
Jimmy K. Eng

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WORK EXPERIENCE

Staff Scientist

Fred Hutchinson Cancer Research Center
1100 Fairview Ave. N., M2-B230
P.O. Box 19024
Seattle, Washington 98109-1024

05/2004 to present

- Director of Scientific Programming, FHCRC Comparative Proteomics.
- Collaborate on primary research with scientists.
- Develop software tools and compute environment for proteomics analysis.

Senior Software Engineer, Proteomics

Institute for Systems Biology
1441 N. 34th St.
Seattle, Washington 98103

01/2000 to 05/2004

- Primary focus on research and development of software tools, applications, and compute systems for automated, high throughput, quantitative proteomics.
- Interface with proteomics core facility, scientists in Ruedi Aebersold's research lab, ISB staff, and external collaborators.
- Organize Seattle-area proteomics software-centric interest group (SPIGOT).
- Instructor for NHLBI sponsored ISB proteomics informatics course.

Software Engineer

Research Consultant

Biological Mass Spectrometry Laboratory of John Yates, III
Department of Molecular Biotechnology
University of Washington
Seattle, Washington 98195

06/1997 to 12/1999

07/1993 to 06/1997

- 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

University of Washington, Seattle, Washington

04/1991 to 03/1993

- 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, Washington
Baccalaureate Honors: Cum Laude.

09/1986 to 08/1990

HONORS/AWARDS/PATENTS

- Phi Beta Kappa National Honor Society, member 1991
 - Eta Kappa Nu Electrical Engineering Honor Society, member 1989
 - University of Washington Certificate of High Scholarship, 1986
 - University of Washington Undergraduate Merit Scholarship, 1987
 - 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
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COMPUTING & AFFILIATIONS

- **Programming:** C
 - **Operating Systems:** *nix, Windows, MacOS
 - **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**, 2004-present
 - **mzXML-associated Standard Solutions Committee**, 2004-present
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PUBLICATIONS

1. "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*, EPUB 01/2005.
2. "Quantitative proteomics of cerebrospinal fluid from Alzheimer disease and controls using isotope-coded affinity tags", Zhang J, Goodlett DR, Quinn JF, Peskind E, Zhou Y, Pan C, Yi E, **Eng J**, Wang Q, Aebersold RH, Montine TJ. submitted
3. "Quantitative proteomic analysis of age-related changes in human cerebrospinal fluid using isotope-coded affinity tag", Zhang J, Goodlett DR, Peskind E, Quinn JF, Zhou Y, Pan Q, Yi EC, **Eng J**, Aebersold RH, Montine T. *Neurobiol Aging*, 26(2), 207-227, 2/2005.
4. "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*, 6:R9, 12/2004.
5. "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*. 22(11), 1459-1466, 11/2004.
 6. "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*, 5, R54, EPUB 07/2004.
 7. "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*, EPUB 07/2004, 3(10), 960-9, 10/2004.
 8. "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*, 76: 3856-60, 07/2004.
 9. "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*, 36: 707-13, 07/2004.
 10. "Identification of androgen-coregulated protein networks from the microsomes of human prostate cancer cells", Wright ME, **Eng J**, Sherman J, Hockenberry DM, Nelson PS, Galitski T, Aebersold R. *Genome Biology*, 5, R4, 12/2003.
 11. "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*, 2(11), 1164-1176, 11/2003
 12. "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.*, 14(9), 957-970, 09/2003
 13. "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.*, 185(15), 4593-4602, 08/2003
 14. "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
 15. "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*, 2(7), 428-442, 07/2003
 16. "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*, 2(7), 426-427, 07/2003
 17. "The study of macromolecular complexes by quantitative proteomics", Ranish JA, Yi EC, Leslie DM, Purvine SO, Goodlett DR, **Eng J**, Aebersold R., *Nature Genetics*, 33(3), 349-355, 03/2003
 18. "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*, 100(5), 2771-2776, 03/2003
 19. "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*, 1(4), 323-333, 04/2002
 20. "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*, 19(10), 946-951, 10/2001
 21. "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*, 15(14), 1214-1221, 06/2001

22. "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*, 292(5518), 929-924, 05/2001
23. "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*, 31(5), 1485-94, 05/2001
24. "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*, 410(6832), 1099-1103, 04/2001
25. "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*, 21(16), 3441-3459, 10/2000
26. "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*, 72(4), 757-763, 02/2000
27. "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*, 71(13), 2270-2278, 07/1999
28. "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*, 17(7), 676-682, 07/1999
29. "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*, 70(17), 3557-3565, 09/1998
30. "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*, 7(3), 706-719, 03/1998
31. "Tandem mass spectrometry", Dongre AR, **Eng JK**, Yates JR III, *BIOFUTUR*, 181, 09/1998
32. "Emerging tandem mass spectrometry techniques for the rapid identification of proteins", Dongre AR, **Eng JK**, Yates JR III, *Trends in Biotechnology*, 15(10), 418-425, 10/1997
33. "High throughput analysis of tandem mass spectrometry data for peptides", Yates JR III, Carmack E, **Eng JK**, *Lab Automation*, 2, 28-31, 1997
34. "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
35. "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
36. "Direct analysis and identification of proteins in mixtures by LC/MS/MS and database searching at the low femtomole level", McCormack AL, Scheiltz D, **Eng JK**, Goode B, Yang S, Barnes G, Drubin D, Yates JR III, *Analytical Chemistry*, 69, 767-776, 1997
37. "Search of sequence databases with uninterpreted high-energy collision-induced dissociation spectra of peptides", Yates JR III, **Eng JK**, Clouser KR, Burlingame AL, *Journal for the American Society of Mass Spectrometry*, 7, 1089-1098, 1996
38. "Mining genomes with MS", Yates JR III, McCormack AL, **Eng J**, *Analytical Chemistry*, 68, 534A-540A, 09/1996
39. "Analyzing complex biological systems using micro-LC-ESI-MS-MS", Link AJ, **Eng J**, Yates JR III, *American Laboratory*, 28(11), 27-30, 1996
40. "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
41. "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*, 121(7), 65R-76R, 07/1996
42. "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*, 58(6), 1239-1246, 06/1996
43. "Mining genomes: correlating tandem mass spectra of modified and unmodified peptides to nucleotide sequences", Yates JR III, **Eng JK**, McCormack AL, *Analytical Chemistry*, 67(18), 3202-3210, 09/1995
44. "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*, 67(8), 1426-1436, 04/1995

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- 45. "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*, 9(15), 1546-1551, 1995
 - 46. "Studies of immunological pathways by using tandem mass spectrometry and database searching", Yates JR III, **Eng J**, McCormack AL, Moji TT, Pious D, *Abstracts of Papers of the American Chemical Society*, 209, 122-, 1995
 - 47. "Peptide sequence analysis on quadrupole mass spectrometers", McCormack AL, **Eng JK**, Yates JR III, *METHODS: A Companion to Methods in Enzymology*, 274-283, 1994
 - 48. "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-, 1994
 - 49. "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*, 5, 976-989, 1994
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BOOK CHAPTERS

- 1. 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. (2004) Lipid raft proteins and their identification to T lymphocytes. *Subcell Biochem.*, editor P.J. Quinn, Kluwer Academic Pub., 37:121-52.
 - 2. **Eng JK**, Martin DB, Aebersold R. (2004) Tandem mass spectrometry database searching. *Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics*, eds. Dunn M, Jorde L, Little P, and Subramaniam S, John Wiley & Sons, Ltd, submitted.
 - 3. **Eng JK**, Keller A, Li XJ, Nesvizhskii AI, Aebersold R. (2004) Computational tools for tandem mass spectrometry-based high throughput quantitative proteomics. *Informatics in Proteomics*, Editors Srivastava S and Hanash S, Marcel Dekker Inc., New York, submitted.
 - 4. Tabb DL, **Eng JK**, Yates JR III. (2000) Protein Identification by SEQUEST. *Proteome Research: Mass Spectrometry (Principles and Practice)*, Editor Peter James, ISBN 3-540-67255-9.
 - 5. Yates JR III, Link AJ, Schieltz D, **Eng JK**. (1999) Direct analysis of protein complexes. *Proteome and Protein Analysis*, Editors Kamp et al., Springer-Verlag, ISBN 3-540-65891-2, 53-64.
 - 6. Krishnamurthy T, Rajamani U, Ross PL, **Eng J**, David M, Lee TD, Stahl DS, Yates JR III. (1999) Ch. 6: Bacterial typing, *Symposium Series No. 745/Natural and Synthetic Toxins: Biological Implications*, Editors A.T. Tu and W. Gaffield, ISBN 0-8412-3630-5.
 - 7. Yates JR III, Carmack EB, Hays LG, Link AJ, **Eng J**. (1998) Automated protein identification using micro-column liquid chromatography tandem mass spectrometry. *Methods in Molecular Biology*, Vol.112: 2-D Proteome Analysis Protocols, Editor Andrew J. Link, Humana Press Inc., Totowa, NJ, ISBN 0-89603-524-7.
 - 8. Yates JR III, Carmack E, **Eng JK**. (1997) Direct Database Searching Using Tandem Mass Spectra of Peptides. *Cell Biology: A Laboratory Handbook, Second Edition*, Volume 4, Part 16, Section I, ISBN 0-12-164725-0.
 - 9. McCormack AL, **Eng JK**, DeRoos PC, Rudensky AY, Yates JR III. (1995) 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 A. P. Snyder, ISBN 0-8412-3378-0, 207-225.
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TALKS

- 1. "Challenges in proteomics data management at FHCRC", *1st International Fungal Proteomics Symposium*, Portland OR, 10/2004.
- 2. "Measuring the relevance of MS/MS database search tools?", *NIST/NIH/ISB Peptide Fragmentation and Identification Workshop*, Gaithersburg, MD, 05/2004
- 3. "Computational Tools for the Statistical Validation of High Throughput Proteomics Data", *ABRF 2004*, Portland, OR, 03/2004
- 4. "MS/MS Database Searching", Educational Session, *HUPO 2nd Annual World Congress*, Montreal, CAN, 10/2003

5. "A Suite of Software Tools for Quantitative Proteomics", Computational Analysis of Proteome Data II, *Lorne Proteomics Symposium*, Lorne, AUS, 02/2003
 6. "TUTORIAL: Analyzing Peptides and Proteins with Mass Spectrometry and Database Searching", *Proteome Society Seminar*, Seattle, WA, 01/2002
 7. "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
 8. "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, 06/2000
 9. "Protein Identification by Tandem Mass Spectrometry Database Searching", *International Conference of Electrophoresis Societies '97*, Workshop on Mass Spectrometry Data Analysis, Seattle, WA, 03/1997
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POSTERS

1. "XPRESS™ software for automated quantitation of relative protein expression levels using tandem mass spectrometry of ICAT™ labeled peptides", **Eng J**, Goodlett D, Purvine S, Yi E, Aebersold R, *ABRF 2001*, San Diego, CA, 02/2001
 2. "Protein Database Searching with Ion Trap MSn Spectra", **Eng J**, Yates JR III, Schieltz DM, *43rd ASMS Conference on Mass Spectrometry*, Atlanta, GA, 05/1995
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