

**Reece Hart, Ph.D.**  
*Curriculum Vitae*  
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(CV online at <http://harts.net/reece/cv.pdf>)

## OBJECTIVE

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I seek a leadership position in which to apply my broad expertise in computational biology, data integration, and IT management to the development of practical information systems that improve the pharmaceutical development process. I enjoy personnel management and seek to further develop my disciplined, nurturing management style. The ideal position will enable wide-ranging interactions between scientists and IT professionals in an dynamic, collaborative, and focused environment.

## CAREER SUMMARY

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- 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.
- Four-year manager of Research computing architecture and operations at Genentech (concurrent with scientific role); extensive relationships at all levels in Research and throughout Genentech.
- Responsible for \$8M Research-IT budget, including the approval of all IT-related purchases.

## EDUCATION AND EMPLOYMENT

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- 2008 Jan - present Scientific Manager, Research Computing & Informatics  
Genentech, Inc, South San Francisco, CA**  
Oversee computing strategy, budget and operations for 1300 Research personnel.
- 2001 Jun - 2008 Jan Scientist, Bioinformatics and Protein Engineering (joint appointment)  
Genentech, Inc, South San Francisco, CA**  
Designed and implemented the comprehensive protein annotation and structure prediction pipeline that is currently used for feature-based target discovery, sequence analysis, and protein variant comparisons. Promoted to scientific manager, above.
- 1999 Feb - 2001 Apr Postdoctoral fellow  
IBM T.J. Watson Research Center, Yorktown Heights, NY**  
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. Left to join Genentech.
- 1991 Aug - 1998 Dec Ph.D., Molecular Biophysics  
Washington University School of Medicine, St. Louis, MO**  
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. [PDF](#)  
Advisor: Jay W. Ponder, Ph.D.
- 1991 Aug - 1994 May M.S., Computer Science.  
Washington University in St. Louis, St. Louis, MO**  
Developed C++ classes and implemented of a Bayesian probability model for the analysis of DNA sequencing data. [PDF](#)  
Advisor: David J. States, M.D., Ph.D.
- 1988 Jun - 1991 Jun Research Assistant  
Salk Institute for Biological Studies, La Jolla, CA**  
Assisted with the isolation a polymorphic marker on, and mapped portions of, human chromosome 11.  
Advisor: Glen A. Evans, M.D., Ph.D.

## PUBLICATIONS, PRESENTATIONS, PATENTS, SOFTWARE

Full list available online at <http://harts.net/reece/pubs/>.

### Papers

Unison: An Integrated Platform for Computational Biology Discovery

Hart RK, Mukhyala K.

*Pac Symp Biocomput.* (2009). [PDF](#)

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](#) [WWW](#)

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](#)

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](#)

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](#)

### **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.*

### **Presentations and Posters**

A Tour of Research Computing at Genentech

Invited presentation, Bio-IT World Expo, Boston, April 2009. [PDF](#)

Unison: Enabling easy, rapid, and comprehensive proteomic mining

UCSF / San Francisco PostgreSQL Users' Group, March 2009. [PDF](#)

Integrating Public and Private Data: Lessons Learned with Unison

invited presentation, Molecular Medicine Tri-Conference, San Francisco, February 2009. [PDF](#)

Unison: An Integrated Platform for Computational Biology Discovery

Pacific Symposium on Biocomputing, Hawaii, January 2009. [PDF](#)

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)

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

## **Software**

### 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)

### autoseq - Automated DNA Sequence Analysis

C++ classes for the manipulation of automated sequencing data and the implementation of a Bayesian peak identification model

[autoseq home page](#)

### TINKER - Software Tools for Molecular Design

Co-contributor of potential smoothing and Ewald summation methods to Jay Ponder's TINKER package

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

## HONORS AND AWARDS

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- 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)

## RESEARCH INTERESTS

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- Remote homology detection and protein structure prediction
- Genome sequence/structure variation and disease implications
- Oncology target discovery
- Data integration

## ACADEMIC ACTIVITIES AND SERVICE

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- Editorial services to Nature Genetics, Biocomputing, Bioinformatics, IEEE Computational Biology, IBM Systems Journal, and others
- Current or past memberships: International Society for Computational Biology, AAAS, Protein Society, Biophysical Society
- NIH/NIAID Grant Review RFP-AI2008-010 (Genomic Sequencing Centers for Infectious Diseases)

## PERSONAL INFORMATION AND ACTIVITIES

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

## REFERENCES

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References will be provided upon request.

Informal recommendations may be available through <http://www.linkedin.com/in/reece> .

### **Scientific Activities**

- **Unison data integration tool and applications (2002-)**  
Designed and developed Unison, a database of precomputed predictions on a comprehensive database of sequences. Unison is the source for internal protein annotations at Genentech and enabled most of my group's mining efforts (below). The tool and non-proprietary data are freely available (<http://unison-db.org/>).
- **Zebrafish Bcl-2 remote homolog mining (2006-2007)**  
Directed and contributed to the building of Hidden Markov Models and use of 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.
- **E3 ligase mining (2006)**  
Implemented a computational test of a complex hypothesis regarding E3 ligases involved in apoptotic signaling.
- **NOD protein modeling (2005)**  
Directed the modeling of polymorphisms in NOD2 that led to hypotheses of the mechanistic consequences of these SNPs.
- **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 and subsequently reported by another group.
- **Helical cytokine mining (2002-2003)**  
Directed our structure prediction effort to identify distant homologs of long- and short-chain helical cytokines. No new candidates were identified.
- **Death Domain mining (2002-2003)**  
Directed and contributed to the use of structure prediction to identify death domain-containing proteins from human and pathogenic sequences and gene predictions.
- **Tumor Necrosis Factor (TNF) ligand mining (2001-2003)**  
Led an extensive effort to computationally identify ligands for TNF receptors that had no known cognate ligand. A small number of candidates were identified in human and pathogenic sequences, but Genentech opted to not pursue non-human TNF ligands.

### **Computer Operations & Informatics**

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.

- Advocated for and oversaw the consolidation of independent computing facilities, leading to greatly improved consistency and efficiency for users and streamlined operations for IT staff.
- Developed the technical requirements for centralized Research storage and designed the file system hierarchy in our storage environment.
- Provided critical leadership for the stabilization of several problematic services and one major disk corruption incident that resulted from a vendor bug.
- Indirectly oversaw the activities of ~20 IT personnel.
- Streamlined software contract processes.
- Managed Research's IT budget (\$8M).
- Was primary liaison between enterprise IT and Research scientific staff.