

Michael J. Guertin

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RESEARCH INTERESTS	Transcription factors, genomics, molecular biology, transcription, chromatin structure and function, cancer, pharmacogenomics, nuclear receptors
PROFESSIONAL EXPERIENCE	<p>University of Virginia, School of Medicine, Biochemistry and Molecular Genetics Department, Center for Public Health Genomics, Cancer Center, Assistant Professor, August 1, 2015</p> <p>National Cancer Institute, Bethesda, MD Cancer Research Training Award Fellow, Hager Lab, 2012 – 2015</p>
EDUCATION	<p>Cornell University, Ithaca, NY Ph.D., Genetics and Development, Lis Lab, 2006 – 2012</p> <p>Stony Brook University, Stony Brook, NY Ph.D. program, Molecular Genetics and Microbiology, 2005-2006 (transferred)</p> <p>Cornell University, Ithaca, NY B.S., Genetics and Development, <i>magna cum laude</i> with distinction in research, 2005</p>
PUBLICATIONS	<p>Guertin MJ, Cullen, AE, Markowitz F, Holding AN. Parallel Factor ChIP Provides Essential Internal Control for Quantitative Differential ChIP-seq: <i>Nucleic Acids Research</i>, 2018 (accepted)</p> <p>Wang Z, Civelek M, Miller CL, Sheffield NC, Guertin MJ, Zang C. BART: a transcription factor prediction tool with query gene sets or epigenetic profiles. <i>Bioinformatics</i>, bty194, 2018.</p> <p>Martins AL, Walavalkar NM, Anderson WD, Zang C, Guertin MJ. Universal correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions: <i>Nucleic Acids Research</i>, gkx1053: https://doi.org/10.1093/nar/gkx1053, 2017.</p> <p>Liu Y, Walavalkar NM, Dozmorov MG, Rich SS, Civelek M, Guertin MJ. Identification of Breast Cancer Associated Variants That Modulate Transcription Factor Binding: <i>PLOS Genetics</i> 13(9): e1006761, 2017.</p> <p>Vihervaara A, Mahat DB, Guertin MJ, Chu T, Danko CG, Lis JT, Sistonen L. Transcriptional response to stress is pre-wired by promoter and enhancer architecture: <i>Nature Communications</i> 8(1), 255, 2017.</p> <p>Pooley JR, Flynn BP, Grøntved L, Baek S, Guertin MJ, Kershaw YM, Birnie MT, Pellatt A, Rivers CA, Schiltz RL, Hager GL, Lightman SL, Conway-Campbell BL. Genome-wide identification of basic helix-loop helix and NF-1 motifs underlying GR binding sites in male rat hippocampus: <i>Endocrinology</i> en.2016-1929, 2017</p> <p>Duarte FM, Fuda NJ, Mahat DB, Core LJ, Guertin MJ*, Lis JT*. Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation: <i>Genes & Development</i> 30 (15): 1731-1746, 2016. (*co-corresponding authorship)</p> <p>Fuda NJ, Guertin MJ, Sharma S, Danko CG, Martins AL, Siepel A, Lis JT. GAGA factor maintains nucleosome-free regions and has a role in RNA Polymerase II recruitment to promoters: <i>PLOS Genetics</i> 11(3): e1005108, 2015.</p> <p>Sung M[©], Guertin MJ[©], Baek S[©], Hager GL. DNase footprint signatures are dictated by factor dynamics and DNA sequence: <i>Molecular Cell</i> 56(2): 275-285, 2014. (©equal contribution)</p>

- Guertin MJ**[®], Zhang X[®], Anguish L, Kim S, Varticovski L, Lis JT, Hager GL, Coonrod SA. Targeted H3R26 deimination specifically facilitates ER binding by modifying nucleosome structure: *PLoS Genetics* 10 (9), e1004613, 2014.
- Guertin MJ**[®], Zhang X[®], Coonrod SA, Hager GL. Transient ER binding and p300 redistribution support a squelching mechanism for E2-repressed genes: *Molecular Endocrinology* 28(9): 1522-33, 2014.
- Guertin MJ**^{*}, Lis JT^{*}. Mechanisms by which transcription factors gain access to target sequence elements in chromatin. *Current Opinion in Genetics and Development* 23(2): 116-123, 2013.
- Guertin MJ**[®], Martins AL[®], Siepel A, Lis JT. Accurate predictions of inducible transcription factor binding intensities in vivo. *PLoS Genetics* 8(3): e1002610, 2012.
- Zhang X, Bolt M, **Guertin MJ**, Chen W, Zhang S, Cherrington BD, Slade DJ, Dreyton CJ, Subramanian V, Bicker KL, Thompson PR, Mancini MA, Lis JT, Coonrod SA. Peptidylarginine deiminase 2-catalyzed histone H3 arginine 26 citrullination facilitates estrogen receptor α target gene activation. *Proc Natl Acad Sci* 109(33):13331-13336, 2012.
- Guertin MJ**, Petesch SJ, Zobeck KL, Min IM, Lis JT. Drosophila heat shock system as a general model to investigate transcriptional regulation. Cold Spring Harbor symposia on quantitative biology 75, 1-9, 2011.
- Guertin MJ**, Lis JT. Chromatin landscape dictates HSF binding to target DNA elements. *PLoS Genetics* 6(9):e1001114, 2010.
- Carmon A, **Guertin MJ**, Grushko O, Marshall B, MacIntyre R. A molecular analysis of mutations at the complex dumpy locus in *Drosophila melanogaster*. *PLoS ONE* 5(8):e12319, 2010.

TEACHING EXPERIENCE

- Lecture, “Transcription Factors”, Chromatin Course: BIOC 8012, University of Virginia, Spring 2016, 2018.
- Lecture, “Dissecting Transcription Regulatory Networks using Molecular Genomics”, Bioengineering Course: BME 4806/7806, University of Virginia, Fall 2015, 2017.
- Medical Biochemistry: Steroid Biosynthesis (1.5 contact hours), Fall 2017
- Medical Biochemistry: Alcohol Metabolism (1.5 contact hours), Fall 2017
- Lecture: “The Transcriptome: a biological perspective”, Public Health Genomics: PHS 5705, University of Virginia, Spring 2017
- Invited workshop instructor: “Computational analysis of ChIP-seq and RNA-seq data”, Åbo Akademi, Finland, September 1-5, 2014.
- Invited workshop instructor: “Statistical analysis of genomic data using R”, Åbo Akademi, Finland, Jan. 14-20, 2013.
- Guest Lecture, “Protein targets of activators”, The Nucleus, Spring 2011
- Graduate Teaching Assistant, Genetics Laboratory, Cornell University, Spring 2007
- Graduate Teaching Assistant, Microbiology Laboratory, Stony Brook, Spring 2006
- Undergraduate Teaching Assistant, Genetics problem solving, Cornell University, Spring/Fall 2004, Spring 2005

AWARDS AND HONORS

- NCI Stimulating Innovation in Breast Cancer Genetic Epidemiology Challenge: 2nd Place Entry (role: PI –2016)
- Cancer Research Training Award Fellow, NCI (2012 – 2015)
- Cornell University College of Veterinary Medicine Visiting Fellow (2013 – 2015)
- Leukemia and Lymphoma Society Fellowship (2013-2016): \$165,000 (declined)
- NCI Cancer, Genetics, and Signaling Fellowship 2012 (declined)
- NIH Training Grant T32-GM007617 (2008 – 2010)
- United States Air Force Honorable Discharge (2001 – 2007)

Magna Cum Laude Cornell University (2005)
Distinction in Research Cornell University (2005)
Air Force Reserve Meritorious Service Medal (2005)
Armed Forces Expeditionary Medal (2003)
National Defense Service Medal (2001)
Global War on Terrorism Service Medal (2001)

TRAINEES

Graduate Students

Arun Dutta MSTP program. 2018 – current)

Postdoctoral

Fureya Liu (2015 – 2017) Juvenile Diabetes Research Foundation Fellow

Ninad Walavalkar (2015 – current) supported by a DP3 and ACS award until 2019

Warren Anderson (joint with Civelek lab, 2016 – current) supported by an Institutional Cardiovascular Research Center training grant September 2016 –August 2018

Sathyan Kizhakke Mattada (2017 – current) DoD Visionary Postdoctoral Fellow

Undergraduate Researchers

Nancy Lee (2015 – current) Harrison Award fellow

May Saito (2016)

Tracy Dien (2016)

Sumeet Sharma (Spring 2008 – Summer 2012)

Shifang Wang (Fall 2007 - Fall 2008)

COLLABORATORS

Stephen Rich, University of Virginia (2016 – present)

Mete Civelek, University of Virginia (2016 – present)

Suna Onengut, University of Virginia (2016 – present)

Lea Sistonen Lab, Åbo Akademi (Turku, Finland) (2012 – 2015)

Michael Stallcup Lab, University of Southern California (2014 – 2015)

Scott Coonrod Lab, Cornell University (2012 – 2014)

David Gross Lab, Louisiana State University (2013 – 2016)

Adam Siepel Lab, Cornell University (2011-2012)

JOURNAL REVIEWS

Ad hoc peer reviewer for *Bioinformatics*, *Cell*, *Developmental Biology*, *Developmental Cell*, *EMBO Journal*, *Epigenetics and Chromatin*, *FEBS Letters*, *Genome Biology*, *Genome Research*, *Molecular and Cellular Biology*, *Molecular Cell*, *Nature*, *Nature Genetics*, *PLOS Biology*, *PLOS Genetics*, *PLOS ONE*, *PNAS*, *RNA*, and *Scientific Reports*.

TALKS

“Transcription factors involved in drug resistance and disease susceptibility”

Harvard University, hosted by Dr. Martha Bulyk. June 18, 2018-scheduled

“Correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions” Brown University, hosted by Dr. Erica Larschan. July 21, 2017

“Transcription factors involved in drug resistance and disease susceptibility” Cancer Molecular Genetics Program, Massey Cancer Center at VCU. Feb. 3, 2017

“Transcription factors involved in drug resistance and correcting biases in genomics data” Genome Sciences Seminar, Center for Public Health Genomics, UVA. Feb. 22, 2017.

“Transcription factors involved in drug resistance” UVA Cancer Center Seminar. Dec. 2, 2016.

“Transcription factors GAF and HSF act at distinct regulatory steps to modulate stress-induced gene activation” Post-Initiation Activities or RNA polymerase: 18th Biennial Blue Ridge Mountains, October 27-30 2016

“Mechanisms of Transcription: Pausing to Celebrate John T. Lis” Cornell University, Ithaca, NY, July 2016. *Symposium Organizer.

“Systematic identification of predictive causal GWAS SNPs within TF binding sites”
Epigenomics, NIH Common Fund Conference, Rio Grande, Puerto Rico, February 2016

“Mechanisms of transcription factor binding and interpreting DNase signatures”
Centre for Molecular Medicine Norway, Oslo, Norway, December 2014.

“Characterization of regulatory networks using unbiased molecular methodologies”
Danish Nortic EMBL Partnership, Copenhagen, Denmark, December 2014

“Unbiased genome-wide molecular surveys reveal novel hormone signaling mechanisms”
Unraveling Genome-wide Transcription Mechanisms Symposium. Turku, Finland,
August, 2014.

“Transient ER binding and cofactor redistribution support a physiological squelching
model for immediate E2-repressed genes” Center of Excellence in Chromosome
Biology Symposium, NIH, Bethesda, MD. June 2014.

Targeted H3R26 deimination specifically facilitates ER binding by modifying
nucleosome structure” Chromatin-DECODE Seminar Series, NCI, Bethesda, MD.
September 2013.

“Discrete, estrogen-stimulated H3R26 deimination specifically marks and stabilizes ER
binding to enhance gene expression” Cold Spring Harbor Mechanisms of Eukaryotic
Transcription. August 2013.

“Unbiased genome-wide molecular surveys reveal novel hormone signaling mechanisms”
Baker Institute for Animal Health, Cornell University. Ithaca, NY, July 2013.

CONFERENCE
ABSTRACTS
AND POSTER
PRESENTATIONS

Guertin MJ, Duarte F, Vihervaara A, Zhang X, Sistonen L, Coonrod SA, Lis JT, Hager, GL. Chromatin landscape and promoter context dictate transcription factor binding and gene activation and repression. Cold Spring Harbor Meeting: Mechanisms of Eukaryotic Transcription, September 2015.

Guertin MJ, Zhang X, Coonrod SA, Hager GL. Transient ER binding and p300 redistribution are associated with immediate E2-repressed genes. Keystone: Nuclear Receptors, January 2014.

Guertin MJ, Martins AL, Core LJ, Sharma S, Lis JT. Genomic Features that Predict Transcription Factor Binding and Gene Activation. Nutrition, Metabolism, and Disease Symposium. Cornell University. October 2012.

Guertin MJ, Martins AL, Lis JT. Accurate predictions of inducible transcription factor binding intensities in vivo. Cold Spring Harbor Meeting: Mechanisms of Eukaryotic Transcription, September 2011.

Guertin MJ, Martins AL, Lis JT. Accurate predictions of inducible HSF binding intensities in vivo using genome-wide binding energies and chromatin landscape. PENN State 30th Summer Symposium in Molecular Biology: Chromatin and Epigenetic Regulation of Transcription, June 2011.

Guertin MJ, Lis JT. Chromatin landscape dictates heat shock factor binding to target DNA elements. Gordon Conference on Chromatin Structure and Function, 2010.

Guertin MJ, Lis JT. Chromatin landscape dictates heat shock factor binding to its target DNA elements. *Drosophila* Research Conference, 2010.

Carmon, A, **Guertin MJ**, MacIntyre RJ. Characterization of *dumpy* mutations at the molecular level. *Drosophila* Research Conference, 2005.

ONGOING SUPPORT	1DP3DK111906-01	Rich (PI)	12/16-11/21
	<i>Systematic identification of functional T1D-associated non-coding SNPs using genetic, transcriptomic and epigenetic methods</i> (15% salary support/50% postdoctoral fellow support ~\$60,000/year to the Guertin lab)		
	Role: Co-Investigator		
PENDING SUPPORT	R21HL135230	Guertin/Civelek (co-PI)	07/01/2018 - 06/30/2020
	<i>Functional Characterization of Coronary Artery Disease Loci</i>		
	\$75000/year direct cost; review council meets in the spring of 2018		
	R35GM128635	Guertin (PI)	07/01/2018 - 06/30/2023
	<i>Mechanisms of coordinate gene regulation by transcription factors</i>		
	\$250000/year direct costs; review council meets in the spring of 2018		
COMPLETED SUPPORT	ACS-IRG #81-001-29-IRG	Abounader (PI)	11/15-12/17
	<i>Defining molecular signatures of lymphoblast and lymphocyte cells to identify critical transcription networks</i>		
	Role: Pilot Project PI (\$30,000/year)		
	5P30CA044579-24	Loughran (PI)	2015-2017
	<i>Identification of transcription factors that propagate the glucocorticoid-induced apoptotic cascade in acute lymphoblastic leukemia (ALL) cells and mediate differential drug sensitivity</i>		
	Role: Pilot Project PI		
	Leukemia & Lymphoma Society Fellowship	Guertin, M (PI)	2013-2016
	<i>Genomic Identification of Molecular Signatures within the Glucocorticoid Network</i> (declined)		
	NCI Cancer, Genetics, and Signaling Fellowship	Guertin (PI)	2013-2016
	<i>Genomic Identification of Molecular Signatures within the Glucocorticoid Network</i> (declined)		
	T32-GM007617	Cornell Genetics and Development Training Grant	2008-2010