Jimmy K. Eng

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WORK EXPERIENCE

Software Engineer 07/2007 to present
Proteomics Resource
Dept. of Genome Sciences
University of Washington
Seattle, Washington 98109

- Member of the proteomics team focusing on the software and data analysis needs for the local proteomics community.

Staff Scientist 05/2004 to 07/2007
Public Health Sciences
Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., M2-B230
Seattle, Washington 98109-1024

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

Senior Software Engineer, Proteomics 01/2000 to 05/2004
Institute for Systems Biology 20% subcontract to present
1441 N. 34th St.
Seattle, Washington 98103

- 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 06/1997 to 12/1999
Research Consultant 07/1993 to 06/1997
Dept. of Molecular Biotechnology
University of Washington
Seattle, Washington 98195

- 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.
- WWW/intranet development including the creation of an HTML/CGI package 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 04/1991 to 03/1993
University of Washington, Seattle, Washington

- 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 09/1986 to 08/1990
University of Washington, Seattle, Washington
Baccalaureate Honors: Cum Laude.

HONORS/AWARDS/PATENTS

- 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
- **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

PUBLICATIONS

1. “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.

2. "MaRiMba: A Software Application for Spectral Library-Based MRM Transition List Assembly", Sherwood CA, Eastham A, Lee LW, Peterson A, Eng JK, Shteynberg D, Mendoza L, Deutsch EW, Risler J, Tasman N, Aebersold R, Lam H, Martin DB. *J Proteome Res*. 2009 Aug 24. [Epub ahead of print]
3. "Analysis of RP-HPLC loading conditions for maximizing peptide identifications in shotgun proteomics", Peterson A, Hohmann L, Huang L, Kim B, Eng JK, Martin DB. *J Proteome Res*. 2009 Aug;8(8):4161-8.
4. "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.
5. "Building consensus spectral libraries for peptide identification in proteomics", Lam H, Deutsch EW, Eddes JS, Eng JK, Stein SE, Aebersold R. *Nat Methods*. 2008 Oct;5(10):873-5. Epub 2008 Sep 21.
6. "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.
7. "MRMer: An interactive open-source and cross-platform system for data extraction and visualization of multiple reaction monitoring experiments", Martin DB, Holzman T, May D, Peterson A, Eastham A, Eng J, McIntosh M. *Mol Cell Proteomics*. 2008 Jul 18.
8. "Quantification of the compositional information provided by immonium ions on a quadrupole-TOF mass spectrometer", Hohmann L, Eng J, Gemmill A, Klimek J, Vitek O, Reid G, Martin D. *Analytical Chemistry*, 2008 Jul 15;80(14):5596-606. Epub 2008 Jun 20.
9. "A multidimensional chromatography technology for in-depth phosphoproteome analysis", Albuquerque CP, Smolka MB, Payne SH, Bafna V, Eng J, Zhou H. *Mol Cell Proteomics*. 2008 Jul;7(7):1389-96. Epub 2008 Apr 11.
10. "Integrated pipeline for mass spectrometry-based discovery and confirmation of biomarkers demonstrated in a mouse model of breast cancer", Whiteaker JR, Zhang H, Zhao L, Wang P, Kelly-Spratt KS, Ivey R, Piening BD, Feng L, Kasarda E, Gurley KE, Eng JK, Chodosh LA, Kemp CJ, McIntosh MW, Paulovich AG. *J Proteome Res*, 2007 Oct;6(10):3962-75. Epub 2007 Aug 21.
11. "Contribution of Protein Fractionation to Depth of Analysis of the Serum and Plasma Proteomes ", Faca V, Pitteri SJ, Newcomb L, Glukhova V, Phanstiel D, Krasnoselsky A, Zhang Q, Struthers J, Wang H, Eng J, Fitzgibbon M, McIntosh M, Hanash S. *J Proteome Res,* 2007 Sep;6(9):3558-65. Epub 2007 Aug 16.
12. "Global survey o f human T leukemic cell by integrating proteomic and transcriptomic profiling", Wu L, Hwang SI, Rezaul K, Lu LJ, Mayya V, Gerstein M, Eng JK, Lundgren DH, Han DK. *Mol Cell Proteomics*, 2007 Aug;6(8):1343-53. Epub 2007 May 21.
13. "A platform for accurate mass and time analysis of mass spectrometry data", May D, Fitzgibbon M, Liu Y, Holzman T, Eng J, Kemp CJ, Whiteaker J, Paulovich A, McIntosh M. *J Proteome Res*, 2007 Jul;6(7):2685-94. Epub 2007 Jun 9.
14. "The Standard Protein Mix Database: A Diverse Data Set To Assist in the Production of Improved Peptide and Protein Identification Software Tools", Klimek J, Eddes JS, Hohmann L, Jackson J, Peterson A, Letarte S, Gafken PR, Katz JE, Mallick P 3, Lee H, Schmidt A, Ossola R, Eng JK, Aebersold R, Martin DB. *J Proteome Res,* 2008 Jan;7(1):96-103. Epub 2007 Aug 21.
15. "Proteomic analysis of human coronary atherosclerotic plaque: A feasibility study of direct tissue proteomics by liquid-chromatography and tandem mass spectrometry", Bagnato C, Thumar J, Mayya V, Hwang SI, Zebroski H, Claffey KP, Haudenschild C, Eng JK, Lundgren DH. *Mol Cell Proteomics*, 2007 Jun;6(6):1088-102. Epub 2007 Mar 5.
16. "An integrated chemical, mass spectrometric and computational strategy for (quantitative) phosphoproteomics: application to Drosophila melanogaster Kc167 cells", Bodenmiller B, Mueller LN, Pedrioli PG, Pflieger D, Junger MA, Eng JK, Aebersold R, Tao WA. *Mol Biosyst*, 2007 Apr;3(4):275-86. Epub 2007 Feb 19.
17. "Development and validation of a spectral library searching method for peptide identification from MS/MS", Lam H, Deutsch EW, Eddes JS, Eng JK, King N, Stein SE, Aebersold R. *Proteomics*, 2007 Mar;7(5):655-67.
18. "Head-to-head comparison of serum fractionation techniques", Whiteaker JR, Zhang H, Eng JK, Fang R, Piening BD, Feng L, Lorentzen TD, Schoenherr RM, Keane JF, Holzman T, Fitzgibbon M, Lin C, Zhang H, Cooke K, Liu T, Camp DG, Anderson L, Watts J, Smith RD, McIntosh MW, Paulovich AG. *J Proteome Res*, 2007 Feb;6(2):828-36.
19. "A combined dataset of human cerebrospinal fluid proteins identified by multi-dimensional chromatography and tandem mass spectrometry", Pan S, Zhu D, Quinn JF, Peskind ER, Montine TJ, Lin B, Goodlett DR, Taylor G, Eng J, Zhang J. *Proteomics*, 2007 Feb;7(3):469-73.
20. "Analysis of the S. cerevisiae proteome with PeptideAtlas", King NL, Deutsch EW, Ranish JA, Nesvizhskii AI, Eddes JS, Mallick P, Eng J, Desiere F, Flory M, Martin DB, Kim B, Lee H, Raught B, Aebersold R. *Genome Biology*, 2006;7(11):R106.

21. "Identification of putative androgen receptor interaction protein molecules: Cytoskeleton and endosomes modulate AR signaling in prostate cancer cells", Jasavala R, Martinez HD, Thumar J, Andaya A, Gingras AC, Eng JK, Aebersold R, Han DK, Wright ME. *Mol Cell Proteomics*, 2007 Feb;6(2):252-71. Epub 2006 Oct 18.

22. "UniPep, a database for N-lined glycosites: a resource for biomarker discovery", Zhang H, Loriaux P, Eng J, Campbell D, Keller A, Moss P, Bonneau R, Zhang H, Zhou Y, Wollscheid B, Cooke K, Yi EC, Lee H, Peskind ER, Zhang J, Smith RD, Aebersold R. *Genome Biology*, 2006;7(8):R73. Epub 2006 Aug 10.

23. "General framework for developing and evaluating database scoring algorithms using the TANDEM search engine", MacLean B, Eng JK, Beavis RC, Mclintosh M. *Bioinformatics*, 2006 Nov 15;22(22):2830-2. Epub 2006 Jul 28.

24. "A suite of algorithms for the comprehensive analysis of complex protein mixtures using high-resolution LC-MS", Bellew M, Coram M, Fitzgibbon M, Igra M, Randolph T, Wang P, May D, Eng J, Fang R, Lin C, Chen J, Goodlett D, Whiteaker J, Paulovich A, McIntosh M. *Bioinformatics*, 2006 Aug 1;22(15):1902-9. Epub 2006 Jun 9.

25. "Direct cancer tissue proteomics: a method to identify candidate cancer biomarkers from formalin-fixed paraffin-embedded archival tissues", Hwang SI, Thumar J, Lundgren DH, Rezaul K, Mayya V, Wu L, Eng J, Wright ME, Han DK. *Oncogene*, 2007 Jan 4;26(1):65-76. Epub 2006 Jun 26.

26. "Quality control metrics for LC-MS feature detection tools demonstrated on Saccharomyces cerevisiae proteomics profiles", Piening BD, Wang P, Bangur CS, Whiteaker J, Zhang H, Feng L, Keane JF, Eng JK, Tang H, Prakash A, McIntosh M, Paulovich A. *J Proteome Res*, 2006 Jul;5(7):1527-34.

27. "Characterization of proteome of human cerebrospinal fluid", Xu J, Chen J, Peskind ER, Jin J, Eng J, Pan C, Montine TJ, Goodlett DR, Zhang J. *Int Rev Neurobiol*, 73:29-98, 2006.

28. "Systematic characterization of nuclear proteome during apoptosis: a quantitative proteomic study by differential extraction and stable isotope labeling", Hwang SI, Lundgren DH, Mayya V, Rezaul K, Cowan AE, Eng JK, Han DK. *Mol Cell Proteomics*, 2006 Jun;5(6):1131-45. Epub 2006 Mar 14.

29. "Challenges in deriving high-confidence protein identifications from data gathered by a HUPO plasma proteome collaborative study", States DJ, Omenn GS, Blackwell TW, Fermin Damian, Eng J, Speicher DW, Hanash SM. *Nature Biotechnology*, 2006 Mar;24(3):333-8.

30. "Computational Proteomics Analysis System (CPAS): An extensible open-source analytic system for evaluating and publishing proteomics data and high throughput biological experiments", Rauch A, Bellew M, Eng J, Fitzgibbon M, Holzman T, Hussey P, Igra M, Maclean B, Lin CW, Detter A, Fang R, Faca V, Gafken P, Zhang H, Whitaker J, States D, Hanash S, Paulovich A, McIntosh M. *J Proteome Res*, 2006 Jan;5(1):112-21.

31. "The PeptideAtlas project", Desiere F, Deutsch EW, King NL, Nesvizhskii AI, Mallick P, Eng J, Chen S, Eddes J, Loevenich SN, Aebersold R. *Nucleic Acids Research*, 2006 Jan 1;34(Database issue):D655-8.

32. "The *Pseudomonas aeruginosa* proteome during anaerobic growth", Wu M, Guina T, Brittnacher M, Nguyen H, Eng J, Miller S. *Journal of Bacteriology*, 2005 Dec;187(23):8185-90.

33. "Pancreatic cancer proteome: the proteins that underlie invasion, metastasis, and immunologic escape", Chen R, Yi EC, Donohoe S, Pan S, Eng J, Cooke K, Crispin DA, Lane Z, Goodlett DR, Bronner MP, Aebersold R, Bretnall TA. *Gastroenterology*, 2005 Oct;129(4):1187-97.

34. "A uniform proteomics MS/MS analysis platform utilizing open XML file formats", Keller A, Eng J, Zhang N, Li X, Aebesold R. *Molecular Systems Biology*, 2005;1:2005.0017. Epub 2005 Aug 2.

35. "Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database", Omenn GS, States DJ, Adamski M, Blackwell TW, Menon R, Hermjakob H, Apweiler R, Haab BB, Simpson RJ, Eddes JS, Kapp EA, Moritz RL, Chan DW, Rai AJ, Admon A, Aebersold R, Eng J, Hancock WS, Hefta SA, Meyer H, Paik YK, Yoo JS, Ping P, Pounds J, Adkins J, Qian X, Wang R, Wasinger V, Wu CY, Zhao X, Zeng R, Archakov A, Tsugita A, Beer I, Pandey A, Pisano M, Andrews P, Tammen H, Speicher DW, Hanash SM. *Proteomics*, 2005 Aug;5(13):3226-45.

36. "Quantitative phosphoproteome analysis using a dendrimer conjugation chemistry and tandem mass spectrometry", Tao W, Wollscheid B, O'Brien R, Eng JK, Li X, Bodenmiller B, Watts JD, Hood L, Aebersold R. *Nature Methods*, 2005 Aug;2(8):591-8.

37. "Investigation of neutral loss during collision-induced dissociation of peptide ions", Martin DB, Eng JK, Nesvizhskii AI, Gemmill A, Aebersold R. *Analytical Chemistry*, 2005 Aug 1;77(15):4870-82.

38. “Human Plasma PeptideAtlas”, Deutsch EW, Eng JK, Zhang H, King NL, Nesvizhskii AI, Lim B, Lee H, Yi EC, Ossola R, Aebersold R. *Proteomics*, 2005 Aug;5(13):3497-500.

39. “An evaluation, comparison, and accurate benchmarking of several publicly available MS/MS search algorithms: Sensitivity and specificity analysis”, Kapp EA, Schutz F, Connolly LM, Chakel JA, Meza JE, Miller CA, Fenyo D, Eng JK, Adkins JN, Omenn GS, Simpson RJ. *Proteomics*, 2005 Aug;5(13):3475-90.

40. “Proteomic analysis of synaptosomes using isotope-coded affinity tags and mass spectrometry”, Schrimpf S, Meskanaite V, Brunner E, Rutishauser D, Walther P, Eng J, Aebersold R, Sonderegger P. *Proteomics*, 2005 Jul;5(10):2531-41.

41. “Quantitative proteomics of cerebrospinal fluid from patients with Alzheimer disease”, Zhang J, Goodlett DR, Quinn JF, Peskind E, Kaye JA, Zhou Y, Pan C, Yi E, Eng J, Wang Q, Aebersold RH, Montine TJ. *J Alzheimer’s Disease*, 2005 Apr;7(2):125-33.

42. “An alternative sampling algorithm for use in liquid chromatography/tandem mass spectrometry experiments”, Kohli BM, Eng JK, Nitsch RM, Konietzko U. *Rapid Communications in Mass Spectrometry*, 2005;19(5):589-96.

43. “High-throughput proteome-screening for biomarker detection”, Pan S, Zhang H, Rush J, Eng J, Zhang N, Patterson D, Comb MJ, Aebersold R. *Mol Cell Proteomics,* 2005 Feb;4(2):182-90. Epub 2005 Jan 5..

44. “Quantitative proteomic analysis of age-related changes in human cerebrospinal fluid”, Zhang J, Goodlett DR, Peskind E, Quinn JF, Zhou Y, Pan Q, Yi EC, Eng J, Aebersold RH, Montine T. *Neurobiol Aging*, 2005 Feb;26(2):207-27.

45. “Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry”, Desiere F, Deutsch EW, Nesvizhskii AI, Mallick P, King NL, Eng JK, Aderem A, Boyle R, Brunner E, Dohonoe S, Fausto N, Hafen E, Hood L, Katze MG, Kennedy KA, Kregenow F, Lee H, Lin B, Martin D, Ranish JA, Rawlings DJ, Samelson LW, Shiio Y, Watts JD, Wollscheid B, Wright ME, Yan W, Yang L, Yi EC, Zhang H, Aebersold R. *Genome Biology*, 2005;6(1):R9. Epub 2004 Dec 10.

46. “A Common Open Representation of Mass Spectrometry Data and its Application in a Proteomics Research Environment”, Pedrioli PGA, Eng JK, Hubley R, Vogelzang M, Deutsch EW, Raught B, Pratt B, Nilsson E, Angeletti R, Apweiler R, Cheung K, Costello CE, Hermjakob H, Huang S, Julian RK Jr, Kapp E, McComb ME, Oliver SG, Omenn G, Paton NW, Simpson R, Smith R, Taylor CF, Zhu W, Aebersold R. *Nature Biotechnology*. 2004 Nov;22(11):1459-66.

47. “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. *Subcell Biochem.*, editor P.J. Quinn, 2004;37:121-52.

48. “System-based proteomic analysis of the interferon response in human liver cells”, Yan W, Lee H, Yi EC, Reiss D, Shannon P, Kwieciszewski BK, Coito C, Li XJ, Keller A, Eng J, Galitski T, Goodlett DR, Aebersold R, Katze MG. *Genome Biology*, 2004;5(8):R54. Epub 2004 Jul 224.

49. “Integrated genomic and proteomic analyses of gene expression in mammalian cells”, Tian Q, Stepaniants SB, Mao M, Weng L, Feetham MC, Doyle MJ, Yi EC, Dai H, Thorsson V, Eng J, Goodlett D, Berger JP, Gunter B, Linseley PS, Stoughton RB, Aebersold R, Collins SJ, Hanlon WA, Hood LE. *Mol Cell Proteomics*, 2004 Oct;3(10):960-9. Epub 2004 Jul 6.

50. “A tool to visualize and evaluate data obtained by liquid chromatography-electrospray ionization-mass spectrometry”, Li J, Pedrioli PG, Eng J, Martin D, Yi EC, Aebersold R. *Analytical Chemistry*, 2004 Jul 1;76(13):3856-60.

51. “Identification of TFB5, a new component of general transcription and DNA repair factor IIH”, Ranish JA, Hahn S, Lu Y, Yi EC, Li XJ, Eng J, Aebersold R. *Nature Genetics*, 2004 Jul;36(7):707-13. Epub 2004 Jun 27.

52. “Proteomic analysis of the intestinal epithelial cell response to enteropathogenic Escherichia coli”, Hardwidge PR, Rodriguez-Escudero I, Goode D, Donohoe S, Eng J, Goodlett DR, Aebersold R, Finlay BB. *J. Biol. Chem.*, 279(19):20127-20136, 05/2004.

53. "Identification of androgen-coregulated protein networks from the microsomes of human prostate cancer cells", Wright ME, Eng J, Sherman J, Hockenbery DM, Nelson PS, Galitski T, Aebersold R. *Genome Biology*, 2003;5(1):R4. Epub 2003 Dec 23.

54. "PROTEOME-3D: An interactive bioinformatics tool for large-scale data exploration and knowledge discovery", Lundgren DH, Eng J, Wright ME, Han DK. *Mol Cell Proteomics*, 2003 Nov;2(11):1164-76. Epub 2003 Sep 7.

55. "Identification of 2D-gel proteins: a comparison of MALDI/TOF peptide mass mapping to mu LC-ESI tandem mass spectrometry", Lim H, Eng J, Yates JR 3rd, Tollaksen SL, Giometti CS, Holden JF, Adams MW, Reich CI, Olsen GJ, Hays LG. *J Am Soc Mass Spectrom.*, 2003 Sep;14(9):957-70.

56. "Initial proteome analysis of model microorganism Haemophilus influenzae strain Rd KW20", Kolker E, Purvine S, Galperin MY, Stolyar S, Goodlett DR, Nesvizhskii AI, Keller A, Xie T, Eng JK, Yi E, Hood L, Picone AF, Cherny T, Tjaden BC, Siegel AF, Reilly TJ, Makarova KS, Palsson BO, Smith AL. *J Bacteriol.*, 2003 Aug;185(15):4593-602.

57. "Proteomic analysis of Pseudomonas aeruginosa grown under magnesium limitation", Guina T, Wu M, Miller SI, Purvine SO, Yi EC, Eng J, Goodlett DR, Aebersold R, Ernst RK, Lee KA. *J Am Soc Mass Spectrom.*, 14(7):742-751, 07/2003.

58. "The application of new software tools to quantitative protein profiling via isotope-coded affinity tag (ICAT) and tandem mass spectrometry: II. Evaluation of tandem mass spectrometry methodologies for large-scale protein analysis, and the application of statistical tools for data analysis and interpretation", Von Haller PD, Yi E, Donohoe S, Vaughn K, Keller A, Nesvizhskii AI, Eng J, Li XJ, Goodlett DR, Aebersold R, Watts JD. *Mol Cell Proteomics*, 2003 Jul;2(7):428-42. Epub 2003 Jun 25.

59. "The application of new software tools to quantitative protein profiling via isotope-coded affinity tag (ICAT) and tandem mass spectrometry: I. Statistically annotated datasets for peptide sequences and proteins identified via the application of ICAT and tandem mass spectrometry to proteins copurifying with T cell lipid rafts", Von Haller PD, Yi E, Donohoe S, Vaughn K, Keller A, Nesvizhskii AI, Eng J, Li XJ, Goodlett DR, Aebersold R, Watts JD. *Mol Cell Proteomics*, 2003 Jul;2(7):426-7. Epub 2003 Jun 25.

60. "The study of macromolecular complexes by quantitative proteomics", Ranish JA, Yi EC, Leslie DM, Purvine SO, Goodlett DR, Eng J, Aebersold R. *Nature Genetics*, 2003 Mar;33(3):349-55. Epub 2003 Feb 18.

61. "Quantitative proteomic analysis indicates increased synthesis of a quinolone by Pseudomonas aeruginosa isolates from cystic fibrosis airways.", Guina T, Purvine SO, Yi EC, Eng J, Goodlett DR, Aebersold R, Miller SI. *Proc Natl Acad Sci*, 2003 Mar 4;100(5):2771-6. Epub 2003 Feb 24.

62. "Complementary profiling of gene expression at the transcriptome and proteome levels in Saccharomyces cerevisiae", Griffin TJ, Gygi SP, Ideker T, Rist B, Eng J, Hood L, Aebersold R. *Mol Cell Proteomics*, 2002 Apr;1(4):323-33.

63. "Code developments to improve the efficiency of automated MS/MS spectra interpretation", Sadygov RG, Eng J, Durr E, Saraf A, McDonald H, MacCoss MJ, Yates JR 3rd. *J Proteome Res*, 2002 May-Jun;1(3):211-5.

64. "Proteome analysis of low-abundance proteins using multidimensional chromatography and isotope-coded affinity tags", Gygi SP, Rist B, Griffin TJ, Eng J, Aebersold R. *J Proteome Res*, 2002 Jan-Feb;1(1):47-54.

65. "Quantitative profiling of differentiation-induced microsomal proteins using isotope-coded affinity tags and mass spectrometry", Han DK, Eng J, Zhou H, Aebersold R. *Nature Biotechnology*, 2001 Oct;19(10):946-51.

66. "Differential stable isotope labeling of peptides for quantitation and de novo sequence derivation", Goodlett DR, Keller A, Watts JD, Newitt R, Yi EC, Purvine S, Eng JK, von Haller P, Aebersold R, Eugene Kolker. *Rapid Communications in Mass Spectrometry*, 2001;15(14):1214-21.

67. "Integrated genomic and proteomic analyses of a systematically perturbed metabolic network", Ideker T, Thorsson V, Ranish JA, Christmas R, Buhler J, Eng JK, Bumgarner R, Goodlett DR, Aebersold R, Hood L. *Science*, 2001 May 4;292(5518):929-34.

68. "In vivo MHC class II presentation of cytosolic proteins revealed by rapid automated tandem mass spectrometry and functional analyses", Dongre AR, Kovats S, deRoos P, McCormack AL, Nakagawa T, Paharkova-Vatchkova V, Eng J, Caldwell H, Yates JR III, Rudensky AY. *European Journal of Immunology*, 2001 May;31(5):1485-94.

69. "The innate immune response to bacterial flagellin is mediated by Toll-like receptor 5", Hayashi F, Smith KD, Ozinsky A, Hawn TR, Yi EC, Goodlett DR, Eng JK, Akira S, Underhill DM, Aderem A. *Nature*, 2001 Apr 26;410(6832):1099-103.

70. "Proteomics of rat liver Golgi complex: Minor proteins are identified through sequential fractionation", Taylor RS, Wu CC, Hays LG, Eng JK, Yates JR III, Howell KE. *Electrophoresis*, 2000 Oct;21(16):3441-59.

71. "Automated identification of amino acid sequence variations in proteins by HPLC/microspray tandem mass spectrometry", Gatlin CL, Eng JK, Terashita ST, Detter JC, Yates JR III. *Analytical Chemistry*, 2000 Feb 15;72(4):757-63.

72. "Mass spectral investigations on microorganisms", Krishnamurthy T, Rajamani U, Ross PL, Jabhour R, Nair H, Eng J, Yates J, Davis MT, Stahl DC, Lee TD. *Journal of Toxicology – Toxin Reviews*, 19(1):95-117, 2000.

73. "Identification of proteins in complexes by solid-phase microextraction/multistep elution/capillary electrophoresis/tandem mass spectrometry", Tong W, Link A, Eng JK, Yates JR III. *Analytical Chemistry*, 1999 Jul 1;71(13):2270-8.

74. "Direct analysis of protein complexes using mass spectrometry", Link AJ, Eng J, Schieltz DM, Carmack E, Mize GM, Morris DR, Garvik BM, Yates JR III. *Nature Biotechnology*, 1999 Jul;17(7):676-82.

75. "Method to compare collision-induced dissociation spectra of peptides: potential for library searching and subtractive analysis", Yates JR III, Morgan SF, Gatlin CL, Griffin PR, Eng JK. *Analytical Chemistry*, 1998 Sep 1;70(17):3557-65.

76. "High throughput protein characterization by automated reverse-phase chromatography/electrospray tandem mass spectrometry", Ducret A, van Oostveen I, Eng JK, Yates JR III, Ruedi Aebersold. *Protein Science*, 1998 Mar;7(3):706-19.

77. "Tandem mass spectrometry", Dongre AR, Eng JK, Yates JR III. *BIOFUTUR*, 181, 09/1998.

78. "Emerging tandem mass spectrometry techniques for the rapid identification of proteins", Dongre AR, Eng JK, Yates JR III. *Trends in Biotechnology*, 1997 Oct;15(10):418-25.
79. "High throughput analysis of tandem mass spectrometry data for peptides", Yates JR III, Carmack E, Eng JK. *Lab Automation*, 2:28-31, 1997.
80. "Mining genomes and proteomes with tandem mass spectrometry", Yates JR III, Link AJ, Schieltz D, Hays L, Eng J. *Abstracts of Papers of the American Chemical Society*, 214:110-, 1997.
81. "Protein identification from 2-DGE and protein mixtures using tandem mass spectrometry", Yates JR III, Link AJ, Hays L, Carmack E, Eng J. *FASEB Journal*, 11, Supplement S., 1997.
82. "Direct analysis and identification of proteins in mixtures by LC/MS/MS and database searching at the low femptomole level", McCormack AL, Scheiltz D, Eng JK, Goode B, Yang S, Barnes G, Drubin D, Yates JR III. *Analytical Chemistry*, 69:767-776, 1997.
83. "Search of sequence databases with uninterpreted high-energy collision-induced dissociation spectra of peptides", Yates JR III, Eng JK, Clauser KR, Burlingame AL. *Journal for the American Society of Mass Spectrometry*, 7:1089-1098, 11/1996.
84. "Mining genomes with MS", Yates JR III, McCormack AL, Eng J. *Analytical Chemistry*, 1996 Sep 1;68(17):534A-540A.
85. "Analyzing complex biological systems using micro-LC-ESI-MS-MS", Link AJ, Eng J, Yates JR III. *American Laboratory*, 28(11):27-30, 07/1996.
86. "Protein database searching with MSn spectra of polypeptides", Eng JK, Yates JR III. *Proceedings of SPIE: Ultrasensitive Biochemical Diagnostics, Editors Gerald E. Cohen, Steven A. Soper, and C.H. Winston Chen*, 2680:378-382, 1996.
87. "Future prospects for the analysis of complex biological systems using micro-column liquid chromatography-electrospray tandem mass spectrometry", Yates JR III, McCormack AL, Link AJ, Schieltz D, Eng J, Hays L. *The Analyst*, 1996 Jul;121(7):65R-76R.
88. "Testing the feasibility of DNA typing for human identification by PCR and an oligonucleotide ligation assay", Delahunty C, Ankener W, Deng Q, Eng J, Nickerson DA. *American Journal of Human Genetics*, 1996 Jun;58(6):1239-46.
89. "Mining genomes: correlating tandem mass spectra of modified and unmodified peptides to nucleotide sequences", Yates JR III, Eng JK, McCormack AL. *Analytical Chemistry*, 1995 Sep 15;67(18):3202-10.
90. "Method to correlate tandem mass spectra of modified peptides to amino acid sequences in the protein database", Yates JR III, Eng JK, McCormack AL, Schieltz D. *Analytical Chemistry*, 1995 Apr 15;67(8):1426-36.
91. "Direct database searching with MALDI-PSD spectra of peptides", Griffin PR, MacCoss MJ, Eng JK, Blevins RA, Aaronson JS, Yates JR III. *Rapid Communications in Mass Spectrometry*, 1995;9(15):1546-51.
92. "Peptide sequence analysis on quadrupole mass spectrometers", McCormack AL, Eng JK, Yates JR III. *METHODS: A Companion to Methods in Enzymology*, 274-283, 1994.
93. "An approach to correlate tandem mass spectral data of peptides with amino acid sequences in a protein database," Eng JK, McCormack AL, Yates JR III. *Journal of the American Society for Mass Spectrometry*, 1994 5:976-989.
94. "Microcapillary liquid-chromatography electrospray-ionization tandem mass-spectrometry of complex-systems", Yates JR III, McCormack AL, Eng J. *Abstracts of Papers of the American Chemical Society*, 207:101-, 03/1994.

BOOK CHAPTERS

1. Myers T, Law W, Eng JK, McIntosh M. Installation and Use of the Computational Proteomics Analysis System (CPAS). *Current Protocols in Bioinformatics*, Chapter 13:Unit 13.5, 2007.
2. Lundgren DH, Eng JK, Han DK. Protein Identification Using TurboSEQUEST. *Current Protocols in Bioinformatics*, editor Baxevanis AD, ISBN 0471250937, 13.3.1-13, 2005.
3. Eng JK, Martin DB, Aebersold R. Tandem mass spectrometry database searching. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, editors Dunn M, Jorde L, Little P, and Subramaniam S, ISBN 0470849746, EPUB 04/2005, 09/2005.
4. Eng JK. Tutorial on tandem mass spectrometry database searching. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, editors Dunn M, Jorde L, Little P, and Subramaniam S, ISBN 0470849746, EPUB 04/2005, 09/2005.

5. Eng JK, Keller A, Li XJ, Nesvizhskii AI, Aebersold R. Chapter 16. Computational tools for tandem mass spectrometry-based high throughput quantitative proteomics. *Informatics in Proteomics*, editor Srivastava S, ISBN 1574444808, 335-352, 05/2005.
6. Tabb DL, Eng JK, Yates JR III. Protein Identification by SEQUEST. *Proteome Research: Mass Spectrometry (Principles and Practice)*, editor James P, ISBN 3540672559, 12/2001.
7. Yates JR III, Link AJ, Schieltz D, Eng JK. Direct analysis of protein complexes. *Proteome and Protein Analysis*, editors Kamp et al., ISBN 3540658912, 53-64, 12/1999.
8. Krishnamurthy T, Rajamani U, Ross PL, Eng J, David M, Lee TD, Stahl DS, Yates JR III. Ch. 6: Bacterial typing and identification by mass spectrometry. *Symposium Series No. 745/Natural and Synthetic Toxins: Biological Implications*, Editors Tu AT and Gaffield W, ISBN 0841236305, 2/2000.
9. Yates JR III, Carmack EB, Hays LG, Link AJ, Eng J. Automated protein identification using micro-column liquid chromatography tandem mass spectrometry. *Methods in Molecular Biology, Vol.112: 2-D Proteome Analysis Protocols*, Editor Link AJ, ISBN 0896035247, 1999;112:553-69.
10. Yates JR III, Carmack E, Eng JK. Direct Database Searching Using Tandem Mass Spectra of Peptides. *Cell Biology: A Laboratory Handbook, Second Edition*, Volume 4, Part 16, Section I, ISBN 0121647250, 01/1998.
11. McCormack AL, Eng JK, DeRoos PC, Rudensky AY, Yates JR III. Microcolumn liquid chromatography - electrospray ionization tandem mass spectrometry: analysis of immunological samples. *Biochemical and Biotechnological Applications of Electrospray Ionization Mass Spectrometry, ACS Symposium Series 69*, Editor Snyder AP, ISBN 0841233780, 207-225, 09/1996.

TALKS

1. "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.
2. "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.
3. "Software/Initiatives in Proteomics", *ASMS 2006 Computer Applications Workshop*, Seattle, WA, 05/2006.
4. "Open Source Proteomics - Computational Proteomics Laboratory", *Proteome Informatics Workshop*, NRPP & US HUPO, Ann Arbor, MI, 06/23/2005.
5. "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.
6. "Challenges in proteomics data management at FHCRC", *1st International Fungal Proteomics Symposium*, Portland OR, 10/23/2004.
7. "Measuring the relevance of MS/MS database search tools?", *NIST/NIH/ISB Peptide Fragmentation and Identification Workshop*, Gaithersburg, MD, 05/2004
8. "Computational Tools for the Statistical Validation of High Throughput Proteomics Data", *ABRF 2004*, Portland, OR, 03/2004
9. "MS/MS Database Searching", Educational Session, *HUPO 2nd Annual World Congress*, Montreal, CAN, 10/03/2003
10. "A Suite of Software Tools for Quantitative Proteomics", Computational Analysis of Proteome Data II, *Lorne Proteomics Symposium*, Lorne, AUS, 02/2003
11. "Tutorial: Analyzing Peptides and Proteins with Mass Spectrometry and Database Searching", *Proteome Society Seminar*, Seattle, WA, 01/2002
12. "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
13. "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
14. "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, Statistics in Functional Genomics and Proteomics, Summer Institute in Statistical Genetics (UW Biostatistics), 06/2007.
2. Lecturer, US HUPO short course on analysis and interpretation of tandem mass spectrometry data, 03/2007.
3. Instructor, FHCRC proteomics short course, 2005, 2006.
4. Lecturer, University of Washington, MEDCHEM 541 Mass Spectrometry Based Proteomics, 2005, 2007.
5. Instructor, ISB/SPC Computational Proteomics Course, 2003-present.
6. Lecturer, ETH Zurich, Proteomics course, 2002, 2003, 2004.
7. Lecturer, University of Washington, MBT 520, 1998, 2001