

Curriculum Vitae

(Revised 6/12/23)

Name: Michael P. Epstein

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Citizenship: US citizen

Current Titles and Affiliations

a) Academic appointments

Assistant Professor, Department of Human Genetics, Emory University School of Medicine, 09/09/2002 to 08/31/2009

Adjunct Professor, Department of Biostatistics, Emory University Rollins School of Public Health, 01/01/2003 to present

Associate Professor, Department of Human Genetics, Emory University School of Medicine, 09/01/2009 to 08/31/2015

Professor, Department of Human Genetics, Emory University School of Medicine, 09/01/2015-present

Director, Center for Computational and Quantitative Genetics, Emory University School of Medicine, 09/01/2016-present

Education

1996, B.S. in Mathematics and Biological Anthropology, Duke University

1998, M.S. in Biostatistics, University of Michigan

2002, Ph.D. in Biostatistics, University of Michigan
Advisors: Drs. Michael Boehnke and Xihong Lin

Committee Memberships

a) Institutional

Faculty Recruitment Committee, Department of Biostatistics, 2004, 2008, 2010, 2017, 2022-2023

Information Technology Committee, Department of Human Genetics, 2006-present

Organizing Committee: BGIN program, Department of Biostatistics and Bioinformatics, 2006 -2010

Recruitment Committee, Population Biology, Ecology, and Evolution Program, Emory University, 2011-2013

Executive Committee, Population Biology, Ecology, and Evolution Program, Emory University, 2011-2015

Curriculum Committee, Population Biology, Ecology, and Evolution Program, Emory University, 2011-2013

Oral Examination Committee, Genetics and Molecular Biology Program, Emory University, 2015-present

Faculty Recruitment Committee, Department of Human Genetics 2016-present

Emory University Senate, 2019-2022

Emory University Faculty Council, 2020-2022

Working Group for Program Enhancement, Genetics and Molecular Biology Program, Emory University, 2020-present

Genetics and Molecular Biology DEI Committee (Chair), Emory University, 2021-present

Scientific Director, Emory Integrated Computational Core, Emory University, 2021-present

a) National

Nominating Committee, American Society of Human Genetics, 2016-2019

External Advisory Board, OPPERA Project, 2016-present

External Advisory Board, UNC IDDRC Center, 2019-present

Member, National Institute of Dental and Craniofacial Research-Clinical Study Oversight Committee, 2020-present

Peer Review Activities

a) Grants

i) National and International

Michael Smith Foundation for Health Research, Reviewer, 2004
Wellcome Trust, Reviewer, 2005
NIDDK, Special Emphasis Panel, 2006, 2007
NIH, BMRD Study Section, Ad-hoc member 2007
NIDDK, DDK-C Study Section, Ad-hoc member 2008
NIH, GCAT Study Section, Ad-hoc member 2009
NIH, GCAT Study Section, Regular member, 2010-2017
Ontario Genomics Institute, 2012
NIH, Special Emphasis Panel, 2013
Chilean National Commission for Science and Technology, Reviewer, 2015
NIH, CIDR Access Committee, Regular member, 2015-2019
Canadian Statistical Sciences Institute, Reviewer, 2015
US-Israel Binational Science Foundation, Reviewer, 2016
NIDDK, DDK-D Study Section, Ad-hoc member 2017
NIH, Special Emphasis Panel, 2018, 2020
NIH/NIGMS, ESI MIRA panel, 2019
NIH/NIMH, Special Emphasis Panel, 2019
NIH, BMRD Study Section, Ad-hoc member 2020
VA, Mental Health and Behavioral-A (MHBA) panel, Ad-hoc member 2023

b) Manuscripts

i) National and International

From 2002-present, ad hoc reviewer for

American Journal of Epidemiology
American Journal of Human Genetics
Annals of Human Genetics
Annals of Neurology
Bioinformatics
Biometrics
Biometrical Journal
Biostatistics
BMC Bioinformatics
BMC Genetics
Computational Statistics & Data Analysis
Genetic Epidemiology

Genetics
Genes & Immunity
Genome Research
Human Heredity
Human Molecular Genetics
JAMA Psychiatry
Journal of the American Statistical Association
Nature
Nature Communications
Nature Genetics
Obesity
PLoS Genetics
PLoS One
Proceedings of the National Academy of Sciences
Science Advances
Statistical Applications in Genetics and Molecular Biology
Statistics in Medicine
Statistical Methods in Medical Research
Theoretical Population Biology

c) Conference Abstracts

i) National and International

American Society of Human Genetics: Statistical Genetics and Genetic Epidemiology section, 2008, 2020

Consultantships

Ontario Genomics Institute, Scientific Advisory Board, 2012-present
Amnion Laboratories, Consultant, 2013-2015

Editorships and Editorial Boards

American Journal of Human Genetics, 2005-2008
F1000 Prime, 2016-present
Genetic Epidemiology, 2011-present
PLoS Genetics, 2016-present
Human Genetics and Genomics Advances, 2020-present
Proceedings of the National Academy of Sciences (Guest Editor), 2020-2021

Honors and Awards

University of Michigan Outstanding First-Year Student in the
Department of Biostatistics, 1997

National Institutes of Health Genome Science Pre-Doctoral Traineeship, 1996-
1999

University of Michigan Horace H. Rackham School of Graduate Studies Pre-
Doctoral Fellowship, 2000

Woodruff Leadership Academy selection, 2018

Society Memberships

American Society of Human Genetics, 2000-present

American Statistical Association, 2002-present

International Biometric Society, 2002-present

International Genetic Epidemiology Society, 2003-present

Organization of Conferences

a) National and International

i) Administrative Positions

Organizer, Junior Faculty Workshop, International Biometric Society: Eastern
North American Region, 2006

Program Committee, IEEE International Conference on Bioinformatics and
Biomedicine, 2012

Lead Organizer, Banff International Research Station Workshop 14w5011,
'Emerging Statistical Challenges and Methods for Analysis of Massive Genomic
Data in Complex Human Disease Studies', 2014

Lead Organizer, American Association for the Advancement of Science,
'Genetics, Statistics, and Precision Medicine', 2018

b) Session as chair

'Molecular Basis of Disorders with Complex Inheritance II: Phenotypes and
Haplotypes', American Society of Human Genetics, Salt Lake City, Utah,
October 2005

'Statistical Methods for Analysis of Gene-Environment Interaction', International
Biometric Society: Eastern North American Region, Austin, Texas, March 2005

‘Recent Advances in Statistical Methods for Genetic Epidemiology’, International Statistical Institute, Lisbon, Portugal, August 2007

‘Statistical Genetics and Genetic Epidemiology’, American Society of Human Genetics, Philadelphia, Pennsylvania, November 2008

‘Next-Generation Sequencing and Rare Variation’, International Genetic Epidemiological Society Meeting, Heidelberg, Germany, September 2011

‘Rare Variant Analysis’, Banff International Research Station Workshop, ‘Emerging Statistical Challenges and Methods for Analysis of Massive Genomic Data in Complex Human Disease Studies’, Banff, Canada, June 2014

‘Genomic Studies of Schizophrenia and Bipolar Disorder’, American Society of Human Genetics, San Diego, California, October 2014

‘Genetics, Statistics, and Precision Medicine’, American Association for the Advancement of Science, February 2018

Formal Teaching

a) Medical Student Training

MEDI545 (Human and Molecular Genetics), Small Group Facilitator, 2003-2006
MD501 (Foundations of Medicine: Normal Human), Small Group Facilitator, 2007

MD500 (Foundations of Medicine: Normal Human), Lecturer, 2010-2011

b) Graduate Program

IBS736 (Genetic Epidemiology), Co-instructor and Co-Organizer, 2002-present

IBS746 (Graduate Human Genetics), Lecturer, 2003, 2005, 2009-present

IBS515 (Current Topics in Human Genetics), Co-instructor and Co-organizer, 2004

IBS592 (Quantitative Methods), Lecturer, 2010-present

EPI552 (Human Genome Epidemiology), Lecturer, 2013-present

BIOS770 (Advanced Statistical Genetics), Lecturer, 2019

BIOS770 (Advanced Statistical Genetics), Organizer and Lead Instructor, 2022

Supervisory Teaching

a) Ph.D. Students Directly Supervised

Lydia Kwee, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University (received Ph.D. Summer, 2008), 2005-2008

Current Position: Biostatistician, Duke Molecular Physiology Institute, Duke University Medical Center

K. Elaine Broadaway, Graduate Student, Population Biology, Ecology, and Evolution program, Emory University (mentored jointly with Dr. Stephanie Sherman), 2010-2015

Current Position: Postdoctoral Fellow, Department of Genetics, University of North Carolina

Yunxuan Jiang, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University (mentored jointly with Dr. Karen Conneely), 2011-2017

Current Position: Statistical Geneticist, 23andMe

Aaron Holleman, Graduate Student, Department of Epidemiology, Emory University (mentored jointly with Dr. Jennifer Mulle), 2017-2022

Current Position: Statistical Geneticist, Alynlam Pharmaceuticals

S. Taylor Fischer, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University, 2018-present

Current Position: Graduate Student

Shijia Bian, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University, 2021-present

Current Position: Graduate Student

Qile Dai, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University (mentored jointly with Dr. Jingjing Yang), 2020-present

Current Position: Graduate Student

Jing Huang, Graduate Student, Genetics and Molecular Biology program, 2021-present

Current Position: Graduate Student

b) Post-doctoral Fellows Directly Supervised

Jessica Hunter, Postdoctoral Researcher, Emory University, 2012-2014

Current Position: Senior Research Public Health Analyst, RTI International

Claudia Solis-Lemus, Postdoctoral Researcher, Emory University, 2017-2019

Current Position: Assistant Professor, Wisconsin Institute for Discovery,
University of Wisconsin-Madison.

Anke Huels, Postdoctoral Research, Emory University, 2018-2019

Current Position: Assistant Professor, Department of Epidemiology, Emory
University

Sarah Curtis, Postdoctoral Researcher, Emory University (mentored jointly with
Dr. Elizabeth Leslie), 2019-

Current Position: Postdoctoral Researcher

Andrew Bass, Postdoctoral Researcher, Emory University (mentored jointly with
Dr. David Cutler), 2021-

Current Position: Postdoctoral Researcher

c) Thesis Committee

Kevin Viel, Graduate Student, Department of Epidemiology, Emory University
(received Ph.D. Fall, 2007), 2004-2007

Current Position: Senior Statistical Programmer, inVentiv Health Clinical

Tiffany Oliver, Genetics and Molecular Biology Program (received Ph.D. Spring,
2008), 2005-2008

Current Position: Associate Professor of Biology, Spelman College

Kira Taylor, Graduate Student, Department of Epidemiology, Emory University
(received Ph.D. Fall, 2009), 2006-2009

Current Position: Associate Professor of Epidemiology and Public Health,
University of Louisville

Jessica Hunter, Genetics and Molecular Biology Program (received Ph.D. Spring
2009), 2006-2009

Current Position: Senior Research Public Health Analyst, RTI International

NaTasha Hollis, Genetics and Molecular Biology Program (received Ph.D. Spring
2010), 2007-2010

Current Position: Epidemiologist, Centers for Disease Control and Prevention

Adam Locke, Genetics and Molecular Biology Program (received Ph.D. Spring 2011), 2007-2011

Current Position: Statistical Geneticist, Regeneron Pharmaceuticals

Benjamin Rambo-Martin, Genetics and Molecular Biology Program, 2012-present

Current Position: Bioinformatics specialist, Battelle

Liz Kennedy, Genetics and Molecular Biology Program, 2014-2018

Current Position: Postdoctoral fellow, Emory University

Peizhou Liao, Department of Biostatistics and Bioinformatics, 2014-2018

Current Position: Postdoctoral Fellow

Chloe Robins, Population Biology, Ecology, and Evolution Program, 2014-2018

Current Position: Human Genetics Investigator, GSK

Kelly Shaw, Genetics and Molecular Biology Program, 2014-2018

Current Position: CDC researcher

Crystal Grant, Genetics and Molecular Biology Program, 2015-2019

Current Position: Christine Mirzayan Science and Technology Policy Graduate Fellow

Sarah Curtis, Genetics and Molecular Biology Program, 2016-2019

Current Position: Postdoctoral fellow

Cristina Trevino, Genetics and Molecular Biology Program, 2015-2020

Current Position: TBD

Trenell Mosley, Genetics and Molecular Biology Program, 2016-2020

Current Position: Postdoctoral fellow

Becky Pollak, Genetics and Molecular Biology Program, 2016-2020

Current Position: Postdoctoral fellow, Icahn School of Medicine at Mount Sinai

Nick Johnson, Population Biology, Ecology, and Evolution Program, 2018-2021

Current Position: TBD

Holly Poore, Department of Psychology, 2018-2021

Current Position: Postdoctoral Fellow

Yemko Pryor, Genetics and Molecular Biology Program, 2019-present

Current Position: Graduate Student

Kimberly Diaz-Perez, Genetics and Molecular Biology Program, 2018-present

Current Position: Graduate Student

Kelsey Robinson, Genetics and Molecular Biology Program ,2020-present

Current Position: Graduate Student

Elizabeth Feldman, Genetics and Molecular Biology Program, 2020-present

Current Position: Graduate Student

Cynthia Perez, Genetics and Molecular Biology Program, 2020-present

Current Position: Graduate Student

d) Ph.D. students: Laboratory rotation

NaTasha Hollis, Genetics and Molecular Biology Program, Spring 2006

Morna Ikeda, Genetics and Molecular Biology Program, Spring 2006

Brandy Wade, Genetics and Molecular Biology Program, Fall 2008

Kelsy Broadway, Population Biology, Evolution, and Ecology Program, Spring 2010

Valery Baranets, Genetics and Molecular Biology Program, Fall 2011

Trenelle Mosley, Genetics and Molecular Biology Program, Spring 2016

Sarah Curtis, Genetics and Molecular Biology Program, Spring 2016
Hari Somnineni, Genetics and Molecular Biology Program, Spring 2016
Nick Johnson, Population Biology, Evolution and Ecology Program, Spring 2017
Beverly Petilli, Genetics and Molecular Biology Program, Spring 2018
Amanda Shurzinske, Genetics and Molecular Biology Program, Spring 2018
Cynthia Perez, Genetics and Molecular Biology Program, Fall 2020
Jing Huang, Genetics and Molecular Biology Program, Fall 2021

e) Masters' students: Directly supervised Masters' theses

Christian Kelly, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University, Spring, 2006

Hemu Nair, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University, Spring, 2007

Yunxuan Jiang, Graduate Student, Department of Biostatistics and Bioinformatics, Emory University, Spring, 2011

Michelle Ivy, Graduate Student, Department of Epidemiology, Emory University, Spring, 2018

Lectureships, Seminar Invitations, and Visiting Professorships

a) National and International

2003: 'Variance-Component Linkage Methods for Complex Traits': Medical Statistics-Current Developments in Statistical Methodology for Genetic Architecture of Complex Diseases, Oberwolfach, Germany

2003: 'Haplotype Analysis in Case-Control Studies': Department of Biostatistics, University of Alabama-Birmingham

2003: 'Variance-Component Methods for Linkage Analysis of General Quantitative Traits': Center for Statistical Science, Brown University.

2004: 'Haplotype Analysis in Case-Control Studies': Department of Biostatistics, University of North Carolina

2004: 'Genetic Association Analysis of Trios and Unrelated Subjects': Department of Biostatistics, Yale University

2005: ‘Genetic Association Analysis of Trios and Unrelated Subjects’: Department of Biostatistics, University of North Carolina

2006: ‘Haplotypes and Fine Mapping’: NIAMS Short Course in Statistical Genetics, Atlanta, GA

2006: ‘Improved Association Analysis of Case-Parent Trios’: Department of Epidemiology, Columbia University

2006: ‘Improved Association Analysis of Case-Parent Trios’: Department of Statistics, University of Georgia

2006: ‘A Simple and Improved Correction for Population Stratification in Case-Control Studies’: Division of Cancer Epidemiology and Genetics, National Cancer Institute

2007: ‘Multilocus Association Methods for Quantitative Traits’: Department of Epidemiology and Biostatistics, Sloan-Kettering Cancer Center,

2008: ‘Fast and Robust Association Tests of Untyped Variants in Case-Control Studies’: NHGRI Conference on Haplotype Analysis of Population & Pedigree Data in Association Studies, Birmingham, AL

2008: ‘Multilocus Association Methods for Quantitative Traits’: Department of Biostatistics, University of Alabama-Birmingham

2008: ‘Fast and Robust Association Tests of Untyped Variants in Case-Control Studies’: DIMACS Workshop on Computational Issues in Genetic Epidemiology, Rutgers University

2008: ‘Fast and Robust Association Tests of Untyped Variants in Case-Control Studies’: Department of Epidemiology and Biostatistics, University of Pennsylvania

2008: ‘Fast and Robust Association Tests of Untyped Variants in Case-Control Studies’: Center for Statistical Genetics, Department of Biostatistics, University of Michigan

2009: ‘Fast and Robust Association Tests of Untyped Variants in Case-Control Studies’: Wellcome Trust Genome Center, Hinxton, United Kingdom

2010: ‘A Matching Approach to Correct for Population Stratification in Case-Control Studies’: Department of Human Genetics, University of California-Los Angeles

2011: ‘Novel Approaches to Correct for Population Stratification in Case-Control Studies’: Department of Statistics, Yale University

2011: ‘Novel Approaches to Correct for Population Stratification in Case-Control Studies’: Department of Epidemiology and Public Health, University of Miami

2012: ‘Novel Approaches to Correct for Population Stratification in Case-Control Studies’: Department of Statistics, George Mason University

2013: ‘Improved Methods for Design and Analysis of Resequencing Studies’: Department of Biostatistics, Columbia University

2013: ‘Statistical Approaches for Gene Mapping in the 22q11DS Sample’: International 22q Consortium, Dublin, Ireland

2014: ‘Statistical Methods for Rare Variant Testing in Affected Sibships’: Section of Biostatistics and Epidemiology, Dartmouth School of Medicine

2014: ‘GE Brings Good Things to Life? Lesson Learned from Gene-Environment Interaction Studies of Psychiatric Traits’: Genomics Grand Rounds, Dartmouth School of Medicine

2014: ‘Statistical Methods for Rare Variant Testing in Affected Sibships’: Section of Biostatistics and Epidemiology, Dartmouth School of Medicine

2014: ‘Statistical Methods for Rare Variant Testing in Affected Sibships’: Institute of Human Genetics, University of California-San Francisco

2015: ‘Statistical Methods for Rare Variant Testing in Affected Sibships’: 4th Workshop on Biostatistics and Bioinformatics, Georgia State University

2016: ‘Assessing Cross-Phenotype Effects of Rare Variants’: Department of Biostatistics, Columbia University

2017: ‘Genetic Analysis of Multivariate Phenotypes’: Division of Biostatistics, University of Minnesota

2021: ‘Novel TWAS Techniques for Studying Complex Human Diseases’: Department of Public Health Sciences, Pennsylvania State University

2021: ‘Novel TWAS Techniques for Studying Complex Human Diseases’: Department of Biostatistics, Johns Hopkins University

2022: ‘A TWAS Framework Leveraging Summary-Level Reference Data’: Department of Biostatistics, University of Michigan

b) Institutional

2003: ‘Variance-Component Methods for Linkage Analysis of General Quantitative Traits’: Department of Biostatistics and Bioinformatics

2007: ‘A Simple and Improved Correction for Population Stratification in Case-Control Studies’: Department of Human Genetics

2008: ‘A Simple and Improved Correction for Population Stratification in Case-Control Studies’: Department of Mathematics and Computer Science

2014: ‘GE Brings Good Things to Life? Lesson Learned from Gene-Environment Interaction Studies of Psychiatric Traits’: Department of Human Genetics

Invitations to Conferences

a) National and International

2004: ‘Case-Control Association Analysis Using Haplotype Similarity’: International Conference on Statistics in Health Sciences, Nantes, France

2005: ‘Association Methods for Complex Traits’: Genetics Special Interest Group, American Epilepsy Society, Washington DC

2007: ‘Multilocus Association Methods for Quantitative Traits’: International Chinese Statistical Association Conference, Raleigh, NC

2007: ‘A Simple and Improved Correction for Population Stratification in Case-Control Studies’: Joint Statistical Meetings, Salt Lake City, UT

2007: ‘A Simple and Improved Correction for Population Stratification in Case-Control Studies’: International Statistical Meetings, Lisbon, Portugal

2008: ‘Multilocus Association Methods for Quantitative Traits’: International Biometric Society Meeting: ENAR region, Crystal City, VA

2008: ‘Fast and Robust Association Tests of Untyped Variants in Case-Control Studies’: International Society of Clinical Biostatistics Meeting, Copenhagen, Denmark

2010: ‘A Matching Approach to Correct for Population Stratification in Case-Control Studies’: International Chinese Statistical Association Meeting, Indianapolis, IN

2010: ‘Kernel Approaches for Gene Mapping of Complex Traits’: Joint Statistical Meetings, Vancouver, BC

2011: ‘A Permutation Approach to Correct for Confounders in Case-Control Resequencing Studies’: Joint Statistical Meetings, Miami, FL

2012: A Matching Approach to Correct for Population Stratification in Case-Control Studies’: IEEE International Conference on Bioinformatics & Biomedicine, Atlanta, GA

2012: ‘A Permutation Approach to Correct for Confounders in Case-Control Resequencing Studies’: International Biometric Society Meeting: ENAR region. Washington DC

2012: ‘Association Mapping in Familial Samples Using Kernel Functions’: Joint Statistical Meetings, San Diego, CA

2014: ‘Statistical Methods for Rare Variant Testing in Affected Sibships’: International Biometric Society Meeting: ENAR region. Baltimore, MD

2014: ‘Statistical Methods for Rare Variant Testing in Affected Sibships’: Banff International Research Station Workshop 14w5011, ‘Emerging Statistical Challenges and Methods for Analysis of Massive Genomic Data in Complex Human Disease Studies’

2015: ‘Assessing Cross-Phenotype Effects of Rare Variants’: Recent Developments in Statistical Methods with Applications to Genetics and Genomics. Oberwolfach, Germany

2016: ‘Rare Variant Analysis of Complex Disease in Pedigrees’: International Biometric Society Meeting: ENAR region, Austin, TX

2016: ‘Assessing Cross-Phenotype Effects of Rare Variants’: International Congress of Human Genetics, Kyoto, Japan

2016: ‘Assessing Cross-Phenotype Effects of Rare Variants’: Mathematical and Computational Medicine International Conference, Columbus, OH

2016: ‘Assessing Cross-Phenotype Effects of Rare Variants’: Joint Statistical Meetings, Chicago, IL

2016: ‘Assessing Cross-Phenotype Effects of Rare Variants’: International Indian Statistical Association, Corvallis, OR

2017: ‘Genetic Analysis of Multivariate Phenotypes’: Third Annual Kliakhandler Conference on Bayesian Inference in Statistics and Statistical Genetics, Houghton, MI

2018: ‘Genetic Analysis of Multivariate Phenotypes’: Joint Statistical Meetings, Vancouver, Canada

2019: ‘Flexible Strategies for Identifying Factors Influencing Pathway Dysregulation’: Banff International Research Station Workshop, ‘Role of Genomics and Metagenomics in Human Health: Recent Developments in Statistical and Computational Methods’

2020: ‘Improved Mediation Analyses in Case-Control Studies’: International Genetic Epidemiological Society Meeting, Virtual

Research Focus

My research focuses on statistical techniques for human gene mapping of complex traits. This work involves two synergistic components: a methodological component focused on developing statistical techniques for improved gene mapping and an applied component focused on mapping genes involved in diseases such as Alzheimer’s disease, breast cancer, epilepsy, and schizophrenia.

Grant Support

a) Active support

i) Federally Funded

R01 AG071170 (NIH/NIA)	09/11/20-8/31/24
Role: MPI	\$480,000
Quantitative Genetic Models for Exploring Missing Heritability of Alzheimer’s Disease	

R01 MH126449 (NIH/NIMH)	9/01/21-09/01/26
Role: MPI	\$3,845,978 (total)
The schizophrenia-associated 3q29 deletion: Genetic architecture of behavioral phenotypes	

R35 GM138313 (NIH/NIGMS)	09/01/20-06/30/25
Role: Co-I (Yang, PI)	\$250,000
Novel Bayesian statistical tools for integrating multi-omics data to help elucidate the genomic etiology of complex phenotypes	

P50 HD104463 (NIH/NICHD)	09/01/20-08/31/25
Role: Co-I (Nelson/Todd MPI)	\$10,147,351 (total)
Fragile X Premutations, Mechanisms, and Modifiers	
Project 3: FXPOI: Mechanisms and Modifiers	

R01 DE030342 (NIH/NIDCR)	09/01/21-05/01/26
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Role: Co-I (Leslie, PI) Genomics of Cleft Palate	\$3,546,618 (total)
R01 CA237318 (NIH/NCI) Role: Co-I (Schildkraut/Lawson MPI) Ovarian Cancer Survival in African-American Women	07/01/20-06/30/25 \$6,839,897 (total)
R01 DE028342 (NIH/NIDCR) Role: Co-Investigator (Leslie, PI) Genetic modifiers of Van der Woude syndrome	08/01/19-07/1/24 \$405,628
R03 DE030118 (NIH/NIDCR) Role: Co-Investigator (Leslie, PI) The role of noncoding regulatory variants in orofacial clefts	08/1/21-07/01/23 \$312,958 (total)
R03 HD106123 (NIH/NICHHD) Role: Co-Investigator (Hunter, PI) Capturing and characterizing variability of cognition and behavior in Down syndrome	09/1/21-06/1/23 \$105,922 (total)
R01 AG072120 (NIH/NIA) Role: Co-Investigator (Wingo, Wingo MPI) A brain multi-omic approach to identify key molecular drivers of neuropsychiatric symptoms in Alzheimer's dementia	09/1/21-09/1/26 \$3,920,696 (total)
R01 AG075827 (NIH/NIA) Role: Co-Investigator (Wingo, Wingo MPI) Integrative genomic, transcriptomic, and proteomic analyses to investigate sex-specific differences in Alzheimer's Disease	09/1/21-09/1/26 \$3,830,232 (total)

b) Pending Support

R01 AG077224 (NIH/NIA) Role: Co-I (Wingo, Wingo MPI) Shared mechanisms between mid-life psychiatric illnesses and late-life AD/ADRD	04/01/22-03/31/27 \$3,786,282 (total)
R01 AG073254 (NIH/NIA) Role: Co-I (Wingo, PI) Integrating human brain proteomes with AD GWAS to identify novel AD causal genes	04/01/22-03/31/27 \$3,793,596 (total)

c) Previous Support

Emory URC 2003037 Role: PI Variance-Component Statistical Methods for Gene Mapping of Complex Diseases and Surrogate Traits	06/01/2003 – 06/01/2004 \$30,000
R01 GM046331-13 (NIH/NIGMS)	03/01/2005-02/28/2009

Role : Co-Investigator (D. Reines, PI)	\$182,361
RNA Polymerase II Elongation Complex: Structure & Function	
Merit Review Grant (VA)	10/01/2005-9/01/2010
Role: Co-Investigator (E. Duncan, PI)	\$129,900
Sensorimotor gating in schizophrenia	
R01 MH076439-03 (NIH/NIMH)	09/30/2005-07/31/2010
Role: Co-Investigator (M. Zwick, PI)	\$361,045
Identifying Autism Susceptibility Genes By High-Throughput Chip Resequencing	
P50 MH077083-02 (NIH/NIMH)	07/14/2006-06/30/2008
Role: Co-Investigator (C. Nemeroff, PI)	\$1,219,693
Predictors of Antidepressant Treatment Response: The Emory CIDAR	
R21 MH076024-02 (NIH/NIMH)	08/15/2006-07/31/2008
Role: Co-Investigator (E. Binder, PI)	\$135,000
Peri-Partum Depression and Genetic Variation in Regulating Genes	
R01 HG003618-02 (NIH/NHGRI)	09/27/2006-08/31/2011
Role: PI	\$200,000
Novel Statistical Methods for Human Gene Mapping	
R01 MH080129-01 (NIH/NIMH)	04/01/2007-03/31/2012
Role: Co-Investigator (S. Warren, PI)	\$448,556
Schizophrenia Susceptibility by Copy Number Variation in the Ashkenazim	
P50 MH077928-01A1 (NIH/NIMH)	09/01/2007-08/31/2012
Role: Co-Investigator (Z. Stowe, PI)	\$1,389,445
Perinatal Stress and Gene Influences: Pathways to Infant Vulnerability	
U01 HL089856-01 (NIH/NHLBI)	09/01/2007-07/01/2012
Role: Consultant (E. Silverman, PI)	\$7,400,000
Genetic Epidemiology of COPD	
R01 MH083722 (NIH/NIMH)	07/01/2008-06/30/2012
Role: Co-Investigator (S. Warren, PI)	\$485,917
Bipolar I susceptibility by copy number variation in an isolated population	
5 U19 MH069056-07(NIH/NIMH)	06/01/2009-05/31/2014
Role: Co-Investigator (Mayberg, PI)	\$1,717,858
Emory-MSSM-GSK-NIMH Collaborative Mood and Anxiety Disorders Initiative	
R01 MH092923-01 (NIH/NIMH)	08/30/2011-07/31/2014
Role: Co-Investigator (B. Hopkins, PI)	\$291,749
Vasopressin Receptor Polymorphism and Social Cognition	

U01-NS077303-01 (NIH/NINDS) 10/01/2011-09/30/2016
 Role: Co-Investigator (Goldstein, PI) \$1,617,056
 3 of 7 Epi4K: Gene discovery in 4,000 epilepsy genomes
 Sequencing, Biostatistics, and Bioinformatics Core

R01 AR060893-01 (NIH/NIAMS) 09/01/2011-08/31/2015
 Role: Co-Investigator (S. Prahalad, PI) \$250,000
 Segmental chromosome sharing in affected relatives with Juvenile Arthritis

R01 MH071537-03 (NIH/NIMH) 09/01/2010-02/29/2016
 Role: Co-Investigator (K. Ressler, PI) \$821,246
 Genetic and Trauma-Related Risk Factors for PTSD

U01 NS077367-01 (NIH/NINDS) 10/01/2012-09/30/2016
 Role: MPI \$315,000
 5 of 7 Epi4K: Gene discovery in 4,000 epilepsy genomes
 Whole Genome Sequencing in Multiplex Families and Pairs

R01 HG007508-01 (NIH/NHGRI) 09/01/2013-06/30/2016 (NCE)
 Role: PI \$250,528
 Enhanced Gene Identification in Complex Traits Using Kernel Machines

5 T15 HL098122-05 (NIH/NHLBI) 03/01/2013-02/28/2016
 Role: Co-Investigator (L. Waller, PI) \$238,892
 Atlanta Summer Institute for Training in Biostatistics

U01 MH101720-01 (NIH/NIMH) 09/26/2013-07/31/2017
 Role: Co-Investigator (Warren, PI) \$1,524,233
 2/5 International Consortium in Brain and Behavior in 22q11.2 Deletion Syndrome

R01 MH105561-01 (NIH/NIMH) 09/25/14-7/31/18
 Role: Co-Investigator (Guo/Kang) \$250,000
 Statistical ICA Methods for Analysis and Integration of Multi-Dimensional Data

R01 MH100917-01 (NIH/NIMH) 05/01/2014-04/30/2018
 Role: Co-Investigator (Warren/Mulle MPI) \$430,430
 1/2 Targeted Sequencing and Functional Evaluation of Mutations in Schizophrenia

R01 HD081274 (NIH/NICHHD) 09/10/2014-05/30/2019
 Role: Co-Investigator (Trumbower, PI) \$250,000
 Mechanisms of Intermittent Hypoxia-Induced Motor Recovery in Persons with SCI

CER-1408-19941 (Fridovich-Keil, PI) 07/01/15-6/01/19
 Patient Centered Outcomes Research Institute
 Intervention and Outcomes in Duarte Galactosemia

U54 NS091859 (NIH/NINDS/NICHHD) 09/22/14-05/31/20

Role: Co-Investigator (Warren, PI) \$1,155,338
Modifiers of FMR1-associated Disorders: Application of High Throughput Technologies

R01 GM117946 (NIH/NIGMS) 02/01/16-12/31/20
Role: MPI \$225,000
Statistical Tests for Mapping Genetic Determinants of Complex Traits

R21 DE029698 (NIH/NIDCR) 04/01/20-03/31/23 (NCE)
Role: PI \$150,000
Improved Mediation Analyses in Case-Control Studies

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a) Peer-reviewed Research Articles (published and in press)

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