

Wilfred H. Tang, Ph.D.

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SUMMARY:

Expertise in:

- Developing bioinformatics software and scientific software
- Answering scientific questions using informatics
- Developing robust, commercial software
- Developing and optimizing algorithms
- Mathematical modeling

PROFESSIONAL EXPERIENCE:

Protein Metrics, Cupertino, CA

Sr. Software Engineer (and first non-founder employee), 2012 – present

- Led development of:
 - Supernovo software for *de novo* sequencing of antibodies (<https://www.proteinmetrics.com/products/supernovo/>)
 - Hydrogen-deuterium exchange software for studying protein higher-order structure
 - Software for analyzing disulfide-bonded proteins and crosslinked proteins
 - Integration of Protein Metrics software with external workflow software – that is, integration of Protein Metrics Byonic and Preview as nodes in Thermo Fisher Scientific's Proteome Discoverer (<https://www.proteinmetrics.com/support-information/#proteome-discoverer-nodes-download>)
- Key contributor to development of software suite for protein and glycoprotein characterization using mass spectrometry data

Agilent Technologies (LC/MS R&D), Santa Clara, CA

R&D Software Engineer, 2009 – 2012

- Developed software for characterizing proteins for biopharmaceutical applications.
- Implemented false discovery rate calculations for proteomics database search software.
- Developed software enabling targeted MS/MS data acquisition in complex mixtures.
- Improved mass spectrometer firmware speed, enabling customers to take full advantage of ~10-fold improvement in the mass spectrometer's sensitivity.

Applied Biosystems (Mass Spectrometry Informatics R&D), Foster City, CA

Staff Software Engineer, 2007 – 2009

Sr. Software Engineer, 2002 – 2007

Bioinformatics Consultant, 2001 – 2002

- Developer for all phases of ProteinPilot, starting from research prototype and culminating in several releases of commercial software (for large-scale protein identification and biomarker discovery from mass spectrometry data – <http://tinyurl.com/ProteinPilot>).
- Responsible for implementing ProteomicS PEP, a tool for estimating false discovery rates in protein identification.
- Used ProteomicS PEP to validate ProteinPilot's performance and to help craft proof statements demonstrating the improvements offered by ProteinPilot over competing products.
- Developed algorithms for:
 - Identifying peptides by database search

- Inferring proteins from peptide identifications without getting fooled by protein homology
- Biomarker discovery using isotopic labels (such as iTRAQ, ICAT, SILAC)
- Compensating for a mistuned mass spectrometer
- Peak detection
- Algorithm optimization to overcome critical bottlenecks
- Responsible for integrating Pro ICAT (protein identification and biomarker discovery software) and Spotfire DecisionSite for Functional Genomics (data visualization software).
- Served as a bridge between the scientists and the software group.
- Filed invention disclosures/patents, published papers, and presented posters/talks related to proteomics software.
- Constructed Oracle database-backed system for storing annotated LC/MS data.

Thermo Finnigan (Proteomics Group), San Jose, CA
Bioinformatics Scientist, 2000 – 2001

- Participated in the initial design and implementation of software for storing and analyzing high-throughput proteomics data obtained from mass spectrometry.
- Implemented the loading of data from Genbank flat files into Oracle.

Newark Memorial High School, Newark, CA
Teacher, 1999 – 2000

- Taught physics, chemistry, and algebra.

Genetics Computer Group, Madison, WI
Software Engineer, 1998 – 1999

- Designed and coded new applications for GCG's Wisconsin Package, including a program for predicting protein secondary structure and a template program to facilitate the development of future GCG applications.
- Fixed bugs in/developed enhancements for existing Wisconsin Package applications.

University of Chicago, Chicago, IL
Research Assistant/Teaching Assistant, 1993 – 1998

- Theoretical chemistry/physics: research on polymers using statistical mechanics
- Wrote software for performing Brownian dynamics simulations on polymers.
 - Created stochastic models for efficiently approximating the Brownian dynamics of polymers.
 - Studied diblock copolymer thin films using both analytical methods and computational (Scheutjens-Fleer) methods.
 - Teaching assistant for physical chemistry laboratory class.

University of California, Berkeley, CA
Teaching Assistant, summer 1992

- Supervised laboratory work and led discussion section for introductory chemistry course.

Lawrence Berkeley National Laboratory, Berkeley, CA
Student Assistant, 1990 – 1991

- Research in experimental biochemistry and biophysics: energy transfer in photosynthesis
- Studied phycoerythrin and allophycocyanin from cyanobacteria using absorption, fluorescence, and time-resolved fluorescence spectroscopy.

Metropolitan Transportation Commission, Oakland, CA
Technical Services Intern, summer 1989

- Wrote computer programs for mining data from an airport flight traffic database.

EDUCATION:

University of Chicago, Chicago, IL
 Ph.D., Chemistry, June 1999
 M.S., Chemistry, August 1993
 GPA: 4.00

University of California, Berkeley, CA
 B.A., Computer Science, May 1992
 B.S., Chemistry, May 1992
 GPA: 3.95

TECHNICAL SKILLS:

Computer languages: C#, C++, Java, Python, Perl, Fortran, Matlab, Mathematica, SQL

HONORS AND SCHOLARSHIPS:

National Defense Science and Engineering Graduate Fellowship (Department of Defense),
 1993-1996
 Graduate Assistance in Areas of National Need Fellowship (Department of Energy), 1992-1993
 Robert R. McCormick Fellowship (University of Chicago), 1996-1998
 William Draper Harkins Fellowship (University of Chicago), 1992-1993
 Chancellor's Scholarship (University of California, Berkeley), 1988-1992

PUBLICATIONS: (available at <http://www.wilfredtang.com/Publications/publications.html>)

1. M. Bern, T. Caval, Y. J. Kil, **W. Tang**, C. Becker, E. Carlson, D. Kletter, K. I. Sen, N. Galy, D. Hagemans, V. Franc, A. J. R. Heck, "Parsimonious Charge Deconvolution for Native Mass Spectrometry," *Journal of Proteome Research* **17**, 1216 (2018).
2. K. I. Sen, **W. H. Tang**, S. Nayak, Y. J. Kil, M. Bern, B. Ozoglu, B. Ueberheide, D. Davis, C. Becker, "Automated Antibody De Novo Sequencing and Its Utility in Biopharmaceutical Discovery," *Journal of the American Society for Mass Spectrometry* **28**, 803 (2017).
3. L. Martens, M. Chambers, M. Sturm, D. Kessner, F. Levander, J. Shofstahl, **W. H. Tang**, A. Römpf, S. Neumann, A. D. Pizarro, L. Montecchi-Palazzi, N. Tasman, M. Coleman, F. Reisinger, P. Souda, H. Hermjakob, P. A. Binz, E. W. Deutsch, "mzML – a Community Standard for Mass Spectrometry Data," *Molecular & Cellular Proteomics* **10**, 1 (2011).
4. **W. H. Tang**, I. V. Shilov, and S. L. Seymour, "Nonlinear Fitting Method for Determining Local False Discovery Rates from Decoy Database Searches," *Journal of Proteome Research* **7**, 3661 (2008).
5. I. V. Shilov, S. L. Seymour, A. A. Patel, A. Loboda, **W. H. Tang**, S. P. Keating, C. L. Hunter, L. M. Nuwaysir, and D. A. Schaeffer, "The Paragon Algorithm, a Next Generation Search Engine That Uses Sequence Temperature Values and Feature Probabilities to Identify Peptides from Tandem Mass Spectra," *Molecular & Cellular Proteomics* **6**, 1638 (2007).
6. **W. H. Tang**, B. R. Halpern, I. V. Shilov, S. L. Seymour, S. P. Keating, A. Loboda, A. A. Patel, D. A. Schaeffer, and L. M. Nuwaysir, "Discovering Known and Unanticipated Protein Modifications Using MS/MS Database Searching," *Analytical Chemistry* **77**, 3931 (2005).
7. **W. H. Tang**, "Confinement of symmetric diblock copolymer thin films," *Macromolecules* **33**, 1370 (2000).
8. **W. H. Tang**, K. S. Kostov, and K. F. Freed, "Theory for the nonequilibrium dynamics of flexible chain molecules: Relaxation to equilibrium of pentadecane from an all-trans conformation," *Journal of Chemical Physics* **108**, 8736 (1998).
9. **W. H. Tang** and T. A. Witten, "Quenched degrees of freedom in symmetric diblock copolymer thin films," *Macromolecules* **31**, 3130 (1998).
10. **W. H. Tang** and T. A. Witten, "Inducing and measuring bridging in telechelic polymer brushes," *Macromolecules* **29**, 4412 (1996).

11. **W. H. Tang**, X. Y. Chang, and K. F. Freed, "Theory for long time polymer and protein dynamics: Basis functions and time correlation functions," *Journal of Chemical Physics* **103**, 9492 (1995).

SELECTED POSTERS AND TALKS:

(available at <http://wilfredtang.com/PostersAndTalks/PostersAndTalks.html>)

1. **W. H. Tang**, M. Bern, C. Becker, K. I. Sen, Y. J. Kil, E. Carlson, H. Rohrs, E. Bergman, Y. Huang, M. Plasencia, J. Adhikari, M. Barrow, D. Fremont, G. Bowman, M. L. Gross, "Integrated Software Platform for Analyzing Hydrogen-Deuterium Exchange and Oxidative Footprinting Data," *66th ASMS Conference on Mass Spectrometry* (2018), poster.
2. **W. H. Tang**, M. Bern, A. Nichols, K. I. Sen, Y. J. Kil, E. Carlson, T. Caval, V. Franc, A. J. R. Heck, "Automated Detection of Clipped Monoclonal Antibodies from High-Resolution Native Mass Spectrometry," *66th ASMS Conference on Mass Spectrometry* (2018), poster.
3. **W. H. Tang**, Y. J. Kil, K. I. Sen, M. Bern, S. Nayak, B. Ueberheide, D. Fenyö, G. Silverman, "Automatic End-to-End De Novo Sequencing (Including I/L) of Antibodies with ETHcD Fragmentation," *65th ASMS Conference on Mass Spectrometry* (2017), poster.
4. **W. H. Tang**, M. Bern, C. Becker, K. I. Sen, "Automatic Antibody Sequencing Software," *64th ASMS Conference on Mass Spectrometry* (2016), poster.
5. **W. H. Tang**, Y. J. Kil, K. L. Crowell, M. Bern, E. Carlson, C. Becker, M. Ford, S. Saveliev, K. Pisupati, R. Ackermann, A. Schwendeman, "Rapid Identification and Quantitation of Disulfide Bonds in Infliximab (Remicade vs Remsima)," *63rd ASMS Conference on Mass Spectrometry* (2015), poster.
6. **W. H. Tang**, Y. J. Kil, C. Becker, M. Bern, "Automated Parameter Setting for Protein Database Searches," *62nd ASMS Conference on Mass Spectrometry* (2014), poster.
7. **W. H. Tang**, "Robust Method for Calculating the Local FDR for Database Search Results," *58th ASMS Conference on Mass Spectrometry* (2010), poster.
8. **W. H. Tang**, "Superior searching: The Paragon algorithm and ProteinPilot software for the identification of native (non-tryptic) peptides within a complex sample," webinar (2007).
9. **W. H. Tang**, C. L. Hunter, F. R. Rooney, N. A. Williamson, and A. W. Purcell, "Assessing the Proportion of Post-Translationally Modified Peptides in the Immunopeptidome," *HUPO 5th Annual World Congress* (2006), talk.
10. **W. H. Tang**, S. L. Seymour, and A. A. Patel, "False Positive Assessment in Database Search," *54th ASMS Conference on Mass Spectrometry* (2006), poster.
11. **W. H. Tang**, S. L. Seymour, A. Loboda, C. L. Hunter, and D. A. Schaeffer, "Recognition of Distinct Protein Isoforms and Isoform-Specific Quantitation," *53rd ASMS Conference on Mass Spectrometry* (2005), poster.
12. **W. H. Tang**, I. V. Shilov, S. L. Seymour, S. P. Keating, A. Loboda, A. A. Patel, and D. A. Schaeffer, "Discovery of Unanticipated Protein Modifications Using MS/MS Database Search," *52nd ASMS Conference on Mass Spectrometry* (2004), poster.
13. **W. H. Tang**, S. L. Seymour, S. P. Keating, I. V. Shilov, A. A. Patel, C. L. Hunter, and D. A. Schaeffer, "Estimation and Optimization of the Accuracy of Peptide Identifications Obtained by MS/MS Database Searching," *51st ASMS Conference on Mass Spectrometry* (2003), poster.

PATENTS:

1. I. V. Shilov and **W. H. Tang**, "Methods and systems for analysis and correction of mass spectrometer data," US 7982180.
2. I. V. Shilov and **W. H. Tang**, "Methods and systems for background correction in tandem mass spectrometry based quantitation," US 7919745.
3. S. L. Seymour, A. Loboda, and **W. H. Tang**, "Methods and systems for protein and peptide evidence assembly," US 2009/0053819.