

# TIMOTHY E. REDDY

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## CURRENT POSITION

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### **Assistant Professor of Genome Sciences**

**2011 – present**

Duke University Medical School  
Institute for Genome Sciences & Policy and,  
Department of Biostatistics & Bioinformatics, Durham, NC  
Lab website: <http://reddylab.org>

### **Secondary Appointment**

**2012 – present**

Duke Department of Molecular Genetics and Microbiology, Division of Human Genetics

The long-term goal of my lab is to understand how genetic changes in gene regulation contribute to recent human evolution. To break new ground on this long-standing problem, we develop and use cutting-edge genomic technologies that enable us to identify and characterize regulatory mutations across the human genome. Because of the massive datasets that we generate, the research demands an interdisciplinary combination of computational and molecular techniques. That interdisciplinary approach sets our lab apart and, we believe, will be the key to understanding how humans have and continue to evolve.

## EDUCATION AND TRAINING

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### **Postdoctoral Fellow, Stanford University and HudsonAlpha Institute**

**2007 – 2011**

Using sequencing-based functional genomics, I researched the relationship between genome sequence and gene expression, both in the context of allele-specific gene expression in an individual, and in the genome-wide response to glucocorticoids.

Advisor: Richard Myers

### **Ph.D. in Bioinformatics, Boston University**

**2003 – 2007**

*“Advances in the Prediction and Understanding of Transcriptional Regulation in Yeast”*

Advisor: Charles DeLisi

### **B.S. in Computer Science, Stanford University**

**1999 – 2003**

## PREVIOUS RESEARCH EXPERIENCE

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### **Postdoctoral Fellow under Dr. Richard Myers**

**2007 – 2011**

My postdoctoral research focuses on using comprehensive genomic measurements of transcriptional regulation and epigenetic marks to understand biological questions. First, to better understand the link between genome sequence and gene expression, I produced the most comprehensive map of human allele-biased transcription factor occupancy and allele-biased expression to date. The results revealed several new discoveries that may have important consequence in our understanding of gene regulation, imprinting, X-inactivation, and the functional consequence of variants identified in GWAS studies. Second, through a detailed comprehensive study of glucocorticoid receptor (GR) occupancy and related gene expression, I discovered and characterized a novel behavior of the GR that allows it to specifically express the key circadian gene PER1 at a targeted low dose of corticosteroid.

### **Boston University Bioinformatics Program under Dr. Charles DeLisi**

**2003 – 2007**

In my thesis, entitled “Advances in the prediction and understanding of transcriptional regulation in yeast,” I developed novel computational strategies to identify transcription factor binding sites.

Using a novel graph theoretical technique, I identified *cis*-regulatory sites across the yeast genome. Applying our approach to human sequences, we identified and validated specific transcription factor binding sites in the promoters of GABAA receptor subunit genes. Finally, I worked on using comparative genomics to study fundamental and evolutionarily conserved mechanisms of transcriptional initiation.

### Stanford Hematology Department under Dr. Peter Lee

2001 – 2003

Collaborated on the design and development of a molecular simulation of the initial stages of T cell Activation. Using the model, we explored the ability of the T cell to integrate signals from tens of thousands of peptide-MHC molecules presented on the surface of Antigen Presenting Cells; and evaluated the effects of various endogenous peptide mixtures on T cell recognition and sensitivity.

## PUBLICATIONS

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\* Indicates corresponding author

22) Gertz J., D. Savic, K. E. Varley, E. C. Partridge, A. Safi, P. Jain, G. M. Cooper, **T. E. Reddy**, G. E. Crawford & R. M. Myers. Distinct properties of cell type-specific and shared transcription factor binding sites. *Molecular Cell*. In Press.

21) Hayes, M. G., M. Urbanek, M. F. Hivert, L. L. Armstrong, J. Morrison, C. Guo, L. P. Lowe, ..., **T. E. Reddy**, N. J. Cox, W. L. Lowe Jr; HAPO Study Cooperative Research Group. "Identification of Hkdc1 and Bace2 as Genes Influencing Glycemic Traits During Pregnancy through Genome-Wide Association Studies." *Diabetes* (Jul 31 2013).

20) Perez-Pinera, P., D. D. Kocak, C. M. Vockley, A. F. Adler, A. M. Kabadi, L. R. Polstein, P. I. Thakore, ..., **T.E. Reddy**, C.A. Gersbach. "Rna-Guided Gene Activation by Crispr-Cas9-Based Transcription Factors." *Nat Methods* (Jul 25 2013).

19) Gao, X., C. M. Vockley, F. Pauli, K. M. Newberry, Y. Xue, S. H. Randell, **T. E. Reddy\***, and B. L. Hogan\*. "Evidence for Multiple Roles for Grainyheadlike 2 in the Establishment and Maintenance of Human Mucociliary Airway Epithelium." *Proc Natl Acad Sci U S A* (May 20 2013).

18) Urbanek, M., M. G. Hayes, L. L. Armstrong, J. Morrison, L. P. Lowe, S. E. Badon, D. Scheftner, ..., **T. E. Reddy**, N. J. Cox, W. L. Lowe Jr; HAPO Study Cooperative Research Group. "The Chromosome 3q25 Genomic Region Is Associated with Measures of Adiposity in Newborns in a Multi-Ethnic Genome-Wide Association Study." *Hum Mol Genet* (Apr 24 2013).

17) Varley, K. E., J. Gertz, K. M. Bowling, S. L. Parker, **T. E. Reddy**, F. Pauli-Behn, M. K. Cross, *et al.* "Dynamic DNA Methylation across Diverse Human Cell Lines and Tissues." *Genome Res* 23, no. 3 (Mar 2013): 555-67.

16) Gertz, J., **T. E. Reddy**, K. E. Varley, M. J. Garabedian, and R. M. Myers. "Genistein and Bisphenol a Exposure Cause Estrogen Receptor 1 to Bind Thousands of Sites in a Cell Type-Specific Manner." *Genome Res* 22, no. 11 (Nov 2012): 2153-62.

15) Dunham, I., A. Kundaje, S. F. Aldred, P. J. Collins, C. A. Davis, F. Doyle, C. B. Epstein, *et al.* "An Integrated Encyclopedia of DNA Elements in the Human Genome." *Nature* 489, no. 7414 (Sep 6 2012): 57-74.

**+ Article recommended by the "Faculty of 1000"**

14) Gerstein, M. B., A. Kundaje, M. Hariharan, S. G. Landt, K. K. Yan, C. Cheng, X. J. Mu, *et al.* "Architecture of the Human Regulatory Network Derived from Encode Data." *Nature* 489, no. 7414 (Sep 6 2012): 91-100.

**+ Article recommended by the "Faculty of 1000"**

13) Landt, S. G., G. K. Marinov, A. Kundaje, P. Kheradpour, F. Pauli, S. Batzoglou, B. E. Bernstein, *et al.* "Chip-Seq Guidelines and Practices of the Encode and Modencode Consortia." *Genome Res* 22, no. 9 (Sep 2012): 1813-31.

**+ Article recommended by the "Faculty of 1000"**

12) **Reddy, T. E.**, J. Gertz, G. E. Crawford, M. J. Garabedian, and R. M. Myers. "The Hypersensitive Glucocorticoid Response Specifically Regulates Period 1 and Expression of Circadian Genes." *Mol Cell Biol* 32, no. 18 (Sep 2012): 3756-67.

**+ Cover of Molecular and cellular biology and recommended by the "Faculty of 1000"**

11) **Reddy, T. E.**, J. Gertz, F. Pauli, K. S. Kucera, K. E. Varley, K. M. Newberry, G. K. Marinov, *et al.* "Effects of Sequence Variation on Differential Allelic Transcription Factor Occupancy and Gene Expression." *Genome Res* 22, no. 5 (May 2012): 860-9.

10) Kucera, K. S., **T. E. Reddy**, F. Pauli, J. Gertz, J. E. Logan, R. M. Myers, and H. F. Willard. "Allele-Specific Distribution of Rna Polymerase Ii on Female X Chromosomes." *Hum Mol Genet* 20, no. 20 (Oct 15 2011): 3964-73.

9) Gertz, J., K. E. Varley, **T. E. Reddy**, K. M. Bowling, F. Pauli, S. L. Parker, K. S. Kucera, H. F. Willard, and R. M. Myers. "Analysis of DNA Methylation in a Three-Generation Family Reveals Widespread Genetic Influence on Epigenetic Regulation." *PLoS Genet* 7, no. 8 (Aug 2011): e1002228.

8) The ENCODE Project Consortium "A User's Guide to the Encyclopedia of DNA Elements (Encode)." *PLoS Biol* 9, no. 4 (Apr 2011): e1001046.

7) Brunner, A. L., D. S. Johnson, S. W. Kim, A. Valouev, **T. E. Reddy**, N. F. Neff, E. Anton, *et al.* "Distinct DNA Methylation Patterns Characterize Differentiated Human Embryonic Stem Cells and Developing Human Fetal Liver." *Genome Res* 19, no. 6 (Jun 2009): 1044-56.

6) **Reddy, T. E.**, F. Pauli, R. O. Sprouse, N. F. Neff, K. M. Newberry, M. J. Garabedian, and R. M. Myers. "Genomic Determination of the Glucocorticoid Response Reveals Unexpected Mechanisms of Gene Regulation." *Genome Res* 19, no. 12 (Dec 2009): 2163-71.

5) **Reddy, T. E.**, B. E. Shakhnovich, D. S. Roberts, S. J. Russek, and C. DeLisi. "Positional Clustering Improves Computational Binding Site Detection and Identifies Novel Cis-Regulatory Sites in Mammalian Gabaa Receptor Subunit Genes." *Nucleic Acids Res* 35, no. 3 (2007): e20.

4) **Reddy, T. E.**, C. DeLisi, and B. E. Shakhnovich. "Binding Site Graphs: A New Graph Theoretical Framework for Prediction of Transcription Factor Binding Sites." *PLoS Comput Biol* 3, no. 5 (May 2007): e90.

3) Casal, A., C. Sumen, **T. E. Reddy**, M. S. Alber, and P. P. Lee. "Agent-Based Modeling of the Context Dependency in T Cell Recognition." *J Theor Biol* 236, no. 4 (Oct 21 2005): 376-91.

2) **Reddy, T. E.**, C. DeLisi, and B. E. Shakhnovich. "Assessing Transcription Factor Motif Drift from Noisy Decoy Sequences." *Genome Inform* 16, no. 1 (2005): 59-67.

1) Shakhnovich, B. E., **T. E. Reddy**, K. Galinsky, J. Mellor, and C. Delisi. "Comparisons of Predicted Genetic Modules: Identification of Co-Expressed Genes through Module Gene Flow." *Genome Inform* 15, no. 1 (2004): 221-8.

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## RESEARCH SUPPORT

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- R01 1R01DK099820-01** Lowe (PI) 10/01/2013-09/30/2018  
**Genetics and Genomics of Maternal Glycemia During Pregnancy**  
 Goal: identify gene regulatory mechanisms that contribute to human fetal adiposity.  
 Role: Investigator
- R01 1R01DA036865-01** Gersbach (PI) 10/01/2013-09/30/2018  
**Engineering Targeted Epigenetic Modifiers for Precise Control of Gene Regulation**  
 Goal: develop new technologies for the targeted control of the human epigenome.  
 Role: Investigator
- R01 1R01DK099820-01** Lowe (PI) 06/01/2013-05/31/2018  
**Genetics and Evolution of Fetal Human Fat Accretion During Development**  
 Goal: identify gene regulatory mechanisms that contribute to human fetal adiposity.  
 Role: Investigator
- U54 1U54HG006998-02** Myers (PI) 09/21/2012-07/31/2016  
**Toward a comprehensive functional annotation of the human genome**  
 Goal: comprehensively identify the binding sites for all regulatory factors in the human genome.  
 Role: Investigator

## AWARDS AND FELLOWSHIPS

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- Featured in Genome Technology's "Young Investigators" issue** 2012
- Postdoctoral Scholar Training Fellowship** 2009 – 2011  
 University of Alabama School of Medicine, Division of Clinical Immunology and Rheumatology
- Travel Fellowship** 2007  
 International Conference on Intelligent Systems for Molecular Biology (ISMB)
- Departmental Award for Excellence in Teaching** 2007  
 Boston University
- Graduate Research Assistantship and University Scholarship** 2005 – 2006  
 Boston University
- Presidential Fellowship** 2004 – 2005  
 Boston University

## INVITED TALKS (selected)

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- Triangle Statistical Genetics Meeting** 2013
- Genomic Sciences Seminar Series, University of Virginia** 2013
- Boston University Student Organized Symposium** 2013
- Population Architecture using Genomics and Epidemiology Steering Committee** 2012
- Duke Center for Human Genome Variation, Human Genetics Evening** 2012
- Biochemistry Seminar Series, North Carolina State University** 2012
- Duke Epigenetics and Epigenomics Program Colloquium** 2012

## TEACHING

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- Instructor for "UPGEN 778: Solutions in Gene Regulation" at Duke University** 2012

<b>Instructor for “UPGEN 532: Human Genetics” at Duke University</b>	<b>2012</b>
<b>Instructor for “BF821: Bioinformatics Graduate Seminar” at Boston University</b>	<b>2007</b>
<b>Teaching Assistant “BF527: Bioinformatics Applications” at Boston University</b>	<b>2005</b>
<b>Teaching Assistant “BE777: Computational Genomics” at Boston University</b>	<b>2004</b>

## ACADEMIC SERVICE AND OUTREACH

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<b>Head Organizer</b>	<b>2013</b>
Duke Interdisciplinary Colloquium on Functional Genomics and Genetics	
<b>Admissions Committee</b>	<b>2012, 2013</b>
Duke University Program in Computational Biology & Bioinformatics	
<b>Student Mentor</b>	<b>2010</b>
HudsonAlpha Institute for Biotechnology BioTrain Series	
<b>Journal Guest Editor</b>	
PLoS Genetics	
<b>Journal Peer Reviewer</b>	
Genome Research, PLoS Computational Biology, PLoS Genetics, Epigenetics, BMC Genomics	

## REFERENCES

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### **Huntington Willard, Ph.D.**

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### **Richard Myers, Ph.D.**

President and Director  
HudsonAlpha Institute for Biotechnology  
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### **William Lowe Jr, M.D.**

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Professor of Medicine, Department of Endocrinology, Metabolism, and Molecular Medicine  
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