

Daryl J. Thomas

658 Tenth Avenue
Menlo Park, California 94025
(650) 366-6234

daryljthomas@gmail.com
daryl@soe.ucsc.edu
www.soe.ucsc.edu/~daryl

Employment History

- 2007- *Senior Bioinformatics Scientist* **Navigenics, Inc.**
Personal genomics company aimed at empowering individuals to reduce their disease risk by developing products to reveal genetic predisposition for important health conditions.
- Development of the Genetic Composite Index (GCI) to estimate the association of a condition with the combined effect of a set of genetic variants.
 - Development of Affymetrix GW 6.0 and Applied Biosystems TaqMan Genotyping assays with validation against reference HapMap samples and customer saliva samples.
 - Analysis of complex genomic regions (*e.g.*, HLA and APOE) using linkage disequilibrium to identify assayable variants across all populations.
 - Integration of disease-level data (heritability, prevalence, life time risk) with locus-specific details (risk/non-risk alleles, genotype frequencies, odds ratios) to support GCI calculations for all conditions in our products.
 - Creation and development of multiple reference databases and interfaces.
- 2003-2006 *Ph.D. Candidate in Bioinformatics* **University of California, Santa Cruz**
Advisors: David Haussler, John Tamkun, and W. James Kent
Using Variation and Constraint to Understand Functional Elements in the Human Genome
- Collaborative development of three primary data sources*
- HapMap Liasion at UCSC: developed methods for data storage, display, and QA.
 - ENCODE Lead: guided a team of developers to develop features within the UCSC Genome Browser to support storage, display, QA, and analysis of new data types.
 - Evolutionary Conservation: early adoption of phastCons for use in identifying regions of evolutionary constraint in disease-associated loci.
- Analyses that intersect these datasets to produce results in genomic biology*
- Genome-wide sliding-window calculation of Tajima's D from HapMap genotypes with validation against full resequencing data identified regions of strong, recent selective sweeps in all populations and confirmed that selected regions were rarely shared between populations.
 - Comparison of linkage disequilibrium (LD) between populations and with functional element classes showed that LD is similar among populations, low near telomeres, but elevated in centromeres and duplicated regions. Regions of strong LD are GC-poor, have reduced polymorphism, are enriched for LINE repeats, and have fewer SINE, DNA, and simple repeats. Immunity and sensory genes are in regions of low LD; housekeeping genes are have high LD.
 - Derived allele frequencies of HapMap data show selective constraint in evolutionarily conserved noncoding regions, thus harboring functionally important variation and not fewer mutations.
 - ENCODE functional elements show enrichment for evolutionarily constraint but incomplete overlap suggests that some functional elements are uncharacterized or constraint is not encoded in the primary sequence.
- 2001-2003 *M.S. Student in Computer Science* **University of California, Santa Cruz**
Advisors: David Haussler, Carol Rohl, and W. James Kent
Sequence Variation in the UCSC Genome Browser
- Development of human and mouse SNP tracks in the UCSC Genome Browser.
 - Addition of scalable haplotype tracks to the UCSC Genome Browser.
 - Coursework in algorithms, Bayesian statistics, machine learning, and bioinformatics.

Employment History (continued)

- 2001-2002 *Bioinformatics Engineer* **Perlegen Sciences, Inc.**
- Development of client/server tools to manage query sequences, find their location in the genome, store this information for subsequent retrieval, and display the results with related annotations in a database-driven GUI browser.
 - Creation, loading, and quality assurance of genomic annotations.
 - Development of a semi-automated pipeline for sequence processing, including acquisition, repeat masking, primer design, primer ordering, and primer tracking.
- 1999-2001 *Data Analyst in Single Nucleotide Polymorphism Discovery* **Affymetrix, Inc.**
- Tracking and analyzing data generated by the Polymorphisms group.
 - Liaison to internal colleagues and to external clients and collaborators.
 - Used in-house applications to analyze chip image data for SNP identification.
 - Developed methods for improving data access, used these tools to track progress.
 - Coordinated ongoing and retrospective analyses of data quality and validation rates to identify inconsistencies in data quality and identify sources of variability.
 - Trained users on in-house software and worked with developers to make functional enhancements.
- 1997-1998 *Senior Research Associate in Product Development* **Sentinel Biosciences, Inc.**
- Purified and characterized antigens for immunization and antibody screening.
 - Developed IgG quantitation ELISA to increase sensitivity and decrease cost.
 - Established tissue culture facility and selected optimum growth conditions for hybridoma cell lines by IgG quantitation ELISA and antigen binding ELISA.
 - Screened polyclonal antisera from five rabbits for antibody titer and specificity.
- 1995-1997 *Graduate Student in Neuroscience* **University of California, Davis**
- Prepared an electroencephalogram using specialized software to record, compile, and average the responses from each of five individuals.
 - Completed analysis of visually evoked single neuron responses by writing new algorithms and using existing statistical tools.
 - Measured effects of pesticide impurities on membrane potential and conductance.
 - Grant proposal to study the involvement of NMDA receptor expression during the critical period of retinal ganglion cell development.
 - Labeled and isolated single retinal ganglion cells for use in differential gene expression and synthesized cDNA from one cell equivalent of total RNA.
- 1992-1995 *Research Technician II in Signal Transduction and Gene Regulation*
Howard Hughes Medical Institute, Stanford University
- Biochemical purification and cloning of the transcription factor NF-ATc and paralogs.
 - Characterized NF-ATc clones by RNase protection, Northern and Southern blot analysis, eukaryotic transienttransfection, reporter gene assays, cytosolic and nuclear protein extraction, and electrophoretic mobility shift assays.
 - Curated and submitted nucleotide sequence data, searched databases for homologs and orthologs using BLAST, evaluated similarity using ALIGN.
 - Created monoclonal antibodies using recombinant protein purification, mouse immunization, antiserum characterization, and Western blots.
- 1991-1992 *Research Associate in DNA Synthesis Chemistry*
Protein and Nucleic Acid Facility, Stanford University
- Increased synthesis capacity three-fold to over 400 oligonucleotides per month.
 - Developed processes and protocols for new reagents and instrumentation.
- 1990-1991 *Research Associate in Organic Chemistry* **Clontech Laboratories, Inc.**
- Developed protocols for synthesis of Biotin-ON phosphoramidite and related reagents for incorporating chemical labels into synthetic oligonucleotides.

Education

2006	Ph.D.	Bioinformatics	UC Santa Cruz
2003	M.S.	Computer Science	UC Santa Cruz
2001	Certificate	Bioinformatics	UC Santa Cruz Extension
2000	Certificate	Database Systems	UC Santa Cruz Extension
1997	M.S. (abd)	Neuroscience	UC Davis
1994	Coursework	Molecular Biology and Biochemistry	Stanford University
1990	B.S.	Chemistry	Carnegie Mellon University

Computational Skills

Operating Systems	RedHat Linux, Solaris Unix, Windows NT, Windows XP, Max OS X.
Languages	C/C++/C#, Java, Perl/CGI, Ruby/Rails, HTML, PL/SQL, MySQL, R, L ^A T _E X.
Clusters	Parasol for Linux and Platform LSF for Linux and Windows.
Office	Word, Excel, PowerPoint, Project; GoogleDocs.
Engineering	CVS, SVN, SourceSafe, NetBeans, OOA/OOD, modular design, integrated testing.
Web	UCSC (Genome Browser, Tables, ...), Ensembl, NCBI, HapMap, ENCODE.
Specialized	Affymetrix DMET and Genotyping; AB Sequence Detection System

Grants

2003-2006	W. James Kent, <u>Daryl J. Thomas</u> , and David Haussler ENCODE graduate research grant NHGRI and University of California, Santa Cruz
1997	<u>Daryl J. Thomas</u> and Leo M. Chalupa Jastro Shields Research Grant University of California, Davis <i>Regulation of the critical period of plasticity in retinal development by expression of NMDA receptor subunit 2b</i>
1986-1990	<u>Daryl J. Thomas</u> University tuition grant Carnegie Mellon University

Patents

John B. Sheehan, Daryl J. Thomas, and Wade A. Barrett
Algorithms for Selection of Primer Pairs
Filed January 9, 2002; assigned May 24, 2005
United States Patent 6,898,531; Assigned to Perlegen Sciences

Karin Au, Jingwen Chen, Nila Patil, and Daryl J. Thomas
Genetic Compositions and Methods
Filed November 10, 2000; assigned May 17, 2001
International Publication Number WO/2001/034840; Assigned to Glaxo-Wellcome

Professional Activities

2005-	American Association for Cancer Research	Member
2003-	International Genetic Epidemiology Society	Member
2000-	International Society for Computational Biology	Member
2000-	American Society for Human Genetics	Member
2000-2001	UCSC Extension Bioinformatics Certificate Steering Committee	Member
1999-2004	Bay Area Bioinformatics Discussion Group	Co-founder
1995-1998	Society for Neuroscience	Member
1993-	American Association for the Advancement of Science	Member
1987-1997	American Chemical Society	Member

Publications

Presymptomatic risk assessment for complex genetic disease

Eran Halperin, Badri Padhukasahasram, Jennifer Wessel, Daryl Thomas, Elana Silver, Heather Trumbower, Nicholas J. Schork, Michele Cargill, Dietrich A. Stephan

2009 *submitted*.

Genome-wide detection and characterization of positive selection in human populations

Pardis C. Sabeti, Patrick Varilly, Ben Fry, Jason Lohmueller, Elizabeth Hostetter, Chris Cotsapas, Xiaohui Xie, Elizabeth H. Byrne, Steven A. McCarroll, Rachele Gaudet, Stephen F. Schaffner, Eric S. Lander, and The International HapMap Consortium

Nature 2007 October 18, 449(7164):913-918. PMID: 17943131; doi:10.1038/nature06250

A second generation human haplotype map of over 3.1 million SNPs

The International HapMap Consortium

Nature 2007 October 18, 449:851-861; doi:10.1038/nature06258

Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project

The ENCODE Project Consortium

Nature 2007 June 14, 447:799-816; doi:10.1038/nature05874

Fast-evolving non-coding sequences in the human genome

Christine P. Bird, Barbara E. Stranger, Maureen Liu, Daryl J. Thomas, Catherine E. Ingle, Claude Beazley, Webb Miller, Matthew E. Hurles, and Emmanouil T. Dermitzakis

Genome Biology 2007 Jun, 8(6):R118; doi:10.1186/gb-2007-8-6-r118

Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome

Elliott H. Margulies*, Gregory M. Cooper*, George Asimenos*, Daryl J. Thomas*, Colin N. Dewey*, Adam C. Siepel, Ewan Birney, Damian Keefe, Ariel S. Schwartz, Minmei Hou, James Taylor, Sergey Nikolaev, Juan I. Montoya-Burgos, Ari Löytynoja, Simon Whelan, Fabio Pardi, Tim Massingham, James B. Brown, Peter Bickel, Ian Holmes, James C. Mullikin, Abel Ureta-Vidal, Benedict Paten, Kate R. Rosenbloom, W. James Kent, NISC Comparative Sequencing Program, Baylor College of Medicine Human Genome Sequencing Center, Washington University Genome Sequencing Center, Broad Sequencing Platform, UCSC Genome Browser Team, Stylianos Antonarakis, Serafim Batzoglou, Nick Goldman, Ross Hardison, David Haussler, Webb Miller, Lior Pachter, Eric D. Green, and Arend Sidow

Genome Research 2007 Jun; 17:760-774

PhenCode: Connecting ENCODE Data with Mutations and Phenotype

Belinda Giardine, Cathy Riemer, Tim Hefferon, Daryl Thomas, Fan Hsu, Julian Zielenski, Yunhua Sang, Laura Elnitski, Garry Cutting, Heather Trumbower, Andy D. Kern, Robert M. Kuhn, George Patrinos, Jim Hughes, Doug Higgs, David Chui, Charles Scriver, Manyphong Phommarinh, Santosh K. Patnaik, Olga Blumenfeld, Bruce Gottlieb, Mauno Vihinen, Jouni Väliäho, W. James Kent, Webb Miller, and Ross C. Hardison

Human Mutation 2007 Jun; 28(6):554-562; doi:10.1002/humu.20484

The ENCODE Project at UC Santa Cruz

Daryl J. Thomas, Kate R. Rosenbloom, Hiram Clawson, Angie S. Hinrichs, Heather Trumbower, Brian J. Raney, Donna Karolchik, Galt P. Barber, Rachel A. Harte, Jennifer Hillman-Jackson, Robert M. Kuhn, Brooke L. Rhead, Kayla E. Smith, Archana Thakkapallyil, Ann S. Zweig, The ENCODE Project Consortium, David Haussler, and W. James Kent

Nucleic Acids Research 2007 Jan; 35:D663-D667; doi:10.1093/nar/gkl1017

Variation resources at UC Santa Cruz

Daryl J. Thomas, Heather Trumbower, Andrew D. Kern, Brooke L. Rhead, Robert M. Kuhn, David Haussler, and W. James Kent

Nucleic Acids Research 2007 Jan; 35:D716-D720; doi:10.1093/nar/gkl953

The UCSC Genome Browser Database: update 2007

Robert M. Kuhn, Donna Karolchik, Ann S. Zweig, Heather Trumbower, Daryl J. Thomas, Archana Thakkapallyil,

Charles W. Sugnet, Mario Stanke, Kayla E. Smith, Adam Siepel, Kate R. Rosenbloom, Brooke L. Rhead, Brian J. Raney, Andy Pohl, Jakob S. Pedersen, Fan Hsu, Angie S. Hinrichs, Rachel A. Harte, Mark Diekhans, Hiram Clawson, Gill Bejerano, Galt P. Barber, Robert Baertsch, David Haussler and W. James Kent
Nucleic Acids Research 2007 Jan; 35:D668-D673; doi:10.1093/nar/gkl928

Conserved noncoding sequences are selectively constrained and not mutation cold spots
 Jared A. Drake*, Christine Bird*, James Nemesh*, Daryl J. Thomas*, Christopher Newton-Cheh, Alexandre Raymond, Laurent Excoffier, Homa Attar, Stylianos E. Antonarakis, Emmanouil T. Dermitzakis, and Joel N. Hirschhorn
Nature Genetics 2006 Feb; 38(2):223-227

The UCSC Genome Browser Database: update 2006
 Angie S. Hinrichs, Donna Karolchik, Robert Baertsch, Galt P. Barber, Gill Bejerano, Hiram Clawson, Mark Diekhans, Terry S. Furey, Rachel A. Harte, Fan Hsu, Jennifer Hillman-Jackson, Robert M. Kuhn, Jakob S. Pedersen, Andy Pohl, Brian J. Raney, Kate R. Rosenbloom, Adam Siepel, Kayla E. Smith, Charles W. Sugnet, Ali Sultan-Qurraie, Daryl J. Thomas, Heather Trumbower, Ryan J. Weber, Matthew Weirauch, Ann S. Zweig, David Haussler, and W. James Kent
Nucleic Acids Research. 2006 Jan; 34:D590-D598

Common deletion polymorphisms in the human genome
 Steven A McCarroll, Tracy N Hadnott, George H Perry, Pardis C Sabeti, Michael C Zody, Jeffrey C Barrett, Stephanie Dallaire, Stacey B Gabriel, Charles Lee, Mark J Daly, David M Altshuler, and The International HapMap Consortium
Nature Genetics 2006 Jan; 38(1):86-92. doi:10.1038/ng1696

Sequence features in regions of weak and strong linkage disequilibrium
 Albert Vernon Smith*, Daryl J. Thomas*, Heather M. Munro, Gonçalo R. Abecasis
Genome Research 2005 Nov; 15(10):1519-1534

Genomic regions exhibiting positive selection identified from dense genotype data
 Christopher S. Carlson, Daryl J. Thomas, Michael Eberle, Robert Livingston, Mark Rieder, Deborah A. Nickerson
Genome Research 2005 Nov; 15(10):1553-1565

A haplotype map of the human genome
 The International HapMap Consortium
Nature 2005 Oct 27; 437(7063):1299-1320

LS-SNP: large-scale annotation of coding non-synonymous SNPs based on multiple information sources
 Rachel Karchin, Mark Diekhans, Libushka Kelly, Daryl J. Thomas, Ursula Pieper, Narayanan Eswar, David Haussler, and Andrej Sali
Bioinformatics 2005 Jun 15; 21(12):2814-2820

The ENCODE (ENCyclopedia Of DNA Elements) Project
 The ENCODE Project Consortium
Science 2004 Oct 22; 306(5696):636-640

Finishing the euchromatic sequence of the human genome
 International Human Genome Sequencing Consortium
Nature 2004 Oct 21; 431(7011):931-945

The UCSC Genome Browser Database
 Donna Karolchik, Robert Baertsch, Mark Diekhans, Terry S. Furey, Angie Hinrichs, Yontao Lu, Krishna Roskin, Matt Schwartz, Charles W. Sugnet, Daryl J. Thomas, Ryan Weber, David Haussler, W. James Kent
Nucleic Acids Research. 2003 Jan 1; 31(1):51-54. PMID:12519945; PMCID: 165576

Blocks of limited haplotype diversity revealed by high-resolution scanning of human chromosome 21
 Nila Patil, Anthony J. Berno, David A. Hinds, Wade A. Barrett, Jigna M. Doshi, Coleen R. Hacker, Curtis R. Kautzer, Danny H. Lee, Claire Marjoribanks, David McDonough, Bich T. Nguyen, Michael C. Norris, John B. Shee-

han, Naiping Shen, David Stern, Renee P. Stokowski, Daryl J. Thomas, Mark O. Trulson, Kanan R. Vyas, Kelly A. Frazer, Stephen P. Fodor, David P. Cox
Science. 2001 Nov 23; 294(5547):1719-1723. PMID: 11721056

Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse
Kerstin Lindblad-Toh, Ellen Winchester, Mark J. Daly, David G. Wang, Joel N. Hirschhorn, Jean-Philippe Laviolette, Kristin Ardlie, David E. Reich, Elizabeth Robinson, Pamela Sklar, Nila Shah, Daryl Thomas, Jian-Bing Fan, Thomas Gingeras, Janet Warrington, Nila Patil, Thomas J. Hudson, Eric S. Lander
Nature Genetics. 2000 Apr; 24(4):381-386. PMID: 10742102

NFATc3, a lymphoid-specific NFATc family member that is calcium-regulated and exhibits distinct DNA binding specificity
Steffan N. Ho, Daryl J. Thomas, Luika A. Timmerman, Xu Li, Uta Francke, Gerald R. Crabtree
Journal of Biological Chemistry. 1995 Aug 25; 270(34):19898-19907. PMID: 765004

Cloning and chromosomal localization of the human and murine genes for the T-cell transcription factors NFATc and NFATp
Xu Li, Steffan N. Ho, Jac Luna, Joe Giacalone, Daryl J. Thomas, Luika A. Timmerman, Gerald R. Crabtree, Uta Francke
Cytogenetics and Cell Genetics. 1995; 68(3-4):185-191. PMID: 7842733

NF-AT components define a family of transcription factors targeted in T-cell activation
Jeffrey P. Northrop, Steffan N. Ho, Lei Chen, Daryl J. Thomas, Luika A. Timmerman, Garry P. Nolan, Ari Admon, Gerald R. Crabtree
Nature. 1994 Jun 9; 369(6480):497-502. PMID: 8202141

Oligonucleotide labeling methods. 3. Direct labeling of oligonucleotides employing a novel, non-nucleosidic, 2-aminobutyl-1,3-propanediol backbone
Paul S. Nelson, Mary Amputch, Mark A. Kent, Sylvester Muthini, Daryl J. Thomas
Nucleic Acids Research. 1992 Dec 11; 20(23):6253-6259. PMID: 1475185

Posters

Curating Genetic Association Literature for Common Diseases
Elana Silver, Eran Halperin, Kord M. Kober, Badri Padhukasahasram, Nila Patil, Michelle Sommargren, Dietrich A. Stephan, Daryl J. Thomas, Heather Trumbower, and Michele Cargill
3rd International Biocuration Conference
April 16, 2009; doi:10.1038/npre.2009.3174.1

Pre-symptomatic risk assessment for complex genetic diseases
Badri Padhukasahasram, Eran Halperin, Jennifer Wessel, Daryl J. Thomas, Elana Silver, Heather Trumbower, Nicholas J. Schork, and Michele Cargill, and Dietrich A. Stephan
American Society for Human Genetics
November 14, 2008 [2497/F]
<http://www.ashg.org/2008meeting/abstracts/fulltext/f20399.htm>

Variation and Selection in the UCSC Genome Browser
Daryl J. Thomas, Heather Trumbower, Andrew D. Kern, David Haussler, W. James Kent
American Society for Human Genetics
October 12, 2006

Genome-wide Distribution of Genes and Sequence Features in Regions of Weak and Strong Linkage Disequilibrium
Albert Vernon Smith, Daryl J. Thomas, Heather Munro, and Goncalo Abecasis
Genome Informatics, CSHL
October 31, 2005

Genome-wide Distribution of Genes and Sequence Features in Regions of Weak and Strong Linkage Disequilibrium

Albert Vernon Smith, Daryl J. Thomas, Heather Munro, and Goncalo Abecasis
American Society for Human Genetics
October 28, 2005

ENCODE and HapMap data in the UCSC Genome Browser
Daryl J. Thomas, Kate Rosenbloom, Adam Siepel, Hiram Clawson, Jim Kent, Webb Miller, David Haussler
6th Annual UC System-Wide Bioengineering Symposium
June 26, 2005

HapMap Data in the UCSC Genome Browser
Daryl J. Thomas, Jim Kent, and David Haussler
Biology of Genomes, CSHL
May 14, 2005

The Analysis of ENCODE Data at UCSC
Daryl J. Thomas, Kate Rosenbloom, Adam Siepel, Hiram Clawson, Jim Kent, David Haussler, and Webb Miller
Biology of Genomes, CSHL
May 14, 2005

HapMap Data in the UCSC Genome Browser
Daryl J. Thomas, Jim Kent, and David Haussler
Genomic Studies and the HapMap, Oxford
March 17, 2005

Large-scale annotation of coding SNPs based on structure considerations
Rachel Karchin, Ursula Pieper, Fred Davis, Narayanan Eswar, Andrea Rossi, Marc Marti-Renom, Andrej Sali, Mark Diekhans, Daryl J. Thomas, David Haussler
Genomic Studies and the HapMap, Oxford
March 15, 2005

Large-scale annotation of coding nsSNPs based on structure considerations
Rachel Karchin, Ursula Pieper, Mark Diekhans, Daryl J. Thomas, Fred Davis, Eswar Narayanan, Marc Marti-Renom, Andrea Rossi, David Haussler, Andrej Sali
ISMB 2004
August 2, 2004

Single nucleotide polymorphism discovery in candidate genes for rheumatoid arthritis
Coleen Hacker, Daryl J. Thomas, Jigna Doshi, Robert P. Kimberly, Thomas R. Gingeras, Nila Patil
American Journal of Human Genetics. 2000 Oct 2; 67(4):1864 (Suppl.)

High specificity immunoassays to detect *Chlamydia trachomatis*
Teresa Y. Yang, Vivian Laitila, Daryl J. Thomas, and Helen H. Lee.
American Society for Microbiology Annual Meeting
1998

Presentations

Comparative Genomics at the University of California, Santa Cruz
Daryl J. Thomas, Heather Trumbower, Fan Hsu, David Haussler, and W. James Kent
Stanford Bioinformatics Week
June 15, 2006

Comparative Genomics at the University of California, Santa Cruz
Daryl J. Thomas, Heather Trumbower, Fan Hsu, David Haussler, and W. James Kent
American Association of Cancer Research Annual Meeting
April 1, 2006

What Are We Made Of? An active presentation of how DNA makes proteins, the building blocks of life
Daryl J. Thomas, Heather Trumbower, and Robert Baertsch
Science Alive! Tutorial at Gavilan College
January 29, 2005

Identification of Functional Elements and Integration of ENCODE data
Daryl J. Thomas, Kate Rosenbloom, Jim Kent, and David Haussler
ENCODE Consortium Meeting
November 10, 2004

Genome Browser Tutorial
Daryl J. Thomas
IEEE Computational Systems Bioinformatics 2004
August 16, 2004

UCSC Genome Browser
Daryl J. Thomas, Jim Kent, and David Haussler
Comparative Genomics Group, NHGRI
July 1, 2004

Comparative Analysis of Mammalian Genomes: Multiple Alignment, Phylogenetic Analysis, and Evolutionary Conservation
Daryl J. Thomas, Kate Rosenbloom, Adam Siepel, Jim Kent, David Haussler, and Webb Miller
ENCODE Consortium Meeting
June 28, 2004

Sequence-Based Data Management at UCSC for the ENCODE Project: Data Submission, Visualization, Analysis, and Public Access
Daryl J. Thomas, Kate Rosenbloom, Hiram Clawson, Angie Hinrichs, Jim Kent, David Haussler, and Webb Miller
ENCODE Consortium Meeting
June 28, 2004

ENCODE data management
Daryl J. Thomas, Kate Rosenbloom, Jim Kent, and David Haussler
Center for Comparative Genomics and Bioinformatics at Pennsylvania State University
June 25, 2004

Connecting sequence conservation, experimental data, and functional annotation: Visualizing ENCODE on the UCSC Browser
Daryl J. Thomas, Kate Rosenbloom, Jim Kent, and David Haussler
ENCODE Consortium Meeting
December 19, 2003

UCSC Genome Browser presentation
Daryl J. Thomas, Jim Kent, and David Haussler
The Tech Museum Awards
October 14, 2003