

Theresa M. (Terry) Farrah  
206-913-3790  
[terry.farrah@gmail.com](mailto:terry.farrah@gmail.com)

## SUMMARY

Bioinformatics scientist with strong background in macromolecular sequence, structure, and function. Enjoys simultaneously developing software and applying it to a specific research project. Experienced in understanding key gene/protein families and using this knowledge to guide research. Skilled at implementing and refining algorithmic methods. Productive and flexible team player. Excellent writing and communication skills. Produces clean, well-documented code.

## EMPLOYMENT

Institute for Systems Biology, Seattle: Proteomics Software Engineer, August 2008 to present.

Software developer for PeptideAtlas, a global proteomics data repository. Implemented a protein inference system and collaborated with others in the proteomics community to develop terminology standards for protein identifications. Created PASSEL, a repository for targeted (SRM) proteomics data, now a key resource for researchers designing SRM experiments. Used PeptideAtlas to perform a meta-study of 91 human plasma experiments and to assess the status of the Human Proteome Project.

University of California at Berkeley: Research Associate, October 2007-July 2008.

As a member of Kimmen Sjölander's lab, developed phylogenomic methods to produce highly accurate sequence alignments for twilight zone homology-based protein structure prediction.

Meridian Geographics, Seattle: Principal, 2003-2007.

Founded a successful and ongoing business that produces 30 unique active outdoor events annually, each with up to 600 participants. Coordinated all aspects of event production; managed volunteer and contract workers; cultivated relationships with sponsors and partner organizations. Brought business to profitability.

Millennium Pharmaceuticals, Cambridge, MA: Knowledge Management Consultant, 2001-2002.

Member of development team for Compass, a web-based catalog of internal information resources.

ZymoGenetics, Seattle: Bioinformatics Scientist, 1994-1998.

Developed and applied a suite of software to discover new therapeutic proteins in cDNA databases. Extended Gribskov's profile technique to enhance selectivity, allowing detection of a new cytokine receptor. By combining automated searches and manual evaluation, I discovered ztnf4 (known as BAFF), a member of the TNF family, leading to development of Atacicept, a B-cell inhibitor currently in development at Merck.

Immunex Corporation, Seattle: Scientific Programmer/Analyst, 1989-1994.

Developed bioinformatics software. Collaborated with scientific staff. Worked extensively with cytokines and their receptors. My exploration of the TNF and TNF receptor families supported the development of Enbrel, a breakthrough drug for rheumatoid arthritis. Implemented a software pipeline to examine viral genomes, and discovered several promising genes that were put into product development.

## EDUCATION

**University of Washington, Seattle, WA**, M.S. Computer Science. National Science Foundation Fellow.

**University of California at Berkeley**, B.A. with honors, Biochemistry and Computer Science. Phi Beta Kappa.

## GENERAL SKILLS

Strong in Unix/Linux, Perl, and Python; also familiar with R, SQL, object-oriented programming and web programming. Have learned and used many other programming languages. Experience with a wide variety of bioinformatics tools.

**PUBLICATIONS, PATENTS, & REFERENCES:** See addendum.