

## OBJECTIVE

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I seek to collaborate on the development of technologies that enable personalized medicine. I have extensive scientific, computational, and management experience in academic and industrial settings coupled with exceptional decision making, communication, and interpersonal skills. The ideal position will provide leadership opportunities in an agile, energetic, entrepreneurial, and focused environment.

## CAREER SUMMARY

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- Computational biologist with graduate degrees in biophysics (Ph.D.) and computer science (M.S.).
- Seven-year scientist at Genentech with deep knowledge of computational biology and high-performance computing needs for genomics, protein structure analysis, computational chemistry, and high-content screening.
- Four-year manager of Research computing architecture and operations at Genentech (concurrent with scientific role); extensive relationships and communications at all levels in Research and across Genentech.
- Responsible for \$8M Research-IT budget, including the approval of all IT-related purchases.

## EDUCATION AND EMPLOYMENT

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### **Sep 2009 – present: Chief Scientist, The Genome Commons, UC Berkeley**

QB3 and Center for Computational Biology, Celera-TCS Innovation Fellow

Collaborating with UC Berkeley and UC San Francisco faculty to build tools and databases for genome interpretation. I have prototyped our data integration platform and analysis pipelines, written four funding proposals to expand project, and communicated goals to diverse audiences since starting.

### **Jun 2001 – Sep 2009: Scientist and Scientific Manager, Genentech, South San Francisco, CA**

Scientist, Bioinformatics and Protein Engineering (joint appointment)

Scientific Manager, Research Computing & Informatics

Responsible for major target discovery initiative using protein structure prediction; designed and implemented Unison ([unison-db.org](http://unison-db.org)), a comprehensive protein database that is the basis for feature-based target discovery and protein variant comparisons; managed Research's computing strategy, budget and operations. Left to join UC Berkeley.

### **Feb 1999 – Apr 2001: 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 prediction, and protein structure prediction. Left to join Genentech.

### **Aug 1991 – Dec 1998: Ph.D. student, Molecular Biophysics, Washington University School of Medicine, St. Louis, MO**

Developed a “deformable” potential function based on AMBER/OPLS and demonstrated its use for molecular structure prediction and protein docking; learned basic techniques of protein expression, purification, and crystallography. [PDF](#)

Advisor: Jay W. Ponder, Ph.D.

### **Aug 1991 – May 1994: 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.

### **Jun 1988 – Jun 1991: 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.

### **Sep 1986 – Jun 1990: B.A., Molecular Biology, University of California, San Diego**

## PUBLICATIONS, PRESENTATIONS, PATENTS, SOFTWARE

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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  
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)

## 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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- Celera-TCS Innovation Fellow (2009-current)
- Genentech Joint Appointment in Protein Engineering (2002-2008)
- 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
- Biological 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: Human Genome Organization, Human Variome Project, International Society for Computational Biology, AAAS, Protein Society, Biophysical Society
- NIH Grant Review experience

## 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
- Hobbies: ultimate frisbee, remote controlled planes

## REFERENCES

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- References will be provided upon request.
- Informal recommendations may be available through <http://www.linkedin.com/in/reece> .

## MAJOR ACTIVITIES AT GENENTECH

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The majority of my professional career was spent at Genentech, where I had an unusual combination of scientific and operational responsibilities. My scientific responsibilities were typically focused projects to apply protein structure prediction or modeling in support of target discovery initiatives. Out of this grew Unison, a database and related tools that provide a continually updated environment for target mining and protein analysis and that is still the primary source of such data internally. I was also responsible for Research's computing strategy, architecture, budget, and operations; this environment serves approximately 1300 scientists in Research, as well as those in Development and Legal divisions.

### Scientific Activities (reverse chronological)

- 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 Activities

- 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.
- Directly or indirectly oversaw numerous multi-quarter upgrades to database, application server, computing, and operating system environments in a complex ecosystem of developers and competing priorities.
- 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.