Curriculum Vitae – 9/28/2018

Name	Paul S. de Vries		
Nationality	Dutch		
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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 study designs 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

08/2017 – Present	*Assistant Professor* Human Genetics Center, School of Public Health, University of Texas Health Science Center at Houston, Houston, TX, USA
04/2016 – 07/2017	*Postdoctoral Research Fellow* Human Genetics Center, School of Public Health, University of Texas Health Science Center at Houston, 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

	Cardiovascular Group, Department of Epidemiology Erasmus Medical Center, 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 authors.*

1. Ligthart S, Vaez A, Võsa U, et al. Genome-wide association analyses of >200,000 subject identifies 42 novel genetic loci for chronic inflammation and highlights causal pathways that link inflammation and complex disorders. *American Journal of Human Genetics*. Article in press.
2. Sabater-Lleal M[*], Huffman JE[*], **de Vries PS**[*], et al. Genome-wide association trans-ethnic meta-analyses identifies novel associations regulating coagulation Factor VIII and von Willebrand Factor plasma levels. *Circulation*. Article in press.
3. Franceschini N, Giambartolomei C, **de Vries PS**, et al. (2018) Genome-wide association study of carotid intima media thickness and plaque identifies novel loci for atherosclerosis and cardiovascular outcomes, and downstream regulatory effects in vascular tissue. *Nature Communications*. Article in press.
4. Ward-Caviness CK, Huffman JE, Evertt K, et al. (2018) DNA methylation age is associated with an altered hemostatic profile in a multi-ethnic meta-analysis. *Blood*. Epub ahead of print.
5. Merino J, Dashti HS, Li SX, et al. (2018) Genome-wide Meta-Analysis of Macronutrient Intake Identifies Two Novel Loci: Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. *Molecular Psychiatry*. Epub ahead of print.
6. 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.
7. Wolters FJ, Boender J, **de Vries PS**, et al. (2018) Von Willebrand factor and ADAMTS13 activity in relation to risk of dementia: a population-based study. *Scientific Reports*. 8(1):5474.
8. Ghanbari M, Peters MJ, **de Vries PS**, et al. (2018) A systematic analysis highlights multiple long non-coding RNAs associated with cardiometabolic disorders. *Journal of Human Genetics.* 63(4):431-446.
9. Guo L, Akahori H, Harari E, et al. (2018) Alternative CD163 Macrophages Promote Intraplaque Angiogenesis, Vascular Permeability and Inflammation, and Plaque Progression in Atherosclerosis. *Journal of Clinical Investigation.* 128(3):1106-1124.
10. Smith CE, Follis JL, Dashti HS, et al. (2018) Genome-wide interactions with dairy intake for body mass index in adults of European descent. *Molecular Nutrition & Food Research.* 62(3).
11. Pirastu N, Joshi PK, **de Vries PS**, et al. (2017) GWAS for male-pattern baldness identifies 71 susceptibility loci explaining 38% of the risk. *Nature Communications.* 8(1):1584.

12. **de Vries PS**, Yu B, Feofanova EV, et al. (2017) Whole-genome sequencing study of serum peptide levels: the Atherosclerosis Risk in Communities study. *Human Molecular Genetics*. 26(17):3442-3450.
13. Nano J, Ghanbari M, Wang W, et al. (2017) Epigenome-wide Association Study Identifies Methylation Sites Associated With Liver Enzymes and Hepatic Steatosis. *Gastroenterology*. 153(4):1096-1106.
14. Braun KVE, Dhana K, **de Vries PS**, et al. (2017) Epigenome-wide association study (EWAS) on lipids: The Rotterdam Study. *Clinical Epigenetics*. 9:15.
15. **de Vries PS**, Sabater-Lleal M, Chasman DI, et al. (2017) Comparison of HapMap and 1000 Genomes reference panels in a large-scale genome-wide association study. *PLOS O*ne. 12(1):e0167742.
16. **de Vries PS**, van Herpt TTW, Ligthart S, et al. (2017) ADAMTS13 activity as a novel risk factor for incident type 2 diabetes mellitus: a population-based cohort study. *Diabetologia*. 60(2):280-286.
17. Morrison AC, Fu YP, O'Donnell CJ, et al. (2016) Variants in ANGPTL4 and the risk of coronary artery disease. *New England Journal of Medicine*. 375(23):2303
18. Yu B[*], **de Vries PS**[*], Metcalf GA, et al. (2016) Whole genome sequence analysis of serum amino acid levels. Geno*me Biology*. 17(1):237.
19. Karaman I, Ferreira DL, Boulange CL, et al. (2016). Workflow for Integrated Processing of Multicohort Untargeted ^{1}H NMR Metabolomics Data in Large-Scale Metabolic Epidemiology. *Journal of Proteome Research.* 15(12):4188-4194.
20. Sedaghat S[*], **de Vries PS**[*], Boender J, et al. (2016). Von Willebrand factor, ADAMTS13 activity and decline in kidney function: a cohort study. *American Journal of Kidney Diseases.* 68(5):726-732.
21. **de Vries PS**, Chasman DI, Sabater-Lleal M, et al. (2016). A meta-analysis of 120246 individuals identifies 18 new loci for fibrinogen concentration. *Human Molecular Genetics.* 25(2):358-70.
22. Nikpay M, Goel A, Won HH, et al. (2015) A comprehensive 1000 genomes-based GWAS meta-analysis of coronary artery disease. *Nature Genetics.* 47(10):1121-30.
23. Huffman JE, **de Vries PS**, Morrison, AC, et al. (2015) Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood.* 126(11):e19-29.
24. Hägg S, Fall T, Ploner A, et al. (2015) Adiposity as a cause of cardiovascular disease: a mendelian randomization study. *International Journal of Epidemiology.* 44(2):578-86.
25. **de Vries PS**, Boender J, Sonneveld MAH, et al. (2015) Genetic variants in the ADAMTS13 and SUPT3H genes are associated with ADAMTS13 activity. *Blood.* 125(25):3949-55.
26. **de Vries PS**, Kavousi M, Ligthart S, et al. (2015) Incremental predictive value of 152 single nucleotide polymorphisms in the 10-year risk prediction of incident coronary heart disease: the Rotterdam Study. *International Journal of Epidemiology.* 44(2):682-8.
27. Ligthart S, **de Vries PS**, Uitterlinden AG, et al. (2015) Pleiotropy among common genetic loci identified for cardiometabolic disorders and C-reactive protein. *PLOS One*. 10 (3):e0118859.
28. Fall T, Hägg S, Ploner A, et al. (2015) Age- and sex-specific causal effects of adiposity on cardiovascular risk factors. *Diabetes.* 64(5):1841-51.
29. Yu B, Li AH, Muzny D, Veeraraghavan N, et al. (2015) Association of Rare Loss-Of-Function Alleles in HAL, Serum Histidine Levels and Incident Coronary Heart Disease. *Circ Cardiovasc Genet.* 8(2):351-5.

30. Ghanbari M, **de Vries PS**, de Looper H, et al. (2014) A genetic variant in the seed region of miR-4513 shows pleiotropic effects on lipid and glucose homeostasis, blood pressure, and coronary artery disease. *Hum Mutation.* 35(12):1524-31.
31. **de Vries PS**, Gielen M, Rizopoulos D, et al. (2014) Association between polyunsaturated fatty acid concentrations in maternal plasma phospholipids during pregnancy and offspring adiposity at age 7: the MEFAB cohort. *Prostaglandins, Leukotrienes & Essential Fatty Acids.* 91(3):81-5.

Submitted Manuscripts

1. **de Vries PS**, Scholz M, Jansen R, et al. Association of genome-wide gene expression levels in blood with carotid intima media thickness: meta-analysis of 5,647 individuals.
2. **de Vries PS**, Sabater-Lleal M, Huffman JE, et al. A genome-wide association study identifies new loci for Factor VII and implicates Factor VII in ischemic stroke etiology.
3. **de Vries PS**, Brown MR, Bentley AR, et al. Multi-ancestry genome-wide association study incorporating gene-alcohol interactions identifies new lipid loci.
4. Ward-Caviness CK, **de Vries PS**, Wiggins KL, et al. Evaluation of causal associations between fibrinogen and incident coronary heart disease: a meta-analysis of Mendelian Randomization studies.
5. Petty LE, Highland HM, Hu H, et al. Tissue-specific trans-ancestral analysis of genetically regulated expression identifies 114 known and 28 novel genes across 15 metabolic and cardiovascular traits.
6. Tzoulaki I, Castagné R, Boulangé CL, et al. Serum metabolic signatures of atherosclerosis.
7. Pankratz N, Wei P, Brody JA, et al. Whole exome sequencing of 14,389 individuals from the ESP and CHARGE consortia identifies novel rare variation associated with hemostatic factors.
8. Bentley AR, Sung YJ, Brown MR, et al. Multi-ancestry genome-wide smoking interaction study of 387,283 individuals identifies novel lipid loci.
9. Bennett JA, Mastrangelo MA, Ture SK, et al. Slc44a2 increases platelet activation and thrombosis by controlling levels of reactive oxygen species and ATP.
10. Kilpeläinen TO, Bentley AR, Raymond Noordam R, et al. Multi-Ancestry Study of Blood Lipid Levels Identifies Four Loci Interacting with Physical Activity.
11. Chen H, Huffman JE, Brody JA, et al. Efficient variant set mixed model association tests for continuous and binary traits in large-scale whole genome sequencing studies.
12. Flannick J, Mercader JM, Fuchsberger C, et al. Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries.

Conference Presentations

1. Multi-ancestry genome-wide association study of incident coronary heart disease. *Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Investigator Meeting*. Rotterdam, 18-19 April 2018 (poster).
2. Association of rare variants specific to pancreatic islets with type 2 diabetes (T2D). *Trans-Omics for Precision Medicine (TOPMed) Investigator Meeting*. Tysons, 29 November - 1 December 2017 (platform).
3. Multi-ancestry genome-wide association study incorporating gene-alcohol intake

interactions identifies 18 new lipid loci. *American Society of Human Genetics Meeting.* Orlando, 17-21 October 2017 (platform).
4. Mendelian randomization for precision medicine: causal effect of fibrinogen on coronary heart disease. *Precision Medicine Day*. Houston, April 13 2017 (invited speaker).
5. Multi-ethnic genome-wide association study of hemostasis phenotypes. *CHARGE Investigator Meeting*. New York City, 23-24 March 2017 (poster).
6. Whole-genome sequencing study of serum peptides: the Atherosclerosis Risk in Communities (ARIC) study. *American Society of Human Genetics Meeting.* Vancouver, 18-22 October 2016 (platform).
7. Multi-ethnic genome-wide association study of incident coronary heart disease. *CHARGE Investigator Meeting.* Charlottesville, 28-29 September 2016 (poster).
8. GWAS of circulating fibrinogen using 1000 genomes imputed data. *CHARGE Investigator Meeting.* Los Angeles, 22-24 January 2014 (poster).

Awards

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

2017	*Course Coordinator and Lecturer* Foundations of Public Health Genetics Department of Epidemiology, Human Genetics, and Environmental Sciences, University of Texas Health Science Center at Houston
2016	*Teaching Assistant and Guest Lecturer* Applied Genetic Methods in Public Health Department of Epidemiology, Human Genetics, and Environmental Sciences, University of Texas Health Science Center at Houston
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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Active Research Support

NIH/NHLBI: R01 HL139553 (Morrison/Smith) 02/05/18-01/31/21
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

NIH/NHLBI: R01 HL134894 (Smith) 08/19/17-07/31/21
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)

NIH: 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)

NIH: 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)

Completed Research Support

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

Professional Memberships

National Associations

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

Research Consortia

2016 – Present	Investigator, Trans-Omics for Precision Medicine (TOPMed) Program
2016 – Present	Investigator, ARIC Study
2012 – Present	Investigator, CHARGE Consortium

Peer Reviewing

Served as a reviewer for the following journals: Circulation, European Journal of Clinical Investigation, PLOS One, Journal of Diabetes and Its Complications, JAMA Cardiology, Genetic Epidemiology, Scientific Reports, Circulation Cardiovascular Genetics, and European Journal of Epidemiology.
