

Michael J. Guertin

DEPARTMENT OF PRIMARY APPOINTMENT

Center for Cell Analysis and Modeling, Department of Genetics and Genome Sciences

ACADEMIC APPOINTMENTS

starting July 2, 2021

Associate Professor

UConn Health

PROFESSIONAL EXPERIENCE (prior to appointment at UConn Health)

August 2015 – June 2021

Assistant Professor

University of Virginia SOM

EDUCATIONAL BACKGROUND

<u>Years</u>	<u>Degree</u>	<u>Institution</u>	<u>Degree conferred</u>
2006-2012	PhD (John Lis Lab)	Cornell University	January 2012
2006	no degree	Stony Brook Uni.	NA
2005	BS (magna cum laude)	Cornell University	May 2005

<u>Additional training</u>	<u>Position</u>	<u>Institution</u>
Nov 2012- Aug 2015	Cancer Research Training Award Fellowship	National Cancer Institute

PRINT AND ORAL SCHOLARSHIP

1. Publications

1a. Peer reviewed journal articles

*corresponding authorship

•equal contribution

- 1) Wolpe JB, Martins AL, **Guertin MJ***. Correction of transposase sequence bias in ATAC-seq data with rule ensemble modeling. *Nucleic Acids Research Genomics and Bioinformatics* 5(2): lqad054, 2023.
- 2) Dutta AB, Lank DS, Przanowska RK, Przanowski P, Wang L, Nguyen B, Walavalkar NM, Duarte FM, **Guertin MJ***. Kinetic networks identify Twist2 as a key regulatory node in adipogenesis *Genome Research* 33: 1-18, 2023.
- 3) Przanowski P*, Przanowska RK, **Guertin MJ***. ANKLE1 cleaves mitochondrial DNA and contributes to cancer risk by promoting apoptosis resistance and metabolic dysregulation. *Communications Biology* 6: 231, 2023. *Note: Dr. Piotr Przanowski was a senior postdoc in my group and it is my policy to permit senior postdocs and senior staff scientists to publish as corresponding or co-corresponding authors.*
- 4) Hu SS, Liu L, Li Q, Ma W, **Guertin MJ**, Meyer CA, Deng K, Zhang T, Zang C. Intrinsic bias estimation for improved analysis of bulk and single-cell chromatin accessibility profiles using SELMA. *Nature Communications* 13: 5533, 2022.
- 5) Przanowska RK, Weidmann CA, Saha S, Cichewicz MA, Jensen KN, Przanowski P, Irving PS, Janes KA, **Guertin MJ**, Weeks KM, Dutta A. Distinct MUNC lncRNA structural domains regulate transcription of different promyogenic factors. *Cell Reports* 38(7):110361, 2022
- 6) Smith JP, Dutta AB, Sathyan KM, **Guertin MJ***, Sheffield NC*. Quality control and processing of nascent RNA profiling data. *Genome Biology* 22, 155, 2021.
- 7) Burchfiel ET, Vihervaara A, **Guertin MJ**, Gomez-Pastor R, Thiele DJ. Comparative interactomes of HSF1 in stress and disease reveal a role for CTCF in HSF1-mediated gene regulation. *Journal of Biological Chemistry* 296, 100097. 2021

- 8) 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.
Note: Dr. Sathyan Mattada was a senior scientist in my group, and it is my policy to permit senior postdocs and senior staff scientists to publish as corresponding or co-corresponding authors. My role in this publication was comparable to any other publication from my group in which I was the corresponding or co-corresponding author.
- 9) Anderson WD*, Duarte FM, Civelek M, **Guertin MJ***. Defining data-driven transcript annotations with primaryTranscriptAnnotation in R. *Bioinformatics*, (36)9: 2926–2928, 2020.
- 10) 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.
- 11) Pincus D, Anandhakumar J, Thiru P, **Guertin MJ**, Erkin 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.
- 12) 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.
- 13) **Guertin MJ**, Cullen, AE, Markowitz F, Holding AN*. Parallel Factor ChIP Provides Essential Internal Control for Quantitative Differential ChIP-seq: *Nucleic Acids Research*, gky252, <https://doi.org/10.1093/nar/gky252>, 2018.
Note: Dr. Andrew Holding was a visiting scholar from the University of Cambridge who embedded in my group during the summer of 2017.
- 14) 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*, bty194, 2018.
- 15) 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), gkx1053, 2018.
- 16) 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.
- 17) 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.
- 18) 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
- 19) 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.
- 20) 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.
- 21) 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)

- 22) **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.
- 23) **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.
- 24) **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.
- 25) **Guertin MJ**[®], Martins AL[®], Siepel A, Lis JT. Accurate predictions of inducible transcription factor binding intensities in vivo. *PLoS Genetics* 8(3): e1002610, 2012.
- 26) 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.
- 27) **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.
- 28) **Guertin MJ**, Lis JT. Chromatin landscape dictates HSF binding to target DNA elements. *PLoS Genetics* 6(9):e1001114, 2010.
- 29) 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.

1d. Preprint journal articles

- 1) Scott TG, Martins AL, **Guertin MJ**^{*}. Processing and evaluating the quality of genome-wide nascent transcription profiling libraries. *bioRxiv* doi: <https://doi.org/10.1101/2022.12.14.520463>, 2022. (under review)

2. Oral Presentations

a. Invited Presentations

i. At professional conferences

- 1) “Kinetic networks and compartment modeling reveal mechanistic functions of transcription factors” The 22nd International Conference on Systems Biology: October 2023.
- 2) “Kinetic networks and compartment modeling reveal that Glucocorticoid Receptor induces pause release” Post-Initiation Activities of RNA polymerase: 20th Biennial Blue Ridge Mountains. November 11, 2022.
- 3) “Kinetic networks identify key regulatory nodes and transcription factor functions in early adipogenesis” Experimental Biology (Programming Society: American Society for Biochemistry and Molecular Biology). April 5, 2022.
- 4) “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.
- 5) “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.

- 6) "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
- 7) "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
- 8) "Systematic identification of predictive causal GWAS SNPs within TF binding sites" Epigenomics, NIH Common Fund Conference, Rio Grande, Puerto Rico, February 2016
- 9) "Discrete, estrogen-stimulated H3R26 deimination specifically marks and stabilizes ER binding to enhance gene expression" Cold Spring Harbor Mechanisms of Eukaryotic Transcription. August 2013.

ii. At another college or university or scholarly institution

- 1) "TRPS1 regulates the estrogen response and cholesterol biosynthesis through transcription factor redistribution" University of Utah, Department of Human Genetics seminar series. scheduled: March 19, 2024
- 2) "Kinetic networks identify Twist2 as a key regulatory node in adipogenesis" Cornell University, Molecular Biology & Genetics seminar series. scheduled: October 13, 2023
- 3) "Kinetic networks identify key regulatory nodes and transcription factors in differentiation cascades" University of Iowa, host: Dr. David Price: March 30, 2023
- 4) "Kinetic networks identify key regulatory nodes and transcription factors in differentiation cascades" Institute for Systems Genomics seminar, UConn Health. June 22, 2023
- 5) "Kinetic networks identify key regulatory nodes and transcription factors in differentiation cascades" 17th Musculoskeletal Institute Research Day, UConn Health. March 24, 2023
- 6) "Kinetic networks of differentiation cascades identify key regulatory nodes and transcription factor functions" Fragile Nucleosome Series. host: Dr. Benjamin Martin, Harvard University. December 21, 2022
- 7) "Coupling molecular biology and genomics to address basic questions in the transcription field" Universidad de Puerto Rico Río Piedras, invited by Dr. José Rodríguez-Martínez. October 26, 2022
- 8) "Mechanisms of Gene Regulation by Transcription Factors" CSHL summer course on Chromatin, Epigenetics and Transcription. August 10, 2022
- 9) "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*
- 10) "Mechanisms of Gene Regulation by Transcription Factors" Northwestern University. Biochemistry and Molecular Genetics. March 9, 2020.
- 11) "Mechanisms of Gene Regulation by Transcription Factors" University of Houston. Biology and Biochemistry. February 17, 2020.
- 12) "Mechanisms of Gene Regulation by Transcription Factors" Penn State University. Biochemistry and Molecular Biology. January 27, 2020.
- 13) "Transcription factors involved in drug resistance and disease susceptibility" Harvard University, hosted by Dr. Martha Bulyk. June 18, 2018.
- 14) "Correction of enzymatic sequence bias reveals molecular signatures of protein/DNA interactions" Brown University, hosted by Dr. Erica Larschan. July 21, 2017
- 15) "Transcription factors involved in drug resistance and disease susceptibility" Cancer Molecular Genetics Program, Massey Cancer Center at VCU. Feb. 3, 2017
- 16) "Transcription factors involved in drug resistance and correcting biases in genomics data" Genome Sciences Seminar, Center for Public Health Genomics, UVA. Feb. 22, 2017.

- 17) "Transcription factors involved in drug resistance" UVA Cancer Center Seminar. Dec. 2, 2016.
- 18) "Mechanisms of transcription factor binding and interpreting DNase signatures" Centre for Molecular Medicine Norway, Oslo, Norway, December 2014.
- 19) "Characterization of regulatory networks using unbiased molecular methodologies" Danish Nortic EMBL Partnership, Copenhagen, Denmark, December 2014
- 20) "Unbiased genome-wide molecular surveys reveal novel hormone signaling mechanisms" Unraveling Genome-wide Transcription Mechanisms Symposium. Turku, Finland, August, 2014.
- 21) "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.
- 22) Targeted H3R26 deimination specifically facilitates ER binding by modifying nucleosome structure" Chromatin-DECODE Seminar Series, NCI, Bethesda, MD. September 2013.
- 23) "Unbiased genome-wide molecular surveys reveal novel hormone signaling mechanisms" Baker Institute for Animal Health, Cornell University. Ithaca, NY, July 2013.

b. Poster presentations

i. Peer reviewed

- 1) Identifying Transcription Factors that Dictate Drug-Resistance in Acute Lymphoblastic Leukemia, Walavalkar N, Lee N, **Guertin M**, Clinical Lymphoma, Myeloma and Leukemia 17, S258-S259. Presented at the Society of Hematologic Oncology, September 2017.

ii. Invited

- 1) **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.
- 2) **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.
- 3) **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.
- 4) **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.
- 5) **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.
- 6) **Guertin MJ**, Lis JT. Chromatin landscape dictates heat shock factor binding to target DNA elements. Gordon Conference on Chromatin Structure and Function, 2010.
- 7) **Guertin MJ**, Lis JT. Chromatin landscape dictates heat shock factor binding to its target DNA elements. *Drosophila* Research Conference, 2010.
- 8) Carmon, A, **Guertin MJ**, MacIntyre RJ. Characterization of *dumpy* mutations at the molecular level. *Drosophila* Research Conference, 2005.

GRANTS

Current

R35GM128635

Guertin (PI)

08/18 – 11/28

Mechanisms of coordinate gene regulation by transcription factors

Role: PI (6 calendar months) (\$1,250,000 direct costs over first 5 years)

update The renewal funding is not official until council meets. The renewal received an impact score of 29. Based on NIGMS data below (<https://loop.nigms.nih.gov/2023/04/application-and-funding-trends-in-fiscal-year-2022/>), this application will likely be renewed. Note that unfunded applications with very low (good) overall impact scores are often unfunded because they are declined due to restrictions associated with the R35 mechanism (\$1,681,200 direct costs requested over years 6-10)

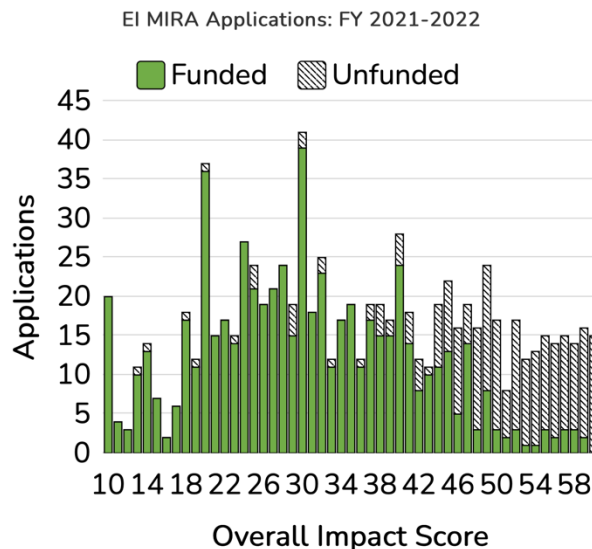


Figure 6. Number of Funded and Unfunded EI MIRA Applications by Overall Impact Score, FY 2021-2022. The funded applications are represented by the solid green bars, and the unfunded applications are represented by the striped bars. Most applications with an overall impact score of 47 or under were funded while a majority those above 47 were not. Applications with an overall impact score greater than 60 were not included on this chart.

Completed

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 salary support per year in direct costs)

R21HL135230

Civelek/Guertin (MPI)

08/18 - 07/20

Functional Characterization of Coronary Artery Disease Loci

Role: Co-PI (0.5 calendar months) (\$150,000 direct costs)

R01 NS105630

Cliffe (PI)

03/18-03/21

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 salary support per year in direct costs))

R01 DK118287

Civelek (PI)

08/18 – 06/20

The role of adipocyte KLF14 in Metabolic Syndrome

Role: Co-Investigator (0.2 calendar months salary support per year in direct costs)

ADDITIONAL ACADEMIC ACCOMPLISHMENTS

National Competitions

NCI Stimulating Innovation in Breast Cancer Genetic Epidemiology Challenge: 2nd Place Entry (role: PI –2016)

External thesis committee member

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

United States-Israel Binational Science Foundation (February 2022)

Worldwide Cancer Research (September 2019)

Cancer Research UK (January 2018)

Peer review

Ad hoc peer reviewer for BBA-Gene Regulatory Mechanisms, Bioinformatics, Cell, Cell Reports, Communications Biology, Developmental Biology, Developmental Cell, EMBO Journal, eLife, Epigenetics and Chromatin, FEBS Letters, Genome Biology, Genome Research, JCI Insight, Molecular and Cellular Biology, Molecular Cell, Nature, Nature Communications, Nature Genetics, Nucleic Acids Research, PLOS Biology, PLOS Genetics, PLOS ONE, PNAS, RNA, Science Advances, and Scientific Reports.

Symposium Organizer

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

Departmental Symposium Organizer

2019

Training Grant outreach

UVA CMB training grant representative at SACNAS 2018

UVA CMB training grant representative at ABRCMS 2020

UConn BMS Systems Biology/Genomics representative at ABRCMS 2021

UConn BMS Systems Biology/Genomics representative at SACNAS 2022

Development of course materials

Before arriving at UConn Health I developed four comprehensive analysis vignettes to analyze molecular genomics data: 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. Together, the preparation of these documents represent hundreds of hours of my investment. These vignettes have been used extensively by graduate students across UVA as they generate data and develop their projects. Each vignette is step-by-step procedure for analyzing data. These guides contain the code and rationale for each analysis so the user can adapt the principles to their system and start analyzing their own data.

The following are static links to the online documents:

http://guertinlab.org/wp-content/uploads/2019/09/Genomic_ATAC-seq_analysis_190912.pdf

http://guertinlab.org/wp-content/uploads/2019/09/Genomic_PRO-seq_analysis.pdf

http://guertinlab.org/wp-content/uploads/2019/09/Genomic_ChIP_RNA-seq_analysis.pdf
https://github.com/stefbekir/bioc8145/raw/master/Guertin_week4/vignette.pdf

These materials were the foundation for a course that I developed and offered at UConn Health in 2022 and 2023: MEDS5420, Molecular Genomics Practicum. The link to all course material is here:

http://guertinlab.cam.uchc.edu/meds5420_2023/MEDS5420_2023_landing.html

Training

Graduate Students

Jinhong Dong, UCHC MD/PhD Systems Biology program (2022 – current)
Rudradeep Mukherjee, UCHC PhD Systems Biology program (2022 – current)
Siyu Sun, UCHC PhD Systems Biology program (2022 – current)
Thomas Scott, UVA MD/PhD program—T32 trainee (2019 – current)
Jacob Wolpe, UVA Cell Biology PhD graduate—Bureau of Indian Education
Scholarship (2020 – 2023)
Arun Dutta, UVA MD/PhD graduate—T32 trainee (2018 – 2023)
Anna Cetnarowska, UVA Visiting Fulbright Student Masters program (2019 – 2020)

Postdoctoral

Piotr Przanowski (2019 – 2021)
Sathyan Kizhakke Mattada (2017 – 2021) 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

Summer students (excluding undergraduates below)

Mia Aglieco (2022)
Carlos Ayala Santos (2019)
Amy Boles (2018)

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)