Michael J. Guertin

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RESEARCH INTERESTS

Transcription factors, genomics, molecular biology, transcription, chromatin structure and function, computational biology, nuclear receptors, cancer biology, stress response

PROFESSIONAL EXPERIENCE

University of Virginia, School of Medicine, Biochemistry and Molecular Genetics Department, Center for Public Health Genomics, Cancer Center.
Assistant Professor, August 1, 2015 – present

National Cancer Institute, Bethesda, MD
Cancer Research Training Award Fellow, Hager Lab, 2012 – 2015

EDUCATION

Cornell University, Ithaca, NY
Ph.D., Genetics and Development, Lis Lab, 2006 – 2012

Stony Brook University, Stony Brook, NY
Ph.D. program, Molecular Genetics and Microbiology, 2005-2006 (transferred)

Cornell University, Ithaca, NY
B.S., Genetics and Development, *magna cum laude* with distinction in research, 2005

PUBLICATIONS

Smith JP, Dutta AB, Sathyan KM, **Guertin MJ*,** Sheffield NC*, Quality control and processing of nascent RNA profiling data. *bioRχiv* https://doi.org/10.1101/2020.02.27.956110, 2020. (*co-corresponding authorship)

Sathyan KM, Scott TG, **Guertin MJ**. ARF-AID: A rapidly inducible protein degradation system that preserves basal endogenous protein levels. *Current Protocols in Molecular Biology* 132(1): e124, 2020.

Anderson WD*, Duarte FM, Civelek M, **Guertin MJ*.** Defining data-driven transcript annotations with primaryTranscriptAnnotation in R. *Bioinformatics*. 36(9): 2926-2928, 2020.

Sathyan KM, McKenna BD, Anderson WD, Duarte FM, Core LJ, and **Guertin MJ**. An improved auxin-inducible degron system preserves native protein levels and enables rapid and specific protein depletion: *Genes & Development.* 33: 1441-1455, 2019.

Pincus D, Anandhakumar J, Thiru P, **Guertin MJ**, Erkine AM, Gross DS. Genetic and epigenetic determinants establish a continuum of Hsf1 occupancy and activity across the yeast genome: *Mol Biol Cell.* (26): 3168-3182, 2018.

Pfister K, Pipka JL, Chiang C, Liu Y, Clark RA, Keller R, Skoglund P, **Guertin MJ**, Hall IM, Stukenberg PT. Identification of Drivers of Aneuploidy in Breast Tumors: *Cell Rep.* 23(9): 2758-2769, 2018.

Guertin MJ, Cullen, AE, Markowetz F, Holding AN. Parallel Factor ChIP Provides Essential Internal Control for Quantitative Differential ChIP-seq: *Nucleic Acids Research*. 46(12): e79, 2018.

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: *Bioinformatics*. 34(16): 2867-2869, 2018.

Martins AL, Walavalkar NM, Anderson WD, Zang C, **Guertin MJ.** Universal correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions: *Nucleic Acids Research*. 46(2): e9, 2018.

Liu Y, Walavalkar NM, Dozmorov MG, Rich SS, Civelek M, **Guertin MJ**. Identification of Breast Cancer Associated Variants That Modulate Transcription Factor Binding: *PLOS Genetics.* 13(9): e1006761, 2017.

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: *Nature Communications.* 8(1): 255, 2017.

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: *Endocrinology.* en.2016-1929, 2017

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: *Genes & Development.* 30 (15): 1731-1746, 2016.

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: *PLOS Genetics.* 11(3): e1005108, 2015.

Sung M☯**, Guertin MJ**☯, Baek S☯, Hager GL. DNase footprint signatures are dictated by factor dynamics and DNA sequence: *Molecular Cell.* 56(2): 275-285, 2014. (☯equal contribution)

Guertin MJ☯, Zhang X☯, Anguish L, Kim S, Varticovshi 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 Genet*ics. 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

University of Virginia teaching:

Instructor BIOC (Biochemistry) 8145 UVA Spring 2020

Bioinformatics

Biochemistry 8145 provides the statistical and programming background as well as introduction to software tools that enable analysis of functional genomics data sets. The course focuses on identifying single nucleotide and structural variants from genomic data, gene expression changes from RNA-seq and PRO-seq data, factors that regulate gene expression including transcription factors (TFs), histone modifications and chromatin state from ChIP-seq and ATAC-seq data and cellular composition and single cell gene expression from scRNAs-seq. Students will learn UNIX basics, statistics associated with each analysis approach, programming in R, and analysis of RNA-seq, PRO-seq, scRNA-seq, ChIP-seq and ATAC-seq data using R/Bioconductor and UNIX-based software tools. Students learn how to perform TF DNA motif and GO/pathway enrichment analysis.

Director Cell and Molecular Biology (CMB) Training Grant research talks

CMB TG PI: Todd Stukenberg 2017-present

Every month, current and past appointees to the CMB training grant meet and two trainees present their latest research. Students meet with a faculty advisor outside their field to prepare the presentations, with an emphasis on communicating their research to scientists from diverse academic backgrounds. My role as the director of the research in progress talks is to facilitate student discussion and provide constructive feedback to the presenters.

Instructor Cell Biology 8450 Fall 2019-2020

Scientific Writing

As the instructor of this scientific writing for grants and fellowship course, I lead five graduate students in discussion and provide feedback for students who develop an F30/F31 style research proposal. The 10 week course is designed to train students on how to develop a competitive research proposal. The students are able to submit polished proposals to the NIH or a relevant funding agency at the conclusion of the class.

Course Director BIOC 8150 Fall 2017-2020

Research in progress

Every week all Biomedical Sciences (BIMS) Biochemistry and Molecular Genetics (BMG) students meet to listen to either two seminars from other students or a single research seminar. All students are required to present their research once a year. Students are encouraged to engage with the speaker through questions and all students provide feedback for the presenting students. These seminars also expose trainees to a diversity of scientific topics and presentation styles.

Lecture, Public Health Sciences (PHS) 5705, course director: Charles Farber

Spring 2017/Spring 2020

The Transcriptome: a biological perspective

The lecture provided an overview of various genomic technologies used to measure transcription and chromatin structure. I also highlighted examples of scientific findings that used these methods to inform on basic biological processes, such as development and disease biology.

Lectures (2), BIOC 8012, course director: Jeff Smith Spring 2016/Spring 2018

Transcription Factors

My instruction in the Chromatin Course focused on basic principles of transcription factors, including their roles in development and their mechanistic properties. The lecture introduced the students to the importance of transcription factors, experimental methodologies that were used to discover their properties, and genomics methods that interrogate their roles in disease. A relevant journal article was assigned and we discussed this in depth during the second meeting.

Medical Biochemistry: Steroid Biosynthesis (Medical Students) Fall 2017
I introduced fundamentals of steroid biosynthesis and led active learning discussions among students.

Medical Biochemistry: Alcohol Metabolism (Medical Students) Fall 2017
I introduced fundamentals of alcohol metabolism and led active learning discussions among students.

Lecture Biomedical Engineering (BME) 4806/7806, course director Brent French
Fall 2015/ Fall 2017
Dissecting Transcription Regulatory Networks using Molecular Genomics
I designed this lecture for biomedical engineering students, therefore in this lecture I emphasized quantitative methods in genomics and recent genomic technologies.

Åbo Akademi teaching:
Invited workshop instructor Åbo Akademi, Finland September 1-5, 2014
Computational analysis of ChIP-seq and RNA-seq data
I designed and developed an intensive 40 hour hands-on workshop that provided 20 students with practical knowledge and skills for processing of ChIP-seq and RNA-seq data.

Invited workshop instructor Åbo Akademi, Finland Jan. 14-20, 2013
Statistical analysis of genomic data using R
I designed and developed an comprehensive 40 hour workshop outlining in depth ChIP-seq data analysis, focusing on integration of ENCODE ChIP data.

Cornell University teaching:
Lecture, course: The Nucleus. Course Director: John Lis Spring 2011
Protein targets of activators

Graduate Teaching Assistant, Genetics Laboratory Spring 2007

Undergraduate Teaching Assistant, Genetics problem solving, Cornell University, Spring/Fall 2004, Spring 2005

DEVELOPING TEACHING RESOURCES

To facilitate genomics research at UVA, I developed four comprehensive molecular genomics data analysis vignettes: 1) Computational analysis of ChIP-seq data; 2) Analysis of PRO-seq data; 3) Analysis of RNA-seq data; and 4) Analysis of ATAC-seq data. These are the foundation for a new course that I will offer in the spring of 2021. These vignettes have been used extensively by graduate students across UVA as they generate data and develop their projects. Each document is a step-by-step procedure for data analysis and they contain the code and rationale for each analysis so the user can adapt the principles to their system and begin to analyze their own data. These resources are publicly available and I routinely work through these documents with UVA graduate students:

1) http://guertinlab.org/wp-content/uploads/2019/09/Genomic_ChIP_RNA-seq_analysis.pdf
2) http://guertinlab.org/wp-content/uploads/2019/09/Genomic_PRO-seq_analysis.pdf
3) https://github.com/stefbekir/bioc8145/raw/master/Guertin_week4/vignette.pdf
4) http://guertinlab.org/wp-content/uploads/2019/09/Genomic_ATAC-seq_analysis_190912.pdf

AWARDS AND HONORS

Dean's Excellence in Teaching Award (student-nominated—*pending decision*) (2020)
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

Jacob Wolpe, Cell Biology PhD program (2020 – current)
Arun Dutta, MSTP program (2018 – current)
Thomas Scott, MSTP program (2019 – current)
Anna Cetnarowska, Visiting Fulbright Student program (2019 – 2020)

Postdoctoral

Piotr Przanowski (2019 – current)
Sathyan Kizhakke Mattada (2017 – current) DoD Visionary Postdoctoral Fellow
Brian McKenna (2018 – 2019) F32 Ruth L. Kirschstein Fellow
Warren Anderson (joint with Civelek lab, 2016 – 2018) AHA Fellow
Ninad Walavalkar (2015 – 2018)
Fureya Liu (2015 – 2017) Juvenile Diabetes Research Foundation Fellow

Undergraduate Researchers

Bao Ngyuen (2019 – present)
Ashley Ewing (2018)
Nancy Lee (2015 – 2018) Harrison Award fellow
May Saito (2016)
Tracy Dien (2016)
Sumeet Sharma (Cornell University, Spring 2008 – Summer 2012)
Shifang Wang (Cornell University, Fall 2007 – Fall 2008)

NON-UVA COLLABORATORS

Dennis Thiele Lab, Duke University (2019 – 2020)
Andrew Holding, CRUK (Cambridge, England) (2017 – 2018)
Lea Sistonen Lab, Åbo Akademi (Turku, Finland) (2012 – 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 *BBA-Gene Regulatory Mechanisms, Bioinformatics, Cell, Developmental Biology, Developmental Cell, EMBO Journal, eLife, 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.*

ADVOCACY AND INCLUSION

My commitment to diversity and inclusion in education began in Air Force basic training after being exposed to a diversity of cultures and backgrounds. I had joined the Air National Guard and I was set to matriculate at Cornell University after basic training. I became an expert in the process of navigating the military bureaucracy to receive the appropriate educational reimbursement and stipend benefits. I developed a reputation as an education benefits advocate for enlisted personnel on my base. Throughout Air Force Technical School and while stationed at the 174th Fighter Wing, I helped dozens of service members capitalize on educational benefits and navigate higher education opportunities.

As a faculty member, I view inclusion and diversity through three overlapping lenses: mentorship, policy, and culture. Every summer I mentor students as a part of UVA's R21 to provide research opportunities to underrepresented students. I directly mentor these students over the summer as they develop in their careers as scientists. I facilitate the recruitment of a diverse student population by attending conferences such as SACNAS and ABRCMS, which offer career development opportunities for individuals from demographic groups that are under-represented in science. My outreach at these conferences is aimed to increase representation of people of color and underserved populations in STEM through engagement and encouragement of students. To this end, I also became involved in shaping our graduate student recruitment, admissions, and training. I am a member of the biomedical sciences admissions committee, I run the Cell and Molecular Biology Training Grant research in progress seminars, and I am the course director for the biomedical sciences student journal club.

Within my department, I advocated for changes to reimbursement policies for graduate student travel, conference registration, and accommodations. While I was unable to change the policy, I found that we can facilitate the option to have travel and registration fees covered up front with a departmental purchasing card. This alleviates hardships for our students who are not economically comfortable.

Culture is the most challenging issue to address from a diversity and inclusion perspective. Fortunately, there is a critical mass of faculty and students within the department who realize the importance of having a diverse workplace that is also inclusive. An effective way to encourage a more inclusive culture is exposure. In order to facilitate a more inclusive culture within a department that is composed of only 10% women faculty, I have volunteered to be on the Departmental Symposium organizing committee for the past two years. In 2019 I led the organization to ensure a speaker list that was diverse and representative. I remained on the committee this past year with the purpose of ensuring that the speaker list is balanced.

Academia needs to better recognize the financial and familial hardships of young scientists who choose to have children, especially women. I experienced and witnessed these struggles first-hand, as my spouse and I had two children as graduate students/postdoctoral fellows. I am sensitive to the challenges with balancing work and family in academia and encourage open communication and share my experiences with my trainees. This is another way that I aim to increase the diversity of the workforce, by encouraging and retaining parents (and specifically women) who drop out of the scientific career track at high rates after years of school, research, and training.

TALKS/SEMINARS

"Mechanisms of Gene Regulation by Transcription Factors" National Cancer Institute. Transcription Factor Interest Group, invited by Dr. Dan Larson. May 2020 *canceled due to COVID19*

"Mechanisms of Gene Regulation by Transcription Factors" Northwestern University. Biochemistry and Molecular Genetics. March 9, 2020.

"Mechanisms of Gene Regulation by Transcription Factors" University of Houston. Biology and Biochemistry. February 17, 2020.

"Mechanisms of Gene Regulation by Transcription Factors" Penn State University. Biochemistry and Molecular Biology. January 27, 2020.

"An improved inducible degron system defines the role of ZNF143 in transcription" Molecular Biosystems: Eukaryotic Gene Regulation and Functional Genomics, Puerto Varas, Chile, October 2019

"An improved inducible degron system defines the role of ZNF143 in maintaining promoter-proximal RNA polymerase pausing" Penn State 38th Summer Symposium in Molecular Biology: Chromatin and Epigenetic Regulation of Transcription, June 2019.

"Leveraging Rapidly Inducible Systems to Define Transcription Factor Target Steps" Post-Initiation Activities of RNA polymerase: 19th Biennial Blue Ridge Mountains, October 25-28, 2018

"Transcription factors involved in drug resistance and disease susceptibility" Harvard University, hosted by Dr. Martha Bulyk. June 18, 2018.

"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 of 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.

COMMITTEES/ SERVICE

UVA School of Medicine

Faculty advisory committee for research computing infrastructure	2016-2018
R21 SRIP reviewer	2018, 2019, 2020

Department

Departmental Symposium Organizing Committee	2019, 2020
CMB training grant representative at SACNAS	2018
CMB training grant representative at ABRCMS	2020 (Fall)
BIMS PhD graduate program admissions committee member	2018, 2019, 2020
Co-director of the CMB training grant research in progress	2016-present

Internal (UVA) thesis committees

Elisa Enriquez Hesles (Dr. Jeff Smith's lab—current)
Jason Smith (Dr. Nathan Sheffield's lab—current)
Róża Przanowska (Dr. Anindya Dutta's lab—current)
Cassie Robertson (Dr. Stephen Rich's lab—current)
Annie Carlton (graduated from Dr. John Bushweller's lab May 2018)

External thesis committees

Colin Waters (graduated from Dr. Martha Bulyk's lab at Harvard in June 2018)
Emily Kaye (graduated from Dr. Erica Larschan's lab at Brown in July 2017)

Grant reviewer for international foundations
Cancer Research UK (January 2018)
Worldwide Cancer Research (September 2019)

ONGOING SUPPORT

R35GM128635 **Guertin** (PI) 08/18 – 07/23
Mechanisms of coordinate gene regulation by transcription factors
Role: PI (6 calendar months) ($1,250,000 direct costs over 5 years)

R01DA048638 Lynch (PI) 03/20-12/24
Genetic and hormonal contributions to sex differences in vulnerability to drug use
Role: Co-Investigator (~$150,000 direct costs over final 2 years of grant)

DP3DK111906 Rich (PI) 12/16-11/21
Systematic identification of functional T1D-associated non-coding SNPs using genetic, transcriptomic and epigenetic methods
Role: Co-Investigator (1.8 calendar months)

R01 NS105630 Cliffe (PI) 03/18-02/23
Cell stress-mediated changes in the Herpes simplex virus type 1 chromatin structure during reactivation from latent infection
Role: Co-Investigator (0.6 calendar months)

R01 DK118287 Civelek (PI) 08/18 – 06/23
The role of adipocyte KLF14 in Metabolic Syndrome
Role: Co-Investigator (0.2 calendar months)

COMPLETED SUPPORT

R21HL135230 **Guertin**/Civelek (MPI) 08/18 - 07/20
Functional Characterization of Coronary Artery Disease Loci
Role: Co-PI (0.5 calendar months) ($150,000 direct costs over 2 years)

P30CA044579 Loughran (PI) 09/18 – 12/19
Functional characterization of the breast and ovarian cancer susceptibility locus 19p13.1
Role: Pilot Project PI ($94,561 direct costs)

ACS-IRG #81-001-29-IRG Abounader (PI) 11/15-12/17
Defining molecular signatures of lymphoblast and lymphocyte cells to identify critical transcription networks
Role: Pilot Project PI

5P30CA044579-24 Loughran (PI) 2015-2017
Identification of transcription factors that propagate the glucocorticoid-induced apoptotic cascade in acute lymphoblastic leukemia (ALL) cells and mediate differential drug sensitivity
Role: Pilot Project PI

Leukemia & Lymphoma Society Fellowship **Guertin** (PI) 2013-2016
Genomic Identification of Molecular Signatures within the Glucocorticoid Network
(declined)

NCI Cancer, Genetics, and Signaling Fellowship **Guertin** (PI) 2013-2016
Genomic Identification of Molecular Signatures within the Glucocorticoid Network
(declined)

T32-GM007617 Cornell Genetics and Development Training Grant 2008-2010