Kenneth E. Westerman, Ph.D.

Instructor
Massachusetts General Hospital
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EDUCATION

Ph.D., Biochemical & Molecular Nutrition *Jun 2016 - Aug 2019*
Tufts Friedman School of Nutrition Science and Policy, Boston, MA

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

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

RESEARCH EXPERIENCE

Instructor *Jul 2022 - present*
Postdoctoral Fellow *Sep 2019 - Jun 2022*
Massachusetts General Hospital, Boston, MA
Broad Institute of MIT and Harvard, Cambridge, MA
Harvard Medical School, Boston, MA
Advisor: Alisa K. Manning, Ph.D.

Develop methods for gene-environment interaction analysis in large-scale consortia and biobanks, including TOPMed, All of Us, and the UK Biobank. Apply these methods to nutrition and lifestyle exposures to find potential genetic modification of the relationship between these behaviors and cardiometabolic disease risk. Implement and share open-source software tools, cloud workflows, and analysis results to advance the field and promote reproducible science.

Doctoral Student *Oct 2016 - Aug 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

Uncovered novel epigenomic signals predictive of incident cardiovascular disease and assembled associated predictive models. 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.

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

Master’s Practicum *Sep 2014 - Jan 2015*
Analyzed 16S metagenomic data to uncover dietary effects on murine microbiome patterns.

GRANTS AND FUNDING

K01 Research Scientist Development Award (NIDDK) – PI ($750k over 5 years)	*2022-present*
Harvard T32 Training Program in Endocrinology (NIDDK) – funded trainee	*2020-2021*
BioData Catalyst Fellowship (NHLBI) – PI ($60k for 1 year)	*2020*
Gerald Cassidy Student Research Award (JM-USDA HNRCA at Tufts University) – MPI	*2018*
Tufts T32 Training Program in Nutrition and Cardiometabolic Disorders (NHLBI) – funded trainee	*2016-2019*

HONORS AND AWARDS

Early Career Abstract-based Travel Award – CHARGE Consortium	*2024*
Abstract-based Travel Award – Precision Nutrition Forum	*2024*
Early Career Abstract-based Travel Award – CHARGE Consortium	*2023*
Advocacy Certificate for Human Genetics and Genomics – ASHG	*2022*
Early Career Investigator Achievement Award – CHARGE Consortium	*2022*
Early Career Abstract-based Travel 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*
Honos Civicus Society – Tufts University civic honor society	*2015*

PUBLICATIONS

Published

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.

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.

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 empirical evidence for the established theoretical model of 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.

Manuscripts

Reviews

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

PRESENTATIONS

Oral

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

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

"Polygenic scores reflect genetic modification of the adiposity-cardiometabolic risk factor relationship". Southern California Polygenic Risk Score Symposium, Virtual. *2024*

"Dissection of a known gene-physical activity interaction using metabolomics". CHARGE Consortium Meeting, Boston, MA. *2023*

"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 Business Meeting, American Society for Nutrition Virtual Meeting. *2022*

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

"Creating a research portal for vQTL and gene-by-environment associations". Common Metabolic Disease Knowledge Portal Network Webinar. *2021*

"Systematic discovery of gene-environment interactions for metabolic serum biomarkers". American Society for Human Genetics Virtual Conference. *2021*

"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*

"Identification of genetic loci impacting COVID-19 severity via gene-environment interaction analysis incorporating known risk factors". International Genetic Epidemiology Society Virtual Conference, Lightning Talk. *2021*

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

"Systematic discovery of gene-environment interactions for cardiometabolic serum biomarkers". CHARGE Consortium Virtual Meeting. *2021*

Panel moderator: “Nutrigenetics, nutrigenomics, and precision nutrition”. Tufts Research and Data Symposium, Virtual.	*2021*
“Epigenome-wide association study of plasma phylloquinone response to phylloquinone supplementation”. American Society for Nutrition Conference, Baltimore, MD.	*2019*
“DNA methylation-based cardiovascular risk assessment”. Nutritional Genomics Organization Conference, Varna, Bulgaria.	*2017*
“A chemogenomics approach defines novel food, chemical and genetic mediators of triglyceride homeostasis”. Nutritional Genomics Organization Conference, Barcelona, Spain.	*2015*

Poster

Precision Nutrition Forum, Copenhagen, DK	*2024*
American Heart Association Epi|Lifestyle Meeting, Chicago, IL	*2024*
American Society for Nutrition Meeting, Boston, MA (Poster Theater)	*2023*
American Diabetes Association Scientific Sessions, San Diego, CA (ePoster Theater)	*2023*
American Society of Human Genetics Meeting, Los Angeles, CA	*2022*
CHARGE Consortium Meeting, Seattle, WA	*2022*
American Society for Nutrition Virtual Conference	*2022*
CHARGE Consortium Meeting, Virtual	*2021*
American Heart Association Epi|Lifestyle Virtual Conference (ePoster Theater)	*2021*
American Society for Human Genetics Virtual Conference	*2020*
American Society for Nutrition Virtual Conference	*2020*
CHARGE Consortium Meeting, Houston, TX	*2020*
American Society of Human Genetics Conference, Houston, TX	*2019*
American Society for Nutrition Conference, Baltimore, MD	*2019*
RECOMB Conference, Washington, DC	*2019*
Experimental Biology Conference, San Diego, CA	*2018*
Tufts Data Intensive Studies Center Symposium, Medford, MA	*2017*

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

Paul Hanson, Analyst, Massachusetts General Hospital Supervise on genetic epidemiology projects (50% FTE)	*2024-present*
Julie Gervis, Research Fellow, Massachusetts General Hospital Mentor on genetic epidemiology and gene-diet interactions.	*2023-present*
Richa Jain and **Rachel Sussman,** Master’s students, Harvard School of Public Health Co-supervised Health Data Science capstone project (with Dr. Tamar Sofer).	*2024*
Joanna Lin, Undergraduate, Bowdoin College Mentored on genetic epidemiology and the scientific publication process. Resulted in our co-first author publication exploring gene-environment interactions for COVID-19 severity.	*2020-2021*

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)
Independently led twice-weekly review sessions for classes of 15+ students.

UNIVERSITY SERVICE

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

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

Co-founder and Coordinator, "NewTrition" talk series at the Tufts Friedman School *2015 - 2018*

Research Working Group Member, Tufts Friedman School Strategic Plan *2015*

Research Committee, Tufts Friedman School Student Research Conference *2014 - 2017*

PEER REVIEW

Selected Journals

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 *Jan 2016 - Dec 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 *Jun 2019 - Aug 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.

Harvard Medical School, Boston, MA *Jun 2015 - May 2016*
Technical Outreach Coordinator
Worked with biological research groups to find gaps in computational workflows and identified relevant resources within the IT department; projects ranged from RNA-Seq analysis in R to system administration.