry-based proteomics and bioinformatics”, 5th Annual Pathology Research Symposium, Department of Pathology, University of Michigan, Ann Arbor, November 10th, 2006
3. “Analysis and statistical validation of shotgun proteomics datasets”, Bioinformatics Workshop, Department of Biostatistics, University of Michigan, 2 February, 2007

Bibliography

Peer Reviewed Publications

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