
John T. Prince

Education | Experience | Publications | Contact

Education

HHMI Research Specialist (Post-doctoral)

May 2008 – present. University of Colorado (CU), Boulder, Colorado.

- Mass spectrometric identification of transient protein complexes
- Advisor: Natalie Ahn

PhD, Cell and Molecular Biology (Bioinformatics and Computational Biology)

Aug 2001 – May 2008. University of Texas (UT), Center for Systems and Synthetic Biology, Austin, Texas.

- GPA 4.00/4.00

B.S., National Merit Scholar, Microbiology (Chemistry Minor)

Dec. 2000. Brigham Young University (BYU), Provo, Utah.

- Graduated Magna Cum Laude (3.89/4.00)

Scientific Experience

Signal Transduction

May 2008 – present. Dr. Natalie Ahn Lab, CU.

- *in vivo* cross-linking and mass spectrometry analysis of transient protein-protein interactions

Proteomics & Bioinformatics

Jan. 2002 – May 2008. Dr. Edward Marcotte Lab, UT.

- Computational analysis of mass spectrometry proteomics data
- Maintenance and operation of 2D-LC nanoelectrospray LTQ-Orbitrap and Ion Trap mass spectrometers
- Creator and curator of the Open Proteomics Database (OPD)

Computational Phylogenetics

Mar. – May 2002. Dr. David Hillis Lab, UT.

- Investigation of site-likelihood parameters of Maximum Likelihood models
- Wrote programs and performed computer simulations

Antibody Engineering

Oct. 2001 – Jan. 2002. Dr. George Georgiou Lab, UT.

- Directed evolution of heat stable antibodies by Phage Display

Organic Synthesis

Jun. 1999 – Aug. 2001. Dr. Merritt Andrus Lab, BYU.

- Synthesis of Multi-Drug Resistance reversal agents (cancer research)
- Worked out a mass spectrometry screening assay
- Performed NMR, column and radial chromatography, TLC

Molecular Biology

Fall 2000. Dr. Michael Leavitt Lab, BYU.

- Isolated large, high adherence plasmid in *E. coli* for design of bacterial interference agents in poultry
- Performed gel electrophoresis, plasmid preps, electroporation, high adherence assay, fluorescence microscopy

Publications, Presentations, & Posters

Sample bias validation to examine the accuracy of large scale mass spectrometry proteomics peptide identification error estimates. Prince JT and Marcotte EM. *Analytical Chemistry* (manuscript submitted).

mspire: Mass spectrometry proteomics in Ruby. Prince JT and Marcotte EM. *Bioinformatics* (manuscript submitted).

Chromatographic alignment of ESI-LC-MS proteomics datasets by bijective interpolated dynamic time warping. Prince JT and Marcotte EM. *Analytical Chemistry*. **2006**, *78*(17), 6140-52.

Mass spectrometry of the *M. smegmatis* proteome: protein expression levels correlate with function, operons, and codon bias. Wang R, Prince JT, Graham DE, Marcotte EM. *Genome Research*. **2005**, *15*(8), 1118-26.

The need for a public proteomics repository. Prince JT, Carlson MW, Wang R, Lu P, Marcotte EM. *Nature Biotechnology*. **2004**, *22*(4), 471-2.

A fast course filtering method for peptide identification by mass spectrometry. Ramakrishnan SR, Rui M, Nakorchevskiy AA, Prince JT, Willard WS, Xu W, Marcotte EM, Miranker DP. *Bioinformatics*. **2006**, *22*(12), 1524-31.

Contact

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