CURRICULUM VITAE

MOLLY HALL, PHD

E-mail Address: mah546@psu.edu

Education

PhD 2015	Pennsylvania State University (Biochemistry & Molecular Biology)
MS 2011	Columbia University (Neuroscience & Education)
BS 2005	Cornell University (Human Development)

Professional Employment

2017-present	Assistant Professor (Tenure-track) Department of Veterinary and Biomedical Sciences Huck Institutes of the Life Sciences Pennsylvania State University
2015-2017	Postdoctoral Researcher – Moore Laboratory Institute for Biomedical Informatics Perelman School of Medicine University of Pennsylvania
2011-2015	Graduate Research Assistant – Ritchie Laboratory Department of Biochemistry & Molecular Biology Pennsylvania State University

Teaching Positions & Courses Taught

2021-present	BMB/VBSC 485 – Human Genomics and Biomedical Informatics (3 credits) Instructor Pennsylvania State University
2020	CAMB 698 – Cell & Molecular Biology Graduate Group Guest Lecturer University of Pennsylvania
2018-present	MCIBS 503 – Critical Elements of Molecular and Cellular Biology (4 credits) Instructor and Course Organizer Pennsylvania State University
2011-2013	Teaching Assistant – Microbiology Laboratory Department of Biochemistry & Molecular Biology Pennsylvania State University
2007-2009	Middle School Science Teacher Williamsburg Collegiate Charter School, Uncommon Schools, Inc. Brooklyn, NY
2005-2007	Middle School Science Teacher Teach For America (TFA) Bronx, NY

Fellowships/Professorships

2019	Dr. Frances Keesler Graham Early Career Professorship for Neural Development Research
2015	Ruth L. Kirschstein National Research Service Award (NRSA) Individual Predoctoral Fellowship (Parent F31)
2011	Braddock-Roberts Fellowship (Penn State University, Department of Biochemistry and Molecular Biology)

Awards

2021	Environmental influences on Child Health Outcomes (ECHO) Opportunities and Infrastructure Fund (OIF) (funded by NICHD)
2021	NIH Loan Repayment Program Recipient (Renewal, funded by NHGRI)
2020	Joan Luerssen Faculty Enhancement Fund (College of Agricultural Sciences, Penn State University)
2019	NIH Loan Repayment Program Recipient (funded by NHGRI)
2019	Roy C. Buck Faculty Award for Outstanding Publication, College of Agricultural Sciences, Penn State University
2016	Wedler Outstanding Doctoral Dissertation Thesis Award
2014	Pacific Symposium on Biocomputing Travel Award, funded through the National Library of Medicine/National Institutes of Health
2013	Paul M. Althouse Outstanding Teaching Assistant Award
2012	Cold Spring Harbor Laboratory Programming for Biology Course Scholarship
2012	Genetic Analysis of Complex Human Disease Travel Scholarship, funded through the National Institutes of Health

Service

2021-Present	Review Editor, Editorial Board of Applied Genetic Epidemiology, *Frontiers in Genetics*
2021-Present	Member, Biobehavior Health Department Faculty Search Committee Precision Population Health Faculty Search
2020-2021	Session organizer, “What about the environment? Leveraging multi-omic datasets to characterize the environment’s role in human health”, 2021 Pacific Symposium on Biocomputing (PSB), Hawaii, HI
2020	Reviewer, NIH, U01 NIDDK Special Emphasis Panel (ZDK1 GRB-G(03))
2019	Session Moderator, “What about the phenotype? Integrating electronic health records to drive discovery in precision health”, American Society of Human Genetics (ASHG), Houston, TX
2018-present	Member, Center for Computational Biology and Bioinformatics (CCBB) Committee, Penn State
2019-present	Member, Molecular, Cellular, and Integrated Biosciences (MCIBS) Candidacy Committee, Huck Institutes, Penn State
2019-present	Member, Pathobiology Graduate Program Selection Committee, Department of Veterinary & Biomedical Sciences, Penn State

2019-present	Member, Bioinformatics and Genomics Program Committee, Huck Institutes, Penn State
2019-2020	Member, College of Agricultural Sciences Nominations and Elections Committee
2018-2019	Member, Penn State High Performance Computing Working Group
2017-Present	Member, Department of Veterinary & Biomedical Sciences Undergraduate and Graduate Scholarship Committee
2017-2020	Founder, Penn State College of Agriculture Sciences Women Faculty Group
2017-2018	Member, Penn State Data Life Course Working Group
2015-Present	Reviewer, *PLoS One*, *BioData Mining, Scientific Reports, Bioinformatics, American Journal of Human Genetics*
2014	Conference session co-organizer for *Pacific Symposium of Biocomputing* session, Characterizing the Importance of Environmental Exposures, Interactions between the Environment and Genetic Architecture and Genetic Interactions
2014-2015	Biochemistry & Molecular Biology Department Climate and Diversity Committee – Graduate Student Liaison
2012-2015	Biochemistry & Molecular Biology Graduate Student Association – Vice President
2012-2015	Biochemistry & Molecular Biology Graduate Student Association – Mentor to incoming first-year students
2011-Present	Cornell University – Alumni Mentor to undergraduate students
2007-2015	Teach For America – Recruitment support, Columbia University
2005-2007	Teach For America – Corps Member

Major Research Interests

The Exposome
Genomics
Metabolomics
Gene-Environment Interactions
Environment-Wide Association Studies
Gene-Gene Interactions
Personalized Medicine
Complex Disease
Psychosocial outcomes
Neurodevelopmental disorders
Genetic Epidemiology
Phenome-Wide Association Studies

Publications

Molly A. Hall, John Wallace, Anastasia M. Lucas, Yuki Bradford, Shefali S. Verma, Bertram Müller, Myhsok, Kristin Passero, Jiayan Zhou, John McGuigan, Beibei Jiang, Sarah A. Pendergrass, Yanfei Zhang, Peggy Peissig, Murray Brilliant, Patrick Sleiman, Hakon Hakonarson, John B. Harley, Krzysztof Kiryluk, Kristel Van Steen, Jason H. Moore, Marylyn D. Ritchie. Novel EDGE encoding method enhances ability to identify genetic interactions. *PLoS Genetics* 17(6): e1009534. https://doi.org/10.1371/journal.pgen.1009534

Li JC, **Hall MA**, Shalev I, Schreier HMC, Gonzalez Zarzar T, Marcovici I, Putnam FW, Noll JG. (2021) Hypothalamic-pituitary-adrenal axis attenuation and obesity risk in sexually abused females. *Psychoneuroendocrinology* 129 1055254.

Passero K, Setia-Verma S, McAllister K, Manrai A, Patel C, **Hall MA**. (2021) What About the Environment? Leveraging Multi-Omic Datasets to Characterize the Environment's Role in Human Health. *Pac Symp Biocomput*, 26: 309-315. https://doi.org/10.1142/9789811232701_0029

Aguilar MA, McGuigan J, **Hall MA**. (2021) Semi-automated NMR Pipeline for Environmental Exposures: New Insights on the Metabolomics of Smokers versus Non-smokers. *Pac Symp Biocomput*, 26: 316-327. https://doi.org/10.1142/9789811232701_0030

Zhou J, Passero K, Palmiero N, Mueller-Myhsok B, Kleber M, Maerz W, and **Hall MA**. (2020) Investigation of gene-gene interactions in cardiac diseases and serum fatty acid levels in LURIC cohort. *PLOS ONE* 15(9): e0238304. https://doi.org/10.1371/journal.pone.0238304

Passero K, He X, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, and **Hall MA**. (2020). Phenome-wide association studies on cardiovascular health and fatty acids considering phenotype quality control practices for epidemiological data. *Pac Symp Biocomput*, 25: 659-670

Lucas AM*, Palmiero N*, McGuigan J, Passero K, Zhou J, Orie D, Ritchie MD, and **Hall MA**. (2019) CLARITE facilitates the quality control and analysis process for EWAS of metabolic-related traits. *Frontiers in Genetics*, 10: 1240. https://doi.org/10.3389/fgene.2019.01240

Manduchi E, Chesi A, **Hall MA**, Grant SFA, Moore JH. (2018) Leveraging putative enhancer-promoter interactions to investigate two-way epistasis in type 2 diabetes GWAS. *Pac. Symp. Biocomput.* 23:548-558.

Hall MA, Cole B, Moore JH. (2018) Gene-Gene Interactions: An Essential Component to Modeling Complexity for Precision Medicine. *Encyclopedia of Bioinformatics and Computational Biology*: 171-177.

Cole B, **Hall MA**, Urbanowicz RJ, Gilbert-Diamond D, Moore JH (2018) Analysis of Gene-Gene Interactions. *Current Protocols in Human Genetics*: 95(1), 1-14.

Hall MA, Wallace J, Lucas A, Kim D, Basile AO, Verma SS, McCarty CA, Brilliant MH, Peissig PL, Kitchner TE, Verma A, Pendergrass S, Dudek S, Moore JH, Ritchie MD (2017) PLATO provides analytic framework for investigating complexity beyond genome-wide association studies. *Nature Communications:*1167.

Manrai AK, Cui Y, Bushel PR, **Hall MA** Karakitsios S, Mattingly CJ, Ritchie M, Schmitt C, Sarigiannis DA, Thomas DC, Wishart D, Balshaw DM, Patel CJ (2017) Informatics and data analytics to support exposome-based discovery for public health. *Annual Review of Public Health*: 38, 279-294.

Kim D, Volk H, Girirajan S, Pendergrass S, **Hall MA**, Verma SS, Schmidt RJ, Hansen RL, Ghosh D, Ludena-Rodriguez Y, Kim K, Ritchie MD, Hertz-Picciotto I, and Selleck SB (2017) The joint effect of air pollution and copy number variation on risk for autism. *Autism Research* 10(9): 1470-1480.

De R, Verma SS, Holzinger ER, **Hall MA**, Burt A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Lange LA, Lanktree MB, Larson EB, North KE, Reiner AP, Tragante V, Tromp G, Wilson JG, Asselbergs FW, Drenos F, Moore JH, Ritchie MD, Keating B, Gilbert-Diamond D (2017) Identifying gene-gene interactions that are highly associated with four quantitative lipid traits across multiple cohorts. *Human Genetics* 136(2): 165-178.

Holzinger ER, Verma SS, Moore CB, **Hall M**, De R, Gilbert-Diamond D, Lanktree MB, Pankratz N, Amuzu A, Burt A, Dale C, Dudek S, Furlong CE, Gaunt TR, Kim DS, Riess H, Sivapalaratnam S, Tragante V, van Iperen EPA, Brautbar A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Larson EB, Rasmussen-Torvik LJ, Tromp G, Baumert J, Cruickshanks KJ, Farrall M, Hingorani AD, Hovingh GK, Kleber ME, Klein BE, Klein R, Koenig W, Lange LA, März W, North KE, Charlotte Onland-Moret N, Reiner AP, Talmud PJ, van der Schouw YT, Wilson JG, Kivimaki M, Kumari M, Moore JH, Drenos F, Asselbergs FW, Keating BJ, Ritchie MD. Discovery and replication of SNP-SNP interactions for quantitative lipid traits in over 60,000 individuals. *BioData Min*. 2017 Jul 24;10:25

Hall MA, Moore JH, Ritchie MD (2016) Embracing complex associations in common traits: Critical considerations for precision medicine. *Trends in Genetics*: 32, 470-484

Li R, Dudek S, Kim D, **Hall MA**, Bradford Y, Peissig P, Brilliant B, Linneman JG, McCarty CA, Bao Le, Ritchie MD (2016) Identification of genetic interaction networks via an evolutionary algorithm evolved Bayesian network. *BioData Mining* 9:18.

Hall MA, Verma A, Brown-Gentry KD, Goodloe R, Boston J, Wilson S, McClellan B, Sutcliffe C, Dilks HH, Gillani NB, Jin H, Mayo P, Allen M, Schnetz-Boutaud N, Crawford DC, Ritchie MD, Pendergrass SA (2014) Detection of pleiotropy through and phenome-wide association study (PheWAS) of epidemiologic data as part of the Environmental Architecture for Genes Linked to Environment (EAGLE) study. *PLoS Genetics*: 10.

Hall MA, Verma SS, Wallace J, Lucas AM, Berg RL, Connolly J, Crawford DC, Crosslin DR, de Andrade M, Dohen KF[7], Haines JL, Harley JB, Jarvik GP, Kitchner T, Kuivaniemi H, Larson EB, Carrell DS, Tromp G, Vrabec TR, Pendergrass SA, McCarty CA, Ritchie MD (2015) Biology-driven gene-gene interaction analysis of age-related cataract in the eMERGE Network. *Genetic Epidemiology*: 39 376-384.

Hall MA, Verma SS, Wall DP, Moore JH Keating B, Campbell DB, Gibson G, Asselbergs FW, Pendergrass S (2015) Session Introduction: Characterizing the the importance of environmental exposures, interactions between the environment and genetic architecture, and genetic interactions. *Pac. Symp. Biocomput.*

Pendergrass SA, Verma A, Okula A, **Hall MA**, Crawford DC, Ritchie MD (2015) Phenome-wide association studies (PheWAS): Embracing complexity for discovery. *Human Heredity* 79:111-123.

De R, Verma SS, Drenos F, Holzinger ER, Holmes MV, **Hall MA,** Burt A, Carrell DS, Crosslin DR, Jarvik GP, Kuivaniemi H, Kullo IJ, Lange LA, Lanktree MB, Larson EB, North KE, Reiner AP, Tragante V, Tromp G, Wilson JG, Asselbergs FW, Drenos F, Moore JH, Ritchie MD, Keating B, Gilbert-Diamond D. (2015) Identifying gene-gene interactions that are highly associated with body mass index using quantitative multifactor dimensionality reduction (QMDR) *BioData Mining* 8: 4.

Hall MA, Dudek SM, Goodloe R, Crawford DC, Pendergrass SA, Peissig P, Brilliant M, McCarty CA, Ritchie MD (2014) Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield Personalized Medicine Research Project Biobank. *Pac Symp Biocomput*: 200-211

Ritchie MD, Verma SS, **Hall MA**, Goodloe RJ, Berg RL, Carrell DS, Carlson CS, Chen L, Crosslin DR, Denny JC, Jarvik G, Li R, Linneman JG, Pathak J, Peissig P, Rasmussen LV, Ramirez AH, Wang X, Wilke RA, Wolf WA, Torstenson ES, Turner SD, McCarty CA (2014) Electronic medical records and genomics (eMERGE) network exploration in cataract: Several new potential susceptibility loci. *Molecular Vision*: 20.

Pendergrass SA, Verma SS, **Hall MA**, Holzinger ER, Moore CB, Wallace JR, Dudek SM, Huggins W, Kitchner T, Waudby C, Berg R, McCarty CA, Ritchie MD (2013) Next-generation analysis of cataracts: determining knowledge driven gene-gene interactions using Biofilter, and gene-environment interactions using the PhenX Toolkit. *Pac Symp Biocomput*: 147-58.

Revise and Resubmit:

Lingyao Li, Lei Gao, Jiayan Zhou, Zihui Ma, **Molly A. Hall**. Crowdsourcing through social media for early warning of infectious disease outbreak: Covid-19 pandemic in the US (Revise & Resubmit at *IEEE Access*)

Submitted/Under Review:

Zhou J, Palmiero N, Passero K, McGuigan J, Aguilar MA, Prabhu KS, and **Hall MA**. Risk assessments for the common types of anemia from exposome through a series of environment-wide association studies (EWASs) in NHANES 1999-2006. (In Preparation)

In Preparation:

McGuigan J, Veturi Y, Li B, Verma A, Le T, Fu W, Haas D, Ritchie MD, **Hall MA***, Moore JH*. Automated machine learning for rare variant analysis of response to antiretroviral therapy in patients infected with HIV

Kristin Passero, Nicole Palmiero, Jennie G Noll, Idan Shalev, Lisa Gatzke-Kopp, and **Molly A. Hall.** Phenome-by-environment-wide association study (PheEWAS) finds multiple associations between early-life psychosocial exposures and later child emotional-behavioral traits (in preparation)

Palmiero N, Zhou J, Passero K, McGuigan J, Aguilar MA, and **Hall MA**. Phenome-wide environment wide association study to evaluate the complexity of the exposome. (In Preparation)

Jiayan Zhou, Kris.n Passero, Xi He, Nicole E. Palmiero, Bertram Müller-Myhsok, Marcus E. Kleber, Winfried Maerz, and Molly A. Hall. (2021) Gene-environment interaction analysis for cardiac-related traits in the Ludwigshafen Risk and Cardiovascular (LURIC) Health Study.

Gonzalez T, Palmiero N, Hall M (2021) Sex differences in the effect of exposures in NHANES.

Lingyao Li, Jiayan Zhou, Sang Gyu Lee, Zihui Ma, Molly A. Hall. (2021) The COVID-19 vaccine hesitancy in the United States from the social media.

Additional Information: Research Support and/or Scholastic Performance

Complete List of Published Work in MyBibliography

https://www.ncbi.nlm.nih.gov/sites/myncbi/18sXnah7uHfQb/bibliography/46095730/public/?sort=date&direction=descending

Active:

1R01CA239256-01A1 (co-investigator) (PI: Peters, Patterson) 12/01/2019 to 11/30/2024
National Institutes of Health
Unique Targeting of Pparb/d Regulation for Cancer Prevention and Therapy
Goals: The goals of this project it to determine the feasibility of selectively repressing PPARb/d activity in colon cancer models to determine the mechanisms by which this pathway inhibit tumorigenesis, to identify metabolic signatures indicative of modulating this pathway, and potentially identify novel biomarkers of efficacy.

Completed Research Support

5F31HG008588-02 05/16/2015-09/30/15

NIH/NHGRI

The primary goal of this project is to develop novel methods to identify and replicate complex interactions in common disease

Role: PI

Conference Talks:

Aguilar MA, McGuigan J, **Hall MA** (Jan 2021) Semi-automated NMR Pipeline for Environmental Exposures: New Insights on the Metabolomics of Smokers versus Non-smokers. Paper presented at the Pacific Symposium on Biocomputing. Virtual.

Passero K, Setia-Verma S, McAllister K, Manrai A, Patel C, **Hall MA** (Jan 2021) What About the Environment? Leveraging Multi-Omic Datasets to Characterize the Environment's Role in Human Health. Paper presented at the Pacific Symposium on Biocomputing. Virtual.

Hall MA, Dudek SM, Goodloe R, Crawford DC, Pendergrass SA, Ritchie MD (2014) Environment-wide association study (EWAS) for type 2 diabetes in the Marshfield Personalized Medicine Research Project Biobank. *2014 Pacific Symposium on Biocomputing (PSB)*

Hall MA, Verma SS, Holzinger ER, Ritchie MD (2013) Replication of gene-gene interaction models associated with cataracts in the eMERGE Network. *American Society for Human Genetics (ASHG)*

Hall MA, Verma A, Brown-Gentry KD, Pendergrass SA (2012) A Phenome-Wide Association Study (PheWAS) using multiple National Health and Nutritional Surveys (NHANES) to identify pleiotropy. *2012 Translational Biology Conference (TBC)*

Invited Talks

Hall MA (Presenter & Author). (2/25/2021). "Knowledge-based gene-environment interaction modeling for neurodevelopmental outcomes". ECHO Cohort PI Meeting, Johns Hopkins University.

Hall MA (Presenter & Author). (11/5/2020). "Computational approaches for modeling complexity in common disease". Animal Science Department Seminar, Penn State University

Hall MA (Presenter & Author). (12/6/2019). "Modeling the complexity of common disease". Roy C. Buck Faculty Award Bortree Seminar, Penn State University

Hall MA (Presenter & Author). (12/4/2019). "Modeling the complexity of common disease". KINES PhD program seminar 12/6/19, Penn State University

Hall MA (Presenter & Author). (February 25, 2019). "Methods for identifying complex associations predictive of common disease". Biobehavioral Health Seminar Series, Penn State University.

Hall MA (Presenter & Author). (November 15, 2018). "Methods for identifying complex associations with diet predictive of common disease". Big Data Workshop, Department of Nutritional Sciences, Penn State University.

Hall, MA (Presenter & Author). (November 14, 2018). "Big data genomics methods for identifying complex associations predictive of common disease". Genomics Seminar Series, Penn State University.

Hall, MA (Presenter & Author). (September 21, 2018). "Leveraging the exposome in health data for identifying complex associations predictive of common disease". Mechanism of Carcinogenesis Retreat, Penn State Cancer Institute, Penn State University.

Hall MA (Presenter & Author). (June 18, 2018). "Quality control is essential to ensuring reproducibility in genotype and non-genetic data". Reproducibility Data Boot Camp, Bioinformatics & Genomics, Penn State University.

Hall MA, Noll J, Patterson A. (May 5, 2018) "Metabolomics: Bridging the divide between life and social sciences". University Health Sciences Council, Penn State University.

Hall MA (Presenter & Author). (October 16, 2017). "Gene-environment interactions predictive of common disease". Genomics Lecture, Department of Biochemistry and Molecular Biology, Penn State University.

Hall MA (Presenter & Author). (September 23, 2017). "Emerging methods for complex associations beyond GWAS". Bioinformatics & Genomics Retreat, Penn State University.

Hall MA (Presenter & Author). (June 11, 2015). "Beyond GWAS: Emerging methods for complex associations for common disease". Department of Biomedical Informatics, Harvard Medical School.

Hall MA (Presenter & Author). (May 5, 2015). "Beyond GWAS: Emerging methods for complex associations for common disease". Institute for Biomedical Informatics, Perelman School of Medicine, University of Pennsylvania.

Posters

Aguilar M, **Hall MA**. Secondary NMR analysis of estrogen receptor positive breast cancer: diagnosis, histology, and years-to-relapse prediction. *2020 MidAtlantic Bioinformatics Conference.*

Aguilar M, McGuigan. J, **Hall MA**. Semi-automated environmental exposure phenotyping: a case for smoking. *2020 American Medical Informatics Association (AMIA).*

McGuigan J, Veturi Y, Li B, Verma A, Le T, Fu W, Haas D, Ritchie MD, **Hall MA***, Moore JH*. Automated machine learning for rare variant analysis of response to antiretroviral therapy in patients infected with HIV. *2020 American Society of Human Genetics (ASHG)*. San Diego, CA.

Aguilar M, McGuigan. J, **Hall MA**. Secondary metabolic analysis of breast cancer nanoparticle chemotherapy: fatty acid metabolism perturbation with newly quantified metabolites and high fidelity classification models. *2020 American Society of Human Genetics (ASHG)*. San Diego, CA.

Hall MA, Palmiero NE, Zhou J, Aguilar M, McGuigan J, Kolli P, Brosius D, Vijay A, Tian Y, Koo I, Allman E, Patterson A, Noll J. Metabolomics reveals novel biomarkers in children who experienced maltreatment. *2020 American Society of Human Genetics (ASHG).*

Zhou J, Palmiero N, Passero K, McGuigan JR, Aguilar MA, and **Hall MA**. Interaction between genes and fatty acids for cardiac-related traitis in LURIC cohort. *2020 American Society of Human Genetics (ASHG).*

Palmiero N, Passero K, Zhou J, McGuigan J, Aguilar M, Ludman A, and **Hall MA**. Environment-wide association study of the phenome to evaluate the complexity of the exposome. *2020 American Society of Human Genetics (ASHG).*

Palmiero N, Passero K, Zhou J, McGuigan J, Aguilar M, Ludman A, and **Hall MA**. Phenome-wide environment wide association study to evaluate the complexity of the exposome. *2020 NYC Exposome Symposium.* New York, NY.

Zhou J, Palmiero N, Passero K, McGuigan JR, Aguilar MA, Prabhu KS, and **Hall MA**. Risk assessments for the common types of anemia from exposome through a series of environment-wide association studies (EWASs) in NHANES 1999-2006. *2020 NYC Exposome Symposium.* New York, NY.

Zhou J, Palmiero N, Passero K, McGuigan JR, Aguilar MA, and **Hall MA**. Gene-environment interaction analysis for cardiac-related traits in the Ludwigshafen Risk and Cardiovascular (LURIC) Health Study. *2020 NYC Exposome Symposium.* New York, NY.

Passero K, Palmiero N, Gatzke-Kopp L, **Hall MA**. Leveraging Environment-wide, Longitudinal Data to Discern How Early-life Exposures Affect Child Health and Development. *2020 NYC Exposome Symposium.* New York, NY.

Aguilar M, McGuigan J, **Hall MA**. Automated NMR Preprocessing and Predictive Modeling of Smoking Exposure with Random Forests. *2020 NYC Exposome Symposium.* New York, NY.

Passero K, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, **Hall MA**. Establishing quality control practices for phenome-wide association studies (PheWAS). *2020 Pacific Symposium on Biocomputing*. Hawaii, HI.

Passero K, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, **Hall MA**. Establishing quality control practices for phenome-wide association studies (PheWAS). *2019 American Society for Human Genetics (ASHG)*. Houston, TX.

Passero K, He X, Zhou J, Mueller-Myhsok B, Kleber ME, Maerz W, **Hall MA**. Phenome-wide association studies on cardiovascular health and fatty acids considering phenotype quality control practices for epidemiological data. *2019 American Society of Human Genetics (ASHG).*

Zhou J, Passero K, Müller-Myhsok B, Kleber ME, Maerz W, **Hall MA**. Investigation of gene-gene interactions in cardiac diseases and fatty acids in LURIC. *2019 American Society of Human Genetics (ASHG).*

Lucas AM, Palmiero N, Orie D, Ritchie MD, **Hall MA**. CLARITE facilitates the quality control and analysis process for EWAS of metabolic-related traits. *2018 American Society of Human Genetics Conference (ASHG).*

Palmiero NE.*, Lucas A.*, Ritchie MD, Vazquez-Vidal I, Peter JH, **Hall MA**. The Utility of CLARITE While Prioritizing Environment-Environment Interactions Relating to HDL-C. *2018 American Society of Human Genetics (ASHG).*

Hall MA, Wallace JR, Pendergrass SA, Ritchie MD. EWAS to GxE: A robust strategy for detecting gene-environment interaction models for age-related cataract. *2014 American Society for Human Genetics (ASHG)*.

Hall MA, Verma A, Brown-Gentry KD, Pendergrass SA. A Phenome-Wide Association Study (PheWAS) using multiple National Health and Nutritional Surveys (NHANES) to identify pleiotropy. *2012 American Society for Human Genetics (ASHG).*

Ph.D. Dissertation Advisor

Morris Aguilar (Bioinformatics & Genomics, MD/PhD) 2018-Present
Kristin Passero (Molecular, Cellular, and Integrative Biosciences) 2018-Present
Jiayan Zhou (Pathobiology) 2018-Present

Ph.D. Dissertation Committee Member

Latisha Franklin (BMMB) 2017-Present
Corinna Moro (BMMB) 2017-Present
Tracy Yu (BMMB) 2020-Present

Research Supervision/Mentoring

Laura Etzel-House (PhD student BBH, Penn State) – 2020-2021
Deven Orie (Undergraduate, Dartmouth College) – Spring 2018
Bryan Almonte (Undergraduate, Bates College) – Summer 2018
Nicole Palmiero (Intern) – Summer 2018
Tuyen Pham (Graduate Intern, West Virginia University) – Summer 2018