

JIMMY K. ENG

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WORK EXPERIENCE

Software Engineer
UW Proteomics Resource and Dept. of Genome Sciences
University of Washington
Seattle, WA

07/2007 to present

- Software engineer at the Proteomics Resource focusing on algorithms development, software tools, and data analysis.
- Collaborate with Proteomics Resource users, various research labs, and the global proteomics community.

Staff Scientist
Public Health Sciences
Fred Hutchinson Cancer Research Center
Seattle, WA

05/2004 to 07/2007

- Member of the Computational Proteomics Laboratory of Dr. Martin McIntosh.
- Collaborate on primary research with scientists focused on the Early Detection of Cancer initiative.
- Develop software tools and compute environment for proteomics analysis.
- Participate in cross institute projects collating mass spectrometry data and performing data analysis.
- Supervised software developers and research scientists.

Senior Software Engineer
Institute for Systems Biology
Seattle, WA

01/2000 to 05/2004

- Member of the proteomics group of Dr. Ruedi Aebersold.
- Primary focus on research and development of software tools, applications, and compute systems for automated, high throughput, quantitative proteomics. This includes the Sashimi SourceForge project and the Trans-Proteomic Pipeline.
- Interface with proteomics core, scientists in proteomics research lab, ISB staff, and external collaborators.

Software Engineer
Research Consultant
Dept. of Molecular Biotechnology
University of Washington
Seattle, WA

06/1997 to 12/1999
07/1993 to 06/1997

- Member of the Biological Mass Spectrometry Laboratory of Dr. John Yates, III.
- Primary focus on research and development of proteomics software.
- Developed SEQUEST, a commercially licensed software program which performs automated protein sequencing by correlating tandem mass spectral data to amino acid sequences in protein and nucleotide databases.
- Created an HTML/CGI package of web tools and related support programs to facilitate mass spectral data analysis with point-and-click access to internal and external data analysis tools.
- Developed a distributed processing version of SEQUEST which performs parallel database searching using the Parallel Virtual Machine (PVM) software. Configured as a single master, multiple slave virtual machine ... features include concurrent, multiple, heterogeneous workstation support and automatic load sharing.
- Assembled a dedicated cluster of Digital Alpha workstations as a high performance Beowulf compute server for parallel, distributed database searching.
- UNIX, DOS/Windows, Macintosh systems administration including hardware, software, and network evaluation, installation, configuration, backup, maintenance, and support.
- Supervised undergraduate, assistant software developers.

EDUCATION

Master of Science in Electrical Engineering
University of Washington, Seattle, WA

- Primary focus included signal processing, neural networks, speech recognition, and expert systems.
- Masters project involved programming, training, and testing a neural network in the application of speech recognition.

Bachelor of Science in Electrical Engineering
University of Washington, Seattle, WA
Baccalaureate Honors: Cum Laude

HONORS, AWARDS, PATENTS

- US Human Proteome Organization (HUPO) Gilbert S. Omenn Computational Proteomics Award, 2020
- Phi Beta Kappa National Honor Society, member 1991
- Eta Kappa Nu Electrical Engineering Honor Society, member 1989
- University of Washington Undergraduate Merit Scholarship, 1987
- University of Washington Certificate of High Scholarship, 1986
- Nellie Martin Carmen Scholarship, 1986-1990
- United States Patent 5,538,897
 - Title: "Use of Mass Spectrometry Fragmentation Patterns of Peptides to Identify Amino Acid Sequences in Databases"
 - Assignee: University of Washington
 - Inventors: John R. Yates, III and Jimmy K. Eng
 - Date Issued: 07/23/1996
- United States Patent 6,017,693
 - Title: "Identification of nucleotides, amino acids, or carbohydrates by mass spectrometry"
 - Assignee: University of Washington
 - Inventors: John R. Yates, III and Jimmy K. Eng
 - Date Issued: 01/25/2000
- European Patent EP1239288
 - Title: "Identification of nucleotides, amino acids, or carbohydrates by mass spectrometry"
 - Applicant: University of Washington
 - Inventors: Eng, Link, Yates
 - Publication Date: 09/11/2002

COMPUTING & AFFILIATIONS

- Programming: C, C++
- Operating Systems: Linux, Windows
- Training:
 - Introduction to ORACLE: SQL and PL/SQL Using Procedure Builder, 1/24/97
 - ORACLE7 Database Administration, 1/17/97
 - SANS 1997: UNIX and NT Security and JAVA programming, 4/20/97-4/26/97
- US HUPO Open Source Committee, Associate Chair for Implementation, 2004-2006

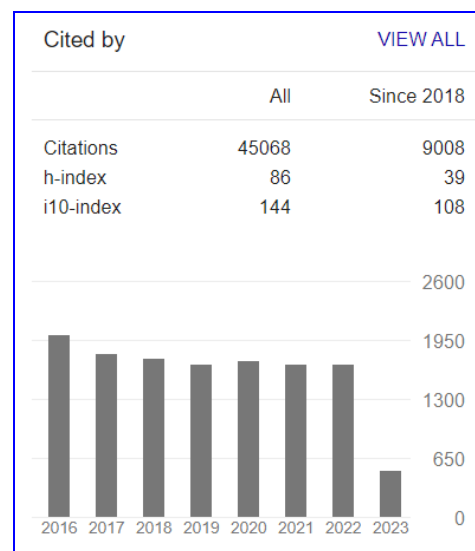
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PUBLICATIONS

1. Trans-Proteomic Pipeline: Robust Mass Spectrometry-Based Proteomics Data Analysis Suite. Deutsch EW, Mendoza L, Shteynberg DD, Hoopmann MR, Sun Z, Eng JK, Moritz RL. *J Proteome Res.* 2023 Feb 3;22(2):615-624. doi: 10.1021/acs.jproteome.2c00624. Epub 2023 Jan 17.
2. The Crux Toolkit for Analysis of Bottom-Up Tandem Mass Spectrometry Proteomics Data. Kertesz-Farkas A, Nii Adoquaye Acquaye FL, Bhimani K, Eng JK, Fondrie WE, Grant C, Hoopmann MR, Lin A, Lu YY, Moritz RL, MacCoss MJ, Noble WS. *J Proteome Res.* 2023 Feb 3;22(2):561-569. doi: 10.1021/acs.jproteome.2c00615. Epub 2023 Jan 4.
3. Coisolation of Peptide Pairs for Peptide Identification and MS/MS-Based Quantification. Smith IR, Eng JK, Barente AS, Hogrebe A, Llovet A, Rodriguez-Mias RA, Villén J. *Anal Chem.* 2022 Nov 8;94(44):15198-15206. doi: 10.1021/acs.analchem.2c01711. Epub 2022 Oct 28.
4. HCN Channel Phosphorylation Sites Mapped by Mass Spectrometry in Human Epilepsy Patients and in an Animal Model of Temporal Lobe Epilepsy. Concepcion FA, Khan MN, Ju Wang JD, Wei AD, Ojemann JG, Ko AL, Shi Y, Eng JK, Ramirez JM, Poolos NP. *Neuroscience.* 2021 Apr 15;460:13-30. doi: 10.1016/j.neuroscience.2021.01.038. Epub 2021 Feb 9.
5. Systemic Proteome Alterations Linked to Early Stage Pancreatic Cancer in Diabetic Patients. Peng H, Pan S, Yan Y, Brand RE, Petersen GM, Chari ST, Lai LA, Eng JK, Brentnall TA, Chen R. *Cancers (Basel).* 2020 Jun 11;12(6):1534. doi: 10.3390/cancers12061534.
6. Full-featured, real-time database searching platform enables fast and accurate multiplexed quantitative proteomics. Schweppe DK, Eng JK, Yu Q, Bailey D, Rad R, Navarrete-Perea J, Huttlin EL, Erickson BK, Paulo JA, Gygi SP. *J Proteome Res.* 2020 May 1;19(5):2026-2034. doi: 10.1021/acs.jproteome.9b00860. Epub 2020 Apr 6.
7. Extending Comet for global amino acid variant and post-translational modification analysis using the PSI extended FASTA format (PEFF). Eng JK, Deutsch EW. *Proteomics.* 2020 Nov;20(21-22):e1900362. doi: 10.1002/pmic.201900362. Epub 2020 Apr 2..
8. In Vivo Cross-Linking MS Reveals Conservation in OmpA Linkage to Different Classes of β -Lactamase Enzymes. Zhong X, Wu X, Schweppe DK, Chavez JD, Mathay M, Eng JK, Keller A, Bruce JE. *J Am Soc Mass Spectrom.* 2020 Feb 5;31(2):190-195. doi: 10.1021/jasms.9b00021. Epub 2019 Nov 21.
9. Predictive proteomic signatures for response of pancreatic cancer patients receiving chemotherapy. Peng H, Chen R, Brentnall TA, Eng JK, Picozzi VJ, Pan S. *Clin Proteomics.* 2019 Jul 17;16:31. doi: 10.1186/s12014-019-9251-3. eCollection 2019.
10. Proteomics Standards Initiative Extended FASTA Format. Binz PA, Shofstahl J, Vizcaíno JA, Barsnes H, Chalkley RJ, Menschaert G, Alpi E, Clauser K, Eng JK, Lane L, Seymour SL, Sánchez LFH, Mayer G, Eisenacher M, Perez-Riverol Y, Kapp EA, Mendoza L, Baker PR, Collins A, Van Den Bossche T, Deutsch EW. *J Proteome Res.* 2019 Jun 7;18(6):2686-2692. doi: 10.1021/acs.jproteome.9b00064. Epub 2019 May 23.
11. In Vivo Proteome of *Pseudomonas aeruginosa* in Airways of Cystic Fibrosis Patients. Wu X, Siehnel RJ, Garudathri J, Staudinger BJ, Hisert KB, Ozer EA, Hauser AR, Eng JK, Manoil C, Singh PK, Bruce JE. *J Proteome Res.* 2019 Jun 7;18(6):2601-2612. doi: 10.1021/acs.jproteome.9b00122. Epub 2019 May 22.
12. A Tandem Mass Spectrometry Sequence Database Search Method for Identification of O-Fucosylated Proteins by Mass Spectrometry. Swearingen KE, Eng JK, Shteynberg D, Vigdorovich V, Springer TA, Mendoza L, Sather DN, Deutsch EW, Kappe SHI, Moritz RL. *J Proteome Res.* 2019 Feb 1;18(2):652-663. doi: 10.1021/acs.jproteome.8b00638. Epub 2018 Dec 21.
13. Tools for 3D Interactome Visualization. Keller A, Chavez JD, Eng JK, Thornton Z, Bruce JE. *J Proteome Res.* 2019 Feb 1;18(2):753-758. doi: 10.1021/acs.jproteome.8b00703. Epub 2018 Dec 18.



14. Bifunctional Immunity Proteins Protect Bacteria against FtsZ-Targeting ADP-Ribosylating Toxins. Ting SY, Bosch DE, Mangiameli SM, Radey MC, Huang S, Park YJ, Kelly KA, Filip SK, Goo YA, Eng JK, Allaire M, Veesler D, Wiggins PA, Peterson SB, Mougous JD. *Cell*. 2018 Nov 15;175(5):1380-1392.e14. doi: 10.1016/j.cell.2018.09.037. Epub 2018 Oct 18.
15. Mango: A General Tool for Collision Induced Dissociation-Cleavable Cross-Linked Peptide Identification. Mohr JP, Perumalla P, Chavez JD, Eng JK, Bruce JE. *Anal Chem*. 2018 May 15;90(10):6028-6034. doi: 10.1021/acs.analchem.7b04991. Epub 2018 Apr 27.
16. Sipros Ensemble improves database searching and filtering for complex metaproteomics. Guo X, Li Z, Yao Q, Mueller RS, Eng JK, Tabb DL, Hervey WJ 4th, Pan C. *Bioinformatics*. 2018 Mar 1;34(5):795-802. doi: 10.1093/bioinformatics/btx601.
17. Extracellular Matrix Proteins Mediate HIV-1 gp120 Interactions with α 4 β 7. Plotnik D, Guo W, Cleveland B, von Haller P, Eng JK, Guttman M, Lee KK, Arthos J, Hu SL. *J Virol*. 2017 Oct 13;91(21). pii: e01005-17. doi: 10.1128/JVI.01005-17. Print 2017 Nov 1.
18. Large-Scale and Targeted Quantitative Cross-Linking MS Using Isotope-Labeled Protein Interaction Reporter (PIR) Cross-Linkers. Zhong X, Navare AT, Chavez JD, Eng JK, Schweppe DK, Bruce JE. *J Proteome Res*. 2017 Feb 3;16(2):720-727. doi: 10.1021/acs.jproteome.6b00752. Epub 2016 Nov 30.
19. A General Method for Targeted Quantitative Cross-Linking Mass Spectrometry. Chavez JD, Eng JK, Schweppe DK, Cilia M, Rivera K, Zhong X, Wu X, Allen T, Khurgel M, Kumar A, Lampropoulos A, Larsson M, Maity S, Morozov Y, Pathmasiri W, Perez-Neut M, Pineyro-Ruiz C, Polina E, Post S, Rider M, Tokmina-Roszyk D, Tyson K, Vieira Parrine Sant'Ana D, Bruce JE. *PLoS One*. 2016 Dec 20;11(12):e0167547. doi: 10.1371/journal.pone.0167547. eCollection 2016.
20. Quantitative Proteomics Based on Optimized Data-Independent Acquisition in Plasma Analysis. Nigjeh EN, Chen R, Brand RE, Petersen GM, Chari ST, von Haller PD, Eng JK, Feng Z, Yan Q, Brentnall TA, Pan S. *J Proteome Res*. 2017 Feb 3;16(2):665-676. doi: 10.1021/acs.jproteome.6b00727. Epub 2017 Jan 3.
21. In vivo protein interaction network analysis reveals porin-localized antibiotic inactivation in *Acinetobacter baumannii* strain AB5075. Wu X, Chavez JD, Schweppe DK, Zheng C, Weisbrod CR, Eng JK, Murali A, Lee SA, Ramage E, Gallagher LA, Kulasekara HD, Edrozo ME, Kamischke CN, Brittnacher MJ, Miller SI, Singh PK, Manoil C, Bruce JE. *Nat Commun*. 2016 Nov 11;7:13414. doi: 10.1038/ncomms13414.
22. In Vivo Conformational Dynamics of Hsp90 and Its Interactors. Chavez JD, Schweppe DK, Eng JK, Bruce JE. *Cell Chem Biol*. 2016 Jun 23;23(6):716-26. doi: 10.1016/j.chembiol.2016.05.012.
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24. Spectral library searching to identify crosslinked peptides. Schweppe DK, Chavez JD, Navare AT, Wu X, Ruiz B, Eng JK, Lam H, Bruce JE. *J Proteome Res*. 2016 Sep 1;32(17):2716-8. doi: 10.1093/bioinformatics/btw232. Epub 2016 Apr 29.
25. Visualization of Host-Poliovirus Interaction Topologies Using Protein Interaction Reporter Technology. DeBlasio SL, Chavez JD, Alexander MM, Ramsey J, Eng JK, Mahoney J, Gray SM, Bruce JE, Cilia M. *J Virol*. 2015 Dec 9;90(4):1973-87. doi: 10.1128/JVI.01706-15.
26. Quantitative interactome analysis reveals a chemoresistant edgotype. Chavez JD, Schweppe DK, Eng JK, Zheng C, Taipale A, Zhang Y, Takara K, Bruce JE. *Nat Commun*. 2015 Aug 3;6:7928. doi: 10.1038/ncomms8928.
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28. A deeper look into Comet--implementation and features. Eng JK, Hoopmann MR, Jahan TA, Egertson JD, Noble WS, MacCoss MJ. *J Am Soc Mass Spectrom*. 2015 Nov;26(11):1865-74. doi: 10.1007/s13361-015-1179-x. Epub 2015 Jun 27.
29. Dynamic Proteome Response of *Pseudomonas aeruginosa* to Tobramycin Antibiotic Treatment. Wu X, Held K, Zheng C, Staudinger BJ, Chavez JD, Weisbrod CR, Eng JK, Singh PK, Manoil C, Bruce JE. *Mol Cell Proteomics*. 2015 Aug;14(8):2126-37. doi: 10.1074/mcp.M115.050161. Epub 2015 May 27.
30. Probing the protein interaction network of *Pseudomonas aeruginosa* cells by chemical cross-linking mass spectrometry. Navare AT, Chavez JD, Zheng C, Weisbrod CR, Eng JK, Siehnell R, Singh PK, Manoil C, Bruce JE. *Structure*. 2015 Apr 7;23(4):762-73. doi: 10.1016/j.str.2015.01.022. Epub 2015 Mar 19.
31. Crux: Rapid Open Source Protein Tandem Mass Spectrometry Analysis. McIlwain S, Tamura K, Kertesz-Farkas A, Grant CE, Diament B, Frewen B, Howbert JJ, Hoopmann MR, Käll L, Eng JK, MacCoss MJ, Noble WS. *J Proteome Res*. 2014 Oct 3;13(10):4488-91. doi: 10.1021/pr500741y. Epub 2014 Sep 9.

32. Protein Kinase PKN1 represses Wnt/beta-catenin signaling in human melanoma cells. James RG, Bosch KA, Kulikauskas RM, Yang PT, Robin NC, Toroni RA, Biechele TL, Berndt JD, von Haller PD, Eng JK, Wolf-Yadlin A, Chien AJ, Moon RT. *J Biol Chem*. 2013 Nov 29;288(48):34658-70. doi: 10.1074/jbc.M113.500314. Epub 2013 Oct 10.
33. Protein interactions, post-translational modifications and topologies in human cells. Chavez JD1, Weisbrod CR, Zheng C, Eng JK, Bruce JE. *Mol Cell Proteomics*. 2013 May;12(5):1451-67. doi: 10.1074/mcp.M112.024497. Epub 2013 Jan 25.
34. In Vivo Protein Interaction Network Identified with a Novel Real-Time Cross-Linked Peptide Identification Strategy. Weisbrod CR, Chavez JD, Eng JK, Yang L, Zheng C, Bruce JE. *J Proteome Res*. 2013 Apr 5;12(4):1569-79. doi: 10.1021/pr3011638. Epub 2013 Feb 28.
35. XLink-DB: Database and Software Tools for Storing and Visualizing Protein Interaction Topology Data. Zheng C, Weisbrod CR, Chavez JD, Eng JK, Sharma V, Wu X, Bruce JE. *J Proteome Res*. 2013 Apr 5;12(4):1989-95. doi: 10.1021/pr301162j. Epub 2013 Mar 5.
36. Systematic measurement of transcription factor-DNA interactions by targeted mass spectrometry identifies candidate gene regulatory proteins. Mirzaei H, Knijnenburg TA, Kim B, Robinson M, Picotti P, Carter GW, Li S, Dilworth DJ, Eng JK, Aitchison JD, Shmulevich I, Galitski T, Aebersold R, Ranish J. *Proc Natl Acad Sci U S A*. 2013 Feb 26;110(9):3645-50. doi: 10.1073/pnas.1216918110. Epub 2013 Feb 6.
37. Comet: an open source tandem mass spectrometry sequence database search tool. Eng JK, Jahan TA, Hoopmann MR. *Proteomics*. 2013 Jan;13(1):22-4. doi: 10.1002/pmic.201200439. Epub 2012 Dec 4.
38. A likelihood-based scoring method for peptide identification using mass spectrometry. Li Q, Eng JK, Stephens M. *Ann Appl Stat*. 2012. Vol. 6, No. 4, 1775-1794, DOI: 10.1214/12-AOAS568.
39. De novo correction of mass measurement error in low resolution tandem MS spectra for shotgun proteomics. Egertson JD, Eng JK, Bereman MS, Hsieh EJ, Merrihew GE, Maccoss MJ. *J Am Soc Mass Spectrom*. 2012 Dec;23(12):2075-82. doi: 10.1007/s13361-012-0482-z. Epub 2012 Sep 25.
40. A mass spectrometry proteomics data management platform. Sharma V, Eng JK, Maccoss MJ, Riffle M. *Mol Cell Proteomics*. 2012 Sep;11(9):824-31. Epub 2012 May 18.
41. Cross-linking measurements of the potato leafroll virus reveal protein interaction topologies required for virion stability, aphid transmission, and virus-plant interactions. Chavez JD, Cilia M, Weisbrod CR, Ju HJ, Eng JK, Gray SM, Bruce JE. *J Proteome Res*. 2012 May 4;11(5):2968-81. Epub 2012 Mar 30.
42. Accurate peptide fragment mass analysis: multiplexed peptide identification and quantification. Weisbrod CR, Eng JK, Hoopmann MR, Baker T, Bruce JE. *J Proteome Res*. 2012 Mar 2;11(3):1621-32. Epub 2012 Feb 21.
43. In vivo application of photocleavable protein interaction reporter technology. Yang L, Zheng C, Weisbrod CR, Tang X, Munske GR, Hoopmann MR, Eng JK, Bruce JE. *J Proteome Res*. 2012 Feb 3;11(2):1027-41. Epub 2012 Jan 9.
44. Sites of ubiquitin attachment in *Saccharomyces cerevisiae*. Starita LM, Lo RS, Eng JK, von Haller PD, Fields S. *Proteomics*. 2012 Jan;12(2):236-40. doi: 10.1002/pmic.201100166. Epub 2011 Dec 20.
45. iProphet: Multi-level integrative analysis of shotgun proteomic data improves peptide and protein identification rates and error estimates. Shteynberg D, Deutsch EW, Lam H, Eng JK, Sun Z, Tasman N, Mendoza L, Moritz RL, Aebersold R, Nesvizhskii AI. *Mol Cell Proteomics*. 2011 Dec;10(12):M111.007690. Epub 2011 Aug 29.
46. A face in the crowd: recognizing peptides through database search. Eng JK, Searle BC, Clauser KR, Tabb DL. *Mol Cell Proteomics*. 2011 Nov;10(11):R111.009522. Epub 2011 Aug 29. Review.
47. Installation and use of LabKey Server for proteomics. Eckels J, Hussey P, Nelson EK, Myers T, Rauch A, Bellew M, Connolly B, Law W, Eng JK, Katz J, McIntosh M, Mallick P, Igra M. *Current Protocols in Bioinformatics*. 2011 Dec:Chapter 13:Unit 13.5.
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50. Cross-linking measurements of in vivo protein complex topologies. Zheng C, Yang L, Hoopmann MR, Eng JK, Tang X, Weisbrod CR, Bruce JE. *Mol Cell Proteomics*. 2011 Oct;10(10):M110.006841. Epub 2011 Jun 22.
51. Fast parallel tandem mass spectral library searching using GPU hardware acceleration. Baumgardner LA, Shanmugam AK, Lam H, Eng JK, Martin DB. *J Proteome Res*. 2011 Jun 3;10(6):2882-8. Epub 2011 May 5.

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56. ChromEval: a software application for the rapid evaluation of HPLC system performance in proteomic applications. Sigmon I, Lee LW, Chang DK, Krusberski N, Cohen D, Eng JK, Martin DB. *Anal Chem*, 2010 Jun 15;82(12):5060-8.
57. Quantitative analysis of the secretome of TGF-beta signaling-deficient mammary fibroblasts. Xu BJ, Yan W, Jovanovic B, An AQ, Cheng N, Aakre ME, Yi Y, Eng J, Link AJ, Moses HL. *Proteomics*. 2010 May 1;82(9):3556-66.
58. A photocleavable and mass spectrometry identifiable cross-linker for protein interaction studies. Yang L, Tang X, Weisbrod CR, Munske GR, Eng JK, von Haller PD, Kaiser NK, Bruce JE. *Anal Chem*, 2010 May 1;82(9):3556-66.
59. Differential protein expression profiles in estrogen receptor-positive and -negative breast cancer tissues using label-free quantitative proteomics. Rezaul K, Thumar JK, Lundgren DH, Eng JK, Claffey KP, Wilson L, Han DK. *Genes Cancer*. 2010 Mar;1(3):251-71.
60. A guided tour of the Trans-Proteomic Pipeline. Deutsch EW, Mendoza L, Shteynberg D, Farrah T, Lam H, Tasman N, Sun Z, Nilsson E, Pratt B, Prazen B, Eng JK, Martin DB, Nesvizhskii AI, Aebersold R. *Proteomics*. 2010 Mar;10(6):1150-9.
61. Trans-Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. Deutsch EW, Shteynberg D, Lam H, Sun Z, Eng JK, Carapito C, von Haller PD, Tasman N, Mendoza L, Farrah T, Aebersold R. *Proteomics*. 2010 Mar;10(6):1190-5.
62. Proteomics data repositories. Riffle M, Eng JK. *Proteomics*. 2009 Oct;9(20):4653-63.
63. Quantitative phosphoproteomic analysis of T cell receptor signaling reveals system-wide modulation of protein-protein interactions. Mayya V, Lundgren DH, Hwang SI, Rezaul K, Wu L, Eng JK, Rodionov V, Han DK. *Sci Signal*. 2009 Aug 18;2(84):ra46.
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66. Proteomic analyses using *Grifola frondosa* metalloendoprotease Lys-N. Hohmann L, Sherwood C, Eastham A, Peterson A, Eng JK, Eddes JS, Shteynberg D, Martin DB. *J Proteome Res*. 2009 Mar;8(3):1415-22.
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68. A fast SEQUEST cross correlation algorithm. Eng JK, Fischer B, Grossmann J, MacCoss MJ. *J Proteome Res*. 2008 Oct;7(10):4598-602. Epub 2008 Sep 6.
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BOOK CHAPTERS

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2. Tandem mass spectrometry database searching. Eng JK, Martin DB, Aebersold R. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, editors Dunn M, Jorde L, Little P, and Subramaniam S, ISBN 0470849746, EPUB 04/2005, 09/2005.
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4. Lipid raft proteins and their identification to T lymphocytes. Wollscheid B, von Haller PD, Yi E, Donohoe S, Vaughn K, Keller A, Nesvizhskii AI, Eng J, Li XJ, Goodlett DR, Aebersold R, Watts JD, Quinn P.J. *Membrane Dynamics and Domains. Subcellular Biochemistry*, editor P.J. Quinn, 2004:37:121-52.
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6. Bacterial typing and identification by mass spectrometry. Krishnamurthy T, Rajamani U, Ross PL, Eng J, David M, Lee TD, Stahl DS, Yates JR III. *Natural and Synthetic Toxins: Biological Implications*, editors Tu AT and Gaffield W, ISBN 0841236305, 2/2000.
7. Direct analysis of protein complexes. Yates JR III, Link AJ, Schieltz D, Eng JK. *Proteome and Protein Analysis*, editors Kamp et al., ISBN 3540658912, 53-64, 12/1999.
8. Automated protein identification using micro-column liquid chromatography tandem mass spectrometry. Yates JR III, Carmack EB, Hays LG, Link AJ, Eng J. *Methods in Molecular Biology, Vol.112: 2-D Proteome Analysis Protocols*, editor Link AJ, ISBN 0896035247, 1999:112:553-69.
9. Microcolumn liquid chromatography electrospray ionization tandem mass spectrometry: analysis of immunological samples. McCormack AL, Eng JK, DeRoos PC, Rudensky AY, Yates JR III. *Biochemical and Biotechnological Applications of Electrospray Ionization Mass Spectrometry, ACS Symposium Series 69*, editor Snyder AP, ISBN 0841233780, 207-225, 09/1996.

TALKS

1. "Algorithms, optimizations, peaks, peptides, and a journey through computational proteomics", *McElvain Seminar Series*, Analytical Chemistry, University of Wisconsin. 2/16/2017.
2. "Twenty Years in Computational Proteomics", *2nd Proteomics Meeting of the Brazilian Proteomics Society and 2nd Pan American HUPO Meeting*, Búzios, Rio de Janeiro State, Brazil. 12/09/2014.
3. "Tools for MS and MS/MS Analysis Using Integrated, Open Source Platforms", *Gordon Research Conference: New Frontiers in Cancer Detection & Diagnosis*, Ventura, CA, 01/26/2007.
4. "Open source software: free tools to analyze your mass spectrometry data", *3rd Joint BSPR/EBI Proteomics Meeting - Integrative Proteomics: Structure, Function, Interaction*, Hinxton, UK, 07/13/2006.
5. "Software/Initiatives in Proteomics", *ASMS 2006 Computer Applications Workshop*, Seattle, WA, 05/2006.
6. "Open Source Proteomics - Computational Proteomics Laboratory", *Proteome Informatics Workshop*, NRPP & US HUPO, Ann Arbor, MI, 06/23/2005.
7. "mzXML: A file format for the open representation of raw mass spectral data", *Spring 2005 Proteome Society Meeting and Informatics Workshop*, PNNL, Richland, WA, 04/01/2005.
8. "Challenges in proteomics data management at FHCRC", *1st International Fungal Proteomics Symposium*, Portland OR, 10/23/2004.
9. "Measuring the relevance of MS/MS database search tools?", *NIST/NIH/ISB Peptide Fragmentation and Identification Workshop*, Gaithersburg, MD, 05/2004

10. "Computational Tools for the Statistical Validation of High Throughput Proteomics Data", *ABRF 2004*, Portland, OR, 03/2004
11. "MS/MS Database Searching", Educational Session, *HUPO 2nd Annual World Congress*, Montreal, CAN, 10/03/2003
12. "A Suite of Software Tools for Quantitative Proteomics", Computational Analysis of Proteome Data II, *Lorne Proteomics Symposium*, Lorne, AUS, 02/2003
13. "Tutorial: Analyzing Peptides and Proteins with Mass Spectrometry and Database Searching", *Proteome Society Seminar*, Seattle, WA, 01/2002
14. "Data Analysis and Management for Proteomics Studies", Education Session I 'Proteomics: The Final Frontier?', *51st American Society of Human Genetics*, San Diego, CA, 10/2001
15. "Protein identification via tandem mass spectrometry database searching using the SEQUEST algorithm", Keynote Speaker, Bioinformatics Session, *6th International Congress of Plant Molecular Biology*, Quebec, Canada, 06/20/2000
16. "Protein Identification by Tandem Mass Spectrometry Database Searching", *International Conference of Electrophoresis Societies '97*, Workshop on Mass Spectrometry Data Analysis, Seattle, WA, 03/1997

TEACHING, LECTURES

1. Lecturer, The 1st SNU International Computational Bioinformatics Workshop 2014, Seoul, South Korea, 10/13/2014.
2. Lecturer, Proteomics course, Cold Springs Harbor Laboratory, 2009 to 2012.
3. Lecturer, Advanced Proteomics Data Analysis Course, The Parc Cientifica de Barcelona and the Instituto Nacional de Proteomica, ProteoRed, 01/2010.
4. Lecturer, Bioinformatics for Protein Discovery, ASMS Fall Workshop, 11/2009.
5. Lecturer, Statistics in Functional Genomics and Proteomics, Summer Institute in Statistical Genetics (UW Biostatistics), 06/2007.
6. Lecturer, US HUPO short course on analysis and interpretation of tandem mass spectrometry data, 03/2007.
7. Instructor, FHCRC proteomics short course, 2005, 2006.
8. Lecturer, University of Washington, MEDCHEM 541 Mass Spectrometry Based Proteomics, 2005, 2007, 2009.
9. Instructor, ISB/SPC Computational Proteomics Course, 2003 to 2009.
10. Lecturer, ETH Zurich, Proteomics course, 2002 to 2004.
11. Lecturer, University of Washington, MBT 520, 1998, 2001.