Kenneth E. Westerman, Ph.D.

Instructor
Massachusetts General Hospital
Harvard Medical School
Broad Institute of MIT and Harvard

1069 Beacon St.
Brookline, MA 02446
kewesterman@mgb.org
ken.e.westerman@gmail.com
kwesterman.github.io

EDUCATION

Ph.D., Biochemical & Molecular Nutrition *2016 - 2019*
Tufts Friedman School of Nutrition Science and Policy, Boston, MA
Dissertation: Genomic and epigenomic prediction of cardiovascular risk and modulation by diet

M.S., Biochemical & Molecular Nutrition, with concentration in Systems Genomics *2014 - 2016*
Tufts Friedman School of Nutrition Science and Policy, Boston, MA

B.S., Chemical Engineering – *Magna cum laude* *2010 - 2014*
Tufts University, Medford, MA

RESEARCH EXPERIENCE

Instructor, Massachusetts General Hospital, Boston, MA *2022 - present*
Affiliations: Harvard Medical School, Broad Institute of MIT and Harvard

First independent faculty role at MGH and Harvard Medical School, supported by a K01 award from the NIDDK. Lead an interdisciplinary research program focused on gene-environment interaction analysis for cardiometabolic disease prevention. Methodological research explores polygenic scores for interaction and the modeling of molecular 'omics mediators. Applied research investigates genetic modification of the cardiometabolic response to omega-3 fatty acids and other dietary and lifestyle exposures. Also lead consortium efforts and working groups (TOPMed, CHARGE) and mentor trainees in genetic epidemiology and informatics.

Postdoctoral Fellow, Massachusetts General Hospital, Boston, MA *2019 - 2022*
Advisor: Alisa K. Manning, Ph.D.

Developed methods for gene-environment interaction analysis in large-scale consortia and biobanks, including TOPMed and the UK Biobank. Applied these methods to find genetic modification of the relationship between nutrition and lifestyle exposures and cardiometabolic disease risk. Implemented and shared open-source software tools, cloud workflows, and analysis results to advance the field and promote reproducible science.

Doctoral Student *2016 - 2019*
JM-USDA Human Nutrition Research Center on Aging at Tufts University, Boston, MA
Advisor: José M. Ordovás, Ph.D.
Doctoral Thesis: Integration of genomics, epigenomics, and diet for cardiovascular risk prediction

Assembled epigenome-wide predictive models for incident cardiovascular disease that are synergistic with traditional risk scores. Demonstrated that DNA methylation may act as a "molecular recorder" of cumulative risk factor exposure and that epigenomic risk predictors may be synergistic with traditional risk scores. Provided proof-of-concept for the prediction of response to dietary fat using genome-wide gene-diet interaction results.

Master's Student
JM-USDA Human Nutrition Research Center on Aging at Tufts University, Boston, MA
Master's Directed Study *2015 - 2018*
Developed a pipeline based on quantitative structure-activity relationship machine learning models to identify targeted uses of food compounds. Published an open-source software tool and an associated manuscript.

GRANTS AND FUNDING

K01 Research Scientist Development Award (NIDDK) – PI ($750k over 5 years) *2022 - present*
BioData Catalyst Fellowship (NHLBI) – PI ($60k for 1 year) *2020*

Gerald Cassidy Student Research Award (JM-USDA HNRCA at Tufts University) – MPI *2018*

Training fellowships

Harvard T32 Training Program in Endocrinology (NIDDK) – funded trainee *2020 - 2021*
Tufts T32 Training Program in Nutrition and Cardiometabolic Disorders (NHLBI) – funded trainee *2016 - 2019*

HONORS AND AWARDS

Early Career Abstract-based Travel Awards – CHARGE Consortium *2022,2023,2024,2025*
Abstract-based Travel Award – Precision Nutrition Forum *2024*
Advocacy Certificate for Human Genetics and Genomics – ASHG *2022*
Early Career Investigator Achievement Award – CHARGE Consortium *2022*
Early Career Educational Travel Award – American Society for Nutrition *2021*
Semifinalist, Charles J. Epstein Trainee Award – American Society for Human Genetics *2021*
Emerging Leaders in Nutrition Science Award – American Society for Nutrition *2021*
Finalist, Postgraduate Research Award Competition – American Society for Nutrition *2021*
IMPACT Fellowship – MIT IMPACT program *2018*

PUBLICATIONS

Primary publications

Westerman KE, Patel CJ, Meigs JB, Chasman DI, Manning AK. Decomposed interaction testing improves detection of genetic modifiers of the relationship of dietary omega-3 fatty acid intake and its plasma biomarkers with hsCRP in the UK Biobank. *Genes Nutr*. 2025; 20(1):3.

- Showed that incorporating molecular data improves the discovery of gene-diet interactions

Westerman KE, Kilpeläinen TO, Sevilla-Gonzalez M, Connelly MA, Wood AC, Tsai MY, et al. Refinement of a published gene-physical activity interaction impacting HDL-cholesterol: role of sex and lipoprotein subfractions. *Genet. Epidemiol*. 2025; 49:e22607.

Francis M, **Westerman KE**, Manning AK, Ye K. Gene-vegetarianism interactions in calcium, estimated glomerular filtration rate, and testosterone identified in genome-wide analysis across 30 biomarkers. *PLoS Genet.* 2024; 20(7):e1011288.

Westerman KE, Sofer T. Many roads to a gene-environment interaction. *Am. J. Hum. Genet.* 2024; 111(4):626-635.

- Describes a set of biological and statistical mechanisms leading to a detected gene-environment interaction

Smith K, Deutsch AJ, McGrail C, Kim H, Hsu S, Huerta-Chayoga A, …, **Westerman KE**, et al. Multi-ancestry polygenic mechanisms of type 2 diabetes. *Nat. Med.* 2024; 30:1065-1074.

Pham DT*, **Westerman KE***, Pan C, Chen L, Srinivasan S, Isganaitis E, et al. Re-analysis and meta-analysis of summary statistics from gene-environment interaction studies. *Bioinformatics*. 2023; 39(12):btad730.

Hasbani NR, **Westerman KE**, Kwak SH, Chen H, Li X, DiCorpo D, et al. Type 2 diabetes modifies the association of CAD genomic risk variants with subclinical atherosclerosis. *Circ. Genom. Precis. Med.* 2023; 16(6):e004176.

Tobias DK, Manning AK, Wessel J, Raghavan S, **Westerman KE**, et al. Clonal hematopoiesis of indeterminate potential (CHIP) and incident type 2 diabetes risk. *Diabetes Care*. 2023; 46(11):1978-1985.

Tian C, Bürki C, **Westerman KE**, Patel CJ. Association between time and consistency of physical activity and type 2 diabetes – a cohort study on participants of the UK Biobank. *Diabetologia*. 2023; 66(12):2275-2282.

Westerman KE, Walker ME, Gaynor SM, Wessel J, DiCorpo D, Ma J, et al. Investigating gene-diet interactions impacting the association between macronutrient intake and glycemic traits. *Diabetes*. 2023; 72(5):653-665.

- First example of an analytical modeling strategy incorporating the complexity of rare genetic variants, gene-environment interactions, and nutritional epidemiology

Kim H, **Westerman KE**, Smith K, Chiou J, Cole JB, Majarian T, et al. High-throughput genetic clustering of type 2 diabetes loci reveals heterogeneous mechanistic pathways of metabolic disease. *Diabetologia.* 2023; 66(3):495-507.

Cole JB, **Westerman KE**, Manning AK, Florez JC, Hirschhorn JN. Genetic heritability as a tool to evaluate the precision of 24-hour recall dietary questionnaire variables in UK Biobank. *Front. Genet.* 2023; 13:1070511.

Sevilla-Gonzalez M, Manning AK, **Westerman KE**, Aguilar-Salinas CA, Deik A, Clish CB. Metabolomic markers of glucose regulation after a lifestyle intervention in prediabetes. *BMJ Open Diabetes Res. Care.* 2022; 10:e003010.

DiCorpo D, Gaynor SM, Russell EM, **Westerman KE**, Raffield LM, Majarian TD, et al. Whole genome sequence association analysis of fasting glucose and fasting insulin levels in diverse cohorts from the NHLBI TOPMed program. *Commun. Biol.* 2022; 5(1):756.

Westerman KE, Majarian TD, Giulianini F, Jang DK, Florez JC, Chen H, Chasman DI, Udler MS, Manning AK, Cole JB. Variance-quantitative trait loci enable systematic discovery of gene-environment interactions for cardiometabolic serum biomarkers. *Nat. Comm.* 2022; 13:3993.

- First demonstration of an "exposome-wide" approach to gene-environment interaction testing
- Altmetric score of 29 (93rd percentile of tracked articles of a similar age)

Gaynor SM, **Westerman KE**, Ackovic LL, Li X, Li Z, Manning AK, Philippakis A, Lin X. STAAR Workflow: A cloud-based workflow for scalable and reproducible rare variant analysis. *Bioinformatics.* 2022; 38(11):3116-3117.

Westerman KE*, Lin J*, Sevilla-Gonzalez M, Tadess B, Marchek C, Manning AK. Gene-environment interaction analysis incorporating sex, cardiometabolic diseases, and multiple deprivation index reveals novel genetic associations with COVID-19 severity. *Front. Genet.* 2022; 12:782172.

Westerman KE, Miao J, Chasman DI, Florez JC, Chen H, Manning AK, Cole JB. Genome-wide gene-diet interaction analysis in the UK Biobank identifies novel effects on hemoglobin A1c. *Hum. Mol. Genet.* 2021; 30(18):1773-1783.

Westerman KE, Pham DT, Hong L, Chen Y, Sevilla-González M, Sung YJ, Sun YV, Morrison AC, Chen H, Manning AK. GEM: scalable and flexible gene-environment interaction analysis in millions of samples. *Bioinformatics.* 2021; 37(20):3514-3520.

Christensen JJ, Ulven SM, Thoresen M, **Westerman K** et al. Associations between dietary patterns and gene expression pattern in peripheral blood mononuclear cells: A cross-sectional study. *Nutr. Metab. Cardiovas. Dis.* 2020; 30(11):2111-2122.

Liu Y, Shen Y, Guo T, Parnell LD, **Westerman KE**, Smith CE, Ordovás JM, Lai C-Q. Statin use associates with risk of type 2 diabetes via epigenetic patterns at *ABCG1*. *Front. Genet.* 2020; 11:622.

Westerman K, Liu Q, Liu S, Parnell LD, Sebastiani P, Jacques P, DeMeo DL, Ordovás JM. A gene-diet interaction-based score predicts response to dietary fat in the Women's Health Initiative. *Am. J. Clin. Nutr.* 2020; 111(4):893-902.

- Provided proof-of-concept for polygenic scores based on interaction effects rather than main effects

Westerman KE, Harrington S, Ordovás JM, Parnell LD. PhyteByte: Identification of foods containing compounds with specific pharmacological properties. *BMC Bioinformatics.* 2020; 21:238.

Westerman K, Fernández-Sanlés A, Patil P, Sebastiani P, Jacques P, Starr JM, Deary IJ, Liu Q, Liu S, Elosua R, DeMeo DL, Ordovás JM. Epigenomic assessment of cardiovascular disease risk and interactions with traditional risk metrics. *J. Am. Heart Assoc.* 2020; 9(8):e015299.

Westerman K*, Kelly J* et al. Epigenome-wide association study reveals a molecular signature of response to phylloquinone (vitamin K1) supplementation. *Epigenetics.* 2020; 15(8):859-870.

- One of the first demonstrations of epigenetic prediction of response to dietary inputs

Westerman K, Sebastiani P, Jacques P, Liu S, DeMeo DL, Ordovás JM. DNA methylation modules associate with incident cardiovascular disease and cumulative risk factor exposure. *Clin. Epigenetics*. 2019; 11:142.

- Provided support for DNA methylation as a "molecular readout" of cumulative risk factor exposure

Reaver A, Hewlings S, **Westerman K**, Blander G, Schmeller T, Heer M, Rein D. A Randomized, Placebo-Controlled, Double-Blind Crossover Study to Assess a Unique Phytosterol Ester Formulation in Lowering LDL Cholesterol Utilizing a Novel Virtual Tracking Tool. *Nutrients*. 2019; 11(9):2108.

Westerman K, Reaver A, Roy C, Ploch M, Sharoni E, Nogal B, Sinclair DA, Katz DL, Blumberg JG, Blander G. Longitudinal analysis of biomarker data from a personalized nutrition platform in healthy subjects. *Sci. Rep.* 2018; 8(1):14685.

Horowitz AI, **Westerman K**, and MJ Panzer. Formulation influence on the sol–gel formation of silica-supported ionogels. *J. Sol-Gel Sci. Technol.* 2016; 78:34-39.

Koh YW, **Westerman K,** and Manzhos S. A computational study of adsorption and vibrations of UF6 on graphene derivatives: Conditions for 2D enrichment. *Carbon.* 2015; 81:800-806.

Preprints

Westerman KE, Gervis JE, O'Connor LJ, Udler MS, Manning AK. Polygenic scores capture genetic modification of the adiposity-cardiometabolic risk factor relationship. *medRxiv*. 2025. doi: 10.1101/2025.04.09.25324066.

Other publications and book chapters (non-peer-reviewed)

Liu Y, **Westerman KE**, Ordovás JM, Lai C-Q. Diet, DNA methylation, and cardiovascular diseases. In: *Nutrition in the Control of Inflammation*, Elsevier. 2024.

Westerman KE and Ordovás JM. DNA methylation and incident cardiovascular disease. *Curr. Opin. Clin. Nutr.* 2020; 23(4): 236-240.

PRESENTATIONS

Invited

Panel discussant: Complementing and not competing: how 'omics informed approaches can, and cannot, enhance nutritional epidemiology. *Nutritional Epidemiology Forum, American Society for Nutrition Meeting*, Orlando, FL. *2025*

Molecular and polygenic approaches to improve the detection of cardiometabolic gene-lifestyle interactions. *Cardiovascular Institute, Beth Israel Deaconess Medical Center*, Boston, MA. *2024*

Asking better questions to improve discovery of gene-lifestyle interactions. *Johns Hopkins University MD-GEM program Genetics Research Day*, Baltimore, MD. *2024*

Genome-wide gene-lifestyle interaction analysis for cardiometabolic health. *Division of Preventive Medicine Faculty Seminar, Brigham and Women's Hospital*, Boston, MA. *2023*

Gene-macronutrient interactions impacting glycemic traits in the TOPMed cohorts and beyond. *Nutrient-Gene Interactions Research Interest Group, American Society for Nutrition Meeting*, Virtual. *2022*

Identification of gene-diet interactions impacting glycemic biomarkers in the multi-ethnic TOPMed cohorts. *2nd International Conference on Precision Nutrition and Metabolism in Public Health and Medicine*, Rhodes, Greece. *2021*

Panel moderator: Nutrigenetics, nutrigenomics, and precision nutrition. *Tufts Research and Data Symposium*, Virtual. *2021*

Abstract-based (selected; 13+ total)

Metabolomic mediators partially explain an observed gene-physical activity interaction impacting HDL-cholesterol. *CHARGE Consortium Meeting, Gene-Lifestyle Interactions Working Group*, Bethesda, MD. *2025*

Alternative polygenic score approaches aid in detecting genetic modification of the relationship between adiposity and cardiometabolic risk. *American Society for Human Genetics Annual Meeting*, Denver, CO. *2024*

Polygenic scores reflect genetic modification of the adiposity-cardiometabolic risk factor relationship. *2024*
CHARGE Consortium Meeting, Rotterdam, Netherlands.

Efficient derivation of summary statistics from multi-exposure, genome-wide, gene-environment interaction studies. *CHARGE Consortium Meeting*, Philadelphia, PA. *2022*

Systematic discovery of gene-environment interactions for metabolic serum biomarkers. *American Society for Human Genetics Annual Meeting,* Virtual. *2021*

Identification of gene-diet interactions impacting glycemic biomarkers in the multi-ethnic TOPMed cohorts. *2021*
American Society for Nutrition Annual Meeting, Virtual.

Epigenome-wide association study of plasma phylloquinone response to phylloquinone supplementation. *2019*
American Society for Nutrition Annual Meeting, Baltimore, MD.

Posters (selected; 17+ total)

American Society for Nutrition Meeting, Boston, MA (Poster Theater) *2023*

American Diabetes Association Scientific Sessions, San Diego, CA (ePoster Theater) *2023*

American Heart Association Epi|Lifestyle Virtual Conference (ePoster Theater) *2021*

PATENTS

LD Parnell, MS Obin, and **KE Westerman**. "Methods of Identifying and Formulating Food Compounds That Modulate Phenotype-Related Targets." US Provisional Patent Pending. *2016*

MENTORSHIP AND TEACHING

Mentorship

James Hu, Intern (planned), Broad Institute *2025*
Primary mentor for upcoming summer project focused on genetic epidemiology.

Paul Hanson, Analyst, Massachusetts General Hospital *2024 - present*
Supervise on genetic epidemiology projects (50% FTE)

Julie Gervis, Research Fellow, Massachusetts General Hospital *2023 - present*
Mentor on genetic epidemiology and gene-diet interactions.

Richa Jain and **Rachel Sussman,** master's students, Harvard School of Public Health *2024*
Co-supervised Health Data Science capstone project (with Dr. Tamar Sofer).

Caiwei Tian and Charlyne Burki, master's students, Harvard Medical School *2022 - 2023*
Co-supervised master's thesis projects (with Dr. Chirag Patel). Resulted in one publication pers student, focusing on physical activity in the UK Biobank.

Joanna Lin, Undergraduate, Bowdoin College *2020 - 2021*
Resulted in co-first author publication on gene-environment interactions for COVID-19 severity.

Teaching

Guest Lecturer, Friedman School of Nutrition at Tufts University *2025*
Course: Precision Nutrition (NUTR 248)
Taught a class focused on gene-diet interaction concepts.

Guest Lecturer, Harvard School of Public Health *2025*
Course: Precision Nutrition (NUT 250)
Taught a class focused on innovations in gene-diet interaction analysis.

Instructor, Harvard School of Medicine *2024*
Course: Pathways, Genetics Discipline (PWY 100)
Led 2 classes on polygenic disease mapping and analysis for first-year medical students.

Teaching Assistant, Tufts Friedman School *2015 & 2016*
Course: Graduate biochemistry (BCHM 0223)
Led twice-weekly review sessions for classes of 15+ students.

LEADERSHIP AND SERVICE

Director of Analytics, EPICORE Biobank and Analytics core, Department of Medicine, MGH *2024 - present*

Founder and convener, Environment and Social Determinants of Health Working Group, TOPMed Program *2024 - present*

Chair, TOPMed Program Annual Meeting, Bethesda, MD *2025*

Reviewer, Pre-selection committee, Broad Institute Summer Research Program (for college students underrepresented in science) *2023 - 2024*

Founder and organizer, Nutritional genomics discussion group, MGH/Broad Institute *2020 - 2024*

Organizer, Omics in epidemiology journal club, MGH *2019 - 2021*

Co-founder and organizer, "NewTrition" talk series, Tufts Friedman School (recognized with *Honos Civicus* university service award) *2015 - 2018*

PEER REVIEW

Selected Journals (ad hoc)

Nature Communications
American Journal of Human Genetics
American Journal of Clinical Nutrition
Diabetologia
Diabetes
Genes and Nutrition
Journal of Nutrition
Clinical Epigenetics
Arteriosclerosis, Thrombosis, and Vascular Biology

Meeting Abstracts

American Society for Nutrition Annual Meeting

PROFESSIONAL EXPERIENCE

InsideTracker, Cambridge, MA *2016 - 2019*
Data Scientist
Analyzed large behavior and blood biomarker datasets from a commercial personalized nutrition platform. Led the statistical modeling and manuscript preparation for the company's first peer-reviewed publication. Developed a software tool for automated analysis and visualization of biomarker data that is now used across the company.

Tufts Medical Center, Boston, MA *2019 - 2019*
Bioinformatician
Consulted on the content of reports for a machine learning-based biological analytics platform being developed within the Tufts Clinical and Translational Science Institute.