

Curriculum Vitae

Reece Hart, Ph.D.

<http://harts.net/reece/cv.pdf>

<http://www.linkedin.com/in/reece>

1 Sussex Street, San Francisco, California 94131

home: 415-452-9916, work: 650-225-6133, email: reece@harts.net

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OBJECTIVE

I seek to apply my broad expertise in computational biology to the development of tools and analysis of data that ultimately improve our understanding of biology and disease. The ideal position will afford me leadership, learning and hands-on opportunities with diverse projects in a vibrant, focused environment.

CAREER SUMMARY

- Computational biologist with graduate degrees in biophysics (PhD) and computer science (MS).
- Seven-year scientist at Genentech with deep knowledge of computational biology and high-performance computing; broad exposure to many other scientific computing applications, including computational chemistry.
- Four-year manager of Research computing architecture and operations at Genentech; extensive relationships at all levels in Research and throughout Genentech.
- Responsible for \$6M Research-IT budget, including the approval or recommendation of all IT-related purchases.

ACADEMIC AND EMPLOYMENT HISTORY

period	position and institution	objectives and achievements
2001 June - present	Scientist (2001-2007) Bioinformatics (primary) Protein Engineering (joint appointment) and Manager, Research Computing (2008-present) Genentech, Inc. South San Francisco, California	Protein Function Annotation and Structure Prediction. Designed and developed the comprehensive functional annotation and structure prediction pipeline that is currently used for feature-based target discovery, sequence annotation, and protein variant analysis. Research Computing Architecture and Operations. Manage the computing architecture, operations, and budget for Research. Reports: 2 direct, 4 "dotted-line", >20 project-based
1999 February - 2001 May	Postdoctoral scientist Computational Biology Center IBM T. J. Watson Research Center Yorktown Heights, New York	Functional Genomics and Proteomics. Refined methods for the automated discovery of protein sequence patterns and demonstrated their use in functional classification, anonymous sequence annotation, fold-family prediction, and protein structure prediction.
1991 June - 1998 December	Doctoral student Molecular Biophysics Washington University School of Medicine St. Louis, Missouri	Ph.D. in Molecular Biophysics. Thesis topic: Theory of potential function smoothing and applications to predictions of molecular conformation and association. Also learned basic techniques of protein expression, purification, and crystallography. Advisor: Jay W. Ponder, Ph.D.
1991 June -1994 May	Masters student in computer science Washington University St. Louis, Missouri	M.S. in Computer Science. Developed C++ classes and implemented of a Bayesian probability model for the analysis of DNA sequencing data. Advisor: David J. States, M.D., Ph.D.
1988 June -1991 June	Research Assistant Salk Institute for Biological Studies La Jolla, California	Human Genome Project and Molecular Biology Laboratory Experience. Isolated a polymorphic marker on and mapped portions of 11q13 and 11q22. Advisor: Glen A. Evans, M.D., Ph.D.
1986 September -1990 June	Undergraduate student University of California, San Diego La Jolla, California	B.A. Molecular Biology

SKILLS

- Communication: I have terrific writing, speaking and organizational skills.
- Leadership: I nurture people; I articulate the balance of business value and technical feasibility well.
- Motivation: I thrive in cooperative environments and work well independently.
- Computational biology acumen: I have deep knowledge of computational biology methods and databases; I am also familiar with many computational chemistry methods and databases.
- Computing experience: I am fluent in Perl, C, shell scripting, CGI, and HTML (and knowledge of others); I have extensive experience with database design, and large, multiplatform software development projects.
- Laboratory experience: I have experience with basic molecular biology protocols, genome mapping, x-ray crystallography, and protein isolation and analysis;

PUBLICATIONS

Patent

Methods and Compositions Relating to ZPA Polypeptides

Avi Ashkenazi, Reece Hart, Erika Kratz, Kiran Mukhyala

Filed May 4, 2006

Provides new model systems for investigating apoptosis in vivo and in vitro, and provides methods for identifying agents that modulate apoptosis.

Papers

Functional characterization of the Bcl-2 gene family in the zebrafish.

Kratz E, Eimon PM, Mukhyala K, Stern H, Zha J, Strasser A, Hart R, Ashkenazi A.

Cell Death Differ. 13(10):1631-40 (2006). [PubMed PDF](#)

Computational identification and Experimental Validation of Novel Zebrafish Bcl2 Family Members

Mukhyala K, Kratz E, Ashkenazi A, Hart RK

unpublished manuscript (2005). [PDF supplementary data](#)

Systematic and Fully Automatic Discovery of Protein Sequence Patterns

Hart RK, Stolovitzky G, Royyuru AK, and Califano A

J Comput Biol. 7(3-4):585-600 (2000). [PubMed PDF](#)

Automatic Discovery of PROSITE Motifs

Hart RK, Stolovitzky G, Royyuru AK, and Califano A

Proceedings of the RECOMB 2000 Conference, Tokyo, Japan (2000).

Note: The J Comput Biol paper above subsumes most of these results.

Exploring the Similarities Between Potential Smoothing and Simulated Annealing.

Hart RK, Pappu RV, and Ponder JW

J. Comput. Chem. 21(7):531-52 (2000). [Abstract PDF](#)

Potential Function Smoothing with Application to Molecular Docking (Ph.D. Thesis)

Hart RK, Ph.D.

Thesis in Molecular Biophysics, 1998 December [Abstract PDF](#)

Analysis and Application of Potential Energy Smoothing for Global Optimization

Pappu RV, Hart RK, and Ponder JW

J. Phys. Chem. B 102:9725-9742 (1998). [Abstract PDF](#)

An Object-Oriented System for the Analysis of Automated DNA Sequencing Data

Masters Thesis in Computer Science, 1994 May [PDF WWW](#)

Isolation, localization, and physical mapping of a highly polymorphic locus on human chromosome 11q13.

Eubanks JH, Selleri L, Hart R, Rosette C, Evans GA

Genomics 11(3):720-9 (1991 Nov) [PubMed](#)

Presentations, Posters, and Software

Mining for Novel TNF Ligands using Unison, an Open Source Database for Target Discovery

poster at ISMB, 2005; Detroit, MI [PDF](#)

Introduction to and Applications of Unison, an Open Source Database for Target Discovery

poster at Automated Function Prediction 2005; Detroit, MI [PDF](#)

Structuring Structural Biology with PostgreSQL

presentation at OSCON (O'Reilly OpenSource Conference) 2004; Portland, OR [PDF](#)

Mining for protein sequences with Unison

poster at Gordon Research Conferences, Queen's College, England. (2003)

Unison Protein Database

Unison is an open source project that provides an easily-updated infrastructure for protein sequence analysis, feature-based mining, and other common tasks. (2003)

<http://unison-db.org/>

Prospect Interface

Perl module for manipulating protein threading results

Available via <http://sourceforge.net/projects/prospect-if> and CPAN. (2002)

Systematic and Automated Discovery of Patterns in PROSITE Families

Hart RK, Califano A, Stolovitzky G, Kumar AR

presentation at RECOMB 2000, April 7-11; Tokyo, Japan

SPLASH: Completely Automatic Discovery of PROSITE motifs

Hart RK, Califano A, Stolovitzky G, Kumar AR

poster presentation at the Proteins Gordon Research Conference, Holderness, New Hampshire (1999)

A Detailed Analysis of Potential Smoothing, Analogies with Simulated Annealing, and Applications to Molecular Docking

Invited presentation to the American Chemical Society, Computational Chemistry Subsection <

1998 October 28, St. Louis

autoseq - Automated DNA Sequence Analysis

C++ classes for the manipulation of automated sequencing data and the implementation of a Bayesian peak identification model (1993-1998).

[autoseq home page](#)

TINKER - Software Tools for Molecular Design

1991-1998; Acknowledged co-contributor of potential smoothing and Ewald summation methods to Jay Ponder's TINKER package

<http://dasher.wustl.edu/tinker/>

Development of a Laboratory Database for Physical Chromosome Mapping

Hart RK and Evans GA

1991 Department of Energy Annual Grantees' Conference

Santa Fe, New Mexico.

Physical Map and Overlapping Cosmid Set for Human Chromosome 11

Evans GA, et al.

1990 Department of Energy Annual Grantees' Conference

Santa Fe, New Mexico.

AWARDS AND FUNDING SOURCES

- Genentech Joint Appointment in Protein Engineering (2002-current)
- Carl and Gerty Cori Graduate Student Fellowship (1995-1996)
- National Library of Medicine grant (LM07049; 1991-1994)
- NIH Training Grant (1994-1998)

PROFESSIONAL ACTIVITIES

- Editorial services to Nature Genetics, Bioinformatics, IEEE Computational Biology, IBM Systems Journal and others
- Current or past memberships: AAAS, Protein Society, Biophysical Society, and ISCB

PERSONAL INFORMATION AND ACTIVITIES

- Hobbies: ultimate frisbee, remote controlled planes, aviation (instrument-rated pilot with 500 hours), volleyball, Go (a strategy board game)
- Weekly parent teacher in daughters' preschool
- United States Citizen
- Born Nov 22, 1968
- Married to Hanna, with three children, Madeline, Margot, and Graham

PORTFOLIO OF MAJOR ACTIVITIES AT GENENTECH

Scientific Activities

- Tumor Necrosis Factor (TNF) ligand mining (2001-2003)
I undertook an extensive effort to identify ligands for TNF receptors that had no known cognate ligand. I used Hidden Markov Models built from manually aligned sequences and several variants of protein threading against Genentech proprietary sequences, public sequences, gene predictions, and six-frame translations. Several unlikely human candidates and one excellent pathogenic candidate were found, but the TNF discovery effort at Genentech was ultimately discontinued.
- Helical Cytokine mining (2002-2003)
I directed our bioinformatics effort to identify distant homologs of long- and short-chain four helix cytokines. One new candidate appeared in the literature during our effort. We did not identify any new candidates.
- Death Domain mining (2002-2003)
I directed a bioinformatics effort to identify death domain-containing proteins from human and pathogenic sequences and gene predictions using protein threading. One Pyrin domain-containing candidate was identified from a pathogenic bacterium but our external partner discontinued this effort and Genentech opted to drop the candidate.
- Immunoreceptor Tyrosine Activating/Inhibitory/Switch Motif (ITxM) mining (2003-2004)
We used our Unison mining platform to continually search for ITxM family proteins. One novel candidate was found but was reported in the literature by another group shortly afterward.
- NOD protein modeling (2005)
I oversaw the modeling of several polymorphisms in NOD2 that led to hypotheses of the mechanistic consequences of these variants.
- Bcl-2 Family Members (2006-2007)
We used manually built Hidden Markov Models and our Unison mining platform (below) to identify five novel proapoptotic Bcl-2 family members in Zebrafish. Four of these candidates were shown experimentally to strongly induce apoptosis.
- E2/E3 protein modeling (2007)
I oversaw the modeling of an E2/E3 interface in a specific ubiquitylation complex and the prediction of critical residues; the importance of the majority of the predicted residues was subsequently validated by mutagenesis.
- Data Integration, Proteomic Analyses, and Protein Mining Tool (2002-)
I designed and developed Unison, a database of diverse precomputed proteomic predictions on a comprehensive database of sequences. Mining by database queries has greatly improved our ability to generate and refine hypotheses. The tool and non-proprietary data are freely available (<http://unison-db.org/>). Unison has become the primary source for protein annotations within Genentech Research. It is also used extensively for mining efforts by my group and others within the Bioinformatics department.

Computer Architecture and Operations Activities

In my role as the manager of Research Computing Architecture and Operations, I was involved in all aspects of strategic planning, architecture, budgeting, project management, and operational issues related to our environment. Examples of my experience are below.

- Initiated (and current chairs) the steering committee that oversees Research's computing priorities.
- Advocated for and oversaw the consolidation of independent computing platforms, leading to improved consistency and efficiency for users and streamlined operations for IT staff.
- Identified the strategic need and solution for authentication within Research's computing environment.
- Directed major hardware and software upgrades of our database, web, storage, and computing infrastructure.
- Advocated for and designed the Research file system hierarchy in our consolidated storage environment. This storage now serves all Research systems.
- Provided critical leadership for the stabilization of several problematic services and one major disk corruption incident that resulted from a vendor bug.
- Oversaw the activities of ~30 CIT personnel
- Streamlined software contract processes.
- Coordinated and approved consolidated Research IT budget and expenditures.
- Provide timely and appropriate communications to CIT, Research, and Bioinformatics staff.
- Represent Research interests to CIT via Genentech's enterprise-wide Technology Council.