Curriculum Vitae – 10/11/2024

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Research Interests

I work on large scale genomic studies within a variety of international consortia to unravel the genetic determinants of cardiovascular disease and its risk factors, with a special emphasis on hemostatic factors. I believe that, as genetic epidemiologists, we have the responsibility to not only discover new associations, but to also translate them into meaningful biological and clinical insights. As such I am particularly interested in approaches such as Mendelian randomization, which has the potential to transform our understanding of disease etiology, and genetic risk prediction, which may give us new tools to prevent disease.

Experience

09/2023 – Present	*Associate Professor with Tenure* Human Genetics Center, Department of Epidemiology, Human Genetics, and Environmental Sciences (EHGES), School of Public Health, University of Texas Health Science Center at Houston (UTHealth-SPH), Houston, TX, USA
11/2018 – 09/2023	*Tenure Track Assistant Professor* Human Genetics Center, Department of EHGES, School of Public Health, UTHealth-SPH, Houston, TX, USA
08/2017 – 11/2018	*Non-Tenure Track Assistant Professor* Human Genetics Center, Department of EHGES, UTHealth-SPH, Houston, TX, USA
04/2016 – 07/2017	*Postdoctoral Research Fellow* Human Genetics Center, Department of EHGES, UTHealth-SPH, Houston, TX, USA
05/2014 – 06/2014	*Visiting Researcher* Faculty of Medicine, School of Public Health, Imperial College, London, United Kingdom
08/2012 – 01/2016	*Doctoral Research Fellow* Cardiovascular Group, Department of Epidemiology, Erasmus Medical Center, Rotterdam, the Netherlands
02/2012 – 08/2012	*Research Intern*

School of Nutrition and Translational Research in Metabolism, Maastricht University, Maastricht, the Netherlands

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Education

08/2012 – 01/2016	*Molecular Epidemiology* PhD Erasmus University Rotterdam, Rotterdam, the Netherlands
08/2011 – 08/2012	*Public Health: Specialization in Epidemiology* MSc Maastricht University, Maastricht, the Netherlands
02/2008 – 06/2011	*Life Sciences* BSc – Honours Program University College Maastricht, Maastricht, the Netherlands

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Published Manuscripts

*Contributed equally as first or last authors.

Mentored trainees from UTHealth are underlined.

Manuscripts with > 20 authors are shown with condensed author lists.

H-index: 40 (Google Scholar, 10/11/2024)

Citations: 8386 (Google Scholar, 10/11/2024)

1. Huffman JE, Nicholas J, Hahn J, Heath AS, Raffield LM, Yanek LR, Brody JA, Thibord F, Almasy L, Bartz TM, Bielak LF, Bowler RP, Carrasquilla GD, Chasman DI, Chen MH, Emmert DB, Ghanbari M, Haessler J, Hottenga JJ, Kleber ME, [...] **de Vries PS***, Sabater-Lleal M*, Morrison AC*, Smith NL*. (2024) Whole-genome analysis of plasma fibrinogen reveals population-differentiated genetic regulators with putative liver roles. *Blood*. Online ahead of print.
2. Hahn J, Temprano-Sagrera G, Hasbani NR, Ligthart S, Dehghan A, Wolberg AS, Smith NL, Sabater-Lleal M, Morrison AC, **de Vries PS.** (2024) Bivariate genome-wide association study of circulating fibrinogen and C-reactive protein levels. *Journal of Thrombosis and Haemostasis*. Online ahead of print.
3. Dobson DA, Fish RJ, **de Vries PS**, Morrison AC, Neerman-Arbez M, Wolberg AS. (2024) Regulation of fibrinogen synthesis. *Thrombosis Research*. Online ahead of print.
4. Kwak SH, Hernandez-Cancela RB, DiCorpo DA, Condon DE, Merino J, Wu P, Brody JA, Yao J, Guo X, Ahmadizar F, Meyer M, Sincan M, Mercader JM, Lee S, Haessler J, Vy HMT, Lin Z, Armstrong ND, Gu S, Tsao NL, et al. (2024) Time-to-Event Genome-Wide Association Study for Incident Cardiovascular Disease in People With Type 2 Diabetes. *Diabetes Care*. Online ahead of print.
5. Zhu X, Yang Y, Lorincz-Comi N, Li G, Bentley AR, **de Vries PS**, Brown M, Morrison AC, Rotimi CN, Gauderman WJ, Rao DC, Aschard H; CHARGE Gene-lifestyle Interactions Working Group. (2024) An approach to identify gene-environment interactions and reveal new biological insight in complex traits. Nature Communications. 15(1):3385.
6. **de Vries PS**, Reventun P, Brown MR, Heath AS, Huffman JE, Le NQ, Bebo A, Brody JA, Temprano-Sagrera G, Raffield LM, Ozel AB, Thibord F, Jain D, Lewis JP, Rodriguez BAT, Pankratz N, Taylor KD,

Polasek O, Chen MH, Yanek LR, et al. (2024) A genetic association study of circulating coagulation Factor VIII and von Willebrand Factor levels. *Blood.* 143(18):1845-1855.

7. Guirette M, Lan J, McKeown NM, Brown MR, Chen H, **de Vries PS**, Kim H, Rebholz CM, Morrison AC, Bartz TM, Fretts AM, Guo X, Lemaitre RN, Liu CT, Noordam R, de Mutsert R, Rosendaal FR, Wang CA, Beilin LJ, Mori TA, et al. (2024) Genome-Wide Interaction Analysis With DASH Diet Score Identified Novel Loci for Systolic Blood Pressure. *Hypertension*. 81(3):552-560.
8. Armstrong ND, Srinivasasainagendra V, Ammous F, Assimes TL, Beitelshees AL, Brody J, Cade BE, Ida Chen YD, Chen H, **de Vries PS**, Floyd JS, Franceschini N, Guo X, Hellwege JN, House JS, Hwu CM, Kardia SLR, Lange EM, Lange LA, McDonough CW, et al. (2023) Whole genome sequence analysis of apparent treatment resistant hypertension status in participants from the Trans-Omics for Precision Medicine program. *Frontiers in Genetics*. 14:1278215.
9. Reventun P, Toledano-Sanz P, Alcharani N, Viskadourou M, Morrison AC, Sabater-Lleal M, Wolberg AS, **de Vries PS**, Smith NL, Osburn WO, Arvanitis M, Lowenstein CJ. (2024) CD36 regulates factor VIII secretion from liver endothelial cells. Blood Advances. 8(1):143-149.
10. **de Vries PS**, Conomos MP, Singh K, Nicholson CJ, Jain D, Hasbani NR, Jiang W, Lee S, Cardenas CLL, Lutz SM, Wong D, Guo X, Yao J, Young EP, Tcheandjieu C, Hilliard AT, Bis LC, Bielak LF, Brown MR, Musharoff S, et al. (2023) Whole-genome sequencing uncovers two loci for coronary artery calcification and identifies ARSE as a regulator of vascular calcification. *Nature Cardiovascular Research*. 2:1159-1172.
11. Gallego-Fabrega C, Temprano-Sagrera G, Cárcel-Márquez J, Muiño E, Cullell N, Lledós M, Llucià-Carol L, Martin-Campos JM, Sobrino T, Castillo J, Millán M, Muñoz-Narbona L, López-Cancio E, Ribó M, Alvarez-Sabin J, Jiménez-Conde J, Roquer J, Tur S, Obach V, Arenillas JF, et al. (2023) A multi-trait genetic Study of Hemostatic factors and Hemorrhagic transformation after stroke treatment. *Journal of Thrombosis and Haemostasis.* S1538-7836(23)00870-X
12. de Las Fuentes L, Schwander KL, Brown MR, Bentley AR, Winkler TW, Sung YJ, Munroe PB, Miller CL, Aschard H, Aslibekyan S, Bartz TM, Bielak LF, Chai JF, Cheng CY, Dorajoo R, Feitosa MF, Guo X, Hartwig FP, Horimoto A, Kolčić I, et al. (2023) Gene-educational attainment interactions in a multi-population genome-wide meta-analysis identify novel lipid loci. *Frontiers in Genetics*. 14:1235337.
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16. Lee MP, Dimos SF, Raffield LM, Wang Z, Ballou AF, Downie CG, Arehart CH, Correa A, **de Vries PS**, Du Z, Gignoux CR, Gordon-Larsen P, Guo X, Haessler J, Howard AG, Hu Y, Kassahun H, Kent ST, Lopez JAG, et al. (2023) Ancestral diversity in lipoprotein(a) studies helps address evidence gaps. *Open Heart*. 10(2):e002382.
17. van de Vegte YJ, Eppinga RN, van der Ende MY, Hagemeijer YP, Mahendran Y, Salfati E, Smith AV, Tan VY, Arking DE, Ntalla I, Appel EV, Schurmann C, Brody JA, Rueedi R, Polasek O, Sveinbjornsson G,

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26. Li X, Quick C, Zhou H, Gaynor SM, Liu Y, Chen H, Selvaraj MS, Sun R, Dey R, Arnett DK, Bielak LF, Bis JC, Blangero J, Boerwinkle E, Bowden DW, Brody JA, Cade BE, Correa A, Cupples LA, Curran JE, et al. (2022) Powerful, scalable and resource-efficient meta-analysis of rare variant associations in large whole-genome sequencing studies. *Nature Genetics.* 55(1):154-164.
27. Majarian TD, Bentley AR, Laville V, Brown MR, Chasman DI, **de Vries PS**, Feitosa MF, Franceschini N, Gauderman WJ, Marchek C, Levy D, Morrison AC, Province M, Rao DC, Schwander K, Sung YJ, Rotimi CN, Aschard H, Gu CC, Manning AK. (2022) Multi-omics insights into the biological mechanisms underlying gene-by-lifestyle interactions with smoking and alcohol consumption detected by genome-wide trans-ancestry meta-analysis. *Frontiers in genetics*. 13:954713.
28. Elgart M, Goodman MO, Isasi C, Chen H, **de Vries PS**, Xu H, Manichaikul AW, Franceschini N, Psaty BM, Rich SS, Rotter JI, Lloyd-Jones DM, Fornage M, Correa A, Heard-Costa NL, Vasan RS, Hernandez R,

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Published Invited Editorials

1. **de Vries PS** (2024) Early life cardiovascular risk factors and midlife epigenetic aging: an enduring legacy. *JACC: Basic to Translational Science*. 9(5):5901-592.
2. **de Vries PS**. (2023) Genetics of predicted platelet activity. *Blood*. 142(22):1851-1852.
3. **de Vries PS**. (2023) Polygenic risk, lifestyle and the lifetime risk of coronary artery disease. *Heart*. 109(10):730-731.
4. Assimes T, **de Vries PS.** (2018) Making the most out of Mendel's laws in complex coronary artery disease. *Journal of the American College of Cardiology*. 72(3):311-313.

Invited Presentations

1. Harmonization and analysis of atherosclerosis phenotypes in the Trans-Omics for Precision Medicine (TOPMed) program. *COnsortium of METabolomics Studies (COMETS) Cardiovascular Working Group*. Virtual. November 9th 2023.
2. Grans as a junior principal investigator in CHARGE. *CHARGE Investigator Meeting*. San Antonio. October 10th 2023.
3. Using results from genome-wide association studies for genetic risk prediction. *Center for Heart Care Data Team Inservice Seminar Series, Department of Management, Policy, and Community Health, The University of Texas Health Science Center at Houston*. Houston. July 12th 2023.
4. Opportunities and challenges in researching the genomics of hemostasis and thrombosis. *Human Genetics Center Seminar Series, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston*. Houston. November 7th 2022.
5. Whole genome sequencing study of coronary artery calcification: the Trans-Omics for Precision Medicine (TOPMed) program. *Human Genome Sequencing Center Virtual Seminar Series, Baylor College of Medicine*. Virtual. June 17th 2021.
6. Genome-wide association studies of coronary artery calcification. *Human Genetics Center Seminar Series, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston*. Houston. September 14th 2020.
7. Trans-ancestry whole genome sequencing analysis of coronary artery calcification. *Framingham Heart Study OMICS Conference Series*. Virtual. November 5th 2019.
8. Multi-ancestry whole genome sequencing analysis of coronary artery calcification in the Trans-Omics for Precision Medicine (TOPMed) program. *NHLBI's Harnessing the New Frontier of Imaging Genomics for Heart, Lung, Blood, and Sleep Disorders workshop*. Bethesda, October 25th 2019.
9. Genetics of hemostasis: new biology and links to cardiovascular disease. *Human Genetics Center Seminar Series, Department of Epidemiology, Human Genetics, and Environmental Sciences, School of Public Health, The University of Texas Health Science Center at Houston*. Houston, October 9th 2017.
10. Mendelian randomization for precision medicine: causal effect of fibrinogen on coronary heart

disease. *Precision Medicine Day*. *Center for Precision Health, School of Biomedical Informatics, The University of Texas Health Science Center at Houston.* Houston, April 13th 2017.

11. Exploring the role of genetic variation in hemostasis: updates from the CHARGE Hemostasis Working Group. *Framingham Heart Study OMICS Conference Series*. Virtual. November 1st 2016.

Conference Presentations

1. Cross-population meta-analysis of 1 million participants identifies variant-by-alcohol consumption interactions at 3 new and 10 known lipid loci. *CHARGE Investigator Meeting*. Denver, May 22nd–24th 2024 (working group presentation).
2. Whole genome sequencing study of coagulation factor VIII and von Willebrand factor reveals new genetic associations. *International Society of Thrombosis and Haemostasis*. Virtual, July 12th–14th 2020 (poster).
3. Multi-ancestry whole genome sequencing analysis of coronary artery calcification. *American Heart Association Scientific Sessions*. Philadelphia, November 16th–18th 2019 (moderated digital poster).
4. Whole genome sequencing and associations with coagulation factors VII and VIII and von Willebrand factor: the Trans-Omics for Precision Medicine (TOPMed) program. *American Society of Human Genetics Meeting*. Houston, October 15th–19th 2019 (poster).
5. Genetically Determined Fibrinogen, Gamma Prime Fibrinogen and Risk of Venous Thromboembolism and Ischemic Stroke: Evidence From Mendelian Randomization. *American Heart Association Epidemiology, Prevention, Lifestyle & Cardiometabolic Health*. Houston, March 5th–8th 2019 (poster).
6. Trans-ancestry whole genome sequencing analysis of coronary artery calcification. *Trans-Omics for Precision Medicine (TOPMed) Investigator Meeting*. Tysons, December 5th–7th 2018 (platform).
7. Trans-ancestry whole genome sequencing analysis of coronary artery calcification. *Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Investigator Meeting*. Baltimore, October 11th–12th 2018 (poster).
8. Multi-ancestry genome-wide association study of incident coronary heart disease. *CHARGE Investigator Meeting*. Rotterdam, April 18th–19th 2018 (poster).
9. Association of rare variants specific to pancreatic islets with type 2 diabetes. *Trans-Omics for Precision Medicine (TOPMed) Investigator Meeting*. Tysons, November 29th–December 1st 2017 (platform).
10. Multi-ancestry genome-wide association study incorporating gene-alcohol intake interactions identifies 18 new lipid loci. *American Society of Human Genetics Meeting.* Orlando, October 17th–21st 2017 (platform).
11. Multi-ethnic genome-wide association study of hemostasis phenotypes. *CHARGE Investigator Meeting*. New York City, March 23rd–24th 2017 (poster).
12. Whole-genome sequencing study of serum peptides: the Atherosclerosis Risk in Communities (ARIC) study. *American Society of Human Genetics Meeting.* Vancouver, October 18th–22nd 2016 (platform).
13. Multi-ethnic genome-wide association study of incident coronary heart disease. *CHARGE Investigator Meeting.* Charlottesville, September 28th–29th 2016 (poster).
14. GWAS of circulating fibrinogen using 1000 genomes imputed data. *CHARGE Investigator Meeting.* Los Angeles, January 22nd–24th 2014 (poster).

Trainee Conference Presentations

Mentored trainees from UTHealth are underlined.

Manuscripts with > 3 authors are shown with condensed author lists.

1. Heath AS, Brown MR, Sabater-Lleal M, […] **de Vries PS**. A genome-wide association study of coagulation Factor VII levels uncovers 14 new loci and provides evidence for regulation by lipid levels. *CHARGE Consortium Investigator Meeting*. Denver. May 22nd-24th 2024 (working group presentation).
2. Braendle SS, Heath A, **de Vries PS**. Longitudinal fasting glucose trajectories in type 2 diabetes patients: associations with polygenic score and atherosclerotic cardiovascular disease. *CHARGE Consortium Investigator Meeting*. San Antonio. October 10th–12th 2023 (poster).
3. Godbole, AR, Heath A, **de Vries PS**. Genome-wide association study of circulating ADAMTS13 levels leveraging publicly available proteomics summary statistics. *Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Investigator Meeting*. Boston. May 9th–11th 2023 (poster).
4. Hahn J, Bressler J, Fornage M, […], **de Vries PS**. Epigenome-wide association study of DNA methylation in blood and coagulation factor VIII and von Willebrand factor plasma levels. *European Society of Human Genetics Meeting*. Glasgow, Scotland. June 10th–13th 2023 (poster).
5. Hahn J, Bressler J, Fornage M, […], **de Vries PS**. Epigenome-wide association study of DNA methylation in blood and coagulation factor VIII and von Willebrand factor plasma levels. *CHARGE Consortium Investigator Meeting*. Boston. May 9th–11th 2023 (poster).
6. Braendle SS, Hasbani NR, Morrison AC, […], **de Vries PS**. Polygenic scores and longitudinal trajectories of cardiometabolic phenotypes. *American Heart Association Scientific Sessions*. Chicago. November 5th–7th 2022 (poster).
7. Hasbani NR, Hahn J, Heath AS, […], **de Vries PS**. Multi-trait analysis genome-wide association study of atherosclerosis phenotypes. *American Society of Human Genetics Meeting*. Los Angeles. October 25th–29th 2022 (poster).
8. Hasbani NR, Hahn J, Heath AS, […], **de Vries PS**. Multi-trait analysis genome-wide association study of atherosclerosis phenotypes. *CHARGE Consortium Investigator Meeting*. Seattle. October 12th–14th 2022 (platform).
9. Friedman R, Heath AS, Johnsen JM, […] **de Vries PS**. Genome-wide association study of low von Willebrand factor levels. *CHARGE Consortium Investigator Meeting*. Seattle. October 12th–14th 2022 (poster and poster blitz).
10. Braendle SS, Hasbani NR, Morrison AC, […], **de Vries PS**. Polygenic scores and longitudinal trajectories of cardiometabolic phenotypes. *CHARGE Consortium Investigator Meeting*. Seattle. October 12th–14th 2022 (poster and working group presentation).
11. Hahn J, Bressler J, Domingo-Relloso, […], **de Vries PS**. Epigenome-wide association study of DNA methylation and fibrinogen: CHARGE Consortium. *International Fibrinogen Research Society Workshop*. Vevey, Switzerland. June 12th–16th 2022 (platform).
12. Hasbani NR, Ligthart S, Brown, MR, [...], **de Vries PS**. Lifetime risk of coronary heart disease: American Heart Association's Life's Simple 7 lifestyle recommendations and polygenic risk. *CHARGE Consortium Investigator Meeting*. Philadelphia. April 27th–29th 2022 (poster and working group presentation).
13. Hahn J, Temprano-Sagrera G, Smith NL, […], **de Vries PS**. Bivariate genome-wide association study of circulating fibrinogen and C-reactive protein (CRP) levels. *American Society of Human Genetics Meeting*. Virtual. October 18th–22nd 2021 (poster).
14. Hasbani NR, Meigs J, Kwak SH, **de Vries PS**. The genetics of coronary artery calcification in individuals with type 2 diabetes. *American Society of Human Genetics*. Virtual. October 18th–22nd 2021 (poster).
15. Hahn J, Temprano-Sagrera G, Smith NL, […], **de Vries PS**. Bivariate genome-wide association study of circulating fibrinogen and C-reactive protein (CRP) levels. *CHARGE Consortium Investigator Meeting*. Virtual. October 7th–8th 2021 (poster, and poster blitz: awarded "best poster").

16. Hasbani NR, Meigs J, Kwak SH, **de Vries PS**. The genetics of coronary artery calcification in individuals with type 2 diabetes. *CHARGE Consortium Investigator Meeting*. Virtual. October 7th–8th 2021 (poster and poster blitz).
17. Hahn J, Bressler J, Domingo-Relloso, […], **de Vries PS**. Epigenome-wide association study of DNA methylation and fibrinogen: CHARGE Consortium. *Congress of the International Society on Thrombosis and Haemostasis (ISTH)*. Virtual. July 17th–21st 2021 (poster).
18. Hahn J, Bressler J, Domingo-Relloso, […], **de Vries PS**. Epigenome-wide association study of DNA methylation and fibrinogen: CHARGE Consortium. *CHARGE Consortium Investigator Meeting*. Virtual. May 6th–7th 2021 (poster and poster blitz).
19. Hasbani NR, Ligthart S, Brown MR, [...], **de Vries PS**. Lifetime risk of coronary heart disease: American Heart Association's Life's Simple 7 lifestyle recommendations and polygenic risk. *Program in Quantitative Genomics Conference*. Virtual. November 5th–6th 2020. (poster).
20. Hasbani NR, Broome JG, Terry JG, [...], **de Vries PS**. Multi-ancestry whole genome sequencing study of carotid intima media thickness and carotid plaque. *American Society of Human Genetics*, Houston. October 15th–19th 2019 (poster).

Active Research Support

NIH/NIA: R01 AG079108 (Sedaghat) 04/01/23-03/31/27
Early onset Alzheimer's disease and related dementias: a population-based approach to identify characteristics and risk factors.
We propose here to pool and rigorously harmonize data to create a cohort with a sizable number of early onset dementia events to estimate its incidence in the general population, identify predisposing or protective physiologic and behavioral risk factors, and study whether a favorable midlife risk profile in the presence of genetic predisposition delays its occurrence.
Role: Subcontract PI Total Subcontract Amount: $273,880

NIH/NHLBI: R01 HL139553 (Morrison/de Vries/Smith) 04/01/23-03/31/27
Analysis of whole genome sequence and hemostasis phenotypes.
We will expand our knowledge of the genetics of FVIII and VWF levels in multi-ethnic populations, and explore complex regulatory mechanisms influencing FVIII and VWF levels such as epistasis and epigenetics.
Role: Multi-PI Total Award Amount: $2,205,101

NIH/NHLBI: R01 HL162928 (Malhotra/de Vries) 04/01/23-03/31/27
Role of Arylsulfatase in vascular calcification.
This proposal aims to enhance our mechanistic insights of vascular disease by focusing on a novel biological pathway, the sulfatase family, that contributes to the development of calcified arteries and plaque development in the blood vessels of humans.
Role: Multi-PI Total Subcontract Amount: $347,248

NIH/NIDDK: U01DK078616 (Meigs) 09/01/20-08/31/25
TOPMed Omics of Type 2 Diabetes and Quantitative Traits
We will investigate type 2 diabetes and quantitative traits by leveraging (1) the biracial Atherosclerosis Risk in Communities Study (ARIC) phenotype, omics, and genetic data; (2) strong TOPMed analytic expertise and leadership, and (3) an ongoing track record of successful collaboration with all investigators that are a part of this competing renewal.

Role: Co-investigator (subcontract) Total Subcontract Amount: $234,000

NIH/NHLBI: R01 HL105756 (Psaty) 07/01/22-06/30/25
CHARGE Consortium: gene discovery for CVD and aging phenotypes
The aims of this competing renewal application are: 1) to provide coordinating-center-like administrative support; 2) to organize two major meetings per year; 3) to provide travel awards to CHARGE meetings for new investigators; 4) to provide support for fellowship exchanges; 5) to provide modest support for cohort participation.
Role: Co-investigator Total Subcontract Amount: $93,600

NIH/NHLBI: R01 HL156991 (Rao) 04/27/21-03/31/25
A Multi-Ancestry Study of Gene-Lifestyle Interactions and Multi-Omics in Cardiometabolic Traits
The primary goal of the proposed research is to leverage existing genomic and –omic data from large multi-ethnic cohorts to discover additional genetic loci for cardiovascular traits by modeling gene-lifestyle interactions.
Role: Co-investigator (subcontract) Total Award Amount: $436,800

NIH/NHLBI: R01 HL146860 (de Vries) 3/17/20-02/28/25
Whole-genome sequencing analysis of coronary atherosclerosis and related traits
This project aims to integrate whole-genome sequence information to study subclinical atherosclerosis and coronary heart disease (CHD). Aims include discovering novel associated genetic variants, studying the underlying genetic architecture, determining the genetic correlation among the phenotypes, and exploring the use of rare variants in genetic risk prediction.
Role: PI Total Award Amount: $2,483,493

NIH/NHLBI: R01 HL151855 (Meigs) 04/01/20-03/31/24 (NCE)
TOPMed Omics of Cardiovascular Disease in Diabetes
We will utilize large-scale whole genome sequence variation, whole blood DNA methylation, transcription, proteomics, and metabolomics to elucidate pathways that contribute to the increased risk of cardiovascular disease in people with type 2 diabetes.
Role: Subcontract PI Total Subcontract Amount: $291,968

NIH/NHLBI: R01 HL141291 (Morrison/Wolberg) 02/01/19-01/31/24 (NCE)
Using genomics and functional biology to understand fibrinogen and its effect on thrombotic and atherosclerotic outcomes
Through this interdisciplinary collaboration between genetic epidemiologists and functional biologists, we will investigate fibrinogen-associated loci to characterize the genomic regulation of fibrinogen, assess epigenetic association with fibrinogen levels, and translate results of genomic studies into a clear understanding of fibrinogen's role in thrombotic and atherosclerotic disease.
Role: Co-investigator Total Award Amount: $3,152,180

Completed Research Support

NIH/NHLBI: R01 HL134894 (Smith) 08/19/17-07/31/23
Population Genomic Variation, Functional Biology, and the Risk of Venous Thrombosis
The goals of this project are a) to coordinate and advance new genetic discovery in the setting of two international consortia on hemostasis and venous thrombosis, and b) to integrate population work with

functional biology work.
Role: Co-investigator (subcontract) Total Subcontract Amount: $344,376

NIH/NHLBI: R01 HL139553 (Morrison/Smith) 02/05/18-01/31/23
Analysis of Whole Genome Sequence and Hemostasis Phenotypes
To expand our knowledge of the genetic factors contributing to the plasma levels of 7 hemostasis phenotypes, we aim to use whole genome sequence data and imputed genotypes to facilitate new genomic discovery for these measured traits and to determine how genetic variation influencing these traits affects susceptibility to clinical outcomes such as venous thromboembolism and cardiovascular events.
Role: Co-investigator Total Award Amount: $2,205,101

NIH/NHLBI: R56 HL155528 (Newman) 09/20/21-08/31/22
Molecular predictors of resistance and vulnerability to cardiovascular events in stable ischemic heart disease
The objective of the proposed research is to determine which molecular assays could help predict cardiovascular disease events in stable ischemic heart disease patient and to better identify and treat high-risk patients.
Role: Subcontract PI Total Subcontract Amount: $23,111

NIH/NHLBI: R01 HL105756 (Psaty) 07/01/18-06/30/22
CHARGE Consortium: gene discovery for CVD and aging phenotypes
The aims of this competing renewal application are: 1) to provide coordinating-center-like administrative support; 2) to organize two major meetings per year; 3) to provide travel awards to CHARGE meetings for new investigators; 4) to provide support for fellowship exchanges; 5) to provide modest support for cohort participation.
Role: Co-investigator Total Subcontract Amount: $291,947

AHA: 18CDA34110116 (de Vries) 07/01/18-06/30/21
Genomic discoveries for understanding and predicting coronary heart disease incidence and prognosis
Using the results of ongoing GWAS of incident CHD, incident myocardial infarction (MI), and incident mortality after MI, we will use whole-genome sequencing to study regions highlighted by our GWAS in more detail and to see whether these findings improve risk prediction of CHD. We will also perform Mendelian randomization analyses to estimate the causal effect of hemostatic factors on CHD and MI, and of traditional cardiovascular risk factors, hemostatic factors, and inflammatory factors on mortality after incident MI.
Role: PI Total Award Amount: $231,000

NIH/NHGRI: UM1HG008898 (Gibbs) 01/14/16-11/30/20
Genomic Architecture of Common Disease in Diverse Populations
The goal of this project is to perform whole genome sequencing to identify genomic regions influencing the human serum metabolome and cardiovascular disease.
Role: Co-investigator (subcontract) Total Subcontract Amount: $2,756,196

NIH/NIDDK: 2U01 DK78616 (Meigs) 06/01/15-05/31/20
Rare Sequencing Variation and Diabetes Quantitative Traits
Genome-wide rare variant scans of whole genome sequence data will be used to define genetic variant architecture of type 2 diabetes and related quantitative traits.
Role: Co-investigator (subcontract) Total Subcontract Amount: $182,355

UTHealth School of Public Health: PRIME award (de Vries) 09/01/18-09/01/19

Multi-ancestry whole-genome sequencing analysis of atherosclerosis phenotypes
This is an internal award of the School of Public Health meant to help early stage investigators gather and analyze pilot data in preparation for a R01 submission.
Role: PI Total Award Amount: $24,940

NIH/NIDDK: U01 DK105554 (Florez) 05/01/17-10/30/18
AMP T2D-GENES Data Coordination Center and Web Portal
This project aims to utilize TOPMed whole genome sequence data for discovery of genomic variation influencing type 2 diabetes and related traits.
Role: Co-investigator (subcontract) Total Subcontract Amount: $46,200

AHA: 17POST3335004 (de Vries) 01/01/17-07/31/17
Genomic discovery for improved risk prediction of coronary heart disease
The goal of this study was to identify new genomic determinants of coronary heart disease and translate these findings into improved risk prediction.
Role: PI Total Award Amount: $95,450

Awards

2023	UTHealth-SPH: Research Mentor-Mentee Award
2018	CHARGE Consortium: Travel Award for the 2018 Investigator Meeting in Baltimore
2017	American Society of Human Genetics: Charles J. Epstein Trainee Award for Excellence in Human Genetics Research, Semifinalist
2017	CHARGE Consortium: Early Career Award
2017	CHARGE Consortium: Travel Award for the 2017 Investigator Meeting in New York City
2016	American Society of Human Genetics: Charles J. Epstein Trainee Award for Excellence in Human Genetics Research, Semifinalist
2014	Erasmus Trust Fund: Travel Award
2013	Erasmus Trust Fund: Travel Award

Teaching Experience

2021 – present	*Guest Lecturer* Molecular Epidemiology (Instructor: Abbas Dehghan) Imperial College London, London, UK

2019 – present	*Co-instructor (50%)* Epidemiology 1 (Online) Department of EHGES, UTHealth-SPH, Houston, TX, USA
2017 – present	*Course Coordinator and sole instructor* Foundations of Public Health Genetics (Online since 2019) Department of EHGES, UTHealth-SPH, Houston, TX, USA
2018	*Guest Lecturer* Epidemiology 1 (Instructor: Alan Nyitray) Department of EHGES, UTHealth-SPH, Houston, TX, USA
2016 & 2018	*Guest Lecturer* Applied Genetic Methods in Public Health (Instructor: Bing Yu) Department of EHGES, UTHealth-SPH, Houston, TX, USA
2013 – 2015	*Teaching Assistant* Study Design Netherlands Institute of Health Sciences Erasmus Medical Center, Rotterdam, the Netherlands
2013 – 2015	*Teaching Assistant* Methodological Topics in Epidemiologic Research Netherlands Institute of Health Sciences Erasmus Medical Center, Rotterdam, the Netherlands
2013	*Organizer and Lecturer* Exome Chip Analysis Workshop Erasmus Medical Center, Rotterdam, the Netherlands

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Current Mentoring Experiences

Student	**Program**	**Role**
Natalie Hasbani	PhD	Thesis supervisor
Benjamin Cristol	PhD	Thesis committee member
Emily Mason	PhD	Thesis committee member
Jessica Rodriguez	PhD	Thesis committee member
Julie Hahn	PhD	Thesis committee member
Rinitha Rajan	MPH	Academic advisor
Odinakachukwu Dimgba	MPH	Academic advisor
Annmaria Joseph	MPH	Academic advisor
Lauren Mignogna	MPH	Academic advisor

Dharmiben Patel	MPH	Academic advisor
Jamie Rose	MPH	Academic advisor

Previous Mentoring Experiences

Student	Program	Role	Graduation
Hanxiao Sun	PhD	External reviewer	2024
Suha Soni	MPH	Academic advisor	2024
Alondra Cueto Valadez	MPH	Academic advisor	2024
Kiana Hunte	MPH	Academic advisor	2024
Alexandra Jordan	MPH	Academic advisor	2023
Aisha Mahmoud	MPH	Academic advisor	2023
Rachel Friedman	MPH	Thesis supervisor and academic advisor	2023
Anuja Godbole	MPH	Independent integrative learning experience advisor	2023
MacIntosh Cornwell	PhD	External reviewer at NYU Grossman School of Medicine	2023
Stephen Thomas	MPH	Academic advisor	2023
Audrey-Carelle Wandji	MPH	Academic advisor	2023
Sara Butt	MPH	Academic advisor	2023
Timothy Cruz	MPH	Academic advisor	2023
Iain Forrest	PhD	External reviewer at Icahn School of Medicine at Mt Sinai	2022
Chandler Childress	MPH	Academic advisor	2022
Nicole Linnard	MPH	Academic advisor	2022
Allison Bebo	MS	Thesis supervisor	2021
Xinyu Wang	PhD	External reviewer	2021
Kalen Blackburn	MPH	Academic advisor	2021
Mrinalini Buddha	MPH	Academic advisor	2021
Ricardo Gutierrez	MPH	Academic advisor	2021
Justin Muller	MPH	Academic advisor	2021
Hayley Snider	MPH	Academic advisor	2021
Andy Castaneda	MPH	Thesis supervisor	2020
Rahema Aman	MPH	Academic advisor	2020
Gregory Ware	MPH	Academic advisor	2020
Jillian Maners	MPH	Thesis supervisor	2019

Professional Memberships

National Associations

2016 – Present	American Heart Association, Council of Epidemiology and Prevention

2016 – Present	American Society of Human Genetics

Research Consortia

2022 – Present	Co-convener, TOPMed Atherosclerosis Working Group
2021 – Present	Co-convener, TOPMed-CHARGE Hemostasis Working Group
2017 – Present	Investigator, Centers for Common Disease Genomics (CCDG) Program
2016 – Present	Investigator, Trans-Omics for Precision Medicine (TOPMed) Program
2016 – Present	Investigator, ARIC Study
2012 – Present	Investigator, CHARGE

Institutional Service at UTHealth-SPH

2022	Reviewer, UTHealth-SPH PRIME award
2020 – Present	Member, Epidemiology Preliminary Exam Committee
2019 – 2020	External Reviewer, Epidemiology Preliminary Exam Committee
2019 – 2020	Member, Human Genetics Center Search Committee (2 positions)
2018 – Present	EHGES Representative, Faculty Council

Professional Service

2022 – Present	Co-convener of the TOPMed Atherosclerosis Working Group
2021 – Present	Co-convener of the TOPMed-CHARGE Hemostasis Working Group
2022	Session moderator at the 2022 CHARGE investigator meeting in Seattle
2020	Member of the organizing committee of the 2020 CHARGE investigator meeting in Houston

-Served as a reviewer for the following journals:

Cardiology journals: Circulation, JACC, JACC: Basic to Translational Science, Heart, Journal of the American Heart Association, JAMA Cardiology, Circulation Genomics and Precision Medicine, Circulation Cardiovascular Genetics.

Hemostasis journals: Blood, Journal of Thrombosis and Haemostasis, Blood advances, Research and Practice in Thrombosis and Haemostasis, Thrombosis Update.

Genetics journals: Cell Genomics, Bioinformatics, PLOS Genetics, Genetic Epidemiology, and Human Molecular Genetics.

Other journals: Med, JAMA, Communications Biology, eBioMedicine, Nature Communication, Nature Medicine, Diabetes Care, Journal of Diabetes and Its Complications, Hypertension Research, European Journal of Clinical Investigation, PLOS One, Scientific Reports, and European Journal of Epidemiology.

-Served as a grant reviewer for the Austrian Science Fund in 2020.

-Served as an ad hoc NIH grant reviewer for the Hemostasis, Thrombosis, Blood Cells and Transfusion (HTBT) study section on February 16-17th, 2023.

-Served as an ad hoc NIH grant reviewer for the Neurological, Mental and Behavioral Health (NMBH) study section on February 21-22nd, 2024.

-Served as abstract reviewer for the American Diabetes Association meeting in 2021 and 2022.
